

FIMH 2021 Benchmark

December 20, 2021

Main clarifications in version v3

1. Figure 3 has been updated to clarify the convention used for data storage.
2. Accordingly, the note for data storage in section 4.1, point 8, has been clarified.
3. Figure 6 has been added to illustrate the regional subdivision per each subject according to the schematic provided in Figure 5C.

Main additions/changes in version v2

1. Several clarifications and modifications have been added to the output section 4.
2. The plan to host a special issue with publications related to the Cardiac Kinematics Benchmark has been postponed. We are still pursuing the option to publish a collective paper on the benchmark results (please see section 5).
3. Results' submission is welcome any time until May 21, 2021.
4. Group comparison results will be presented in the Cardiac Kinematics Benchmark special session on June 23, 2021 (12:00 to 13:30 PDT). Individual participants will also present their methods in this special session.

Main additions/changes in version v1.1

1. A paragraph and Fig. 1 have been added to section 3.1.2 to clarify the short axis slices location along the longitudinal axis at the beginning of systole.
2. A paragraph and Fig. 3 have been added to section 3.1.2 to clarify the convention chosen to store phase data from the computational phantom in matrix form.

Main additions/changes in version v1

1. Information on the computational phantom data has been updated, please see section 3.1 for detailed description of the computational phantom.
 2. Computational phantom DICOM files have been uploaded to the GitHub repository [BenchmarkData](#). Participants should analyze the DICOM images directly. Previous .mat and .dns files have been removed from the repository.
 3. The output description has been updated.
 4. Task for participants: please download the DICOM images for the computational phantom and import the images to your preferred analysis platform to ensure the DICOM images can be successfully loaded. If not, please notify the organizers: Vicky Wang (vywang66@stanford.edu) and Luigi Perotti (Luigi.Perotti@ucf.edu).
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Background

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 selected output data for comparison
5. Dissemination of the cardiac kinematics benchmark study

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 selected output data for 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 data 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

Synthetic cine DENSE imaging data are generated from a computational cylindrical phantom whose deformation is analytically defined so that exact analytical displacements and strains can be computed

3.1.1 Computational phantom: Analytical motion

In this benchmark, we prescribed a deformation field in cylindrical coordinates of the form:

$$r(R, \Theta, Z) = a_1 + (1 + a_2)R + a_3 R^2; \quad (1a)$$

$$\theta(R, \Theta, Z) = \Theta + a_4 \frac{Z - Z_{\text{bot}}}{Z_{\text{top}} - Z_{\text{bot}}}; \quad (1b)$$

$$z(R, \Theta, Z) = (1 + a_5)Z, \quad (1c)$$

where the values of the parameters a_1 to a_5 and the physical dimension of the phantom are reported in tables 1 and 2, respectively.

Table 1: Computational phantom deformation parameters.

a_1	a_2	a_3	a_4	a_5
-21.301899	0.875377	-0.009475	0.079924	-0.141489

Table 2: Computational phantom geometrical dimensions and synthetic myofiber preferential orientation at endo (inner), mid, and epi (outer) phantom surfaces

R_{endo} [mm]	R_{epi} [mm]	Z_{bot} [mm]	Z_{top} [mm]
25	35	0	28
θ_{inner} [deg]	θ_{mid} [deg]	θ_{outer} [deg]	
70	-6	-42	

From eq. 1, the deformation gradient tensor \mathbf{F} can be computed analytically, for example following the notes available [here](#). Subsequently, the Green-Lagrange strain tensor can also be analytically computed from the deformation gradient tensor \mathbf{F} .

3.1.2 Computational phantom: synthetic cine DENSE DICOM images

The DICOM files corresponding to three short axis slices are provided. The bottom face of the phantom is fixed in Z ($Z_{\text{bot}} = 0$ mm) and the short axis slices locations are $z = 4$ mm, $z = 12$ mm, and $z = 20$ mm. At peak systole, these spatial locations correspond to the following Z coordinates in the reference configuration: $Z = 4.6592$ mm, $Z = 13.9777$ mm, and $Z = 23.2961$ mm, respectively, computed as $Z = \frac{z}{1+a_5}$ from eq. 1 (see also Fig. 1).

