

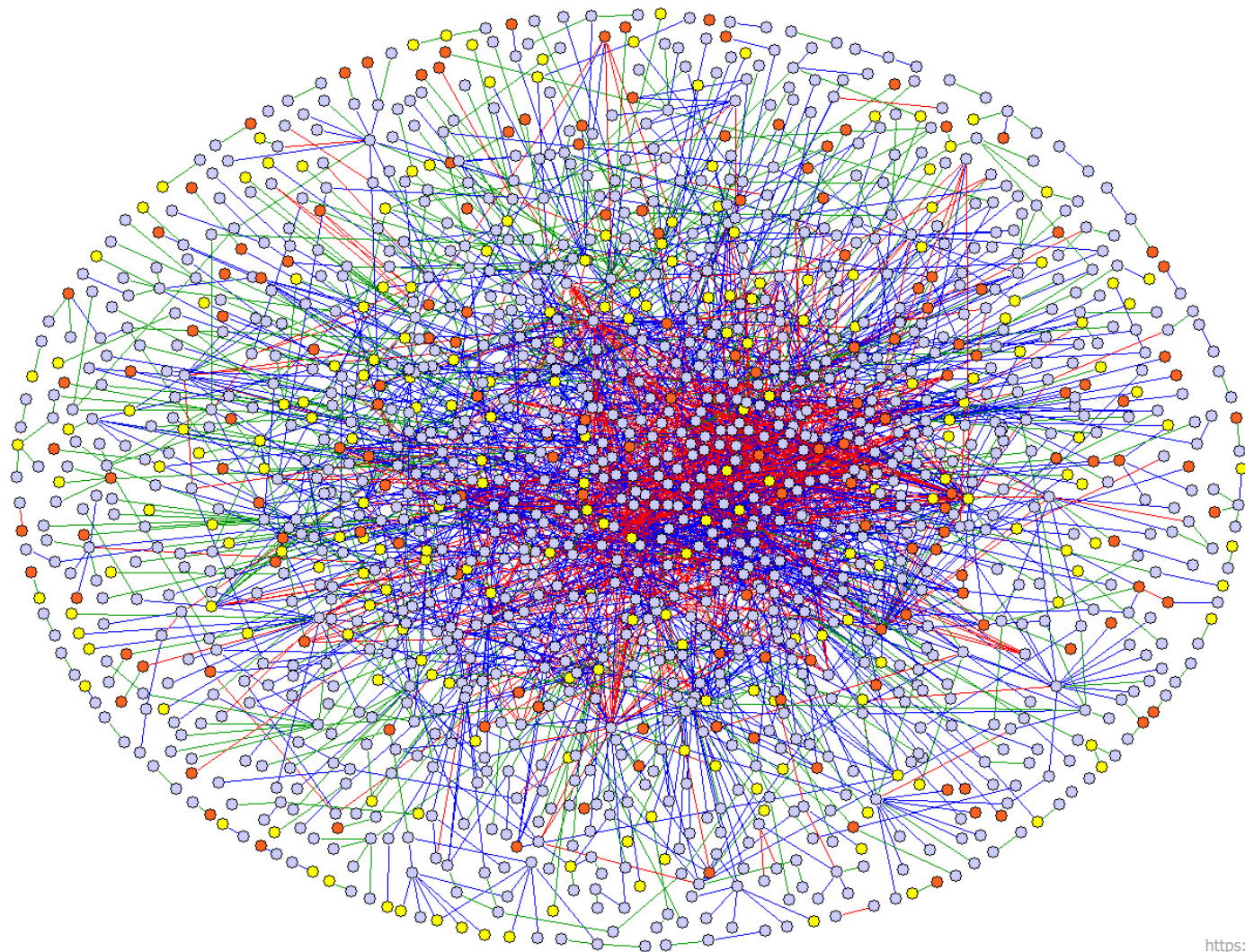


JOHNS HOPKINS

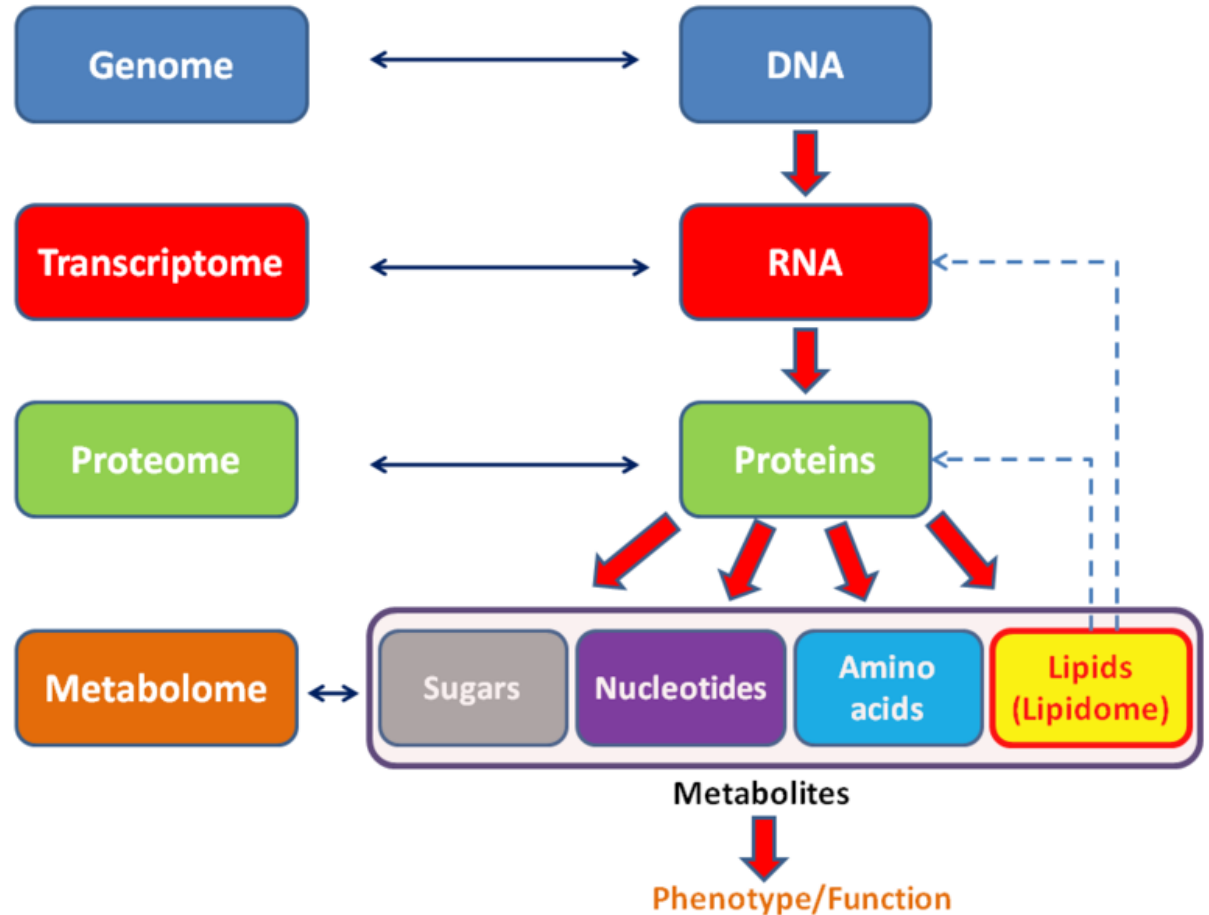
WHITING SCHOOL
of ENGINEERING

Cell and Tissue Engineering

High Throughput Data



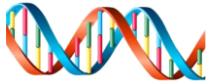

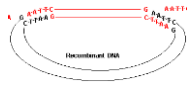
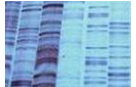

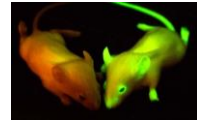

Phenomics



Genomics

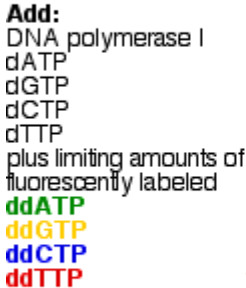
pharmacogenomics

Adapted from Tissue Engineering, Palsson & Bhatia
www.astrochem.org
www.millerandlevine.com
www.ocf.berkeley.edu
