

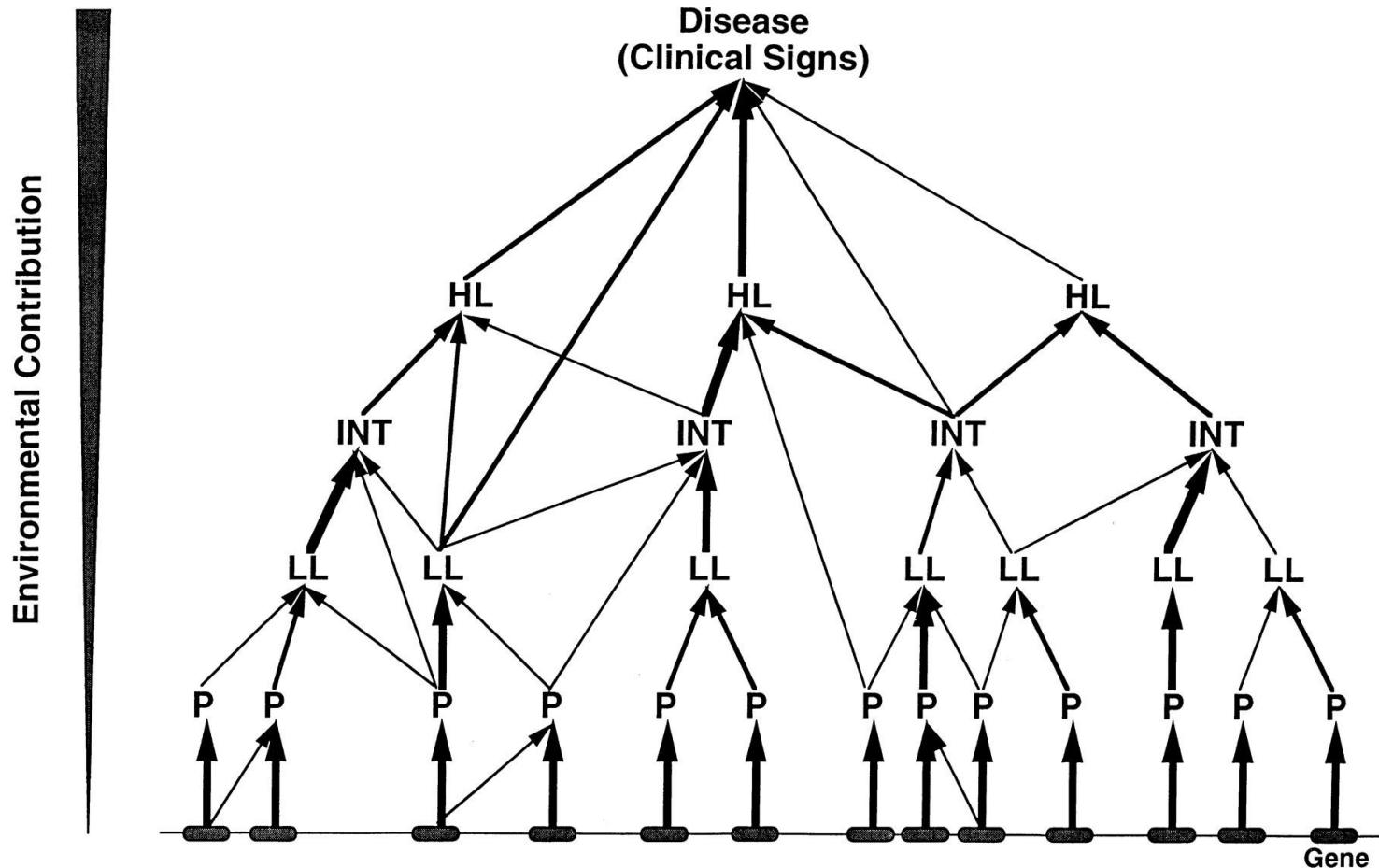
Fenomika

All about Eve (well, Adam too)

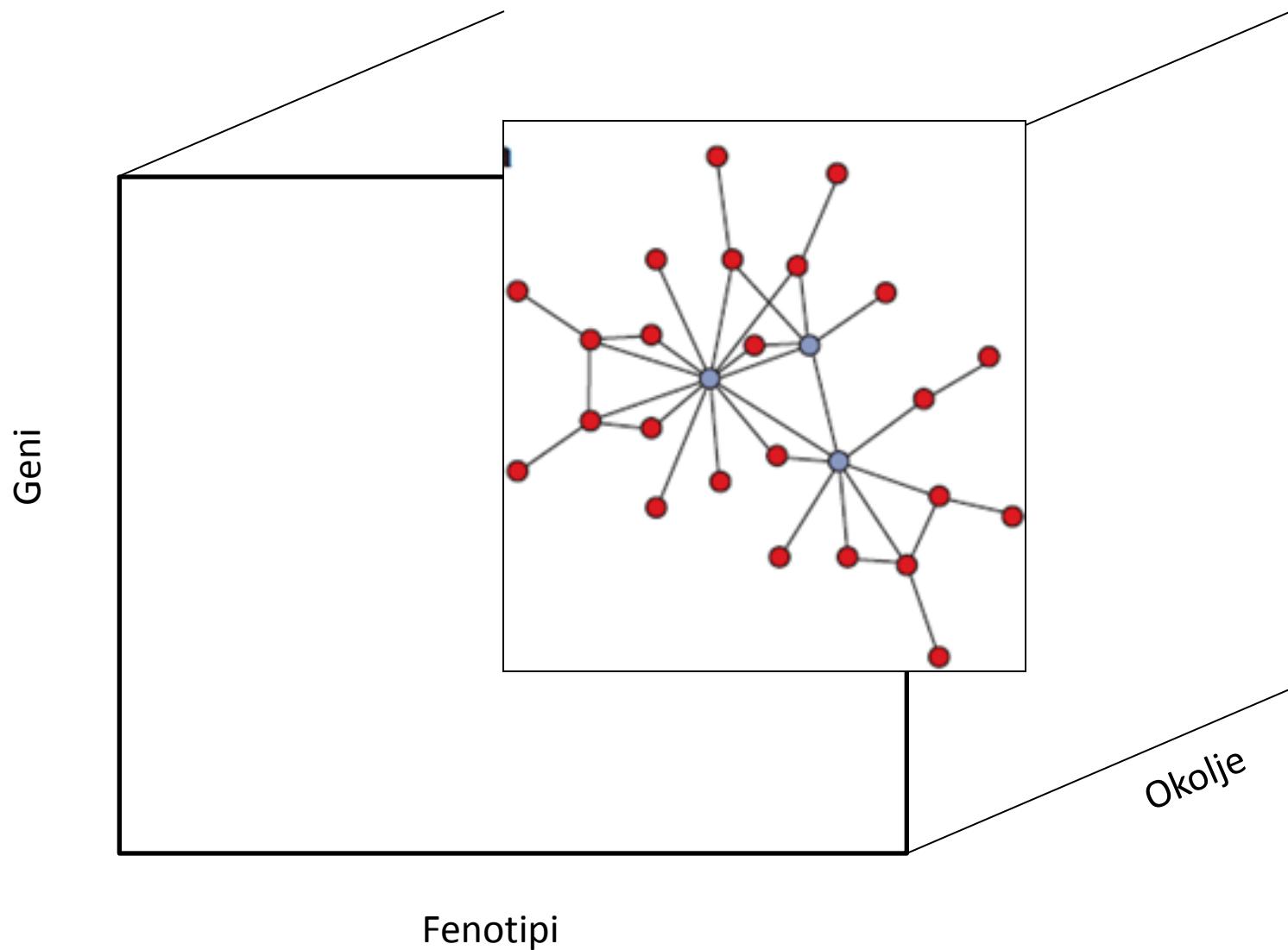


Nicholas J. Shork (1997) Genetics of complex disease: approaches, problems, and solutions.
Am J Respir Crit Care 156:S10

'In addition, a new discipline, "phenomics" or "phenometrics," could be initiated that would complement genomic research as presently performed.'



