Resting state fMRI allows tracking of functional connectivity on an individual level

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Background: Resting state fMRI (rsfMRI) studies have demonstrated changes of functional connectivity in groups of patients afflicted with neuropsychiatric disorders (Greicius, 2008). Translating results from group studies into the real clinical scenario is gaining interest. To show that rsfMRI can generate statistical biomarkers on an individual level we compare individual measures of within- and between network coherence, and of hierarchical functional organization of a 59 yr old female patient with semantic dementia (SD) to distributions of the same measures computed from a freely available dataset of healthy controls (Yeo et al., 2011).

Methods: We acquired 7 minutes of rsfMRI data (TR=3s, TE=50ms, FA=90°, FOV=192mm, matrix size=64x64, 36 slices, slice thickness=3mm, gap=0.75mm, acquisition order: ascending-interleaved even-odd) and a T1-weighted scan on a 1.5T Siemens Aera scanner. Data were preprocessed according to the standard Freesurfer pipeline. Average timeseries were extracted from each region of interest (ROI) of three atlases (7-rs-nets, 17-rs-nets, and aparc). For computation of within-network coherence, each ROI was segregated hemisphere-wise into three spatially distinct sub-clusters with k-means clustering. We computed within-network coherence hemisphere-wise as the partial correlation of the sub-clusters in each ROI using motion-correction parameters, average signal of CSF, average signal of WM, and the global average signal as confounds. For between-network coherence we averaged timeseries from corresponding ROIs in the left and right hemisphere, and computed pairwise partial correlations using the same confounds as before. For the patient and each control we computed the functional organization with a hierarchical cluster analysis based on the between-network partial correlations. We then assessed the dissimilarity of each resulting dendrogram with the dendrogram based on the average between-network correlation (leaving out the respective target subject) to create a Null-distribution of dendrogram-dissimilarity using the CLUE-library in R.

Results: The patient has a reduced within-network coherence compared to healthy controls, and a severe reduction of within network coherence after one year, but only between hemispheres, not within hemispheres. The dorsal attention network decouples from other networks within a year. Hierarchical functional connectivity of the patient becomes dissimilar to the healthy control group (percent rank 100).

Conclusions: Individual fMRI-based diagnostic and prognostic information is the basis of Precision Medicine. This study showed selective functional network decoupling within one year in a patient with SD. Hierarchical organization and its changes can be tracked by means of a 7 min rsfMRI scan and may have potential for improved understanding of pathophysiology of disease and prognosis.