www.prism.gatech.edu
www.australiangeographic.com.au
www.glogster.com

Decade	Milestone	
1950s	Structure of DNA discovered	
1960s	Genetic code broken	
1970s	Recombinant DNA technology	
1980s	DNA sequencing technology	
1990s	Whole-genome sequencing DNA Chip technology Patient-specific treatment	
2000s	Biodiversity Designer organisms	
>2000s	Sequencing the human genome Genotype-phenotype relationship	

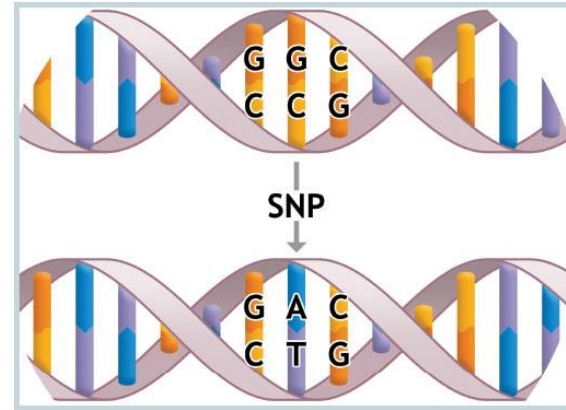
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Single-stranded DNA
to be sequenced



