Day 5
sampling - clustering

SAMPLE POPULATION

SAMPLING: IS ESTIMATING THE CHARACTERISTICS OF THE WHOLE POPULATION USING INFORMATION COLLECTED FROM A **SAMPLE** GROUP.

The sampling process comprises several stages:

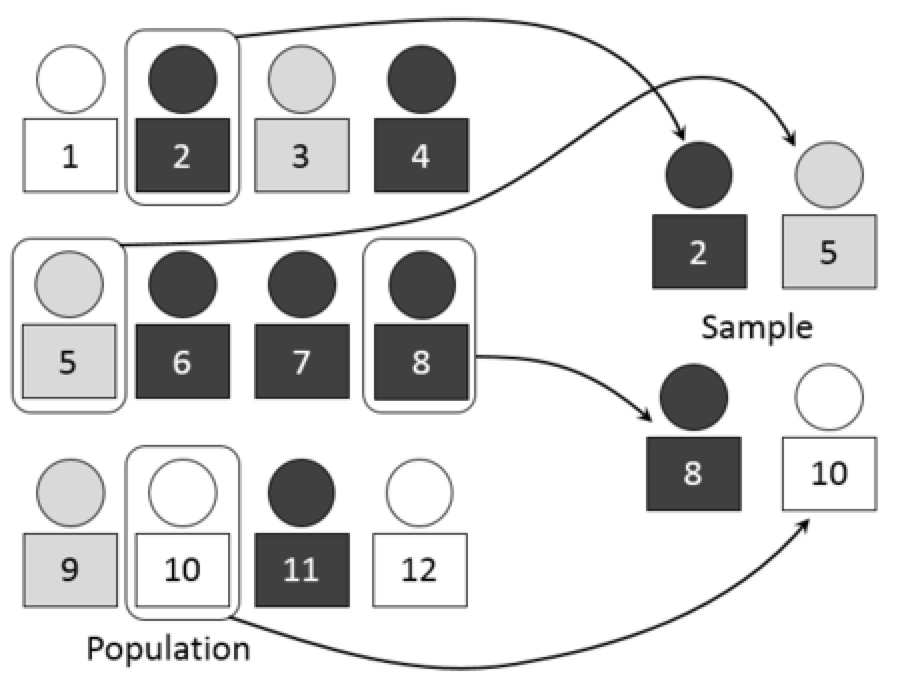
- Defining the population of concern
- Specifying a sampling frame, a set of items or events possible to measure
- Specifying a sampling method for selecting items or events from the frame
- Determining the sample size
- Implementing the sampling plan
- Sampling and data collecting

Simple random sampling

In a simple random sample (SRS) of a given size, all such subsets of the frame are given an equal probability.

In particular, the variance between individual results within the sample is a good indicator of variance in the overall population, which makes it relatively easy to estimate the accuracy of results.

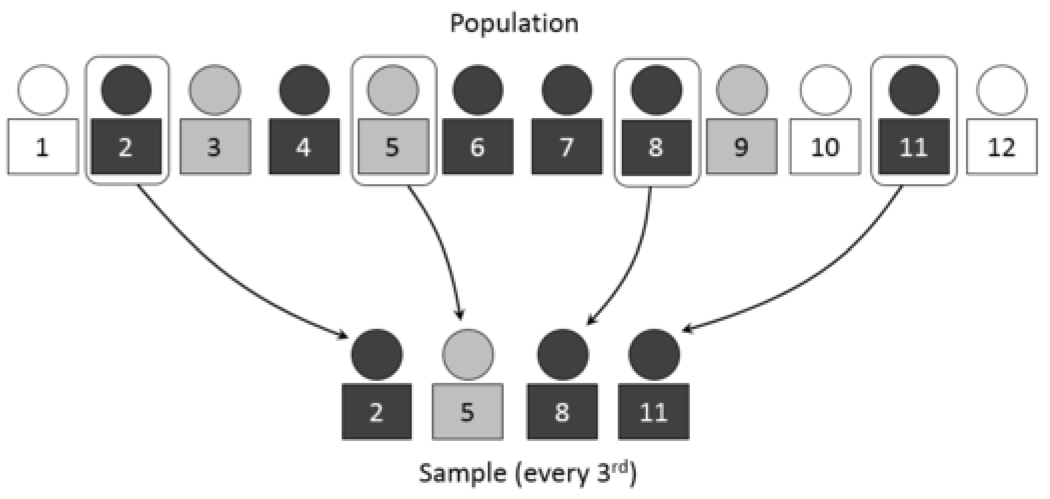
SRS can be vulnerable to sampling error because the randomness of the selection may result in a sample that doesn't reflect the makeup of the population.



Systematic sampling

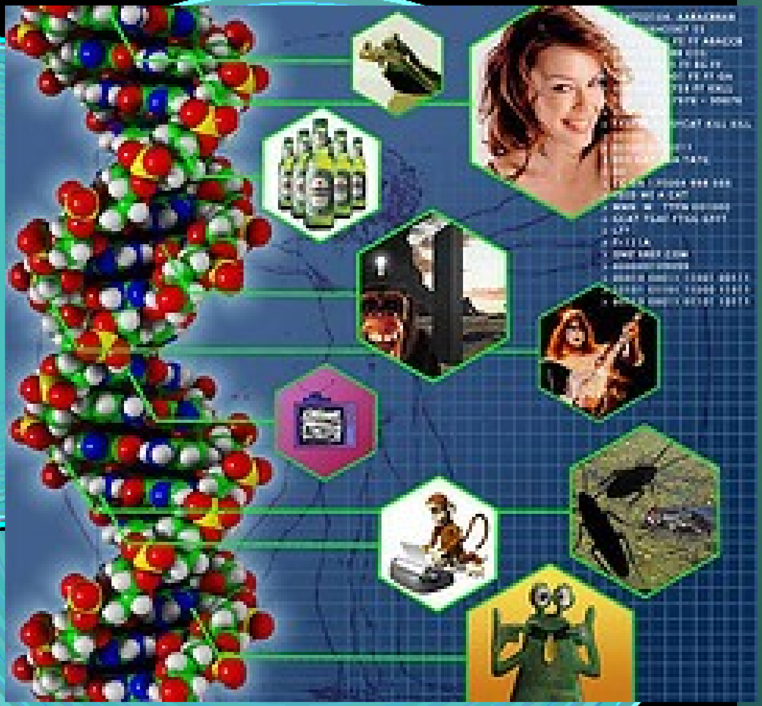
Systematic sampling (also known as interval sampling) relies on arranging the study population according to some ordering scheme and then selecting elements at regular intervals through that ordered list

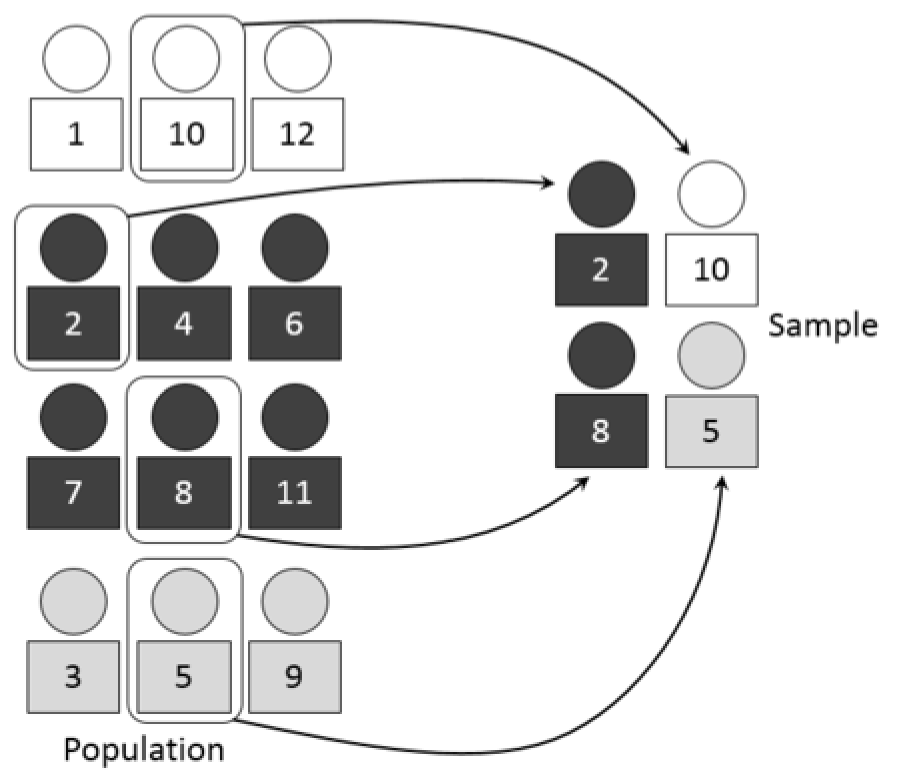
Systematic sampling involves a random start and then proceeds with the selection of every *k*th element from then onwards. In this case, *k*=(population size/sample size). It is important that the starting point is not automatically the first in the list, but is instead randomly chosen from within the first to the *k*th element in the list.



