

Meeting abstract

Open Access

I 124 Automated soft segmentation of the left ventricle using myocardial effusion threshold reduction and intravoxel computation (METRIC)

Noel Codella*, Jonathon W Weinsaft, Matthew D Cham, Matthew Janik, Martin R Prince and Yi Wang

Address: Weill Medical College of Cornell University, New York, NY, USA

* 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):A249 doi:10.1186/1532-429X-10-S1-A249

This abstract is available from: <http://jcmr-online.com/content/10/S1/A249>

© 2008 Codella et al; licensee BioMed Central Ltd.

Introduction

An automated partial voxel left ventricular segmentation algorithm is presented. The algorithm, termed LV-METRIC (Left Ventricular Myocardial Effusion Threshold Reduction with Intravoxel Computation), measures the blood volume of the LV from cardiac cine MRI images, for all phases and slices. Papillary muscle and trabecular muscles are accounted for through partial voxel interpolation. Minimal interaction is required in some basal slices for which the valve plane must be defined.

Algorithm

1) A Hough transform is performed on the subtraction of images from phases 1 and 10 of a mid-ventricular slice [1–4]. 2) Edge-based region-growth is performed to discover the mean and standard deviation (μ_b/σ_b) of full-blood voxels. 3) A planar surface is fit to full-blood voxels to compensate for coil sensitivity variations. 4) Successive lower-bound threshold based region-growth processes are run for an iteratively decreasing threshold to estimate the myocardial mean. Eventually, region-growth breaks through the myocardium, "effusing" into surrounding structures. This effusion threshold is strongly related to the mean (μ_m). 5) The total blood volume is determined by the summation of the histogram multiplied by a linear weighting function between ($\mu_b - 2\sigma_b$) and ($\mu_m + 2\sigma_b$). 6) An energy function of distance from the center of mass and intensity difference is used to find the next seed point.

Materials and methods

The study included 38 randomly selected patients (15 male, mean age 52.4 years \pm 15.1 standard deviation), including 20 referred for clinical cardiac MRI and 18 with normal systolic function (based on a-priori MT). The most common clinical indications for referral were assessment of presence or pattern of myocardial scar. This study was approved by our IRB. Scans were performed using a GE Signa 1.5 T scanner, imaging parameters TR 3.3–4.5 ms, TE 1.1–2.0 ms, flip angle 55–60, matrix size 192 \times 192 – 256 \times 256, image dimensions 256 \times 256, receiver bandwidth 125 kHz, FOV 290–400 \times 240–360, slice thickness and slice gap 6–8 mm & 2–4 mm, respectively (total 10 mm). The LV in each patient was imaged in 6–10 slices, 20–28 cardiac phases. Two LV-METRIC volume measurements were compared to expert manual tracing (MT) measurements that excluded papillary muscles from the blood volume according to established criteria [5,6]. In the first measurement, LV-METRIC linearly interpolated the blood content of voxels. In the second, all partial-blood voxels are considered full-blood. Student's t-test was used to determine statistical significance.

Results

Figures 1 and 2 show example LV-METRIC and manual segmentations. Blue to green denotes blood content from least to most. The absolute and relative differences between MT and LV-METRIC linearly interpolating partial-blood voxels are shown in Table 1. All differences

