

Sparse Data Representations with Applications to Multiscale Integrative Genomic Informatics

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Abstract

In the current post-genome era, high resolution genetic probes evolved from Human Genome Sequencing Project have been developed. When combined with imaging techniques, they provide multiscale structural information about genome variations and add a new dimension to gene expression analysis. The combination of multiscale genomic information promises a comprehensive and systematic approach for the study of multiscale biological systems. However, fulfilling the promise calls for powerful analytic techniques to handle and mine the vast amount of signal and image data generated by these multiscale and multi-modality genomic platforms. As a powerful statistical and computational approach recently developed in statistics and signal processing, sparse data representations or compressive sensing provides a promising way to address the challenges facing multiscale genomic informatics. In this talk, I will talk our research on the development of sparse models with the applications to a variety of genomic informatics problems such as the estimation of copy number variations (CNVs) from array and sequencing data, cancer subtyping, chromosome image classification and integration of SNP and fMRI data for diseases diagnosis.