

## Speakers

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Dr. Bittner received his B.A. from the College of the Holy Cross, and his Ph.D. from Princeton University in Biochemistry. He is currently the Head of the Teleonomics Unit within the Cancer Genetics Branch of the National Human Genome Research Institute. Dr. Bittner has been involved in a variety of genetic and cytogenetic strategies to study the range of complex changes characterizing the development and progression of cancer, and other complex disorders. He has particularly concentrated his recent efforts on developing hybridization-based analytical tools which will allow profiling of structure/expression changes at multiple loci in a single experiment, including cDNA microarrays. This technology requires a broad range of hardware, analytical software, statistical methodology, biological resources and biochemical methodologies which have had to be both developed and routinized in order to make this technology readily applicable to the large number of questions for which it is likely useful.

### Evaluating the analytical foundation of gene expression profiling with cDNA microarrays

Microarray-based analysis of gene expression requires the assembly of a complex system of biological reagents, hardware, software and laboratory and analytic procedures. A variety of reported methodologies and commercial products offer an often-confusing plethora of choices to groups contemplating commencing large-scale analysis of gene expression. Regardless of the methodology or technology chosen, there are, in fact, central necessities for successful gene expression analysis. This talk will survey core requirements for producing microarrays, using them to determine comparative levels of gene expression between samples and carrying out comparisons of expression levels across multiple samples. Emphasis will be focused on comparison of quantitative values obtained from microarray data and reproducibility of microarray results.