Co-activation pattern analysis on resting-state fMRI data in people with Huntington's Disease

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Huntington's Disease (HD) is a neurodegenerative disorder caused by an inherited monogenic autosomal dominant mutation, namely a cytosine-adenosine-guanine (CAG) trinucleotide repeat expansion in the Huntingtin (HTT) gene. The CAG expansion encodes for a long poly glutamine tract, leading to the production of mutant HTT (mHTT) protein, toxic and prone to aggregate. Due to a selective vulnerability of the medium spiny neurons to mHTT, normal striatal functioning is disrupted, which eventually leads to movement dysfunction. Resting state functional MRI (RS-fMRI) can be used to capture fluctuations in spontaneous neural activity via the blood oxygenation level dependent (BOLD) contrast. Distant brain regions show high temporal correlations, referred to as functional connectivity (FC), between their BOLD signals forming resting state networks (RSNs). Temporal fluctuations in FC can be observed within these networks and have been shown to be altered in some neurodegenerative diseases. However, no study has investigated the temporal fluctuations in the brain's functional dynamics in people with HD (PwHD). We plan to bridge this gap by using co-activation patterns (CAPs), which are transient sub-components of RSNs and have proven to accurately distinguish in between HD model mice and wild type mice. In this project, RS-fMRI scans were made with a 3 T Magnetom ALLEGRA (Siemens) head MRI system on a population sample of healthy controls (n=56), pre-manifest patients (n=23) and manifest patients (n=32). We aim to extract CAPs and their metrics from controls and PwHD, to compare spatial and temporal properties of the identified CAPs and to feed the CAP metrics into a classifier to train it to accurately predict the disease state in individual participants.