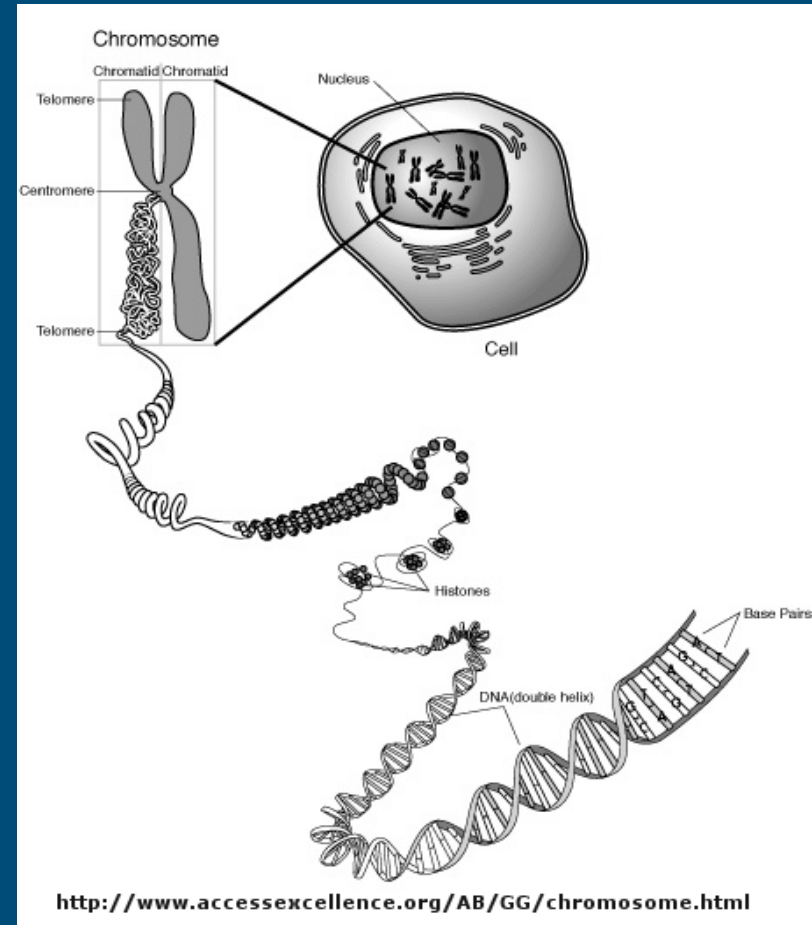
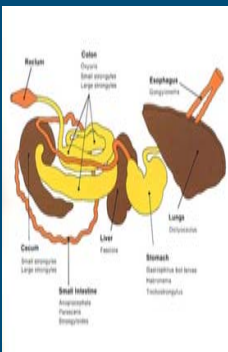
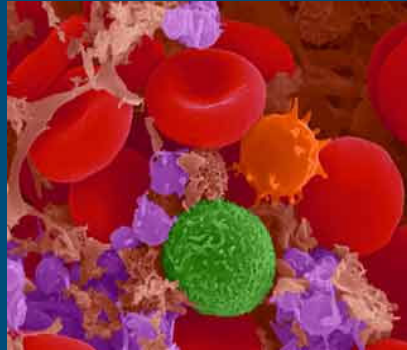
