Development of multiple tests interface using R shiny

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Abstract

In the field of genetics, sometimes we want to know the difference between two groups. When extracting and comparing genes to know the difference between these two groups, there may be many genes. Numerous hypotheses arise about this, and we have to reject the hypotheses corresponding to the different genes in response.

A representative method for this is the Bonferroni method, which divides the overall error rate of the experiment by the number of hypotheses to control the error rate for each comparison. However, because Bonferroni's method is too conservative to make a judgment, the number of rejected hypotheses may decrease, which may reduce the power of the experiment. To overcome these shortcomings, a method of controlling the FDR (False Discovery Rate) has emerged.

Methods for controlling FDR are performed under different constraints and produce different results, but there are times when it is desired to compare the results of different methods at the same time. This process is complex and can take a long time. To overcome this limitation, the statistical program R is used to compare and visualize the results of various methods through an easy manipulation method.

Keywords

Mutiple testing, FDR(False Discovery Rate), Interpace

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