metaMA : an R package implementing meta-analysis approaches for microarrays

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Microarrays have been widely used to detect differentially expressed genes, for example between normal and tumoral samples. Due to the high cost of these experiments, results often rely on small sample size designs. Since more and more microarray data are available in the public domain, meta-analysis, which consists in combining summary statistics from different studies, is of great interest in this field. Thus, meta-analysis offers the possibility to considerably increase the statistical power and gives more accurate results. The package metaMA implements moderated effect size combinations, as proposed by Marot et al.(2009) as well as inverse normal p-value combinations, with p-values calculated from moderated t-tests.

We compared all these meta-analysis methods in an extensive simulation for various amounts of inter-study variability. We found that

1. moderated effect size combination improved existing gene-by-gene effect size approaches

2. effect size combination is more conservative than the p-value combination method, i.e. it stays much below the nomimal FDR. This is also reflected in the fact that the effect size combination eliminates more false positives than the p-value combination among the genes which are significant in at least one individual study but not in the meta-analysis.

3. p-value combination outperformed the other classical meta-analysis methods in terms of sensitivity and gene ranking (larger areas under the ROC curves).

References

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