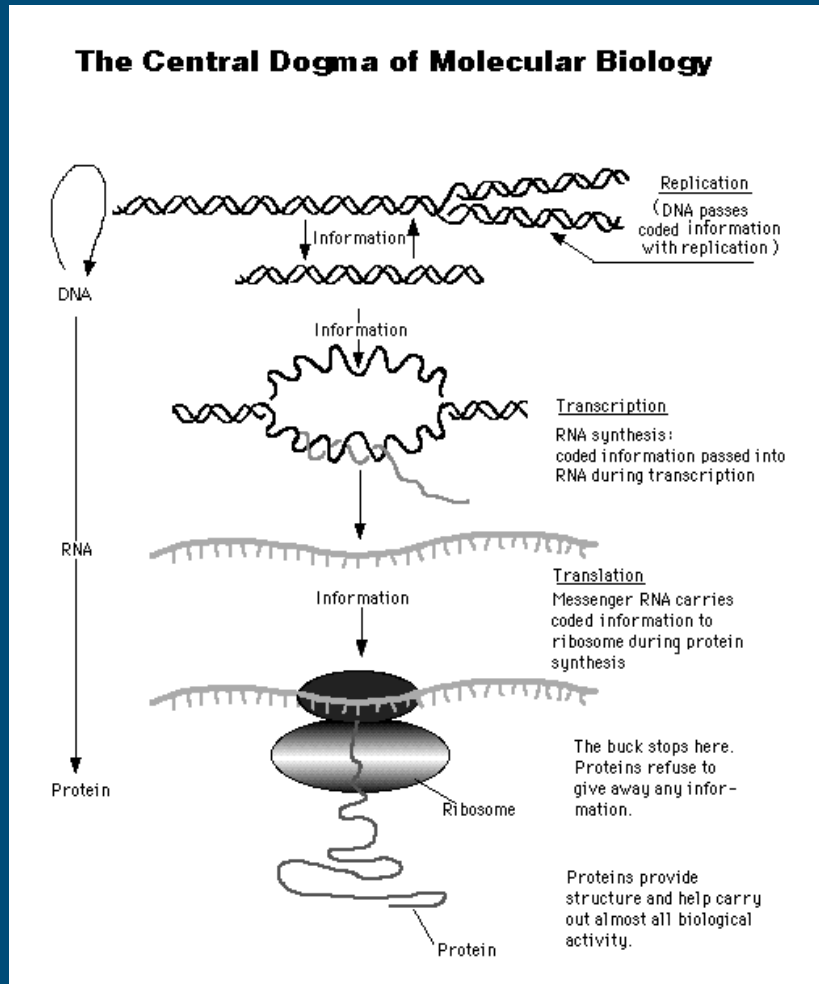
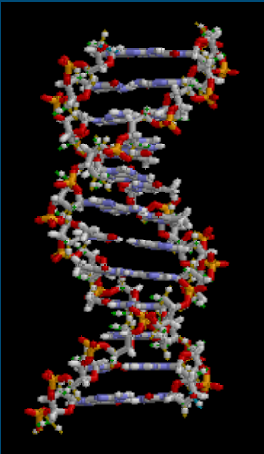
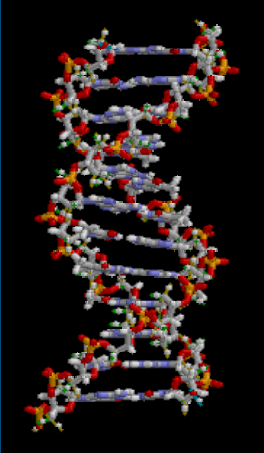


