



The Virtual Embryo Project: **a computational framework for** **developmental toxicity**



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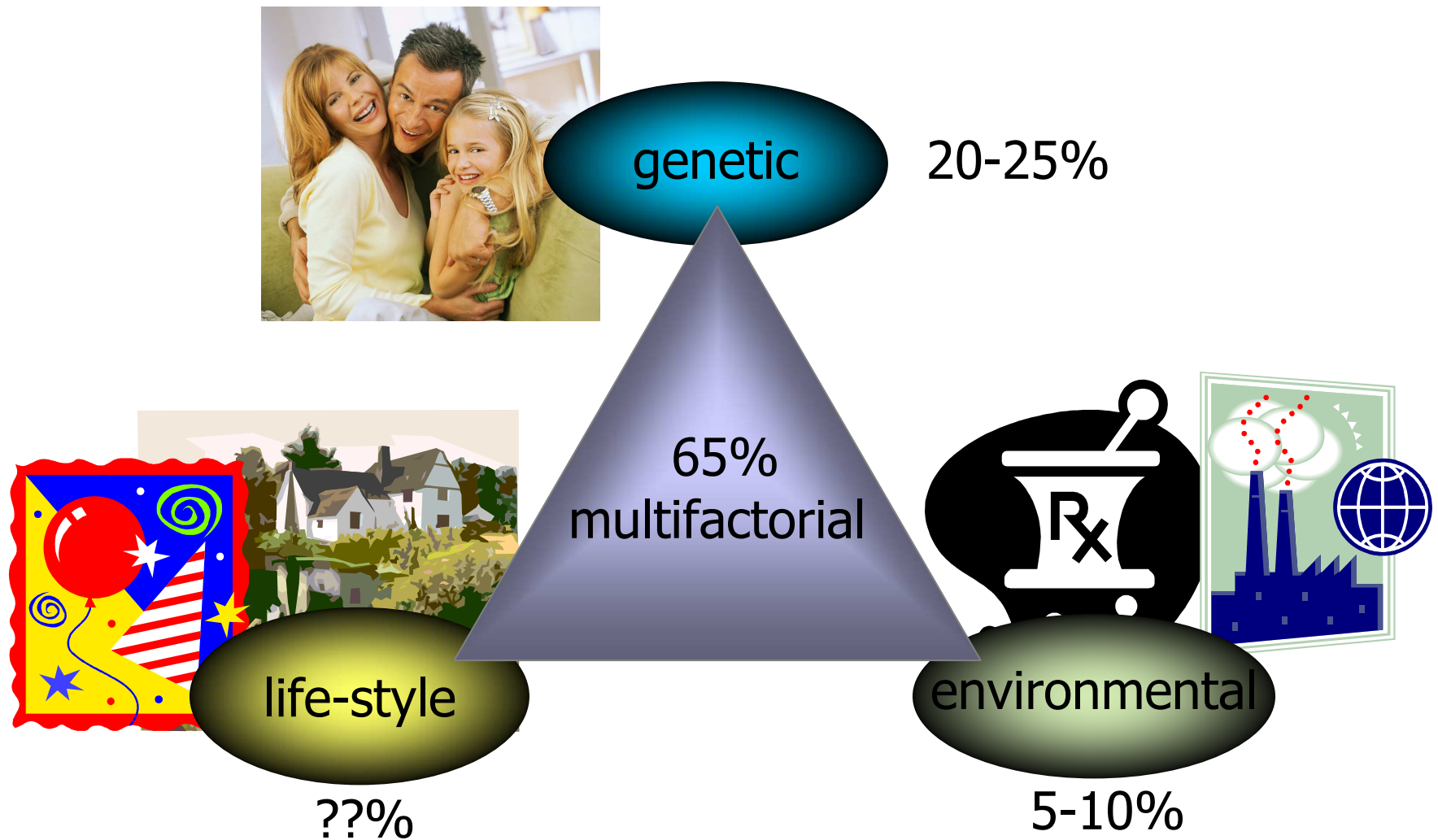


Outline

- ❖ scope of the problem
- ❖ new vision and strategy
- ❖ v-EmbryoTM
- ❖ developmental systems biology
- ❖ virtual tissues and simulators



Scope of the Problem: developmental (prenatal) defects





Limitations of the current strategy

- ❖ developmental endpoints are likely sensitive to many chemicals a fetus may be exposed to via the environment
- ❖ testing methods for developmental endpoints are expensive, time consuming, and use lots of animals
- ❖ not sensitive to developmental endpoints such as subtle malformations, functional defects or fetal programming
- ❖ nos. of chemicals requiring evaluation for developmental toxicity far exceeds what has and can be delivered



New strategy: systems biology

- ❖ genome-based technologies coupled with advances in robotics generates data comprehensively and efficiency
- ❖ use bioinformatics and computational biology to build systems-based models of detailed embryological events
- ❖ potential to significantly accelerate understanding of chemical mechanisms and toxicity pathways *in vitro*
- ❖ Holy Grail: revolutionize the way scientifically defensible predictions of toxicity *in vivo* can be based



high-throughput bioactivity profiling

Biological spectra analysis: Linking biological activity profiles to molecular structure

Anton F. Fliri*, William T. Loging, Peter F. Thadeio, and Robert A. Volkman*†

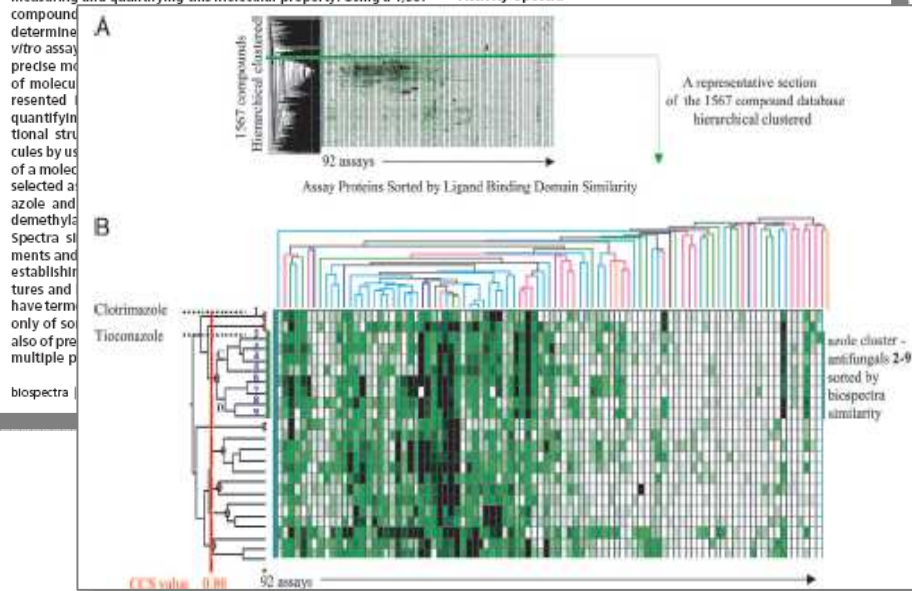
Pfizer Global Research and Development, Groton, CT 06340

Communicated by Larry E. Overman, University of California, Irvine, CA, October 25, 2004 (received for review September 4, 2004)

Establishing quantitative relationships between molecular structure and broad biological effects has been a longstanding challenge in science. Currently, no method exists for forecasting broad biological activity profiles of medicinal agents even within narrow boundaries of structurally similar molecules. Starting from the premise that biological activity results from the capacity of small organic molecules to modulate the activity of the proteome, we set out to investigate whether descriptor sets could be developed for measuring and quantifying this molecular property. Using a 1,567-

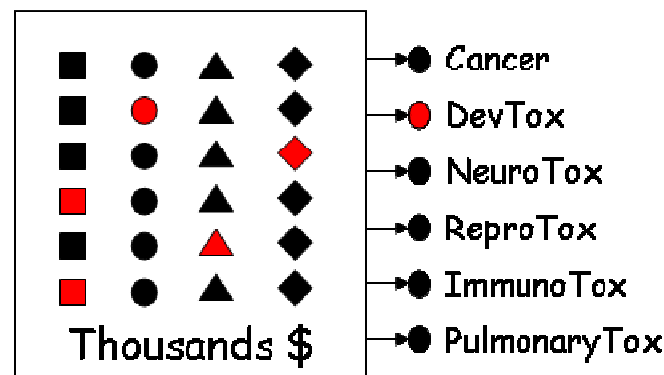
differences in biological environments (8). Considering the complexity of this requirement, computational solutions that precisely link molecular structure to broad biological response are currently not possible (9, 10). We report here an approach to structure-function studies that is based on measurements of the capacity of molecules to interact with the proteome (11).