STRATIFIED SAMPLING

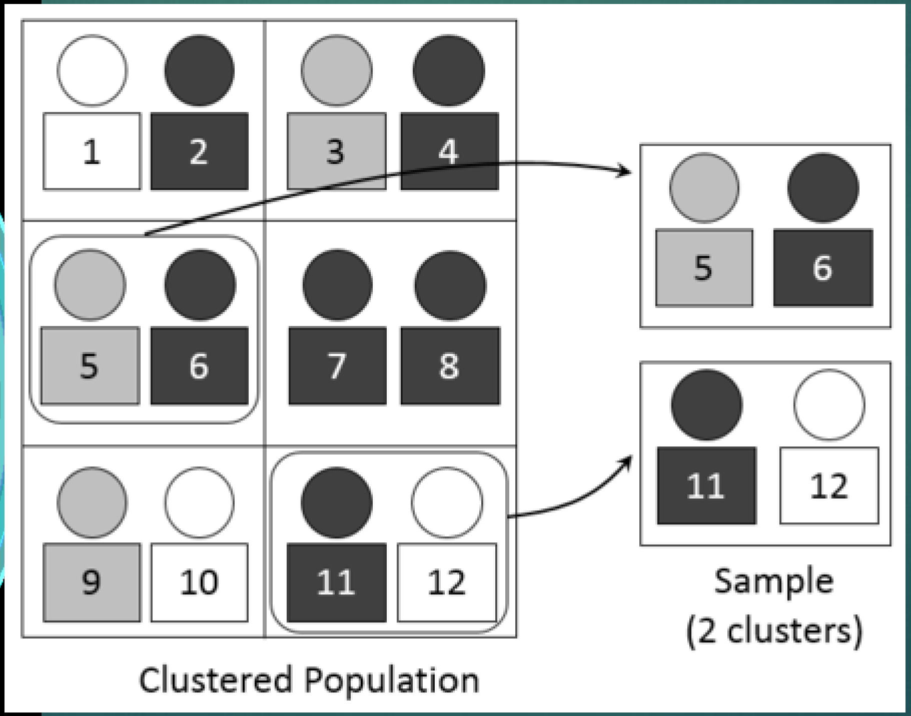
WHEN THE POPULATION EMBRACES A NUMBER OF DISTINCT CATEGORIES, THE FRAME CAN BE ORGANIZED BY THESE CATEGORIES INTO SEPARATE "STRATA." EACH STRATUM IS THEN SAMPLED AS AN INDEPENDENT SUB-POPULATION, OUT OF WHICH INDIVIDUAL ELEMENTS CAN BE RANDOMLY SELECTED





Cluster sampling

- Sometimes it is more cost-effective to select respondents in groups ('clusters')



Quota sampling
Minimax sampling
Accidental sampling
Voluntary Sampling

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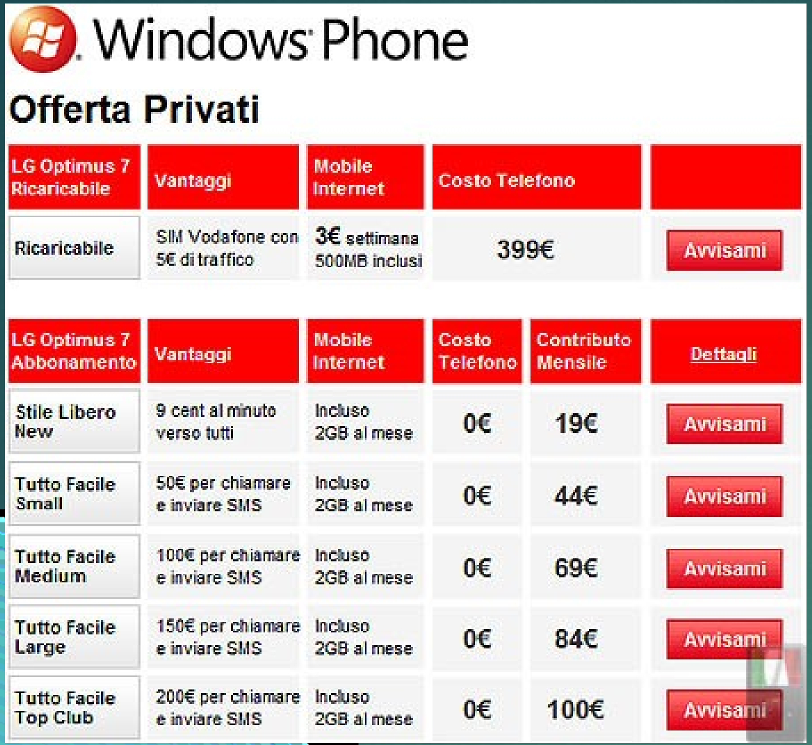


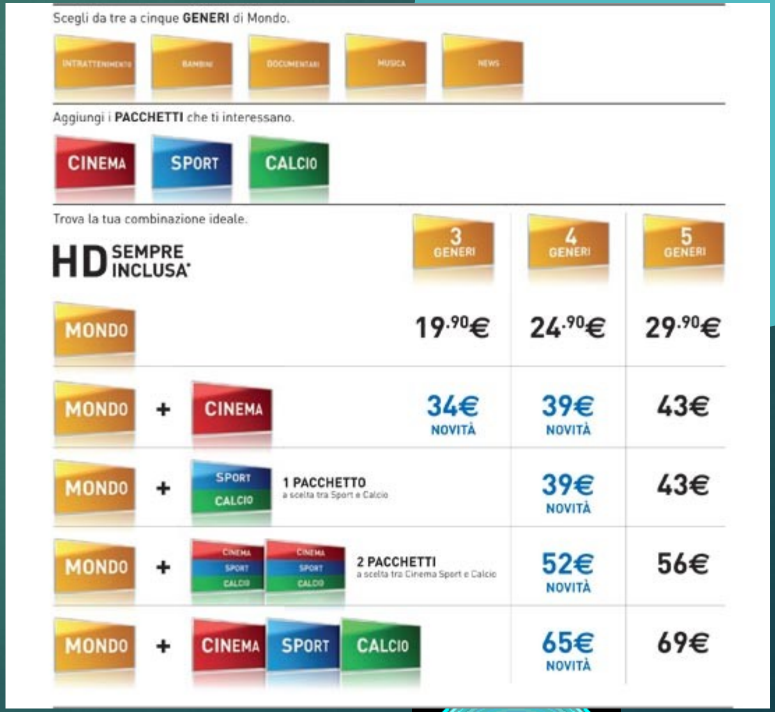
Windows Phone

Offerta Privati

LG Optimus 7 Ricaricabile	Vantaggi	Mobile Internet	Costo Telefono	
Ricaricabile	SIM Vodafone con 5€ di traffico	3€ settimana 500MB inclusi	399€	Avvisami

LG Optimus 7 Abbonamento	Vantaggi	Mobile Internet	Costo Telefono	Contributo Mensile	Dettagli
Stile Libero New	9 cent al minuto verso tutti	Incluso 2GB al mese	0€	19€	Avvisami
Tutto Facile Small	50€ per chiamare e inviare SMS	Incluso 2GB al mese	0€	44€	Avvisami
Tutto Facile Medium	100€ per chiamare e inviare SMS	Incluso 2GB al mese	0€	69€	Avvisami
Tutto Facile Large	150€ per chiamare e inviare SMS	Incluso 2GB al mese	0€	84€	Avvisami
Tutto Facile Top Club	200€ per chiamare e inviare SMS	Incluso 2GB al mese	0€	100€	Avvisami

sky



Scegli da tre a cinque **GENERI** di Mondo.

INTRATTENIMENTO BAMBINI DOCUMENTARI MUSICA NEWS

Aggiungi i **PACCHETTI** che ti interessano.

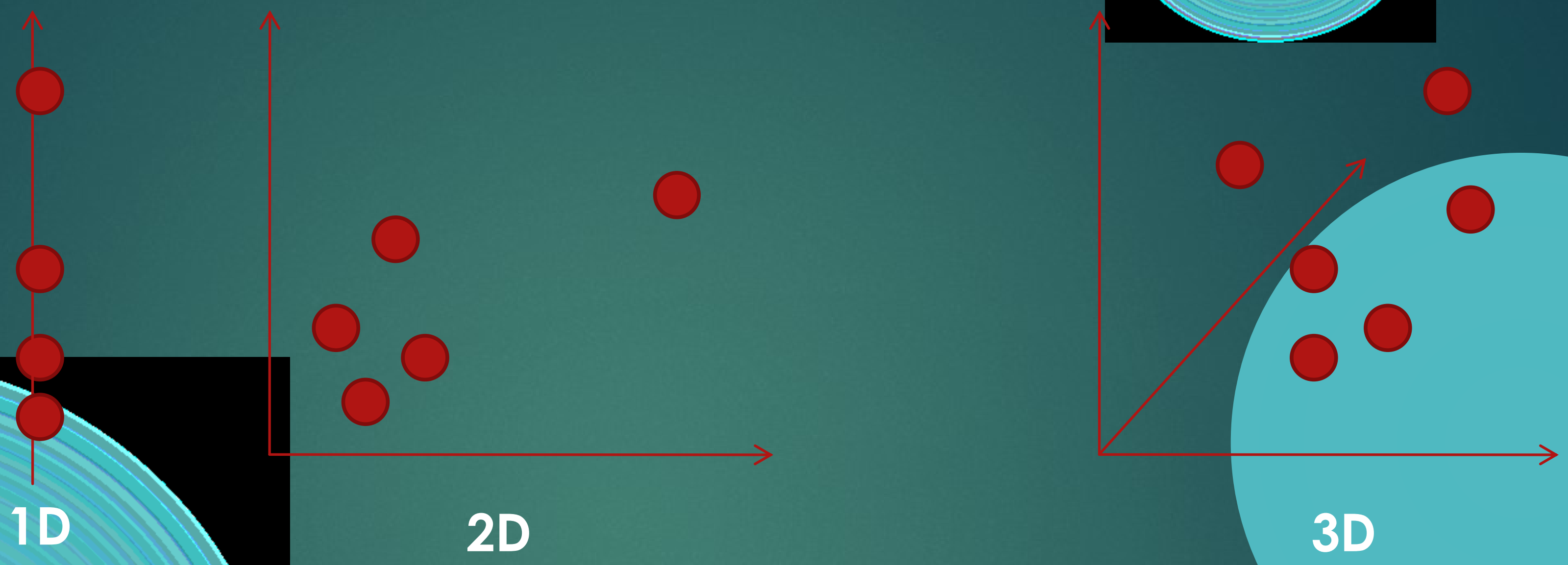
CINEMA SPORT CALCIO

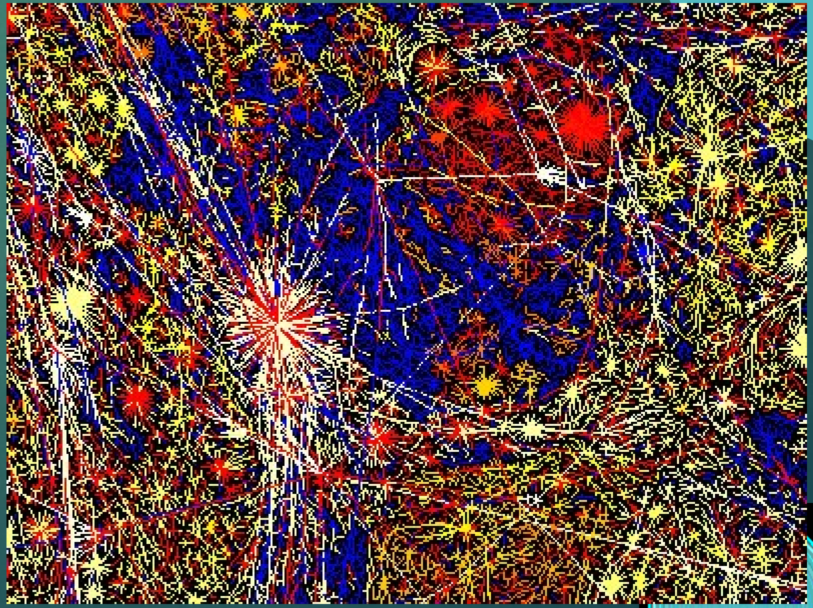
Trova la tua combinazione ideale.

