

# Pre-processing and Clustering Algorithms for Microarray Data in Cancer Research

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## **Abstract**

*The development of microarray technologies makes it possible to understand the molecular basis of human diseases, like cancer. Microarray experiments may be used to simultaneously assess gene expression values for thousands of genes. Along with bioinformatics and data mining techniques, they are important in finding relationships between gene expression values and clinical outcomes. One of these techniques is represented by the clustering analysis. This paper describes a typical workflow for microarray data and different hierarchical clustering algorithms for DNA microarray data, underlining their advantages and disadvantages.*