Translation of Chemical Property Information into Biological Activity Spectra



SOURCE: Fliri et al. (2005) PNAS 102: 261–266

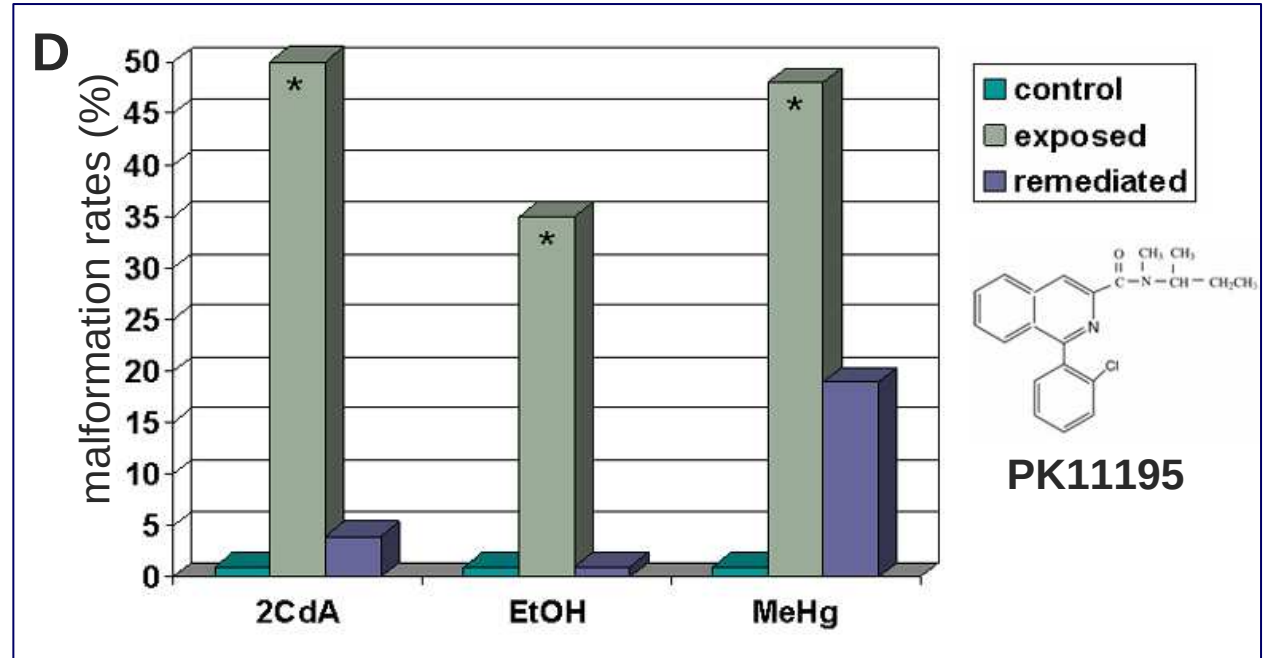
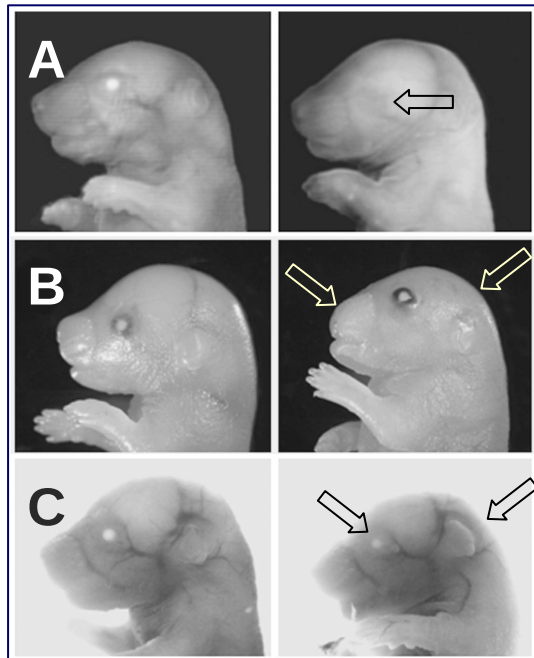
EPA's ToxCast™ Research Program: predictive signatures for thousands of environmental chemicals



SOURCE: David Dix, NCCT



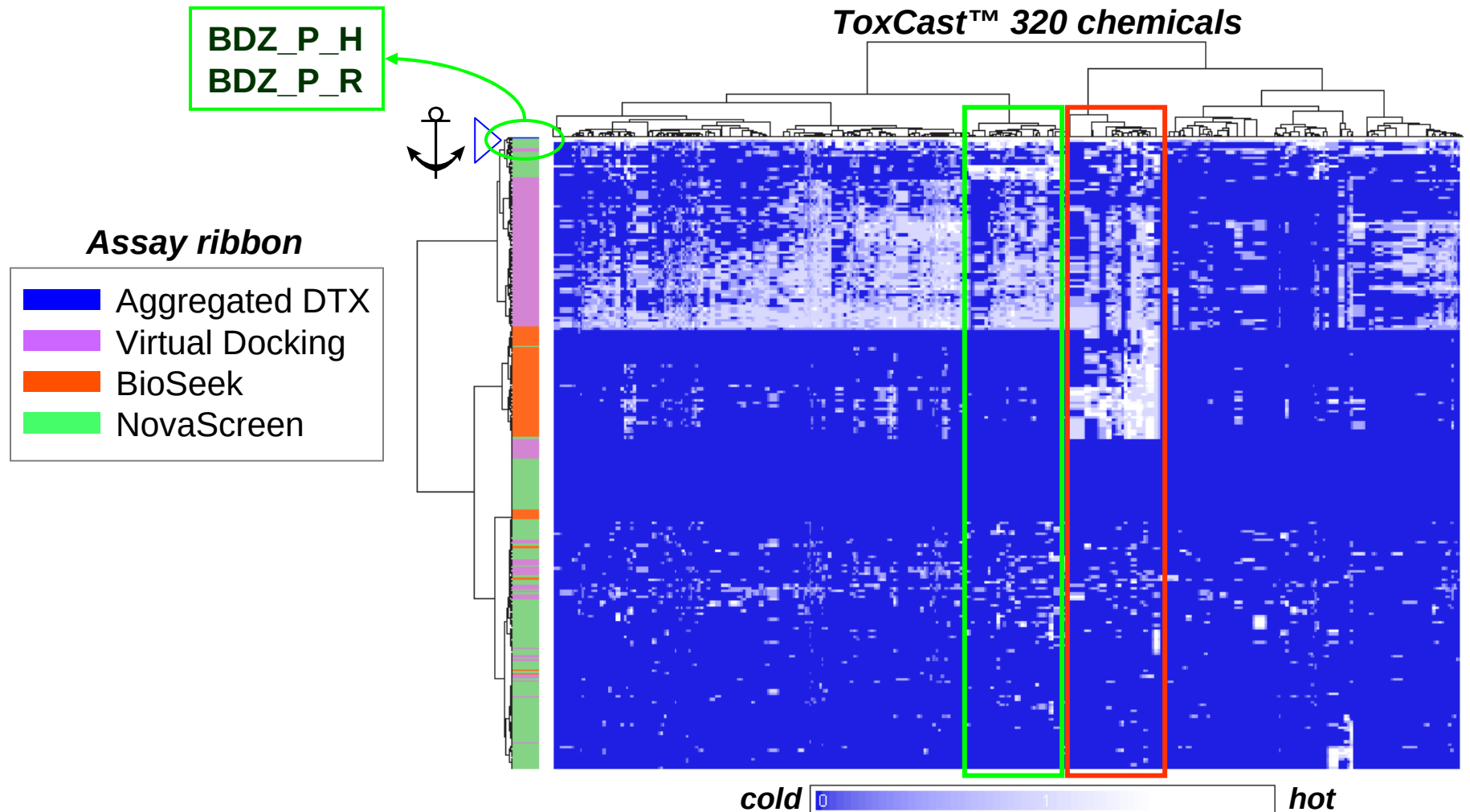
in vivo animal models



- (A) Eye Reduction Defects (ERD) with 2-chloro-2'-deoxyadenosine (**2CdA**) on day 8
- (B) Fetal Alcohol Syndrome (FAS) with ethanol (**EtOH**) exposed on gestation day 8
- (C) Fetal Minamata Disease (FMD) with methylmercury (**MeHg**) exposed on day 9
- (D) Remediation: co-exposed to mitochondrial *BDZ_P* ligand (**PK11195**) on day 8 or 9

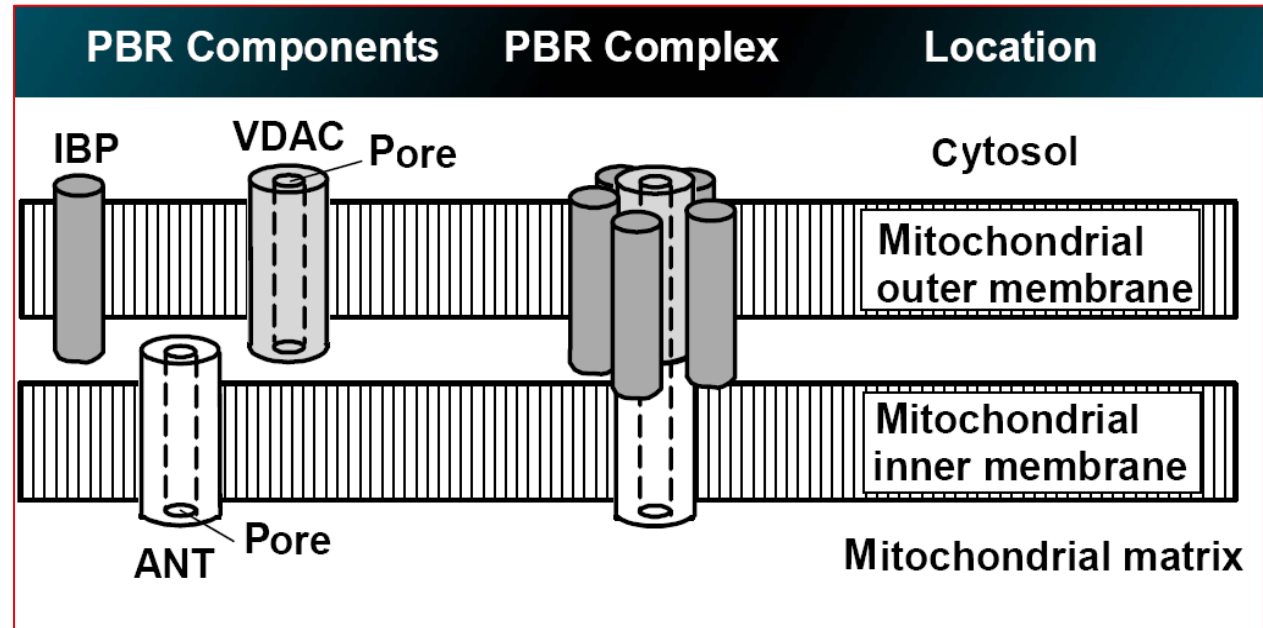
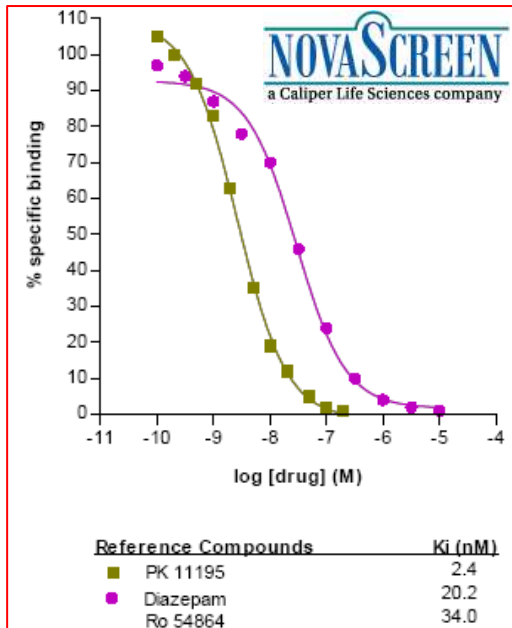


bioactivity profile: ~280 chemicals from ~1300 prenatal studies (ToxRefDB_3700) clustered by ~380 assays and anchored to aggregate developmental toxicity