The following parameters are used to convert the phantom displacement field to three sets of phase images and magnitude images: 2.5×2.5 mm² in plane resolution, 8 mm slice thickness, $k_e = 0.08$ cycles/mm for all three phase encoding directions, the acquisition matrix size is 32×32 .

Watermarks are added in the bottom right corner of the magnitude and phase images to ensure images are orientated correctly upon data loading. An increasing watermark length along the right vertical edge of the image corresponds to images at increasingly higher z location (see Fig. 2).

The phase data is stored as illustrated in Fig. 3 with the X and Y phases swapped. Accordingly, the “Swap XY” option has already been selected in the provided DICOM files.

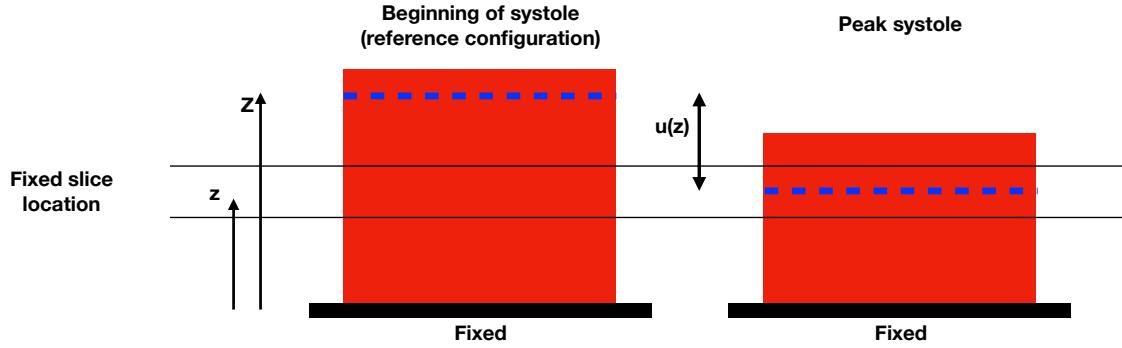


Figure 1: The location of the short axis slices along the phantom longitudinal axis is fixed in space. As the base of the phantom moves downward during contraction, the slices Z position in the reference configuration is higher as shown above, i.e., the slice at position Z in the reference configuration will be at position z at peak systole (dashed blue line).

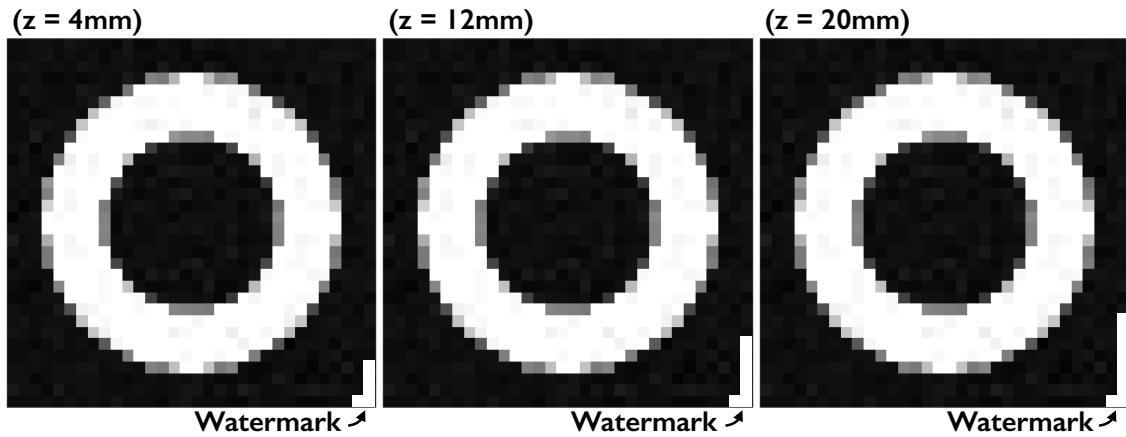


Figure 2: A watermark indicates the bottom right corner of the images. An increasing watermark length along the right vertical edge of the image corresponds to images at increasingly higher z location, e.g., $z = 4$ mm, $z = 12$ mm, and $z = 20$ mm.

