



PHILIPS

Pinnacle³

Planning

Instructions for Use

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Medical Device Directive

Pinnacle³ Radiation Therapy Planning System is CE Marked to the Medical Device Directive 93/42/EEC.

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Device Description

The Pinnacle³ Radiation Therapy Planning (RTP) software is composed of several modules including the core Pinnacle³ functionality, Syntegra[™], P³IMRT[®], P³MD[®], and AcQSim^{3™}. The Pinnacle³ RTP software runs on a Solaris UNIX (or UNIX compliant) computer, which allows qualified medical personnel to enter patient data into the system, use that data to construct a plan for radiation therapy, and evaluate the plan. Optionally, the qualified medical personnel may output the plan in an electronic or printed form for use by other systems in the delivery of treatment to a patient.

Pinnacle³ includes networking capabilities to provide connectivity to other Pinnacle³, Syntegra, PC Access Point (remote planning), P³MD, AcQSim³, or P³IMRT workstations, input devices and output devices, as well as access to the Pinnacle³ database from any Pinnacle³ workstation available on the network. The system can be run from a single workstation but has network capability to other Pinnacle³ workstations and to both input and output devices via local area network (LAN) or wide area network (WAN). The Pinnacle³ RTP System also has an enterprise configuration for larger sites requiring a centralized data center environment. This system consists of one or multiple rack mountable servers on which Pinnacle³ sessions run which enables display on any network accessible computer.

Installation instructions appear on the DVD insert included with the software DVD. You only need to load the software on the systems designated as the servers at your site.

To enable use of the software, a licensing key must be issued by a Customer Support representative or your local distributor. You may contact Customer Support at 1-800-722-9377 (US and Canada) or your local distributor for assistance with installation or licensing.

Intended Use

Pinnacle³ Radiation Therapy Planning System is a software package intended to provide planning support for the treatment of disease processes, utilizing photon, proton, electron and brachytherapy techniques.

Indications for Use

Pinnacle³ Radiation Therapy Planning System is a software package intended to provide planning support for the treatment of disease processes. Pinnacle³ Radiation Therapy Planning System incorporates a number of fully integrated subsystems, including Pinnacle³ Proton, which supports proton therapy planning. The full Pinnacle³ Radiation Therapy Planning System software package provides planning support for the treatment of disease processes, utilizing photon, proton, electron and brachytherapy techniques.

Pinnacle³ Radiation Therapy Planning System assists the clinician in formulating a treatment plan that maximizes the dose to the treatment volume while minimizing the dose to the surrounding normal tissues. The system is capable of operating in both the forward planning and inverse planning modes. Plans generated using this system are used in the determination of the course of a patient's radiation treatment. They are to be evaluated, modified and implemented by qualified medical personnel.

Contraindications

There are no known contraindications regarding the use of the Pinnacle³ RTP system.

Intended Audience

This manual is written for qualified medical personnel trained as users of Pinnacle³ RTP systems. You should make sure that you have thoroughly read and completely understand the manuals and release notes that are delivered with the software. Keep this manual and all other manuals delivered with the software near your Pinnacle³ system and review them periodically. The initial installation procedure will be performed by a Field Service Engineer. If you suspect that your system has an error, discontinue its use and contact Customer Support or your local distributor.



General Device Warnings

Do not load non-system software onto the computer used by this system without the direct authorization of Philips Medical Systems. Feature performance and safety may be compromised.

To assure proper treatment, it is critical that a qualified medical person review and verify all system treatment plan parameters using an independent verification method prior to treating patients using the plan.

We recommend that you review TG40, TG53, and other pertinent radiation therapy treatment standards and incorporate those methods into your clinical practice to ensure that your use of the system results in the most accurate treatment plans. TG40, TG53, and other reports are available publicly at the American Association of Physicists in Medicine (AAPM) website.

- Comprehensive QA for radiation oncology: Report of AAPM Radiation Therapy Committee Task Group 40. *Medical Physics* 21(4), 1994.
- American Association of Physicists in Medicine Radiation Therapy Committee Task Group 53: Quality assurance for clinical radiotherapy treatment planning. *Medical Physics* 25(10), 1998.

The following clinical practices are recommended to verify the accuracy of each treatment plan:

- An independent calculation of the monitor units for each beam of a plan and treatment time for each brachytherapy plan.
- Acquisition and review of portal images or review of multi-leaf collimator (MLC) leaf positions after import to the treatment system.
- A chart check prior to the plan being delivered or during the first week of treatment.
- Independent review of the treatment plan prior to the delivery.
- Cross-functional review of the plan in a weekly chart round.
- Manual verification of record and verify settings after transfer to the treatment machine.
- Verification of the SSD and field shape during patient setup.

These reviews should be performed for a new plan or when a change is made to any component of a plan.

U.S.A. law: CAUTION: Federal law restricts this device to sale by or on the order of a physician.

Only qualified medical personnel should operate the system. New personnel should receive training prior to unsupervised operation of the system. For more information, contact Customer Support or your local distributor.

Serious injury to patients can result due to the misapplication of this product. Make sure that you thoroughly understand all the user instructions prior to using this device.

Pinnacle³ treatment plans may include the statement NOT FOR CLINICAL USE. Based on the machine or isotope data and the treatment plan, the software determined that the plan cannot be delivered clinically. Do not treat patients with plans that are not for clinical use.

Pinnacle³ includes sample data. This information is for reference purposes only. Do not treat patients with plans based on sample machines or other sample data.

Use of Symbols in Labeling

Philips Healthcare complies with International Standards and FDA requirements for the use of symbols in labeling. An online glossary of symbols used by Philips Healthcare is available at <http://www.symbols.philips.com>.

Notes

Equipment specifications are subject to alteration without notice. All changes will be in compliance with regulations governing manufacture of medical equipment.

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1 Getting Started

Introduction

The Pinnacle³ treatment planning system provides a comprehensive set of tools for setting up and evaluating treatment plans. The software includes options for simulation, and photon, electron, stereotactic radiosurgery, proton, and brachytherapy treatment planning.



CAUTION

If you purchase Pinnacle³ without the dose calculation features and you try to open a plan that already has dose computed, you will get an error message that dose will be invalidated. You can still view the plan. If you do not save the plan, the dose will still be intact. If you save the plan, you will have to go back into Pinnacle³ (with dose) to recompute dose. We recommend that you make a copy of the plan and work on the copy so the dose in the original plan does not get invalidated.

NOTE

The Pinnacle³ system should not be used within the space where surfaces may come into contact with the patient or with an attendant who can touch the patient. This space is defined as 1.83 meters (6 feet) outside the perimeter of the intended location of the treatment table and 2.29 meters (7.5 feet) above the floor.

Classic Pinnacle³

Classic Pinnacle³ refers to the multi-window interface included with the Pinnacle³ treatment planning system.

Planning

Planning refers to the basic, single-window interface included with the Pinnacle³ treatment planning system.

AcQSim³

AcQSim³ is a simulation tool that allows you to do the following tasks:

- perform absolute localization at the time of scan acquisition because AcQSim³ can determine table coordinates corresponding to where the patient should be marked (available for approved Philips scanners only)
- use advanced DCR (digitally composited radiograph) display and manipulation tools
- set up volumes of interest to eliminate image data that would impede visualization
- add a user-defined default set of orthogonal beams and a customized set of viewing windows upon starting your simulation plan

- set independent window/level values, set up laser lookup tables, display 2D reference lines, and set other visualization parameters
- create separate preferences for simulation and planning
- use AcQSim³ as a stand-alone CT simulation system or add dose and IMRT for a complete simulation and planning system networked to a single database

**CAUTION**

Some of the AcQSim³ features are available only for DICOM image sets. You must have DICOM Image 4.2 or later installed to use those features. The features that require DICOM Image 4.2 state that you must be using a DICOM image.

Syntegra and Image Fusion

Syntegra and Image Fusion allow you to correlate, or register, multiple patient image sets using the image fusion features. You can view correlated images in 2D and 3D.

NOTE

The Syntegra features are available only if you are licensed for Syntegra.

DICOM conformance

DICOM (Digital Imaging and Communications in Medicine) is a standard for the electronic transfer of digital images and associated information, developed by the American College of Radiology and the National Electrical Manufacturers Association. The Pinnacle³ software operates within DICOM standards and within the standards of the manufacturer's Conformance Statement for DICOM. The DICOM conformance statement is available on the Philips Healthcare website (www.healthcare.philips.com).

Log in to the workstation

Your workstation is ready to use when the power is turned on and the log-in prompt appears on the screen. The log-in prompt appears whenever you turn on the power, reset the system, or log out.

- 1 At the log-in prompt, enter your user name, then press the **Return** key. The password window appears.
- 2 Type your password, then press the **Return** key. To keep passwords secret, the password is not shown as you type it.

When you are logged in, the Pinnacle³ screen background appears on the desktop.

User accounts

The standard account is p3rtp. Individual user accounts can be set up by your system administrator.

When a new user account is created it uses the default factory settings. Your account includes your own home directory. You can view and copy the files in another user's directory, but you cannot

save to the other user's directory. Once you log in to your user account and make any change, that change is specific only to your account. Scripts you create are specific to your account, too.

So, you could create a script and save it in your home directory, then have other users copy it to their own directories. (You can still save scripts to the common script directory under Pinnacle³ where everyone can use them.)

Patient and plan files are not located in individual user home directories so all users can work on all patients and plans.

Start the software

After you are logged in to your workstation, you can start the software.



- 1 Click the Pinnacle³ icon in the front panel at the bottom of the screen.

The **Launch Pad** window appears. For more information, see *Launch Pad window*.

NOTE

The Pinnacle³ icon that appears in the front panel will be one of the two icons shown here. The icon varies depending on the version of the Solaris operating system that your system is running.

- 2 To select an institution, click the **Institutions** button in the **Launch Pad** window. The **Select Institution** window appears.
- 3 Highlight the name of the institution you want and then click **Close**. The **Launch Pad** window appears.

If you do not make a selection, the software uses the default institution shown at the bottom of the **Select Institution** window.

NOTE

To add institutions and learn how to add patients and plans, see the *Launch Pad Instructions for Use*.

- 4 Click the **Planning** button to add patients, acquire and import patient images, and add plans. The **Patient Select** window appears.

If you want to review an existing plan, select the patient and plan.

- 5 At the bottom of the **Patient Select** window click the appropriate button:

- **AcQSim**—Start AcQSim³.
- **Fusion**—Start Syntegra or Image Fusion. See the *Image Fusion* chapter.
- **Planning**—Start the planning software. Depending on your preference settings, you will go into Classic Pinnacle³ (multi-window interface) or the **Planning** window (single-window interface).

The default viewing windows display a transverse, sagittal and coronal view.

Launch Pad window

The first screen you see when you start Pinnacle³ is the **Launch Pad** window. This window provides access to patient database operations for the current institution.

The following options are available from the **Launch Pad** window.

- **Institutions**—Add, select, or delete institutions. See the *Launch Pad Instructions for Use* for details.
- **Planning**—Proceed to the patient planning software. See the *Launch Pad Instructions for Use* for details.
- **Physics**—Access the physics tool. The physics tool is described in the *Pinnacle³ Physics Instructions for Use*.
- **Configure**—Access system administration functions. See the *Launch Pad Instructions for Use* for information about system administration.
- **Backup**—Archive patient and physics data to tape or across the network. See the *Launch Pad Instructions for Use* for details.
- **Restore**—Restore archived patient and physics data. See the *Launch Pad Instructions for Use* for details.
- **Exit**—Exit the **Launch Pad** window. See the *Exit the software* section for details.

Locked data in Launch Pad

If data in Launch Pad is locked, no other users can modify the data until the lock is released or the user exits Launch Pad. Locking is employed in several areas:

- While any institution data is being modified, that institution and all patients in that institution are locked. If one institution is locked, you can still make changes to or work in another institution.
- While any patient information is being modified, including plan or image set information, the patient is locked.
- While physics information is being modified, the physics module is locked.
- While a plan is being modified in the software, the patient is locked. The plan and patient are not available to other users on the network until the person editing the plan exits the planning session.
- Once the software has been run on a plan, the primary CT image set and plan type are locked.

Exit the software

When you are finished with your treatment planning session, you should exit the planning software.

- 1 Select **File - Exit**.

The **Save Confirmation** window appears.

- 2 Select the appropriate option:
 - **Exit without saving**—Exit the software without saving the plan.
 - **Save and exit**—Save the plan before exiting.
 - **Delete auto-saved computed files**—Delete any computed files that were created during the planning session. Plan elements that will be deleted include (but are not limited to) the following items: dose grid, control point dose, brachytherapy dose, DRRs, and compensators.
 - **Delete stored control point dose for dynamic arc beams**—Remove dose from all control points in the plan. This option appears only if your plan contains a dynamic arc beam.
 - **Cancel**—Close the Save Confirmation window and return to the software.
- 3 When prompted: **End planning session. Are you sure?**, select **Yes** to quit planning. The **Patient Select** window appears.
- 4 Click the **Close** button in the **Patient Select** window.
-  5 Click the **Exit** button to exit **Launch Pad**. A confirmation window appears.
- 6 Click the **Yes** button to exit the software, or click the **No** button to return to **Launch Pad**.

If you chose to exit **Launch Pad** and you do not plan to use the system again soon, you should end your session and log out of the system.

Log out of the system

The procedure for logging out of the system varies depending on the version of the Solaris operating system that your system is running.

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- 1 Click the **EXIT** button on the front panel.
A **Logout Confirmation** window asks you to confirm or cancel the exit procedure.
- 2 Click the **OK** button to verify your selection.
When you click the **OK** button, the current screen workspace layouts are saved. The log-in prompt appears.

NOTE

You can also log out by right-clicking the desktop and selecting **Log out** from the menu.

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- 1 From the **System** menu on the Solaris desktop, click **Log Out**. A confirmation window appears.
- 2 Click the **Log Out** button to log out of the system. The log-in prompt appears after you have successfully logged off of the system.

Shutdown procedures



CAUTION

You must shut down system components in the proper order. All users must be logged out of all workstations before you shut down the system power for any component.

We recommend that you shut down your systems on a weekly, biweekly, or monthly basis. UNIX systems are robust, but there are file maintenance and “housekeeping” procedures that occur only during system shutdown and startup.

You should shut down your system for the following reasons:

- To deal with system issues that you cannot address otherwise.
- To guard against system damage in case of severe electrical storms, hurricanes, and other weather issues such as extremely high humidity and temperatures.
- To occasionally “flush” clogged system resources, including memory leaks, printer daemons, and the mail daemon.

If your site has just one or two workstations, you might want to shut down your system each Friday evening and then bring it back up on Monday morning. If a weekly shutdown is impractical, do it once a month. If your site has a large network with multiple workstations, you should shut down your system once a month.

For information on the shutdown procedures for your system, please consult the instructions for use for your system’s server. If you need assistance, please contact Customer Support or your local distributor.

2 Setup

Overview

The procedures and information in this chapter assume that you have set up a patient, imported one or more image sets, and created a plan in Launch Pad. For information on how to perform those tasks, see the *Launch Pad Instructions for Use*.



CAUTION

If you are starting a plan that you restored from Pinnacle³ 4.0b or earlier (only SunOS versions), the software displays an error that the .ImageInfo file has been modified outside of the software. Since those software versions did not include information about patient position, this is expected behavior. You can ignore this error. The software assumes the patient is head-first, supine.

The initial setup of the patient is the same for stereotactic radiosurgery, photon, electron, or proton beam treatment planning. For stereotactic radiosurgery treatment plans, you can also set the frame coordinates.

New plan setup for image-based planning

In accordance with International Atomic Energy Agency (IAEA) recommendations and International Electrotechnical Committee (IEC) 62083 standards, you must confirm all patient and plan setup information prior to delivering treatment.

When you open an image-based plan for the first time, the **Confirm Plan Setup** window appears. You cannot begin planning until you verify that the information in this window is correct for the primary image set. If you have secondary image sets in the plan, you must use the viewing windows in Pinnacle³ to confirm that the patient orientation is correct for each image set.



CAUTION

If no CT scanner, CT to density table, or CT to stopping power table is available, notify the physicist who commissioned the software. The manufacturer name, model name, or kVp for the scanner may have been entered incorrectly during commissioning.

- 1 Verify that the patient setup information is correct. Use the viewing window in the **Confirm Plan Setup** window to view the image set.

Patient orientation is detected from the original image data file. If the patient orientation is unavailable, the software assumes that the CT scan was obtained with the patient positioned on their back, head first into the scanner with the table moving into the scanner.

If the patient setup information is not correct, click the **Cancel and Exit** button to return to Launch Pad. Use the **Data Set Editor** window to change the patient orientation information. For more information, see the *Launch Pad Instructions for Use*.

- 2 Verify that the scanner and CT to density table are correct, or select a CT to density table if one is not already selected.

The software uses the data file for the image set to determine which scanner was used to acquire the images. The CT to density table that the physicist selected for that scanner during commissioning appears in the **CT-Density Table for Dose Calculation** field. If the software is unable to determine which scanner was used to acquire the images, then you must select the appropriate CT to density table from the **CT-Density Table for Dose Calculation** option list.

The selected CT to density table is shown in the **Confirm Plan Setup** window. You cannot modify the table, but you can select a different table from the **CT-Density Table for Dose Computation** option list.

If the image set is a maximum intensity projection (MIP) or minimum intensity projection (MinIP) image set, then the software does not associate a scanner with the plan.

- 3 If you are licensed for proton treatment planning, verify that the CT to stopping power table is correct, or select a CT to stopping power table if one is not already selected.

The CT to stopping power table that the physicist selected for the scanner during commissioning appears in the **CT-Stopping Power Table for Dose Calculation** field. If the software is unable to determine which scanner was used to acquire the images, then you must select the appropriate CT to stopping power table from the **CT-Stopping Power Table for Dose Calculation** option list.

The selected CT to stopping power table is shown in the **Confirm Plan Setup** window. You cannot modify the table, but you can select a different table from the **CT-Stopping Power Table for Dose Calculation** option list if necessary.



- 4 If the CT scanner information and the patient setup information are correct, click the **Accept** button. If not, click the **Cancel and Exit** button to delete the plan and return to Launch Pad.
- 5 Click the **Initialize** button at the top of the window to display the **Patient Setup** panel. Continue to the sections that follow in this chapter for additional setup information.

Change the CT to density table

You can select a different CT to density table at any time during planning. By default, the software uses the CT to density table that you accepted in the **Confirm Plan Setup** window.

Click the **View** button to view the CT to density table. You cannot edit the table, but you may need to see it in order to choose the correct one for your plan.

If you select a different CT to density table, you are prompted to accept the new table when you compute dose for a beam. If dose has already been computed and you select a different CT to density table, dose is invalidated.

Change the CT to stopping power table

NOTE

The information in this section is only applicable if you are licensed for proton treatment planning.

You can select a different CT to stopping power table at any time during planning. By default, the software uses the CT to stopping power table that you accepted in the **Confirm Plan Setup** window.

Click the **View** button to view the CT to stopping power table. You cannot edit the table, but you may need to see it in order to choose the correct table for your plan.

If you select a different CT to stopping power table after you have computed dose for a beam, dose is invalidated.

Set window/level

Use the window/level feature to identify values that provide good contrast for viewing images. For more information about setting the window and level, see the *View Patient Data* chapter.

Set the body board

NOTE

If you are licensed for proton treatment planning, you will not be able to compute dose for a proton beam if you use a body board.

You can specify most of the patient position options in the **Data Set Editor** window, as described in the *Launch Pad Instructions for Use*. However, there is one more patient positioning parameter you can set: the use of a body board.

- 1 Are you using a body board?
 - If yes, in the **Use body board** field, select **Yes**. A field appears for you to set the angle of the board.
 - If no, in the **Use body board** field, select **No**. This procedure is complete.
- 2 In the **Angle** field, set the angle (-10 to 90 degrees) of the body board as you will use it during treatment.

NOTE

If you alter the body board settings, computed dose for beams set to laser localization will be invalidated and the beam display will be updated.

Remove the couch



CAUTION

If you are licensed for proton treatment planning, we recommend that you do not remove the couch from the patient data. The presence of the couch in the beam changes the effective range of the beam, and the resulting delivery may be different than what you intend. Use one of the following options to plan with the couch in the patient data.

- Make sure that the couch that will be used during treatment is the couch that is used when the patient data is collected.
- Set up the beam geometries to avoid the couch.
- Model the couch using regions of interest and density overrides to account for the couch attenuation. For information about this method, contact Customer Support and request Application Note 2009-01, or download the document from InCenter.



WARNING

During photon planning, the couch interferes with SSD measurements and dose computation unless it is removed from the patient data. If the couch was not removed as part of the new plan setup, you should remove it before adding beams and computing dose.



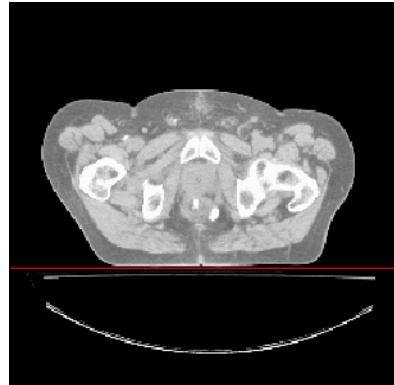
WARNING

When removing the couch, observe the couch removal plane in the transverse and sagittal windows. Verify that the couch does not bisect any part of the patient. If the couch removal plane erroneously bisects the patient, dose calculations may be incorrect, bolus may appear incorrectly, and lungs and other cavities may be replaced with air, among other problems.

Because the patient CT scans include the couch on which the patient is scanned, the couch appears to the software to be an extension of the patient data. You can remove the couch from the patient data so it does not affect SSD and dose computation. The location of the couch removal plane is indicated by a line in 2D images and by a plane in 3D images.

The couch removal plane removes the CT couch from the scan, which is sufficient for most plans. You should always check the location of the couch removal plane to verify that it is in the correct

location for computation. If a plan requires that you treat through the couch at oblique angles and you want to create a more accurate representation of the couch on the linear accelerator, contact Customer Support and request Application Note 2009-01 or download the document from InCenter.



- 1 Click the **Couch Removal** tab.
- 2 Select **Yes** at **Remove couch from scan**.
- 3 To remove the couch, do one of the following options:
 - Enter the Y coordinate for the top of the couch (the distance from the “bottom” of the data set to the couch top).
 - Click the **Move couch removal plane** tool and in the 2D viewing windows remove the couch by dragging the couch removal line until it is placed at the point where the patient ends and the couch top begins.
- 4 You can lock and unlock the position of the couch removal plane. Click the buttons shown at left to lock or unlock the couch.
- 5 If you want to change the color of the couch removal line, use the **Display color** option list to select a different color.



Set the outside air threshold



WARNING

Specifying an incorrect outside-patient air threshold can result in incorrect SSD calculation and inaccurate dose calculation. Verify that the outside-patient air threshold is set correctly before computing dose. Values should be 0.6 to 0.85 g/cm³.

Pinnacle³ does not require you to define external patient contours for image-based plans. Instead, it uses the density information in the image scans to differentiate between the patient and the air surrounding the patient.

Use the outside-patient air threshold to specify the density threshold to differentiate between the patient and the air. Voxels outside the patient below this threshold are considered to be air; dose is zero in these voxels. If this threshold is not specified correctly, dose may appear in low-density objects, such as blankets or positioning devices, that are present in the CT scan.

- 1 In the **Outside-patient air threshold** field, enter the density that should be considered air (not part of the patient data set).
- 2 Click the button next to the threshold to select the unit of measure.

**CAUTION**

Remove the couch prior to generating an external ROI. If you do not remove the couch, it may be included as part of the patient.

- 3 If you want to generate a region of interest (ROI) for the patient-air threshold (a skin contour), click the **Display as ROI** button. The software generates patient-air contours on each slice. The ROI appears in the list on the **Regions of Interest** panel with a default name of External ROI #, where # is a number.

If you change the outside-patient air threshold, click the button again to generate a new ROI using the new value.

NOTE

A new ROI is generated each time you click the **Display as ROI** button. To remove external ROIs that you do not want, go the **Regions of Interest** panel and delete them.

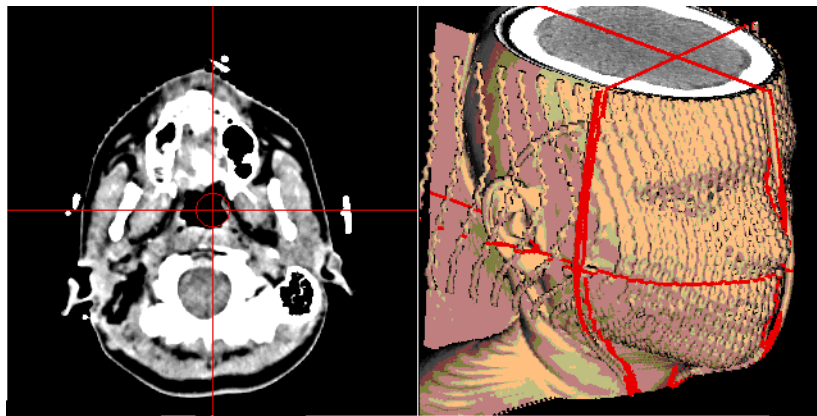
Use lasers to align the patient

Laser alignment localization lets you use the CT data to simulate laser alignment of the patient. Laser alignment allows you to position the laser center in the patient data set as it will be positioned during treatment. You can then determine the offset between the planning isocenter and the laser center and reposition the patient accordingly.

NOTE

If you export plan information, relative couch shifts between the patient setup and the treatment positions are exported if the lasers have been set for a plan and the plan contains only one isocenter. If the plan contains multiple isocenters, then the shifts are not exported (see the *Export* chapter).

You set the laser alignment system in the **CT Scanner Configuration** window in the physics tool. The system may have either one or three moveable lasers. The one moveable laser is in the X (sagittal) direction. The three moveable lasers consist of one in the X direction and two in the Y (coronal) direction (one on each side of the table). For more information, see the *Pinnacle³ Physics Instructions for Use*.



Set the laser center



CAUTION

If lasers are not positioned correctly, inaccurate patient setup information may be reported. Be careful when positioning the lasers.



- 1 Click the **Initialize** button to display the **Patient Setup** panel, then click the **Localization** tab.
- 2 There are several ways you can specify the position of the laser center.
 - Interactively position the laser center in viewing windows. Use the 2D or 3D laser positioning tools to drag the laser center to the desired position in either 2D or 3D windows.
 - Enter the coordinates of the laser center in the **CT Lateral**, **Ant-Post**, and **Sup-Inf** fields.
 - If you have defined a point of interest that corresponds with the laser center position, you can select the POI and click the **Copy from POI** button.
- 3 Do you want the lasers always shown in the viewing windows?

- If yes, in the **Display after localization complete** field select **Yes**. From the **Display color** option list, select the laser color.
- If no, in the **Display after localization complete** field select **No**.

View coordinate details

After you localize the patient, you can use the **Beam Isocenter** window to view details about the laser localization coordinates. The lower portion of the window displays how the table and patient will be set up with respect to the point of interest. For more information about the **Beam Isocenter** window, see *Obtain coordinates for the isocenters* in the *Beams* chapter.



- 1 Display the **Beams** panel.
- 2 Select the POI that is at the laser center.
- 3 Click the **Details** button. The **Beam Isocenter** window appears.

Stereotactic frame localization

NOTE

All length dimensions in Pinnacle³, including stereotactic coordinates, are shown in centimeters in all software displays and printouts. This is required to comply with International Atomic Energy Agency (IAEA) 1540 standards.

Stereotactic frame localization allows you to specify the frame position and transform CT coordinates to stereotactic frame coordinates. Once you have performed the localization, the isocenter coordinates can be displayed using the stereotactic frame coordinate system.

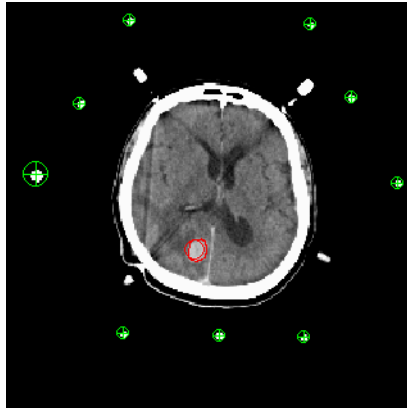
NOTE

This section uses a BRW frame as an example for the frame localization process. The system also supports Compass, Fischer, and Leksell frame localization.

NOTE

Pinnacle³ properly accounts for tilt in its stereotactic frame transformations.

The rods from the stereotactic frame appear as cross sections on each transverse CT image. The locations of these cross sections determine the transformation from the CT to the frame coordinate system.



CAUTION

Each isocenter specified in CT coordinates is converted to the frame coordinates using the transformation for the closest CT slice.

The transformation is also used to properly orient beams, which are specified with respect to the frame and must be reoriented with respect to the CT coordinate system to account for any rotation between the coordinate systems.

Automatic stereotactic frame localization

In most instances, the software can automatically locate the frame rods and then compute a separate transformation for each slice.

**CAUTION**

The automatic frame localization can fail when the CT scan includes a head ring or when a rod is touching the patient or another high-density object. If the automatic rod localization fails, you have to manually position the rods in the patient data.

- 1 On the **Localization** tab of the **Patient Setup** panel, click the **Stereo Localization** button.

The **Stereotactic Frame Localization** window appears.

- 2 Select the stereotactic frame type.

NOTE

You can use the **Preferences** utility to set up a default frame for stereotactic frame localization. For more information on setting up a default frame, see *Preferences* in the *Utilities* chapter.

- 3 Click the **Find Rods and Compute Transformations** button. When the rods are found, the rod positions appear on each slice. When the transformation is complete, the software displays the number of slices having valid transformations.

NOTE

For information on the status of the transformation on each slice, click the **Examine Detail** button. See *Individual slice localization* for an explanation of this function.

**CAUTION**

For accurate dose computation the frame rods must be digitally removed from the patient data set. Verify that the software has found each rod on each slice.

- 4 Click the **Remove Frame** button. The status displays under the button.
- 5 Click the **Close** button to close the **Frame Localization** window.

Individual slice localization

In the **Individual Slice Data** window you can view the transformation information for individual slices. You can also localize the frame rods and compute the transformations on individual slices using the options in this window.

**CAUTION**

The automatic frame localization can fail when the CT scan includes a head ring or when a rod is touching the patient or another high-density object. If the automatic rod localization fails, you have to manually position the rods in the patient data.

For Fischer frame localization, you may need to adjust the **Rod Search Threshold** so that the metal frame rods can be distinguished from the high-density plastic of the frame. You can use the **Show image value 2D** tool or the **Profile** tool to determine the correct CT number for this threshold.

- 1 Click the **Examine Detail** button in the **Stereotactic Frame Localization** window. The **Stereotactic Localization Individual Slice Data** window appears.

**CAUTION**

When using individual slices for frame localization and transformation, you should use the slice closest to the isocenter and a minimum of one slice above and one slice below the slice closest to the isocenter.

- 2 In the **Slice List**, select the desired slice.
- 3 Click the **Find Rods For Slice** button.
- 4 Click the **Compute Transformation** button to compute the transformation on the selected slice.

Manually position rods

You must attempt to compute transformations prior to starting this procedure. If you do not, you cannot enter some of the windows.

- 1 Click the **Examine Detail** button in the **Stereotactic Frame Localization** window. The **Stereotactic Localization Individual Slice Data** window appears.
- 2 Click the **Edit/View Rod Positions** button. The **Stereo Slice Rod Positions** window appears.
- 3 In a transverse viewing window, display the slice on which you want to manually position the frame rods.



- 4 Select the **Manually position rod** tool from the **Stereo Slice Rod Positions** window.
- 5 In the viewing window, click and drag the rod indicator to position it on the correct rod.

NOTE

If you want to see the numbers of the rods in the viewing window, set the **Frame 2D Display** option to **Label** in the **Stereotactic Frame Localization** window.

**CAUTION**

For accurate dose computation, the frame rods must be digitally removed from the patient data set. Verify that the software has found the rod correctly.

- 6 If the rod is not in contact with another high-density object, click the **Find rod center from current position** button. The software automatically locates the rod center from the manually defined position.
- 7 Repeat steps 5 and 6 for each rod you need to position on that slice.
- 8 When the rods have been positioned, return to the **Stereotactic Localization Individual Slice Data** window and click the **Compute Transformation** button to compute the coordinate system transformation for that slice.

**CAUTION**

Do not click the **Find Rods for Slice** button; it will reposition all the rods on the slice.

- 9 Repeat steps 2-8 for all other slices that need manual rod positioning.

Angiographic frame localization

Angiographic frame localization allows you to reconstruct the intracranial target position and magnification from orthogonal angiographic films. The coordinates can be entered manually into the software.

Two films are required for entering the localization frame coordinates: Anterior-Posterior and Lateral.



CAUTION

Before using the angiographic frame localization options, you must obtain valid CT frame transformations.

Find the rods

- 1 On the **Localization** tab of the **Patient Setup** panel, click the **Stereo Localization** button.
The **Stereotactic Frame Localization** window appears.
- 2 Select the type of headframe used.
- 3 Click the **Angiographic Localization** button. The **Angiographic Frame Localization** window appears.
- 4 Select the correct film orientation.



CAUTION

The coordinates determine the position of the patient in the frame. Verify your coordinates after you enter them into Pinnacle³. Entering invalid coordinates may affect beam placement and, therefore, dose calculation.

- 5 Enter the coordinates.

Complete the frame reconstruction

Once the angiographic frame coordinates have been entered, frame reconstructions can be computed, magnification factors reviewed, and you can copy target coordinates to beam isocenters.

- 1 In the **Stereotactic Frame Localization** window, click the **Angiographic Localization** button. The **Angiographic Frame Localization** window appears.
- 2 Click the **Reconstruct** button. The Lateral, AP, and Vertical reconstructions compute and appear in the window. The error factor is also computed and listed on the window.



CAUTION

The automatic frame localization can fail when the CT scan includes a head ring or when a rod is touching the patient or another high density object. If the automatic rod localization fails, you have to manually position the rods in the patient data.

- 3 Click the **Magnification** button. The **Angio Film Magnification** window appears. Magnifications and Source to Film Distance are provided for both orientations of the film.



CAUTION

Before copying the target angiographic frame coordinates to the beam isocenter, you must obtain valid CT frame transformations.

- 4 Click the **Beam Isocenter** button. The **Beam Isocenter** window appears. The isocenter coordinates are translated into physical coordinates in relationship to the headframe.
- 5 Click the **Copy Angio** button to copy the target coordinates to the beam isocenter.

3 View Patient Data

Overview

The software allows you to display two-dimensional (2D) and three-dimensional (3D) images of both patient data and treatment planning data.

In this chapter you will learn to use the visualization tools to display 2D and 3D images of patient anatomy and the regions of interest, points of interest, and beams.

The software contains a number of useful visualization tools. You can use these tools in any order:

- 2D and 3D viewing windows
- **Tools** window, which appears when you right-click a viewing window
- **Side Tools** window, which can appear along the right side of the screen (if you are licensed for AcQSim³)
- Cutplane tools, which allow you to define a plane that cuts through the 3D data set to reveal a feature of the patient anatomy

Viewing windows

All 2D and 3D images are displayed in viewing windows. The viewing windows remain displayed regardless of which panel you select from the buttons at the top of the window.

When the planning tool starts, a set of viewing windows appears by default: transverse, sagittal, and coronal image orientations.

View menu

Use the **View** menu to change the configuration of the viewing windows.

Item	Description
	Display one large 2D transverse viewing window. You can choose a different orientation from the option list at the bottom of the window.
	Display a large, 2D transverse viewing window; a small, 2D sagittal window; and a small, 2D coronal window. This is the default layout.
	Display nine 2D viewing windows. The top windows are transverse, the middle are sagittal, and the bottom are coronal. The windows in each row are synchronized, meaning that the images zoom, scroll, and pan together. By default, windows in each row display consecutive slices, but you can specify a custom slice separation for each row in the Slice increment fields at the bottom of the window if desired.
	Display nine 2D transverse viewing windows. The windows are synchronized, meaning that the images zoom, scroll, and pan together. You can choose a different orientation from the option list at the bottom of the window.
	Display one 2D transverse, one 3D, and two DRR viewing windows.
	Display one 2D transverse, 2D sagittal, 2D coronal, one 3D, one beam's eye view, and one large DRR viewing window.
	Display one large beam's eye view window.
	Display one 2D transverse, 2D sagittal, 2D coronal, and one 3D viewing window.
	Display one large beam's eye view window with a small room's eye view window in the corner.
	Display two large 2D windows in the same orientation for comparing the primary and secondary studies side by side. The layout also has controls to let you view the primary image, the secondary image, or both at once (fusion). These two windows are always synchronized, so there is only one slice selection slider.
	Display two rows of 2D windows: a 2D transverse, 2D sagittal, and 2D coronal window. The top row displays the primary image set and the bottom row displays the current secondary image set. You can change the image set shown in each row.

Viewing options

Use the **Primary**, **Secondary**, and **Fusion** radio buttons to choose what image sets display in the windows. If you choose **Secondary** or **Fusion**, the current secondary image set is used for display. The **Fusion** option displays both the primary and secondary image set.

If you change to an oblique view in a viewing window, use the **Reset T/S/C** button to change back to an orthogonal view.

Maximize the viewing area

To expand the viewing area on screen, you can hide the panel on the left side of the screen so that the viewing windows expand into that space.

- « To expand the viewing area, click the **Hide** button. The panel is hidden, and the viewing windows expand to the left.
- » To restore the panel, click the **Show** button. The viewing windows return to their original size and the panel reappears.

Maximize a viewing window

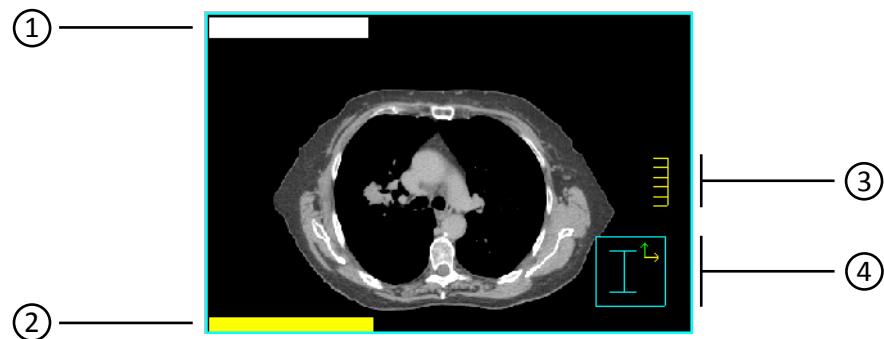
You can expand a viewing window so that it fills the entire viewing layout.

- 1 Click the viewing window that you want to expand.
- 2 Press the **m** key. The viewing window expands to fill the viewing area.
- 3 To return the viewing window to its original size, click the **m** key again.

Switch between 2D and 3D modes

You can switch the display mode between 2D and 3D in most windows. To switch a viewing window between 2D and 3D, open the **Tools** window and select **2D - Enter 3D Mode** or **3D - Enter 2D Mode**. Some windows do not allow you to switch the display mode between 2D and 3D. In these windows, an error message appears if you try to do so.

2D viewing windows



1	The trial name or record name displays in white text.
2	The slice number, slice position, image set name, and image-related information display in yellow text. For transverse images, slices are numbered from 1 starting at the end of the image set. The Z position corresponds with the scanner Z position for each slice. For sagittal and coronal images, the index number in the image set is used as the slice number.
3	Ruler, which measures five centimeters and is scaled when the image is zoomed in and out
4	The orientation cube uses letters and arrows to indicate patient orientation. The letter in the box indicates the side of the image that is displayed: • A = Anterior • P = Posterior • S = Superior • I = Inferior • L = Left • R = Right Color-coded arrows on the box indicate patient orientation: • Green arrow is anterior-facing • Yellow arrow is left-facing • Orange arrow is superior-facing

NOTE
A change in the aspect ratio of your screen will distort the 2D images. However, this does not affect printed images.

Change the slices that appear

You can choose the slices displayed in 2D windows by either specifying particular slices or using 2D tools and menu options to browse through the images.

Display a specific image in a viewing window

- 1 Right-click in a 2D viewing window. The **Tools** window appears.
- 2 Select **2D - Choose Slice**. The **Image Selection** window appears.
- 3 In the **Image to Display** field, enter the slice number and then click **Close**. That slice appears in the viewing window.

Scroll through images



- If you do not know the number for the slice you want to display, use the **Scroll through slices** tool to find it. See the *Tools* chapter for more information about this tool.
- To move through an image set one slice at a time, use the **Next Slice** and **Previous Slice** options in the **2D** menu of any viewing window or the **Next Slice** and **Previous Slice** options in the **2D** menu of the *Tools* window. Keyboard shortcuts are also available. When the cursor is in a viewing window, press **n** or the up arrow key to display the next slice in the series of slices. Press **p** or the down arrow key to display the previous slice in the series of slices. You can toggle the direction that the arrow keys scroll through the image set in the **Preferences** window.

Display the slice position in other windows

You can display the position of any currently displayed slice as a line in other 2D windows. For example, if you have three 2D windows and the image orientation is different for each, you can indicate the position of the currently displayed transverse slice by a line in the sagittal and coronal images.

To turn the display line on or off for a single viewing window, in the **Tools** window select **2D - 2D Slice Position On/Off**.

To turn the display line on or off for all viewing windows, in the **Tools** window select **2D - Global 2D Slice Position On/Off**.



Use the **Correlated pointer** tool shown at the left to select the orthogonal slices that are displayed in a viewing window set. See the *Tools* chapter for more information about this tool.

2D menu options

To display the **Tools** window, right-click in a viewing window. See the *Tools* chapter for information about the 2D tools.

Menu option	Description
Enter 3D Mode	Change the 2D viewing window to a 3D display.
Next Data Set	View the next image set in the viewing window. You can also type a v in a viewing window to see the next image set. To scroll through image sets while skipping the dose image set, use the left and right arrow keys.
Orientation	View a transverse, sagittal, or coronal image in the 2D viewing window. You can also type an a to view a transverse (axial) view, an s for a sagittal view, or a c for a coronal view.
Interpolation	Select Nearest Neighbor Interpolation or Bi-linear Interpolation . Bi-linear interpolation takes longer to display, but provides better display quality.
Zoom	Use the following selections to magnify an image. • Zoom—This label shows the current zoom factor. • Fill Window—Set the zoom factor so the entire image fits in the window. • Double Zoom—Double the current zoom factor. • Half Zoom—Cut the current zoom factor in half. • Life Size—Produce a life size image, meaning that the patient anatomy could be measured by measuring the image on the screen.

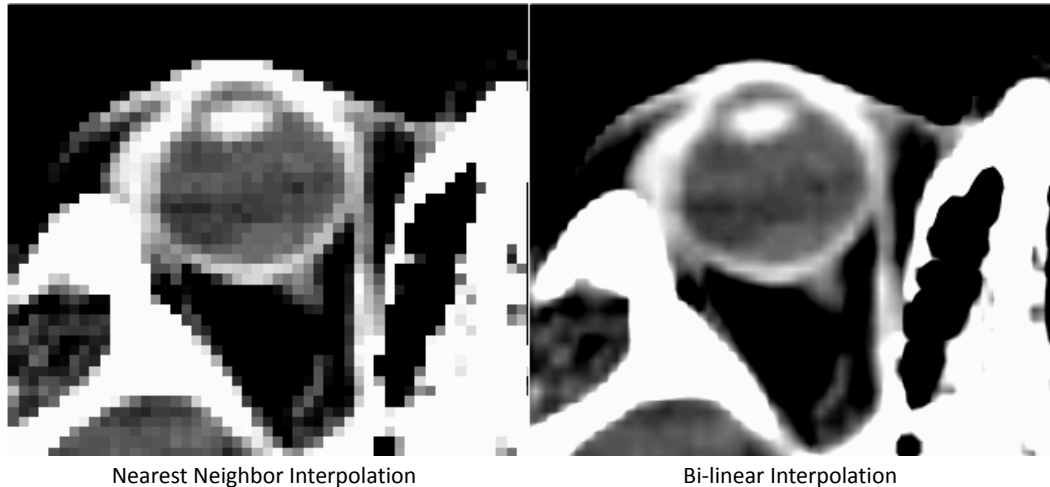
Menu option	Description
2D Slice Position	Turn the display of slice positioning on or off in the selected 2D window. A check mark appears next to this option when it is turned on. To display slice positions, you can also use the Correlated pointer tool.
Global 2D Slice Position	Turn the display of slice positioning on or off in all viewing windows. A check mark appears next to this option when it is turned on. To display slice positions, you can also use the Correlated pointer tool.
Set Slice To Current POI	This displays the slice that contains the currently selected POI. Select a POI in the Points of Interest panel.
Reference Ind. 2D	This changes the behavior of the Correlated pointer tool. A check mark appears next to this option when it is turned on. See the <i>Tools</i> chapter for an explanation of the tool.
3D Slice Position	Turn the display of slice positioning on or off in 3D windows. A check mark appears next to this option when it is turned on. To display slice positions, you can also use the Correlated pointer tool.
Clear Annotation	Remove all annotations from the image.
2D Measurement Grid	Turn the display of the measurement grid on or off in the selected 2D window. A check mark appears next to this option when it is turned on. Set the grid size in the Preferences window. See <i>Preferences</i> in the <i>Utilities</i> chapter.
Global 2D Measurement Grid	Turn the display of the measurement grid on or off in all 2D windows. A check mark appears next to this option when it is turned on. Set the grid size in the Preferences window. See <i>Preferences</i> in the <i>Utilities</i> chapter.
Choose Slice	Display a specific slice in a 2D viewing window. In the window that appears, enter the number of the slice you want to display.
Next Slice	View the next slice in the image set.
Previous Slice	View the previous slice in the image set.
Next Trial (or Next Record)	If using multiple trials or records, view the next trial or record. You can also type a t in a viewing window to see the next trial or record.

Specify the interpolation method

As you zoom in on an image, individual pixels become visible. The interpolation method determines the smoothness of the transition between adjoining pixels. The software offers two types of interpolation:

- **Nearest Neighbor Interpolation**—the greyscale value displayed is that of the closest pixel in the original image. Images may appear somewhat blocky.

- **Bi-linear Interpolation**—the displayed value is interpolated linearly from the four original image pixels surrounding the display position. Images appear smoother, but take longer to display.



Specify the interpolation method

- 1 Right-click in a 2D viewing window. The **Tools** window appears.
- 2 Select **2D - Interpolation**. Then select the interpolation method.

Set the default interpolation method

- 1 Open the **Preferences** window. See *Preferences* in the *Utilities* chapter.
- 2 Next to **Default interpolation for 2D display**, select **Bi-linear** or **Nearest neighbor** interpolation as the default method.

Set the window and level

You can set the window and level parameters to adjust the amount of contrast in each image set. A color scale, typically ranging from black through gray to white, is used to display the images. (You can change the display from greyscale to color in the **Data Set Specifications** window.) The

“window” specifies the range of values to be mapped into the color ramp. The “level” specifies the image value at which the range begins.

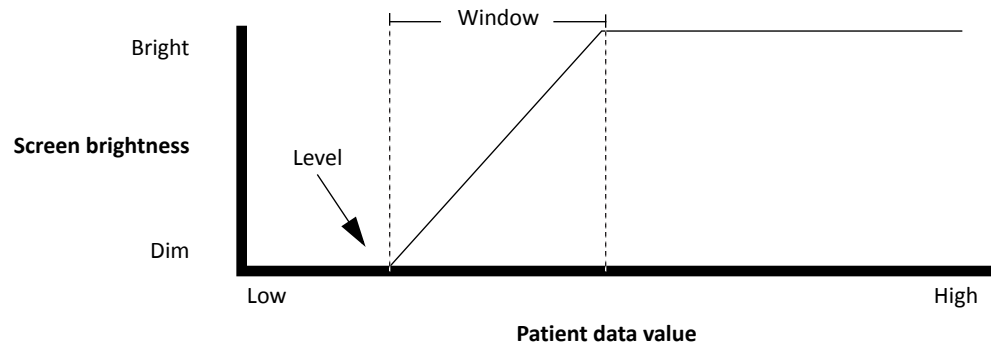


Image values below the level are set to the dimmest color (black). Image values above the level plus the window are set to the brightest color (white). Image values between these endpoints are set based on a linear ramp.

Exponential and logarithmic ramps assign more colors to the higher and lower values, respectively. Since hot spots in some types of images are so hot, linear ramps sometimes show only the hotspot. For exponential and logarithmic ramps, the straight line in the diagram above is replaced with an exponential or logarithmic curve.

The histogram equalization ramp is an optimal assignment of the color shades to the data. It accentuates all details, including some details you may not want accentuated, like noise.

If you have the **Default middle mouse window/level** preference set to **Yes**, you can use the middle mouse button in the viewing window to set the window and level.

- 1 Open the **Window/Level** window in any of the following ways:
 - Right-click in a 2D viewing window and click the **Window/Level** button.
 - Click the **Initialize** button at the top of the window and then click the **Window/Level** button in the **Patient Setup** panel.
- 2 Do you want the window and level settings to be the same for all images with the same modality?
 - Yes—Set **Link window/level by modality** to **Yes**. The next time you modify the window and level settings for one image set, those settings are applied to all other image sets with the same modality. Continue to step 3.
 - No—Set **Link window/level by modality** to **No**. Continue to step 3.
- 3 In the **Data set** list, select the image set for which you want to set the window and level.
- 4 Drag the sliders to change the values of the **Window**, **Level**, or **Level + Window**. You can also reset the window and level by typing the desired image values in the fields beside the sliders.

To use one of the standard window and level values, click your choice in the **Presets** list.

NOTE

When you manually change the window or level values, the selection in the **Presets** list changes to “--” because you are no longer using window and level values that are defined by a preset.

- 5 In the **Color ramp function** list, select the type of color ramp to be used with the image set or viewing window. This distributes color map entries through the full range of values in the image set.

If you select **Histogram Equalization**, you can better view two or more areas in which image set values are concentrated, but the areas are far apart. The equalized table uses more colors in areas with higher concentrations of values, but very few where the histogram falls to zero, thus allowing more contrast in both areas.

- 6 In the **Distribution of data set values** section of the window, use the histogram to view the distribution of image set values to see where the greatest concentrations of CT values lie.
 - To interactively change the window and level in the histogram to emphasize concentrations of CT values, drag the red and green markers, respectively.
 - To change the display range of the histogram, enter new values in the **Min** and **Max** fields. For example, you can decrease the range to magnify an area of the histogram.
- 7 When you finish setting the window and level, click **Close**.

Edit the presets

In the **Window/Level** window, click the **Edit Presets** button.

You have the following options:

- To develop a new preset, click the **Add Preset** button, type a name for the new preset in the **Name** field, and enter settings for it in the **Window** and **Level** fields.
- To edit an existing preset, select the preset in the list and then enter new settings in the **Window** and **Level** fields.
- To delete presets that you created yourself, select the preset in the list and then click the **Delete preset** button. You cannot delete a preset that came with the software.
- To save your edited presets for use in future sessions, click the **Save presets** button. If you do not, your edited presets will be lost as soon as you end your current session.
- To cancel your edited presets and return to the original settings, click the **Load factory presets** button. Presets that you created yourself are unaffected.

When you finish editing the presets, click **Close**.

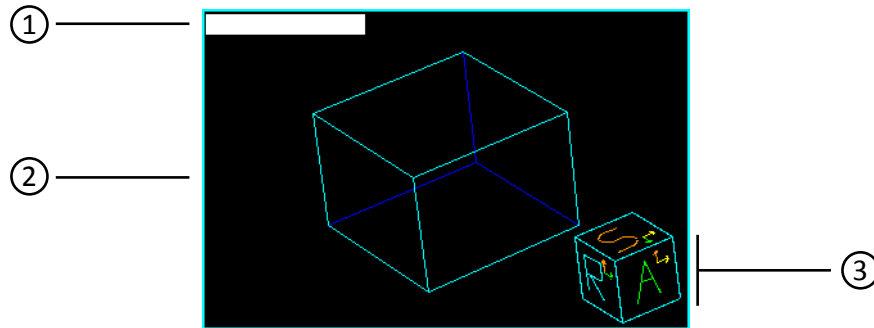
Window and level tools

In addition to the Window/Level commands described in the previous section, you can use tools on the **Tools** panel to interactively change the window and level. See the *Tools* chapter for information about the window and level tools.

NOTE

When you finish setting the window and level, you should select a different 2D tool to avoid accidentally changing the window and level settings.

3D viewing windows



1	The trial name or record name displays in white text.
2	Data set limits display as a blue cube.
3	The orientation cube uses letters and arrows to indicate patient orientation. The letter in the box indicates the side of the image that is displayed: • A = Anterior • P = Posterior • S = Superior • I = Inferior • L = Left • R = Right Color-coded arrows on the box indicate patient orientation: • Green arrow is anterior-facing • Yellow arrow is left-facing • Orange arrow is superior-facing

- 1 To switch to 3D viewing mode, right-click in a viewing window. The **Tools** window appears. Select **2D - Enter 3D Mode**.
- 2 To render a 3D image, right-click in the viewing window and select **3D - Render**.
You can also position the cursor in the viewing window and press **r** to render the image. Clicking the cursor in the 3D window during rendering cancels the rendering operation.
- 3 To change the rendering method, right-click in the viewing window and select **3D - Image Type**.
Selections include skin, bone, and digitally reconstructed radiographs (DRRs) of varying image qualities. High-quality methods take longer to render.
- 4 Use the 3D tools and menu options to control the appearance of the 3D image. The tools are described in the *Tools* chapter.
For example, you can change the viewpoint of an image using selections from the **3D - Viewpoint** menu option. To specify when new 3D images are rendered, use the **3D - Render New Image** options.

3D image display options

The software provides powerful 3D imaging features for viewing patient data. You can specify some 3D parameters in the **Data Set Specifications** window. To open this window, select **Utilities - Data Sets**.

The top portion of the window displays the data sets that are available for your plan. To select a data set, click the radio button next to the data set that you want to select.

NOTE

The window displays **Variable** in the **Sup-Inf Voxel Size** field for variably-spaced data sets.

The bottom left portion of the window displays the details for the selected data set. You cannot modify these values. The bottom right portion of the window displays the fields for the selected data set. These fields are described in the following tables.

The following fields allow you to choose how the data set is rendered.

Option	Description
2D Color	The color to be used in 2D viewing windows to display the image set.
3D Color	The color to be used in 3D viewing windows to display the image set.
Render	Specify whether the current volume should be rendered in 3D images. You should set the Render option to No when you do not want to render the patient data set in 3D windows.
Data set limits	Specify which line segments making up the outer volume limits should be displayed.

The following fields allow you to set the rendering threshold and step size.

Option	Description
Lower Limit Upper Limit	Set limits of the range of CT numbers that are used when rendering images. By changing these limits, you can determine which structures are displayed when images are rendered. Structures within the threshold limits are visible.
Step Size	Refers to the steps taken along each ray during volume rendering. A lower value produces a more accurate image but takes longer to generate. The values for these parameters can be set by typing a value into the box or by clicking the left mouse button on the slider and dragging it to a new value. The default step size is 0.1 cm. If you change this value to be rather large (for example, 1.0), you may “lose” parts of the image since the software will render a very coarse image in a 3D window.

Select a 3D image type for all images

The **View 3D** menu in the **Data Set Specifications** window lets you access 3D rendering parameters. From this menu, you can select the type of image that is rendered and control its appearance.

- 1 Select **Utilities - Data Sets**.

The **Data Set Specifications** window appears.

- 2 Select **View 3D - Standard Images**.

- 3 Choose the image type from the menu that appears. This image type is used to render all 3D images until a different image type is selected.

Standard image types include skin, bone, and digitally reconstructed radiographs (DRRs) of varying image quality. Lower-quality images take less time to generate because a simpler interpolation method is used for the image generation. However, as the name suggests, the image quality is not as good.

- 4 Right-click on the viewing window in which you want to view the image and select **2D - Enter 3D Mode**.
- 5 Right-click on the viewing window and select **3D - Render**, or position the cursor in the 3D viewing window and press **r** to render the image.

Clicking the cursor within the 3D window while the image is being rendered cancels the rendering operation.

NOTE

Increasing the size of the window to be rendered increases the amount of time it takes to complete the rendering.

Select a 3D image type for a viewing window

The procedure above sets the rendering for all 3D images. To render images using different rendering methods in each viewing window (for example, a **Skin** rendering in one viewing window and a **Bone** rendering in the next), use the following steps.

- 1 Right-click in a 3D viewing window. A **Tools** window appears.
- 2 Select **3D - Image Type**, and then select the rendering method for that window.

Repeat these steps for the other viewing windows.

3D menu options

You can select when a 3D volume renders, the image type, and how regions of interest appear inside the volume using the 3D tools and the options in the **3D** menu of the **Tools** window. See the *Tools* chapter for information about the 3D tools.

For details on creating BEV displays and room's eye view (REV) displays in viewing windows, see *Beam's eye views* and *Room's eye view*.

Menu option	Description
Enter 2D Mode	Change the 3D viewing window to a 2D display.
Render	Render the image in 3D.

Menu option	Description
Render New Image	The following options determine when an image is rendered: • When requested—The 3D image is rendered only when you select the Render command. • After motion complete—The 3D image is rendered after you complete any change in the orientation of the data set. • After any view change—The 3D image is rendered continuously, even as you make changes to the orientation of the volume. If you want to view a rendered image even while you are rotating the volume and don't care how fast or slow the software performs, you may want to choose this option. • After any view change (Low-Res)—This option only affects data sets rendered in a surface image type, such as Bone-Default, Skin-Default, Bone-High or Skin-High. The data set is rendered as a low-resolution voxel projection while it is moved. When motion is complete, the data set is rendered using its normal image type. If the data set is already using a low-resolution or voxel project image type, or is being rendered as a DRR, this option works like the After any view change option. The Render 3D images automatically preference overrides the initial setting upon plan start-up. If you select a different Render New Image option, it becomes the current rendering method.
Image Type	Select a type of rendering. Selections include skin, bone, and digitally reconstructed radiographs of varying image qualities. High-quality methods take longer to render.
Viewpoint	Change the viewpoint for a 3D image. If you reposition the data set so that it is no longer visible in the viewing window, you can choose Move focus to volume center to reposition the center of the volume in the middle of the viewing window.
Clear Annotation	Remove all annotations from the image.
Transparent Dataset On	When the patient volume is rendered using skin or bone rendering, regions of interest (ROIs) are often obscured from view because of the patient data. When you want to see the ROIs and patient data together in a 3D image, you can make the patient surface transparent. A check mark appears next to this option when it is turned on.
Next Trial (or Next Record)	If using multiple trials or records, view the next trial or record. You can also type a t in a viewing window to see the next trial or record.

Access 2D and 3D tools

You have different ways to display the 2D and 3D tools:

- You can right-click in a viewing window to display the **Tools** window.
- The **Side Tools** window can appear along the right side of the screen (if you are licensed for AcQSim³). This window provides quick access to tools appropriate to the currently selected viewing window (2D, 3D, BEV, BUnit 100078 Rev. DRV, or REV).

This section describes the various tool windows. For information about specific tools, see the *Tools* chapter.

Tools window

By clicking your right mouse button in a 2D or 3D viewing window, you open a window that features tools specific to a 2D or 3D window.

 The **Tools** window closes after you select a tool. If you want the **Tools** window to remain open after you make a selection, click the **Pin window** button shown at left.

More tools may appear in the window depending on the planning task you are performing (for example, ROIs).

For details about each tool, see the *Tools* chapter.

Side Tools window

You can choose to display a **Side Tools** window along the right side of the main window (if you are licensed for AcQSim³). This window provides quick access to tools appropriate to the currently selected viewing window (2D, 3D, BEV, BRV, or REV).

To display the **Side Tools** window, click the **Side Tools** button in the **Tools** window. To display the **Side Tools** window as a default, set the **Display Side Tools window** preference in the **Preferences** window to **Yes**. See *Preferences* in the *Utilities* chapter for more information.

For details about each tool, see the *Tools* chapter.

Program the middle mouse button

To program the middle mouse button to a particular tool, click the tool with the middle mouse button. Subsequently, each click of the middle mouse button in a viewing window activates the selected tool. To cancel the middle-mouse button programming, either select a different tool with the middle mouse button or use the **2D cursor select** tool or **3D cursor select** tool. For details about each tool, see the *Tools* chapter.

Cine viewing options

If you imported a 4D image set, you can use the **Cine** tool to create a movie of all the phases that are associated with the patient. You can create a movie in 2D or 3D viewing windows.

To use the **Cine** tool in a 2D viewing window, set the viewing mode to Transverse, Sagittal, or Coronal. To use the **Cine** tool in a 3D viewing window, render the image as a DRR.

- 1 Right-click in a viewing window. The **Tools** window appears.



- 2 In the **Cine** portion of the window, click the **Play** button. The viewing window cycles through all the phases associated with the patient. If you are creating a movie in a 3D viewing window, it may take a few minutes for all the phases to render.

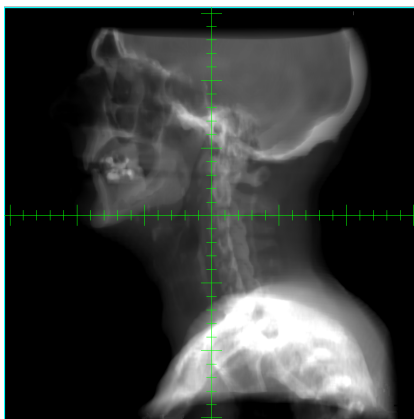
After the movie has started, you can use the scroll bar next to the **Stop** button to adjust the speed of the movie.



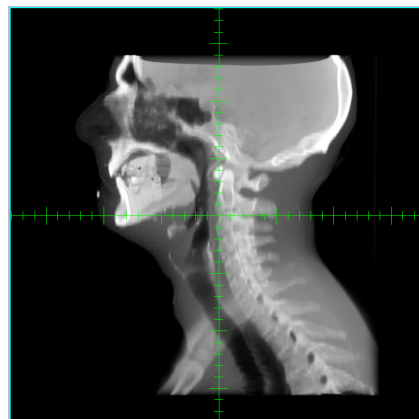
- 3 Click the **Stop** button to stop the movie. If you change the viewing window, the movie automatically stops.

Beam's eye views

Beam's eye view (BEV) displays allow you to view the patient anatomy that lies in the path of a beam. You can view volumetric images of the patient anatomy such as skin and bone rendered images and digitally reconstructed radiographs (DRRs).



BEV DRR



BEV DCR

You can display BEVs for each beam or you can develop multiple BEVs for the same beam.

- 1 Create or go to a 3D viewing window and then right-click it. The **Tools** window appears.
- 2 Select **BEV** and then select the beam you want to view. If you select **Current**, for example, the view is locked to the current beam. The BEV appears in the viewing window.
- 3 Click the **BEV Options** button. The **Beam's Eye View Options** window appears.
- 4 In the **Window** option list, make sure the window you are setting up as a beam's eye view is selected.

To change the background color of the window, click the **Background color** button and select a color in the window that appears.

- 5 In the **Type** option list, select the type of image you want to view. The resulting options vary depending on your selection.
 - If you select **DRR**, continue with the remaining steps of this procedure. Appropriate settings are selected by default, but you can change them if necessary. The DRR settings apply to the selected beam, not to the selected viewing window.
 - If you select **2D Orthogonal Plane**, set the offset of the isocenter from the center of the viewing window, and set the interpolation. These settings apply to the selected viewing window only. This procedure is complete.
 - If you select **3D Image**, a regular skin-rendered 3D image is shown in the BEV. The perspective in a 3D BEV is different from that of a regular 3D window, and is defined so that the projected field size is correct with respect to the image's anatomical features. If you select **3D Image**, you have the option of turning the display of other beams on or off in the BEV. This procedure is complete.
- 6 Set the **Display grid?** option to turn on or off the measurement grid. As a default, the measurement grid is turned off.

To customize the measurement grid, enter a resolution in the **Grid resolution** field, and select a style and color from the **Grid style** and **Grid color** option lists.

- 7 On the **Window/Level** tab, set the window and level to gain the best DRR contrast and brightness for your plan.

These window and level settings are based on the maximum DRR value. For more information, see *Set the window and level*.

- 8 In the **Color ramp function** option list, select the type of color ramp.
- 9 Set the **Automatic brightness** option to turn on or off the automatic brightness processing. As a default, **Automatic brightness** is turned on for DRRs.
- 10 On the **Settings** tab, adjust the settings described in the table below as needed.

Setting	Description
Step size Resolution	Set the step size and resolution for computation. Step size refers to the steps taken along each ray during volume rendering. A lower value produces a more accurate image but takes longer to generate. The Fast settings are used during interactive rendering (e.g., during gantry rotation) when a faster DRR is desirable. Otherwise, the Normal settings are used.
Energy (MeV)	Select the beam energy used for computation. An energy of 0.025 to 0.03 MeV has been shown to generate the best DRRs. The default value is 0.03 MeV. Use a higher energy for thicker image sets, or when you want to simulate a port film.
Brightness	Select the brightness factor used when rendering. Try a brightness value from 0.7 to 0.8 for the best DRR image quality. Values between 1.0 and 2.0 make the image brighter. Values between 0.1 and 1.0 make the image darker.
Interpolation	Select the method for generating the DRR. • Coarse uses nearest neighbor interpolation. It is less smooth than the other options, but faster. • Smooth uses linear interpolation in the Z dimension only. This is the default selection; it is smoother than Coarse and faster than Smoothest. • Smoothest uses linear interpolation in all three dimensions, but is slower than the Smooth option. If you want to set the default method of DRR interpolation to always be Coarse or Smoothest, use the Preferences window.
CT to density table	Select the table to be used when computing the DRR. This table is only used for the DRR; it is not used in the calculations performed in your plan. For each image type (CT, MR, PET), make sure you have a CT to Density Table that can properly render that type. See the <i>Pinnacle³ Physics Instructions for Use</i> for information on setting up a table.
Automatically generate DRRs	Select: • Yes if you want the software to automatically generate the DRR any time you modify the display settings. • No if you only want to render the DRR yourself. This setting applies to all the DRRs in your plan. You can also set this option in the Preferences window.
Speed up collimator movements	Select Yes to speed up collimator movement when adjusting a collimator on a BEV with the mouse.

Setting	Description
Speed up BEV translation	Select Yes to speed up BEV translation by only rendering the current BEV during translation. When this option is set to Yes , only the current BEV renders as you translate the BEV using the mouse, while any other BEV windows display only the axis lines that represent the isocenter location. Once you release the mouse, the other BEVs render completely.

11 When you finish setting the BEV parameters, click the **Close** button.

12 To render the BEV, press the “r” key in the viewing window.

NOTE

If the image does not appear, go to the **Data Set Specifications** window and make sure the **Render** option for the patient data is set to **Yes**.

NOTE

To quickly turn on or off a DRR for the current beam, right-click the BEV and click the **BEV On/BEV Off** button in the **Tools** window.

Room's eye view

In a room's eye view (REV), you can see the location of the patient in relationship to the machine. This can be helpful in determining if the patient orientation is correct. However, small data sets may be difficult to interpret given the small amount of the patient that you see in proportion to the room.

You can display REVs for each beam in the plan or you can develop multiple REVs for the same beam. Only one beam is shown per window.

The gantry, accelerator, table, and room floor appear, too. If you want to change the display of these components, see the *Pinnacle³ Planning Reference Guide*.

The geometry of these objects is associated with the beam's machine. When the beam geometry is modified, the REV updates appropriately. The gantry rotates, the couch rotates, and the patient shifts when the isocenter or the laser center is modified.

- 1 Display a 3D window or beam's eye view window.
- 2 Right click in the 3D or beam's eye view window. The **Tools** window appears.
- 3 Select **REV**.
- 4 Select the beam to be viewed. The window changes to a room's eye view. If you select **Current**, for example, the view is locked to the current beam. The REV appears in the viewing window.

Beam relative views

Beam relative views (BRVs) are 2D views that are based on a beam's position and orientation. BRVs are generally oblique with respect to transverse, coronal, and sagittal patient geometry. Use BRVs to examine the spatial relationships between a beam, patient anatomy, POIs, and ROIs. BRV orientations are parallel to the central axis of the beam (back/front), parallel to the beam's x-axis, or parallel to the beam's y-axis.

BRVs are available for any beam, and are useful in several situations. For example:

- You can use BRVs for simulations involving cancers of the head and neck when a non-coplanar beam arrangement is needed. For proper field matching, you can quickly locate a projection that is sagittal or coronal to the central axis of the supra clavicular or head fields, then manipulate the gantry collimator or couch of an alternate beam to correctly match the divergence to a fixed beam.
- When simulating half-beam breast tangents in which the treatment couch must be angled, you can graphically match the diverging beams throughout the patient. Select the beam axial slice of the medial tangent field, then turn on the display for the lateral beam on the 2D BRV axial slice of the medial beam. Use gantry and collimator adjustments to align the lateral beam with the medial tangent beam.

- 1 Create a 2D viewing window and right-click it. The **Tools** window appears.
- 2 From the **BRV** menu, select the beam you want to view. The default BRV orientation is **Front/Back**. The BRV appears in the viewing window. The lines across the image represent the beam.
- 3 To select a different BRV orientation, right-click the viewing window and select **2D - BRV Orientation**.
- 4 To change the slice plane of the BRV, right-click the viewing window and select **2D - BRV Options**.

The **Beam-Relative View (BRV) Options** window appears.

- 5 Make sure the correct beam and window are selected.

The **Window** option list contains all BRVs, BEVs, and room's eye views (REVs) for the current beam. If you select a BEV or REV in this window, all BRV-specific options will be unavailable.

- 6 Set the orientation of the BRV.

When setting orientation, you can select either **Front/Back**, the names assigned to the machine's top and bottom jaws (for example, Y1/Y2), or the names assigned to the machine's right and left jaws (for example, X1/X2). Changing the orientation results in the BRV offset being reset to 0.

- 7 Use the **Offset**, **Index**, and **Step Size** fields to specify the plane displayed in the BRV.

The offset, a slice increment that corresponds to the distance from the isocenter plane, is the **Step Size** multiplied by the **Index**. You can enter a negative or positive offset value or use the slider to pan smoothly through the BRV. The **Step Size** must be between 0 and 2 cm.

In BRVs with **Front/Back** orientation, a negative offset corresponds to a plane on the source side of the isocenter; a positive offset corresponds to the other side. Thus, the BRV offset works like the 2D BEV offset.

- 8 Set the display rotation of the BRV.

This rotation is only available for **Front/Back** BRVs. You can set this rotation to any angle.

