Public Abstract

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The present dissertation contains two parts. In the first part, we develop a new Bayesian analysis of functional MRI data. We propose a novel triple gamma Hemodynamic Response Function (HRF) including the component to describe the initial dip. We use HRF to inform voxel-wise neuronal activities. Then we devise a new model selection procedure with a nonlocal pMOM prior for joint detection of neuronal activation and estimation of HRF, in order to time the activation time difference between visual and motor areas in the brain.

In the second part, we develop a new Bayesian analysis of RNA-Seq Time Course experiments data. We propose to use Bayesian Principal Component regression model and based on that, devise a model selection procedure by using nonlocal piMOM prior in order to identify differentially expressed genes. Most current existing methods for RNA-Seq Time Course experiments data are from static view of point and cannot predict temporal patterns. Our method estimate the posterior differentially expressed probability for each gene by borrowing information across all subjects. Use of nonlocal prior in the model selection procedure reduces false discovered differentially expressed genes.