

Predictive Models and Computational Toxicology

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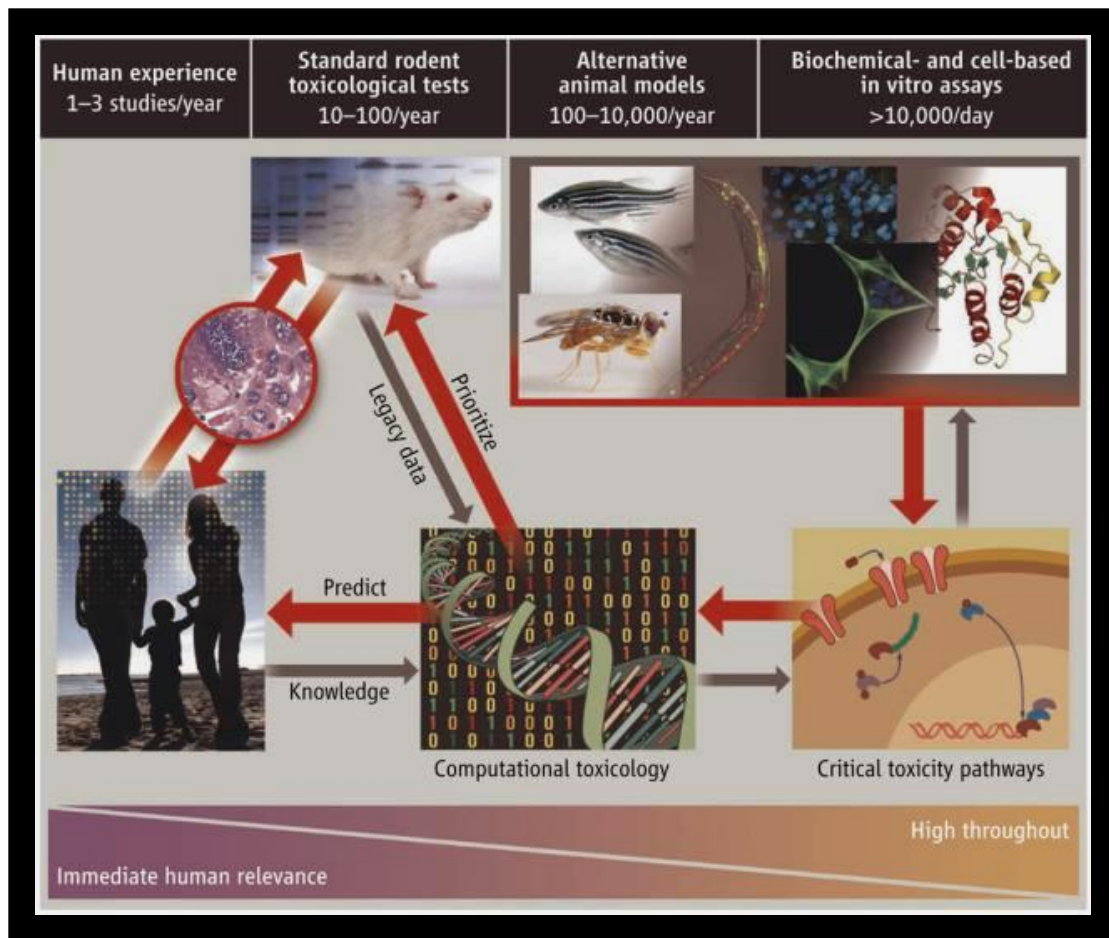


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Problem Statement

- ❖ tens of thousands of chemicals, most lack toxicity information especially for reproduction and development
- ❖ standard paradigm for toxicity testing is low throughput: animal-based studies focus on 'apical endpoints'
- ❖ emerging 21st paradigm: focus on pathways tested *in vitro* using assays amenable to high-throughput screening (HTS)
- ❖ computational challenge: to integrate vast arrays of *in vitro* data into *in silico* models predictive of *in vivo* toxicity

Tox21 Vision: Transforming Toxicity Testing



**National Center for Advancing
Translational Sciences (NCATS)**
<http://www.ncats.nih.gov/>

**SOURCE: Collins, Gray and Bucher (2008) Toxicology. Transforming
environmental health protection. Science 319: 906**

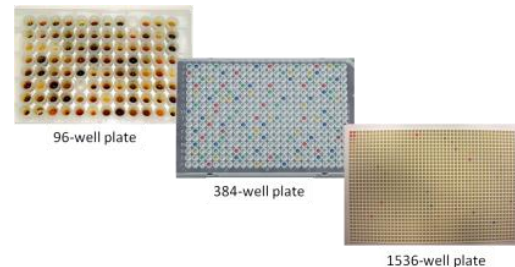
Computational Toxicology: high-throughput screening (HTS)



- ❖ **ToxCast:** EPA research effort profiling >1060 chemicals across >700 *in vitro* assays (27M data points). <http://www.epa.gov/ncct/toxcast/>
 - **Phase-I**: 310 data-rich chemicals (primarily pesticides) having over 30 years of traditional animal studies valued at \$2B (completed 2011).
 - **Phase-II**: adds 767 chemicals (eg, industrial and consumer products, food additives, failed drugs) extend the broader chemical landscape (Sept 2013).
 - **Phase-III**: adds 1001 compounds in a subset of assays (2014).
- ❖ **Tox21:** partnership of federal agencies.
 - brings chemical inventory to 10,000
 - >50 HTS *in vitro* assays (ongoing)



ToxCast Assays



Assay Provider

ACEA
Apredica
Attagene
BioReliance
BioSeek
CeeTox
CellzDirect
Tox21/NCATS
NHEERL MESC
NHEERL Zebrafish
NovaScreen (Perkin Elmer)
Odyssey Thera
Vala Sciences

Biological Response

cell proliferation and death
cell differentiation
Enzymatic activity
mitochondrial depolarization
protein stabilization
oxidative phosphorylation
reporter gene activation
gene expression (qNPA)
receptor binding
receptor activity
steroidogenesis

Target Family

response Element
transporter
cytokines
kinases
nuclear receptor
CYP450 / ADME
cholinesterase
phosphatases
proteases
XME metabolism
GPCRs
ion channels

Assay Design

viability reporter
morphology reporter
conformation reporter
enzyme reporter
membrane potential reporter
binding reporter
inducible reporter

Readout Type

single
multiplexed
multiparametric

Species

human
rat
mouse
zebrafish
sheep
boar
rabbit
cattle
guinea pig

Tissue Source

Lung	Breast
Liver	Vascular
Skin	Kidney
Cervix	Testis
Uterus	Brain
Intestinal	Spleen
Bladder	Ovary
Pancreas	Prostate
Inflammatory	Bone

Detection Technology

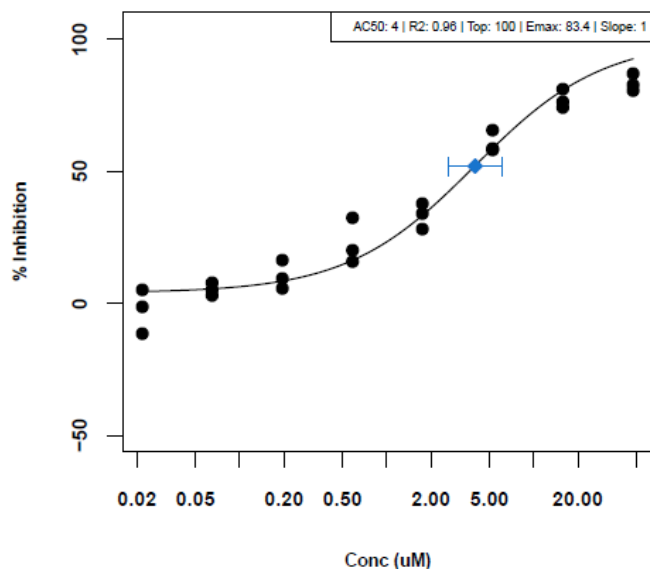
qNPA and ELISA
Fluorescence & Luminescence
Alamar Blue Reduction
Arraysan / Microscopy
Reporter gene activation
Spectrophotometry
Radioactivity
HPLC and HPEC
TR-FRET

Cell Format

cell free
cell lines
primary cells
complex cultures
free embryos

ToxCastDB

<http://actor.epa.gov/actor/faces/ToxCastDB/DataCollection.jsp>



AC50 concentration producing a 50% change
LEC lowest effect concentration

ToxCastDB
 You are here: EPA Home » National Center for Computational Toxicology » ToxCastDB » Data Collection

Home | Basic Info | Data Collection List | Chemical List | Genes Associated with Assays | Help

Data Collection: Novascreen

Name: Novascreen
 Description: Novascreen / Caliper - receptor binding and enzyme inhibition assays
 Number of Chemicals: 329
 Number of Assays: 273
 Number of Data Points: 93440

Data Collection Summary

Name	Assay Name	Description	Substances	Components	Species	Gene
NVS_ENZ_XTA2	Novascreen Human TxA2	Human TxA2 Fluorescein-peptide	320	1	Homo sapiens	TXA2
NVS_ENZ_XTAA	Novascreen Human TAA	Human TAA Fluorescein-labeled peptide	320	2	Homo sapiens	NTSR1
NVS_ENZ_XVEGR1	Novascreen Human VEGFR1	Human VEGFR1 Fluorescein-labeled peptide	320	2	Homo sapiens	PLT1
NVS_ENZ_XVEGR2	Novascreen Human VEGFR2	Human VEGFR2 Fluorescein-labeled peptide	320	1	Homo sapiens	KDR
NVS_ENZ_XVEGR3	Novascreen Human VEGFR3	Human VEGFR3 Fluorescein-labeled peptide	320	1	Homo sapiens	PLT4
NVS_ENZ_XZAPR1	Novascreen Human ZAPR1	Human ZAP-70 Fluorescein-peptide	320	1	Homo sapiens	ZAP70
NVS_ENZ_XCO1	Novascreen Ome CO1	Ome CO1 Acaribonic acid TMPD	320	1	Ovis aries	PTGS1
NVS_ENZ_XCO2	Novascreen Ome CO2	Ome CO2 Acaribonic acid TMPD	320	1	Ovis aries	PTGS2
NVS_ENZ_XMTHFR	Novascreen Pig MTHFR	Pig MTHFR 5,14C-MeTHF	320	1	Sus scrofa	MTHFR
NVS_ENZ_XR62C	Novascreen Rabbit R6	Rabbit R6 3H-2-DB1	320	1	Oryctolagus cuniculus	MTHFR
NVS_ENZ_XCF3KBinding	Novascreen Rat AC-F3K Binding	Rat AC-F3K Binding 3H-Forskolin	320	1	Rattus norvegicus	Adenyly

ToxCastDB
 You are here: EPA Home » National Center for Computational Toxicology » ToxCastDB » Assay

ACTuR ToxCastDB ToxCastDB ExporCastDB BISTox

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Assay: Novascreen Human VEGFR2

Assay Id: 978
 Source: Novascreen
 Source Name AID: NVS_ENZ_hVEGFR2
 Name: Novascreen Human VEGFR2
 Description: Human VEGFR2 Fluorescein-labeled peptide
 Number of Substances: 320
 Number of Components: 1
 Species: Homo sapiens

