A biclustering algorithm based on a Bicluster Enumeration Tree: application to DNA microarray data

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In a number of domains, like in DNA microarray data analysis, we need to cluster simultaneously rows (genes) and columns (conditions) of a data matrix to identify groups of rows coherent with groups of columns. This kind of clustering is called biclustering. Biclustering algorithms are extensively used in DNA microarray data analysis. More effective biclustering algorithms are highly desirable and needed.

Liens
[1] http://okina.univ-angers.fr/publications?f[author]=7471
[2] http://okina.univ-angers.fr/publications?f[author]=7472
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[4] http://okina.univ-angers.fr/publications/ua4245
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