

## Development and quality assessment of neuroimaging-based biomarkers for brain disorders

A considerable body of literature applying deep learning techniques to clinical neuroimaging data has emerged in recent years (see Litjens et al., 2017); however, the field must be considered to be still in its infancy. Published techniques are usually bound to single measurement modalities and single datasets with moderate sample sizes. The generalizability of the reported results to data from different centers, as well as their robustness to measurement errors, missing data, outliers, etc., is thus often not clear. Besides the relatively small sample sizes that are prevalent, a factor that has further hampered the development of diagnostic markers in this field is the strong heterogeneity of mental disorders. This project aims to advance the field of neuroimaging-based biomarker identification for brain diseases by 1) harmonizing, combining and cross-checking data from different centers, 2) developing standardized performance assessment protocols for assessing not only average prediction accuracy but also additional dimensions such as fairness, robustness, uncertainty calibration and interpretability on a single-patient level, and 3) developing novel multi-modal machine learning and deep learning methodologies that provide competitive performance in the above-mentioned quality dimensions.

The project will initially focus on the prediction of (co-) occurrences of psychiatric disorders in a large adolescent sample obtained from three centers (Alexander et al., 2017). Structural (T1-weighted MRI) and functional (EEG and fMRI) neuroimaging data as well as behavioural and questionnaire data will be used for prediction. Age-, and sex-dependent normative models for data features of interest will be derived from healthy cohorts, based on which the degree of abnormality in individual diseased patients will be quantified. Novel machine learning based predictive models incorporating such multimodal normative data will be devised and validated.

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### References

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