If the open source cine DENSE post-processing toolbox found at [cine DENSE analysis tool](#) [1] is used for data analysis, the “Swap XY” option should already appear as selected.

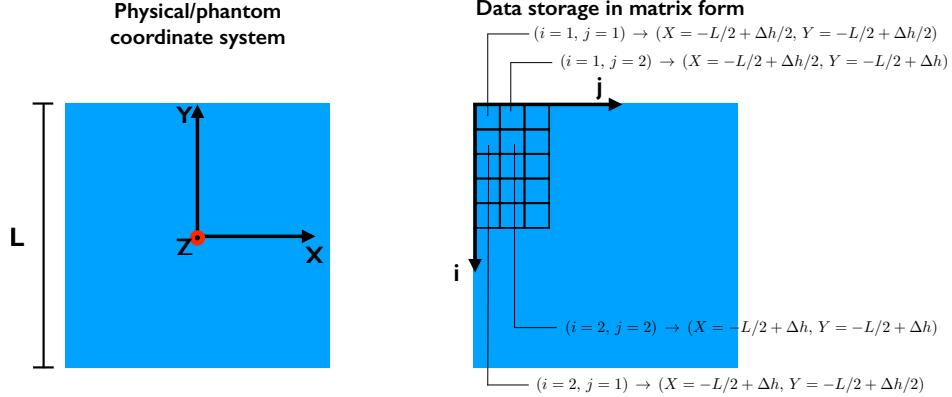


Figure 3: Physical coordinate system versus system chosen for data storage. Δh represents the sampling resolution (Here $\Delta h = 0.5$ mm, see also section 4.1)

Additional information about the computational phantom can be found in [2], although the parameters and the deformation equations reported here should be used as reference.

3.2 Healthy subjects

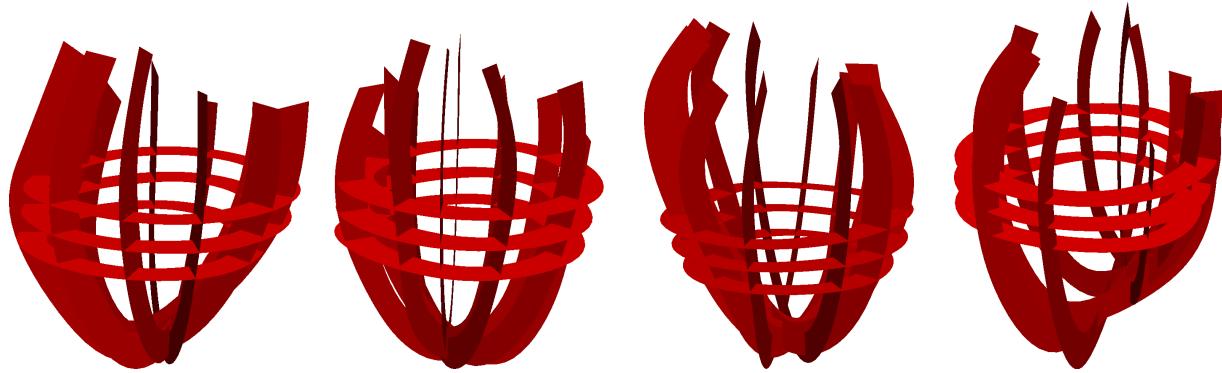
Cine DENSE data was acquired using a 3T (Prisma, Siemens) scanner following animal protocol #2015-124 as approved by the UCLA Chancellor’s Animal Research Committee. Three mid-ventricular, 8 mm apart, cine DENSE short axis slices are provided per subject using the following sequence parameters: 15 ms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

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 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.



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

Figure 4: Short axis slices location for healthy subjects TR-1242 and TR-1264, and for subjects TR-1434 and TR-1493 with myocardial infarction.

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. 4.