HD SEMPRE INCLUSA*	3 GENERI	4 GENERI	5 GENERI
MONDO	19.90€	24.90€	29.90€
MONDO + CINEMA	34€ NOVITÀ	39€ NOVITÀ	43€
MONDO + SPORT / CALCIO 1 PACCHETTO a scelta tra Sport e Calcio		39€ NOVITÀ	43€
MONDO + CINEMA SPORT CALCIO / CINEMA SPORT CALCIO 2 PACCHETTI a scelta tra Cinema Sport e Calcio		52€ NOVITÀ	56€
MONDO + CINEMA SPORT CALCIO		65€ NOVITÀ	69€

vodafone

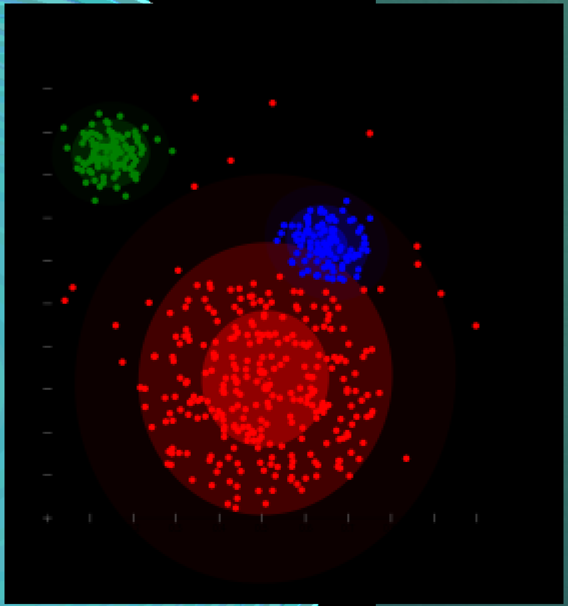
CLUSTERING

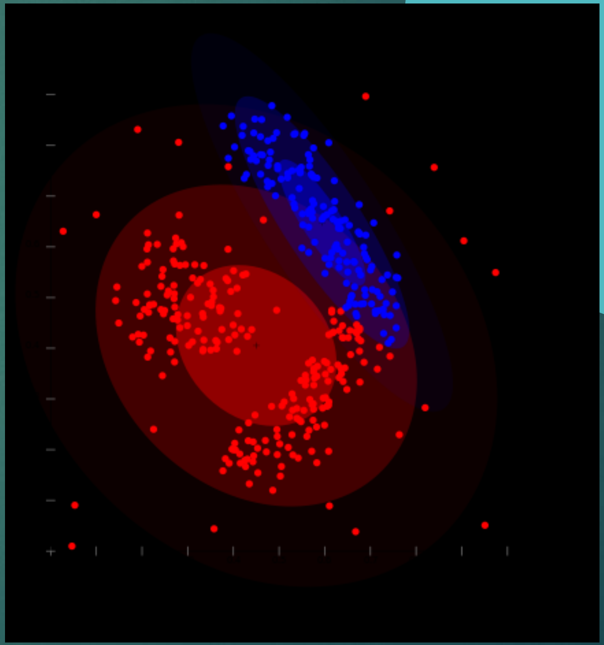




Clustering techniques are based on measures of similarity between elements. In many approaches this similarity is conceived in terms of distance in a multidimensional space.

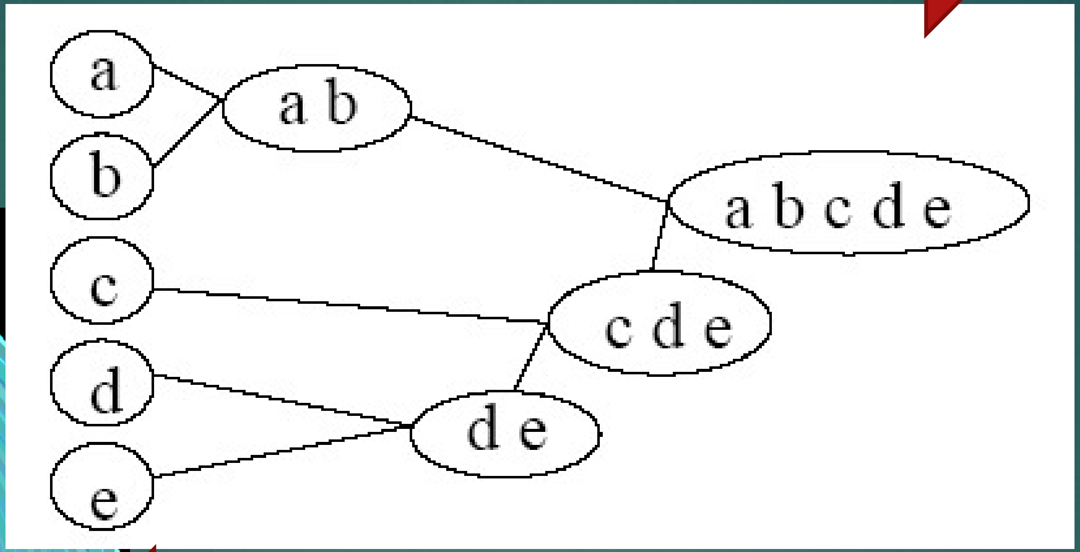
The notion of a "cluster" cannot be precisely defined, which is one of the reasons why there are so many clustering algorithms.There is a common denominator: a group of data objects





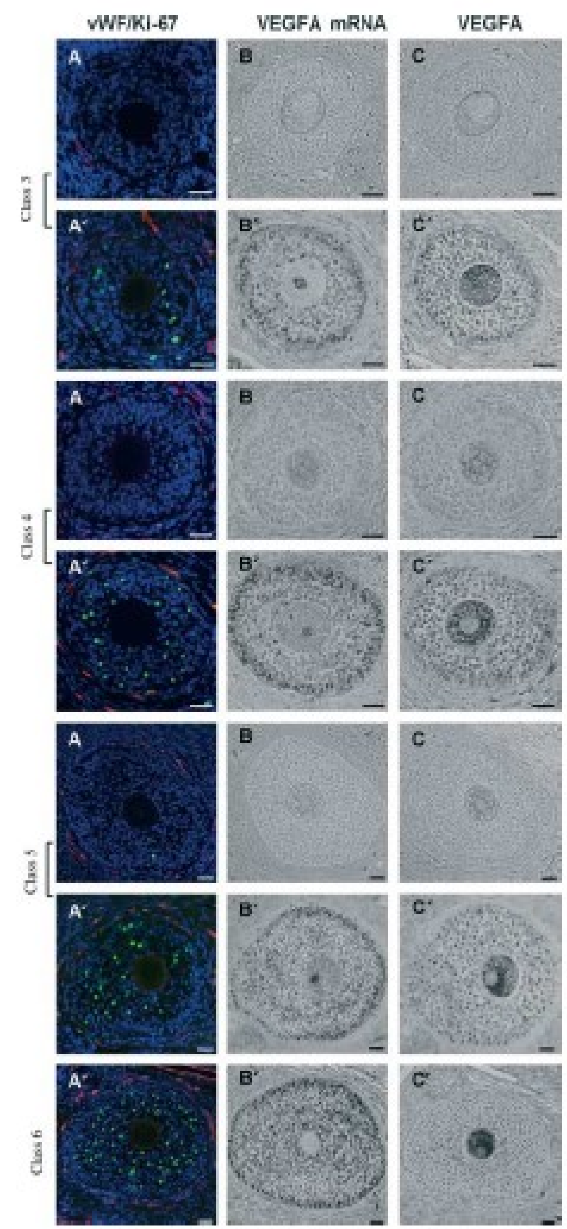
Clustering

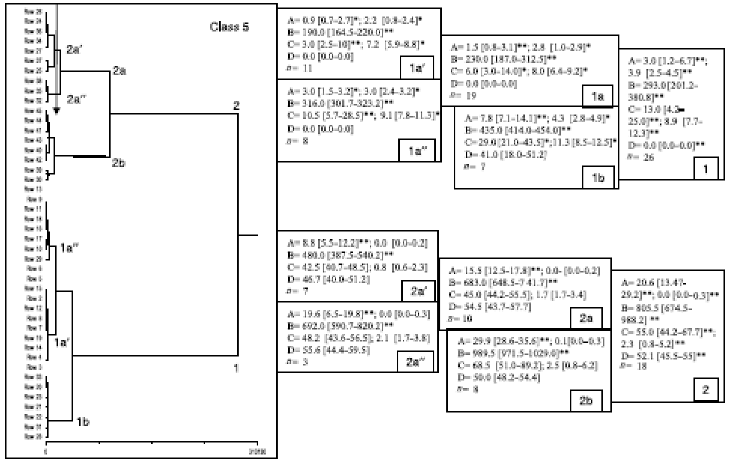
Bottom-up



Top-Down

dendogramma





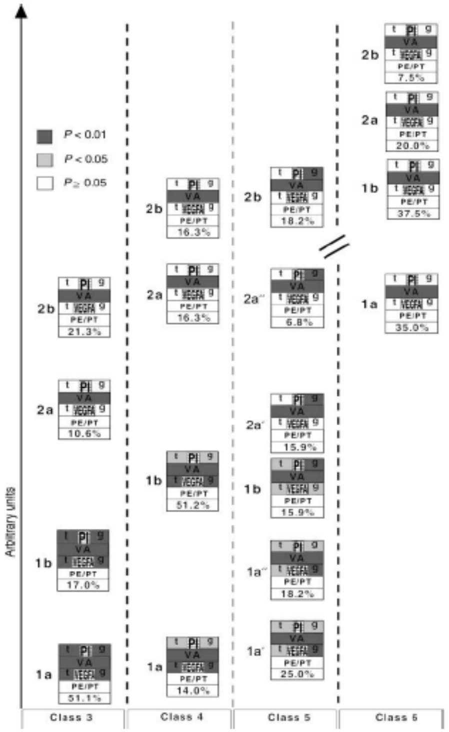


Figure 5 A general model that describes the distribution of the follicular subpopulations identified inside each follicular class by using cluster analysis. The subpopulations were represented within each class and arranged on the *y*-axis by considering the distances between the bifurcation obtained in the dendograms. The grey scale represents significant differences recovered for somatic and vascular parameters. The thickness of the dotted line represents the statistical difference among classes. t PI, theca proliferation index; g PI, granulosa proliferation index; VA, vascular area; t VEGFA, theca *VEGFA* mRNA; g VEGFA, granulosa *VEGFA* mRNA; PE/PT, proportion of proliferating endothelial cells; % value, percentage of preantral follicles belonging to the subpopulation.