- 9 When you finish setting the BRV parameters, click the **Close** button.



- 10 To display dose distribution in the BRV as a colorwash, click the **Eval** button at the top of the **Planning** window. Then, in the **Dose Display & Analysis** section, next to **2D Colorwash Display** select **On**.

To turn the BRV back into a standard 2D window, right-click the BRV and select **None** from the **BRV** menu.

BRV tools

Other than the exceptions listed below, 2D tools work in BRVs as they do in any other 2D window. For more details about using 2D tools, see the *Tools* chapter.

- You cannot use the POI tools to move the isocenter of the BRV's beam. The BRV image plane is determined by this isocenter.
- When a beam is being viewed in a BRV, you cannot use the **2D Beam Angle** tool to position the beam on 2D images.
- You must close the BRV before changing the trial.

Digitally reconstructed radiograph options

If you display images as DRRs, you can set your own parameters for generating them instead of using the standard DRR images.

NOTE

These DRR settings do not apply in beam's eye views. If you want to make DRR settings in BEVs, right-click a BEV window and click the **BEV Options** button. For more details, see *Beam's eye views*.

NOTE

The software can only create composite 3D renderings of surface images, not of DRR images or of DRR/surface combinations. The DRR blocks out the surface rendering at spots where the two would appear instead of merging.

- 1 Select **Utilities - Data Sets**.

The **Data Set Specifications** window appears.

- 2 Select **View 3D - Image Type - Digitally Reconstructed Radiograph**. The **DRR Options** window appears.
- 3 Enter the DRR parameters:
 - **DRR Energy**—The beam energy used for computation. An energy of 0.025 to 0.03 MeV has been shown to generate the best DRRs.
 - **CT to Density Table**—The CT to Density table to be used when computing the DRR. The CT to Density table maps the CT numbers to density, and the mass attenuation coefficients for these densities are used to generate the DRRs.
 - **Brightness Factor**—Brightness values from 0.7 to 0.8 produce the best DRR image quality. Values between 1.0 and 2.0 make the image brighter. Values between 0.1 and 1.0 make the image darker.
 - **Use Rendering Threshold**—Use the upper and lower rendering thresholds in the **Data Set Specifications** window to set the range of CT numbers for generating the DRR. The values between the lower and upper limits are used to generate the DRR. For example, to see less soft tissue in the DRR, raise the lower limit.

NOTE

DRRs look best when generated from slices with a thickness less than 5 mm. If you generate DRRs with thicker slices, their appearance might seem “stepped”.

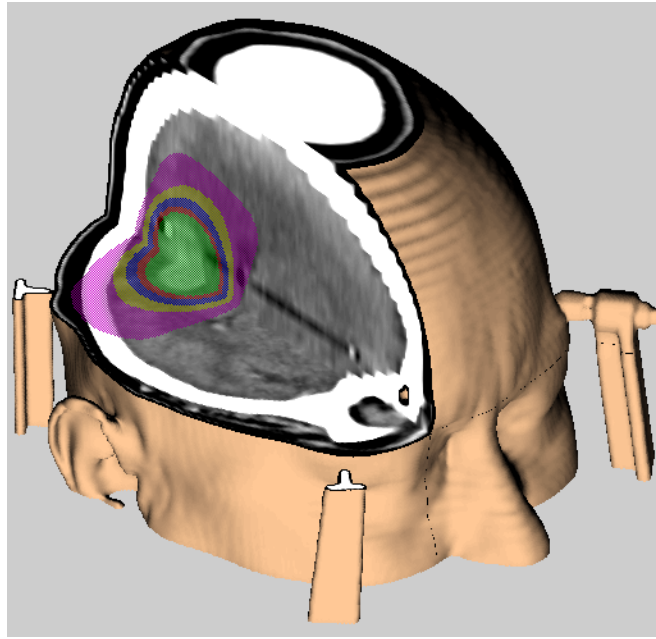
- 4 If you want to specify faster DRR rendering, in the **Data Set Specifications** window select **View 3D - Interpolation - Nearest XY, Linear Z**.

This interpolation does not adversely affect image quality, because X-Y resolution is typically much finer than the Z resolution.

- 5 To close the **Data Set Specifications** window, select **Close**.

Add cutplanes to 3D images

Cutplanes allow you to define a plane that cuts through the three-dimensional image set to reveal a feature of the patient anatomy. For the best cutplane effect, select a case on which you have drawn a number of ROIs.



NOTE

The **After Motion Complete** rendering option, which renders the 3D image after you complete any change in the orientation of the image set, does not apply to the movement of cutplanes.

The following procedure is an example of how to use cutplanes.

- 1 Choose a **Poly Surf** or similar rendering option for the ROIs you want to display in 3D.
- 2 If necessary, right-click in a viewing window and select **Enter 3D Mode** from the **2D** menu of the **Tools** window that appears.
- 3 Right-click in the viewing window again, select **3D - Image Type**, and then select a **Skin** rendering option.
- 4 Select **Utilities - Cutplanes**.

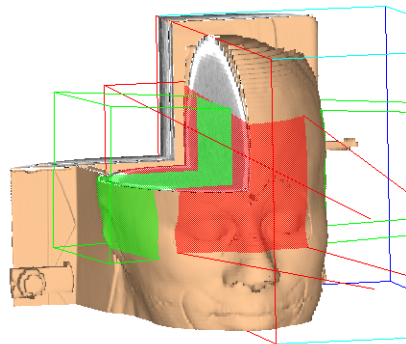
The **Cutplanes** window appears.

- 5 Select **Options - Add X Cutplane** (transverse, sagittal, or coronal) to add a cutplane through the center of the image set in the desired orientation.

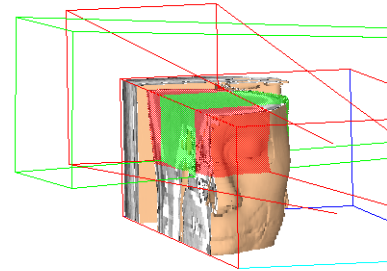
If you want to add a cutplane to all image sets, select **All Data Sets** from the **Data Set Name** option list.

- 6 Turn on or off the cutplane display using the toggle button next to the **Mark** column. If you turn off a cutplane it is automatically unmarked so you cannot move it accidentally. If you mark a cutplane it automatically displays.

- 7 At the bottom of the window, select the display mode for the cutplanes. Cut out displays the whole image set with a plane cut out of it. **Box** displays only the portion of the image set that is left after the plane cuts through it.



Cut out display



Box display

- 8 Change the orientation or position of the cutplane using the cutplane tools.

These tools operate on “marked” cutplanes. To mark the cutplane, click the box in the **Mark** column of the spreadsheet. The marked cutplane displays in yellow in 2D viewing windows and in red in the 3D viewing windows.



Then, for example, you can click the **Move cutplane 3D** tool shown at left, put the cursor on the red line, and then click and drag the red box left or right to set the intersection position. You can try intersecting through the center of some ROIs.

You can use the other cutplane tools to rotate the cutplanes about the X, Y, and Z axes, or to move the cutplane along one axis in 2D. To create a complex cutplane display, you must select and render each segment without overwriting other segments.



- 9 To specify non-normalized cutplane vectors, click the **Edit Normal** button.

The software automatically normalizes vectors according to the values in the **Cutplane Normal** fields. When you click **Edit Normal**, you can assign your own normal values without having the software re-normalize them. Enter the non-normalized vectors in the **New Normal** fields, click the **Accept** button to save the new vectors, and then click the **Done** button.

- 10 With the cursor in the 3D window, press the **r** key to render the plane. You will see a skin rendering in the marked volume and some protruding ROIs on the unmarked side.
- 11 Right-click in the viewing window, select **3D - Image Type**, and then select a **Bone** rendering option.
- 12 In the **Cutplanes** window, select **Options - Reversed Marked Cutplanes**. The cutplane reverses its position.
- 13 Render the cutplane again, as described in step 10. You will see a bone rendering in the marked volume, this time on the other side of the patient.

Sample cutplane display

To create a complex cutplane display, use the following settings and then apply the cutplanes.

Field	Setting
Image Set	Both
Display Mode	Cut-Out
Transverse Cut	On
Sagittal Cut	On
Coronal Cut	On
3D Colorwash (in Syntegra)	Show Secondary on Primary (This projects the secondary image set on the surface of the primary image set.)

General display options

Set the display of all beams

The **All Beam Display** option in the **Utilities** menu allows you to override the display settings for individual beams. You can display or hide all the beams in the 2D viewing windows. And, you can display or hide all the beams in the 3D viewing windows.

Set the display of all ROIs and POIs

The **All ROI Display** and **All POI Display** options in the **Utilities** menu allow you to override the display settings for individual ROIs and POIs. You can display or hide all the ROIs and POIs in the 2D viewing windows. And, you can display or hide all the ROIs and POIs in the 3D viewing windows.

4 Image Fusion

Overview

NOTE

The **Registration** panel is available only if you are licensed for Syntegra, and the **Deformation** panel is available only if you are licensed for Syntegra and Dynamic Planning. Contact Customer Support for licensing information.

Pinnacle³ and Syntegra allow you to correlate, or register, multiple patient image sets using the image fusion features. You can view correlated images in 2D and 3D, and you can correlate multiple patient image sets even if they use different modalities.

After you register a secondary image set to the primary set, you can also create a deformed image set that represents the mapping of the secondary image set to the primary image set based on the computed deformation vector field (DVF).

The **Image Fusion** window uses two reconstructed studies of the same organ or system; you reorient an active image to align with a stationary reference image in any direction. Syntegra uses multiple reconstructed studies of the same organ or system. You can select more than one secondary image set for image fusion, but you can only view fusion of one secondary image set at a time with the primary image set.

You can save the reoriented, aligned image data as part of your plan.

NOTE

The **Image Fusion** and **Syntegra** windows display images in absolute coordinates (in centimeters). Thus, if one study is acquired in the standard CT matrix of 512x512 with a pixel size of 1 mm and another is acquired in a 128x128 matrix with a pixel size of 4 mm, both studies have the same size in the display.

Image fusion limitations

- If the position of the patient on the table is not the same in the image sets that you want to register, you may not be able to accurately align the image sets.
- If you are registering multiple secondary image sets that are not pre-registered or that use different fields of view, you must register each image set separately.

The fusion window

On the **Utilities** menu, click **Image Fusion** to open the **Image Fusion** or **Syntegra** window.

The **Image Fusion** and **Syntegra** windows are each one large window that allows you to register multiple image sets. The main icons along the top show the different panels for **Setup**, **Registration**, **Deformation**, and **Contours**. When you open a fusion window, by default a 2D

transverse, coronal, and sagittal viewing window set and 3D viewing window appear in the right panel (you can change the default in your preferences).

Main icons

Icon	Panel	Description
	Setup	Displays the Setup panel. Use it to set up the display of your image sets, determine which image sets are moveable, and perform manual registration.
	Registration	Displays the Registration panel. This is only available if you are licensed for Syntegra. Use it to automatically register the secondary image sets to the primary image set.
	Deformation	Displays the Deformation panel. This is only available if you are licensed for Dynamic Planning. Use it to create a deformed image set and assess the quality of the deformed image set.
	Contours	Displays the Regions of Interest panel. Use it to draw contours of tumors and anatomical structures.

Setup panel

Options menu

Menu Item	Function
Global Thick Slice Display	Turn on or off the display of thick slices in 2D viewing windows.
2D Tool Parameters	Set the increments to use with the shift and rotation tools.
Registration Parameters	View the translation and rotation offsets between the primary and selected secondary image set.

Fields

Field	Description
Primary Image Set	The image set to which all other image sets are registered.
Secondary Image Set	An image set that will be registered to the primary image set.
2D Color	The color to be used in 2D viewing windows to display the image set.
Available Fusion Image Sets	The list of available secondary image sets that can be registered to the primary image set. All moveable fusion image sets are moved when you use the interactive registration tools.
Copy this transformation to	Copy the transformation parameters of the current secondary image set to another secondary image set. You can only copy the parameters to moveable image sets.
Image thickness	The requested thickness for the thick slice display. This setting applies to all image sets.
Fusion display method	If you select Alpha Blending (only available in Syntegra), the Alpha field appears. If you select Checkerboard , the Tile size field appears.

Field	Description
Alpha	Use the Alpha slider to set the transparency of the primary image set. This feature is only available in Syntegra.
Tile size	The size of the squares to use when displaying the “checkerboard” view of the image sets. This setting applies to the current viewing window.

NOTE

ALL secondary images that are moveable are moved together when you use the registration tools or the automated registration.

Registration panel

The **Registration** panel is available only if you are licensed for Syntegra.

Options menu

Menu Item	Function
Global Thick Slice Display	Turn on or off the display of thick slices in 2D viewing windows.
2D Tool Parameters	Set the increments to use with the shift and rotation tools.
Registration Parameters	View the translation and rotation offsets between the primary and selected secondary image set.

Fields

Tab	Field	Description
Images	Use defaults for	Set the default automated image registration type. The combination you select configures Syntegra to use a recommended algorithm. The order of the modalities in the list is not relevant: CT-MRI would be the same as MRI-CT.
Images	Algorithm	Algorithms to determine the best registration for all the image sets. You can set the default algorithm as a user preference. • Cross correlation makes direct comparisons between image set values. It is effective for registering image sets of the same modality. • Local correlation makes comparisons of many areas of the image sets. It works best for image sets with differing modalities in which equivalent features can easily be seen (for example, CT-MR). • Normalized mutual information uses probability concepts to optimize the data between image sets. It does not assume a functional relationship between the values, so it is effective for multi-modality image sets.
Images	Show intermediate transformations	As each transformation step is complete, display that transformation in the viewing windows.
Images	Elapsed time	Displays how long the fusion has been running.
Images	Time limit	The maximum time Syntegra should work on fusing the image sets.
Images	Similarity score	This number shows the progress of the transformation (like a “percent complete” number). It does not define the accuracy of the transformation, merely its state. It appears during the registration process.

Tab	Field	Description
Images	Use common bounding box	Select whether to limit both data sets at once or limit them separately. • Yes—Use a common bounding box for both image sets. • No—Use separate bounding boxes for the primary and secondary image sets.
Images	Limit both data sets	If Use common bounding box is set to Yes , select the method for limiting both data sets: • No—Use a combination of both image sets. • Existing ROI—Set the Margin around the combined ROIs. • Bounding Box—Limit the image sets to a rectangle you define.
Images	Limit Primary data	Limit fusion of the primary image set to the defined subvolume or one of its regions of interest. • No—Use the whole image set. • Existing ROI—Limit the image set to an ROI. • Bounding Box—Limit the image set to a rectangle that you define.
Images	Limit Secondary data	Limit fusion of the secondary image set to the defined subvolume or one of its regions of interest. • No—Use the whole image set. • Existing ROI—Limit the image set to an ROI. • Bounding Box—Limit the image set to a rectangle that you define.
Points	Fiducial Points	Displays the fiducial point sets (one point each on the primary image set and a secondary image set). Also displays the distance between the two points.
Points	2D Display for All Fiducial Pairs	Turn on or off the display of the points in 2D viewing windows.
Points	3D Display for All Fiducial Pairs	Turn on or off the display of the points in 3D viewing windows.
Points	Mean distance between points	The average distance between all primary/secondary fiducial point sets.

Deformation panel

The **Deformation** panel is available only if you are licensed for Dynamic Planning. See *Deformable image registration* in this chapter.

Regions of Interest panel

See the *Regions of Interest* chapter for information about contouring.

Viewing windows

2D and 3D viewing windows are used to view the patient anatomy, fusion of the image sets, fiducial markers, and regions of interest.

Default viewing window



Next to the default viewing window set, the following fields allow you to control the display.

Field	Description
Render	Specify whether the current volume should be rendered in 3D images. You should set the Render option to No when you do not want to render the patient data set in 3D windows.
3D Color	Set the color to be used when displaying the image set in 3D.
Image Type	Specify the image type. The image types are surface and maximum intensity projection (MIP).
Render Threshold	Use the upper and lower rendering thresholds to determine the range of values used when generating the image. Threshold values do not apply to the MIP image type.
3D Colorwash	Select how the software shows the primary and secondary image sets in 3D displays.

NOTE

You cannot combine surface and MIP image types in one viewing window.

Other viewing windows

Use the **View** menu to change the configuration of the viewing windows.

Menu Item	Function
	Display one large 2D window for viewing the primary image, the secondary image, or both at once (fusion). The layout also features a smaller 2D window, which always displays the primary image as a reference. The larger and smaller windows stay synchronized as you change their orientation.
	Display two large 2D windows in the same orientation for comparing the primary and secondary studies side by side. The layout also has controls to let you view the primary image, the secondary image, or both at once (fusion). These two windows are always synchronized, so there is only one slice selection slider. This layout is good for reviewing registration and drawing contours after the image sets are registered.
	The default view contains transverse, sagittal, and coronal 2D views in the top row, and a 3D view. This layout includes 3D viewing window options. This layout is good for manual- or image-based registration. It allows the best view of image alignment.
	Display three 2D windows: transverse, sagittal, and one large coronal window. There are no slice selection bars in this window so you will have to use the n and p keys or the scroll tool to change slices.

Menu Item	Function
	Display two rows of 2D windows: a 2D transverse, 2D sagittal, and 2D coronal window. The top row displays the primary image set and the bottom row displays the current secondary image set. You can change the image set shown in each row. This layout is good for placing points for point-based registration.
	Display three sets of 2D viewing windows. Each set is a sequence of slices. The first row is the primary image set. The second row is the secondary image set. The third row is the fusion view (both image sets). This layout is good for reviewing the image sets after registering them.
	Display three 2D windows (transverse, sagittal, and coronal) and one 3D window.
	Display three rows of 2D windows of each orientation: transverse, sagittal, and coronal. The rows are synchronized. You can change the slice separation in each row.

Viewing options

Use the **Primary**, **Secondary**, and **Fusion** radio buttons to choose what image sets display in the windows. If you chose **Secondary** or **Fusion**, the current secondary image set is used for display. Use the **Reset to T/S/C** button to set the display back to one transverse, sagittal, and coronal 2D view.



The **Fusion** option displays both the primary and secondary image set. While using the **Fusion** mode for the viewing windows, you can use the **Show secondary image cutout** tool to create a “cutout” in the primary image set that shows the secondary image set. This view can help you determine if your images are aligned.

Set up the image sets



CAUTION

View your image sets as single slices before transforming and registering the image sets. Doing so should allow you to see if there are any anomalies in the image sets you intend to use.

The following is the basic procedure for setting up your image sets. For detailed information and procedures, see the sections that follow.



- 1 Click the **Setup** icon at the top of the window to display the **Registration Setup** panel.
- 2 For the primary image set, change the 2D color, if necessary.
- 3 If the window and level are not optimal, click the **Window/Level** button. The **Window/Level** window appears. Change the settings so the image set appears correctly for your needs. See *Modify the window and level*.
- 4 For the secondary image sets, select the image set for which you want to set the color, window, and level.
- 5 Change the 2D color if necessary.
- 6 If the window and level are not optimal, click the **Window/Level** button. The **Window/Level** window appears. Change the settings so the image set appears correctly for your needs. See *Modify the window and level*.
- 7 Repeat steps 3-5 for each secondary image set.
- 8 Under **Available Fusion Image Sets**, click on the **Moveable/Not Moveable** toggle button next to each image set until the proper image sets are moveable or unmoveable.

NOTE

The **Undo previous transformation** button can be used while an image set is moveable. Once you change the image set to not moveable, the registration changes you have made cannot be undone. The **Redo** button can be used to re-do an action you just chose to undo and will work only for those changes that are still in memory.



- 9 In Syntegra only: Use the **Move Secondary Center to Primary Center** and **Reset Secondary to Initial Position** buttons to move the secondary image sets if necessary. The **Move Secondary Center to Primary Center** button moves the geometric center of the secondary image set to the geometric center of the primary image set.
- 10 To change the 2D checkerboard view, use the **Tile Size** field to set the size of the squares.
- 11 In Syntegra only: Under **2D View Parameters**, if you want to use the alpha blending view, select **Alpha Blending** then use the **Alpha** slider or field to set the transparency of the primary image set.



Now you can manually adjust the registration, or if you are licensed for Syntegra you can use the automatic registration tools in the **Registration** panel.

Set the color map



At the top of the **Registration Setup** panel you can select the color map for each image set.

The default color map for the primary image set is greyscale. The default color map for all secondary image sets is thermal. If you have different default color maps selected as preferences, those will be used as the defaults.

For the primary image set, from the **2D Color** option list, select the color map.

For secondary image sets, from the **Image Set** option list, select the desired image set. Then from the **2D Color** option list, select the color map.

Modify the window and level

The “window” specifies the range of values to be mapped into the color ramp. The “level” specifies the image value at which the range begins. Image set values are mapped to colors based on a ramp function that can be selected in the **Window/Level** window. The default is a linear function, but you can set a new default in the **Preferences** window.

You can set the window and level for each image set. In the **Preferences** window you can set default window and levels for the primary image set and all secondary image sets.

In the **Syntegra** or **Image Fusion** window, select the image set for which you want to set the window and level. Use the table that follows to set the window and level that you prefer.

Field	Description
Sliders	Use the long sliders to interactively set the window and level for the primary image set and all secondary image sets. The red line sets the window. The green line sets the level and window. Click between the lines and drag to adjust the level. Use the radio buttons below each slider to make changes to the desired image.
Window	Use the slider or enter the window number you want for the image set.
Level	Use the slider or enter the level number you want for the image set.
Units	Specify the window and level units: percentage of max (maximum value in the image set), actual image set values, or standard uptake values (SUVs). SUV units are available when there is SUV information in Philips PET image sets. For the actual image set, the range of values is zero to the maximum volume value. When you select SUV, the range of values becomes 0-10. The software converts each image set value to an SUV before mapping it to a color. The two SUV color maps (SUV2 and SUV3) each have 10 discrete colors. If you set the level to zero and the window to 10, then all SUVs in the range 0-0.5 map to the first color, 0.5-1 to the second color, 1-2 to the third, 2-3 to the fourth, etc. You can use the full range or decrease the window. You can use other color maps with SUV, but the other maps do not have discrete colors.
Ramp	The function to use to distribute color map entries through the full range of values in the image set. The functions are: linear, logarithmic, exponential, and histogram equalization.
Presets	Use standard or custom window and level settings. To create or edit a preset, see <i>Window and level presets</i> .

NOTE

When you manually change the **Window** or **Level** values, the selection in the **Presets** list changes to “--” because you are no longer using window and level values that are defined by a preset.

Click the **More** button to change the way the window is displayed. The window includes a histogram as an additional tool for setting the window and level.

Use the histogram to view the distribution of data set values and identify where the greatest concentrations of values lie.

- To interactively change the window and level in the histogram to emphasize concentrations of values, drag the red and green markers, respectively. (If you do not see them, the window marker is at the very left edge and the level marker is at the very right edge.)
- To change the display range of the histogram, enter new values in the **Min** and **Max** fields. For example, you can decrease the range to magnify an area of the histogram.

Window and level presets

To use one of the standard window and level values, select from the **Presets** option list.

If you want to edit the window and level of the preset values, click the **Edit** (or **Edit Presets**) button. The **Edit Window/Level Presets** window appears.

- To develop a new preset, click the **Add Preset** button, type a name for the new preset in the **Name** field, and enter settings for it in the **Window** and **Level** fields.
- To edit an existing preset, select it in the list and then enter new settings in the **Window** and **Level** fields.
- To delete presets that you created yourself, select the preset in the list and then click the **Delete Preset** button. You cannot delete a preset that came with the software.
- To save your edited presets for use in future sessions, click the **Save Presets** button. If you do not save, your edited presets will be lost as soon as you end your current session.
- To cancel your edited presets and return to the original settings, click the **Load Factory Presets** button. Presets that you created yourself are unaffected.

When you finish editing the presets, click the **Close** button.

Make image sets moveable



In the middle of the **Registration Setup** panel you can choose which image sets are moveable or stationary. Any image set that is moveable is changed by the registration and transformations you perform. All changes to secondary image sets are relative to the coordinate system of the primary image set.

Click the button next to the image set name to toggle between moveable and unmoveable.

NOTE

ALL secondary images that are moveable are moved together when you use the registration tools or the automated registration.

Set 2D fusion display

Checkerboard

To achieve the illusion of fusing images in the 2D views, alternating tiles of the active and reference images appear in the fusion window. The “tile size” allows you to vary the amount of mixing between the pixels of the active and reference studies when they are fused and can be useful when evaluating the registration between image sets. The default setting is alternating one pixel from each image set. To display a different overlay in the selected view, enter a new number in the **Tile size** field and press **Enter**, or click and drag the slider.

Alpha blending

This feature is only available if you are licensed for Syntegra. If you are licensed, this is the default display mode.

Alpha blending is used in computer graphics to create the effect of transparency. In computer graphics, each pixel has three channels of color—red, green, and blue—and a fourth channel called the alpha channel. The alpha channel controls graphics display methods such as levels of transparency or opacity. You can use alpha blending to simulate the transparency of the primary image set so you can “see through it” to the secondary image set.

The alpha value is used to blend the red, green, and blue values from each image set. A value of zero (0) makes the primary image set completely transparent. A value of one (1) makes the primary image set completely opaque.

Use the **Alpha** slider to set the alpha value of the primary image set. The default value is 0.5 (50%).

Copy a transformation

This feature is only available if you are licensed for Syntegra. If you have multiple secondary image sets that were acquired on the same machine, with the same patient position, and with the same field of view, you can copy the fusion transformation from the first image set to the second image set.

To copy a completed fusion transformation to another image set, make the image sets moveable. Under **Copy this transformation to**, select the image set, then click the **Go** button.

Use thick slices

The “thick” slice feature is only available if you are licensed for Syntegra.

Use the **Image Thickness** field under **2D View Parameters** to set how “thick” each slice should be in the image set. This feature allows you to decrease the “noise” in the image set.

Syntegra averages all of the image data over the range of slices that makes up that thickness. When displayed in the viewing window the range of slices is displayed (Z = 10.0 to 12.20) since it is not a specific slice.

The value that you enter may not always be the actual slice thickness. The actual thickness can be seen by looking at the range of slices displayed in the viewing window. Syntegra determines the thickness by taking the original slice you displayed in the viewing window and adding an equal number of slices to either side so that the total thickness is less than or equal to your entered value. The voxel size plays a large part. For image sets with

- standard slices: for example if your voxel size is 0.3 cm, Syntegra can only add slices in increments of 0.3 cm to either side of the current slice. If you enter 1.0 cm, you will get a thick slice of 0.9 cm, not 1.0 cm (the original slice and a slice on either side = $0.3 + 0.3 + 0.3 = 0.9$). To get a thick slice that is the same as the value you enter, make the value a multiple of the voxel size.
- inconsistent slices (only affects transverse views since inconsistent spacing is only allowed in the Z direction): the thickness is your entered value. Syntegra uses a weighted average to combine the slices, where the weight is the percentage of the slice that fits inside the thick slice.
- oblique slices: the original oblique slice is averaged with parallel oblique slices at increments of 0.4 cm from the original slice so the distance from the first to last slice is less than or equal to your entered value.

When using thick slices please note that:

- you can change a thick slice back to the individual slices at any time.
- ROIs cannot be created on thick slices and existing ROIs are not displayed.
- the maximum thickness allowed is 16 mm.
- points for point-based registration cannot be placed on thick slices.
- you *can* use the zoom, pan, and scroll tools in viewing windows displaying thick slices.
- you *can* use the cutout window tool in viewing windows displaying thick slices.

Automatic registration

The features in this section are available only if you are licensed for Syntegra.



CAUTION

View your image sets as single slices before transforming and registering the image sets. Doing so should allow you to see if there are any anomalies in the image sets.

Image-based registration

For image-based registration you do not have to define any points (fiducial markers). Syntegra registers the image sets based on the image data.

- 1 Select the secondary image set that you want to register.
- 2 From the **Use defaults for** list, select the combination to be used.

The combination that you select configures Syntegra to use a recommended algorithm but you can select a specific algorithm (or set one as a user preference).

- 3 If necessary, from the **Algorithm** list, select the algorithm that Syntegra should use to align the image sets.
- 4 In the **Show intermediate transformations** field select **Yes** or **No** to view the transformations as they occur.
- 5 In the **Time limit** field set the maximum length of time you want the software to run transformations.
- 6 You can limit the volume of the primary or secondary image set that should be used for registration. Select the appropriate option in the **Use common bounding box** field:
 - **Yes**—Use one common bounding box for both the primary and secondary image sets.
 - **No**—Use separate bounding boxes for the primary and secondary image sets.
- 7 Define how the image sets should be limited.
 - **No**—Do not limit the image set.
 - **Existing ROI**—Limit the image set to an ROI. Select the ROI from the list that appears.



- **Bounding Box**—Limit the image set to a rectangle that you define. Limit the volume by using the **Adjust bounding box** tool to draw a rectangle on the image set. See *Define the sub-volumes*.
- 8 Click **Register Images**. The **Stop and Accept** button appears in place of the **Register Images** button. The **Similarity Score** field appears and updates after each iteration so that you can see how close the registration is to completion.

If you want to stop the registration before the software considers the registration complete, click **Stop and Accept**. If you stop the registration before the software is finished, the current iteration of the registration is used and shown.



CAUTION

Verify the accuracy of your registration before proceeding. If it is not accurate enough, use the manual tools or image- or point-based registration to refine it further.

Define the sub-volumes



Using the **Adjust bounding box** tool, you can define one sub-volume (box or region of interest) on each image set that the software uses for registration. Sub-volumes let you eliminate some of the “extra” parts of the image set that are not vital for registration because the software ignores all of the data points outside of the sub-volume. For example, when fusing head scans in which one image set contains a portion of the neck and torso, create a sub-volume that excludes the neck and torso.

You can draw sub-volumes while using the fusion view on transverse, sagittal, or coronal views, or you can select an ROI to use as the sub-volume.

NOTE

You can draw the sub-volume as large as you want, but the software will not let you cover the image set and slice information in the bottom of the viewing window.

Point-based registration

You can use fiducial markers to help align the images. To register image sets, you must set up fiducial marker pairs: one marker on the primary image set (displays in red) and one on a secondary image set.

These markers can be moved at any time. If you move the image set, the markers move with the image set. In 2D views a marker appears as a crosshair inside a circle. In 3D views a marker appears as a sphere.

Syntegra displays the distance between each pair so that you can identify misplaced or un-registered markers.

- 1 Select the secondary image set that you want to register.
- 2 On the **Points** tab, click **Add New Fiducial Pair**. The software adds a set of fiducial markers to the list.



- 3 In a viewing window, use the **Place fiducial markers** tool to place each marker at the appropriate spot on the image set.
- 4 Repeat steps 2 and 3 for each pair you want to add.

You must place a minimum of 3 pairs of markers. You can place a maximum of 10 pairs of markers.

- 5 Click **Register Images**. After the registration is complete, the mean distance of all the points appears at the bottom of the panel.



CAUTION

Verify the accuracy of your registration before proceeding. If it is not accurate enough, use the manual tools or image- or point-based registration to refine it further.

Registration parameters

To view the translation and rotation offsets of each secondary image set, on the **Options** menu, click **Registration Parameters**. The window displays the information for the current secondary image set. To change the image set, select it from the **Secondary Image Set** list.

You can change the translation vector by modifying the X, Y, or Z offsets. If you set the **Rotation** field to **Angles**, you can change the rotation.

Manual registration

Use the 3D tools first to begin correlating the images, then use the 2D tools to fine-tune the registration process.

Adjustments in 3D

The 3D tools are available only in Image Fusion.



- 1 In the **Setup** panel, set up the transverse, sagittal, and coronal viewing windows so you can see the image sets in all three orientations.
- 2 If the secondary image set does not appear, it might be completely outside the CT image. Click on the **Moveable/Not Moveable** toggle button next to the secondary image set to make it moveable, then use the 3D registration controls to shift and rotate the 3D images.



- Use the **Move secondary** tool to shift the 3D image.
- Use the **Rotate secondary** tool to rotate the 3D image.



- 3 Repeatedly shift and rotate the active image with respect to the reference image until the studies appear to be correlated.

3D rendering



After you register the images, you can render reference and active studies in 3D using the 3D window controls. These controls only appear in the default layout of the **Image Fusion** window.

The 3D view displays a blue and a green wireframe, representing the field of view (FOV) of the reference and active studies, respectively. If the FOVs of the active and reference studies are the same, wireframes have the same size and overlap.

As you move the active image, watch the effect on the wireframes in the 3D view. The green wireframe reflects the transformations. The reference wireframe, in blue, does not change because the reference study is static spatially.



To change the orientation of the 3D view, right-click it and use the **3D rotate**, **3D pan**, and **3D zoom** tools. See the *Tools* chapter for details about these tools.

- 1 Change the display colors of the image sets using the **Primary 3D Color** and **Secondary 3D Color** option lists.

You can set the display colors to see a clear distinction between the CT images and the MRIs. We recommend the **Thermal** selection for secondary PET images and secondary MRIs.

- 2 If you want to render the secondary image set with the primary image set, select **Yes** in the **Secondary Render** field.

By default, the secondary image set is rendered with the primary image set.

- 3 Set the rendering thresholds for both image sets.

The thresholds determine the limits of the pixel values that are included in the 3D reconstruction. Pixel values outside the limits are not rendered.

- 4 Use the **3D Colorwash** option menu to select how the software shows the primary and secondary image sets in 3D displays.
- 5 To render the image sets, click the **Render** button.

To view the image from another angle, change its rotation and render it again.

Adjustments in 2D

Use the following tools to make manual adjustments or manually fuse image sets.



- To shift the image set in small increments, click the **2D fine-tune shift** tool shown at left, then click in the top, bottom, left, or right part of the image, depending on the shift you want. For example, click the left side of the image set to shift it to the left.



- To rotate the image set, click the **2D fine-tune rotation** tool shown at left, then click the right half of the image for clockwise rotation and the left half for counterclockwise rotation.

The rotation controls are based on the center of the image. Watch the effect on the active image in the target plane and other planes.



CAUTION

Verify the accuracy of your registration before proceeding.

Deformable image registration

After you register a secondary image set to the primary image set, you can choose to create a deformed image set. A deformed image set is a new image set that is mapped to the primary image set based on the computed displacement vector field (DVF) between the primary and secondary image sets.

Rigidly register the image sets

Before you create a deformed image set, rigidly register the secondary image set to the primary image set.



- 1 Click **Deformation** in the **Syntegra** window to open the **Deformation** panel.

NOTE

The **Deformation** panel is available only if you are licensed for Syntegra and Dynamic Planning.

- 2 In the **Rigid Registration** section of the **Deformation** panel, select the secondary image set that you want to register.
- 3 In the **Limit Image Sets** section of the **Deformation** panel, you can limit the volume of the primary or secondary image set that should be used for registration. In the **Use common bounding box** field select **Yes** or **No** to use one common bounding box for both the primary and secondary image sets, and then define how the image sets should be limited.
 - **No**—Do not limit the image set.
 - **Existing ROI**—Limit the image set to an ROI. Select the ROI from the list that appears.
 - **Bounding Box**—Limit the image set to a rectangle that you define. Limit the volume by using the **Adjust bounding box** tool to draw a rectangle on the image set. See *Define the sub-volumes*.
- 4 If necessary, select the algorithm that Syntegra should use to align the image sets from the **Rigid Registration Algorithm** list.
- 5 Click **Register Images**. The software registers the images.



Create a deformed CT image set

- 1 In the **Rigid Registration** section of the **Deformation** panel, select the secondary image set that you want to use for deformation.

NOTE

The secondary image set must be a CT or cone beam CT (CBCT) image set. Also, deformed image sets cannot be deformed again, so do not select a deformed image set as the secondary image set.

- 2 In the **Limit Image Sets** section of the **Deformation** panel, you can limit the volume of the primary or secondary image set that should be used for deformation. In the **Use common**

bounding box field select **Yes** or **No** to use one common bounding box for both the primary and secondary image sets, and then define how the image sets should be limited.

- **No**—Do not limit the image set.
- **Existing ROI**—Limit the image set to an ROI. Select the ROI from the list that appears.
- **Bounding Box**—Limit the image set to a rectangle that you define. Limit the volume by using the **Adjust bounding box** tool to draw a rectangle on the image set. See *Define the sub-volumes*.



- 3 In the **Deformable Registration** section of the **Deformation** panel, select the modality of the primary image set from the **Primary Image Modality** options.
- 4 In the **Filter images** field, select **Yes** or **No** to exclude extraneous data from the images.

If you select **Yes**, the software attempts to exclude everything outside of the patient from the images, including the table, blankets and other patient coverings, and head frames, masks, and other positioning devices. This is particularly important when one image set includes a head frame, for example, and the other image set does not. Excluding artifacts outside of the patient can improve the resulting deformation.

- 5 If necessary, change the amount of smoothing that is applied during deformation by typing a value in the **Smoothing** field. For the initial deformation we recommend that you use the default value, which will be sufficient for the majority of deformations. If you notice that your deformation is too constrained or is not smooth enough, you can change the **Smoothing** value and deform the images again. For example, if there has been a dramatic change in the patient between the acquisition of the primary and secondary image sets, you may need to adjust this value to obtain a more satisfactory image deformation.

Smoothing controls the amount of Gaussian smoothing that is used to reduce deformation irregularities, but it also limits the resolution of the deformation. A small **Smoothing** value results in more variation in deformation than a large value. If you set the value too low, the software could produce unnatural deformations. If you set the value too high, you could smooth the deformation too much and reduce the accuracy of local deformations.

- 6 Click **Create Deformed Image**. The software creates a new deformed image set that represents the mapping of the secondary image set to the primary image set based on the computed DVF.

Registration QA tools



Click **Deformation** in the **Syntegra** window to open the **Deformation** panel. The **Deformable Registration** and **Registration Validation** sections of the panel provide several tools that you can use to assess the quality of the deformation.

NOTE

The **Deformation** panel is available only if you are licensed for Syntegra and Dynamic Planning.

View the deformation

You can view the displacement vector field (DVF) that is computed between the primary image set and the selected secondary image set. The DVF displays as either arrows or a grid on the following image sets:

- Primary image set
 - Secondary image set that was used to generate the DVF
 - Deformed image set
 - Fusion views of the primary image set and either the secondary image set or the deformed image set
- 1 In the **Rigid Registration** section of the **Deformation** panel, verify that the secondary image set for which you want to display the DVF is selected in the **Secondary Image** field.
 - 2 In the **Deformable Registration** section of the **Deformation** panel, set **Deformation Display** to either **Arrows** or **Grid**.
 - 3 If necessary, adjust the **Deformation Display Spacing** value to set the spacing of the DVF display.
 - 4 If you set the **Deformation Display** to **Arrows**, you can set two additional options:
 - **Limit arrows to patient?**—Limit the deformation display to the patient volume as defined by the outside-patient air threshold.
 - **Minimum Arrow Length**—Set the minimum length of arrow to display. This filters out the display of arrows that are shorter than the minimum length, which helps you to visualize the regions with the largest displacements between image sets.

Validate the registration

In the **Registration Validation** section of the **Deformation** panel, click **Validate** to open the **Registration Validation** window. The information shown in the window is the registration information for the secondary image set that is listed in the **Secondary Image** field. To show information for a different image set, select the image set from the **Secondary Image** list.

The **Registration Information** section of the window contains details about the registration, including the specific primary and secondary image sets used in the registration and the rigid translation and rigid rotation parameters that were applied to the secondary image set in relation to the primary image set.

NOTE

If the secondary image set is a deformed image set, “--” appears in the **Secondary Image Date** field.

The **Validation Information** section of the window lists the **Target Registration Error** value, if you calculated this value, and information about the approval of the registration. (See *Calculate the Target Registration Error*.) Comments that you type in the **Comment** field are saved with the trial and are included in the plan report.

Calculate ROI Similarity

The **ROI Similarity** section of the window lets you assess the quality of the image deformation by measuring the mapping between deformed ROIs and non-deformed ROIs.

NOTE

You can use the **Propagate ROI** feature to propagate ROIs from a record to your primary image set and then use the propagated ROIs as reference ROIs when you use the **ROI Similarity** feature. See *Propagate ROIs from a record*.

- 1 Click **Add** to add a row to the **ROI Similarity** table.
- 2 Define a pair of ROIs to compare by selecting one of the ROIs in the **Reference ROI** column and the second ROI in the **ROI to Validate** column.

Repeat steps 1 and 2 until you have defined all of the pairs of ROIs that you want to compare.

- 3 Click **Compute** to calculate the **Dice Score**, **Mean Distance to Agreement**, and **Max Distance to Agreement** values for the ROI pairs.

The **Dice Score (DSC)** (Dice Similarity Coefficient) is a measure of how well the two ROI volumes overlap one another. The results are reported as a value between 0.00 and 1.00: A value of 0.00 indicates no overlap of the ROI volumes, and a value of 1.00 indicates a perfect overlap of the two volumes.

The distance to agreement value is calculated by first determining the shortest distance between each point on one ROI and the closest point on the other ROI. Then the maximum of these distances is chosen for each slice. **Mean Distance to Agreement** is the mean of these values across all slices. **Max Distance to Agreement** is the maximum of these values across all slices.

NOTE

The **Max Distance to Agreement** and **Mean Distance to Agreement** values may be slightly larger than expected because they are computed slice-by-slice. This may be most noticeable when the superior or inferior end of one ROI spans more slices than its corresponding ROI, or similar situations.

- 4 To delete an ROI pair, click the **Delete** check box for the pair and click **Delete Selected**. To delete all of the ROI pairs, click **Select All** and then **Delete Selected**.

Click **Clear All** to remove all of the check marks from the **Delete** check boxes.

Calculate the Target Registration Error

You can assess the quality of the image deformation by calculating the Target Registration Error (TRE). TRE is the average of the distances between pairs of points: one point located on the primary image set and one point located on the deformed secondary image set.

- 1 In the **Registration Validation** section of the **Deformation** panel, click **Place TRE Points**. The **Registration** panel opens.
- 2 From the **Image Set** list in the **Secondary** section of the panel, select the deformed image set.
- 3 On the **Points** tab in the **Automated Registration** section of the panel, click **Add New Fiducial Pair**. The software adds a set of markers to the list.

To display the fiducial markers in the viewing windows, set the 2D and 3D display options as appropriate.



- 4 In a viewing window, use the **Place fiducial markers** tool to place each marker at the appropriate spot on the image set.

Select **Primary** below the viewing windows to move the point on the primary image set, and select **Secondary** to move the point on the secondary image set.

- 5 Repeat steps 3 and 4 for each pair of markers that you want to add.
- 6 To delete a pair of markers, select the pair in the table and click **Delete Current Fiducial Pair**.



- 7 Click **Deformation** at the top of the **Syntegra** window to open the **Deformation** panel.
- 8 In the **Registration Validation** section of the panel, click **Validate**. The **Registration Validation** window opens. The **Target Registration Error** value is shown in the **Validation Information** section of the window.

NOTE

The TRE value is also shown in the **Mean distance between points** field on the **Points** tab in the **Registration** panel.

Modify the registration

If you are not satisfied with the results of the registration, you can make modifications and register the image sets again.

- Rigid registration—return to the **Deformation** panel, make adjustments to the rigid registration settings as necessary, and register the image sets again. Additionally, if you used a bounding box to limit the volume, you can change the dimensions and location of the bounding box before you register the image sets again.

- Deformable registration—return to the **Deformation** panel, verify that the deformed secondary image set that you want to modify is selected in the **Secondary Image** field, and click **Reset Deformation**. The following actions occur:

Image Deformation Being Reset	Actions
CT image set	- The deformed CT image set and the displacement vector field (DVF) that were generated during the deformation are deleted. - The CT image set that was the source for the deformed CT image set becomes Moveable unless the image set has an approved rigid registration, in which case it remains Approved.
CT image set that includes prior dose	The actions listed for the CT image set occur. In addition, the following also occur to remove prior dose: - In the Prescriptions window, the Dose Display Mode is set to Current Dose Only for all trials. - In the Manage Prior Dose window, the Scale Mode is set to Scale Factor for all trials. - In the Manage Prior Dose window for all records in all trials, the setting in the Include column is set to None, the Scale Factor value is set to 1, and the Delivered Fractions value is set to the total fractions of the record.

See *Deformable image registration* for information about registering and deforming image sets.

Approve the rigid registration

When you are satisfied with the results of the rigid registration, you can approve the registration.

- In the **Registration Validation** section of the **Deformation** panel, type your name or initials in the **Approved By** field.
- Click **Approve Registration**. The following actions occur:
 - The secondary image set is labeled “Approved” in the **Setup** panel, and it cannot be moved.
 - You can include the record dose for this secondary image set in prior dose.
 - When you generate your plan report, information about the approved rigid registration is included in the plan report.

Reject the rigid registration

Once you have approved a rigid registration, if you need to remove the approval from the registration or set the secondary image set to **Moveable**, you must reject the rigid registration.

NOTE

When you reject a rigid registration, no changes are made to the rigid registration itself. The primary and secondary image sets remain registered as they were prior to your approval.

- In the **Rigid Registration** section of the **Deformation** panel, verify that the secondary image set for which you want to reject the registration is selected in the **Secondary Image** field.

- 2 In the **Registration Validation** section of the **Deformation** panel, click **Reject Registration**. The following actions occur:

Image Registration Being Rejected	Actions
CT image set	• The approval is removed from the rigid registration. • The selected secondary CT image set becomes Moveable unless the image set has an approved deformed registration, in which case it remains Not Moveable.
CT image set that includes prior dose	The actions listed for the CT image set occur. In addition, the following also occur to remove prior dose: • In the Prescriptions window, the Dose Display Mode is set to Current Dose Only for all trials. • In the Manage Prior Dose window, the Scale Mode is set to Scale Factor for all trials. • In the Manage Prior Dose window for all records in all trials, the setting in the Include column is set to None, the Scale Factor value is set to 1, and the Delivered Fractions value is set to the total fractions of the record.
PET image set	• The approval is removed from the rigid registration. • The selected secondary PET image set becomes Moveable.

Approve the deformation

When you are satisfied with the results of the deformation, you must approve the deformation in order to deform dose using this deformation.

- 1 In the **Registration Validation** section of the **Deformation** panel, type your name or initials in the **Approved By** field.
- 2 Click **Approve Registration**. The following actions occur:
 - The deformed image set is labeled “Approved” in the **Setup** panel, and it cannot be moved.
 - You can include the record dose for this secondary image set in prior dose.
 - When you generate your plan report, information about the approved deformed secondary image set is included in the plan report.

Reject the deformation

If you need to remove the approval from a deformation, you must reject the deformation.

- 1 In the **Rigid Registration** section of the **Deformation** panel, verify that the deformed secondary image set for which you want to reject the deformation is selected in the **Secondary Image** field.

- 2 In the **Registration Validation** section of the **Deformation** panel, click **Reject Deformation**. The following actions occur:

Image Deformation Being Rejected	Actions
CT image set	• The approval is removed from the deformed CT image set. • The CT image set becomes Not Moveable.
CT image set that includes prior dose	The actions listed for the CT image set occur. In addition, the following also occur to remove prior dose: • In the Prescriptions window, the Dose Display Mode is set to Current Dose Only for all trials. • In the Manage Prior Dose window, the Scale Mode is set to Scale Factor for all trials. • In the Manage Prior Dose window for all records in all trials, the setting in the Include column is set to None, the Scale Factor value is set to 1, and the Delivered Fractions value is set to the total fractions of the record.

5 Auto-Segmentation

Overview

Auto-Segmentation is a tool that automatically produces contours for normal tissues in CT image sets. Unlike model-based segmentation, Auto-Segmentation does not require you to position the anatomical structures on the CT image set. It uses probability-based atlases and a segmentation algorithm to find the regions of interest.

Auto-Segmentation comes pre-loaded with factory atlases, which include the abdomen, head and neck, male pelvis, and thorax atlases. After you select an atlas, Auto-Segmentation automatically segments the CT image set.

NOTE

The Auto-Segmentation features are available only if you are licensed for Auto-Segmentation. Contact Customer Support for licensing information.

Terminology

- *Atlas* is a group of organs or structures that are used by Auto-Segmentation to define the regions of interest.
- *Structures* are the anatomical regions of interest. They are a sub-unit of an atlas.
- *Factory atlas* is a default atlas that is installed with the Auto-Segmentation tool.
- *Custom atlas* is a copy of a factory atlas that you have modified to fit the needs of your clinic.
- *Loading an atlas* refers to adding the segmented ROIs to a plan so that you can view the segmented CT image sets.

Supported images



CAUTION

Your segmentation results may be inaccurate if your image set contains any of the following characteristics:

- **Contrast media**
- **Metal artifacts**
- **A derived image set (MIP, AvgIP, or MinIP)**

You can use Auto-Segmentation on these image sets, but it is your responsibility to verify the results.

Auto-Segmentation supports the following types of image sets:

- CT image sets
- Maximum Intensity Projection (MIP), Average Intensity Projection (AvgIP), and Minimum Intensity Projection (MinIP) CT image sets
- Concatenated image sets

Image sets must meet the following requirements. For more information, see the *Patients and Plans* chapter of the *Launch Pad Instructions for Use*.

- Patient orientation must be head-first supine, except for the **Male Pelvis** atlas. For the **Male Pelvis** atlas, the patient orientation can be head-first supine or head-first prone.
- The label for the patient scan orientation (for example, head-first supine, or feet-first supine) should match the patient orientation at acquisition. Using a patient orientation that is not supported can cause Auto-Segmentation to fail.

Set up Auto-Segmentation Preferences

In the **Preferences** window you can select a factory atlas or customize an atlas based on the needs of your clinic. You can perform the following tasks:

- Determine if you want to use a specific atlas in your clinic by setting it to active or inactive. An inactive atlas does not appear in the list of atlases when you use the Auto-Segmentation tool.
- Create a custom atlas. You can copy an atlas and activate the structures that you want to segment. You can change the structure names and colors. In addition, you can delete structures from a custom atlas.
- Reorder the appearance of the atlases in the list. You may want to move the most frequently used atlases to the top of the list.

NOTE

Because preferences are specific to a software version, the default settings are used unless you change the Planning and AcQSim³ Preferences for this software version. The **Auto-Seg** panel in the **Preferences** window is password-protected to prevent accidental changes. For more information, see the *System Administration* chapter of the *Launch Pad Instructions for Use*.

Open the Auto-Seg panel in the Preferences window

- 1 Click the **Configure** button in the **Launch Pad** window or click the **Utilities** menu in the **Planning**, **AcQSim**, or **Image Fusion** windows.
- 2 Select **Preferences** from the list.
- 3 Select **Auto-Segmentation** from the **Category** list on the left side of the **Preferences** window.
- 4 Enter the password. The default password is Atlas. You can change the password after entering the correct password by clicking the **Change Auto-Seg Password** button and following the prompts. If you have any difficulties with your password, please contact Customer Support or your local distributor.

If you have a separate login name, you will create your own preferences. If all users log in using the same name, one set of preferences is used for all system users.

Set the atlas to active or inactive

Auto-Segmentation requires that you specify at least one active atlas and structure. To activate an atlas in the **Preferences** window, select the check box after an atlas's name. To make a structure active or inactive, see *Customize the atlas*.

Customize the atlas

You can modify the list of structures that are displayed and segmented by activating or deactivating them. Factory atlases can be active or inactive, but you cannot make specific factory structures active or inactive. Since you cannot change a factory atlas, you will make a copy and then change the structures of the copied atlas. Then you can activate your custom atlas.

- 1 To copy or view the names and colors for an atlas's structures, select the radio button in front of an atlas's name.
- 2 Click the **Copy** button. The copied atlas appears at the end of the atlas list. The structures that are included in the copied atlas are listed in the right side column.
- 3 Select the check boxes in the **Active** column for the structures that you want to segment.
- 4 To rename an atlas or structure, click on the **Name** field and type a new name. If you do not change the name, the copied atlas name and the original structure names will be displayed. You cannot change the name of an original factory atlas or structure.
- 5 To change the color of a structure, click on the **Color** field for a structure and select a different color.
- 6 To delete an atlas from **Preferences**, select the radio button next to the atlas name in the **Select** column and click the **Delete** button. You cannot delete an original atlas and its structures.
- 7 Click the **Save Planning Preferences** button or the **Save AcQSim Preferences** button to save the modifications, or click the **Close** button to exit without saving.

Reorder the list of atlases

You can set the order of the atlases that display.

- 1 Select the radio button in front of the atlas that you would like to move. You can only reorder atlases, not structures.
- 2 Click the up and down buttons next to the **Copy** button to position this atlas in the list.
- 3 Click the **Save Planning Preferences** button or the **Save AcQSim Preferences** button.

Use Auto-Segmentation

Before using Auto-Segmentation for the first time, you can set up your preferences to determine which atlases and structures will be available for your clinic's use. If you do not set up your preferences, you can still use the default factory atlases. See *Set up Auto-Segmentation Preferences*.

You can use Auto-Segmentation after creating a plan or from Launch Pad. After creating a plan and starting either Planning or AcQSim³, perform the following steps:

- If you want to segment a new atlas, click the **Auto-Seg** button and continue to *Start Auto-Segmentation for a plan*.
- If segmented atlases are available, and you want to use one of the completed atlases, click the **Auto-Seg** button and continue to *Load completed Auto-Segmentation atlases into a plan*.
- If Auto-Segmentation is already started, the **Auto-Segmentation Status** window is displayed and you must wait until it is finished. You can safely exit Pinnacle³ during segmentation. The segmentation continues to run even though you have ended your Pinnacle³ session. See *Check Auto-Segmentation Status*.

Atlases can be backed up and restored along with other Pinnacle³ data. For more information, see the *Backup and Restore* chapter in the *Launch Pad Instructions for Use*.

To delete an atlas from a plan, see *Delete ROIs and ROI contours*.

Start Auto-Segmentation for a plan

- 1 In the **Auto-Segmentation** window, select an atlas.
- 2 Click the **Start** button. The **Auto-Segmentation Status** window opens.
- 3 After the segmentation is finished, click the **Close** button to close the **Auto-Segmentation Status** window. The **Load Atlas ROI** window opens.
- 4 In the **Load Atlas ROI** window, select one or more atlases that segmented successfully.

A status message notifies you whether the segmentation was successful. If the segmentation was not successful, see *Analyze a failed segmentation*.

If there are multiple structures in the atlases, click the **Details** button to verify the segmentation status of each structure.

- 5 Click the **Load** button. The software prompts you to verify the position and accuracy of the generated list of ROIs, as well as the ROI names and colors.



CAUTION

Before loading an atlas into a plan, check the status of the structures. Failed structures will not be loaded into the plan.

Load completed Auto-Segmentation atlases into a plan

- 1 In the **Auto-Segmentation** window, click the **Load Completed Atlases** button.

- 2 Select an atlas that segmented successfully. If the automatic segmentation was unsuccessful because of memory constraints, you can try to segment the atlas again when your system has fewer processes running.
- 3 Click the **Load** button. The software prompts you to verify the position and accuracy of the generated list of ROIs, as well as the ROI names and colors.
- 4 Make any necessary adjustments to the ROIs.

**CAUTION**

After the atlases are loaded, verify all structures for position and accuracy before continuing the planning process in Pinnacle³.

Use Auto-Segmentation with Launch Pad

You can launch Auto-Segmentation before creating a plan.

- 1 In the **Patient Select** window in Launch Pad, add or select a patient.
- 2 Click the **Images** button to select the image set. A previously Auto-Segmented image set has the value **Yes** in the **Auto-Seg** column. The column's value is either **Yes** or empty. For more information about selecting images, see the *Patients and Plans* chapter in the *Launch Pad Instructions for Use*.
- 3 Click the **Auto-Seg** button. The **Auto-Segmentation** window opens.
- 4 Select an atlas.
- 5 Click the **Start** button. The **Auto-Segmentation Status** window opens. You can click the **Close** button to close the window.
- 6 Once the segmentation is finished, the **Auto-Segmentation Status** window reopens.
- 7 Check the segmentation status.

NOTE

You can return to the **Auto-Segmentation Status** window at any time by clicking an **Auto-Seg** button on a window. For more information, see *Check Auto-Segmentation Status*.

Troubleshooting

If you want to use Auto-Segmentation, you must have at least one active atlas. See *Set up Auto-Segmentation Preferences*. If all of the factory and custom atlases are set to inactive, then the **Auto-Seg** button in the **Image Select** window will be grayed out.

If the automatic segmentation was unsuccessful because of memory constraints, you can try to segment the atlas again when your system has fewer processes running.

Sometimes the atlas cannot be successfully segmented because of factors in the image (for example, dental artifacts) or unusual patient anatomy (for example, a missing lung). In these cases, it is unlikely that trying to segment the atlas again will yield different results. For more information, see *Supported images*.

Check Auto-Segmentation Status

The **Auto-Segmentation Status** window allows you to check on the progress or cancel the segmentation.

If the segmentation is running and you want to perform other tasks, you can click the **Close** button to hide the **Auto-Segmentation Status** window. This will not affect the segmentation. You can return to the **Auto-Segmentation Status** screen at any time by clicking an **Auto-Seg** button on a window.

You can use Auto-Segmentation on different image sets at the same time. The number of image sets on which you use Auto-Segmentation at the same time is limited by the number of processors on the platform. For example, if you have four processors, you can start two instances of Auto-Segmentation from Launch Pad on two image sets at the same time.

Analyze a failed segmentation

If the segmentation fails, the reason for the failure displays in the **Auto-Segmentation Status** window. Otherwise you can view the status for all of the atlases by clicking the **Details** button in the **Load Atlas ROI** window. The **Auto-Segmentation Details** window lists all the atlases and indicates whether their structures were successfully or unsuccessfully segmented.

6 Model-Based Segmentation

Overview

NOTE

The organ model library is available in the **Planning**, **AcQSim**, and **Syntegra** windows only if you are licensed for Model-Based Segmentation (MBS).

The organ model library provides pre-defined ROIs for common structures. You can load single organ models into a plan, or you can load a group of organ models at the same time. Standard organ models in the organ model library are designed to adapt to CT data.

While traditional ROIs are built on contours, organ models are ROIs built on 3D polygonal surface meshes, or *meshes*. A mesh is defined by a collection of vertices. You can edit the vertices in a mesh manually and then automatically adapt the mesh to the patient image set. After adaptation, you can convert the mesh to the contours used in traditional ROIs.

NOTE

Standard ROI tools are unavailable until you convert a mesh to contours.

You can propagate meshes to secondary image sets. This allows you to adapt a mesh using data from another image set.

You can add new organ models to the library or add new samples to existing organ models. You can also create new organ model groups to match your clinical practices.

Use the organ model library

Load an organ model or group

To load an organ model or group, first display the **Regions of Interest** panel to the left of the viewing windows by clicking the **Contours** button at the top of the window.

Set up the display

While you can load organ models or groups in any view, we recommend the following four-window view.



1 From the **View** menu, select the view shown at the left.



2 Click the **Zoom correlated pointer 2D** tool.



3 Click and drag on a 2D window to define the area into which to load an organ model or group. When you release the mouse, the **Correlated pointer** tool is automatically selected.

4 Click in a 2D window to define the center of the first organ model or group you want to load.

Load the organ model or group

The software loads the organ models at the intersection of the transverse, coronal, and sagittal views, which you can define using the **Correlated pointer** tool as described above. If there is no intersection, the software loads the organ models at the center of the selected window (2D windows) or at the center of the image set (3D windows).

When you load a group, the spatial relationships among the organ models in the group are not maintained; rather, the organ models are all loaded at the same center point. Manually position the organ models after you load the group.

- 1 Click the **Load Organ** button. The **Load Organ Model** window opens.
- 2 Select an organ model or group.

The software adds a new mesh for each organ model. The meshes are listed in the **Regions Of Interest** list and appear in the viewing windows in the same orientation as the image set. All organ models are centered where you defined in *Set up the display*.



The **Load Organ Model** window closes after you select an organ model or group. If you want the **Load Organ Model** window to remain open after you make a selection, click the **Pin window** button.

Manually position a mesh

A mesh must be positioned near the organ so that the software can adapt it to fit the organ. You can edit a mesh in order to position it closely to the organ. Select the mesh you want to manually position, then select the appropriate 2D editing tool.

NOTE
Editing a mesh does not change the organ model in the library; editing only affects the ROI in the current plan. To modify an organ model, see *Customize the organ model library*.

Please remember these points when manually positioning a mesh:

- You can toggle among the editing tools using the middle mouse button. You must set the **Middle mouse window/level** preference to **No** in order to use this feature. See *Preferences* in the *Utilities* chapter.
- You can undo the most recent edit by clicking the **Undo mesh edit** button.
- The mesh editing tools affect only the currently selected mesh. You have the option of clicking a mesh to select it for editing. To do so, set the **Allow mesh tools to set current mesh** preference to **Yes**. See *Preferences* in the *Utilities* chapter.

If you must make extreme changes to the mesh, we recommend you set the **Replace mean mesh before adaptation** setting to **Yes** in the **Organ Model Settings** window. See *Create an organ model*.

Tool	Name	Function
	Move mesh	Move the selected mesh to a new location. Select the mesh that you want to move, then drag it to the new location.

Tool	Name	Function
	Scale mesh	Scale the selected mesh. Select the mesh that you want to scale, then drag left and right to scale it horizontally or drag up and down to scale it vertically.
	Rotate mesh	Rotate the selected mesh. Select the mesh that you want to rotate, then drag clockwise or counterclockwise to rotate the mesh around its center.
	Undo mesh edit	Undo the last action that you performed on the mesh. Click the Undo mesh edit button again to redo the action.
	Pull mesh	Pull the surface of the mesh. Set the radius of the tool, then drag the cursor to pull the mesh. As you drag the cursor, vertices farther away from the original cursor location move in the direction you drag, but with a distance weighted by a Gaussian function and the radius of the tool. A dashed-line circle indicates the range of vertices affected as you drag the cursor. The Mesh Modeling Options section on the Edit Options tab of the Regions of Interest panel contains a Lock edited vertices option. To prevent edited vertices from moving during adaptation, set the Lock edited vertices option to Yes before using this tool. Setting the Lock edited vertices option to Yes can be useful if the mesh is shifting toward neighboring organs during adaptation. Please note that the lock is not absolute; the edited vertices may still move slightly during adaptation. Locked edited vertices display in a different color from other vertices. Click the Reset button to unlock all vertices in the mesh.

Adapt a mesh

After you have edited the mesh so that it is positioned near the organ, you can automatically adapt it to match the image set to which the ROI is assigned.

NOTE

You can adapt a mesh to one image set while viewing another image set. See *Propagate a mesh to secondary image sets* for information on using organ models in plans with multiple image sets.

- 1 Click the **Edit Options** tab, and select the mesh you want to adapt.
- 2 Do you want to set custom adaptation settings or use default settings?
 - Custom adaptation settings—go to step 3.
 - Default settings—go to step 4.
- 3 Click the **Organ Model Settings** button. Adjust the adaptation settings in the **Organ Model Settings** window as needed. See *Create an organ model*.
- 4 If you want the adapted mesh to attempt to avoid a certain ROI, select the ROI in the **Avoid ROI** option list.
- 5 Do you want contours to be automatically updated as the mesh changes?
 - Yes—set the **Auto-update contours** option to **Yes**.
 - No—set the **Auto-update contours** option to **No**.

NOTE

If you set this option to **No**, you can still update the contours manually by clicking the **Update** button next to this option.

If you convert a mesh to contours, edit the contours, change back to mesh display, and then edit the mesh, the edits you made to the contours are lost if the **Auto-update contours** option is set to **Yes**.

- 6 Click the **Adapt Mesh** button. The progress meter displays the percentage of the adaptation completed. Click the **Stop** button to stop the adaptation at any time.

After adaptation is complete, you can edit the mesh if needed and adapt it again.

NOTE

You can undo the adaptation by clicking the **Undo mesh edit** button.

Convert a mesh to contours

NOTE

You must convert a mesh to contours before performing many common ROI-related tasks, such as computing ROI statistics, generating dose volume histograms (DVHs), or setting IMRT objectives and constraints.

You have several options for converting a mesh to contours:

- Automatically convert a mesh to contours after each edit—set the **Auto-update contours** option to **Yes**.
- Convert a mesh to contours—click the **Update** button (next to the **Auto-update contours** option).
- Convert all meshes to contours—click the **Convert All Mesh to Contours** button.

After conversion, review the contours and edit them as needed. See *Edit ROI contours* in the *Regions of Interest* chapter.

NOTE

The most superior and/or inferior contours commonly require editing.

You can correct small contouring anomalies by selecting **Options - Clean ROI**. See *Clean ROIs* in the *Regions of Interest* chapter.

Propagate a mesh to secondary image sets

When a plan has multiple image sets, you can propagate a mesh from the primary image set to the secondary image sets, as long as the source and target image sets are not the same. Once the mesh has been propagated, you can manually position and adapt the meshes on the secondary image sets.

NOTE

Before you propagate ROIs to secondary image sets, the image sets must be registered.

If the image sets are not automatically registered (such as phased respiratory image sets), use Syntegra or Image Fusion to register the image sets. See the *Image Fusion* chapter.

- 1 In the **Regions of Interest** panel, load, manually position, and adapt organ models in the primary image set. See *Load an organ model or group*, *Manually position a mesh*, and *Adapt a mesh*.

**NOTE**

While you can load organ models or groups in any view, we recommend the four-window view shown at left.

- 2 Select **Options - Propagate ROIs**. The **Propagate ROIs** window opens.
- 3 Select the **Propagate Mesh ROIs** tab.
- 4 Select the check boxes for the meshes you want to propagate.
- 5 To automatically adapt the meshes after propagation, select the **Adapt after Propagation** check boxes for the meshes to be propagated.
- 6 Select the secondary image sets to which you want to propagate the meshes in the **Select target data sets** list.
- 7 Click the **Propagate** button.

Use the options below the viewing windows to display the different image sets, then change the colors of the ROIs so that they are easier to distinguish from one another.

To review, manually position, and adapt propagated meshes, first select the image set to which you propagated the organ. At the bottom of the window, select the **Secondary** option, then select the image set to which you propagated the organ from the **Secondary** option list.

After you manually position and adapt the meshes on the secondary image sets, you can use ROI expansion/contraction tools to combine the different ROIs for a particular structure into one composite ROI in the primary image set. You can use two different methods:

- Use ROI expansion/contraction tools to combine the ROIs from the different image sets into a single ROI in the primary image set. This method is slower, and results in only one additional ROI (the new composite ROI) in the primary image set. See *Expand and contract ROIs* in the *Regions of Interest* chapter.
- Propagate the ROIs from secondary image sets back to the primary image set, then use ROI expansion/contraction tools to combine the ROIs into a single ROI. This method is faster, and results in multiple additional ROIs (the new composite ROI and the propagated ROIs) in the primary image set.

Customize the organ model library

You can create custom organ models, add samples to existing organ models, and add or delete organ models and groups.

The organ model library is password-protected to prevent accidental overwriting of mesh data. The default password is p3mbs.

NOTE

After you enter the default password, you can set a custom password by clicking the **Change Password** button in the **Organ Model Library** window.

Create an organ model

You can create custom organ models to use as organs or as dose-shaping ROIs.

NOTE

Organ models are saved in head-first supine orientation. When you load an organ, the software orients it correctly to match the patient image set, allowing you to use a single organ model for multiple treatment orientations.

- 1 How do you want to create the new organ model?
 - From a new ROI—create an ROI and draw contours as needed. Go to step 2.
 - From an existing ROI—modify the ROI contours as needed and go to step 2.
 - From an existing organ model—load the organ model and go to step 5.
 - 2 Select **Options - Convert Contours to Mesh**. The **Mesh Generation** window appears.
- The window displays the current ROI volume and suggested number of vertices for the mesh.

NOTE

You can continue to edit the ROI with the **Mesh Generation** window open. When you are finished editing, click the **Recompute** button to update the ROI volume and suggested number of vertices.

- 3 Enter the number of vertices for the mesh in the **Requested # of vertices** field, or accept the value that the software suggests. The minimum number of vertices is 200.

NOTE

Setting an extremely large number of vertices increases the adaptation time for an organ model and may not produce better results. The practical limit for the largest organ models is around 3,000 vertices.

- 4 Click the **Generate New Mesh** button. A status window appears while the software generates the mesh.
- 5 Name the ROI with the name you want to appear in the organ model library.
- 6 Set the following default settings for the new mesh:
 - Color
 - 2D and 3D display modes (must be mesh display modes)

- Line width
 - 3D editing tool radius
- 7 Adjust the mesh (if necessary) using the mesh editing tools. See *Manually position a mesh*.
 - 8 Click the **Organ Model Settings** button on the **Edit Options** tab. The **Organ Model Settings** window appears. Adjust the settings as needed.

Setting	Description
Replace mean mesh before adaptation?	Replaces the mean mesh with the displayed mesh before adaptation. Set this option to Yes only when the edited mesh differs significantly from the original mesh.
Clean ROI after adaptation?	Removes small contour anomalies after adaptation. Set the Minimum contour area to a value appropriate for the size of the mesh. You must set the Auto-update contours option to Yes for ROI cleaning to occur.
Smooth mesh after adaptation?	Smooths the mesh by moving vertices based on the averages of surrounding vertices. You can also manually smooth the mesh by clicking the Smooth Mesh button on the Edit Options tab of the Regions of Interest panel.
Organ Flexibility	Sets the amount of shape variation allowed during adaptation. Use higher values for organs with significant variation (for example, the rectum) and lower values for organs with less variation (for example, the femur).
Proximity Weight	As the software searches for the features that define the organ, this field sets the importance of features detected at greater distances from the mesh. Enter a higher setting to prevent the mesh from attracting to features that are farther away from the mesh.
Min CT Value	Sets the minimum CT value the software uses when searching for features during adaptation.
Max CT Value	Sets the maximum CT value the software uses when searching for features during adaptation.
Gradient Direction	Sets how the software determines which gradients are strong or weak when it searches for features during adaptation. Strong features are those that define the organ. Select one of the following: • Positive—Software treats a positive gradient as a strong feature and a negative gradient as a weak feature. Choose this option for a structure that has a lower CT value than the surrounding tissue, such as the brain. • Negative—Software treats a negative gradient as a strong feature and a positive gradient as a weak feature. Choose this option for a structure that has a higher CT value than the surrounding tissue, such as the bladder. • Unsigned—Software treats gradients with larger magnitudes as strong features and gradients with smaller magnitudes as weak features.
Gradient Clipping	Sets whether the software uses hard or soft clipping in relation to the Max Gradient CT#/mm and Gradient Direction when searching for features during adaptation. Hard clipping finds fewer features; soft clipping finds more features.
Max Gradient CT#/mm	Sets the maximum gradient value the software uses when searching for features during adaptation.
Avoid CT Values	Sets a threshold value and instructs the software to avoid CT values either greater than or less than that value when searching for features during adaptation.

