HeartIC
Image-based data assimilation for an HPC model of the heart

Gautier Bureau, Dominique Chapelle, Radomir Chabiniok, Sebastien Gilles, Philippe Moireau, M3DISIM team, Inria Saclay Île-de-France
Alexandra Groth, Philips Hamburg
Jiri Minarcik, Katerina Solovsk, Czech Technical University in Prague

Context

- Motivations
  - A personalised model typically for a patient
  - Can be used for predictive purposes: providing diagnosis and prognosis assistance
- Starting point
  - MΞDISIM heart model can be calibrated to represent cardiac cycles of patients with various pathologies.
  - Data assimilation strategies to register this type of model on actual data extracted from medical images – typically Cine-MRI.

Objectives

- Drawbacks of previous strategy
  - Discrepancy measure between the data and the model requires a segmentation step of the data and is based on a simple definition of the distance between boundaries.
- Objectives
  - Propose a new discrepancy measure that can be constructed without prior segmentation of the image data using the expertise of Philips Hamburg.
  - Transfer from the old simulation code the first strategy and develop the new strategy in a new HPC code.
  - Applying the state estimator in processing other types of cardiac MR data, which might be corrupted due to typical issues in cardiac MRI (motion of the subject, not-perfect periodicity of cardiac cycles)

Outline

- Cardiac modeling and data assimilation
- State estimation using pre-segmented surfaces
- State estimation with Philips discrepancy
- Applying the state estimator in processing other types of cardiac MR data

Cardiac modeling and data assimilation

Myocardium modeling summary

- Principle of dynamics in total Lagrangian formulation

$$\int_{\Omega_0} \rho \ddot{\underline{y}} \cdot \delta \underline{v} \, d\Omega_0 + \int_{\Omega_0} \underline{\underline{\Sigma}} : \delta \underline{\underline{e}} \, d\Omega_0 + \int_{\Gamma} P_V \, \underline{\nu} \cdot \underline{\underline{F}}^{-1} \cdot \delta \underline{v} \, J \, d\Gamma = 0, \quad \forall \delta \underline{v} \in V$$

- Constitutive law

$$\underline{\underline{\Sigma}} = \frac{\partial W^e}{\partial \underline{\underline{e}}} + \frac{\partial W^\eta}{\partial \dot{\underline{\underline{e}}}} + \sigma_{ID}(e_{ID}, e_c) \underline{n} \otimes \underline{n}$$

- Hyperelastic term $W^e = c_0 \, e^{c_1 (J_1 - 3)^2} + c_2 \, e^{c_3 (J_4 - 1)^2} + \kappa \left[(J - 1) - \ln J \right]$
  with reduced invariants $J_1 = \left(\mathrm{tr} \underline{\underline{C}} \right) J^{-\frac{2}{3}}, \quad J_4 = \left(\underline{n} \cdot \underline{\underline{C}} \cdot \underline{n} \right) J^{-\frac{2}{3}}$
- Viscous term $W^\eta = \frac{\eta}{2} \, \mathrm{tr}(\dot{\underline{\underline{e}}}^2)$
- Active part (fiber directed)

Data assimilation strategy

- We a model defined by the following systems

$$\begin{cases} \dot{u}(t) &= A(u,t), \\ u(0) &= u_\diamond + \zeta^u, \end{cases}$$

- We have some observations at our disposal.

- There exists a discrepancy operator allowing to compare the observation associated with with any other state.

- We define a new dynamic model called ***observer*** or ***state estimator***

$$\begin{cases} \dot{\hat{u}}(t) &= A(\hat{u},t) + G_u\left(D(z_u,\hat{u})\right), \\ \hat{u}(0) &= u_\diamond, \end{cases}$$

State estimation using pre-segmented surfaces

Increase predictivity of biophysical heart model (model personalization / patient-specific medicine e.g. to plan therapy)

Coupling physical model-based & cine MRI

- 3D biomechanical heart model can be calibrated to represent patients' heart contraction
- A discrepancy exists when directly comparing the boundary of model with the patient's cine MRI

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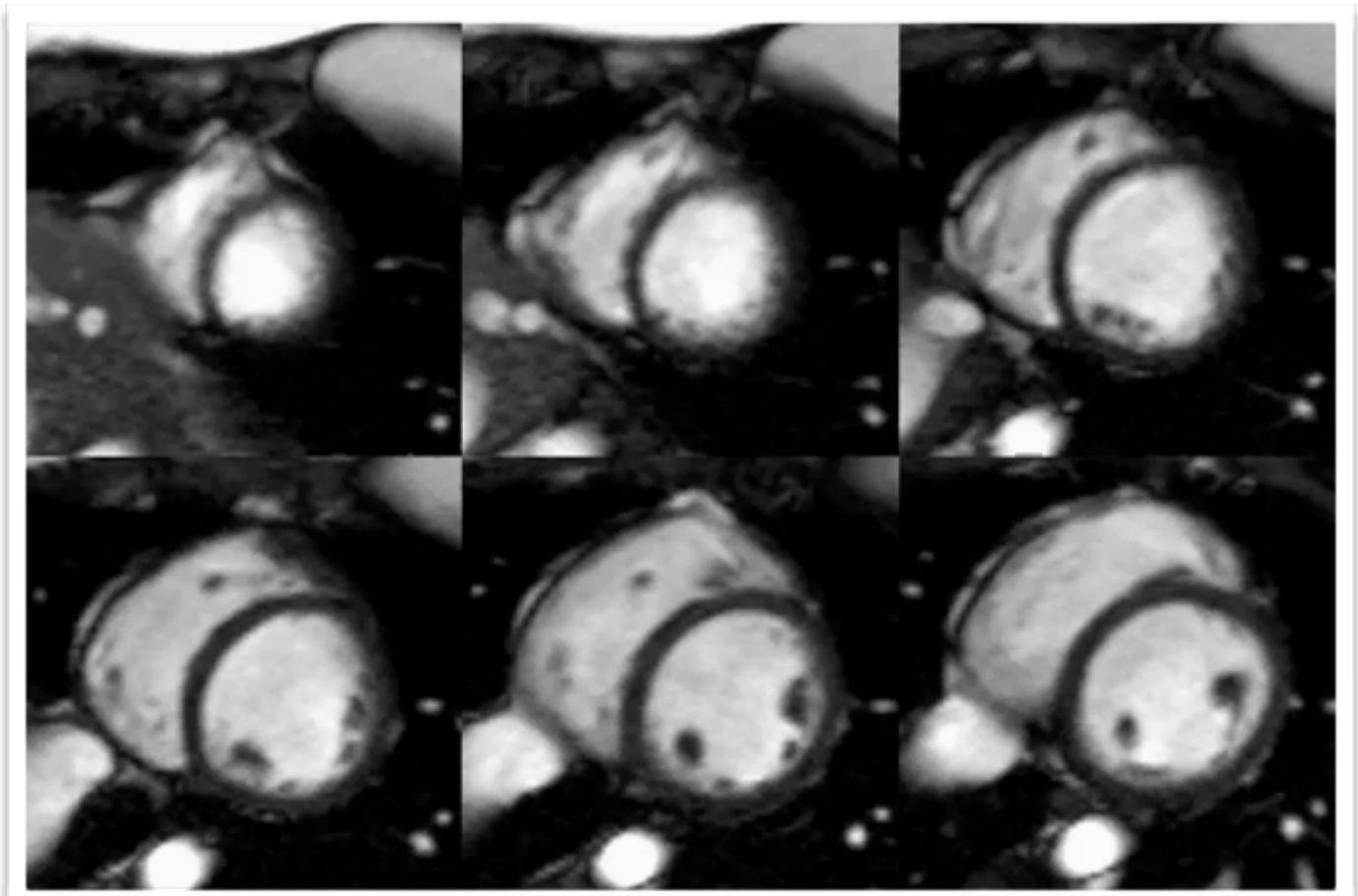


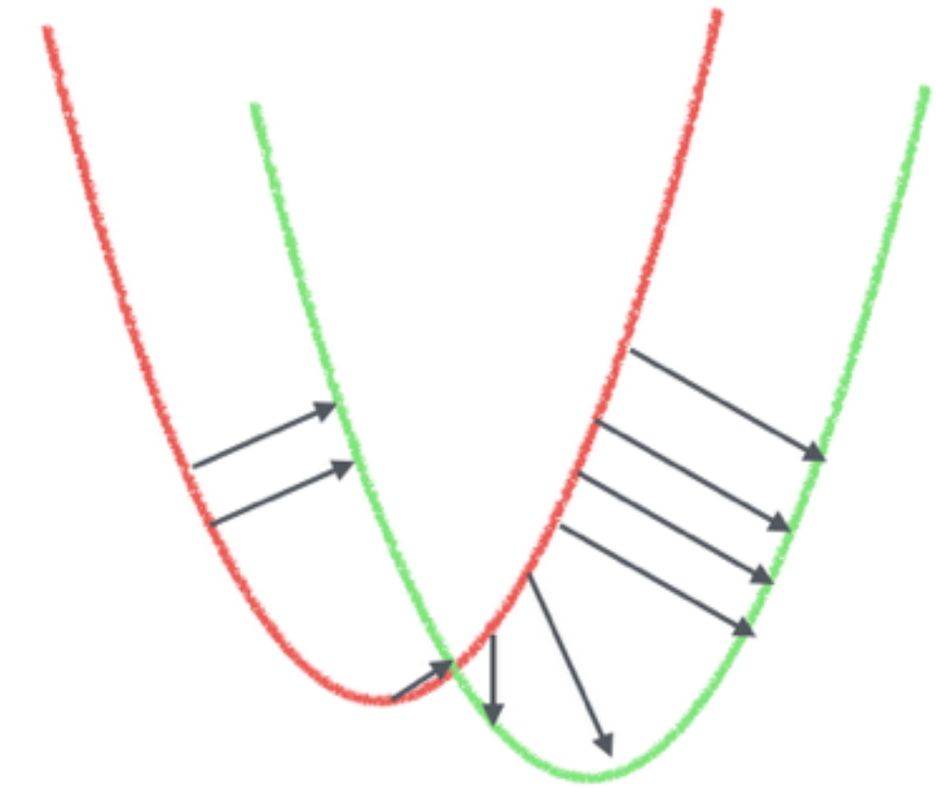
Example of cine MRI in short axis of heart: typically covers whole heart in ~15 slices with temporal resolution ~15-30ms

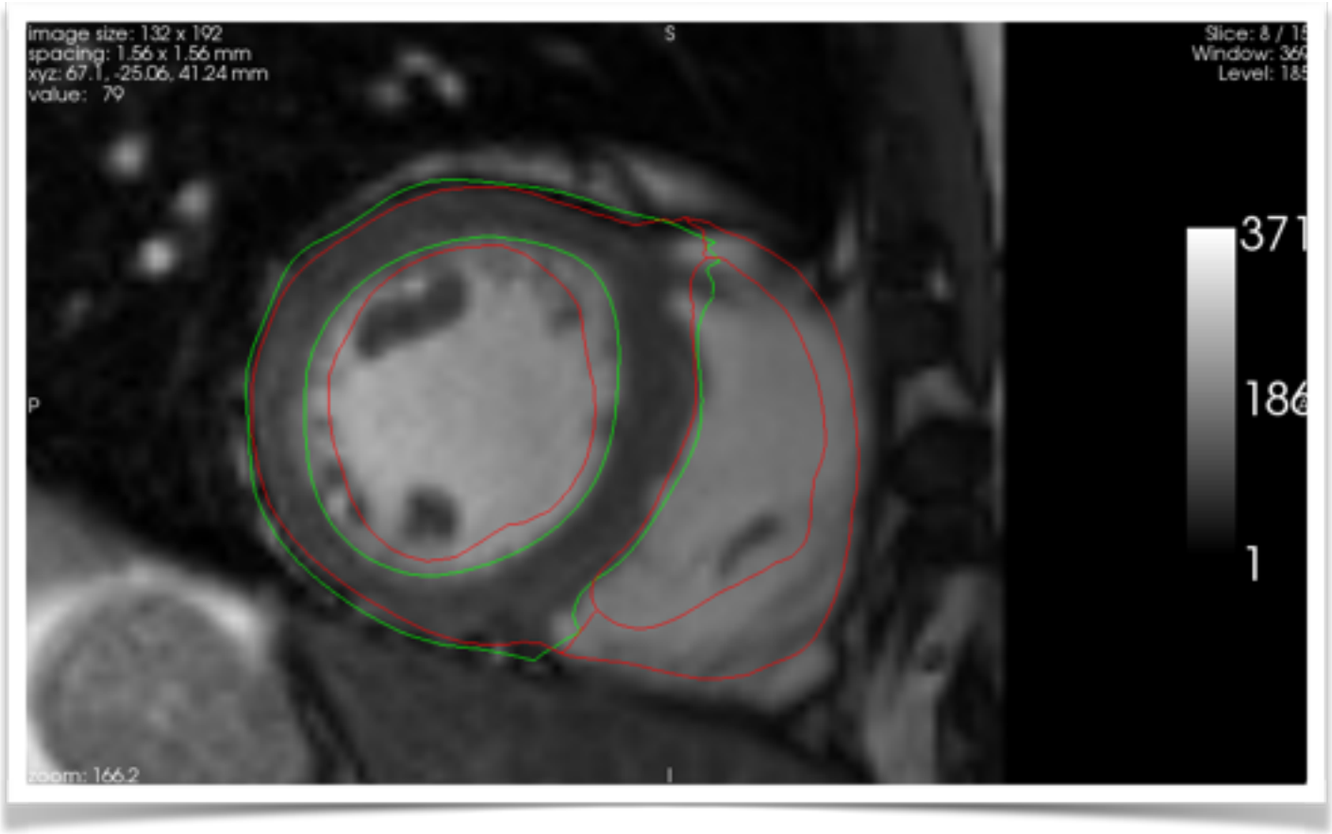
Coupling physical model-based & cine MRI

- 3D biomechanical heart model can be calibrated to represent patients' heart contraction
- A discrepancy exists when directly comparing the boundary of model with the patient's cine MRI
- Data assimilation introduces feedback of the image data to correct the state of physical model (state estimation)
- A natural discrepancy measure between 3D model and time-resolved cine MRI sequences is the surface-to-surface distance (endo/epi-cardium of model vs. corresponding surface in cine MRI)

State estimation using pre-segmented boundary surfaces

- Correction based on a term of the form $-\gamma \int_{\Gamma} \text{dist}(\underline{x}, \Gamma) \cdot \underline{n} \cdot \underline{w}\, d\Gamma$
- Computes the distance between the simulated model and a target surface mesh.

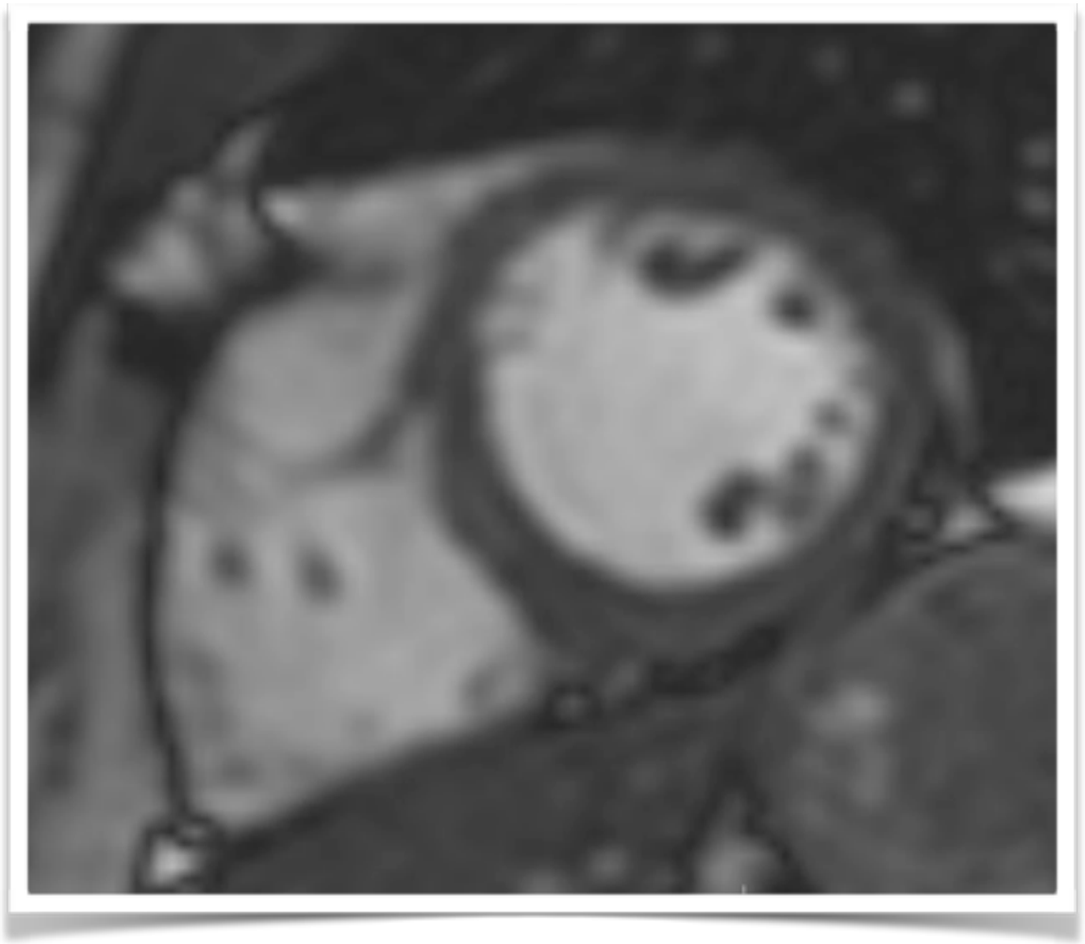




Green: observations (target)
Red: simulated model

P. Moireau, D.Chapelle, and P. Le Tallec:
Filtering for distributed mechanical systems using position measurements:
Perspectives in medical imaging, Inverse Problems, 25(3), 2009.

