

BAYESIAN ANALYSIS OF SKEW NORMAL MIXED MODELS IN GENE EXPRESSION DATA FROM A COMPLEX PEDIGREE

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- **ABSTRACT:** *Estimates of heritability for gene expression are scarce and commonly originated from family structures, in which the variability of responses among and within families is provided under a uniform covariance structure for related individuals. Gauss-Markov normal mixed models are the usual choice for such estimates, but in microarrays studies it is common to find asymmetry in residuals of the adjustment of data previously normalized. This, by itself, justifies the use of skew models. In this study it was analyzed a family based pedigree with gene expression measured by microarrays for all individuals. Thus, this work deals with the development and computational implementation of skew normal additive-dominance model for the analysis of microarrays by complex pedigrees, that allows skewness in all distributions of random effects. It was calculated the Bayes factors for the selection of the best models and HPD intervals for marginal estimates. Results are shown for two of the analyzed probes. For these probes, there was more evidence in favor of skew normal additive-dominance model.*
- **KEYWORDS:** *MCMC; mixed models; multivariate skew normal distribution; Bayesian inference.*

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