Setting	Description
Limit Feature Search	Limits the search for features along a triangle normal. When the software finds no features after a specific number of consecutive steps (based on the feature searching settings Min CT Value, Max CT Value, and Gradient Direction), the software ignores potential features farther out along the triangle normal. Select None if you do not want to limit the search for features along a triangle (from 10 mm inside the mesh to 10 mm outside, with steps every 1 mm). Select Half to stop the search for features when 11 consecutive steps find no features, or Full to stop the search when 3 consecutive steps find no features. The standard setting is None; select Half or Full when the mesh is attracting to features that may be false features because they are located in areas where the CT value is outside the range defined by the Min CT Value and Max CT Value.
Settings acceptable for adaptations?	Sets whether the organ model can be adapted. Select No when creating a mesh to be used as a dose-shaping ROI. This prevents you from unintentionally adapting this mesh to the patient data. For example, you might use this setting for a nodal neck volume.

- 9 Select **Options - Organ Model Library**. When the software prompts you, enter the password. The default password is p3mbs. The **Organ Model Library** window appears.

NOTE

After you enter the default password, you can set a custom password by clicking the **Change Password** button in the **Organ Model Library** window.

- 10 Select the group to which you want to add the new organ model.

NOTE

You can create a custom group at a later time and move the mesh to this group. See *Create a group*.

- 11 Click the **Save ROI <Organ_Name> as New Model** button.
- 12 When the software prompts you, enter your name and click the **Done** button.

The new mesh is labeled with your name and the current date and time, and is saved in the group you selected. The **Samples** field is set to one sample. The **Samples** field will update as you add more samples to the mesh.

Add a sample to an organ model

You can generate a sample to add to an existing organ model from two sources: from image data or from existing contours.

The software adds samples to an organ model in a weighted fashion; as you add more samples, each sample has progressively less influence on the organ model. We have found that after the first five to ten samples, adding samples does not improve substantially the effectiveness of the organ model.

NOTE

The mesh must have the same number of vertices as the organ model to which you wish to add the sample. Begin by loading the organ model to which you want to add a sample in order to ensure the sample you create has the same number of vertices.

Add a sample generated from image data

Generate a sample by loading an organ model, editing it, and adapting it to the patient image set.

- 1 Load into a plan the organ model to which you want to add a sample. See *Load an organ model or group*.
- 2 Manually position and adapt the mesh. See *Manually position a mesh* and *Adapt a mesh*.
- 3 Select **Options - Organ Model Library**. When the software prompts you, enter the password. The **Organ Model Library** window appears.
- 4 Select the organ model to which you will add a sample.
- 5 Click the **Add ROI <Organ_Name> as New Sample** button. The software averages the current mesh into the mean mesh for the organ model in the organ model library.

NOTE

You can display the mean mesh at any time by setting the **Show Mean** option in the **Organ Model Settings** window to **Yes**.

Add a sample generated from contours

Generate a sample from contours you have already created by loading an organ model and automatically modifying the mesh to match the contours.

- 1 Load into a plan the organ model to which you want to add a sample. See *Load an organ model or group*.
- 2 Set the **2D Display** mode to **Contour**.
- 3 Delete, create, and edit contours as necessary to create the desired shape.
- 4 If necessary, check the relative positions of the contours and the mesh. A mesh must be positioned near the contours so that the software can adapt it to fit the contours.
 - a Set the **2D Display** mode to **Mesh**.
 - b Click the **Organ Model Settings** button on the **Edit Options** tab. In the **Organ Model Settings** window, set the **Show Colorwash** option to **Yes**.
 - c Compare the relative positions of the contours and the mesh and adjust the position of the mesh if necessary.
- 5 Select **Options - Fit Mesh to Contours**.

The software modifies the existing mesh to fit the new contours while keeping the number of vertices constant. The display switches to a mesh display when the process is complete.

You can compare the mesh to the contours by setting the **Show Contours** and/or **Show Colorwash** options in the **Organ Model Settings** window to **Yes**. If the new contours differ significantly in size and shape from the original mesh, you may need to select **Options - Fit Mesh to Contours** several times to achieve the desired result.

- 6 Select **Options - Organ Model Library**. When the software prompts you, enter the password. The **Organ Model Library** window appears.
- 7 Select the organ model to which you will add a sample.

- Click the **Add ROI <Organ_Name> as New Sample** button. The software averages the current mesh into the mean organ model in the organ model library.

Manage the organ model library

Select **Options - Organ Model Library**. When the software prompts you, enter the password. The **Organ Model Library** window appears.

Once the organ model library is open, you can perform several different tasks as described below.

Change the password

The default password is p3mbs. Click the **Change Password** button, and when the software prompts, enter the old password, then enter the new password, then re-enter the new password to confirm it.

Import an organ model

You can load an organ model into a plan from a file. Once the organ model is loaded, you can also save it to the library.

- On the **Organ Models** tab, click the **Import Organ** button. The **Select ROI File** window appears.
- Navigate to and select the appropriate *.template.roi* file for the organ model, then click the **OK** button.

Delete an organ model

On the **Organ Models** tab, select the organ to be deleted and click the **Delete Model <Organ_Name> from Library** button.

Create a group

- On the **Groups** tab, click the **Create New Group** button. A new group appears in the list.
- Select the new group and enter a name in the **Edit Group Name** field.

Rename a group

On the **Groups** tab, select the group and enter a new name in the **Edit Group Name** field.

Delete a group

- On the **Groups** tab, select the group and click the **Delete Group** button.
- When the software prompts you to confirm the deletion, click **Yes**.

Move an organ model to a different group

- On the **Groups** tab, select the organ model to be moved from the **Model to Move** option list.
- Select the group to which you want to move the organ model from the **Destination Group** option list.

Back up and restore organ models

You can back up and restore the organ model library in Launch Pad. See the *Launch Pad Instructions for Use*.

Restore original organ models and groups

In addition to restoring organ models that you have backed up, you can also restore the original, unmodified organ models and groups. As you restore the original organ models and groups, you can choose whether to overwrite modified organ models and groups with the original versions.

NOTE

If you choose to overwrite modified organs and groups with the original versions, all changes you have made to the organs and groups are lost.

Click the **Restore Factory Settings** button, and when the software prompts, choose whether to overwrite specific organ models and groups.

7 Regions of Interest

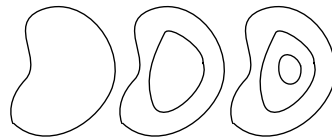
Overview

A region of interest (ROI) is a contour or set of contours that defines the limits of an area which is important in treatment planning, such as the target volume or a radiation-sensitive structure. When using CT images for planning, only the structures for which you want to generate volumetric or statistical information need to be defined as ROIs. In contour-based planning, all structures to be defined by contours should be entered as ROIs and assigned densities.

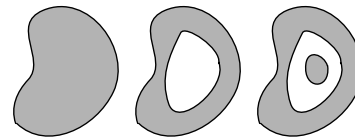
Any number of contours can be used to define an ROI, and any number can be drawn on a single image slice. You can draw contours on transverse, sagittal, or coronal 2D images, but all contours for a single ROI should be drawn on slices with the same orientation.

The volume units (voxels) inside the ROI contours may or may not be included in the ROI volume, depending on how you define the contours. If a contour is entered within another contour, the area bounded by the two contours is included in the ROI. The gray areas in the illustration below indicate portions of the ROI that are included in the ROI volume.

These ROI contours...



translate to these ROI volumes.



NOTE

You can quickly define ROIs by loading organ models, adapting them to the image set, and then converting them to contours. The organ model library is available in the **Planning**, **AcQSim**, and **Syntegra** windows only if you are licensed for Model-Based Segmentation (MBS). See *Model-Based Segmentation*.

You can also quickly define ROIs by using the Auto-Segmentation tool, which automatically produces contours for normal tissues in CT image sets. The Auto-Segmentation tool is available in the **Image Select**, **Planning**, and **AcQSim** windows only if you are licensed for Auto-Segmentation. See *Auto-Segmentation*.



CAUTION

Be careful when creating ROIs that approach the surface of the patient. Incorrect positioning of ROIs, particularly when assigning densities or using bolus, can affect the accuracy of the plan. For example, if a lung contour touches the surface of a patient and the air/tissue threshold is higher than the lung density, the lung will be filled with air. Review the placement of all ROIs, whether manually or automatically generated.



Click the **Contours** button at the top of the window to display the **Regions of Interest** panel.

Sort ROIs

You can manually order the list of ROIs.

- 1 Select **Options - Sort**.

The **Sort** window appears.

- 2 Click the **ROI** tab.
- 3 Select an item and use the arrows to move it:

Control	Description
	Move item to the top
	Move item up
	Move item down
	Move item to the bottom

Display ROIs on all image sets

To toggle the **Display ROIs on all data sets** option, select **Options - Display ROIs on all data sets**. You can also toggle the default setting for this option in the **Preferences** window.

When the **Display ROIs on all data sets** option is turned on, ROIs that you draw appear on every image set in the plan. When the **Display ROIs on all data sets** option is turned off, ROIs that you draw appear only on the image set in which the ROI was drawn.

NOTE

If the 2D display mode for the ROI is **Contour** and the **Display ROIs on all data sets** option is turned on, the ROI only appears on other image sets if the slices in the image sets align exactly with the slices in the image set on which the ROI was drawn.

Draw contours

Follow the steps below to begin drawing contours. Then you can manually contour structures using the **Create contour paintbrush** tool, **Create contour freehand** tool, and **Create contour point by point** tool.

Begin to draw contours

- 1 Click the **Add ROI** button. A new ROI is added to the ROI list with a default name.
Select the ROI to which you want to add contours.
- 2 In a 2D viewing window, display the image you want to use for contouring. You may want to zoom in on the structure to facilitate drawing.
- 3 If you want to rename the ROI, delete the automatically generated name (e.g., ROI_1) and type a new one in the **ROI Name** field.
- 4 If you have multiple image sets, select the image set to associate with the ROI.
- 5 In the **ROI Type** option list, select the type to associate with the ROI.
- 6 Draw the contours as needed. The following sections explain how to use the drawing tools. The number of contours you define appears as you complete the contours.

You can use the **n** and **p** keys (next and previous slice) to scroll through the slices of the image set. You can also press the down arrow key to move to the next image or the up arrow key to move to the previous image. You can toggle the direction that the arrow keys scroll through the image set in the **Preferences** window.

- 7 To update the volume display and the volume for the selected ROI, click the **Recompute** button.



CAUTION

Review all contours to verify that they are correct for your plan.

The gray area around the perimeter of the viewing window represents the edge of the density grid; do not draw ROIs outside this grid. The software does not compute areas of ROIs that are outside the density grid.

You can edit ROIs using the procedures described in the *Edit ROI contours* section.

Use the Create contour paintbrush tool



Use the **Create contour paintbrush** tool to “paint” an ROI on a slice. The tool provides contour drawing, editing, and deleting functions, depending on where you use it.

- 1 Follow the steps in *Begin to draw contours*.
- 2 Enter the diameter (mm) of the brush that you use to “paint” the ROI in the field below the **Create contour paintbrush** tool.
- 3 On the **Edit Options** tab of the **Regions of Interest** panel, set the **Auto-close painted contours** option. If you want painted contours to be closed and filled automatically, leave this option set to **Yes**. In some situations, such as the contouring of organ walls, you may want to set this option to **No**.

- 4 Select the **Create contour paintbrush** tool, then position the cursor at the point on the slice where you want to start, edit, or delete the contour.

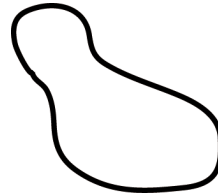
The tool works differently depending on where you click.

- If you click on an image where there is no contour, a new, circular contour appears. Drag to create a thick line; wherever you move the cursor, the circle is filled in for the ROI.
 - By clicking inside the edge of an existing contour, you can push out the edges of the contour.
 - If you click outside, but near, an existing contour, the tool functions as an eraser, and the contour is erased wherever you move the tool. You can use this method to push in the edges of a contour.
- 5 Go to the next slice, draw a contour for the ROI, and repeat the previous steps.

Draw continuous line contours



Use the **Create contour freehand** tool to define contours by drawing a continuous line like the one shown below.

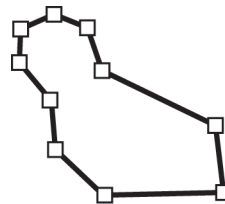


- 1 Follow the steps in *Begin to draw contours*.
- 2 Select the **Create contour freehand** tool, then drag around the limits of the region until you have closed the contour.
- 3 Go to the next slice and repeat the previous steps to draw a contour for the ROI.

Draw point-by-point contours



Use the **Create contour point by point** tool to define contours by “dropping” a series of points, as shown below.



- 1 Follow the steps in *Begin to draw contours*.
- 2 Select the **Create contour point by point** tool and click where you want to start the contour. A small box appears and indicates the point you defined.
- 3 Click where you want to add the next point to the contour. You can also drag the point to the position you want. A line is drawn between the two points. Define the remaining points in the same manner.

- 4 To close the contour, click on the first point you defined. The square point markers disappear.

Change the ROI display

The options on the **Display Options** tab of the **Regions of Interest** panel let you select different display options for the selected ROI, including color, 2D display method, 3D display method, box size, and line width.

For information on ROI precision, see the *Pinnacle³ Planning Reference Guide*.

Color

The ROI display color is automatically selected when the ROI is added. The ROI is displayed in the same color in both 2D and 3D images. To change the display color, select the ROI and make a selection from the **Color** list.

2D display

To select a different 2D display method for an ROI, select the ROI and make a selection from the **2D Display** list. You have the following options:

- **Contour**—The ROI is shown as a line contour. This is the default 2D display setting. The contours are only visible in the orientation used to draw contours.
- **Colorwash**—The ROI is shown only as a colorwash. Although the ROI is visible in all three orientations, you cannot manually draw contours in this display mode.
- **Both**—The ROI is shown as both a polygonal wire surface and colorwash, and it is visible in all three orientations. The polygonal wire surface will appear in oblique views.
- **Poly**—A polygonal wire surface is generated for the ROI, and a contour is drawn on the 2D slices where the polygonal wire surface intersects the slice. Use this display to see a contour for the ROI on other orthogonal slices, or to view an ROI on oblique slices and in multiple data sets. When displaying large ROIs, you may notice a significant decrease in system speed.
- **Mesh**—The ROI is shown as a mesh.

NOTE

Mesh display is available only if you are licensed for Model-Based Segmentation (MBS). See the *Model-Based Segmentation* chapter.

- **Off**—The ROI is not displayed in 2D images. You can contour with the display off, but each contour will “disappear” until you turn on the 2D display for that ROI.

When manually drawing ROI contours, you need to select a drawing mode (**Contour**, **Both**, or **Poly**). To view ROIs on 2D images in all three orientations (transverse, sagittal and coronal), select **Colorwash**, **Both**, or **Poly** as the display mode.

3D display

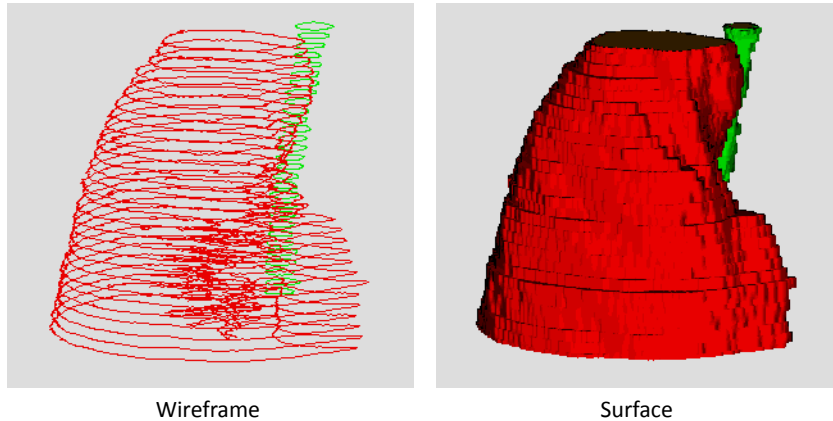
ROIs can be displayed in 3D mode with or without the patient data. The 3D display mode determines how the ROI appears in all 3D windows. For all display modes, a wireframe is used when rotating the volume and when the 3D image is not rendered.

To select a different 3D display method for an ROI, select the ROI and make a selection from the **3D Display** list.

If you select any 3D display mode besides **Wireframe**, you must render the image before the ROI surface will be visible. To do this, right-click the viewing window in which you want to render the ROI and select **3D - Render**.

You have the following 3D display options:

- **Wireframe**—Each contour in the ROI is drawn as a wireframe.



- **Surface**—The ROI appears as a solid surface after rendering. Use this option to generate surface displays of large ROIs.
- **Trans Surf** (Transparent Surface)—The ROI is rendered as a transparent surface. Any ROIs or other objects within or behind the transparent ROI are visible.

NOTE

The default step size for rendering ROIs is 0.1 cm. If you increase this value in the **Data Set Specifications** window (for example, to 1.0), you may “lose” parts of the image, since the software will render a very coarse image in a 3D window. This affects **Surface** and **Trans Surf** displays only.

- **Poly Wire** (Polygonal Wire)—The ROI is rendered with a polygonal wireframe.

NOTE

In order to add annotations to wireframe ROIs, you must click directly on one of the wires.

- **Poly Surf** (Polygonal Surface)—The ROI is rendered using a solid polygonal surface. This option can slow display speed when rendering large ROIs.
- **Trans Poly** (Transparent Polygonal Surface)—The ROI is rendered using a transparent polygonal surface. Any ROI within or behind the transparent ROI is visible.
- **Mesh Wire**—The ROI is rendered with a polygonal wireframe mesh.
- **Mesh Surf**—The ROI is rendered using a solid polygonal surface mesh.
- **Trans Mesh**—The ROI is rendered using a transparent polygonal surface mesh.

NOTE

Mesh display is available only if you are licensed for Model-Based Segmentation (MBS). See the *Model-Based Segmentation* chapter.

NOTE

Because mesh displays render quickly, you may want to choose an automatic rendering option when viewing meshes. For information on rendering options, see *3D menu options* in the *View Patient Data* chapter. For information on meshes, see the *Model-Based Segmentation* chapter.

- **Off**—The ROI is not displayed in 3D images.

Display ROI without patient data

- 1 Select **Utilities - Data Sets**.

The **Data Set Specifications** window appears.

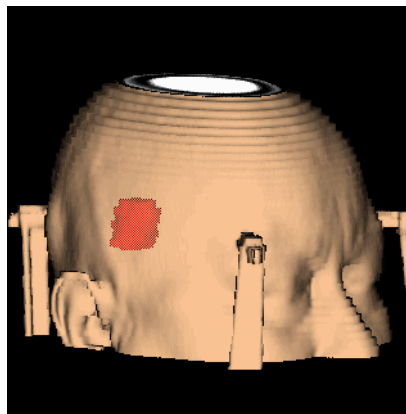
- 2 Select **No** for the **Render** parameter setting.
- 3 Right-click the viewing window in which you want to render the ROI and select **3D - Render**.

NOTE

If the patient data already appears in the viewing window, you must make a change to the display (for example, use the **Rotate** tool to rotate the display) in order for the patient data to disappear.

Display ROI with transparent patient data

When patient volumes are rendered using skin or bone rendering, ROIs are often obscured from view because of the patient data. To see ROIs and patient data together in a 3D image, as shown, you can make the patient surface transparent.



- 1 Create a 3D viewing window or enter 3D mode in an existing viewing window.
- 2 Select the 3D display mode for the ROIs to be displayed with the patient data.
- 3 Right-click the viewing window where you want to display the patient data and select **3D - Transparent Dataset On**.
- 4 Right-click the viewing window again and select **3D - Render**.

Box size and line width

Click the **Box Size** list to change the size of the points on a selected contour. Use the **Small** box size, for example, on continuously drawn curves to edit individual points in the curve more easily.

Click the **Line Width** list to change the line width for a selected ROI.

Display the contour outline in BEVs

To display ROIs in beam's eye view DRRs, in the **Display outline in BEV DRR** field select **Yes**. In each BEV window, the outlines of the contours appear.

Propagate ROIs from a record

If a plan has a record as a result of copying another plan, you can propagate ROIs from the record to the primary image set with or without deformation.

NOTE

You can only propagate from a record if you have the Dynamic Planning option.

- 1 Open the **Propagate ROIs** window using one of the following methods:
 - From the **Regions of Interest** panel or the **Record Viewer** window, select **Options - Propagate ROIs**.
 - From the **Registration Validation** section of the **Deformation** panel in **Syntegra**, click **Propagate ROIs**.

The **Propagate ROIs** window opens.

- 2 Select the **Propagate Dynamic Planning ROIs** tab.
- 3 Select the **ROI Source** to use.
- 4 Select the check boxes for the ROIs that you want to propagate.
- 5 Specify whether to apply deformation when the ROI is propagated from the record.
- 6 Specify whether to replace existing ROIs in the plan with ROIs that are propagated from the record.
 - **Yes**—one of the following will occur:
 - If the name of an ROI that you selected to propagate matches the name of an ROI on the primary image set in the plan, then the ROI in the plan will be replaced with the propagated ROI.
 - If none of the ROI names match, then the propagated ROI will be added as a new ROI in the plan.
 - If the name of an ROI that you selected to propagate matches the name of an ROI in the plan, but that ROI is not on the primary image set, then the propagated ROI will be added as a new ROI on the primary image set in the plan.
 - **No**—the propagated ROI will be added as a new ROI on the primary image set in the plan.
- 7 Click the **Propagate** button.

If you selected **Yes** to replace existing ROIs with propagated ROIs, dose may become invalidated or your dose distribution may change if replacing the existing ROI changes the shape of a block that is based on the ROI or if you use prescriptions that prescribe to an ROI, for example. Review dose, prescriptions, DVHs, scorecard goals, and other elements of the plan that rely on ROIs after you propagate the ROIs.

After you propagate, you can use ROI expansion/contraction tools to combine the different ROIs for a particular structure into one composite ROI in the primary image set.

Delete ROIs and ROI contours

You can remove entire ROIs or particular ROI contours with the following tools and menu options.

Delete ROIs

- 1 Click the **Delete ROI** button.

The **ROI Delete** window opens.

- 2 Select the ROIs that you want to delete:
 - Select an ROI by selecting the check box to the left of the ROI name.
 - Click the **Select Auto-Seg** button to select all ROIs that were created by the Auto-Segmentation tool. For information about Auto-Segmentation, see the *Auto-Segmentation* chapter.
 - Click the **Select Auto-Planning** button to select all ROIs that were created by the Auto-Planning tool. For information about Auto-Planning, see the *P³IMRT Instructions for Use*.

If the ROI cannot be deleted due to a dependency, the name of the ROI appears in the panel on the right side. To view a list of the objects that are associated with the ROI, click the **Examine objects** button.

NOTE

You cannot delete an ROI that has a prescription, beam, dose volume histogram (DVH), or IMRT objective/constraint associated with it.

- 3 Click the **Delete Selected ROIs** button.

Delete a contour from an ROI



- 1 To delete one or more contours from a slice associated with the current ROI, click the **Delete contour** tool. Drag to draw a box over any contours that you want to delete that are associated with the current ROI.
- 2 To remove all contours for an ROI without removing the ROI from the list, select **Options - Delete All Contours**.

The software prompts you for confirmation before removing the contours.

- 3 To remove the last contour or set of contours you added to an image, click the **Undo last contouring** button on the **Edit Options** tab of the **Regions of Interest** panel.

Copy ROI contours

You can copy existing contours from the current slice to adjacent slices or to a range of slices. You can transfer ROI contours from one data set to another. In addition, you can create a copy of an entire ROI. The following sections describe your options.

Copy contours from last slice

You can copy all the contours from a slice you just edited to another slice.

- 1 Click the **Edit Options** tab in the **Regions of Interest** panel.
- 2 To copy all the contours to the
 - previous slice, click the **Previous** button.
 - next slice, click the **Next** button.
 - current slice, click the **Current** button.

Contours are not copied if the slice to which you want to copy contours already contains contours for the ROI.

If you have a transverse 2D viewing window active, the software displays the slice onto which you just copied the contours.

Copy a contour to a range of slices



- 1 Select the **Select contour** tool and click on the contour to be copied.
- 2 Select **Options - Copy Contour to Slices**.

The **Copy Contour** window appears.

- 3 Enter the minimum and maximum coordinates for the slices to which you want to copy the selected contour.
- 4 Click the **OK** button to copy the contour to the specified slices. Click the **Cancel** button if you do not want to copy the contour.



CAUTION

Review the copied contour(s) to verify that it is correct for your plan. Make any necessary changes.

Transfer contours to another data set

You can transfer ROI contours from one data set to another. If you select a different data set for an ROI in the **Data Set** option list of the **Regions of Interest** panel, a window appears. Select whether to replace the ROIs existing contours or create an ROI that contains the transferred contours.

Note that contours cannot be transferred exactly because data sets can have different orientations and resolutions. Instead, new contours are generated by autocontouring the 3D shape enclosed by the original contours. The new contours are always transverse.

Create a copy of an ROI

- 1 At the top of the **Regions of Interest** panel, select the ROI to copy.
- 2 Select **Options - Copy Current ROI**. The new ROI appears in the list with “_COPY” appended to its name.

If the ROI had a mesh associated with it, the mesh is copied too. See the *Model-Based Segmentation* chapter.

Edit ROI contours

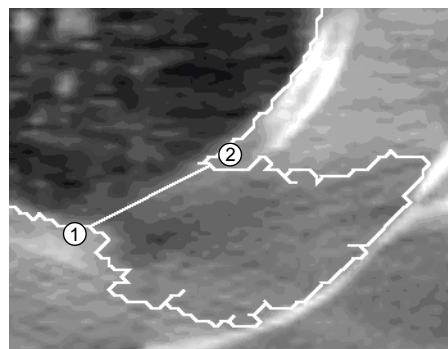
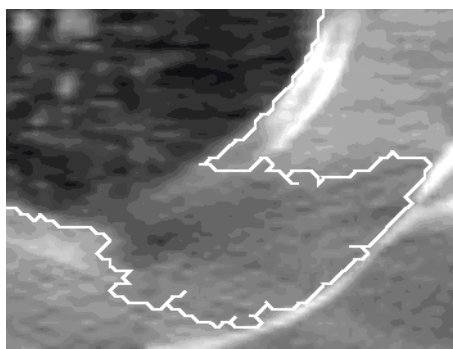
The following sections explain your options for editing ROI contours.

Delete a section of a contour



You can use the **Split contour** tool to divide a single contour into two contours on the current ROI and then delete the unwanted portion of the contour. This tool is most useful for editing contours generated using the autocontouring tools.

In the following example, some soft tissue was included in an automatically generated lung contour. To separate the lung from the soft tissue, select the **Split contour** tool and position the cursor on point 1 of the current ROI. Click and drag the cursor to point 2 to create two separate contours. If a line does not appear between the two contours, try again. The starting and ending points for defining the separation line must be outside (not on) the contour you are attempting to separate.



After separating the contours, you can delete the unwanted contour using the **Delete contour** tool.

Edit ROI contours using the editing tools

- 1 Click on the contour to select it. When the contour is selected, all of the points in the contour are displayed with square point markers.

NOTE

When editing a contour, zoom in on it to see the points to be edited.

- 2 Select an editing tool to edit the contour.
 - When adding or removing points, click at the position of the point to be added or removed.
 - When using the **Edit contour** or **Move contour** tools, click on the point or contour to be moved and drag the point to the new position.

You can use the following editing tools.

Tool	Description
	The Select contour tool allows you to select a contour for editing by clicking it.
	After selecting a contour with the Select contour tool, use the Add contour point tool to add a point after the last point that was added.
	Use the Edit contour tool to move points in the selected contour using a “rubber band” effect. Click on the point you want to reposition and then drag the point to the new location.
	After selecting a contour with the Select contour tool, use the Insert contour point tool to place a point between two previously defined contour points. To insert a point, position the cursor between the two points and press the left mouse button. You can then position the point as desired.
	After selecting a contour with the Select contour tool, use the Remove contour point tool to remove points from the contour. Position the cursor on the point you want to remove and press the left mouse button to remove it.
	Use the Move contour tool to move the contour to a new location on the same slice. (If you do not select the contour first but just click on this tool, the points do not appear, which allows you to place the contour accurately.) Click the contour you want to move and drag it to a new location.
	Use the Scale contour tool to scale the selected contour. (If you do not select the contour first but just click on this tool, the points do not appear, which allows you to scale the contour accurately.) Select the contour you want to scale, click on a point, then drag it left and right to scale it horizontally or drag up and down to scale it vertically.

Interpolate contours

If you do not want to draw contours for a structure on every slice of a data set, you can use the program's interpolation features to generate contours between contours you drew on non-consecutive transverse slices. The individual interpolated contours that are displayed indicate where the edge of the interpolated volume intersects the transverse slices.

Interpolating between contours

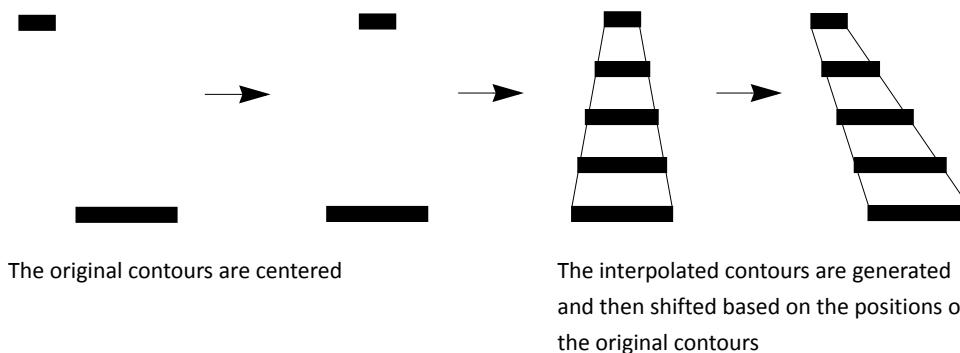
- 1 Draw contours on at least the first and last slices that contain the ROI. The more contours you draw within the ROI, the more accurate the interpolation will be.
- 2 On the **Edit Options** tab, click the **Interpolate Between Contours** button.
- 3 Once the interpolated contours have been generated, you can use the ROI editing tools to move and reshape the contour.
- 4 If you are not satisfied with the results, you can edit the contours or click the **Delete All Interpolated Contours** button to delete them.

Advanced interpolation

- 1 Use one of the ROI drawing tools to draw two or more contours for the structure that you want to interpolate. Using more contours will produce better results from the interpolation.
- 2 Select **Options - Advanced Interpolation**.

The **Contour Interpolation** window appears.

- 3 Select the ROI to be interpolated.
- 4 Select the type of interpolation to generate the contours:
 - **Based on overlap, without curve centering**—This option generates interpolated contours only if the defined contour pairs overlap.
 - **Based on overlap, with curve centering**—With this option, contours are interpolated regardless of whether they overlap. Contour pairs are first centered, the interpolated volume is generated, and the drawn contours are shifted to their correct positions, as illustrated below.



When contours overlap, there is little difference between these two methods.

- 5 Select whether to load the contours into a new ROI. If you set this option to **Yes**, all of the interpolated contours, along with copies of the original contours, are moved to a new “destination” ROI. The name for the new ROI is generated by appending “_INTERP” to the original ROI name.
- 6 Click the **Interpolate between all contours of ROI** button to generate the interpolated contours.

**CAUTION**

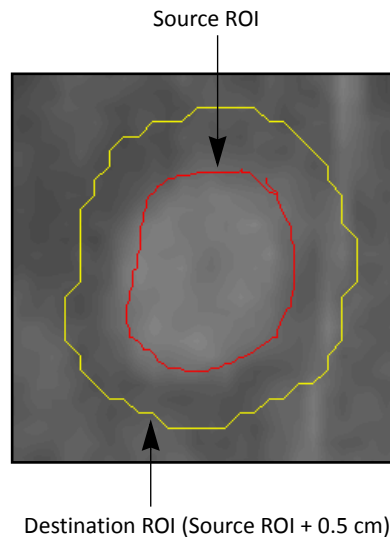
Review the contours to verify that they are correct for your plan. The interpolation might produce unexpected results if the ROIs do not have the same approximate shape.

- 7 Once the interpolated contours have been generated, you can use the ROI editing tools to move and reshape the contour. If you are not satisfied with the results, you can click the **Delete Interpolated Contours** button to delete the interpolated contours, or you can edit the appropriate contours.

Expand and contract ROIs

You can use the expansion and contraction feature to generate the following:

- New contours based on existing ROIs, plus or minus a margin. In the example below, the software creates a new ROI by expanding the source ROI by a uniform margin of 0.5 cm.



- New contours that are combinations of existing ROIs. The existing ROIs are unaffected by this operation.

When you expand or contract an ROI group, the action is performed on the exterior border of all the ROIs combined.

- 1 Click the **ROI Expansion/Contraction** button on the **Edit Options** tab.

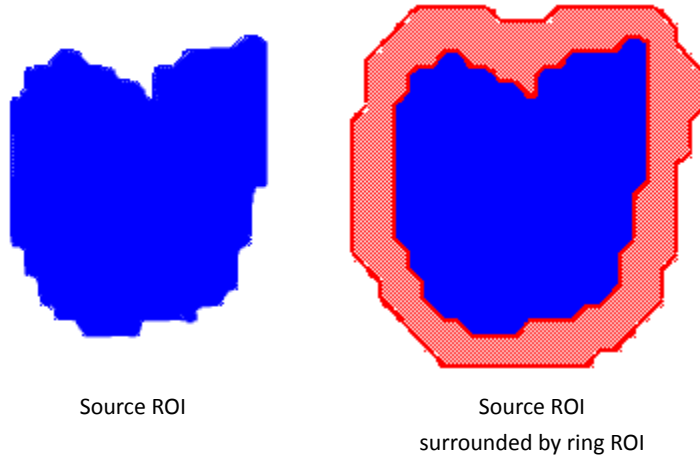
The **ROI Expansion/Contraction** window appears.

- 2 Click the appropriate tab to use individual ROIs or ROI Groups.
- 3 Select the **Source** check box for the ROI to be used as the source. To combine two or more ROIs, select the **Source** check boxes for multiple ROIs.
- 4 If you want to prevent the new ROI from overlapping an existing one, you can define a limiting ROI by selecting one of these options:
 - **Avoid Interior**—the new ROI will avoid the region inside this ROI.
 - **Avoid Exterior**—the new ROI will avoid the region outside this ROI. For example, you can contour the skin surface, then select the **Avoid Exterior** check box for the patient surface ROI in order to keep the new ROI within the patient volume.
- 5 Set the destination ROI:
 - **Select ROI to modify**—From the option list, select the ROI for which the new contours will be drawn. All contours in this ROI will be replaced by new contours.
 - **Create new ROI**—Enter the name for the new ROI.

- 6 Define the margin of expansion or contraction of the source ROI(s):
 - **Uniform margin**—Enter the margin for expansion or contraction in all directions.
 - **Variable margin**—Enter the right and left margins, anterior and posterior margins, and superior and inferior margins.
- 7 Click one of the following buttons to complete the expansion or contraction:
 - **Expand**—Expand the source ROI(s) by the margin.
 - **Contract**—Contract the source ROI(s) by the margin.
 - **Create Ring ROI**—Create a new “ring” ROI around the source ROI. The margin you defined sets the thickness of the ring. A ring ROI can be useful for surface structures such as the rectum wall.

NOTE

When creating a ring ROI with a uniform margin, set the margin at least 1.5 times the minimum voxel size of the image set.



The software performs the expansion or contraction. This may take a few minutes for large volumes.

**CAUTION**

Review the contours to verify that they are correct for your plan.

Autocontour ROIs

Use the autocontouring tools to generate contours automatically based on the CT values in the patient images.

Autocontouring tips

The autocontouring function uses the point in the image where you click as a starting point (or “seed” point). It then searches to the right of the seed point for pixels having CT values above or below the limits you define with the upper and lower thresholds.

- If the CT value of the seed point is within the range of the thresholds, the contour is drawn on the pixels just before the values cross out of the threshold range.
- If the seed point CT value is outside the range of the thresholds, the contour is drawn on the first pixels whose values cross into the threshold range.

Because the software searches to the right, you should generally choose a seed point directly on the structure or to the left of it.

For example, the contour shown in the following figure was generated with a seed point indicated by the asterisk, using thresholds of 800 and 4096. Notice that the contour is drawn on the first pixel that crosses the lower threshold. For images from most CT scanners, the CT values shown in the table below the figure should work well for commonly autocontoured structures. These are recommended values; you may need to change them for your plan.

1505	1174	792	450	296	337	336	369
1395	1418	876	554	337	304	340	354
1446	1661	1360	989	614	397	357	435
1290	1387	1401	989	696	439	354	298
1132	1180	1384	1262	1026	677	400	422
1203	1239	1262	1343	1245	999	655	391
1353	1242	1172	1212	1207	1093	856	593

Structure	Lower Limit	Upper Limit
Lung	100	800
Bone	1300	4096
Skin	500	4096



CAUTION

When autocontouring, you can inadvertently create contours that may lead to incorrect definition of the ROI volume. The correct definition of this volume is critical to the calculations of dose volume histograms and statistics for the ROI.

**CAUTION**

Review the contours to verify that they are correct for your plan.

For information on 2D tools you can use to assist in autocontouring, see the *Pinnacle³ Planning Reference Guide*.

NOTE

You can also autocontour a structure on all slices using the single contour autocontouring tool and pressing the **n** or **p** keys on the keyboard to move from one slice to the next. Using this method, you can control the seed point on each slice and thus control the position of the generated contours.

Set an autocontour bounding box

You can create a bounding box to specify a smaller area for the software to use when automatically creating contours. This can prevent the software from contouring the couch or artifacts in the image set.

You can also apply an isodensity colorwash to the image. The colorwash appears in the image set where the values are within the autocontouring thresholds.

- 1 Click the **Autocontour Options** button on the **Edit Options** tab. The **ROI Bounding Box** window appears.
- 2 Next to **Apply Bounding Box** select **Yes**. The default bounding box size is the image set volume.
- 3 Use the origin fields to set the starting point of the bounding box. Then set the width, length, and height.

OR

Use the bounding box tools to create and adjust a bounding box.

- 4 Set the bounding box color.
- 5 Next to **Display Isodensity** select **Yes** if you want to display an autocontouring colorwash.

Autocontour ROIs



- 1 Display the image you want to use for autocontouring in a 2D viewing window.
- 2 Click the **Contours** button.
- 3 Select an existing ROI or create a new one.
- 4 If the image set is a PET image set, click the **Autocontour Options** button on the **Edit Options** tab. The **ROI Bounding Box** window appears.

In the **Threshold Unit** option list, select either **Raw Values** or **SUV**.

NOTE

The software can only import SUV values from Philips PET scanners. If you did not import the image set from a Philips PET scanner, you cannot change the threshold units.

- 5 Enter the upper and lower autocontour threshold.

6 Select one of the following autocontour tools:



- To generate a single contour on a single slice automatically, select the **Autocontour structure on current slice** tool. Next, click the left mouse button at an appropriate seed point in the image. The software searches in the direction of the arrow until it finds the first structure with CT values within the specified density range, then automatically draws a contour around the structure.



- To generate contours automatically for all structures on a single slice that have densities within the specified range, select the **Autocontour all on current slice** tool. Next, click the left mouse button within the image. All structures on the slice within the threshold are contoured. If the 2D image is zoomed, the autocontouring may include contours that are not visible in the window.



- To autocontour a single contour on all slices that include the structure, select the **Autocontour structure on all slices** tool. Next, click the left mouse button at an appropriate seed point in the image. The tool uses the specified autocontouring thresholds to generate a contour on the current slice, then does the same on adjoining slices for any connected structure that has a density within the threshold range.



- To generate contours automatically for all structures on all slices, select the **Autocontour all on all slices** tool. Next, click the left mouse button at an appropriate seed point in the image. The tool uses the specified autocontouring thresholds to generate contours on the current slice, then does the same on adjoining slices for any connected structure that has a density within the threshold range.

Override ROI density

NOTE

If you are not licensed for proton treatment planning, you can disregard the references to stopping power in this procedure.

NOTE

For electrons, the maximum density override for ROIs is 11.3 gm/cm³. If you enter a value greater than 11.3 gm/cm³, the software still uses 11.3 gm/cm³ for dose computation. For shielding structures directly on the surface of the patient, make sure the ROI is thick enough to stop all primary electrons. When shielding structures are used, high overrides that correspond to the density of lead may compromise the integrity of the algorithm used in the dose computation.



WARNING

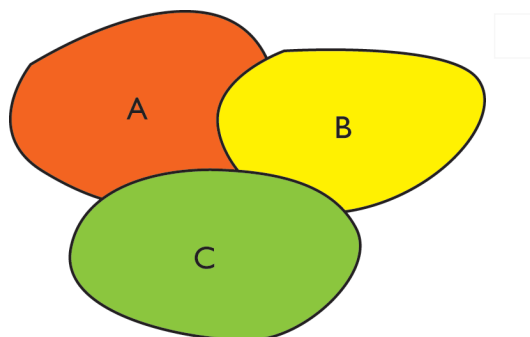
Changing the density or stopping power changes the dose calculation. Verify that the override values you enter are correct. If you change the override values, recompute dose.

The density or stopping power information that you enter is used in the dose calculation, and it overrides the density and stopping power information in the CT image set; however, the CT data is not permanently altered. You can always return to the CT data by setting the **Override Density** option to **No**.

The software uses the density and stopping power override data instead of the CT data when autocontouring and when computing ROI statistics for the density data set. See *Compute statistics on ROIs* and *Autocontour ROIs*.

- 1 In the **Regions of Interest** panel, select **Options - Density Override**.
- 2 If you want to specify an override value for one or more ROIs, set **Override Density** to **Yes** for those ROIs. The order in which you turn on the Density Override option for the ROIs determines the default **Override Sequence**.
- 3 If necessary, change the **Override Sequence** as appropriate for your plan. The **Override Sequence** is the order in which the software overrides the density and stopping power for the ROIs. For example, if multiple ROIs overlap each other, the software uses the density of the ROI

with the largest **Override Sequence** value for the overlapping volume of the ROI (see example below).



ROI	Override Sequence value
A	1
B	2
C	3

- 4 If you want to set the density and stopping power of the voxels outside of the ROI instead of inside of it, click the **Inside ROI** button in the **Load Voxels** column. This option can remove objects from outside a given ROI. For example, if you want to remove all densities around the patient, you can autocontour the skin and load the voxels outside the ROI with a density of zero.
- 5 Are you licensed for proton treatment planning?
 - No—go to step 6 to continue.
 - Yes—go to step 8 to continue.
- 6 In the **Density** field, type the density value.
Density values must be within the range specified by the CT to Density table for this patient.
- 7 Select the density units, either g/cm³ or CT numbers.
This procedure is complete.
- 8 Type the override value in the **Density**, **Stopping Power**, or **CT Number** field. The values in the other two fields are adjusted accordingly.
 - If you override the density, the CT number corresponding to the density that you specified will be used to set the stopping power for the ROI based on the CT to stopping power table.
 - If you override the stopping power, the CT number corresponding to the stopping power that you specified will be used to set the density for the ROI based on the CT to density table.
 - If you override the CT number, the density and stopping power for the ROI will be set based on the table values corresponding to the CT number that you specified.

This procedure is complete.

NOTE

Range and modulation are recomputed when you change the density, stopping power, or CT number values. In addition, dose is invalidated when these values are changed.

View ROI density overrides

You can view ROI overrides in a separate window.

In the **Density** tab of the **Regions of Interest** window, click the **View Density Overrides** button. The **Density Override Display** window appears.

The **Density Override Display** window displays an ROI with its density overridden



- 123** The grayscale CT image within the ROI is replaced with a solid color corresponding to the density value of the override. Use the **Show image value 2D** tool to display the image value of a density override.

NOTE

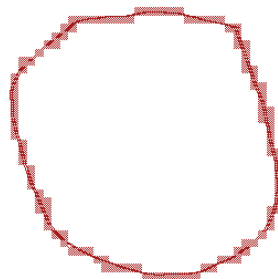
An error message appears if the density override display is invalid. Click the **Recompute** button to recompute the density override display.

Correct contouring problems

Clean ROIs

Use the **Clean ROI** option to correct the following contouring problems.

- When copying ROI contours, you can accidentally copy a contour on top of itself. When this happens, nothing is “inside” the two contours. The resulting volume contains only the voxels through which the contour passes, as shown below.



- When autocontouring, you can generate many small, unnecessary contours in addition to the contour for the structure, or you can inadvertently generate duplicate contours for the same structure.



CAUTION

When autocontouring or copying ROIs, you can inadvertently create contours that lead to an incorrectly defined ROI volume. This volume is critical in calculating dose volume histograms and ROI statistics. Check the autocontoured ROIs to verify that they are correct.

- 1 Select the ROI you want to correct.
- 2 Select **Options - Clean ROI**.

The software scans the selected ROI to detect problems, and the **ROI Curve Cleanup Results** window appears.

All contours with an area smaller than the **Minimum Contour Area** are listed in the window, as are contours that have more overlap than the **Overlap Threshold**.

- 3 If necessary, change the **Minimum Contour Area** and **Overlap Threshold** and click the **Rescan** button to check again for problems using the new parameters.
- 4 To delete problem contours, click the **Delete Curves** button. To move contours to a different ROI, click the **Move Curves to New ROI** button.
- 5 When you finish, click the **Close** button.

Smooth ROIs

Autocontouring can produce small filaments where the curve loops back upon itself. While these filaments are the correct behavior for autocontouring and cause no problems for treatment planning, they present problems for RTOG output. To eliminate these filaments, use an ROI smoothing method called erosion/dilation.

NOTE

You cannot use this method on ROIs that have sagittal or coronal contours.

- 1 Select **Options - Smooth Contours**.

The **ROI Erode/Dilate** window appears.

- 2 Select the ROI you want to smooth.
- 3 Specify the margin as a fraction of voxel size.

The default margin, 0.5, is sufficient to eliminate filaments. The range of allowable margins is 0.1 to 10.0. The larger the fraction, the smoother the result.

- 4 Click the **Erode/Dilate ROI** button.

The ROI is first contracted by a small margin to eliminate the filaments and other small features, then expanded by the same margin to restore the original structure (now smoothed).

- 5 Click the **Close** button when you finish the smoothing operation.

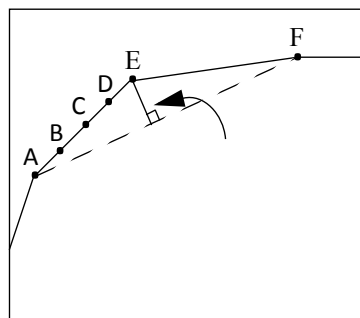
Reduce ROI points

Contours generated using continuous line contouring and autocontouring can contain a large number of points, which can slow the display speed. The software provides three methods for eliminating unnecessary points in contours, especially in regions of little curvature, to improve the display speed.

Reduce points by distance

- 1 Select the ROI to be reduced.
- 2 Select **Options - ROI Point Reduction - Reduce Current ROI by Distance**.
- 3 The software prompts you to enter the maximum distance to reduce the points. The default value should work well in most cases. Enter a value, then click the **OK** button.

In the following illustration, if the distances between point B and the dotted line, point C and the dotted line, and point D and the dotted line are less than the maximum distance you assign, and the distance between point E and the dotted line is greater than the maximum distance, then points B, C, and D will be removed.

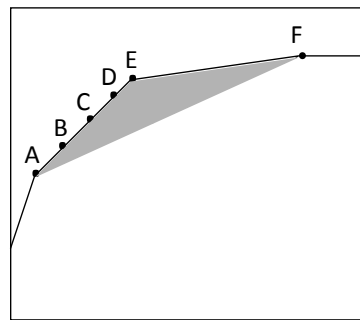


Maximum Distance Method

Reduce points by area

- 1 Select the ROI to be reduced.
- 2 Select **Options - ROI Point Reduction - Reduce Current ROI by Area**.
- 3 The software prompts you to enter the maximum area to reduce the points. The default value should work well in most cases. Enter a value, then click the **OK** button.

The maximum area method is similar to the maximum distance method. In the following illustration, if the area of the shaded region is greater than the maximum area you assign, then points B, C, and D will be removed. Both methods reduce the number of points significantly. However, the maximum area method is better in most situations, as it retains the shape of the ROI more accurately.



Maximum Area Method

Reduce points for all ROIs

If you intend to use DICOM RT to export ROIs to a system that limits the number of points in a contour, you can use this feature to reduce the number of points in all the ROIs.

- 1 Select **Options - ROI Point Reduction - Reduce Points for All ROIs**.
- 2 The software prompts you to enter the maximum number of points per contour. Enter a value, then click the **Reduce Points** button.

This method applies both the maximum distance and maximum area methods to reduce the number of points in all ROIs. The software uses default maximum distance and area values and iteratively increases the values until all contours in all ROIs contain no more than the number of points that you specified.

Patch and Through

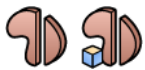
Patch and Through is a technique that lets you treat a target volume that has a U or V shape and surrounds a critical organ. In this technique, the target ROI is split into two ROIs using the **Part ROI** tool. Two beams are then assigned to the ROIs to ensure that dose is delivered to the entire target volume while sparing the critical structure. The Through beam covers as much of the target ROI as possible, and the Patch beam covers the rest of the target ROI.

- 1 Create the target ROI.

NOTE

Set the **2D Display** to **Contour**, **Colorwash**, **Poly**, or **Both** when you use the patch and through technique. The **Part ROI** tool only works with one of those display options.

- 2 Select **Part ROI** from the **Options** menu. The **ROI Parting Tool** window opens.
- 3 Select the target ROI from the **ROI to Part** option list.
- 4 Click the **Part ROI 2D** tool if you are viewing the images in 2D, or click the **Part ROI 3D** tool if you are viewing the images in 3D. The **ROI Parting Tool** window closes.



NOTE

The **Part ROI 2D** tool and the **Part ROI 3D** tool are used to split ROIs in 2D and 3D views, respectively. For example, you cannot split an ROI in a 2D viewing window if you use the **Part ROI 3D** tool.

- 5 Draw a line across the target ROI at the location at which you want to split the ROI. When you release the mouse after you draw the line, the software divides the ROI into two ROIs along the plane in which the line is drawn. The new ROIs keep the name of the original ROI and are appended with “_large” and “_small”.

NOTE

You can irradiate the target while sparing the critical structure by distributing the dose from the Patch and Through beams that are treating the target. Ideally, the distal penumbra of the Patch beam is summed with the lateral penumbra of the Through beam to provide a uniform dose to the target. Typically, the 50% lateral and 50% distal doses are overlapped. However, you can choose 75% lateral and 25% distal doses, or some other combination.

Create a beam-specific ROI

NOTE

This feature is only available if you are licensed for proton treatment planning.

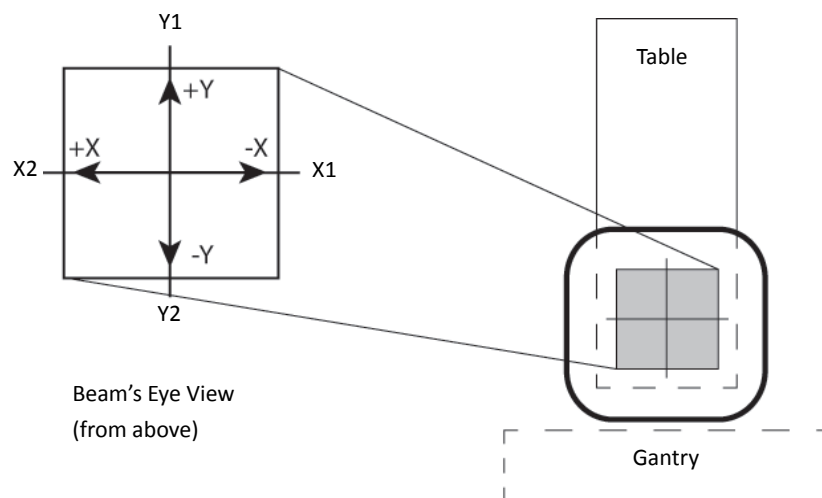
The beam-specific ROI feature lets you create a new ROI by expanding the target ROI in the beam's coordinate system using margins that are specific to the beam. (In contrast, ROIs that are expanded using the **ROI Expansion/Contraction** tool are expanded and contracted using the Pinnacle³ patient coordinate system.) You can specify beam-specific proximal, distal, and lateral margins that help to mitigate range uncertainty and target motion while the beam is being delivered. You can use the new ROI for optimization objectives and for plan evaluation in the presence of uncertainties.

The following must be true before you can create a beam-specific ROI.

- You must have defined a target ROI for the beam.
 - The target ROI must be displayed in a mode other than mesh mode.
- 1 In the **Beams** panel, click the **Modifiers** tab and click the **Beam Specific ROI** button.

The **Beam Specific ROI** window opens.

- 2 In the **Beam** option list, select the beam for which you want to create the ROI.
- 3 Type the lateral margins in the **Left**, **Right**, **Top**, and **Bottom** fields. The X and Y directions are shown in the following graphic for the beam coordinate system.



- 4 Type the proximal and distal margins.
- 5 Click the **Create Beam Specific ROI** button. A new ROI is created and is added to the ROI list. The new ROI is named *beam name_target ROI name*. For example, if the name of the target ROI is "PTV" and the name of the beam is "AP", then the name of the new beam-specific ROI is "AP_PTV".
- 6 To view information about the beam-specific ROI, click the **Contours** button to open the **Regions Of Interest** panel.

Manage ROI groups

ROI groups are managed automatically when you use Dynamic Planning. However, an ROI Group Manager is provided to allow you to make changes when a manual ROI group is preferred over an automatic one, for example, or when ROI groups are not working as you wish. This feature allows you to add and delete ROIs and ROI groups and adjust their colors.

NOTE

If you make changes using the ROI Group Manager, ROI Trending and ROI Group DVH could be affected as well leading to undesirable behavior. For this reason, you should only use the ROI Manager as a last resort.

NOTE

This feature is available only if you are licensed for Dynamic Planning.

The ROI Group Manager is available in the **Regions of Interest** panel by selecting **Options - ROI Group Manager**, and in the **ROI Expansion/Contraction** window by clicking the **ROI Group manager** button on the **ROI Group** tab.

When the **ROI Group Manager** window opens, you can perform the following actions.

Add an ROI group

- 1 Click **Add ROI Group**.
- 2 Type a **Name** for the group.

When you propagate ROIs or use Dynamic Planning, the **Color** is automatically assigned based on the “source” ROI. This ensures that planning ROI colors match **ROI Group** colors. This is clinically desirable. However, if you need to change the color, you can do so.

- 3 Select a **Color** for the group.

Add an ROI to a group

- 1 Select a group to which you want to add an ROI from the **ROI Groups** list.
- 2 In the list of **Available ROIs** below the **ROI Groups**, select the source for the ROIs from the **ROI List**. The source is either the current plan (**Planning**) or a record.
- 3 Select the ROIs to add to the group and click **Add To ROI Group**.

Remove an ROI from a group

Other than deleting a record, this is the only way to delete an ROI from a group.

- 1 Select a group from the **ROI Groups** list.
- 2 In the list of **Grouped ROIs**, select the ROIs to remove.
- 3 Click **Remove From ROI Group**.

Delete an ROI group

- 1 Select a group to delete from the **ROI Groups** list.
- 2 Click **Delete ROI Group**.

Set the color of an ROI group

- 1 Select a group from the **ROI Groups** list.
- 2 Select a **Color** from the list.

Compute statistics on ROIs

- 1 In the **Regions of Interest** panel, select **Options - Statistics**.



CAUTION

Any part of the ROI that is outside the dose grid will not have dose calculated. To obtain accurate statistics for ROI dose, the entire ROI must be included in the dose grid. To ensure accurate density statistics, the entire ROI must be included in the patient density volume.

- 2 Select the data set for which you want to compute statistics from the **Data Set To Compute Stats On** option list. If you select **Density**, statistics are computed by looking up values from the primary data set and passing them through the selected CT to density table.
- 3 Select **Recompute Statistics** from the **Statistics** menu.

NOTE

Initially, the software is set up to calculate statistics only when you select the **Recompute Statistics** option. To have statistics update whenever any change is made to an ROI, select **Statistics - Update Stats When - Any ROI Altered**.

The statistics computed for the ROI are volume, minimum and maximum value, mean value, sum value, SUV value, standard deviation, and percent outside grid. The last value is the percentage of the ROI that is outside the grid for which statistics were calculated.

The sum value is the sum of the image set voxel values for those that are within the ROI.

The **% Outside Grid** value displays the percentage of the grid that is outside the data set for which statistics were calculated. If you are computing dose statistics, the **% Outside Grid** refers to the dose grid. If you are computing density statistics, the value refers to the density grid. If the grid fully encompasses the ROI, this value is zero.

The **% Outside Grid** is only correct if the entire ROI is within the data set to which it is assigned. In most cases, this distinction is not important, but keep the point in mind if you use image fusion with multiple patient volumes. Image fusion is described in the *View Patient Data* chapter.

8 Points of Interest

Overview

You can use points of interest (POIs) as isocenters, as reference points for 2D and 3D viewing, and to generate profiles between two known coordinates. Once dose has been computed, you can use POIs to obtain point dose information, including the total dose at the point and the dose contribution from each beam to the point.

An isocenter is a POI at which a beam is aimed. You can add any number of POIs or isocenters to a plan. For isocentric setups, you will usually have only one POI for a given set of beams. For SSD beams, you need to add an isocenter for each beam, plus a calculation POI.

Precise positioning of isocenters is required, especially for stereotactic radiosurgery. Be careful in your placement of isocenters: if there is too much overlap, you could apply a larger than intended dose to one area (a “hot spot”).

You can place POIs in 2D, 3D, and BEV viewing windows. A number of tools help you interactively and automatically place isocenters after they have been added.



Display the **Points of Interest** panel to the left of the viewing windows by clicking the **Points** button at the top of the window.

Place a point of interest

NOTE

If you want to use a POI for beam placement or dose evaluation, you must place the POI on the primary image set.

- 1 Click the **Add Point** button. A new POI is added to the list with a default name.
- 2 Make sure the new POI is highlighted in the list.
- 3 In the **POI Name** field, change the name of the POI to something appropriate for your plan and according to your clinical practices.
- 4 If you have multiple image sets, select the image set to associate with the POI.
- 5 In the **POI Type** option list, select a type to associate with the POI.
- 6 Position the POI using any of the following options:
 - If you know the CT coordinates of the POI, enter its position in the **Lateral**, **Ant-Post**, and **Sup-Inf** fields.
 - Use the point of interest tools to interactively position the POI.
 - Use the **Autoplace POI** tool, as described in the next section.

NOTE

The DICOM coordinates appear in the **Points of Interest** panel below the CT coordinates. The DICOM coordinates do not appear if any of the following statements are true.

- The image set is not a DICOM image set.
- You modified the image set using the **Data Set Editor** window.
- The plan uses a water phantom or synthetic data.

- 7 Set the diameter of the POI, in centimeters.

The diameter is for visualization only, except for stereotactic plans, where diameter reflects the default cone size. For more information on this setting, see *Specify POI diameters*.

- 8 Set the 2D display mode, 3D display mode, and color that is assigned to the POI. For more information on these settings, see *Change the POI display*.

Position isocenters automatically

You can automatically place an isocenter so that it covers regions of interest (ROIs). The placement algorithm uses the smallest possible box or centroid to cover the ROIs. The POI is then placed at the center of this construct.

Place a POI in one ROI

- 1 Click the **Add Point** button. Then click the **Autoplace POI** button. The **POI Automatic Positioning** window appears.
- 2 Select the ROI that you want to cover from the **Region of Interest** list.
- 3 Select **Box** or **Centroid** as the POI placement method.
- 4 Click the **Automatically Place Point** button.

**CAUTION**

Verify that the automatically placed POI is in the correct location. Change its position or diameter if necessary.

Place a POI in multiple ROIs

- 1 Click the **Add Point** button. Then click the **Set Inside Multiple Regions** button. The **Select Multiple ROIs** window appears.
- 2 Select the check box for the desired ROI. Repeat for each ROI that you want to cover.
- 3 Select **Box** or **Centroid** as the POI placement method.
- 4 Click the **Autoplace POI** button.

**CAUTION**

Verify that the automatically placed POI is in the correct location. Change its position or diameter if necessary.

Make a POI a reference point

If you are licensed for AcQSim³ and relative coordinates are enabled, the **Set Reference Point** button is enabled on the **Points of Interest** panel. If you use a beam isocenter as the reference point, you can see the location of other beams relative to the beam assigned to the reference point.

If you click this button, the selected POI coordinates are set to 0,0,0 and all other plan element coordinates (beam isocenters, 3D bounding box, cubic VOIs, dose grid, other POIs, and the laser coordinate origin) are relative to the POI.



CAUTION

If you set relative coordinates after computing dose, the dose is made invalid.

Delete a POI

- 1 Click the **Delete Point** button.
The **POI Delete** window appears.
- 2 Select the POI that you want to delete.
- 3 Click the **Delete Selected POI** button to delete the POI.

If the POI is an isocenter for any treatment beams or setup beams, you cannot remove the POI. To delete such a point, you must delete the beams or specify a different isocenter for the beams. If necessary, click the **Examine objects** button to view the objects that rely on the selected POI.



CAUTION

Deleted beams cannot be undone and will change your treatment plan. Verify that you are deleting the correct beam or selecting the correct isocenter.

Lock a POI

You can lock a POI to prevent it from being modified.



To lock a POI, select it from the list and click the **Lock POI** button. The button image changes from unlocked to locked, and you cannot modify the POI.



To unlock a POI, select it from the list and click the **Unlock POI** button. The button image changes from locked to unlocked, and you can modify the POI.

Point of interest utilities

Sort POIs

You can manually order the list of POIs.

- 1 Select **Options - Sort**.
The **Sort** window appears.
- 2 Click the **POI** tab.
- 3 Select an item and use the arrows to move it:

Control	Description
	Move item to the top
	Move item up
	Move item down
	Move item to the bottom

Point of interest coordinate precision

You can select the precision used to display the coordinates of all POIs.

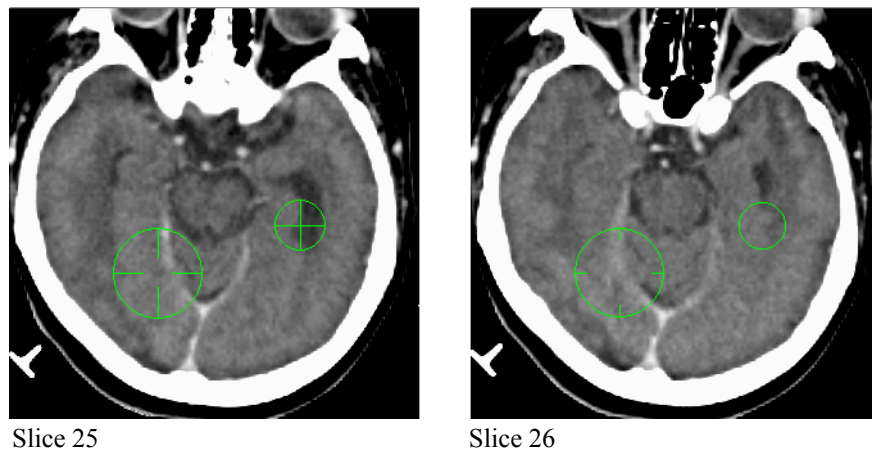
- 1 Select **Options - POI Spreadsheet**.
The **Points Of Interest** window appears.
- 2 Select **Options - Coord Display Precision**. Select the precision you want from the list that appears.

Change the POI display

You can display POIs in both 2D and 3D images. The color of the POI in 2D and 3D images corresponds to your selection in the **Color** list of the **Points of Interest** panel.

In 2D images, the intersection of the POI and the slice is displayed as a circle. The crosshairs on the POI and the size of the circle indicate closeness to the center of the sphere. If the POI is positioned directly on an image slice, a complete crosshair is drawn. If the POI does not lie directly on the slice, partial crosshairs are drawn. Record POIs are indicated by dashed circles.

The following figure shows a set of transverse images. A small isocenter is positioned directly on slice 25. The larger isocenter is positioned between the images. The crosshair on slice 25 is more complete, indicating that the large isocenter is closer to slice 25 than to the slice 26.



In 3D images, POIs are displayed as surface, transparent or wireframe spheres the size of the specified diameter.

- 1 Make sure the POI you want to change is highlighted in the list.
- 2 To change the color of the POI, select an option from the **Color** option list.
- 3 From the **2D Display** option list, select **On**, **Off**, or **Label** to set the 2D display mode for the POI.
- 4 From the **3D Display** option list, select **Surface**, **Transparent**, **Wireframe**, or **Off** to set the 3D display mode for the POI.

Specify POI diameters

You can change the diameter of a POI. For stereotactic radiosurgery, the isocenter display can be useful in selecting the appropriate collimator size. By changing the isocenter diameter size, you can see how well the circular collimator covers the target volume.

Using the **Autoplace POI** function you can have the software select the nearest diameter size that covers the specified ROI. You can also use the **POI Diameter** list to determine the available diameters, as described in the following steps. The diameter values in this list can be set to any diameter size or limited to the available collimators on a given machine.

- 1 Select **Options - POI Diameter List**. The **POI Diameter List** window appears.
- 2 To set up an arbitrary list of diameters, you can add and delete diameters on the list using the **Add Diameter** and **Remove Current Diameter** buttons. You can change the diameter values by typing in the boxes.
- 3 If you want to set up the diameter list to correspond with available collimators on a machine, click the **Copy from Machine** button.

In the **Machine** field of the next window, select the machine from which you want to copy the circular collimator values. The available circular collimators for the machine are listed. Click the

Set the POI diameter list to machine collimator diameters button to change the diameter list, and then click the **Close** button.

- 4 If you want to sort the list so that diameters are listed from smallest to largest, click the **Sort By Diameter** button in the **POI Diameter List** window.
- 5 If you want this diameter list to be the default selection for automatic isocenter placement, click the **Save As Default** button.
- 6 When you finish, click the **Close** button.

Calculate the distance between points of interest

- 1 Select **Options - POI Spreadsheet**.

The **Points Of Interest** window appears.

- 2 Select **Options - POI Distance Window**. The **Distance** window appears.
- 3 Select the two points from the **First POI** and **Second POI** option lists. The distance between the points is shown at the bottom of the window.

Position points of interest interactively

You can use the following tools to interactively position POIs in 2D or 3D images.

Position isocenters on 2D slices



Select the **Move POI** tool to place a POI directly on a transverse, sagittal, or coronal slice.

On the 2D slice where you want to place the isocenter, position the cursor and click the left mouse button to place the POI on the slice. You can also position the POI by holding down the left mouse button and dragging the POI to the new position.

Position isocenters between slices



If you want to place an isocenter between CT slices, select the **Nudge POI toward you** tool or the **Nudge POI away from you** tool.

Click in the viewing window that shows the images you want to use for positioning. Continue to click in the window until the isocenter is positioned properly.

For example, to move the isocenter between two transverse slices, click in the viewing window that shows transverse images. Clicking the **Nudge POI toward you** tool moves the isocenter 1/10 of the voxel height toward you in the volume. Clicking the **Nudge POI away from you** tool moves the isocenter 1/10 of the voxel height away from you in the volume.



If a POI is positioned between CT slices and you want to reposition it without changing the slice, you can use the **Translate POI** tool to move the POI within the current plane without moving it to the slice where you click.

Position isocenters in 3D images



Select the **Move POI 3D** tool to position POIs on the surface of a rendered image. This tool is useful for setting up SSD treatments.

NOTE

3D POI positioning does not work unless a surface image (skin or bone) is rendered in a 3D viewing window.

Open a 3D viewing window and then render the 3D image. Then position the cursor and click the left mouse button to place the POI in the volume. You can also position the POI by holding down the left mouse button and dragging it to the new position.

9 Beams

Overview

This chapter explains how to set up plans for all external beam treatment modalities. Plan setup includes patient localization and beam setup.

For stereotactic radiosurgery and photon or electron beam treatment planning, you perform the initial setup of the beams and the beam geometry in the same manner.

The basic process for the initial beam setup is as follows:

- 1 Add a beam.
- 2 Set the beam display.
- 3 Set the beam isocenter.
- 4 Set the angles (this includes setting the couch, gantry, and collimator angles).
- 5 Set up the jaws.
- 6 Match beam edges.

After you finish setting up the beams, you can add the beam modifiers to your plan. See the *Beam Modifiers* chapter for more information.

For proton beam treatment planning, the basic process for the initial beam setup is as follows:

- 1 Add a beam.
- 2 Set the beam display.
- 3 Set the beam isocenter.
- 4 Set the couch and gantry angles.
- 5 Set the snout.
- 6 Match beam edges.

The software adds a default aperture and compensator to proton beams that use the double scattering or uniform scanning modalities. See the *Beam Modifiers* chapter for more information.



Click **Beams** at the top of the window to display the **Beams** panel.

Sort beams

You can manually order the list of beams.



- 1 Click **Beams** at the top of the window. The **Beams** panel opens.
- 2 Select **Options - Sort**.

The **Sort** window opens.

- 3 Click the **Beam** tab.

4 Select an item and use the arrows to move it:

Control	Description
	Move item to the top.
	Move item up.
	Move item down.
	Move item to the bottom.

Preparing to add, copy, and delete beams

About the machines

Only commissioned machines are available in planning and simulation. The software uses the most recent machine version unless you specifically change the version. See the *Pinnacle³ Planning Reference Guide* for more details.



CAUTION

The default machine is selected automatically when you add a beam. Because beam geometry is machine-dependent, verify that the correct machine is being used for each beam before you set the beam parameters.



CAUTION

The current POI is selected automatically as the isocenter when you add a beam. Verify that the correct POI is being used as the isocenter for each beam.

View machine information

You can view the physics information for the machine that is used by the current beam. In the **Beams** panel, select **Options - Machine/Energy** or right-click the machine name in the **Setup** tab. (Due to the behavior of the Pinnacle³ windowing environment, the **Num Lock** and **Caps Lock** functions must be turned off in order for the right-click behavior to work properly.)

