

POSTER PRESENTATION

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Statistical analysis of multiple significance test methods for differential proteomics

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Background

In current proteomics research, a big challenge is to differentiate the correlative proteins for a given biological function from all existing proteins, and if it does, how strong is the relationship between the proteins and function. Statistical significance testing can be used to address this question. However, every traditional statistical test method may suffer from the inability to identify important differentially expressed proteins if the biological samples do not completely meet the assumptions of each test method [1]. To detect the regulated proteins for differential proteomics, we analyze multiple significance test methods and discover some significance proteins.

Results

We use the four statistical methods, i.e., Kolmogorov-Smirnov test (KS-test), Baumgartner-Weib-Schindler test (BWS-test), T-test, Brunner-Munzel test (BM-test) to measure the difference of the expression level of individual protein under two experimental conditions, respectively. The results had been successfully used for the discovery of protein biomarkers in breast cancer.

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