



Computational Modeling and Simulation of Developmental Toxicity

What can we learn from a virtual embryo?

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Chemical Safety for Sustainability Research Program



Virtual Tissue Models (VTM) project

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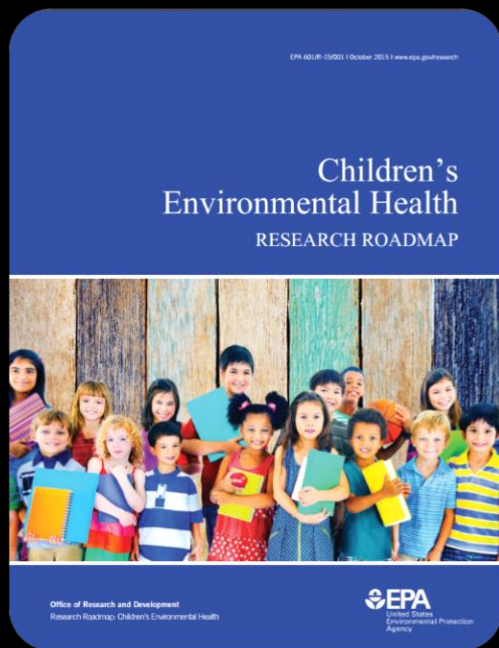
RIVM, Bilthoven NL

February 17, 2017



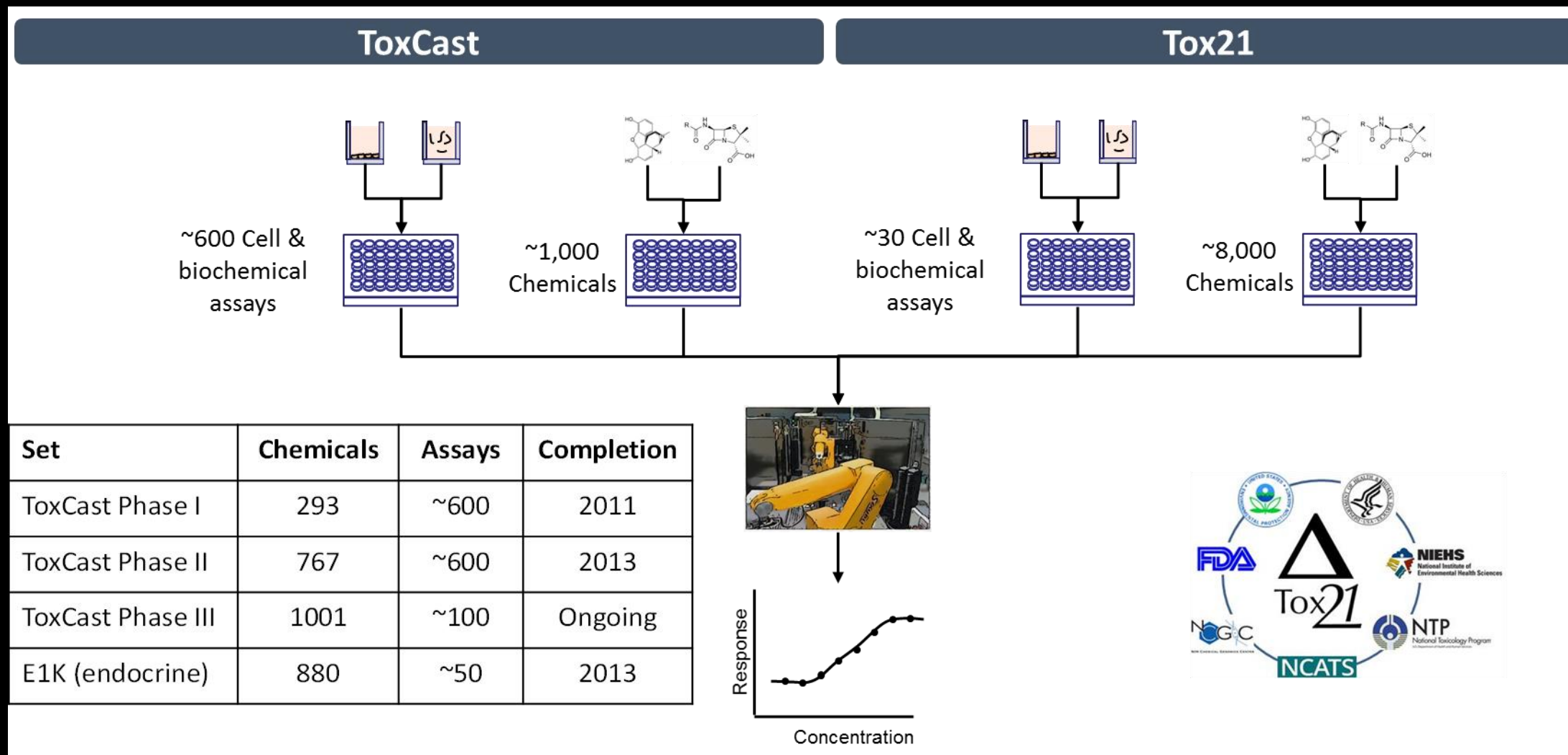
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Developmental and Reproductive Toxicity (DART)