You cannot change the information in the **Machine Information** window, but you can use it to confirm that you have selected the correct machine. For detailed information about the machine parameters, see the *Pinnacle³ Physics Instructions for Use*.

Add a beam

- 1 In the **Beams** panel, click **Add Beam**. The software adds a new beam to the list.

NOTE

If a POI does not exist when you add a beam, the software places one in the center of the CT image set and automatically selects it as the isocenter.

- 2 Make sure the new beam is highlighted in the list.

NOTE

To more efficiently set up the plan, you can enter the parameters for the first beam and then use one of the copy commands to add the remaining beams.

- 3 In the **Name** field, change the name to something appropriate for your plan according to your clinical practices.
- 4 If you will export plan information to a Record and Verify system, enter a unique ID for each beam in the **Field ID** field.

- 5 In the **Machine** field, select the machine to be used for treatment. The version of the machine appears after you select it.
- 6 In the **Modality** field, select the mode to be used for treatment.
- 7 In the **Energy** field, select the energy to be used for treatment.

**CAUTION**

The Sliding Window beam type appears in the Beam Type field for beams that were converted using the sliding window algorithm in P³IMRT. **Do not change this beam type.** If you change the beam type, the software invalidates dose for the beam and removes all but the first control point from the beam. Also, you will not be able to change the beam back to a Sliding Window beam using the Beam Type field. You will have to convert it again using P³IMRT.

- 8 In the **Beam Type** field, select type of beam that you want to use:
 - For fixed beams, choose **Static**.
 - For arced beams, choose **Arc**.
 - To perform forward planning and set up control points, choose **Step & Shoot MLC**.
 - To create a conformal arc plan, choose **Conformal Arc**. See the *Beam Modifiers* chapter for more information.
 - For beams with motorized wedges, choose **Motorized Wedge**. See the *Beam Modifiers* chapter for more information.
 - To create a SmartArc plan, choose **Dynamic Arc**. See the *P³IMRT Instructions for Use* for more information on how to create a SmartArc plan.
- 9 In the **Dose Rate** field, select the dose rate to be used for the beam.

NOTE

If the High-Dose Technique is enabled for the machine, and the MU of the beam is greater than the MU threshold that was specified for this beam type in Physics when your machine was commissioned, then the value is exported as “SRS” in the High-Dose Technique tag (300A,00C7) of the DICOM export.

- 10 In the **Delivery Time Multiplier** field, enter the value (1 to 5) to be used to calculate the maximum treatment delivery time for the plan.
- 11 If you are using the Stereotactic Radiosurgery (SRS) technique for the treatment and your machine is enabled for the High-Dose Technique, select **Yes** for the **SRS Technique** option. This setting exports a value of “SRS” in the High-Dose Technique tag in the DICOM export.

Add a proton beam

- 1 In the **Beams** panel, click **Add Beam**. The software adds a new beam to the list.

NOTE

If a POI does not exist when you add a beam, the software places one in the center of the CT image set and automatically selects it as the isocenter.

- 2 Make sure the new beam is highlighted in the list.

NOTE

To more efficiently set up the plan, you can enter the parameters for the first beam and then use one of the copy commands to add the remaining beams.

- 3 In the **Name** field, change the name to something appropriate for your plan according to your clinical practices.
- 4 If you will export plan information to a Record and Verify system, enter a unique ID for each beam in the **Field ID** field.
- 5 In the **Machine** field, select the machine to be used for treatment. The version of the machine appears after you select it.
- 6 In the **Modality** field, select the mode to be used for treatment.
- 7 In the **Target ROI** field, select the target ROI for this beam.
- 8 To adjust the range or modulation, set proximal or distal margins, and view general beam parameters, click **Details**. The **Proton Beam Parameters** window opens.

The **Proton Beam Parameters** window displays the set range and set modulation values and the target range and target modulation values:

- The **Range** and **Modulation** fields show the set range and set modulation values, which are the values that the beam would exhibit if it was delivered to water. For double scattering and uniform scanning beams, these values are sent to the machine for delivery. For spot scanning beams, these values are used to generate the layers and spots that are sent to the machine for delivery.
 - The **Target Range** and **Target Modulation** fields show range and modulation values that are determined by ray tracing through the target. Target range is the deepest depth of the target in terms of water equivalent distance. Target modulation is the greatest longitudinal thickness of the target in terms of water equivalent distance.
- 9 Choose one of the following:
 - If this beam is a double scattering or uniform scanning beam, continue to step 10.
 - If this beam is a spot scanning beam, continue to step 13.
 - 10 Choose one of the following:
 - To use the **Target Range** and **Target Modulation** values, do not make any changes to the beam parameters. Go to step 13.
 - To use the **Range** (set range) and **Modulation** (set modulation) values, go to step 11.
 - 11 To add margins to the proximal or distal edge of the target ROI in order to adjust the longitudinal dose to the target, set the **Enter Margins** field to **Yes** and go to step 13. Otherwise, set the **Enter Margins** field to **No** and go to step 12.
 - 12 If necessary, change the range and modulation values by typing new values in the **Range** field and the **Modulation** field. Then go to step 14.
 - 13 Specify either **Automatic** or **Manual** margins by clicking the appropriate button.
 - If you specify **Automatic** margins, the software computes the optimal margins and displays the values in the **Proximal** and **Distal** fields. For information, see “Methodologies and tools

for proton beam design for lung tumors”, by M.F. Moyers, et al, *International Journal of Radiation Oncology * Biology * Physics* 49:1429–1438 (2001).

- If you specify **Manual** margins, specify the appropriate margins by typing values in the **Proximal** and **Distal** fields.

14 Choose one of the following:

- If this beam is a double scattering or uniform scanning beam, go to *Set beam parameters for double scattering and uniform scanning*.
- If this beam is a spot scanning beam, go to *Set beam parameters for spot scanning*.

Set beam parameters for double scattering and uniform scanning

- 1 If the selected machine supports full plateau delivery and you want to enable that option for this beam, select **Yes** in the **Full Plateau** field. The software sets the modulation to be equal to the range, and the software will calculate dose to the surface of the patient.

NOTE

The full plateau option is only available if it was enabled for this machine during the commissioning process. Full plateau delivery means that the 100% dose level extends to the patient surface, while full modulation means that the proximal level of the SOBP extends to the patient surface. For full modulation, if the proximal level is 95%, then 95% of plateau dose extends to the patient surface.

- 2 The **Model Parameters** section of the window includes information about the range band that the software selected for the beam. Click **SOBP** to view the **Cumulative Weight** and the components for this range band.
- 3 To lock the beam, continue to *Lock a beam*.

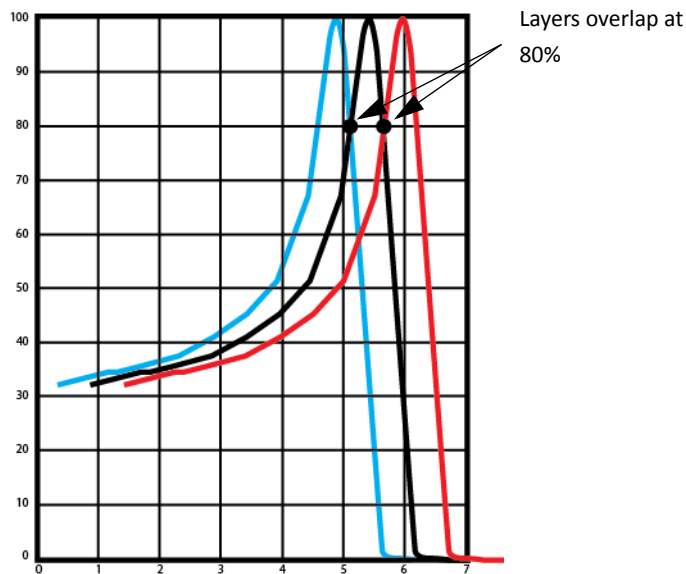
Set beam parameters for spot scanning

- 1 If necessary, select the range shifter that should be used for the beam from the **Range Shifter** list. The thickness of the range shifter is shown in the **Range Shifter Thickness** field.
- 2 If necessary, you can record the range modulator ID value so that the value will be included when you export to DICOM. Select **Yes** in the **Enter Range Modulator ID** field and type the **Range Modulator ID** value for the range shifter that you selected. The ID value is defined by the manufacturer of the machine.
- 3 The **Spot Parameters** section of the window lets you define several parameters that are specific to spots. Select **Automatic** or **Manual** for spot pattern generation:
 - **Automatic**—The software determines the pattern for the layers and spots based on your specifications for layer overlap and spot spacing. Continue to *Generate layer and spot patterns automatically*.
 - **Manual**—Manually import layers and spot patterns. Continue to *Import layer and spot patterns*.

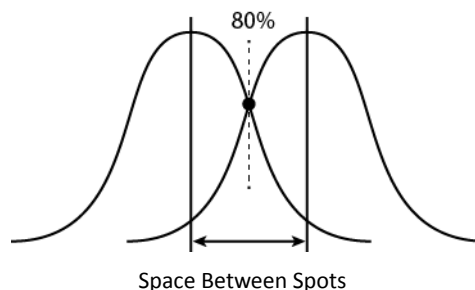
Generate layer and spot patterns automatically

- 1 Select **Uniform** or **Variable** for the lateral target margin:

- **Uniform**—Specify the appropriate margin by typing a value in the **Margin** field. A uniform margin is applied to the top, bottom, left, and right directions for the spots as viewed from the beam's eye view.
 - **Variable**—Specify the appropriate margins in the fields. The margins are applied to the top, bottom, left, and right directions for the spots as viewed from the beam's eye view.
- 2 In the **Layer Overlap** field, type the percentage of overlap that should be allowed for each layer. The percentage that you specify is the percentage at which the integral depth dose curves overlap each other. For example, a **Layer Overlap** value of 80% means that two adjacent layers will overlap where the 80% proximal point of integral depth dose curve meets the 80% distal point of another integral depth dose curve, as shown in the following image.



- 3 Select **Automatic** or **Manual** for spot spacing.
- **Automatic**—The software determines the spacing for the spots in each layer based on your specifications. In the **Overlap** field, type the percentage of overlap in the lateral directions that should be allowed for each spot. The software will place spots based on this setting when you compute dose. The spacing is computed for the maximum energy at the isocenter, and this spacing value is used for all of the layers. For example, for symmetric fluence, an **Overlap** value of 80% means that two adjacent spots will be placed at a spacing where their in-air fluence profiles intersect at 80% as shown in the following image. For asymmetric fluence, the spacing is calculated based on the X and Y profiles, and the smaller spacing value is used for all of the spots.



- **Manual**—Type the absolute physical distance in centimeters that you want to use between adjacent spots in the field. The software will place spots in each layer based on this setting when you compute dose.
- 4 If you want to add extra spots near the edges of the spot pattern of the layer, select **Yes** for the **Double Density** option. When you add extra spots to the field, the optimizer will have better control of the dose distribution at the edges of the layer.
 - 5 Click **Generate** to generate the spots and layers according to the settings that you specified. The **Spot Viewer** window opens. For information about the **Spot Viewer** window, see *View spots for spot scanning beams*.

NOTE

You are not required to generate the spots and layers at this time. Spots and layers are automatically generated when you compute dose for the beam or process the spots in the beam. However, generating the spots now allows you to view the spots before you compute dose.

NOTE

If the energy defined for a beam is not sufficient to completely cover the target ROI, the software generates spots for the beam for as much of the ROI as possible. Review all of the spots for the trial to confirm that spots have been generated for the entire ROI, and adjust the plan if necessary.

- 6 To lock the beam, continue to *Lock a beam*.
- 7 When you are finished generating the layers and spots, you can review the locations of the spots in the **Spot Viewer** window and, if necessary, make adjustments before you compute dose. See *View spots for spot scanning beams*.
- 8 To export the layers and spots, continue to *Export layers and spots*.

Import layer and spot patterns

- 1 Click **Spot Details** to import layers and spots. The **Spot Details** window opens.
- 2 Click **Import** to import files. The **Select File(s)** window opens.
- 3 Use the **Directory** list at the right to locate directories and pattern files on your hard disk.

The current directory is displayed at the top of the list. To go up one directory, click the double dots (..) in the list. To go down one directory, click the directory name in the list.

- 4 Select the file to import and click **OK**. The layers and spots that are included in the file appear in the **Spot Details** window. The energy and range values for the layer that is selected in the list appear in the **Energy** and **Range** fields. The number of spots that are included in the selected layer appear in the **Number of Spots** field.

NOTE

The spot positions in the file must be valid so the software can successfully import the file. The position for each spot must be divisible by a common number that is greater than 0.10 cm.

The weights of the spots shown in the **Spot Details** window may not be the same as the weights of the spots in the file. When you import spots, the software normalizes the

weights of the spots so that the sum of the weights of the spots in each beam equals 1.0.

- 5 To sort the layers in the list from the lowest energy to the highest energy, click **Sort Layers**.
- 6 To lock the beam, continue to *Lock a beam*.
- 7 When you are finished generating the layers and spots, you can review the locations of the spots in the **Spot Viewer** window and, if necessary, make adjustments before you compute dose. See *View spots for spot scanning beams*.
- 8 To export the layers and spots, continue to *Export layers and spots*.

Export layers and spots

NOTE

This section applies only to spot scanning beams.

- 1 In the **Proton Beam Parameters** window, click **Spot Details**. The **Spot Details** window opens.
- 2 Select the layer that you want to export and click **Export**. The **Select File(s)** window opens.
- 3 Use the **Directory** list on the right to locate the directory to which you want to export the layer.

The current directory is displayed at the top of the list in the **Directory** field. To go up one directory, click the double dots (..) in the list. To go down one directory, click the directory name in the list.

- 4 In the **File Name** field, type a name for the file that you are exporting.



CAUTION

Do not use the following characters in the file name. If you use any of these characters in the file name, the export may fail.

. " ' ~ & () | < > + * \ / ; : @ ! [] # ^ % \$ = { } , ?

- 5 Click **OK** to export the file to the directory that you selected. The software exports the layer that you selected as a text file. Click **Cancel** to close the **Select File(s)** window without exporting the layer.

NOTE

Spots with a weight of zero are not exported.

Lock a beam

To lock a proton beam when you are finished setting the beam parameters and defining the aperture and compensator, select **Yes** in the **Lock Beam** field in the **Proton Beam Parameters** window. (To define an aperture for double scattering beams and uniform scanning beams, see *Apertures*. To define a compensator, see *Compensators*.)

When the beam is locked, the only parameters that you can change are the couch and gantry angles, isocenter, and SSD. You can also process the spots for a locked beam. The other beam parameters are locked and cannot be changed unless the beam is unlocked:

- You cannot change the number of layers or spots.
- You cannot change the minimum and maximum MU used for processing the spots.
- You cannot change the range, modulation, snout, proximal margin, distal margin, the CT to density table or the CT to stopping power table.
- You cannot choose a different machine, modality, or target ROI for the beam.
- You cannot copy and oppose beam.
- You cannot edit the aperture or compensator.
- The aperture, range, and modulation are not updated if the target ROI is modified.

NOTE

When you unlock a beam, the range and modulation values are automatically updated, and the computed dose is invalidated. Also, the aperture and compensator are not automatically unlocked. You must manually unlock those modifiers if you want to edit them.

Copy a beam

**CAUTION**

Including two identical beams in your plan can cause dose to be higher than intended. Make sure you modify the copied beam appropriately.

- 1 In the list of beams, select the beam you want to copy.
- 2 From the **Options** menu, select **Copy Beam**. A beam with the same settings as the selected beam is added to the plan.

Copy and oppose a beam

NOTE

You cannot copy and oppose a dynamic arc or conformal arc beam. You also cannot copy and oppose proton beams when the beam is locked, when the beam contains ROIs that are used for distal blocking, or for a machine that uses discrete gantry angles.

- 1 In the list of beams, select the beam you want to copy.
- 2 From the **Options** menu, select one of the following:
 - **Copy & Oppose Beam**—A new beam whose gantry angle is opposed to the selected beam is added to the plan.
 - **Copy & Oppose Beam w/ Table**—A new beam whose gantry and couch angles are opposed to the selected beam is added to the plan.

NOTE

Copy & Oppose Beam w/ Table is not available for proton machines that use discrete gantry angles.

Delete a beam



WARNING

You cannot restore beams after you have deleted them. Be careful when deleting a beam necessary to your plan. Make sure that you are deleting the beam from the correct trial.

- 1 Click **Delete Beam**. The **Select Beam to Delete** window opens.
- 2 Delete the beams.
 - To delete one beam, select the beam and click **Delete Selected Beam**.
 - To delete all beams, click **Delete All Beams in List** and confirm the deletion in the window that opens.

Use stored beam files

NOTE

The following information does not apply to proton beams.

You can access stored beam configurations using the **Standard Plans** command in the **Options** menu of the **Beams** panel.

Several beam configuration files have been provided with the software:

- *FourField.Beam.Script* is set up as a standard four-field box.
- *FourFieldProstate.Beam.Script* is set up as a standard four-field box with the region of interest named “prostate” automatically blocked with a 1 cm margin.
- *StereoFiveArc.Beam.Script* is a stereotactic radiosurgery plan with five arcs.
- *StereoSevenArc.Beam.Script* is a stereotactic radiosurgery plan with seven arcs.

You can create your own stored beam files using the scripting functions. See the scripting information in the *Utilities* chapter for more information.

- 1 Select **Options - Standard Plans**. The **Standard Beam Plans** window opens.
- 2 By default, the window lists the beam configurations that are provided with the software. If you want to use a beam configuration that you created using the scripting functions, click **User Std Plans**.

To switch back to the list of configurations that are provided with the software, click **System Std Plans**.

NOTE

New scripts do not appear in the **Standard Beam Plans** window until you exit the current plan and re-enter it.

- 3 Select the plan from the list and click **Proceed**. The **Confirm Standard Plan** window opens.

- 4 Select the isocenter and the treatment machine to be used for the beams, then click **Add New Beams**.

The software creates the beam setup for the selected plan.

**CAUTION**

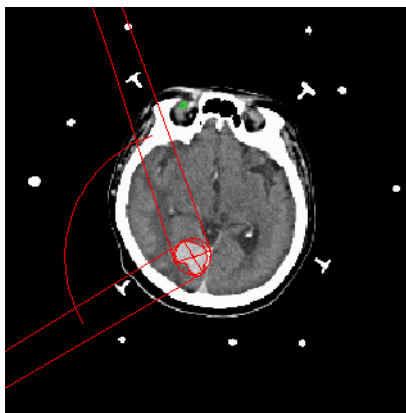
The beams added to your plan may not be exactly correct for your plan. Verify each beam's placement and settings after adding stored beams.

Beam visualization

Initially, the software displays all beams in both 2D and 3D viewing windows. As you add beams to the plan, each beam appears in a different color. To help you associate information in the **Beams** panel with the beam display in the viewing windows, the beam name is framed in the beam's display color.

2D images display the intersection of the beam with the slice. The limits of the beam field are indicated by a solid line. The central axis for the beam is indicated by a dashed line. When the beam is orthogonal to the image plane, the central axis position is indicated by intersecting cross hairs.

Stereotactic arcs are indicated by their starting and ending beams in the arc and a curved rotation indicator, which shows the direction of rotation between the starting and ending beams.



In 3D images, you can display the beam as a solid surface or wireframe. You can also see the intersection of the beam with anatomical surfaces.

Set the beam display

- 1 Make sure the beam you want to change is highlighted in the list.
- 2 In the **Display Options** area, click the **Color** option list to select a different color.
- 3 Next to **2D Display**, select **Yes** if the beam should appear in 2D viewing windows, or **No** if it should be hidden.
- 4 Next to **3D Display**, select **Yes** if the beam should appear in 3D viewing windows, or **No** if it should be hidden.

You can also choose to display all the beams in 2D or 3D viewing windows. The **All Beam Display** option in the **Utilities** menu allows you to override the display settings for the individual beams. You can display or hide all beams in 2D or 3D viewing windows.

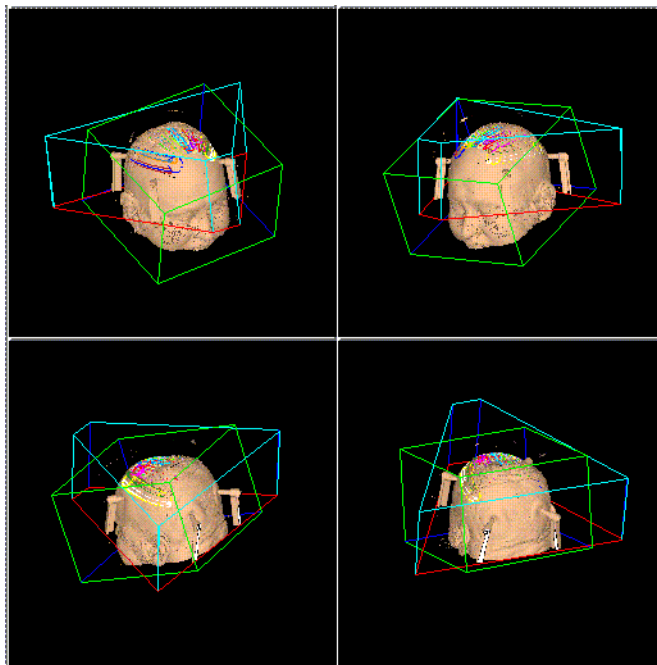
For more details on beam display parameters, see *Set the beam display parameters* in the *Pinnacle³ Planning Reference Guide*.

Specify beam orientation and collimation

Although beam geometry setup is similar for all treatment modalities, you should consult the section below that applies to your modality. Beam geometry is limited by the physical machine parameters entered in the physics tools. Collimator jaw positions are set in the physics tool.

Beam orientation and collimation for stereotactic arcs

To determine the best placement of stereotactic arcs, you can create a set of 3D viewing windows and display 3D skin surface images of the patient from different viewpoints so the entire head is visible. As you add arcs to the plan, the surface path of the beam displays on the skin surface.



See the *View Patient Data* chapter for more 2D and 3D display information. See *Beam visualization* for details on setting beam display options.

Set the couch and gantry angles

- 1 In the **Beams** panel, click the **Geometry** tab.
- 2 Are you using a C-Arm machine?
 - Yes—Go to step 3.
 - No—Go to step 4.

NOTE

If you are licensed for C-Arm, it is available for photon and stereotactic beams and can be used with static, step-and-shoot, arc, and conformal arc beam types.

NOTE

The couch angle is set to 0 degrees for machines that are commissioned with a C-Arm, and it cannot be changed.

NOTE

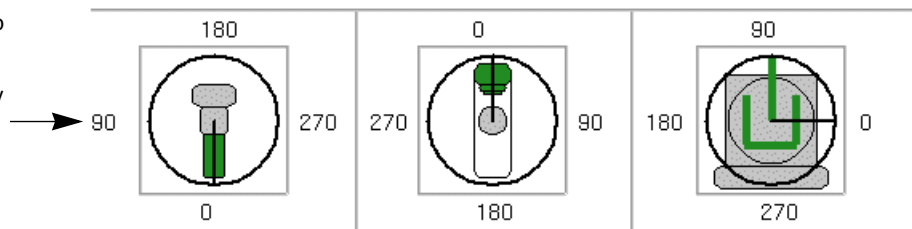
Mitsubishi DME 2.2e or later is required to export plans that contain C-Arm beams.

- 3 To set the angle for the C-Arm, do one of the following:
 - Enter the degree of the angle. Go to step 6.
 - Click and drag the head of the accelerator in the C-Arm graphic to change the C-Arm angle. Go to step 6.
- 4 To set the angles for the couch, do one of the following:
 - Enter the degree of the angle.
 - Use the up and down arrows to set the angle. The couch in the graphic moves to that angle.
 - Click and drag the outer portion of the couch in the graphic to the desired angle.

NOTE

If you are licensed for proton treatment planning and are defining the geometry for a proton beam, the collimator angle graphic is not shown.

Use these graphics to interactively change the couch and gantry angles.



- 5 Click **Set Couch Positions** to view the couch position information for the selected beam. The **Couch Positions** window opens. The default values that were commissioned in Physics are shown in the window. Verify that these values are correct for the beam, and change them as necessary for the plan.

If you change the values and want to propagate them to all beams that use the same isocenter as the selected beam, click **Apply to related beams**.

- 6 Are you using an arc?
 - If yes, go to the next step.
 - If no, go to step 9.

NOTE

Electron arcs are not available in Pinnacle³.

- 7 Click the **Gantry Rotation Direction** icon to toggle the rotation to the proper direction (clockwise or counterclockwise). The icon changes to show the direction.

NOTE

The **Gantry Rotation Direction** icon is not available for proton beams.

- 8 Set the starting and stopping gantry angles in one of the following ways:
 - Enter the starting and stopping angles. The gantry in the graphic moves to show those angles.
 - Use the up and down arrows to set the angles. The gantry in the graphic moves to those angles.
 - Click and drag the green gantry in the graphic to the desired starting angle. Click and drag the red gantry to set the stopping angle.

Do not continue; this procedure is complete.

- 9 Set the gantry angle in one of the following ways (the starting and stopping angles are the same):
 - Enter the starting angle. The gantry in the graphic moves to that angle.
 - Use the up and down arrows to set the angle. The gantry in the graphic moves to that angle.
 - Click and drag the green gantry in the graphic to the desired angle.

For proton beams that use a machine with discrete gantry angles, use one of the following methods:

- Select the desired angle from the **Angle** list.
- Click and drag the green gantry in the graphic to the desired angle.



CAUTION

For a static beam, make sure the start and stop angles match. This is the default configuration.

Set the isocenter

- 1 In the **Beams** panel, click the **Setup** tab.



CAUTION

Because most electron beam isocenters will be on the skin, we recommend that you add a point of interest at a specified depth for use as a reference point in the prescription and dose calculations.

- 2 Specify the isocenter by selecting it from the **Isocenter** list. Only the POIs that are assigned to the primary image set appear in the list.



CAUTION

Changing the SSD moves the isocenter of the beam and all attached beams. If necessary, you can use multiple isocenters to avoid this situation.

- 3 Set the SSD. The isocenter for that beam moves to the SSD you specify. You can use the isocenter placement tools to graphically move the isocenter.

For stereotactic and photon arcs, the SSD listed is the starting SSD for the arc. For electron and proton beams, the SSD listed is the nominal SSD. The nominal SSD is the distance from the skin surface to a fixed reference location upstream in the beam line.

- 4 If the displayed localization system is not correct, select the localization method from the **Localization System** list.

If you localize the patient in the software and then change the localization method, you must localize the patient again.

Set the collimator angle and jaws

NOTE

If you are working with a proton beam, you do not need to follow the procedure in this section. Collimator angles and jaws do not apply to proton beams.

- 1 In the **Beams** panel, click the **Geometry** tab.

NOTE

If you want to add control points and perform forward planning in Pinnacle³, see the *Forward-Planning IMRT* chapter.

- 2 Set the collimator angle (looking down from the machine at the patient) in one of the following ways:
 - Enter the degree of the angle. The collimator in the graphic moves to the angle you set.
 - Use the up and down arrows to set the angle. The collimator in the graphic moves to the angle you set.
 - Click and drag the collimator in the graphic to the desired angle.

NOTE

If you change the machine, the software may change the collimator angle to keep the tray opening in the same orientation. If the angle is not allowed for the machine, the software uses the closest allowable angle. Check your collimator settings after changing machines.

- 3 Is this a photon, stereo, or electron beam?
 - If stereo or electron, go to step 7.
 - If photon, go to step 4.
- 4 Enter the jaw positions. Are the jaws symmetric (dependent/jaw position is the same on both sides) in the horizontal or vertical directions?
 - If yes, click the button beneath **Symmetric** so a **Yes** appears next to the direction that is symmetric. Set the width and height of the jaws.
 - If no, click the button beneath **Symmetric** so **No** appears next to the direction that is asymmetric. Enter the position of the jaw from the central axis.

NOTE

For fixed jaw machines, you cannot edit the jaw information.

- 5 If you want the jaw positions applied to all photon beams, click **Apply to All Beams**.

NOTE

If a machine does not allow asymmetric (independent) jaws, the asymmetric jaw options are not available.

NOTE

When you export a beam with independent jaws to a Record and Verify system, the beam exports as asymmetric even when the jaws are positioned symmetrically.

- 6 For fixed jaw machines, use the **X1**, **X2**, **Y1**, and **Y2** fields to specify the width and height of the rectangle that the MLC leaves define (if necessary).
- 7 Is this a stereo or electron beam?
 - Stereo—from the **Circular Field** list select the appropriate size. (The collimator is initially set to match the isocenter diameter.)
 - Electron—from the **Electron Cone** list select the appropriate size.

Set the snout

NOTE

The snout options are only available if you are licensed for proton treatment planning.

- 1 In the **Beams** panel, click the **Geometry** tab.
- 2 In the **Snout** section of the panel, select the snout that you want to use from the **Name** list. For double scattering beams and uniform scanning beams, the software selects the smallest snout that will cover the field size by default. For spot scanning beams, the software selects the largest snout by default.

NOTE

For spot scanning beams, **Field Radius** values are not shown because apertures are not supported for use with spot scanning beams. Also, you can only change the snout setting if you set the **Spot Pattern Generation** option to **Automatic** in the **Proton Beam Parameters** window.

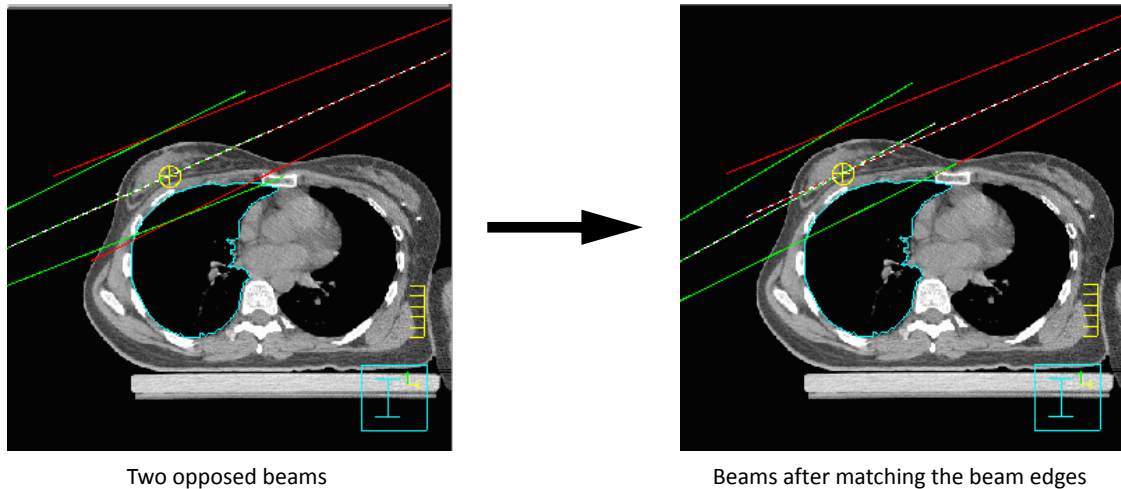
- 3 If necessary, adjust the **Air gap along central axis** value. The initial value in this field is the maximum allowable air gap.

This value is the distance between the distal end of the snout and the surface of the patient that is measured along the central axis of the field. If this value is too small and the software detects a collision between the snout and the patient or the snout and the table, a collision indicator appears in the **Snout** section of the panel. In addition, the point at which the collision will occur is shown on the patient image.

If you change the **Air gap along central axis** value, the software recalculates the **Minimum air gap within field** value, which is the minimum air gap between the patient surface and the snout across the entire field.

Match beam edges

You can match the beam edge for two opposed beams using the **Match Edge** command. The beams should be opposed prior to using the **Match Edge** command. The edge of the beams that is closest to the center of the patient is the edge that is matched.



- 1 In the **Beams** panel, select **Options - Match Edge**.
The **Beam Edge Matching** window opens.
- 2 Select the opposed beams for which you want to center or match the edge.
- 3 Click **Center Opposed Beams** to set the SSD for both beams so that the isocenter is centered between them.
- 4 Click **Match Edge of Opposed Beams**.

Center beam in field

You can move the isocenter of a beam (usually an asymmetric field) to the center of the field to make it symmetric. If you have already set up asymmetric jaws for the beam, centering the beam makes the jaws symmetric but does not change the field size.

- 1 Select the beam that has the isocenter you want to center in the field.
- 2 Select **Options - Center Beam in Field**. The isocenter is moved to the center of the field.

Obtain coordinates for the isocenters

After setting up the isocenter for each beam, you can view the isocenter position in the CT coordinate system and the frame coordinate system or the corresponding motion needed to align the patient. The coordinates for all isocenters are included on the printed plan reports.

Stereotactic frame coordinates

- 1 On the **Setup** tab of the **Beams** panel, click **Details** next to the **Isocenter** field.

The **Beam Isocenter** window opens.

- 2 If other beams use a different isocenter, select the beams from the **Beam** list to view the frame coordinates for the additional isocenters.

NOTE

If the stereotactic frame coordinates are known, you can enter the frame coordinates in the three fields at the center of the window.

Laser alignment coordinates

- 1 On the **Setup** tab of the **Beams** panel, click **Details** next to the **Isocenter** field.

The **Beam Isocenter** window opens.

- 2 If other beams use a different isocenter, select the beams from the **Beam** list to view the laser or table motion for the additional isocenters.
- 3 If the laser alignment system is not correct, select the correct laser alignment system.

**WARNING**

If you are upgrading from a previous version of Pinnacle³ software, make sure that the method for displaying the isocenter shift is consistent with your expectations. If necessary, you can change the default setting in the CT to density table in the physics tool. See *CT Scanner Configuration* in the *Pinnacle³ Physics Instructions for Use*.

- 4 Select how to display the isocenter shift:

- **Table**—Displays isocenter shifts relative to the table.
- **Laser**—Displays table motion in the X and Y direction as laser motion for simulation. Laser motion is the inverse of table motion and is specified per beam.

If you select a laser alignment system with a “1” in the name, you will have one moveable laser for simulation. If you select a laser alignment system with a “3” in the name, you will have three moveable lasers.

The one moveable laser is in the X direction (left/right). The three-laser system has one laser in the X direction and two in the Y (up/down) direction, one on each side of the table.

Change the machine for a beam



CAUTION

After you select a new machine for a beam, verify that all beam modifiers, beam geometry, and dose rate settings are correct.

When you change the machine for a beam, the software attempts to preserve all beam modifiers, beam geometry, and dose rate settings:

- If the new machine does not support a beam modifier that is associated with the beam, the software removes that beam modifier from the beam.
- If the new machine does not support the geometry of the beam, the software attempts to accommodate for the capabilities of the new machine, which may result in beam geometry that is different from the original beam geometry.
- If the new machine can use the same dose rate, then the dose rate is retained. If the same dose rate is not available on the new machine, then the default dose rate for the new machine is used.

If you optimized the beam in IMRT, you may need to optimize the trial again after you change the machine for a beam. If you optimized the plan with the **Intensity Modulation** optimization type, the software removes the ODM if you have not converted the trial. If you optimized the beam with the **DMPO** or **SmartArc** optimization type, you may want to run the optimization again for at least 5 iterations so that the MLC positions can adjust for the new machine.

- 1 Click the **Beams** button. The **Beams** panel opens. Select the **Setup** tab.
- 2 Select the beam for which you want to change the machine.
- 3 In the **Machine** list, select the machine that you want to associate with the beam.

View spots for spot scanning beams

NOTE

This section only applies to proton beams that use the spot scanning modality.

The **Spot Viewer** window lets you view the details of the spots in a layer. Tools included in this window let you visualize the spots with respect to the beam and the image set. In addition, data included in the window show which spots will deliver dose. You can change which spots will deliver dose to spare critical structures.

NOTE

If the energy defined for a beam is not sufficient to completely cover the target ROI, the software generates spots for the beam for as much of the ROI as possible. Review all of the spots for the trial to confirm that spots have been generated for the entire ROI, and adjust the trial if necessary.

NOTE

In order to view ROI contours on each of the slices in the viewing window, ROIs must be displayed using the **Poly** display option. If ROIs are displayed using one of the contour display options, ROI contours may not appear on each slice.

- 1 From the **Options** menu in the **Beams** panel, select **Spot Viewer**.

Information about the spots is shown in the window in three ways:

- A graph shows the position of each spot at the isocenter plane. The rows are the X position and the columns are the Y position of the spot. The X and Y position of a spot is the projection of the spot's central axis on the isocenter plane.
- A 2D viewing window shows the location of the spots on the image set. The location of the spot that is currently selected in the graph and highlighted in the table is indicated by crosshairs in the 2D viewing window. The spots are shown in the viewing window at the point along the central axis of the beam where the integral depth dose (IDD) peak occurs.
- Specific information about each spot in the layer appears in the table. In addition to the X and Y position and the relative weight information, the table also includes the MU and the status of each spot. If a spot is **On**, then that spot will deliver dose during treatment. If a spot is **Off**, then the weight and MU for that spot are zero and that spot will not deliver dose during treatment.

Click on a spot in one of the three display methods to highlight information about the spot in the other two views. For example, click on a spot in the graph to highlight information about the spot in the table, and the location of the spot in the 2D viewing window is indicated by crosshairs.

The display color of a spot is determined by the weight of the spot. Spots that are turned on are assigned a color according to the color legend that is shown in the upper-right corner of the viewing window. Spots that are turned off or have a weight of zero are white.

- 2 To view spots for a beam, select the beam from the **Beam** list.
- 3 To view spots for a layer, select the layer from the **Layer** list.

- 4 Click the **Layer Details** tab to view the following information about the layer:
 - number of spots in the layer
 - size (resolution) of the spot grid
 - number of spots that are turned on in the layer
 - nominal range value for the layer
- 5 Click the **Beam Details** tab to view the following information:
 - number of spots in the trial
 - number of spots in the beam
 - MU/fraction value for the beam
 - number of layers in the beam
 - number of repaints supported for the beam
- 6 On the **Beam Details** tab, type the number of repaints that should be exported to DICOM in the **Number of Repaints** field. The machine interprets and splits the spots by the number of repaints that you specify.

NOTE

If the machine associated with the beam does not support repainting, then one repaint is exported to DICOM and you cannot change the value in the **Number of Repaints** field.

- 7 Click the **Spot Processing** tab to access the spot processing options.
- 8 Specify the minimum spot MU/fraction and maximum spot MU/fraction values that should be used for each spot.

NOTE

If the machine associated with the beam does not support repainting, you can simulate repainting of the spots by specifying a low value in the **Maximum MU/Fraction** field to cause more spots to be split.

- 9 To turn on spots, select one or more rows in the table and click **Turn On Selected Spots**.

NOTE

Even if you select more than one row in the table, only one spot is highlighted in the grid and the viewing window.

If you manually turn off a spot and then turn it back on, the software sets the weight for the spot to zero.

- To select multiple spots that are contiguous in the table, press and hold the **Shift** key and select the first and last rows that you need to change. All rows in between are selected as well.
 - To select multiple spots that are not contiguous in the table, press and hold the **Ctrl** key and select the rows that you need to change.
 - To turn on all of the spots in the layer, click **Turn On All Spots**.
- 10 To turn off spots, select one or more rows in the table and click **Turn Off Selected Spots**. When you turn off spots, the total MUs for the beam is reduced by the number of MUs that were

represented by the spots that you turned off, and the weights of the remaining spots are adjusted so that the sum of their weights equals 1.0.

- To select multiple spots that are contiguous in the table, press and hold the **Shift** key and select the first and last rows that you need to change. All rows in between are selected as well.
- To select multiple spots that are not contiguous in the table, press and hold the **Ctrl** key and select the rows that you need to change.
- To turn off all of the spots in the layer, click **Turn Off All Spots**.

NOTE

Dose will not be delivered to a spot that has been turned off.

You cannot turn off all of the spots for a layer if you have already turned off all of the spots in the other layers in the beam. At least one spot must remain turned on in a beam, and that spot will have a weight of 1.0.

11 Process the spots.

- To process the spots for the selected beam, click **Process Beam**.
- To process the spots for all of the beams, click **Process All Beams**.

When the software processes spots, it confirms that the MU for each spot is within the minimum and maximum spot MU limits:

- If the MU for a spot is less than one-half of the minimum spot MU that you specified, then the MU for that spot is set to zero.
- If the MU for a spot is greater than one-half of the minimum spot MU that you specified, then the MU for that spot is set to the minimum spot MU value.
- If the MU for a spot is greater than the maximum spot MU that you specified, then the spot is split so that the MU of each of the split spots is within the minimum and maximum spot MU limits.

NOTE

If you process the spots after dose has been computed for the beam, then the MUs for the individual spots may change and the dose for the beam may be adjusted to account for the changes in the MUs of the spots. Spots that you have processed are invalidated if any of the following actions occur, and you will need to process the spots again:

- The minimum or maximum spot MU is changed.
- The beam MU is changed.
- The beam weight is changed.
- The prescription is changed.
- You optimize the plan.

12 To view and process spots for other beams or layers, return to step 2.

Viewing window menu options

Additional tools for the viewing window in the **Spot Viewer** window are displayed when you right-click in the viewing window.

Menu option	Description
Select Spot	Click on a spot in the viewing window to view the corresponding information about the spot in the table and the grid view.
Scroll	Drag the cursor to the left and right within the viewing window to scroll through the transverse, sagittal, or coronal images. Click on the far left to move to the beginning of the series of slices. Click on the far right to move to the end of the series. When the cursor is in the viewing window, you can also press the N key to display the next image in the series and press the P key to display the previous image.
Pan	Drag the cursor within the viewing window to reposition the 2D image. The image moves as you move the cursor.
Zoom	Drag the cursor across the viewing window to increase and decrease the magnification of the image. Move the cursor to the left to shrink the image. Move the cursor to the right to magnify the image. The image remains centered in the viewing window, so you may need to use the Pan tool to change the region of the image that is displayed.
Show Dose/Hide Dose	Click Show Dose to display the dose colorwash for the trial on the viewing window. The menu item changes to Hide Dose . Click Hide Dose to turn off the dose colorwash. The menu item changes to Show Dose .
Orientation	View a transverse, sagittal, or coronal image in the 2D viewing window. You can also press the A key to view a transverse (axial) view, the S key for a sagittal view, or the C key for a coronal view.
Box Zoom	Drag diagonally across the image until the region you want to zoom is within the box.
CT/Dose	Display the image value for the point in the image that corresponds to the cursor position. The image values appear when you click the left mouse button. If the dose has been computed, the computed dose and density at the cursor position also appear. The stopping power and the Water Equivalent Thickness (WET) are also shown. Values are computed using the nearest-neighbor method.
Distance	Measure distances on an image: As you drag across the image, a line is drawn showing the distance being measured. The distance (in centimeters) is listed at the bottom of the image. The Water Equivalent Thickness (WET) is also shown.

10 Beam Modifiers

Overview

This chapter covers the beam modifiers you can add to a treatment plan.

Display the beams panel to the left of the viewing windows by clicking on the **Beams** button at the top of the window. You will use the **Modifiers** tab to add modifiers to your beams.

NOTE

The **ODM** field in the **Modifiers** tab displays whether an opening density matrix (ODM) in the field is valid (**Yes** when ODM is valid, **No** when ODM is invalid). Dose computed with an ODM in the field results in approximate MUs, and the plan cannot be used clinically or exported. Approximate monitor units are identified with a tilde (~) after dose is computed. You can invalidate the ODM by clicking the **Reset** button or converting the beam using P³IMRT. After you invalidate the ODM, the plan can be used clinically or exported. See the *P³IMRT Instructions for Use* for information on converting a beam with an ODM to a deliverable beam.

Stereotactic radiosurgery modifiers

For stereotactic radiosurgery there are typically no modifiers added to the plan. For some newer treatment systems mini multi-leaf collimators (MLCs) are used. If you have mini-MLC capabilities that can be set up for your machine in the physics tool and set up in planning, see *Multi-leaf collimators*.

Electron beam modifiers

For electron beam planning you can add blocks and bolus. To add these to your plan, see the following sections:

- Blocks
- Bolus

Photon beam modifiers

For photon beam planning you can add blocks, MLCs, wedges, compensators, and bolus. To add these to your plan, see the following sections:

- Blocks (including the AutoSurround feature available for photon beams)
- Multi-leaf collimators
- Wedges
- Compensators
- Bolus

Proton beam modifiers

Proton treatment planning uses apertures and compensators to modify beams. See the following sections for information:

- Apertures
- Compensators

NOTE

The aperture and proton-specific compensator options are only available if you are licensed for proton treatment planning.

Blocks

This feature can only be used with electron and photon beams. When adding beam blocks, you can draw the block in a beam's eye view window or generate blocks automatically based on a region of interest.

Beam blocks are added from the **Modifiers** tab of the **Beams** panel.

Add a block

- 1 Click the **Modifiers** tab of the **Beams** panel.
- 2 Select the beam from the **Beam** list.
- 3 Click the **Add Block** button. You can click on it a number of times to add the total number of blocks you want to set up.
- 4 In the blocks list, select the one on which you want to work.



CAUTION

For a photon arc, automatic blocks are generated at the starting angle for the arc. The block is not modified as the gantry rotates.

- 5 Do you want the software to automatically generate the block based on a region of interest or do you want to manually define the block?
 - Automatic—From the **Structure** option list select the region of interest to associate with the block.
 - Manual—From the **Structure** option list select **Manual**.



CAUTION

Verify that the automatically placed blocks are correct for the beam. Modify them as appropriate for your plan. You can edit automatically generated blocks by changing the block type to Manual and then using the editing tools to adjust the block shape.

If you switch from Automatic to Manual, the block's contours are copied to the new manual block and the block's margin is set to 0.0. Any existing manual contours are lost.



CAUTION

If the beam geometry is changed during automatic blocking, the software automatically reshapes the block to conform to the ROI shape.

While the block shape is correctly maintained regardless of the beam angle, the collimator jaws are not adjusted to surround the specified ROI. Check your block and adjust the field size as necessary.

- 6 From the **Action** option list, select whether to expose or block the region of interest.
- 7 From the **Rest of Field** option list, select whether to expose or block the field outside of the region of interest, or to take no action (**As Is**).
- 8 Do you want the manually defined block to move with the collimator?
 - If yes, in the **Rotate with Collimator** field select **Yes**.
 - If no, in the **Rotate with Collimator** field select **No** so the block remains stationary.

Blocks will not rotate with the collimator during optimization of MLCs, regardless of your selection.

- 9 Do you need an extra margin around the block?
 - If yes, in the **Margin** field enter the extra amount to be added to all four sides.
 - If no, go to 10.
- 10 Are you using an MLC?
 - If yes, in the **Use MLC?** field select **Yes**. Go to 12.
 - If no, in the **Use MLC?** field select **No**. In the **Tray #** field, enter the block tray number/name (up to 16 characters). The name is "--" by default.

NOTE

For fixed jaw machines, the **Use MLC?** field is set to **Yes** and cannot be changed.

NOTE

When you print or export a plan using DICOM RT, the **Tray #** value is included with each block.



CAUTION

Default values are used initially for the tray transmission factor and block and tray transmission factors. Verify that these values are correct and change them as necessary for your plan.

- 11 Are you setting up a block in a photon beam?
 - If yes, enter the transmission factors in the **Tray** and the **Block and Tray** fields. Then go to 12.
 - If no, go to 12.
- 12 Are you going to manually define the block or do you need to edit the block?
 - If yes, continue to *Manually define the block*.
 - If no, this procedure is complete.

NOTE

When creating blocks and MLCs for an ROI, be aware that the ROI display mode affects its appearance, especially for small field sizes. The **Colorwash** and **Poly** modes more accurately represent the ROI than the **Contour** display. For details on ROI precision, see the *Pinnacle³ Planning Reference Guide*.

NOTE

If your machine has MLC leaves that track the jaws, you can click the **MLC Options** button to view and verify the MLC leaves as they will be positioned at the linac.

Manually define the block

- 1 Change the viewing window to a beam's eye view (BEV).
- 2 In the viewing window, turn on the 3D display for all structures you want to see while defining the block.
- 3 Select the block from the block list.
- 4 In the **Structure** option list select **Manual** if it is not already selected.



- 5 Select the **Create block point by point** or **Create block paintbrush** tool.
 - For the **Create block point by point** tool, click on the BEV where you want to start drawing the block. A small box appears at the point you defined. Continue to define the remaining points in the same manner. To close the contour for the block, click on the first point that you defined.
 - For the **Create block paintbrush** tool, drag on the BEV to draw the block. As you draw, the contour of the block appears.
- 6 To specify a margin (cm) for the block, enter it in the **Margin** field.

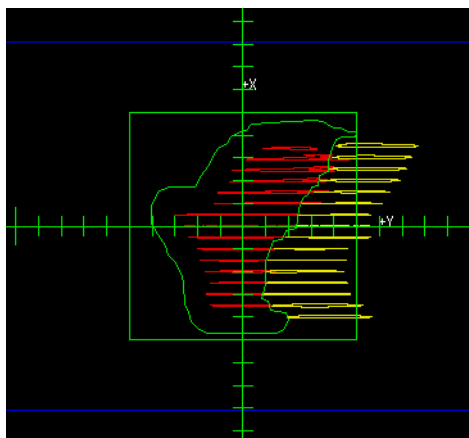
Use the tools along the beam panel to edit the block. For more information, see the *Tools* chapter.

Now you can set blocking priorities, set up multi-leaf collimators (MLCs), and export block and MLC data.

Set the blocking priorities

The priority option allows you to set up a beam block that always blocks a specific structure while always exposing another. By using this option and selecting the appropriate combination of the **Action** and **Rest of Field** options, you can effectively create a hierarchy of structures and can spare sensitive structures while exposing the tumor.

For example, if you have a sensitive structure near your target volume and you want to always block the sensitive structure but expose the target volume, you can set the priority of the sensitive structure to 1 and the priority for the target volume to 2. This set of blocking priorities would generate the block shown below.



- 1 On the **Modifiers** tab in the list of blocks, select the block you want to set as the top priority (the exposure or blocking that is most important).
- 2 From the option list that appears next to the block, select **1**.
- 3 For each additional block, select it and set the priority.

Use the AutoSurround feature

NOTE

The AutoSurround feature is not available for fixed jaw machines.

This feature can only be used with photon beams. Use AutoSurround to make the collimator jaws automatically move to the boundaries of the blocks or to a margin around the block edge. The AutoSurround feature may be used with a block or with an MLC.

If MLC leaves have been manually positioned, the software warns you that the positioning will be lost if you use AutoSurround. When using AutoSurround with an MLC, the jaws push to either the block or the MLC-defined field, whichever is more limiting. Leaves that are above or below the block area and never touch the block are not affected.

- 1 Set the **AutoSurround blocks** field to **Yes**. The **AutoSurround margin** field appears.
- 2 In the **AutoSurround margin** field, set the offset between the jaws and blocking mask.

Unlock the blocks in a beam

If you have copied a plan to a new image, all blocks whose beams have at least one control point are locked by default to prevent any changes from taking place during the copying process. To make changes to the blocks in the plan you must unlock them.

When blocks are locked for a beam and you change the beam's geometry (by moving the isocenter, for example), the existing block shape is unaffected and rotates with the collimator. However, you can still edit individual MLC leaf positions.

When blocks are locked, you cannot perform the following tasks:

- change the beam machine, energy, modality, or type
- copy and oppose a beam
- change the electron cone
- turn the MLC on or off
- use leaf pushing and similar operations that affect the entire MLC
- change the jaw positions and jaw symmetry
- add, delete, or insert a control point
- add, delete, or change the angle and orientation of a wedge, compensator, or a block associated with the beam
- export blocks for the beam
- regenerate an arc beam
- reset the ODM
- use the AutoSurround feature

If a beam's blocks are locked, you can unlock them by selecting the beam and setting the **Lock Blocks** field to **No**. This field affects all the blocks in a beam.

When optimizing an IMRT plan, blocks are unlocked automatically before optimization begins.

Delete a block

- 1 In the blocks list, select the one you want to delete.
- 2 Click the **Delete block** button.



The block tray number changes to **No block**.

Wedges

You can add wedges to photon beams. You can choose from the wedges (physical, dynamic, or motorized) that were defined in the physics tool for the selected machine. In beam's eye view displays, a label appears indicating which jaw the thick end is facing. These labels and the available wedges vary depending on the names entered in the physics tool.

The wedge orientation icons are designed to look like the actual wedges as they appear when added to the wedge tray. The small tab shows the placement of the tab that is inserted into the machine.

- 1 On the **Modifiers** tab, select the wedge to be used for treatment from the **Wedge** list.

NOTE

To use a dynamic wedge, you must use a static beam type.

- 2 Is the wedge physical (static) or dynamic?
 - Physical—the angle is fixed; you cannot set it.
 - Dynamic—in the **Angle** field, specify the angle.

You can type any angle within the allowable range of 0 to 80 degrees if you specified continuous wedge angles when setting up the dynamic wedge in the physics tool. If you specified discrete angles in the physics tool, then you select one of the angles from a list.

- 3 In the **Orientation** field, select the wedge orientation.

The wedge icons and their corresponding wedge orientations are explained in the *Pinnacle³ Planning Reference Guide*.



CAUTION

Verify that the wedge angle and orientation are correct for your plan prior to treating the patient.

To display additional information about the current wedge click the right mouse button on the **Wedge** field, **Angle** field, or **Orientation** field for the beam. For more information, see the *Pinnacle³ Planning Reference Guide*.

Set up a beam with a motorized wedge



CAUTION

If you create a plan that contains a beam with a motorized wedge, you will only be able to export the plan using DICOM RT.

- 1 Add a beam to the plan.
- 2 Specify the machine, modality, and energy. (A motorized wedge must be defined for the machine you select.)
- 3 From the **Beam Type** list, select **Motorized Wedge**. Two control points are added to the beam: one wedged and one open. Each has a default relative weight of 50%.
- 4 Set up the beam display, beam isocenter, angles, and jaws.
- 5 Click the **Modifiers** tab.

- 6 From the **Wedge** list, select the wedge that you want to use. Only wedges that can be used as motorized wedges appear in the **Wedge** list.

NOTE

If you had not selected **Motorized Wedge** as the beam type and you select a motorized wedge, the software prompts you to confirm that it is okay to change the beam type to **Motorized Wedge**. Click **Yes** to proceed. If you click **No**, no wedge is added.

- 7 In the **Orientation** field, select the wedge orientation, if necessary.

NOTE

Motorized wedges are not available in irregular field planning or planar dose calculation.

Change the angle of the motorized wedge

You can change the synthesized angle of the motorized wedge by adjusting the weights of the control points or by typing an angle value.

Adjust the control point weights

- 1 Compute dose for the beam that contains the motorized wedge you want to change.
- 2 Select **Options - Control Points**.

The **Control Points** window opens. The two control points for the beam are listed in the window.

- 3 Adjust the weights of the control points as necessary.
- 4 If necessary, repeat this procedure for other beams that contain motorized wedges.

Set the angle

- 1 Select the beam that contains the motorized wedge that you want to change.
- 2 Click the **Modifiers** tab.
- 3 Type the necessary angle in the **Angle** field. The software adjusts the weights of the two control points so MUs are correctly distributed to achieve the angle you typed. See the synthesized wedge angle information in the *Pinnacle³ Physics Instructions for Use* for details about how the wedge angle is calculated.

NOTE

Pinnacle³ computes dose based on the weights of the control points, not the angle you type in the **Angle** field. The angle you specify determines the relative weights of the control points. Also, the maximum angle Pinnacle³ uses is the one entered in the **Wedge Angle** field of the **Wedge Editor** window in the photon physics tool. Refer to the *Pinnacle³ Physics Instructions for Use* for more information.

Multi-leaf collimators

This feature can only be used with photon beams and only if the MLC physics data has been entered for the machine.

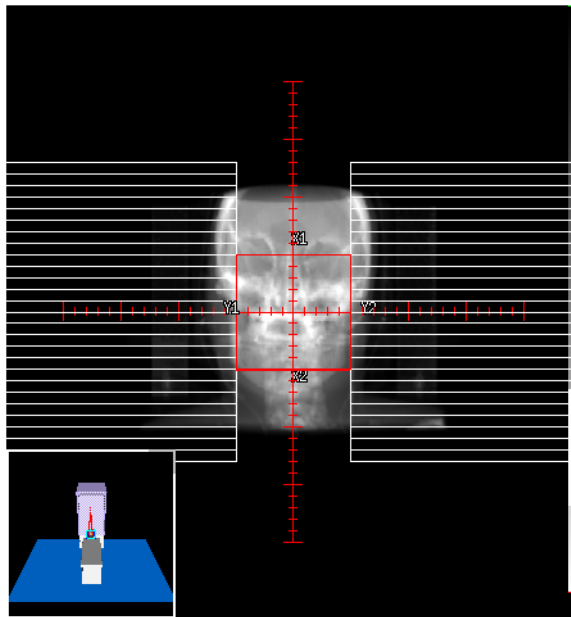
If your radiation therapy machine has a multi-leaf collimator (MLC), you can use the MLC controls in Pinnacle³ to help shape the radiation beam. The jaw transmission is set in the physics tool during modeling. For partial transmission jaws, the value used is the combination of the jaw and MLC transmissions.

When a beam contains a block and uses MLCs, you can define the MLC leaf positions automatically according to the definition of the beam block or manually by shaping the MLC leaf by leaf.

- 1 Click the **Modifiers** tab.
- 2 Define a block, if necessary.
- 3 In the **Use MLC?** field select **Yes**. MLC leaves are automatically pushed to the jaw positions or to the block if there is one.

NOTE

For fixed jaw machines, the **Use MLC?** field is set to **Yes** and you cannot change it.



- 4 Click **MLC Options**. The **Beam MLC Leaf Position Editor** window opens.
- 5 Make sure the correct beam is selected in the **MLC for beam** field.
- 6 If you modify the jaw positions for a beam that uses MLCs with control points and no block, on the **Leaf Pushing** tab click **Push Leaves to Jaws** to move the leaves to the current jaw position. If the beam contains multiple control points, you will have to do this for each control point.
- 7 Define the MLC leaves automatically or manually:
 - Automatically—continue to *Automatically define the leaf positions*.
 - Manually—continue to *Manually define the leaf positions*.

NOTE

If the beam type is **Step & Shoot MLC**, a list of control points appears in the **Beam MLC Leaf Position Editor** window. To use the control points, see *Forward-Planning IMRT*.

Automatically define the leaf positions

- 1 Make sure the correct beam is selected from the **MLC for beam** list in the **Beam MLC Leaf Position Editor** window.

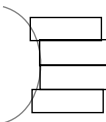
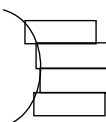
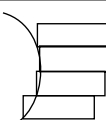
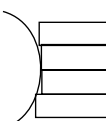
**CAUTION**

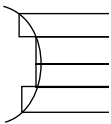
You must define blocks before setting the MLC leaf positions. Verify the placement of the automatically placed MLC leaves.

**CAUTION**

For fixed jaw machines, the machine must treat with the closed leaves pushed behind the jaws. The software tries to force this to happen when you click **Push Leaves to Block** or when a change to the plan automatically causes the leaves to be pushed to the block. Verify that the closed leaves are behind the jaws before you compute dose.

- 2 On the **Leaf Pushing** tab, click **Push Leaves to Block**. The MLC leaves are automatically configured to match the beam block you defined, as shown in the beam's eye view.
- 3 In the **Push Leaves To Leaf** list, select the appropriate option to cover exposed areas just outside the perimeter of the beam block. These options give you another measure of automatic control over the leaf positions, which may be necessary since the ROI is not rectangular and the MLC leaves are rectangular.

Position		Description
	Center	Make the MLC leaves stop at the first intersection point of the center of each leaf with the beam block.
	Top	Make the MLC leaves stop at the first intersection point of the top of each leaf with the beam block.
	Bottom	Make the MLC leaves stop at the first intersection point of the bottom of each leaf with the beam block.
	Average	Set the leaf to make underexposed and overexposed regions of the beam block equivalent. In the illustration at left, the overexposed and underexposed areas are equal.
	Minimum	Make the MLC leaves stop at the first intersection point with the beam block. This option ensures that the beam block is not overlapped, but more exposed area remains around the block.

Position	Description	
	Maximum	Make the MLC leaves stop at the first intersection point with the beam block <i>after</i> covering all exposed area around it. The MLC leaves will also cover some of the block.

- 4 For machines that allow interdigitation and for which the MLC is not set to replace the jaws, you can move the closed leaf pairs behind the jaws to minimize leakage through the closed leaf pairs.

In the **Close Leaves For** list, select **Current Trial** to move the closed leaf pairs behind the jaws for all beams in the trial, or select **Current Beam** to move the closed leaf pairs only in the current beam. Then click **Close Leaves Behind Jaws** to push the closed leaf pairs behind the jaws.

NOTE
If the maximum tip position for the machine is less than or equal to the maximum jaw position and the beam is a static, arc, or motorized wedge beam, then the MLC leaves will not be pushed behind the jaws.

NOTE
For step and shoot or conformal arc beams, if the maximum tip position from the jaw for the machine is smaller than the field size along the direction of leaf travel, then clicking **Close Leaves Behind Jaws** will position the closed leaf pairs at different locations for different control points.

 **CAUTION**
Verify the automatically selected collimator angle.

- 5 Click **Optimize Collimator Angle**. The software selects the angle with the lowest error.

NOTE
Optimize Collimator Angle is available if there is at least one block.

The geometrical data updates and the optimized results appear as a plot of error versus collimator angle. To close the histogram, click **Close**.

The **Error** field displays the MLC error, in cm². The error is the sum of unblocked regions that should be blocked and of blocked regions that should be exposed. If you think the error is too high, you can refine the leaf positions by editing them manually.

- 6 If you want to add a skin flash adjustment, enter a value in the **Shift leaves** field and click either **Shift A bank** or **Shift B bank**. The software opens the leaves in the bank by the specified amount. If necessary, the software also shifts the jaw associated with the bank you are opening.

NOTE
The labels on the **Shift A bank** and **Shift B bank** buttons are the bank names that you entered in the **MLC Editor** window in the physics tool. For example, if the banks are named **Left** and **Right**, the buttons read **Shift Left bank** and **Shift Right bank**.

You can use the skin flash adjustment only for step-and-shoot MLC beams that do not use the AutoSurround feature. The adjustment affects only the selected control point, and moves only

those leaf pairs that are open by more than their minimum opposing leaf gap. For more information, see *Forward-Planning IMRT*.



WARNING

Verify the accuracy of your MLC settings before continuing. To check, visually verify the correctness of the MLC leaves. Incorrect MLC settings and leaf positions can result in incorrect dose.

Manually define the leaf positions

The leaves extend from the edges of the beam's eye view if you have them defined to move parallel to the left/right jaws. The table in the **Beam MLC Leaf Position Editor** window shows the left and right position of each leaf pair. These positions update as you define the MLC settings.

NOTE

If the **AutoSurround blocks** option is on, manual editing of MLC leaves only affects the left and right jaws (assuming that the leaves move parallel to the left/right jaws), and only affects leaves that overlap the field. You can still move leaves above and below the field, but the top and bottom jaws will not widen to enclose those leaves.

NOTE

If you move a leaf so that it violates the maximum tip difference settings with which the machine is commissioned, other leaves may also move so that the maximum tip difference restrictions are satisfied.

- 1 Make sure the correct beam is selected from the **MLC for beam** list in the **Beam MLC Leaf Position Editor** window.
- 2 Enter the coordinates of the leaf positions or graphically place the leaves:
 - Enter coordinates—first click a position coordinate. Next, enter the new position in the field above the table. This procedure is complete.
 - Graphically move leaves—go to step 3.
- 3 Click the **Move MLC manually** tool.
- 4 Click an empty area between the leaves to extend the closest leaf to the clicked point, or reposition leaves by dragging their edges.



Leaves appear by default as white bars after you click in the beam's eye view. Use the jaw labels to help orient yourself in the beam's eye view.

NOTE

If a block automatically conforms to an ROI and you manually change the MLC leaf positions, and then you change the plan such that the block shape must be updated, the MLC leaf positions revert to the shape of the block. For example, if a block exposes a target ROI and you move the beam's isocenter, the software updates the block shape and the MLC leaves conform to the new block shape. In this case, if you want to retain the MLC leaf positions that you defined manually, you must delete the block before you change the plan.

- 5 To change the color of the leaves, click **Options - Display Parameters** to open the **Beam Display** window. Then select **MLC Leaves** from the **Component** list and choose the color from the **Component 2D/3D Color** list.

**WARNING**

Verify the accuracy of your MLC settings before continuing. To check, visually verify the correctness of the MLC leaves. Incorrect MLC settings and leaf positions can result in incorrect dose.

MLC leaf display options

The **Display Options** tab in the **Beam MLC Leaf Position Editor** lets you set leaf display options for the current beam:

- **Clip leaves**—Select **Yes** to view only the section of the MLC that is within the rectangular field limits in the BEV window. When this setting is **No**, the entire MLC is displayed in the BEV window.
- **Fill in leaves**—Select **Yes** to fill in the MLC leaves with color. If you select **No**, the MLC leaves are displayed with outlines.
- **Maximum leaf motion**—Select **Yes** to display the maximum extent of the MLC leaf openings across all control points for step-and-shoot, sliding window, and conformal arc beams. A dashed line showing the maximum extent of the leaf motion appears in the BEV DRR display.

NOTE

In the **Utilities** menu, you can set these same MLC leaf display options for all beams and override the settings of individual beams.

Create conformal arc plans

A conformal arc plan calculates new sets of MLC positions at specified intervals through a treatment arc. When you build a conformal arc, you define the start and stop angles for the arc as well as the degrees between control points. The software creates a control point at the start angle and intermediate control points that are separated by the specified angle increment. A final control point is created at the stop angle. After the software creates the conformal arc, control points cannot be added or deleted.

At each control point, the MLC leaves are pushed to conform to the specified blocking mask. Control points for conformal arc beams are weighted so as to deliver a constant monitor unit (MU) per degree. However, the first and last (and sometimes the second to last) control points receive fewer MUs and have a smaller arc length.

You can export conformal arc plans by using the following methods:

- In DICOM RT export format
- In the Toshiba MLC export format
- To a Toshiba MLV Record & Verify system
- To the Varian Shaper system via the Shaper protocol/file format
- To Mitsubishi accelerators via DME

The following procedure explains how to create a conformal arc plan. The procedure assumes that you have already used the **Photon Physics Tool** to commission a machine that has an MLC and can deliver conformal arc beams. For details, see the *Pinnacle³ Physics Instructions for Use*.

- 1 Add a conformal arc beam to a plan. See *Preparing to add, copy, and delete beams* in the *Beams* chapter.
- 2 Click the **Modifiers** tab of the **Beams** panel.
- 3 Select the beam for which you want to set up a block from the **Beam** list.
- 4 Add blocks for the ROIs to be exposed or blocked. At least one ROI must be exposed, and manual blocks may not be used.
- 5 Click **Conformal Arc**.

The **Conformal Arc** window opens.

- 6 Set the rotation direction and gantry angles.
- 7 Enter a value in the **Degrees Between Control Points** field. If the arc length is 90 degrees or greater, use a value of 1-10 degrees. If the arc length is less than 90 degrees, use a value of 1-5 degrees. (Arc length is the angular distance from the start angle to the stop angle in the direction of rotation.)

NOTE

The software will generate exact monitor units for each control point if you use the values described in step 7. For a quick calculation of the dose distribution, use a value of 11-20 degrees if the arc length is 90 degrees or greater, or 6-10 degrees if the arc length is less than 90 degrees. When you use these values, the resulting monitor units are approximate and the plan cannot be used clinically or exported. Approximate monitor

units are identified with a tilde (~). When you are satisfied with the dose distribution, use the values described in step 7 to generate exact monitor units.

- 8 Do you want the collimator jaws to move automatically using the AutoSurround Blocks feature?
 - Yes—go to step 9.
 - No—go to step 10.
- 9 Set the **AutoSurround Blocks** option to **Yes**.

NOTE

The **AutoSurround Blocks** option does not appear for fixed jaw machines.

- 10 Click **Create Conformal Arc**. The software creates the conformal arc control points.

NOTE

You cannot manually add or delete individual control points or modify control point weights.



- 11 To view control points in the **Conformal Arc Multiple BEV** window, click **Display consecutive MLC control point BEV** in the **Conformal Arc** window.
- 12 To view detailed information for each control point, select **Options - Control Points**.

The **Control Points** window opens. The software displays the monitor units and weights of each control point in a conformal arc beam as a cumulative value from the starting point up to the control point.

- 13 Repeat steps 1-10 as needed to create additional conformal arc beams.



CAUTION

After you export a conformal arc plan to a Record and Verify system or MLC treatment unit, verify that the exported plan information is consistent with the software's plan.

MLV beam export

Toshiba MLV export requires that an MLC shape be exported for every 2 degrees of gantry motion throughout the arc. Unless you create the conformal arc with an increment of 2 degrees, the software does not create a control point for every gantry angle that must be exported. In order to address this, the export linearly interpolates the MLC positions for the required angles based on the actual control points of the conformal arc.

Varying jaw positions

Consider how you will export a conformal arc plan before varying jaw positions between MLC control points. Plans in which jaw positions vary between control points cannot be exported using Toshiba MLC export or Mitsubishi DME export. However, Toshiba plans with varying jaw positions can be exported using Toshiba MLV export.

Apertures

NOTE

Aperture options are only available if you are licensed for proton treatment planning. Apertures are only available for use in double scattering beams and uniform scanning beams.

If a beam is locked, the aperture for that beam is also locked. If you cannot access the aperture options, unlock the beam and the aperture, if necessary. See *Lock a beam*.

The software adds a default aperture (the target aperture) to each double scattering beam and uniform scanning beam after you select a target ROI.

When calculating the milled aperture, the software applies the milling algorithm taking into account the physical milling tool diameter to ensure that the aperture created in planning should be achievable at the milling machine.

- 1 Change the viewing window to a beam's eye view (BEV) so that you can visualize the aperture.
- 2 Click the **Modifiers** tab of the **Beams** panel.
- 3 Select the beam from the **Beams** list.
- 4 Select the structure that you want to expose from the **Structure** list.

If you select the **Manual** structure, go to *Manually change the aperture* to change the shape of the aperture opening.

- 5 Click **Properties**. The **Aperture Properties** window opens.
- 6 Specify an aperture ID in the **Aperture ID** field.

NOTE

The default ID for the aperture is generated based on the Medical Record Number of the patient, the Field ID, and the beam name.

- 7 Verify that the aperture material that is shown in the **Material** field is the correct material for this aperture. To change the material, select a different material from the **Material** list.
- 8 If necessary, specify a margin for the aperture opening in the **Margin** field. The software exposes the structure that you selected plus the margin that you specify when it creates the aperture opening. We recommend that you specify a margin of 0.30 cm or more.

