

## A Bayesian Approach for the Joint Analysis of fMRI and SNP Data

Francesco C. Stingo<sup>1</sup>, Michele Guindani<sup>1</sup>, Marina Vannucci<sup>2</sup> and Vince D. Calhoun<sup>3</sup>

<sup>1</sup>*Department of Biostatistics, University of Texas MD Anderson Cancer Center,*

<sup>2</sup>*Department of Statistics, Rice University,*

<sup>3</sup>*Depts. of Electrical and Computer Engineering, University of New Mexico*

### Abstract

In this work we develop a Bayesian hierarchical modeling approach for imaging genetics. We have available data from a study on schizophrenia. Our interest lies in identifying brain regions of interest (ROIs) with discriminating activation patterns between schizophrenic and control subjects, and in relating the ROIs activations with available genetic information from single nucleotide polymorphisms (SNPs) on the subjects. For this task we develop a hierarchical mixture model that includes several innovative characteristics: first, it incorporates the selection of features (ROIs) that discriminate the subjects into separate components, allowing for a direct assessment of the uncertainties in the estimates of the model selection parameters. Second, it allows the mixture components to depend on selected covariates, i.e., the SNPs data. In this sense, our proposed model is integrative, in that it combines the activation patterns with the subjects specific genetic information. Third, it incorporates prior knowledge via network models that capture structural dependencies among the variables. More specifically, it employs spatially based selection process priors that capture available knowledge on connectivity among regions of the brain, so that regions belonging to same activation patterns are more likely to be selected together. Furthermore, our hierarchical formulation accounts for additional spatial correlation among selected features. Applied to the schizophrenia data, the model leads to the simultaneous selection of a set of discriminatory ROIs and the relevant SNPs, together with the reconstruction of the correlation structure of the selected regions. To the best of our knowledge, our work represents the first attempt at a rigorous modeling strategy for imaging genetics data that incorporates all such features.

**Keywords:** Bayesian Hierarchical Model, fMRI, Imaging Genetic, Markov Random Field, Variable Selection

**AMS subject classifications:** 62H30, 62H35.