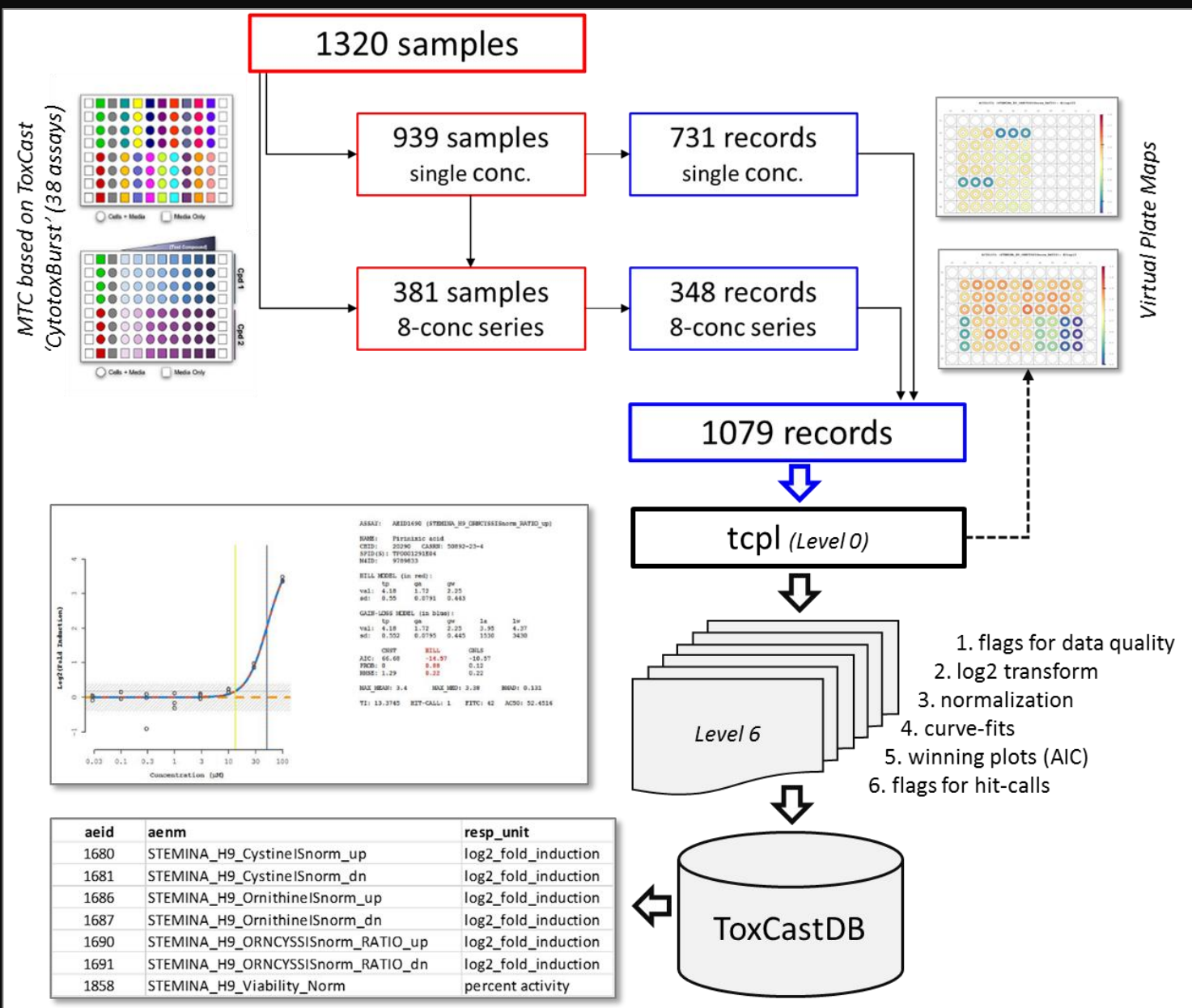


- DART testing is important for assessing the potential consequences of drug and chemical exposure on human health and well-being.
- Complexity of pregnancy and the reproductive cycle makes DART testing challenging and costly for traditional (animal-based) methods.
- A compendium of *in vitro* data from ToxCast/Tox21 high-throughput screening (HTS) programs is available for predictive toxicology.
- 'Predictive DART' will require an integrative strategy that mobilizes HTS data into *in silico* models that capture the relevant embryology.

Shifting to Molecular/Pathway Approaches



Stemina (STM): hESC (WA09) targeted biomarker (ORN/CYSS secretome)



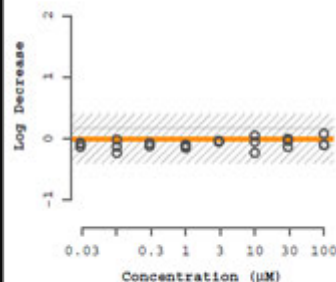
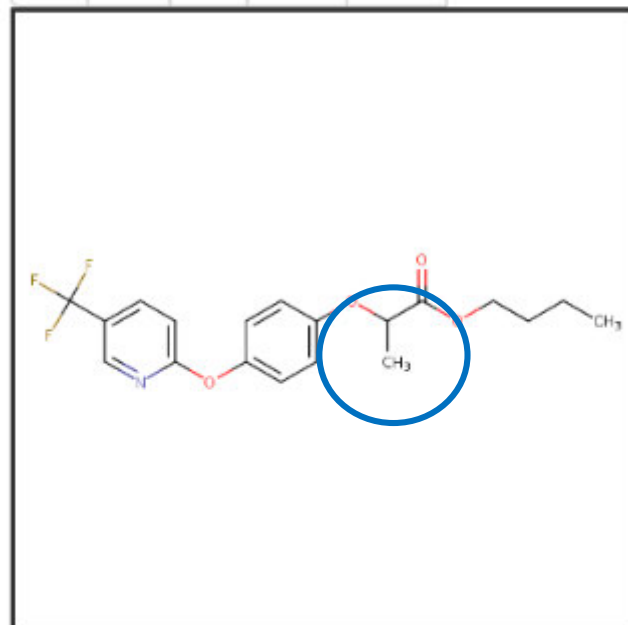
- **Prediction models:** range from 87-91% BA (sens 0.80 to 0.86, spec 0.93 to 1.00 depending on anchor)
- **Initial analysis:** revealed 177 actives (16.4% tested) with several known teratogens and many unknowns
- **ToxRefDB:** preliminary model vs skeletal defects ($dLEL \leq 50$ mg/kg) : sensitivity (0.36), specificity (0.86) for BA = 79.3%

Example of “unknown teratogenicity” - stereoisomer pair

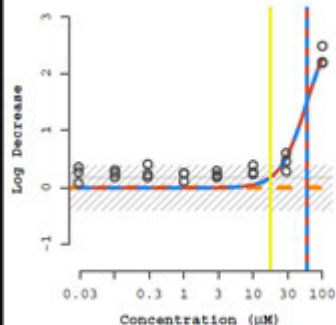
Fluazifop-butyl

69806-50-4 | DTXSID3034612 ⓘ

ⓘ Searched by Integrated Source Name: Found 1 result for 'fluazifop butyl'.



ASSAY: ARID1690 (STEMINA_H9_ORNCTSSISnorm_RATIO_up)
NAME: Fluazifop-butyl
CHID: 34612 CASRN: 69806-50-4
SPID(S): TP0001297F08
MAID: 11032862
HILL MODEL: Not applicable.
GAIN-LOSS MODEL: Not applicable.
CNST
AIC: -34.09 HILL NA GNLS
PROB: 1 NA NA
RMSE: 0.1 NA NA
MAX_MEAN: -0.0286 MAX_MRD: -0.0265 RMAD: 0.135
TI: NA HIT-CALL: 0 FITC: 4 ACSO: NA
FLAGS:

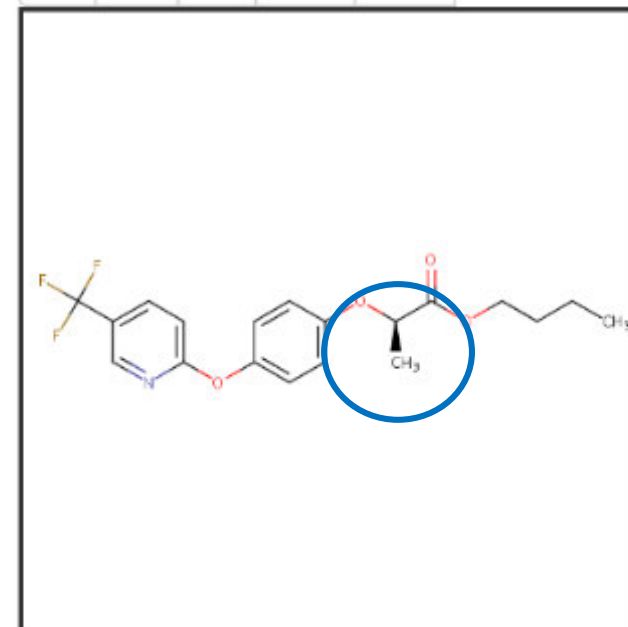


ASSAY: ARID1690 (STEMINA_H9_ORNCTSSISnorm_RATIO_up)
NAME: Fluazifop-P-butyl
CHID: 34855 CASRN: 79241-46-6
SPID(S): TP0001297B10
MAID: 11032878
HILL MODEL (in red):
tp ga gw
val: 3 1.78 2.23
sd: 1.41 0.253 1.33
GAIN-LOSS MODEL (in blue):
tp ga gw la lw
val: 3 1.78 2.23 3.89 6.39
sd: 1.41 0.253 1.33 152000 511000
CNST
AIC: 52.53 HILL 11.66 GNLS 19.66
PROB: 0 0.88 0.12
RMSE: 0.87 0.24 0.24
MAX_MEAN: 2.3 MAX_MRD: 2.22 RMAD: 0.135
TI: 17.7 HIT-CALL: 1 FITC: 42 ACSO: 60.1
FLAGS:
10