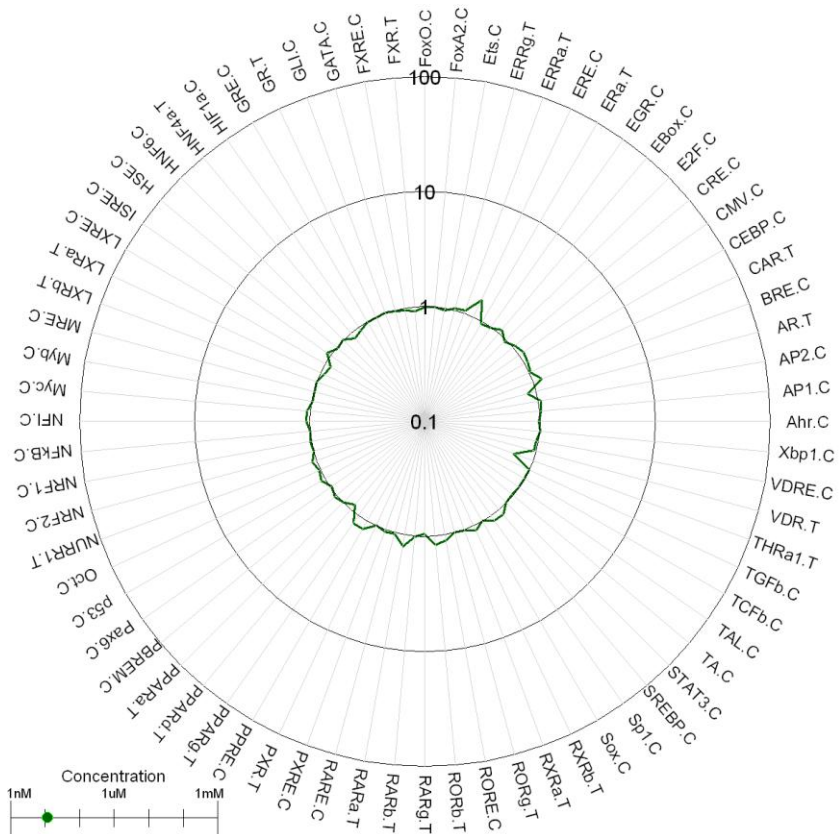
Parameters

Parameter	Value
CATALOG NUMBER	200-0768
ASSAY CATEGORY	Enzyme Inhibition
ASSAY CATEGORY	In vitro (Biochemical)
ASSAY TARGET	VEGFR2
ASSAY TARGET FAMILY	Kinase
ASSAY TARGET SOURCE	Recombinant
ASSAY TARGET SOURCE TYPE	amino acid 805 to 1356
ASSAY GENE ID	3791
ASSAY GENE NAME	KDR
ASSAY REFERENCE COMPOUND	Staurosporine
ASSAY NOTE	KINASE
ASSAY SUBSTRATE NAME	receptor tyrosine kinase
ASSAY ATP CONCENTRATION (M)	NCCT_v2
ASSAY ENZYME AFFINITY ATP KM (M)	Fluorescein-labeled peptide
ASSAY LIGAND NAME	1.50E-06
ASSAY LIGAND CONCENTRATION (M)	1.20E-05
ASSAY BMAX	Fluorescein-peptide + ATP -> fluorescein-phosphopeptide + ADP

Data

Name	CASRN	NVS_ENZ_hVEGFR2 (uM)
Mancozeb	8018-01-7	5.9
Maneb	12427-38-2	31.0
Metiram-zinc	9006-42-2	45.0
Oxytetracycline dihydrate	6153-64-6	19.0

EXAMPLE: reporter gene activation (Attagene)



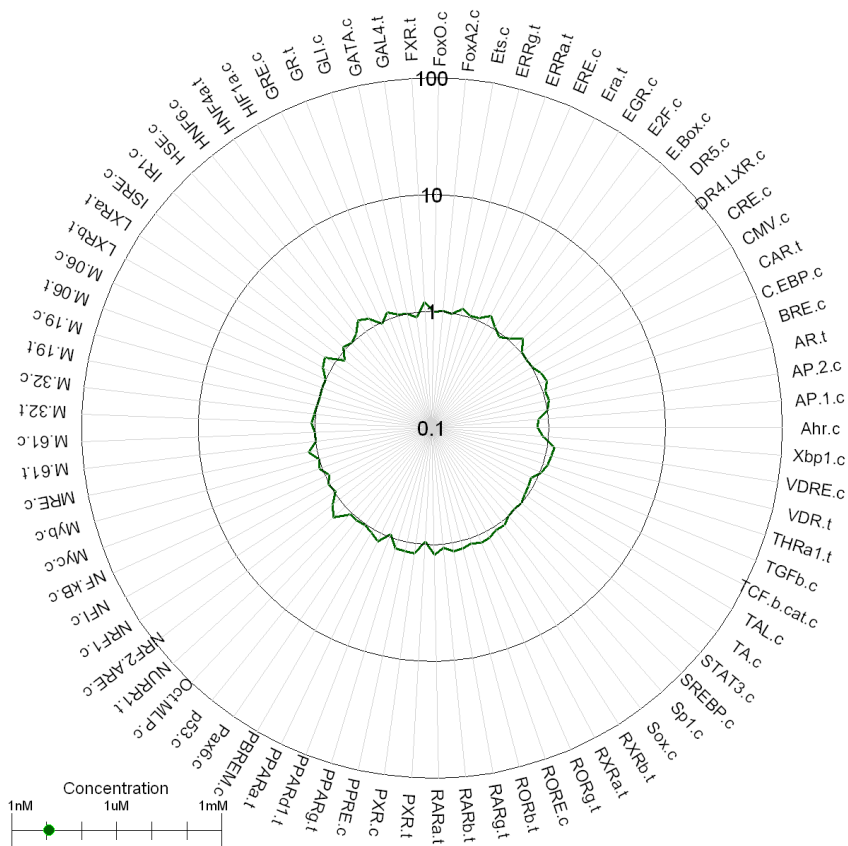
Spider plot maps the activity of 72 reporter gene pathways tested in ToxCast

Animation shows concentration response

Example: a pharmaceutical tested in ToxCast Phase II

Sunburst: loss of specificity

EXAMPLE: reporter gene activation (Attagene)

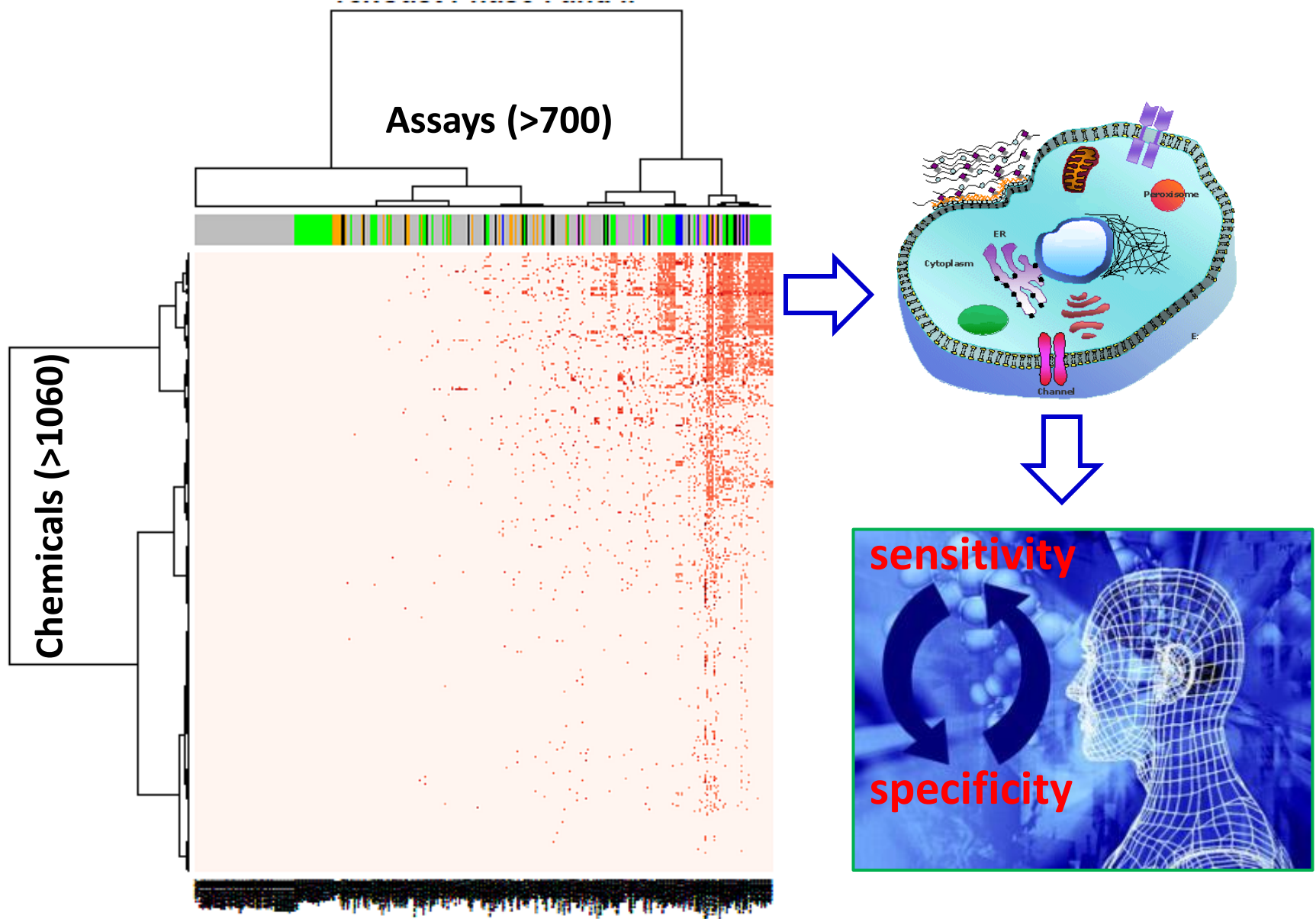


Spider plot maps the activity of 72 reporter gene pathways tested in ToxCast

Example: concentration response for an environmental chemical (Pentachlorophenol)

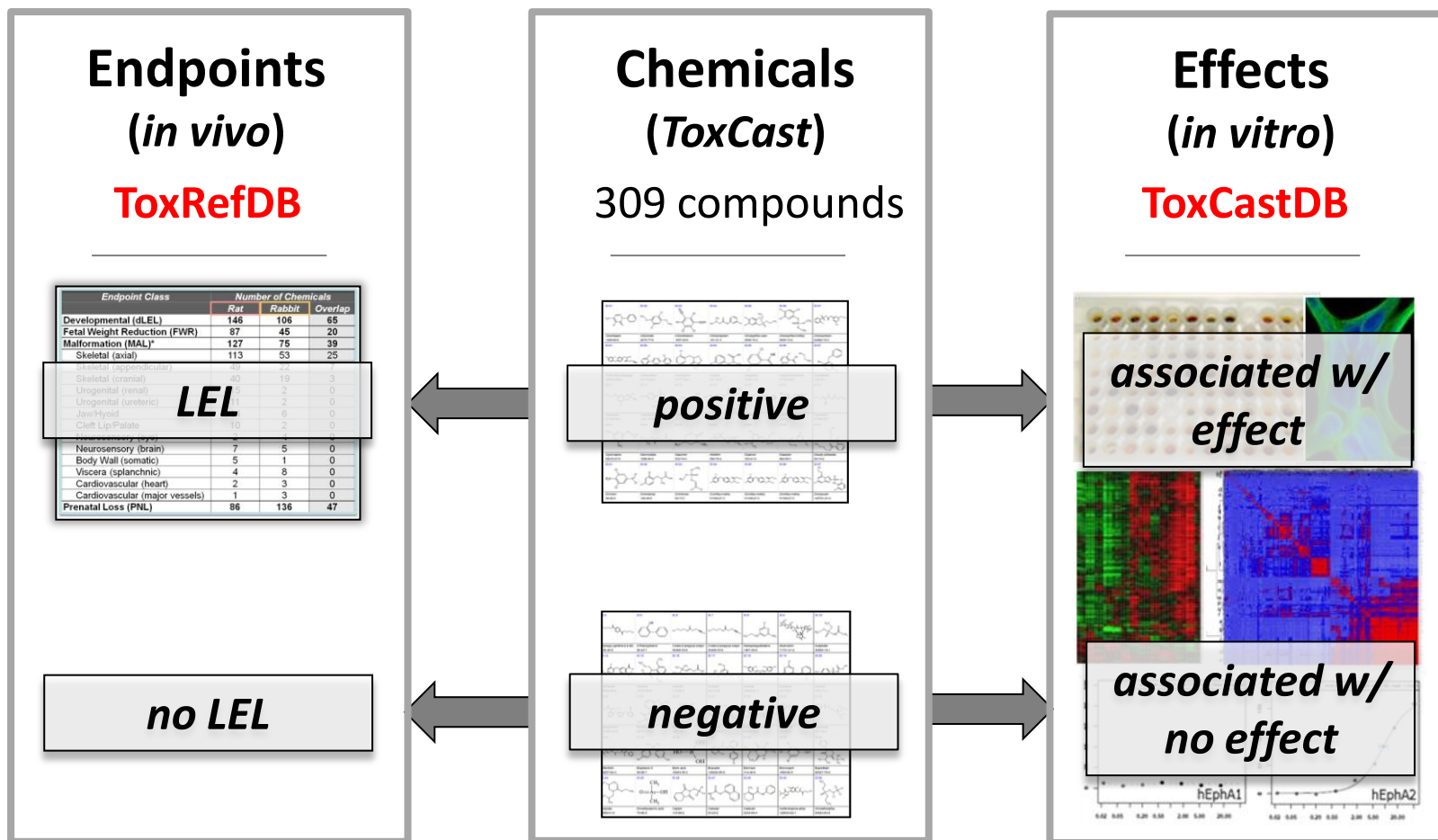
Sunburst: approaching cytotoxicity

***In vitro* profiling:** we can now begin to group chemicals by their **'bioactivity profiles'** and look for signatures that predict toxicity.



