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data, some genes in a gene expression study are differentially expressed but their biological significance is not clear, and therefore these genes may be considered non-significant. In such cases, setting the threshold at 0.05 would result in falsely considering these genes as significant. On the other hand, setting the threshold at 0.05 could result in failing to consider some significant genes as significant. To address this problem, EMD may compute a q-value for each gene. As before, we denote by \$D\$ the set of genes that are differentially expressed, and by \$S\$ the set of genes that are not differentially expressed. In this paper, we set the threshold on the q-value to 0.05. We call the threshold-based method denoted by "T". In the context of identifying differentially expressed genes, the false discovery rate may be of interest as it represents the expected proportion of type I errors in the set of identified differentially expressed genes. A q-value is an analogue of a p-value for testing the difference between groups, and it is defined as the expected proportion of false discoveries among all the identified differentially expressed genes. The q-value is in between 0 and 1. 82157476af

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