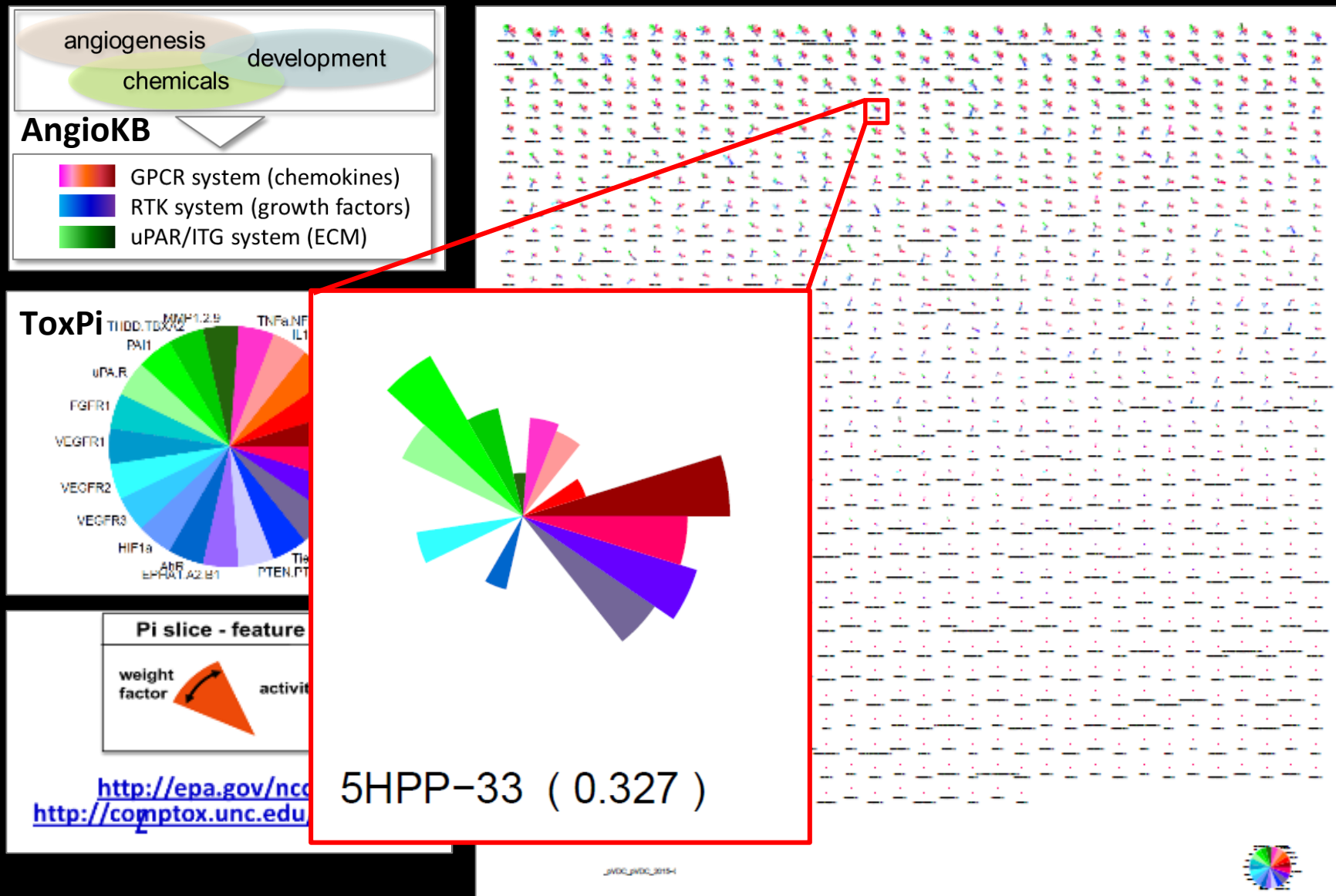
Fluazifop-P-butyl

79241-46-6 | DTXSID0034855 ⓘ

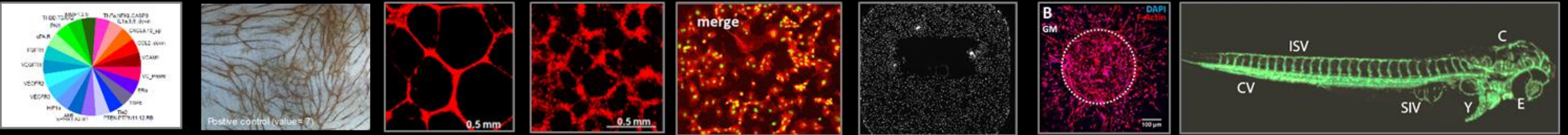
ⓘ Searched by Approved Name: Found 1 result for 'fluazifop-p-butyl'.



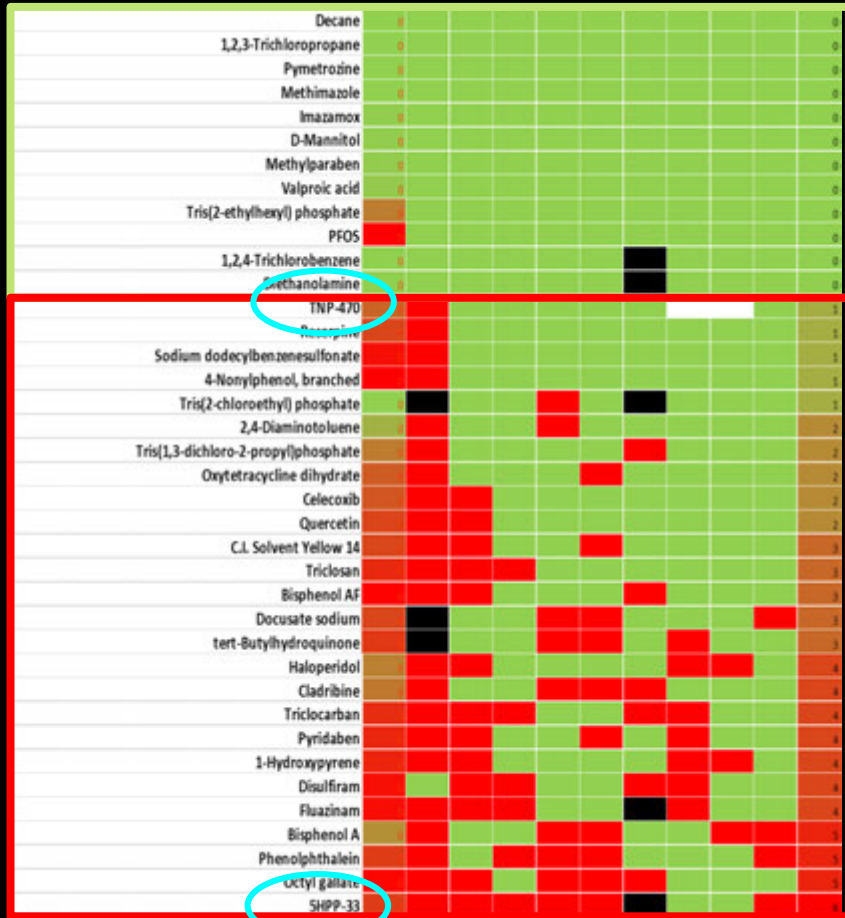
Angiogenesis: chemicals sorted by predicted potential to disrupt angiogenesis (pVDCs)



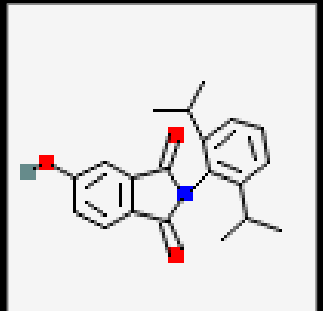
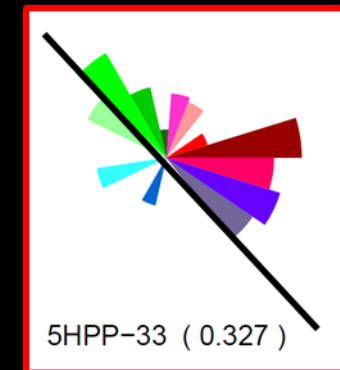
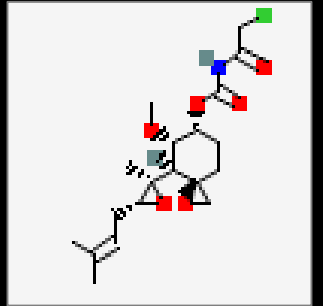
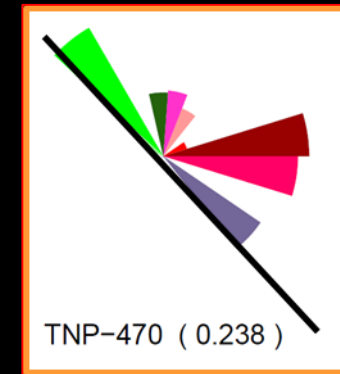
Validation: 38 pVDCs and non-pVDCs evaluated across 8 angiogenic platforms