Using Genomics

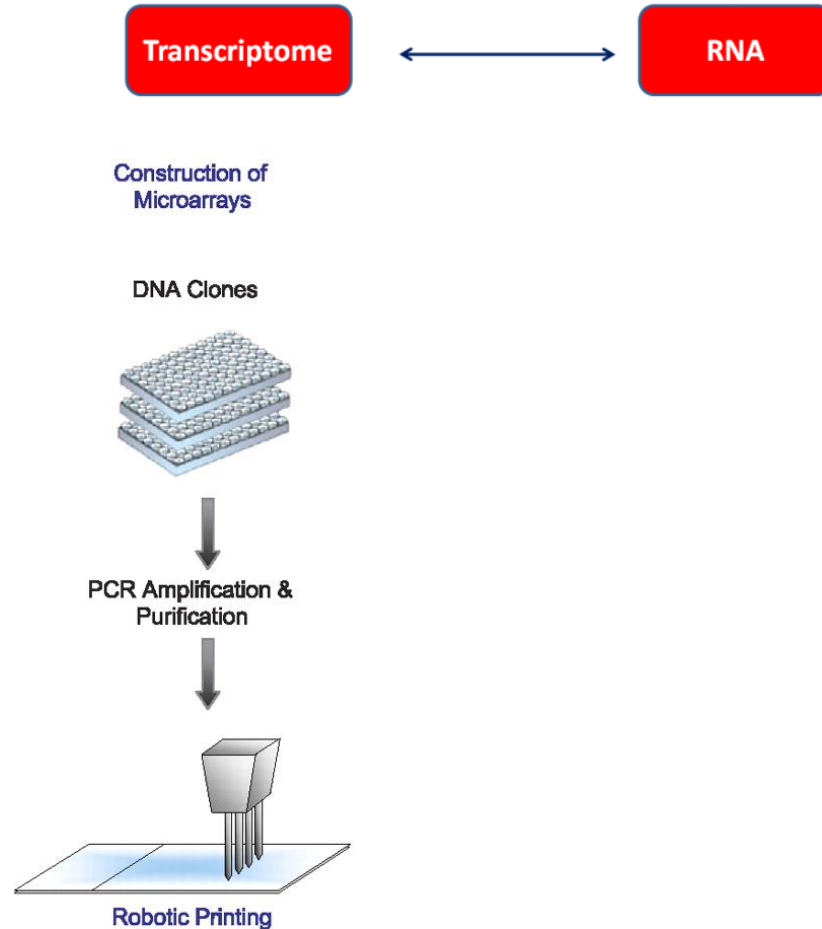
- Sequencing Similarity
- Sequence Variation
- SNPs – single nucleotide polymorphisms