NOTE

The data shown in the **Stopping power relative to water** field and the **Slab thickness** field are the data that were commissioned in the physics tool for this aperture material. You cannot change this data in planning.

- 9 Specify the number of slabs required for this aperture.

NOTE

The system verifies that the total thickness of the aperture slabs is sufficient to stop the radiation for the given range and modulation. The thickness safety margin of the aperture should be greater than or equal to 0.30 cm.

- 10 Specify a conversion method by selecting the **Over** or **Under** option.
 - **Over**—the aperture exposes the entire target ROI. In this conversion method, the opening of the milled aperture is always the same size or larger than the opening of the target aperture.
 - **Under**—the aperture exposes as much of the target ROI as possible but might miss some sharp points or angles. In this conversion method, the opening of the milled aperture will be smaller than the opening of the target aperture.
- 11 Specify the milling tool diameter in the **Milling tool diameter** field.

NOTE

The initial value that is shown in the **Milling tool diameter** field is the default milling tool diameter value that was commissioned in the physics tool for this aperture material.

The field radius calculation that is displayed in the **Snout** section of the **Geometry** tab is based on the aperture milling diameter. If the aperture has an irregular shape, then the radii along the X and Y axes and the maximum radius are displayed.

- 12 Choose one of the following:
 - To define the aperture for another beam, return to step 3.
 - If you have defined the apertures for all of the double scattering beams and uniform scanning beams, continue to step 13.
- 13 Click **Close** to close the **Aperture Properties** window.
- 14 When you are finished defining the apertures, we recommend that you lock the apertures to prevent unwanted changes to the shape of the aperture. Go to *Lock the aperture*.

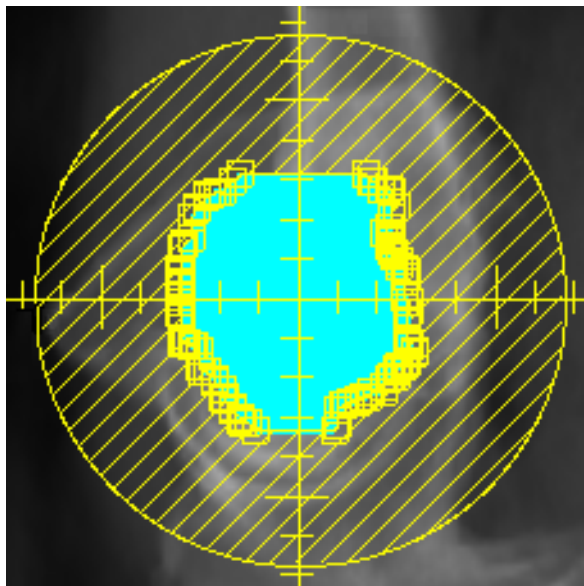
Manually change the aperture

When you select the **Manual** option from the **Structure** list, editing tools appear in the **Beams** panel that let you change the shape of the aperture opening.



- 1 Click **Select block** from the list of editing tools.

- 2 Click the inside edge of the aperture. All of the points in the aperture are displayed with square point markers as shown in the following illustration.



- 3 Use the editing tools to modify the shape of the aperture opening. For information about using these tools, see the *Tools* chapter.
- 4 When you are finished modifying the shape of the aperture opening, we recommend that you lock the aperture to prevent unwanted changes to the shape of the aperture. Go to *Lock the aperture*.

Lock the aperture

- 1 In the **Beams** panel, click the **Setup** tab and then click the **Details** button.
The **Proton Beam Parameters** window opens.
- 2 In the **Beam** list, select the beam that contains the aperture that you want to lock.
- 3 Select **Yes** in the **Lock Aperture** field.

When the aperture is locked, you cannot change the snout or the air gap. In addition, you cannot choose a different machine, modality, or target ROI. You can change the other beam parameters, however.

Compensators

Compensators can be used with photon and proton beams:

- Photon beams—see *Create compensators for photon beams*.
- Proton beams—see *Define compensators for proton beams*.

NOTE

Proton compensator options are only available if you are licensed for proton treatment planning.

Create compensators for photon beams

The software can automatically design missing tissue and dose compensators or, if you have another means of designing compensators, you can enter the compensator thickness array manually. For information on designing compensators manually, see the *Pinnacle³ Planning Reference Guide*.

To open the **Compensator Editor** window, click **Edit** in the **Compensator** section of the **Modifiers** tab on the **Beams** panel.

If you use the automatic compensator design option, the software can compensate for missing tissue, primary dose, or full 3D dose (primary and scatter). The software determines the shape of the compensator as follows:

- 1 You define the density of the compensation material, the width, height, and resolution for the compensator, and the depth of the plane for the compensator shape optimization.
- 2 The software creates a series of points on the optimization plane with one point per cell in the compensator array.
- 3 The software computes dose using the following rules:
 - Missing Tissue Compensator—The energy fluence is computed using SSDs, thus obtaining just a patient surface shape.
 - Primary Dose Compensator—The energy fluence is computed using density-corrected primary fluence.
 - Full 3D Dose Compensator—The density-corrected primary fluence is computed, and then a CC Convolution calculation is performed on the fluence.
- 4 The software computes mean dose in the 2D array of points and the dose statistics for the optimization plane are displayed in the **Compensator Editor** window.

The fields under **Plane Dose Statistics** show how well you are achieving the same dose/energy fluence to all points. The software attempts to create a uniform dose/energy fluence to the points on the optimization plane. The values are relative because they depend on the monitor units, which are variable. Points beneath blocks or outside the patient are excluded.

The **Min**, **Max**, and **Mean** fields display the minimum, maximum, and mean dose/energy fluence to all points in the plane. The **Std Dev** field displays the standard deviation from the mean of all the points.

- 5 The thickness of compensation material in each cell of the compensator array is adjusted using one of the following equations, depending on the type of compensator you are using:
- **Missing Tissue** compensators:

$$Thickness_{(i,j)} = (SSD_{(i,j)} - SSD_{min}) / \text{Compensator density}$$

- For **Primary Dose** and **Full 3D Dose** compensators, the system uses an iterative process to get a uniform TERMA or dose, respectively, to the user-specified plane:

$$Thickness_{(i,j)} = Thickness_{(i,j)} - \frac{\log(\text{MeanDose} / \text{Dose}_{(i,j)})}{\text{MeanAttenuation}}$$

MeanAttenuation is the mean μ/ρ for the beam energy spectrum and the compensator density.

- 6 The software repeats steps 3-5 for the specified number of iterations.

To fill the compensator pixels outside the optimized area of the compensator, the software uses the option you specify for the **Thickness Outside Field** in the **Design Options** window. This field and other compensator design options are described in the *Pinnacle³ Planning Reference Guide*.

Compensator attributes

The compensator attributes allow you to define the compensator.

- **Density**—Specifies the density of the compensator material (in g/cm³).
- **Source To Comp Dist**—Specifies the distance from the source to the top of the compensator tray.
- **Actual Width** and **Actual Height**—Defines the actual dimensions of the compensator in the X and Y directions (in cm). If you select SAD for the scale width/height display in the next field, then the width and height are projections to SAD. If you enter the **X Dimension**, **Y Dimension**, and **Resolution** (as described below), the **Actual Width** and **Actual Height** are calculated using the following equations:

$$\text{Actual Width} = (\text{X Dimension} - 1) \cdot \text{Resolution}$$

$$\text{Actual Height} = (\text{Y Dimension} - 1) \cdot \text{Resolution}$$

- **Scale Width/Height Display To**—Specify whether the width and height of the compensator should be set based on the source-to-axis distance (SAD) or source-to-compensator distance (SCD). If you select SAD, the **Actual Width** and **Actual Height** labels change to **Width at SAD** and **Height at SAD**.
- **Resolution**—Sets the compensator output resolution. The compensator is divided into a grid with this resolution, and thicknesses are determined for each section of the grid.
- **X Dimension** and **Y Dimension**—Sets the number of pixels in each direction. If you have entered the **Actual Width**, **Actual Height**, and **Resolution**, the **X Dimension** and **Y Dimension** are calculated automatically.

- **Round Thickness Values**—If you want to round the values in the compensator thickness array, select **Yes** and then specify a rounding value from 0.001 to 30 in the **Round to Nearest** field that appears. Rounding to the closest even multiple of the rounding value occurs after the last iteration of optimization or when you enter values manually in the compensator array. For example, if the rounding value that you specify is 0.200, a compensator thickness value of 0.250 is rounded to 0.200 because 0.250 is closer to 0.200 than it is to 0.400, and a compensator thickness value of 0.320 is rounded to 0.400.
- **OF Correction Factor**—Enter a correction factor for the output factor if you measure dose with your compensator and you think that a correction is needed. A correction factor is not required; enter one only if you think it is necessary. Generally, the **OF Correction Factor** should be set to 1.0.

If an **OF Correction Factor** is used, it is multiplied by the collimator output factor (OF_c) to give a total **Collimator Output Factor** for the compensated field:

$$OF_c = \text{Collimator OF} \cdot \text{Compensator OF Correction Factor}$$

See the *Pinnacle³ Planning Reference Guide* for more information about calculating the correction factor.

Define compensators for proton beams

NOTE

The following information only applies to double scattering beams or uniform scanning beams. Compensators are not used in spot scanning beams.

If a beam is locked, the compensator for that beam is also locked. If you cannot access the compensator options, verify that the beam is not locked, and unlock the beam and the compensator if necessary. See *Lock a beam*.

The software adds a compensator to each double scattering beam and uniform scanning beam after you select a target ROI for the beam.

NOTE

The software will not add a compensator to the beam if it cannot find a valid range band for the beam. For more information, see *Preparing to add, copy, and delete beams*.

- 1 Click the **Modifiers** tab in the **Beams** panel, and select the beam from the **Beams** list.
- 2 Click **Edit** in the **Compensator** section of the **Beams** panel. The **Compensator Editor** window opens.
- 3 Verify that **Yes** is selected in the **Use Compensator** field.
- 4 Set the following attributes as appropriate.

NOTE

The resolution of a proton compensator is calculated using the diameter of the milling tool. You cannot change the resolution values in the **X Resolution** or **Y Resolution** fields.

- **Scale Width/Height Display To**—Specify whether the width and height of the compensator should be set based on the virtual source-to-axis distance (SAD) or virtual source-to-

compensator distance (SCD). If you select SAD, the software displays the **Width at SAD** and **Height at SAD** values. If you select SCD, the software displays the **Actual Width** and **Actual Height** values.

NOTE

The SAD is the distance from the isocenter to the virtual source. The SCD is the distance from the compensator to the virtual source.

- **Round Thickness Values**—If you want to round the values in the compensator thickness array, select **Yes** and then specify a rounding value from 0.001 to 30 in the **Round To Nearest** field that appears. Rounding to the closest even multiple of the rounding value occurs after the last iteration of optimization or when you enter values manually in the compensator array. For example, if the rounding value that you specify is 0.200, a compensator thickness value of 0.250 is rounded to 0.200 because 0.250 is closer to 0.200 than it is to 0.400, and a compensator thickness value of 0.320 is rounded to 0.400.
- 5 Click **Properties**. The **Compensator Properties** window opens.
 - 6 Type an ID for the compensator in the **Compensator ID** field if you do not want to use the default ID assigned by the software.
 - 7 Verify that the compensator material that is shown in the **Material** field is the correct material for this compensator. To change the material, select a material from the **Material** list.

NOTE

The data shown in the **Stopping power relative to water** field and the **Minimum thickness** field are the data that were commissioned in the physics tool for this compensator material. You cannot change this data in planning.

- 8 Specify whether edge processing should be applied to the compensator.
 - **Yes**—An average thickness value is assigned to compensator pixels that are unblocked by the aperture and that do not intersect the target ROI. The value assigned is the average thickness of all of the pixels that fall within a radius that you specify from the pixel.
 - **No**—The compensator pixels that fall outside of the target ROI are assigned the maximum compensator thickness value.
- 9 Specify whether smearing should be applied to the compensator.

When you apply smearing, each compensator pixel thickness value is reassigned to the lowest value among its nearest neighbors within the radius that you specify. Smearing mitigates patient motion and setup errors as well as dose “undershoot.”

- **Yes**—Specify a smearing margin between 0 cm and 5 cm.
- **No**—Smearing is not applied to the compensator.

NOTE

If you apply smearing or change the smearing settings after you have manually edited the compensator, the changes that you made to the compensator are lost when the software recomputes the compensator to apply the new smearing settings.

- 10 Specify whether distal blocking should be applied to the compensator.

Distal blocking increases the thickness of certain pixels in the compensator to pull the dose back from organs that are distal to the target ROI.

- **Yes**—Click **Edit**. The **Distal Blocking Editor** window opens. Continue to step 11.
- **No**—Distal blocking is not applied to the compensator. Continue to step 15.

NOTE

If you add or remove distal blocking or change a margin after you have manually edited the compensator, the changes that you made to the compensator are lost when the software recalculates the compensator to apply the distal blocking changes.

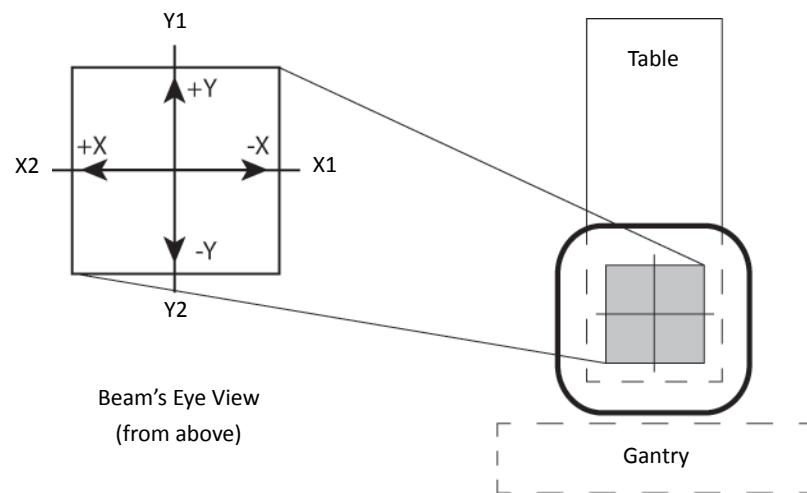
- 11 In the **Distal Blocking Editor** window, select the check boxes for the ROIs that you want to use for distal blocking and click **Add to distal blocking list**. The ROIs appear in the **Distally blocked ROIs** list.
- 12 Type a margin from 0 cm to 5 cm that should be applied to the distally blocked ROIs.
- 13 To remove an ROI from the **Distally blocked ROIs** list, select the check box for the ROI you want to remove from the list and click **Remove from distal blocking list**.
- 14 When you are finished, click **Close** to close the **Distal Blocking Editor** window.
- 15 Specify whether the compensator should be truncated.
- **Yes**—The maximum thickness value of the unmilled compensator area is overwritten with the maximum thickness value of the milled compensator area that is generated by the system.
 - **No**—The compensator is not truncated. The maximum thickness value of the unmilled compensator area that was specified during snout creation is retained.
- 16 Specify a milling method by selecting the **Plunge** or **Continuous** option.
- **Plunge**—The milling tool is a non-zero radius tool. Specify the milling tool diameter after you select this option.

NOTE

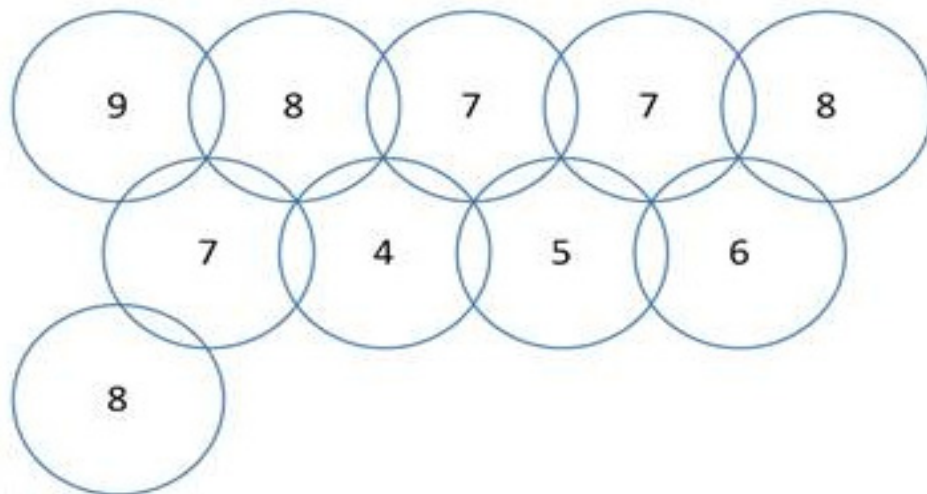
The initial value shown in the **Milling tool diameter** field is the value that was commissioned in the physics tool.

- **Continuous**—The milling tool is a zero-radius tool.
- 17 Click **Close** to close the **Compensator Properties** window.
- 18 To view the thickness array for the compensator, click **Edit Thickness Array**. The **Compensator Array Editor** displays the physical thickness values in the table, in centimeters. These values are calculated based on the snout that you specified for this beam, the shape of the aperture, and the compensator properties. The column and row headings are the coordinates of the X axis and the Y axis based on the graphic that follows. You cannot edit the values in the array from

this window. They are shown only for reference. To edit the thickness array, see *Edit compensators for proton beams*.



If you selected the **Plunge** milling method, every other row of the compensator thickness array is shifted in the positive X direction. The amount of the shift is half of the X step size (resolution). This shift ensures that all of the plunges fully overlap (there are no gaps of unmilled material). The shift is necessary because a circular cutting tool of finite diameter is used to mill the compensator. The graphic that follows illustrates a plunge milling method (a hexagonal milling pattern). This milling technique helps achieve the least overlap between milling bits while covering the compensator area completely. The numbers inside the circles represent the depth at a particular point in centimeters.



If you selected the **Continuous** milling method, no shift is applied.

Edit compensators for proton beams

The **Compensator Editor** lets you adjust the dose distribution by changing the thickness values of a compensator so that you can compare different dose scenarios and create an optimal compensator for the treatment.

NOTE

If the beam is unlocked but the compensator is locked, you can make changes to the compensator and view the results of the changes, but you cannot save your changes. To save changes, you must unlock the compensator before you make your changes. See *Lock the compensator for proton beams*.

- 1 Click the **Modifiers** tab in the **Beams** panel, and select the beam from the **Beams** list.
- 2 Click **Edit** in the **Compensator** section of the **Beams** panel. The **Compensator Editor** window opens.
- 3 Click **Advanced Editing**. The **Advanced Compensator Editor** window opens.

NOTE

The **Advanced Editing** button is only active if dose is computed for the beam.

The window contains two 2D viewing windows. The viewing window at the top shows the location and shape of the compensator. The viewing window at the bottom shows the dose distribution. You can display the isodose levels as a colorwash and as isodose lines.

The window also contains two tabs.

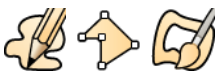
- **Edit**—Contains tools that let you edit the compensator. Continue to step 4.
 - **Display**—Contains tools that let you change the display of the dose distribution. See *Change the display*.
- 4 Click the **Edit** tab if the **Edit** panel is not already shown.

The thickness array at the bottom of the **Edit** panel shows the thickness of each pixel in the compensator. When you click on a pixel in the thickness array, the location of that pixel is marked in the 2D viewing window. After you specify the isothickness settings and colors for the compensator on the **Display** tab, the pixels in the thickness array are color-coded according to their thickness.

- 5 From the **Region** list, select a method for editing the compensator.



- **Pixel**—Select **Pixel** to edit the compensator one pixel at a time. To edit a pixel, either select the **Edit pixel** tool shown at left and click on the pixel in the viewing window that you want to edit or select the pixel that you want to edit in the thickness array at the bottom of the **Edit** panel. Then enter the new thickness value in the **Value at cursor** field in the **Settings** area of the **Edit** tab.



- **Area**—Select **Area** to edit multiple pixels at one time. To select the pixels to edit, select one of the drawing tools shown at left and draw around the area that you want to edit.

NOTE

To change the diameter of the paintbrush for the **Create contour paintbrush** tool, type a value in the **Diam. (mm)** field.

- **Flat**—Changes the thickness values for all of the selected pixels to the new thickness value that you enter in the **Value** field.
- **Average**—Calculates the average thickness of the selected pixels, and then changes the thickness values of the selected pixels to the average thickness value. For example, if you select two pixels with thickness values of 1.2 cm and 2.0 cm, the new thickness value for both of the pixels is 1.6 cm.
- **Percentage**—Changes the thickness values of the selected pixels by adding or subtracting the percentage that you enter in the **Value (+/-)** field from the original thickness values. Enter a positive value to add to the thickness, or enter a negative value to subtract from the thickness. For example, if you select two pixels with thickness values of 4 cm and 8 cm and then enter a value of “25” in the **Value (+/-)** field, the new thickness values for the pixels are 5 cm and 10 cm respectively.
- **Add or subtract**—Changes the thickness values of the selected pixels by adding or subtracting the value that you enter in the **Value (+/-)** field from the original thickness values. Enter a positive value to add to the thickness values, or enter a negative value to subtract from the thickness values.

6 Click **Compute** to calculate dose.

7 Continue to edit the compensator and compute dose until you are satisfied with the dose distribution.



8 If you selected the **Area** option in step 5 and drew contours and want to remove them from the image of the compensator, click the **Delete contour** tool and drag the cursor over any contours associated with the current ROI that you want to delete.

9 When you are finished editing the compensator, select **File – Save and Close Window** to save your changes and close the **Advanced Compensator Editor** window.

To close the window without saving your changes, select **File – Reject and Close Window**.

NOTE

The **Save and Close Window** option only saves the compensator for the current planning session. You must also save the trial when you exit the planning session to save the compensator to the trial.

10 When you are finished defining the compensator, we recommend that you lock the compensator to prevent unwanted changes to the shape of the compensator. Go to *Lock the compensator for proton beams*.

Change the display

- 1 Click the **Display** tab. The **Display** panel opens.
- 2 Drag the **Anatomy - Compensator** slider to change the opacity of the anatomy and the compensator in the viewing window.
- 3 Select **On** or **Off** in the **Beam Display** field to show or hide the beam in the viewing windows.
- 4 To view the thickness distribution of the compensator, click **Add a new isothickness** to add an isothickness line. A new row appears in the isothickness table.
- 5 Enter a thickness value in the **Isothickness** field.
- 6 To change the isothickness line display color, select a color from the **Color** list.

- 7 To turn the display of the isothickness line on or off, click **Display Color** for the isothickness line.
- 8 To remove an isothickness line from the display, select the line that you want to remove and click **Remove isothickness**.
- 9 To view the dose distribution, select an option from the **Isodose lines are** list.
 - **Percent of Max Dose**—The isodose lines are displayed as a percentage of maximum dose, and the maximum dose is listed.
 - **Percent of POI Dose**—The isodose lines are displayed as a percentage of the dose at a selected point of interest (POI). When you select the POI, the dose at that normalization point is displayed.
- 10 Click **Add a new isodose line** to add one isodose line, or click **Add/set lines at 98, 90, 80, ..., 20, 10%** to add multiple isodose lines at the percent of the dose normalization point you selected in step 9.

Rows are added to the isodose table. The dose distribution is displayed in the viewing window as per the dose percentage.
- 11 To change the value for an isodose line, type a new value in the **Value** field for that line.
- 12 To change the isodose line display color, select the color from the **Color** list for that line.
- 13 To turn the 2D display of an isodose line on or off, click **2D Display** for the line.
- 14 To display colorwash for the dose distribution, click **Yes** next to **2D Colorwash Display**.
- 15 To remove an isodose line, select the line that you want to remove and click **Remove isodose line**.
- 16 To change the orientation of the image in the second viewing window, select an orientation from the list below the viewing window.
- 17 If the orientation of the image in the viewing window is **Perpendicular BRV** and you want to change the rotation of the image, type a value in the **Display Rotation** field.

Lock the compensator for proton beams

When you are finished editing the compensator, we recommend that you lock the compensator to prevent unintended changes to the compensator.

- 1 In the **Beams** panel, click the **Setup** tab and then click **Details**.

The **Proton Beam Parameters** window opens.
- 2 In the **Beam** list, select the beam that contains the compensator that you want to lock.
- 3 Select **Yes** in the **Lock Compensator** field.

When the compensator is locked, you cannot make any changes to the compensator itself. In addition, you cannot change the snout, air gap, beam modality, or target ROI. You also cannot choose a different machine. You can change the other beam parameters, however.

Print compensators for proton beams

The compensator printing feature lets you generate a printout of the compensator so you can verify that the compensator produced by the software and the physical compensator that was milled using the same specifications are comparable prior to treatment.

- 1 Click **Print Compensator** in the **Compensator Editor** window. The **Compensator Printing** window opens.

NOTE

The dots in the **Compensator Printing** window represent the center of the milling bit. The shape of the snout, either circular or rectangular, is also displayed.

- 2 Set up the isothickness lines as needed before printing. For more information, see *Change the display*.
- 3 Click **Print**. The **Compensator Print** window opens.
- 4 Click **Select Printer** to select a printer. The **Color Printer Selection** window opens.
- 5 Select the printer that you want to use and click **Close**.
- 6 Click **Proceed** to print the compensator. The paper size and the number of pages to be printed are determined by the size of the compensator.

The printout represents the milling pattern. If you used the plunge milling technique, then the compensator is represented by circular milling bits in the printout. If you used the continuous milling technique, then the compensator is represented by continuous lines on the printout.

Display measurement points

The **Measurement Points** section of the **Compensator Printing** window lets you view different thicknesses across the compensator and their distances from the X and Y axes.



- 1 To view the thickness at a particular point, click the **Annotate compensator thickness** tool and click the point that you want to measure on the compensator. The thickness of the compensator at that point and the distance of that point from the X and Y axes are displayed in the **Measurement Points** section of the window and in the upper right corner of the compensator viewing window.



- 2 To delete an annotated point, click the **Delete annotation** tool and click the thickness and distance information that you want to delete in the upper right corner of the compensator viewing window.

Remove compensators from proton beams

The software adds a compensator to each double scattering beam and uniform scanning beam after you select a target ROI for the beam. If you do not want to use a compensator with a beam, you must manually remove the compensator from the beam.

- 1 Click the **Modifiers** tab in the **Beams** panel, and select the beam from the **Beams** list.
- 2 Click **Edit** in the **Compensator** section of the **Beams** panel. The **Compensator Editor** window opens.

- 3 Select **No** in the **Use Compensator** field. The software removes the compensator from the beam.

Set proton beam modifier information for export

If you enabled the export of DICOM sequences for lateral spreading devices and range modulators when you commissioned the machine in physics, you can define the information to be exported on the **Modifiers** tab of the **Beams** panel. The information differs based on the type of beam that you are defining.

Define export settings for a uniform scanning beam

If the current beam is a uniform scanning beam, the **Range Modulator Export Settings** section appears on the **Modifiers** tab. Specify the start and stop gating angles of the range modulator in the appropriate fields.

Define export settings for a double scattering beam

If the current beam is a double scattering beam, the **Range Modulator Export Settings** and **Lateral Spreading Device Export Settings** sections appear on the **Modifiers** tab.

- 1 In the **Range Modulator Export Settings** section, specify the start and stop gating angles of the range modulator.
- 2 In the **Lateral Spreading Device Export Settings** section, specify the settings for the lateral spreading devices. Type a value for each lateral spreading device based on the settings of your machine. Some machines require you to type “IN” or “OUT” while others require you to type a sequence of 0’s or 1’s, where “0” indicates an “OUT” setting and “1” indicates an “IN” setting. For example, if a lateral spreading device has plates set as “100”, this indicates that the first plate is “IN” and the other two plates are “OUT”. Refer to the documentation that was provided by the machine vendor to determine the correct value.

Define export settings for a spot scanning beam

If the current beam is a spot scanning beam, the list of lateral spreading devices that are defined for the machine appears on the **Modifiers** tab.

- 1 Select a device from the **Lateral Spreading Device Configuration** list.
- 2 In the **Settings** field, specify the setting for the lateral spreading device. Type a value based on the settings of your machine. Some machines require you to type “IN” or “OUT” while others require you to type a sequence of 0’s or 1’s, where “0” indicates an “OUT” setting and “1” indicates an “IN” setting. For example, if a lateral spreading device has plates set as “100”, this indicates that the first plate is “IN” and the other two plates are “OUT”. Refer to the documentation that was provided by the machine vendor to determine the correct value.

Bolus

The bolus feature can only be used with electron and photon beams.



CAUTION

Make sure you verify that the bolus is correct for your plan prior to using the bolus when treating the patient.

You can add boluses to the plan at any time. Boluses appear on the image as soon as they are created, and they are created at the resolution of the patient image data, not the dose grid. Boluses are generated independent of jaw size, so a bolus can be wider than the beam size, if necessary.

Before you create a bolus, try to remove artifacts from the area where you want to create the bolus. You can remove artifacts such as patient markers, CT artifacts, and immobilization devices by creating a contour around the artifact and then setting the density override value to 0. You can also contour the external patient outline, override the density outside of the contour, and set the density to zero. The software will create the bolus without including the artifacts in its calculations.

Bolus limitations

- When you add bolus to an electron beam, and the source to bolus distance is less than the SSDs included in your output factor table, monitor units will not be available. If you want to add a bolus that is closer than the minimum SSD defined for the machine, we recommend that you add data measured with SSDs less than the current minimum to your output factor table.
- You cannot build a bolus if it extends outside of the image set or if the image set has 2 rows and columns, or less, of pixels in the air space outside of the patient.
- You cannot build a constant-thickness bolus if the patient does not appear in the center of the image set. However, you can still draw the bolus manually using the **Create bolus point by point** tool. For more information, see *Variable thickness bolus*.
- You cannot build a bolus on a single-slice image set. If your plan uses a single-slice image set, you must create an additional slice superior and inferior to the contoured slice. The center slice must be thicker than the bolus will extend.
- A bolus cannot extend to cover any part of the most superior and inferior slices.
- The software invalidates the bolus if you do any of the following:
 - Move the couch removal plane so that it intersects with the bolus.
 - Restore or remove a stereotactic frame.
 - Change the outside-patient air threshold.
 - Change the CT to Density table.
 - Change the status of density override for one of the ROIs that the bolus intersects or touches.
 - Change the status of whether to load voxels **Inside ROI** or **Outside ROI** for one of the density-overridden ROIs.
 - Change the density across the patient-air threshold for one of the density-overridden ROIs that the bolus intersects or touches.

- Change the density unit so that the density changes across the patient-air threshold for one of the density-overridden ROIs the bolus intersects or touches.
- Change the shape of a density-overridden ROI that intersects or touches a bolus.

NOTE

If you open a plan that was created in Pinnacle³ 7.6 or earlier, boluses in the plan are invalidated. You must recreate the boluses in order to include them in the plan.

Add a bolus

- 1 On the **Modifiers** tab on the **Beams** panel, click **Edit** in the **Bolus** column at the bottom of the panel, or select **Options - Bolus**. The **Bolus** panel opens.
- 2 Click **Add Bolus**. The bolus options appear in the panel.
- 3 Change the name of the bolus in the **Name** field, if necessary.

NOTE

Use only alphanumeric characters and underscores when you name the bolus. Do not use the following characters: ' " ~ &) (| < > + * / \ ; : @ ! [] .

- 4 Create the bolus:
 - To create a constant thickness bolus, go to *Constant thickness bolus*.
 - To create a variable thickness bolus, go to *Variable thickness bolus*.

Constant thickness bolus

- 1 In the **Edit Options** section of the **Bolus** panel, select **Yes** in the **Constant thickness** field.
- 2 Do you want to create a bounding box to limit the data used to generate the bolus?
 - Yes—select **Yes** in the **Define skin boundaries** field and go to step 3.
 - No—select **No** in the **Define skin boundaries** field. The software will use data from the entire image set when it generates the bolus. Go to step 4.
- 3 Click the **Skin boundary** tool, then click and drag to draw a bounding box. The bounding box defines the patient surface area that will be covered by the bolus.



The software only uses data from inside the bounding box when it generates bolus, so you can use the bounding box to keep things such as CT artifacts and the couch from being used to generate the bolus.

NOTE

You can only draw the bounding box on a 2D transverse image. The software applies the bounding box when you define a bolus on a 3D BEV image, but the box itself does not appear in the 3D viewing window.

- 4 Do you want to define the bolus on a 2D transverse image or a 3D BEV?
 - If 2D transverse image, go to *Define bolus on 2D transverse image*.
 - If 3D BEV, go to *Define bolus on 3D BEV*.

Define bolus on 2D transverse image

NOTE

To define a wrap-around bolus, go to *Define wrap-around bolus*.



- 1 From the **Define bolus in** list, select **2D Transverse**.
- 2 Click the **Add bolus edge** tool.
- 3 On the transverse image, define the left and right edges of the bolus: Click and drag on the image to draw a line to define the left edge of the bolus, and then draw another line to define the right edge of the bolus. The edges of the bolus must be defined in a clockwise direction around the patient and must intersect the outside-patient air threshold.

The **Bolus edges defined on slice** field displays the slice on which the bolus is defined. Lines appear on the sagittal and coronal images to show the center, inferior, and superior borders of the bolus that will be built.



If you need to reposition a line, you must remove the line from the image and then redraw it. To remove a line, click the **Delete bolus edge** tool and then click and drag a rectangle around the line you want to remove. When you release the mouse button, the line disappears.

- 4 In the **Density** field, enter the density of the bolus.
- 5 In the **Thickness** field, enter the thickness of the bolus.
- 6 In the **Distance** fields, enter the distances that are needed between the current slice and the superior and inferior ends of the bolus.
- 7 Click **Build Bolus**. The bolus appears on the image. In addition, the 2D display option and additional buttons appear in the **Bolus** panel.

NOTE

If the software has difficulty finding the patient surface, adjust the outside-patient air threshold value and build the bolus again. See *Set the outside air threshold* in the *Setup* chapter.

NOTE

When the software begins to build the bolus, a **Cancel** button appears next to the **Build Bolus** button. Click **Cancel** to stop the build process, if necessary.

- 8 Click the 2D display option to turn on and turn off the bounding box.

For information about the buttons that appear on the **Bolus** panel or to edit the bolus, go to *Edit a bolus*.

Define wrap-around bolus

- 1 From the **Define bolus in** list, select **2D Transverse**.
- 2 In the **Encompass data** field, select **Yes**.
- 3 In the transverse viewing window, display the slice you want to use as the center slice for the bolus.
-  4 Click the **Select the center slice** tool, and click on the transverse image to select that slice as the center slice. The slice number displays in the **Selected center slice** field. The bolus will extend in the superior and inferior directions from this slice.
- 5 In the **Density** field, enter the density of the bolus.
- 6 In the **Thickness** field, enter the thickness of the bolus.
- 7 In the **Superior Distance** field, enter the distance that is needed between the center slice and the superior end of the bolus.
- 8 In the **Inferior Distance** field, enter the distance that is needed between the center slice and the inferior end of the bolus.
- 9 Click **Build Bolus**. The bolus appears on the image. In addition, the 2D display option and additional buttons appear in the **Bolus** panel.

NOTE

If the software has difficulty finding the patient surface, adjust the outside-patient air threshold value and build the bolus again. See *Set the outside air threshold* in the *Setup* chapter.

NOTE

When the software begins to build the bolus, a **Cancel** button appears in place of the **Build Bolus** button. Click **Cancel** to stop the build process, if necessary.

- 10 Click the 2D display option to turn on and turn off the bounding box.

For information about the buttons that appear on the **Bolus** panel or to edit the bolus, go to *Edit a bolus*.

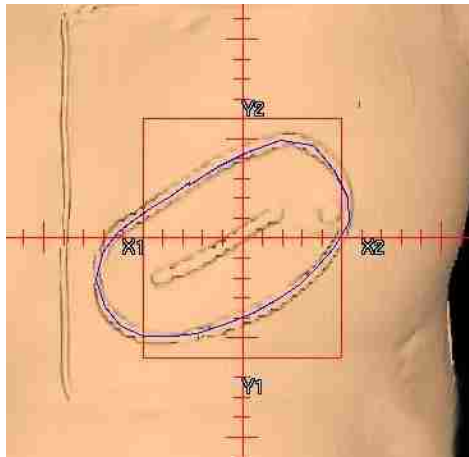
Define bolus on 3D BEV

- 1 From the **Define bolus in** list, select **3D BEV**.

- 2 Set up a BEV window for the current beam. You can use any of the BEV options (**DRR**, **DCR**, **2D Orthogonal Plane**, or **3D Image**).

NOTE

The **DCR** option is only available if you are licensed for AcQSim³.



- 3 Click the **Create bolus point by point** tool to define the contour of the bolus.
- 4 Click on the BEV where you want to start the contour. A small box appears and indicates the point you defined. Define the remaining points in the same manner. You can also click and drag a point to the position you want.

NOTE

Any points drawn outside the patient data will not be used to generate the bolus.

- 5 To close the contour, click the first point you defined. The small boxes disappear.

NOTE

The bolus contour is displayed based on the selected beam's BEV coordinate system, so any changes you make to the selected beam's geometry (couch angle, gantry angle, or collimator angle) after the contour is drawn will change the position of the bolus relative to the patient data, even if you do not change the shape or location of the contour. Once the bolus is built, the bolus is fixed to the patient data coordinate system, and changes to the selected beam's geometry or selecting a different beam will not affect the bolus.

- 6 If you need to delete the contour, click **Delete Curve**.
- 7 In the **Density** field, enter the density of the bolus.
- 8 In the **Thickness** field, enter the thickness of the bolus.
- 9 Click **Build Bolus**. The bolus appears on the image. In addition, the 2D display option and additional buttons appear in the **Bolus** panel.

NOTE

If the software has difficulty finding the patient surface, adjust the outside-patient air threshold value and build the bolus again. See *Set the outside air threshold* in the *Setup* chapter.

NOTE

When the software begins to build the bolus, a **Cancel** button appears in place of the **Build Bolus** button. Click **Cancel** to stop the build process, if necessary.

- 10 Click the 2D display option to turn on and turn off the bounding box.

For information about the buttons that appear on the **Bolus** panel or to edit the bolus, go to *Edit a bolus*.

Variable thickness bolus

NOTE

You can display a grid on a 2D image to help you draw the bolus. To display the grid, right-click in a 2D viewing window and select **2D - 2D Measurement Grid On**. You can change the size of the grid in the **Preferences** window. For more information, see the *View Patient Data* chapter.

- 1 In the **Edit Options** section of the **Bolus** panel, select **No** in the **Constant thickness** field.

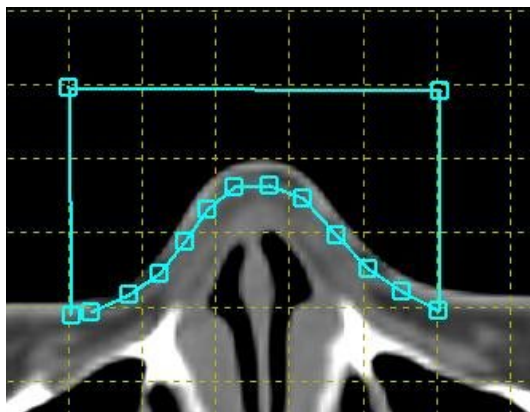


- 2 Click the **Create bolus point by point** tool to define the contour of the bolus.

NOTE

The contour of the bolus must intersect the outside-patient air threshold at two locations.

- 3 Click on the image where you want to start the contour. A small box appears and indicates the point you defined. Define the remaining points in the same manner. You can also click and drag a point to the position you want.

**NOTE**

Any points drawn outside the patient data will not be used to generate the bolus.

- 4 To close the contour, click the first point you defined. The small boxes disappear. The slice number on which the contour is defined displays in the **Bolus edges defined on slice** field.
- 5 If you need to delete the contour, click **Delete Curve**.
- 6 In the **Density** field, enter the density of the bolus.

- 7 In the **Superior Distance** field, enter the distance you want between the current slice and the superior end of the bolus.
- 8 In the **Inferior Distance** field, enter the distance you want between the current slice and the inferior end of the bolus.
- 9 Click **Build Bolus**. The bolus appears on the image and additional buttons appear in the **Bolus** panel. For information about these buttons or to edit the bolus, go to *Edit a bolus*.

Edit a bolus

Once you have built a bolus, you can edit it to remove contours, smooth edges, or change the contour of the bolus. You can also convert a constant thickness bolus to a variable thickness bolus.

NOTE

Bolus contours must appear on contiguous slices. You cannot create a contour on a slice that would leave an empty slice in the bolus, and you cannot delete a slice from the middle of a bolus.

Invalidate a bolus

If you need to change the parameters of the bolus, click **Invalidate Bolus**. The edge markers or contours you defined remain on the image, as does the bounding box. Change the parameters as necessary, and then click **Build Bolus**.

NOTE

If you invalidate a bolus that has been applied to a beam, the bolus is no longer applied to any beam. Make sure you reapply the bolus to a beam after you build the bolus again.

Remove contours

Click **Delete Superior End** to remove the first contour on the superior end of the bolus.

Click **Delete Inferior End** to remove the first contour on the inferior end of the bolus.

You can click the buttons repeatedly to remove more than one contour.

Delete a bolus

To delete a bolus, click **Delete Bolus**. The bolus and the bounding box are removed from the image, and the name of the bolus is removed from the **Bolus** list.

Clean a bolus

The **Clean Bolus** feature lets you remove very small curves from your bolus.

- 1 Click **Clean Bolus**. The **Bolus Curve Cleanup Results** window opens.
- 2 In the **Minimum Bolus Curve Area** field, enter the necessary minimum bolus curve area.
- 3 Click **Scan Bolus**. The software searches the bolus for curves that are smaller than the minimum bolus curve area you specified and displays these curves in the **Bolus Curve Cleanup Results** window.
- 4 Click **Delete Problem Curves** to delete the curves that are listed in the window.

NOTE

If you modify the bolus after cleaning it, you may need to clean it again.

Convert a bolus to a variable thickness bolus

Click **Set to Variable** to convert a constant thickness bolus to a variable thickness bolus. You can now edit the bolus with the tools available for editing a variable thickness bolus.

Edit a variable thickness bolus

Use the **Create bolus paintbrush** tool to edit the shape of a variable thickness bolus. This tool appears after you build a variable thickness bolus or convert a constant thickness bolus to a variable thickness bolus.

NOTE

You can display a grid on a 2D image to help you edit the bolus. To display the grid, right-click in a 2D viewing window and select **2D - 2D Measurement Grid On**. You can change the size of the grid in the **Preferences** window. For more information, see the *View Patient Data* chapter.



- 1 Click the **Create bolus paintbrush** tool.
- 2 Position the cursor at the point where you want to start, edit, or delete a contour.
- 3 Use one of the following methods to edit the contour.
 - If you click on a section of the image where there is no bolus, a new, circular bolus appears. Click and drag to create a thick line; wherever you move the cursor, the circle is filled in for the bolus.
 - If you click inside an existing bolus, you can push out the edges of the bolus.
 - If you click outside, but near, an existing edge of the bolus, the tool functions as an eraser, and the bolus is erased wherever you move the cursor. You can use this method to push in the edges of the bolus.

NOTE

If the diameter of the paint brush is too large or too small, enter a new diameter value in the **Diam (mm)** field.

- 4 When you finish editing the contour, go to the next slice on which you want to edit the shape of the bolus and repeat the process.

Add a scanned bolus

If the image set includes a bolus in the CT scan, you can add a scanned bolus to a beam so that the DICOM export will indicate that a bolus was present in the scan. A scanned bolus is a virtual bolus that is created as a ROI with a volume of zero. The density and thickness values of the scanned bolus are set to zero so that the bolus will not impact the dose computation. You cannot change the density or thickness values, or any of the other parameters, for a scanned bolus.

- 1 In the **Modifiers** tab on the **Beams** panel, click **Edit** in the **Bolus** column at the bottom of the panel, or select **Options - Bolus**. The **Bolus** panel opens.
- 2 Click **Add Scanned Bolus**. A new bolus is added to the **Bolus** list, and **_Scanned** is appended to the name of the bolus to indicate that it is a scanned bolus.
- 3 Change the name of the bolus in the **Name** field, if necessary.

NOTE

Use only alphanumeric characters and underscores when you name the scanned bolus. Do not use the following characters: ' " ' ~ &) (| < > + * / \ ; : @ ! [] .

- 4 To delete a scanned bolus, go to *Delete a bolus*. To apply the scanned bolus to a beam, go to *Apply a bolus to a beam*.

Apply a bolus to a beam

You must apply a bolus to one or more beams in order to include the bolus in dose calculations.

- 1 In the **Bolus** list, select the bolus that you want to apply to a beam.
- 2 In the **Beam** list, click in the **Apply current bolus?** column to toggle the **Yes/No** option for the beam to which you want to apply the bolus. If **Yes** appears next to a beam, then the bolus is applied to that beam.

You can apply the same bolus to multiple beams, and you can apply multiple boluses to one beam. However, if you create overlapping boluses, the overlapping boluses cannot be applied to the same beam.

Once you apply a bolus to a beam, the **SSD With Bolus** value displays on the **Setup** tab in the **Beams** panel.

NOTE

If you invalidate a bolus that has been applied to a beam, that bolus is no longer applied to any beam. Make sure to reapply the bolus to a beam after you build the bolus again (or reapply the scanned bolus directly to a beam). Also, dose for the beam is invalidated when a bolus is invalidated.

NOTE

For IMRT plans, if all of the beams that will be optimized are not applied to the same bolus(es), or if some of the beams have bolus applied and some do not, the optimization will be significantly slower than if all of the beams have the same bolus(es) (or no bolus) applied to them.

- 3 To display a list of the boluses applied to a beam, go to the **Beams** panel and select the beam from the **Beams** list. Then, from the **Modifiers** tab, click **List** in the **Bolus** column at the bottom of the panel.

The **Beam Reliant Boluses** window opens.

Bolus display options

The bolus display options (**Color**, **2D Display**, **3D Display**, **Box Size**, and **Line Size**) function the same as the display options for ROIs. For information about the display options, see *Change the ROI display* in the *Regions of Interest* chapter.

NOTE

The mesh options and the **Display outline in BEV DRR** field described in the *Change the ROI display* section do not apply to bolus.

Bolus report

The plan printout contains a separate bolus information page that includes the thickness of each bolus (or “None” if the bolus is variable thickness), the density of each bolus, and the beams to which the boluses are applied. The SSD with bolus value appears in the Beam Geometry section of the plan printout.

11 Calculate Dose

Overview

Once the beams are set up as desired, you can specify the dose grid and compute dose for the plan. If you want to change the dose computation options, such as homogeneous or heterogeneous dose, you can do so using the dose computation parameters. You can also set the prescription and optimize the beam weights to that prescription.

The basic process for computing dose is:

- 1 Set up the dose grid (this includes defining the grid and setting its resolution)
- 2 Extend the image set (if necessary)
- 3 Set the dose computation parameters
- 4 Compute dose
- 5 Set the prescriptions
- 6 Assign beams to prescriptions
- 7 Set the beam weighting

If your plan contains records, you can display the dose from those records to assess the impact of the prior dose on the current trial. See *Assess the impact of prior dose*.

NOTE

Dose can be displayed in either cGy or Gy. The dose display preference is set in the **Preferences** window. If you are licensed for proton treatment planning, all dose quantities are presented in units of cGy (RBE) or Gy (RBE). This chapter uses cGy when referring to dose.



CAUTION

If you purchase Pinnacle³ without the dose calculation features and you try to open a plan that already has dose computed, you will get an error message that dose will be invalidated. You can still view the plan. If you do not save the plan, the dose will still be intact. If you save the plan, you will have to go back into Pinnacle³ (with dose) to recompute dose. We recommend that you make a copy of the plan and work on the copy so the dose in the original plan does not get invalidated.



Click on the **Dose** button at the top of the window to see the dose computation options.

Dose

All dose in Pinnacle³ is presented in terms of cobalt-equivalent effective dose, and not physical dose. The two doses are related through the Relative Biological Effect (RBE) factor. For photon and electron beams, the two doses are numerically equivalent because the RBE factor is 1. That is not the case for proton beams.

When the system is not licensed for proton treatment planning, dose is presented as cGy or Gy because the RBE is 1. When the system is licensed for proton treatment planning, all dose quantities in Pinnacle³ are presented in units of cGy (RBE), according to the convention described in “The RBE issues in ion-beam therapy: conclusions of a joint IAEA/ICRU working group regarding quantities and units,” A. Wambersie, et. al, *Radiation Protection Dosimetry*, 122:463-470 (2006). Because the software uses this approach, you can create composite plans that include beams from protons, as well as other modalities, so that you correctly account for the biological effect of the entire course of treatment in the total dose.

Pinnacle³ does not directly calculate beam quantity calibration coefficients (dose per MU) for proton beams. You must enter a coefficient value that you calculate or measure outside the system in order to calculate absolute dose. It is important that the value that is entered is the effective dose per MU, taking the RBE into account. The value should not be obtained from a measured physical proton dose.

The prescription associates a dose value in cGy to a point at which the cGy/MU is known or to some other known cGy/MU value such as the maximum dose. The total monitor units required to produce the prescribed dose can be computed and divided between the beams based on the beam weights. You can create multiple prescriptions for a plan to determine the total dose from an initial treatment and a boost, or from a prior treatment and a current treatment.

Photon-specific dose information

While it can be difficult to manually compute the monitor units in a complex patient geometry, the software lets you analyze how the patient anatomy affects the final monitor unit calculation. You can trace through the changes in dose and monitor units as the patient surface curvature is considered, then as the primary scatter is modified by patient density, and finally as the secondary scatter is modified by heterogeneities. After performing a full 3D computation, you can turn off the heterogeneity corrections for the secondary scatter computation and recompute the monitor units. This gives the change in monitor units due to the effects of the patient density on secondary scatter. Similarly, the dose can be recomputed with heterogeneity corrections turned off for the primary TERMA computation, and the effect of the patient density on the primary dose can be assessed. Finally, the flat water phantom option allows the dose to be computed without any corrections for curvature of the patient surface. This final computation will match a simple manual computation for the water phantom.

The following dose engines are available:

- **Fast Convolve** computation performs a convolution superposition calculation with fewer ray directions used for the scatter calculation than are used for **Adaptive Convolve** computation. The **Fast Convolve** computation is less accurate near the surface and in the penumbra region, with the maximum error typically being less than 5%. The software does not let you use this dose engine to compute dose for use clinically.
- **Adaptive Convolve** computation performs adaptive sampling during convolution dose calculation. Use this engine to reduce computation time by sampling every fourth point in the dose grid and interpolating dose in flat areas. If the dose grid cannot be interpolated accurately enough by sampling every fourth point, the software automatically switches to **CC Convolution** and samples every point in the dose grid.

- **CC Convolution** computation performs a full convolution superposition calculation. We recommend that you use this option for all monitor unit calculations.

Set up the dose grid



CAUTION

Before computing dose, you must specify the size and location of the dose grid. The allowable size of the dose grid is dependent on the amount of RAM in your system. If an error message indicates that there is insufficient memory to create the dose grid, decrease the size or resolution of the dose grid.

Use the 3D dose grid to specify where in the patient you want dose to be computed. The dose grid also specifies the resolution to use for dose computation.

Placement of the dose grid is as important as the grid resolution. You can define the dose grid manually or place the grid automatically to cover a range of slices.



CAUTION

Position the dose grid to cover all critical structures. Otherwise, you may not have enough information to properly assess the plan. Dose volume histograms might be calculated erroneously if the entire region of interest is not included in the dose grid.

Manually place the dose grid



- 1 Click **Dose** at the top of the window to display the **Dose** panel.



- 2 Select the **Draw dose grid** tool.

If a dose grid already exists for the plan when you select this tool, the grid is displayed as a dashed green line on the 2D patient images.

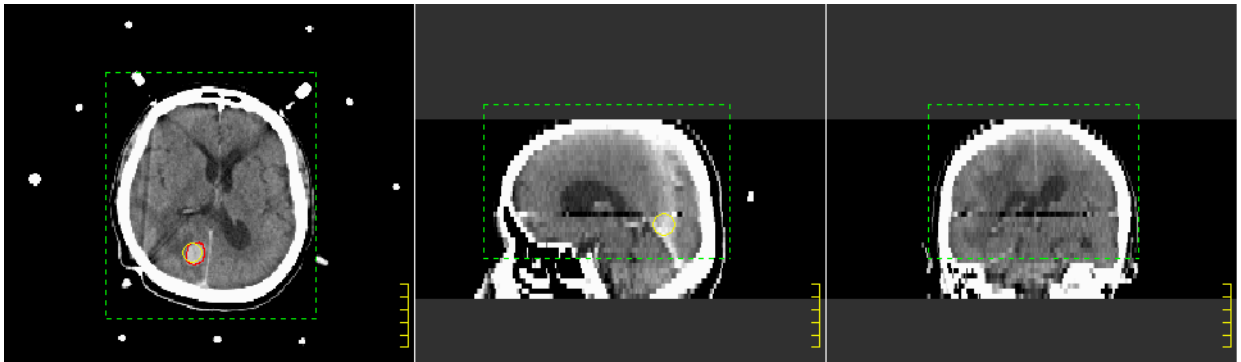
NOTE

If you do not see the dose grid on the display, it may be because the displayed image does not lie within the dose grid. Scroll through the 2D images until you see the dashed green line that indicates the dose grid.

If prior dose is included, the boundary of the dose distribution for each record that is included in prior dose is displayed with a thick orange line. If more than one record is included in prior dose, a separate thick orange line is displayed for each boundary. See *Assess the impact of prior dose*.

- 3 Define the lateral and anterior-posterior dimensions of the dose grid by drawing the dose grid in a transverse slice. Drag diagonally to draw the dose grid.
- 4 To define the superior-inferior dimensions of the dose grid, draw the dose grid in either a sagittal or coronal 2D slice.

The following figure shows the dose grid displayed in all three orientations. You may find it easier to see the dose grid with the 2D beam display turned off.



- 5 If you need to adjust the placement of the dose grid, select the **Move dose grid** tool and drag the grid to the desired location.

Automatically place the dose grid

Cover a range of slices

Click **Cover Range of Slices**. The **Automatic Grid Placement** window opens. Enter the slices to cover in the fields, and then click **OK**.

Cover a specific region of interest

- 1 Click **Cover Selected ROIs**. The **Automatic Grid Placement Using Target** window opens.
- 2 In the **Specify ROI to cover** field, select the region of interest that should be contained within the dose grid.
- 3 In the **Additional padding** field, set the additional amount of space that should be contained within the dose grid outside of the area of the region of interest.
- 4 Click **OK**.

Set the dose grid resolution

The dose grid resolution specifies the size of the voxels for which the dose is computed. The dose grid dimensions and origins are set when you place the dose grid.

When you set up the dose grid resolution, there is always a trade-off between high resolution and computation time. To get better resolution, the voxel size must be decreased. This increases the number of voxels required to cover all of the regions of interest and increases the amount of time required to compute dose.

Dose grid resolution also affects how quickly a plan opens. For example, if you compute dose for a plan with a dose grid resolution of 0.3 cm³, save and exit the plan, and then reopen the plan, the plan could take several minutes to load. We recommend that you use a dose grid resolution of

0.4 cm³ for preliminary dose computations, and then increase the dose grid resolution to 0.3 cm³ for the final dose computation.

Using an unnecessarily large dose grid can also increase the calculation time without yielding any additional information for plan evaluation. For example, if the dose grid extends 5 cm beyond the patient in the lateral, anterior, and posterior directions, a significant percentage of the dose calculation time may be spent calculating dose in the air surrounding the patient.



WARNING

Using a coarse dose grid resolution provides less accurate monitor unit calculations than the default or higher-resolution dose grids. A dose grid resolution of 0.4 cm³ or smaller is recommended. If the resolution is greater than 0.5 cm in any dimension, monitor units appear with a tilde (~) to indicate that the values are approximate.

You can use the default dose grid resolution settings (0.4, 0.4, 0.4) for most dose computations. For smaller field sizes, you may need a smaller voxel size (higher resolution). For plan evaluation, you could use a low-resolution dose grid (0.5 to 1.0) to quickly obtain a general idea of the dose distribution for a given plan. However, using a low resolution provides less accurate results.

NOTE

If the current trial contains proton beams, you will not be able to compute dose for the proton beams if you set a dose grid resolution that is coarser than 0.4 cm in any dimension.



CAUTION

The dose grid resolution must be an even multiple of the density/fluence grid resolution, and different dimensions can have different voxel sizes. If you enter an invalid resolution, Pinnacle³ will not allow you to compute the dose.

If the density/fluence grid resolution matches the dose grid resolution, changing the resolution of either grid can adversely affect the accuracy at each point.

You can also specify the resolution of the density/fluence grid. For example, if a coarse dose grid is adequate for your plan, but the dose at each point in the grid must be accurate, you need to set a high-resolution density/fluence grid. To make the density/fluence grid match the dose grid, choose the **Match Dose Grid** option in the **Density/Fluence Grid Resolution** field.

Extend the image set

Ideally, a plan image set extends far enough above and below the beams so that dose calculations are correct with respect to primary and scatter effects. However, if the patient image set is not large enough, you can extend it on both ends by extrapolating the end CT slices for dose calculation.

Although there is no display of the additional slices, the software extends the density information in the top and bottom slices of the image set by the specified number of centimeters. This density information is included in the dose calculations.

Be aware that extending the image set increases computation time. If the image set does not need to be extended, set the top and bottom values to 0. If the image set needs to be extended in only one direction, set the value in the opposite direction to 0.



WARNING

Make sure you will not affect the accuracy of the dose computations before selecting extension values for a plan. If you are treating using vertex fields, extending the image set in the superior direction could result in misleading SSD and dose calculations. If you think you may use non-coplanar or vertex fields, you should acquire CT data that extends to the top of the head, and you should make sure the image set extension in the superior direction is set to 0.

NOTE

You can also use this feature to extend image sets for contour-based planning. But if no density is defined for either of the end slices, extending the image set has no affect on the scatter dose and the extension results in larger MUs.

- 1 In the **Extend top slice of CT** field, enter the number of centimeters to extend the top slice beyond the end of the image set.
- 2 In the **Extend bottom slice of CT** field, enter the number of centimeters to extend the bottom slice beyond the end of the image set.

The effects of dose grid geometry on dose calculation time

For details on these effects, see the *Pinnacle³ Planning Reference Guide*.

Set the dose computation parameters

The dose computation parameters control how dose is computed. The dose computation options vary depending on the treatment modality.

For all beam types that are not proton beams, see the following sections for dose computation options.

For proton beams, the dose computation parameters cannot be modified. For double scattering beams and uniform scanning beams, the dose engine is always **Pencil Beam**. For spot scanning beams, the dose engine is always **Spot Scanning**. For all proton beams, the density correction is always heterogeneous.

Select the dose engine

You can select the dose engines for the beams without setting all of the specific dose computation parameters. In the **Dose Computation** section of the **Dose** panel, select a dose engine for each beam from the beam's dose engine list. The engine is assigned to the beam with the default dose parameters.

See the *Overview* section for more information about each type.

Set all the parameters



CAUTION

Unless you specify otherwise, all dose calculations for photon and electron beams assume a heterogeneous patient.

- 1 From the **Dose** panel, select **Options - Dose Comp Parameters**. The **Dose Computation Parameters** window opens.
- 2 From the **Beam** list, select the beam you want to set.
- 3 Select the correct dose engine.
- 4 For the type of beam, set the appropriate dose parameters.

**CAUTION**

The Zenith and Azimuthal Bin Count parameters set the number of ray directions for the scatter calculation in polar coordinates. You cannot change these settings.

Photon beam	Electron beam	Stereotactic beam
In the Primary Homogenous and Scatter Homogeneous fields, specify the density correction for each calculation. See <i>Photon density correction options</i> for more information.	In the Density Correction field, specify whether the computation should be heterogeneous (density correction) or homogeneous (no density correction).	In the Arc Increment for Dose Computation field, set the distance (degrees) between sub-beams.
In the Arc Increment for Dose Computation field, set the distance (degrees) between sub-beams for photon arcs.		

NOTE

A greater number of degrees for arcs will speed up dose calculations because dose is calculated less frequently in each arc. However, as the number of degrees increases, the accuracy of the dose decreases.

Photon density correction options

**CAUTION**

The Water Phantom at SSD option is not intended to be used for clinical dose calculations. If you use this option when the field edge lies outside the density grid, the software will not allow dose computation.

For photon beams, these are the density correction options:

- **Primary Homogeneous**—The primary fluence portion of the convolution superposition computation ignores all heterogeneities in the patient and instead uses a density of 1.0 gm/cm³ throughout the patient.
- **Scatter Homogeneous**—The scatter portion of the convolution superposition computation ignores all heterogeneities in the patient and instead uses a density of 1.0 gm/cm³ throughout the patient.
- **Water Phantom at SSD**—The dose is computed for the beam in a flat water phantom positioned at the beam's SSD.

Compute dose

Dose is computed for each beam individually. If you modify a beam after computing dose, only the modified beam must be recomputed.



WARNING

You should use Adaptive Convolve or CC Convolution for photon beam monitor unit calculations. Fast Convolve dose calculation is designed for use during plan evaluation; using Fast Convolve or a dose grid resolution of more than 0.5 cm in any dimension adversely affects the accuracy of monitor units. In such cases, monitor units appear with a tilde (~) to indicate that the values are approximate.



CAUTION

Before computing dose you must specify the dose grid size and location. Also, you cannot compute dose (profiles or output factors) for a machine that has output factors or measurement geometries with jaw setting violations.



CAUTION

Currently, the software computes only relative dose for Cobalt 60 machines. At this time, absolute dose calculation for Cobalt 60 is not supported because the software reports machine controls in monitor units only, does not handle source decay for teletherapy sources, and does not handle corrections for timer error.

- 1 In the **Dose Computation** section of the **Dose** panel, make sure the appropriate dose engine is selected for each beam.
- 2 Do you want to compute dose for all of the beams?



- If yes, click **Compute** for the first beam, then click **Redo Spreadsheet** to trigger dose calculation for all of the other beams.
- If no, click **Compute** for the beam for which you want to compute dose.



CAUTION

If any parameter which affects dose is modified during dose computation, the computation is cancelled for the beam.

You can continue to work in the software during dose computation. After dose calculation has started, the **Compute** button turns into a **Cancel** button which you can click at any time to cancel the dose computation. The word **Done** appears in place of the **Cancel** button when dose computation is complete.

For spot scanning beams: During the commissioning of a spot scanning machine, the minimum and maximum Z-plane values are defined. These values indicate the range of the beam within which the in-air fluence models are valid for dose computation. In some instances, the setup of the plan and the spot scanning beams may be such that dose needs to be computed in a Z plane that lies outside of the minimum and maximum Z-plane values that were defined during commissioning. If this occurs, a warning message appears indicating that dose could not be computed. The best way to correct the problem is to increase the distance between the minimum and maximum Z-plane values in the machine model and commission the machine again. If this is not practical, you can shift the location of the isocenter along the beam axis, or

you can decrease the dimensions of the dose grid or change the location of the dose grid so that the entire dose grid lies within the range of the Z-plane values.

Set the prescriptions

You can prescribe dose before or after dose computation. If you change the prescription after dose computation, the dose values are retained and recalculation is not required.

You can create multiple prescriptions for a plan, allowing you to determine the total dose from an initial treatment and a boost, or the total dose from a prior treatment and a current treatment. You can also copy a beam to other beams and split the dose among them, or adjust the prescription.

The software computes dose as cGy/MU. The prescription associates a dose value in cGy to a point at which the cGy/MU is known or to some other known cGy/MU value such as the maximum dose. The total monitor units required to produce the prescribed dose can be computed and divided between the beams based on the beam weights.

NOTE

If you are licensed for proton treatment planning, dose is computed as cGy (RBE)/MU. For more information, see *Dose*.

When prior dose is included for the selected trial, the prior dose information is included in the **Description** column for the prescriptions in the **Prescriptions** window. In addition, the **Prior Dose** section of the **Prescriptions** window displays the prescriptions from records that are included in prior dose. See *Assess the impact of prior dose*.



CAUTION

If you do not specify a prescription prior to dose calculation, a default prescription (200 cGy to the maximum dose for a single fraction) is used initially. You should change to the correct value before finishing the plan.



CAUTION

Dose can be misleading if computed with a prescription that is beyond the machine's limitations. In the physics tool, you must specify limits for monitor units and also specify whether to allow these limits to be exceeded for a machine.

If the software is set up so that the limits cannot be exceeded and the prescribed dose requires a monitor unit setting which exceeds the limits, the monitor units are set to the limits and the actual dose may not match the prescription. When this occurs, the Monitor Units are highlighted in red.

If a beam has invalid MUs, and multiple beams are assigned to more than one prescription, then the software will not calculate a total dose. If all of the beams have invalid MUs, the isodose lines and point dose readings are percentages. If all of the beams are assigned to the same prescription and a beam has invalid MUs, the software displays relative dose and dashes (--) for the beam weights.

Prescribe dose

- 1 Click **Edit Prescriptions** in the **Dose** panel, or press **Ctrl + P**. The **Prescriptions** window opens.

When dose is computed, the **Description** indicates the actual dose computed by the system. The **Monitor Units per Fraction** and **Total Fractions** columns indicate the actual MUs per

fraction and total number of fractions. Because MUs may be constrained values, the actual dose may differ slightly from the prescribed dose.

- 2 Select the appropriate trial from the list at the top of the window.
- 3 Add or edit a prescription:
 - Add—Click **Add**. A new prescription is added to the list. In the **Name** field, type a new name for the prescription.
 - Edit—Go to step 4.
- 4 Select a prescription and then click **Edit**. The **Edit Prescription** window opens.
- 5 In the **Prescribe** field, type the dose in cGy or Gy and specify whether it should be the overall (total) dose or dose per fraction.



CAUTION

Maximum dose refers to the absolute maximum for the entire 3D volume of the patient, not for a given slice. Verify that your prescription is correct for the patient volume.

- 6 Use the table below to set up your prescription.

Prescribe to max dose	Prescribe to an ROI	Prescribe to a POI
In the Prescription percentage field, set the percentage of the maximum dose to receive this prescription.	In the Prescription percentage field, set the percentage of the ROI minimum, maximum, or mean dose to receive this prescription.	In the Prescription percentage field, set the percentage of the point dose to receive this prescription.
Select Max Dose as the Percentage of option.	Select ROI Min , ROI Max , or ROI Mean as the Percentage of option. Select the region of interest. The MU for each beam assigned to the prescription is set to deliver the specified minimum, maximum, or mean dose to the selected region of interest. Relative beam weights are proportional to MUs when you prescribe to an ROI.	Select Point Dose as the Percentage of option. Select the point of interest to be used as the prescription point. Only POIs that are assigned to the primary image set appear in the list. Select the proportional beam weighting option. When the beam weights are proportional to MUs, the total monitor units delivered to the point is divided among the total number of beams based on the beam weights. When the beam weights are proportional to point dose, the contribution of each beam's dose to the total point dose is proportional to each beam's weight. If you change the proportional beam weighting option after you assign beam weights, the software may adjust the relative beam weight values in order to maintain the same dose and monitor units.

- 7 In the **Number of Fractions** field, type the total number of fractions.
- 8 Click **Close**. The list of prescriptions for the trial is updated to reflect your changes.

- 9 By default, the first prescription listed in the **Prescriptions** window is designated as the current prescription. All new beams that you add to the trial will be assigned to that prescription. If you have multiple prescriptions and want to change the current prescription, click the radio button to the left of the prescription that you want to set as the current prescription.

Set total monitor units

- 1 In the **Edit Prescription** window, select the **Set Monitor Units** option.
- 2 In the **Total Monitor Units** field, type the number of monitor units per fraction.
- 3 In the **Number of Fractions** field, type the total number of fractions.
- 4 Click **Close**.

NOTE

If the prescription changes, the software updates the value in the **Total Monitor Units** field to indicate the actual number of monitor units in the prescription.

Assess the impact of prior dose

Note

The prior dose feature is available only if you are licensed for Dynamic Planning.

If your plan contains records, you can include the dose from those records to assess the impact of prior dose on the current trial.

In order to include dose from a record, the record must meet the following requirements:

- Either the secondary image set that is associated with the record has been rigidly registered or deformably registered to the primary image set (and the registration has been approved), or the record was created by accumulating dose or importing dose to the primary image set.
- The record does not have **No** in either the **Selected for Treatment** or **Clinically Valid** columns in the **Manage Prior Dose** window.
 - The **Selected for Treatment** column indicates whether the trial that was used to create the record was selected for treatment in the original plan. (If the original plan had only one trial, it is automatically selected for treatment.)
 - The **Clinically Valid** column indicates whether the trial that was used to create the record was included the statement NOT FOR CLINICAL USE in the original plan.

See *Deformable image registration* and *Use the Record Viewer and the Treatment Navigator*.



CAUTION

Verify that records where the **Selected for Treatment** value is **Yes** represent trials that were actually delivered clinically. The **Selected for Treatment** value is confirmation only of the trial being selected for treatment in the original plan, not of treatment delivery.

- 1 Click **Edit Prescriptions** in the **Dose** panel. Or, in the **Plan Evaluation** window, click **Prescriptions** on the **Options** menu. The **Prescriptions** window opens.
- 2 In the **Dose Display Mode** section at the bottom of the **Prescriptions** window, select the appropriate option:
 - **Current Dose Only**—Include only computed dose for the current trial. No prior dose is included.
 - **Prior Dose Only**—Include only prior dose. No dose for the current trial is included.
 - **Current Dose and Prior Dose**—Include both computed dose for the current trial and prior dose.
- 3 If you chose **Prior Dose Only** or **Current Dose and Prior Dose**, click **Manage Prior Dose** to select the record dose to include. The **Manage Prior Dose** window opens.
- 4 If you want to scale the record dose before including it in prior dose, set the **Scale Mode**:
 - **Scale Factor**—Type a scale value. The record dose that will be included in the prior dose is the record dose multiplied by the scale value.
 - **Fractions Delivered**—Type the number of fractions that were delivered. The record dose that will be included in the prior dose is the dose that was delivered in that number of fractions. This option is only available if a record contains a **Total Fractions** value and if each record has a single prescription.

- 5 Select the record dose that you want to include in the prior dose by selecting an option from the **Include** column for each record:
 - **Rigid**—Include the record dose without deformation. For secondary image sets, this option appears only if you have approved the rigid registration in the **Syntegra** window. See *Registration QA tools*.
 - **Deformed**—Include the record dose with deformation. This option appears only if you have approved the deformation in the **Syntegra** window. See *Registration QA tools*.
 - **None**—Include no dose from this record.