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

Each participant will be assigned a Google folder with a name identifier limited to less than 10 characters. This identifier may be based on the group name, institute, and/or key participant’s last name. Please send this identifier as soon as possible to the benchmark organizers. Once this identifier is provided, we will create a main Google folder using the identifier and the following sub-folders:

1. Computational_Phantom
2. Pre_clinical

4.1 Computational Phantom folder

Results of the computational phantom analysis should be uploaded to the **Computational_Phantom** folder according to the guidelines listed below:

1. Although 4 SNR levels are provided, only results for SNR=20 and SNR=inf will be compared across all groups.
2. Results will be reported separately for each of the 3 slices: S04, S12, S20.
3. Peak systolic Lagrangian displacement dx , dy , and dz should be reported.

4. Peak systolic Green-Lagrange strain components E_{cc} , $E_{\ell\ell}$, E_{rr} should be reported (Reporting all strain components is not mandatory to participate in the benchmark). Additional strain components that can be reported are $E_{cl\ell}$, $E_{rl\ell}$, E_{rc} , and E_{ff} .
5. Definition of the local wall coordinate system (circumferential, longitudinal, and radial) should agree with the following:
 - 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 (see Fig. 5A).
 - At every point X_q in a short axis slice, the circumferential direction is defined along the line perpendicular to the radial direction (see Fig. 5A).
 - The longitudinal direction is identified as perpendicular to the short axis slice plane (see Fig. 5A).
6. E_{vv} represents 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 ℓ along the \mathbf{z} axis in the reference configuration.
7. 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 θ with respect to the short axis plane. The helix angle θ is rule based and varying quadratically from 70° at endocardium, to -6° at midwall, and -42° at epicardium. Accordingly, the helix angle θ is defined transmurally as

$$\theta = 2\theta_{endo}(r - 0.5)(r - 1) - 4\theta_{mid}(r)(r - 1) + 2\theta_{epi}(r)(r - 0.5), \quad (2)$$

$r = (R - R_{endo})/(R_{epi} - R_{endo})$ varies from 0 at endocardium to 1 at epicardium.

8. All strains and displacement measures are sampled at the centers of the voxels defined by a grid with in plane resolution equal to 0.5 mm. The grid covers the entire short axis plane. As the image matrix size is 32×32 voxels and each voxel measures 2.5mm, the image size is $80\text{mm} \times 80\text{mm}$. Therefore, the resultant grid is 160×160 with a 0.5mm spacing. Note: according to Fig. 3, the center of the sampled voxel stored at $(i=1,j=1)$ is at $(-39.75\text{mm}, -39.75\text{mm})$, the center of the sampled voxel stored at $(i=1,j=2)$ is at $(-39.75\text{mm}, -39.25\text{mm})$, and so on. For group comparison, only voxels in the phantom/myocardium at the reference configuration will be considered (see Fig. 5B). Therefore, the voxels outside the phantom should be filled with ‘NaN’.
9. All quantities for comparison should be reported in a .mat file with the following naming convention:
 - NameIdentifier_CompPham_SNR#_SliceID_QuantityReported.mat

For example:

- SFVA_CompPham_SNR20_S04_dx.mat

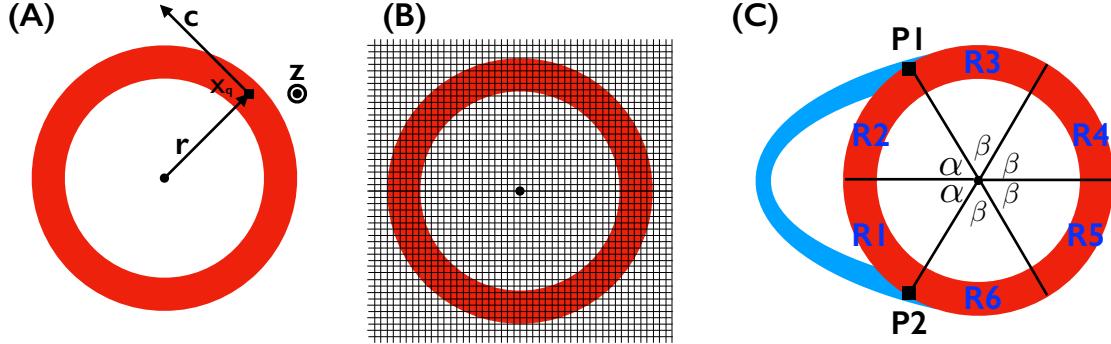


Figure 5: (A) Cylindrical coordinates system used to project the strain tensor \mathbf{E} along the radial, circumferential, and longitudinal directions. (B) Schematic of sample grid overlaid to short axis slice. (C) Regional subdivision per slice (see also Fig. 6)