Mining the Predictive Signatures:

What assays best correlated with selected endpoints?



ToxCast predictive signatures (1st generation)

❖ machine-learning models anchored to apical endpoints

liver tumors: Judson et al. 2010, Env Hlth Persp 118: 485-492

hepatocarcinogenesis: Shah et al. 2011, PLoS One 6(2): e14584

developmental tox: Kleinstreuer et al. 2011, Tox App Pharm 257(1):111-21

rat-rabbit prenatal devtox: Sipes et al. 2011, Tox Sci 124: 109-127

rat fertility: Martin et al. 2011, Biol Reprod 85: 327-339

zebrafish development: Sipes et al. 2011, Birth Defects Res C 93: 256-267

cancer hallmarks: Kleinstreuer et al. 2012, Tox Sci, doi:10.1093/toxsci/kfs285

❖ prediction models anchored to pathways or processes

endocrine disruption: Reif et al. 2010, Env Hlth Persp 118: 1714-1720

microdosimetry: Wambaugh and Shah 2010, PLoS Comp Biol 6: e1000756

mESC differentiation: Chandler et al. 2011, PLoS One 6(6): e18540

HTP risk assessment: Judson et al. 2011, Chem Res Toxicol 24: 451-462

angiogenesis: Kleinstreuer et al. 2011, Env Hlth Persp 119: 1596-1603

vascular AOP: Knudsen and Kleinstreuer, 2011, Birth Def Res C 93:312-323

multi-scale simulation: Kleinstreuer et al., 2013, PLoS Comp Biol (in press)

Predictive signature for developmental toxicity

Feature	Description	Weight
RAR	Retinoic Acid receptor	0.58
GPCR	G-Protein-Coupled Receptors	0.55
TGFβ	Transforming Growth Factor β	0.38
MT	Microtubule organization	0.30
SENS_CYP	Cytochrome P450 (sensitive)	0.26
AP1	Activator protein 1	0.24
SLCO1B1	Organic anion transporter 1B1	0.11
CYP	CYPs (other)	0.06
HLA-DR	MHC complex	-0.38
PXR	Pregnane X receptor	-0.24
IL8	Interleukin 8	-0.23
PGE2	Prostaglandin E2 response	-0.18

Feature	Description	Weight
CCL2	Chemokine ligand 2 (MCP1)	1.15
IL	Interleukin (1a and 8)	0.39
CYP	Cytochrome P450	0.24
TGFβ	Transforming Growth Factor β	0.28
MESC	Mouse ES cells (J1)	0.13
SULT2A1	Sulfotransferase	-0.26
PGE2	Prostaglandin E2 response	-0.15

*Multivariate **Rat** Model*
71% balanced accuracy

Phase-I models
connected to relevant
biological processes in
prenatal DevTox

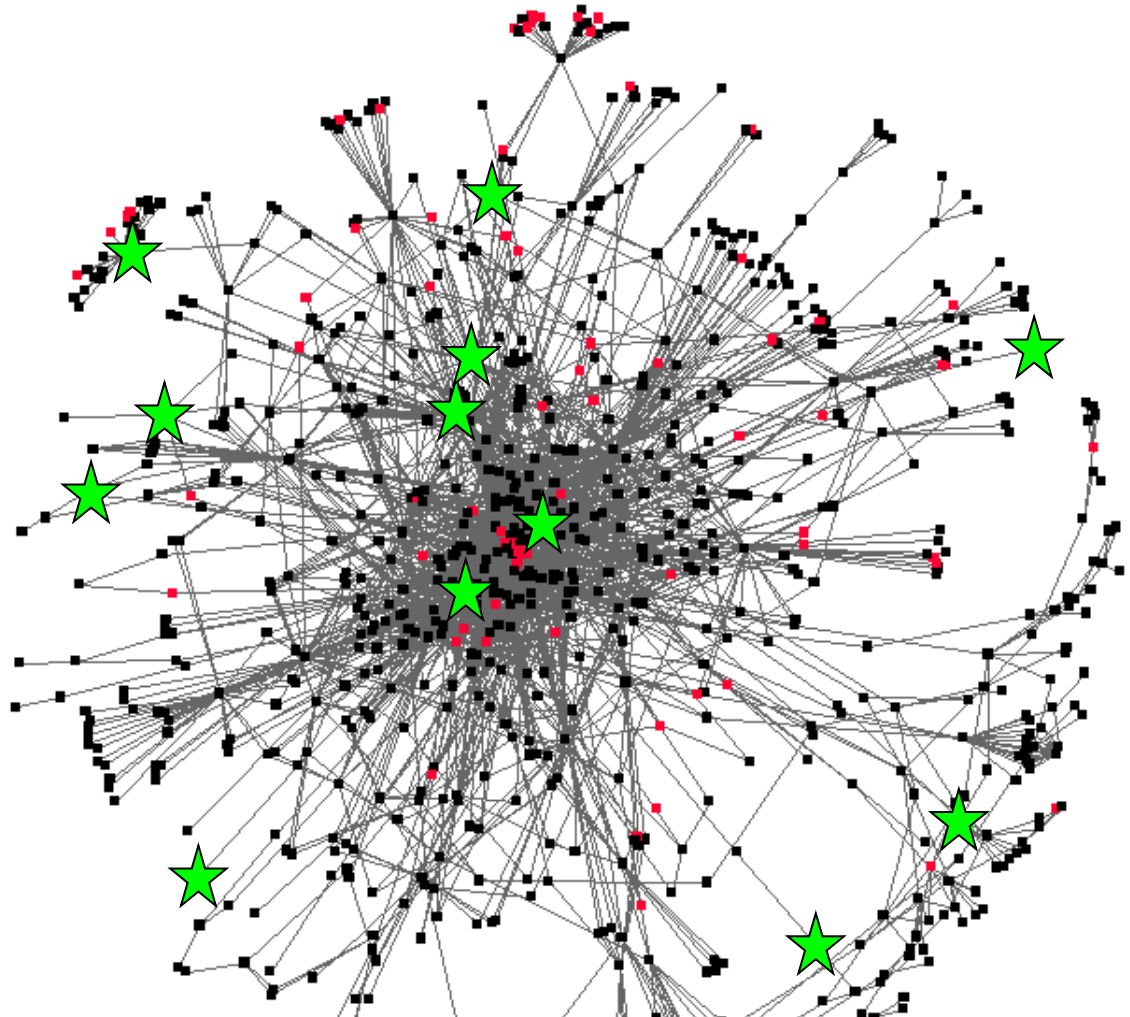
*Multivariate **Rabbit** Model*
74% balanced accuracy

Features mapped by 'biological process'

univariate DevTox features
multivariate DevTox features

★ *processes related to neovascularization (vasculogenesis and/or angiogenesis)*

Feature	Description	Weight
RAR	Retinoic Acid receptor	0.58
GPCR	G-Protein-Coupled Receptors	0.55
TGFβ	Transforming Growth Factor β	0.38
MT	Microtubule organization	0.30
SENS_CYP	Cytochrome P450 (sensitive)	0.26
AP1	Activator protein 1	0.24
SLCO1B1	Organic anion transporter 1B1	0.11
CYP	CYPs (other)	0.06
HLA-DR	MHC complex	-0.38
PXR	Pregnane X receptor	-0.24
IL8	Interleukin 8	-0.23
PGE2	Prostaglandin E2 response	-0.18
Feature	Description	Weight
CCL2	Chemokine ligand 2 (MCP1)	1.15
IL	Interleukin (1a and 8)	0.39



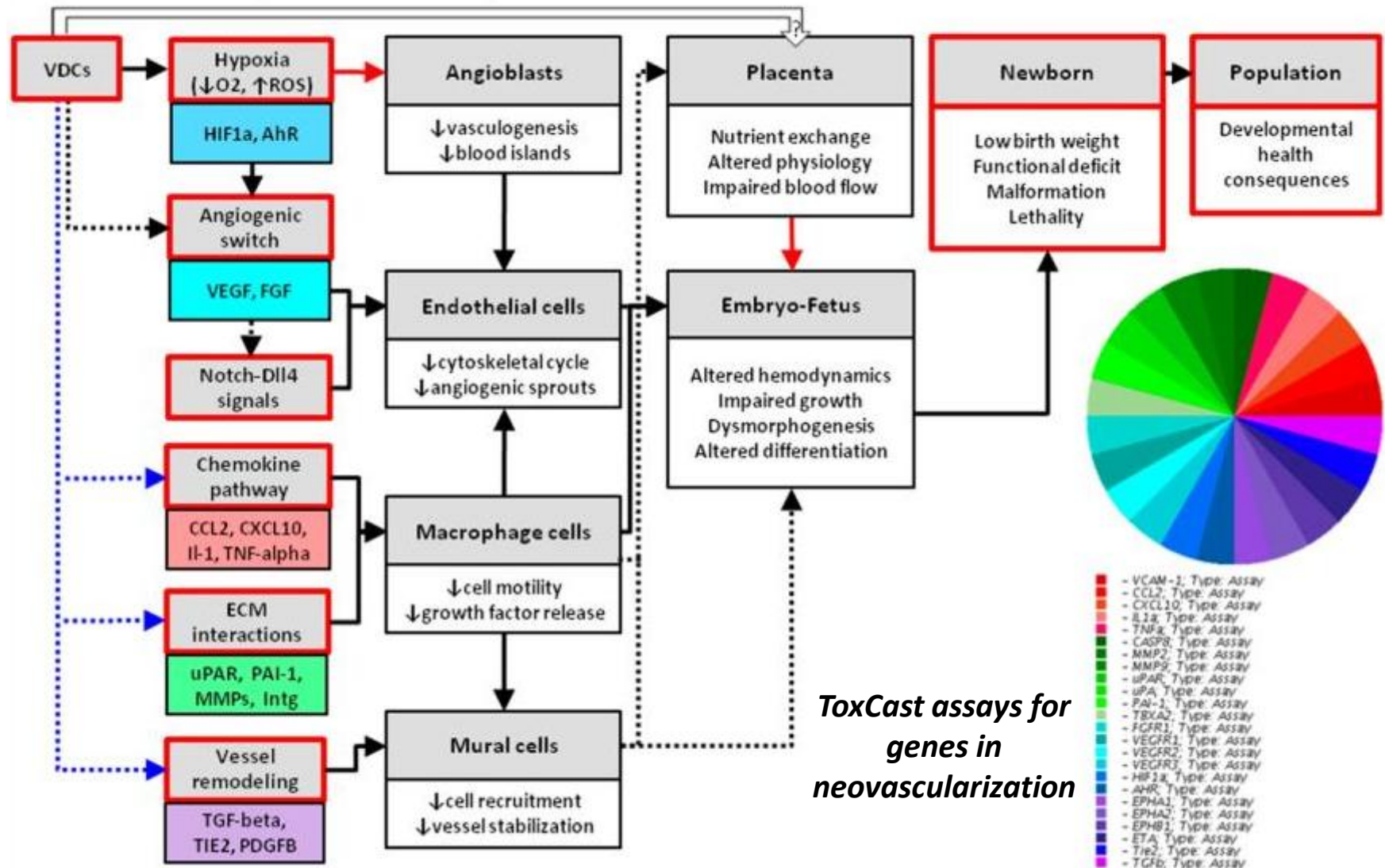
HYPOTHESIS: disruption of embryonic blood vessel formation is a direct target for some developmental effects

- ❖ Gene Ontology (GO) and Mammalian Phenotype (MP) browsers of MGI database (<http://www.informatics.jax.org/>) for **neovascularization**:
 - abnormal vasculogenesis [MP:0001622; 72 genotypes, 73 annotations]
 - abnormal angiogenesis [MP:0000260; 610 genotypes, 894 annotations]
- ❖ 65 genes with roles in vasculogenesis or angiogenesis linked to ToxCast assays, 50 had evidence of abnormal embryonic vascular development in MGI

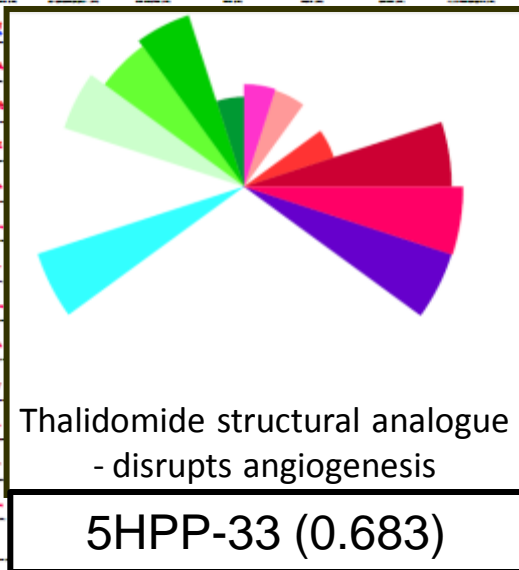
Overlap between ToxCast assay targets and abnormal vascular phenotypes from genetic mouse models.