From living systems to DNA



DNA is the carrier of all genetic information



DNA

RNA

Protein

Metabolites

Structure

Transport

Regulation

Communication

Genomics: analysis of all genes instead of one

Sequencing

Microarrays

Proteomics

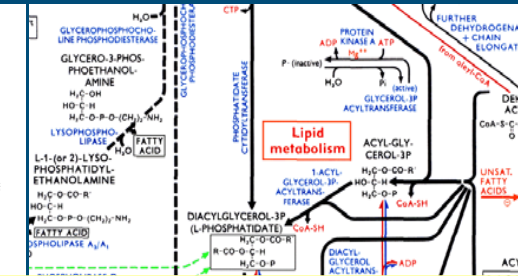
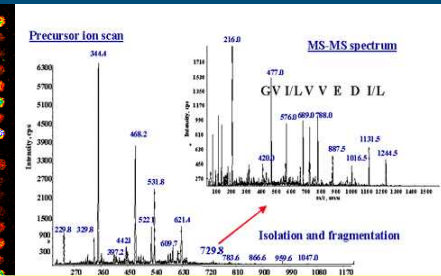
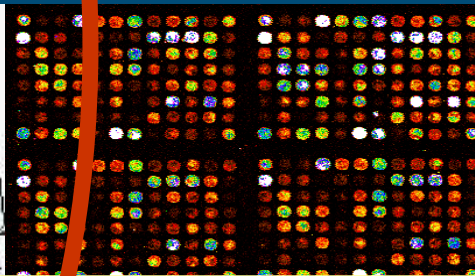
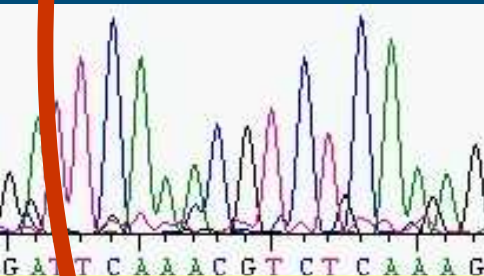
Metabolomics

DNA sequence

Gene activity

Proteins

Metabolites



Bioinformatics



Knowledge

Applications

Analysis of DNA sequence

■ Large sequencing centers

- Genome sequence of human (3,253,037,807), chicken, cow, (pig), dog, cat, mouse, rat chimpanzee, frog, etc.
- We know the genes/proteins and their structures

