

Statistical Models to Study Transcriptome and Proteome Data

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Abstract:

The analysis and interpretation of transcriptome and proteome data provide numerous challenges due to the complexity of the biological systems studied. I will present examples of statistical models suitable for two complex biological cases. In one case, proteins often undergo extensive post-translational processing such that the final biologically active product is not readily identified from the initial form. I will show how generalized linear models can be used to solve this problem.

In another case, simultaneous study of expression of thousands of genes using microarray technology generates large quantities of data. I will present a semiparametric approach to profile gene expression patterns across time.