A B C D E F G H I J

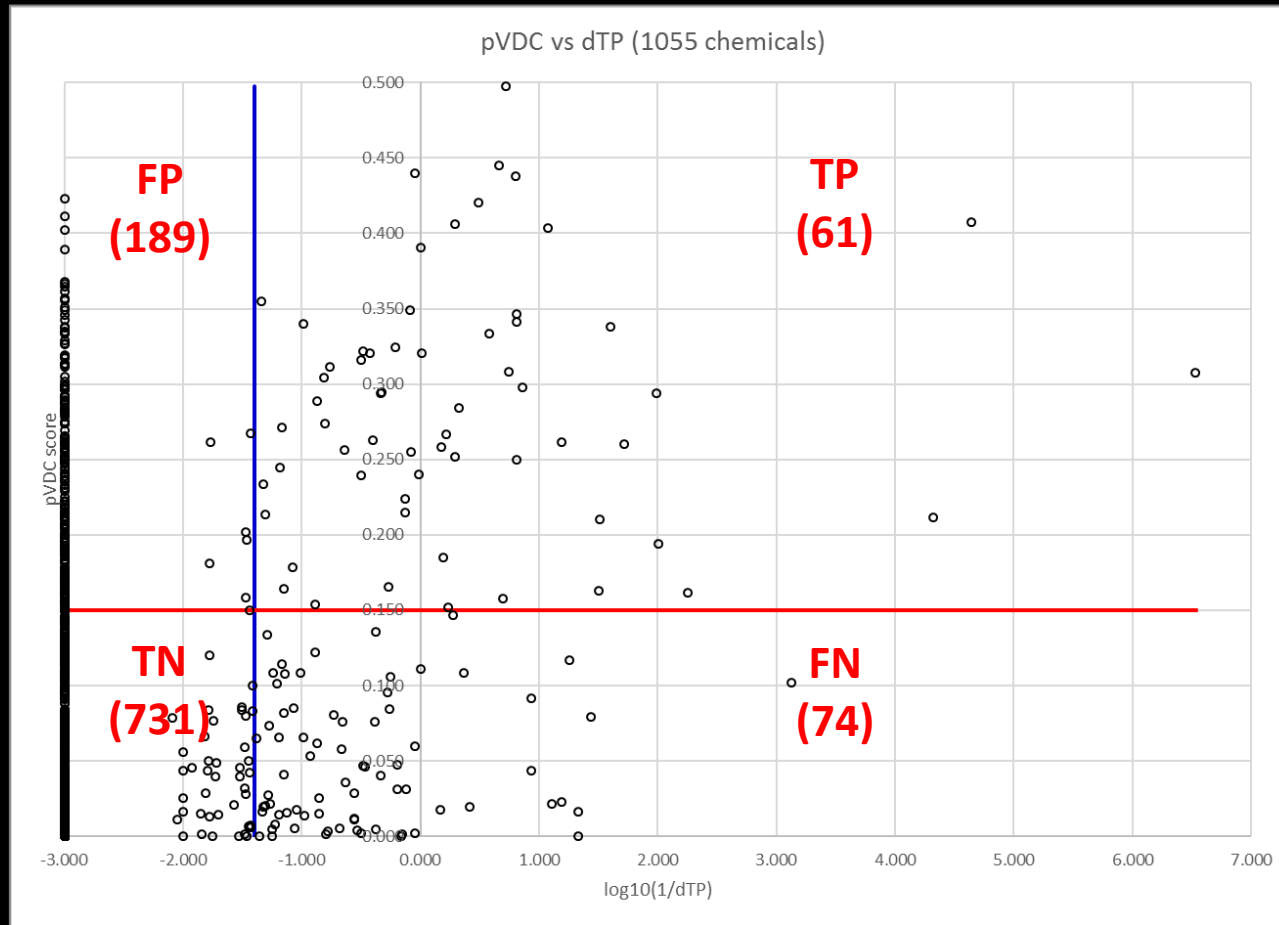


- A ToxPi [1]
- B FICAM tubulogenesis [2]
- C Synthetic tubulogenesis [3]
- D Matrigel tubulogenesis [3]
- E nuCTNB [4]
- F EC migration [4]
- G angiogenic sprouting [5]
- H TG-zebrafish [1]
- I Vala tubulogenesis [2]
- J aggregate (B to I)



[1] Tal et al. *Reprod Toxicol* (submitted); [2] Knudsen et al., *in prep*; [3] Nguyen et al. *Nature Bioengineering* (submitted); [4] Belair et al. (2016) *Acta Biomaterialia*.

DevTox: how well does pVDC score match teratogenic potential in a human system?



AOP-based **pVDC** score vs **DevTox** potential from the STM hES cell platform

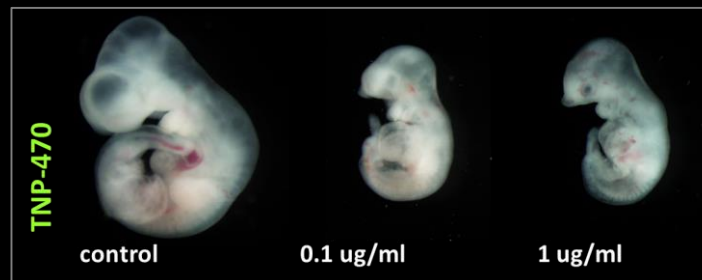
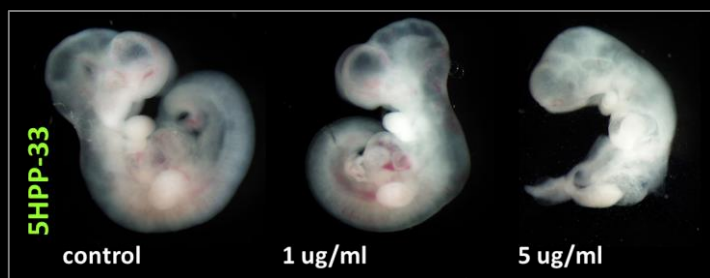
Balanced Accuracy = 75.1%
(modeled on the 38-test set)

24.4% pVDC(+) also STM(+)
90.8% pVDC(-) also STM(-)

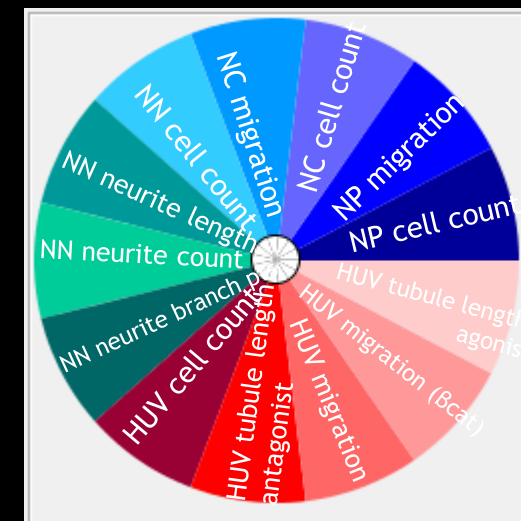
5HPP-33: DevTox (WEC) AC50 = 21.2 μ M; STM predicts human teratogenicity at ≥ 4.37 μ M

TNP-470: DevTox (WEC) AC50 = 0.038 μ M; STM predicts human teratogenicity at ≥ 0.01 μ M

