Recent progress in biotechnology has been fueled by advances in biosensing platforms. High-throughput and high performance biosensors, in particular, have become essential research tools in genomics, and are a rapidly growing segment of the life sciences industry. Among the most prominent of such technologies are DNA microarrays and quantitative (real-time) polymerase chain reaction (QPCR) systems.

DNA microarrays are primarily used to measure gene expression levels, i.e., to quantify the process of DNA transcription. However, the probabilistic nature of the biochemical processes (e.g., hybridization) involved in the preparation and conducting of microarray experiments causes a high level of measurement uncertainties. In this talk, we describe the use of probabilistic techniques to model these uncertainties and, based on the model, employ optimal algorithms to detect and estimate the quantities of the targets, and to analytically find the fundamental limits of their performance. These techniques may considerably increase the signal-to-noise ratio, dynamic range, and resolution of DNA and protein microarrays as well as other affinity-based biosensors. We also describe a similar statistical signal processing approach to QPCR systems.

A major limitation of conventional microarrays is their reliance on a single measurement taken ostensibly after the hybridization reaches steady-state. To overcome this, we have developed a novel real-time microarray (RT-$\mu$Array) platform, a fluorescent-based biosensor assay capable of quantifying the kinetics of the hybridization process. By processing the much larger amount of acquired data, the real-time microarray systems achieve higher signal-to-noise ratio, smaller estimation error, broader detection dynamic range and much more reliable performance in the face of systematic errors such as array-printing/synthesis variations as well as washing/scanning imperfections. As a result, RT-MU Array systems suggest many new applications for biological discovery and open up many signal processing possibilities. We briefly touch upon a very promising approach for multiplex QPCR in a single well and its various