Diabetes
Cancer
Alzheimer's
disease

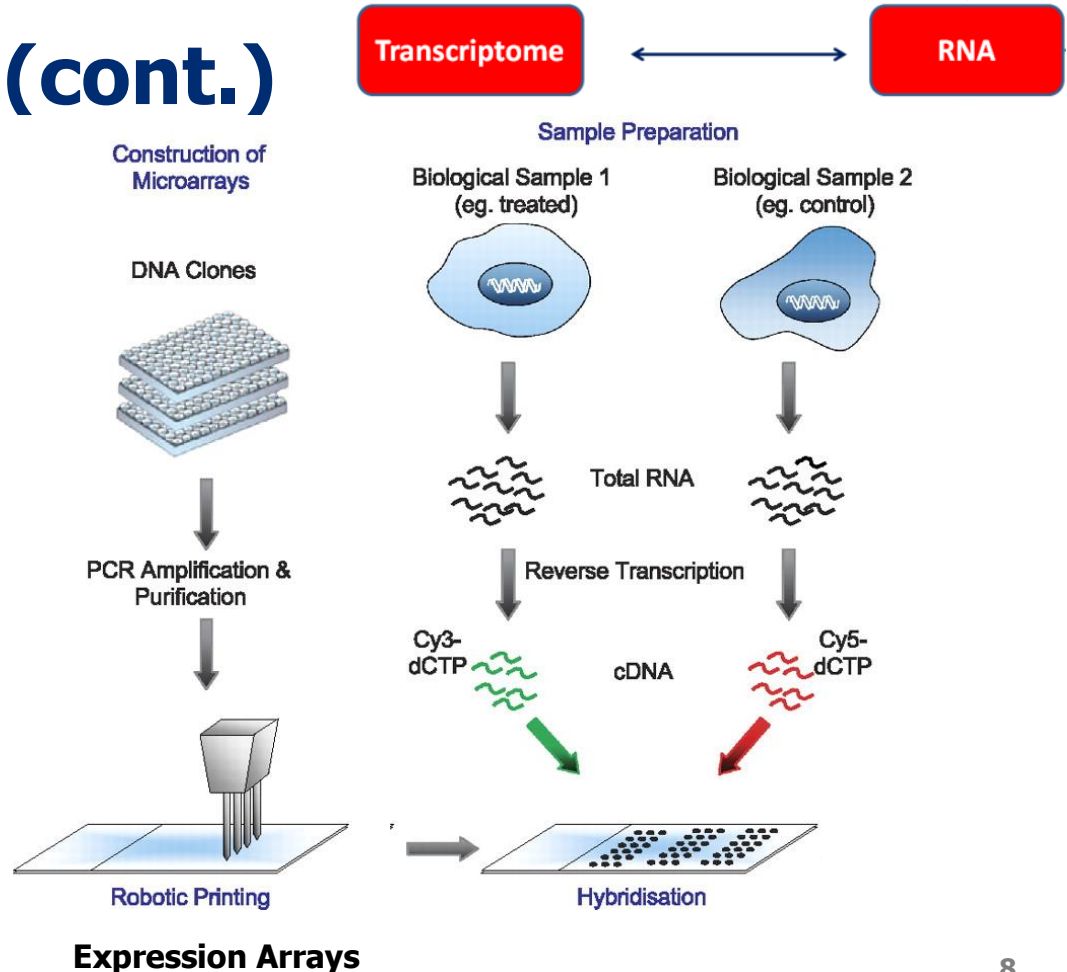
Transcriptomics

- Expression Arrays

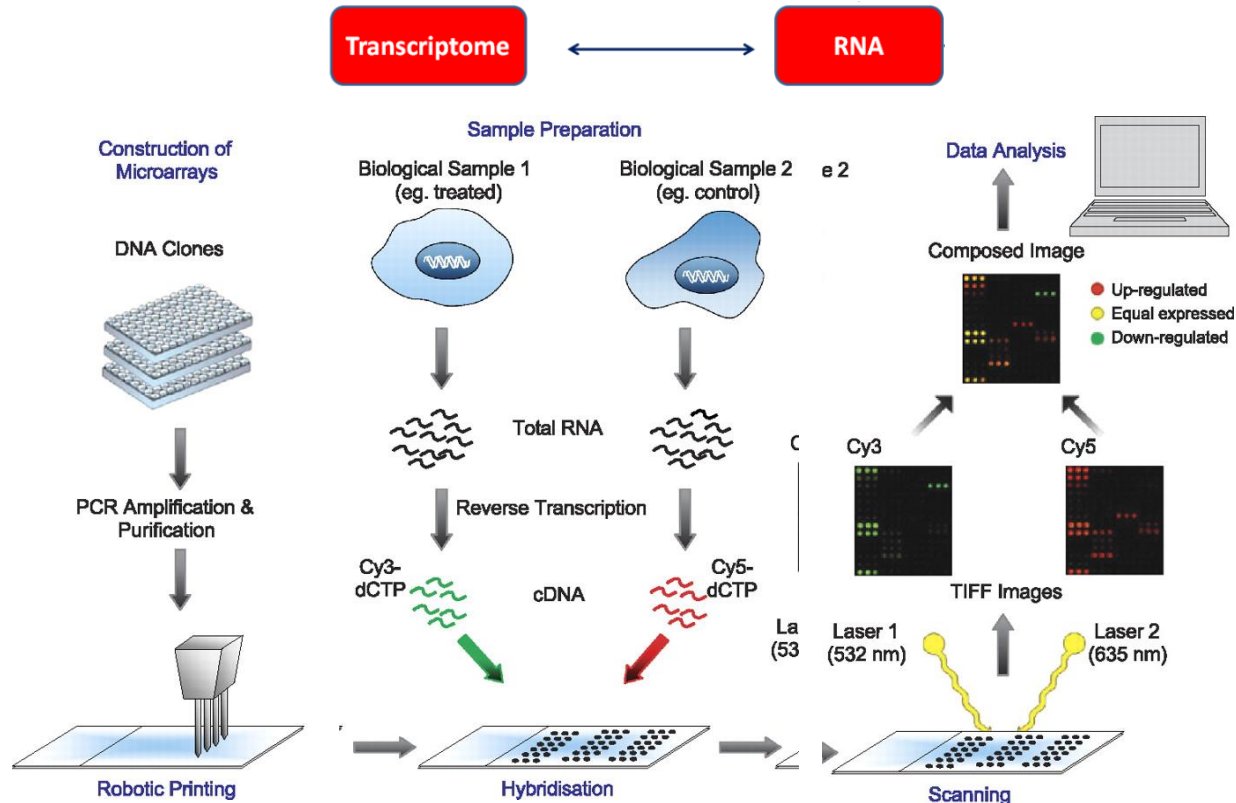


