

From Image to Personalized Cardiac Simulation: STACOM Encoding Anatomical Structures into a Model-Based Segmentation Framework

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Summary

- Setting: Organ-scale biophysical simulations are important.
 Personalization is needed for patient specific results.
- Problem: The pipeline from image to simulation is complicated.
 Some structures invisible in some modalities eg. CT.
- Solution: Encode simulation relative to segmentation mesh.
 Reconstruct after model-based segmentation.

Surface Correspondence Location

- Average surface distance d_s is 1.6mm.
- Larger than the segmentation error d_M 0.6mm
- Surface correspondence is location dependent.



- Results: Analyzed surface correspondence; error is 1.6mm.
 Encoding simulation mesh into model is promising.
- Conclusion: Surface correspondence has room for improvement.
 Mesh allows to integrate data from different sources.
 Pipeline from CT image to cardiac simulation in place.

Encoding of Simulation Structures

- Encode simulation mesh and structures into mean mesh.
 - * Barycentric coordinates for locations and fiber directions.
 - * Height above a surface along surface triangle normals.
- Model-based segmentation:
 - I) localization
 - 2) parametric adaptation and
 - 3) deformable adaptation of a mean mesh.
- Reconstruct structures after model adaptation to an image.
- No anatomical inter-patient variation relative to mesh captured.

Average Anatomy
Average Location 〇



Underlying Anatomy Real Location *****

Encoded Structures

• Atrial and ventricular muscle fiber directions



Sinus Node (SN), 2) Crista Terminalis (CT), 3) Pectinate Muscles (PM),
 Bachman Bundle (BM), 5) Inferior Isthmus (II)

• Errors obtained the surface correspondence analysis.

Average distances

Mean Mesh ••• Encoded Structure •



Segmented CT Scan Real Location Invisible

Analysis of Surface Correspondence

- Indirect approach to assess quality of surface correspondence.
 I) Segment a set of anatomical images.
 - 2) Adapted meshes become mean meshes for 2nd segmentation set.
 - 3) Compare variation in outcome of 2nd segmentation set.



Euclidean distance d _E [mm]	1.95	1.83	1.82	1.79	1.86
Mesh-to-mesh distance d _M [mm]	0.50	0.51	0.48	0.56	0.48
Surface distance d _s [mm]	1.95	1.84	1.83	1.79	1.87

SN CT CT SN

Example for Simulation Pipeline

- All information integrated into the segmentation mesh.
- Simulation pipeline available after model adaptation.
- Eikonal equation, isotropic (top) versus anisotropic (bottom).
 Anisotropic simulation includes Crista Terminalis.



- Mesh-to-mesh distance d_M
- Euclidean distance d_E



Surface Correspondence Histogram

N=37 CT scans at diastasis with very good segmentation.
 i.e. d_M below 5mm for 99% of the vertices.



Activation time

Transmembrane voltage after 30, 60 and 90 ms

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