Semi-Automatic Segmentation of Tagged Myocardial Short-Axis Images

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Introduction

Myocardial tagging combined with harmonic phase analysis (HARP) [1] has proven to be an accurate and fast method for the quantification of myocardial deformation. As a prerequisite for the calculation of functional indices, the myocardial tissue should be delineated reproducibly and desirably automatically. A method has been described previously [2] to accurately identify endo- and epicardial borders on short-axis CSPAMM [3] images. In this work, this manual approach is further developed and automated. Endo- and epicardial contours are detected automatically on threshold-images, allowing analyses of tagged short-axis images with minimal observer-interaction and increased reproducibility.

Methods

The myocardium is identified on the harmonic magnitude image (HARM) with a few markers set on the myocardial midwall by an observer. A spline is fitted through the markers and signal intensity along this contour is determined. The application of an adaptive threshold in a rotating sector along the spline yields the threshold-image. Starting from 72 landmark points equally distributed on the spline, the edges of the threshold-image are detected in both radial directions. Depending on the radial distance to the center of the spline, outliers are discarded and relocated on a spline through the remaining points. The same procedure is then independently applied in four separate sectors in order to smooth out papillary muscles and other irregularities in the threshold-image. Further smoothing of the epi- and endocardial contours is achieved by relocating all points onto a spline through twelve equally distributed points defined by the mean radius in the respective sector. Based on these endo- and epicardial contours, the centerline is calculated (Fig.1).

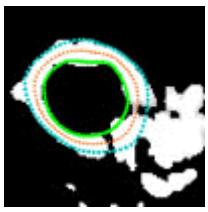

Figure 1: Automatically calculated contours on the threshold-image

To validate the centerline position, CSPAMM images of 5 patients with hypertension and mild ventricular hypertrophy were acquired at three cardiac levels with a 1.5T Philips scanner (Philips Medical Systems, Best, NL) using a single breath hold EPI sequence (EPI-factor:9, FOV:300-330mm, matrix:128x27, ramped flip angles:8-25°, 17 cardiac phases, tag distance: 8mm). Additionally, anatomical images were acquired on the same cardiac levels with an EPI sequence (EPI-factor:9, FOV:192x192 mm^2, matrix:128x80). Identical positioning of the heart was achieved by real time navigator control (acceptance range: ±1.5mm of initial diaphragm position). The midwall contour was identified on the tagged images at the end of the cardiac cycle as described above and compared with the midwall contour calculated from the manually defined endo- and epicardial contours on the anatomical images. For comparison, all 72 points were resampled and the radial differences of the landmark points were calculated.

For the validation of the HARP-tracking results after applying the described method, data from a study by Myers et al. [4] was used. The analysis comprised two apical CSPAMM images (temporal separation of measurements: 2 months) for each of 23 patients with non-ischemic dilated cardiomyopathy acquired on a 1.0T Philips scanner (EPI-factor:9, FOV:310mm, matrix:128x48, 16 cardiac phases, temporal resolution: 35ms, tag distance: 8mm). Data from the two measurements were considered independent for analysis. To compare inter-observer reproducibility, two observers independently identified the midwall contour manually [2] and semi-automatically as described above. The contour was tracked throughout the cardiac cycle using HARP incorporating peak-combination [5] and maximum circumferential shortening was compared.

Results

For one hypertrophic patient the contour detected by the algorithm was unreliable on the equatorial level. For all other measurements the mean radial differences between anatomy- and CSPAMM-images are illustrated in Fig.2 depending on the distance to a reference point which was chosen as the anterior junction of the septal wall with the right ventricle. The mean radius of all midwall contours differed by 1.45±2.93mm (Fig.2).

The differences of the HARP-analysis between two observers could be reduced and hence inter-observer reproducibility improved. Maximum circumferential shortening differed by 0.08±0.88% for a manually identified contour and by 0.03±0.54% for a contour detected by the algorithm (Fig.3).

The difference between the apical peak circumferential shortening for the contour detected semi-automatically compared to the manually drawn contour was increased by 0.75% with a standard deviation of 1.12% ($p<0.0001$, Fig.4).

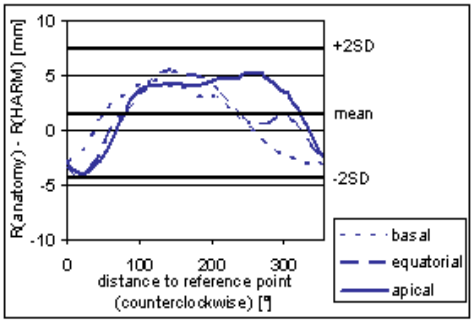

Figure 2: Mean contour radii on anatomic images (by hand) and CSPAMM-images (automatically)

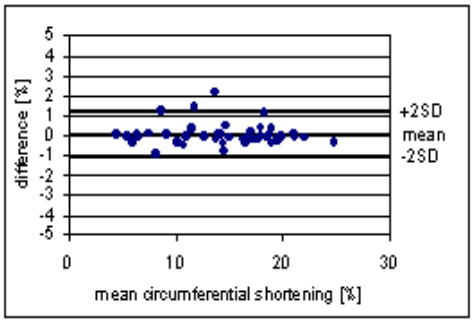

Figure 3: Max. circumferential shortening for two observers applying the algorithm

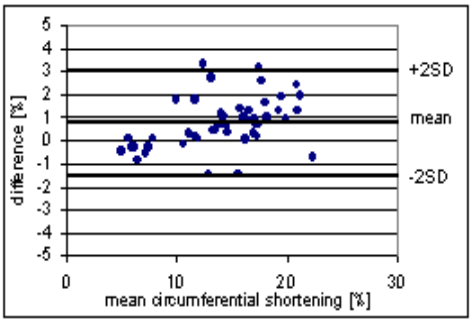

Figure 4: Max. circumferential shortening, contours identified automatically & by hand

Conclusion

Applying the described method, endo- and epicardial contours can be calculated semi-automatically i.e. with minimal user interaction. Peak circumferential shortening on the apical level differs by 2.24% (2xSD) with a bias of 0.75% from the tracking result of manually drawn contours. Inter-observer reproducibility could be clearly improved. The method is robust and allows for a faster and user independent analysis of tagged myocardial short-axis images.

References

[1] Osman NF, et al., 1999, MRM 42(6): 1048-60. [2] Schwitter J, et al., 2002, Proc ISMRM: 1676. [3] Fischer SE, et al., 1993, MRM 30(2): 191-200. [4] Myers J, et al., 2002, Am Heart J. 144(4): 719-25. [5] Ryf S, et al. 2004, Proc SCMR: 451