Pleiotropnost



Fenetika & Fenomika

Ena definicij fenomike: “**the acquisition of high-dimensional phenotypic data on an organism-wide scale**”, ali

pridobivanje visokodimenzionalnih podatkov na ravni celotnega organizma;

Houle D, Govindaraju DR, Omholt S. (2010) Nat Rev Genet. 11:855

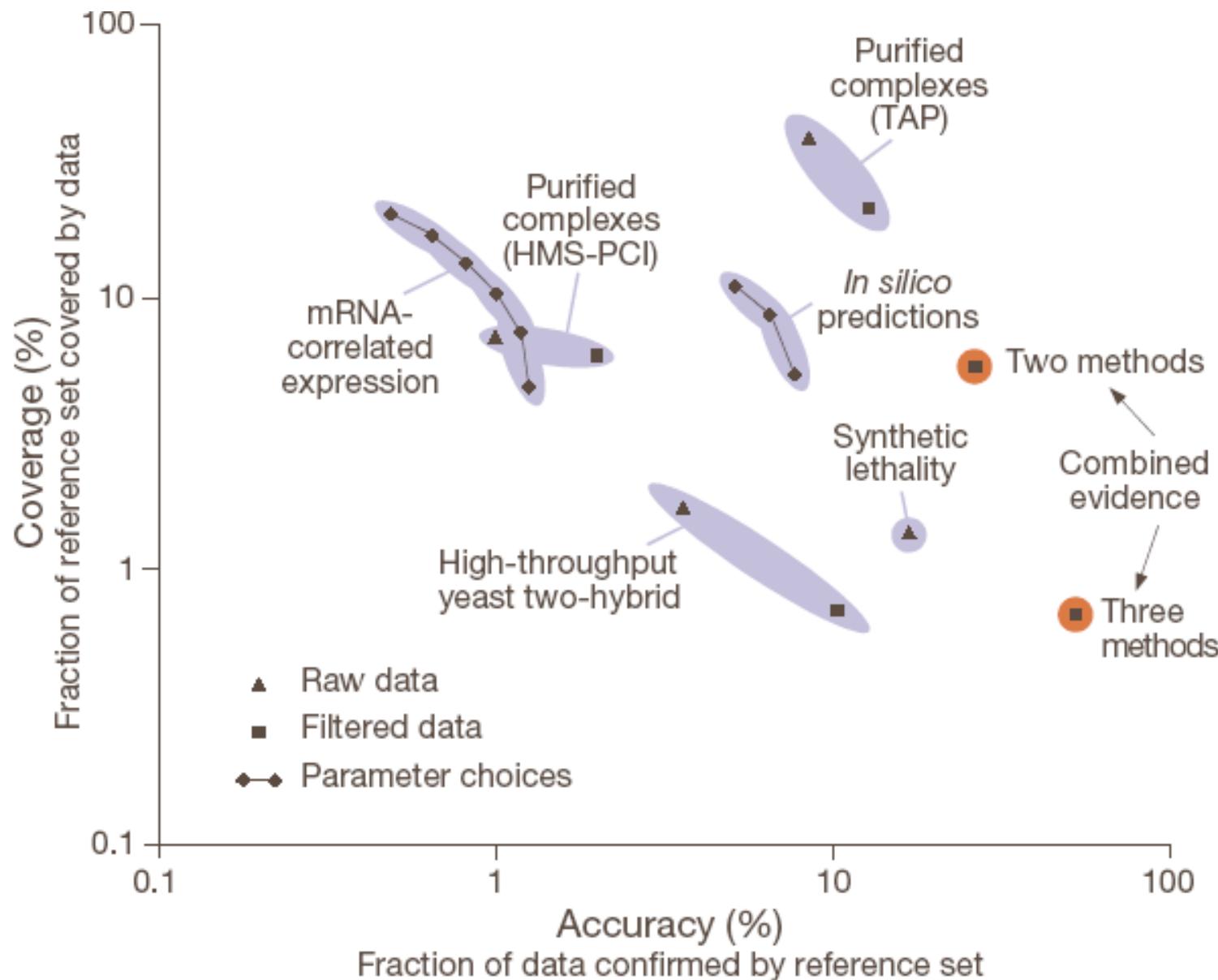
Opcija: merjenje specifične lastnosti pri organizmu, spremenjenem s perturbacijo na ravni celotnega genoma

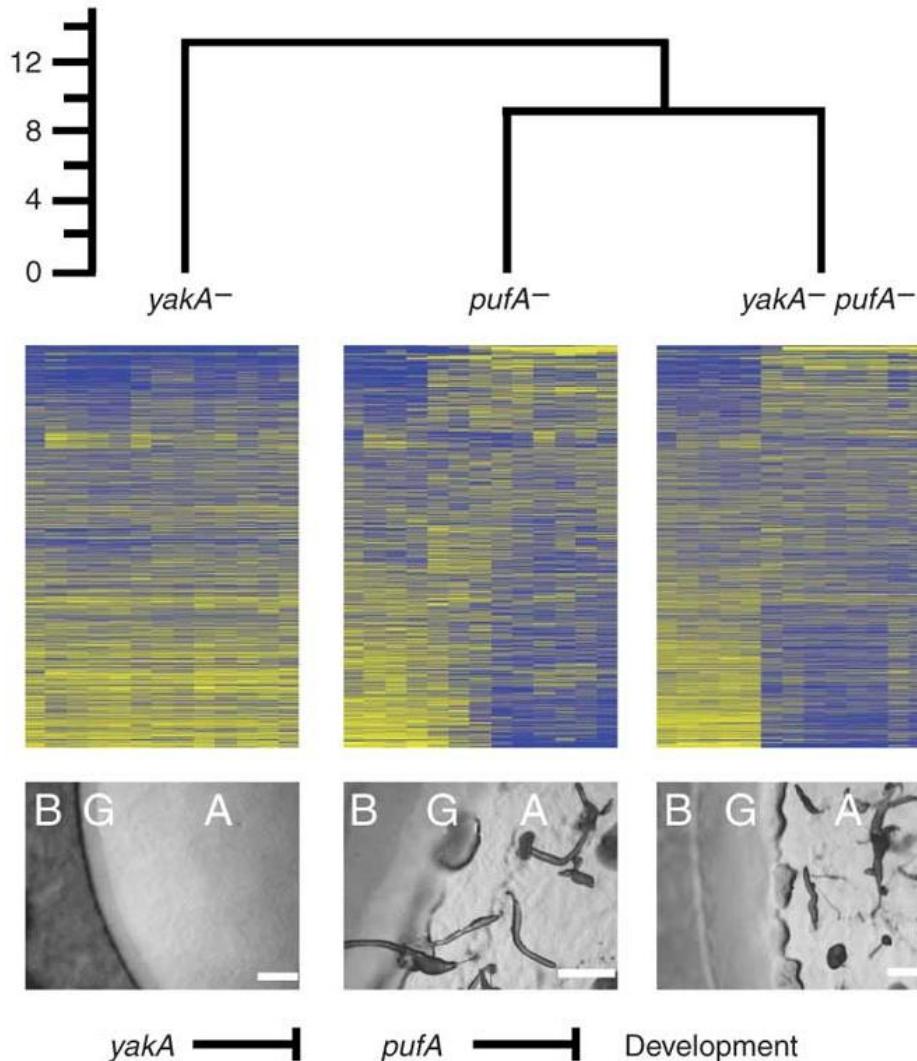
ekstenzivna vs. intenzivna fenomika

eks.: velik nabor fenotipov

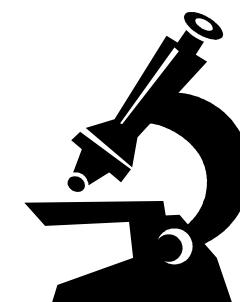
int.: velika globina posameznega fenotipa

