

Methods in Microarray Normalization

Scientists can use molecular profiling microarrays to compare healthy cells with their diseased counterparts and develop gene-specific treatments. Finding the best way to interpret original profiling data into accurate trends, however, continues to drive the development of normalization algorithms and software tools.

Methods in Microarray Normalization compiles the most useful and novel techniques for the first time into a single, organized source. Experts in the field provide a diverse view of the mathematical processes that are important in normalizing data and avoiding inherent systematic biases. They also review useful software, including discussions on key algorithms, comparative data, and download locations.

The book discusses the use of early normalization techniques for new profiling methods and includes strategies for assessing the utility of various normalization algorithms. It contains the latest microarray innovations from companies such as Agilent, Affymetrix, and GeneGo as well as new normalization methods for protein and CGH arrays, many of which are applicable for antibody, microRNA, methylation, and siRNA arrays.

Features

- Explains how pathway analysis, feature selection, and classification results can be used for new profiling techniques
- Reviews the latest advances in peptide, glyco, antibody, expression, and SNP microarrays
- Examines the latest methods for pooling genomic samples to identify disease-specific SNPs
- Illustrates the impact of data normalization on clinical outcomes based on the applications of commercial products such as MammaPrint and OncoTypeDX
- Lists open-source molecular profiling normalization algorithms available and where to access them

Methods in Microarray Normalization provides scientists with a complete resource on the most effective tools available for maximizing microarray data in biochemical research.



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