Functional magnetic resonance imaging (fMRI), a noninvasive neuroimaging method that provides an indirect measure of neuronal activity by detecting blood flow changes, has experienced an explosive growth in the past years. In this talk, I will first discuss a joint analytical framework to detect regions of the brain which exhibit neuronal activity in response to a stimulus and, simultaneously, infer the association of spatially remote voxels that exhibit fMRI time series with similar characteristics. The latter can be viewed as an aspect of functional connectivity, as it naturally captures statistical dependencies among remote neurophysiological events. The model incorporates information on both the spatial and temporal correlation structures of the data. The high-dimensionality of the data and the large amount of parameters pose challenges from a computational point of view. I will then discuss an approximate variational Bayes algorithm for posterior inference, and I will compare its efficiency and estimation results with respect to a full Markov Chain Monte Carlo algorithm. Finally, I will present a Bayesian hierarchical modeling approach for imaging genetics. Here, we have available data from a fMRI study on schizophrenia, and the interest lies in linking brain connectivity to the available genetic information on schizophrenic patients and healthy controls. For this task, I will propose a hierarchical mixture model that includes several features in a unified estimation framework: it incorporates the selection of ROIs that discriminate the subjects into separate groups; it allows the mixture components to depend on selected covariates; it includes prior models that capture structural dependencies among the ROIs. I will investigate the performance of the proposed models on both simulated and real fMRI data.

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