

BICLUSTERING ALGORITHMS: ANALYSING STATISTICAL SYMMETRY

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The purpose is to study inspect the complexities and implementations of biclustering algorithms with intent of analyzing its structural design along with a real-world application and analyze their performance on microarrays of gene expression data for a gene condition. The paper would be majorly focused around areas of biclustering in genetic studies and bioinformatics along the lines of computation required in analysis of gene expression data. It attempts to tackle the limitation of results from the application of classical clustering methods on genes by working on mathematical or asymptotic optimization of the various algorithms that have been proposed.