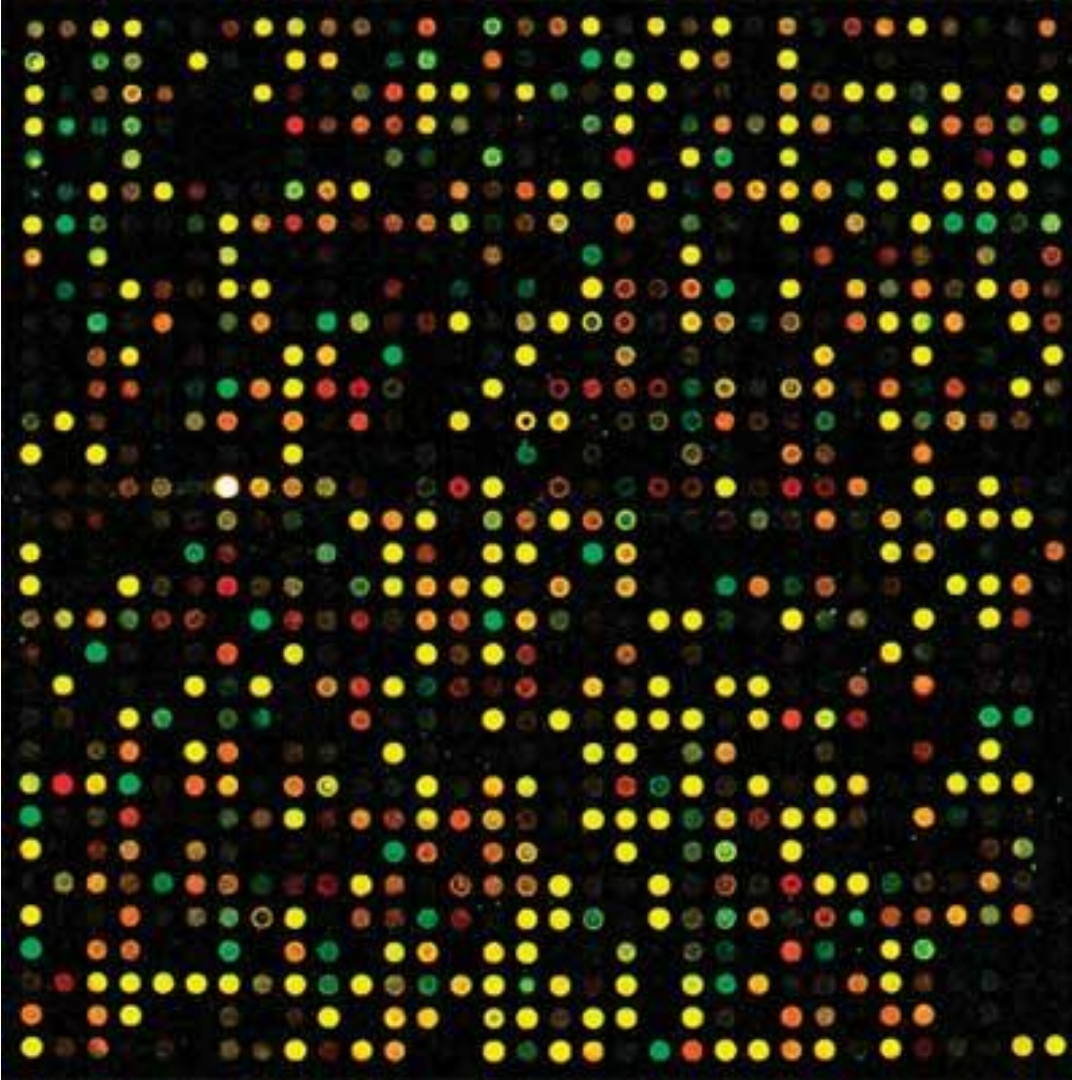
Transcriptomics (cont.)

- Expression Arrays



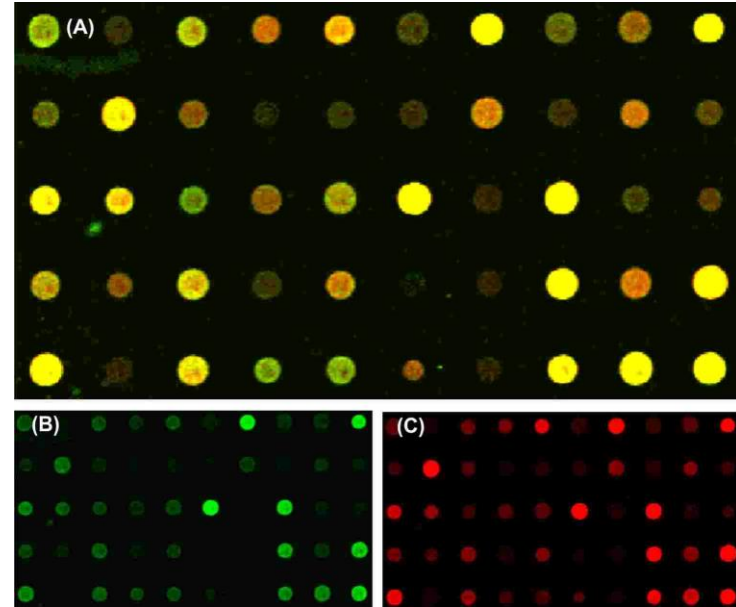
Transcriptomics (cont.)





