1   EEG Data

A central question in neuroscience is understanding the brain's functional architecture. Neuroscientific studies in this context often analyse EEG data [2] which represent brain activity in certain brain regions.

In the present study, we are investigating EEG recordings of 134 patients suffering from major depressive disorder (MDD) at two different times. The first one was recorded before any depression treatment was started (visit 1, day 0), and the second one was recorded 1 week after the treatment start (visit 2, day 7). One subject's EEG data from one visit is a multivariate time series with 19 individual time series corresponding to the 19 EEG channels, which again correspond to certain brain regions. Each series consists of approximately 9 minutes of recording sampled at a frequency of 250 Hz.

2   Coupling Data

These time series are the basis for analysing the functional interplay of these regions. In this context, different connectivity measures have been proposed to quantify this [3], for example, partial correlations between the time series. This results in a connectivity matrix, where the (i,j)-th entry represents the functional connection of region i with region j. More recently, the Kuramoto model for the synchronisation behaviour of mathematical oscillators has been used to derive another measure for connectivity. It is a system of differential equations. By estimating the coefficients $K_{i,j}$ of the differential equation system

$$\dot{\varphi}_i(t) = \frac{\partial \varphi_i(t)}{\partial t} = \frac{1}{r} \sum_{j=1}^{r} K_{i,j} \sin(\varphi_j(t) - \varphi_i(t)) = f(t, \varphi_i(t)) \quad i = 1, \ldots, r. \tag{1}$$

that best fit the recorded data, they as well can be interpreted as a connectivity measure between the time series.

Due to the large number of measure points in the recordings, the Kuramoto connectivity matrix [1] can be calculated for smaller time windows for instance for 250 measure points amounting to 1 second of recording. The structure of the resulting connectivity data for a single patient is depicted in Fig. 1

Performing this for all 134 subjects, the resulting data matrix K of size $134 \times 19 \times 19 \times 380$ consists of the 19×19 connectivity matrices for each of the 380 time windows and each of the 134 patients. This object is the basis for subsequent analysis.

3   Goal

After 4 weeks of treatment, 66 of the patients showed a positive reaction to the treatment (responders) and the remaining 68 patients did not respond to the treatment (non-responders). The goal of this work is to find a way to distinguish the two groups based on the provided K connectivity data derived from the EEG recordings from visit 1 and possibly visit 2 and hence predict the treatment outcome at an early stage.

4   Analysis Tools

There are several possible directions for the analysis of these data. One could perform statistical tests on several measures of the matrices. For instance, one could measure the variability of the connectivity coefficients across windows. One simple way to do so is to calculate the standard deviation across windows. The features of a single subject then consist of a single 19×19 matrix. These matrices might also be used as the features for subsequent clustering/classification.

The Kuramoto coefficients can take on positive as well as negative values translating to attraction and repulsion between the signals. One could analyse the signs of the coefficients in each window in more detail and either view them as features for subsequent clustering/classification or perform statistical tests for significant differences among the groups or visits.
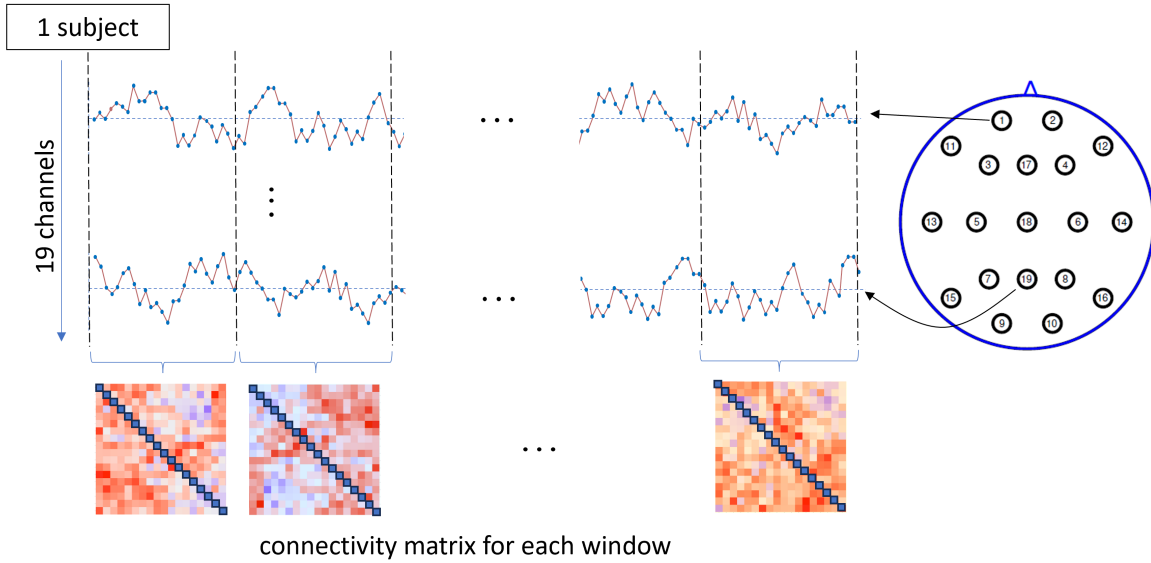
Figure 1: A single subject's data consist of 19 time series from the 19 EEG channels representing the brain activity in 19 brain regions. We cut the time series in equally sized windows (250 measure points, approximately 1 second of recording). For each window the Kuramoto connectivity matrix is calculated.

The Kuramoto coupling matrix is by default not symmetric, but the estimation can be designed to force symmetry. The symmetric form of the coefficients can be interpreted as the affinity matrix of a graph. This enables the analysis with graph-specific data mining algorithms.

References

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