Image processing and simulation of perfusion MRI images for the prediction of the evolution of the ischemic lesion in stroke.

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Stroke – a neurological deficit resulting from blood supply perturbations in the brain – is a major public health issue, representing the third cause of death in industrialized countries. There is a need to improve the identification of patients eligible to the different therapies and the evaluation of the benefit-risk ratio for the patients. During this PhD work, we wish to investigate new biomarkers, extracted from multi-modality images, for the prediction of the ischemic lesion evolution. In this context, Dynamic Susceptibility Contrast (DSC)-MRI, a prominent imaging modality for the assessment of cerebral perfusion, can help to identify the tissues at risk of infarction from the benign oligaemia. However, the entire pipeline from the acquisition to the analysis and interpretation of a DSC-MRI remains complex and some limitations are still to be overcome [1]. As a first step, we therefore proposed to contribute to the DSC-MRI post-treatment pipeline in order to improve tissue classifications.

We notably worked on the step of data deconvolution, one of the steps key to the improvement of DSC-MRI. This step consists in the resolution of an inverse ill-posed problem and allows the computation of hemodynamic parameters which are important biomarkers for the prediction of the ischemic lesion evolution. In order to compare objectively the performances of existing deconvolution algorithms and to validate new ones, it is necessary to have access to information on the ground truth after deconvolution. The PET-MRI hybrid imaging modality, which can provide both MRI images and PET-based quantitative hemodynamic parameter maps, is a very good modality candidate for the validation on real data. However, this hybrid modality is recent and only a few machines are available worldwide. An alternative validation approach which is becoming more and more prominent in medical imaging is the in silico validation approach (i.e. via numerical simulations). In our context, this approach consists in simulating DSC-MRI images from the ground truth after deconvolution and in evaluating the capacity of the deconvolution algorithms to recover this ground truth. One of the main challenges with the in silico validation approach is to inject a sufficient level of realism into the simulator in order to ensure that the simulations allow to evaluate the robustness of the deconvolution algorithms with respect to the different sources of noise and variability in real clinical images. In [2], we discussed the impact of the realism of the noise model used in the simulations. We showed the validity of a gaussian approximation of the log-rician distribution of the MRI data, first via a low-level statistic approach, then via the extraction of high-level information with respect to the processing pipeline, such as the extraction of the cerebral blood flow, a hemodynamic parameter of great clinical interest. We then proposed a new simulator including a realistic model for the noise in the MRI acquisition pipeline as well as realistic tissue distributions and realistic lesion and brain shapes. The use of this simulator is manifold. For example, it allows to evaluate the capacity of the deconvolution algorithms to recover the shape of the ischemic region which has recently been identified as a predictive biomarker of the final infarct volume [3]. Furthermore, the introduction of a new simulator with good shape realism was essential in order to evaluate the performance of certain deconvolution algorithms such as our team's algorithm [4] which include an edge preserving spatio-temporal regularization term and therefore do not deal with the deconvolution of each voxel independently but takes into account the information from neighboring voxels. An illustration of the performance of our team's algorithm is given in Figure 1.

In addition to this work on the deconvolution step, we also studied the normalization step which follows the deconvolution. This step is meant to correct the effect of vascular delay and dispersion on the hemodynamic parameter maps and to facilitate inter-individual quantitative studies. In [5] we compare, on real and simulated data, the performances of the different normalization strategies available in the literature.

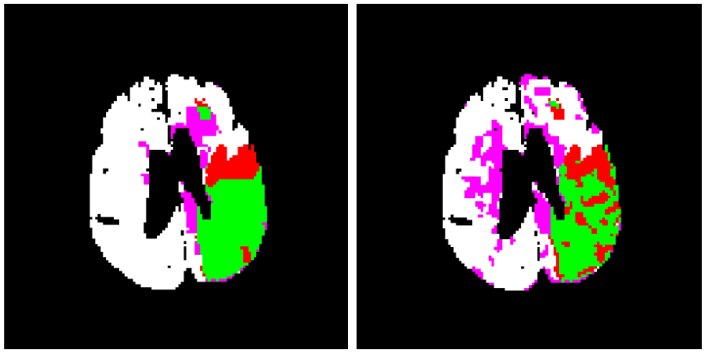

Figure 1: Label images illustrating the quality of the prediction after thresholding of an hemodynamic parameter map, the mean transit time, extracted after deconvolution with (left) our team's algorithm [4] and (right) a deconvolution algorithm with a temporal regularization term only. In green the true positives, in red the false negatives, in magenta the false positives and in white the true negatives.

References

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