CLUSTERING

Comp Clin Pathol

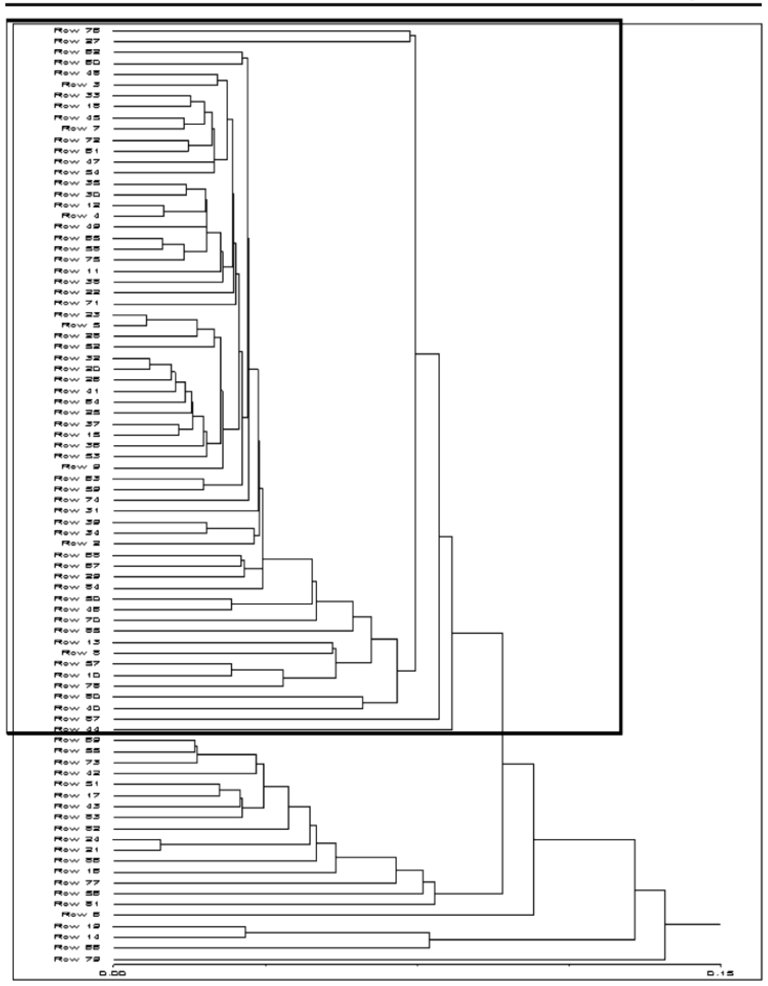


Fig. 2 Multivariate hierarchical cluster analysis of MICRO dogs. The *caption* shows the area of interest where clustering is significant

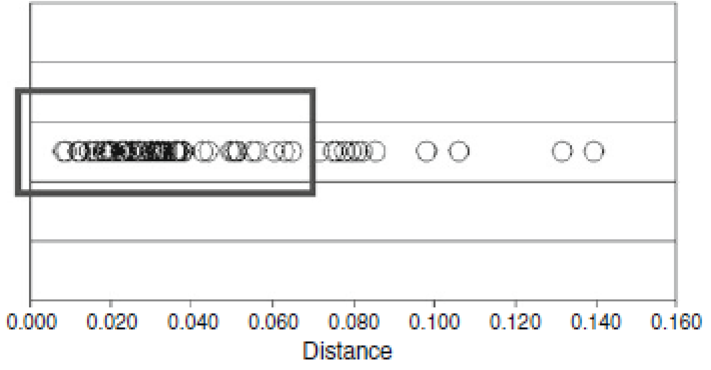
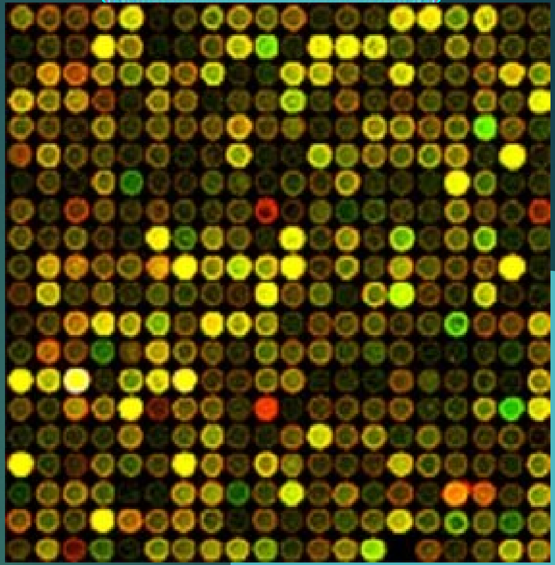


Fig. 3 Mono-dimensional distribution of distances among the dogs as measured by clustering. The *caption* shows a clear subgroup among the MICRO dogs

Inividuality
Complexity



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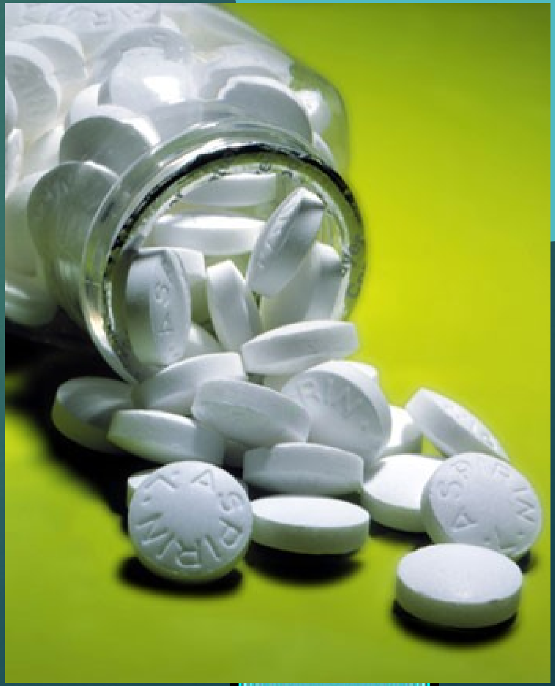
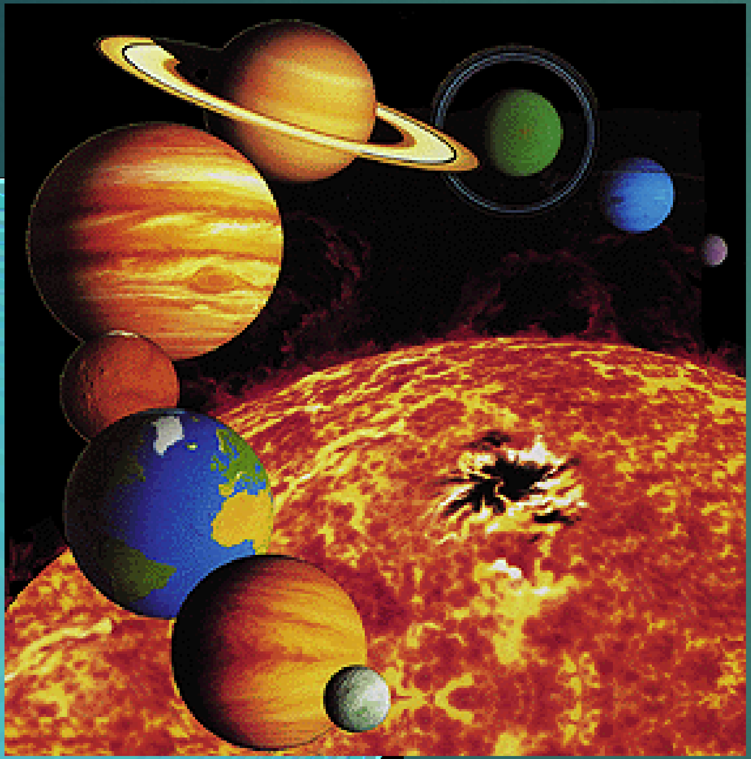
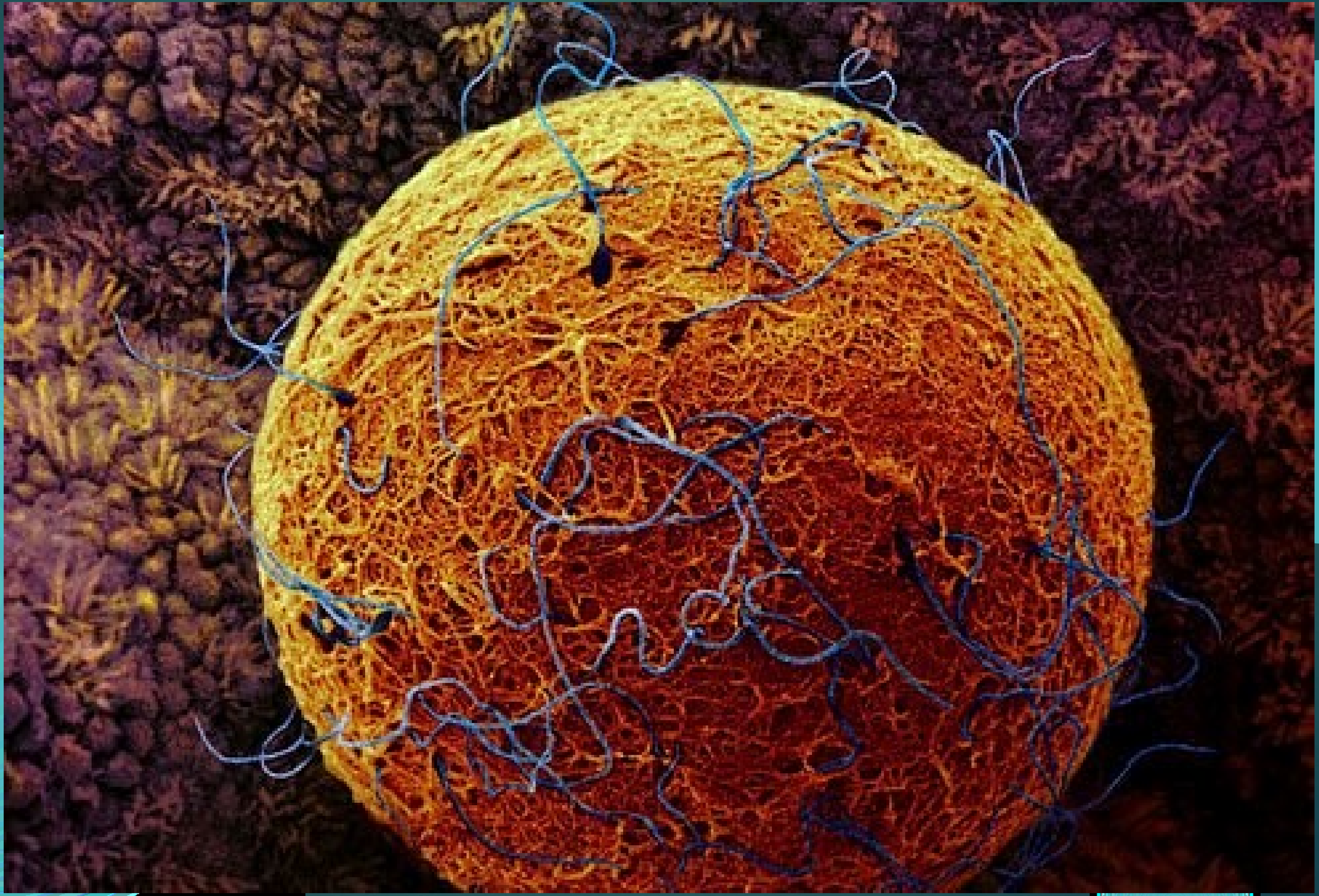