State estimation using pre-segmented boundary surfaces: exemple of results



Green: pre-segmented surfaces (“observations”)
Red: biophysical model (pre-calibrated), physical & physiological but a bit far from the data
Blue: Corrected model by data (model-data coupling) with physics inside and very well wrt. to the data

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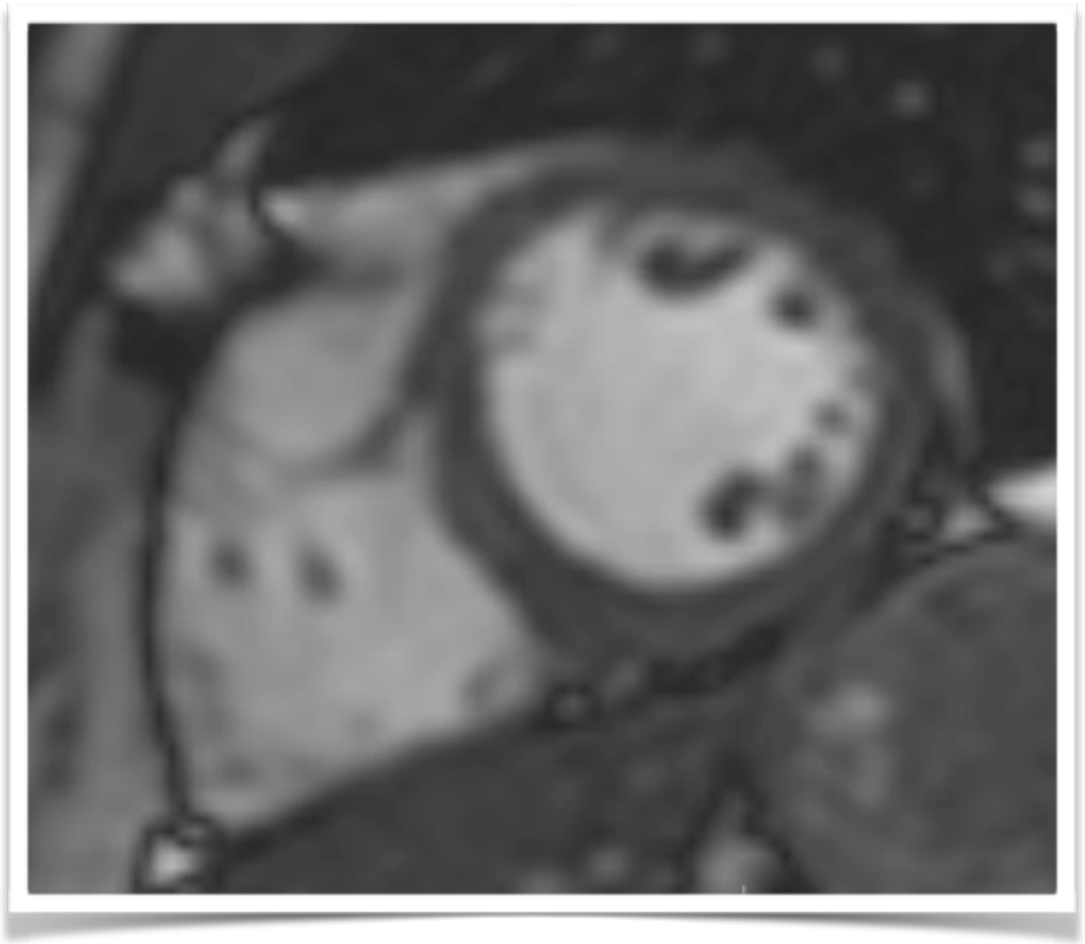

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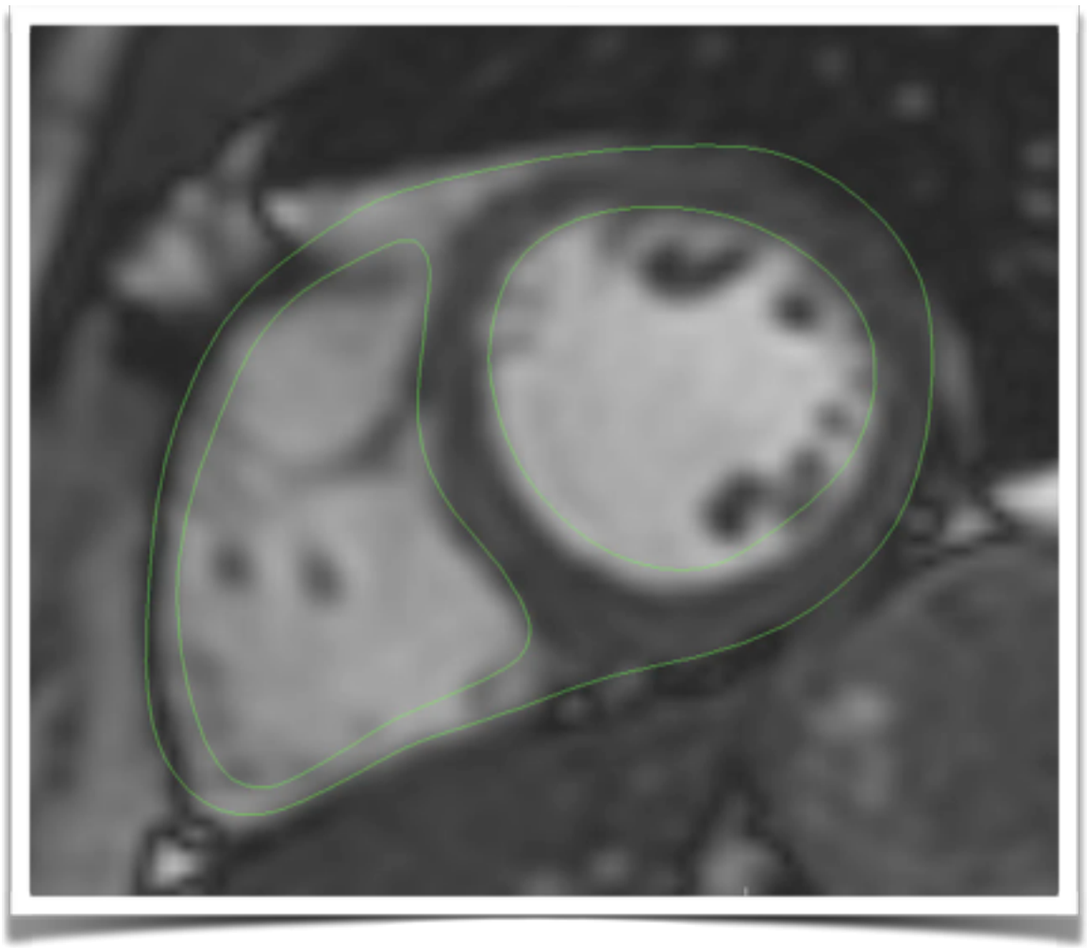

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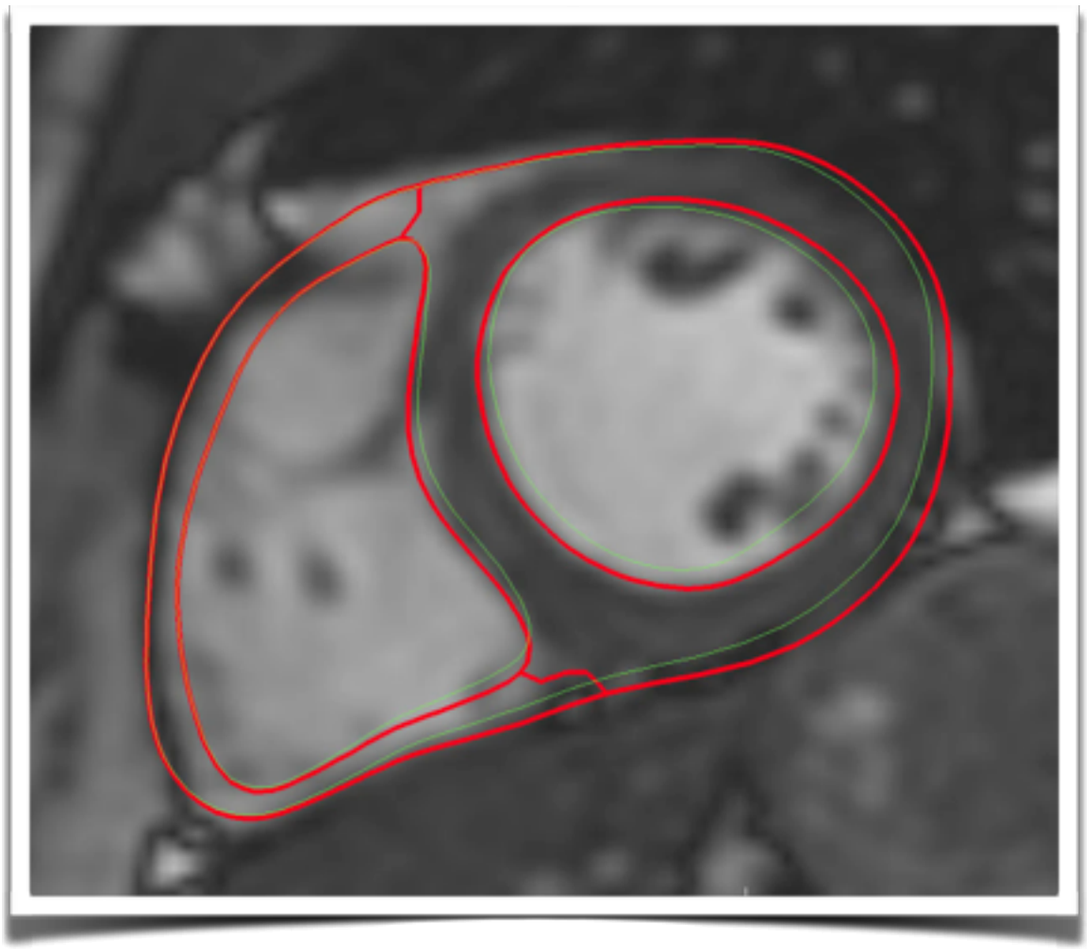

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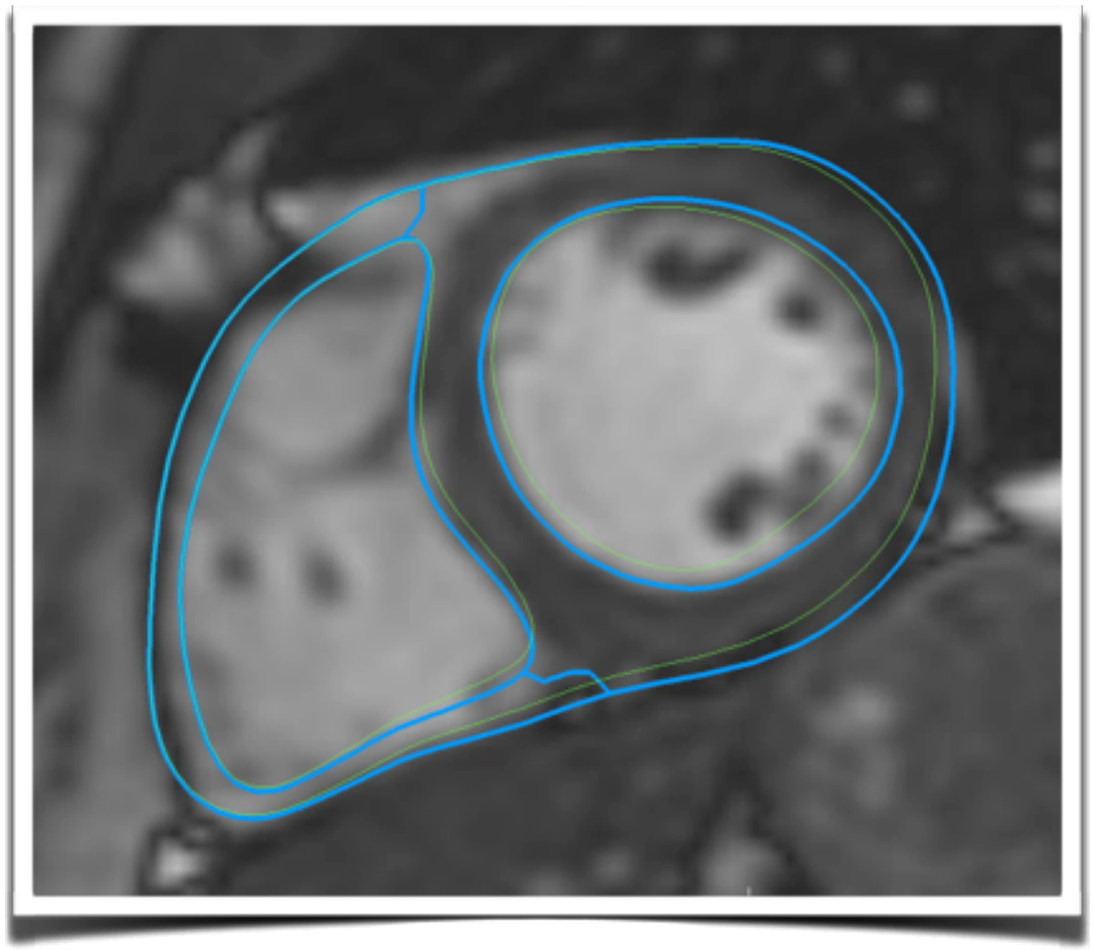

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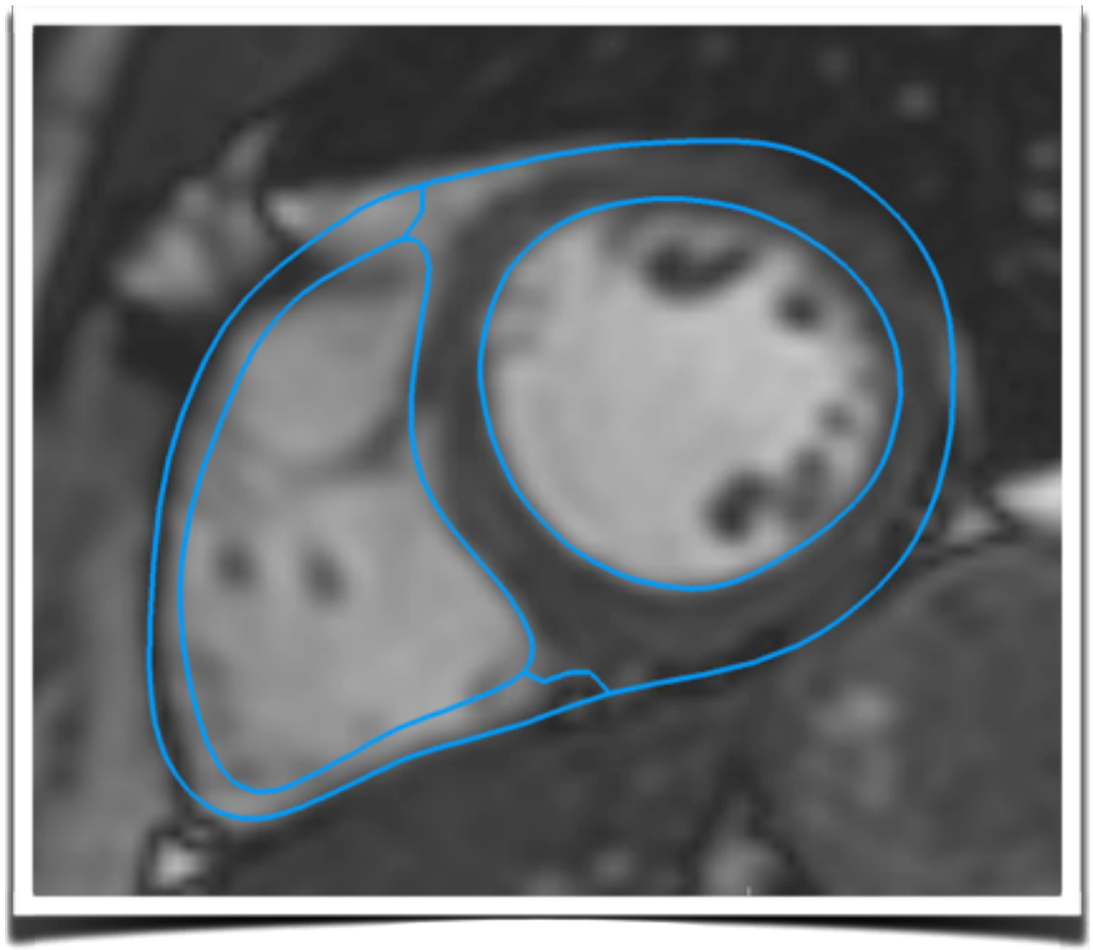

