

Converging to consensus: the end and the beginning of differential gene expression microarray analysis.

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Each step in the analysis and interpretation of microarray data has an impact on both the biological interpretation of the data as well as on the differentially expressed gene set. There is a common perception that sources of variability in microarrays affect the content of a gene set but can be absorbed by the biological interpretation of these results. While the relative impact of sources of variability may be different on the gene set and on the biological interpretation, the value of both is affected. An incomplete biological interpretation and an incorrect gene set are both deleterious to the application of these data in the clinic. We will examine key steps in which we may have an immediate impact to reduce these sources of variability through consensus and standards.