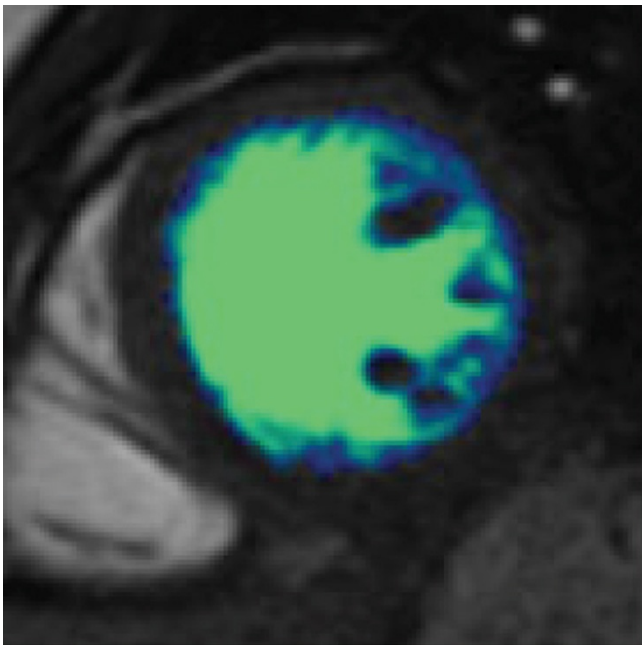


Figure 1

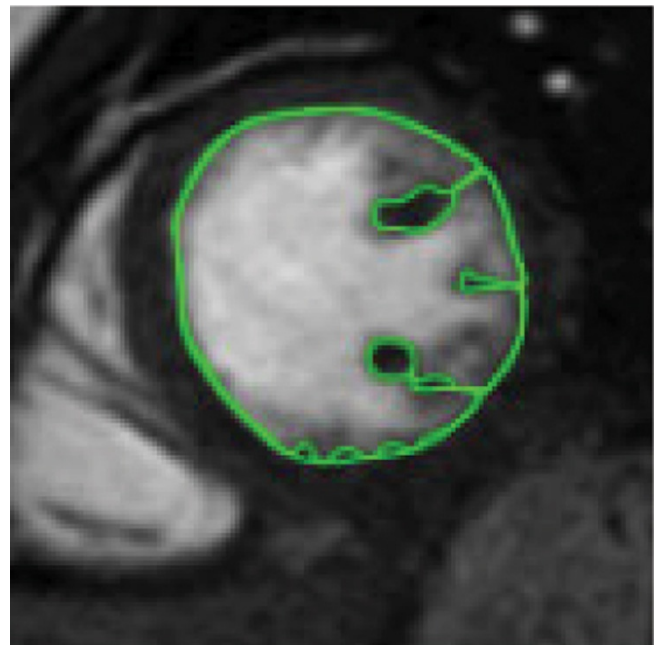


Figure 2

were statistically significant. The differences considering all partial-blood voxels as full-blood voxels are shown in Table 2. No significant differences were observed.

Discussion

While LV-METRIC volumes were smaller than manual tracing (MT) volumes, the LV-METRIC measurements that counted partial-blood voxels as full-blood voxels were similar to MT. Therefore, the difference between MT and LV-METRIC was likely due to partial voxel effects. In current breath hold 2D acquisition of cine SSFP images, the voxel size is limited to $1.4 \times 1.4 \times 10 \text{ mm}^3$. Consequentially, voxels with mixed myocardium and blood are invariably present, which leads to volume overestimation. Further validation using phantoms and high resolution scans as comparison standards must be performed to conclusively show the accuracy of partial voxel measurements.

Table 1: MT minus LV-METRIC with Linear Partial Voxel Interpolation. (x = MT)

	Absolute	Relative	Correlation	Volume Partial Voxels in LV-METRIC (Relative)	Volume Partial Voxels in LV-METRIC (Absolute)
End Diastolic Volume	$23.1 \pm 10.2 \text{ (mL)}$	$16 \pm 4.8 \text{ (%)}$	$y = 0.86x - 2.94$ $R^2 = 0.990$	$8.4 \pm 6 \text{ (%)}$	$21.1 \pm 6.1 \text{ (mL)}$
End Systolic Volume	$11.6 \pm 7.2 \text{ (mL)}$	$20.7 \pm 7.2 \text{ (%)}$	$y = 0.86x - 2.94$ $R^2 = 0.990$	$23.6 \pm 8 \text{ (%)}$	$10 \pm 5.6 \text{ (mL)}$
Ejection Fraction	$-1.9 \pm 2.5 \text{ (%)}$	$-3.0 \pm 4.2 \text{ (%)}$	$y = 1.02x + 0.39$ $R^2 = 0.972$		

Table 2: MT minus LV-METRIC with all partial-blood voxels counted as full-blood voxels. (x = MT)

	Absolute	Relative	Correlation
End Diastolic Volume	0.77 ± 5.1 (mL)	0.1 ± 3.4 (%)	y = 0.98x + 2.88 R2 = 0.992
End Systolic Volume	-1.9 ± 6.1 (mL)	-4.4 ± 9.5 (%)	y = 0.98x + 2.88 R2 = 0.992
Ejection Fraction	1.5 ± 3.3 (%)	-3.0 ± 7.5 (%)	y = 1.01x - 1.94 R2 = 0.949

References

1. Geest RJ van der, et al.: *J Cardiovasc Magn Reson* 2004, **6(3)**:609-617.
2. Pednekar A, et al.: *IEEE Trans Biomed Eng* 2006, **53(7)**:1425-1428.
3. Geest RJ van der, et al.: *Journal of Computer Assisted Tomography* 1997, **21(5)**:756-765.
4. Illingworth J, et al.: *Comput Vision Graph* 1988, **44(1)**:87-116.
5. Papavassiliu T, et al.: *Radiology* 2005, **236(1)**:57-64.
6. Hudsmith LE, et al.: *J Cardiovasc Magn Reson* 2005, **7(5)**:775-782.

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