Različni tipi podatkov





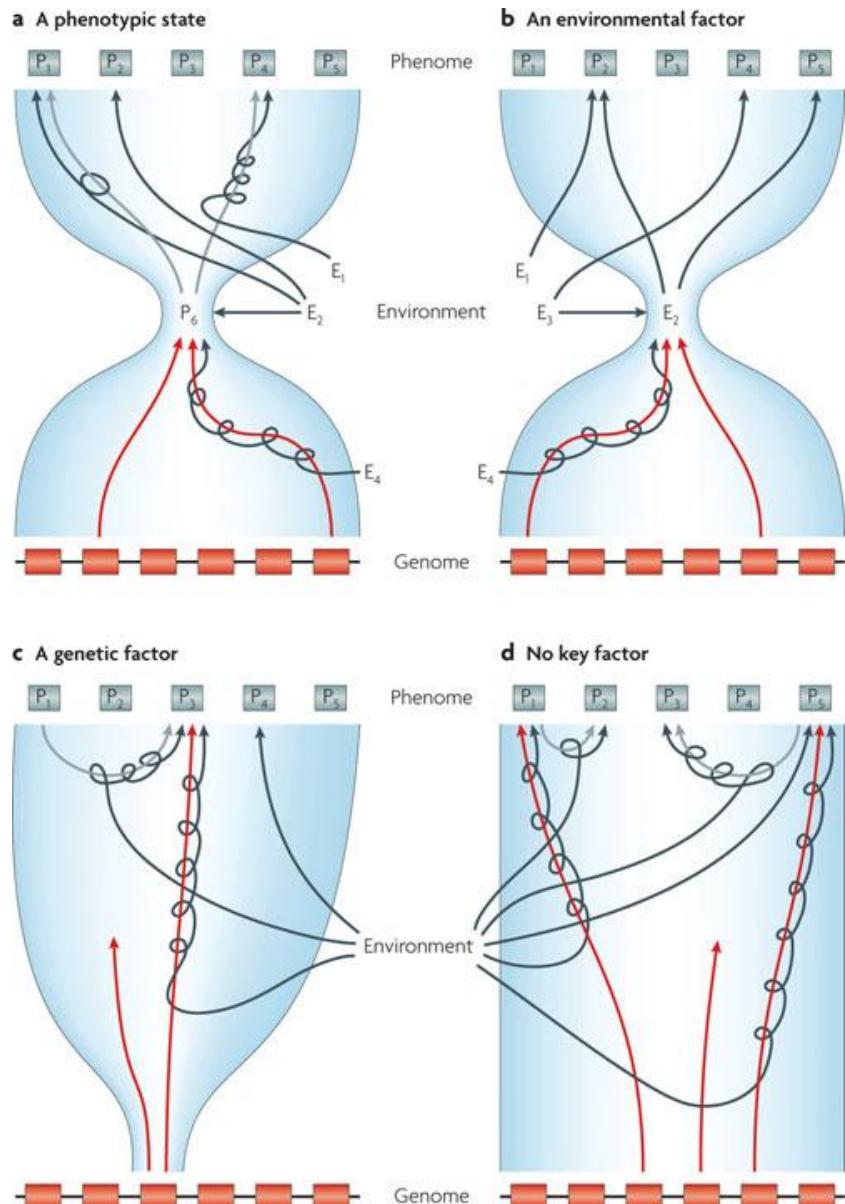
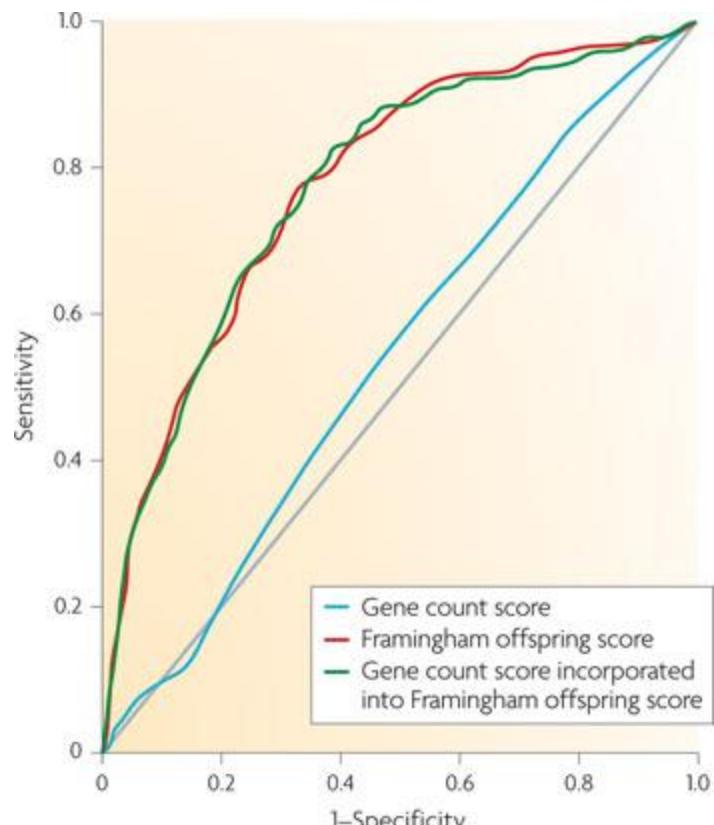
“Mikroskop molekularne biologije”



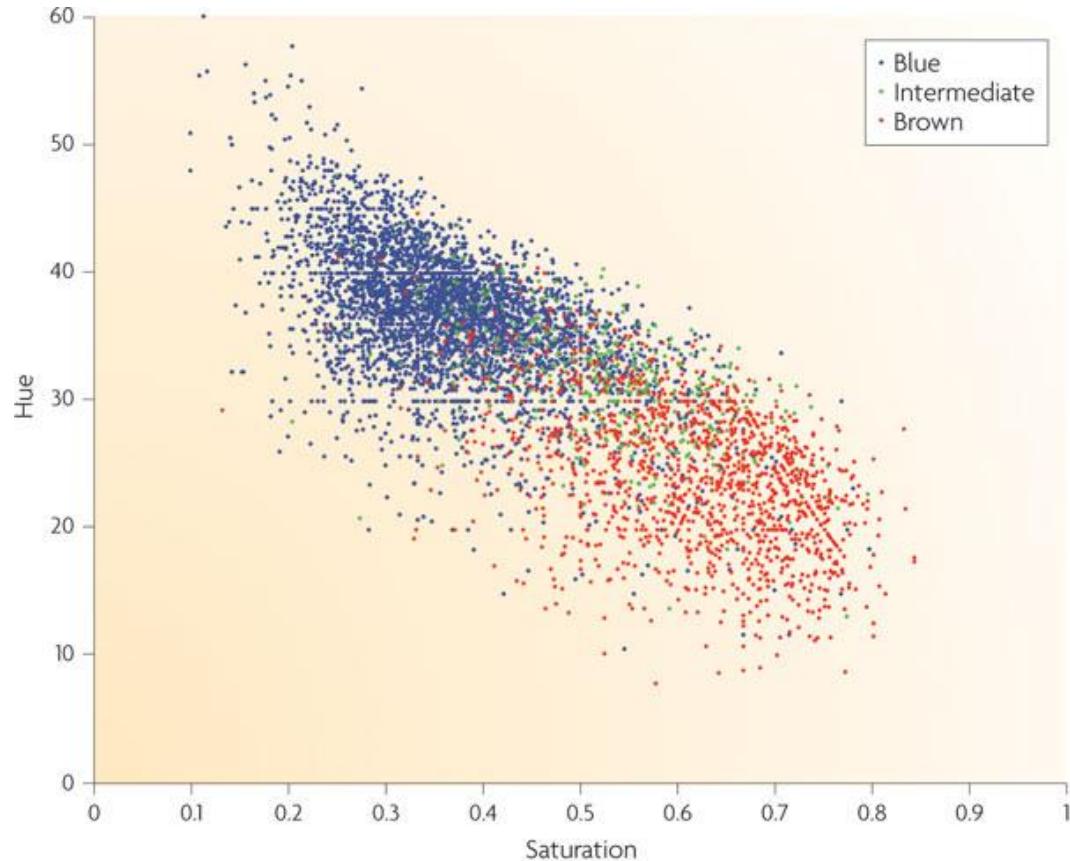
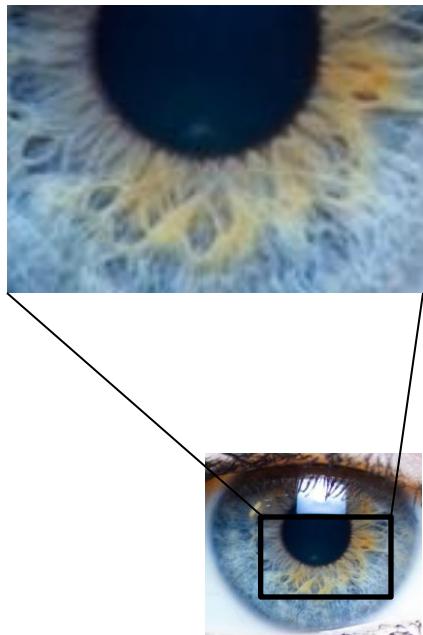
Van Driessche N, Demšar J, Booth EO, Hill P, Juvan P, Zupan B, Kuspa A, Shaulsky G. (2005) *Nature Genetics* 37:471

Ali lahko fenotipe napovedujemo?

Če da, na osnovi česa?