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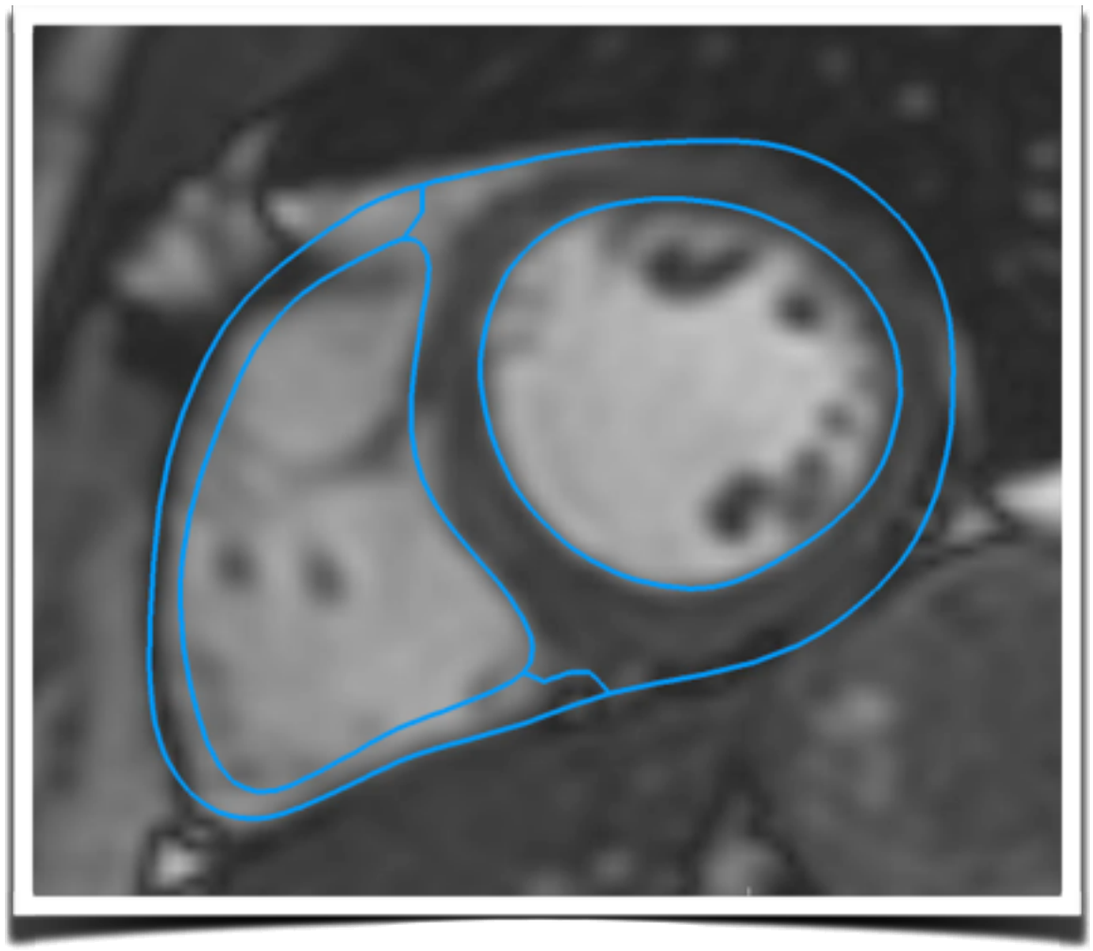

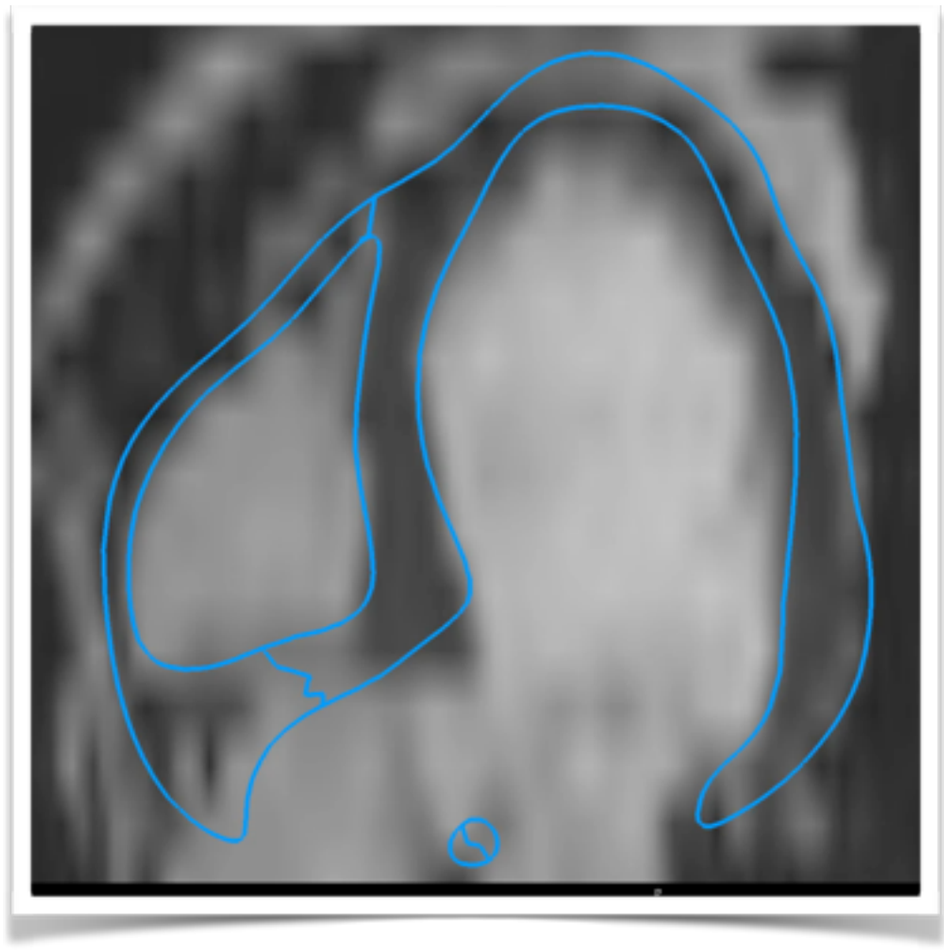

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State estimation using pre-segmented boundary surfaces: drawbacks

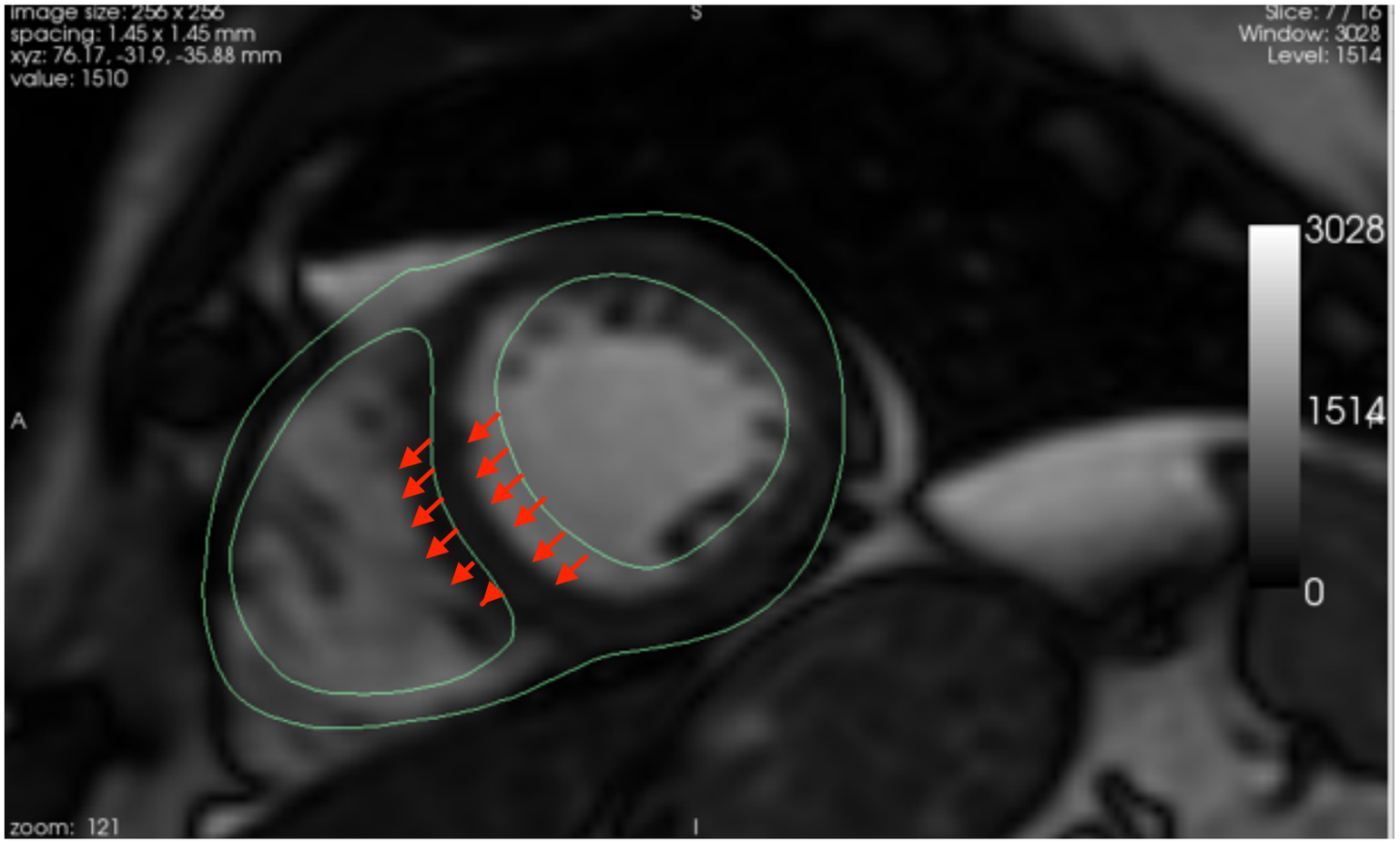
- Manual segmentation from a medical doctor or automatic segmentation from a clever algorithm (rare) is required to pre-process the data

State estimation with Philips discrepancy

Philips discrepancy

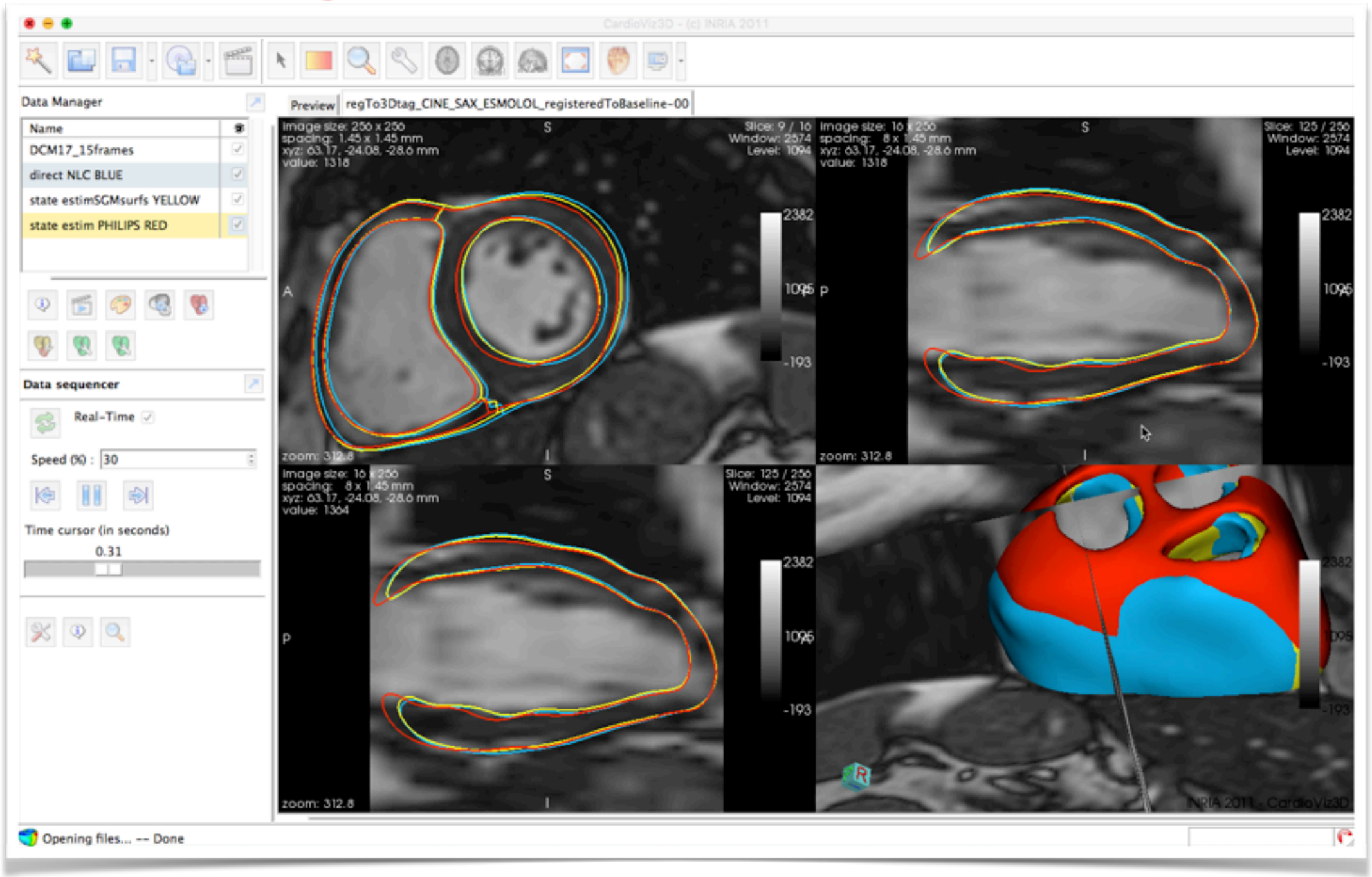
- Philips can compute distances directly in the image

- Our objective:
  - Use this image-based distance instead of a mesh-based distance !



A. Groth, J. Weese, and H. Lehmann. Robust left ventricular myocardium segmentation for multi-protocol MR. In Proc. of SPIE, volume 8314, pages 83142S1–9, 2012.

Results using Philips observator



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Yellow: correction by pre-segmented surfaces (as in the slides before)

Red: correction by Philips discrepancy operator (without prior segmenting)

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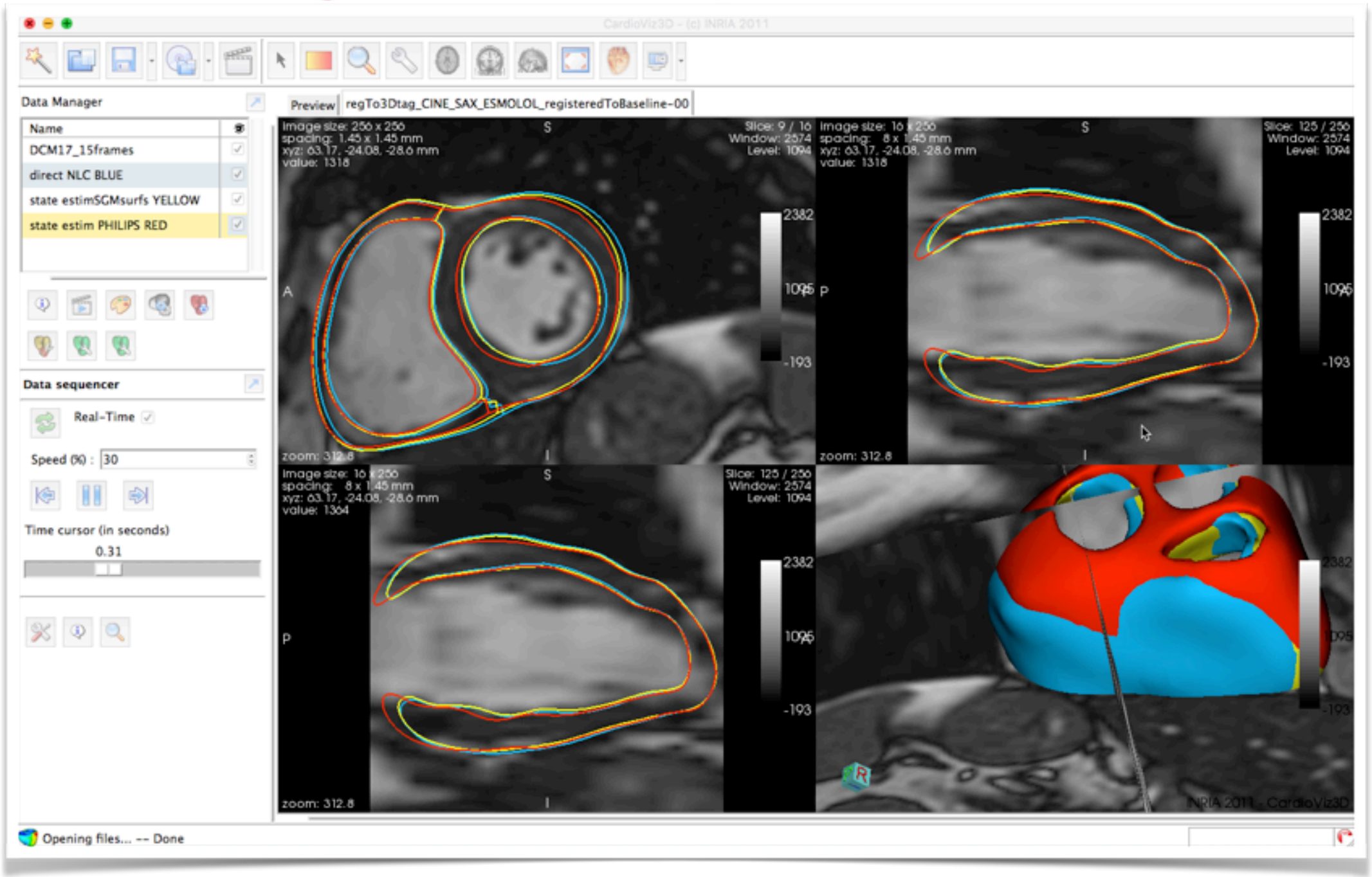

