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Analysis and interpretation of variance in gene expression data

In gene expression profiling with microarrays technical variance refers to the commonly considerable measurement errors. Reasons seem to be manifold. The effect of cross-hybridizations, which means unspecic bindings of RNA-fragments to the probes on the array, is controversially discussed. Some researchers consider this effect the most important source of error while others consider it negligible.

Furthermore variance based on real existing biological differences is denoted biological variance. The analysis of gene expression experiments with methods identifying differences in variance yield possible marker transcripts an analysis based on means does not reveal.

The project aims to get a better understanding of sources of variance in Gene Expression Data.

Publications

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