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# Network models of aberrant brain connectivity for elucidation of the pathophysiology of schizophrenia

Autor: Xiaolong Zhang
Institut / Klinik: Zentralinstitut für Seelische Gesundheit Mannheim (ZI)
Doktormutter: Prof. Dr. H. Tost

Schizophrenia is a serious and chronic mental disorder, which brings not only suffering to patients, but also much burden to families and society. Current diagnosis is mainly based on criterion-based systems, including ICD and DSM, which describe various symptoms of schizophrenia, and antipsychotic drugs are only relatively effective for positive symptoms, but not for negative symptoms and cognitive dysfunction. Previous neuroimaging studies have not provided stable biomarkers for clinical practice. Part of the reason lies in the focus of analysis on group-level, static, and descriptive research approaches.

To improve this situation, I firstly reviewed novel network models and machine learning methods that have the potentials to dig deeply into the mechanisms of disease, define psychopathological subgroups across current diagnostic boundaries, and predict individual response to treatment. Secondly, I chose and applied one promising network tool, generative model, to investigate the altered brain network in schizophrenia. Among the four classes of models, one two-factor model combining spatial constraints and topological facilitation could equally simulate the normal and altered formation of brain networks. By comparing the model parameters, relatives and schizophrenia showed lower spatial constraints and topological facilitation, which is consistent with the topological perturbation in disease. And spatial constraints in healthy controls may be linked to polygenic risk for schizophrenia and cognitive function. In sum, this thesis provides promising analysis approaches and application examples that may help elucidate the complex and dynamic neurodevelopmental process of mental disorders.