Context  When working with signals in a medical context, the scale of the collected databases and the cost of asking a
doctor to annotate them makes the labeling process almost impossible for practical cases. Moreover, some annotation
for the considered task might be hard to assess. For instance, when predicting the consciousness of a patient in a
coma from electroencephalographic recordings, there is no consensus on the ground truth. Another example would
be the early detection of neurological disorder such as Parkinson, as it is very complicated to generate a base of
motor records with enough people who will develop disorders in the following 10 years. Thus, these applications are
particularly in need for unsupervised learning methods.

Unsupervised learning can highlight statistical effects in the structure of the signal which can be used to stratify the
subjects in coherent groups. However, one drawback of unsupervised learning is that to be actionable, one need to
extract the structure of the data that has been learned by the model. A solution to make this extraction easier is to
provided beforehand a form of structure for the signal thanks to domain knowledge. The convolutional sparse linear
model \[2\] is one established framework for unsupervised learning designed for signals. It learns shift-invariant
patterns to sparsely reconstruct a signal. These patterns, also called atoms, correspond to recurrent structures present in the
data. While recent advances have improved the computational tractability of these methods \[5, 4\] and adapted them
to neurophysiological data \[1\], there are still many shortcomings that make them unpractical for applications outside
denoising.

In particular, the classical convolutional model does not account for the relative localization of the activations.
However, neural activity localized in the brain is generated by the information flow between the neurons and thus also
has a temporal structure that reveals connections between functional areas. An interesting question would be to see
how one can model and learn these time dependencies between areas in the brain from the data using unsupervised
or self-supervised learning.

Methods  We propose to answer this question by improving the temporal structure of the activation. While using
the $\ell_1$ norm to penalize non-sparse activation, the underlying assumption is that each activation is independent from
all the others. By changing the regularization for the activations, it would be possible to incorporate a finer temporal
structure. By using either group sparsity – modeling simultaneous activations – or more complex regularization based
on point process models \[3\], it is possible to expand the temporal modeling for the convolutional dictionary learning
framework. This approach would lead to model that are more identifiable as the correlation structure is explicit
and can be analyzed once it is learned. We propose during this internship to explore the benefit of such model
for neurophysiological data in MEG. A particular challenge will be to come up with efficient parameter estimation
techniques – potentially distributed – and to develop a proper validation method based on task MEG.
Environment The internship will take place in Inria Saclay, in the Parietal team. This is a large team working focused on mathematical methods for statistical modeling of brain function using neuroimaging data (fMRI, MEG, EEG). Particular topics of interest include machine learning techniques, numerical and parallel optimization, applications to human cognitive neuroscience, and scientific software development.

Requirements

- Strong mathematical background. Knowledge in numerical optimization is a plus.
- Good programming skills in Python. Knowledge of parallel computing is a plus.

References