

An Automatic Data Processing Pipeline to Reconstruct Coherent 3D Image Volumes From Cardiac Cine MRI Data



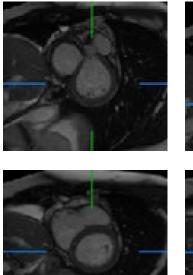
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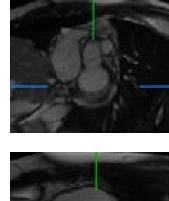
Abstract

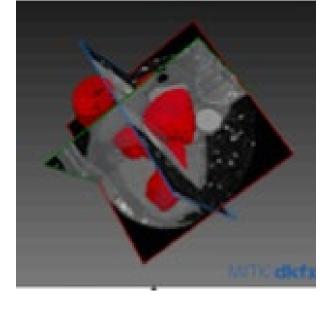
Computational fluid dynamics (CFD) simulations of left ventricle (LV) flow require geometric models of the heart constructed from patient-specific cardiac image scans. Cine magnetic resonance imaging (MRI) produces several time-series 2D image slices from different locations of the heart which must be reconstructed into a 3D image volume before a deep learning model for constructing CFD-ready LV models can utilize it. Thus, we are creating a data processing pipeline that can automatically take in all 2D image slices for a patient and align them to produce a 3D image volume.

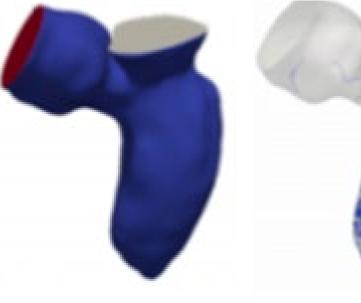
Background

Cardiovascular disease is the leading cause of death worldwide [1]. Computational fluid dynamics (CFD) simulations of left ventricle (LV) flow combined with patient medical imaging data may facilitate a better understanding of cardiovascular diseases so patients can have improved diagnosis and treatments.









2D Cine MRI Images

3D CT Images and Segmentation

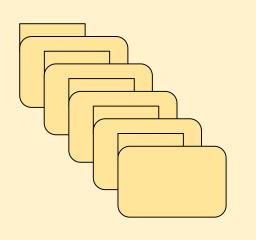
3D CT Model

CFD Simulation

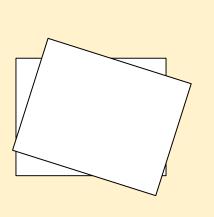
Data and Software

- This study used the "Data Science Bowl Cardiac Challenge Data" which consists of images of over 1000 patients of varying ages and cardiac function. These 2D cine images are in DICOM (Digital Imaging and Communications in Medicine) format.
- We used SimpleElastix and SimpleITK for alignment and registration and Medical Imaging Interaction Toolkit (MITK) for visualization which are free, open source software.

Data Processing Pipeline



Dicom images are sorted by file name



Registration is used to reduce misalignments

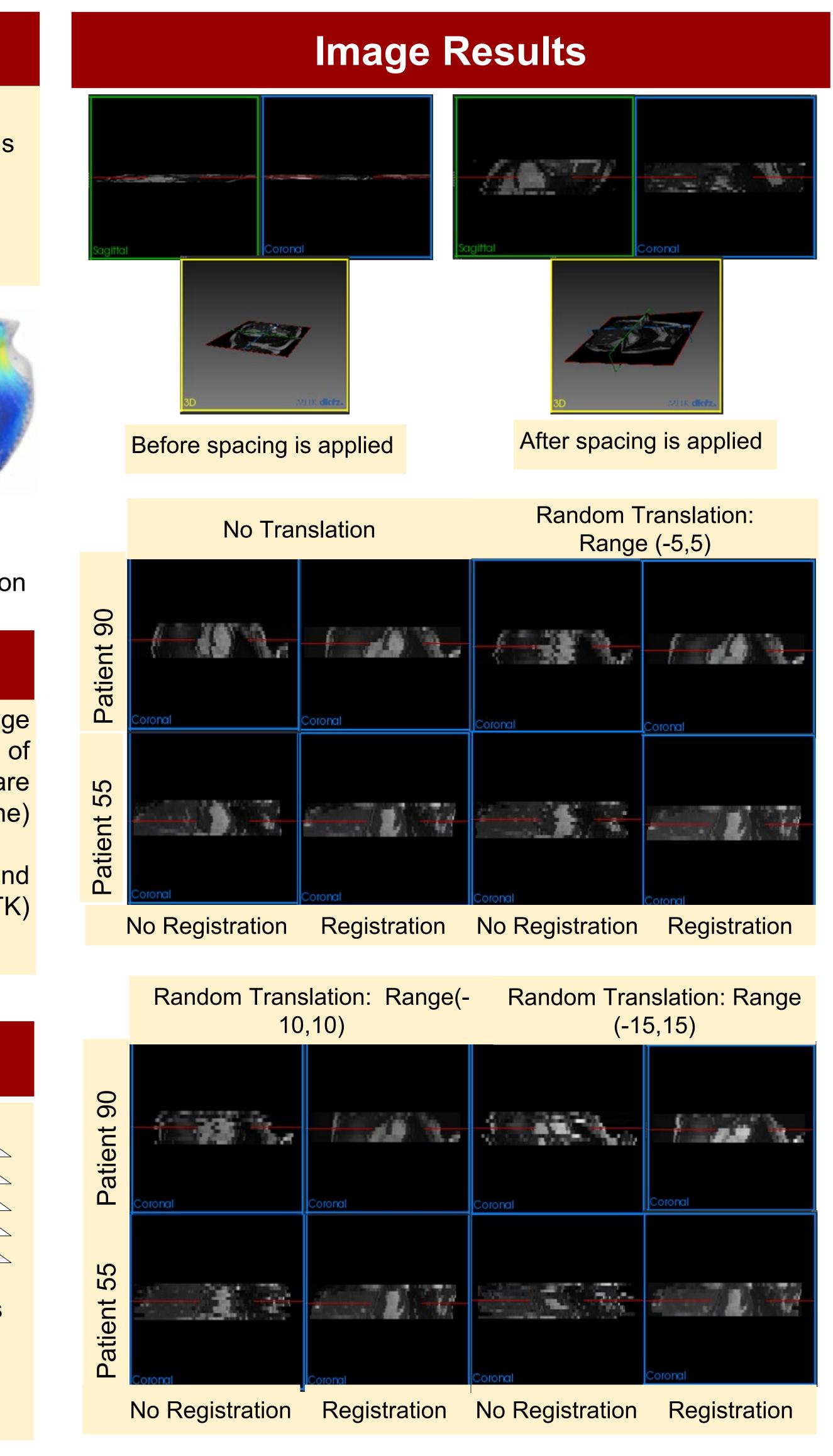
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Images are stacked

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Spacing is adjusted between images

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Quantification Of Registration Error

- artificially corrupted the volume and cause more • We misalignments to better view registration being applied. We used translation to randomly shifted center of images which used parameters that correspond to the x and y direction.
- There is a consistently larger number in the y direction. A larger translation range means a larger amount of error.

Translation Range	Total Mean of Patient Translation Parameters	Standard Deviation
(-5,5)	(3.84, 4.84)	(.298, .382)
(-10,10)	(5.06, 7.02)	(.149, .384)
(-15,15)	(7.71, 8.843)	(.193, .241)

References

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- 4. Lowekamp BC, Chen DT, Ibáñez L and Blezek D (2013) The Design of SimpleITK. Front. Neuroinform. 7:45. doi: 10.3389/fninf.2013.00045
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