

Meeting abstract

Open Access

1092 Automatic tracking of mitral valve motion by non-rigid image registration

Bo Li*¹, Young Alistair^{1,2} and Cowan Brett³

Address: ¹Bioengineering Institute, Auckland, New Zealand, ²Auckland MRI Research Group, Auckland, New Zealand and ³Centre for Advanced MRI, Auckland, New Zealand

* Corresponding author

from 11th Annual SCMR Scientific Sessions
Los Angeles, CA, USA. 1–3 February 2008

Published: 22 October 2008

Journal of Cardiovascular Magnetic Resonance 2008, **10**(Suppl 1):A217 doi:10.1186/1532-429X-10-S1-A217

This abstract is available from: <http://jcmr-online.com/content/10/S1/A217>

© 2008 Li et al; licensee BioMed Central Ltd.

Introduction

Measurement of mitral valve annular motion is important in the study of systolic and diastolic cardiac function, and provides a valuable parameter for the assessment of myocardial contractility. Cardiac MRI is well-known as a non-invasive method for the assessment of ventricular function. It provides an abundant source of detailed, quantitative data for the evaluation of the structure and function of the heart, valves and major vessels. Mitral valve annular measurements are still however generally performed by echocardiography.

Purpose

The purpose of this paper is to present an automatic method for the tracking of mitral valve annular motion from long axis Steady-State Free Precession (SSFP) cines. The results are validated in long axis cines in 36 cases by measuring the distance errors between the automated tracked motion and manual results from trained observers.

Methods

Technical

A new non-rigid image registration algorithm was developed to quantify the deformation (displacement and strain) between a reference frame (I_0) and current frame (I_t), from a SSFP cine. A mathematical model was constructed to define the mapping of material points between the two frames, so that it could be used to map the current image I_t back to the reference image I_0 . If the reference image coordinates are X and the current image coordi-

nates x , then $x = B(X)$ represents the mathematical model, and the mapping process is represented by: $I_0(X) = I_t(B(X))$. An energy function $E = \int (I_0(X, Y) - I_t(B(X, Y)))^2 + S(X, Y)$ was used as objective function to measure the similarity between the original reference image and current image which has been 'warped' to the reference image. It includes a smoothing term (S) to penalize and control model deformation. The Levenberg-Marquardt algorithm was used to optimize the non-linear least squares problem to determine the optimal $B(X)$. Motion was tracked between adjacent frames, and accumulation of the tracked deformation was used to provide an estimate of the motion of all points in the images during the entire cardiac cycle. If B_a^b represents the tracked deformation from frame a to frame b , then the accumulated motion from frame 0 to frame t in cardiac cycle is: $B_{t-1}^t B_{t-2}^{t-1} \dots B_1^2 B_0^1(X, Y)$.

Validation

Points were manually placed on the insertion of the mitral valve leaflets with the Left ventricular/Left atrial intersection at end-diastole and these were then automatically tracked through the cardiac cycle. The positions of the automatic points were then compared with those placed by trained observers and the distance error calculated (mm), calculation of annular velocity is straightforward.

Results

See Figures 1 and 2.