<u>ToxCast</u> Gene Target *	MP Annotated Term	<u>ToxCast</u> Assays
AHR	patent ductus venosus, abnormal vascular regression	<u>ATG_Ahr_CIS</u> , <u>NCGC_Ahr</u>
BMPR2	decreased angiogenesis	ATG_BRE_CIS
CASP8	abnormal vitelline vasculature morphology	NVS_ENZ_hCASP8
CCL2	decreased angiogenesis, abnormal physiological <u>neovascularization</u> , <u>choroidal neovascularization</u>	BSK_3C_MCP1, BSK_4H_MCP1, BSK_KF3CT_MCP1, BSK_LPS_MCP1, BSK_SAg_MCP1, BSK_SM3C_MCP1
CEBPB*	abnormal <u>vasculogenesis</u> , absent organized vascular network	ATG_C_EBP_CIS, ATG_CRE_CIS

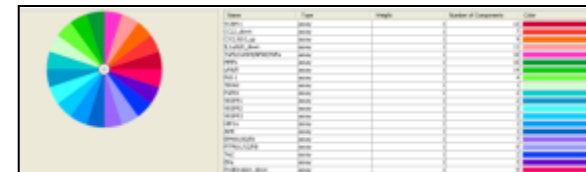
Proposed Adverse Outcome Pathway (AOP) for embryonic vascular disruption: based on what we know



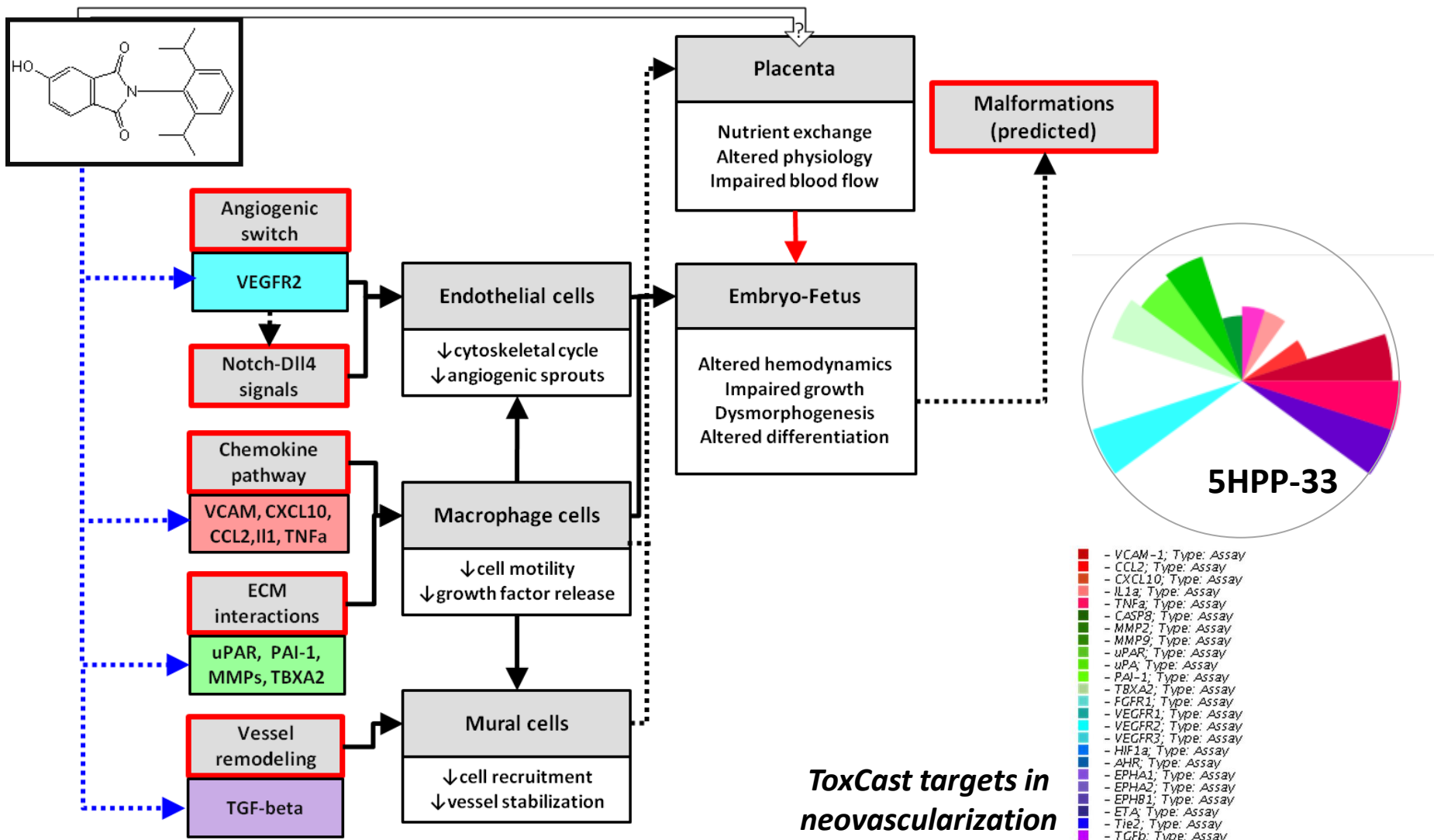
ToxPi ranking by pVDC score: 1060 ToxCast compounds



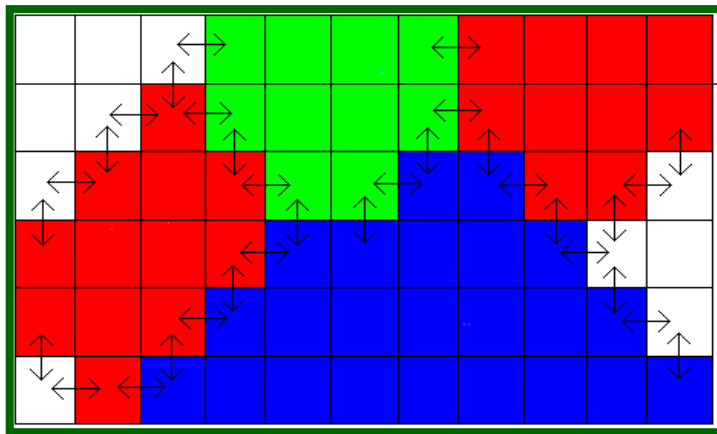
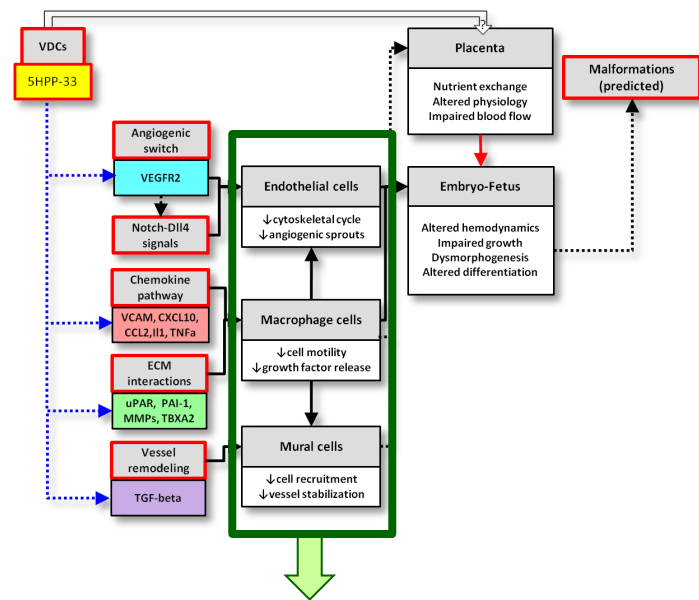
Toxicity Prioritization Index
(ToxPi) for vascular disruption



Proposed AOP for 5HPP-33



cellular *Agent-Based Models* (ABMs)

[illegible]

Core Developmental Processes

- Patterning (Sets up Future Events)
- Timing (Clocks and Oscillators)
- Differentiation (Cell Diversification)
- Morphogenesis (Tissue Organization)

Cellular Primitives

- Growth (Proliferation)
- Growth (Volume Increase)
- Death (Apoptosis)
- Differentiation (Function)
- Adhesion (Differential Hypothesis)
- Shape (Geometry)
- Motility (Cell Migration)
- Extra Cellular Matrix (Remodeling)

Morphogenetic Movement

- Folding
- Epiboly
- Convergent Extension
- Branching Morphogenesis
- Cell Condensation
- Cell Sorting
- Trans-Differentiation
- Cavitation
- Involution/Invagination
- Tractional Forces

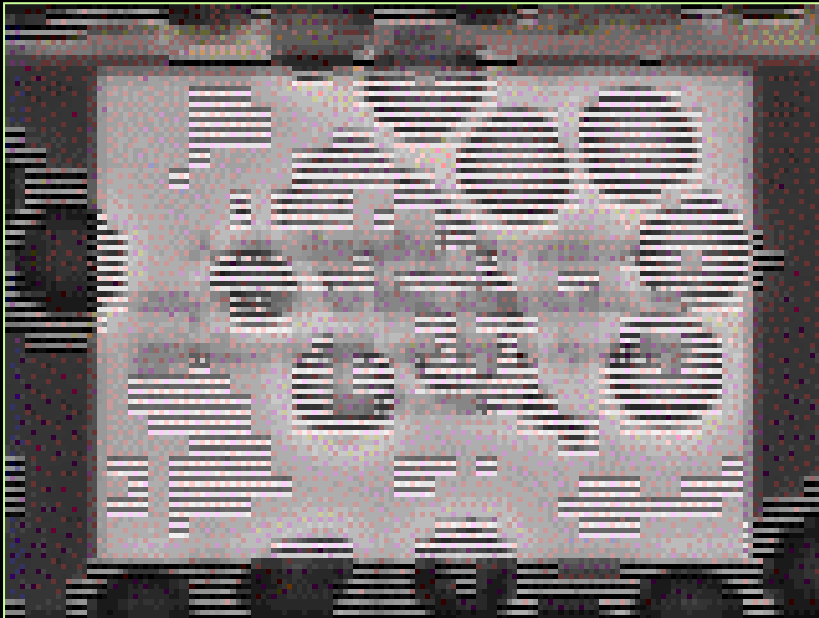
Directed Cell Movement

- Contact Guidance (Boundaries)
- Haptotaxis (ECM Tracks)
- Chemotaxis (Chemical Signals)

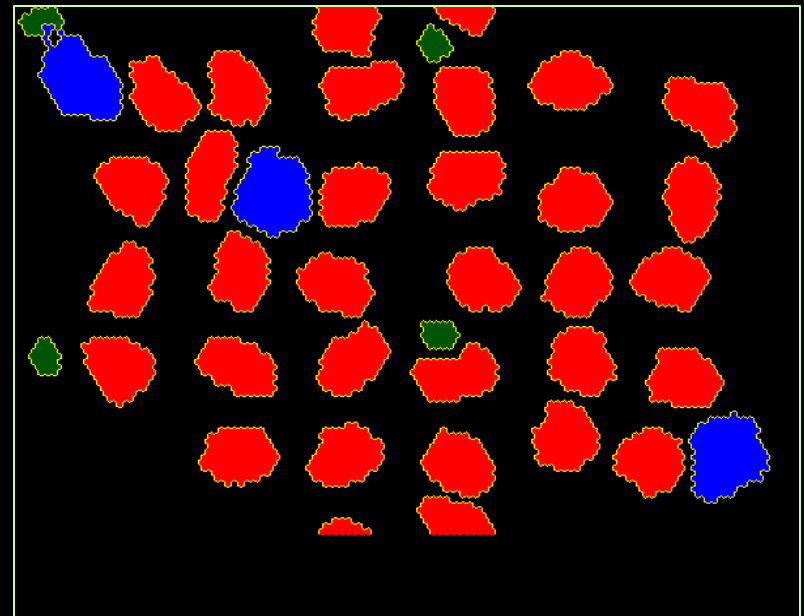
ABMs address cellular systems biology:

