

## *Topics in Gene Microarray Analysis*

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### *Abstract:*

*The first part of this seminar will cover a hierarchical Bayes mixture model of cDNA-spotted gene expression microarrays. Analysis of the comparative expression data is approached as a problem of estimation of a sparse vector. There is an interesting connection between this Bayesian approach and false discovery rate (FDR) thresholding.*

*The second part will cover non-parametric normalization of high-density genotyping microarray data. Following a close analysis of fluorescent intensities from a set of 64 Affymetrix Mapping 10K arrays, a non-parametric slide-to-slide normalization technique is proposed. There is evidence that normalization improves discrimination power in genotype calling.*