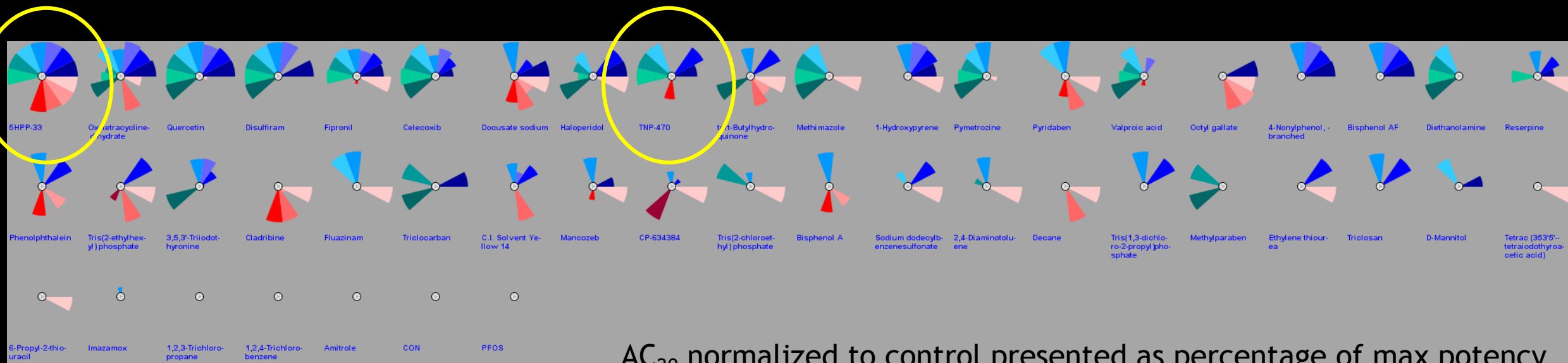
Preliminary: 46 chemicals tested for activity on angiogenesis (Vala) and neurogenesis (Aruna)



Neurogenesis (blue/green)



Angiogenesis (red)



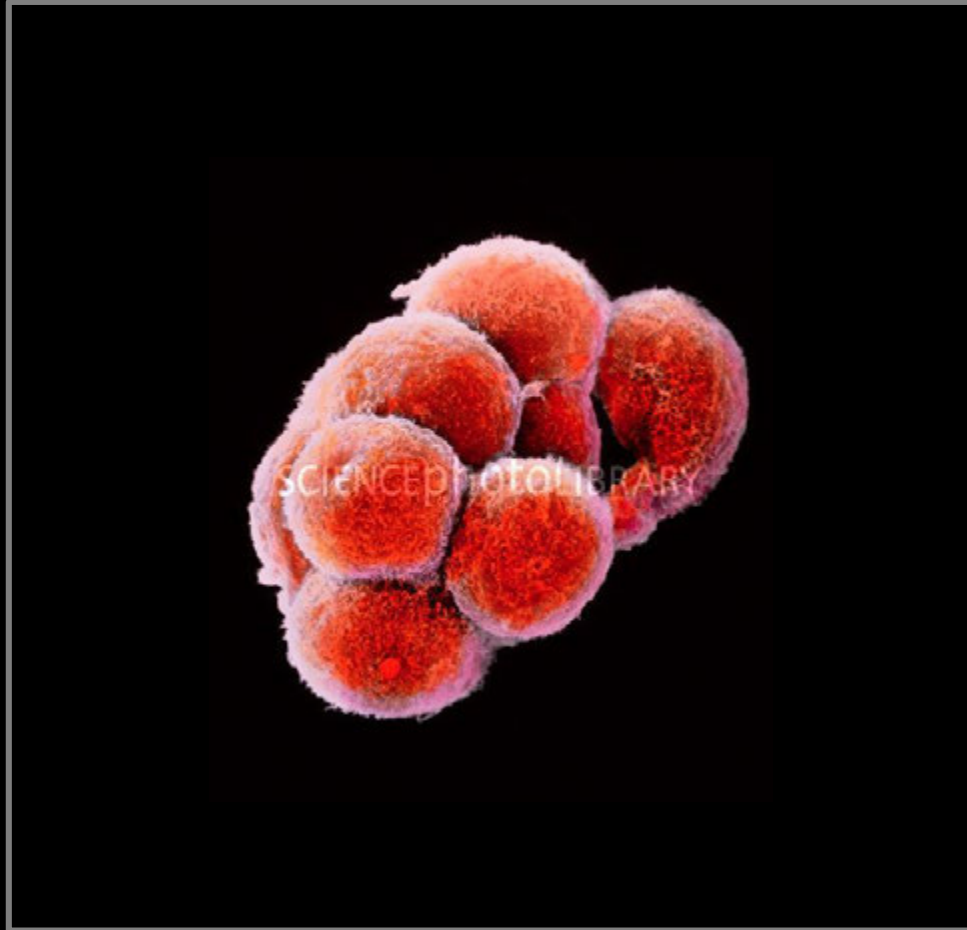
AC₂₀ normalized to control presented as percentage of max potency

Virtual reconstruction of developmental toxicity



- ▶ The question of how tissues and organs are shaped during development is crucial for understanding (and predicting) human birth defects.
- ▶ While ToxCast HTS data may predict developmental toxicity with reasonable accuracy, mechanistic models are still necessary to capture the relevant biology.
- ▶ Subtle microscopic changes induced chemically may amplify to an adverse outcome but coarse changes may override lesion propagation in any complex adaptive system.
- ▶ Modeling system dynamics in a developing tissue is a multiscale problem that challenges our ability to predict toxicity from *in vitro* profiling data (ToxCast/Tox21).

Anatomical homeostasis in a self-regulating Virtual Embryo



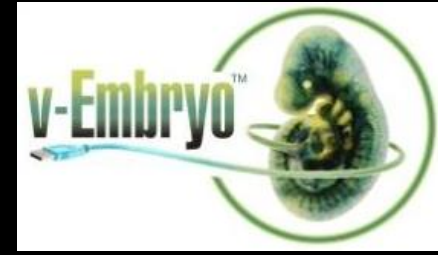
Mouse Morula

SOURCE: Science Photo Library



*SOURCE: Andersen, Newman and Otter
(2006) Am. Assoc. Artif. Intel.*

Breathing life into a 'Virtual Embryo'



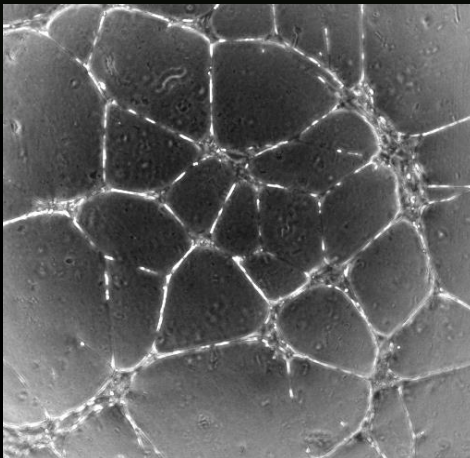
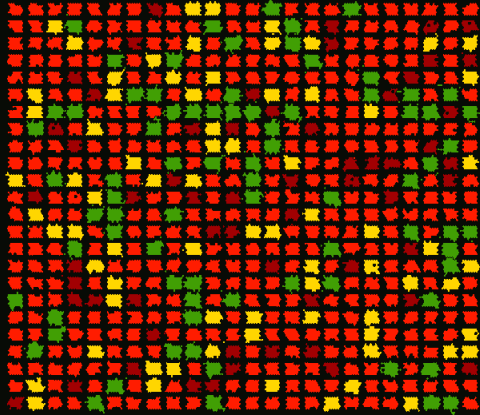
- ▶ **Hypothesis:** computer models that recapitulate a morphogenetic series of events can be used analytically (to understand) and theoretically (to predict) developmental toxicity.
- ▶ **Agent-Based Modeling and Simulation (ABMS):** a heuristic approach to reconstruct tissue dynamics from the bottom-up, cell-by-cell and interaction-by-interaction.
- ▶ **CompuCell3D:** open source modeling environment
 - engineered at Indiana University by James Glazier and colleagues;
 - steppables for distinct cell behaviors (growth, proliferation, apoptosis, differentiation, polarization, motility, ECM, signal secretion, ...);
 - rules coded in Python for cell-autonomous 'agents' that interact in shared microenvironment and self-organize into emergent phenotypes.

