R shiny based interface for multiple testing

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Abstract

When it comes to the discovery of biomarker gene, we need to find some genes which show statistically significant difference between two groups, i.e., disease v.s. normal group. In high-throughput data, since there are numerous genes (variables) which are obtained from each subject, biomarker discovery is categorized as multiple testing problem. Many multiple testing methods, which control false discovery rate (FDR) have been developed.

As a seminal work, Benjamini and Hochberg (BH) develop a method that use ordered p-values. They also show that the proposed method control FDR at the aimed level. Unlike BH, Efron and his colleagues formulate the multiple testing problem into the mixture framework. One dimensional test statistic is used in the two component mixture model. Ploner and his colleagues propose a new method which use two-dimensional test statistic. From another angle, Kim and his colleagues suggest another two-dimensional test statistic. Main difference is that the method test for each one-dimensional statistic separately and then combine both of them by using Bonferroni idea. Recently, Ramos and his colleagues develop a method, which is especially working for spiky null case.

We develop R shiny based interface, which include all multiple testing methods mentioned above.

Keywords

Mutiple testing, FDR(False Discovery Rate), R shiny

References:

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