

Statistics and Data Science Seminar

Bayesian Graphical Models with Application to Integrate TCGA data

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Abstract: The Cancer Genomes Atlas (TCGA) data are unique in that multimodal measurements across genomics features, such as copy number, DNA methylation, and gene expression, are obtained on matched tumor samples. The multimodality provides an unprecedented opportunity to investigate the interplay of these features. Graphical models are powerful tools for this task that address the interaction of any two features in the presence of others, while traditional correlation- or regression-based models cannot. We introduce Zodiac, an online resource consisting of a large database containing nearly 200 million interaction networks of multiple genomics features produced by applying novel Bayesian graphical models on TCGA data through massively parallel computation. Setting a new way of integrating TCGA data, Zodiac, publically available at <http://www.compgenome.org/ZODIAC>, is expected to facilitate the generation of new knowledge and hypotheses by the community.

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