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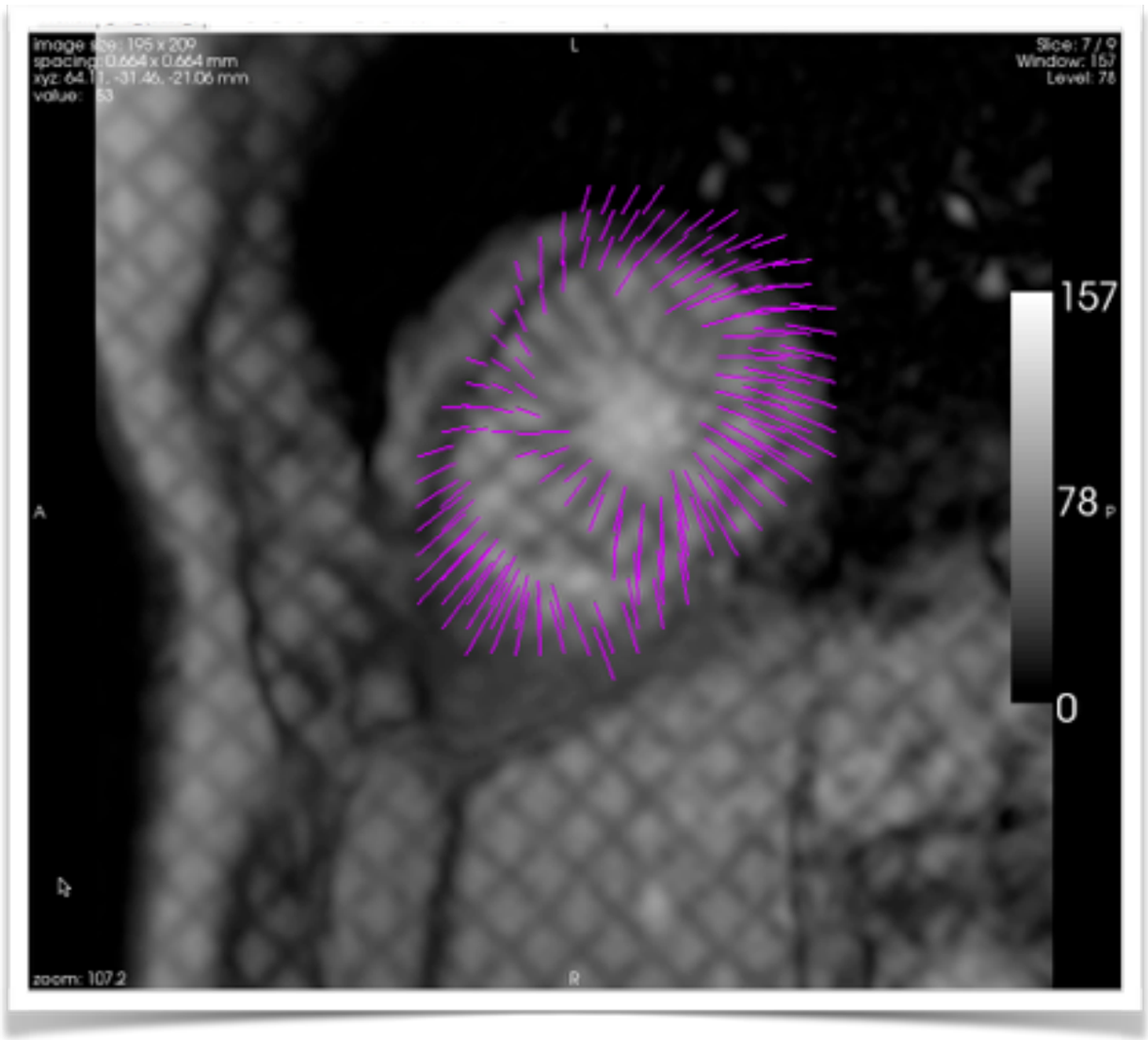
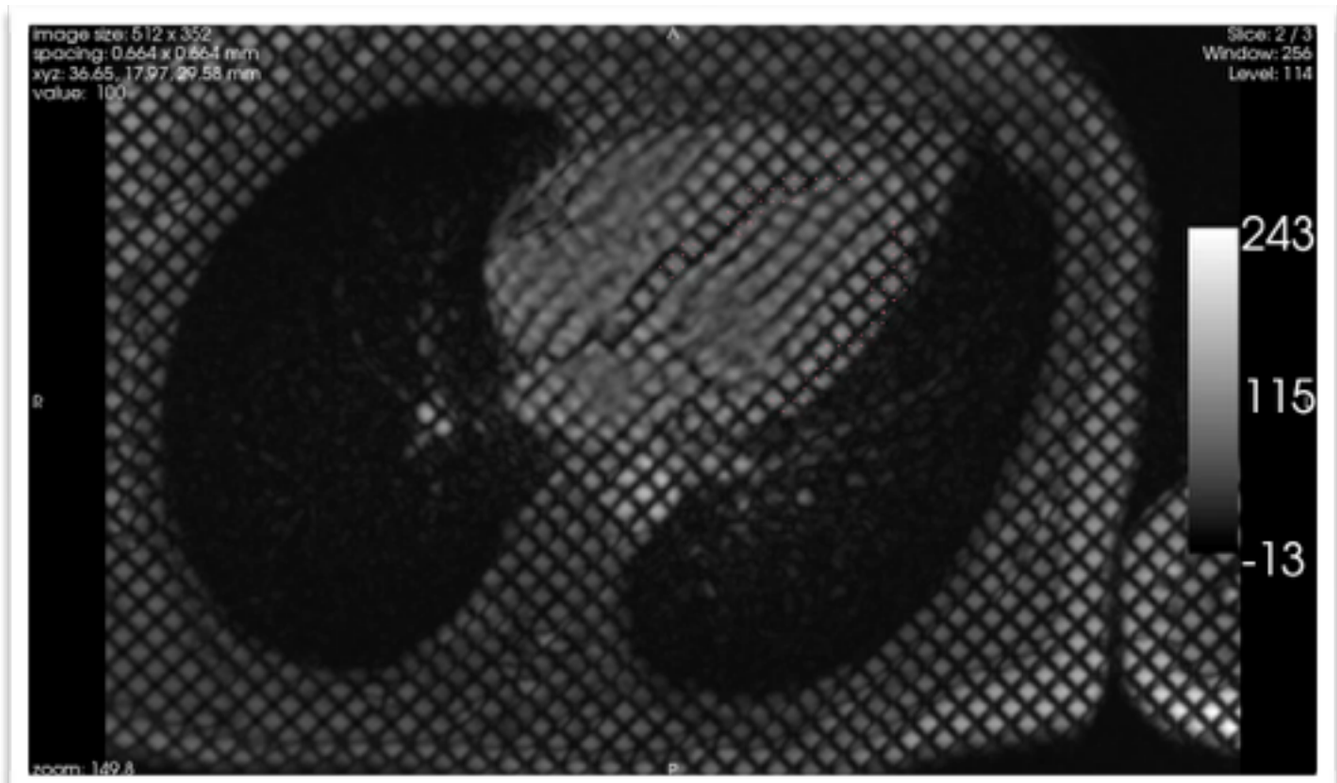
Validation using additional data

- Error assessed by displacement extracted from independently acquired tagged MRI (“pseudo-ground truth”)





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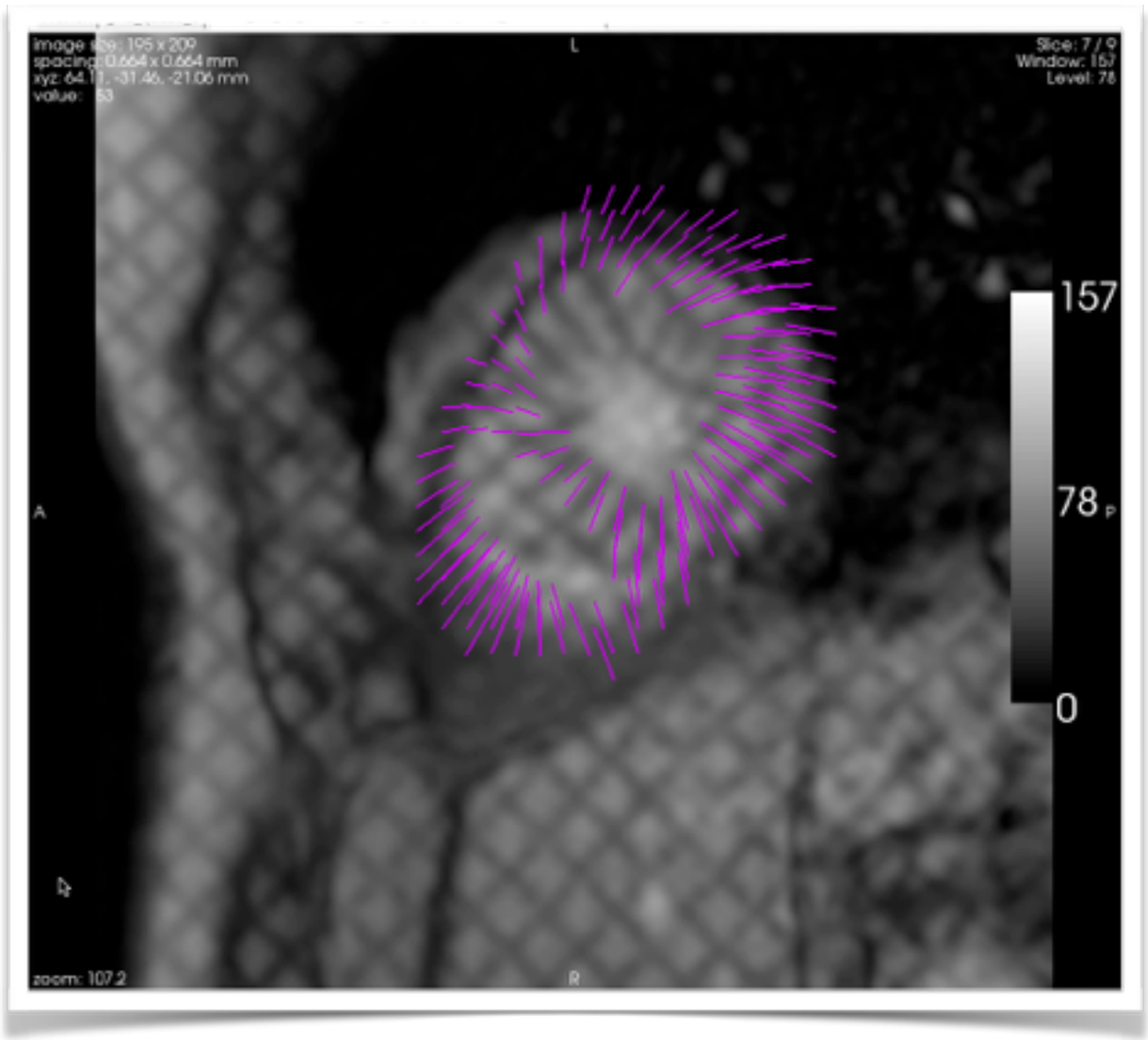