Angiogenesis

VEGF165
MMPs
VEGF121
sFlit1
TIE2
CXCL10
CCL2

ABMS

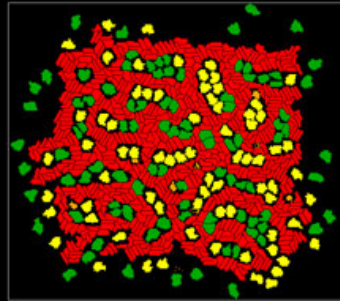
Endothelial Stalk
Endothelial Tip
Mural Cell
Inflammatory Cell



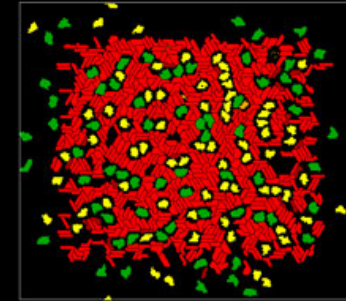
SOURCE: J Glazier, Indiana University

Exposure to 5HPP-33, a synthetic thalidomide analog

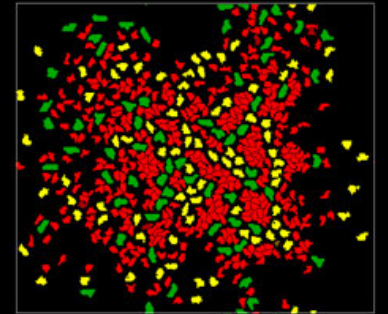
control



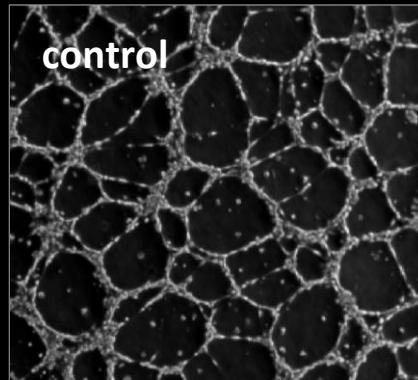
4 μ M



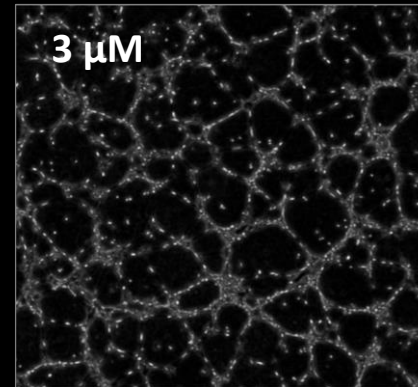
40 μ M



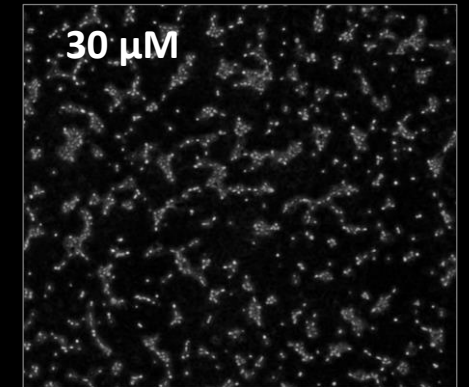
control



3 μ M



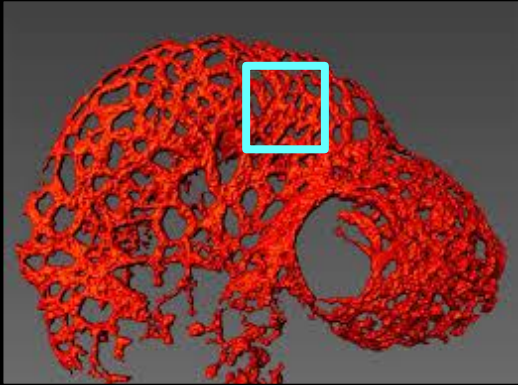
30 μ M



SOURCE: Kleinstreuer et al. 2013, PLoS Comp Biol

Computational Neurovascular Unit (cNVU): simulating brain angiogenesis with microglia.

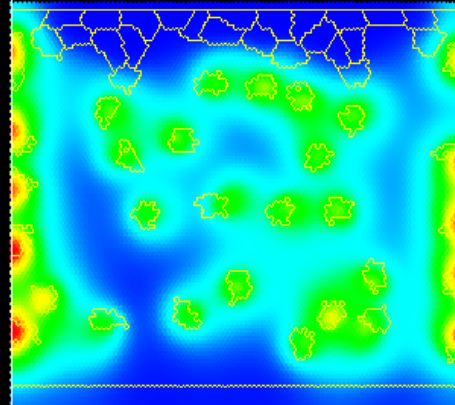
BBB development



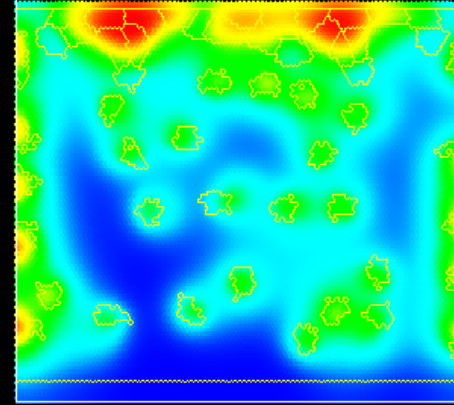
Cell field



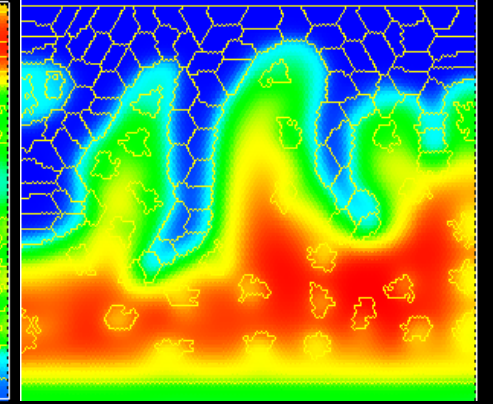
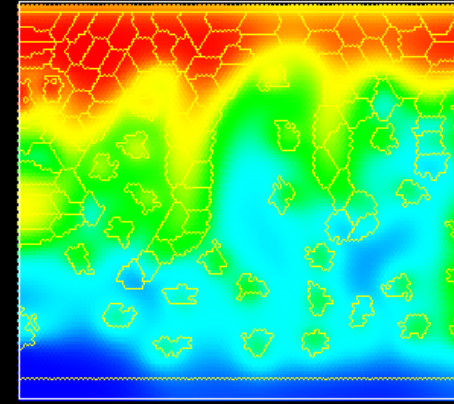
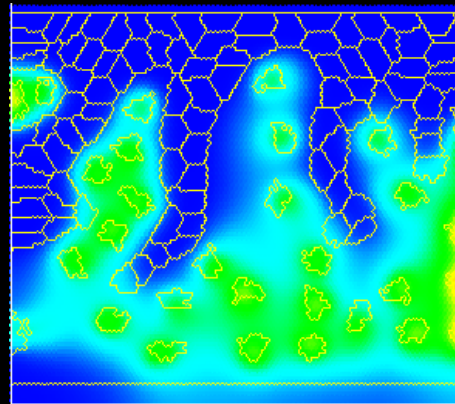
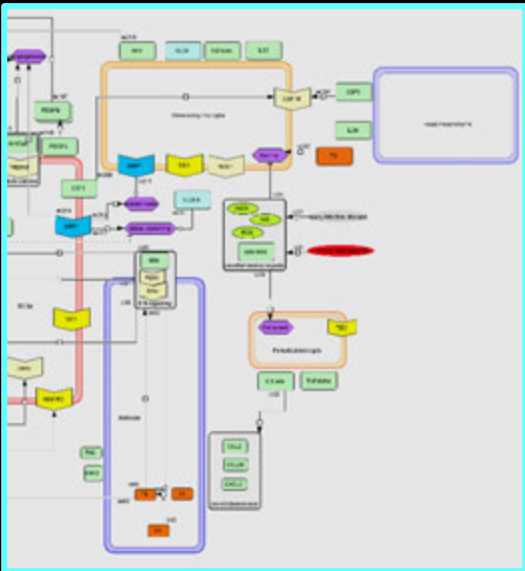
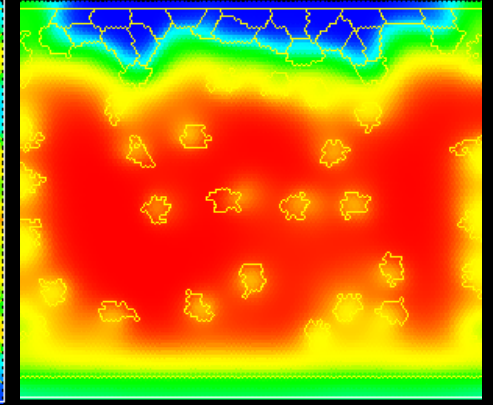
VEGF-C