Diskretni in zvezni fenotipi



Nature Reviews | Genetics

Nat Rev Genet (2010) 11:855

Fenotipizacija preko bioloških hierarhij

Level	Extensive	Intensive
DNA, RNA	Solved and costs declining rapidly. Limited by bioinformatics capabilities	Possible but costly; detailed sampling is challenging
Chromatin	Made possible by chromatin immunoprecipitation but with low precision; costly	Possible but costly; detailed sampling is challenging owing to instability
Proteins, metabolites	Mostly solved and capabilities are still improving for rare constituents	Possible but costly; detailed sampling is challenging
Cells	Huge diversity of assays is possible but most are low throughput. Image-based techniques for high throughput are promising	Many temporally continuous assays. Image-based approaches allow some combination of extensive and intensive measurement
Development	Low-throughput measures are abundant. High-throughput image-based methods are possible for small living individuals (<i>embryos</i> and <i>Caenorhabditis elegans</i>) and sectioned tissues	Temporal depth by repeated sampling or image-based approaches
Physiology	Huge diversity of assays is possible, but most are low throughput, unless based on proteomic or metabolomic data	Many temporally continuous assays. Spatial sampling is often possible
Morphology	Solved in principle with the use of imaging, but assays often require extensive sample preparation. Post-processing to extract and measure features requires specialized informatics capability	Intensive sampling of morphological form is possible with specialized processing. Temporal depth is limited by destructive sampling
Behaviour	Possible with continuous observation of video of confined or local populations, or for humans, self-reporting. Data extraction from video using specialized software or human labour	Extensive sampling gives intensive coverage. Specific aspects of behaviour can be intensively measured with data loggers

Nat Rev Genet (2010) 11:855

Časovni razpon: ~15 velikostnih razredov

Prostorski razpon: ~9 velikostnih razredov

Podatkovne baze za fenotipe

Genotypic and phenotypic databases	Concepts				Relationships				
					Binary		Ternary		
	Gene	Molecular Class	Phenotype	Disease	Gene-Gene	Gene-Molecular Class	Gene-Phenotype	Gene-Disease	Gene-Molecular Class -Phenotype
Curated Phenomic Databases									
MGD (12)	●	●	●			■	■		■
OMIM (3, 69)	●		○	○			◊	◊	
OMIA (55, 71)	●		●	●			□	□	
Other model organism resources (12, 13, 55, 71–76)	●	●	●			□	□		□
Computationally-derived phenomic databases									
www.PhenoGO.org (35)	●	●	●	●	■	■	■	■	■
PhenomicDB (2)	●		○	○			◊	◊	
Genetic Association Database (77)	●		○	○					◊
GeneCards (59–61)	●					□		◊	
Phenomic analyses									
QMR-OMIM (63)	●		●	●			■	■	
Mining OMIM (78)									
GenesTrace (64)	●	●	●	●		■	■	■	■
UMLS-GEO Network (65)	●		●	●			■	■	
Literature-based techniques (19, 57, 62, 79, 80)	●		○	■			◊		□
Rank-based integration / fusion (70, 81)	●	●				■		◊	◊



Minimum Information Standards

From Wikipedia, the free encyclopedia

Contents [hide]

1 MI Standards

- 1.1 MIAME, gene expression microarray
 - 1.1.1 MIAME-env, environmental genomics
 - 1.1.2 MIAME-nut, nutritional genomics
 - 1.1.3 MIAME-tox, toxogenomics
 - 1.1.4 MIAME-Plant, plant
- 1.2 MINI: Minimum Information about a Neuroscience Investigation
 - 1.2.1 MINI: Electrophysiology
- 1.3 MIARE, RNAi experiment
- 1.4 MIACA, cell based assay
- 1.5 MIAPE, proteomic experiments
- 1.6 MIMIx, molecular interactions
- 1.7 MIAPAR, protein affinity reagents
- 1.8 MIABE, bioactive entities
- 1.9 MIGS/MIMS, genome/metagenome sequences
- 1.10 MiFlowCyt, flow cytometry
 - 1.10.1 Minimum Information about a Flow Cytometry Experiment
- 1.11 MISFISHIE, In Situ Hybridization and Immunohistochemistry Experiments
- 1.12 MIAPA, Phylogenetic Analysis
- 1.13 MIAO, ORF
- 1.14 MIAMET, METabolomics experiment
- 1.15 MIAFGE, Functional Genomics Experiment
- 1.16 MIRIAM, Minimum Information Required in the Annotation of Models
- 1.17 MIASE, Minimum Information About a Simulation Experiment
- 1.18 CIMR, Core Information for Metabolomics Reporting

2 References

3 External links

- 3.1 MIBBI Minimum Information for Biological and Biomedical Investigations
- 3.2 FGED Society
- 3.3 HUPO-PSI HUPO Protein Standards Initiative
- 3.4 FuGE Functional Genomics Experiment
- 3.5 MSI The Metabolomics Standards Initiative
- 3.6 MIACA, Minimum Information About a Cellular Assay
- 3.7 MIARE, Minimum Information About an RNAi Experiment
- 3.8 MiFlowCyt, Minimum Information about a Flow Cytometry Experiment
- 3.9 Nature Community Consultation

4 References



PhenomicDB

Enter term(s) or part of a term:
[How to search](#)

Example: [apoptosis](#)
in these sections:

All

 Use wildcard (If unselected wildcard can be used with *)

Select Organisms:

- All
- [Caenorhabditis elegans](#)
- [Dictyostelium discoideum](#)
- [Fruit fly](#)
- [Human](#)
- [Mouse](#)
- [Yeast](#)
- [Zebrafish](#)

Restrict query to:

- genotypes
- phenotypes
- only genotypes with associated phenotypes
- only phenotypes with associated genotypes
- no restriction

Select data fields to show:

- Default
- Official gene symbol
- Gene description
- External genotype ID
- NCBI Gene ID
- mRNA ID
- GO term
- GO ID

PhenomicDB is a multi-organism phenotype-genotype database including human, mouse, fruit fly, *C.elegans*, and other model organisms. The inclusion of gene indeces ([NCBI Gene](#)) and orthologues (same gene in different organisms) from [HomoloGene](#) allows to compare phenotypes of a given gene over many organisms simultaneously.

PhenomicDB contains data from publicly available primary databases: FlyBase, Flyrnai.org, WormBase, Phenobank, CYGD, MatDB, OMIM, MGI, ZFIN, SGD, DicBase, NCBI Gene, and HomoloGene.

[View cluster statistics](#)

Statistics

Organism	Phenotypes	Genotypes	
		all	with orthologues
Caenorhabditis elegans	130777	49436	8678
Dictyostelium discoideum	11230	13893	0
Fruit fly	154223	34679	9263
Human	8944	42562	18832
Mouse	29444	86976	21470
Yeast	80846	7218	4849
Zebrafish	5736	47742	18668
Other	21985	8068897	154383

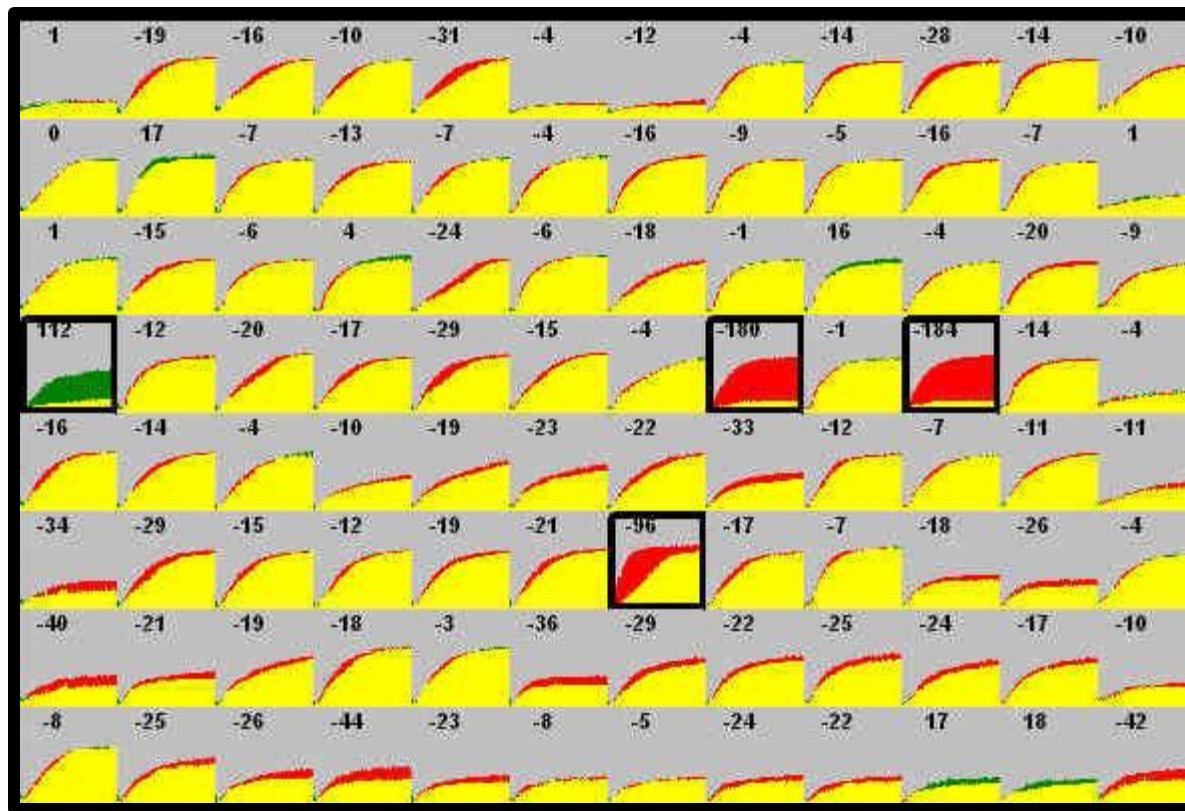
How to link to PhenomicDB using e.g. RefSeq identifiers
 PhenomicDB in Science: [From Gene To Flesh](#),
[Citing PhenomicDB](#)

