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Ultrasound

Measuring cardiac tissue motion and strain

Automated Cardiac Motion Quantification[A.I.] (aCMQ[A.I.])

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Overview

Automated Cardiac Motion Quantification[A.I.] (aCMQ[A.I.]) is a clinically focused tool for measuring cardiac tissue motion and strain. Such measures have been shown to be very useful for evaluating a variety of cardiac motion abnormalities.

Analysis of cardiac motion can be very challenging and prone to significant variability. With its semi-automated approach, aCMQ[A.I.] can reduce the variability of the analysis of cardiac motion and streamline the workflow.

For the last few years, a task force led by the ASE and the EACVI has been working to standardize the strain measurement method and results among vendors with the goal of reducing variability. This task force has made a number of recommendations for standardization and, in response, numerous changes have been made to aCMQ[A.I.].

Measurement of strain

aCMQ[A.I.] provides for the measurement of strain within a segmented Region of Interest (ROI). Previously Philips used a 7-segment ROI for each left ventricle (LV) apical view. This 7-segment model included an apical segment that facilitated combining the segment values for each view into the AHA recommended 17-segment bullseye. The speckle task force consensus document has recommended using six segments for each apical view and an 18-segment model for the bullseye. aCMQ has been changed to follow those recommendations. To segment the ROI of the left ventricle it is first divided into a left half and a right half. The left half extends from the apex to the left basal point. The right half extends from the apex to the right basal point. Each half is then divided into three equal length segments with the length measured along the mid-line of each segment. Within each segment approximately 100 points are tracked. This number of points provides good accuracy with regard to tracking tissue motion while also providing rapid calculation.

aCMQ[A.I.] produces an initial contour starting at a user-specified reference frame. The user can select either the ED or ES frame to be the reference frame. The tracking is then computed throughout the cardiac cycle. The user can either accept this contour tracking or edit the contour at either the ED or ES frame. aCMQ[A.I.] allows the user to edit both the ED and ES frames to obtain the best accuracy of the LVEF and LV GLS. If the user had selected the ED frame as the reference frame then editing the ED frame would require re-running the contour tracking. In this situation, the contour tracking is automatically updated when the ES frame is edited. If the user had selected the ES frame as the reference frame then editing the ES frame would require re-running the contour tracking. In this situation, the contour tracking is automatically updated when the ED frame is edited.

The myocardium is composed of multiple layers and it may be useful to compute the regional strains of the different layers. To provide this capability, aCMQ[A.I.] allows the user to specify where the strain should be computed, either along the endocardium, along the mid-wall, or along the epicardium. Independent of the path along which the strain is calculated, the displacement is measured by tracking points across the entire width of the ROI in all cases.

Using the segmented ROI, a regional longitudinal strain (LS) is generated for each of the segments. The speckle task force has recommended that the longitudinal strain (LS) measurement be provided while also allowing for one of the regional strain measurements to be rejected. To do this, the longitudinal strain (LS) for each apical view is calculated utilizing the entire length of the contour. This approach is referred to as the Length of Line approach. The formula used is **LS for each apical view = (Contour Length at ES – Contour Length at ED)/Contour Length at ED**. The global longitudinal strain (GLS) in the report is the average of the LS from the three apical views.
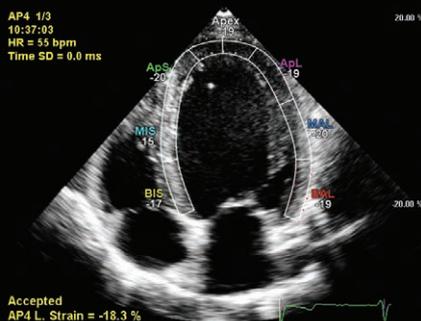
Previous 7 segments per view ROI
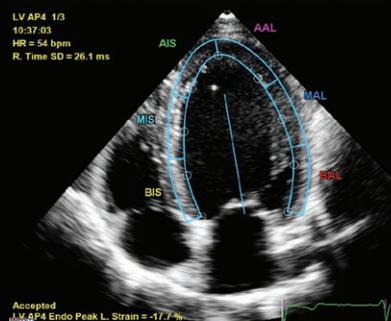
Current 6 segments per view ROI

Layer-specific strain selection

Display of strain results

After approval of the ROI, the strain is calculated throughout the cardiac cycle and the strain results are shown as a parametric image loop. Playing this loop allows the tissue motion to be displayed. The user has the ability to reject any ROI segments that are judged to have inaccurate tracking. The LS will not be displayed for any view having two or more rejected segments.

