# Integrative Analysis of multiple largescale molecular biological data



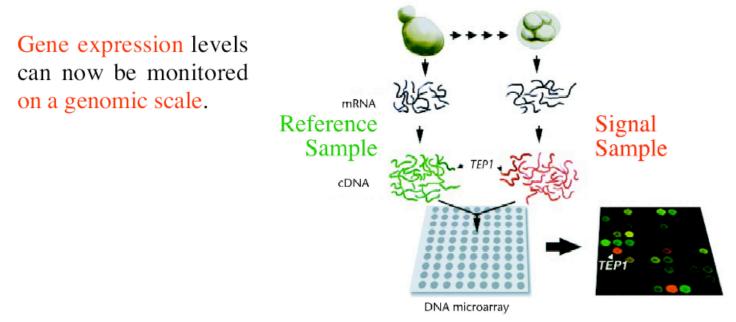
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### **New High Throughput Technologies**

Sequencing of the human genome, and the genomes of other model organisms, such as yeast, is completed or well underway.

DNA microarray hybridization technology allows probing fluorescently tagged cDNA copies of mRNA from a single sample with thousands of DNA targets or synthetic oligonucleotides simultaneously.

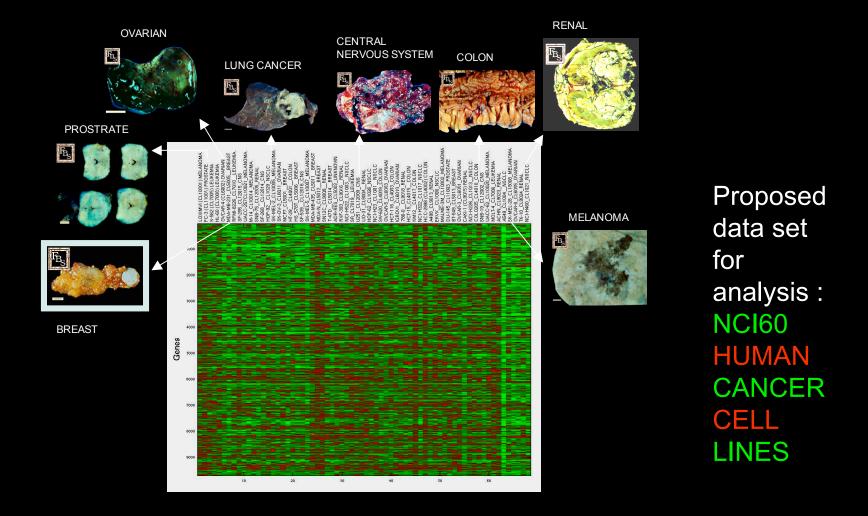


Brown & Botstein, *Nature Genetics* <u>21</u>, 33 (1999); Lipshutz, Fodor, Gingeras & Lockhart, *Nature Genetics* <u>21</u>, 20 (1999).

Slide courtesy: Dr.Orly Alter, Genomic Signal Processing Lab, UT Austin

Motivation: The NCI60 Human cancer cell lines are extensively used as experimental models.

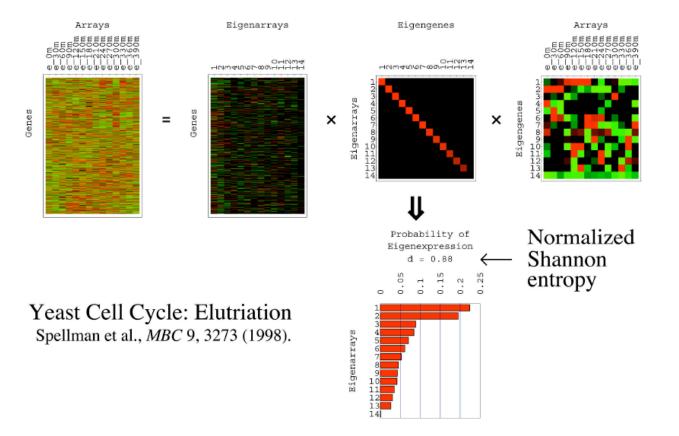
Goal: Perceive relationships between three datasets containing three different types of attributes of the NCI60 – genome-scale expression, sensitivities to more than 70,000 chemical compounds and chemotherapeutics, and proteomic profiles.



#### KEY PAPER 1 : [Alter et al, 2000]

#### **Singular Value Decomposition (I)**

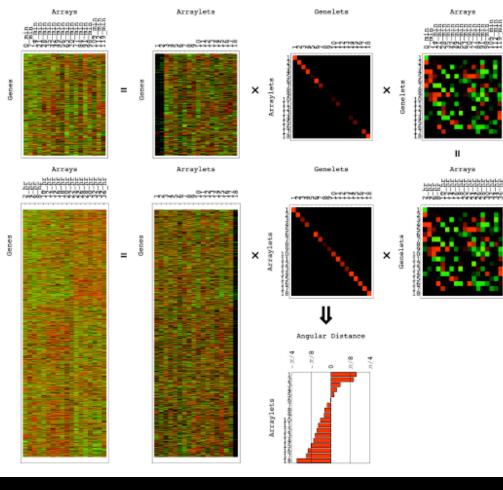
Linear transformation of gene expression data from genes  $\times$  arrays space to reduced diagonalized "eigengenes"  $\times$  "eigenarrays" space.



### Generalized SVD (I)

Linear transformation of two datasets from two genes × arrays spaces to two reduced diagonalized "genelets" × "arraylets" spaces.

#### Yeast Cell Cycle: Alpha Factor Spellman et al., *MBC* <u>9</u>, 3273 (1998).



## KEY PAPER 2 : [ Alter et al, 2003 ]

#### KEY PAPERS 3,4 & 5: Data Sets

Proteomic Profiling of the NCI-60 Cancer Cell Lines
Using New High-density Reverse-phase Lysate
Microarrays

[Nishizuka et al ,2003]

•A Gene Expression Database for the Molecular Pharmacology of Cancer

[Scherf et al, 2000]

•Systematic variation in gene expression patterns in human cancer cell lines

[Ross et al, 2000]