

## Clustering of microarray data using K-means

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The microarray is a technique used by biologists to perform many genome experiments which produces very large datasets; analysis of those datasets is a challenge for scientists as the number of genome datasets increasing rapidly every year. K-means clustering is an unsupervised data mining technique used widely by bioinformaticians to analyze Microarray data. The clustering of these microarray data can greatly boost the research works of the biologist. However, K-means can take between a few seconds to several days to process Microarray data depending on the size of these datasets which puts limit on the complexity of biological problems and results in incomplete solution to the problem. In order to overcome such problems, this project proposes a resource sharing mechanism of client-server model.

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