Bayesian Integrated Functional Analysis of Microarray Data

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Abstract

The statistical analysis of microarray data usually proceeds in a sequential manner, with the output of the previous step always serving as the input of the next one. However, the methods currently used in such analyses do not properly account for the fact that the intermediate results may not always be correct, then leading to cumulating error in the inferences drawn based on such steps. Here we show that, by an application of hierarchical Bayesian methodology, this sequential procedure can be replaced by a single joint analysis, while systematically accounting for the uncertainties in this process. Moreover, we can also integrate relevant functional information available from data bases into such an analysis, thereby increasing the reliability of the biological conclusions that are drawn. We illustrate these points by analysing real data and by showing that the genes can be divided into categories of interest, with the defining characteristic depending on the biological question that is considered. We contend that the proposed method has advantages at two levels. First, there are gains in the statistical and biological results from the analysis of this particular data set. Secondly, it opens up new possibilities in analysing microarray data in general.