Biobar features PhenomicDB

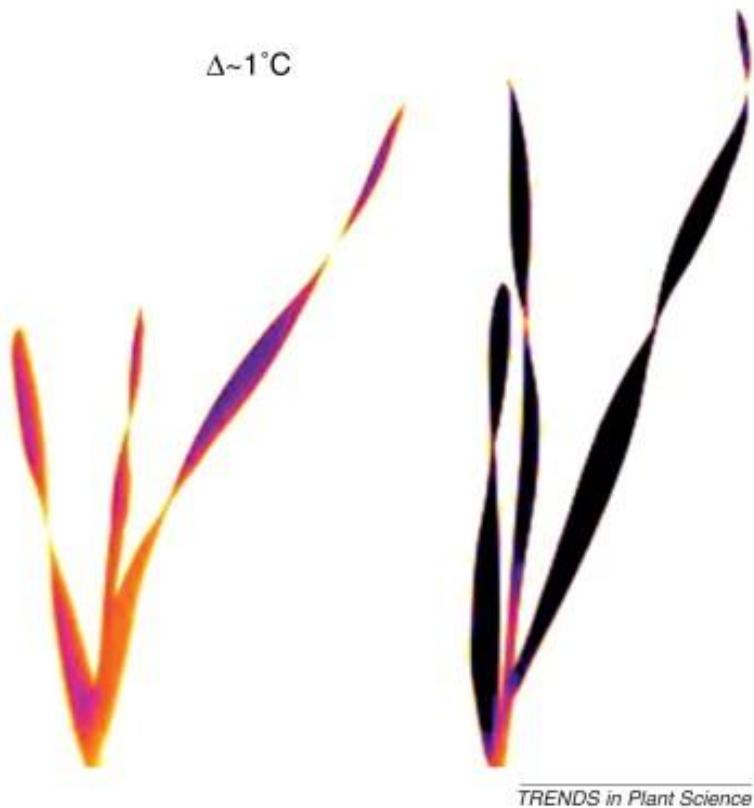


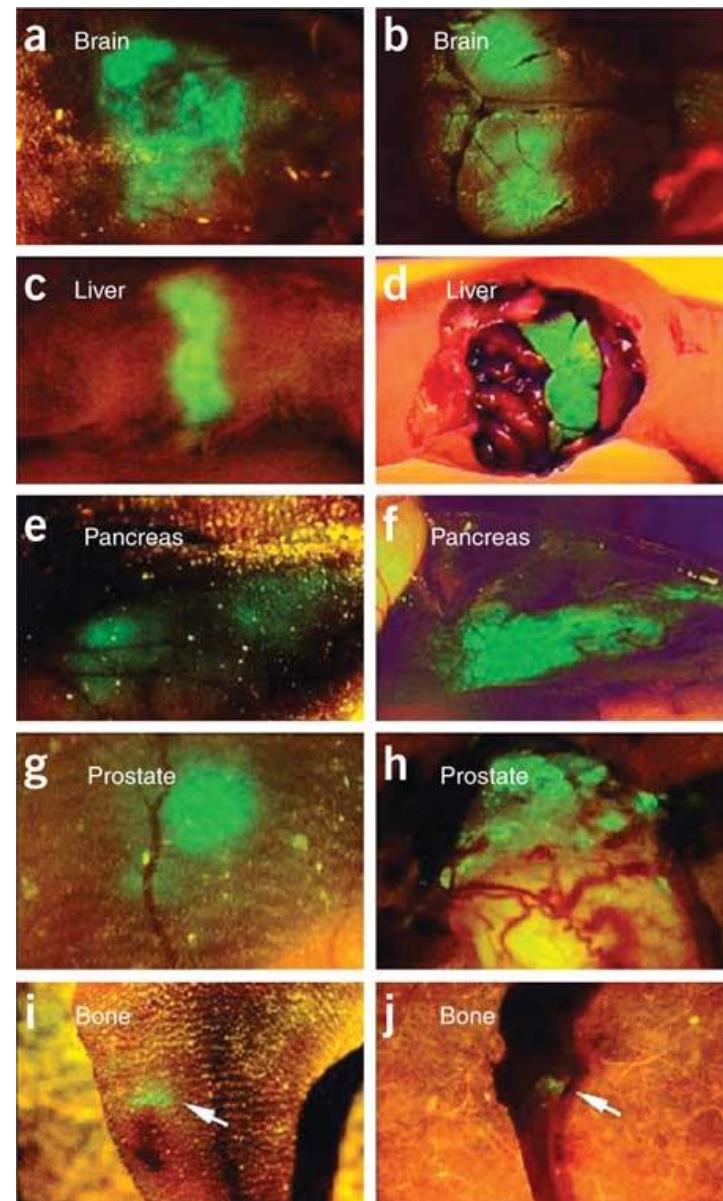
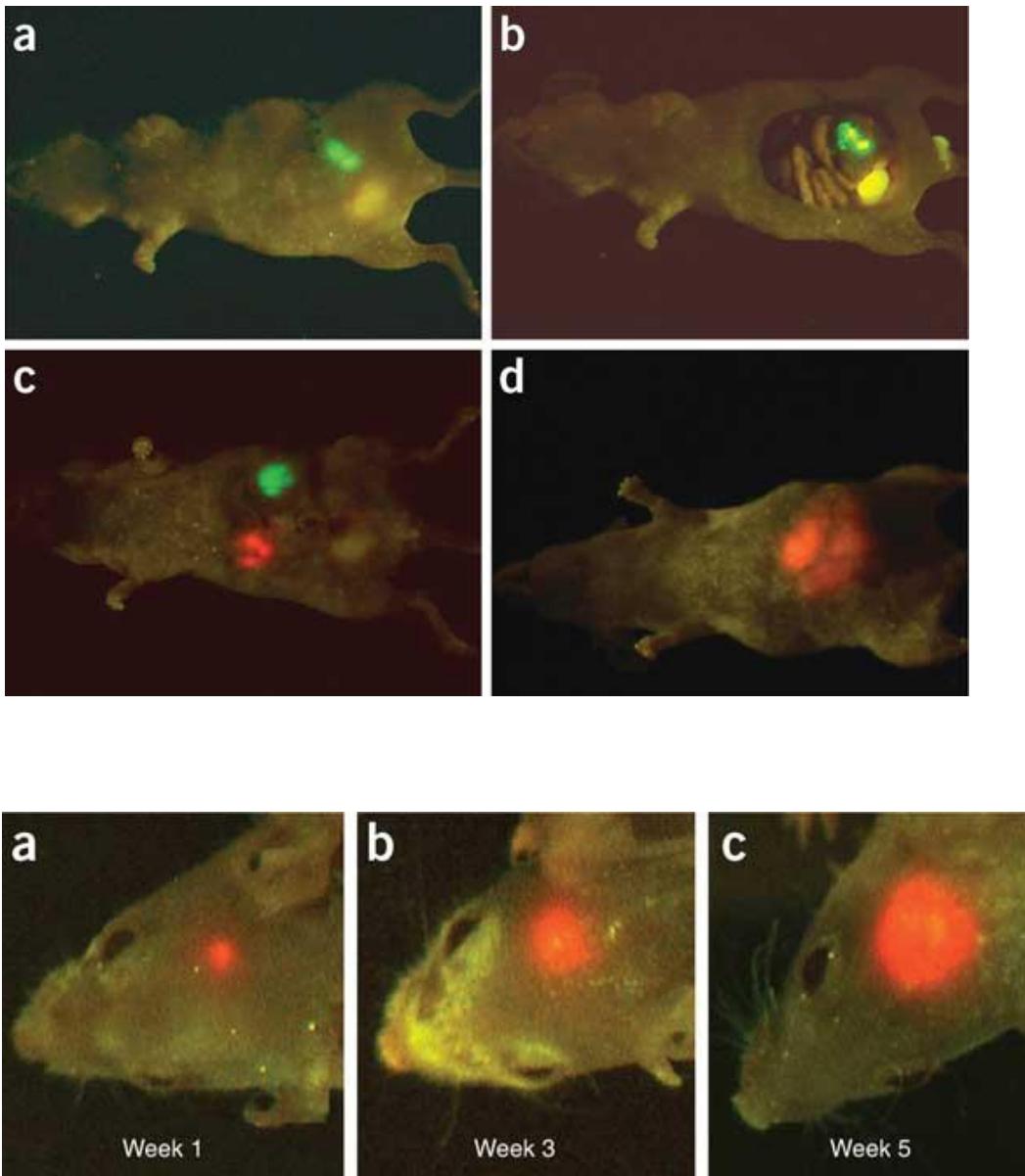
Analiza posameznih celic vs. analiza populacije

