FIMH 2021 Benchmark

December 24, 2020

The goals of this benchmark are: 1) discussing the variability in calculation of cardiac kinematics (displacements and strains); 2) validating kinematics analysis tools using a computational phantom; 3) comparing strains and displacements computed from pre-clinical swine data across different analysis tools; and 4) improving our confidence in cardiac strain estimates as an imaging biomarker to distinguish between healthy and diseased hearts.

We want to emphasize that this benchmark is *not* meant as a challenge but simply as a platform for discussion and comparison to improve the calculation of cardiac motion and strains.

This working document is organized as follow:

1. Motivation
2. Method
3. Description of input data
   (a) Computational phantom
   (b) Healthy subjects
   (c) Subjects with myocardial infarct
4. Description of output measures to be collected for submission and group-wise comparison
5. Results dissemination

1 Motivation

Cardiac strains have increasingly become a potential imaging biomarker to characterize cardiac function in health and disease. However, a large range of cardiac strains is reported in the literature, even for healthy volunteers. Several factors could contribute to this large spread, among which the processing methods adopted to compute cardiac strains from acquired displacements. As acquired displacement imaging data are inherently noisy, different processing methods may amplify or reduce the experimental error as well as introduce a bias in the computed strains.

In order to improve our confidence in using cardiac strains as biomarkers for cardiac function and dysfunction and compare strains reported in different studies, it is necessary to evaluate the variability introduced by different processing methods. To this end, the goal of this benchmark study is to characterize cardiac strains — particularly end systolic (ES) strains — variation due to different processing methods and pipelines.

2 Method

We propose to analyze three sets of cine DENSE (Displacement Encoding with Stimulated Echoes) data, from which cardiac strains are computed and compared across participants.

Each participant can use their preferred analysis tool to analyze the input data listed below. The open source cine DENSE post-processing toolbox found at cine DENSE analysis tool [1] can also be used as a starting point to analyze the input data.

Strain results will then be collected according to the guidelines provided in the "Description of output measures to be collected for submission and group-wise comparison" section listed below and summarized by the benchmark organizers.

3 Description of input data

Three sets of input data are provided: 1) synthetic cine DENSE images generated from a computational cylindrical phantom in which displacements are analytically defined such that exact analytical strains are also known; 2) mid-ventricular cine DENSE images for $N = 2$ healthy swine subjects ($Tr - 1242$ and $Tr - 1264$); and 3) mid-ventricular cine DENSE images for $N = 2$ swine subjects with an infarct ($Tr - 1434$ and $Tr - 1493$).

The data can be downloaded from: BenchmarkData

3.1 Computational phantom

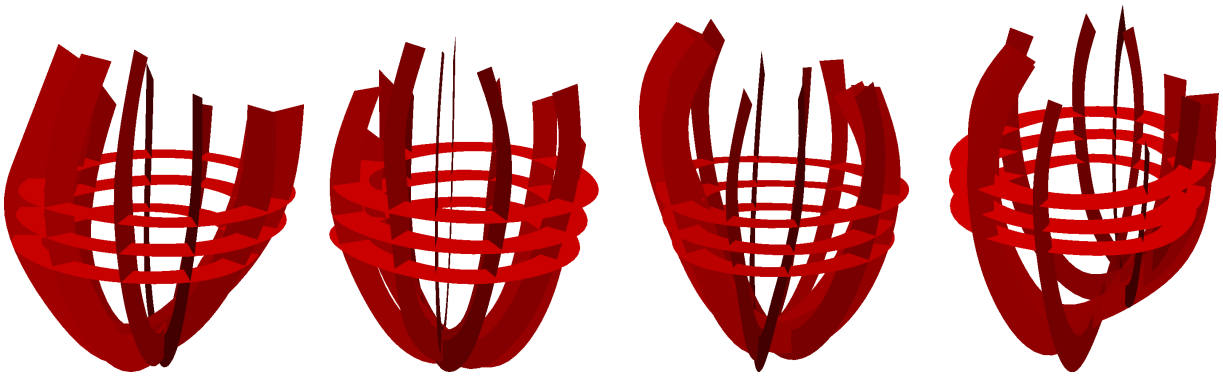
Data description will be added soon.

3.2 Healthy subjects

Cine DENSE data was acquired using a 3T (Prisma, Siemens) scanner following animal protocol #2015-124 as approved by the UCLA Chancellor's Animal Research Committee. Three mid-ventricular, 8 mm apart, cine DENSE short axis slices are provided per subject using the following sequence parameters: 15 ms view shared temporal resolution, $2.5{\times}2.5 mm^2$ in plane resolution, balanced 4-point phase encoding in x, y, z, TE/TR = 1.04/15, k_e = 0.08 cycles/mm, $N_{\text{avg}} = 3$, spiral interleaves = 10.

An image of the location of the cine DENSE short axis slices for subjects $Tr - 1242$ and $Tr - 1264$ is reported in Fig. 1.

Conventional cine cardiac magnetic resonance (CMR) short axis images are also included for reference. The cine CMR images are acquired with a different temporal resolution, early on during the MR exams, and in some cases with a different trigger delay. Therefore there is no frame-to-frame correspondence between cine DENSE and cine CMR images. If



(a) Subject $Tr-1242$. (b) Subject $Tr-1264$. (c) Subject $Tr-1434$. (d) Subject $Tr-1493$.