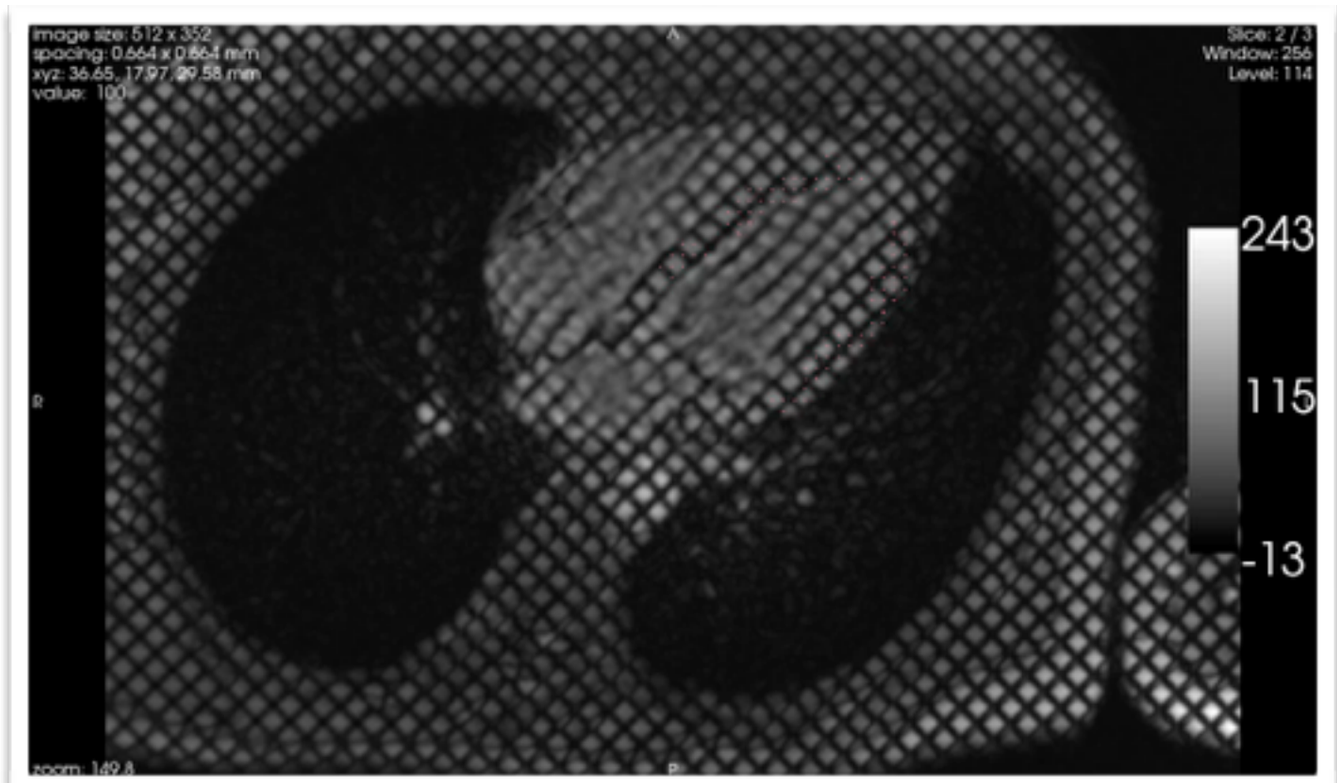

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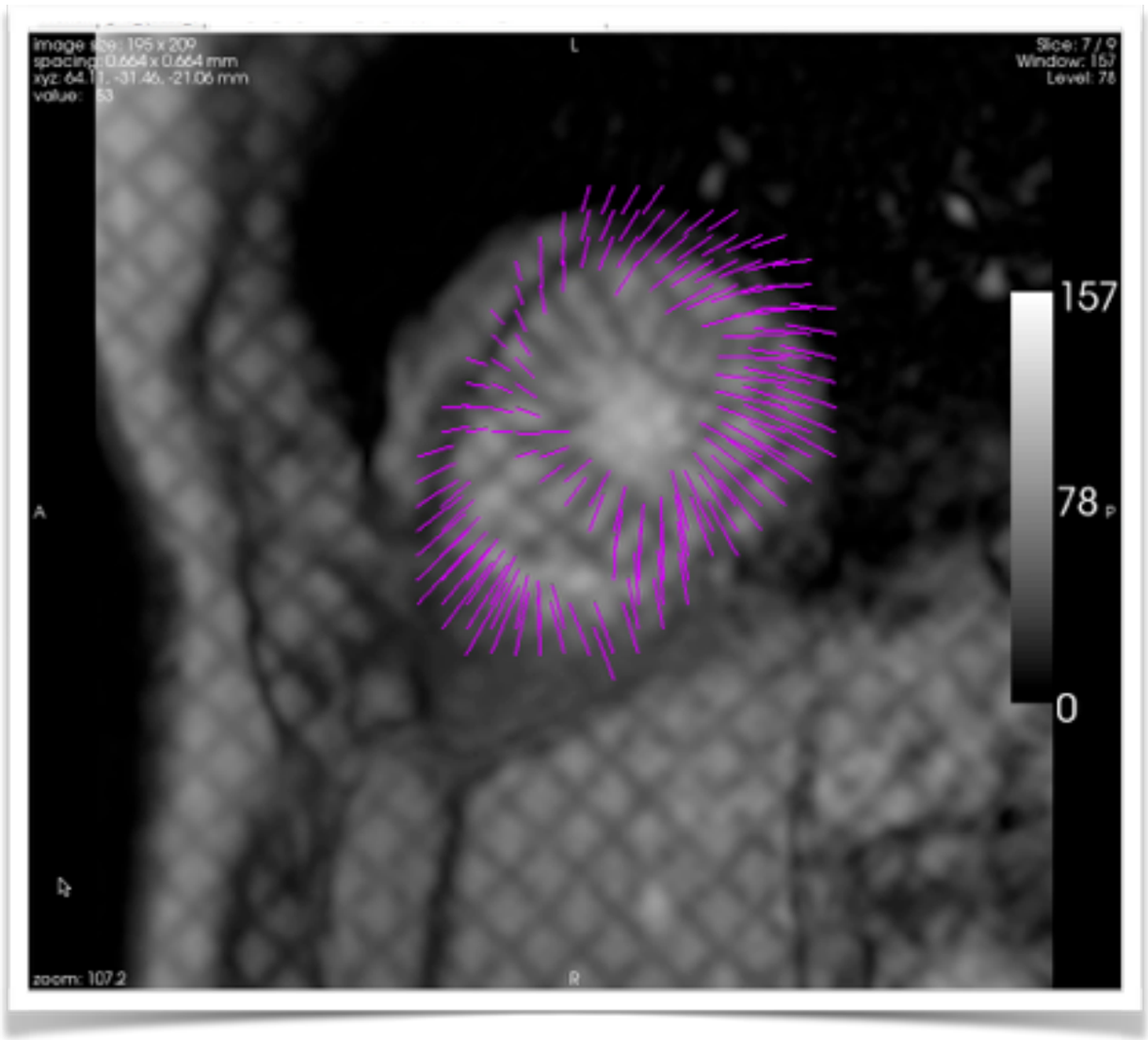
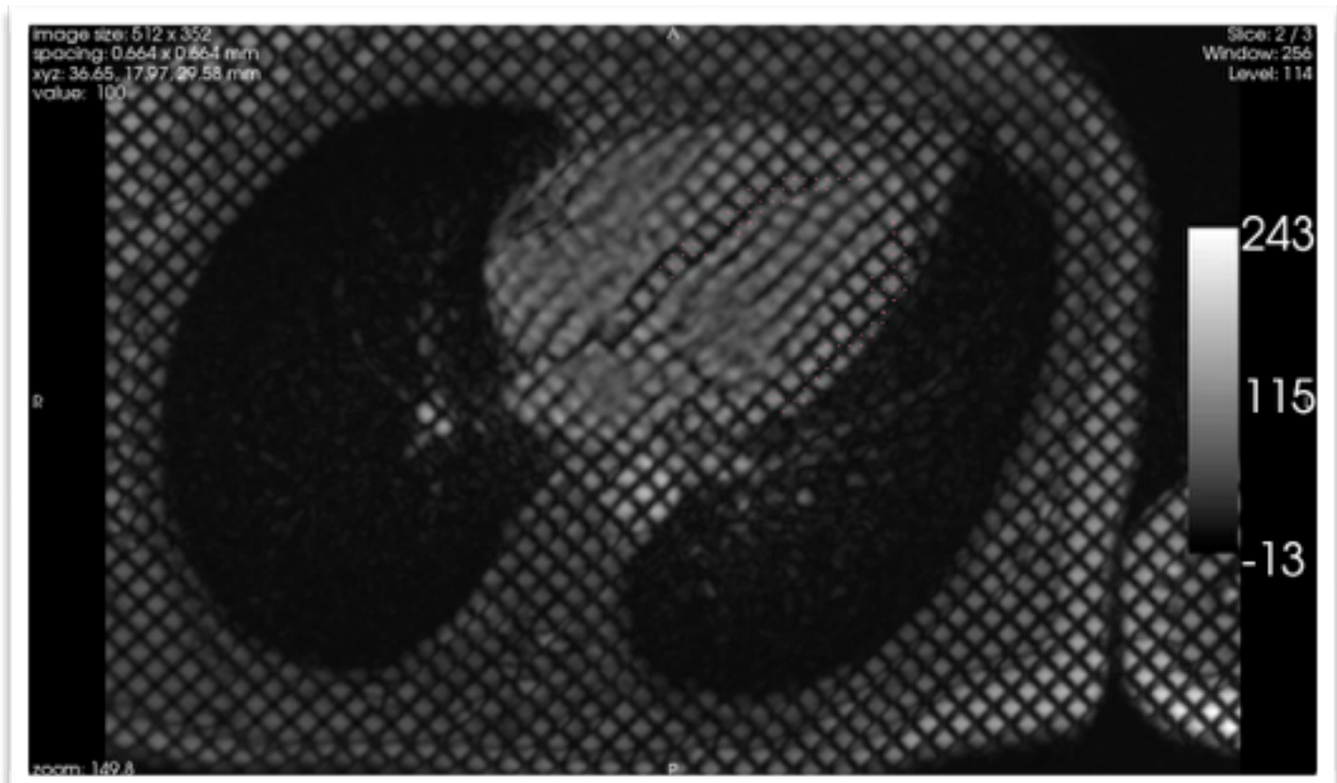
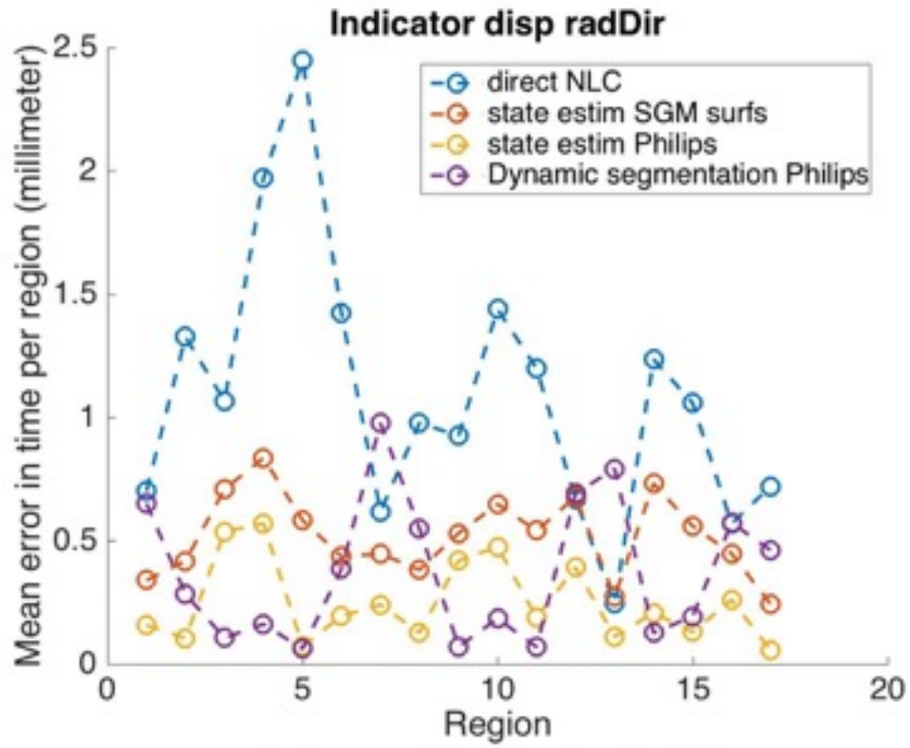
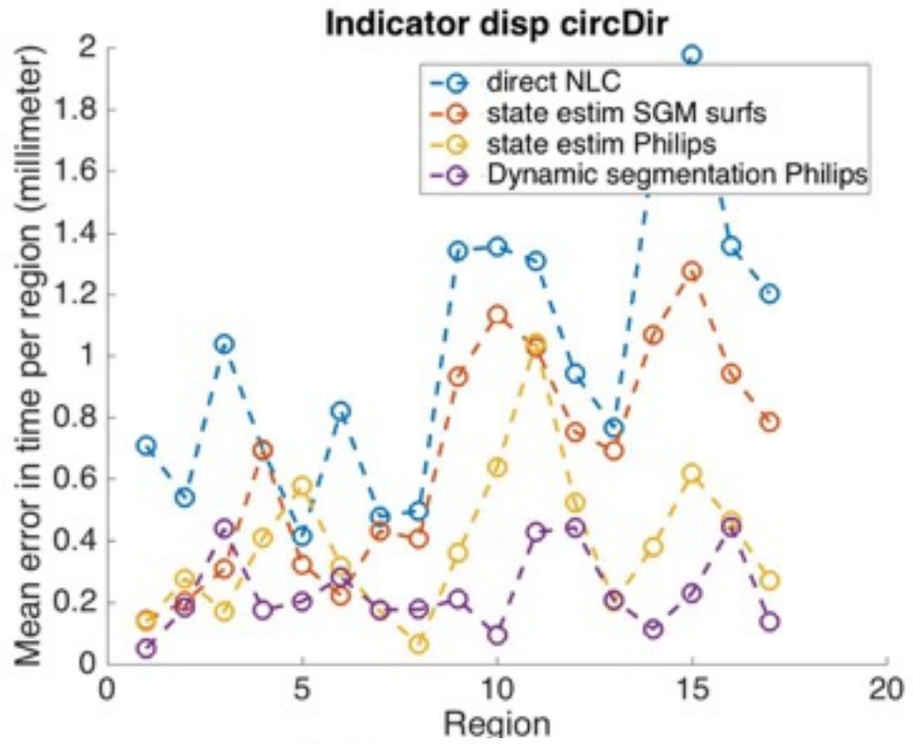
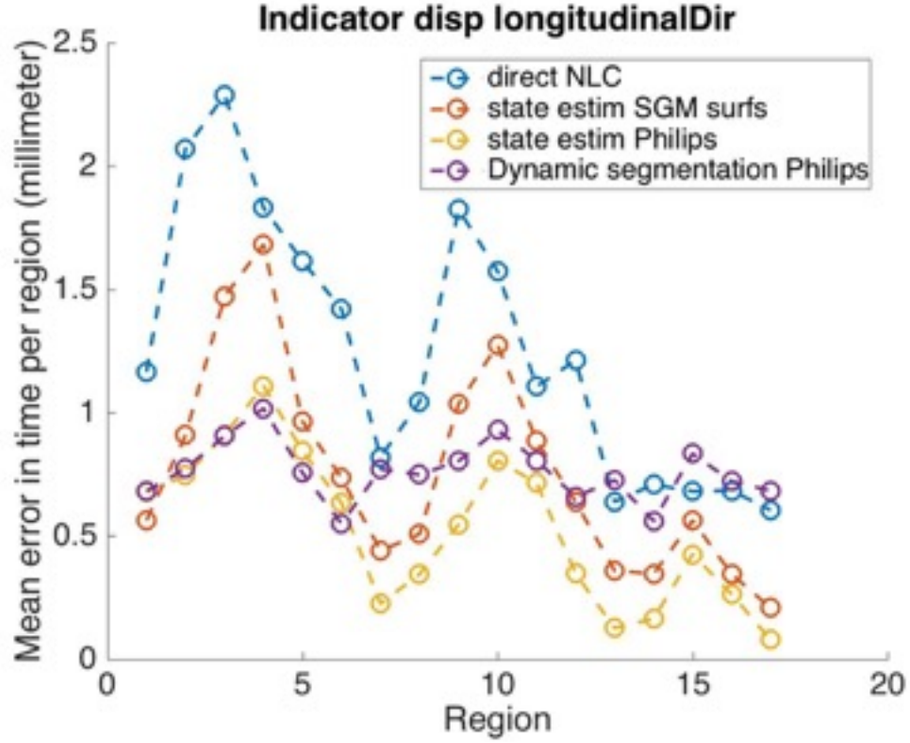


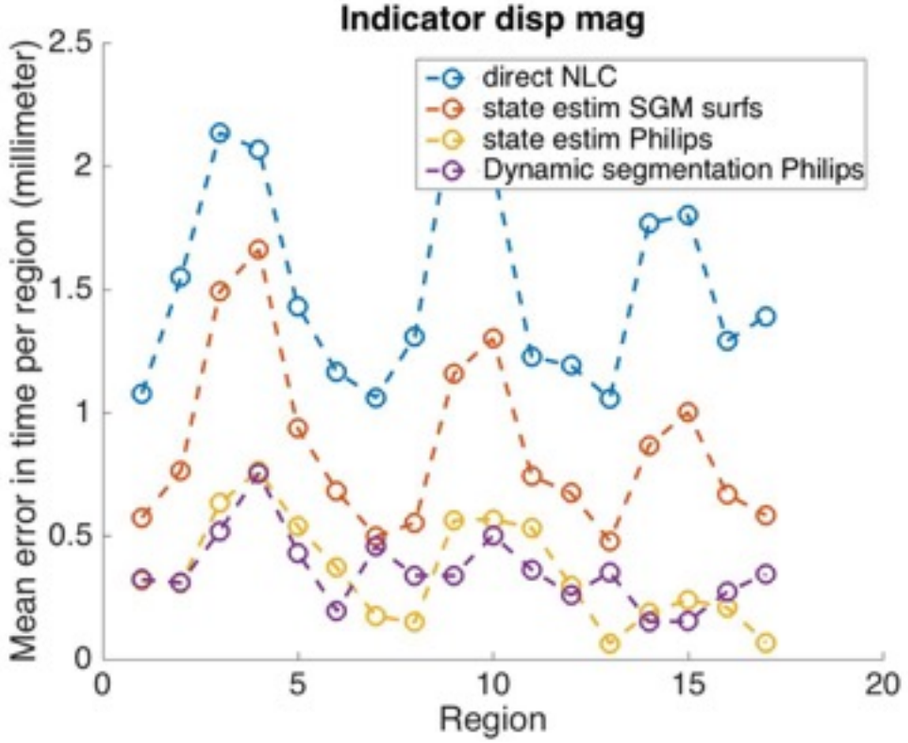


Validation results









IK+E
M

FJFI

informatics mathematics
Inria

Applying the state estimator in processing other types of cardiac MR data

Provide directly some clinically important information

Motion compensation in T1-mapping MRI sequence

- T1 relaxation time is one of the intrinsic MRI contrasts characterising each tissue
  - Fibrosis (Damaged tissue) : T1 ↘

- Effective T1-mapping MR imaging sequences (ex: MOLLI sequence) are relatively widely used non-invasive assessment of myocardium.

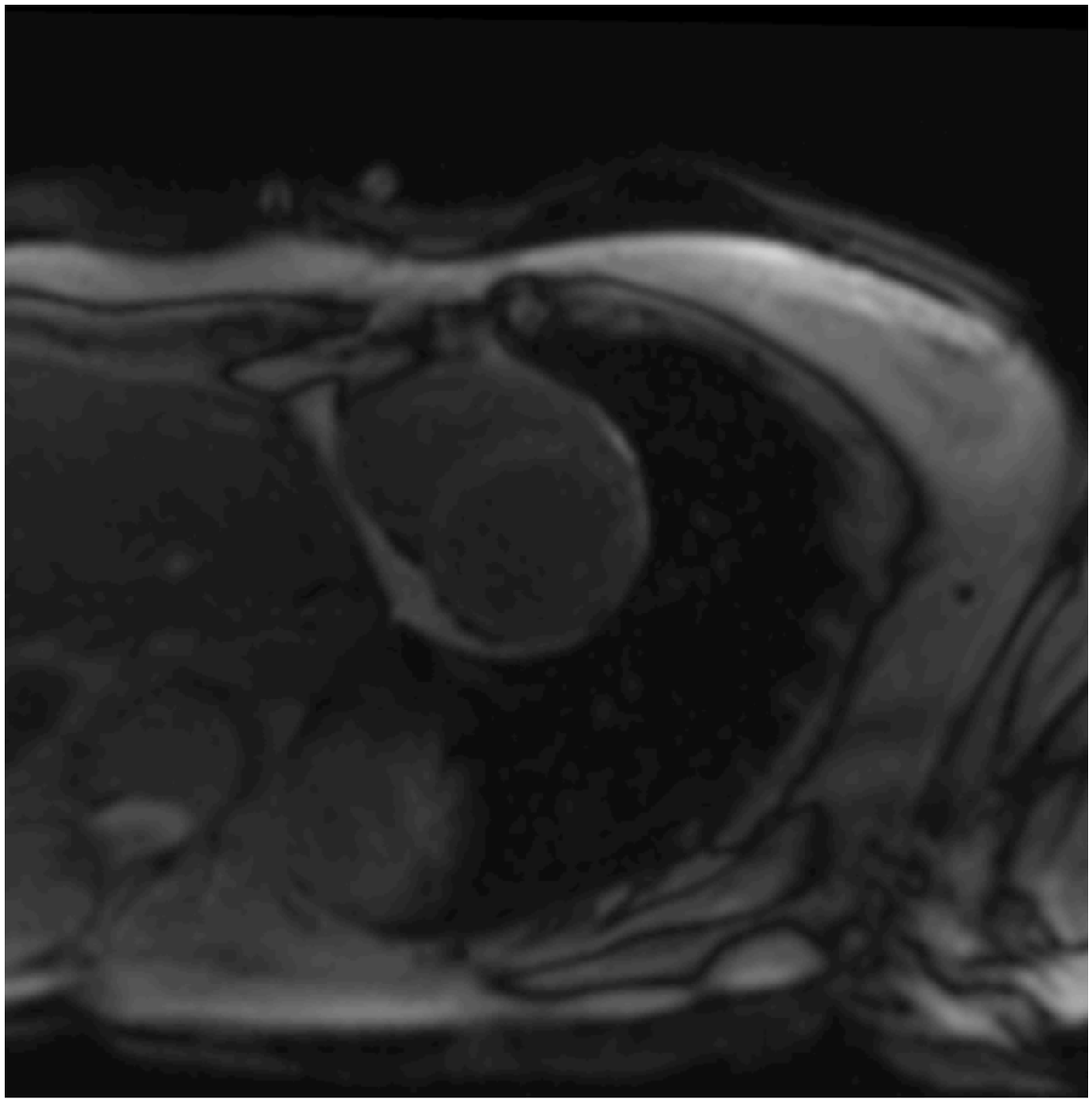
Difficulty:

- How to register this sequence (eulerian in nature) with the more classical MRI sequence of the patient (eulerian also) ?

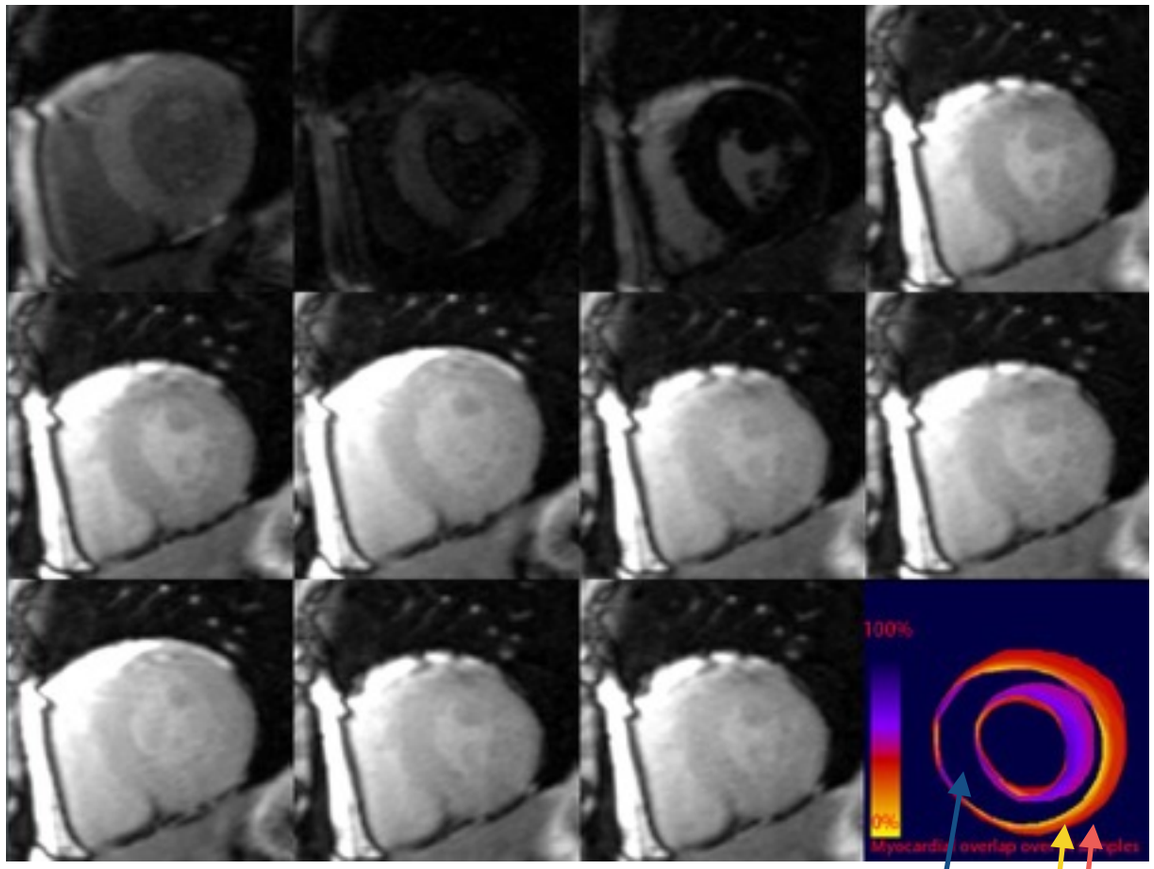
Idea:

- Use a state estimation of the trajectory.

