Sparse Matrix-Valued Regression Models: Theory and Methodologies

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Data with a matrix-valued response for each experimental unit are commonly encountered in contemporary statistical applications. For example, drug synergy effects can be treated integrally as a matrix-valued variable by designating rows and columns to be doses of two drugs respectively. Image data and data from cross-over designs also generate matrix-valued responses. A complete description of cancer related DNA variants will provide profound insights into the origins, evolution and progression of cancer and will act as an impetus for the development of new anticancer drugs. To exploit this development, a number of studies have demonstrated that pharmacogenomic profiling in cancer cell lines can be used as a biomarker discovery platform to guide the development of new cancer therapies.

In this project, we will develop some sparse matrix-variate regression models for describing the nonlinear link patterns between cancer genomic data and drug synergy data. We will develop the so-called beamforming approach for model estimation and variable selection, and nonparametric testing. The proposed applications aim to improve our understanding of cancer-related molecular mechanisms.

References
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