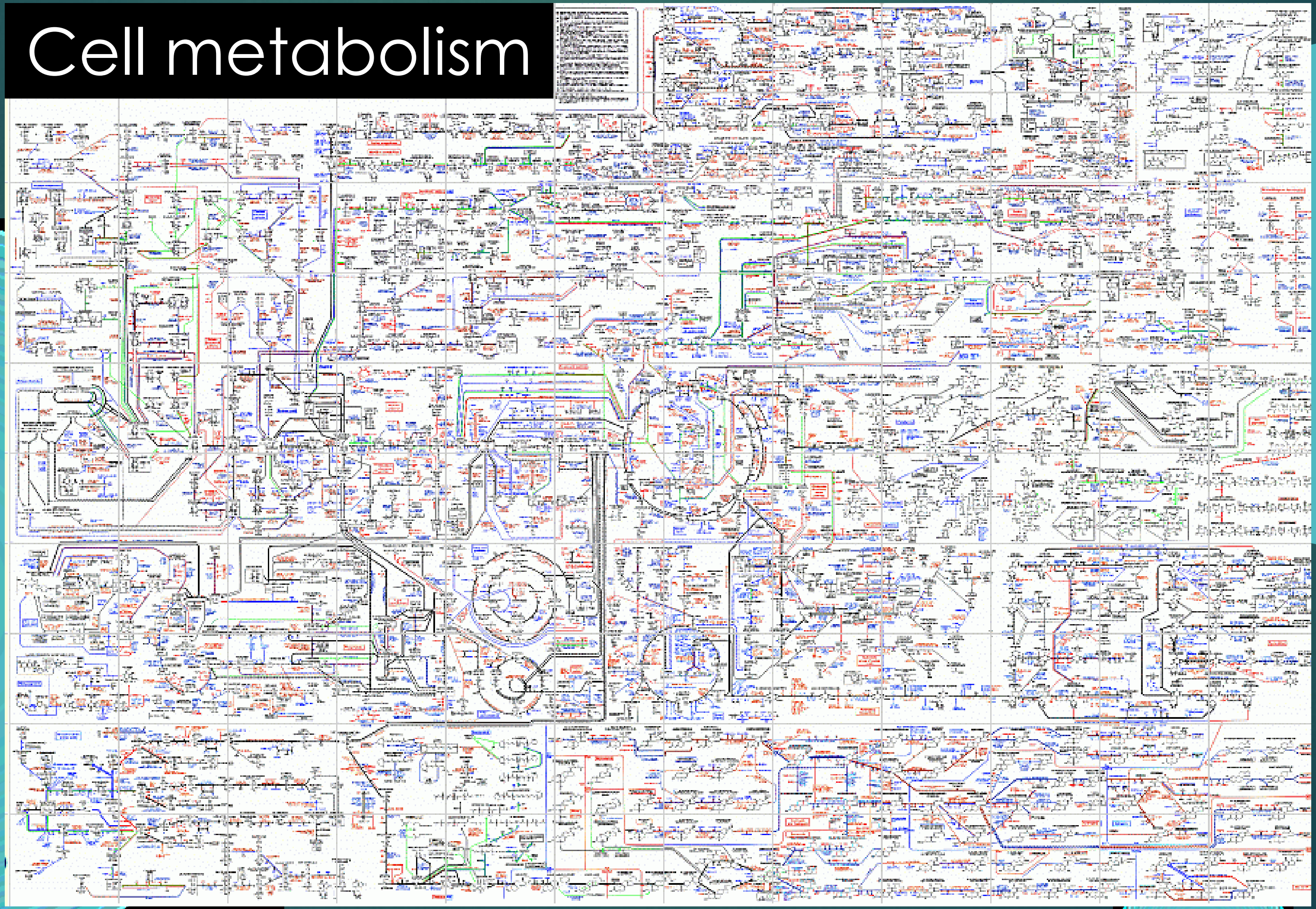
Complicated vs. complex



fertility



Biological complexity

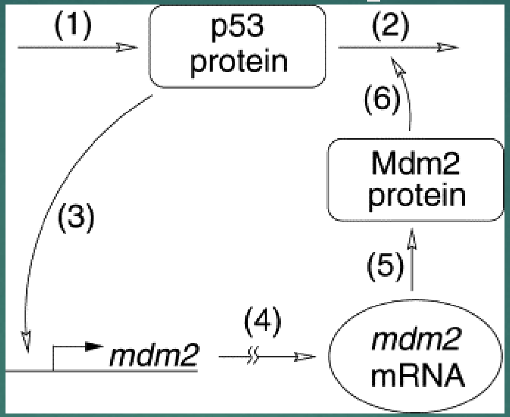


Cell metabolism

Complexity:

non-linearity of interactions:

An example…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(2)
(6)
Mdm2 protein
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(5)
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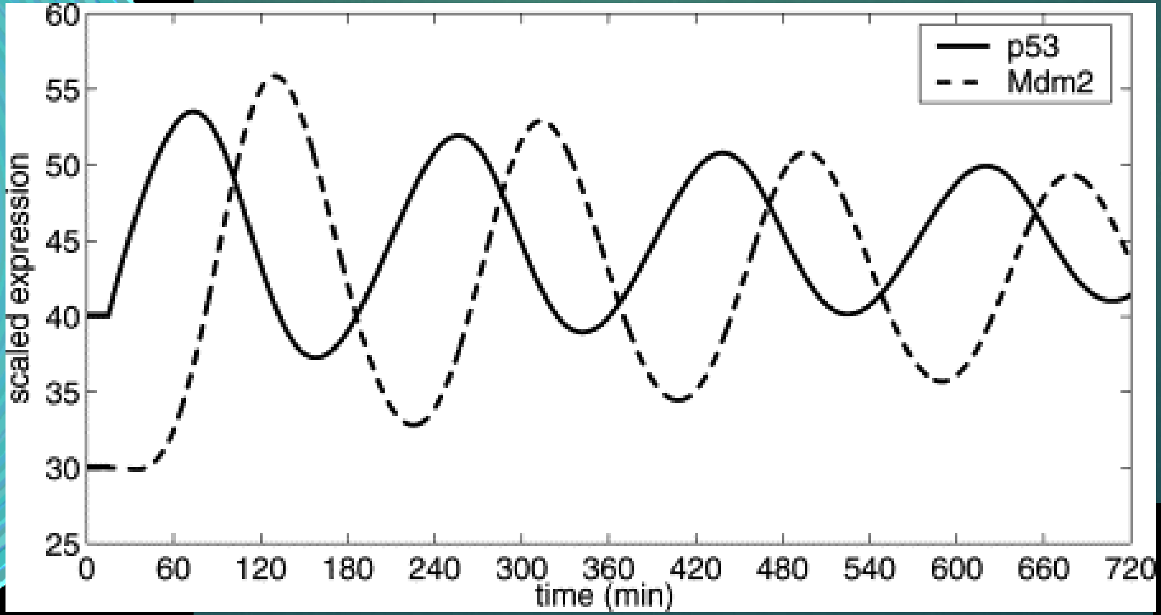
mdm2
mdm2 mRNA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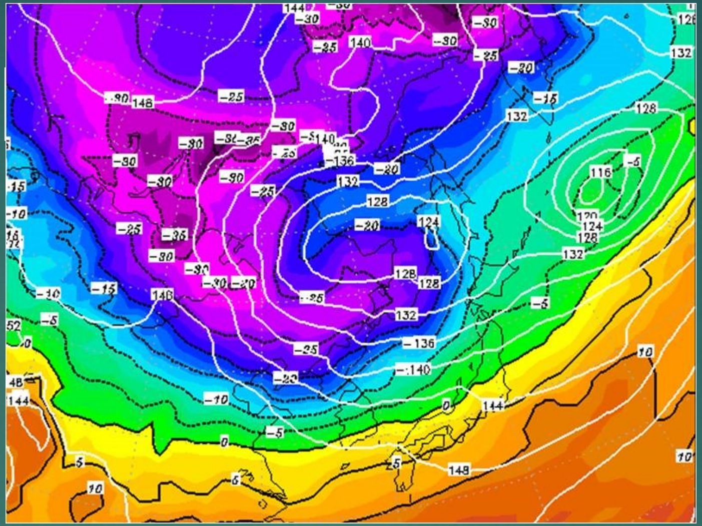
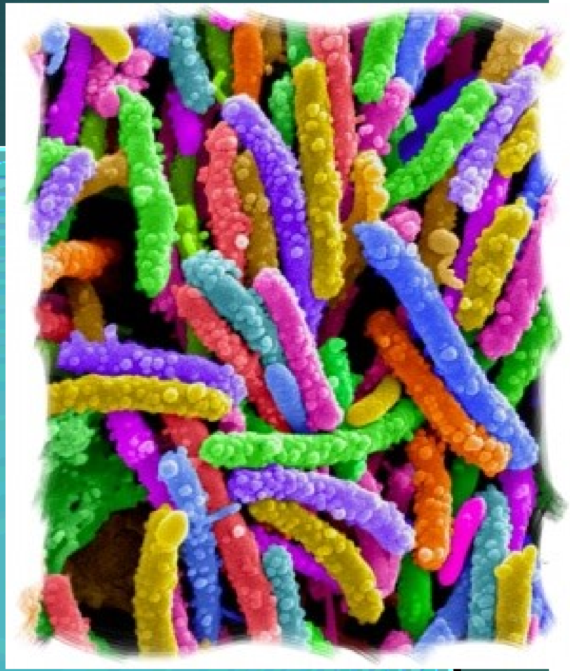
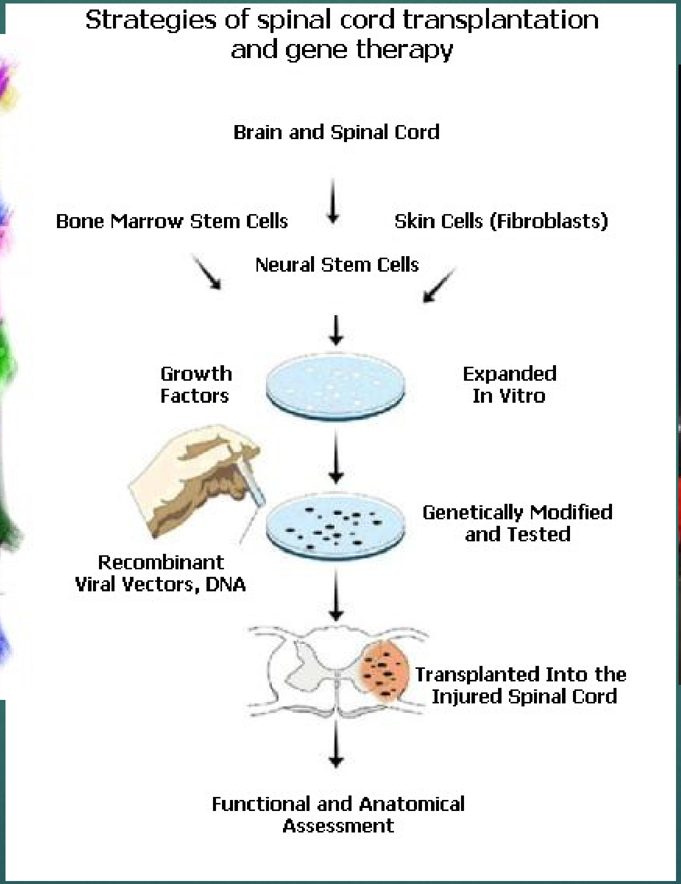