A MOLLI sequence



A single 2D slice of MOLLI: movie of 11 IR-“samples” showing the heart not being perfectly still



The need of motion correction demonstrated when overlying all IR samples

- *yellow-red where the myocardium is present only on 1-4 of IR samples*
- *even in the location with myocardium in 100% of IR samples (typically septum), the assumption of each pixel corresponding to a given material point over all IR-samples is clearly wrong*

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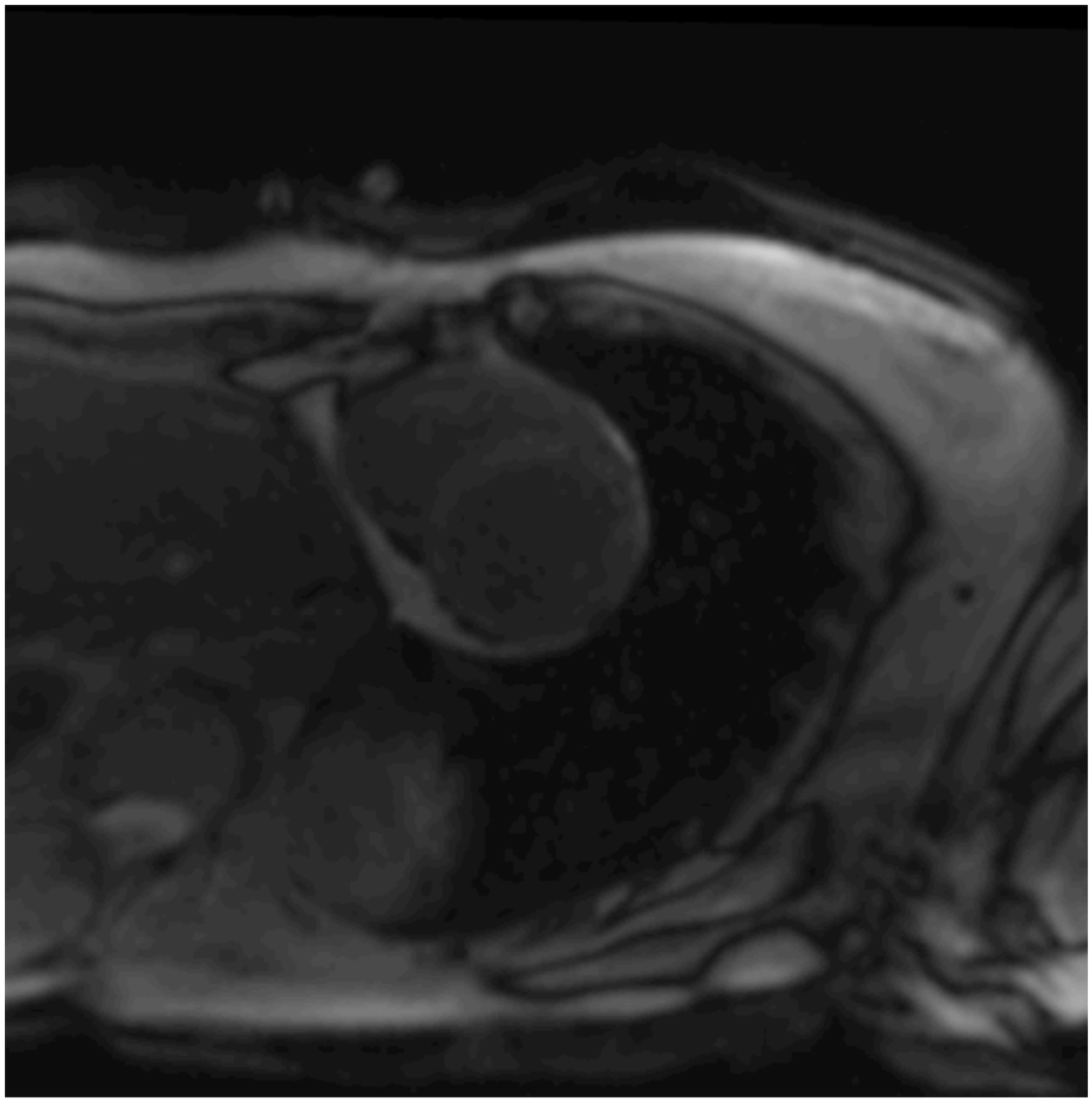

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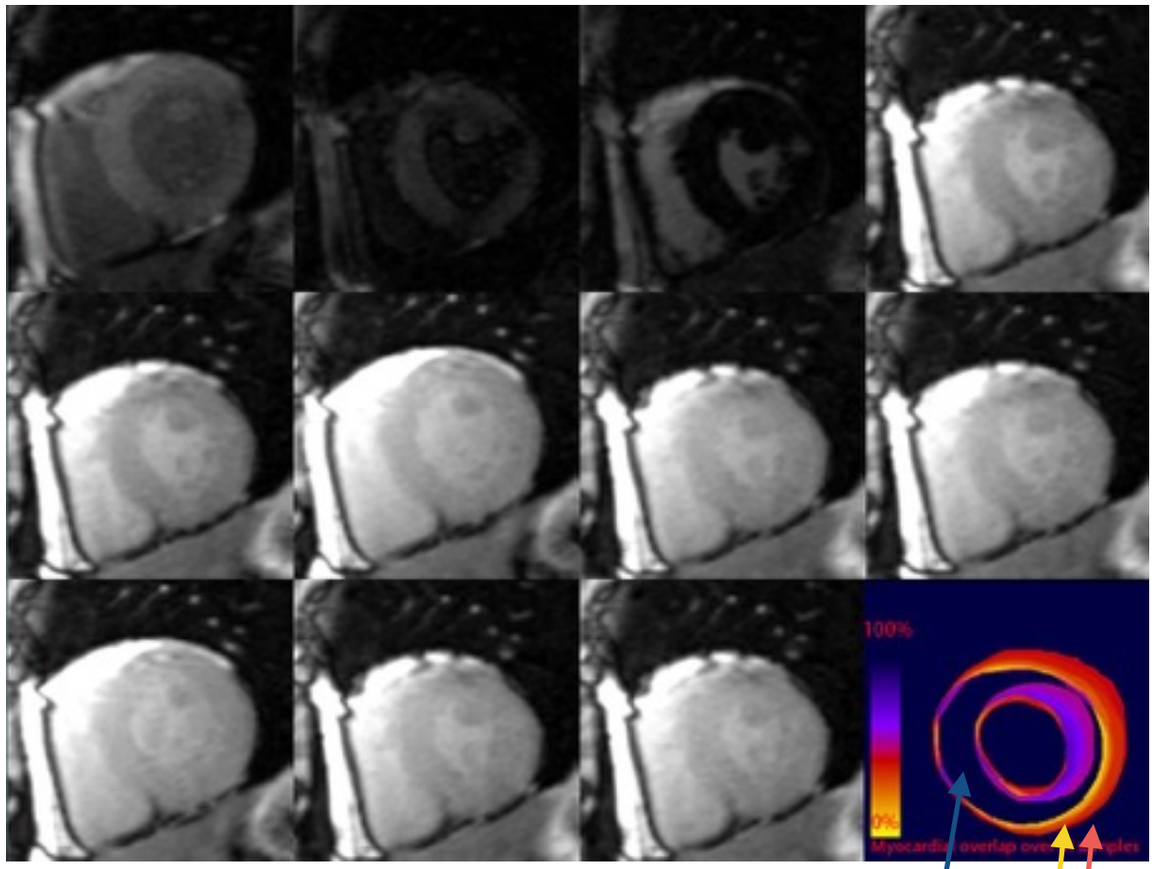

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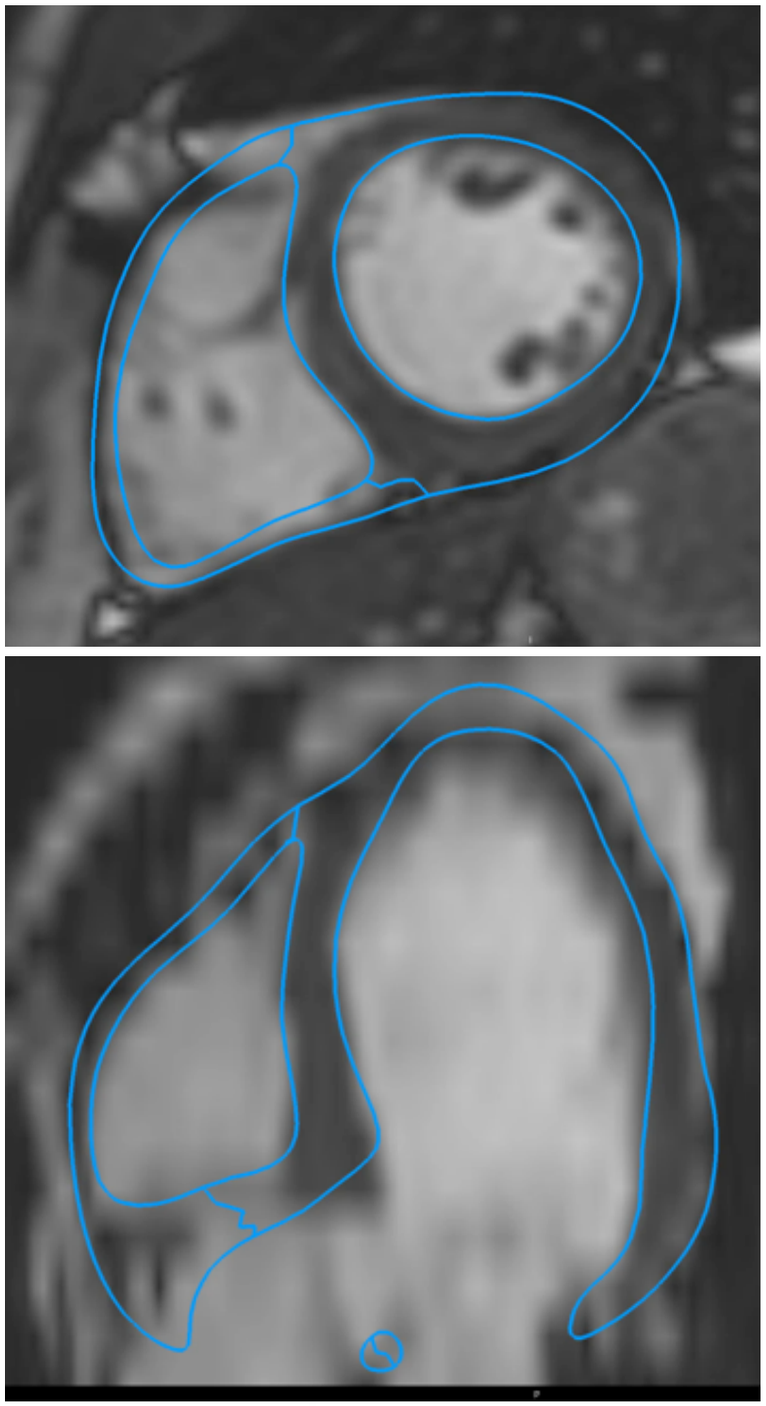
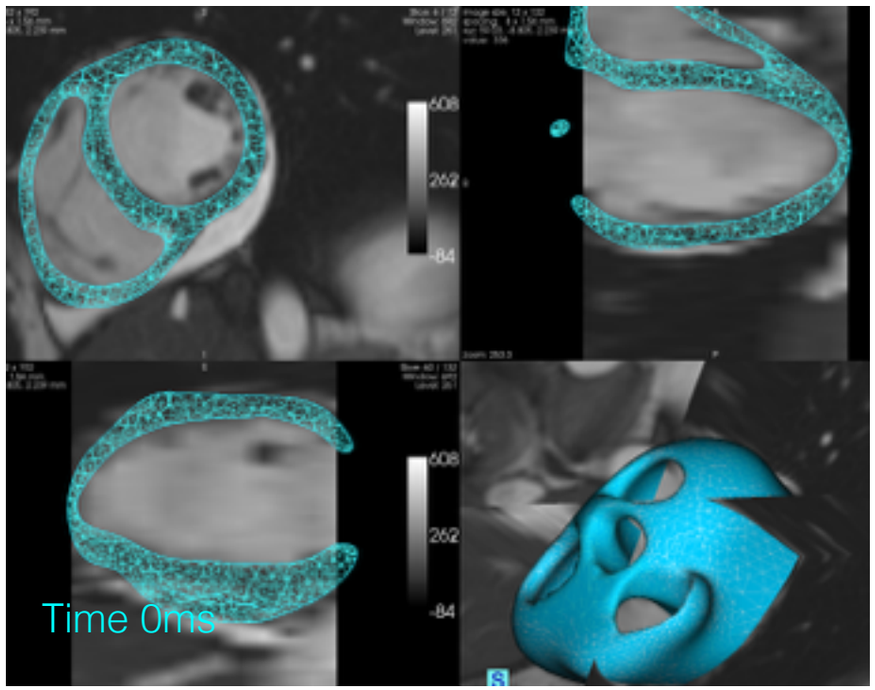
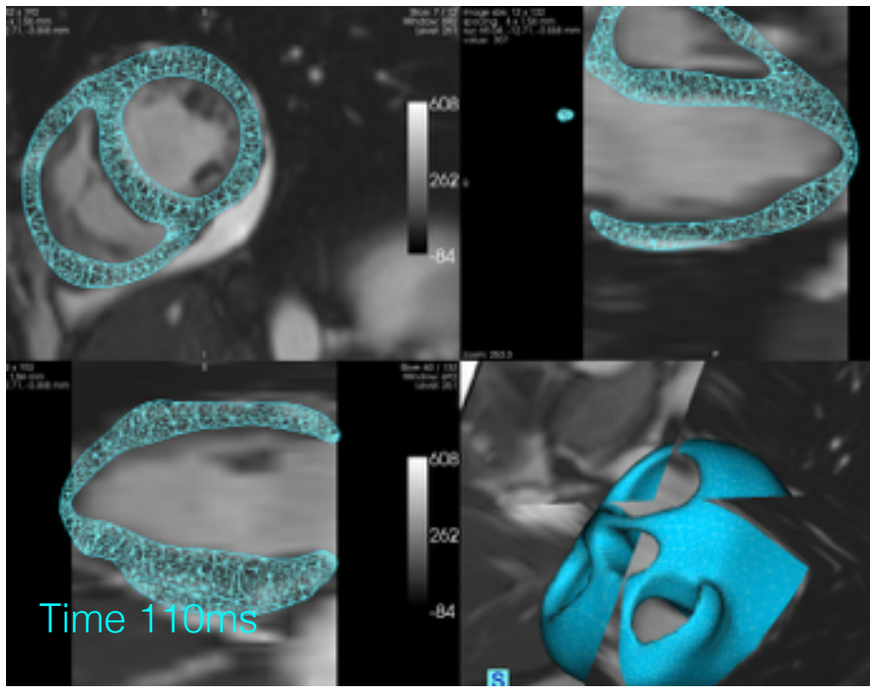
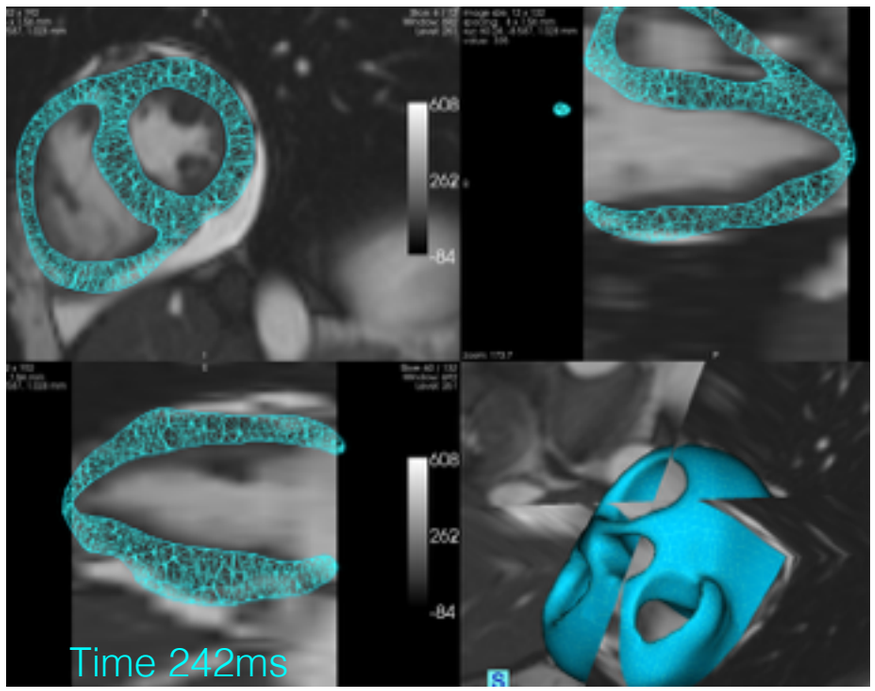
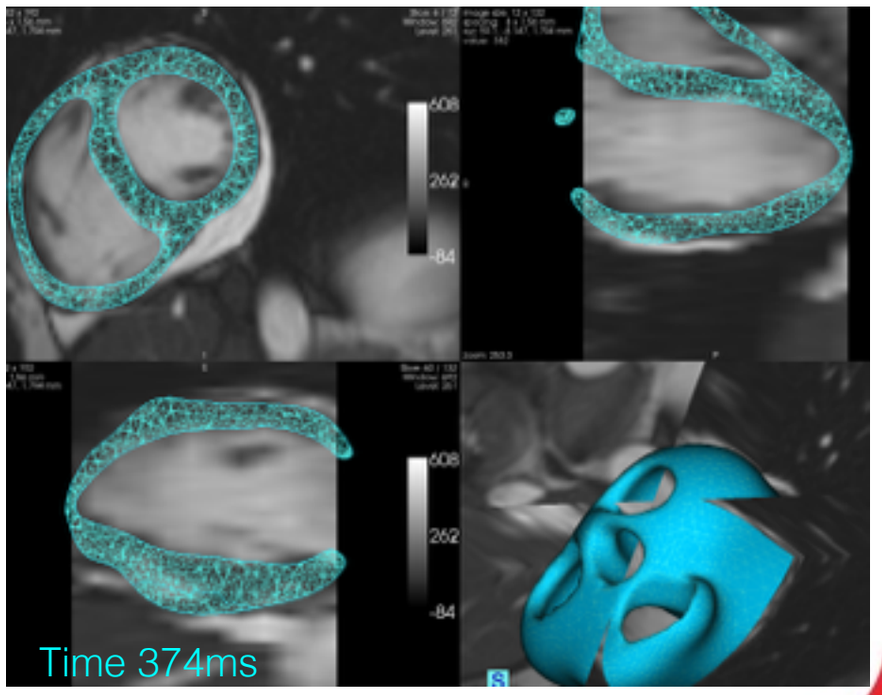
- State estimator from the first HeartIC objectives is an excellent 3D+t representation of heart in Lagrangian sense (as per volume mesh nodes)