- each cell is an 'agent' (unit of autonomous decision)
- simulation is driven by biological networks and rules

In vitro

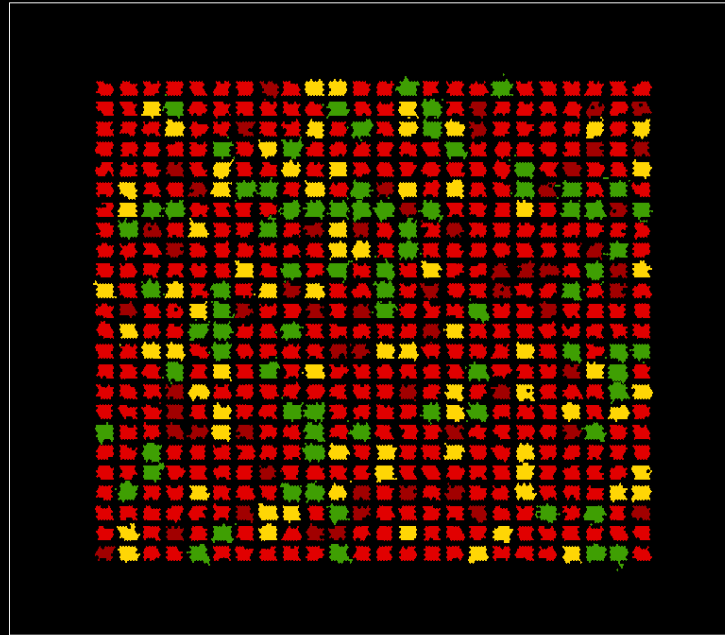


In silico



● *macrophage*
● *RBC*
● *bug*

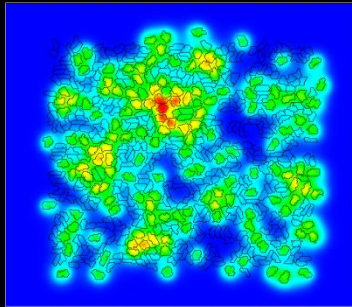
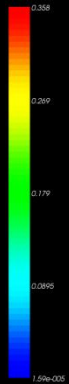
Multicellular ABM of vasculogenesis



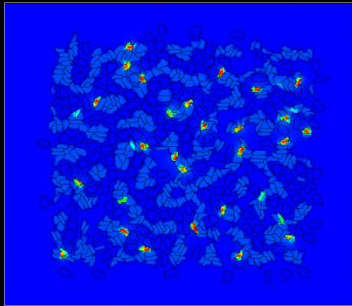
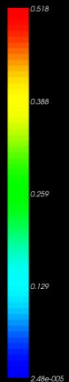
- ABM forms capillary network from endothelial cells (red), inflammatory cells (yellow), and mural cells (green)

Multicellular ABM of vasculogenesis

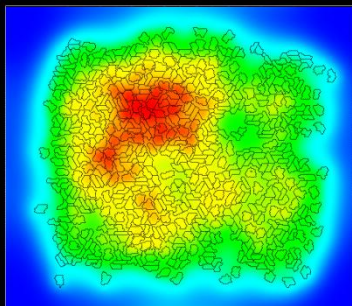
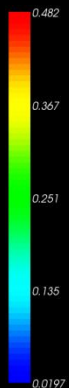
**VEGF
165**



MMPs

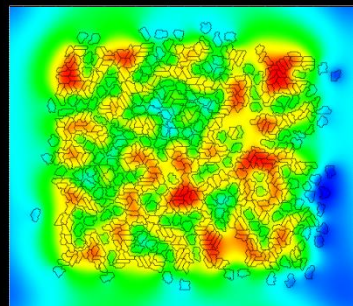
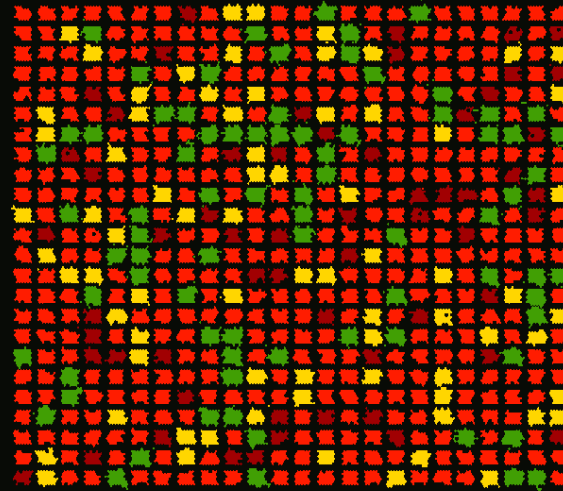


**VEGF
121**

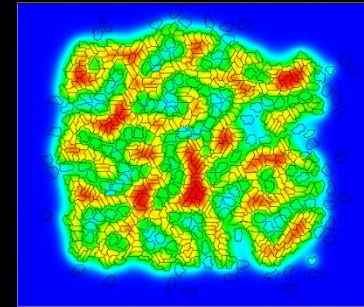
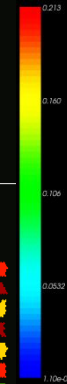


ECs
ECt

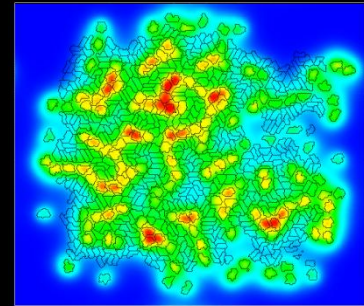
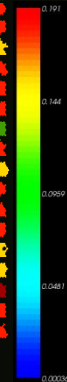
MC
IC



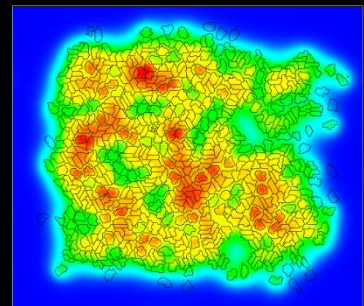
sFlt1



**Ang1/
Tie2**

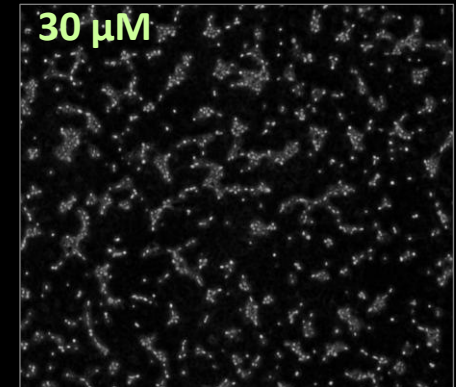
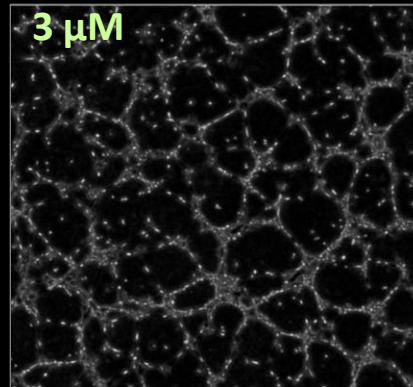
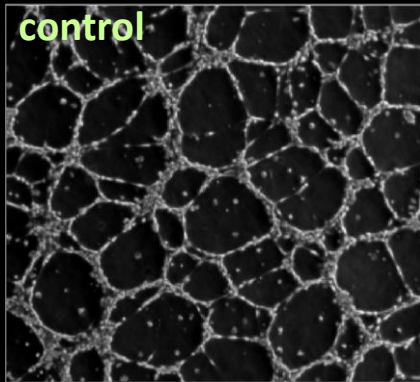
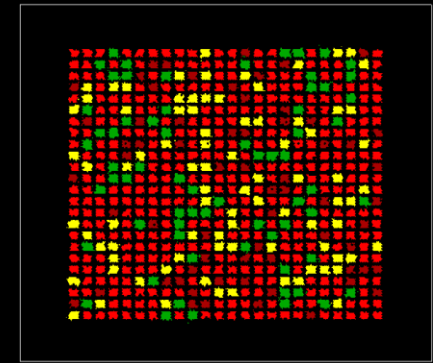
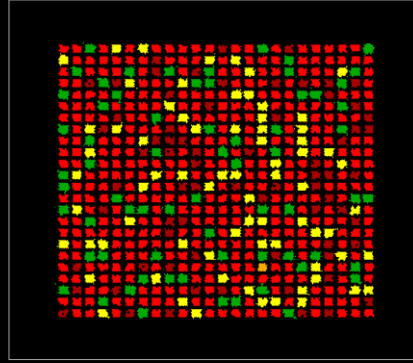
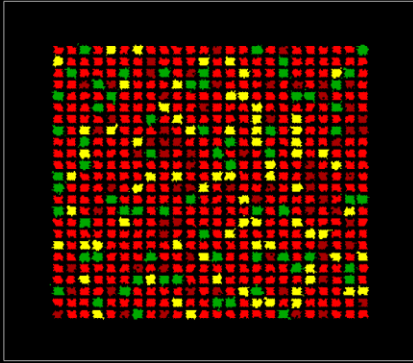


CXCL10

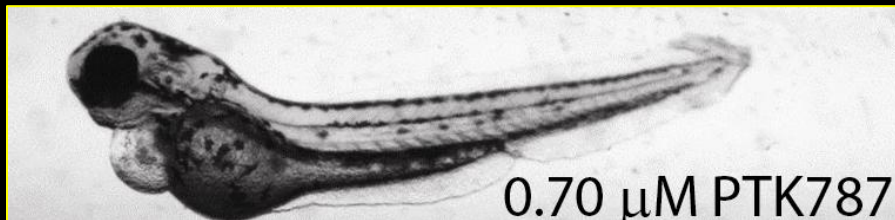
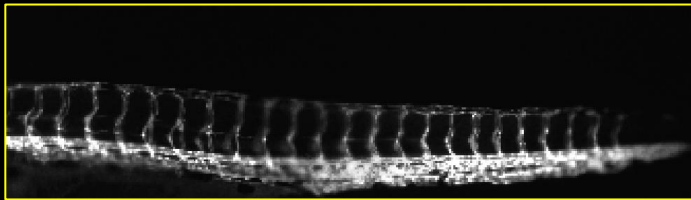
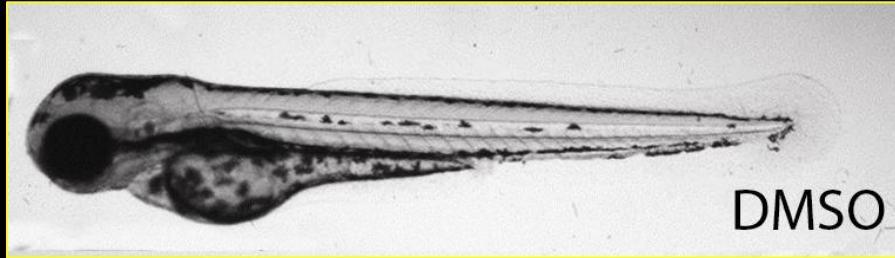


CCL2

- Cell ABM simulation perturbed with ToxCast HTS data captures the 5HPP-33 effect and concentration-response

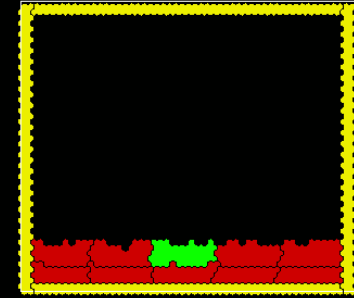


VEGFR2 inhibitor: transgenic zebrafish embryos



*T Tal, S Padilla
US EPA*

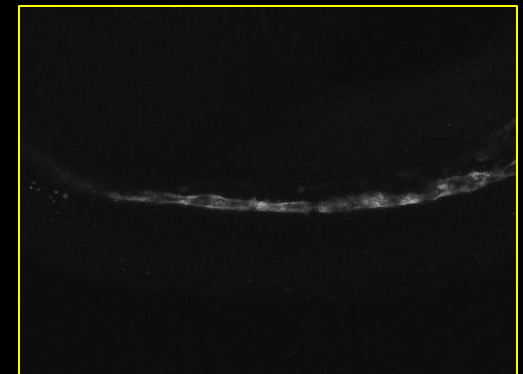
sprouting



DMSO



0.70 μ M
PTK787



*C McCollum, M Bondesson
University of Houston*

Case for Thalidomide Embryopathy

CRBN
cereblon (proteasome)

