

Department Of Statistics Purdue University, West Lafayette, IN

Myra Samuels Memorial Lecture 2017

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Statistical Challenges Modeling Transcriptional Patterns in the Brain

Abstract

The transcriptional pattern of the developing brain is of great interest in humans. Recent developments have made it possible to measure transcription of single cells rather than bulk tissue, and to obtain a dense temporal sampling of prenatal and postnatal periods measured on fine anatomical division of the brain. We discuss various statistical challenges arising in the analysis of these data.

Technological advanced have enabled the measurement of RNA levels for individual cells. Compared to traditional bulk RNA-seq data, single cell sequencing yields valuable insights about gene expression profiles for different cell types, which is potentially critical for understanding many complex human diseases. However, developing quantitative tools for such data remains challenging because of technical noise. We propose a unified statistical framework for both single cell and bulk RNA-seq data, formulated as a hierarchical model.

Co-expression networks reveal gene communities and provide insight into the nature of genes involved in risk for genetic disorders. While it is well documented that gene expression varies dramatically over developmental periods in the brain, the associated changes in gene communities over time remain poorly understood. Recently a rich source of data from rhesus monkey brains has become available pertaining to this question. Once the data are divided by cell type and developmental period, however, sample sizes are very small, making inference quite challenging. We develop a global community detection method that combines information across a series of networks, longitudinally, to strengthen the inference for each time period. Our method is derived from evolutionary spectral clustering and degree correction methods.