BDZP: peripheral-type benzodiazepine receptor (new name TSPO for mitochondrial 18K TranSPOrter)

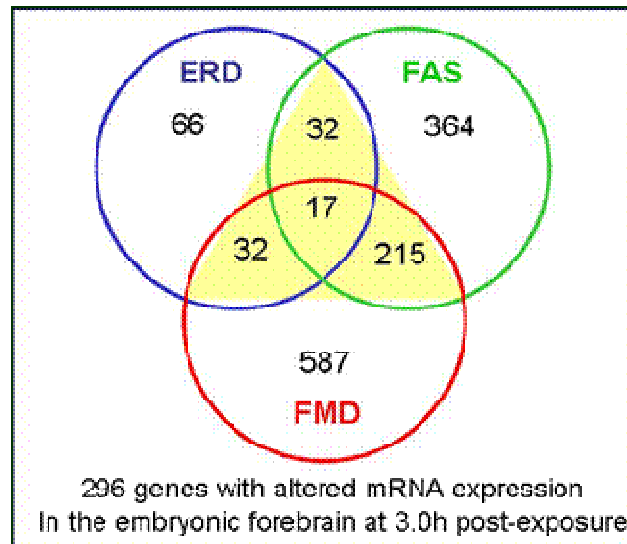


Putative functions:

steroidogenesis (StAR)
oxygen sensing (NRF1)
apoptosis (BCL2)
genomic signals (p53)

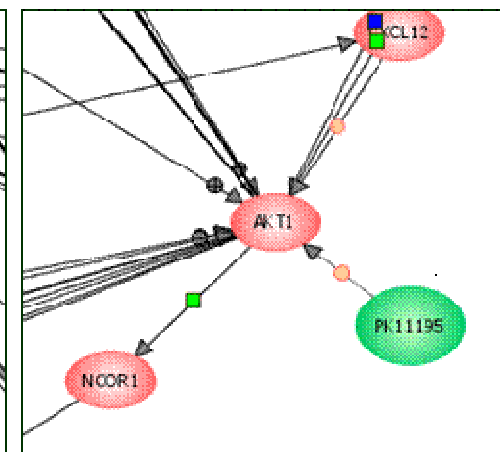
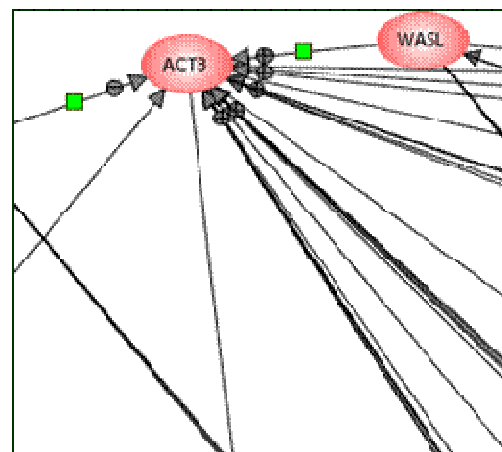
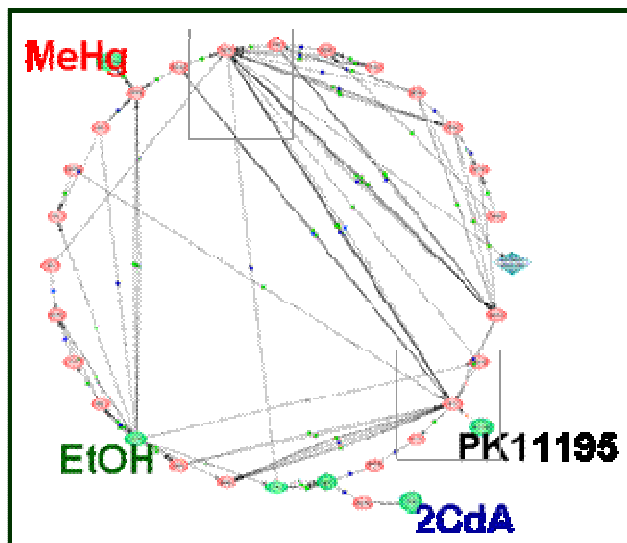


core gene network in early embryos



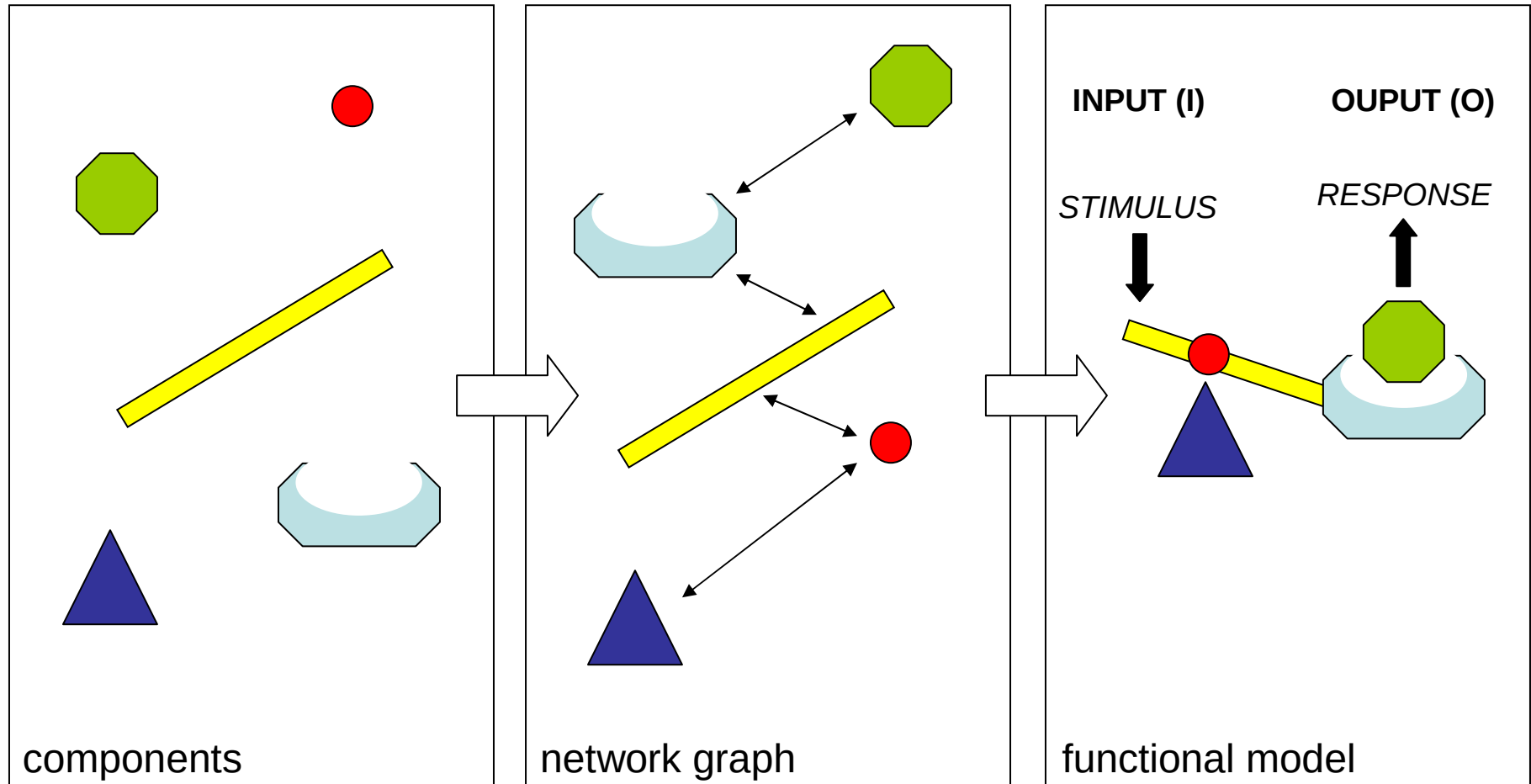
KEGG PATHWAY

	LIST	P value
RIBOSOME	55	2.52E-06
FOCAL ADHESION	41	0.010225
CALCIUM SIGNALING PATHWAY	36	0.006316
INSULIN SIGNALING PATHWAY	27	0.034363
PHOSPHATIDYLINOSITOL SIGNALING SYSTEM	23	0.005534
GAP JUNCTION	20	0.037796
LONG-TERM DEPRESSION	18	0.016329
ADHERENS JUNCTION	17	0.045554
GLYCOLYSIS / GLUCONEOGENESIS	16	0.011854
LONG-TERM POTENTIATION	15	0.029993
PROTEASOME	12	0.003279
TYPE II DIABETES MELLITUS	12	0.028197





computational systems models: why mathematical modeling is urgently needed



Based on MW Covert (2006) Integrated regulatory and metabolic models. In: Computational Systems Biology, edited by A Kriete and R Eils, Elsevier Academic Press (page 194)



in the new vision ...