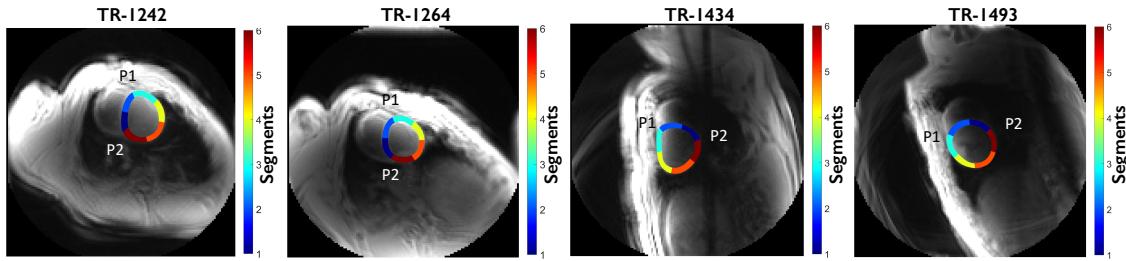


Figure 6: Regional subdivision per each subject according to Fig. 5C

- SFVA_CompPham_SNR20_S04_dy.mat
- ...
- SFVA_CompPham_SNR20_S12_Ecc.mat
- SFVA_CompPham_SNR20_S12_Err.mat
- ...
- SFVA_CompPham_SNRinf_S20_Ecc.mat

These .mat files will be further analyzed by the benchmark organizers and can be tested by the participants using the available ComparisonCode.

4.2 Pre_clinical data folder

1. In the **Pre_clinical** folder, a Google spreadsheet will be created for each participant.
2. Each Google spreadsheet, will have 4 tabs, one per each subject, i.e., TR-1242, TR-1264, TR-1434, and TR-1493.
3. Each tab will contain a table as Table 3 in this document. Other Green-Lagrange strain components (e.g., E_{cr} , E_{cl} , E_{lr}) may also be reported.
4. Q1 and Q3 in table 3 refer to the 25th and 75th percentiles, respectively.

	E_{cc}			$E_{\ell\ell}$			E_{rr}			E_{ff}		
	Q1	Median	Q3	Q1	Median	Q3	Q1	Median	Q3	Q1	Median	Q3
Endo												
Mid												
Epi												
R1												
R2												
R3												
R4												
R5												
R6												
Total												
Peak systole frame												

Table 3: Strain output measures for preclinical data

5. The endocardial (endo), midwall (mid), and epicardial (epi) regions are defined by dividing the wall into 3 equal transmural segments.
6. In order to compute regional strains, six regions are defined as follow (recalling the six mid-ventricular AHA regions). On each slice, the right-ventricle (RV) insertion points P1 and P2 are identified together with the barycenter of the left ventricle. The septal region contained between points P1 and P2 is subdivided into two equal regions (R1 and R2) spanning the same angle with respect to the LV barycenter. The remaining of the myocardial wall is subdivided into four equal regions (R3 to R6) spanning the same angle with respect to the LV barycenter (See Fig 5C).
7. The first phase recorded in the DENSE data will be used as reference configuration.
8. Peak systole is identified as the cardiac frame 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 participants.

5 Dissemination of the cardiac kinematics benchmark study

The plan to host a special issue has been postponed to when additional imaging data will be included in the benchmark (e.g., tag MRI data).

We are still pursuing the option to publish a collation paper on the benchmark results in a journal publication authored by all participants. Participating in the collection paper is *not* a requirement to participate in the benchmark. More details about authorship (e.g., number of authors from each group) will be decided after the benchmark session at FIMH 2021.

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.
- [2] Ilya A Verzhbinsky, Luigi E Perotti, Kévin Moulin, Tyler E Cork, Michael Loecher, and Daniel B Ennis. Estimating aggregate cardiomyocyte strain using in vivo diffusion and displacement encoded MRI. *IEEE Transactions on Medical Imaging*, 39(3):656–667, 2019.