

Mixture-Regression Cluster Model applied to Longitudinal Microarray Experiments

Emma Holian, *emma.holian@ul.ie*

Department of Mathematics and Statistics, University of Limerick, Limerick, Ireland.

Keywords: Microarray; Longitudinal; Mixtures; Regression; Random effects.

AMS: 60J80

Abstract

The aim of this work is to explore various statistical techniques to identify genes which contribute to some change in phenotype level. For example, the response of fish kept under stressful conditions for various lengths of time. We aim to assess the level of *differential* expression of each gene in the tissue samples and also attempt to model the expression patterns of genes over time, not only to classify genes by similarities in expression patterns, but also to model these patterns as specified functions.

The proposed Mixture-Regression Cluster Model is developed to model *and* cluster the genes into groups according to their expressions measured over time. This model is similar to that of the multivariate normal mixture model in that clusters are identified by the EM algorithm but is adapted to incorporate the flexibility of regression curves to fit the trends. In this way, additional features such as covariates, random effects and correlation structures can be incorporated into the model while potentially offering a considerable saving on the number of parameters required to model the trends.

Acknowledgements: Special Thanks to colleagues working at the National Diagnostics Centre, and in the Mathematics Department of National University of Ireland, Galway, where the work was carried out.

References

- [1] Wit, E., and McClure, J. (2004). *Statistics for Microarrays: design, analysis and inference*. John Wiley & Sons.
- [2] Diggle, P.J., Heagerty, P., Liang, K., and Zeger, S.L. (2002). *Analysis of Longitudinal Data*. Oxford University Press.
- [3] McLachlan, G.J., and Peel, D. (2000). *Finite Mixture Models*. New York: John Wiley & Sons.