Phenotype microarray (Fenotipska ‘mikromreža’)

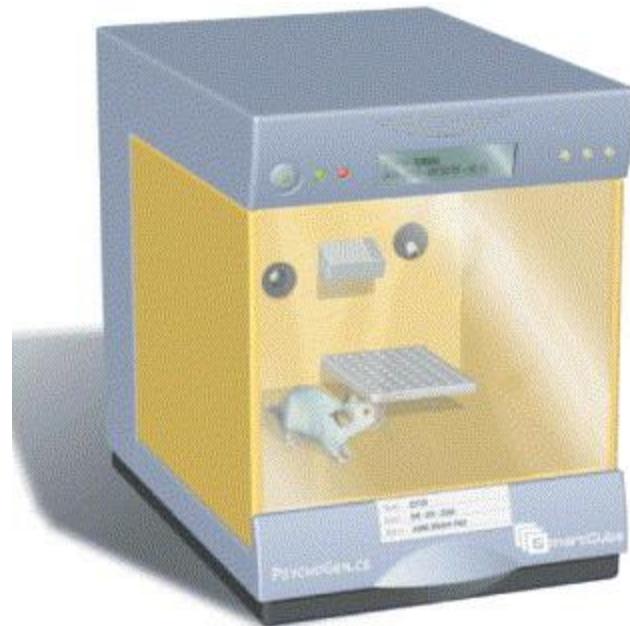


Abiotski stres – termalna fotografija



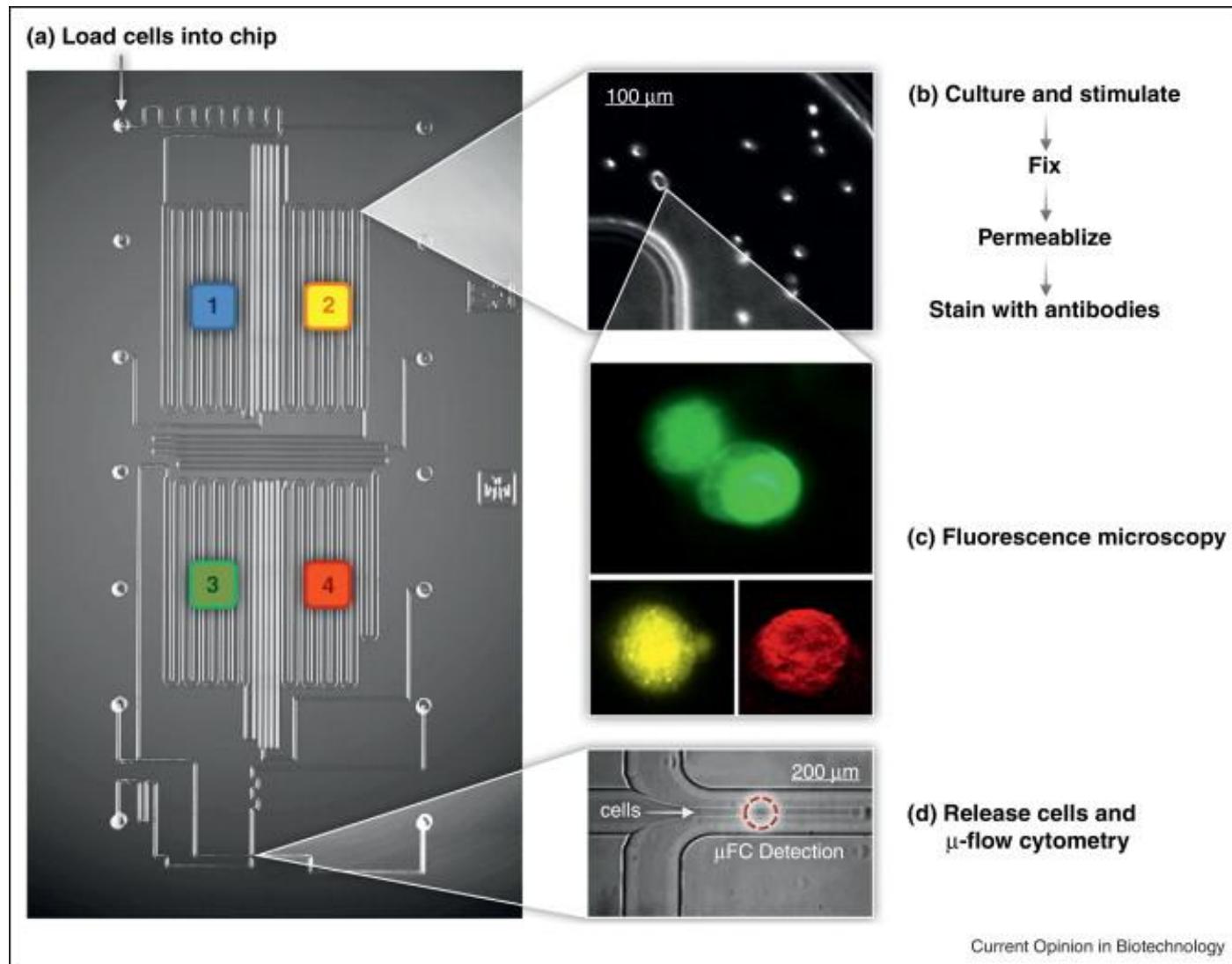


Sistematično testiranje obnašanja



SmartCube™ (PsychoGenics, Inc.)

Mikrotekočinski sistemi



Analiza podatkov

- Analiza slik (*Image analysis*)
- Problem LPSN (*large p, small N*)



Statistične metode
*(SVM, Random forest,
Partial least-square
regression)*



**“A imate še kaj
drugega na zalogi?”**

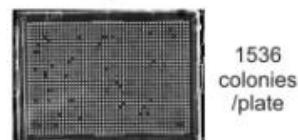
cG-P modeli

HCM - natančnost

Integration of GFP fusion protein into ~4900 haploid yeast deletion strains. Pinning of yeast colonies on solid media plates (→robotics).



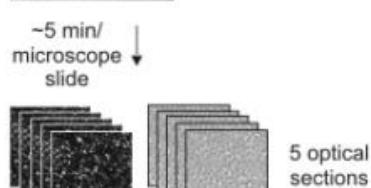
~20 days



Creation of high-density arrays of yeast colonies on solid media plates (→robotics).



