Bayesian Latent Class Modelling of Microarray Data

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Abstract

Evolution of microarrys has opened up opportunities to study gene and gene expression in a way never imagined before. Most microarray experiments produces a wide range of changes in the expression level of the genes involved, and determining which of these changes are physiologically relevant in the system is an essential part of the analysis. Microarray data analysis is typically performed in several distinct steps of operations: (1) normalization, (2) classification, and (3) functional analysis of the identified genes. Although the outcome of any of these steps crucially depends on how the previous steps were carried out, this point has been in general not been considered in the literature. In this paper an integrated method using gene expression and ontology data is proposed, based on Bayesian latent class modelling which combines all these three steps into one. We illustrate our approach by analysing a real life data set, and show that the expression changes of genes could be interpreted in a way that agrees with the biological functionalities involved.