

Multi-modal cardiac MRI analysis using diffusion models

Laboratory: laboratoire CREATIS - <https://www.creatis.insa-lyon.fr/>

Research team: Equipe Myriad - <https://creatis-myriad.github.io/>

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Length: 3 years starting in September/October 2023

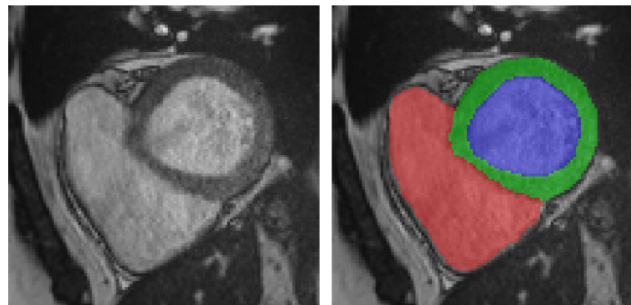
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Position: Already funded by a national grant



Context

Obtaining a robust segmentation of the different cardiac chambers is essential for the diagnosis and follow-up of cardiac pathologies in order to extract quantitative measures such as myocardial mass, left ventricle and right ventricle volumes, and ejection fraction or the volume of damaged myocardium. The scientific community is currently focused on segmenting cine MR images, the most common type of MR sequence used in clinical routine. There are numerous public databases of cine MRI images that can be used to train robust and performant artificial intelligence (AI) algorithms for segmentation tasks, as illustrated in the figure below.



Examples of automatic segmentation of cardiac structures in cine MRI imaging [1]

However, there are other crucial biomarkers for characterizing the myocardial state, such as intramyocardial fibrosis, which cannot be extracted from cine images alone. These biomarkers necessitate the utilization of additional types of MR sequences, such as T1, T2, and T2* sequences for analyzing tissue content, as well as LGE sequences for identifying areas of myocardial scar, and EGE sequences for assessing myocardial perfusion. Unfortunately, algorithms designed for cine images do not demonstrate robust generalization to other types of MRI sequences. Moreover, retraining an algorithm from scratch for a specific type of MRI sequence can be a time-consuming and challenging process, primarily due to the requirement of establishing sufficiently large and well-referenced databases.

Objectives

The main objective of this thesis is to develop approaches based on style transfer methods in order to leverage the quality of AI algorithms trained on cine sequences

to efficiently obtain equivalent results for other MR sequences. In addition, we will investigate the development of accurate AI architectures for the quantification of damaged myocardial volume.

Methodology

The methods of style transfer are techniques derived from natural image analysis. Several approaches are now well established, among which GAN (Generative Adversarial Network) methods are the most commonly used [2]. Recently, new AI techniques based on diffusion [3] and flow models [4] have shown spectacular results, but their relevance in medical imaging remains to be demonstrated. In this context, we propose to study the ability of these methods (the Glow model [4] being one potential candidates), to transform any MR sequences into cine images. The resulting images will be segmented using in-house AI algorithms trained on real cine images. Finally, the results will be applied to the original MR sequences and compared using ground truths made by expert radiologists.

In parallel, we will investigate segmentation methods dedicated to the quantification of the volume of damaged myocardium. Indeed, numerous studies have shown a strong link between the amount of intra-myocardial fibrosis and the state of progress of cardiac pathologies. This task is particularly difficult because of the diffuse appearance of areas with fibrosis. To address this problem, we will develop solutions also based on diffusion models (see [5] for some examples) to learn the inter-expert variability of regions with intramyocardial fibrosis, the interest being to capacity in providing a family of plausible segmentation maps of areas with fibrosis taking into account the learned expert variability. This will allow the generation of efficient segmentation and confidence maps of fibrosis that can be used for predictive models developed by authors PhD students in our lab.

Applicant profile

- Data analysis
- Specific motivation for the medical field
- Good Python programming skills
- Good English skills

Application

To apply, send your CV, covering letter and transcripts to

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References

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- [2] Y. Zhao, Unpaired Image-to-Image Translation Using Adversarial Consistency Loss. ECCV, 2020.
- [3] P. Dhariwal, Diffusion models beat gans on image synthesis. arXiv preprint arXiv:2105.05233, 2021.
- [4] D. P. Kingma, Glow: Generative Flow with Invertible 1x1 Convolutions. NeurIPS 2018.
- [5] <https://github.com/WuJunde/MedSegDiff>

