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Abstract Title: Incorporating Spatial Dependence into Bayesian Multiple Testing of Statistical Parametric Maps in Functional Neuroimaging

Abstract: The analysis of functional neuroimaging data often involves the simultaneous testing for activation at thousands of voxels, leading to a massive multiple testing problem. This is true whether the data analyzed are time courses observed at each voxel or a collection of summary statistics such as statistical parametric maps (SPMs). It is known that classical multiplicity corrections become strongly conservative in the presence of a massive number of tests. Some more popular approaches for thresholding imaging data, such as the Benjamini-Hochberg step-up procedure for false discovery rate control, tend to lose precision or power when the assumption of independence of the data does not hold. Bayesian approaches to large scale simultaneous inference also often rely on the assumption of independence. We introduce a spatial dependence structure into a Bayesian multiple testing model for the analysis of SPMs. By using SPMs rather than the voxel time courses, much of the computational burden is mitigated. Increased power is demonstrated by using the dependence model to draw inference on a real dataset collected in a fMRI study of cognitive control. The model also is shown to lead to improved identification of neural activation patterns known to be associated with eye movement tasks.

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Abstract Title: Binary Classification Using Significant Features of fMRI Data

Abstract: Binary classification is the task of using information from individuals to place them into one of two distinct groups. An example is classifying patients as having a certain illness or not. A related question is the identification of features which determine the classification. One approach to answer these questions is called linear discriminant analysis (LDA), which creates a linear function to determine group placement. Additionally the function helps identify which features (variables) contribute more information towards class placement. In order to properly estimate the function the number of observations cannot be less than the number of variables. In the context of fMRI data the individual voxels are treated as the variables and the individual as the observation, which results in the large p small n problem and prevents the use of LDA. Our goal is to

develop a method that allows us to use all the observations to create a binary classification scheme, which would allow us to classify new individuals based on an fMRI scan. We will show how a singular value decomposition (SVD) can be used to reduce the data dimension in order to utilize ridge linear discriminant analysis (RLDA) to create a classification rule. Furthermore this approach allows us to incorporate a threshold value and back transformation to identify the parts of the brain which are behaving differently between groups. We will also demonstrate the use of this method with fMRI scans of people with schizophrenia and people without.

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Abstract Title: Antisaccade trial probability modulates circuitry activation in event-related fMRI: comparison of hemodynamic response functions

Abstract: Cognitive control is a process that modulates neural functioning to ensure successful performance based on current goals. Saccades provide a simple model for measuring cognitive control in the laboratory: basic, visually guided prosaccades are reflex-like glances towards a newly appearing cue, while complex antisaccades are glances to the mirror location of the cue and require greater levels of cognitive control to inhibit a prepotent glance towards the cue and to generate a volitional saccade. Saccades are supported by well-defined neural circuitry including visual cortex, posterior parietal cortex, frontal and supplementary eye fields, and prefrontal cortex, in which activation differs between trial types in both strength and extent. Furthermore, the context in which saccades are performed may affect response characteristics and neural activation patterns. The current study investigated the impact of varying the probability of anti- versus pro-saccades across runs. Seventeen healthy UGA undergraduates performed three mixed runs of saccades (a. 25% anti/ 75% pro; b. 50% anti/ 50% pro; c. 75% anti/25% pro) in the functional magnetic resonance imaging environment. A 3x2 (Run by Trial Type) ANOVA was performed to determine differences in BOLD activity across conditions. Two parallel analyses were conducted using separate basis functions to model the hemodynamic response (HRF), which were then convolved with stimulus timing to create regressors for the general linear model. One method used a canonical, pre-determined HRF shape (Gamma function) that estimated only a single amplitude value per voxel, while the second method estimated the HRF shape along multiple time points based on the current data (TENT function). A comparison of the results from both ANOVAs indicated that while the two methods produced similar regions with

significant effects in some instances, there were also a number of areas where the two methods differed. For the Run x Type interaction, both methods revealed significant clusters in right occipital/temporal and right parietal cortices; however, clusters in right prefrontal and left occipital/temporal cortices were identified only by the Gamma method, whereas a cluster in left occipital cortex was identified only by the TENT method. These differences may have been due to invalid assumptions about the nature of the HRF using the Gamma function or a lack of power when using the TENT function. In either case, the current results demonstrate the importance of appropriately selecting an HRF model when analyzing and interpreting fMRI data.

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Abstract Title: Exploring Functional Brain Dynamics Via a Bayesian Connectivity Change Point Model

Abstract: Multiple recent neuroimaging studies have demonstrated that the human brain's function undergoes remarkable temporal dynamics. However, quantitative characterization and modeling of such functional dynamics have been rarely explored. To fill this gap, we presents a novel Bayesian connectivity change point model (BCCPM), to analyze the joint probabilities among regions constituting brain networks between different time periods and statistically determine the boundaries of temporal blocks to estimate the change points. Such regions are modeled by the method based on brain structural connectome, namely the DICCOL system. Intuitively, the determined change points represent the transitions of functional interaction patterns within the brain networks and can be used to investigate temporal functional brain dynamics. The BCCPM has been evaluated and validated by synthesized data. Also, the BCCPM has been applied to a real block-design task-based fMRI dataset and interesting results were obtained.

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Abstract Title: Model-Based Time Series Clustering using CHOMP

Abstract: Time series clustering has attracted a lot of interest in recent years because of its ability to cluster the temporal patterns in data. Among all approaches, our focus is on model-based algorithms due to its ability to study the statistical properties that is usually unknown in other clustering algorithms. Previous work has used models such as ARIMA, simple Markov Chain, and Hidden Markov Model (HMM). However, these models can only account for simple dependence structure in the time series. This may result in errors in the clustering stage since the complicated data structure is not characterized appropriately by the model. In this paper, we propose a model-based time series clustering using the Copula-based Higher Order Markov Process (CHOMP) which allows for higher order non-linear dependence structure and accepts continuous random variables. The algorithm combines the finite mixture model approach and iterative relocation method to obtain the most probable clustering based on the likelihood. We further relax the stationary condition in the CHOMP so that it can be applied to some non-stationary time series. Results from a simulation study using the proposed method will be presented in the talk.

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Abstract Title: Comparison of the activation pattern differences between two occasions using ROIs analysis

Functional Magnetic Resonance Imaging (fMRI) studies can be divided into two streams depending on the goal: a whole-brain voxelwise analysis and a regions of interest (ROIs) analysis. The method based on a whole-brain voxelwise analysis is a common approach for exploring the brain areas related to specific cognitive processes. A voxelwise analysis, however, does not permit us to examine specific statistical hypotheses about the subregions of the brain. If brain regions involved in specific cognitive processes are detected in the primary research, then it is usual to investigate the detected brain regions (i.e., ROIs) to determine how specific neural regions within whole brain may have been differentially affected. In this work, we conduct an analysis using 11 bilateral neural ROIs previously identified using saccade task; our analysis is built in the wavelet domain to take temporal correlation into account. First, we analyze the fMRI data acquired on two occasions while the participants are engaged in eye movement tasks: antisaccades (generating glance away from a cue), prosaccades (glancing toward a target), or fixation (maintaining gaze on a target). We attempt to compare the activation pattern differences between the two occasions by using the bootstrap resampling-based test and by using the feature extraction approach.

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