~10 min



~5 min/ microscope slide

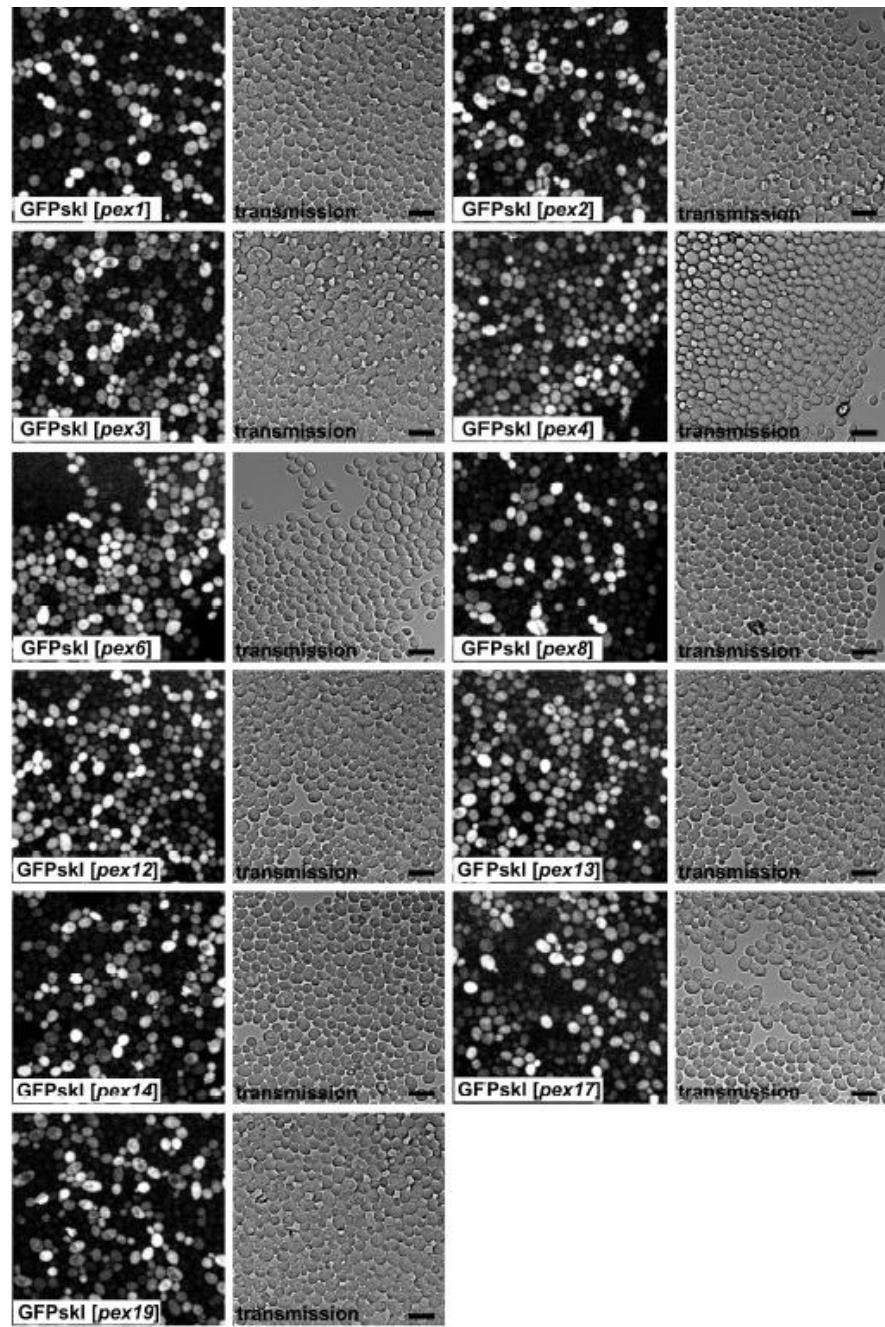
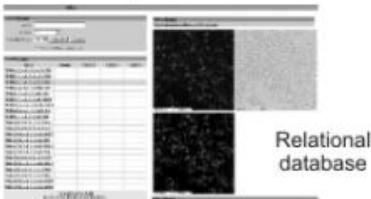
~30 min/ 96 samples



Semi-automated acquisition of 3d fluorescence and 3d transmission data. (→custom-made microscope control software).

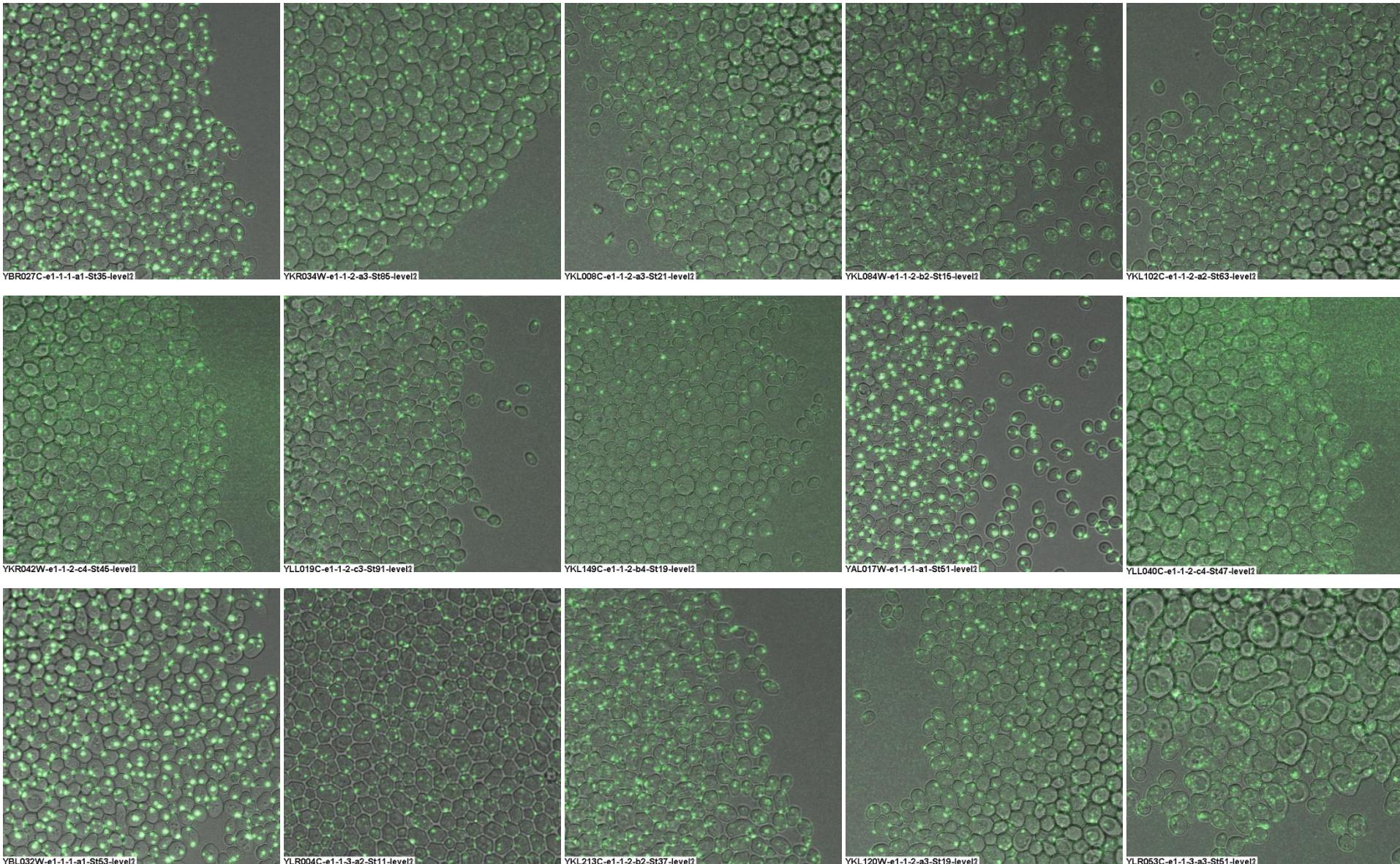
Automated filtering, visualization and quantification of generated 3d image data (→custom-made software).

