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Statistical View of Popular Biclustering Algorithms

Recently, several biclustering algorithms have been proposed to reveal submatrices of the data matrix whose rows exhibit similar behaviour across a set of columns, and conversely. These have important applications to gene expression analysis, for example, to find genes that are co-regulated across a subset of conditions. Few of these algorithms are based on explicit models. This work proposes some underlying statistical models associated with some of the most popular biclustering algorithms. It shows that these algorithms can be justified within a Bayesian framework and can be derived from Bayesian computational techniques.