■ Ultra high throughput sequencers

- 20.000.000 – 100.000.000 / run



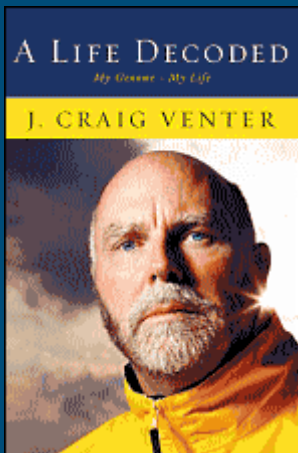
DNA sequencing revolution

genome sequence of individuals come of age

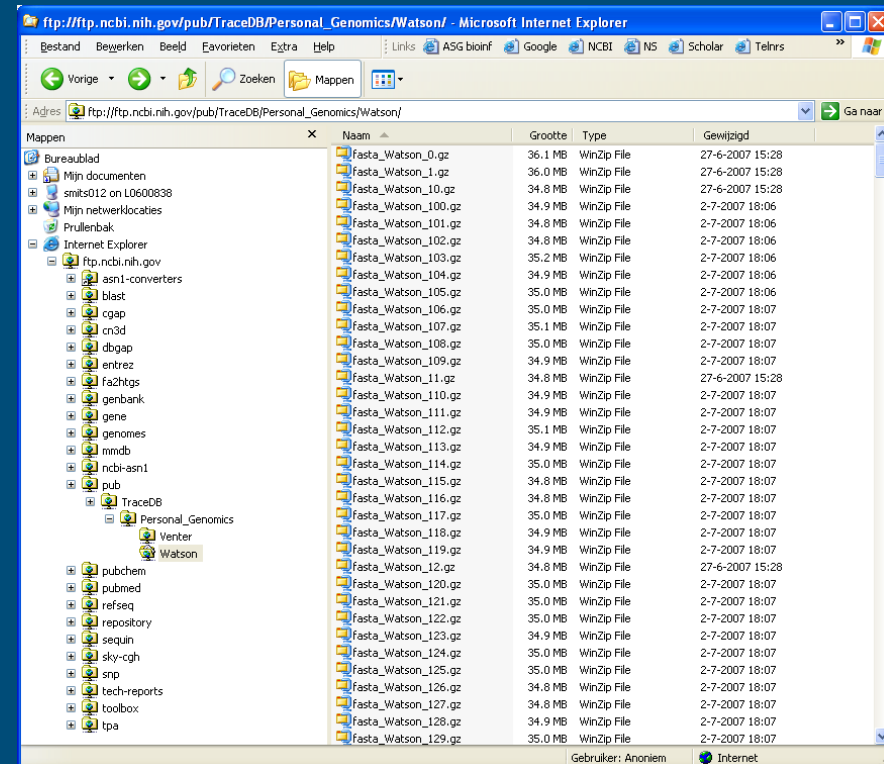


James Watson, June 2007

2 months vs 13 years
1 million vs 3 billion \$



Levy S, et al.,
The Diploid Genome Sequence of an Individual Human.
PLoS Biol. 2007 Sep 4;5(10):e254



Analysis of genetic variation (SNP)

- 1 SNP per 1000 bp

```
---AAGCTTTGCGGTACTT---  
| | | | | | | | | | | | | | |  
---AAGCTTTACGGTACTT---
```

- Identification

- By sequence analysis
- We know the genetic variation

- Challenge: which SNPs linked to trait X, Y, Z

Genome sequence Bos taurus

Statistics

Assembly:	Btau_3.1, Aug 2006
Genebuild:	Ensembl, Sep 2006
Database version:	44.3a
Known genes:	16,945
Projected genes:	1,610
Novel genes:	3,725
Pseudogenes:	1,264
RNA genes:	1,671
Genscan gene predictions:	59,639
Gene exons:	220,542
Gene transcripts:	29,598
SNPs:	1,792,456
Base Pairs*:	3,247,285,296
Golden Path Length**:	3,033,353,239

Btau_3.1 is an assembly of the cow, *Bos taurus*, Hereford breed.



http://www.ensembl.org/Bos_taurus/index.html

Genomic Selection

Principle

Large number of markers across the genome

Breeding values are estimated for pieces of the genome

These values are combined to “total” breeding value

Genome of animal X (“genomic pieces” A,B,...,J):

