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A POPULATION-BASED APPROACH TO THE SIMULATION OF REALISTIC 3D MYOCARDIAL INFARCTION

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Introduction

Large amounts of data with ground truth are generally needed for training and/or validating machine learning algorithms. In medical imaging, image datasets are often of limited size, hence the high interest in simulated data. However, for the effective use of such data, the simulation models should be personalized to the real population.

Population-wise personalization recently showed as a viable alternative to individual personalization, which is not always possible, in particular, for models involving randomness [1]. The optimization in the method presented in [1] relies on a gradient-free algorithm, namely CMA-ES (Covariance Matrix Adaptation – Evolution Strategy) [2]. This method showed promising results for the personalization of two simple 2D geometrical models of infarction: 1) iterative, consisting of the union of random number of random spheres within the myocardium, and 2) elliptical, consisting of one random ellipsoid within the myocardium. These 2D approaches had a fast computing time and allowed easy visualization to validate the method, but with limited complexity of infarct patterns. In this work, we demonstrate the extension of this 2D method to 3D infarct patterns.

Data and method

The real data for the personalization come from gadolinium enhanced MR images from the MIMI study (ID: NCT01360242) where myocardial infarcts were segmented by experts. Before the personalization, image contents were aligned to a reference anatomy and rotated to match the same coronary territory. Each 3D image consists of 11 z-slices of 80x80 pixels with 12327 elements within the myocardium. We focused on the images from 77 patients without any empty slices.

We chose two 3D geometrical models of infarcts: 1) iterative with 3D spheres and 2 learning parameters (number of spheres and maximal radius of spheres), and 2) elliptical with one ellipsoid with 6 learning parameters for 3 axes (distribution centers and extensions). For the personalization, we evaluated the CMA-ES algorithm with several distances between the distributions of synthetic and real samples: a) Kullback-Leibler (KL) divergence, b) Hellinger distance, c) Maximum Mean Discrepancy.

Results

We observed the convergence in all cases. The computation time varied from 16 to 40 min (500-800

iterations) with an Intel(R) Core(TM) i7-10610U CPU @ 1.80GHz, RAM 16 GB. To compare distributions and main variations of real and generated populations, we used the non-linear dimensionality reduction Isomap (of Python's sklearn) with multi-scale kernel regression [3] to reconstruct high-dimensional samples along the first three latent dimensions.

Synthetic and real data are rather similar, slightly more realistic for the iterative model (see Figure 1). For the iterative model, the solution is rather stable from one distance to another a, b, c (more variability is observed with the elliptical model), the first modes correspond to variations of rotation, position of the center of mass and size in each case. For the real population, the modes are respectively size, position of the center of mass and transmural. So, the infarct patterns roughly coincide in terms of the main geometrical characteristics, but transmural is insufficiently conveyed.

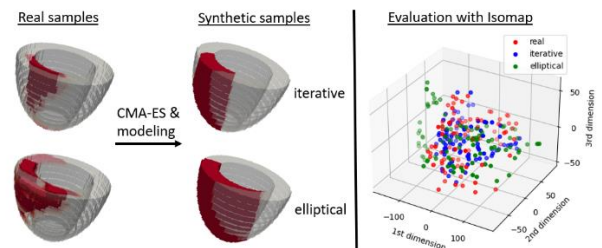


Figure 1: Personalization pipeline: from the input data to learned modeling parameters for the output data with the matching distribution (KL divergence).

Conclusion

The population-wise personalization of such models is possible in 3D in the sense of distributions; however, better realism of individual cases is needed. Our future work includes improving the infarction models and the personalization metrics potentially integrating the dimensionality reduction in the cost function.

References

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