The strain results can be shown as strain waveforms. The characteristics of the strain waveforms can have a significant impact on their utility. To provide for adjusting the waveform characteristics, aCMQ[A.I.] provides three selections of Quantification Smoothness. These settings impact not only the waveform smoothing but also regularization in the 2D speckle tracking.

Peak Systolic Strain is widely used in daily practice. Some users prefer Peak Strain. But End Systolic Strain is very rarely used.

For regional strain measurements:
- **Peak**
- **Peak Systolic** (default setting)
- **End Systolic**
- **Positive Peak Systolic**: positive strain value indicates early systolic expansion
- **Post Systolic**: peak strain happened after AVC indicates delay contraction

Peak Systolic Strain is the most commonly used measurement for segmental strain. Positive Peak and Post Systolic Peak are used by some clinicians performing CRT.
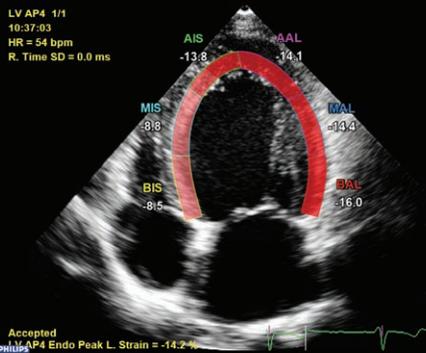
Strain parametric image
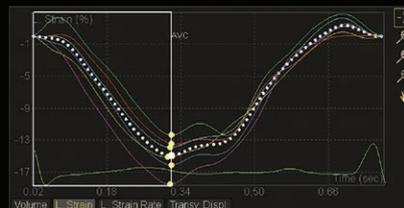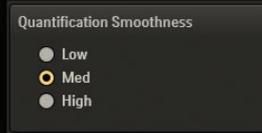

Quantification smoothness selection
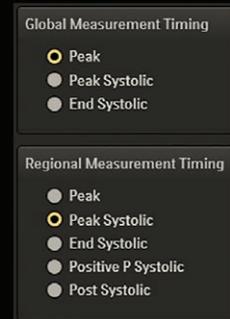
Strain measurement timing selection

When determining the measured strain value, aCMQ[A.I.] allows the user to select the timing of the strain measurement. Different selections are available for global and regional timing.

For global longitudinal strain measurement:
- **Peak:** peak strain from entire heart cycle (Peak between R–R)
- **Peak Systolic**: peak strain within the systolic period (R to AVC)
- **End Systolic:** peak strain at AVC

R–AVC can be set automatically based on the timing of the minimum volume using the AP3 view or the user can enter the timing value.

LS values from the three apical views (AP2, AP3, and AP4) or three short axis views (basal, mid, apex) can be combined into a parametric display known as a bullseye diagram. These bullseye diagrams allow for the quick evaluation of the regional strain behavior of the entire left ventricle.
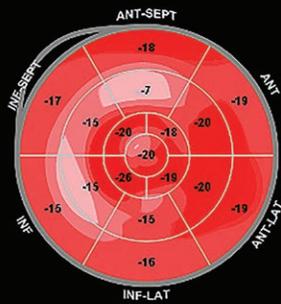
17-segment model
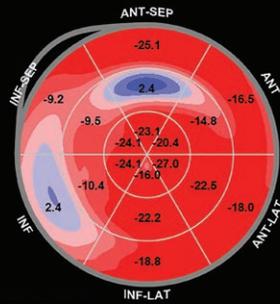
18-segment model
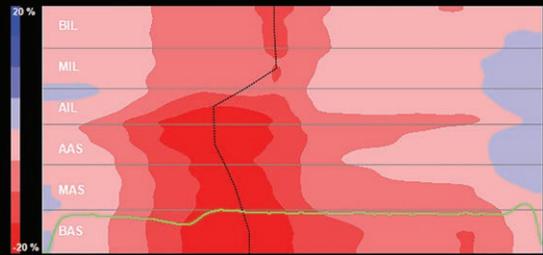
Color M-mode display

Shown above are two different bullseye diagrams that can be selected. One option is the 17-segment model recommended by the AHA and the second option is an 18-segment model recommended by the speckle task force. Both models have six basal and six mid segments. The 18-segment model has six apical segments whereas the 17-segment model has four apical segments and an apical cap segment.

