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**Development of methods, algorithms and applications for the robust and objective delineation of structures in diffusion weighted MR images**

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Diffusion weighted imaging (DWI) derived parameters like the apparent diffusion coefficient (ADC) are known to correlate inversely to tumour-proliferation in brain tumours. In high grade gliomas, the heterogeneity makes it difficult to delineate high and low proliferative areas. Furthermore, this separation is impeded by partial volume effects and blurred borders. In addition to that, necrosis and cerebrospinal fluid increase the uncertainty of a proper delineation. A second parameter derived by diffusion weighted imaging is the perfusion fraction *f* and can be used to differentiate pancreatic diseases like pancreatic carcinoma from healthy tissue and pancreatitis from pancreatic carcinoma, thanks to the hypoperfused nature of pancreatic carcinoma versus pancreatitis and healthy pancreatic tissue, respectively.

In this thesis, we present algorithms and approaches for these two cases to objectively determine the derived parameters. In the glioma case, an approach is presented to automatically delineate the mentioned heterogeneous regions and to probabilistically quantify the tissue inhomogeneity. Two methods were tested to achieve this aim. Firstly, a Gaussian mixture model, solely consisting of Gaussians and a partial volume aware technique using an additional class. Next, an Expectation Maximization algorithm has been applied onto these two models to separate these regions. In the pancreatic case, we used linear rigid image registration, to spatially align the so called **b** value stack, representing the diffusion raw data, and tried to improve the reproducibility of the derived parameters and the plausibility of the anatomical structure.

The results of the first study indicate that the Gaussian model excels the partial volume model in terms of reproducibility by using a systematic initialization routine automatically drawn onto the low and high-proliferative areas. In the second study, we could show that linear image registration significantly improves the plausibility of the spatially alignment of the **b** value stack and furthermore the reproducibility of the IVIM derived parameters such as *f*.

In conclusion, we can say that the first study yields an automatic, rapid, reproducible and objective determination of regions of signal inhomogeneity in high grade gliomas by an automatic initialization whereas the second study results in a reduction of residual motion and artifacts ending up in a degradation of the standard deviation of the perfusion fraction *f* to better delineate between the pancreatic entities. This leads to a development of a pancreatic screening tool which could be eventually expanded onto the usage of other organs.