... our ability to create mathematical models describing the function of **biological networks** will become just as important as traditional lab skills and thinking - D Butler (2001) Nature 409, 758-760

*“Molecular biology took Humpty Dumpty apart ... **mathematical modeling** is required to put him back together again ...”*

– Schnell et al. (2007) Am Sci 95:134

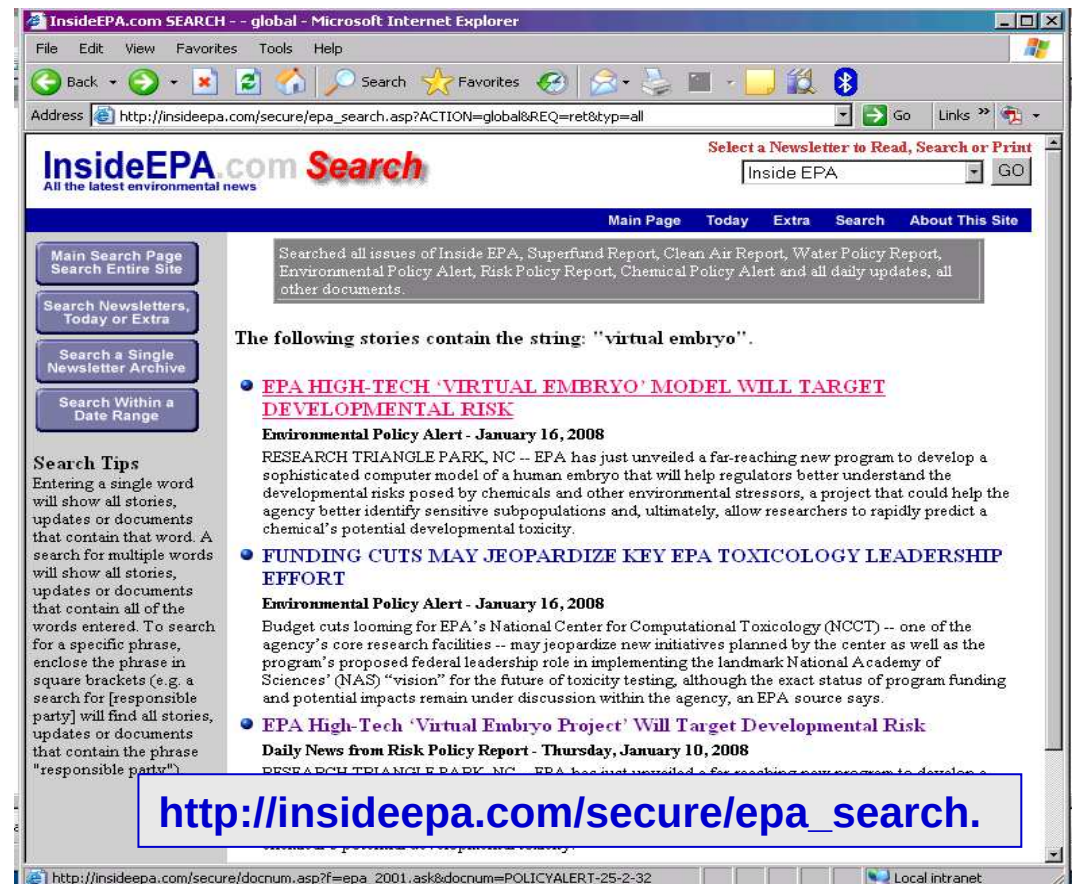




THE VIRTUAL EMBRYO

SOURCE: Matt Shipman, Risk Policy Report, Vol 15, No.2 - January 8 2008

- ❖ far-reaching new program to develop a sophisticated computer model of a human embryo ...

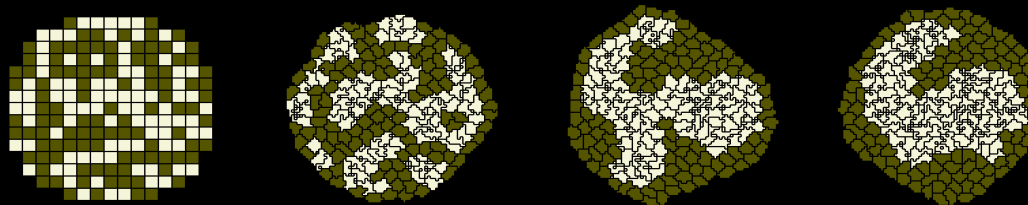


- ❖ help regulators better understand the developmental risks posed by chemicals and other environmental stressors
- ❖ help the agency better identify sensitive subpopulations and, ultimately, allow researchers to rapidly predict a chemical's potential developmental toxicity

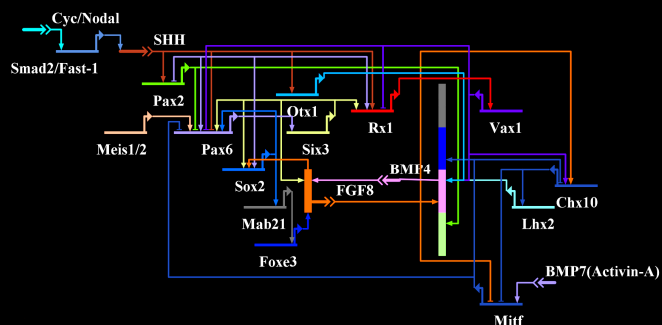
traditional prenatal studies



artificial life simulators

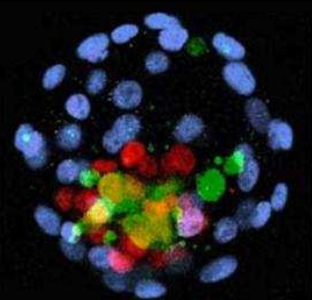


developmental pathways



HTP screening assays

stem cells



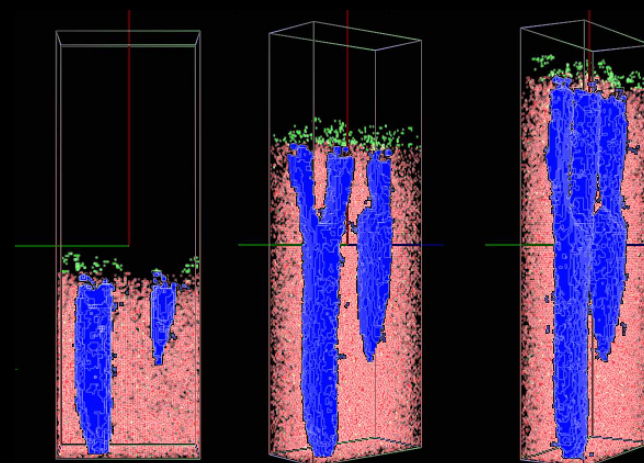
Z-fish embryos

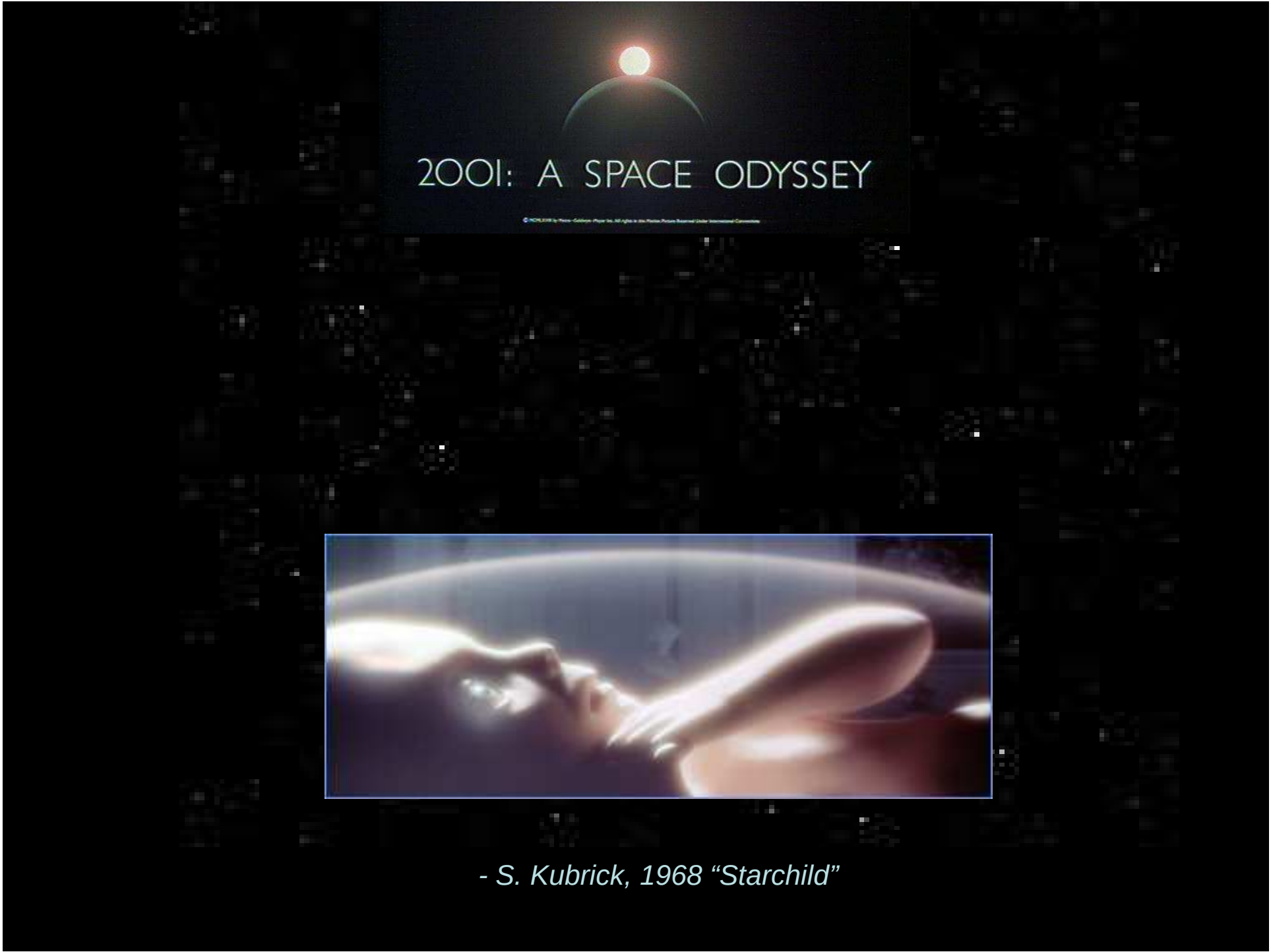


ToxCast™ & BDSM



in silico morphogenesis (CC3D)



The background of the slide is a movie poster for "2001: A Space Odyssey". It features a dark space scene with a bright sun or star partially obscured by the horizon of a planet, creating a lens flare effect. The title "2001: A SPACE ODYSSEY" is centered in a white, sans-serif font. Below the title, there is a small line of fine print.