NOTE

To include dose from records that you created either by accumulating dose or importing dose to the primary image set, select **Rigid** in the **Include** column.

- 6 Click **Close** to close the **Manage Prior Dose** window. The **Prior Dose** section of the **Prescriptions** window indicates the records that are selected for prior dose, and the **Description** text for the prescription indicates that prior dose is included.
- 7 Click **Close** to close the **Prescriptions** window.

When prior dose is included, the following information is provided in the software:

- In 2D and 3D viewing windows, the **Dose Display Mode** (either **Prior Dose Only** or **Current Dose and Prior Dose**) displays in the upper-left corner of the window.
- The boundary of the dose distribution for each record that is included in prior dose is displayed on 2D viewing windows. The boundary is displayed with a thick orange line, and the boundary is displayed only on the primary image set and only when the trial dose grid is displayed. If more than one record is included in prior dose, a separate thick orange line is displayed for each boundary. See *Set up the dose grid*.
- Indicators appear in the **Scorecard** window, **Planar Dose** window, and the **Dose Volume Histogram** and **Biology** panels of the **Plan Evaluation** window. See *Evaluate trials with a scorecard*, *Compute dose to a plane*, *Evaluate plans with dose volume histograms*, and *Generate biological response comparisons*.

When you generate your plan report, you can choose to print a summary of the prior dose information. See *Print plan setup information*.

You can return to the **Prescriptions** window and **Manage Prior Dose** window to change the prior dose settings as needed. To return to the **Prescriptions** window, press **Ctrl+P**.

NOTE

When you include record dose without deformation in a trial, and the dose grid of the trial differs from the dose grid of the included record, the prior dose display may differ from the dose display in the record. For example, if the secondary image set that is associated with a record is heavily rotated due to differences in patient positioning between scans, the dose grids will not be aligned well with each other. To reduce discrepancies like this, ensure that both the record dose grid and the trial dose grid have the same resolution and size, and that they overlay approximately the same part of the patient on each image set.

Restrictions

When prior dose is included, you cannot perform the following tasks:

- Optimize a trial.
- Use Auto-Planning.
- Use robustness analysis.

To perform these tasks, change the **Dose Display Mode** to **Current Dose Only**.

Assign beams to prescriptions

Pinnacle³ assigns all beams to the default prescription (200 cGy to the maximum dose for a single fraction). Once you have created your prescriptions, you can reassign the beams to specific prescriptions.

- 1 Click the **Beam Weighting** button in the **Dose** panel. The **Beam Weighting and Prescription** window opens.
- 2 In the **Prescription** field for the beam that you want to reassign, click the option list and select the prescription for this beam.

Add beams after creating multiple prescriptions

If you add a new beam to the trial after you have created your prescriptions, Pinnacle³ adds the new beam to the current prescription. If the current prescription is not appropriate for that beam, reassign the new beam to a different prescription.

Use prescriptions with proton beams

If you are licensed for proton treatment planning, Pinnacle³ assigns beams to prescriptions differently than if you are not licensed for proton treatment planning.

A prescription cannot have both proton and non-proton beams assigned to it. When you create a new beam or change the modality of an existing beam, the beam is automatically assigned to a prescription as follows:

- If no prescriptions exist, the software creates a new default prescription and assigns the new beam to that prescription.
- If two prescriptions exist (one with non-proton beams assigned and the other with proton beams assigned), the new beam is assigned to the appropriate prescription based on beam modality.
- If multiple prescriptions exist, but the beams assigned to those prescriptions do not match the modality of the new beam, the software creates a new prescription and assigns the new beam to that prescription.
- If multiple prescriptions exist for both non-proton and proton beams, and the beams assigned to the current prescription match the modality of the new beam, the software assigns the new beam to the current prescription.
- If multiple prescriptions exist for both non-proton and proton beams, and the beams assigned to current prescription do not match the modality of the new beam, the software assigns the new beam to the first prescription in the prescription list that matches the modality of the new beam. The software notifies you with the name of the prescription to which the beam was assigned.

NOTE

For IMPT optimization, double scattering beams and uniform scanning beams cannot be assigned to the same prescriptions as spot scanning beams. However, the software does not differentiate between proton beam modalities when it assigns proton beams to

prescriptions and can assign all proton beams to the same prescription. If you are using both double scattering and uniform scanning beams in the same plan with spot scanning beams, you will need to manually assign the proton beams to the appropriate prescriptions.

Verify that all of the beams are assigned to the correct prescriptions before you compute dose.

Set the beam weighting

The beam weights are set by specifying percentages of the total prescription for each beam. Because the beam weights are relative, changing the weight of one beam changes the weights for all other beams. As you modify a beam's weight, other weights of other beams for the same prescription are adjusted so that the total percentage is always 100%. If you want to prevent a beam weight from being changed, you can lock the beam weight.

You can specify beam weighting before or after dose computation. If you change the beam weights after dose computation, the dose values are retained and recalculation is not required.

Monitor units are calculated for each beam and displayed as **MU/Fraction** for static beams and **MU/Degree** for arcs.

NOTE

For plans in which you prescribe dose to a POI, please be aware that when you select a different POI to which you will prescribe dose, the relative beam weighting changes rather than the monitor units. This occurs even when relative beam weights are locked.

Set specific beam weights

- 1 In the **Dose Computation** section of the **Dose** panel, click the **Beam Weighting** button.
- 2 Do you want to set relative weights or MU/Fraction for each beam?
 - Relative weights—go to step 3.
 - MU/Fraction—go to step 6.
- 3 Enter the relative weight for a beam.
- 4 Do you want to lock the weight for this beam?
 - If yes, click the **Weight Lock** button for that beam. Then go to step 5. The button is labeled **Locked** when the beam is locked. Unlock the beam by clicking the button again.
 - If no, go to step 5.
- 5 Repeat steps 3 and 4 for all other beams with the same prescription. Remember that as you set the weight for each beam, the relative weights of all other beams using the same prescription change unless the weight is locked.

This procedure is complete.



CAUTION

Beam weights are assigned using proportional monitor units rather than proportional dose unless point dose prescription with proportional dose is specified.

- 6 In the **MU/Fraction** or **MU/Degree** field, enter the monitor unit value for the beam.
- 7 Repeat step 6 for all other beams that have the same prescription.

Make beam weights equal

You can have the software make the beam weights equal for all unlocked beams assigned to a prescription.

**CAUTION**

When using the **Set Equal Weights** option, the beam weighting is based on Monitor Units instead of dose, unless the prescription was set up for point dose and the beam weighting option is set to be proportional to Point Dose.

- 1 In the **Dose** panel, select **Options - Weighting Options**. The **Weighting Options** window appears.

If you want to see the beam weights change, in the **Dose Computation** section click the **Beam Weighting** button and move the window that appears so you can see it and the **Weighting Options** window.

- 2 Select the prescription for which all beams should be weighted equally.
- 3 Click the **Set Equal Weights for Unlocked Beams** button.

Make beam weight proportional

This feature works for stereotactic radiosurgery arcs. The software makes the beam weights proportional to the arc lengths of the beams.

- 1 In the **Dose** panel, select **Options - Weighting Options**. The **Weighting Options** window appears.

If you want to see the beam weights change, in the **Dose Computation** section click the **Beam Weighting** button and move the window that appears so you can see it and the **Weighting Options** window.

- 2 Select the prescription that should have proportional beam weights.
- 3 Click the **Set Weights Proportional to Arc Length** button.

Optimize the beam weights

The software lets you add constraints to the selected prescription and optimize the beam weights. This feature is important, for example, in a stereotactic radiosurgery application with multiple isocenters within the brain.

- 1 In the **Dose** panel, select **Options - Weighting Options**. The **Weighting Options** window appears.
- 2 Click the **Optimize Weights** button. The **Beam Weight Optimizer** window appears.
- 3 Click the **Add** button to add a new optimization point to the window. Each point you add lets you assign a different constraint to the beam weight optimization.

You can delete a point later by selecting it and clicking the **Delete** button.

- 4 Click one of the **POI** option lists and select a point of interest.
- 5 Use the next option list to specify whether the POI dose should be equal to, less than, or greater than the desired dose.
- 6 Specify the desired dose for the POI. (Actual dose is determined by the dose computation you performed earlier.)

- 7 Use the **Penalty** field to determine which dose constraints are most important.

For example, if you assign three constraints, you can enter 100 in the **Penalty** field for the most important constraint, 10 for the next important constraint, and 1 for the least important one. In this example, the first constraint is 10 times more important than the next one, and so on.

- 8 Do you want to group constraints by isocenter or prescription?
 - No—in the **Group By** option list select **No Grouping**.
 - Isocenter—in the **Group By** option list select **Isocenter**. The relative weights assigned to the isocenter beam group will not change. Only the overall group weighting changes.
 - Prescription—in the **Group By** option list select **Prescription**. The relative weights assigned to the prescription beam group will not change. Only the overall group weighting changes.
- 9 Do you want the prescription modified as part of optimizing the beam weights?
 - If yes, at **Modify Prescription** select **Yes**. The software modifies the prescription to meet the dose constraints.
 - If no, at **Modify Prescription** select **No**. The software may be unable to meet the dose constraints you assign. This is because the software uses the prescription to calculate optimization.
- 10 If you want to specify more than one dose optimization point, repeat steps 3-9 for each point. But, you cannot apply multiple constraints to the same POI.
- 11 Click the **Optimize** button to optimize the beam weights.

Display the dose distribution

The dose distribution can be displayed as isodose lines on any image. A colorwash display of the dose distribution can also be produced in 2D images, and isodose surface displays can be produced in 3D images.



CAUTION

Dose must be computed for all weighted beams in order to display the dose distribution.



To access the dose display options, click the **Eval** button. In the IMRT window you can select **Options - Isodose Lines**.

You can turn the 2D colorwash display on and off, turn all 2D and 3D isodose line displays on and off, and display the **Isodose Line** window to set isodose line display attributes. For more information about isodose displays and specifications, see the *Plan Evaluation Tools* chapter.

Monitor unit calculation

After dose is computed, you can display the **Monitor Unit** window to obtain information which can be used to check the monitor unit calculation. This window reports monitor units using a quantity called normalized dose. The information displayed in the window changes based on the beam modality.

In the **Dose** panel, select **Options - Monitor Units**. The **Monitor Units** window appears.



WARNING

Using Fast Convolve dose computation or a dose grid resolution of more than 0.5 cm in any dimension adversely affects the accuracy of monitor unit calculations. In such cases, monitor units appear with a tilde (~) to indicate that the values are approximate.

For information on traditional, convolution algorithm, or hand monitor unit calculation, see the *Pinnacle³ Planning Reference Guide*.

Fields and buttons

Title	Description
Cal Depth (Calibration Depth)	The depth of the calibration point below the surface of the phantom.
Calibration Dose (D/MU)	The calibration dose per MU.
Central Axis Depth	The depth of the reference point, as projected along the central axis.
Collimator Output Factor (OFc)	The computed correction factor determined during commissioning.
Dose at Ref Point/Fraction	The dose per fraction at the given reference point.
Effective Depth	The radiological depth scaled by density, pixel by pixel, along the line of sight. Pinnacle ³ does not use effective depth but provides it for secondary MU calculations.
Water Equivalent Depth	This field appears only if you are licensed for proton treatment planning. The radiological depth scaled by density, pixel by pixel, along the line of sight. Analogous to effective depth, but scaled by stopping power rather than density.
Equiv Square at SAD for Output Factor lookup (4A/P)	The equivalent square of the field used to look up the OFc.
Exposed Blocked Area at SAD	The area of the beam that is exposed.
Exposed Unblocked Area at SAD	The area of the beam without the block in the beam.
Off Axis Distance (OAD)	The distance from the reference point to the central axis.
Pct of field blocked	The percentage of the area of the field that is blocked by the beam block.
Percent of unblocked field intersecting patient.	The percentage of the area of the field exposed by the beam block and intersecting the patient.
Perimeter at SAD	The perimeter of the beam exposed by the jaws as measured in the isocenter plane.

Title	Description
Monitor Units Per Fraction (MU)	The number of monitor units per fraction.
Normalized Dose at Ref Point (ND)	The normalized dose at the given reference point. This value is equal to the dose divided by the calibration dose.
Total Transmission Factor (TTF)	The total block and tray transmission factor.
Reference Point Depth	The distance from the patient surface to the reference point along the line between the source and the reference point.
SCD	The distance from the source to the calibration point.
Source to Point Distance (SPD)	The distance from the source to the reference point.
SSD to Reference Point	The source to surface distance along the line between the source and reference point.

Photon monitor unit calculation

If bolus was added to the beam, asterisks appear next to fields that do not include bolus in their computed values, such as SSD and depths.

NOTE

If a beam has invalid monitor units, change the reference point dose in the **Monitor Units** window.

NOTE

For fixed jaw machines, the **Equiv Square at SAD for Output Factor lookup (4A/P)** value is computed using the minimum circumscribing rectangle defined either by the jaws or by the edge of the MLC-defined field, whichever is more limiting. For Siemens machines in which the MLC replaces the jaw, it is computed using the rectangle defined by the most open leaves and the jaw positions. In all other cases, it is computed using the rectangle defined by the jaw positions.

Select the reference point for the beam

The reference point is a selectable, beam-specific point where details of the absolute dose computation for the beam are reported, or where absolute dose is specified. This point can be selected after dose is computed since it does not affect the dose distribution shape.

NOTE

Only POIs that are assigned to the primary image set appear in the **Reference Point** option list.



WARNING

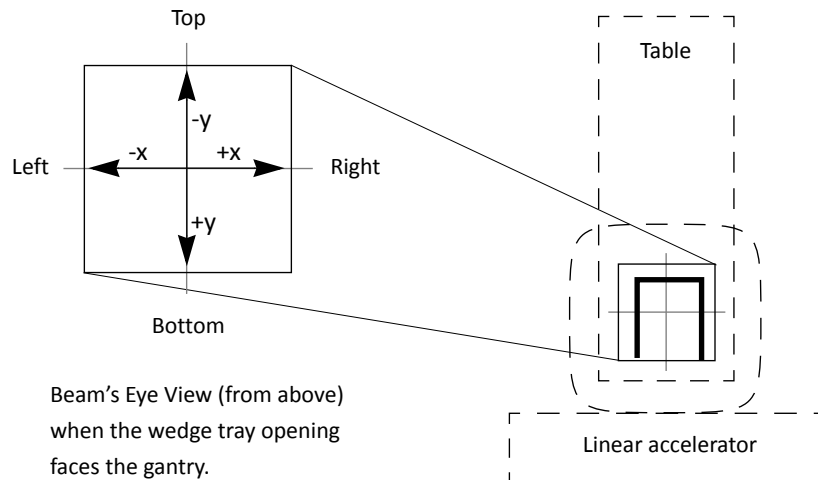
Changing the position or dose of the reference point changes the dose throughout the dose grid. Be careful when positioning the reference point or changing the dose of the reference point.

The **Reference Point** options allow you to select a reference point for the dose calculation. You can choose a point of interest for the reference point, or you can specify the depth and position of the reference point. The system default is to use the isocenter for the beam as the reference point.

To use a point of interest as the reference point, choose **Use POI for Ref Point** and then select the point from the list of points of interest.

To define a reference point, choose **Specify Depth, X, Y**. In the fields that appear, enter the depth and any X and Y axis offset from the central axis.

The X and Y offsets are defined using the coordinate system shown in the following illustration.



Define the dose normalization point for photon dose/MU

You can also define the normalization used for determining the dose per monitor unit. To use the output factor table to calculate the dose per monitor unit at the reference point, choose the **Use OF Table** option. If output factors are not available for a given beam geometry, or if you want to override the software MU computation using a measured absolute dose, you can use the **Specify D/MU** option.

Software MU computation using the OF table

If you choose the **Use OF Table** option and appropriate output factors are available for the beam, the software computes absolute dose (Dose/MU) for the beam. In this case, reference point selection does not affect the dose distribution in any way. Details of the absolute dose computation are reported at the reference point. For detailed information on MU computation, see the *Pinnacle³ Planning Reference Guide*.

The convolution dose engine is capable of computing absolute dose given the beam characteristics and the patient characteristics. Thus, normalized dose includes the effects of beam blocking, patient shape, inhomogeneities, etc.



CAUTION

Reported OF_c and OF_p values may differ from measured values. The phantom output factor is computed using an ideal “measurement” of the scattered TERMA for the field. The software’s

internal normalization accounts for the absolute dose at the calibration point and forces $OF_p = OF_c = 1$ for the calibrated field.

Because all convolution calculations inherently handle the phantom scatter correctly (consistently, and in an ideal fashion), absolute dose normalization is achieved by scaling the incident energy fluence by the internal normalization constant, and the OF_c that matches the field. During commissioning, the software tabulates the OF_c values for all field sizes for which relative output factors were entered.

Overriding the software MU computation

If you use the **Specify D/MU** option, you can specify an absolute dose (cGy/MU) at the reference point. The internal monitor unit equation then simplifies to:

$$D_{ref\ point}/Fraction = MU \cdot (D/MU)_{meas}$$

where $(D/MU)_{meas}$ is the measured absolute dose at the reference point.

NOTE

If you use the Specify D/MU option and dose becomes invalidated or uncomputed, the normalization reverts to the **Use OF Table** option.

Stereotactic radiosurgery monitor unit calculation

This **Monitor Units** window shows the average TAR (**Avg. TAR** field) and d_1 (**D_{air}/MU at iso** field) for the beam. To obtain the D/MU at isocenter, multiply these two values together:

$$TAR \cdot d_1 = D/MU_{iso}$$

The system also displays the D/MU at isocenter obtained directly from the beam's dose distribution. The computed D/MU (d_{iso}) and the value in the dose grid should be approximately equal.

NOTE

In most instances, the isocenter point will not fall directly in the center of one of the dose grid voxels, so the values may not be exactly equal. Using a smaller dose grid should improve this compliance.

NOTE

If you use RadCalc to read information from a Pinnacle³ stereotactic plan, the name of the prescription point in RadCalc may not match the name of the prescription point in Pinnacle³. In a stereotactic plan, the dose and monitor units are calculated using the prescription point you selected in the **Prescriptions** window. However, since the name of the prescription point is not used in the **Monitor Units** window, the software uses the name of the first prescription point that is listed in the **Prescriptions** window when data is transferred to RadCalc.

To display the TAR information for each sub-beam used to compute the current beam, click the **Detail** button. The **Stereotactic TAR Information Per Gantry Angle** window appears.

The fundamental stereotactic dose computation involves determining the dose per monitor unit D/MU (SSD, d, r, Wc) at a point from one of the stereotactic pencil beams that comprise an arc. For detailed information on stereotactic radiosurgery monitor unit calculation, see the *Pinnacle³ Planning Reference Guide*.

Electron beam monitor unit calculation

Electron beam monitor units will be computed by the software for all field sizes and SSDs if you entered the output factor information correctly in the Electron Physics Tool. The SSD and field size for the beam cannot be outside the range of the setup geometries for measured output factors entered in the physics tool.

Proton beam monitor unit calculation

All dose in Pinnacle³ is presented in terms of effective dose, taking the Relative Biological Effect (RBE) into account. Pinnacle³ does not calculate dose per MU directly for protons, but requires you to enter a value that is calculated or measured outside the system in order to calculate absolute dose. It is important that you enter this value as effective dose, taking RBE into account. This is especially important for composite plans in which proton dose will be added to dose from photon or electron beams. (Note that Pinnacle³ assumes that RBE is 1 for photon and electron dose, so effective and physical dose for those modalities are identical.) For information about RBE, see the *Calculate Dose* chapter.

Select the reference point for the beam

The reference point is a selectable, beam-specific point either where details of the absolute dose computation for the beam are reported or where absolute dose is specified. You can select this point after you compute dose because it does not affect the dose distribution shape and it only changes the MU for that beam.

NOTE

Only POIs that are assigned to the primary image set appear in the **Reference Point** option list.



WARNING

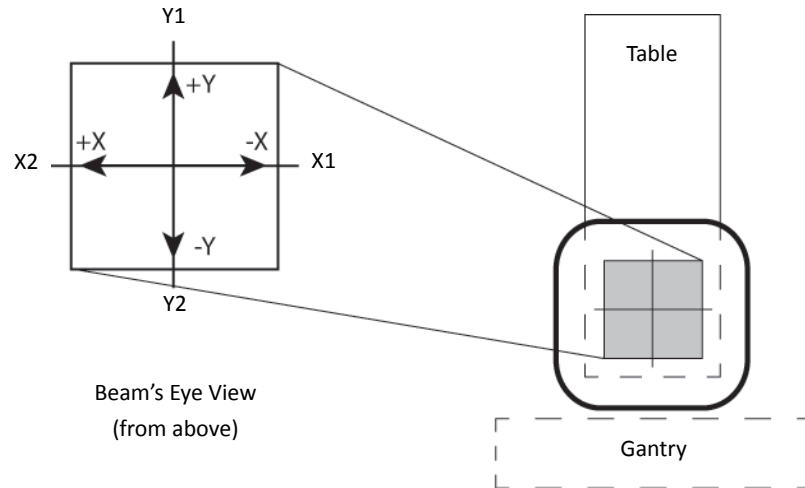
Changing the position or dose of the reference point changes the dose throughout the dose grid. Be careful when positioning the reference point or changing the dose of the reference point.

The **Reference Point** options allow you to select a reference point for the dose calculation. You can choose a point of interest for the reference point, or you can specify the depth and position of the reference point. The system default is to use the isocenter for the beam as the reference point.

To use a point of interest as the reference point, choose **Use POI for Ref Point** and then select the POI from the list.

To define a reference point, choose **Specify Depth, X, Y**. In the fields that appear, enter the depth and any X axis and Y axis offset from the central axis.

The X and Y offsets are defined using the coordinate system in the following illustration.



Define the dose normalization parameter for proton dose/MU

NOTE

The options for defining the normalization parameter for dose/MU do not appear for spot scanning beams. Normalization for spot scanning beams is always absolute dose and cannot be changed.

You can also define the normalization used for determining the dose per monitor unit for double scattering and uniform scanning proton beams. Select the **Use Relative Dose** option for relative dose or the **Specify D/MU** option for absolute dose.

Overriding the software MU computation

For double scattering beams and uniform scanning beams, **Use Relative Dose** is the default option for defining the normalization that is used for determining the dose per monitor unit. The system computes the normalized dose when this option is selected.

For spot scanning beams, **Use Absolute Dose** is the default option for defining the normalization that is used for determining the dose per monitor unit. The system computes the absolute dose when this option is selected.

The **Specify D/MU** option allows you to specify an absolute dose in (cGy (RBE))/MU at the reference point.

The internal monitor unit equation then simplifies to:

$$D_{ref\ point}/Fraction = MU \cdot (D/MU)_{meas}$$

where $(D/MU)_{meas}$ is the measured absolute dose at the reference point.

NOTE

You must specify the dose at the reference point per fraction for proton beams in terms of effective dose per monitor unit, (cGy (RBE)/MU or Gy (RBE)/MU), taking RBE into account. This is particularly important in a composite plan that contains other modalities (photons or electrons) as well as protons, so that the composite dose correctly characterizes the biological effect of the entire course of treatment.

12 Forward-Planning IMRT

Overview

Intensity-modulated radiation therapy (IMRT) is a treatment technique using beams with varying intensities to conform the high dose region to the target volume while sparing normal tissue structures, enabling dose escalation and improved local tumor control.

Forward-planning segmental IMRT is an extension of 3D conformal treatment planning. Beam intensities are modulated using physical, virtual, or dynamic wedges, tissue compensators, full or partial-transmission blocks, asymmetric jaws, and multi-leaf collimators (MLC). Designing the modulated fields is an iterative process that begins after a conventional 3D dose distribution has been computed and evaluated. Beam weights and beam directions may also be modified, in addition to beam intensity, to produce an optimal plan.

The forward-planning segmental IMRT procedures in this guide have are a natural extension of 3D treatment planning. The procedures you use depend on the clinical site being planned, your treatment objectives, and the delivery devices available to you.

The procedures meet the following criteria:

- Achievable using your treatment planning system (software versions 5.0 and higher).
- No significant increase in the complexity of the treatment planning or treatment delivery process.
- Treatment verification is possible using your standard clinical QA procedures.

Before using these procedures, you should become familiar with the basic treatment planning functions.

Techniques



WARNING

Small field sizes are used in forward-planning IMRT. Validate your machines (beam models) at each field size prior to creating plans using the forward-planning techniques.

This chapter describes two different techniques for modulating beam intensities. One technique involves designing beam segments and then optimizing the weight of each segment to obtain the necessary dose distribution (see *Design beam segments*). The other technique involves adding control points to each beam and then optimizing the weights of the control points and beams to obtain the necessary dose distribution (see *Forward planning using control points*).

Control point vs. segment

IMRT uses control points to describe the dynamic aspects of a beam. The term “control point” was adopted from the DICOM RT specification. A control point is a general concept for specifying a point during treatment where the beam changes. Aspects of a control point that may change during

treatment include gantry, collimator, and couch angles, MLC leaf positions, jaw positions, wedge states, and MUs/weight. See the *Forward planning using control points* section for more information about control points.

A segment or multi-leaf collimator (MLC) control point, as the terms are commonly used, is essentially a control point that only allows changes in MLC leaf positions, jaw positions, and MUs/weight during delivery.

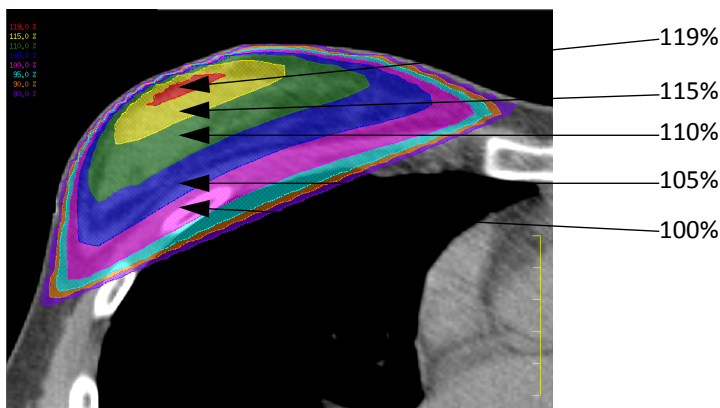
Skin flash adjustment

You can automatically adjust step-and-shoot MLC leaves to account for patient movement during treatment. When you set a skin flash adjustment in the **Beam MLC Leaf Position Editor** window, the software shifts the open MLC leaves on the selected bank by the specified amount. If necessary, the software also shifts the jaw associated with the bank you are opening. For more information, see *Multi-leaf collimators* in the *Beam Modifiers* chapter.

Design beam segments

Segmental IMRT uses multiple, fixed segments or subfields to create the intensity-modulated dose distribution. The beam segments are usually created using static multi-leaf collimators (MLCs). If practical, either full or partial-transmission blocks or asymmetric jaws may be used.

These procedures assume that you have already completed, displayed, and evaluated a conventional treatment plan.



Conventional 3D dose distribution

You have several options for designing beam segments:

- Define segments using dose volumes as ROIs
- Draw segments on 3D DRR displays
- Draw segments on 2D BEV displays
- Define segments using asymmetric jaws
- Define segments using variable block margins

A careful selection of the number of beams and beam angles generally reduces the number of segments required to produce a satisfactory plan.

Define segments using dose volumes as ROIs

If dose regions are outlined as ROIs, you can define beam segments automatically by using the software's auto-blocking functions.

You can automatically create an ROI from an isodose line by clicking the **Create ROI** button for the isodose line in the **Isodose Line Window**. See *Create an ROI from an isodose line* in the *Plan Evaluation Tools* chapter.

After you create ROIs for each appropriate dose range, follow the basic forward-planning procedures and automatically define segments by blocking or exposing the contoured dose ROIs.

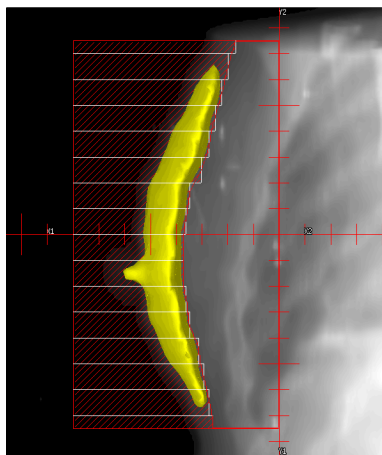
Draw segments on 3D DRR displays

- 1 Copy one of the beams.
- 2 Change the weight for the new beam to zero.

NOTE

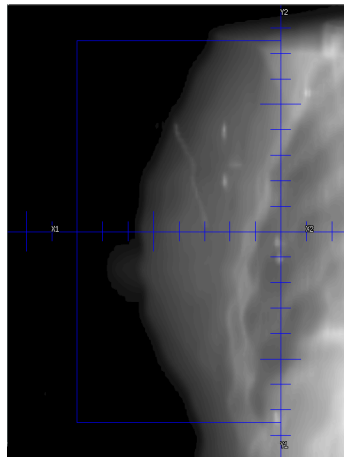
Setting the weight to zero ensures that the dose distribution for the original plan still displays on the screen.

- 3 Display a DRR for the new beam.
- 4 Display the 3D dose cloud corresponding to the first dose level to be blocked or boosted.
- 5 Add a block to the new beam.
- 6 Manually draw a block matching the 3D dose cloud displayed on the DRR. Turn on the MLC leaves.

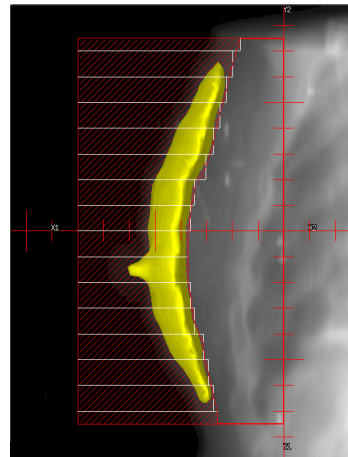


Block drawn to cover 115% dose cloud

- 7 Repeat steps 1-6 for as many segments as necessary. If the beam just created is being opposed, you may use the Copy & Oppose option. Because you copied a beam with a zero weight, the weight for the copied beam is zero.



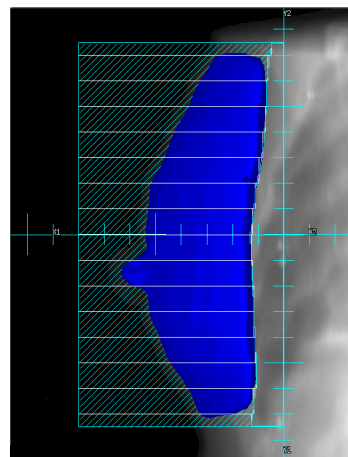
Open segment



115% segment



110% segment



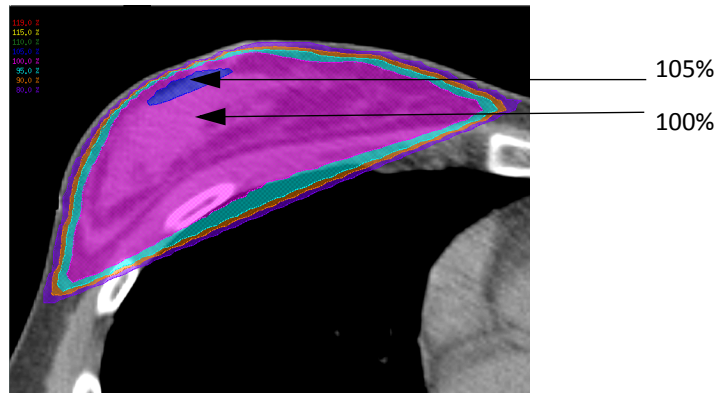
105% segment

Sample set of beam segments

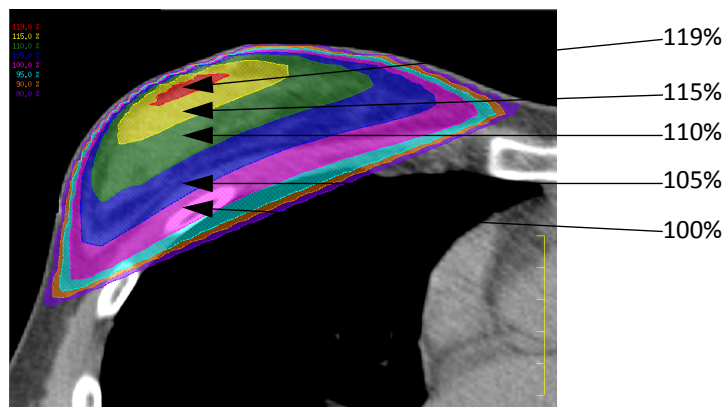
- 8 Recalculate the dose distribution.

- 9 Adjust the beam weights to produce the optimal dose distribution. See *Optimize beam weights*.

Click the **Dose** button. On the **Dose** panel click the **Beam Weighting** button. The **Beam Weighting and Prescription** window appears.



Intensity-modulated dose distribution

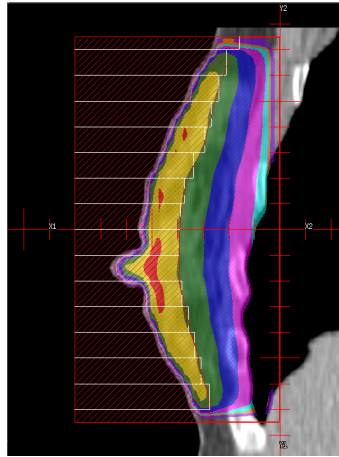


Conventional 3D dose distribution

Draw segments on 2D BEV displays

- 1 Copy one of the beams.
- 2 Change the weight for the new beam to zero.
- 3 Display a 2D BEV for the new beam.
- 4 Right-click in the viewing window. The popup **Tools** window appears.
- 5 Click the **BEV Options** button. The **Beam's Eye View Options** window appears.
- 6 From the **Type** option list, select **2D Orthogonal Plane**.
- 7 Change the offset (cm) if you want to define blocks on a plane other than the isocenter plane.
- 8 Click the **Close** button in the **Beam's Eye View Options** window.
- 9 Turn on the 3D colorwash to display isodose levels on the 2D BEV.
- 10 Add a block to the new beam.

- 11 Manually draw a block matching the dose level displayed on the BEV. Turn on the MLC leaves.



Block drawn to cover 115% dose level

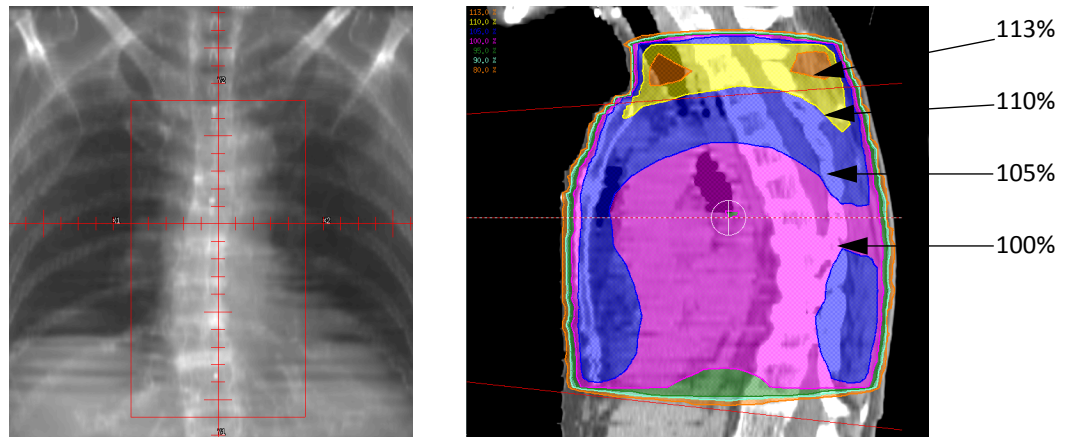
- 12 Repeat steps 1-11 for as many segments as necessary. If the beam just created is being opposed, you may use the Copy & Oppose option. Because you copied a beam with a zero weight, the weight for the copied beam is zero.
- 13 Recalculate the dose distribution.
- 14 Adjust the beam weights to produce the optimal dose distribution. See *Optimize beam weights*.

Define segments using asymmetric jaws

- 1 Copy one of the beams.
- 2 Change the weight for the new beam to zero.
- 3 Display a DRR for the new beam.
- 4 Display a 2D dose distribution (transverse, sagittal, or coronal).
- 5 Move the appropriate asymmetric jaw on the DRR view until the desired dose levels are blocked. You can adjust the jaw by looking at both the DRR and the 2D dose displays.

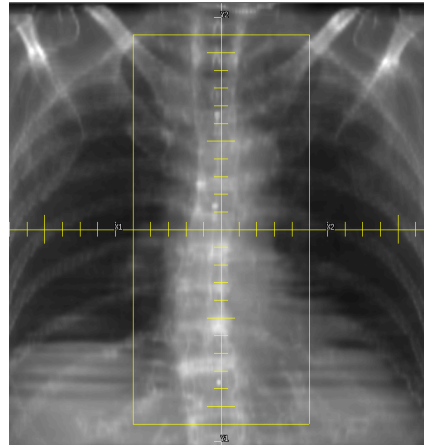
NOTE

You cannot move an asymmetric jaw if **AutoSurround Blocks** is set to **Yes**.

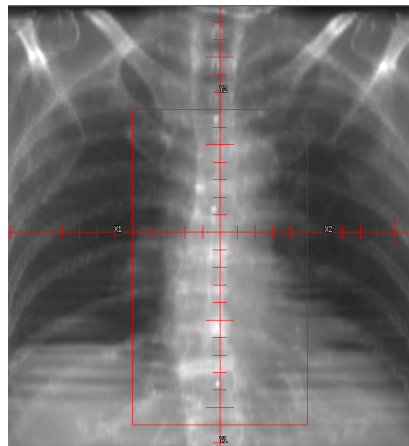


Segment defined to block the first dose level

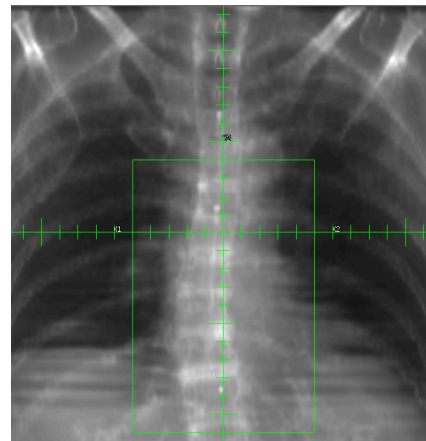
- 6 Repeat steps 1-5 for as many segments as necessary. If the beam just created is being opposed, you may use the Copy & Oppose option. Because you copied a beam with a zero weight, the weight for the copied beam is zero.



Open segment

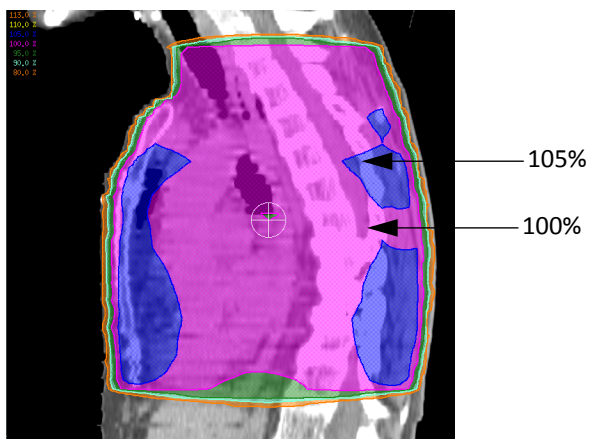


110% segment

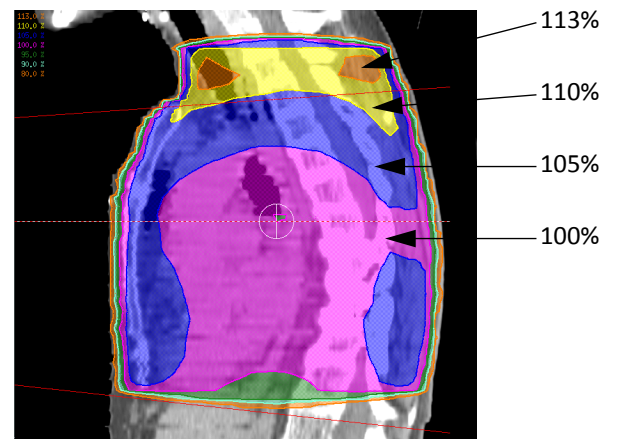


105% segment

- 7 Recalculate the dose distribution.
- 8 Adjust the beam weights to produce the optimal dose distribution. See *Optimize beam weights*.



Intensity-modulated dose distribution



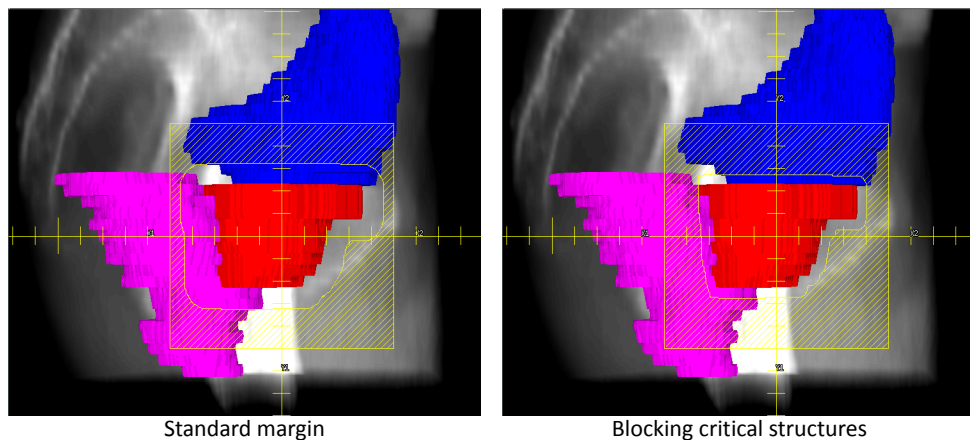
Initial dose distribution

Define segments using variable block margins

The software's blocking functions give you a number of options for designing intensity modulated treatments. For example, you can design an original field that treats the target volume with an appropriate margin. Then you design subfields to differentially block overlapping critical structures.

You can also design segmented fields to deliver simultaneous integrated boost (SIB) treatments, where the volumes of regional, suspected, and gross disease are all treated simultaneously. In many cases, standard subfields can be created using the software's HotScript feature.

- 1 Copy one of the beams.
- 2 Change the weight for the new beam to zero.
- 3 Display a DRR for the new beam.



- 4 Define a new segment with margins that are different from the original beam using the autoblocking function, manual blocking, or a combination of the two techniques. Turn on the MLC leaves.
- 5 Repeat steps 1-4 for as many segments as necessary. If the beam just created is being opposed, you may use the Copy & Oppose option. Because you copied a beam with a zero weight, the weight for the copied beam is zero.
- 6 Recalculate the dose distribution.
- 7 Adjust the beam weights to produce the optimal dose distribution. See *Optimize beam weights*.

Optimize beam weights

Beam weights are set by specifying percentages of the total prescription for each beam. The relative weights for all beams assigned to a prescription always add up to 100%. Beam weights can be adjusted manually or automatically. Because the beam weights are relative, making a change to the weight of one beam changes the weight of all other beams. If you want to prevent a beam weight from being changed, you can lock the weight.

The beam weight optimizer function allows you to specify POI-based dose objectives and have the system determine the optimum weights for each beam required to achieve these objectives.

Beam weight optimization can be used to optimize weights for segmental fields, beam orientations, and wedge angles to deliver uniform dose distributions.



CAUTION

Verify that the dose distribution is correct and does not contain unexpected hot or cold spots. After you have optimized the beam weights, use the dose volume histogram and the maximum dose display to evaluate the dose distribution.

Optimize beam segment weights

Because the software displays dose distribution changes in real time as beam weights are adjusted, it is often easier to optimize segment weights manually. We recommend that you set equal weights for beams before beginning the optimization process to assure that no beams have weights set to zero.

Most of the prescribed dose is delivered by the original beams with the remaining dose given by the subfields. As a result, setting the total weight for all original beams to 90% of the prescription dose gives you a reasonable starting point for optimization.

For example, if there are two original beams, set the initial weight for each beam to 45%. If you lock the first beam after setting the weight to 45%, then set the second beam weight to 45% (without locking it), to keep the beam weight equal to 100%, the software changes the weights of the additional beams. Then you can produce the desired dose distribution by manually fine-tuning the beam weights. Alternatively, you can adjust the weights for the original beams until the high dose region receives the prescribed dose. For the additional beams, adjust the beam weights to deliver the prescribed dose.

There are two ways you can use the beam weight optimizer to determine the segment weights:

- Distribute POIs throughout the target volume and critical structures, specify dose objectives and constraints, and let the system optimize the weights. If necessary, you can manually fine-tune the beam weights after computer optimization is complete.
- Place POIs within the dose regions used to define the segments, specify a uniform dose objective to each of these points, and let the system optimize the weights.



CAUTION

Always evaluate each beam after optimization. Blocking to cover isodose lines may result in fields that are normalized under a block or MLC. For the best accuracy, the prescription point of interest should be exposed by all fields.

NOTE

For additional information on adjusting beam weights and using the beam weight optimizer, please refer to the *Calculate Dose* chapter.

Optimize beam orientations

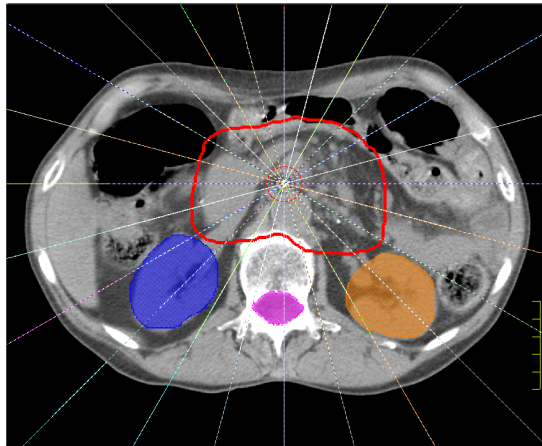
The beam weight optimizer can be used to optimize beam orientations (beam selection). This technique is useful for designing site-specific class solutions or optimal initial beam arrangements for 3D conformal planning.

For example, you may routinely use a standard technique consisting of four, five, or six beams at specified angles to treat a particular site. The beam optimizer may be able to find a better beam arrangement that can be used as a new standard plan.

- 1 Place a large number of coplanar beams around the patient contour at equi-angular increments. An increment of 15° is reasonable.

NOTE

You can record a HotScript to use the new plan as a standard plan to treat similar sites in the future.



24 beams at equi-angular 15° increments

- 2 Compute the dose distribution.
- 3 Set the weights equal for all beams.
- 4 Place POIs throughout the target volume and critical structures.
- 5 Open the beam weight optimizer and specify dose objectives and constraints for each POI.
- 6 Optimize the weights.
- 7 Lock all beams that have weights below a given value (for example, below 5% or below 10%).
- 8 Delete the locked beams.
- 9 Optimize the weights for the remaining beams.
- 10 Repeat steps 6-9 until a reasonable number of beams remain.
- 11 Fine-tune the weights to produce the optimal dose distribution.

NOTE

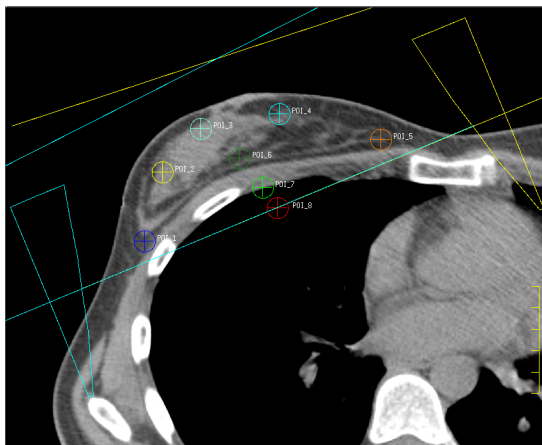
This technique can be extended to optimize non-coplanar beam orientations as well.

Optimize wedge angles

The beam weight optimizer can be used to optimize wedge angles.

- 1 Place an open beam and a 60° wedge beam at each orientation.
- 2 Compute the dose distribution.

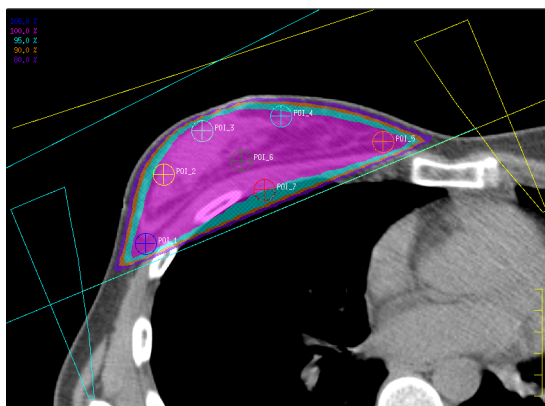
- 3 Set the weights equally for all beams.
- 4 Place POIs throughout the target volume and critical structures.



POIs distributed throughout target area

- 5 Open the beam weight optimizer and specify dose objectives and constraints for each POI.
- 6 Optimize the weights.
- 7 Review the relative weights of the open and 60° wedge beams at each orientation. You can either accept these beams or select an equivalent virtual/dynamic or physical wedge angle to replace both beams and then compute the final dose distribution.

Click the **Dose** button. On the **Dose** panel click the **Beam Weighting** button. The **Beam Weighting and Prescription** window appears.



Optimized dose distribution

NOTE

Optimization can also be performed by manually adjusting the beam weights. You can also optimize wedge orientation by placing an open beam and a 60° wedge beam at each allowable wedge orientation.

Forward planning using control points

Instead of creating multiple beams with different blocking shapes, you can modulate beam intensity by adding control points to a beam. A control point holds the state of the treatment as it progresses. The present state includes gantry, collimator, and couch angles, MLC leaf positions, the dose grid, and modifier descriptions. As any of these aspects of the treatment changes, a new control point is introduced for the beam.

For static beams, there is only one control point. For arc beams, there are two control points (beginning and ending points) and the blocking shape remains the same for both. For step-and-shoot MLC beams, you can set the blocking and store the dose for each control point. Storing the dose allows you to re-weight the individual control points in the beam and see the dose update in real time. If you store dose for each control point, you can optimize the control point weights.

The software invalidates dose for both a control point and the beam if you change a parameter that changes the control point, unless the weight of the control point is zero.

If a parameter affects all control points for a beam, and that parameter is changed, the software invalidates the dose for all control points. For example, changing the isocenter, the dose grid, or the machine, or adding or removing wedges, changes the dose for the beam and all control points.

Define MLC control points

Use the options in the **Beams** panel to add control points to a beam. This procedure assumes that you have already completed, displayed, and evaluated a conventional treatment plan. (An example of a 3D dose distribution is shown in *Design beam segments*.)

- 1 Select the beam to which you want to add MLC control points.
- 2 Set the beam type to **Step & Shoot MLC**.
- 3 Click the **OK** button to confirm that the software should turn on MLC.
- 4 Select **Options - Control Points**. The **Control Points** window appears.



CAUTION

When you store dose for MLC control points, the software calculates dose for each MLC control point when you compute dose for the beam, so calculating dose will take more time than usual. In order to preserve disk space, the software does not save dose for the individual MLC control points when you exit the plan, but does save dose for the entire beam.

If you need to change the MLC control points after you have exited the plan, you have to store dose for the MLC control points and recompute dose for the beams again in order to see the dose update in real time when you make your changes.

- 5 Do you want to store the dose for the MLC control points?
 - If yes, select **Yes** in the **Store Control Point Dose** field.
 - If no, select **No** in the **Store Control Point Dose** field.

If you store the dose, you can re-weight the individual MLC control points in the beam and see the dose update in real time. If you do not store the dose, the software invalidates dose when you add or re-weight MLC control points.

- 6 Click the **Close** button.
- 7 Compute dose for the beam.
- 8 Display a DRR for the beam.
- 9 Display the 3D dose cloud corresponding to the dose level to be blocked or boosted.
- 10 Select **Options - Control Points**. The **Control Points** window appears.
- 11 Do you want to add an MLC control point to the “end” of the beam or insert one after the selected MLC control point?
 - Add to the end—click the **Add Control Point** button. A new MLC control point appears at the end of the list. The new MLC control point is a copy of the one that was previously at the end of the list, except its weight is 0.0.
 - Insert after the selected point—click the **Insert Control Point** button. A new MLC control point appears after the selected point. The new MLC control point is a copy of the previous one, except its weight is 0.0.
- 12 Add a block to the new MLC control point.
- 13 Manually draw a block matching the 3D dose cloud displayed on the DRR. (An example is shown in *Draw segments on 3D DRR displays*.) If necessary, delete the existing block before you draw the new block.
- 14 Repeat steps 9-13 until you have added all the necessary MLC control points to the beam. (Examples are shown in *Draw segments on 3D DRR displays*.)
- 15 Add the necessary MLC control points to the other beams. You can either copy the current beam, copy and oppose the current beam, or repeat steps 1-14 to manually add MLC control points to the other beams.
- 16 When you are finished adding MLC control points to the beams, recalculate dose for all the beams.

**CAUTION**

If you did not store the dose for the MLC control points, the software invalidates dose for a beam when you adjust the relative weights of the MLC control points. You will need to recalculate dose for the beam after you re-weight the MLC control points.

- 17 Adjust the relative weight of each beam and MLC control point, as necessary, to obtain the dose distribution you want. As you change the relative weight, the dose changes in any dose displays you have open for the trial.

NOTE

If you are licensed for P³IMRT, you can use that program to perform segment weight optimization. See the *P³IMRT Instructions for Use* for information.

- 18 If you want to lock the weight of a beam or MLC control point so the software will not change it, set the **Weight Locked** column to **Yes**.
- 19 When you are satisfied with the plan, you can print a hard copy of the plan and export the plan via DICOM RT or Varian Shaper, version G.

NOTE

You can only use DICOM RT or Varian Shaper, version G, to export control points. For more information, see the *Export* chapter.

13 Plan Evaluation Tools

Overview

The software provides a variety of tools for evaluating and comparing treatment plans. This chapter describes how to use the following plan evaluation tools:

- Display dose distribution information
- Obtain point dose information
- Evaluate trials with a scorecard
- Evaluate plans with dose volume histograms
- Obtain ROI dose statistics
- Compare dose
- Generate biological response comparisons
- ROI trending
- Generate dose profiles
- Accumulate dose
- Compare multiple trials
- Compute dose to a plane
- Use the Record Viewer and the Treatment Navigator
- Evaluate plans with QA phantoms
- Evaluate plans with DRRs

Display dose distribution information

Once dose is computed, you can display the dose distribution with the patient data. In 2D displays, you can display isodose levels as a colorwash and as isodose lines. In 3D displays, you can display isodose levels as solid or transparent surfaces.



- 1 Click the **Eval** button at the top of the window to display the **Evaluation** panel.
- 2 Do you have default isodose lines set up from a previous planning session?
 - Yes—Click the **All Lines On** button to display the isodose line. Go to step 4.
 - No—Click the **Add Line(s)** button.
- 3 In the **Isodose Line Addition Window**, click a button to select the isodose lines to display.

Click the **Close** button when you are finished.

NOTE

When normalizing to maximum dose, the 100% line is actually a point, not a line. Therefore, the highest isodose line value is initially set to 98%.

NOTE

If isodose lines are not displayed, check to see that all beams with a weight greater than zero are computed. If all the beams are computed and you still cannot see the isodose lines on the currently displayed 2D slices, scroll through the images. The current slice may not be receiving dose, or it may be outside the dose grid.

NOTE

For spot scanning beams, if the energy defined for a beam is not sufficient to completely cover the target ROI, the software will compute dose for that beam for as much of the ROI as possible. Review the isodose display for the ROI to confirm that the trial dose distribution is what you expect for the ROI, and adjust the plan if necessary.

- 4 To change the value for an isodose line, type a new value in the **Value** field for that line.
- 5 To change the isodose line display color, select the color from the **Color** list.
- 6 To turn the 2D display of a single isodose line on or off, click the **2D Display** button for the isodose line.

NOTE

If you want the system to display the same isodose values using the same display colors each time a plan is created, you can save those lines and display colors. Click the **Line Details** button in the **Evaluation** panel to display the **Isodose Line Window**. Set the isodose line display options that you want to use as the defaults, then click the **Save As Default** button.

NOTE

If you want to apply the same setting to all isodose lines, change the setting for the top isodose line in the table and then click the **Redo spreadsheet** button.

- 7 To display the isodose surface in 3D, select **Surface** or **Transparent** from the **3D Display** option list. Then render the image.

- 8 Click the **Isodose Lines Are** option list at the top of the **Evaluation** panel and select the isodose line display normalization.
 - **Absolute**—the isodose lines show absolute dose values in cGy rather than percentage dose values, and the maximum dose is listed.
 - **Percent of Max Dose**—the isodose lines are displayed as a percentage of maximum dose, and the maximum dose is listed.
 - **Percent of POI Dose**—the isodose lines are displayed as a percentage of the dose at a selected point of interest (POI). When you select the POI, the dose at that normalization point is displayed.
- 9 If desired, turn on the colorwash display for the dose distribution in 2D and 3D.

Click the **On/Off** buttons next to **2D Colorwash Display** and **3D Colorwash Display** in the **Evaluation** panel.

If you have specified isodose lines, the colors used for the colorwash display correspond to the isodose line colors. If you have not specified isodose lines, the colorwash display uses a spectrum from red to purple, with red at the “hot” end of the spectrum.

Create an ROI from an isodose line

You can create an ROI from an isodose line. The software resamples the dose volume at the resolution of the image set, then automatically contours the resampled volume.



- 1 Click the **Eval** button at the top of the window to display the **Evaluation** panel.
- 2 Click the **Line Details** button. The **Isodose Line Window** appears.
- 3 Click the **Create ROI** button for a given isodose line.

The new ROI is named *value (trial name)_y*. For example, the ROI for the 110% isodose line for the second trial is named “110% (Trial_2)_1.”

Remove an isodose line

- 1 In the **Evaluation** panel, click the **Remove Line** button.
The **Isodose Line Removal Window** appears.
- 2 Select the isodose line to delete from the **Isodose Line Window** and then click the **Delete Line** button.

Set up 3D isodose surface displays

When evaluating plans, it is often useful to set up a 3D isodose surface display that shows the target volume and a particular isodose surface.

- 1 To display the target volume and an isodose surface in 3D without patient images, first create a 3D viewing window or enter 3D mode from one of the existing 2D windows.
- 2 Right-click in the viewing window and select **BEV - None**.
- 3 Click the **Contours** button at the top of the window to display the **Regions of Interest** panel.

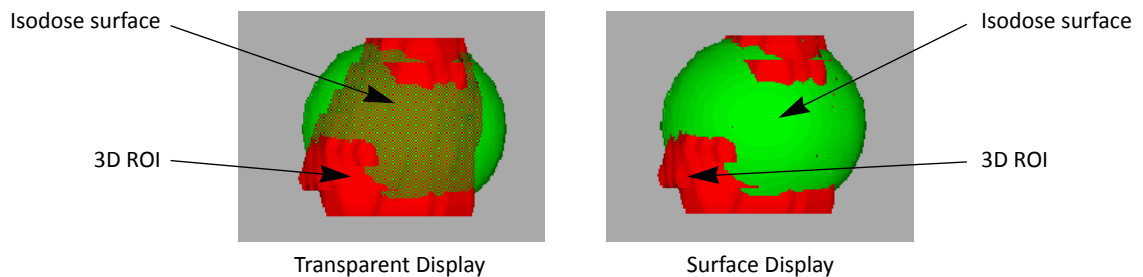


- 4 Select **Surface** or **Poly Surf** as the 3D display mode for all ROIs that you want to see as solid surfaces in 3D.
- 5 Select **Utilities - Data Sets**.
- 6 In the **Data Set Specifications** window, set the **Render** option to **No**.
- 7 Click **Close** to close the **Data Set Specifications** window.

NOTE

To see the isodose surface through the patient data, set the **Render** option to **Yes** and select **Transparent Dataset On** from the **3D** menu of the 3D viewing window in which you want to view the image.

- 8 In the **Evaluation** panel, turn on the 3D display for the isodose value you want to view as an isodose surface.
 - To see through the isodose surface to the target volume, select **Transparent** as the 3D display mode.
 - To see only the portions of the target volume that are not covered by the isodose surface, select **Surface** as the 3D display mode.



- 9 Select **Render** from the **3D** menu of the viewing window you set up in step 1.

NOTE

To have the image update automatically after rotating or zooming the image, open the **3D** menu and select **Render New Image - After motion complete**. To have the image update continuously, select **Render New Image - After any view change**.

Obtain point dose information

Once dose has been computed, you can obtain dose information for any point in the patient volume.



CAUTION

Because isodose lines can be smoothed and interpolated, it is possible that a prescription point will not comply with the isodose lines. Under such conditions, the point should be taken as the sole indicator of dose.



- 1 Click the **Eval** button at the top of the window to display the **Evaluation** panel.
- 2 Click the **Max dose point display** button.

The **Maximum Dose Point Display** window appears.

- 3 To display the maximum dose point within the dose calculation grid in the viewing window, select **On** as the **Display** option.

If you set up multiple trials, use the **Coordinates of max dose point for trial** option list to select the trial you want to use to view the maximum dose point coordinates. To view a different trial in a viewing window, press the **t** key with the cursor in the viewing window.

The maximum dose point displays on the appropriate slice, and the name of the trial or record appears in parentheses after it. Record names are indicated with an asterisk (*).

- 4 Click the **Close** button.



CAUTION

Different trials may have different doses. So that you are aware of which trial's dose you are viewing, check the trial name in the upper corner of the POI dose report.

- 5 To display the dose to any point of interest, click the **Point of Interest Dose Table** button in the **Evaluation** panel.

The **POI Dose** report appears and displays the total dose to each point of interest as well as the dose contribution from each beam to the total dose. Dose is displayed for all POIs in the plan, even for those added after dose is computed. When prior dose is included (the **Dose Display Mode** is either **Prior Dose Only** or **Current Dose and Prior Dose**), the prior dose to each point of interest is also displayed. Click the **Close** button when you finish reviewing the **POI Dose** report.

NOTE

The dose at each point is linearly interpolated from the dose grid.



When dose is computed, right-click in a 2D viewing window and then click the **Show image value 2D** tool to display the dose at the point in the CT image that corresponds to the current cursor position. The CT value and density for the point are also displayed at the bottom of the viewing window.

Evaluate trials with a scorecard

In the **Scorecard** window, you can define clinical goals and then evaluate how well the trials in the plan meet those goals. When you save your plan, the scorecard is saved along with it, although the computed results are not saved.

You can define goals for a plan, and then save those goals to a library to use with other plans.

 You can open the **Scorecard** window by clicking the **Scorecard** button at the top of the **Plan Evaluation** window. You can also open it from the **Utilities** menu in either the **Planning** window or the **Plan Evaluation** window.

About sample scorecards

There are sample scorecards in the scorecard library to provide you with a starting point as you develop your scorecards. These sample scorecards were developed based on RTOG protocols. We recommend that you create copies of the sample scorecards (by saving the sample scorecards with new names that are appropriate for your clinical practices) and then change the copied scorecards as needed.

NOTE
If you reinstall Pinnacle³ or install a new version of Pinnacle³, any changes you have made to the sample scorecards are overwritten and the original samples are restored. To retain your changes to the sample scorecards, save the sample scorecards with new names before you change them.

Create a scorecard

- 1 On the **Utilities** menu in either the **Planning** window or the **Plan Evaluation** window, click **Scorecards**, and then click **Scorecard Library**. The **Scorecard Library** window opens.
- 2 Do you want to create a new scorecard or create a copy of a sample scorecard?
 - Create a new scorecard—Click **New**. The **Scorecard** window opens.
 - Create a copy of a sample scorecard—Select a sample scorecard (or any existing scorecard) from the list and click **Load**. The **Scorecard** window opens. On the **File** menu, click **Save Scorecard to Library**. In the window that opens, type a name for the scorecard and click **OK**. The scorecard name displays in the **Name** field at the top of the **Scorecard** window.
- 3 In the **Description** field, type a description for the scorecard.
- 4 At the bottom of the window, click **Add Goal**, and then set the values for the goal appropriately.

Field	Description
ROI	ROI for which you set a goal (see <i>About ROIs and POIs in treatment techniques and scorecards</i> in the <i>P³IMRT Instructions for Use</i>)

Field	Description
Type	Type of goal. The goal is met under the following conditions: • Min DVH (%)—At the volume (%) that you specify in the goal, the dose that is delivered to the ROI is greater than or equal to the dose value that you specify in the goal. • Max DVH (%)—At the volume (%) that you specify in the goal, the dose that is delivered to the ROI is less than or equal to the dose value that you specify in the goal. • Min DVH (cm³)—At the volume (cm³) that you specify in the goal, the dose that is delivered to the ROI is greater than or equal to the dose value that you specify in the goal. • Max DVH (cm³)—At the volume (cm³) that you specify in the goal, the dose that is delivered to the ROI is less than or equal to the dose value that you specify in the goal. • Min Dose—The minimum dose that is delivered to the ROI is greater than or equal to the dose value that you specify in the goal. • Max Dose—The maximum dose that is delivered to the ROI is less than or equal to the dose value that you specify in the goal. • Mean Dose—The mean dose that is delivered to the ROI is less than or equal to the dose value that you specify in the goal. This goal is intended for use with OARs (organs at risk) rather than targets.
Primary Goal Dose Primary Goal Volume	Dose goal that the trial must meet. For dose goals that require a volume, set the volume for the dose goal.
Secondary Goal Dose Secondary Goal Volume	Dose goal that the trial should meet if the Primary Goal Dose cannot be met. (The Secondary Goal Dose is the goal that is less stringent but still acceptable.) For dose goals that require a volume, set the volume for the dose goal.

5 Continue to add goals and set the values until you are satisfied with the goals.

6 Do you want to use this scorecard for other plans?

- No—Continue to *Compute a scorecard*.
- Yes—On the **File** menu, click **Save Scorecard to Library**. In the window that opens, type a name for the scorecard and click **OK**. The scorecard name displays in the **Name** field at the top of the **Scorecard** window. Continue to *Compute a scorecard*.

Compute a scorecard

Before you compute a scorecard, compute dose for the trial that you want to evaluate. If you have already created a scorecard for this plan, you can open the **Scorecard** window and go to step 3.

When prior dose is included, the **Dose Display Mode** (either **Prior Dose Only** or **Current Dose and Prior Dose**) displays to the left of the trial name. See *Assess the impact of prior dose*.



CAUTION

Scorecard results are intended to be used in conjunction with other plan evaluation tools. We recommend that you follow the established clinical procedures for plan review and approval.

- 1 On the **Utilities** menu in either the **Planning** window or the **Plan Evaluation** window, click **Scorecards**, and then click **Scorecard Library**. The **Scorecard Library** window opens.
- 2 Create a scorecard (see *Create a scorecard*) or load a scorecard from the library. To load a scorecard, select the scorecard from the list and click **Load**.

If you have a large number of scorecards, you can filter the list using search terms. For example:

- To display only those scorecards with the word “breast” anywhere in the name, type “breast” in the **Scorecard Name** field and click **Filter**.
- To display only those scorecards with the words “head and neck” anywhere in the name and the words “DMPO trial” anywhere in the description, type “head and neck” in the **Scorecard Name** field, type “DMPO trial” in the **Description** field, and then click **Filter**.

Click **Show All** to clear the filter and show the full list again.

- 3 In the upper-right corner of the **Scorecard** window, select the trial that you want to evaluate.
- 4 Click **Compute**.

The software analyzes the trial and determines how well the trial meets the clinical goals. The results of the analysis display in the scorecard.

Field	Description
Dose	Dose statistic for the dose to the ROI that is used in the goal. The type of dose statistic that displays varies based on the type of goal: • Min DVH or Min Dose—Minimum dose from the trial to the ROI • Max DVH or Max Dose—Maximum dose from the trial to the ROI • Mean Dose—Mean dose from the trial to the ROI
Volume at Primary Goal Dose	For DVH goals, the actual volume receiving the amount of dose that is specified in the Primary Goal Dose
Result	Result of the goal: • Met—Primary Goal Dose is met • OK—Primary Goal Dose is not met, but Secondary Goal Dose is met • Not Met—Neither Primary Goal Dose nor Secondary Goal Dose is met

- 5 In the upper-right corner of the **Scorecard** window, select a different trial and click **Compute** to display the scorecard results for that trial.
- 6 Continue to select different trials and click **Compute** to see the results of the analysis for each trial and to compare the results of the different trials. You can also click **ROI Statistics** to view the statistics for the ROIs, if needed.
- 7 On the **File** menu, click **Close Window** to close the **Scorecard** window.

NOTE

When you compute a scorecard, the result may be unclear when the goal and the computed result are very close. For dose values, this is more likely to occur when the **Dose Display Decimal places** field in the **Preferences** window has a low value. For example, a goal may display as **Not Met** even when the values for the **Primary Goal Dose** and **Dose** appear to be the same. When this occurs, the two values differ, but the difference is so small that the difference is not evident because there are insufficient decimal places displayed to show the difference. To avoid this issue with regard to dose values, set the **Dose Display Decimal places** field to a higher value.

Delete a scorecard

- 1 On the **Utilities** menu in either the **Planning** window or the **Plan Evaluation** window, click **Scorecards**, and then click **Scorecard Library**. The **Scorecard Library** window opens.
- 2 Select a scorecard from the list and click **Delete**.

Evaluate plans with dose volume histograms



CAUTION

The DVH default is normalized to the percent of maximum dose. The maximum dose is the maximum anywhere in the dose grid and may cause the DVH to be misinterpreted. We recommend that you select absolute dose or specify the maximum dose rather than using the default. For detailed information about how maximum dose is calculated, see the *Pinnacle³ Planning Reference Guide*.

You can summarize the dose distribution for selected regions of interest (ROIs) across multiple trials with dose volume histograms (DVHs). You can also summarize dose distribution for ROI groups across both trials and records. DVHs provide plots of normalized or absolute dose versus normalized or absolute volume. From the DVHs you can determine the distribution of dose within given volumes. However, the DVHs do not provide any spatial information about the dose distribution.

