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**Dataset** **Open**

# Structural and functional connectomes from 27 schizophrenic patients and 27 matched healthy adults

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## Description

**Data Acquisition**

The cohort consists of a total of 27 healthy participants (age 35 ± 6.8 years) and 27 schizophrenic patients (age 41 ± 9.6), scanned in a 3-Tesla MRI scanner (Trio, Siemens Medical, Germany) using a 32-channel head-coil. The schizophrenic patients are from the Service of General Psychiatry at the Lausanne University Hospital (CHUV). All of them were diagnosed with schizophrenic and schizoaffective disorders after meeting the DSM-IV criteria (American Psychiatric Association (2000): Diagnostic and Statistical Manual of Mental Disorders, 4th ed. DSM-IV-TR. American Psychiatric Pub, Arlington, VA22209, USA). The Diagnostic Interview for Genetic Studies assessment was used to recruits the healthy controls (Preisig et al. 1999). 24 out of the 27 schizophrenics were under medication with mean chlorpromazine equivalent dose (CPZ) of 431 ± 288 mg. The written consent was obtained for all subjects - in accordance with institutional guidelines of the Ethics Committee of Clinical Research of the Faculty of Biology and Medicine, University of Lausanne, Switzerland, #82/14, #382/11, #26.4.2005). All subjects were fully anonymised.

The session protocol consisted of (1) a magnetization-prepared rapid acquisition gradient echo (MPRAGE) sequence sensitive to white/gray matter contrast (1-mm in-plane resolution, 1.2-mm slice thickness), (2) a Diffusion Spectrum Imaging (DSI) sequence (128 diffusion-weighted volumes and a single b0 volume, maximum b-value 8,000 s/mm2, 2.2x2.2x3.0 mm voxel size), and (3) a gradient echo EPI sequence sensitive to BOLD contrast (3.3-mm in-plane resolution and slice thickness with a 0.3-mm gap, TE 30 ms, TR 1,920 ms, resulting in 280 images per participant). During the fMRI scan, participants were not engaged in any overt task, and the scan was treated as eyes-open resting-state fMRI (rs-fMRI).

**Data Pre-processing**

Initial signal processing of all MPRAGE, DSI, and rs-fMRI data was performed using the Connectome Mapper pipeline (Daducci et al. 2012). Grey and white matter were segmented from the MPRAGE volume using freesurfer (Desikan et al. 2006) and parcellated into 83 cortical and subcortical areas. The parcels were then further subdivided into 129, 234, 463 and 1015 approximately equally sized parcels according to the Lausanne anatomical atlas following the method proposed by (Cammoun et al. 2012). DSI data were reconstructed following the protocol described by (Wedeen et al. 2005), allowing us to estimate multiple diffusion directions per voxel. The diffusion probability density function was reconstructed as the discrete 3D Fourier transform of the signal modulus. The orientation distribution function (ODF) was calculated as the radial summation of the normalized 3D probability distribution function. Thus, the ODF is defined on a discrete sphere and captures the diffusion intensity in every direction.

**Structural Connectivity**

Structural connectivity matrices were estimated for individual participants using deterministic streamline tractography on reconstructed DSI data, initiating 32 streamline propagations per diffusion direction, per white matter voxel (Wedeen et al. 2008). Structural connectivity between pairs of regions was measured in terms of fiber density, defined as the number of streamlines between the two regions, normalized by the average length of the streamlines and average surface area of the two regions (Hagmann et al. 2008). The goal of this normalization was to compensate for the bias toward longer fibers inherent in the tractography procedure, as well as differences in region size. The number of fibers and fiber length were also included in the dataset. For the quantitative measure of structural connectivity, the generalised fractional anisotropy (gFA, Tuch et al. 2004) and average apparent diffusion coefficient (ADC, Sener et al. 2001) were also computed for each tract.

**Functional Connectivity**

Functional data were pre-processed using routines designed to facilitate subsequent network exploration (Murphy et al. 2009, Power et al. 2012). The first four time points were excluded from subsequent analysis to allow the time series to stabilize. The signal was linearly detrended and further physiological (white-matter and cerebrospinal fluid regressors) and motion artefacts (three translational and three rotational regressors) confounds were regressed. Then, the signal was spatially smoothed and bandpass-filtered between 0.01-0.1 Hz with Hamming windowed sinc FIR filter. To obtain the brain regions for different atlas scales the signal was linearly registered to the MPRAGE image and averaged within a given region (Jenkinson et al. 2012). Functional matrices were obtained by computing Pearson’s correlation between the individual pairs of regions. All of the above was carried out in subject’s native space (Daducci et al. 2012, Griffa et al. 2017).

Brain cortical bert freesurfer rendering for the 5 scales of the Lausanne2008 atlas is available on <https://github.com/jvohryzek/bert4lausanne2008>.

**Additional details**

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## Citation

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