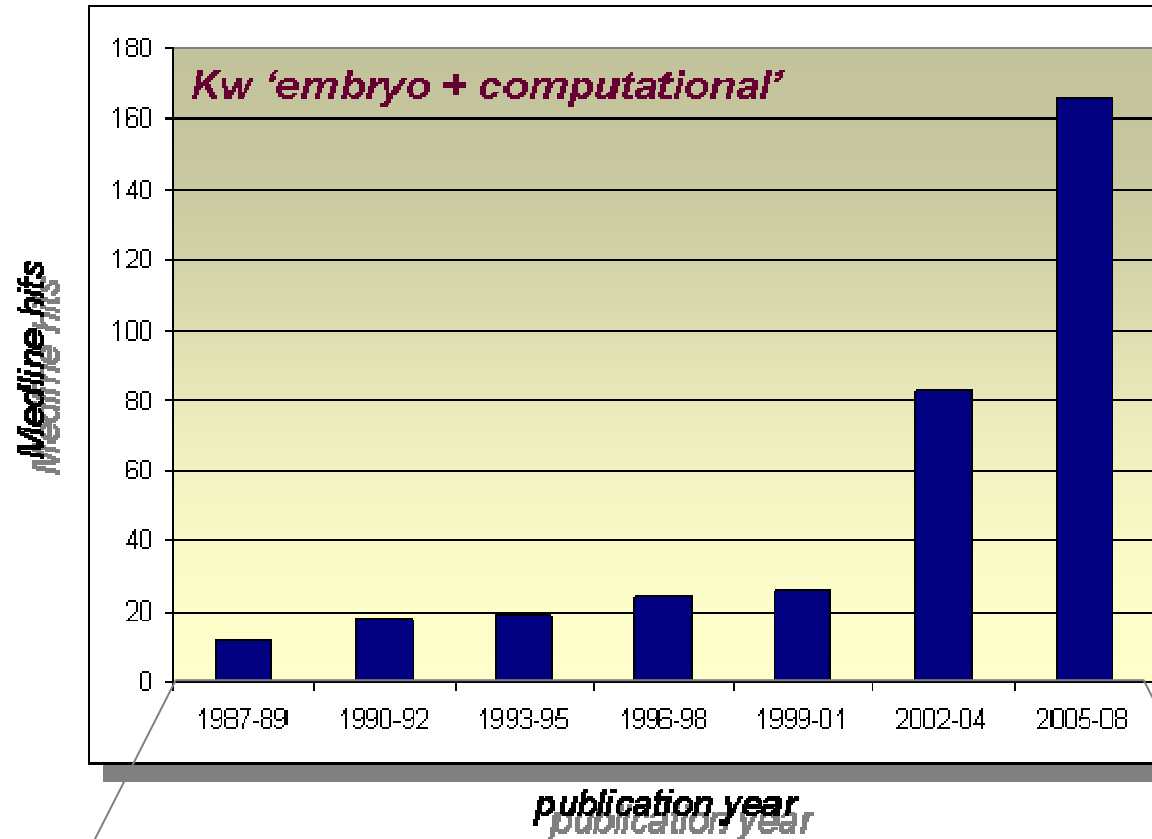
2001: A SPACE ODYSSEY



- S. Kubrick, 1968 "Starchild"



computational embryology: impact of the human genome project



*descriptive
biology*

cell biology
biochemistry

molecular
biology

genomics
bioinformatics

systems
biology

*virtual
biology*



Developmental Systems Biology

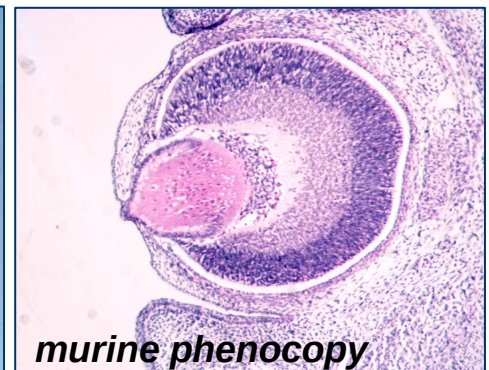
- ❖ virtual tissues and artificial life simulators as models to study morphogenesis and predict defects *in silico*
- ❖ addresses how mechanisms at one scale (cellular) interact to produce higher level (tissue) phenomena
- ❖ just as molecular networks determine local cell behavior, discrete cellular networks drive morphogenesis
- ❖ myriad of agents that can disrupt morphogenesis requires understanding systems at a network-level



research prototype: vertebrate eye development

Attributes:

- ❖ good literature base
- ❖ human relevance
- ❖ reciprocal tissue interactions
- ❖ morphogenetic cell death
- ❖ range of ocular phenotypes
- ❖ often non-syndromic
- ❖ genetic susceptibility
- ❖ environmental sensitivity
- ❖ developmental ontology
- ❖ self-regulating gene networks
- ❖ conservation of cell signaling
- ❖ mitochondrial dependency
- ❖ cellular interaction networks
- ❖ simple/complex



SOURCE: Wubah et al. (2001) *Teratology* 64: 154-169
Charlap et al. (2003) *Birth Def Res A* 67: 108-115



Key event: lens vesicle $\leftrightarrow$ optic vesicle

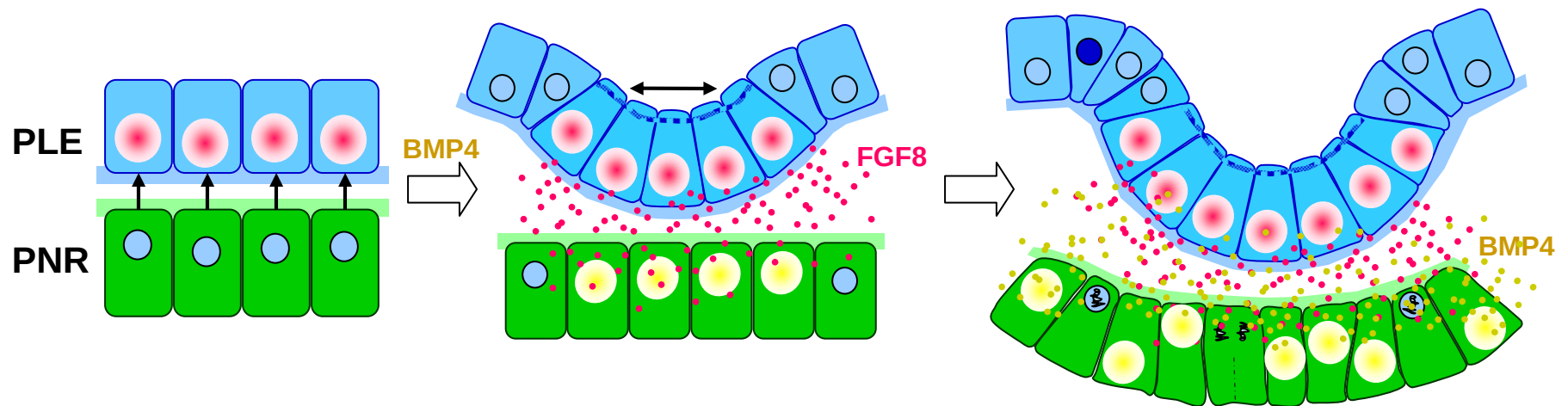
cell-based processes driving the natural system

PATTERNING
cell interaction

MORPHOGENESIS
cytoskeletal remodeling

SELECTIVE GROWTH
proliferation and apoptosis

CELL DIFFERENTIATION
crystallins, Photorec. genes



cell-based processes driving the formal system

NETWORK LOGIC
information flow

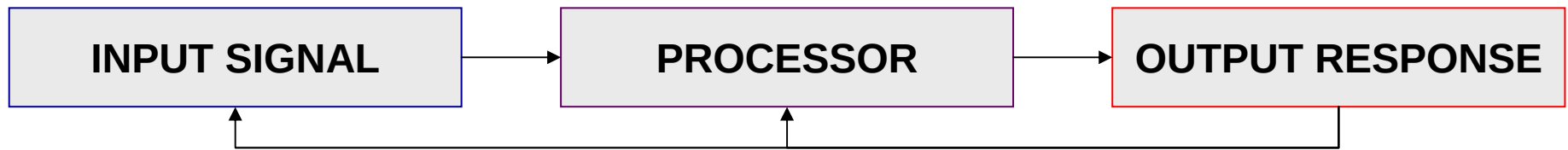
CELLULAR AUTOMATA
cellular Potts model

BIOCHEMICAL FIELDS
Reaction-Diffusion eq.

STATE TRANSITIONS
cell type & state module

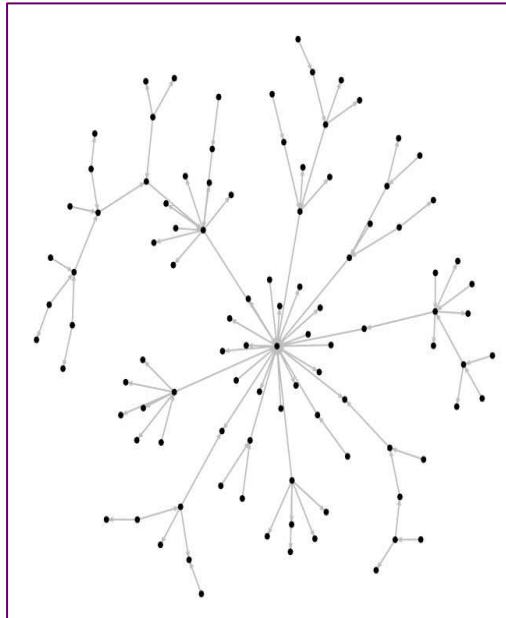


gene regulatory networks (GRNs)



Developmental Signals

Wnt, TGF β , Shh, RTK, Notch-Delta, NF-kB, PCD, nuclear hormone receptors, RPTPs, receptor GC, cytokines, NO, GPCRs, integrins, CADs, gap junction, ligand-gated cation channels, UPR, p53



Morphoregulatory Responses

patterning
proliferation
apoptosis
differentiation
adhesion
motility
shape
ECM remodeling



building developmental GRNs: capturing data from EMAGE database

emap <http://genex.hgu.mrc.ac.uk/> 3D digital atlas | TS14

HOME 3D DIGITAL ATLAS EMAGE DATABASE RESOURCES CONTACT SITE SEARCH

☐ 3D Navigation ☒ Navigation Window ☒ Section Window ☒ Anatomy Window Theiler Stage: TS14

No component selected

TS14

- embryo
 - branchial arch
 - cavities and their linings
 - ectoderm
 - limb
 - mesenchyme
 - notochord*
 - organ system
 - cardiovascular system
 - nervous system
 - sensory organ
 - ear
 - eye
 - nose
 - visceral organ
 - primitive streak
 - tail bud
 - extraembryonic component*

< Contract Expand >

More Theiler 14 (E9) resources:

