University of California, Irvine
Statistics Seminar

Fully Bayesian Analysis of
Hierarchical Count Regression Models

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(Bldg. #314 on campus map)

Heterosis, or hybrid vigor, is the enhancement of the phenotype of hybrid progeny relative to their inbred parents. To identify genes displaying a heterosis pattern in their expression, we construct a gene-specific overdispersed count regression model. Since there are ~40,000 genes and ~10 samples, we build a hierarchical model for the gene-specific parameters to provide a data-based borrowing of information across genes. To implement a fully Bayesian analysis, we construct a novel parallelized Markov chain Monte Carlo algorithm that efficiently utilizes the architecture of a graphical processing unit through embarrassingly parallel computations and parallel reductions. We demonstrate the utility of the method to identify gene expression heterosis through a variety of simulation studies and analyze an RNAseq maize dataset to identify genes with 6 different types of heterosis.

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