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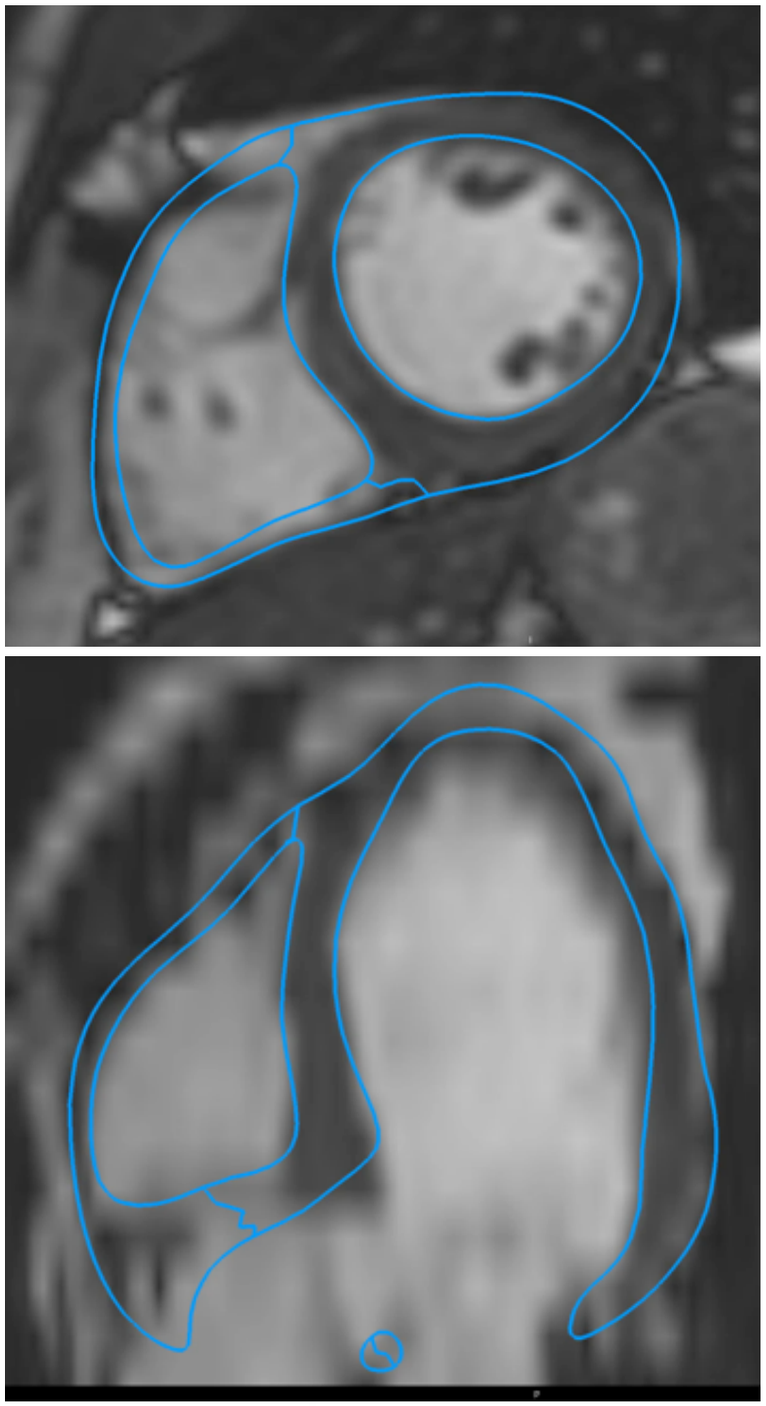
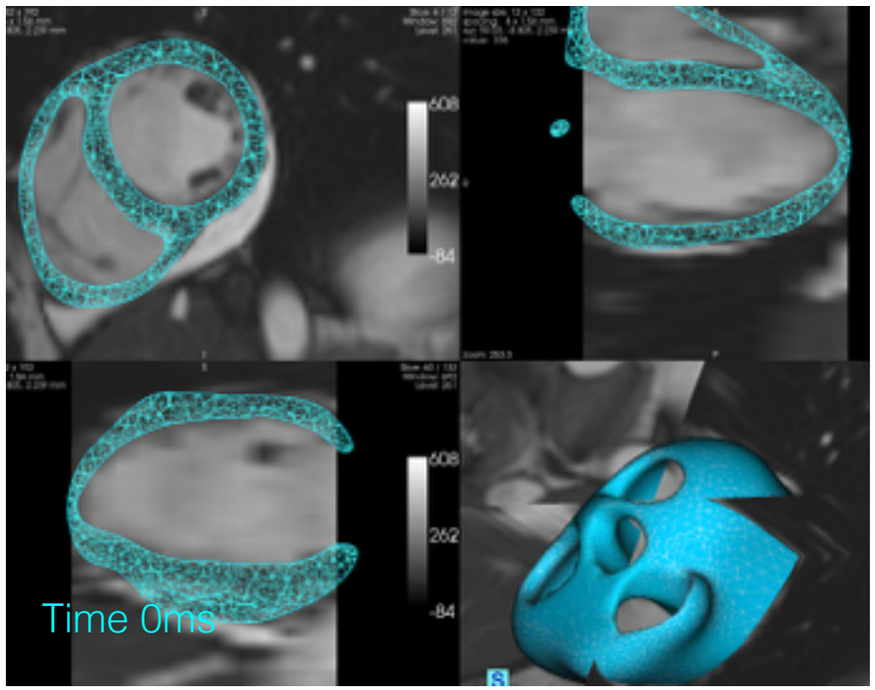
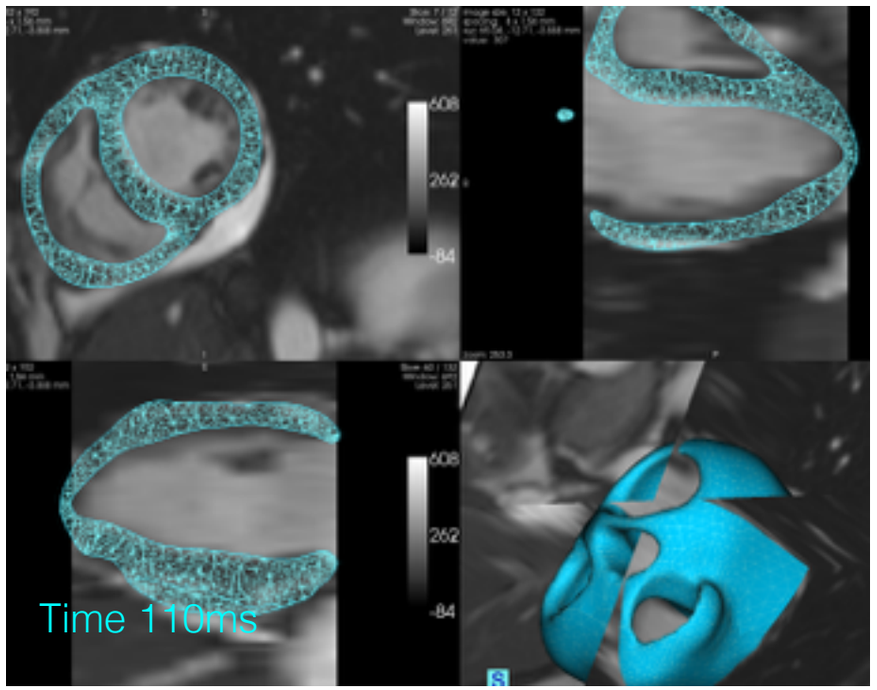
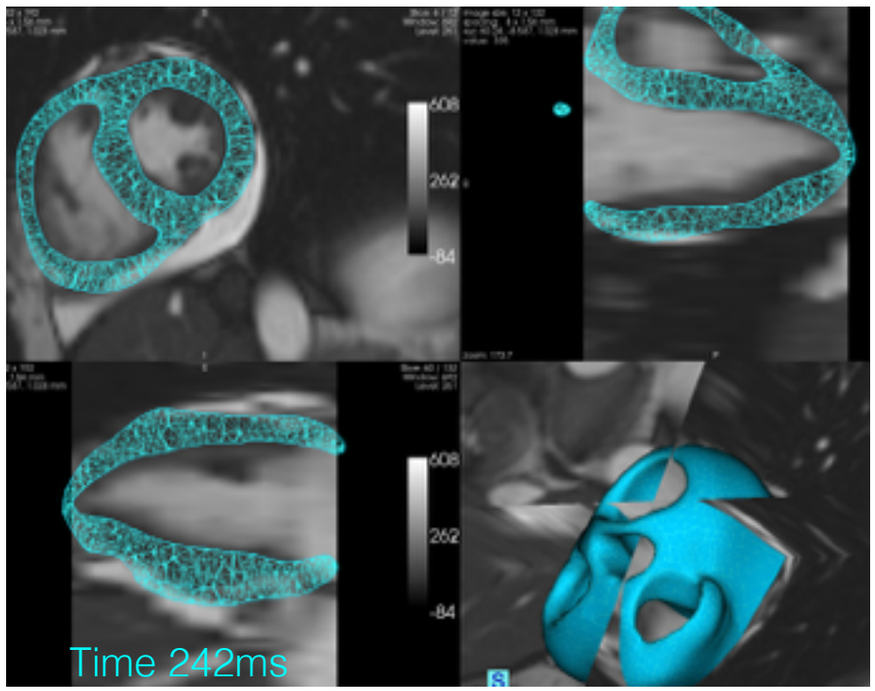
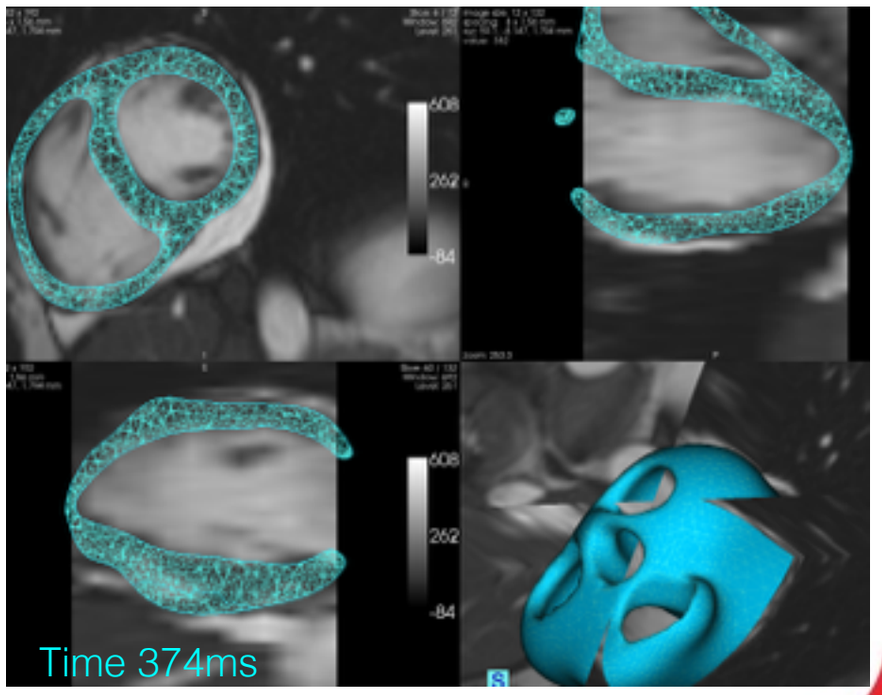




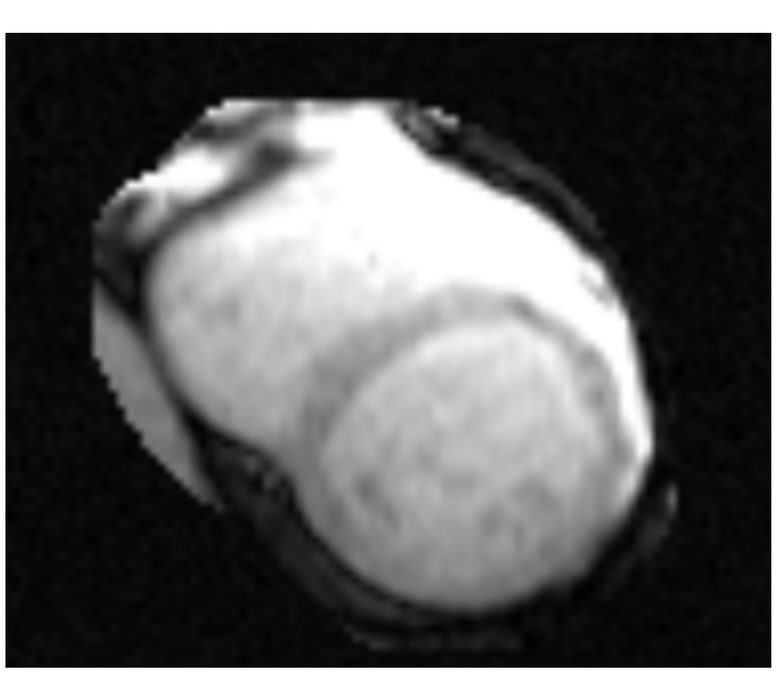




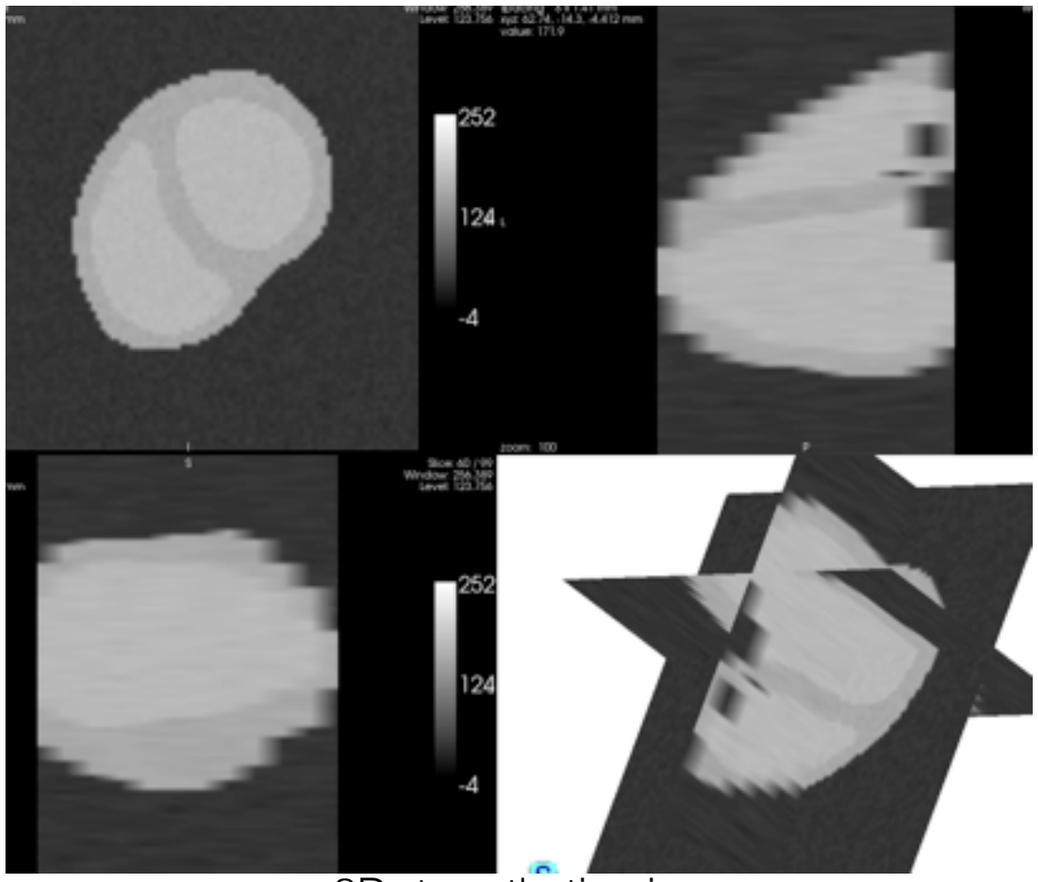


Spatial registration of MOLLI frames using 3D+t state estimator template via creating synthetic cine

- Synthetic MRI created from the set of N meshes of state estimator
  - Corresponds to the motion in real cine MRI (as created via state estimation)
  - Lagrangian displacements are "under control" (we do still know the position of the mesh nodes)
  - Signal ("color") in the myocardium, in left and right ventricle cavities and outside of heart can be chosen accordingly to the mean signal in given region specifically to a given IR-sample of the MOLLI