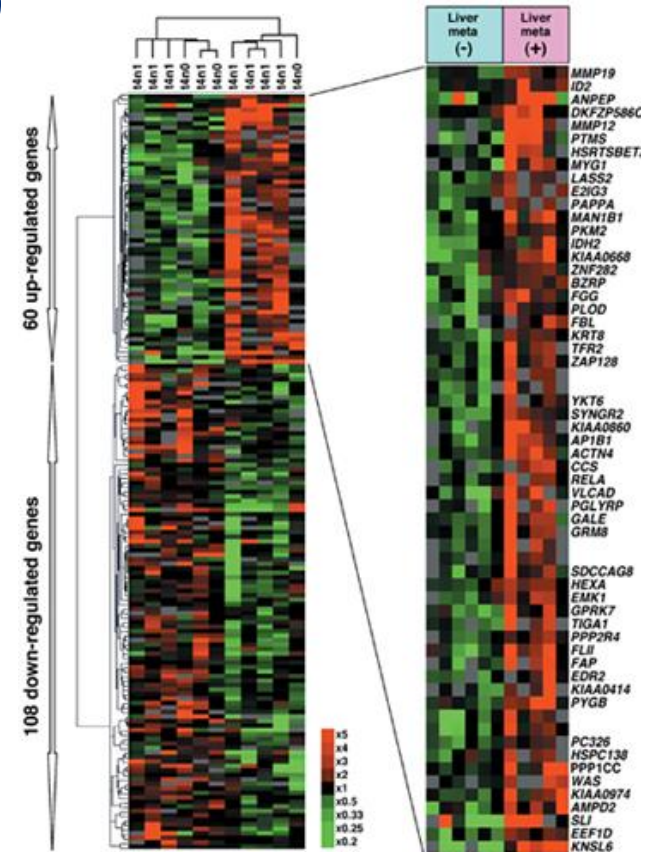
Microarray data analysis

1. Image Processing
2. Normalization
3. Identifying differentially expressed genes
4. Data analysis
5. Choosing a metric



Microarray data analysis (cont.)

1. Image Processing
2. Normalization
3. Identifying differentially expressed genes
4. Data analysis
5. Choosing a metric
 - “guilt by association”



Microarray analysis – gene expression profiling

- **How do we use it?**
 - Classification
 - disease state
 - disease subtype
 - appropriate treatment

oncotype DX[®]
Breast Cancer Assay

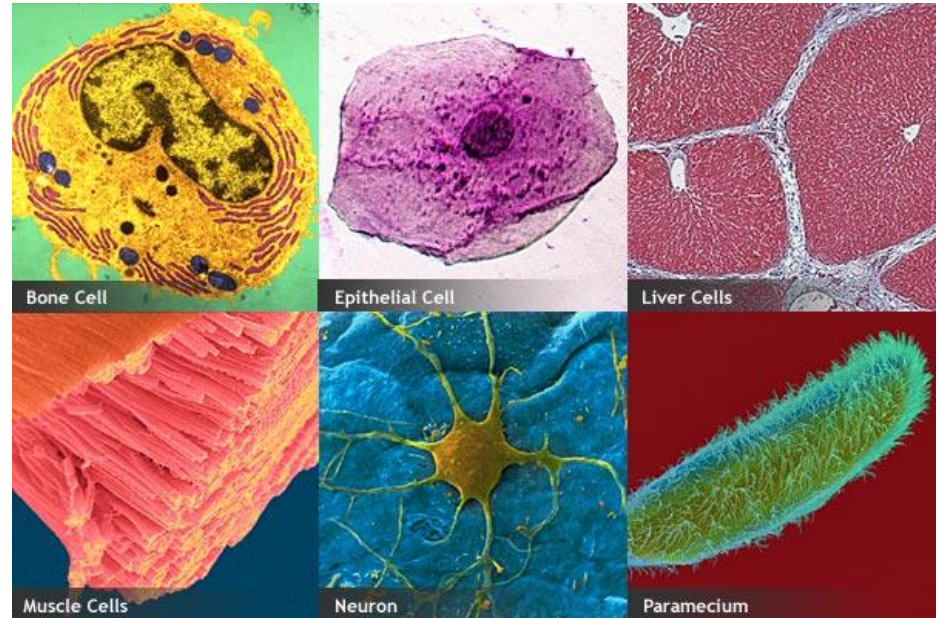


mammaprint™
decoding breast cancer.

Clariant Insight[®] Dx Mammostrat[®]

Microarray analysis – gene expression profiling (cont.)

