

Improving on t-tests or F-tests for a large number of hypothesis with application to Microarray data analysis

by

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Abstract

In the modern day application of Statistics, we often face the problem of testing a large number of hypotheses based on small sample sizes for each test. One primary example is Microarray experiments. In these experiments, the number of genes simultaneously studied could easily be as big as ten thousands and the number of observations for each hypothesis testing is however small typically around 6. This is a large p small n problem. Tests based on separate observations such as traditional t-tests or F- tests have poor power and there is a great need to search for alternative more powerful tests by using all the combined observations.

Recently the research area of improving upon t-tests or F-tests has become very active. A popular example is SAM proposed by Storey and Tibshirani (2003). The newly proposed test by Cui,Hwang, Qiu, Blades, Churchill (Biostatistics 2005), called F_s test, works very well in power. So do the tests proposed by Wright and Simon (Bioinformatics 2003) and Smyth (SAGMB 2004). When F_s is applied to control FDR, it is also more powerful than the corresponding procedure based on the usual F-test. The recent procedure Edge proposed by Storey (2007) seems promising.

We focus on finding a theory that explains why F_s does well. This procedure and virtually all procedures in the literature however only modify or shrink the variances. Should we shrink the means too? An alternative test called F_{ss} tests is developed. Come and find out whether that improves upon the power further. The discussion focuses on theory and is understandable to statisticians even without knowledge in Microarray experiments.