



JOHNS HOPKINS
BLOOMBERG
SCHOOL of PUBLIC HEALTH

Department of Biostatistics

BIOSTATISTICS SEMINAR

Learning from the Transcriptome: analysis of single cell and bulk RNA sequence data

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Abstract:

Quantification of gene expression can be a critical step towards characterizing the etiology of complex diseases. Growth typically involves differentiation from progenitor cells into more specialized descendants, often involving lineages of pure and transitional cells to achieve final form. Recent technology has enabled estimation of gene expression profiles of single cells and these profiles theoretically differentiate pure cell types. What is missing from the analytical toolbox is an efficient technique to classify pure and transitional cells from their profiles. Here I introduce SOUP, for Semi-sOft cLUstering with Pure cells.

While there are many strengths to single cell expression, the data tend to be noisy. Hence we propose a method to glean more insight from bulk gene expression. Our objective is to borrow information across multiple measurements of the same tissue per individual, such as multiple regions of the brain, using an empirical Bayes approach to estimate individual- and cell-type-specific gene expression. To illustrate, we estimate gene co-expression networks in specific brain cell types, which are then interpreted in light of genetic findings in autism spectrum disorder (ASD).

Kathryn Roeder is the UPMC Professor of Statistics and Life Sciences in the Departments of Statistics and Data Science and Computational Biology. She is also Vice Provost for Faculty at Carnegie Mellon University. Dr. Roeder has developed statistical and machine learning methods in a wide spectrum of areas, including high dimensional data problems in genetics. Her work focuses on statistical methods to reveal the genetic basis of complex disease. She is one of the leaders of the Autism Sequencing Consortium, an international organization dedicated to discovering the genetic etiology of autism. In 1997, she received the COPSS Presidents' Award, as well as the COPSS Snedecor Award for outstanding work in statistical applications.

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Room W2008 (Refreshments 12:00pm)

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