Figure 1: Short axis slices location for healthy subjects $Tr-1242$ and $Tr-1264$, and for subjects $Tr-1434$ and $Tr-1493$ with myocardial infarction.

segmentation is performed on the cine CMR images, care should be exerted in temporal alignment between cine DENSE and cine CMR images.

3.3 Subjects with myocardial infarct

Animal care and handling followed protocol #2015-124 as approved by the UCLA Chancellor's Animal Research Committee. In subject $Tr-1434$, the infarct was due to a thrombus formed in the proximal left anterior descending (LAD) coronary artery. In subject $Tr-1493$, an infarct was induced by injecting 2.5˘3.0ml of microspheres (Polybead, Polystyrene 90 micron from Polysciences Inc) in a sub-branch of the left circumflex (LCx) coronary artery. The post-infarction MRI exam was performed eight weeks after infarct induction.

Cine DENSE short axis slices parameters are identical to the ones used in the MR exams of the healthy subjects. An image of the location of the DENSE MRI short axis data for subjects $Tr-1434$ and $Tr-1493$ with myocardial infarction is reported in Fig. **??**.

Short axis cine images are also included for reference (Please see Healthy subjects description for more details.)

4 Description of selected output data for comparison

Once the participant has finished analyzing the cine DENSE images, we ask the participants to export strain estimates to a pre-populated spreadsheet which will be made available to participants soon.

We will focus our comparison on: 1) the Lagrangian displacement of a set of 3D evenly spaced spatial points (0.5mm spacing in x, y, and z); and 2) average sector-based and transmural strains (E_{cc}, E_{ll}, and E_{rr}) for both computational phantom and pre-clinical swine data.

Table **??** contains a preliminary list of strain measures to be collected according to the guidelines below:

- Each entry should report median [$25^{th}-75^{th}$ percentiles].

	Endo	Mid	Epi	AHA-R7	AHA-R8	AHA-R9	AHA-R10	AHA-R11	AHA-R12	Total
E_{cc}										
E_{ll}										
E_{rr}										
E_{ff}										

- The endocardial (endo), midwall (mid), and epicardial (epi) regions are defined by dividing the wall in 3 equal transmural segments.
- At every point X_q in a short axis slice, the radial direction is defined along the line joining X_q with the short axis slice barycenter (Fig. 2).
- At every point X_q in a short axis slice, the circumferential direction is defined along the line perpendicular to the radial direction (Fig. 2).
- The longitudinal direction is identified as perpendicular to the short axis slice plane (Fig. 2).
- AHA-RX identifies mid-ventricular AHA region X, where 'X' is between 7 and 12, given that the three mid-ventricular cine DENSE slices approximately belong to AHA sectors 7-12.
- E_{vv} represent the strain computed by projecting the Green-Lagrange strain tensor $\mathbf{E}$ along the direction $\mathbf{v}$, where $\mathbf{v}$ can represent the circumferential direction $\mathbf{c}$, radial direction $\mathbf{r}$, and longitudinal direction $\boldsymbol{\ell}$ along the $\mathbf{z}$ axis.
- The calculation of myofiber strains is optional. If participants decide to compute myofiber strains, at each location, the "myofiber" direction is defined in the plane identified by the circumferential and longitudinal directions and forming an helix angle α with the short axis plane. The helix angle α is rule based and varying quadratically from 70° at endocardium, to 0° at midwall, and -50° at epicardium.
- All strains and displacement measures are sampled at the centers of the voxels defined by a grid with in plane resolution equal to 0.5mm. The grid covers the entire image short axis plane and only voxels in the myocardium at the reference configuration will be considered (Fig. 2).

The first phase recorded in the DENSE data will be used as reference configuration.

Peak systole is identified as the cardiac phase where E_{cc} is maximum. Although peak systole may be identified in several different ways, this criterion is chosen to have a common standard to report the data for comparison across different groups.

5 Dissemination of the cardiac kinematics benchmark study

We are actively working with *Philosophical Transactions A* to host a special issue on this benchmark study. More details will be available in January 2021.

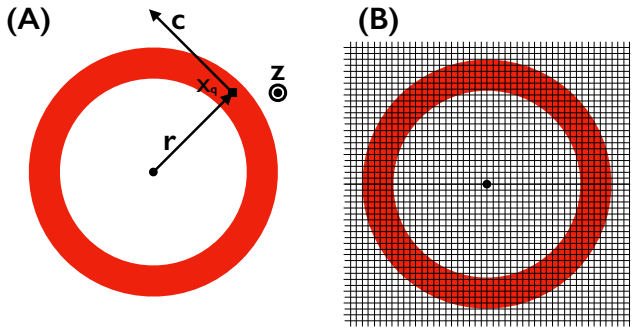


Figure 2: (A) Cylindrical coordinates system used to project the strain tensor **E** along the radial, circumferential, and longitudinal directions. (B) Schematic of sample grid overlaid to short axis slice.

References

[1] Bruce S Spottiswoode, Xiaodong Zhong, Aaron T Hess, CM Kramer, Ernesta M Meintjes, Bongani M Mayosi, and Frederick H Epstein. Tracking myocardial motion from cine DENSE images using spatiotemporal phase unwrapping and temporal fitting. *IEEE transactions on medical imaging*, 26(1):15–30, 2007.