Sources of Variation in Microarray Experiments

Stanislav Zakharkin, Ph.D.
Postdoctoral Fellow
Department of Biostatistics, Section on Statistical Genetics
University of Alabama at Birmingham

Abstract:

Variability in gene expression as measured in microarray experiments arises from different sources including image analysis, biological and technical variability. We performed a microarray experiment using Affymetrix chips to determine relative contributions of various factors. The study included 8 samples from 21-day old Sprague Dawley CD female rats exposed to genistein (a soy isoflavone) from birth to 21 days. Each RNA sample was divided in half to allow separate labeling reactions, and one of the labeling reactions for each sample was further divided in half to produce two technical replicated. Thus, a total of 24 chips were used, which were randomized with respect to processing day and scanning order. A model accounted for biological variability, variability due to labeling, and a residual error. In addition, we used a shrinkage estimator of variance components that provides gene-specific variances but also uses information across all of the genes in dataset to improve estimation. The four different image processing methods, D-Chip, MAS 5.0, RMA, and GCRMA were compared. The results of analysis indicate that biological variability has the greatest contribution emphasizing the necessity of using biological replicates in microarray experiments.