unpredictability





Strategies of spinal cord transplantation and gene therapy

Brain and Spinal Cord

Bone Marrow Stem Cells

Skin Cells (Fibroblasts)

Neural Stem Cells

Growth Factors

Expanded In Vitro

Genetically Modified and Tested

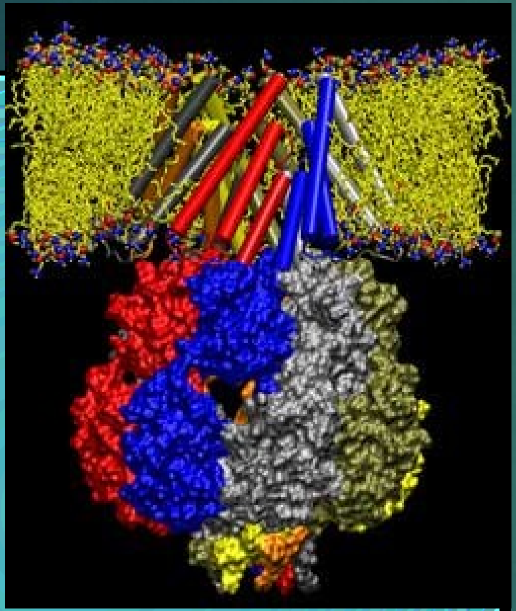
Recombinant Viral Vectors, DNA

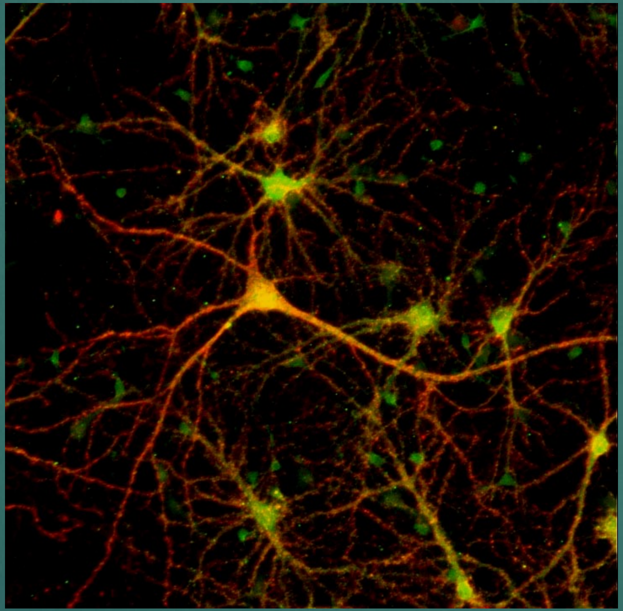
Transplanted Into the Injured Spinal Cord

Functional and Anatomical Assessment

Butterfly effect

Emergence of proprieties





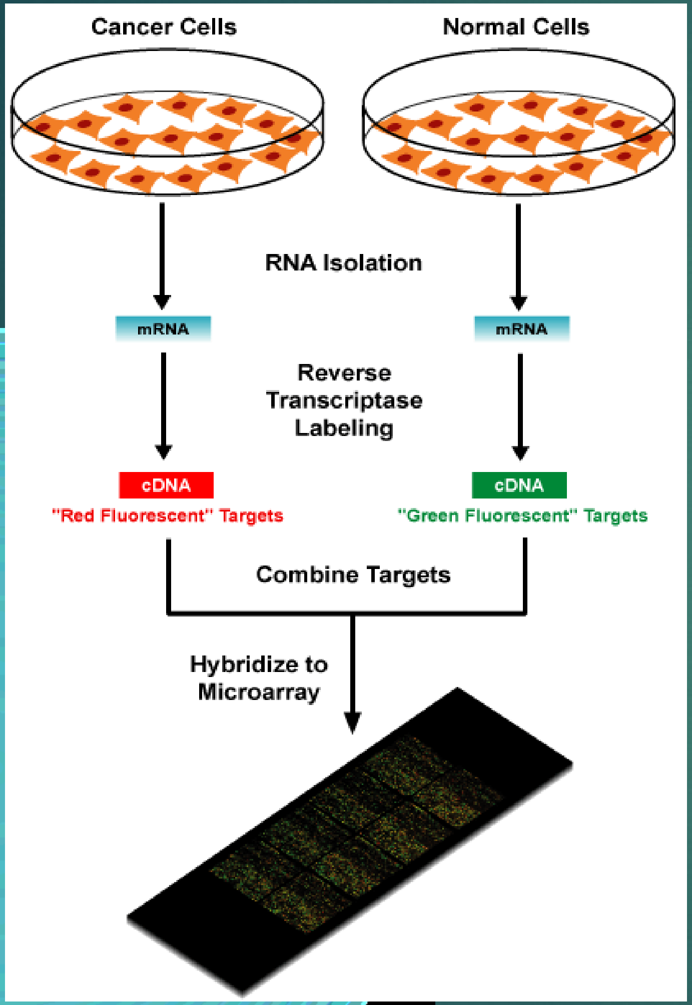
The whole is more (different) than the sum of the individual components

Human Genome Project

Begun formally in 1990, the U.S. Human Genome Project was a 13-year effort coordinated by the U.S. Department of Energy and the National Institutes of Health. The project originally was planned to last 15 years, but rapid technological advances accelerated the completion date to 2003. Project goals

- *identify* all the approximately 20,000-25,000 genes in human DNA,
- *determine* the sequences of the 3 billion chemical base pairs that make up human DNA,
- *store* this information in databases,
- *improve* tools for data analysis,
- *transfer* related technologies to the private sector, and
- *address* the ethical, legal, and social issues (ELSI) that may arise from the project.