Stage Definition	Section Movies:	Embryo View:	High-resolution Section Images:	Anatomy Nomenclature Database	CD-ROM
 Transverse ~Frontal ~Sagittal	Transverse ~Frontal ~Sagittal	 More		Java Browser Plain Text XML	

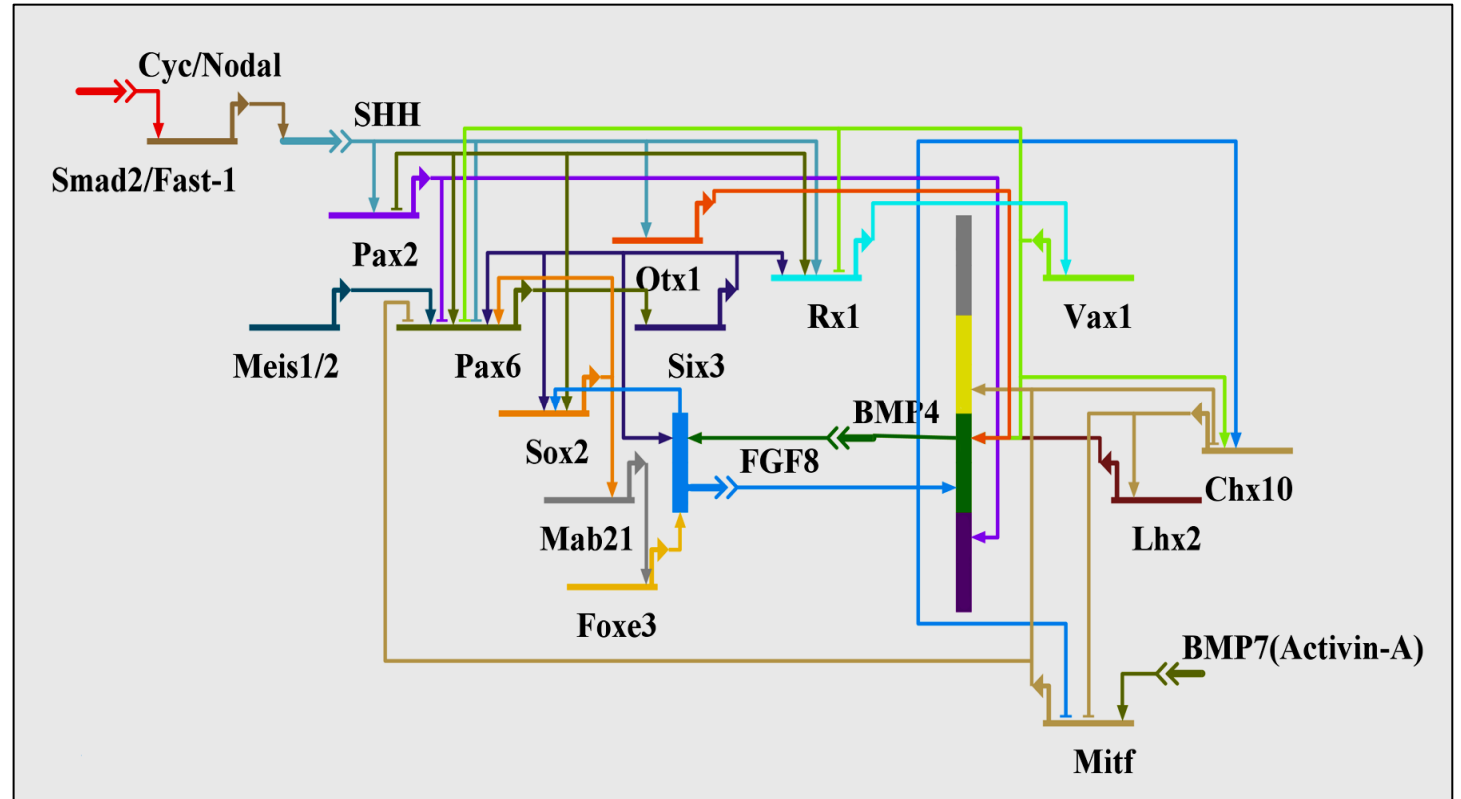
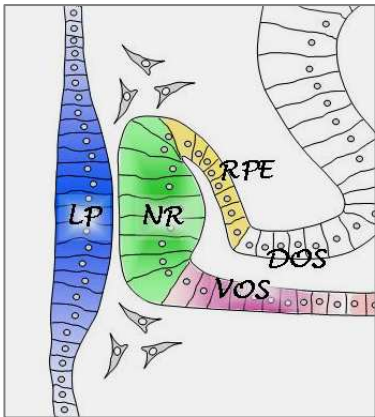
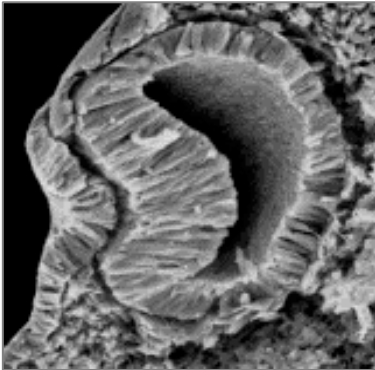
Web page contact: genexweb@hgu.mrc.ac.uk Last modified: 01/03/2004

63 genes (TS12-18)
captures 2164 PMIDs

Sl. No.	Gene 1	Gene 2	Search 1	Search 2	PMID	Web link	Title	Author's	Read	Present	New Inform
1	luc2	luc1	test or embryo	mouse or mic	12783802	New Page	A temperature-sensitive	Van J. Vain	Y	Y	N
2	luc2	luc1	test or embryo	mouse or mic	10858892	New Page	Direct action of the	Stulen P. J	Y	Y	N
3	luc2	luc1	test or embryo	mouse or mic	10934427	New Page	The effects of	Stulen P. J	Y	Y	N
4	luc2	luc1	test or embryo	mouse or mic	8946261	New Page	Expression of	Stulen P. J	Y	Y	N
5	luc2	luc1	test or embryo	mouse or mic	8974416	New Page	Complex expression of	Stulen P. J	Y	Y	N
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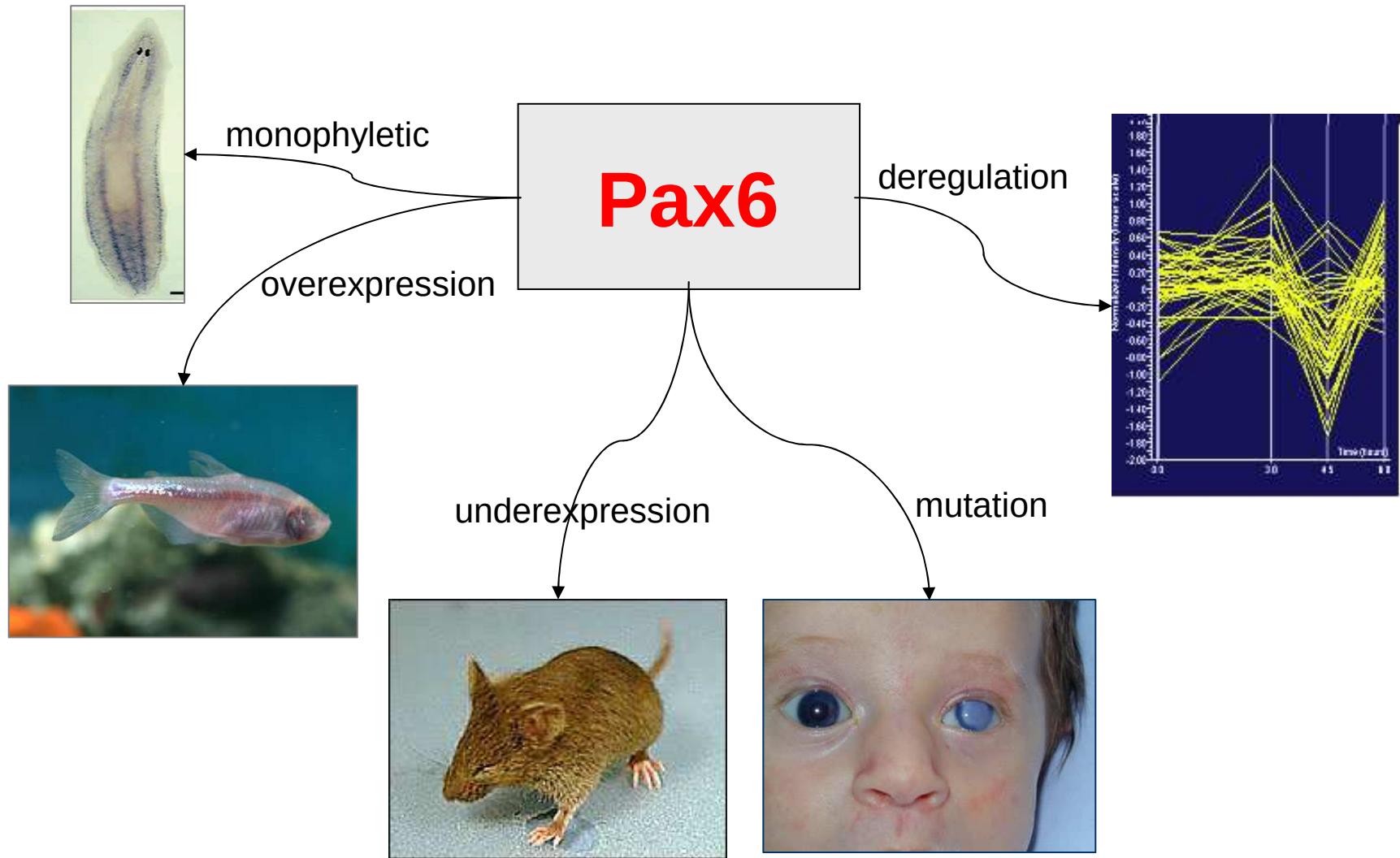
GRN for early eye development: built by semi-automated database + literature mining