MOLLI sample@ IR1195ms



3D+t synthetic cine
(template for rigid registration of the MOLLI sample)

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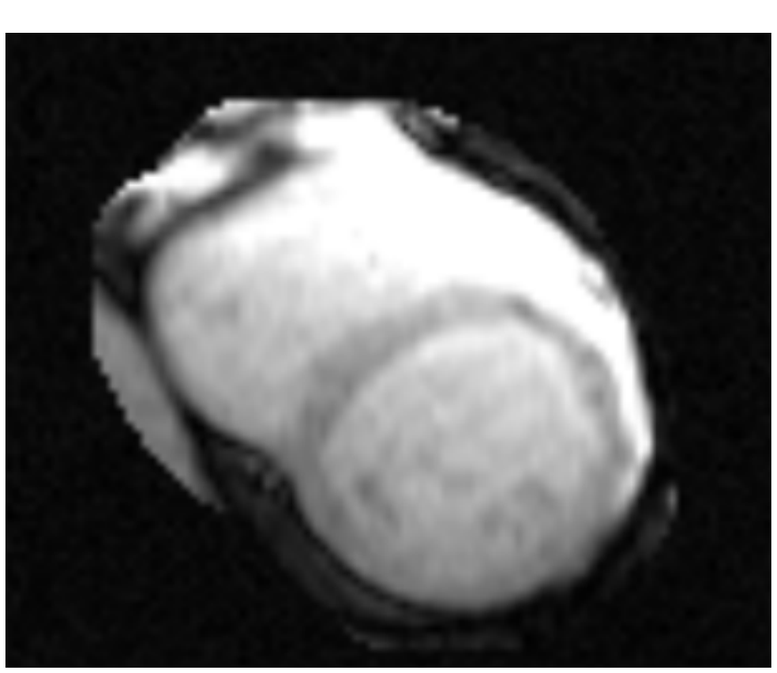

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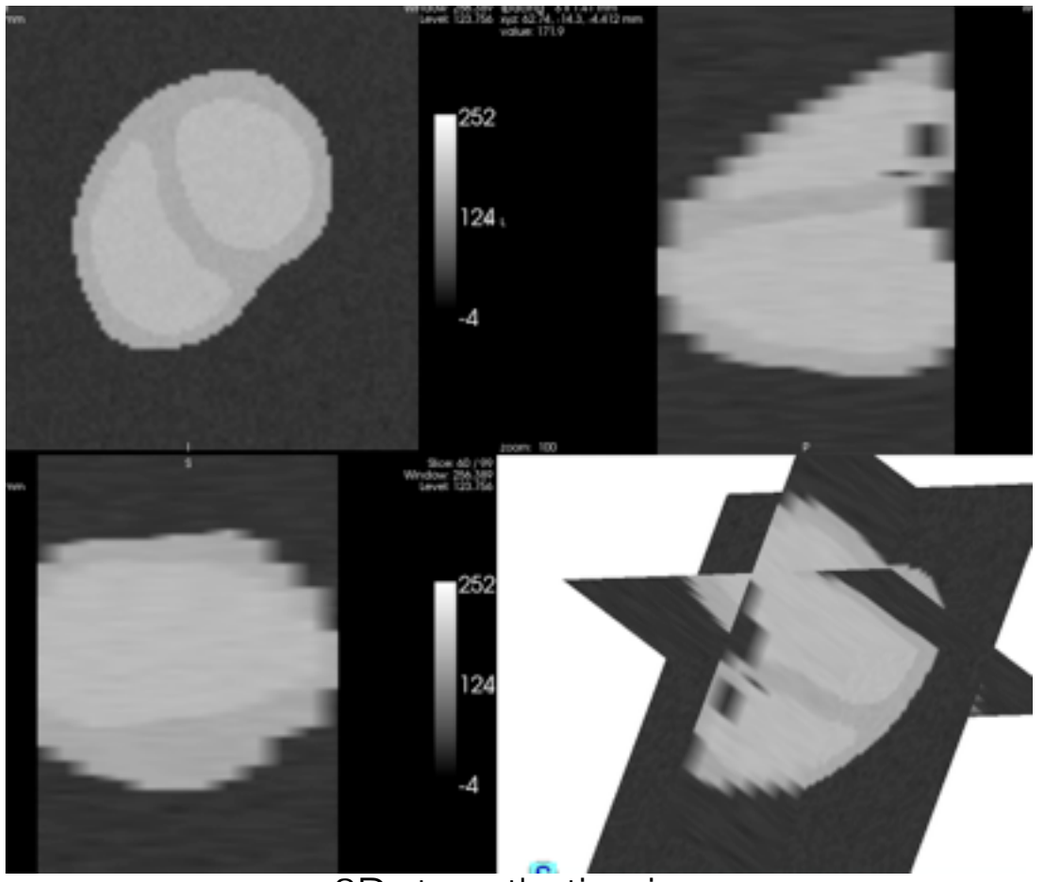

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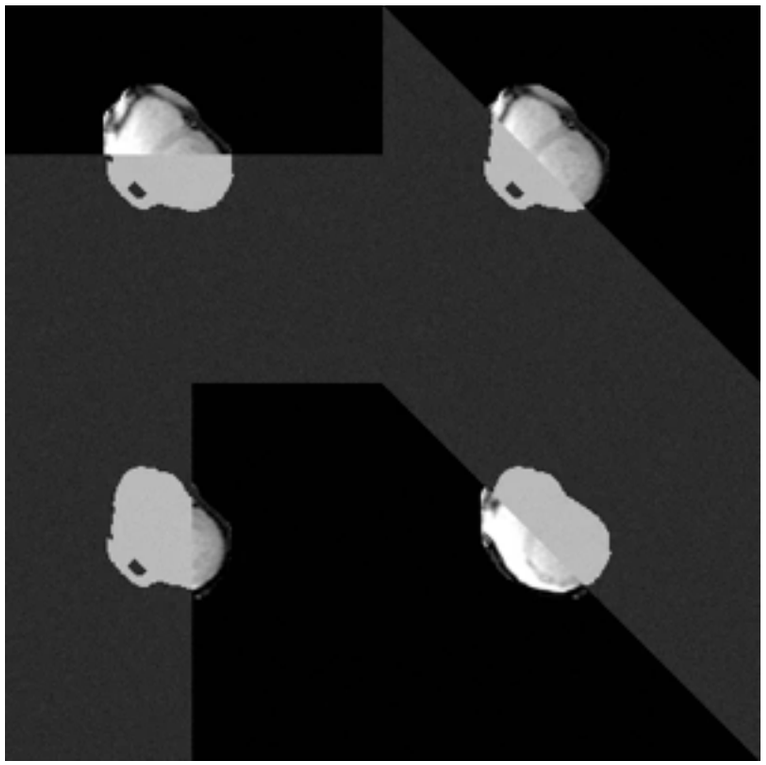
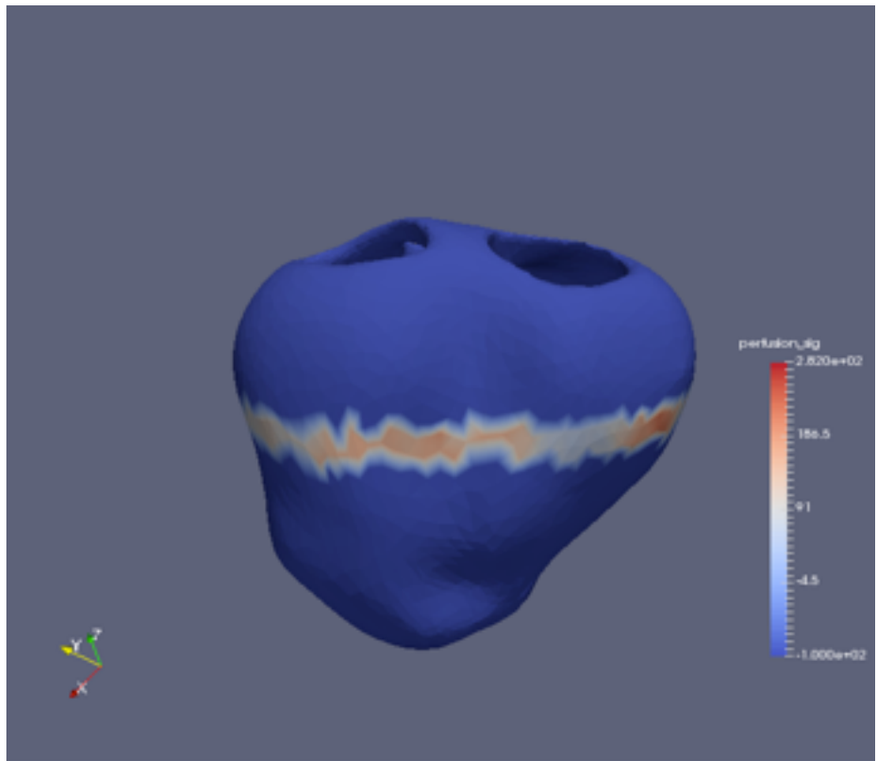
Projection of the MRI signal on the mesh (in the nodes in Lagrangian sense)

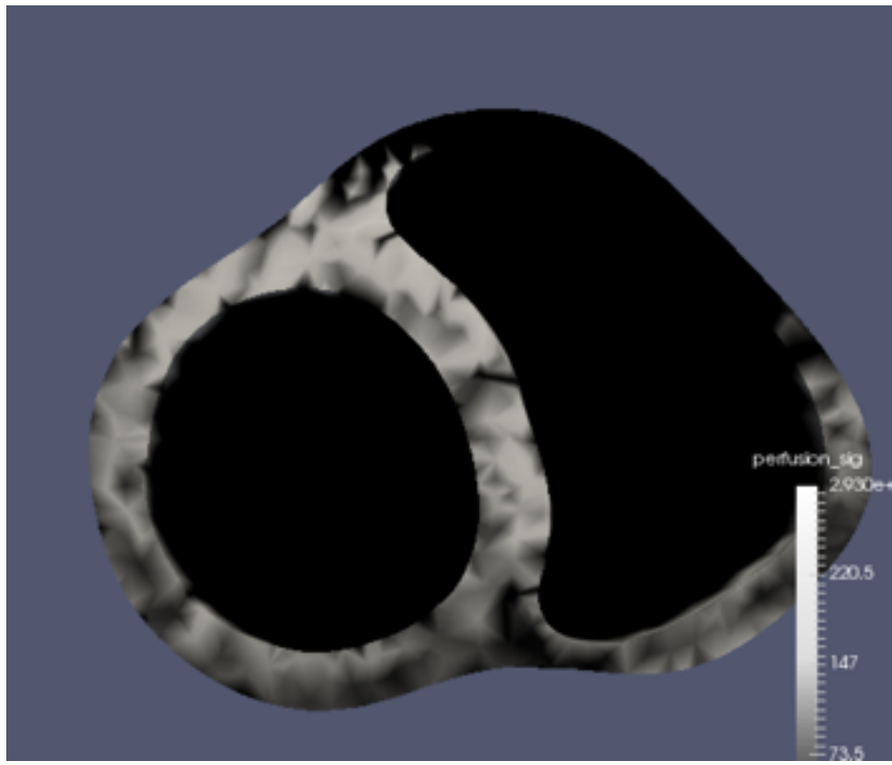
- The final registered 2D planes may vary according to the heart motion / breathing motion



Best fits for each IR time
(the locations of 2D slices vary in 3D space!)



Vizualization in “reference configuration” of the object (mesh)



computed T1 relax times
(by fitting the relaxation exponentials)

Note that number of IR samples in a given node may give a confidence map of the fit.

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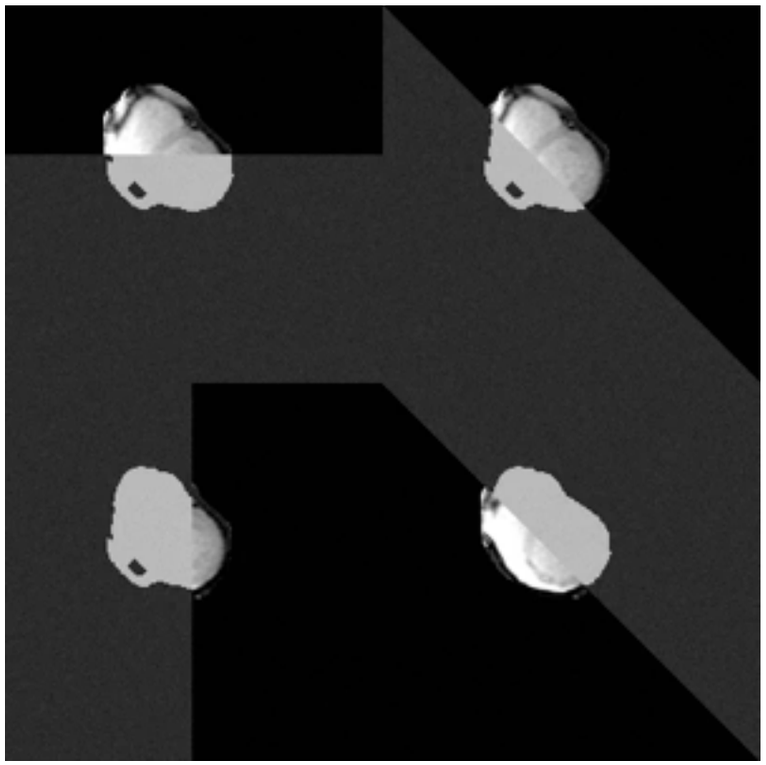

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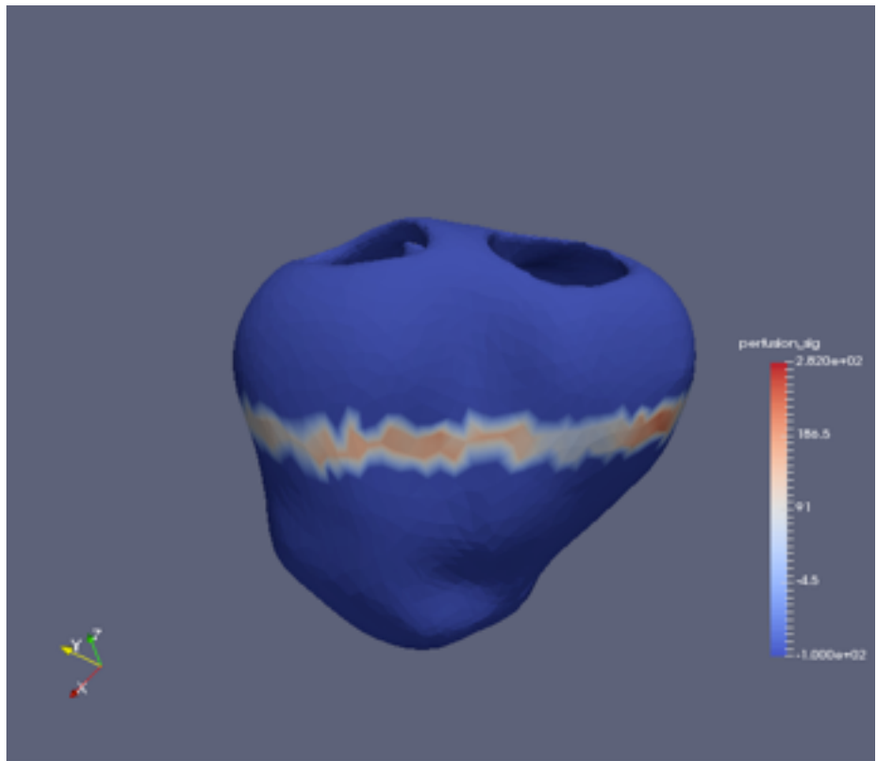

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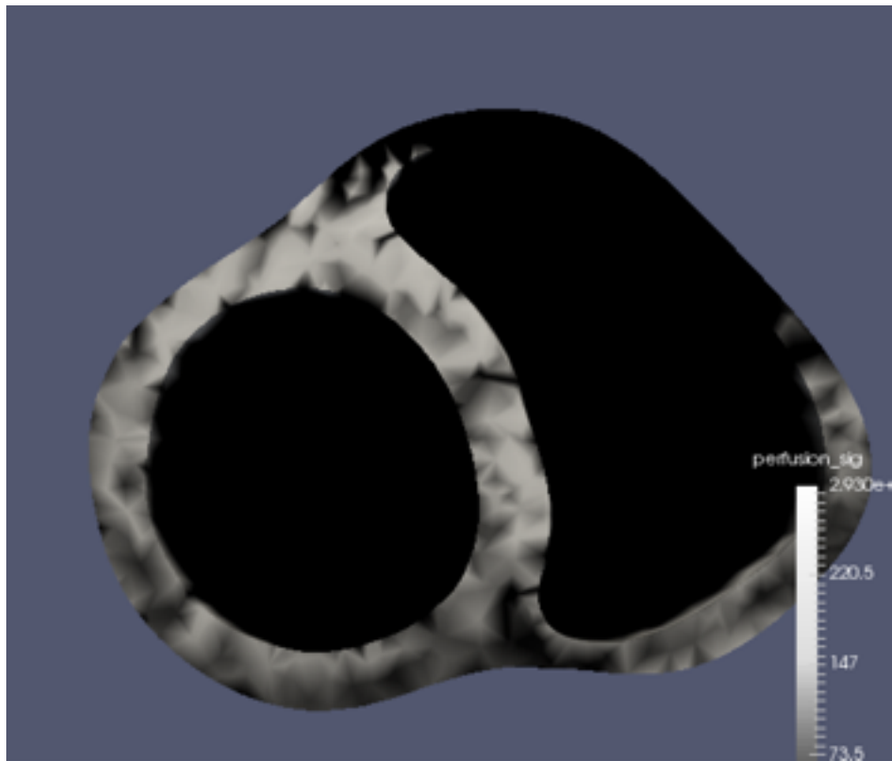

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Thank you for your attention.

Questions ?