1046-92-1421   **Tatiana Valerievna Tatarinova*** (`ttatarin@lmu.edu`), Department of Mathematics, Loyola Marymount University, Los Angeles, CA 90045, and **Alan Schumitzky** (`schum@usc.edu`), Department of Mathematics, USC, Los Angeles, CA 90089. *Kullback-Leibler Markov Chain Monte Carlo – a new Algorithm for Finite Mixture Aanalysis and its Application to Gene Expression Data.*

A number of methods have been developed for clustering gene expression data. We would like to suggest a new Bayesian method for clustering of data-rich time-series observations. Experimental points of the time series observations are ordered and this fact sets them apart from other microarray measurements. In this paper we study Bayesian analysis of nonlinear hierarchical mixture models with a finite but unknown number of components. Our approach is based on Monte Carlo Markov Chain (MCMC) methods. One of the applications of our method is directed to the clustering problem in gene expression analysis. From a mathematical and statistical point of view, we discuss the following topics: Theoretical and practical convergence problems of the MCMC method; Determination of the number of components in the mixture; Computational problems associated with likelihood calculations. In the existing literature, these problems have mainly been addressed in the linear case. One of the main contributions of this paper is developing a method for the nonlinear case. Our approach is based on a combination of methods including Gibbs sampling, Random Permutation sampling, Birth-Death MCMC, and Kullback-Leibler distance. (Received September 15, 2008)