A GPU Accelerated Cardiac Image Segmentation Approach using Diffeomorphic Registration

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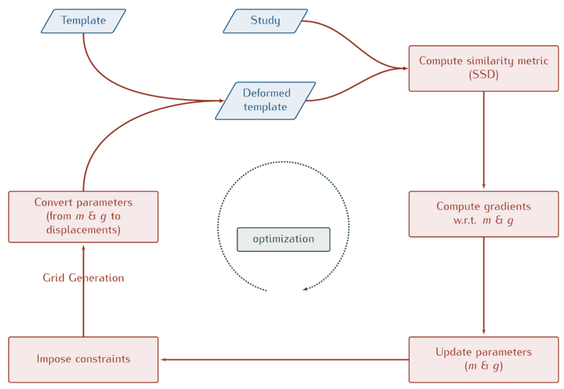
Background

- This study presents a parallel moving mesh correspondence algorithm for the RV segmentation using GPU computing
- Automatic delineation of the RV is difficult because of its complex morphology, thin and ill-defined borders, and the photometric similarities between the connected cardiac regions such as papillary muscles and heart wall
- One solution to the problem is to use a non-rigid registration method to obtain the point correspondence in a sequence of cine MR images [1]
- However, non-rigid registration algorithms involve optimization of similarity functions, and are therefore, computationally expensive
- In a previous study, we proposed GPU computing to accelerate the algorithm
- In this study, we further parallelize the problem by image concatenation
- We also extend the method by computing point correspondence in forward and backward directions and taking the weighted average to improve the accuracy

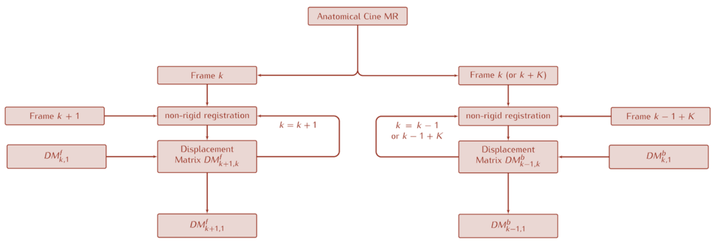
Method

- The proposed approach uses a diffeomorphic nonrigid registration algorithm to find point correspondence between two images in a cardiac sequence

Diffeomorphic Registration Algorithm



Forward-Backward Registration



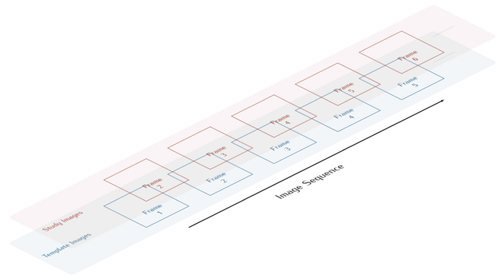
- Weighted average of the displacement matrix at frame k

$$DM^t_{k,1} = (1-w) * DM^f_{k,1} + w * DM^b_{k,1} \qquad w = k/K$$

K — total number of frames in the sequence

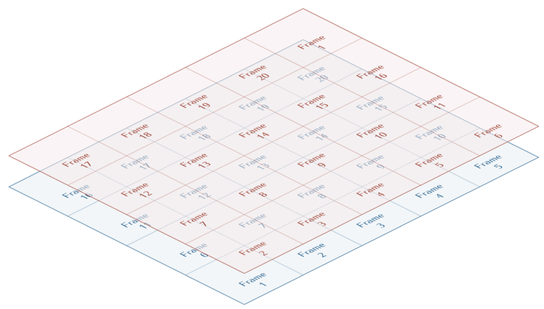
Parallelization

Image Registration - Sequential Order



- The process requires running the registration algorithm $K-1$ times for forward and backward directions.

Parallelization - Image Concatenation



- The process requires running the registration algorithm only once for forward and backward directions.
- Concatenation was performed on the GPU to reduce memory transfer.

Implementation

- The algorithms were implemented using the Python Programming Language
- The GPU CUDA version was implemented using Numbapro (Continuum Analytics, Austin, TX)
- The following Numbapro CUDA submodules were used: cufft and cublas
- The GPU versions of the algorithm were tested on a NVIDIA Tesla K40c

Data

- The proposed method was evaluated over the Training data set provided by the MICCAI 2012 RV segmentation challenge (http://www.litislab.eu/rvsc/)
- The data set consists of short-axis MRI volumes of 16 subjects
- The data was acquired on 1.5T MR scanners

Results

- Performance comparison for different implementations of the algorithm to process a sequence of 20 MR images.

Performance

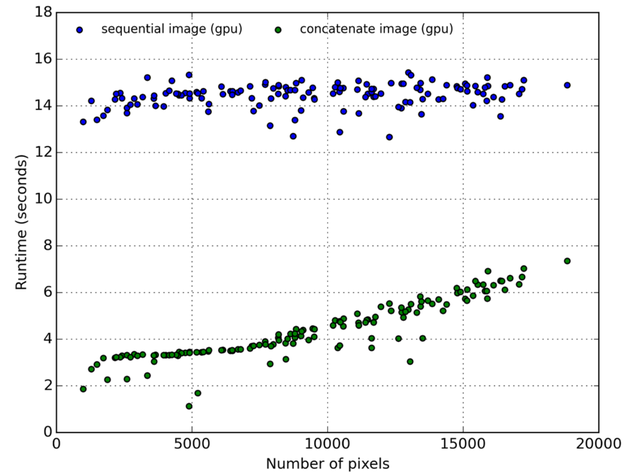
Implementation	Moving mesh computation
GPU — concatenated image	4.36 ± 1.22 seconds
GPU — sequential image	14.45 ± 0.51 seconds
CPU (python)[a]	3991.70 ± 1456.78 seconds

[a]Evaluated only over one subject in the forward direction due to very large runtime, which amounts to approximately half of the computation time for the forward-backward registration.

- The proposed method yielded an additional acceleration of more than 3× of the sequential image CUDA version

Performance

- Number of pixels vs runtime for image sequential and concatenated image implementations



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References

[1] K. Punithakumar and M. Noga and P. Boulanger. "Cardiac Right Ventricular Segmentation via Point Correspondence," in *International Conference of the IEEE Engineering in Medicine and Biology Society*, Osaka, Japan, 2013, pp. 4010–4013