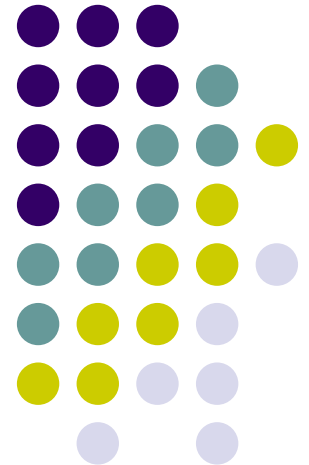


Statistical Methods for Bioinformatics and Computational Biology

Yinglei Lai, Ph.D.

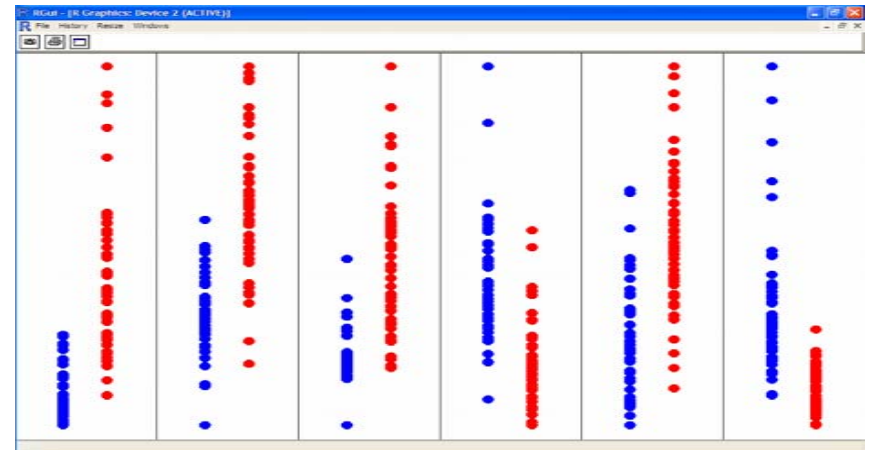
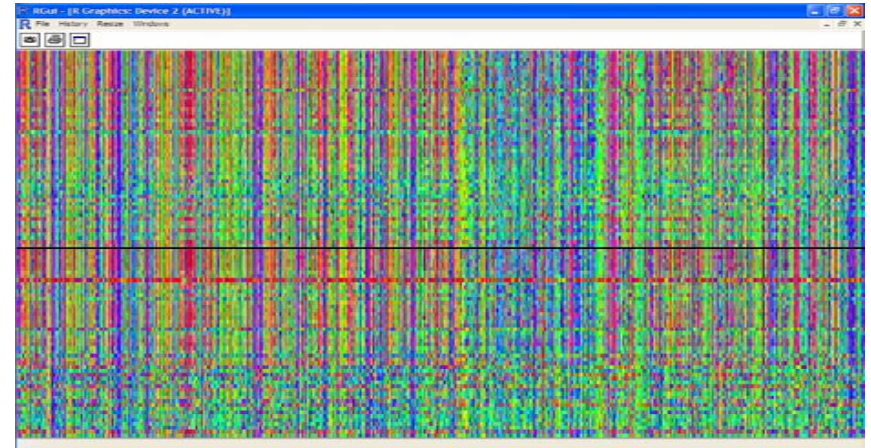
**Department of Statistics and Biostatistics Center
The George Washington University**



Statistical Analysis of Microarray Data in Disease Studies



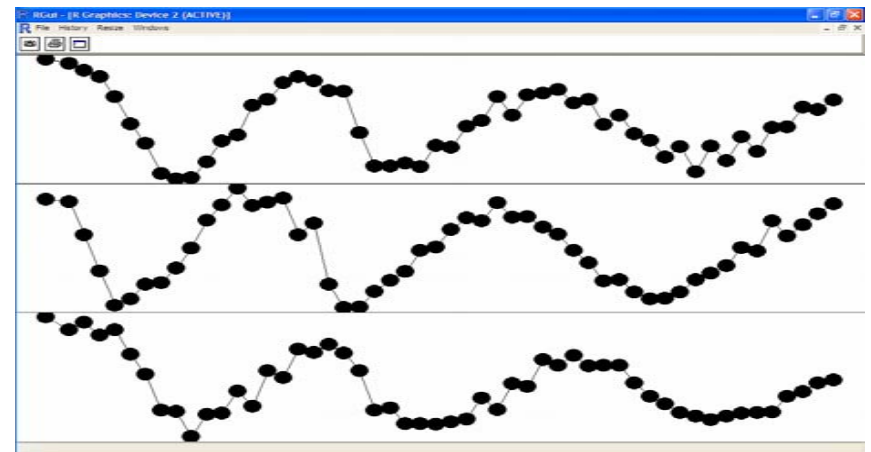
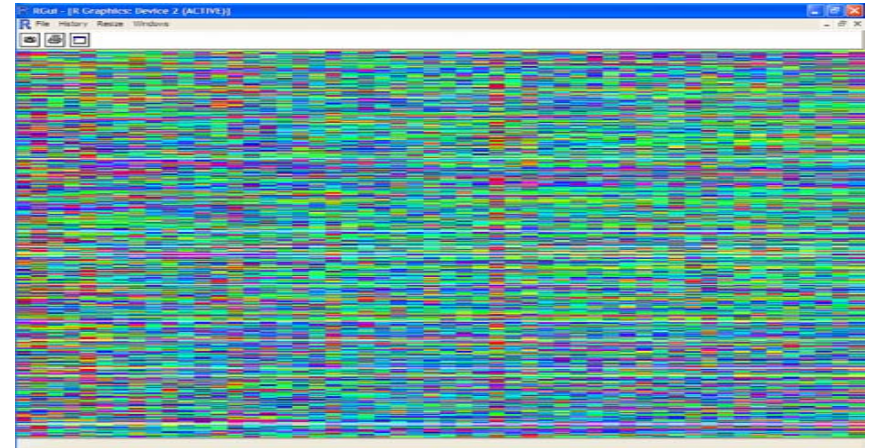
- A large number of genes
1000 ~ 10000
- A small number of samples
100 ~ 100
- Noisy data
- Identification of differential expressions
- Identification of differential co-expressions
- Control of false positives
- Feature selection and classification
- Clustering and class discovery



Statistical Analysis of Microarray Data in Cell Cycle Studies



- A large number of genes
1000 ~ 10000
- A small number of time points
10 ~ 50
- Noisy data
- Identification of cell cycle regulated genes
- Integration of multiple data sets
- Integration of other types of data





Other Research Topics

- **Proteomic Data Analysis**
- **Methodology in Biostatistics**
- **Statistical Genetics**

- *Partially Supported by NIH Grants*

Thank you for your participation!