SOURCE: Knudsen and Singh (2008), manuscript in preparation

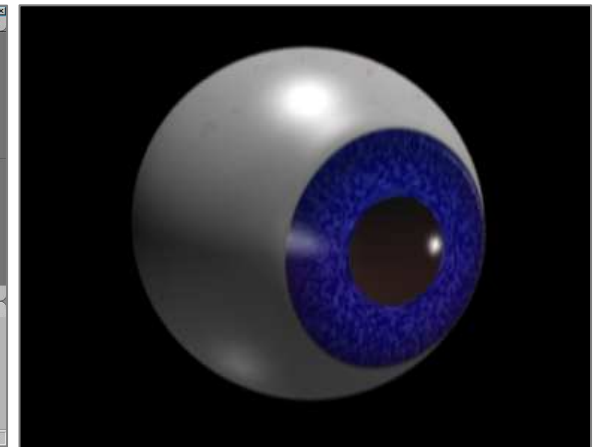
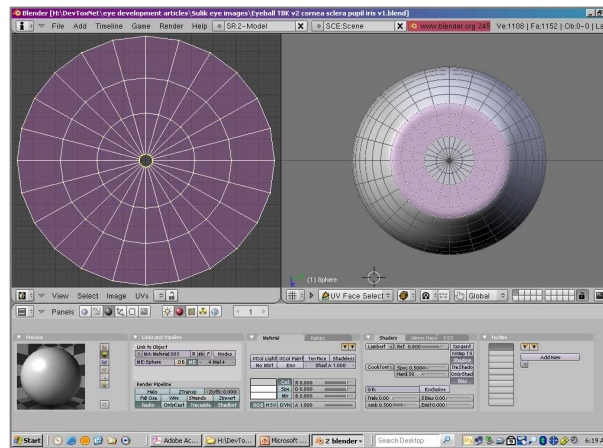
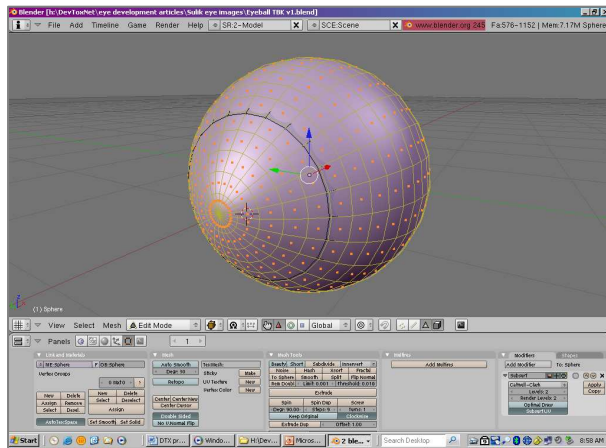


consequences of perturbing GRNs



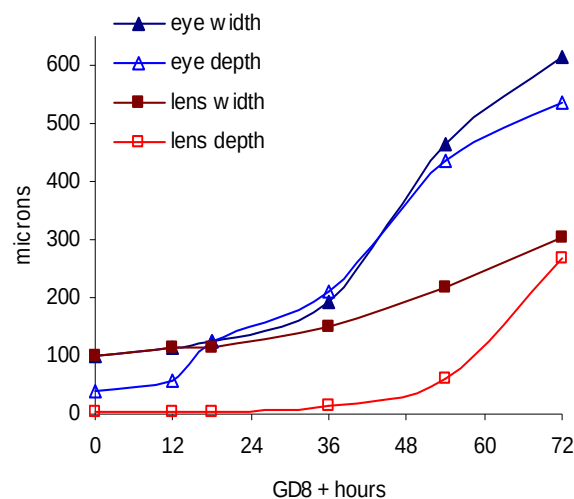


simulation: surface representation



Model of the eye constructed with Blender 2.5 software, **Blender**foundation, <http://www.blender.org>

MORPHOMETRY: on-line atlases and SEM image banks of mouse eye development



$$y = a * b^x$$

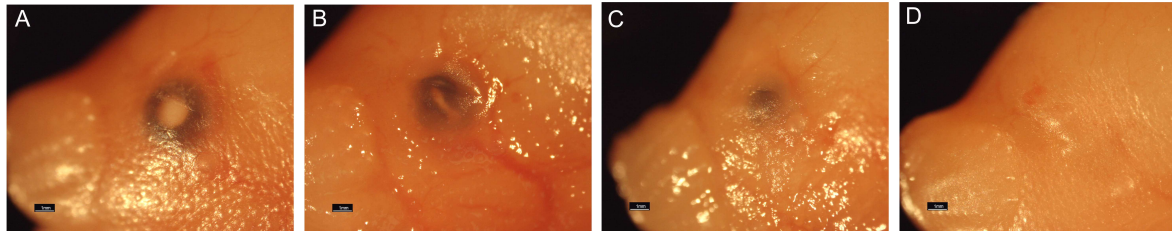
Parameter	Coefficient	Standard error	P	P, adj R ² or
eye width				
variable a	67.8043	18.4709	0.0089	0.98150301
variable b	1.0279	0.0034	< 0.0001	0.95433389
eye depth				
variable a	77.3446	22.6413	0.0269	0.96849494
variable b	1.0282	0.0048	< 0.0001	0.92247805
lens width				
variable a	67.7712	9.0020	< 0.0001	0.99318307
variable b	1.0172	0.0010	< 0.0001	0.98426766
lens depth				
variable a	0.7208	0.1232	0.0043	0.99939671
variable b	1.0887	0.026	< 0.0001	0.99924413



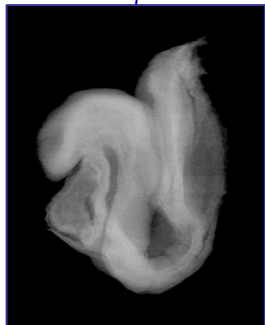
challenge: modeling catastrophe *in silico*