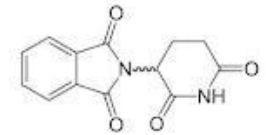
cell-cell signaling
molecular gradients (FGF8)

cellular behaviors
growth and apoptosis

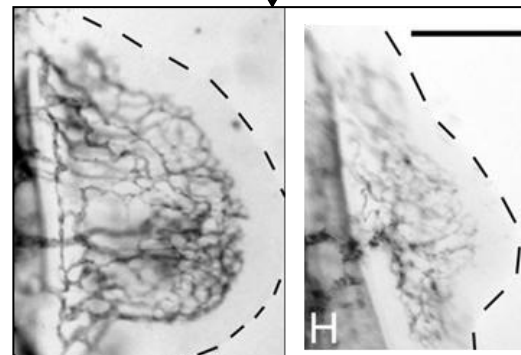
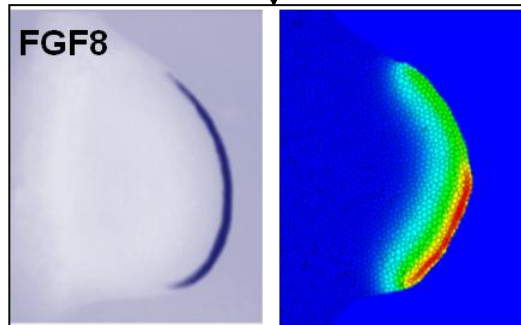
embryonic vasculature
vascular disruption

