Project 4. Functional connectivity analysis during motor imagery using fMRI

Case study
- 5 healthy subjects studied during execution of 2 motor imagery tasks and during rest.
- **Goal:** Estimate and compare the functional connectomes in 2 motor imagery tasks and in resting-state.
- Link to download data.

Data description
- Data was acquired under three conditions: two motor imagery tasks and a resting-state condition. One motor imagery task (Graz task) involved only motor imagery, while the other (NeuRow task) combined motor imagery with motor observation. Each task consisted of three runs, each containing three cycles that alternated between left-arm and right-arm imagery blocks with rest in between. Each block included three trials, alternated with rest periods. A resting-state acquisition was also performed, during which subjects were instructed to lie still.
- Data acquisition:
    - MR Scanner: 3T Siemens Vida using a 64-channel receive RF coil.
    - T1-weighted structural image collected using an MPRAGE sequence (TR = 2300ms, TE = 2.98ms, voxel size = 1.0mm isotropic).
    - fMRI data acquired using a 2D Echo-Planar Imaging (EPI) sequence (TR = 1260ms, TE = 30ms, flip angle = 70◦, voxel size = 2.2mm isotropic, in-plane acceleration with GRAPPA factor 2, simultaneous multi-slice with SMS factor 3, 60 axial slices).
- Data provided:
    - Preprocessed fMRI data resampled to the MNI standard space (*filtered_func_data2standard.nii.gz*). Preprocessing performed included motion correction, B0 unwarping, high-pass temporal filtering and spatial smoothing. For the resting-state data, nuisance regression of motion and physiological confounds was also performed.
    - Labels of the Shaefer 100-parcel atlas in the standard MNI space (*Schaefer2018_100Parcels_7Networks_order_FSLMNI152_2mm.nii.gz*) . Correspondence to Yeo's canonical resting-state networks (RSNs) (*Schaefer2018_100Parcels_7Networks_order.lut*). Link to download atlas.

Data analysis
- **Compute Average Functional Connectomes**
    - Parcellate fMRI data: segment the preprocessed fMRI data into 100 regions according to the Schaefer100 atlas (parcellation in this context refers to dividing the brain into predefined regions based on an atlas, averaging voxel-level time-courses into region-wise time-courses).
    - Compute the pairwise Pearson correlation between the time-courses of all regions to generate a functional connectivity matrix.
    - Sort the regions by their canonical RSN assignment.
    - Compute the average correlation within and between RSNs to obtain a between-RSN functional connectivity matrix.

- o Compare the functional connectomes between each pair of conditions by performing statistical tests on the connectivity values (e.g., pairwise t-tests for region-to-region correlations or RSN-level averages, with corrections for multiple comparisons if necessary).
- **Compute Graph-Based Connectivity Metrics**
  This section can be done using for example the Brain Connectivity Toolbox in MATLAB https://sites.google.com/site/bctnet/, or in Python https://pypi.org/project/bctpy/.
  - o *Obtain a graph from each functional connectivity matrix, by thresholding or weighting it.*
  - o *Compute graph theory metrics for each task, such as global efficiency, characteristic path length, degree.*
  - o *Compare them between pairs of conditions using appropriate statistical tests.*