Statistics for biomedical engineering and multiphysics approaches to study diseases

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Abstract

In this work, we introduce a semi-automated pipeline that transforms raw CT-derived segmentations into simulation-ready cardiac meshes while preserving both anatomical accuracy and topological consistency. The generated meshes are watertight, share identical topology, and maintain consistent point-to-point correspondence across samples. By enabling the creation of anatomically coherent virtual cohorts, this approach supports large-scale in silico studies, facilitates uncertainty quantification, and allows for the exploration of variability-driven aspects of cardiac function.

Keywords: Statistical shape analysis; Principal Components Analysis; Gaussian Mixture Model; Digital heart; Virtual Cohort Generation

1 Introduction

Multiphysics cardiac simulations coupling fluid–structure interaction and electrophysiology (FSEI) [1] can reproduce complex cardiac dynamics, but most studies remain limited to single, often patient-specific anatomies. Incorporating population-level variability is essential for robust modeling, uncertainty quantification, and in silico trials, requiring virtual cohorts of anatomically consistent geometries. Traditional segmentation methods struggle to produce such cohorts due to acquisition and operator-dependent limitations [2], and although deep learning has alleviated some issues, challenges remain. As a result, large-scale segmentation datasets often contain mesh defects and topological inconsistencies (e.g., holes, non-manifold regions) that are unsuitable for multiphysics simulations, particularly in hemodynamics (see Figure 1). Here, we propose a semi-automatic pipeline to generate simulation-ready cardiac meshes directly from CT scans, combining machine learning-based segmentation, principal component analysis [3], and in-house geometric processing tools to ensure watertight surfaces and high-quality meshes compatible with multiphysics solvers.

2 Materials and methods

An initial segmentation is performed on each CT scan using the TotalSegmentator Heart Chambers plugin in 3D Slicer, which automatically identifies and segments the left and right ventricles and atria.

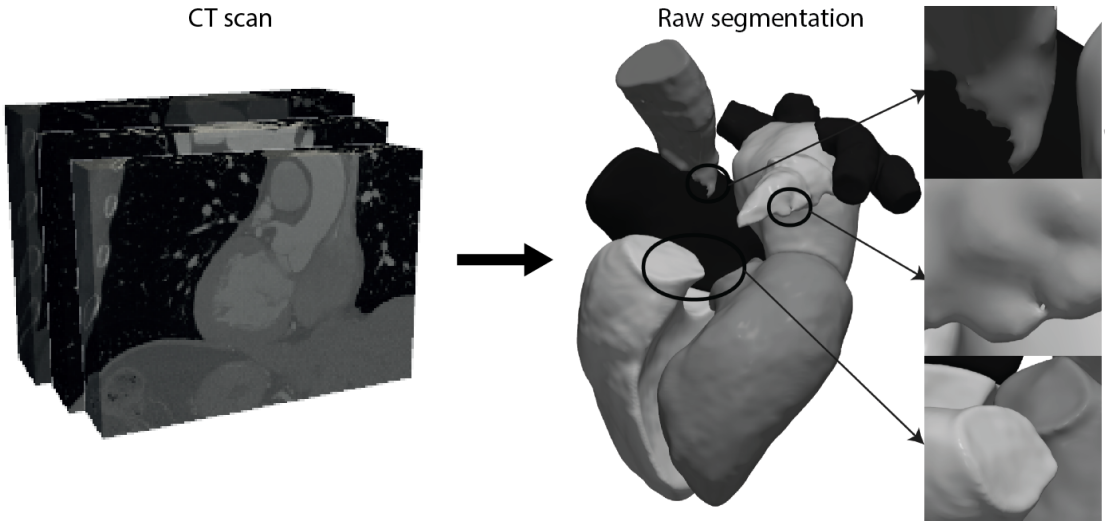

Figure 1: CT scan data (left) and corresponding raw segmented cardiac anatomy (right). The zoomed view on the right highlights typical segmentation artifacts: manual delineation leads to small holes and poor connectivity between neighboring anatomical structures, particularly in junctional regions.