Total breeding value animal X = $A1 + A2 + B4 + B3 + \dots + J6 + J2$

A	B	C	D	E	F	G	H	I	J
1	4	3	2	1	8	4	2	7	6
2	3	5	1	4	5	4	3	7	2

Process

1000+ animals with known
genotypes and reliable performance records



Estimate breeding values for pieces of the genome

+

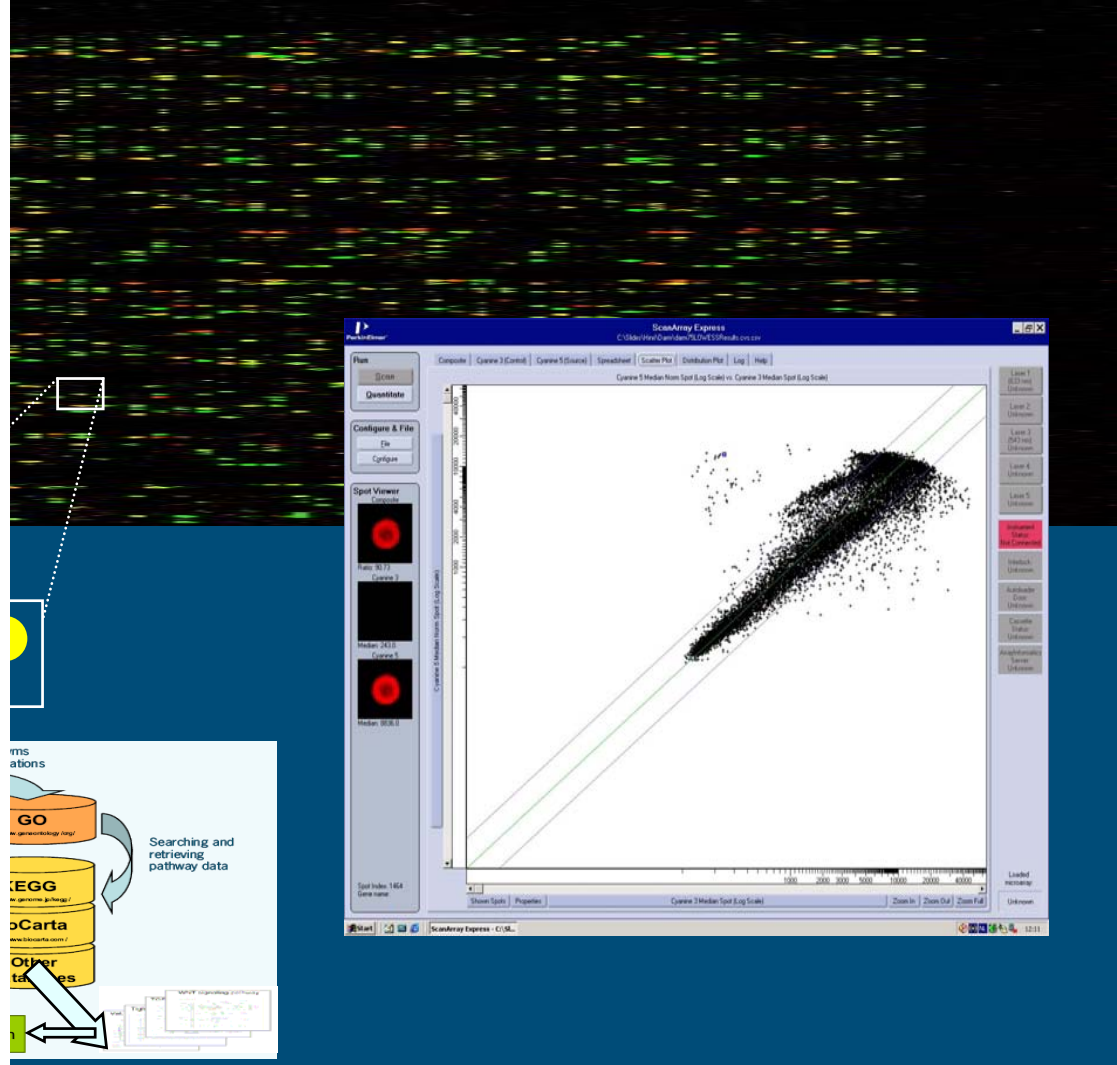
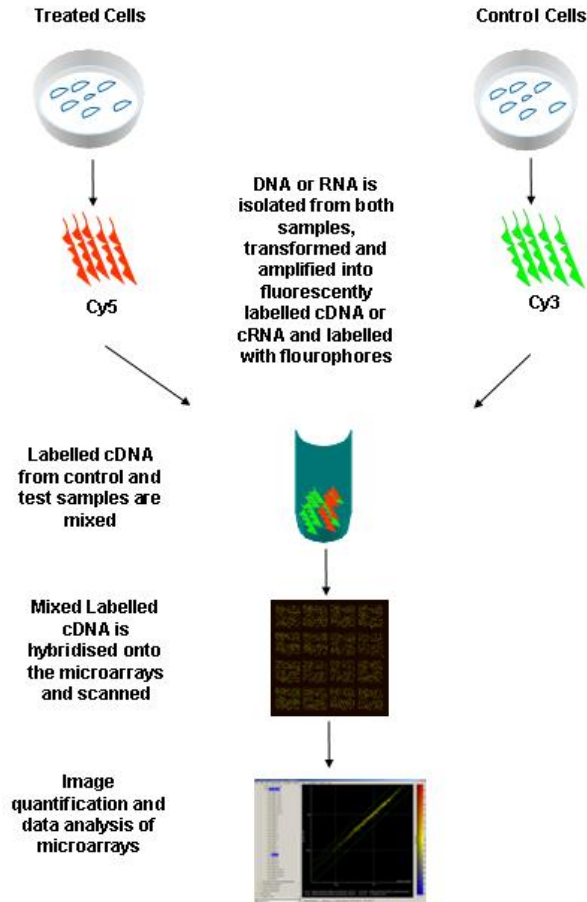
Young animals with known genotypes but
WITHOUT performance records