small changes in nonlinear system → sudden shifts in behavior

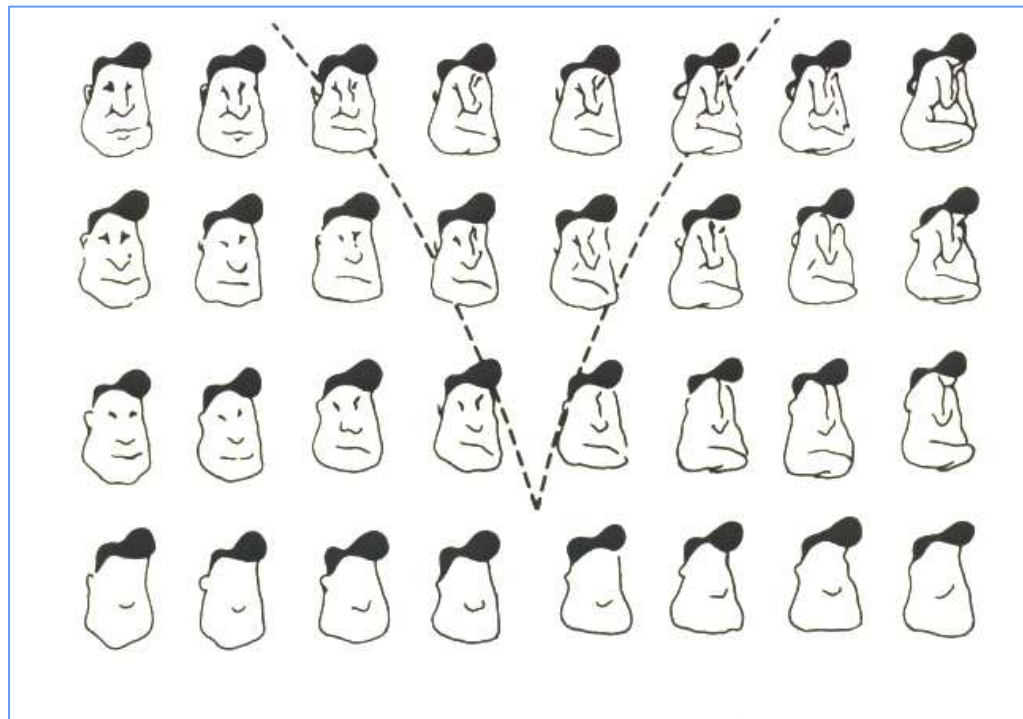
STATE A ←-----→ STATE B



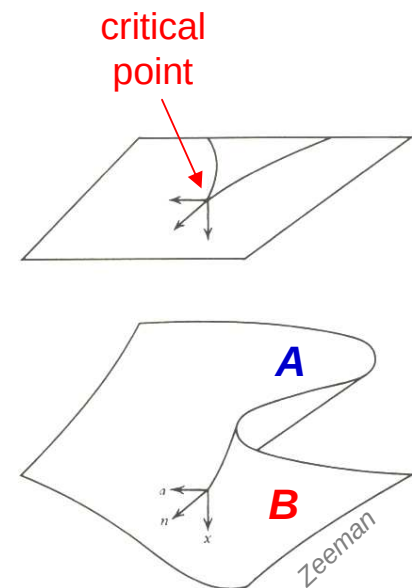
Gestation →



exposure

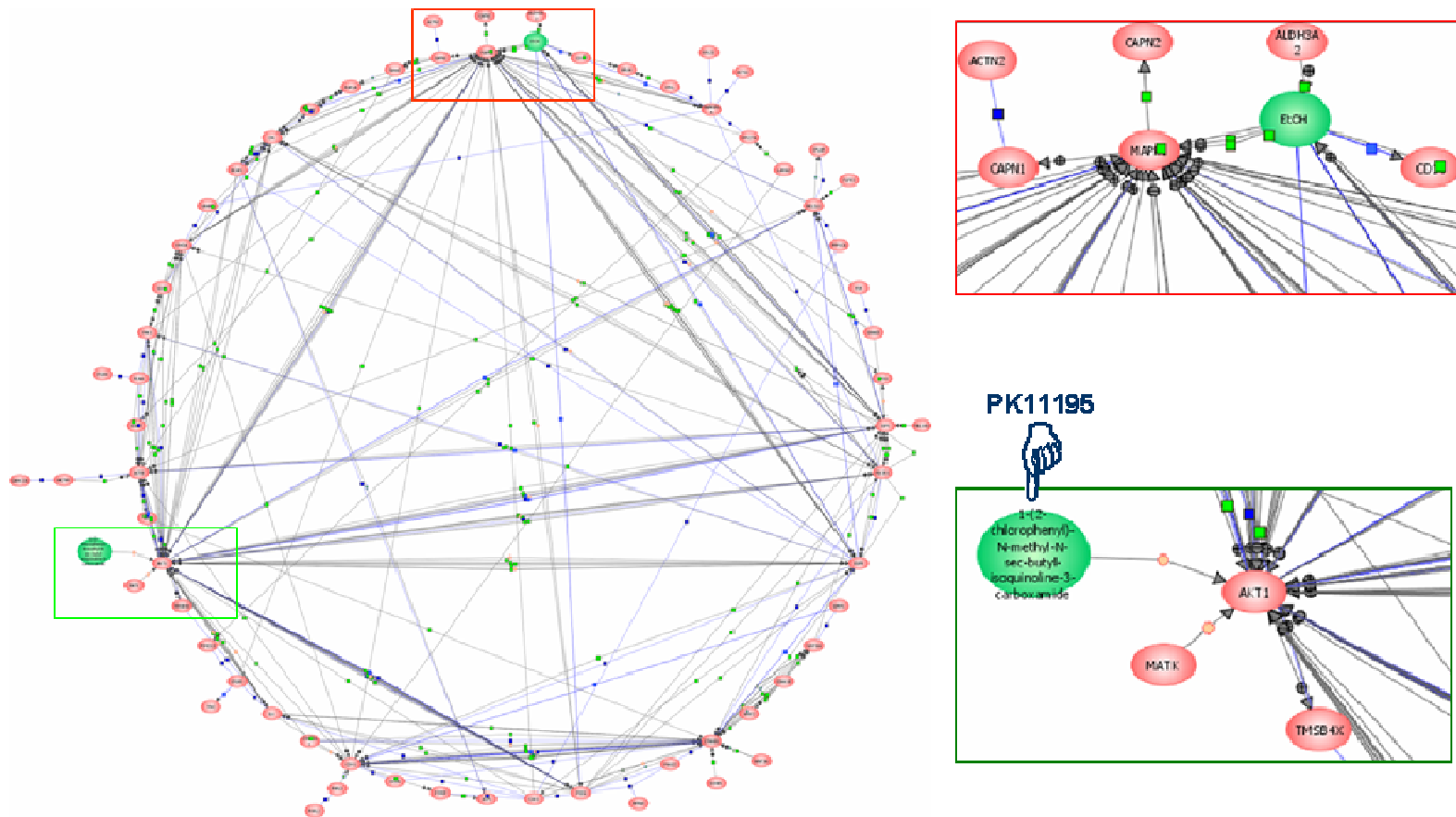


SOURCE: Saunders, 1980, Cambridge University Press NY





FAS network: genes affected in the rudimentary forebrain during maternal alcohol exposure



SOURCE: Green ML, Singh AV, Zhang Y, Nemeth KA, Sulik KK and Knudsen TB (2007) Reprogramming of genetic networks during initiation of the fetal alcohol syndrome. *Devel Dynam* 236: 613-631



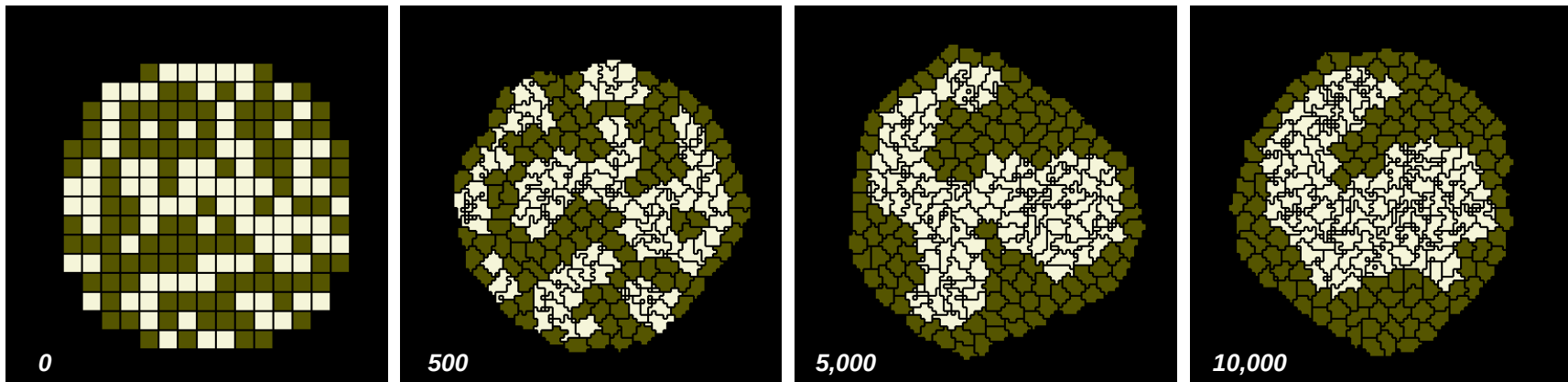
Functional models: differential cell adhesion in mouse embryos modeled *in silico*

Cell autonomous sorting (biological)

		B6J	B6N	B6J-B6N differential
receptor-mediated cell adhesion genes	Gene			
	Procollagen 1 alpha 2	↑	↑	+ 0.12
	Procollagen 6 alpha 2	↑	—	+ 0.74
	Integrin alpha 3	↑	↓	+ 1.09
	Integrin beta 3	↓	—	- 0.42
	Caveolin-1	↑	—	+ 0.75
	L1 cell adhesion molecule	—	↓	+ 0.20
	Focal adhesion kinase (PTK2)	—	↓	+ 1.28
	Ephrin b1	↑	↓	+ 1.38
	Ephrin b2	—	↓	+ 1.61
	Ephrin b3	↑	—	+ 0.88
	Ephrin a5	↑	↓ ↓	+ 2.24
	EPH receptor A2	—	↓	+ 0.68
	EPH receptor A4	—	↓	+ 1.34
	IGF-1	↑	—	+ 0.35
	IGF-1 receptor	—	↓	+ 0.70

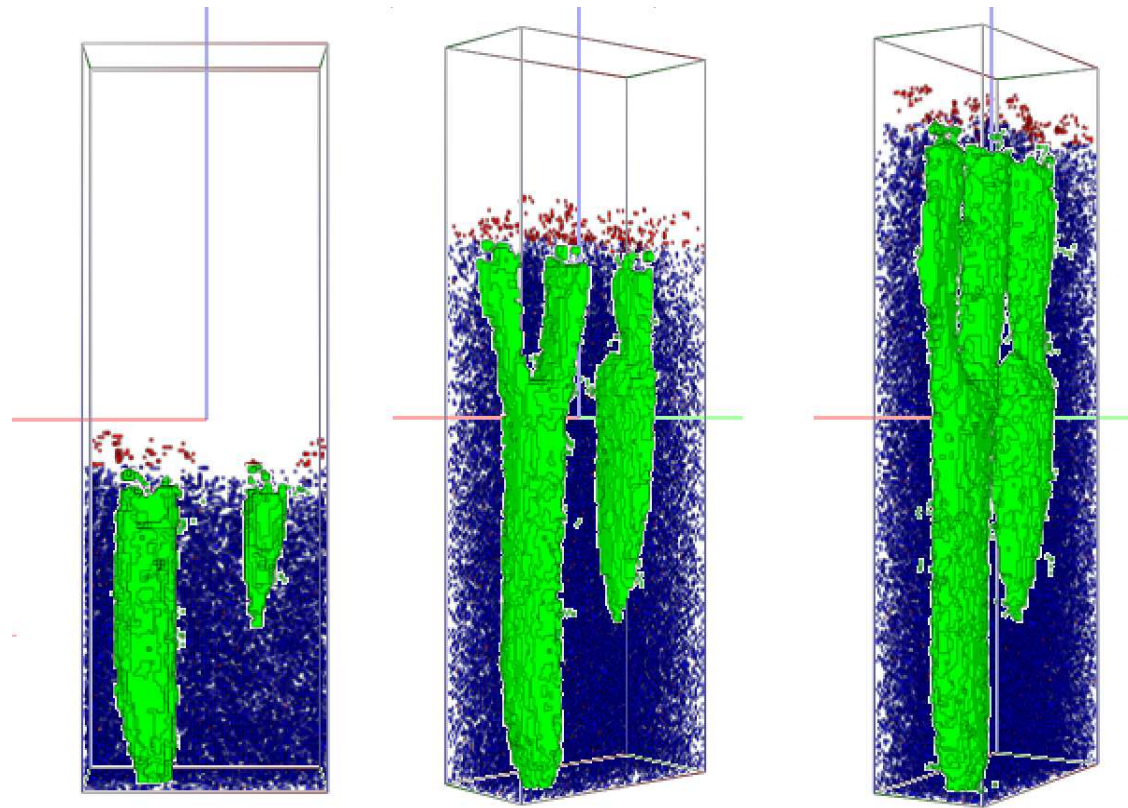
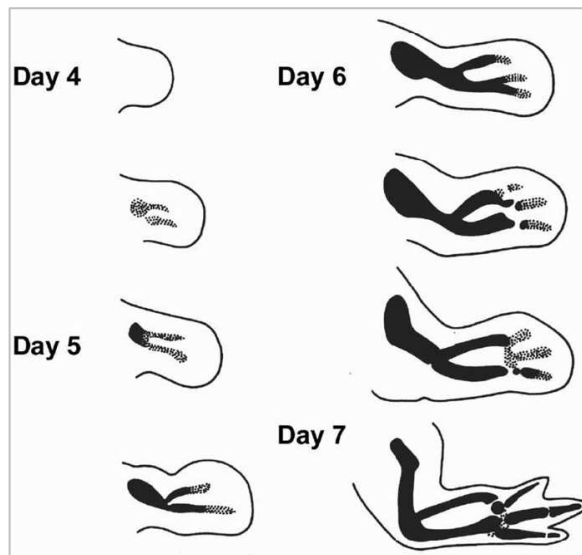
Subset of significantly altered genes in focal adhesion linked by functional classification and expression profile; up-/down regulation at threshold of 0.75-fold change. The differential is given in log(2) units (eg, 1 = two-fold change).

Cell sorting automaton (computational)





toolbox for *in silico* morphogenesis: agent-based model of chick limb development



CompuCell3D Rendering at steps 1750, 2750, 3250

SOURCE: Cickovski et al. (2005) *IEEE/ACM Trans Comput Biol Bioinform* 2: 1-15



Complicated for sure but inevitably ...

- ❖ computational models will be needed to unravel biological complexity
- ❖ virtual tissues and artificial life simulators will become more common research techniques
- ❖ *in silico* experiments can test the complex factors that influence morphogenesis and teratogenesis
- ❖ e-science will need to close the gap between virtual biology and the real world



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