Nonlinear measurement error models for high throughput genomic experiments

Z.Q. John Lu

National Institute of Standards and Technology

While there exist some nice models for the measurement process of scalar and small-scale analytical chemistry experiments, there is lack of understanding and tools for establishing the standards and performance of high throughput biological experiments, such as microarray measurements. An ongoing program at NIST on gene expression microarray experiments has demonstrated some potential approaches, including some performance metrics for scanner microarray measurement, and use of spike-in experiments in calibration and validation. I will describe a class of multiphase and nonlinear regression models used in these studies, and show how these general measurement models can accommodate for the wide exponential range of signal variation while accounting for the background error, multiplicative signal error, instrument saturation at high intensity, and how they can be adapted to model the highly parallel and multivariate nature of modern biochemical experiments.