



**Application number/Title: 44108** - Predictive value of the structural connectome using machine learning

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**Keywords provided by the Applicant PI to describe the research project:**

deep learning, diffusion mri, machine learning, structural connectome, tract-based phenotypes

**Application Lay Summary:**

Using diffusion weighted MRI the axonal pathways of the human brain can be estimated. This gives information on how the different areas of the brain are connected. This is called the 'structural connectome' and contains rich information as many studies have shown. In patients with schizophrenia for example differences in the structural connectome can be observed (Ardekani et al., 2011). However, extracting the structural connectome from the diffusion weighted MRI images is not easy. Many methods for that have been proposed, but results are still quite error-prone (Maier-Hein et al., 2017). Recent advancements in computer science have enable more efficient use of large datasets by letting the computer learn from the data by itself. Those methods are called 'machine learning' and have enabled much more powerful image processing applications. We have developed a new method which uses these new machine learning methods for more accurate reconstruction of the structural connections in the human brain. The methods shows very good results on the popular Human Connectome Project dataset. Now we want to apply this new method at scale and see whether it yields an added predictive value with respect to genetic data, functional connectome or metadata in comparison to traditional methods. Improving our understanding of these relations can help us to detect diseases earlier or to find potential risk factors. Given the enormous size and the number of different modalities of the UK Biobank it is an ideal dataset to investigate these questions.

The estimated runtime of the project is 18 months.