Although the raw segmentations capture cardiac morphological variability, they are not suitable for multiphysics simulations or statistical shape modeling due to geometric defects. To address this, we employ a registration procedure in which a template mesh is deformed to match each anatomy, preserving mesh quality while capturing patient-specific features.

We then define morphogeometric descriptors independent of mesh representation, encoding clinically relevant shape characteristics. After registration, all meshes share the same number of vertices, connectivity, and point-to-point correspondence, enabling statistical shape modeling. To reduce dimensionality, principal component analysis (PCA) is applied to extract the dominant modes of variation. A Gaussian mixture model (GMM) is subsequently fitted to the PCA coefficients to describe the distribution in the latent space, with the number of clusters selected based on inertia and silhouette criteria.

3 Results and discussion

The pipeline is applied to 60 cardiac CT scans to build a statistical shape model that quantifies anatomical variability. This model is further used for data augmentation and the generation of virtual cardiac cohorts. The resulting geometries can be successfully employed in multiphysics simulations of healthy subjects, demonstrating the potential of the framework for population-based modeling and large-scale in silico studies. A subset of the registered meshes is shown in Figure 2, where visual inspection confirms anatomically consistent geometries while preserving subject-specific variability.

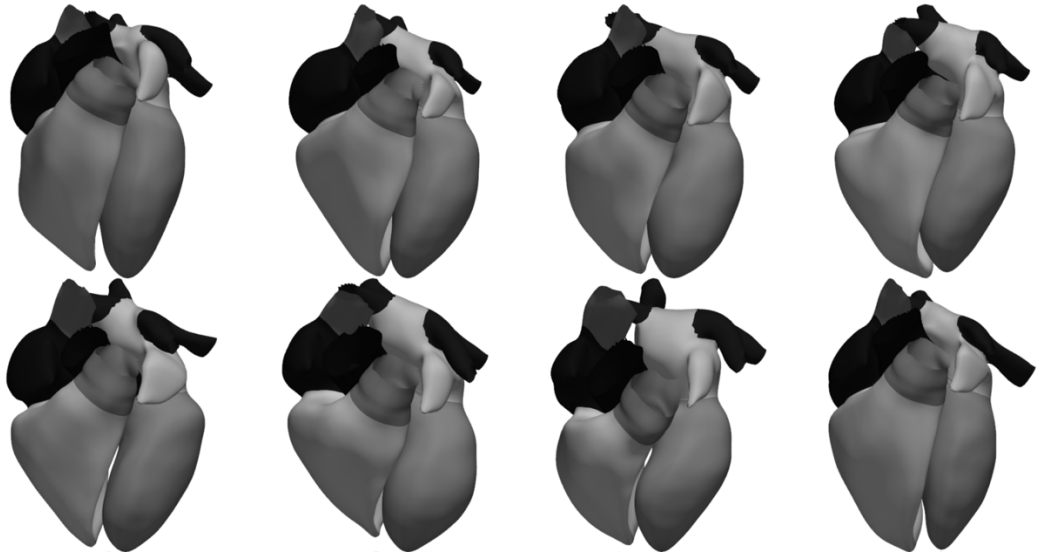

Figure 2: Small cohort of 8 meshes after template-to-anatomical registration. All geometries share an identical topology and point-to-point correspondence, while preserving subject-specific anatomical variability.

4 Final Remarks

This work presents a semi-automatic pipeline for generating simulation-ready cardiac meshes from CT data. By combining a template-based multi-chamber registration approach with multi-scale optimization, the method produces watertight, isotopological meshes that preserve subject-specific anatomy while ensuring numerical robustness and consistency. The code is publicly available as open-source software. Access to consistent meshes with point-wise correspondence enables the integration of electrophysiological and hemodynamic simulations within a unified population-based framework.

References

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