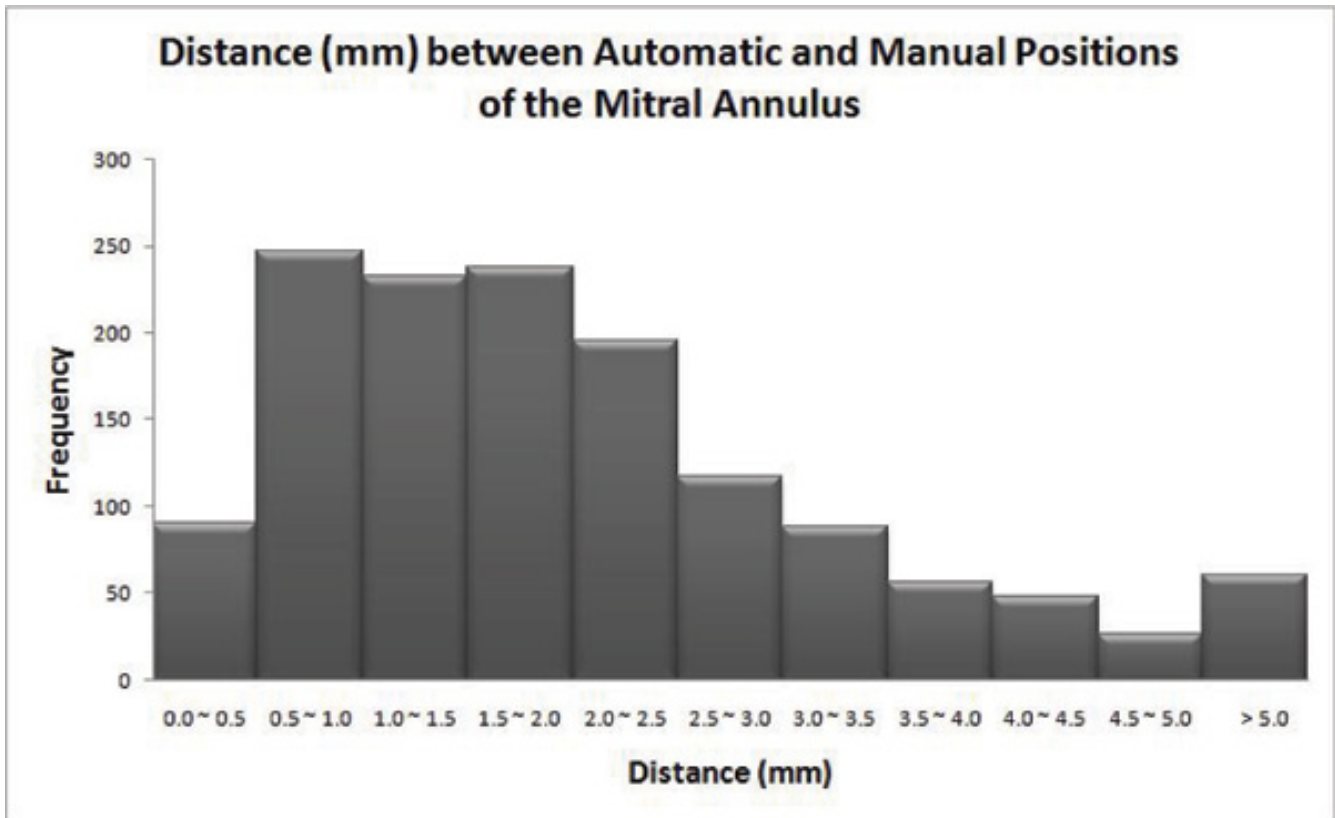


Figure 1
Distance between automatically tracked and manually defined (gold standard) position of the mitral valve annulus.

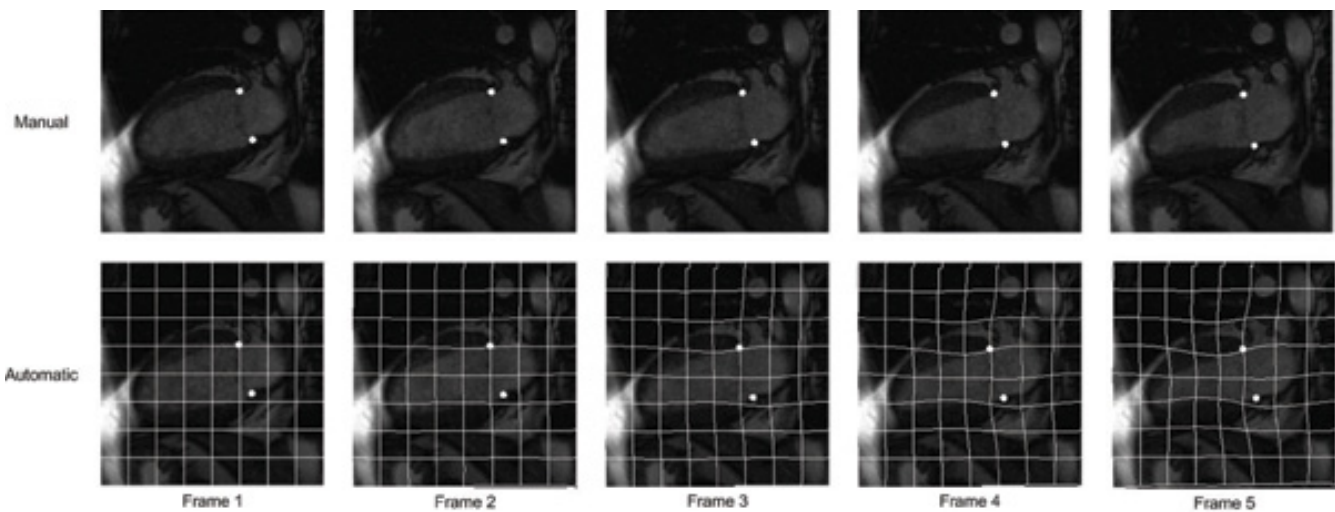


Figure 2
Tracking of end-diastolic points from end-diastole (where they were manually defined) to frames 1 to 5 (second row), compared with manually tracked positions (first row).

Discussion and conclusion

We have demonstrated a generalized automatic method for tracking mitral valve motion from CMR cines. This method can also be extended to track other cardiac structures such as papillary muscles, epicardial and endocardial contours.

Publish with **BioMed Central** and every scientist can read your work free of charge

"BioMed Central will be the most significant development for disseminating the results of biomedical research in our lifetime."

Sir Paul Nurse, Cancer Research UK

Your research papers will be:

- available free of charge to the entire biomedical community
- peer reviewed and published immediately upon acceptance
- cited in PubMed and archived on PubMed Central
- yours — you keep the copyright

Submit your manuscript here:
http://www.biomedcentral.com/info/publishing_adv.asp

