

Nonparametric Bayesian mixture models for identifying clusters from longitudinal and cross-sectional data

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The identification of sets of co-regulated genes that share a common function is a key question of modern genomics. Bayesian profile regression is a semi-supervised mixture modelling approach that makes use of a response to guide inference toward relevant clusterings. Previous applications of profile regression have considered univariate continuous, categorical, and count outcomes. In this work, we extend Bayesian profile regression to cases where the outcome is longitudinal (or multivariate continuous), using multivariate normal and Gaussian process regression response models. The model is applied on budding-yeast data to identify groups of genes co-regulated during the *Saccharomyces cerevisiae* cell cycle. We identify four distinct groups of genes associated with specific patterns of gene expression trajectories, along with the bound transcriptional factors, likely involved in their co-regulation process.

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