

Consensus clustering approach to group brain connectivity matrices

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In the supervised analysis of human connectome data, subjects are usually grouped by high-level clinical categories (e.g., patients and controls). However, the population of healthy subjects (as well as those of patients) is typically highly heterogeneous: clustering algorithms find natural groupings in the data, and therefore constitute a suitable technique for disentangling the heterogeneity that is inherent to many diseases and to the cohort of controls. We present here a new method, rooted on the consensus clustering, where the connectivity pattern of each region is analyzed by a clustering algorithm and a consensus matrix is built by merging the partitions obtained in correspondence of each region. By analyzing publicly available data-sets, as well as a simulated toy system, we demonstrate that the proposed approach allows to robustly identify groups of subjects, or, for longitudinal datasets, groups of physiological or behavioral variables, with similar connectomes, thus providing a partition beyond the measured labels associated to them. Moreover, the proposed approach may also be seen as a preprocessing stage: extracting the natural classes present in data and subsequently performing a supervised analysis between the subgroups found by consensus clustering, allows to identify variables whose pattern is altered in group comparisons, which are not identified when the groups are used as a whole. We present application of the proposed method to fMRI public data, looking for brain regions whose connectivity pattern is altered in the group comparisons.

References

[1] J. Rasero et al., Consensus clustering approach to group brain connectivity matrices, *Network Neuroscience* 2017 1:3, 242-253