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Agglomerative Bayesian Biclustering

In many biological domains such as metabolomics, proteomics, and genetics a data matrix with subjects in rows and variables in columns is produced. For such data simultaneous clustering of subjects and variables, called biclustering, is of interest. For instance, in gene expression data, clustering subjects reflects which subjects have similar genetic make up, and clustering genes reflects which genes might function similarly on the measured subjects. We suggest a fully-automatic biclustering algorithm using a Bayesian model which does not require knowledge about the number of partitions. Furthermore, agglomerative method produces a graphical representation of biclusters through dendrogram.