

Statistical Signal Processing for Gene Microarrays

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Abstract

Over the past decade there has been an explosion in the amount of genomic data available to biomedical researchers due to advances in biotechnology. For example, using gene microarray technology, it is now possible to probe a person's gene expression profile over the more than 30,000 genes of the draft human genome. Signals extracted from gene microarray experiments can be linked to genetic factors underlying disease development and aging in a population. This has greatly accelerated the pace of gene discovery. However, the massive scale and experimental variability of genomic data makes extraction and analysis of useful genetic information very challenging. We will give an overview of some of these challenges and discuss some of our work in developing signal processing tools to meet them.

Full paper was not available at the time of printing.