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On the Application of a Bayesian Infinite Mixture Modelling

In microarray analyses, genes are expressed to varying levels across different cellular conditions. It is believed that the identification of gene with similar expression patterns across conditions demonstrating variable temporal, developmental, topographical, histological and physiological patterns will give insight to their biological functions. The aim is to create clusters which hold genes whose expression levels are inter-related at various conditions. We further develop a recent algorithm based on the Bayesian infinite mixture model; in particular we allow for non-isotropic covariance matrices in order to better reflect reality. Our algorithm is discussed and illustrated on simulated and real data.