

*Comparison of Normalization Methods for cDNA Microarrays*

Liling L. Warren(1,2) and Ben Hui Liu(1,2)

(1) Bioinformatics Program, North Carolina State University, Raleigh, NC 27695, USA

(2) Bio-informatics Group Inc. Cary, NC, 27511, USA

Normalization is an intermediate step that has been routinely carried out after image analysis and before data analysis in gene expression microarray experiments. It is a necessary and important step to remove certain systematic variations that are introduced during different steps in a microarray experiment (Hedge et al., 2000; Yang et al., 2002).

Here in this paper, we will carry out similar gene based ANOVA tests as done by Prichard et al. to identify genes differentially expressed between mice. Before performing gene based ANOVA, different normalization procedures will be applied and we will examine how they influence the final analysis results. Based on different multiple testing criteria, there is strong evidence showing genes are actually differentially expressed between genetically identical mice. We thus perform power analysis to examine how various normalization methods affect the power to identify differentially expressed genes between mice. And finally, we will try to explain the discrepancies caused by different normalization methods and to discuss biological implications from this study.