- omics



Cancer Cells

Normal Cells

RNA Isolation

mRNA

mRNA

Reverse Transcriptase Labeling

cDNA

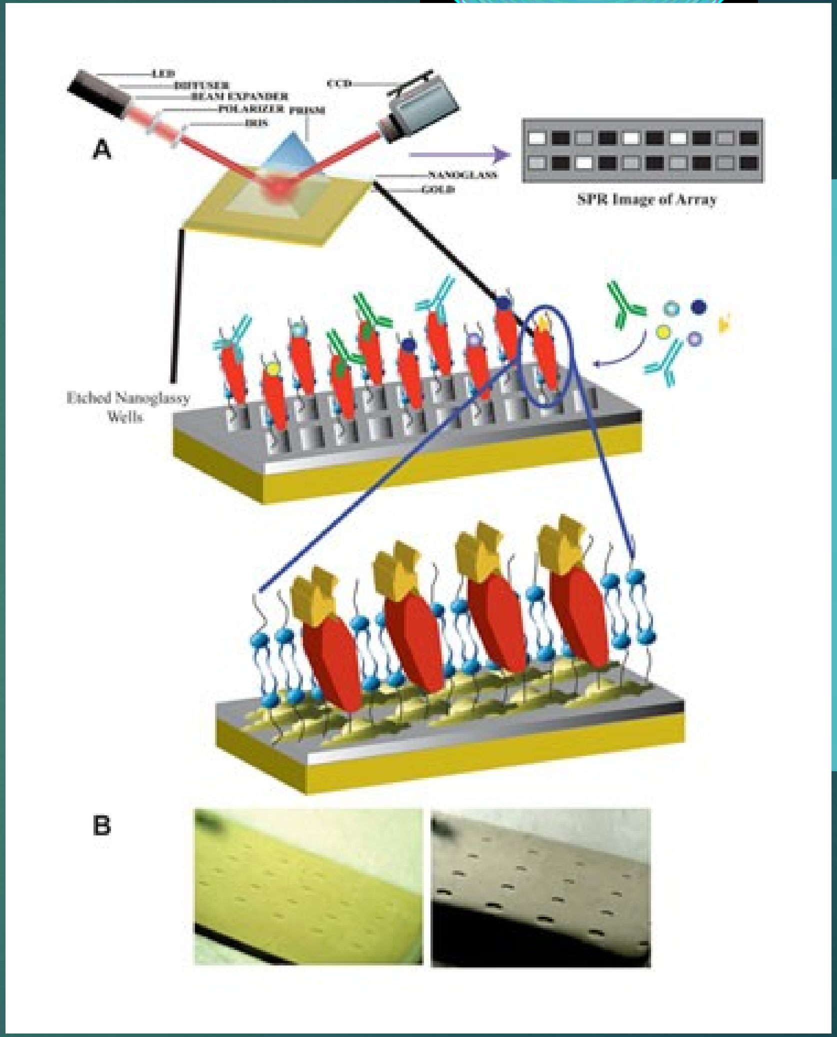
"Red Fluorescent" Targets

cDNA

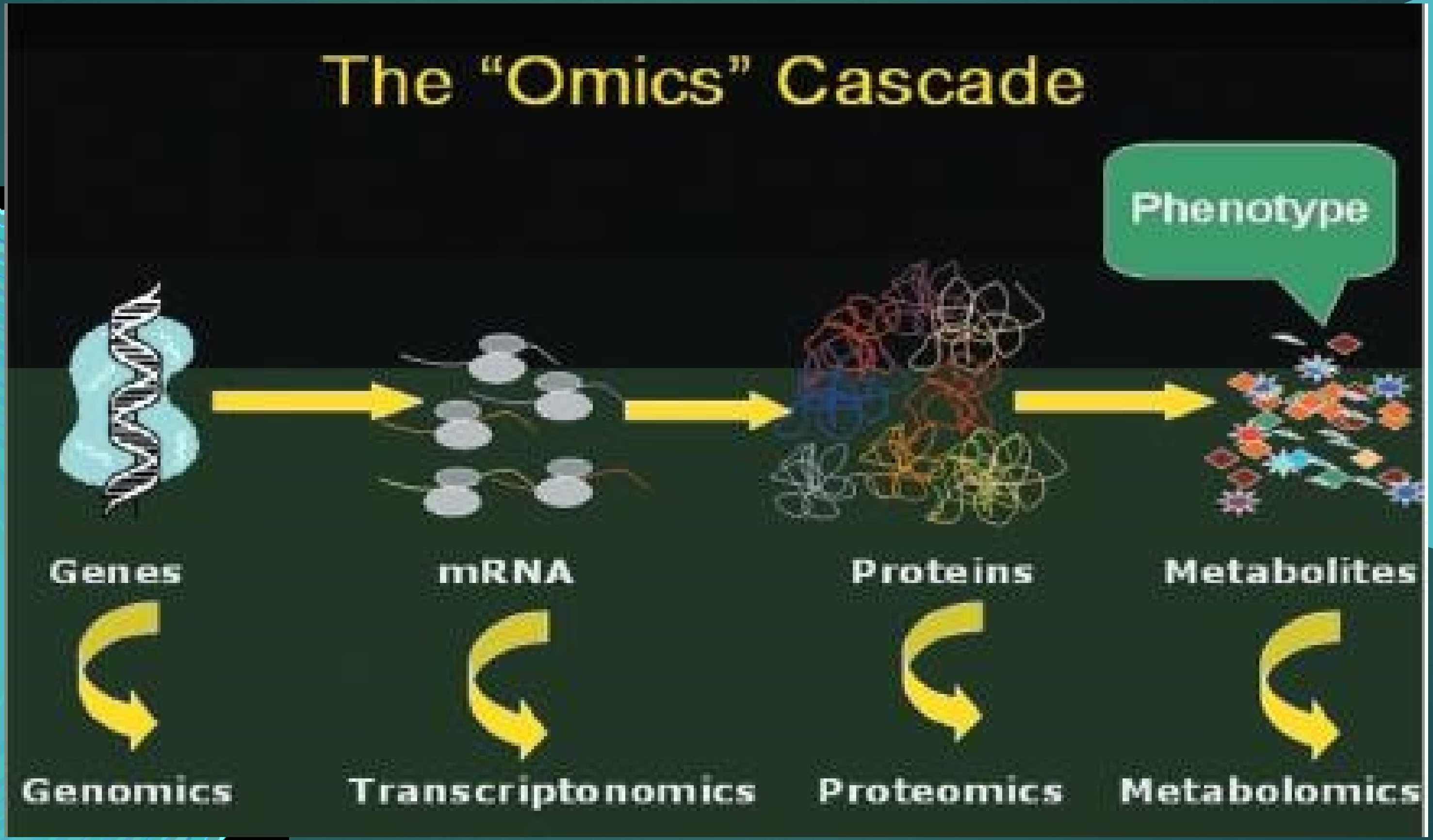
"Green Fluorescent" Targets

Combine Targets

Hybridize to Microarray



- OMICS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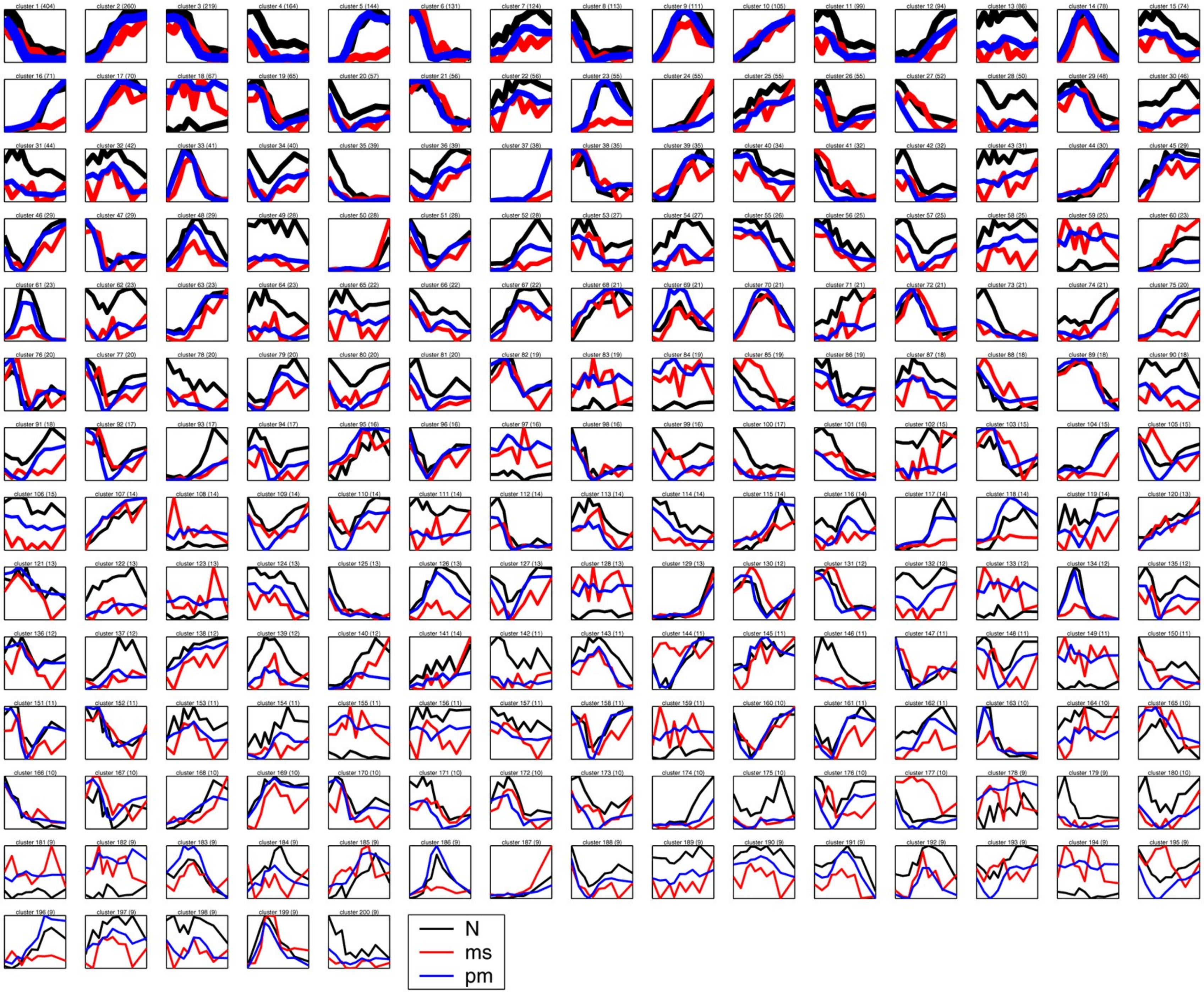
Genes
mRNA
Proteins
Metabolites
Genomics
Transcriptonomics
Proteomics