sVEGFR1



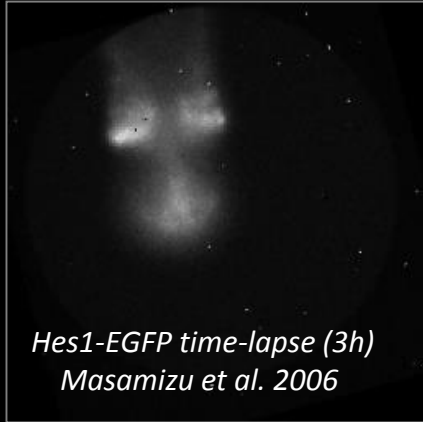
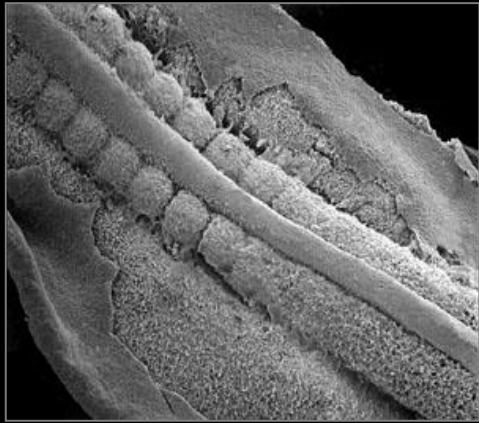
VEGF-A



- Endothelial (Stalk)
- Endothelial (Tip)
- Microglia

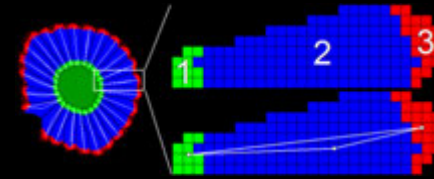
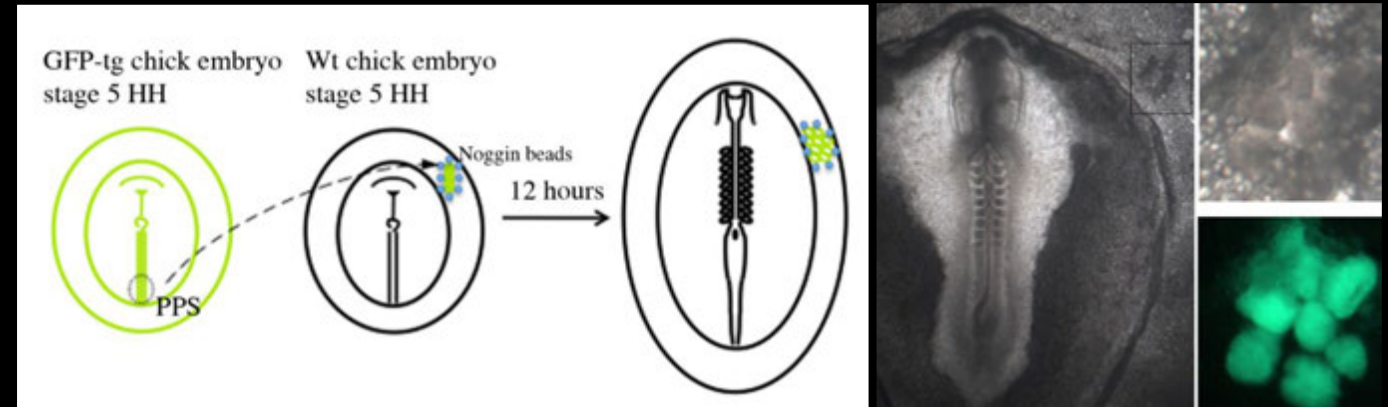
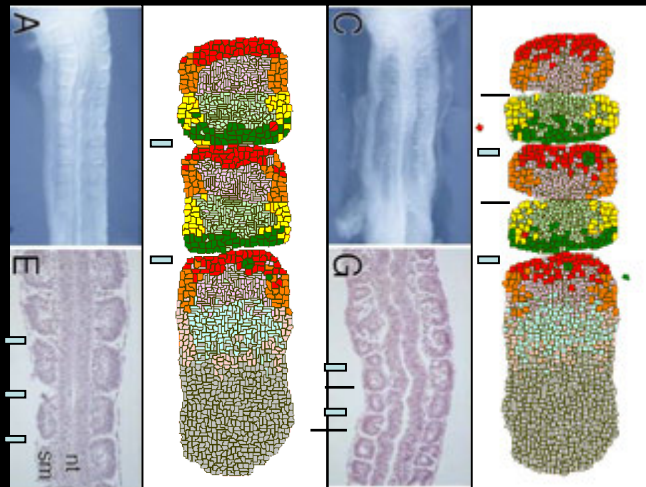
Zurlinden et al. (in preparation)

Somite formation



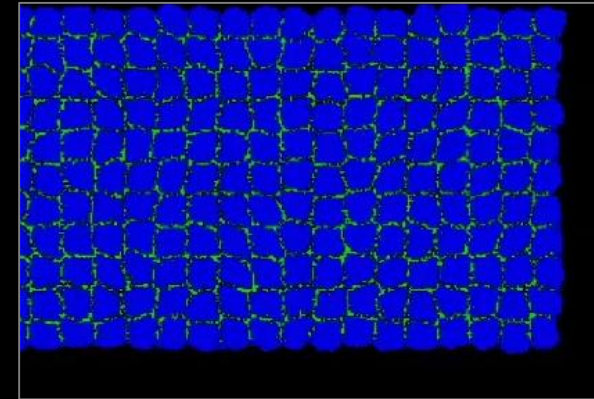
Clock and Wavefront model:

- signal gradients along AP axis (eg, FGF8, RA)
- oscillating gene expression (eg, LNFG, Hes1)
- cell adhesion (eg, ND, ephrin system)



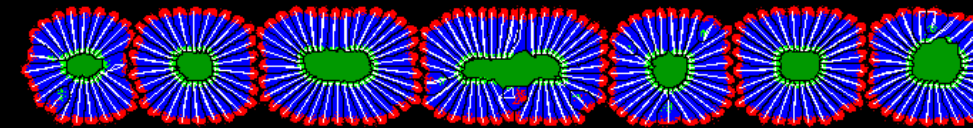
Epithelialization model:

- clock genes do not oscillate
- somites form simultaneously



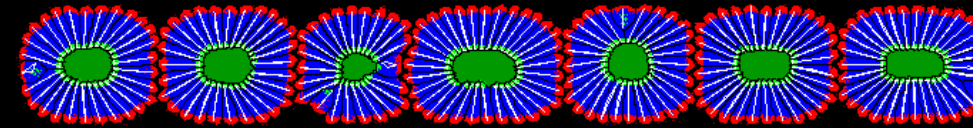
Adding the Wavefront:

