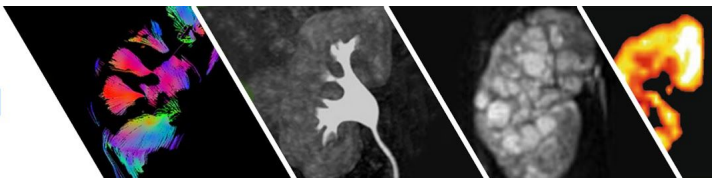


Bridging the gap between data and technology: Building a shared database for machine learning applications in renal MRI

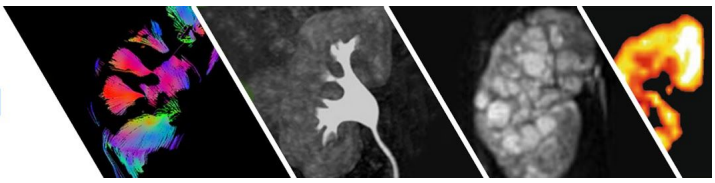
STSM start date 2018/10/01
STSM end date 2018/10/11
Grantee name **Fotios Tagkalakis**

PURPOSE OF THE STSM

The aim of this STSM experience at the Chair for Computer Aided Medical Procedures (CAMP), Technical University of Munich (TUM) was to establish, from a technical perspective, the main requirements of structuring a renal MRI database that can be utilised for transferring ML solutions between various European groups active in this area. This academic visit also aimed towards initiating an interdepartmental cooperation, between TUM and University of Leeds, in order to pave way for improving reproducibility and standardization of methods in renal MRI biomarker quantification with ease of access to pooled imaging data.

DESCRIPTION OF WORK CARRIED OUT DURING THE STSM

At the beginning of the first week of the STSM, we formulated the requirements that an MRI database should meet in order to be suitable for development of Machine Learning pipelines. This included the format of the input data, choice of the Deep Learning(DL) / Machine Learning(ML) framework that could be utilized, and the tools for storing and managing the data.
Additionally, we discussed the challenges of developing reproducible and robust algorithmic pipelines for the quantification of MR imaging biomarkers. One of the first issues addressed was that of motion correction, since the vast majority of the renal biomarkers that can be extracted from MR images require kidney segmentation and/or model fitting procedures. In both cases, having a proper registration pipeline for the imaging sequences leads to more robust final outcome.
On these grounds, a presentation of my work on motion correction for DCE data was relevant, highlighting how this approach has been expanded to address the same issue for other sequences as well (DTI, T1, T2-mapping e.t.c.). Following that, presentations of PhD students



from CAMP TUM showcased the latest developments on the field of deep learning for medical imaging.
The aforementioned was the starting point for some fruitful exchange of ideas and led to the preliminary design of possible deep convolutional neural network architecutres that could assist towards developing a robust multi-parametric MRI motion correction approach.

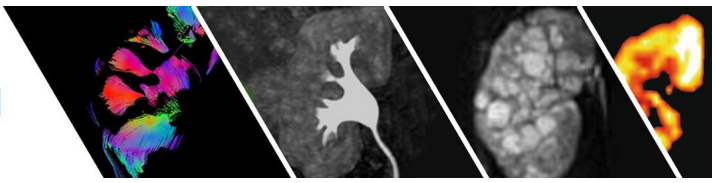
DESCRIPTION OF THE MAIN RESULTS OBTAINED

Out of the available tools that could be utilized for storage and processing of the MRI data, Zenodo, which is a tool for building open access databases seems to be the most appealing choice.Zenodo assigns a unique DOI to the submitted files while providing the opportunity to link code from GitHub with uploaded datasets and make them both directly citable.It can also accept any file format, including DICOM files which is the most suited format for our purpose and of course it provides sufficient space for the large imaging datasets needed (segmentation masks, augmented data, etc.). Additionally, Quibim, a tool specifically designed to allow structured application of advanced modules and algorithms for image analysis and quantification of imaging biomarkers, could be utilized either for deploying DL algorithms directly on the said platform or transferring trained models for integration in existing pipelines.
Furthermore, a series of discussions took place regarding the available DL frameworks that could be utilized to develop DL/ML pipelines for the quantification of MR imaging biomarkers. Two frameworks stood out: Tensorflow and Pytorch. Tensorflow right now seems to be the most popular one since it is highly flexible, it has high performance, a handy visualization tool (Tensorboard) and a strong (academic and industrial oriented) community. However, the main disadvantage for Tensorflow is the use of static computational graphs, which is an issue addressed by Pytorch and the main reason why Pytorch's popularity is exponentially growing over the last months. Pytorch allows quick prototyping, the use of dynamic data structures and dynamic computational graphs, while it is highly modular. The latest version Pytorch 1.0 is going to be a combination of Caffe2's modularity and the production-oriented capabilities of ONNX making the use of this framework even more compelling. Based on the discussions, Pytorch seems to be the right choice for the development of ML applications in combination with Tensorflow wherever suitable.

FUTURE COLLABORATIONS

Out of this STSM two possibilities for future collaboration between the Leeds Imaging Biomarkers Group (LIBG) of the University of Leeds and the Chair for Computer Aided Medical Procedures (CAMP) of the Technical University of Munich came up:

1. CAMP has shown interest in joining the Parenchima cost action, bringing its technical expertise on the development of Deep Learning, Machine Learning solutions in the field of Medical Imaging.



2. A cooperation was initiated between LIBG and CAMP in order to develop a deep convolutional neural network capable of performing robust motion correction for multi-parametric MRI datasets. The core idea is to start from the work conducted already in LIBG on model target driven registration of DCE data and expand it further by incorporating the tracer kinetic models as part of the neural network's cost function. Following the development of the aforementioned concept, submission of a paper with co-authors from both teams is aimed.

Acknowledgement

This STSM was based upon work from COST Action PARENCHIMA (CA16103), supported by COST (European Cooperation in Science and Technology).

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Funded by the Horizon 2020 Framework Programme of the European Union

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