Predict breeding value young animals

Microarray hybridisation

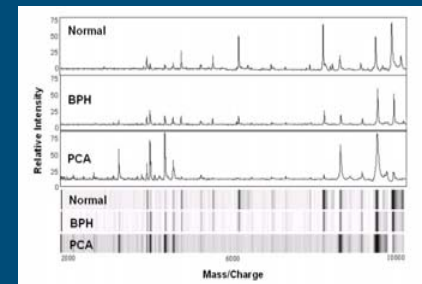
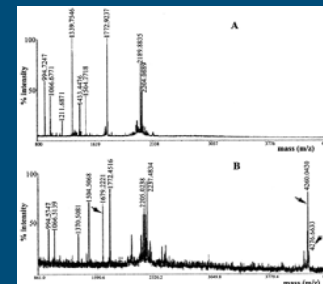
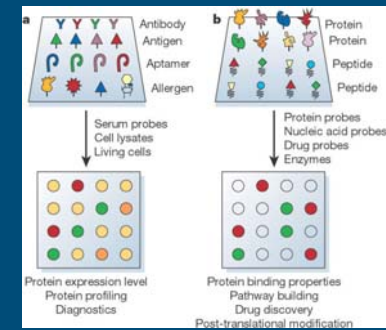
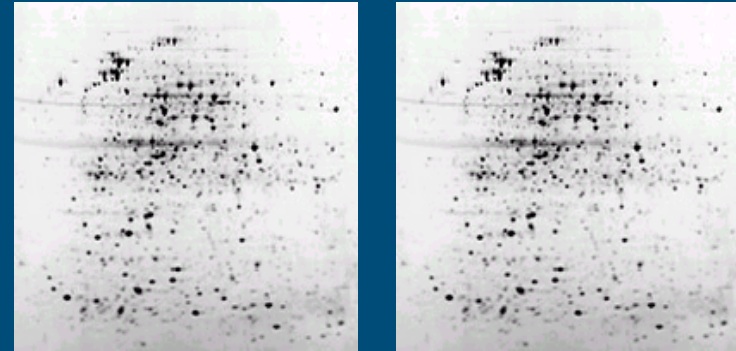
Target preparation and array hybridization



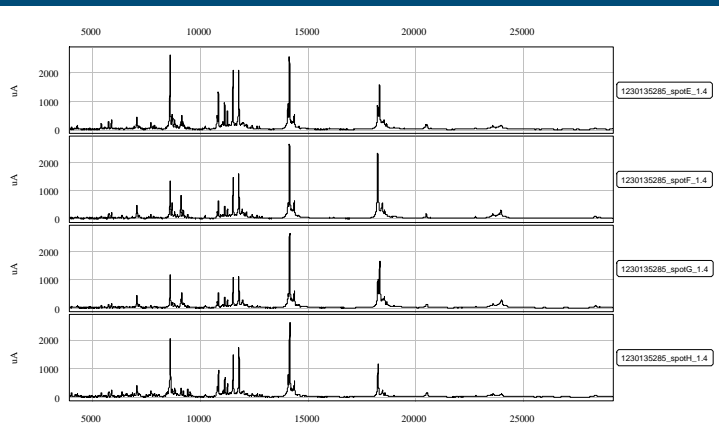
Proteomics (phosphoproteomics, glycoproteomics)