Metabolomics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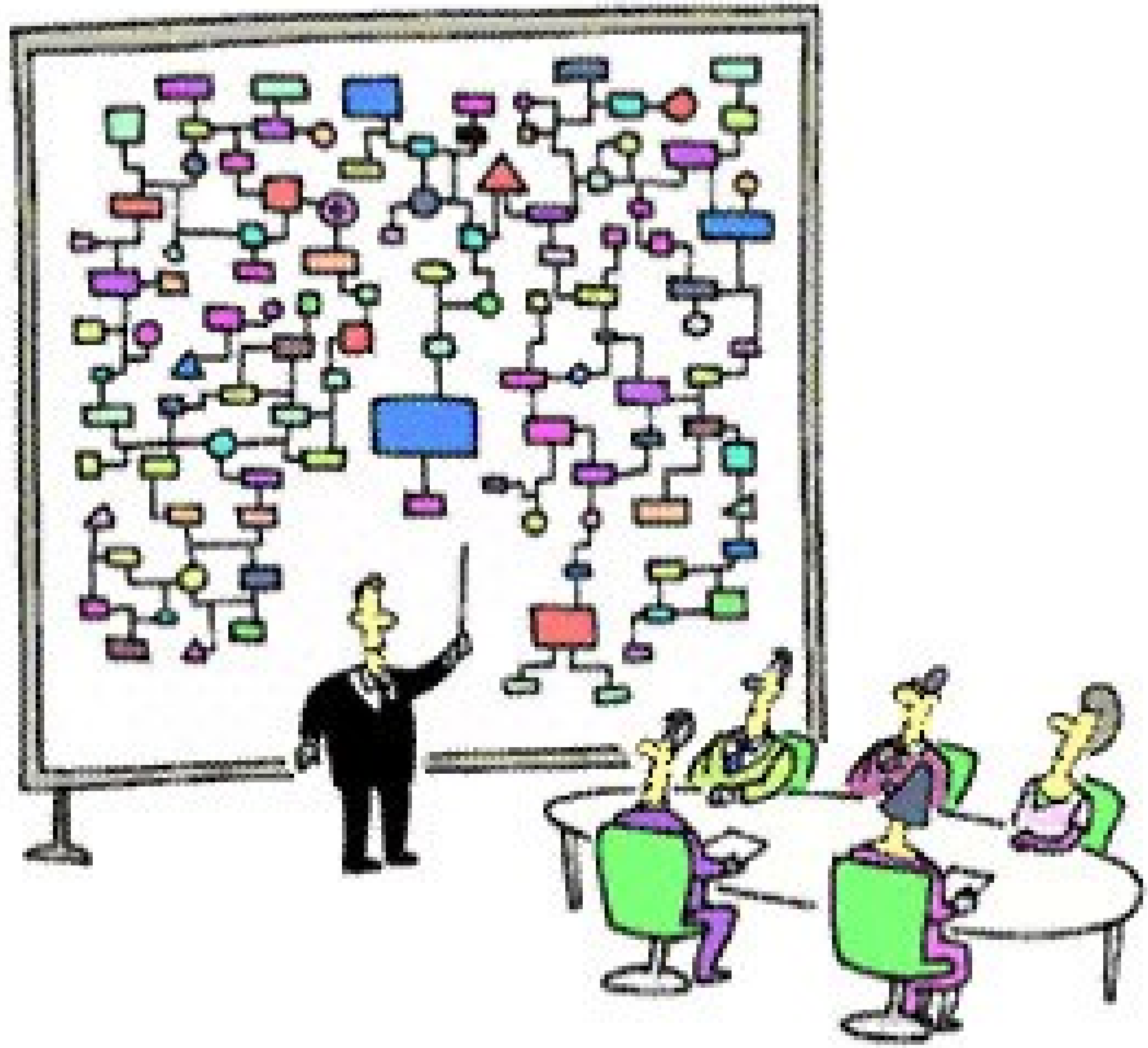
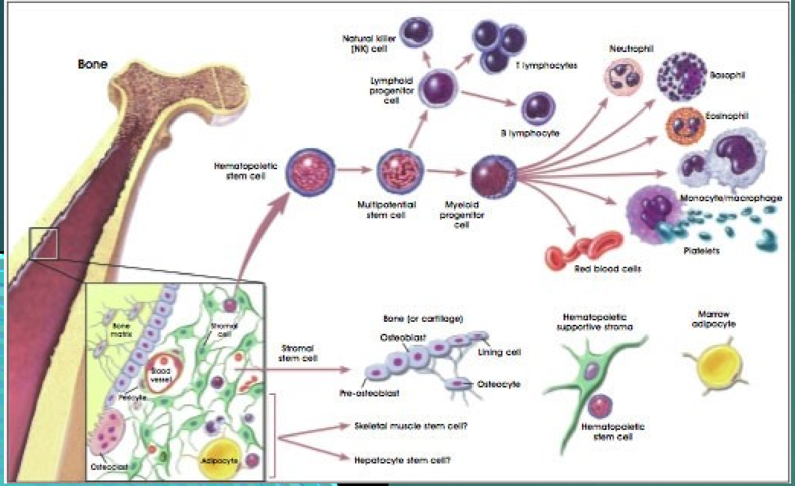
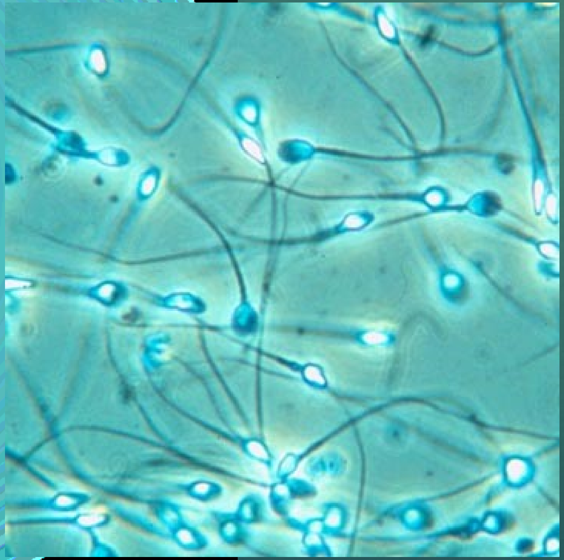
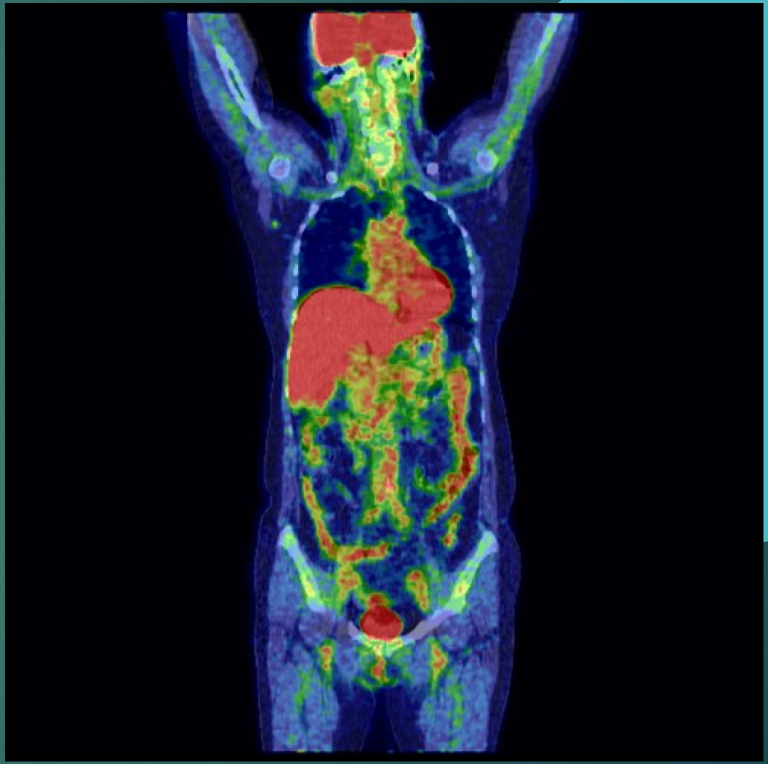


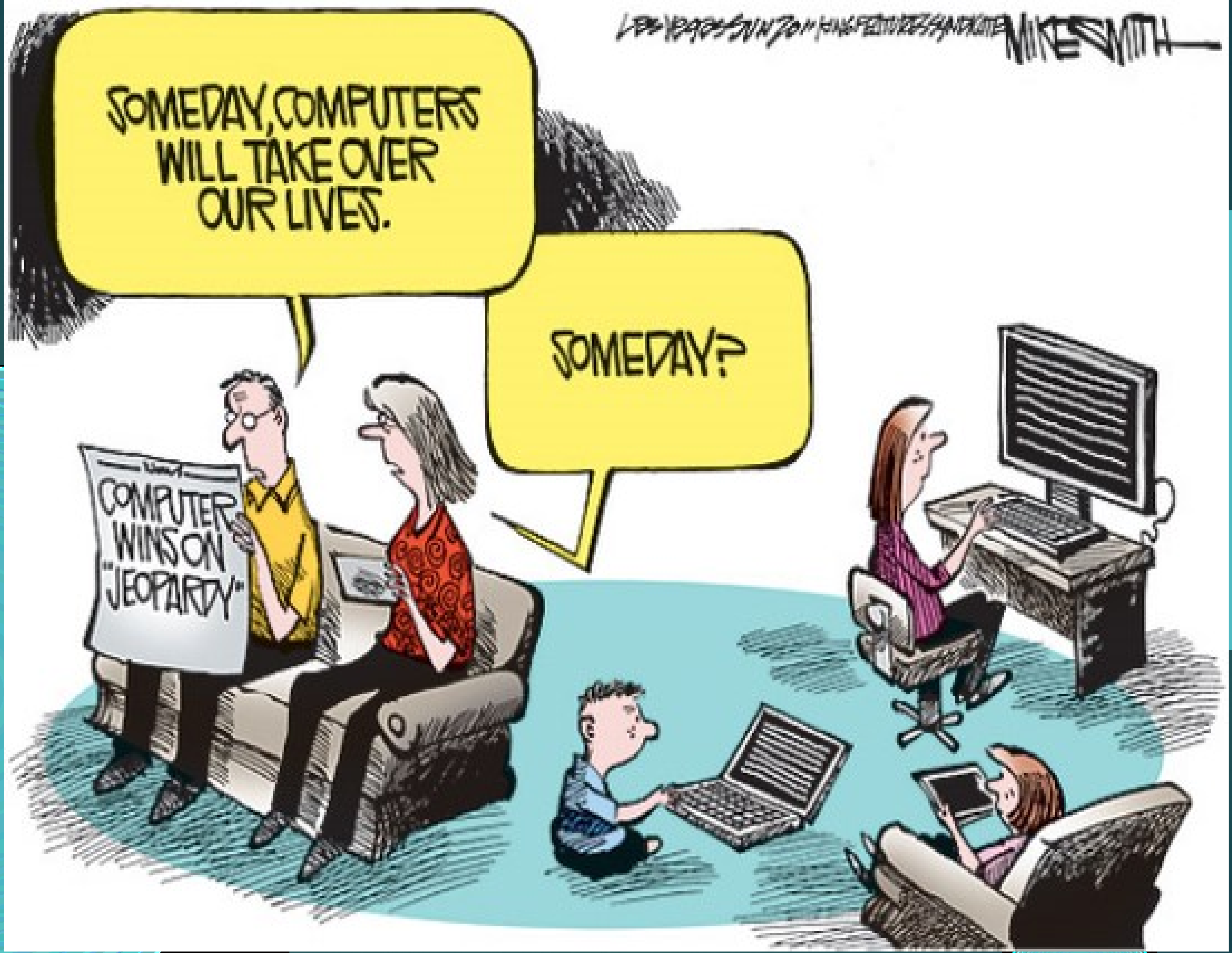
"And that's why we need a computer."

Computational models in biology and medicine








LAS VEGAS SUN 2011 KING FEATURES SYNDICATE MIKE SMITH
SOMEDAY, COMPUTERS WILL TAKE OVER OUR LIVES.
SOMEDAY?
COMPUTER WINS ON "JEOPARDY"