If any of the trials selected in the DVH include prior dose (the **Dose Display Mode** is either **Prior Dose Only** or **Current Dose and Prior Dose**), then those trials are indicated in orange in the **Trials** list, and the text “Includes Prior Dose” displays on the DVH. See *Assess the impact of prior dose*.

NOTE

When you copy a plan to a new image set with or without deformation, prior dose values for the new plan will be slightly different than those of the original plan. Small differences in prior dose values are expected because the resolution, size, and alignment of the dose grid for each plan are inherently different.

- 1 To generate a dose volume histogram for an ROI, click the **Dose Volume Histogram** button near the bottom of the **Evaluation** panel.

The **Plan Evaluation** window appears. The **Dose Volume Histogram** panel is selected.



NOTE

To return to the **Dose Volume Histogram** panel from another panel, at the top of the **Plan Evaluation** window click the **DVH** button.

- 2 In either the **Trials** list or the **Trials and Records** list on the **ROI Group** tab, select the **Display** check box for the trials or records that you want to evaluate. If you want to display multiple items, use the **Line Type** option lists to distinguish among DVH line types.

You can clear the **Display** check box for an item to remove all DVH lines for that trial or record.

- 3 In either the **ROIs** list or the **ROI Groups** list on the **ROI Group** tab, select the **Display** check box for the ROIs or ROI groups that you want to evaluate. The DVHs appear for the ROIs in the selected trials and records using the current DVH calculation and display options.

You can clear the **Display** check box for an ROI or ROI group to remove all DVH lines for that ROI or ROI group.

NOTE

If beams are re-weighted or recalculated or if ROI volumes change, the DVHs are automatically recalculated.

NOTE

The color of the DVH line is linked to the ROI or ROI group color, so the line color cannot be changed.

NOTE

You can obtain NTCP and TCP response values for an ROI using the Lyman-Kutcher model. In the **Plan Evaluation** window, select **Utilities - Edit NTCP/TCP**. For more information, see the *Plan Evaluation Tools* chapter in the *Pinnacle³ Planning Reference Guide*.

NOTE

For proton spot scanning beams, if the energy defined for a beam is not sufficient to completely cover the target ROI, the software will compute dose for that beam for as much of the ROI as possible. Review the DVH for the ROI to confirm that the trial dose distribution is what you expect for the ROI, and adjust the plan if necessary.

- 4 In the **ROIs** list, enter a value for the 'a' parameter for each ROI. The generalized EUD (gEUD) equation requires a single parameter 'a'. The 'a' parameter controls the sensitivity of the gEUD computation to hot or cold dose areas within the specified ROI. (This parameter is not available on the **ROI Group** tab.)

Click the **Compute** button above the **gEUD** column to compute gEUD values. If you change dose or edit an ROI, the software invalidates gEUD values. If you change the 'a' parameter for an ROI after you compute gEUD values, the software automatically recomputes the gEUD value for that ROI.

- **a < 1**—appropriate for ROIs representing targets. As the 'a' value becomes smaller (or more negative), the gEUD computation becomes more sensitive to cold spots.
- **a = 1**—corresponds to the mean dose to the target.
- **a > 1**—appropriate for ROIs representing critical structures. As the 'a' value becomes larger, the gEUD computation becomes more sensitive to hot spots.

NOTE

The 'a' parameter field (in the **ROIs** list) and the **Generalized EUD** field (in the **ROI Statistics** spreadsheet) appear only if you are licensed for Biological Evaluation.

- 5 Select the desired DVH calculation and axis display options. The DVH is automatically recalculated and displayed using the new settings.

Group	Option	Description
DVH Calculation	Cumulative	DVH displays the total volume that has received a given dose or more.
	Differential	DVH displays the distribution of dose received by each volume unit of the specified structure.
Dose Axis Display	Normalized Dose	The dose to the ROI is normalized to 1.0 (100%), and the dose axis of the DVH shows the percent of maximum dose to the specified ROI.
	Absolute Dose	The dose axis of the DVH shows absolute dose to the ROI (in cGy or Gy).
	Auto-Compute Max	Select this option to let the software compute the maximum dose value in the ROI. This option is selected by default.
	Specify Max Dose	Select this option to specify the maximum dose yourself. This option is commonly used with brachytherapy plans, which sometimes have high doses that fall outside the maximum range of the histogram. The percentage of the structure volume with a dose greater than the maximum histogram dose is shown in the % > Max column of the ROI Statistics spreadsheet.
Volume Axis Display	Normalized Volume	The volume is normalized to 1.0 (100%), and the volume axis of the DVH shows the percent of the ROI volume receiving a given dose.
	Absolute Volume	The volume axis of the DVH shows the actual volume (in cm ³) receiving a given dose.

NOTE

The software calculates the **% > Max** value by dividing the volume of all voxels whose values exceed the range of the last histogram bin by the total volume of the ROI. Therefore, the value that the software uses to calculate the **% > Max** value may not be the same as the value that you enter in the **Specify Max Dose** field.

- 6 If you want to view the DVH for an ROI in tabular format, select the ROI in the **ROI Statistics** spreadsheet and click the **Tabular DVH** button.

The tabular DVH display is controlled by the following parameters in the top section of the window. These controls also affect the graphical DVH display.

- **DVH**—Select the DVH for tabular display.
- **Include in plan report**—Choose whether the currently displayed tabular DVH prints with the plan report.
- **Set Number of Bins/Set Bin Size**—Choose how the DVH table is generated. Changes to these parameters also affect the DVH plots.
 - Use the **Set Number of Bins** option to specify the number of bins in the histogram. Bin size is calculated by dividing the maximum dose by the number of bins.
 - If you choose **Set Bin Size**, you can specify the size of the bins in the histogram in cGy. The number of bins are calculated by dividing the maximum dose by the bin size.
- **Columns**—Specify the number of columns used to display and print the tabular DVH.

- **Copy All Settings to Other DVHs**—Click this button to copy the tabular settings for the currently selected DVH to all other DVHs.
- 7 Use the **DVH Tools** to get dose and volume values for a point on a curve and to zoom into the graph.



- Click the **Track** tool, then click on or near a point on a curve. The dose and volume values appear in a box in the upper right corner of the graph. At the bottom of the box are the curve's trial and record information. Moving the mouse allows you to see the changes in values.

To switch to a different curve, click on the curve or select it from the list in the **ROI Statistics** spreadsheet at the bottom of the window. This selects the point on the curve at the same dose. To stop tracking, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click **Reset**.



- Click the **Box Zoom 2D** tool and click and drag to create a rectangle to define a subset of the graph to display. You can zoom further by clicking and dragging again. To reset the zoom level to the default setting, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click **Reset**.

Obtain ROI dose statistics



CAUTION

To obtain accurate statistical information on the dose in an ROI, the entire ROI must be included in the dose grid. Any portion of the ROI that is outside the dose grid is reported in the **% Outside Grid** column of the **ROI Statistics** spreadsheet.

The **ROI Statistics** spreadsheet in the **Dose Volume Histogram** panel of the **Plan Evaluation** window displays statistical information on the dose in a region of interest.

The **Line Type** column shows the line color and style for the corresponding line in the DVH.

NOTE

You can include dose statistics for all ROIs in printed plan reports. Also, the **Generalized EUD** field displays only if you are licensed for Biological Evaluation.

Compare dose

The **Dose Comparison** panel in the **Plan Evaluation** window allows you to compare dose between a trial and another trial, a trial and a record, or a record and another record. The two items to be compared appear side by side in 2D viewing windows.

The windows in the **Dose Comparison** panel work like other viewing windows. For example, you can compare the dose on multiple slices by scrolling through the anatomy.

Note that the two viewing windows do not operate independently. If you pan and zoom in one window, for example, the other window pans and zooms, too.

- 1 Click the **Dose Volume Histogram** button near the bottom of the **Evaluation** panel.

The **Plan Evaluation** window appears.



- 2 At the top of the **Plan Evaluation** window, click the **Compare** button. The **Dose Comparison** panel appears.
- 3 In the **Trial or Record** list above each 2D window, select the trial or record that you want to display. Records are indicated with an asterisk in the **Trial or Record** list.

About records in the Dose Comparison panel

A viewing window that displays a record will display the primary image set for that record, even when this image set is not the same as the primary image set for the current plan. The trial viewing window and record viewing window are synchronized, though, so that when you scroll through either image set, both windows scroll together.

For a record, you set up your display of isodose lines, POIs, and ROIs in the **Record Viewer** window. See *Use the Record Viewer and the Treatment Navigator*.

You can access directly the **Dose Comparison** panel from the **Record Viewer** window. On the **File** menu, click **Records**, then click the **Trial/Record Comparison** button.

Generate biological response comparisons

NOTE

The **Biology** panel is available only if you are licensed for Biological Evaluation. If you do not have this license, you can still obtain NTCP and TCP response values for an ROI using the Lyman-Kutcher model. In the **Plan Evaluation** window, select **Utilities - Edit NTCP/TCP**. For more information, see the *Plan Evaluation Tools* chapter in the *Pinnacle³ Planning Reference Guide*.

You can use the **Biology** panel of the **Plan Evaluation** window to view radiobiological response probabilities based on biological responses for selected ROIs across multiple trials. The responses are evaluated using the Källman S-model.

For information on how the responses are calculated, see the *Plan Evaluation Tools* chapter in the *Pinnacle³ Planning Reference Guide*.

If any of the trials selected in the graph include prior dose (the **Dose Display Mode** is either **Prior Dose Only** or **Current Dose and Prior Dose**), then those trials are indicated in orange in the **Trials** list, and the text “Includes Prior Dose” displays on the **Biological Response** graph. See *Assess the impact of prior dose*.



CAUTION

The data in the software database for calculated biological response probabilities is for reference only. We do not recommend or endorse these numbers for use in treatment decisions.



CAUTION

The software calculates the response values based on the dose grid resolution. However, the software calculates ROI statistics and DVHs based on the primary image set resolution. Therefore, the calculated responses may not match exactly what the ROI statistics or the DVHs would suggest.

- 1 Click the **Dose Volume Histogram** button near the bottom of the **Evaluation** panel.

The **Plan Evaluation** window appears.



- 2 At the top of the **Plan Evaluation** window, click the **Biology** button. The **Biology** panel appears.
- 3 Click the **Add Response** button to add a biological response to the comparison. The new response appears in the **Responses** spreadsheet.
- 4 Select the settings for the biological response. The settings and default values are based on entries in the biological response database. See *Customize the biological response database* for more information.

Field	Description
Display	Select the check box to display this biological response line.
Index	This value is a sequential number assigned to the biological response.
Type	Select either NTCP or TCP.
ROI	Select the ROI on which the biological response will be based.
Organ	If you selected NTCP in the Type field, select the appropriate organ type.

Field	Description
Tumor	If you selected TCP in the Type field, select the appropriate tumor type.
Stage	If you selected TCP in the Type field, select the appropriate tumor stage.
End Point	If you selected NTCP in the Type field, select the appropriate end point.
D50	The dose at 50% probability for avoiding normal tissue damage (NTCP) or controlling the tumor (TCP). This value is derived from the values that you selected in the Organ and End Point or Tumor and Stage fields. You can enter a custom value if desired. Value is in Gy or cGy according to your dose measurement unit selection in the Preferences window.
Gamma	This sets the sensitivity to changes in dose. This value is derived from the values that you selected in the Organ and End Point or Tumor and Stage fields. You can enter a custom value if desired.
Alpha/Beta	This affects the cell survival model. This value is derived from the values that you selected in the Organ and End Point or Tumor and Stage fields. Common Alpha/Beta ratios are 3 or 10 Gy. You can enter a custom value if desired.
Seriality	This indicates the seriality of the organ and end point selected, and it appears only for NTCP responses. You can enter a custom value if desired.

- To evaluate more than one response, repeat steps 3-4 as needed to add responses.

NOTE

To delete a response, select it in the **Responses** spreadsheet and click the **Delete Current Response** button.

- Select composite responses to be displayed from the **Composites** group. Use the option lists next to each one to select colors for the composite response lines.

NOTE

In order to view a **P+** composite response, you must define both **TCP** and **NTCP** responses.

NOTE

The software calculates the composites using all responses, including responses whose lines are not displayed.

- In the **Trials** group, select the **Display** check box for the trials you want to evaluate. If you want to display multiple trials, use the **Line Type** option lists to distinguish among biological response lines.

You can clear the **Display** check box for a trial to remove all biological response lines for that trial.

- Click the **Compute Responses** button. The biological and composite response lines appear in the **Biological Response** graph. Probability values for each response at 100% of dose appear to the right of the graph. The **Line Type** column shows the line color and style for the corresponding line in the **Biological Response** graph.

The graph displays the percent of dose vs. probability. For example, the value at 100% represents the probability for the response at the current dose level for the trial, while the

value at 90% represents the probability for the response if 90% of the trial dose level were delivered.

After you evaluate the responses for a trial, you can adjust the percent of dose delivered in the trial prescription to match the percent dose on the graph for the desired biological response probability.

NOTE

If you make changes to the values in the **Responses** spreadsheet, you may invalidate the computed responses. When a response is invalidated, its response line does not display in the graph, and dashes replace the probability value at 100% dose. Click the **Compute Responses** button to recompute the response.

Customize the biological response database

You can customize the biological response database of normal tissue complication and tumor control probability parameters for the Källman S-Model. You can modify existing organ and tumor profiles or create new ones. The software uses these profiles as default values in the **Biology** panel.

The biological response database installs with original “factory settings.” When you modify values in the database, you have the option of reverting to the factory settings at any time, even if you have saved your modifications to the database.

NOTE

The **Load New Factory Settings** button allows you to update the biological response database when new factory settings are distributed. Contact Customer Support for assistance.



CAUTION

Enter and review these parameters carefully. Most published data does not correspond to in vivo radiation response of normal or diseased tissue, so it is important that you do not use biological response probabilities as the only criteria for plan fitness.

Add or revise an organ profile

- 1 In the **Plan Evaluation** window, select **Utilities - Biological Response DB**. The **Biological Response Database** window appears.
- 2 Click the **Organs** tab.
- 3 To revise an existing organ, select it in the list. To create a new organ, click the **Add Organ** button.

NOTE

To delete an organ, select it in the list and click the **Delete Organ** button.

- 4 Enter the name of the organ in the **Organ** name field.
- 5 To revise an existing end point, select it in the list. To create a new end point, click the **Add End Point** button.
- 6 Complete the fields for the end point. For descriptions of the fields, see *Generate biological response comparisons*.

- 7 Repeat steps 5-6 as needed for each end point.

NOTE

To delete an end point, select it and click the **Delete End Point** button.

- 8 Repeat steps 3-7 as needed for each organ.
- 9 Do you want to use your changes just for this planning session, save your changes to the database, or revert to the original factory settings?
 - Use just for this planning session—Go to step 10.
 - Save to the database—Click the **Save Database** button. Go to step 10.
 - Revert to original factory settings—Select the end point to revert and click the **Revert End Point** button. Repeat for other end points as needed. Go to step 10.

NOTE

You can only use the **Revert End Point** button to revert end points included in the factory settings database; you cannot revert end points that you have added to the database. To revert end points that you have added, exit the plan without saving the biological response database.

- 10 Click the **Close** button.

Add or revise a tumor profile

- 1 In the **Plan Evaluation** window, select **Utilities - Biological Response DB**. The **Biological Response Database** window appears.
- 2 Click the **Tumor Sites** tab.
- 3 To revise an existing tumor, select it in the list. To create a new tumor, click the **Add Tumor Site** button.

NOTE

To delete a tumor, select it in the list and click the **Delete Tumor Site** button.

- 4 Enter the name of the organ in the **Tumor site name** field.
- 5 To revise an existing stage, select it in the list. To create a new stage, click the **Add Stage** button.
- 6 Complete the fields for the stage. For descriptions of the fields, see *Generate biological response comparisons* in this chapter.
- 7 Repeat steps 5-6 as needed for each stage.

NOTE

To delete a stage, select it and click the **Delete Stage** button.

- 8 Repeat steps 3-7 as needed for each tumor.
- 9 Do you want to use your changes just for this planning session, save your changes to the database, or revert to the original factory settings?
 - Use just for this planning session—Go to step 10.
 - Save to the database—Click the **Save Database** button. Go to step 10.

- Revert to original factory settings—Select the stage to revert and click the **Revert Stage** button. Repeat for other stages as needed. Go to step 10.

NOTE

You can only use the **Revert Stage** button to revert stages included in the factory settings database; you cannot revert stages that you have added to the database. To revert stages that you have added, exit the plan without saving the biological response database.

- 10 Click the **Close** button. When the software prompts you to save your changes to the database, click **No**.

ROI trending

You can use the **Trend** panel of the **Plan Evaluation** window to track the motion and view the volume of an ROI group.

NOTE

The **Trend** panel is available only if you are licensed for Dynamic Planning.

- 1 Click the **Dose Volume Histogram** button near the bottom of the **Evaluation** panel.

The **Plan Evaluation** window appears.

- 2 At the top of the **Plan Evaluation** window, click the **Trend** button. The **Trend** panel appears.
- 3 Select an ROI group to view.

NOTE

ROI groups are managed automatically when you use Dynamic Planning. However, an ROI Group Manager is provided to allow you to make changes when a manual ROI group is preferred over an automatic one, for example, or when ROI groups are not working as you wish. For more information, see *Manage ROI groups*.

Information about the motion and volume of the ROI group appears in numerical form in the table, and in graphical form at the bottom of the window. In the table, a record is indicated by an initial asterisk in the **Volume Description**.

The first ROI in the group has an Index value of 0 and is used as the reference, and the motion of the other ROIs in the group is calculated relative to this first ROI.

The **Relative Centroid Position** graph displays the motion in each dimension (**Delta X**, **Delta Y**, and **Delta Z**) and also displays the magnitude of change (**Delta Mag**) in all three dimensions. The **Total Volume** graph represents the total volume of the ROIs. The graphs refer to the ROIs by their index values in the table.

NOTE

If you modify any ROIs in the ROI group while the **Plan Evaluation** window is open, click the **Recompute** button to recompute the data in the window.

Generate dose profiles



CAUTION

Dose profiles cannot be generated until the dose has been computed for the plan.

You can generate dose profiles between any two points of interest.

- 1 Select **Utilities - Profile**.

The **Profile** window appears.

- 2 In the **Title** field, type a title that identifies the profile.
- 3 Select the points of interest to use as the profile's start and end points from the **First POI** and **Second POI** option lists.
- 4 Select the type of data you want to profile by selecting one of the data sets from the **Data set** option list. For a profile of dose values, choose the **Dose** data set.
- 5 Select the interpolation method to use for the dose profile. **Nearest Neighbor** interpolation is more blocky than **Trilinear** interpolation.
- 6 Do you want to view the Water Equivalent Thickness (WET) profile?
 - If yes, select the **Yes** button and specify the beam that you want to use from the **Use Beam** option list.
 - If no, select the **No** button.

NOTE

The **WET profile?** option only appears in the **Profile** window if you are licensed for proton treatment planning.

- 7 Click the **Options** button. The **Profile Options** window appears.
- 8 How do you want to display the bins?
 - To divide the bins of the profile into increments of centimeters, click **Specify Bin Width (cm)**. Then enter the width increment in the **Bin Width** field.
 - To display the bin in terms of the number of profile sampling points, click **Specify Bin Count**. Then use the **Bin Count** field to specify the number of sample points to display in the profile.
- 9 Click the **Close** button.
- 10 Click the **Create Profile** button in the **Profile** window to generate a dose profile.

Accumulate dose

You can calculate the dose accumulated in multiple trials or records associated with the primary image set.

Trials and records are only available for dose accumulation if the following requirements are met:

- The dose grids of the trials or records must overlap. Dose is accumulated only in the overlapping regions of the dose grids.
- The trials must be selected for treatment.
- The dose must be valid. In other words, you cannot accumulate dose from a trial that has approximate monitor units (MUs).
- The dose units must be the same. For example, you cannot accumulate dose from a record in which dose was computed in Gy and a trial in which dose was computed in cGy.
- Prior dose is not displayed. See *Assess the impact of prior dose*.



CAUTION

Accumulating dose creates a record, which contains copies of the ROIs (including boluses) and POIs in the plan. The copies are locked when the record is created. This means that if you edit the planning ROIs and POIs after accumulating dose, the changes will not be reflected in the record ROIs and POIs. If you use the edited ROIs or POIs in planning in conjunction with the unchanged versions in the record, the point doses, dose volume histograms, and inverse planning results may be misleading, as they rely on the accuracy of the objects. For this reason, if you edit ROIs or POIs after accumulating dose be sure to delete the dose accumulation record and create a new one.

- 1 Select **Utilities - Dose Accumulation**.
- 2 Select the trials or records to accumulate. Records are indicated with an asterisk.
- 3 If you want to weight the dose of a trial or record for accumulation, enter a **Scale** value. The default **Scale** value is 1, which will accumulate the dose from that trial or record at 100%. To weight the dose, enter a **Scale** value either less than or greater than 1. For example, a **Scale** value of .5 would accumulate 50% of the dose, or a **Scale** value of 1.2 would accumulate 120% of the dose.
- 4 Click **Accumulate**.

The software creates a new record, which includes the ROIs, POIs, and dose for the accumulated trials and records. POIs that were locked are unlocked. Any boluses in the accumulated trials are converted to ROIs. The new record displays in the **Record Viewer** window with a standard set of isodose lines for the accumulated dose.

To add comment text to the record that describes the trials or records for which you accumulated dose, select **File - Records**, and in the **Records** window, click the **Details** button. See *Manage records*.

Use multiple trials

Using the multiple trials option, you can first prepare aspects of a treatment plan as described elsewhere in this guide. You can then copy the plan, change aspects of it to set up slightly different scenarios, and then compare the plans to see which is more effective. For example, you can compare two beam configurations. For breast treatment planning, you could contrast a trial containing a 15-degree wedge versus a trial with a 30-degree wedge.

You can create as many comparative trials as you want, and the trials you compare can be as similar or dissimilar as you want. The following steps explain a common way to use multiple trials.

- 1 Develop your plan in the software.
- 2 Open the **Trials** window in any of the following ways:
 - Select **File - Trials**.
 - Right-click the **Trial** option list that appears at the top of the window.

If you have not developed a plan yet, you can start from this window by clicking **Add New Trial**. You can then enter a name for the plan in the **Trial Name** field.

- 3 To create a copy of the existing trial, select the trial (plan) you developed and then click the **Copy Current Trial** button.

A generic name for the copied trial appears in the list. Select this name and enter a more descriptive one in the **Trial Name** field.

- 4 Click the **Close** button.



CAUTION

Any changes you make to a plan are applied to the current trial. Verify that you are using the desired trial.

- 5 Click the **Trial** option list and select the copied trial you just created.

The trial you select becomes the current trial throughout the software. Any changes you make to a plan are applied to the current trial. If you print a plan, the information for the selected trial prints.



CAUTION

Viewing windows are not linked to the current trial. You must explicitly select the trial to display in a viewing window. Verify that you are using the correct trial in the viewing windows when planning.

NOTE

If you select a different trial, any beam's eye views (BEVs), room's eye views, or beam-relative views will revert to normal viewing windows, since the software does not know which beam should be referenced in the new trial. The only exceptions to this rule are BEVs and REVs set to display the **Current** beam.

You can view any trial in a 2D viewing window. The name of the current trial is displayed in the upper-left corner of the viewing window. To view a different trial:

- Right-click in a 2D viewing window and select **2D - Next Trial** until you see the trial you want.
- Position the cursor within a viewing window and then press the **t** key.
- Select a trial from the option list in the upper-right corner of the window.

- 6 Change variables of the new trial to create two similar but competing plans.

For example, if your original trial was a 4-field prostate trial, you could change the copied trial to be a 6-field prostate trial.

- 7 To compare the two trials, return to the **Trials** window and click the **Trial/Record Comparison** button. The two trials appear side by side for comparison in the **Plan Evaluation** window. See *Compare dose*.



- 8 To evaluate and compare dose distribution in multiple trials, click the **Eval** button at the top of the **Planning** window.

- **Isodose Line Display**—The isodose line display attributes (line color, 2D and 3D display settings) are common to all trials.
- **Maximum Dose Point Display**—Click this button to display the **Maximum Dose Point Display** window. This window works in conjunction with the **Dose Comparison** panel of the **Plan Evaluation** window. To see the maximum dose point for one of the multiple trials in the **Dose Comparison** panel, select the trial you want from the **Coordinates of max dose point for trial** option list.
- **Point of Interest Dose Table**—Click this button to display the **POI Dose** table. This table displays dose information for all the trials.

- 9 Use dose volume histograms (DVHs) to see which trial is delivering the best dose to the target volume.

Click the **Dose Volume Histogram** button near the bottom of the **Evaluation** panel.

The dose distribution of any ROI can be summarized by a DVH. You can set up the DVH to show each of the multiple trials so you can compare them as overlays in the graph.



WARNING

Selecting the wrong trial for treatment could cause injury to the patient. Verify that the trial you select for treatment is the one you want to use.

- 10 Return to the **Trials** window, select the trial to be used for treatment, and select **Yes** next to **Use selected trial for treatment?** You can select more than one trial for treatment.



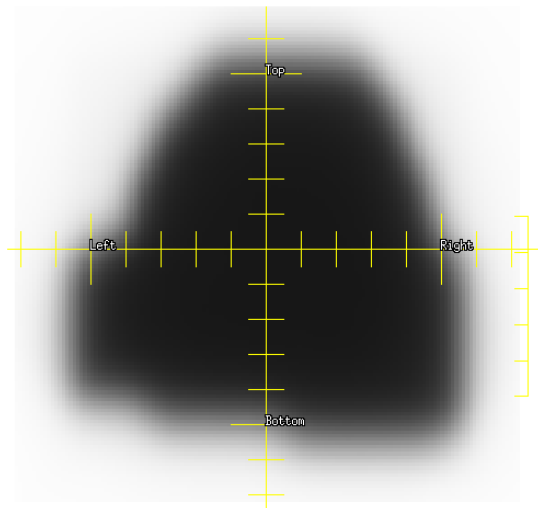
CAUTION

Do not delete the trial you will use for treatment. If you have not saved the treatment plan and you delete the trial, you cannot recover the most recent version of the trial. Verify that you are deleting the correct trial.

- 11 If a trial is no longer useful for comparison, you can select its name in the list and click the **Delete Trial** button. You must keep at least one trial in the plan.
- 12 To exit the **Trials** window, click the **Close** button.

Compute dose to a plane

The Planar Dose option lets you generate a two-dimensional dose array (planar dose) for any beam at a given depth in a flat water phantom or the current image set. The dose map is displayed by default in inverse greyscale. Planar dose maps may be printed or exported to files for comparison with measurements.



NOTE

In the sample dose plane shown above, the negative y-axis points upward in the beam's eye view because the machine was commissioned with the tray opening toward the bottom of the image. Pinnacle³ ignores collimator rotations for planar dose reconstruction, and the negative y-axis is always opposite the tray opening.

NOTE

The planar dose algorithm only computes dose within the volume of the patient or water phantom, including any extension you defined when you set up the dose grid.

See the *Pinnacle³ Planning Reference Guide* for more information on the planar dose settings.

Compute planar dose on static and step-and-shoot beams

- 1 Select **Utilities - Planar Dose**.

The **Planar Dose Computation** window opens.

- 2 Select the appropriate trial from the **Trial** option list.
- 3 Click the **Add Plane** button to add a new dose computation, or click the **Add Plane Per Beam** button to add dose planes for all beams in the trial.

NOTE

To delete the selected dose plane, click the **Delete Plane** button. To delete all dose planes, click the **Delete All** button.

- 4 If you want to label the dose plane, type a name in the **Name** field.

- 5 Click the **Beam** option list and select the beam for which you want to calculate dose.
- 6 Do you want dose calculated as if the beam is being delivered to a flat water phantom or the current patient image set?
 - Flat water phantom—In the image set option list on the **Planes** tab, select **Phantom**. The software computes planar dose based on the geometry of the beam that is selected.
 - Patient image set—Select **Primary data** from the image set option list on the **Planes** tab.

NOTE

If the beam is a proton beam, or if you added a static beam to compute planar dose on a plan that uses arc beams, conformal arc beams, dynamic arc beams, or beams with motorized wedges, select the **Primary data** option from the image set option list on the **Planes** tab.

- 7 If necessary, change the couch angle by typing a new value in the **Couch** field.
- 8 If necessary, change the gantry angle by typing a new value in the **Gantry Start** field.
- 9 If you selected **Primary data** in step 6, then go to step 11. Otherwise, go to step 10.
- 10 Type the source to plane distance (**SPD**) and the source to surface distance (**SSD**) of the beam to the phantom. Go to step 13.
- 11 Type the source to plane distance (SPD) of the beam in the **SPD** field.
- 12 If you selected **Primary data** on the **Planes** tab, the dose grid settings option list appears. You can then select one of the two options that follow:
 - **Compute beam**—The software computes planar dose based on the gantry and couch angles that you enter in the fields available and the geometry of the beam selected.
 - **Sample trial**—The software interpolates planar dose from the trial dose grid. Using the **Sample trial** option is equivalent to a composite dose. When prior dose is included, the **Dose Display Mode** (either **Prior Dose Only** or **Current Dose and Prior Dose**) displays on the planar dose image. See *Assess the impact of prior dose*.

NOTE

If the beam is a proton beam, or if you added a static beam to compute planar dose on a plan that uses arc beams, conformal arc beams, dynamic arc beams, or beams with motorized wedges, select the **Sample trial** option from the image set option list on the **Planes** tab.

- 13 On the **Dose** tab, use the **Resolution** field to set the resolution of the dose distribution. The smaller the resolution, the finer the dose display, and the longer the calculation time.

The TERMA grid resolution is determined by either the trial dose grid or the user-specified resolution. Therefore, you should set the planar dose grid resolution to match the TERMA grid resolution to avoid a loss of resolution in the planar dose image.

- 14 Set the dimensions of the dose map in the **Dimension** fields. As a default, the dose map dimensions are set to include a 1.5 cm margin around the exposed field.
- 15 If necessary, change the display color of the dose map in the **Color** option list.
- 16 Click the **Compute** button. When the planar dose computation is complete, the dose distribution appears in the viewing window.

The planar dose is computed in cGy/MU for the selected beam. If you chose to sample the trial dose grid, the dose values in the plane are in cGy or Gy, depending on the **Dose Display** setting in the **Preferences** window.

NOTE

If you are licensed for proton treatment planning and the trial contains a proton beam, dose values in the plane are computed in cGy(RBE) or Gy(RBE).



To compute multiple dose planes, click the **Compute** button for the first plane, and then click the **Redo spreadsheet** button to compute the remaining planes.

NOTE

The trial dose grid must be large enough to encompass all of the high dose region. Otherwise planar dose may be incorrect.

If necessary, you can use the 2D tools to modify the display and obtain information about the data. Right-click the planar dose viewing window to display the 2D menu and tools. See the *View Patient Data* chapter for details about the 2D tools.

Troubleshoot planar dose

- If the planar dose image appears to be cut off, go to the **Dose Grid** panel in the **Planning** window and extend the top or bottom slice of the CT image. This should make the rest of the planar dose image visible.
- On a plan with uncomputed beams, planar dose may not compute properly. To avoid this issue, compute all beams in the plan before computing planar dose.

Compute planar dose on other beam types



CAUTION

If you select **Primary data** and **Sample trial** for an arc beam, conformal arc beam, or dynamic arc beam, the software uses the gantry start angle for the arc to define the plane.

To compute planar dose on plans that use arc beams, conformal arc beams, dynamic arc beams, or beams with motorized wedges, add a new static beam to the plan and compute planar dose using the geometry of the static beam.

- 1 Compute dose on all beams in the original plan.
- 2 Add a new static beam. Ensure that the relative weight for this beam is zero.
- 3 Compute dose on the new static beam.
- 4 To define a plane within the dose grid, set the couch, collimator, and gantry angle for the static beam to reflect the desired plane orientation.
- 5 Compute planar dose for the new static beam. See *Compute planar dose on static and step-and-shoot beams*.

Use arbitrary point files for defining points on film

You can use a point file that defines the x,y,z locations of the planar dose pixels in world coordinates. This allows you to specify a spiral (or any other shape) phantom and compute dose to each point on the “plane.”

The point file is a space-delimited ASCII text file in the following format:

```
x_dim y_dim resolution
point1.x point1.y point1.z
point2.x point2.y point2.z
...
```

The following is a sample point file:

```
84 13 0.500
15.110 30.680 11.700
14.919 30.189 11.700
15.034 29.658 11.700
15.351 29.215 11.700
15.818 28.980 11.700
...
```

where 84 is the x dimension, 13 is the y dimension and 0.500 is the resolution. In this example there are 84×13 sets of x,y,z coordinates representing the world location of each pixel in the 84×13 pixel array.

NOTE

You can only use point files for dose planes that use the patient image set. You cannot use point files with water phantoms.

- 1 If a dose plane does not exist, create one before proceeding.
- 2 In the **Planar Dose Computation** window on the **Dose** tab, click the **File Input** button. The **Select Point File For Planar Dose** window opens.
- 3 Select the **Yes** radio button to use the point file for plane definition.
- 4 Use the directory tools to locate and select the point file.
- 5 Click the **OK** button.

Print planar dose

After you compute planar dose, you can print the dose plane.

- 1 In the **Planar Dose Computation** window, change the **Scale** value, if necessary, to print a dose display that is smaller or larger than the value currently shown.
A value of “1” creates a life-sized print of the dose distribution.
- 2 Click the **Print Using X:1 Scale** button. The **Print** window opens. Adjust the print settings as needed. For information about the settings, see the *Print* chapter.
- 3 Click the **Proceed** button.

- 4 From the confirmation dialog box that opens, choose **Yes** to print the image. Choose **No** to cancel printing.

Print planar dose to a DICOM printer

After you compute planar dose, you can preview and print the dose plane to a DICOM printer. You can also print the dose plane as a secondary capture or computed radiography image. For more information about how to print DICOM images, see the *Print* chapter.

- 1 In the **Planar Dose Computation** window, click the **DICOM Print Preview** button to preview the dose plane. Click the button again to return to the normal view.

When you print a dose plane using DICOM, the annotations are “burned” onto the image. Before printing, verify that the annotations do not overlap something important. If necessary, you can use the Pinnacle³ 2D tools to modify the display before printing.

You can choose which annotations are included when the dose plane is printed by selecting film annotation options in **Preferences**.

- 2 Click the **DICOM Print** button. The **Print** window opens. Adjust the print settings as needed. For information about the settings, see the *Print* chapter.
- 3 Click the **Proceed** button.
- 4 From the confirmation dialog box that opens, choose **Yes** to print the image. Choose **No** to cancel printing.

Export planar dose

After you compute planar dose, you can export the information to a file.

- 1 In the **Planar Dose Computation** window, type the name of the directory to which you want to export the file. If necessary, click the **Browse** button to locate a directory.
- 2 Select either ASCII or binary as the export format.
- 3 Do you want to export the selected dose plane or all dose planes?
 - Selected dose plane—go to step 4.
 - All dose planes—go to step 6.
- 4 Type a name for the file.
- 5 Click the **Export Plane To File** button. A message confirms that the dose plane was exported successfully. This procedure is complete.
- 6 Click the **Export All Planes To File** button. The software exports a file for each dose plane to the selected directory. File names are based on the dose plane names. A message confirms that the dose planes were exported successfully.

Use the Record Viewer and the Treatment Navigator

About records

A record is a view of data that cannot be changed. It includes information that is either historical in nature, or data that has been imported or generated. Pinnacle³ creates a record after you perform one of these tasks:

Task	Records created	Items in the records	Where to find more information
Copy a plan to a new image set	One record for each trial selected to be copied	ROIs, POIs, prescriptions, and dose	See <i>Create plans with Dynamic Planning</i> in the <i>Launch Pad Instructions for Use</i> .
Accumulate dose	One record	ROIs, POIs, and dose	See <i>Accumulate dose</i> .
Import DICOM RT dose	One record	Dose	See <i>Import plan information</i> .

The primary tool for viewing a record is the **Record Viewer** window. However, you can work with records in other tools, too, such as the **Plan Evaluation** window. Record names are indicated with an asterisk (*), and records display with their dose image set by default.

About the Record Viewer

The **Record Viewer** window is similar to the **Planning** window; it includes a subset of the features in the **Regions of Interest**, **Points of Interest**, and **Evaluation** panels.

Use the **View** menu to change the viewing window setup in the **Record Viewer**. You cannot change individual windows between 2D and 3D mode in this tool.

View a record

- 1 Click **Record Viewer** on the **Utilities** menu. The **Record Viewer** window opens.

You can also open the **Record Viewer** window from the **Treatment Navigator** window. See *Navigate to a trial or record*.

- 2 Select the record that you want to view from the list in the upper-right corner of the window. You can also type a **t** in a viewing window to see the next record.

The **Record Viewer** displays the dose image set associated with the selected record. This dose image set is identified in the **Dose Information** section of the **Evaluation** panel. However, you can display dose data on another image set. Type a **v** in a 2D viewing window or use the left and right arrow keys to see dose data on a different image set.

All ROIs and POIs that are associated with records display with dotted lines.

Compare records and trials

In the **Record Viewer** window, you can compare trials in the current plan and records using the following tools:

- ROI display in Planning—In the **Regions of Interest** panel, select **Yes** next to **Display record ROIs on all data sets** in order to display ROIs from this record on all data sets associated with the plan. For each record ROI that you want to display in the **Planning** window, set the 2D display mode in the **Record Viewer** window to either **Both** or **Poly**. ROIs from records display with dotted lines.
- POI display in Planning—In the **Points of Interest** panel, select **Yes** next to **Display record POIs on all data sets** in order to display POIs from this record on all data sets associated with the plan. POIs from records display with dotted lines in 2D viewing windows.
- ROI or POI display for all records—On the **Utilities** menu, click either **All ROI Display** or **All POI Display** to control the display of all ROIs or POIs in 2D and 3D viewing windows.
- Dose comparison—On the **File** menu of the **Record Viewer** window, click **Records**, then click the **Trial/Record Comparison** button. Records are indicated with an asterisk in the **Trial or Record** list. See *Compare dose*.
- DVH—In the **Plan Evaluation** panel, click the **Dose Volume Histogram** button. Use the options in the **ROI Group** tab to compare ROI groups across trials and records. See *Evaluate plans with dose volume histograms*.
- Isodose lines—In the **Plan Evaluation** panel, display isodose lines on the viewing windows. Click the **Line Details** button to manage the isodose lines and create ROIs from isodose lines. See *Display dose distribution information*.
- Maximum dose point display—In the **Plan Evaluation** panel, click the **Max dose point display** button to display the maximum dose point for any record associated with the plan. See *Obtain point dose information*.

View record prescriptions

If a record contains prescription information, you can view it by clicking **Prescriptions** at the bottom of the **Eval** panel. The **Record Prescriptions** window opens and shows prescription information for the current record. To view prescription information for a different record, select the record from the **Prescriptions for Record** list at the top of the window.

If you choose, you can add comments to the prescription information at the bottom of the **Record Prescriptions** window.

Manage records

- 1 On the **File** menu in the **Record Viewer** window, click **Records**. The **Records** window opens.
- 2 Select a record from the **Record List**.

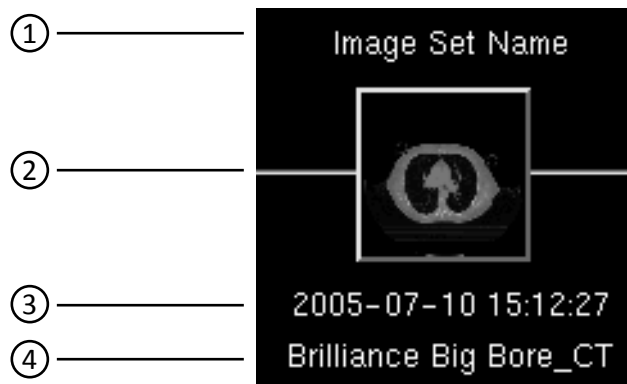
3 Perform any of the following tasks:

- Delete the record—Click the **Delete Record** button.
- Change the name of the record—Select the text in the **Record Name** field and type a new name.
- View record details—Click the **Details** button to view additional information about the record, including the date that the record was created and the dose image set associated with the record. For records that you create by accumulating dose, you can add comment text to describe each trial or record that was accumulated.

About the Treatment Navigator

The **Treatment Navigator** window allows you to navigate between the current plan and the records associated with the plan. The **Treatment Navigator** window opens when a plan has at least one record associated with it.

The **Treatment Navigator** window displays one icon for each image set. The icons are ordered from oldest image set to newest image set, left to right. The right-most icon represents the primary image set of the current plan. Each icon provides access to all records associated with that image set. The right-most icon also provides access to the trials in the current plan. A sample icon appears in the following illustration.



1	Image set name
2	Center slice of the image set
3	Image set date
4	Scanner name and modality

NOTE

The **Treatment Navigator** is only available if you have the Dynamic Planning license.

Navigate to a trial or record

- 1 In the **Treatment Navigator** window, select an icon by clicking it or by using the left and right arrow keys on the keyboard to navigate to it.

- 2 Click the selected icon or press the **Enter** key to open the **Record Viewer** window. For the right-most icon (the primary image set for the current plan), click the icon or press the **Enter** key to toggle between two windows:
 - the **Record Viewer** window for records associated with the image set
 - the **Planning** window for trials in the current plan

Evaluate plans with QA phantoms

The Copy to Phantom option lets you copy the beams from a plan to one of your stored quality assurance (QA) phantoms to verify the dose distribution or the dose at given points of interest.

Define a QA phantom



CAUTION

Define a QA phantom for each patient orientation you expect to treat. When you evaluate a plan, we recommend that the orientation of the QA phantom match the patient orientation in the plan. If the orientations do not match, the plan will be incorrectly oriented with respect to the phantom and you will not be able to accurately verify the dose distribution.



CAUTION

Do not select the Water Phantom option in the Edit Plan Data window when you add a plan to the phantom patient. If you select Water Phantom, you will not be able to save the plan as a phantom.

- 1 In the **Patient Select** window, add a patient in which to store phantoms.
- 2 Import the phantom images.
- 3 Add a plan that uses the images you just imported.
- 4 Click the **Planning** button to enter the treatment planning software.
- 5 In the **Confirm Plan Setup** window, verify that the patient orientation is correct.
- 6 Add POIs and ROIs to the phantom as necessary.

Choose names for the POIs that are different from names used in patient plans. During plan evaluation, it will be easier to differentiate between phantom and patient POIs if they have different names.

- 7 End the planning session and save the data files.
- 8 In the **Patient Select** window, click the **QA Tools** button. The **QA Tools** window appears.
- 9 Click the **Save as Phantom** button. The **Save Phantom** window appears.
- 10 Enter a name for the phantom.
- 11 Click the **Save** button.

Copy a plan to a QA phantom

NOTE

You cannot copy a plan that was created in Pinnacle³ version 8.0 or earlier to a phantom that was created in Pinnacle³ 9 or later.

If you have saved a data set as a QA phantom, you can copy a plan to the phantom for quality assurance and plan verification.

- 1 In the **Patient Select** window, select a patient and the plan you want to copy.

- 2 Click the **QA Tools** button. The **QA Tools** window appears.
- 3 Click the **Copy to Phantom** button. The **CT Patient/Directory List** window appears.
- 4 Select the phantom data set you want to use. We recommend that you use a phantom data set that has the same patient orientation as the patient plan you selected.
- 5 Click the **Import** button.

A new plan is added to the **Plans** list. This new plan is the result of copying the patient plan to the phantom plan. This is the plan you will use to validate your patient plan.

NOTE

When you copy a plan to a QA phantom, the following actions occur:

- The dose is invalidated.
- All boluses are removed from the plan.
- Each prescription in the new plan is set to the **Set Monitor Units** option.
- The MUs for each beam are retained.
- The dose grid is adjusted so that it covers the entire image set in the new plan.

Evaluate the plan



CAUTION

You cannot return to the **Phantom POI Adjust** window once you click the **Close** button. Be sure you are finished aligning the patient and phantom plans before you click the **Close** button.



CAUTION

The software does not prevent you from moving beams or POIs once you close the **Phantom POI Adjust** window. **DO NOT** change any beam or POI locations. If you change these settings, this plan will no longer match your patient plan, and the dose calculations you make will not be valid for your patient plan.

- 1 In the **Patient Select** window, select the plan that was created when you copied the patient's data to a phantom.
- 2 Click the **Planning** button.

The **Phantom POI Adjust** window appears. Use this window to align the coordinate systems of the patient and phantom plans.

- 3 In the **Target POI** option list, select the phantom POI you want to use as the target POI.
- 4 In the **Target Beam** option list, select the beam you want to align to the coordinates of the target POI.
- 5 Click the **Move beams to new position** button. The software aligns the POI of the target beam to the coordinates of the target POI. The spatial relationship between all beams and their associated POIs is maintained.
- 6 Click the **Close** button.
- 7 Adjust the size and location of the dose grid, if necessary.
- 8 Calculate dose for the beams.
- 9 Evaluate the results against film dosimetry, planar dose, or other measurements.

NOTE

When you back up patients that contain QA phantom plans, Pinnacle³ also backs up the phantoms. See the *Launch Pad Instructions for Use* for information on backing up patient data.

Delete a QA phantom

You can delete QA phantoms that do not have patient plans copied to them. If a patient plan is associated with a QA phantom, you must delete the plan before you can delete the QA phantom.

- 1 In the **Patient Select** window, click the **QA Tools** button. The **QA Tools** window appears.
- 2 Click the **Delete Phantom** button. The **CT Patient/Directory List** window appears.
- 3 Select the phantom to be deleted from the list and click the **Delete** button.
- 4 Click the **Close** buttons in the **CT Patient/Directory List** window and the **QA Tools** window.

Evaluate plans with DRRs

Use the **Plan Evaluation DRRs** window to view and print beam's eye views (BEVs) that help you verify the isocenter of a completed plan.

1 Select **Utilities - Plan Eval DRRs**.

If virtual setup beams are not configured, the **Select Setup Beam POI** window appears. In this window, you must select the isocenter and machine that the software uses to create the evaluation DRRs. Then, click the **Plan Eval DRRs** button to access the **Plan Evaluation DRRs** window.

If virtual setup beams are already configured, the **Plan Evaluation DRRs** window appears.

- To create DRRs for non-proton beams, see *Create non-proton beam DRRs*.
- To create DRRs for proton beams, see *Create proton beam DRRs*.

Create non-proton beam DRRs

For non-proton beams, you can display or print AP or PA, Left or Right, and Superior or Inferior DRRs to verify your plan.

1 In the **Plan Evaluation DRRs** window, select an orientation for viewing the DRRs.

NOTE

The software calculates the source to surface distance (SSD) using the CT to density table that you selected in the **Beam's Eye View Options** window. If you use a different CT to Density table in the **Plan Evaluation DRRs** window than you do in Planning, the SSD in the **Plan Evaluation DRRs** window may be slightly different than the SSD in your plan.

2 Specify the jaw positions for each beam. The default jaw names and positions are set in Physics during commissioning.

NOTE

If the machine is commissioned with stereotactic or electron energies and with no photon energies, you are not allowed to change the jaw positions. If the machine is a fixed jaw machine, you cannot change the jaw positions even though the software allows you to enter new values. The jaw position values are set as they were commissioned with the machine and you cannot change them.

3 If necessary, adjust the DRR display parameters in the **Plan Evaluation DRRs** window. Right-click in a viewing window and then click the **BEV Options** button. For more information on the display parameters, see the *View Patient Data* chapter.

NOTE

The window and level settings are percentages of the maximum DRR volume value.

4 To display all multi-leaf collimator (MLC) leaves for all beams in the trial, deselect the **Clip Setup MLCs** check box.

- 5 To change the isocenter or machine, select a different option from the **Isocenter** or **Machine** option list.
- 6 To print the DRRs, click the **Print Window** button. The **Print** window appears. For more information about how to print viewing windows, see the *Print* chapter.
- 7 Click the **Close** button.

NOTE

To delete all setup beams, click the **Delete Setup Beams** button. When you click the **Delete Setup Beams** button, the **Plan Evaluation DRRs** window and the **DICOM Export** window are both closed.

Create proton beam DRRs

For proton beams, you can display or print AP or PA, Left or Right, and Superior or Inferior DRRs to verify your plan, or you can specify an angle from which to create the DRR.

- 1 In the **Plan Evaluation DRRs** window, select an imaging device from the option list.
 - If you selected a continuous imaging device, go to step 2.
 - If you selected a fixed imaging device, go to step 4.

NOTE

The **Angle** and **SAD** values displayed in the window are the values that were commissioned for the imaging device.

- 2 Select an orientation for viewing the DRRs.
- 3 If you selected **Other** as the orientation, specify the angle that should be used to create the DRR.
- 4 If necessary, adjust the DRR display parameters in the **Plan Evaluation DRRs** window. Right-click in a viewing window and then click the **BEV Options** button. For more information on the display parameters, see the *View Patient Data* chapter.

NOTE

The window and level settings are percentages of the maximum DRR volume value.

- 5 To change the isocenter or machine, select a different option from the **Isocenter** or **Machine** option list.
- 6 To print the DRRs, click the **Print Window** button. The **Print** window appears. For more information about how to print viewing windows, see the *Print* chapter.
- 7 Click the **Close** button.

NOTE

To delete all setup beams, click the **Delete Setup Beams** button. When you click the **Delete Setup Beams** button, the **Plan Evaluation DRRs** window and the **DICOM Export** window are both closed.

Perform robustness analysis

NOTE

The robustness analysis option is only available if you are licensed for proton treatment planning.

Robustness analysis is a plan evaluation tool that lets you define different scenarios to evaluate how different setup or range errors will affect dose distribution. Robustness analysis can only be performed for proton beams. If a trial also contains beams that are not proton beams, the dose from those beams is considered as background dose to create scenarios.



- 1 Click the **Eval** button at the top of the window to open the **Isodose Lines** panel. Then click the **Dose Volume Histogram** button near the bottom of the panel.

The **Plan Evaluation** window opens.



- 2 Click the **Robust analysis** button at the top of the **Plan Evaluation** window. The **Robustness Analysis** panel opens.

On the **2D Dose Comparison** tab, you can view and compare the nominal dose and dose due to error side-by-side for each slice of the image set. The window on the left shows the dose distribution from the trial that is selected in the **Trial** option list. The window on the right shows the dose distribution from the scenario that is selected in the **Scenario** option list.

The 2D viewing window tools function the same in these viewing windows as they do in other 2D viewing windows in the software. For example, you can compare the dose on multiple slices by scrolling through the anatomy. Note that the two viewing windows do not operate independently. If you pan and zoom in one window, for example, the other window also pans and zooms.

Use the fields at the top of the panel to specify errors for the scenario.

- **Range Error**—Specify the percent by which the range should be shifted. Dose for each beam is recomputed assuming changes to the Water Equivalent Thickness (WET) based on the percentage that you enter.
- **Setup errors**—Specify errors in the setup by entering values in the **X Error**, **Y Error**, and **Z Error** fields. Dose is recomputed for each beam based on the error values.



NOTE

The **X Error**, **Y Error**, and **Z Error** values use the room coordinate system, not the patient coordinate system. The isocenters do not move with the patient.

Create a scenario

NOTE

In order to create a scenario, the trial must contain at least one proton beam and dose must be computed for all of the beams in the trial.

- 1 From the **Trial** list, select the trial that you want to evaluate.
- 2 In the fields at the top of the panel, enter the error parameters for the scenario.

- 3 Click **Compute Scenarios**. The software recomputes dose for the beams in the trial and displays the dose distribution for the scenario in the viewing window on the right. The scenario is saved to the trial that is selected in the **Trial** list.

NOTE

To cancel the creation of a scenario, click **Cancel** in the **Robustness Analysis Progress** window. The errors that have been computed are retained, but those that are in progress or not yet started are canceled.

NOTE

If a beam has a locked isocenter, that beam will not be shifted when dose is computed for the setup error scenarios. This can be useful when you have junction fields where each beam has a separate isocenter and you want to evaluate the robustness of the trials with individual beams that are shifted independently of the other beams.

NOTE

In some instances, the setup errors that you specified may result in a scenario in which dose needs to be computed in a Z plane that lies outside of the minimum and maximum Z-plane values that were defined for the machine during commissioning. If this occurs, a warning message appears indicating that dose could not be computed. To correct the problem, change the setup error for the scenario that could not be created and then create the scenarios again. Alternatively, you can change the dimensions of the dose grid in the trial so that the entire dose grid including the scenario error lies within the range of the Z-plane values. Dose for the trial is invalidated if you change the dimensions of the dose grid, and you will need to recompute dose for the trial.

Evaluate scenario dose with dose volume histograms

**CAUTION**

The DVH default is normalized to the percent of maximum dose. The maximum dose is the maximum anywhere in the dose grid and may cause the DVH to be misinterpreted. We recommend that you select absolute dose or specify the maximum dose rather than using the default. For detailed information about how maximum dose is calculated, see the *Pinnacle³ Planning Reference Guide*.

On the **DVH** tab in the **Robustness Analysis** panel, you can summarize the dose distribution for selected regions of interest (ROIs) across multiple trials with dose volume histograms (DVHs). DVHs provide plots of normalized or absolute dose versus normalized or absolute volume. From the DVHs you can determine the distribution of dose within given volumes. However, the DVHs do not provide any spatial information about the dose distribution.

- 1 Click the **DVH** tab. The dose volume histogram information appears.
- 2 In the **Scenario** list, select the scenario for which you want to view the DVH.
- 3 In the **Trials or Scenarios** list, select the **Display** check box for the trial or scenarios that you want to evaluate. If you want to display multiple choices, use the **Line Type** lists to set different styles for the DVH lines for each trial or scenario.

NOTE

The trial that is shown in the **Trials or Scenarios** list is the trial that is selected in the **Trial** list at the top of the **Robustness Analysis** panel.

- In the **ROIs** list, select the **Display** check box for the ROIs that you want to evaluate. The DVHs for the ROIs appear in the selected trials and scenarios using the current DVH calculation and display options.

NOTE

If beams are re-weighted or recalculated or if ROI volumes change, the DVHs are automatically recalculated.

NOTE

The color of the DVH line is linked to the ROI color, so the line color cannot be changed.

- Select the desired DVH calculation and axis display options. The DVH is automatically recalculated and displayed using the new settings.

Group	Option	Description
DVH Calculation	Cumulative	DVH displays the total volume that has received a given dose or more.
	Differential	DVH displays the distribution of dose received by each volume unit of the specified structure.
Dose Axis Display	Normalized Dose	The dose to the ROI is normalized to 1.0 (100%), and the dose axis of the DVH shows the percent of maximum dose to the specified ROI.
	Absolute Dose	The dose axis of the DVH shows absolute dose to the ROI (in cGy or Gy).
	Auto-Compute Max	Select this option to let the software compute the maximum dose value in the ROI. This option is selected by default.
	Specify Max Dose	Select this option to specify the maximum dose yourself. This option is commonly used with brachytherapy plans, which sometimes have high doses that fall outside the maximum range of the histogram. The percentage of the structure volume with a dose greater than the maximum histogram dose is shown in the % > Max column of the ROI Statistics spreadsheet.
Volume Axis Display	Normalized Volume	The volume is normalized to 1.0 (100%), and the volume axis of the DVH shows the percent of the ROI volume receiving a given dose.
	Absolute Volume	The volume axis of the DVH shows the actual volume (in cm ³) receiving a given dose.

NOTE

The software calculates the **% > Max** value by dividing the volume of all voxels whose values exceed the range of the last histogram bin by the total volume of the ROI. Therefore, the value that the software uses to calculate the **% > Max** value may not be the same as the value that you enter in the **Specify Max Dose** field.

NOTE

The DVH for a scenario is not saved when the plan is saved.

- 6 Use the **DVH Tools** to obtain dose and volume values for a point on a curve and to zoom into the graph.



- Click the **Track** tool, then click on or near a point on a curve. The dose and volume values appear in a box in the upper right corner of the graph. At the bottom of the box are the curve's trial and record information. Moving the mouse allows you to see the changes in values.

To switch to a different curve, click on the curve or select it from the list in the **ROI Statistics** spreadsheet at the bottom of the window. This selects the point on the curve at the same dose. To stop tracking, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click **Reset**.



- Click the **Box Zoom 2D** tool and draw a rectangle to define a subset of the graph to display. You can zoom further by drawing a rectangle again. To reset the zoom level to the default setting, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click **Reset**.

14 Import

Overview

If you are licensed for DICOM RT, you can import the following DICOM RT data:

- plans
- structure sets
- dose (where Dose Summation Type = PLAN)
- spatial registration

Before you attempt to import plan information into Pinnacle³, you must set up the patient, import the image sets, and create a plan in Launch Pad. For more information, see the *Launch Pad Instructions for Use*. For information about Pinnacle³ DICOM conformance, see *DICOM conformance* in the *Getting Started* chapter.

When you import image sets in Launch Pad with the intent to import plan data from that image set later via DICOM RT, the image set must conform to the following standards:

- To properly match the image data with the plan data, you must enter the correct Medical Record Number (MRN) in Launch Pad for the imported image set. If you do not, you cannot import the plan.

If you do not know the MRN, enter the other information in Launch Pad, open the **Select Images For Import** window and note the MRN that appears in the window. You can then return to Launch Pad and enter the correct MRN. Alternatively, you can choose to import the image set with patient demographics. For more information, see the *Launch Pad Instructions for Use*.

- When you import the image sets in Launch Pad, select the DICOM3File scanner type in the **Image Select** window.
- The **Select Images For Import** window displays the DICOM image sets that you can import. The names in the **Image Name** column will become the patient names for the images in Pinnacle³. Punctuation such as carets (^) indicate breaks in the name. For example, an image name of *FFS^Head^* will be considered a patient with the last name of *FFS* and the first name of *Head* in Pinnacle³. You can reduce error messages by entering the first and last names as the patient names in Launch Pad. However, these errors do not prevent you from importing plans via DICOM RT.

Transfer limitations

- In Launch Pad, if you make any of the following changes to an image set, you cannot import dose, structure sets, or spatial registration to that image set.
 - change the patient position
 - change the patient orientation
 - change the treatment position

- change the X/Y pixel size
- change the Z coordinate for a slice
- delete a slice
- You cannot import structure sets or spatial registration if the original plan was created on a decubitus image set.
- You cannot import structure sets, dose, or spatial registration if the original plan was created on an image set that is not found in the current plan.
- You cannot import structure sets if ROIs have contours that are not on a slice.
- You cannot import plans that contain segmented beams, dynamic wedges, motorized wedges, or sliding window beams.
- You can import plans and structure sets only if you used DICOM Image 4.2d or later to import the images in the plan.
- You can import spatial registration only if you used DICOM Image 9 or later to import the images in the plan.

Import plan information



CAUTION

When the import is complete, verify all information before continuing the planning process in Pinnacle³.

You can import plans (RT Plan), structure sets (RT Structure Set), dose (RT Dose), and spatial registration to any plan.

- 1 On the **File** menu, click **Import** and then click **DICOM**.

The **Import** window appears.

NOTE

If you know that new patients or messages have been transmitted to or deleted from the Pinnacle³ DICOM server since you last opened the window, click the **Refresh Lists** button.

- 2 In the **Patients eligible for import** list, select the patient that contains the information that you want to import.

To delete a patient from the list, select the patient and click the **Delete Patient** button. When you delete a patient, you remove the messages that are associated with the patient but retain any image files.

- 3 The **Available messages** list displays a list of messages that are associated with the selected patient.
 - Import all messages—Do not select any messages. Click the **Import** button. The software imports all messages that are associated with the patient.
 - Import one message—Select the message that you want to import. Click the **Import** button. The software imports only the message that you selected.

- Import multiple messages—Hold down the **Control** key and select the messages that you want to import. Click the **Import** button. The software imports only the messages that you selected.

To delete messages, select the messages that you want to delete and click the **Delete Messages** button. Hold down the **Control** key as you click to select multiple messages.

- 4 Click the **Close** button when the import is complete.

Imported Message Type	Result
RT Plan	The software creates a new trial and imports the plan data to that trial. The new trial becomes the current trial for that plan.
RT Structure Set	The ROIs and POIs in the structure set are added to the plan. If your plan already contains ROIs and POIs, the ROIs and POIs in the structure set are added to the plan in addition to the existing ROIs and POIs.
RT Dose	The software creates a new record and imports the dose data to that record. See <i>Use the Record Viewer and the Treatment Navigator</i> .
Spatial registration	The software registers the image sets in the plan.

Import beams from RadCalc

NOTE

The instructions in this section require the use of RadCalc. To purchase RadCalc, contact your Philips sales representative or local distributor.

If you want to import beams from an RT plan into Pinnacle³ but the beams contain multiple control points, use RadCalc to export a script file that contains the beam data. You can then run the script file to import the beams into Pinnacle³ for use in planning.



CAUTION

When the import is complete, verify all information before continuing the planning process in Pinnacle³.

NOTE

Specific directories are required to transfer files between Pinnacle³ and other software applications such as PlanIQ and RadCalc. For more information about these directories and instructions to change them, see the *System Administration* chapter in the *Pinnacle³ Launch Pad Instructions for Use*.

- 1 After you have exported the script file from RadCalc to the **RadCalc to Pinnacle** directory, click **Import** from the **File** menu, and then click **RadCalc**. The **RadCalc Import** window opens.

The **RadCalc Import** window lists the file name and date for each RadCalc script that matches the patient's MRN. If necessary, click **Refresh** to update the list of script files.

- 2 Select the script file that contains the beams you want to import.

NOTE

When **Delete upon import** is selected, the script file you selected is deleted from the **RadCalc to Pinnacle** directory after the beams are imported into Pinnacle³. This option is selected by default.

- 3 Click **OK** to run the script. The beams are imported into a new trial.

15 Export

Overview



WARNING

Plans may include the statement **NOT FOR CLINICAL USE**. Based on the machine or isotope data and the plan, the software determined that the plan cannot be delivered clinically. Do not treat patients with plans that are not for clinical use.

DICOM RT is the most common method of export. You can also export some plan information without using DICOM RT.

This chapter describes how to export the following:

- Export DICOM plan information
- Export laser localization coordinates
- Export blocks
- Export compensators
- Export MLCs
- Export to Calypso
- Export for record and verify systems
- Export for Mitsubishi DME record and verify systems
- Export files for RTOG submission

Export DICOM plan information



CAUTION

We recommend that you test the output from the software to your receiving DICOM system to confirm that parameters are being transferred correctly. Confirm that the plan information at the receiving system console is the same as the plan information you set up in the software.

For information about Pinnacle³ DICOM conformance, see *DICOM conformance* in the *Getting Started* chapter.

NOTE

You can export DICOM information only if you are licensed for DICOM RT.

NOTE

When you export a plan, DICOM RT samples the dose grid at the reference point specified in the **Monitor Units** window in order to determine the dose per beam to export. If you prescribe to something other than a POI, we recommend that you create a new POI in a region of the patient with the desired prescription dose. Specify this new POI as the dose reference point for each beam.

NOTE

If you are licensed for protons, all dose that you export is assumed to be cobalt-equivalent effective dose, not physical dose. For information, see the *Calculate Dose* chapter. For information about how the software exports dose, see the Pinnacle³ DICOM Conformance Statement, which is available on the Philips Healthcare website (www.healthcare.philips.com).

Transfer limitations

- In Launch Pad, make sure that the patient and plan information does not contain any of the following characters. If the patient or plan information contains these characters, you cannot export the plan.
 . ' ~ & () | < > + * \ / ; : @ ! [] #
- In Launch Pad, you must enter a last name, first name, and medical record number. If any of these fields are blank, you cannot export the plan.
- In Launch Pad, if you make any of the following changes to an image set, you cannot export structure sets, dose, or spatial registration for the modified image set. You can still export a plan, but the software does not include the isocenter in the plan.
 - change the patient position
 - change the patient orientation
 - change the treatment position
 - change the X/Y pixel size
 - change the Z coordinate for a slice
 - delete a slice
- You cannot export a trial that is not selected for treatment or that cannot be delivered clinically.

- You cannot export a locked plan that has been changed.
- You cannot export structure sets, dose, or spatial registration from a decubitus image set.
- You can export structure sets only if you used DICOM Image 4.2d or later to import the images in the plan.
- You can export spatial registration only if you used DICOM Image 9 or later to import the images in the plan.
- You cannot export an entire trial in one export if the trial contains both proton and non-proton beams. You must export the trial prescription-by-prescription in order to export all beams for that trial.
- You cannot export a proton plan for which dose is not computed.

Export plan information

DICOM RT Export must be configured properly before you can export DICOM information. For assistance with configuring DICOM RT Export, contact Customer Support at 1-800-722-9377 (US and Canada) or your local distributor. Contact the appropriate target system representative for details regarding your target system.

- 1 On the **File** menu, click **Export**, and then click **DICOM**.

The **DICOM Export** window opens.

- 2 Select the trial that contains the information that you want to export from the **Trial to export** list.
- 3 Select the destination to which you want to export plan information from the **Destination AE Title** list.

The **Destination AE Title** list identifies the possible DICOM target systems. If no choice is available, obtain the appropriate AE (Application Entity) title from your IT department, and then contact Customer Support or your local distributor for assistance in entering it.

- 4 Select the information that you want to export. See *Fields and buttons*.
- 5 Click **Transmit Data** to export the information to the AE destination.

If the export cannot be completed within the number of seconds you specify in the **DICOM Timeout** field, the export may fail.

NOTE

The Pinnacle³ software does not include a mechanism for the electronic approval of plans prior to export. For this reason, the software always exports the approval status of plans as UNAPPROVED. This information is explicitly stated in the following message that is displayed in the DICOM Export window:

“The Approval Status DICOM tag (300E, 0002) is always sent as UNAPPROVED.”

Fields and buttons

Title	Description
Trial to export	The trial that contains the information that you want to export.
Local AE Title	The local site from which you want to export the information.
Series Number Series Description	Enter a series number and series description to associate with the current export (optional).
Destination AE Title	The remote site to which you want to export the information.
DICOM Timeout	The amount of time (in seconds) before the software cancels the DICOM export.
DRR Resolution	If you will export RT Image or Setup Beams , set the resolution of the DRRs to be exported. The default value is 512, and you can set the value within the range 256–4096.
Plan Intent	Select the purpose for this export. Select None if you do not want to include this information in the DICOM export.
Transmit Data	Transmit (export) the selected information.
RT Plan	Export the prescriptions that you select. Only the prescriptions that have non-proton beams assigned to them will appear in the Prescription list. You can also choose which tolerance table the machine uses for the prescription. If a prescription uses multiple machines, you cannot export a tolerance table for that prescription. Relative couch shifts between the patient setup and the treatment positions are exported if the lasers have been set for the plan and the plan contains only one isocenter. If the plan contains multiple isocenters, then the shifts are not exported.
RT Ion Plan	Export the prescription that you select. Only the prescriptions that have proton beams assigned to them will appear in the Prescription list. The RT Ion Plan check box only appears if you are licensed for proton treatment planning.
Send SSDs in all arc control points	Include the Source to Surface Distance (SSD) for each control point in each arc beam that is in the prescriptions that you select for export. This option applies only to plans that use arc, conformal arc, and dynamic arc beams.
RT Structures	Export the ROIs and POIs that are associated with the image sets that you select. Only valid DICOM image sets appear under RT Structures. A DICOM image set is invalid if you changed any of the following for the image set: patient position, patient orientation, treatment position, X/Y pixel size, or the Z coordinate for a slice.
Select ROI	Click Select ROI to view the list of ROIs that are associated with the selected image sets. The Select ROIs to Export window opens. Select the ROIs that you want to export and then click Close. ROIs that are created by the Auto-Planning tool during optimization appear dimmed in the window if you set the Include Auto-Planning ROIs in plan output preference to No in the IMRT category of the Preferences window. See the <i>Utilities</i> chapter in the <i>Pinnacle³ Planning Reference Guide</i> for more information. Available only if you select the RT Structures and the related image set check boxes.

Title	Description
RT Image	Export a DRR for each treatment beam that is associated with the trial. Available only if you select RT Plan or RT Ion Plan . You can set the resolution of the DRRs to be exported in the DRR Resolution field.
Annotate Images	Annotate the treatment beam DRRs that you export. Available only if you select RT Image .
RT Dose	Export dose grids for the plan. The software allows you to export the following: • Dose per control point—Export a dose grid for each control point in each beam that is associated with the prescriptions that you select for export. (This option is not available if you select RT Ion Plan.) • Dose per beam—Export a dose grid for each beam that is associated with the prescriptions that you select for export. • Dose per prescription—Export a dose grid for each prescription that you select for export. Each dose grid is the sum of the dose grids for all beams in the prescription. • Sum of selected prescriptions—Export one dose grid that is the sum of the dose grids in the prescriptions that you select for export. • Current dose and prior dose—Export both the computed dose and prior dose. This option is available only when the Dose Display Mode in the Prescriptions window is set to Current Dose and Prior Dose. All other DICOM export options except DICOM Image are unavailable when prior dose is included. See <i>Assess the impact of prior dose</i>. The check boxes listed above are available only if you have computed dose and you select RT Plan or RT Ion Plan.
Spatial Registration	Export the spatial registration for each secondary image set.
DICOM Image	Export the DICOM image sets that you select. The software exports the original DICOM image set. Any changes that you made to the image set do not export.
Setup Beams	Export two setup beams for the isocenter that you select. If no setup beams are configured, the Select Setup Beam POI window opens and you must select the isocenter and machine for the setup beams. For proton DRRs, you can select imaging devices and orientations for the setup beams. Available only if you select RT Plan or RT Ion Plan.
Annotate Setup Beams	Annotate the setup beam DRRs that you export. Annotations include a crosshair, an orientation cube, and information about the plan, machine, energy, prescription, patient setup, and beam modifiers. Available only if you select the Setup Beams check box. You can set the resolution of the DRRs to be exported in the DRR Resolution field.
Setup Beam Viewer	Use the Isocenter and Machine lists to define the setup beam DRR that you want to export. For non-proton DRRs, use the orientation lists to view the DRR. However, the software always exports one left and one anterior setup beam DRR for the selected POI, regardless of the settings that you select in the orientation lists. For proton DRRs, use the Imaging Device lists to select imaging devices for the DRRs. If you select a Continuous imaging device, use the orientation list to view the DRR. For an orientation of Other, type an angle for the DRR. Available only if you select the Setup Beams check box.

Export laser localization coordinates

After you localize the patient and set up beams (beams must exist before you can export) or when the plan is completed, you can create files that contain a description of the plan's isocenter geometry using the specific coordinate systems of laser localization systems. These files can be used by the laser localization system to align laser marking devices to correspond to the plan.