- **How do we use it?**
 - Cell differentiation or tissue specification

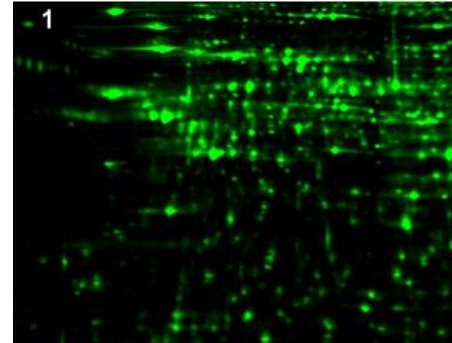


Proteomics

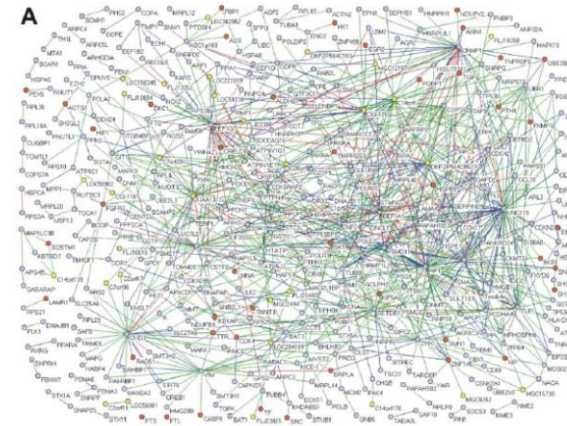
- Structure
- Expression
- Function



Expression Profiling

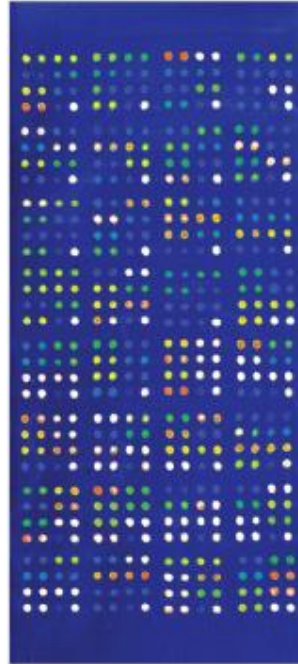


Interaction Maps

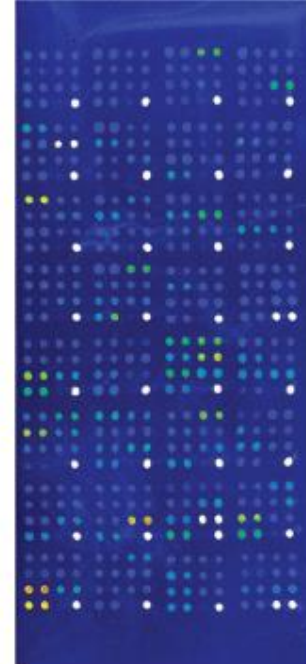


Proteomics (cont.)

- Expression Profiling



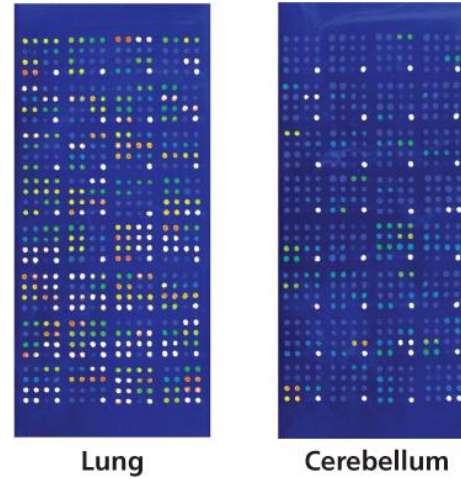
Lung



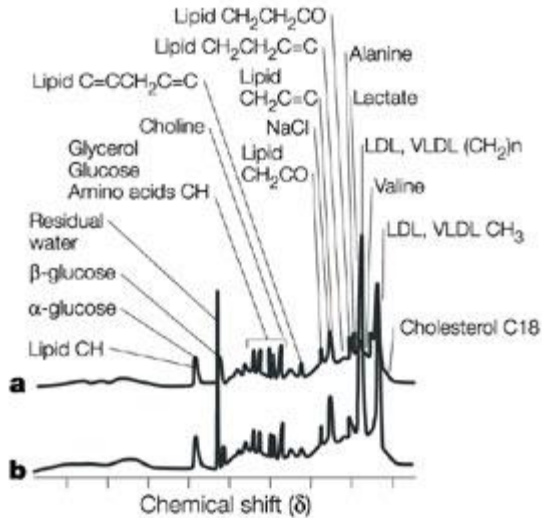
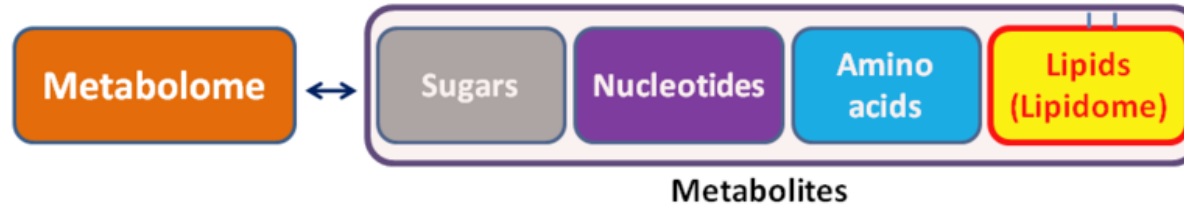
Cerebellum

Proteomics (cont.)