early limb-buds
dysmorphogenesis

birth defects
limb malformations

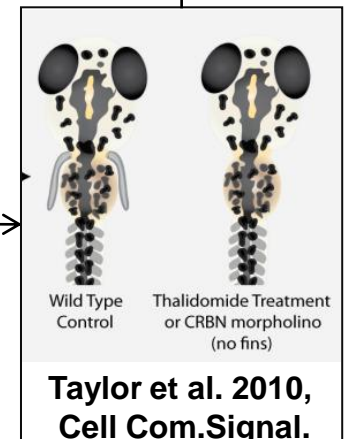


Thalidomide



Therapontos et al. 2009, PNAS 106

**Short or missing
limbs in humans,
monkeys, rabbits,
zebrafish (but not
rodents)**



**Taylor et al. 2010,
Cell Com.Signal.**

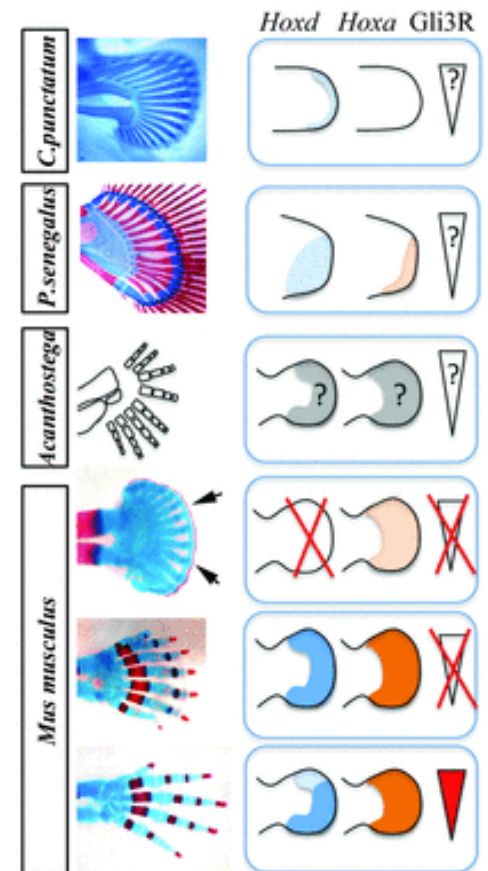
Digital Morphogenesis



Boot et al. (2008) Nat Met 5: 609



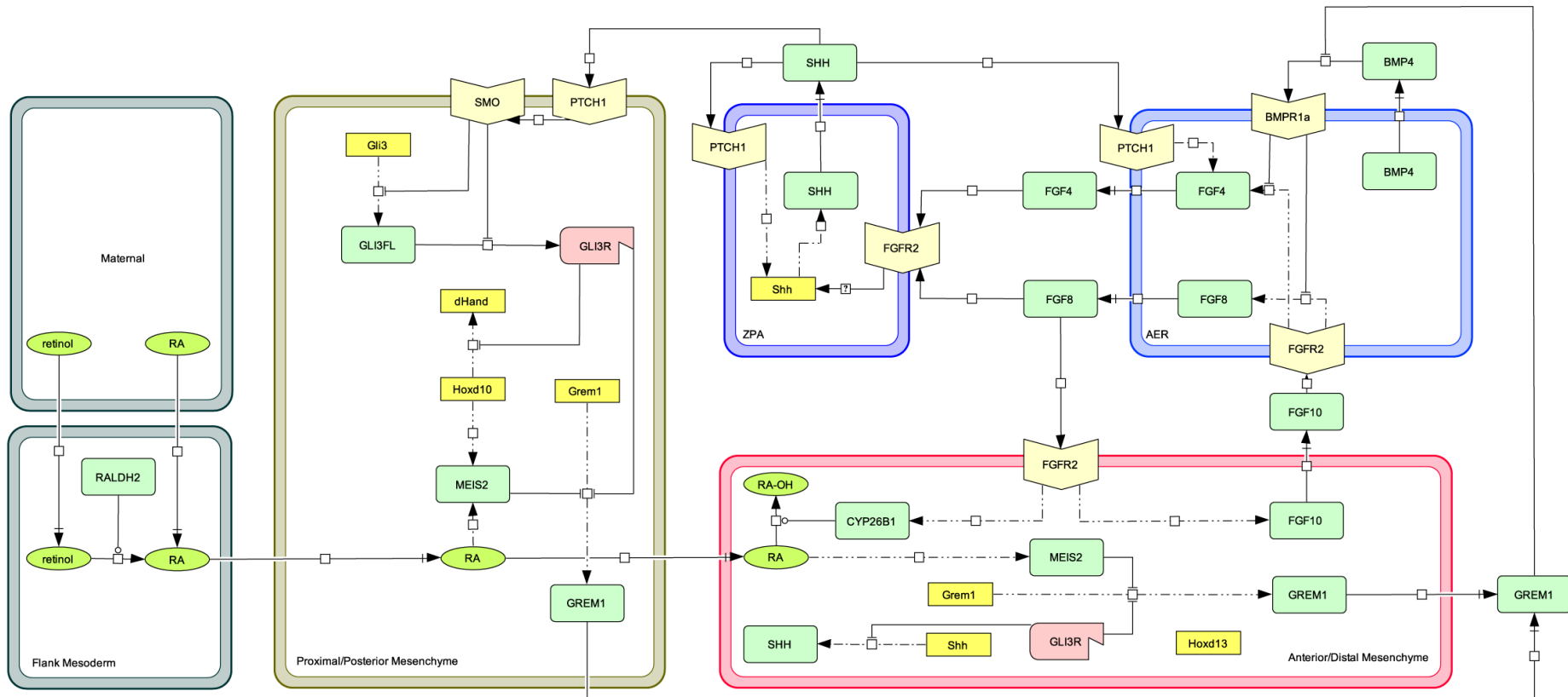
Vogel (2012) Science 338: 1406



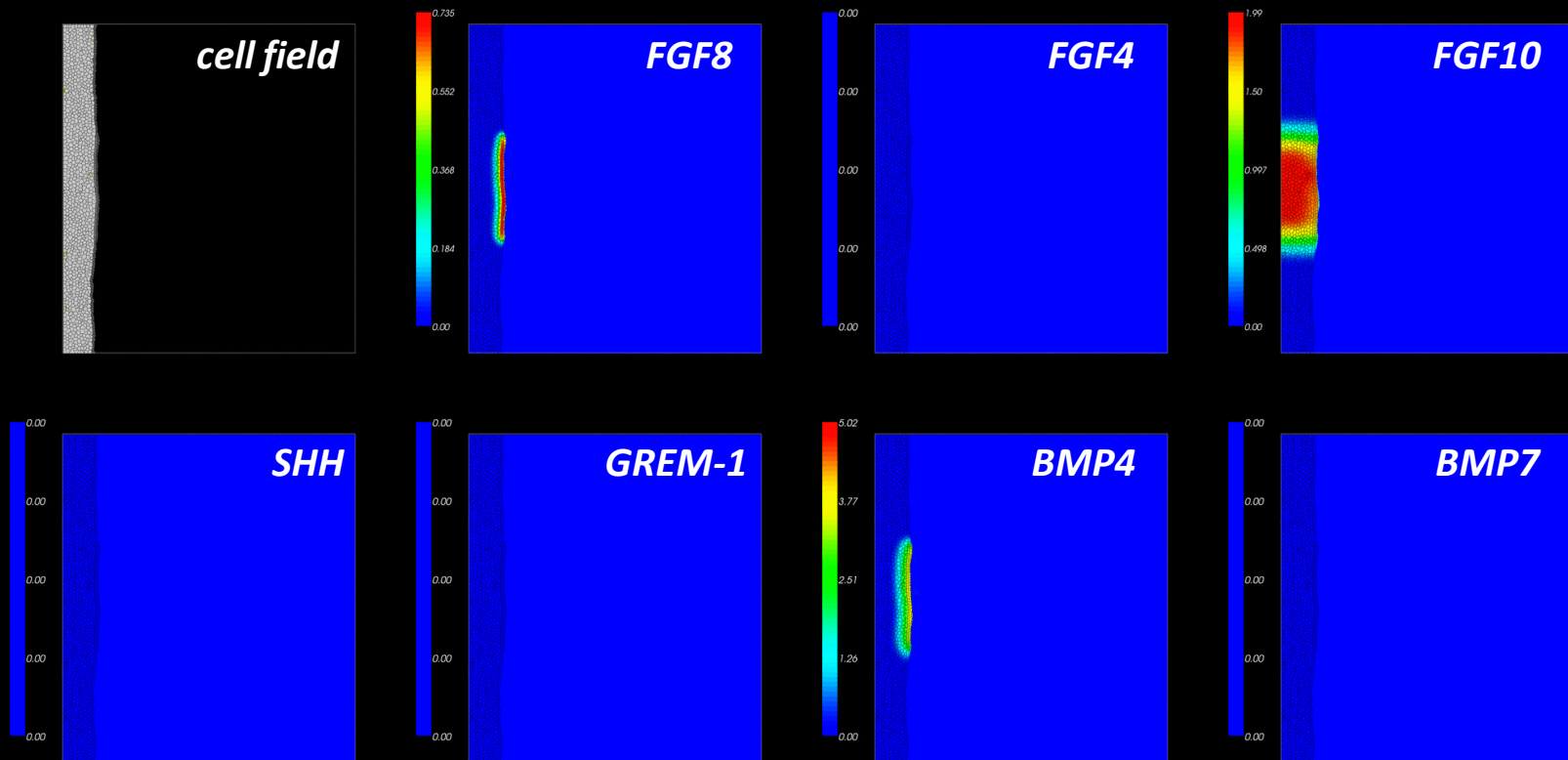
Sheth et al. (2012) Science 338: 1476

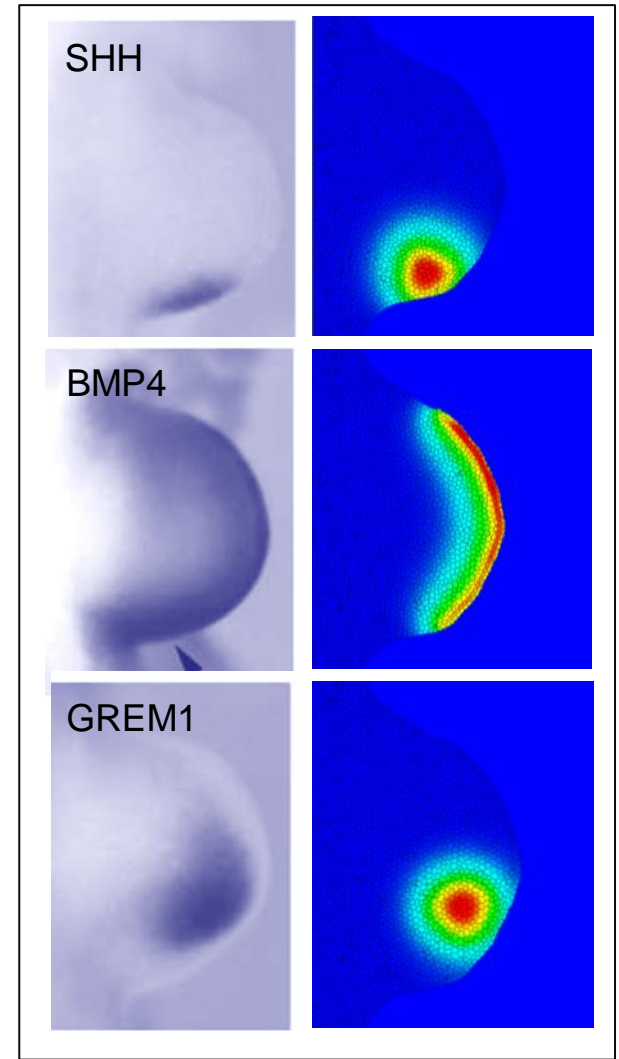
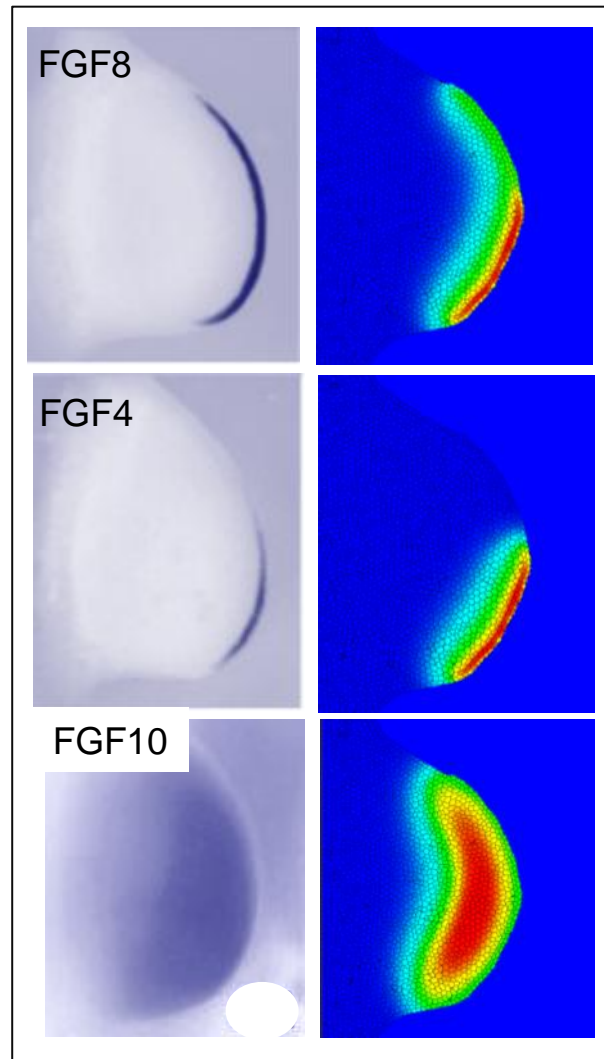
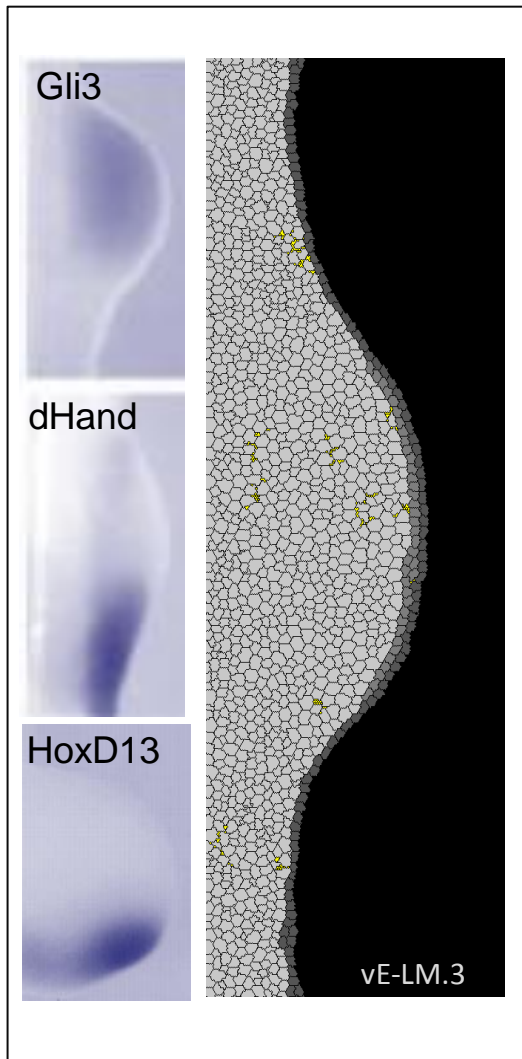
LIMB OUTGROWTH

Control Network



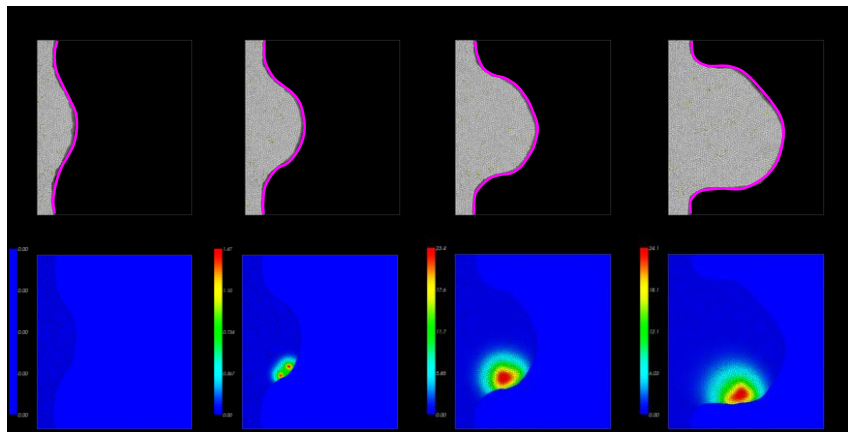
- This cell ABM simulates signal propagation during hindlimb-bud outgrowth in early mouse embryos (~42h)



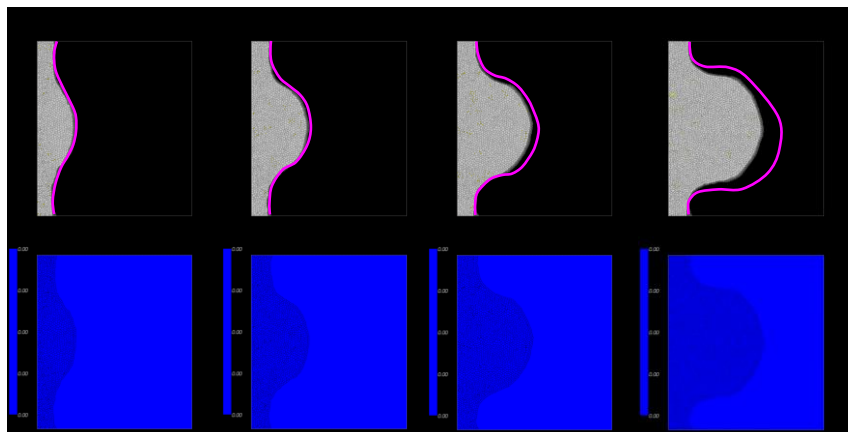


Simulated outgrowth

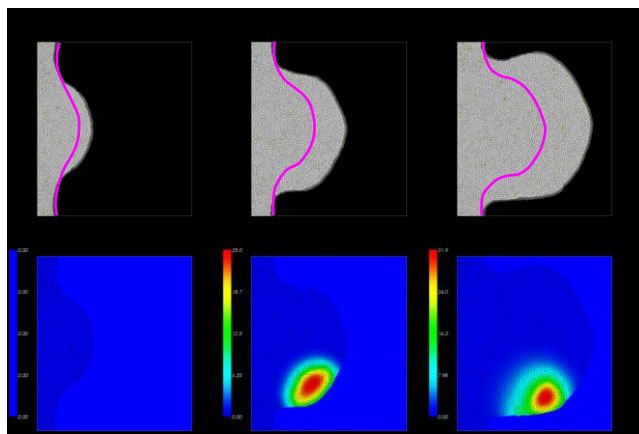
Wild-type



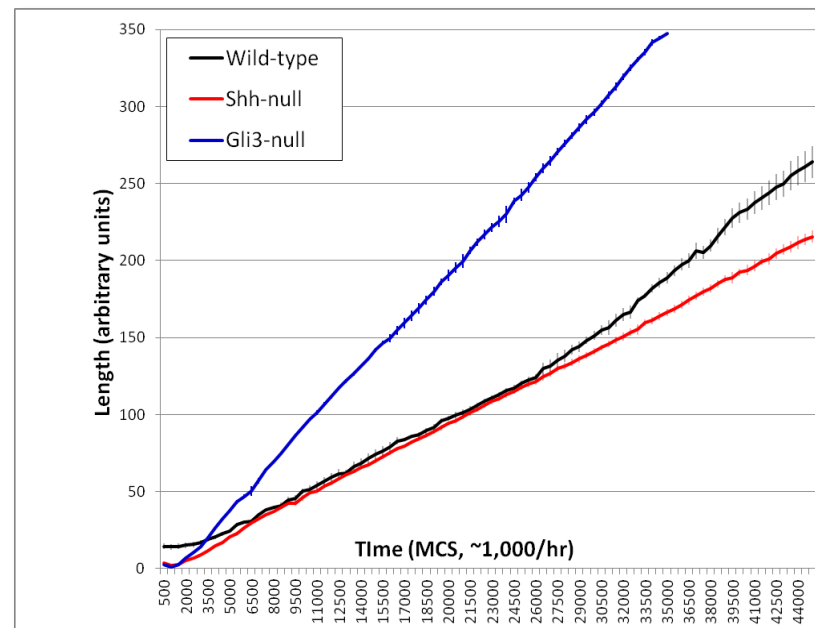
Shh-null



Gli3-null



Rate of elongation ($n=5$)