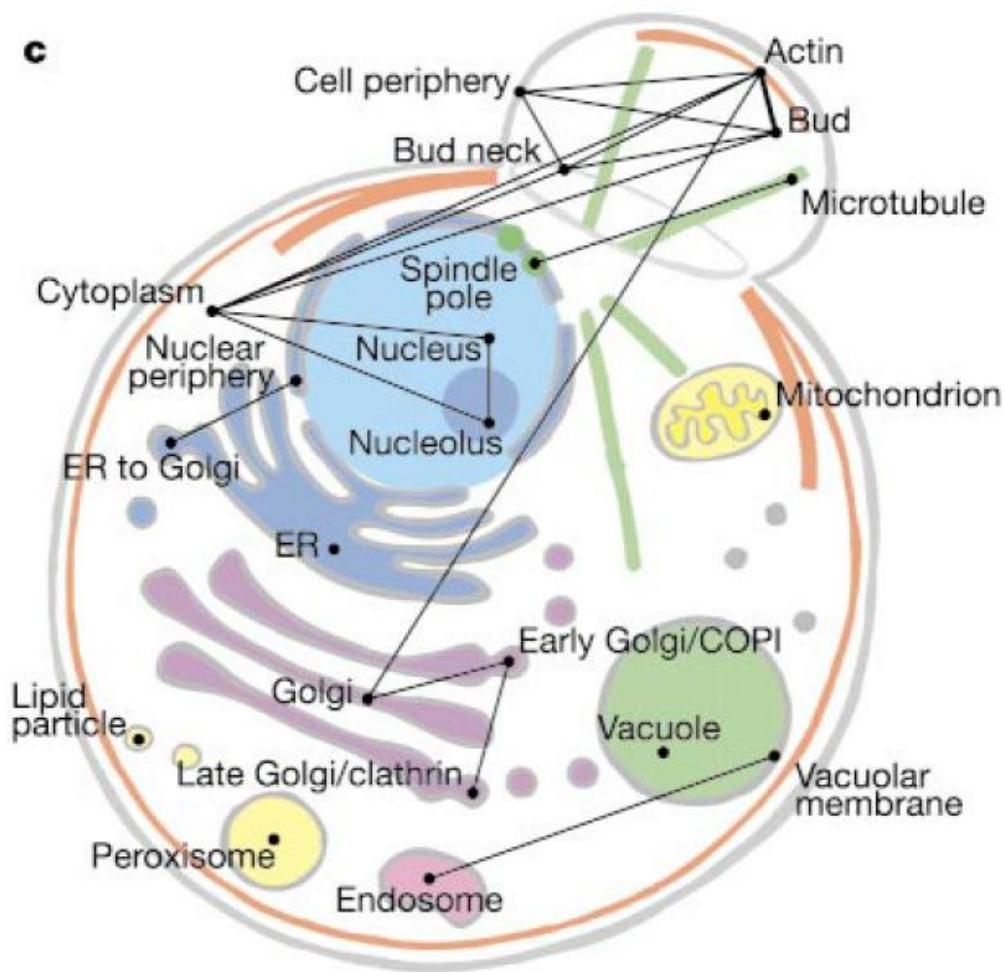
Storage of acquired image data and of numerical data



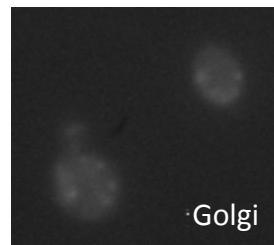
Napake pri metodah funkcijске genomike: kako izvreči lažno pozitivne oziroma kako ujeti lažno negativne

Analiza slike: človek vs. računalnik

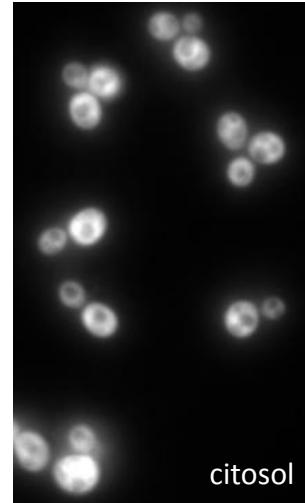


c

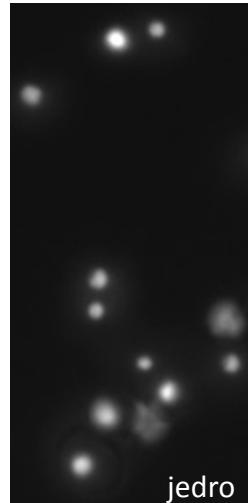
Nature (2003) 425:686



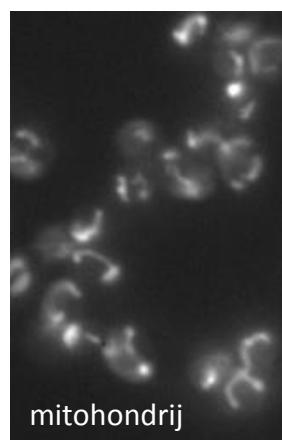
Golgi



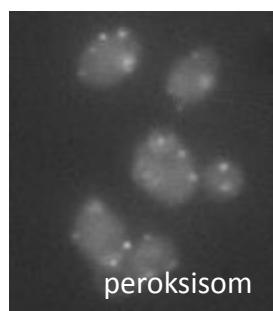
citosol



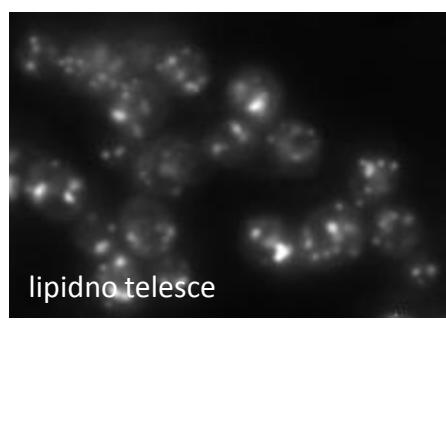
jedro



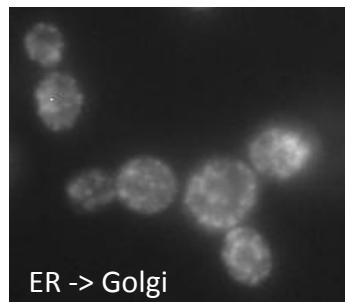
mitochondrij



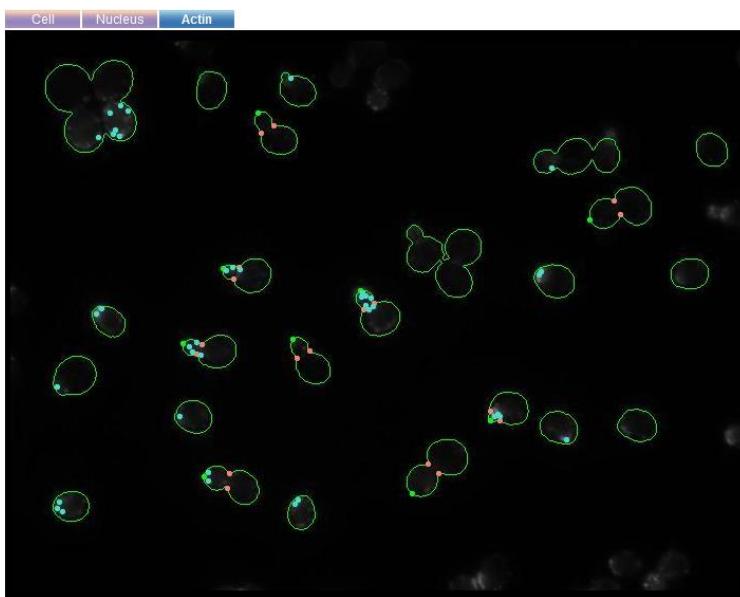
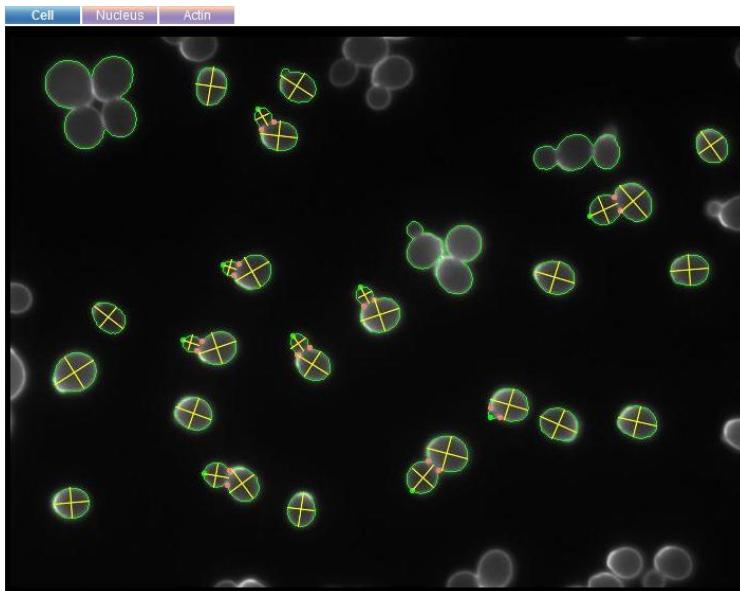
peroksisom



lipidno telesce



ER -> Golgi



~500 morfoloških parametrov

Kateri so **paralelni** in kateri
ortogonalni?