- Separation, purification
- Profiling
- Identification
- Interaction

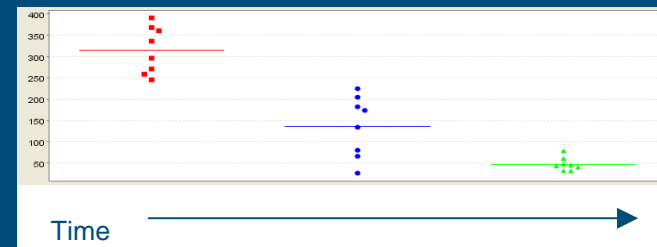
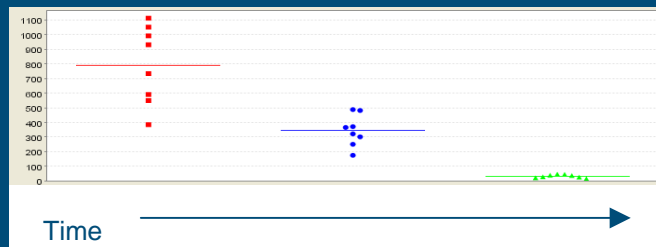
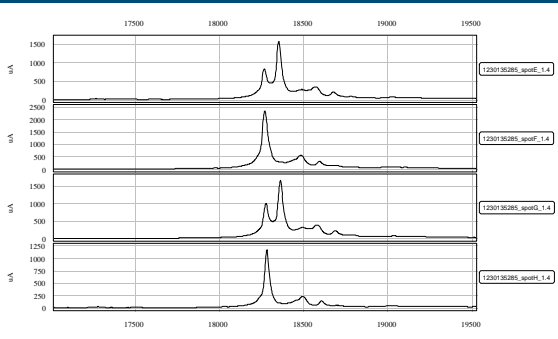
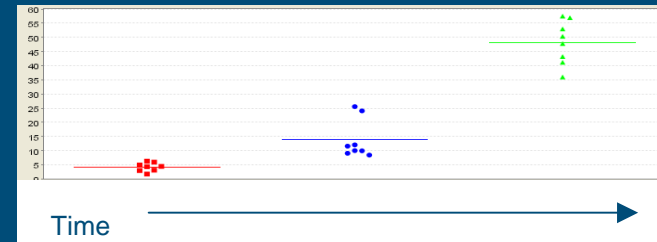
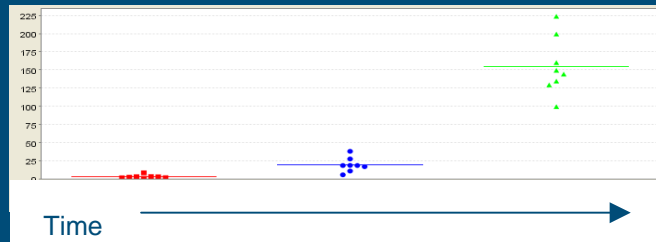
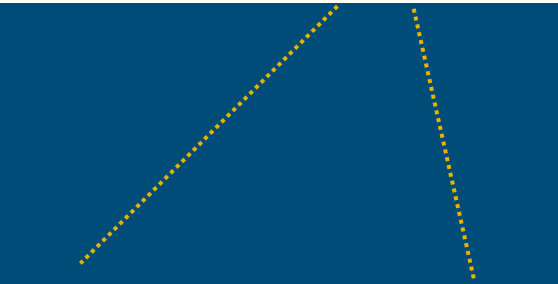
- 1-D gelelectroforese
- 2-D gelelectroforese
- Immune affinity chromatography
- Protein microarrays
- HPLC-MS, HPLC-MS/MS
- Yeast two hybrid
- FRET, SPR
- MALDI-TOF, SELDI-TOF



Milk composition: proteins



Biomarkers for mastitis / quality



homozygous

Potential applications of functional genomics information

- Measure or monitor health or quality parameters (biomarkers)
 - Udder, intestine, immune responsiveness, product quality
 - Deviations from this – early warning
 - Measuring effects of treatments
 - Correlates of protection after vaccination
- Modulation of pathways / biological processes
 - By vaccine adjuvants that work by activating innate immunity and direct the development of the adaptive immunity
 - By feed ingredients that improve “awareness” of innate immune system
 - By other compounds: minerals, receptor-ligands, RNAi, etc
- Development of new tools and methodologies
 - Vaccines or prevention measures
 - Feed or management regimes