Predicted outcomes

digital patterns inferred from the literature; not yet implemented in the model



Wild-type



Shh-null

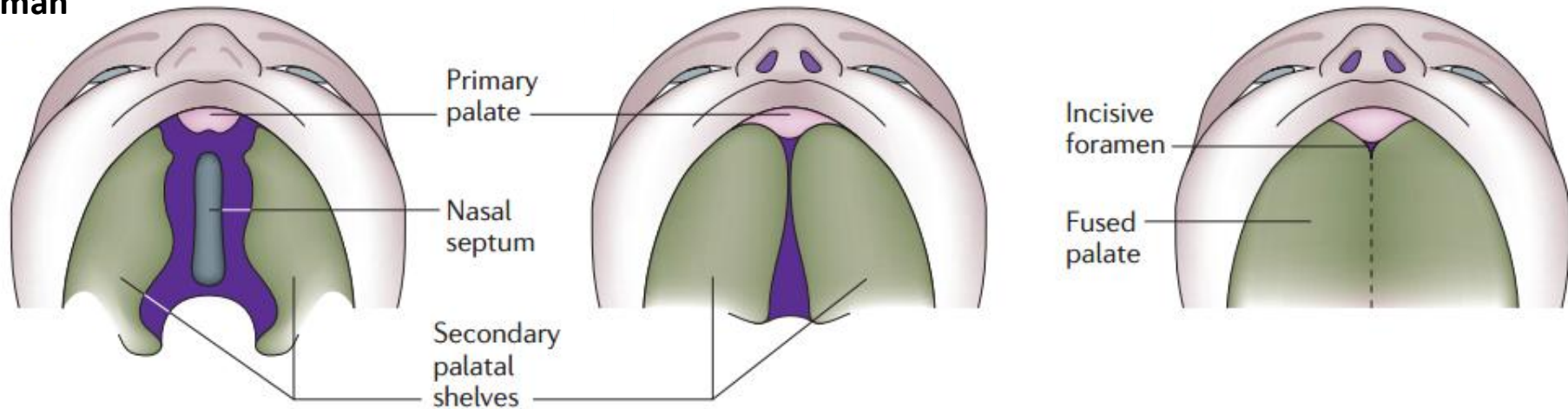


Gli3-null

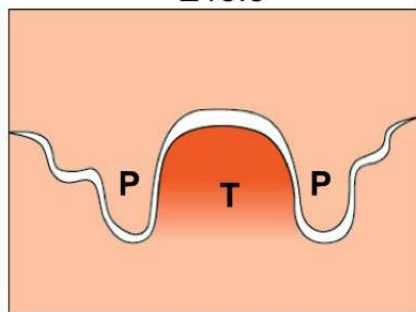
Morphogenetic Fusion

cleft palate affects 1 in 700 births

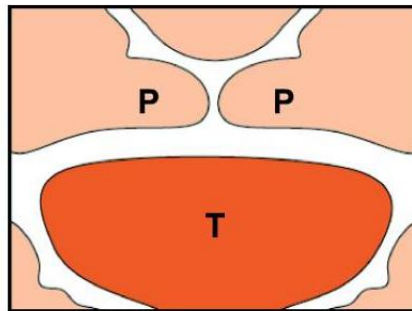
human



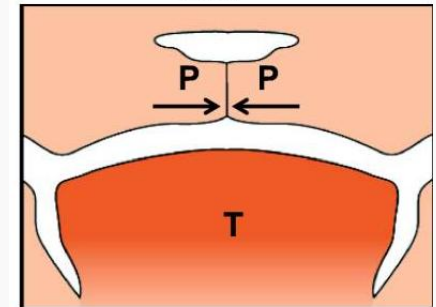
mouse



Growth



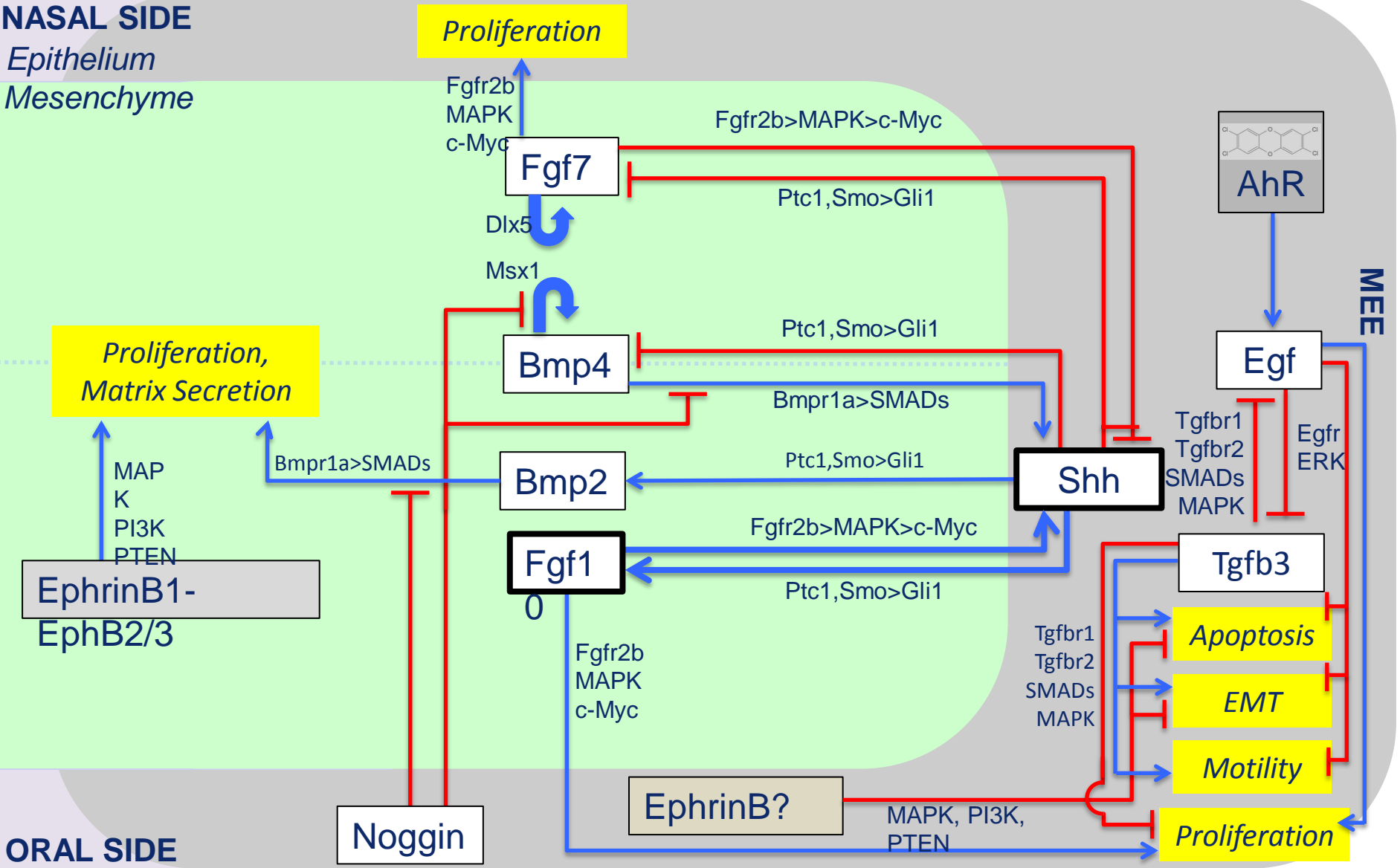
Apposition



Fusion

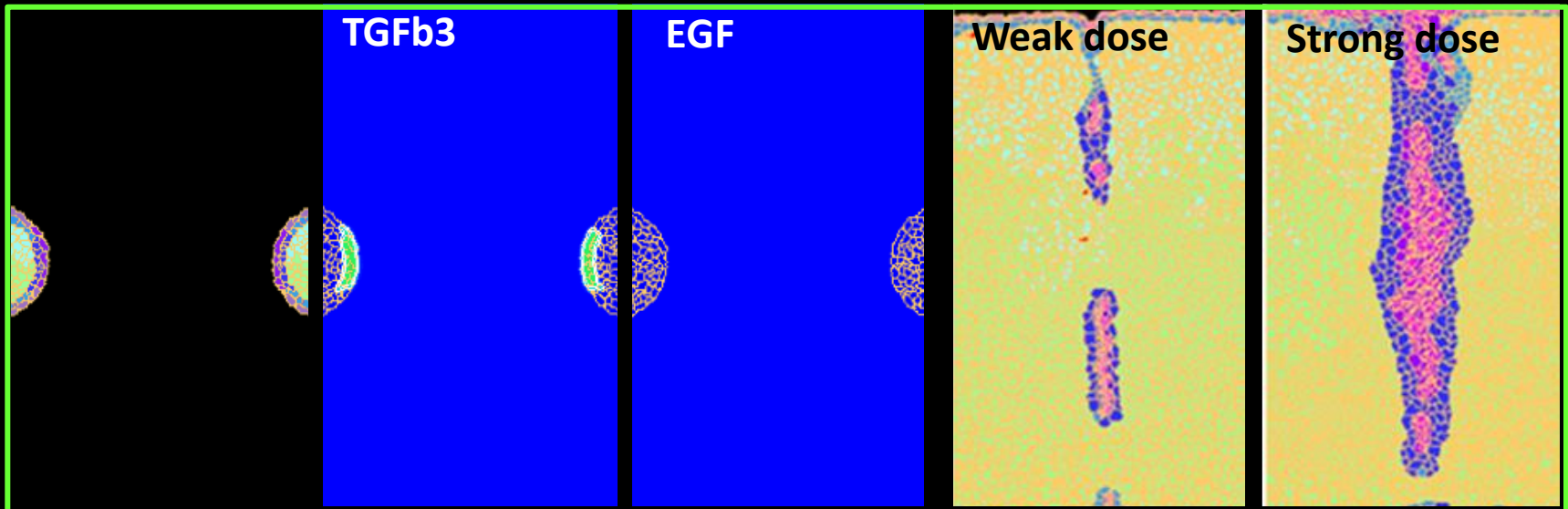
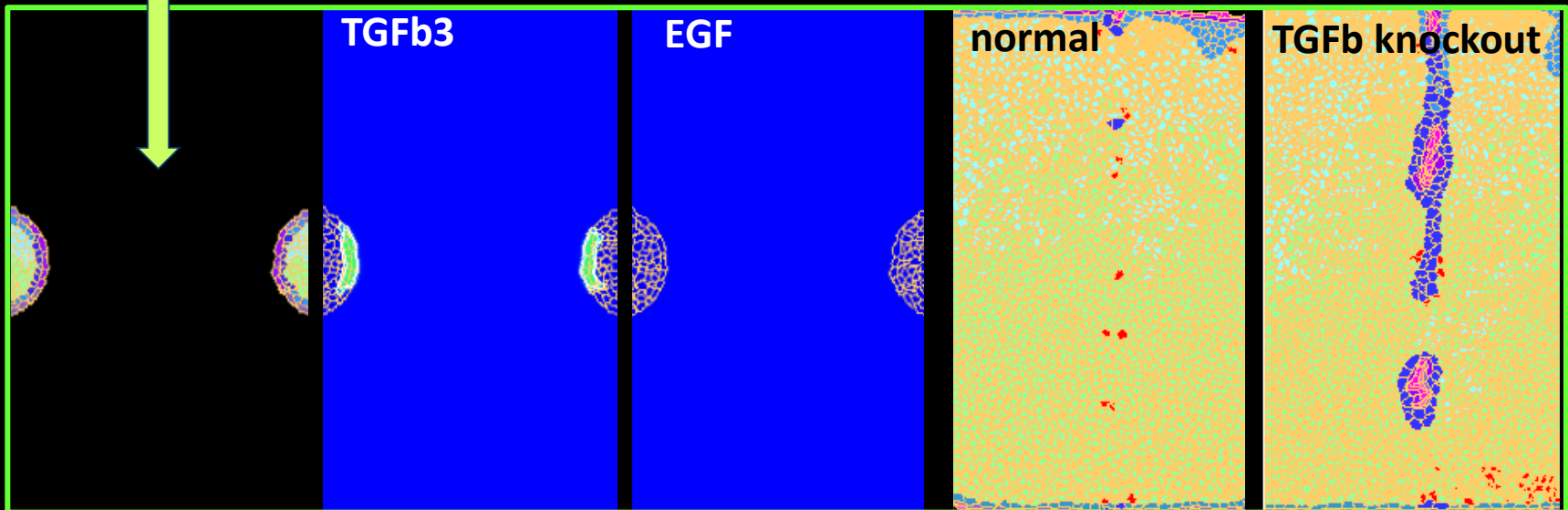
MOUSE PALATAL FUSION: CONTROL NETWORK

NASAL SIDE
Epithelium
Mesenchyme



KEY EVENT:
seam breakdown

Flipping the *TGFb3* / EGF switch



HYPOTHESIS

A computer model that simulates cellular function in the growing embryo can be used to predict the potential impact of chemical exposure during pregnancy and lactation

Executable Biology



Benefits of virtual biology:

- new way to model HTS data
- new tools for quantitative AOP elucidation
- can rapidly sweep many 'what-if' scenarios
- hypothesis generation to inform targeted studies

Challenges to design and implementation:

- not a living entity (can only specify rules as we understand them)
- complexity of network structure and dynamics (systems theory)
- finding the sweet-spot to enable but not overspecify performance

Virtual Embryo Team

<http://www.epa.gov/ncct/v-Embryo/>

Task Management

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S Darney, E Cohen-Hubal (EPA - CSS)
K Crofton, D Wolf, R Highsmith (MIs)
T Knudsen and S Hunter (Task Leads)

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M Firestone (EPA - OCHP)
E Mendez (EPA - OCSPP)

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(LHM), A Singh (Syngenta Corp)

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I Shah, J Wambaugh (EPA-NCCT, CSS 2.2.1)

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S Clendenon, A Shirinifard (TIVS – Indiana U)
E Carney, R Ellis-Hutchings, Raja Settivari (DOW)
T Heinonen, R Sarkanen (FICAM)

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S Hutson (Vanderbilt U)

