Bayesian Characterization Of Natural Variation In Gene Expression

Madhuchhanda Bhattacharjee¹ Mikko J. Sillanpää¹ Colin Pritchard² Elja Arjas¹

¹Rolf Nevanlinna Institute University of Helsinki Finland 2 Division of Human Biology Fred Hutchinson Cancer Research Centre USA $\,$

Abstract

For gene expression data we propose a hierarchical Bayesian method of analysis using latent variables, wherein we have combined normalization and classification in a single framework. The uncertainty associated with classification for each gene can also be estimated based on the posterior distributions of the latent variables applied. The proposed models are implemented using the MCMC algorithm