CAUTION

Verify that you are using the correct trial when you export laser coordinates. And, export the laser coordinates using an appropriate file name so you can identify the patient and plan.

NOTE

You cannot export laser coordinates for a trial that is not selected for treatment or that cannot be delivered clinically.

- 1 Select **File - Export - Other**. The **Export** window appears.
- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the files.
- 3 In the **Category** list, select **Laser**.
- 4 In the **Laser alignment system** option list, select the laser localization system.

You can select a system for a single moveable (sagittal) laser or for three (one sagittal and two coronal) lasers.
- 5 In the **Isocenters to export** field, select the isocenters. Hold down the **Control** key to select more than one.
- 6 In the **Output file name** field, assign a name to the laser localization file.
- 7 Click the **Export Isocenters** button to create the files.

Export blocks

If you have an automatic block cutter, you can generate a file to transfer to the block cutter for block generation.



CAUTION

Verify that the block shape is correct for your treatment plan prior to exporting the block to a file.



CAUTION

Using an old block cutter output file may result in the incorrect blocks being cut for the plan. If you change the plan or use a different trial for your treatment, generate a new block cutter output file.

NOTE

You cannot export block cutter information for a trial that is not selected for treatment or that cannot be delivered clinically.

- 1 Click the **Beams** icon at the top of the window, and in the **Modifiers** tab of the **Beam** panel, click the **Output** button.

The **Export** window appears.

- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the exported file.

You can enter the directory path manually or click the **Browse** button and select the directory path you want.

- 3 Select the export format for the block cutter file.
- 4 Select the beam you want to export.
- 5 In the **Block file name** field, enter a name for the block file.

A default name appears according to the export format you selected.

- 6 In the **Block/Field edge overlap** field, enter the margin of overlap between the block and the edge of the field (if necessary).
- 7 Click the **Export Block** button to save the file to the specified directory.

Export compensators

After you complete your compensator design, you can export it to a file that can be taken to a milling machine.



WARNING

If you modify a compensator parameter without re-optimizing the compensator, the output compensator design will not take into account that change. Make sure the compensator is optimized with the current settings prior to generating an output file.

NOTE

You cannot export compensator information for a trial that is not selected for treatment or that cannot be delivered clinically.

- 1 In the **Compensator Editor** window, click the **Compensator Output** button. The **Export** window appears.
- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the exported file.
- 3 Select the export format for the compensator file.
- 4 Select the beam you want to export.
- 5 In the **Compensator file name** field, enter a name for the compensator design you are exporting.
- 6 Click the **Export Compensator** button to save the file to the specified directory.
- 7 After exporting the file, copy it to a disk for transfer to the milling machine.

Export MLCs

You can export MLC leaf positions to an ASCII text file in a number of formats.



WARNING

After exporting the MLC leaf positions, verify their accuracy by examining them in your MLC software. Incorrect leaf positions can result in incorrect dose.



WARNING

If you commissioned a machine using Pinnacle³ version 4.2f and enabled swapping of MLC leaf pairs and leaf order on export, you must recommission the machine before exporting will be allowed for any native format.



CAUTION

Using incorrect MLC leaf positions can expose or block the incorrect area on a patient. Verify the positions of the MLC leaves before exporting the positions to a file.

NOTE

You cannot export MLC leaf positions for a trial that is not selected for treatment or that cannot be delivered clinically.

- 1 Click the **Export MLC Leaf Positions** button in the **Beam MLC Leaf Position Editor** window. The **Export** window appears.
- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the exported file.

For Philips/Elekta export, the directory specified for export should be NFS-mounted to the Philips/Elekta MLC. By default, `/home/p3rtp` is NFS-exported. Therefore, you can create an Exports directory in `/home/p3rtp`, then specify `/home/p3rtp/Exports` in the **Specify Export Directory** field. The directory is then NFS-mounted to your Philips/Elekta MLC computer, so you can perform a direct import on the Philips/Elekta side. No disk copying is necessary.

- 3 Select the **MLC export format**.
- 4 Which format did you select?
 - **Varian**—enter an **Output ID** number. This ID number is the actual name of the file that is exported. Continue to *Export using the Varian format*.
 - **Philips/Elekta**—enter an **Output ID** number. This ID number is the Patient ID to be imported to the MLC and the name of the default directory. Continue to *Export using the Philips/Elekta format*.
 - **Toshiba**—enter an **Output ID** number. This ID number is the Patient ID to be imported by the MLC. Continue to *Export using the Toshiba format*.

Export using the Varian format



CAUTION

The Varian Shaper software limits block shapes to 100 points. If necessary, the software reduces the number of points during export to meet this requirement, but when blocking to an ROI, you might want to use the ROI point reduction tool to reduce the number of points yourself. You are thus assured that ROIs maintain the shape you want.

- 1 Specify the **File version** as **F** or **G** (F is not available for arc beams). If you select version **G**, enter a value in the **Leaf Position Tolerance** field. This value specifies the position tolerance (in cm) of the leaves during dynamic treatment.
- 2 Select the beams you want to export. Hold down the **Control** key as you click to select multiple beams.
- 3 Click the **Export All** button to export all beams, or click the **Export Selected** button to export only the beams that you selected.

Export using the Philips/Elekta format

- 1 Specify the MLC name in the **MLC Name** field.
- 2 Specify whether you are using an accessory in the beam path. If you select **Yes**, the software prompts you to enter the fitment code assigned to the accessory.
- 3 Select the beams you want to export.

Use the **Treatment** and **Beam Number** menus to specify treatment numbers and beam numbers for each beam you want to export. If you select **No Export** for either the treatment or beam number, the beam will not be exported. You cannot assign two beams to the same treatment/beam number pair.

- 4 Click the **Export** button to save the files to the specified directory.

Export using the Toshiba format

NOTE

You must calculate dose before MLC data can be exported in Toshiba format.

- 1 Select the beams you want to export.

Use the **Plan Number** menu to specify a plan number for each beam you want to export. If you select **No Export** for the plan number, the beam will not be exported. You cannot specify beam numbers; they increment automatically each time you select a plan number. You cannot have more than eight beams per plan, and you cannot assign two beams to the same plan/beam number pair.

- 2 Click the **Export** button to save the files to the specified directory. Toshiba will connect to your system via FTP and retrieve the files.

Export to Calypso

NOTE

When you scan the patient, use slices that are between 1 and 1.5 mm thick. If slices are thicker than 1.5 mm, the transponders may not be visible in the image set.

Contour the transponders

To export the location of each transponder, you must place a POI to mark each transponder's location. To accurately position each POI, we recommend that you contour each transponder and use the Autoplace POI feature to place the POIs.

- 1 Create an ROI for each transponder.
- 2 Contour each transponder on the primary image set.
- 3 Create one POI for each transponder that you contour. You must assign the POIs to the primary image set in order to export to Calypso.
- 4 Use the Autoplace POI feature to place each POI in the center of a transponder ROI. Select **Centroid** as the placement method. For more information, see *Place a point of interest* in the *Points of Interest* chapter.
- 5 If you want to define the treatment isocenter as the center of all transponders, create another POI and use the **Set Inside Multiple Regions** feature to place the POI in the middle of the transponder contours. Select **Centroid** as the placement method.

Export the transponder locations

- 1 Select **File - Export - Other**.
The **Export** window appears.
- 2 In the **Category** list, select **Calypso**.
- 3 In the **Trial to export** option list at the top of the **Export** window, select the trial that you want to export. The trial that you select must be the trial that is selected for treatment.
- 4 In the **Apex**, **Left Base**, and **Right Base** option lists, select the POI that corresponds to the appropriate transponder. You must select at least two transponders to export to Calypso.
- 5 In the **Isocenter** option list, select the treatment isocenter. You can only select a POI that is the isocenter for a beam. Therefore, you must add at least one beam to the plan.

NOTE

Only POIs that are assigned to the primary image set appear in the option lists.

- 6 Click the **Export** button.

Export for record and verify systems

After you calculate dose, you can export to a Record and Verify system. To see a list of the data exported by Record and Verify, see the *Pinnacle³ Planning Reference Guide*.



CAUTION

We recommend that you test the output from the software to your record and verify system to confirm that parameters are being transferred correctly. Confirm that the plan information at the record and verify system console is the same as the plan information you set up in the software.

Note that when exporting data using Record and Verify, the exported dose is the reference point dose (the isocenter, by default). If you prescribe a percentage of the reference point dose, the export data will still report 100% of the dose prescribed to the reference point.

NOTE

You cannot export using Record and Verify for a trial that is not selected for treatment or that cannot be delivered clinically.

NOTE

Before you can export with the Record and Verify feature, machines must first be commissioned for Record and Verify in Physics mode and the patient must have a medical record number assigned in Pinnacle³.

You may want to assign a field identifier to each beam before you export. Open the **Beams** panel and enter the field identifiers in the **Field ID** field.

If you are sending the file to a remote site, the file is first saved to a local drive and then transferred via FTP to the remote site. To make FTP transfers, the Record and Verify computer must be configured as an FTP server with a known login and password.

To use the Mitsubishi DME export format, please see *Export for Mitsubishi DME record and verify systems*.

- 1 Select **File - Export - Other**.

The **Export** window appears.

- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the exported file.
- 3 In the **Category** list, select **R & V**.
- 4 Select the **Record and Verify** format.
- 5 In the **File** name field, enter a name for the file you are exporting.



CAUTION

If you use any of the following characters when you enter a file name, the export may fail. Check the Export data fields for these characters before attempting to export:

. “ ‘ ` ~ & () | < > + * \ / ; : @ ! [] #

- 6 If you do not want to export MLC leaf positions, click the **No** button next to **Transmit MLC leaves**.

If the leaves of an Elekta/Philips accelerator MLC were set closer than the minimum tip distance, the software prompts you to set the leaves to zero before exporting.

- 7 Enter the **Course ID** you want the **Record and Verify** system to use.
- 8 In the **Tolerance table** field, enter the tolerance table value (1-9), which identifies a specific tolerance table on your Record & Verify system.

- 9 In the **Destination** field, select one of the following options:

- **Local**—your file is exported to the specified local directory. Go to step 11.
- **Remote**—several new fields appear. Go to step 10.

- 10 Fill in the fields so that the file can be exported via FTP to the remote site.

If you want to export the file to the top-level FTP directory, specify the directory as a period (.) in the **Directory** field. To export the file to any other existing directory, specify the directory by name.

If you want to save these settings as the default settings for future exports, click the **Save FTP Preferences** button. The password is not saved.

- 11 Click the **Export R & V** button.

If you try to export with a file name you have already used, you are asked if you want to continue. Click **Yes** to continue or **No** to cancel the export. If you cancel, rename the file and perform the export. An *.rtp* extension is added to the file name, and all plan information is sent to an intermediate interface for recording and verification.

Export for Mitsubishi DME record and verify systems

To see a list of the data exported by Mitsubishi DME Record and Verify, see the *Pinnacle³ Planning Reference Guide*.

Export guidelines

- The Mitsubishi Record and Verify software does not support the export of physical modifiers. If you export a trial that includes physical modifiers, a warning appears and the trial is exported without the physical modifier information.
- The Machine Type in the **Machine Editor** window of the physics tool must have “Mitsubishi” as the first word of the Machine Type. Also, if more than one machine type is used in the plan, then no data will be exported.
- The Mitsubishi Record and Verify software does not accept dynamic wedges. Therefore, in the **Wedge Editor** of the physics tool, the Wedge Angle (for RTOG) must be filled in with the wedge angle for the FIXED wedge being edited. If one or more beams contain a dynamic wedge, then no data will be exported.
- The Mitsubishi Record and Verify software only allows export of conformal arc beams if all the jaw positions are the same for all of the control points in a beam.

Export procedure

Before you can export plans using the Record and Verify feature, machines must first be commissioned for Record and Verify in the physics tool.



CAUTION

We recommend that you confirm that the plan information at the Record and Verify system console is the same as the Pinnacle³ plan information.

When you export data using Record and Verify, the exported dose is the reference point dose (the isocenter, by default). If you prescribe a percentage of the reference point dose, the export data still reports 100% of the dose prescribed to the reference point.

- 1 After calculating dose for your plan, in Launch Pad click the **Planning** button. The **Patient Select** window appears.
- 2 Select the patient, image set, and plan as you normally do in Launch Pad. Make sure the patient has a Medical Record Number, or no data will be exported.
- 3 In the **Patient Select** window click the **Planning** button to start Pinnacle³.
- 4 If you want to assign a field identifier to each beam, display the **Machine** tab in the **External Beam Treatment Planning** window. Enter the identifiers in the **Field ID** fields.
- 5 In the **Pinnacle Main Menu** click the **Plan** button. The **Plan Information** window appears.
- 6 Click the **Export Other** button. The **Export** window appears.
- 7 Select the **R & V** Category.
- 8 At the top of the **Export** window select the trial to export, and enter the directory path or click the **Browse** button and select the path in which to store the exported file.

- 9 Select the Mitsubishi record and verify format.
- 10 Click the **Export R & V** button.

If you try to export using an existing file name, you are asked if you want to continue. If you cancel the export, rename the file and perform the export again. Two files are created: TEMP1 (the export file) and TEMPID.dat (the export management file). For remote exports, the file is first saved to a local drive and then transferred via FTP. To make FTP transfers, the Record and Verify computer must be configured as an FTP server with a known login and password.

Export files for RTOG submission

Files can be created for electronic RTOG submission using a special exporting option. All plan information is saved in these files.

NOTE

You cannot export a file for RTOG submission for a trial that is not selected for treatment or that cannot be delivered clinically.

- 1 Select **File - Export - Other**.

The **Export** window appears.

- 2 Use the fields at the top of the **Export** window to select the trial you want to export and specify the directory where you want to store the files.
- 3 In the **Category** list, select **RTOG**.
- 4 In the **RTOG output file name prefix** field, enter the name to be used for the RTOG output files (for example, MSmith).

For compatibility with older PCs, restrict the name to eight characters.

- 5 Click the **Export RTOG Files** button.

Files are created with the prefix (for example, MSmith.001, MSmith.002, MSmith.003) in the specified directory.

16 Print

Overview



WARNING

Plans may include the statement **NOT FOR CLINICAL USE**. Based on the machine or isotope data and the plan, the software determined that the plan cannot be delivered clinically. Do not treat patients with plans that are not for clinical use.

You can generate reports that describe treatment plan setup and prescription, and graphically depict plan setup and isodose distributions.

This chapter describes how to:

- Print plan setup information
- Print viewing windows
- Print DICOM images
- Print blocks
- Print to PDF with P3PDF

Print plan setup information

Using the printer, you can generate reports that describe treatment plan setup and prescription, and graphically depict plan setup and the isodose distributions. Include this information in the patient's chart.



CAUTION

Make sure you verify all setup parameters, dose information, and MLC positions in the report against the same information as it appears on the screen.



CAUTION

On MLC reports, the leaf coordinates are Pinnacle³ coordinates, not the coordinates of the machine you are using. Make sure you review the Pinnacle³ coordinates on the report and how they relate to your machine before setting up your MLCs.



CAUTION

On reports that contain control points, note that jaw-related parameters such as OFc and unblocked equivalent squares are specific to the last control point. Dose-related parameters such as dose, MU, dose/MU, and normalized dose are for the overall beam.

- 1 Select **File - Print Plan**.

The **Trial Print Confirmation** window appears.

- 2 Select the type of report you want to print.
 - **Summary and Text Report**—Select this option to print the entire plan report.
 - **Summary Report Only**—The summary report includes information about beam setup, prescriptions, and isocenters. Go to step 4.
 - **MLC Report**—This report includes information about the multi-leaf collimator (MLC) included with the plan. Go to step 4.
- 3 Choose the plan information to include, such as ROI dose information, MLC information, a summary of an IMRT plan, a summary of the registration information, or a summary of the prior dose information.
- 4 For the beam's page option, select if you want beams grouped by modality or isocenter.

If you select **Modality**, beams of the same modality and using the same machine (and version) are printed on together. If you select **Isocenter**, beams of the same modality and assigned to the same isocenter, prescription, machine (and version), and localization are printed together. Up to three beams are printed per page.
- 5 In the **Comment** field, add any comments you want to include with the report.
- 6 If the plan contains more than one trial, select the trial for which you want to print a report.
- 7 Click the **Print** button.

NOTE

Note the **Revision** field in the report heading. The plan revision numbers show whether the ROIs, POIs, and dose have been modified since the last report was printed. For example, R03.P03.D03 would represent the third revision to ROIs, POIs, and dose.

NOTE

If you are licensed for Dynamic Planning and you chose to include a summary of the registration information in the plan report, information will only be included for those secondary images for which you approved the registration.

Select different printers and paper sizes

From the **Printer Selection** window, you can add and delete printers, edit printer information, and direct reports to a file or a different printer. For details, see the *Pinnacle³ Planning Reference Guide*.

Print viewing windows

The Color Print function provides three methods of printing windows on the color printer:

- **Click on window to be printed**—When the cursor changes to a diamond shape, click on the window you want to print. The window you select is scaled to fit the page.
- **Define rectangular area using cursor**—When the cursor changes to a corner () , click and drag a box to encompass the area of the screen to be printed. The area within the box is scaled to fit the page.
- **Specify a window by the ID number**—You can choose a window to be printed by specifying its ID number, which is in the title bar of the viewing window/window set in Classic Pinnacle³.

NOTE

If any area of the window you want to print is not displayed on the screen, that area will not print. Drag the entire window into view before printing it.

You can resize the image to fill the page or specify a zoom factor for the printed image. You can print a life-size image by specifying a zoom factor of 1. If the image you are printing will be used for cutting blocks, you can calculate the appropriate zoom factor by dividing the source to film distance by the SAD.

If the image does not fit on a page, it prints on multiple pages with registration marks so that the pages can be properly aligned.

Print a viewing window

NOTE

You cannot print DICOM images to film from this window. Use a BEV viewing window, as explained in *Print the DICOM image to film from a BEV window*.

- 1 Select **File - Print Window**.

The **Print** window appears.

- 2 Select a printing method.
- 3 Which print method do you want to use?
 - **Click on window to be printed**—go to step 7.
 - **Define rectangular area using cursor**—go to step 7.
 - **Specify a window by the ID number**—go to step 4.
- 4 Enter the ID number of the window to print. The ID numbers are in the title bar of the viewing window/window set in Classic Pinnacle³. By default, the software enters the ID number of the current window for you.
- 5 Select the window sizing option for the printed image.

**CAUTION**

Specifying a large zoom factor may result in a large number of pages being printed. The confirmation window displays the number of pages. You can decrease the number of pages printed by using the zoom tool to focus on a smaller area before specifying the print zoom factor.

- 6 In the **Zoom Factor** field change the zoom factor to the desired setting.
- 7 Use the **Report Comment** field to add any comments you want to include on the printout.
- 8 If necessary, click the **Select Printer** button and switch to a different color printer or paper size. The **Color Printer Selection** window appears.

For details on this window, see the *Pinnacle³ Planning Reference Guide*.

- 9 Click the **Proceed** button.
- 10 Did you choose to print an image using the window ID?
 - If yes, go to step 11.
 - If no, select the window or area you want to print. Then go to step 11.
- 11 From the confirmation dialog box that appears, choose **Yes** to print the image on the color printer. (Choosing **No** cancels the print job.)

Print a beam's eye view image to scale

You can specify a magnification factor for printing beam's eye view images that are similar to simulator films. This procedure assumes that you have set up a beam's eye view in a viewing window.

- 1 Set up the beam's eye view display for the beam you want to print.
- 2 Select **File - Print Window**. The **Print** window appears.
- 3 Select **Specify a window by the ID number**. The software enters the ID number of the current window for you.
- 4 Select **Resize Image by Zoom Factor** as the output image size.

**CAUTION**

Specifying a large zoom factor may result in a large number of pages being printed. The confirmation window displays the number of pages. You can decrease the number of pages printed by using the zoom tool to focus on a smaller area before specifying the print zoom factor.

- 5 In the **Zoom Factor** field enter the magnification factor. You can use the following equation to determine the zoom factor.

$$\text{Zoom factor} = \frac{\text{Source to film distance}}{\text{Source to axis distance}}$$

- 6 Use the **Report Comment** field to add comments to the printout.
- 7 From the confirmation dialog box that appears, choose **Yes** to print the image on the color printer. Choose **No** to cancel printing.

Print DICOM images

You can print DICOM images to film from a beam's eye view (BEV) window. In addition, you can print planar dose maps to a DICOM printer. See *Print planar dose to a DICOM printer* in the *Plan Evaluation Tools* chapter. For information about Pinnacle³ DICOM conformance, see *DICOM conformance* in the *Getting Started* chapter.

You also can capture DRR images or planar dose maps to send to an R & V system. See *DICOM print setup for delivery to an R & V system*.

NOTE

If you want to add or remove a DICOM printer, call Customer Support.

DICOM BEV print setup

- 1 Select **File - Print Window**.

The **Print** window appears.

- 2 Click the **Select Printer** button. The **Color Printer Selection** window appears.
- 3 Click the **Add Printer** button. The **Edit Color Printer** window appears.
- 4 Click the **Printer Type** option list and select **DICOM Printer**.
- 5 Make the following settings.

NOTE

This information is available in the conformance statement published by the printer manufacturer.

- Select an available DICOM printer from the **Printer AE Title** option list.
- Select whether the printer output is color or grayscale.
- Select the print medium, such as clear film or blue film.
- Select the size of the film.
- Select the destination bin to which the film will print on the selected printer.
- Select whether the printer supports collation.
- Select the magnification type, which specifies the interpolation algorithm used to fill in missing pixel values when magnifying the image.
 - **Cubic**—A polynomial surface algorithm creates a weighted average of the neighboring pixels. This is the slowest method, but produces the highest image quality. If you select **Cubic** magnification, you can specify the smoothing type. The greater the value you enter, the sharper the image appears. The range of values you can enter varies by printer; see your printer conformance statement for more information.
 - **Bilinear**—A bilinear algorithm creates a weighted average of a small neighborhood of four pixels.
 - **Replicate**—A nearest-neighbor algorithm duplicates the closest pixel value. This is the fastest method, but produces the lowest image quality.

- Set the print margin for your printer. The print margin should be documented in your printer's instructions. The software uses this margin to determine the maximum allowable magnification.
 - Specify the maximum density value of the printout. This value varies by printer; see your printer conformance statement for more information.
 - Specify the polarity of the printout, either **Normal** (x-ray) or **Reverse** (negative). When you select **Normal**, pixels with intensities of zero are black; when you select **Reverse**, pixels with intensities of zero are white.
 - Specify whether a trim should be added to the printout.
 - Specify whether empty areas of the image should appear in black or white.
 - If you selected a trim for the printout, specify whether the trim color should be black or white.
 - If any component of a print request is not completed within the number of seconds you specify in the **Timeout** field, the print job is cancelled.
 - If desired, you can enter a configuration string of non-standard options that further optimize printing quality. These strings are specific to the selected printer and manufacturer.
- 6 If you want to test the printer connection, click the **Test Connection** button.

**CAUTION**

We recommend that you measure the feature on the test print to ensure that the scaling is correct.

- 7 If you want to see an example printout, click the **Print Test Image** button.
- 8 When you finish editing the printer settings, click the **Close** button.
- 9 In the **Color Printer Selection** window, click the **Save Printers** button. If you do not click the **Save Printers** button, the printer setup information is lost when you exit the software.
- 10 Click the **Close** button.
- 11 Click the **Cancel** button in the **Print** window.
- 12 Determine which annotations you want to print with DICOM images. Select **Utilities - Preferences**. The **Preferences** window appears.
- 13 Select **Film Annotation** from the **Category** list and specify which annotations you want to include or exclude from the printout:
 - The comment entered with the patient demographic data in Launch Pad.
 - Machine information, including machine name, energy, and modality.
 - Beam geometry, including SSD, gantry start and stop positions, couch angle, collimator angle, and positions and names of each jaw.
 - Beam modifiers, including wedge name and angle, and presence of bolus and compensators.
 - Isocenter information, including isocenter name, explanation of coordinate system, coordinate labels and values, and body board angle. (This text is modified if the plan uses a stereo beam.)
 - Institution information, including the institution name, physician name, and planner's name.

- Prescription information, including prescription name, MU/fraction, number of fractions, and beam weight.
- 14 When you finish, click the **Close** button to use the settings for this session. To save the annotation settings, click the **Save Planning Preferences** button in the **Preferences** window, and then click the **Close** button.

Print the DICOM image to film from a BEV window

- 1 Right-click a 3D viewing window, select the **BEV** menu, and select the beam you want to view.
- 2 Right-click the BEV viewing window and click the **Preview** button.

Annotations appear on the BEV image as they will appear on the printout. If you want to turn some annotations off, open the **Preferences** window. Select **Film Annotation** from the **Category** list and specify which annotations you want to exclude.

Some required annotations appear at the top of the viewing window, including the patient name, patient medical record number, magnification factor, beam name, plan name, trial name, plan revision, Pinnacle³ version, timestamp, and notifications whether the printout may be used clinically and whether the localization system is valid.

Annotations may look small on the viewing window, but they are readable when printed on the film.

- 3 If you are satisfied with the print preview and the annotations, right-click the BEV window again and click the **Print** button. The **Print** window appears.
- 4 Adjust the print settings as needed and click the **Proceed** button.
- 5 Enter the life-size scale factor you want for the printed image. The window shows the maximum scale that will fit the image on a single film.
- 6 Click the **Print** button.
- 7 From the confirmation dialog box that appears, choose **Yes** to print the image. Choose **No** to cancel printing.

If you want to print another film, wait until the print confirmation message appears for the first printout.

DICOM print setup for delivery to an R & V system

You can capture DRR images or dose planes to send to an R & V system.

Contact Customer Support to configure the DICOM Remote AE Title. The representative will need to know the AE Title, host name, and DICOM port of your R & V system.

- 1 Select **File - Print Window**.
The **Print** window appears.
- 2 Click the **Select Printer** button. The **Color Printer Selection** window appears.
- 3 Click the **Add Printer** button. The **Edit Color Printer** window appears.
- 4 Enter the printer name.

- 5 From the **Printer Type** list select **DICOM Network**.
- 6 In the **Remote AE Title** list, select the AE Title of the location to which you are sending images.
- 7 Click the **Send Test Image** button to test the connection and output.
- 8 Click the **Close** button when you finish editing the printer settings.
- 9 In the **Color Printer Selection** window, click the **Save Printers** button. If you do not click the **Save Printers** button, the printer setup information is lost when you exit the software.

Print blocks

You can print the beam's eye view to scale and use the scaled output to cut the block. A scale factor of 1 generates a life-size image. To generate an image with a source-to-film distance (SFD) of 140 cm (assuming the SAD is 100 cm), enter a scale factor of 1.4. To determine a scale factor, divide the SFD by the SAD.



CAUTION

Specifying a large scale factor may result in a large number of pages being printed. Review the confirmation window to determine how many pages will print. You can decrease the number of pages printed by using the zoom tool to zoom in on a smaller area before specifying the print zoom factor.

If the scaled image is too large to fit on a page, the software splits up the image to print on multiple pages. When the image is printed on multiple pages, registration marks are printed on the images so the pages can be properly aligned.



CAUTION

Verify that the block shape is correct for your treatment plan prior to printing the block.

Print the block

- 1 Set up a beam's eye view with the block displayed in it.
- 2 Select **File - Print Window**. The **Print** window appears.
- 3 Select **Specify a window by the ID number**. The software enters the ID number of the current window for you.
- 4 Select **Resize Image by Zoom Factor** as the output image size.
- 5 In the **Zoom Factor** field enter the magnification factor.
- 6 Use the **Report Comment** field to add comments to the printout.
- 7 Click the **Proceed** button.
- 8 In the confirmation dialog box that appears, choose **Yes** to print the image on the color printer. Choose **No** to cancel printing.

Print to PDF with P3PDF

About P3PDF

P3PDF is a set of Pinnacle³ scripts (see *The Scripting utility*) that prints reports and windows to PostScript files and converts the PostScript files to a single PDF file. The reports and windows are grouped by patient so that each PDF file is for a specific patient and trial. P3PDF does not require a separate license.

Using P3PDF

All the settings for the PostScript files and generated PDF files come from the **Trial Print Confirmation** and **Print Window Confirmation** windows. For example, to include a comment, add it in the **Trial Print Confirmation** window and then use P3PDF.

- 1 Select **Utilities - Scripting**.

The **HotScripts** window appears.

- 2 In the **HotScripts** window click **Browse**.
- 3 Browse to `/usr/local/adacnew/p3pdf`.
- 4 Select `P3PDFReportManager.Script` and click **OK**. The **HotScripts** window changes to show a list of buttons that you can use to generate PostScript files and convert them to PDF files.
- 5 Use the list of buttons to create PostScript files and convert them to a PDF file. See the following table for information about each button.
- 6 Click the **Go to HotScript Main Window** button.

NOTE

We recommend that you add to your **HotScript** buttons a button to run `P3PDFReportManager.Script`.

NOTE

Every time that you run the P3PDF HotScript, the script removes PostScript and PDF files that are over a week old.

Field	Description
Create a Trial PS File	Print the report for the current trial to a PostScript file that can be converted to a PDF file.
Create a Window PS File	Select a window and print it to a PostScript file that can be converted to a PDF file. (You can print multiple windows.)
Create a Concatenated PDF File	Convert the PostScript files of the trial report and windows to a single PDF file. The PDF file is saved in the <code>/home/p3reports</code> folder. Each file is named <code>pinnaclePatient_MRN-TrialName.pdf</code> : • <i>MRN</i> is the patient ID (Medical Record Number). • <i>TrialName</i> is the name of the current trial.
Display the PDF File	Open a PDF viewer and display the PDF file that you created for the current patient and trial. You also can use this button to display an existing PDF file.

Field	Description
Delete All Temporary Files	Use this when you do not want the current PostScript files to be part of a PDF file.
Go to HotScript Main Window	Display your list of HotScript buttons again in the HotScript window.

17 Save Plans

Overview

You should save the plan frequently while planning, and before exiting the software. You can save your plan information at any time, set up an automatic save, and recover plans after a system error.

Save the plan



CAUTION

If you lose power to your system while you are saving a plan, it is possible that not all of the plan data was saved, causing anomalies in your plan. For example, when you re-open a plan the beams may not appear in the data set where you had placed them. Review any plan that you had open during a power loss to verify and correct the plan data.

The software provides three methods for saving your plans.

- **Save**—To save your plan while you are still working on it, select **File - Save Plan**.
- **Save on exit**—When you exit the planning software, it prompts you to save your plan. If you do not save the plan while exiting, the plan reverts to the last saved plan. If you do not save your plan at all, the plan reverts to its original, “un-planned” state.

Two additional save options are also available upon exiting the software:

- **Delete auto-saved computed files**—Delete any computed files that were created during the planning session. Plan elements that will be deleted include (but are not limited to) the following items: dose grid, control point dose, brachytherapy dose, DRRs, and compensators.
- **Delete stored control point dose for dynamic arc beams**—Remove dose from all control points in the plan. This option appears only if your plan contains a dynamic arc beam.
- **Save automatically**—In the **Preferences** window, you can set how often the software automatically saves your current plan. The time is set in minutes. The automatically saved plan is used only when there is an abnormal termination and recovery of the plan. You still must save the plan normally when you quit the planning software. See *Preferences* in the *Utilities* chapter.



CAUTION

If you exit normally without saving the plan, you cannot recover what you have done from the automatically saved plan.

Recover the plan

If a power failure or fatal error occurs in the software, the **Plan Recovery** window appears when you reopen the plan. Use the window to attempt to recover the last normally saved plan or the last automatically saved plan. You can review both plans before selecting the plan to accept and save.

The software initially loads the normally saved plan. At this point, you can review the plan. For instance, if you had been adding beams, you can click the **Beams** button to see what beams were saved for the plan. You can open all planning windows for review. If you cover up the **Plan Recovery** window while reviewing the plan, you can bring it forward by selecting **File - Save Plan**.

After you review the normally saved plan, choose one of the options in the **Plan Recovery** window.

- **Exit with No Changes**—Both plans are left intact and you exit the software.
- **Accept and Save Plan**—The currently loaded plan is saved and the other plan (in this case, the last automatically saved plan) is lost.
- **Review Last Auto-Saved Plan**—The software loads the last automatically saved plan, which you can review. The **Plan Recovery** window now lets you choose whether to accept and save this plan or review the last normally saved plan.

NOTE

You can switch between the two plans as many times as you like. You will not lose either plan until you accept and save one of them.

Plan locking

Plans can be locked to preserve the state of the plan. A locked plan is a read-only plan and changes cannot be saved. We recommend you lock a plan after it is approved for treatment.

When a plan is locked, a padlock icon is displayed next to the patient information above the viewing windows.

When you print a treatment plan and window for a locked plan, the printout indicates the locked status. You can print and export an unlocked plan. Prior to printing or exporting, the software may warn you that the plan is unlocked, depending on how you set the **Warn about unlocked plan** preference (see the *Utilities* chapter in the *Pinnacle³ Planning Reference Guide*).



CAUTION

In a locked plan you can make changes that modify the RPD (ROI, POI, and Dose) revision levels, but you cannot print or export plan information. Any changes you make will not be saved (the revision levels will increment while you are in the plan but will return to the locked revision levels when you close the plan).

You can delete, backup, and restore locked plans. During backup and restore, the software maintains the lock status.

Lock the plan

- 1 In Planning: Select **File - Lock Plan**. After you click **Yes**, the **Lock Plan** window appears.

OR

- 1 In Irregular Planning: Click the **Lock Plan** button. The **Lock Plan** window appears.
- 2 Enter your name or initials in the field. (You can use only numbers, letters, and underscores.)
- 3 Click the **Lock Plan** button. The plan is locked. You can still change the plan but you cannot save the changes. If you need to make changes that must be saved, you must copy the plan and modify the copy.

In Launch Pad an asterisk (*) appears next to the plan name to show it is locked. When you select the plan in Launch Pad, the user name, text entered when the plan was locked, and the date and time it was locked appear to the right of the plan list.

Unlock the plan

If you need to unlock a plan, you must copy the plan and modify the copy. The copied plan keeps the same RPD (ROI, POI, Dose) revision levels as the original plan.

18 Utilities

Overview

The table below contains a comprehensive list of the utilities available in Pinnacle³. The utilities that appear in the **Utilities** menu depend on the application that you are using (Planning, AcQSim³, or Image Fusion).

Utility	Description
Cutplanes	Open the Cutplanes spreadsheet. See the <i>View Patient Data</i> chapter.
Profile	Open the Profile window to generate dose profiles between two points of interest. See the <i>Plan Evaluation Tools</i> chapter.
Scripting	Open the scripting window to play or record scripts. This feature is explained in this chapter.
Preferences	Open the Preferences window to change global settings for the software. This feature is explained in this chapter.
Data Sets	Open a window that contains basic parameters for each data set in the plan. See the <i>View Patient Data</i> chapter.
Image Set Slice List	Open a window to see the Z position and SUV (standardized uptake value) scale factor of each slice in a selected image set.
Image Fusion	Open a window that lets you fuse images. See the <i>Image Fusion</i> chapter.
Transform	Display the tools needed to transform/fuse data sets. See the <i>View Patient Data</i> chapter.
Planar Dose	Open the Planar Dose Computation window. See the <i>Plan Evaluation Tools</i> chapter.
Plan Eval DRRs	Open the Plan Evaluation DRRs window. See the <i>Plan Evaluation Tools</i> chapter.
Planning	Open the Planning window. See the <i>Pinnacle³ Planning Instructions for Use</i> .
AcQSim	Open the AcQSim window. See the <i>AcQSim³ Instructions for Use</i> .
Record Viewer	Open the Record Viewer window. See the <i>Plan Evaluation Tools</i> chapter.
Dose Accumulation	Open the Dose Accumulation window, which allows you to select trials or records for dose accumulation. See the <i>Plan Evaluation Tools</i> chapter.
About	Open the information window that displays the software version number and other information.
All ROI Display	Display or hide ROIs in all 2D or 3D windows. This utility allows you to override the display settings for individual ROIs.
All POI Display	Display or hide POIs in all 2D or 3D windows. This utility allows you to override the display settings for individual POIs.
All Beam Display	Display or hide all the beams in 2D or 3D viewing windows. This utility allows you to override the display settings for individual beams.

Utility	Description
Clip MLC Leaves	Override the Clip leaves settings in the Beam MLC Leaf Position Editor window for the individual beams. Display or clip the MLC leaves for all beams in the plan. See the <i>Beam Modifiers</i> chapter.
Fill MLC Leaves	Override the Fill in leaves settings in the Beam MLC Leaf Position Editor window for the individual beams. Display the MLC leaves as outlines or as filled for all beams in the plan. See the <i>Beam Modifiers</i> chapter.
Max MLC Leaf Motion	Override the Maximum leaf motion settings in the Beam MLC Leaf Position Editor window for the individual beams. Display or hide the maximum leaf motion indicators for all beams in the plan. See the <i>Beam Modifiers</i> chapter.

Preferences

In the **Preferences** window you can specify separate preferences for either Classic Pinnacle³ and Planning (**Planning Preferences**) or AcQSim³ (**AcQSim Preferences**).

NOTE

You can only set preferences for the current tool. To set both **Planning Preferences** and **AcQSim Preferences** within the same window, see the *System Administration* chapter of the *Launch Pad Instructions for Use*.

If all users log in using the same name, one set of preferences is used for all system users. If you have separate login names (available with Solaris 8 or later), each user has their own preferences.

NOTE

Because preferences are specific to a software version, the default settings are used unless you change the Planning and AcQSim³ preferences for this software version. This means that the settings in the **Preferences** window revert back to the factory default settings after installation. Please review all preference settings before and after the installation, and save any edits following the installation of a new software version.

- 1 Select **Utilities - Preferences**. The **Preferences** window appears.
- 2 Set the preference options as desired. For more information about Auto-Segmentation preferences, see *Set up Auto-Segmentation Preferences*. The other options are described in detail in the *Pinnacle³ Planning Reference Guide*.
- 3 Click the **Save Planning Preferences** button.

If you do not save the preference settings, they are active for your current session only. If you do not save the preference settings for Auto-Segmentation, they are not active for any session.

The Scripting utility

The Scripting utility allows you to record and play back “scripts” of software operations. These scripts allow you to automate repetitive operations and store protocol plans for easy retrieval.

Scripts are similar to macros in other software products. A script executes a series of software operations when it is run. To create the script, you “record” the software operations you want to include in it. Scripts can be used for everything from repeating simple operations, such as setting the window and level for prostate CT data, to complex beam setup operations.

For details on advanced scripting options, see the *Pinnacle³ Planning Reference Guide*.



CAUTION

We recommend that you save your scripts to the **PinnacleSiteData/Scripts** directory. (This is the default directory when recording scripts.) Scripts you save in system areas such as **/PinnacleStatic** will be inaccessible when a new version of Pinnacle³ is installed.

All scripts that you create must be validated again if you install a new version of Pinnacle³.

Run HotScripts

The **HotScripts** window lets you play back scripts that have been recorded.



CAUTION

Using the incorrect script may add elements to your plan that change the treatment you are trying to achieve. Make sure you select the proper script and verify your plan after running the script.

- 1 Select **Utilities - Scripting**.

The **HotScripts** window appears.

NOTE

In the **Preferences** window, you can set up Pinnacle³ to always display the **HotScripts** window when the system starts.

- 2 Click the button for the HotScript you want to run. The operations specified in the script are performed.

NOTE

See the *Pinnacle³ Planning Reference Guide* for information on using the **Browse** button to play back script files that are not set up in the **Hotscripts** window.

Record HotScripts

To record a script, turn on the recording option, use the software as you normally would to perform the operations you want to record, and turn the recording option off when you are done. Once a script has been recorded, you can replay the script by clicking the appropriate button in the **HotScripts** window.

To make sure you record exactly what you want to record, see the *Pinnacle³ Planning Reference Guide*.

- 1 Select **Utilities - Scripting**.

The **HotScripts** window appears.

- 2 Click the **Edit** button in the **HotScripts** window to display the **Edit HotScript List** window.
- 3 Do you want to record a new script, record over an existing script, or add a script to the list (expand the list with another script)?
 - New script, in one of the fields that says “unassigned” delete the label and type an appropriate name for your script.
 - Record over a script, in the field that you want to record over, delete the label and type an appropriate name for your script.
 - Add a script, click the **Add** button. Replace the “unassigned” text with the appropriate name for your script.

NOTE

Script names cannot contain spaces or the following characters:

+ ? * < > [] | \ ` ' " & , / ! { } ()



CAUTION

Once you start recording, you cannot pause the recorder. You also cannot append one script onto another, so you must record all the steps you want to perform or run multiple scripts separately.

- 4 Click the **Record** button to the right of the HotScript name to begin recording, then perform the operations that you want to include in your script.
- 5 When you finish, click the **End Record** button to stop recording.
- 6 Click the **Done** button to return to the **HotScript** window where you can run the script.

Remove HotScripts from the HotScripts window

You can remove HotScripts from the **HotScripts** window or replace them with new HotScripts.

- 1 Click the **Edit** button in the **HotScripts** window to display the **Edit HotScript List** window.
- 2 Select the HotScript you want to remove and press the **Backspace** or **Delete** key to delete the name.

When you exit the **Edit HotScript List** window, the HotScript is unassigned and the unassigned button is moved to the bottom of the **HotScripts** window.

19 Tools

Data sets

These tools appear in the **Data Set Editor** window.

Tool	Name	Function
	Display one MPR layout	Examine a specific slice. To examine a slice, click on the slice and then click this tool.
	Display multiple MPR layout	Return to a view of multiple images after examining a specific slice.
	Display three MPR, one 3D layout	View a compound layout to help you select the patient orientation. The layout consists of transverse, sagittal, and coronal views in 2D, a 3D window, and a set of basic 3D tools. For details on using the 3D tools, see <i>3D images</i> .

Image Fusion and Syntegra

These tools appear in the Image Fusion and Syntegra windows.

Tool	Name	Function
	Move secondary	Align the secondary image set over the primary image set. When moving an image set in one viewing window, the movement appears in all viewing windows.
	2D fine-tune shift	Shift the secondary image set in small increments by clicking at the top, bottom, left, or right part of the image. To change the increment, select Options - 2D Tool Parameters . The default incremental move is 1 mm.
	Rotate secondary	Correct rotational errors between the images in any of the planes. This tool allows for free rotation of the image set.
	2D fine-tune rotation	Rotate the secondary image set in small increments by clicking the right half of the image for clockwise rotation and the left half for counterclockwise rotation. You can rotate the secondary image with respect to the primary image in any plane. The default rotational increment is 1 degree. To change the increment, select Options - 2D Tool Parameters .
	Undo previous transformation	Undo previous transformations that you have made to the secondary image set. You can undo all actions until you make the image set unmovable. Once it is unmovable, the transformation history is removed from the software's memory.
	Redo	Redo a transformation that you have just "undone."

Tool	Name	Function
	Place fiducial markers	Place fiducial marker pairs (points of interest) on the primary and secondary image sets. To move the primary point, click on the point in the primary image set or the fusion image. To move the secondary point, click on the point in the secondary image set. This tool is only available when you display the Points registration tab.
	Correlated pointer	Change the orthogonal slices that are displayed in the viewing windows. Position the cursor on a viewing window and click, then drag the lines until the desired slices are displayed in the other windows. When the slice position lines are displayed in all three orientations, you can use this tool to quickly display the transverse, sagittal, and coronal planes which cut through structures of interest. If used in a window that is not a transverse, sagittal, or coronal view, the tool displays orthogonal lines intersecting at the selected point, and it does not cause the other viewing windows to change slices.
	Zoom correlated pointer 2D	Change the orthogonal slices that are displayed in the viewing windows while zooming in on a region of an image. Drag diagonally until the region to be zoomed is within the box. The region of the image that is inside the box is magnified in the transverse, sagittal, and coronal viewing windows, and the orthogonal slices that are displayed are adjusted accordingly.
	Show secondary image cutout	In a 2D fusion viewing window, create a rectangular cutout on the primary image set that shows the overlay of the secondary image set just in that cutout. You can resize it by clicking and dragging its edges or corners. Its maximum size is 1/4 of the size of the viewing window. The cutout does not move if you move the image sets within that viewing window. You can move it if you click in the center of it and then drag it. It remains displayed until you click outside of it (with this tool still selected). This tool is available only in Syntegra.
	Adjust bounding box	Place a rectangle on the image set to define a sub-volume for use in automated registration. This is available if Limit Primary data , Limit Secondary data , or Limit both data sets is set to Bounding Box . This tool is available only in Syntegra.

2D images

You can access 2D tools in several locations. See *Access 2D and 3D tools* in the *View Patient Data* chapter for information. Use these tools to modify the display of 2D images and obtain information on the patient data.

Tool	Name	Function
	Scroll through slices	Scroll through the “stack” of transverse, sagittal, or coronal images in a viewing window. To scroll through a stack of images, drag the cursor to the left and right within the 2D viewing window. Clicking on the far left places you at the beginning of the series of slices. Clicking on the far right places you at the end of the series. When the cursor is in a viewing window, you can also press n to display the next image in the series and press p to display the previous image.
	2D pan	Use this tool to reposition the 2D image within the viewing window. Drag the cursor within the window until the image is positioned as desired.

Tool	Name	Function
	2D zoom	Increase and decrease the magnification of the image by dragging the cursor across the viewing window. Dragging to the left shrinks the image. Dragging to the right magnifies the image. The image remains centered in the viewing window, so you may need to use the 2D Pan tool to change the region of the image that is displayed.
	Box zoom	Draw a box around a region of the image that you want to zoom by dragging the cursor diagonally until the region to be zoomed is within the box.
	Show image value 2D	Display the image value for the point in the image that corresponds to the cursor position. The image values appear when you click and hold the left mouse button. If the dose has been computed, the computed dose and density at that cursor position also appear. If you are licensed for proton treatment planning, the stopping power and the Water Equivalent Thickness (WET) are also shown. Values are computed using the nearest-neighbor method.
	Distance display	Measure distances on an image. As you drag across the image, a line is drawn showing the distance being measured. The distance (in centimeters) is listed at the bottom of the image. If you are licensed for proton treatment planning, the Water Equivalent Thickness (WET) is also shown.
	Distance annotation	Use the tool to measure distances on an image and draw a distance indicator and label on the image. As you drag to draw a line, the line that you drew remains on the image and the distance (in centimeters) is listed on the image. If you are licensed for proton treatment planning, the Water Equivalent Thickness (WET) is also shown. Use the Delete annotation tool to remove the label from the image.
	Profile	Generate a profile of the numbers across any portion of the image. You can use the Profile tool to determine threshold values for autocontouring regions of interest or to compute maximum gradients when defining organ models. To generate a profile of image values, drag the cursor across the image. A window appears and shows a plot of the image values along the line that you drew.
	Window/level bar	Set the window and level for displaying 2D images. When you use this tool, the Window/Level color bar appears along the right edge of the viewing window in which you are adjusting the window and level. The green bar in the upper portion of the color bar sets the level. The red bar in the lower portion of the color bar sets the window. To change the level, click the green bar and drag the cursor up and down until the level is set as desired. The green bar does not appear if the level is negative, but clicking near the top of the color bar will make the green bar reappear (and make the level positive). To change the window setting, click the red bar and drag the cursor up and down until the window is set as desired.
	Window/level point	With the Window/level point tool, you can use the current window to set the level by specifying the center point of the window. The level is set so that the current window frames the image value at the cursor position. Position the cursor on the desired point and then drag the cursor to adjust the image.
	Window/level	Use the Window/level tool to specify the window and level by dragging the cursor within the viewing window. To change the level, drag the cursor up and down in the viewing window. To change the window setting, drag the cursor left and right. The window and level values appear at the bottom of the viewing window.

Tool	Name	Function
	Zoom correlated pointer 2D	Drag the cursor to draw a box around a region of the image that you want to zoom. When you release the mouse, transverse, sagittal, and coronal views all zoom to the same selected region. Slice position display is automatically turned on and centered in the selected region, and the Correlated pointer tool is automatically selected. You can use this tool to set up viewing windows before loading an organ model. See the <i>Model-Based Segmentation</i> chapter. Change the orthogonal slices that are displayed in the viewing windows while zooming in on a region of an image. Drag diagonally until the region to be zoomed is within the box. The region of the image that is inside the box is magnified in the transverse, sagittal, and coronal viewing windows, and the orthogonal slices that are displayed are adjusted accordingly.
	Correlated pointer	Change the orthogonal slices that are displayed in the viewing windows. Turn on slice position display, then drag the lines until the desired slices are displayed in the other windows. You can use this tool to quickly display the transverse, sagittal, and coronal planes that cut through structures of interest. You cannot use this tool in BRV windows. For information on slice position display, see <i>Display the slice position in other windows</i> in the <i>View Patient Data</i> chapter.
	2D annotation with label	Use the 2D annotation with label tool to add labels to 2D images.
	Delete 2D annotation	Use the Delete 2D annotation tool to remove annotations from 2D images. Click this tool and then click the annotation that you want to delete.
	2D cursor select	Click the tool with the middle mouse button to return the middle mouse button to its default state. The default state of the middle mouse button is to toggle between the Scroll through slices , 2D zoom , and 2D pan tools. The tool you activate with the middle mouse button is then selected by default when you click the left mouse button in a viewing window.
	Water equivalent thickness (WET) profile	Generates a Water Equivalent Thickness (WET) profile (gm/cm ²) between two points. To generate a WET profile, drag the cursor across the image. A window appears and shows a plot of the WET values for the current beam along the line that you drew.

3D images

You can access 3D tools in several locations. See *Access 2D and 3D tools* in the *View Patient Data* chapter for information. Use these tools to modify the display of 3D images.

Tool	Name	Function
	3D rotate	Rotate the image as if you were holding it in your hand and turning it to look at it from a different angle. With this tool selected, click on an edge of the volume limits to grab the volume and drag the cursor to rotate the volume.
	3D pan	Move the volume up, down, left, or right in the window. The volume's zoom factor and viewpoint do not change.
	3D zoom	Change the field of view for the volume. When you "zoom in" on the volume, the field of view is decreased, and the image appears larger. When you "zoom out" on the volume, the field of view is increased, and the image appears smaller.

Tool	Name	Function
	Rotate XY	Rotate the volume about the viewing coordinate system axes that extend out from the focus point in the middle of the viewing window. To rotate the volume about the y-axis, drag the cursor left or right within the viewing window. To rotate the volume about the x-axis, drag the cursor up and down.
	3D annotation	Label an ROI with its defined name after clicking on the ROI in a 3D viewing window. Annotations are not “linked” to the items you are labelling. For example, if you delete or rename an ROI, you must delete or rename the annotation separately.
	3D cursor select	Click the tool with the middle mouse button to return the middle mouse button to its default state. The default state of the middle mouse button is to toggle between the 3D rotate , 3D zoom , and 3D pan tools. The tool you activate with the middle mouse button is then selected by default when you click the left mouse button in a viewing window.

Localization

Use these tools for patient localization tasks.

Tool	Name	Function
	Manually position rod	Position the stereotactic frame rods on individual slices. After selecting the tool, click on the rods in a 2D viewing window.
	Move couch removal plane	Position the couch plane in a 2D window. This marks where the couch begins so it can be taken out of dose calculations.

Meshes

Use these tools to edit meshes in 2D windows.

Tool	Name	Function
	Move mesh	Move the selected mesh to a new location. Select the mesh that you want to move, then drag it to the new location.
	Scale mesh	Scale the selected mesh. Select the mesh that you want to scale, then drag left and right to scale it horizontally or drag up and down to scale it vertically.
	Rotate mesh	Rotate the selected mesh. Select the mesh that you want to rotate, then drag clockwise or counterclockwise to rotate the mesh around its center.
	Undo mesh edit	Undo the last action that you performed on the mesh. Click the Undo mesh edit button again to redo the action.

Tool	Name	Function
	Pull mesh	Pull the surface of the mesh. Set the radius of the tool, then drag the cursor to pull the mesh. As you drag the cursor, vertices farther away from the original cursor location move in the direction you drag, but with a distance weighted by a Gaussian function and the radius of the tool. A dashed-line circle indicates the range of vertices affected as you drag the cursor. The Mesh Modeling Options section on the Edit Options tab of the Regions of Interest panel contains a Lock edited vertices option. To prevent edited vertices from moving during adaptation, set the Lock edited vertices option to Yes before using this tool. Setting the Lock edited vertices option to Yes can be useful if the mesh is shifting toward neighboring organs during adaptation. Please note that the lock is not absolute; the edited vertices may still move slightly during adaptation. Locked edited vertices display in a different color from other vertices. Click the Reset button to unlock all vertices in the mesh.

Regions of interest

Use these tools to create and edit regions of interest (ROIs).

Tool	Name	Function
	Create contour paintbrush	"Paint" an ROI on a 2D transverse slice. The tool provides contour drawing, editing, and deleting functions, depending on where you use it. Before clicking the tool, use the Diam field to enter the diameter (in millimeters) of the brush. If you want painted contours to be closed and filled automatically, leave the Auto-close painted contours option set to Yes. Sometimes, such as when contouring organ walls, you may want to set this option to No. Next, click the Create contour paintbrush tool and position the cursor at the point where you want to start, edit, or delete a contour. The tool works differently depending on where you click. • If you click on an image where there is no contour, a new, circular contour appears. Drag the cursor to create a thick line; wherever you move the cursor, the circle is filled in for the ROI. • By clicking inside an existing contour, you can push out the edges of the contour. • If you click outside, but near, an existing contour, the tool functions as an eraser, and the ROI is erased wherever you move the tool. You can use this method to push in the edges of the contour. Go to the next slice on which you want to draw a contour for this ROI and repeat the process.
	Create contour point by point	Define contours by "dropping" a series of points. Select the tool and click where you want to start the contour. A small box appears and indicates the point that you defined. Then click where you want to add the next point to the contour. You can also drag the point to the position that you want. A line is drawn between the two points. Continue to define the remaining points in the same way. To close the contour, drop the last point of the contour inside the box of the first point.

Tool	Name	Function
	Create contour freehand	Define contours by drawing a continuous line. Position the cursor at the point on the slice where you want to start the contour. Then drag the cursor to draw a contour around the limits of the region. Release the mouse button when you have closed the contour. Go to the next slice on which you want to draw a contour for this ROI and repeat the steps.
	Autocontour structure on current slice	Generate a single contour on a single slice automatically. The software searches to the right from where you click on the image until the first structure with values within the minimum and maximum threshold values that you specify is found. The software then automatically draws a contour around the structure. After entering the upper and lower thresholds in the Autocontour thresholds fields, select the tool and click at an appropriate seed point in the image. If the seed point has a value within the specified range, the first structure to the right of the seed point with values outside the range is autocontoured. If the seed point has a value outside the range, the first structure to the right of the seed point with values inside the range is autocontoured.
	Autocontour all on current slice	Generate contours automatically for all structures on a given slice that have values within the specified range. After entering the upper and lower thresholds in the Autocontour thresholds fields, select the tool and click within the image. All structures on the slice within the threshold are contoured. If the 2D image is zoomed, this may include contours that are not visible in the window.
	Autocontour structure on all slices	Autocontour a single structure on all slices on which the structure appears. The tool uses the specified autocontouring thresholds to generate a contour on the current slice automatically and then generates a contour on adjoining slices for any structure that is connected to the contour on the previous slice and has a value within the specified range. After entering the upper and lower thresholds in the Autocontour thresholds fields, select the tool and click at an appropriate seed point in the image. If the seed point has a value within the specified range, the first structure to the right of the seed point with values outside the range is autocontoured. If the seed point has a value outside the range, the first structure to the right of the seed point with values inside the range is autocontoured. The software then searches for the structure in adjacent slices and automatically contours the structure on those slices.
	Autocontour all on all slices	Autocontour all structures on all slices. The tool uses the specified autocontouring thresholds to generate contours automatically on the current slice and then generates contours on adjoining slices for any structures that are connected to the contours on the previous slice and have values within the specified range. After entering the upper and lower thresholds in the Autocontour thresholds fields, select the tool and click at an appropriate seed point in the image. If the seed point has a value within the specified range, the first structures to the right of the seed point with values outside the range are autocontoured. If the seed point has a value outside the range, the first structures to the right of the seed point with values inside the range are autocontoured. The software then searches for the structures in adjacent slices and automatically contours the structures on those slices.
	Delete contour	Remove one or more contours from a slice associated with the current ROI. To delete the contours, drag the cursor diagonally over any contours associated with the current ROI you want to delete.
	Split contour	Divide a single contour into two contours on the current ROI. To divide a contour, position the cursor outside the current ROI and drag the cursor to another position outside the ROI.

Tool	Name	Function
	Select contour	Select a contour for editing by clicking it.
	Add contour point	Add a point after the last point that was added.
	Edit contour	Move a point in the selected contour using a “rubber band” effect. Click the point you want to reposition and then drag it to the new location.
	Insert contour point	Place a point between two previously defined points in the selected contour. To insert a point, position the cursor between the two points and click. After the point is inserted it can be dragged until it is positioned as desired.
	Delete contour point	Remove a point from the selected contour. Position the cursor on the point you want to remove and click to remove the point.
	Move contour	Move the selected contour to a new location on the same slice. Click the contour you want to move and then drag it to the new location. (If you do not select the contour first but just click on this tool, the points disappear to allow you to place the contour accurately.)
	Scale contour	Scale the selected contour. Select the contour you want to scale, then drag left and right to scale it horizontally or drag up and down to scale it vertically. (If you do not select the contour first but just click on this tool, the points disappear to allow you to scale the contour accurately.)

Points of interest

Use these tools to position points of interest (POIs).

Tool	Name	Function
	Move POI	Place a POI directly on a transverse, sagittal or coronal slice. Display the 2D slice where you want to place the center of the POI. Next, select the Move POI tool, position the cursor where you want to add the POI, and click to place the POI on the slice. You can also position the POI by dragging it to the new position.
	Translate POI	Move a POI within the current plane without moving it to the slice where you click. Use this tool when a POI is positioned between CT slices and you want to reposition it without changing the slice.
	Move POI 3D	Position POIs on 3D images. First, open a 3D viewing window and render the 3D image you want to use to position the POI. Next, select the Move POI 3D tool, position the cursor where you want to add the POI, and click to place the POI in the volume. You can also position the POI by dragging it to the new position.
	Nudge POI toward you	Move a POI 1/10 of the voxel height toward you in the volume. Click the Nudge POI toward you tool, then click in the viewing window that shows the images that you want to use for positioning. Continue to click in the window until the POI is positioned properly.
	Nudge POI away from you	Move a POI 1/10 of the voxel height away from you in the volume. Click the Nudge POI away from you tool, then click in the viewing window that shows the images that you want to use for positioning. Continue to click in the window until the POI is positioned properly.

Beams

Use these tools to position beams and isocenters.

Tool	Name	Function
	Move POI	Position the isocenter for the current beam. The isocenter is moved to the plane of the CT slice on which it is placed.
	2D aim beam	Position the beam on 2D images. The couch and gantry angles are modified so that the central axis of the current beam intersects the point selected using this tool.
	3D aim beam	Position the beam on 3D images. The couch and gantry angles are modified so that the central axis of the current beam intersects the selected point on the patient's surface.

Collimators

Use these tools to adjust isocenters, collimator jaws, and MLC leaves.

Tool	Name	Function
	Reposition isocenter	Reposition the isocenter of the beam displayed in the BEV window by dragging the isocenter to a new position.
	Place Field	Reposition the isocenter of the beam displayed in the BEV window. Click in the BEV window to move the isocenter to a new location.
	Adjust collimator 3D	Adjust collimator jaw positions in BEV windows by dragging a jaw to change its position. To rotate the collimator, drag the axis.
	Move MLC manually	Move multi-leaf collimator leaves in a BEV window. Click this tool in the Beam MLC Leaf Position Editor window, then click the leaf you want to move and drag it, or click the location where you want the leaf to have the software move it.

Blocks

Use these tools to create, edit, and delete blocks when the **Structure** field is set to **Manual**.

Tool	Name	Function
	Create block paintbrush	"Paint" a block. The tool provides block drawing, editing, and deleting functions, depending on where you use it. Before clicking the tool, use the Diam field to enter the diameter (in millimeters) of the brush. The drawn block is closed and filled automatically. Next, click the Create block paintbrush tool and position the cursor at the point where you want to start, edit, or delete a block. The tool works differently depending on where you click. - If you click on an image where there is no block, a new, circular contour appears. Drag the cursor to create a thick line; wherever you move the cursor, the circle is filled in for the block. - By clicking inside an existing block, you can push out the edges. - If you click outside, but near, an existing block, the tool functions as an eraser, and the block is erased wherever you move the tool. You can use this method to push in the edges of the block.
	Create block point by point	Draw a beam block by defining a series of points. Any number of contours can be drawn for a single block.
	Delete block	Remove a manually drawn block. Drag the cursor over the block to remove it.
	Select block	Select the block outline to be edited by clicking on the outline. If the block has a margin, you must select the original block outline instead of the margin.
	Edit block point	Move points in the selected block.
	Insert block point	Place a point between two previously defined points in the selected block. To insert a point, position the cursor on the outline between the two points and click. After the point is inserted it can be dragged until it is positioned as desired.
	Delete block point	Remove points from the selected block. Position the cursor on the point that you want to remove and click to remove the point.
	Move block	Move the selected block to a new location within the collimator jaws.
	Scale block	Scale the selected block. Click on the block that you want to scale, then drag left and right to scale it horizontally or drag up and down to scale it vertically.
	Copy block	Copy the selected block. Once you have copied the block, you can flip it over either axis to mirror the original block.
	Flip block over X axis	Flip the selected block over the X axis. Use this tool in conjunction with the Copy block tool to create a mirror image of a block.
	Flip block over Y axis	Flip the selected block over the Y axis. Use this tool in conjunction with the Copy block tool to create a mirror image of a block.

Bolus

Use the bolus tools to define the skin boundary and bolus.

Tool	Name	Function
	Skin boundary	For a constant thickness bolus, define the skin boundary in which the bolus will be created. To define the boundary, drag the cursor in a 2D transverse image to draw a rectangle that will be the skin boundary. If you need to adjust the location of the rectangle, draw a new rectangle in the correct location. The old rectangle disappears.
	Add bolus edge	For a constant thickness bolus, define the left and right edges of a bolus on a 2D image. To define the edges, drag the cursor to draw a line where the left edge of the bolus should be. Then drag the cursor to draw a line where the right edge of the bolus should be. The edges must be drawn in a clockwise direction, and the lines must intersect the patient air threshold.
	Delete bolus edge	For a constant thickness bolus, remove a line drawn to define a bolus edge on a 2D image by dragging the cursor to draw a rectangle around the line.
	Create bolus point by point	For a variable thickness bolus, define the contours of the bolus on a 2D image or 3D BEV image by “dropping” a series of points. Select the tool and click where you want to start the contour. A small box appears and indicates the point that you defined. Then click where you want to add the next point to the contour. You can also drag the point to the position that you want. A line is drawn between the two points. Continue to define the remaining points in the same way. To close the contour, drop the last point of the bolus inside the box of the first point.
	Select the center slice	For a constant thickness bolus with Encompass data set to Yes , select the image slice from which the bolus extends in the superior and inferior directions.
	Create bolus paintbrush	Edit the shape of a variable thickness bolus on a slice-by-slice basis. Before clicking the tool, use the Diam field to enter the diameter (in millimeters) of the brush. Next, click the Create bolus paintbrush tool and position the cursor at the point where you want to start, edit, or delete a contour. The tool works differently depending on where you click. • If you click on a section of the image where there is no bolus, a new, circular bolus appears. Drag the cursor to create a thick line; wherever you move the cursor, the circle is filled in for the bolus. • By clicking inside an existing bolus you can push out the edges of the bolus. • If you click outside, but near, an existing edge of the bolus, the tool functions as an eraser, and the bolus is erased wherever you move the cursor. You can use this method to push in the edges of the bolus. Go to the next slice on which you want to edit the shape of the bolus and repeat the process.

Proton compensator

Use these tools to edit and view the thickness of a proton compensator.

Tool	Name	Function
	Edit pixel	Displays the thickness (cm) of a proton compensator at a specific point. With this tool selected, click on the compensator. The thickness at the point on which you clicked appears in the Value at cursor field, and that pixel is highlighted in the Thickness Array .
	Create contour freehand	Define contours by drawing a continuous line. Drawing a contour allows you to edit multiple pixels at one time. You can change the thickness values of all of the pixels within the contour to a single value, update the thickness values of all of the pixels to the average of the thickness values, or modify the thickness values by adding or subtracting a specific value or percentage. After you click the tool, position the cursor at the point on the slice where you want to start the contour. Then drag the cursor to draw a contour around the limits of the region. Release the mouse button when you have closed the contour.
	Create contour point by point	Define contours by “dropping” a series of points. Drawing a contour allows you to edit multiple pixels at one time. You can change the thickness values of all the pixels within the contour to a single value, update the thickness values of all the pixels to the average of the thickness values, or modify the thickness values by adding or subtracting a specific value or percentage. Select the tool and click where you want to start the contour. A small box appears and indicates the point that you defined. Then click where you want to add the next point to the contour. You can also drag the point to the position that you want. A line is drawn between the two points. Continue to define the remaining points in the same way. To close the contour, drop the last point of the contour inside the box of the first point.
	Create contour paintbrush	“Paint” a contour on a slice. Drawing a contour allows you to edit multiple pixels at one time. You can change the thickness values of all the pixels within the contour to a single value, update the thickness values of all the pixels to the average of the thickness values, or modify the thickness values by adding or subtracting a specific value or percentage. The tool provides contour drawing, editing, and deleting functions, depending on where you use it. Before clicking the tool, use the Diam field to enter the diameter (in millimeters) of the brush. Next, click the Create contour paintbrush tool and position the cursor at the point where you want to start, edit, or delete a contour. The tool works differently depending on where you click. • To draw a contour, drag the cursor to create a thick line; wherever you move the cursor, the circle is filled in for the contour. • By clicking inside an existing contour, you can push out the edges of the contour. • If you click outside, but near, an existing contour, the tool functions as an eraser, and the contour is erased wherever you move the tool. You can use this method to push in the edges of the contour.
	Delete contour	Remove one or more contours from the compensator. To delete the contours, drag the cursor diagonally over any contours that you want to delete.

Dose

Use these tools to position and resize the dose grid.

Tool	Name	Function
	Draw dose grid	Position and resize the dose grid in a 2D image.
	Move dose grid	Reposition the dose grid in a 2D image.

Dose volume histogram (DVH)

Use these tools for navigating the DVH graph.

Tool	Name	Function
	Track	Click the Track tool, then click on or near a point on a curve. The dose and volume values appear in a box in the upper right corner of the graph. At the bottom of the box are the curve's trial and record information. Moving the mouse allows you to see the changes in values. You can use this tool in a zoomed window. Changes in the values depend on the resolution of the binning. No interpolation is performed, and thus some of the value changes may appear "jumpy" if the Tabular DVH settings are too small. To switch to a different curve, click on the curve or select it from the list in the ROI Statistics spreadsheet at the bottom of the window. This selects the point on the curve at the same dose. To stop tracking, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click Reset.
	Box Zoom 2D	Click the Box Zoom 2D tool and drag to create a rectangle to define a subset of the graph to display. You can zoom further by dragging again. To reset the zoom level to the default setting, click the tool again to turn it off. To return the DVH to its original state before any tracking or zooming, click Reset.

Brachytherapy

Use the brachytherapy tools to place sources and position catheters.

Tool	Name	Function
	Place source	Place the currently selected source in the patient by clicking on the desired source position.
	Rotate source	Specify the angle of a linear source. When this tool is selected, drag the cursor in a viewing window to change the source orientation.
	Select source	Use this tool if you have difficulty selecting the proper source. When you click this tool, the source that you select becomes the active source in the Brachytherapy windows and the viewing windows.

Tool	Name	Function
	Add/delete source	Add or delete sources. If you click this tool and then click an area that is more than 0.25 cm from an existing source, a new source is added. If you click the tool and then click on a source, the source is deleted.
	Place catheter tip	To position the tip of the catheter, select the tool and click in the image at the position of the tip of the catheter.
	Place catheter base	To position the base of the catheter, select the tool and click in the image at the position of the base of the catheter.
	Add segment	If the catheter is not straight, use the tool to create segments that follow the changes in the catheter positions in the CT. To interactively position the segment tip and base, select the segment from the list of segments and use the tip and base tools to position the tip and base.
	Move all catheters	To reposition the catheter template, select the tool and move the catheter template in any axis. You can use the Catheter Transform tools to rotate and translate the catheter template positions.

Cutplanes

Use these tools for creating cutplanes.

Tool	Name	Function
	Move cutplane 2D	Click the tool to turn on the 2D display of marked cutplanes. Click in a 2D window to move the displayed cutplanes along their tangent.
	Move cutplane 3D	Move a marked cutplane in the direction perpendicular to the plane.
	Rotate cutplane about X-axis	Rotate a marked cutplane about the X-axis to create an oblique cutplane.
	Rotate cutplane about Y-axis	Rotate a marked cutplane about the Y-axis to create an oblique cutplane.
	Rotate cutplane about Z-axis	Rotate a marked cutplane about the Z-axis to create an oblique cutplane.

Additional

The following are additional tools in the software.

Tool	Name	Function
	Redo spreadsheet	Apply the last change to a parameter in a spreadsheet to all entries in that spreadsheet. The Redo spreadsheet tool appears in several of the windows in the software.

Keyboard shortcuts

Use these keyboard shortcuts to perform various functions in Pinnacle³.

Keys	Function
t	View next trial.
n	View next image slice.
p	View previous image slice.
v	View next image set.
a	View transverse (axial) orientation.
s	View sagittal orientation.
c	View coronal orientation.
r	Render BEV or 3D skin.
x	In a 2D viewing window, toggle between the Scroll through slices , 2D zoom , and 2D pan tools. In a 3D viewing window, toggle between the 3D rotate , 3D zoom , and 3D pan tools.
o	Select a slice by number.
z	Set a 2D window back to the default magnification.
u	Increase magnification of the 2D window.
d	Decrease magnification of the 2D window.
m	Expand a viewing window so that it fills the entire viewing layout.
Ctrl + d	Compute dose for all beams.
Ctrl + p	Open the Prescriptions window.
Ctrl + r	Redo spreadsheet.
Ctrl + s	Save plan.
Ctrl + w	Create a 3D viewing window.
Ctrl + x	Exit the software.
Shift + o	Select 2D images by the starting slice and increment.



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