- Expression Profiling
- Interaction Maps



Metabolomics



a – NMR of a health patient

b – NMR of a patient with atherosclerosis

Metabolomics (cont.)

- Target analysis –
 - the effect of one gene on the concentration of one metabolite
- Metabolite profiling –
 - the effect of several genes or a pathway on a metabolite
- Fingerprinting –
 - qualitative measure of a number of metabolites
- Metabolomics –
 - quantitative measure of all metabolites

Metabolomics (cont.)

- Human Metabolome Project
 - Chemical data
 - Clinical data
 - Molecular biology/biochemistry data
 - >40,000 metabolites



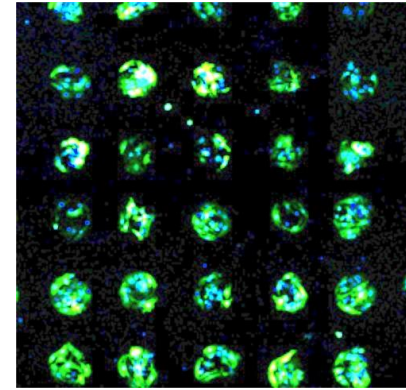
Phenomics

- The study of how genes interact with the environment giving rise to characteristics



Phenomics (cont.)

The study of how genes interact with the environment giving rise to characteristics



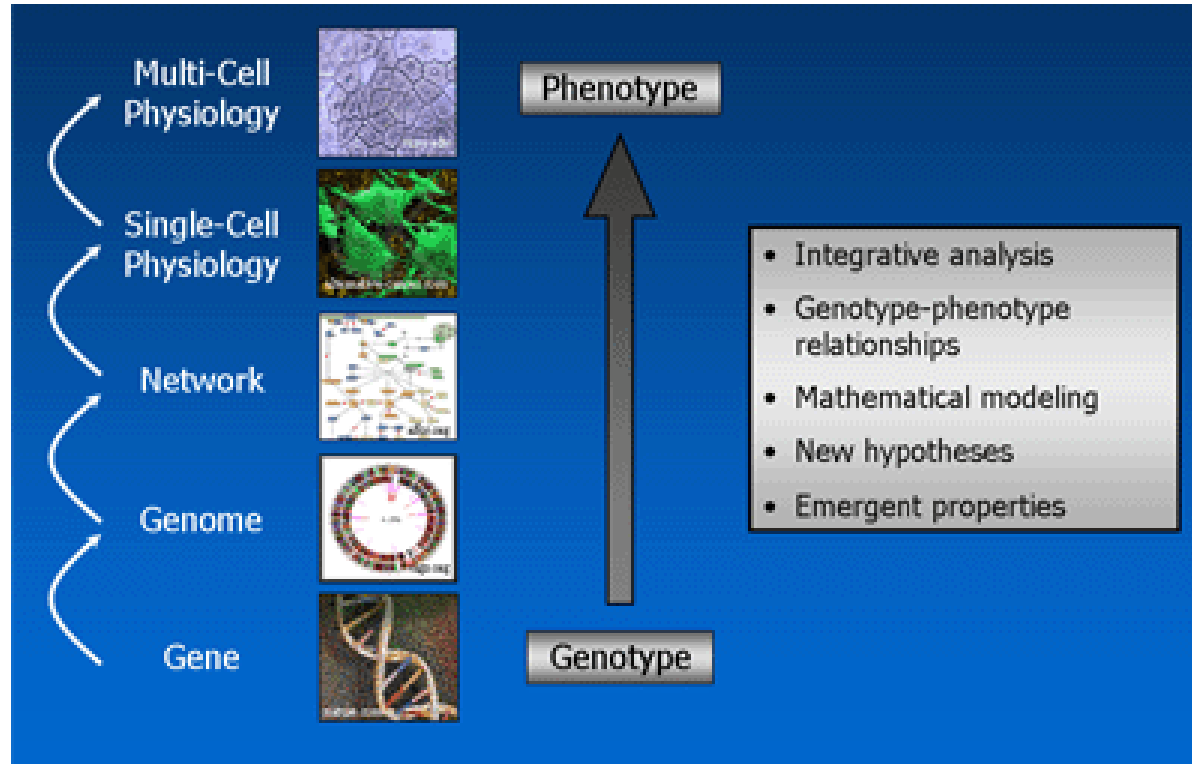
MEETING REPORT

Getting Ready for the Human Phenome Project: The 2012 Forum of the Human Variome Project

Human Mutation



Systems biology





JOHNS HOPKINS

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