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Regressing Covariance Matrix on Vector Covariates for Single Cell Co-expression Analysis

Wednesday, September 25th, 2024

12:00 PM

110 Frelinghuysen Road, Hill Center, Room 116

Zoom Meeting: Meeting ID: 969 0606 4706

Password: 745339

<https://rutgers.zoom.us/j/96906064706?pwd=ZklvbExpRVBJQ3c5dUhhYTFuR2ZrZz09>

Light refreshments will be served in Hill 452, 11:20am

Abstract: Population-level single-cell gene expression data captures the gene expressions of thousands of cells from each individual within a sizable cohort. This data enables the construction of cell-type- and individual-specific gene co-expression networks by estimating the covariance matrices. Understanding how such co-expression networks are associated with individual-level covariates is crucial. This paper considers Fréchet regression with the covariance matrix as the outcome and vector covariates, using the Wasserstein distance between covariance matrices as a substitute for the Euclidean distance. A test statistic is defined based on the Fréchet mean and covariate-weighted Fréchet mean. The asymptotic distribution of the test statistic is derived under the assumption of simultaneously diagonalizable covariance matrices. Results from an analysis of large-scale single-cell data reveal an association between the co-expression network of genes in the nutrient sensing pathway and age, indicating a perturbation in gene co-expression networks with aging. More general Fréchet regression on the Bures-Wasserstein manifold will also be discussed and applied to the same single-cell RNA-seq data.

Bio: Dr. Hongzhe Li is Perelman Professor of Biostatistics, Epidemiology and Informatics at the Perelman School of Medicine at the University of Pennsylvania. He is Vice Chair for Research Integration, Director of Center of Statistics in Big Data and former Chair of the Graduate Program in Biostatistic at Penn. He is also a Professor of Statistics and Data Science at the Wharton School and a Professor of Applied Mathematics and Computational Science at Penn. Dr. Li has been elected as a Fellow of the American Statistical Association (ASA), a Fellow of the Institute of Mathematical Statistics (IMS) and a Fellow of American Association for the Advancement of Science (AAAS). Dr. Li served on the Board of Scientific Counselors of the National Cancer Institute of NIH and regularly serves on various NIH study sections. He served as Chair of the Section on Statistics in Genomics and Genetics of the ASA and Co-Editor-in-Chief of Statistics in Biosciences. Dr. Li's research focuses on developing statistical and computational methods for analysis of large-scale genetic, genomics and metagenomics data and theory on high dimensional statistics. He has trained over 50 PhD students and postdoctoral fellows.