The strain results can also be displayed using a color M-mode display that shows regional strain versus time. The bullseye diagram is created from the color M-mode display by sampling the color M-mode display along the black line and interpolating between views. For each region, the black line is positioned at the time of maximum strain as determined by the user's selection of Regional Strain Timing

Image types supported

aCMQ[A.I.] now can be used for both native and non-native 2D images from Philips Ultrasound products. This will allow users to utilize many previously acquired data sets. The new aCMQ[A.I.] also allows the user to analyze images without an ECG. In those cases the user must manually identify R-R heart cycle.

Validation

Since there is no commercially available strain phantom, Philips created a computerized phantom that begins with an ultrasound image and creates known motion and strain. This phantom was used to validate the accuracy of the strain measurement. In addition the aCMQ[A.I.] results were compared clinically with other vendor's strain tools.

Conclusion

Speckle tracking is an exciting technique which shows a great deal of clinical promise. aCMQ[A.I.] incorporates the latest recommendations of the ASE and EACVI speckle task force with a user-centered workflow to provide a useful tool that is proving to be valuable in evaluating cardiac function.

Frequently asked questions

Q **Does the software track the full thickness of the myocardium?**

A **Yes.** In the Langrangian strain calculation of **Strain = Displacement/Relaxed Length**, the displacement is measured using a full 2D dense speckle tracking across the entire myocardium.

Q **How is the global strain calculated?**

A GLS is calculated using the Length of Line method which utilizes the entire length of the contour.

Q **Does the software perform strain drift correction? And if yes, can we switch it off?**

A The software does perform drift correction to match the diastolic boundary at the beginning and end of the cardiac cycle. This drift correction can't be disabled.

Q **If a segment is tracking so poorly that we need to exclude it (no more than one per view), how does the software calculate the global strain?**

A GLS is calculated using the Length of Line method which utilizes the entire length of the contour. These same comments also apply to Global Circumferential Strain (GCS).

Q **Assessing the quality of a segment's strain curve, what should one look for?**

A There are a number of characteristics to be considered. Is the strain curve for a region consistent with the strain curves of adjacent regions? Is the longitudinal strain curve consistent with the visual assessment of the wall thickening of the region? For a segment in question does the image show any unusual motion?

Q **How is strain calculated in different layers?**

A aCMQ[A.I.] allows the user to specify where the strain should be calculated, either along the endocardium, along the mid-wall, or along the epicardium. Independent of the path along which the strain is calculated, the displacement is measured by tracking points across the entire width of the ROI in all cases.

Q **How does aCMQ[A.I.] set the R-AVC automatically? Can it be changed?**

A R-AVC can be set automatically based on the timing of the minimum volume using the AP3 view or the user can enter the timing value.

Q **Does the software use regularization? Can this be switched off?**

A The software uses regularization to reduce random variations. This regularization can be adjusted using the Smoothness setting in the Preferences.

Q **Can I directly compare the segment strain for the 17-segment vs. 18-segment model?**

A Because the individual segments for the 17-segment model are in slightly different locations than the individual segments for the 18-segment model, the two bullseye diagrams can't be directly compared, segment for segment.

Q **Is the strain measurement consistent in QLAB between different versions of the releases?**

A The aCMQ[A.I.] software is periodically enhanced and minor differences between the strain values may be observed. If feasible, older images should be reanalyzed with the latest software to provide for maximum consistency of results.

Q **Is aCMQ[A.I.] global longitudinal strain (GLS) validated?**

A At the present time, there is no objective standard, such as a phantom, with which to validate the strain results. But there are published clinical papers and abstracts that compared aCMQ[A.I.] to other vendors' GLS with very favorable results, such as "Head-to-Head Comparison of Global Longitudinal Strain Measurements among Nine Different Vendors The EACVI/ASE Inter-Vendor Comparison Study" (J Am Soc Echocardiogr 2015;28:1171-81.)", and "Improvement in Strain Concordance between Two Major Vendors after the Strain Standardization Initiative" (J Am Soc Echocardiogr 2015;28:642-8.)".

Q **How should serial studies be handled?**

A When doing serial studies, it is recommended to use the same level of software to analyze all the images. Even small variations in the behavior of different levels of the same software could impact the study results.

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