- restores sequentiality

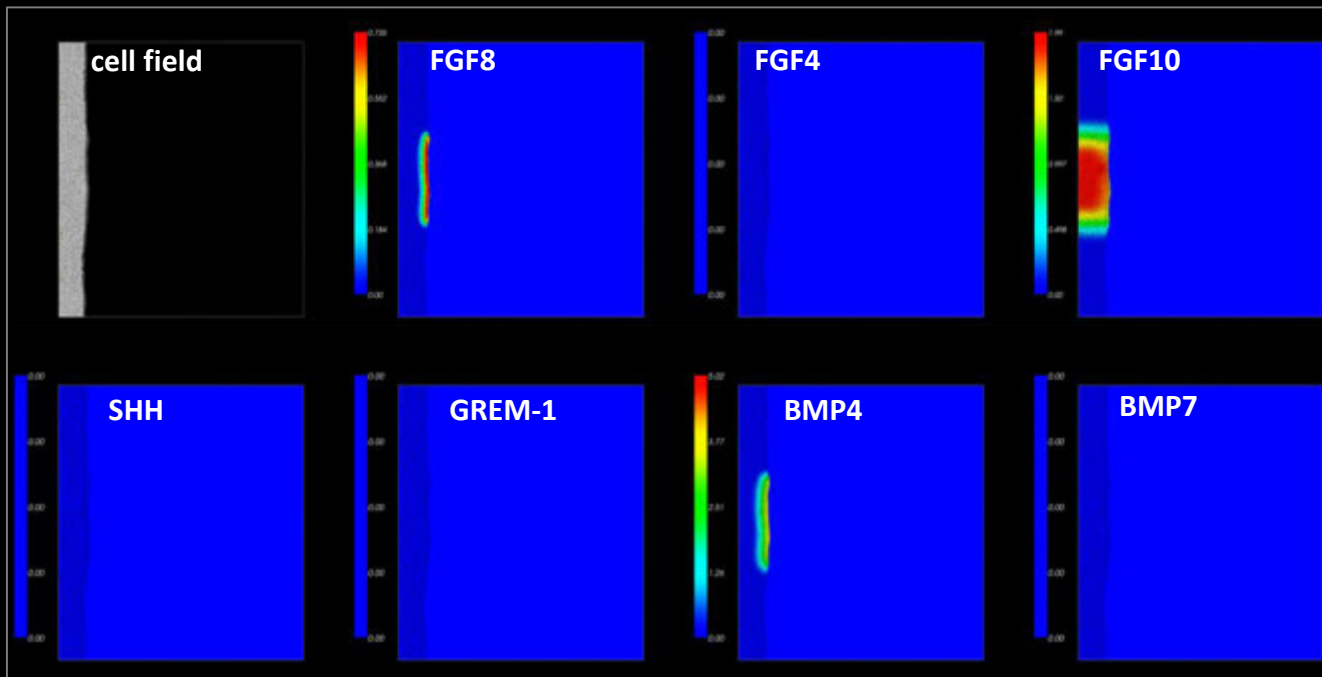
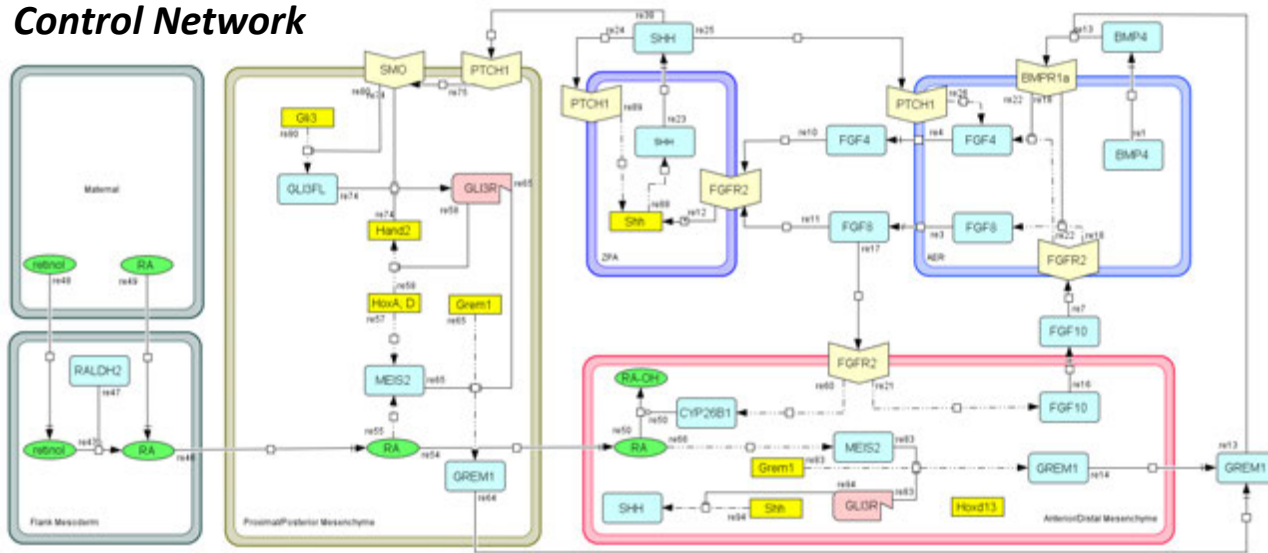


And adding the Clock:

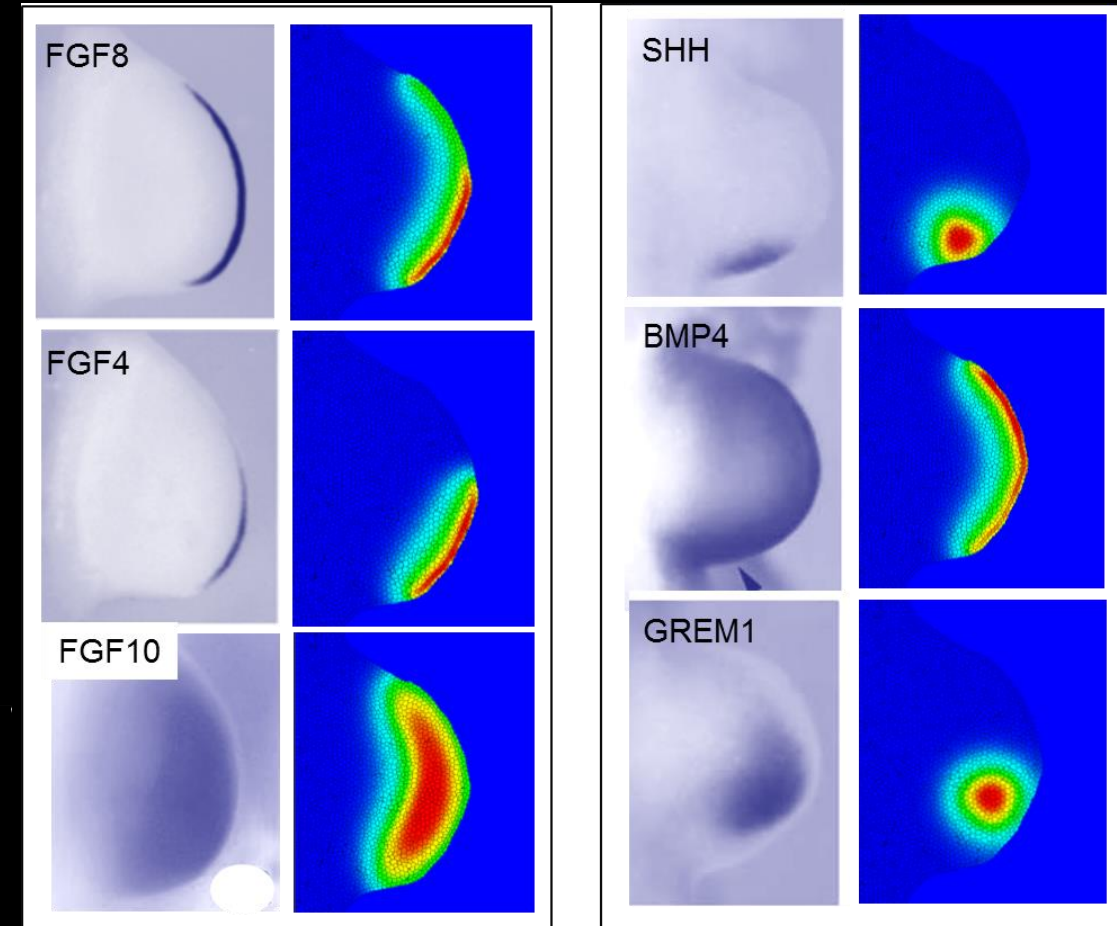
- improves regularity



Control Network

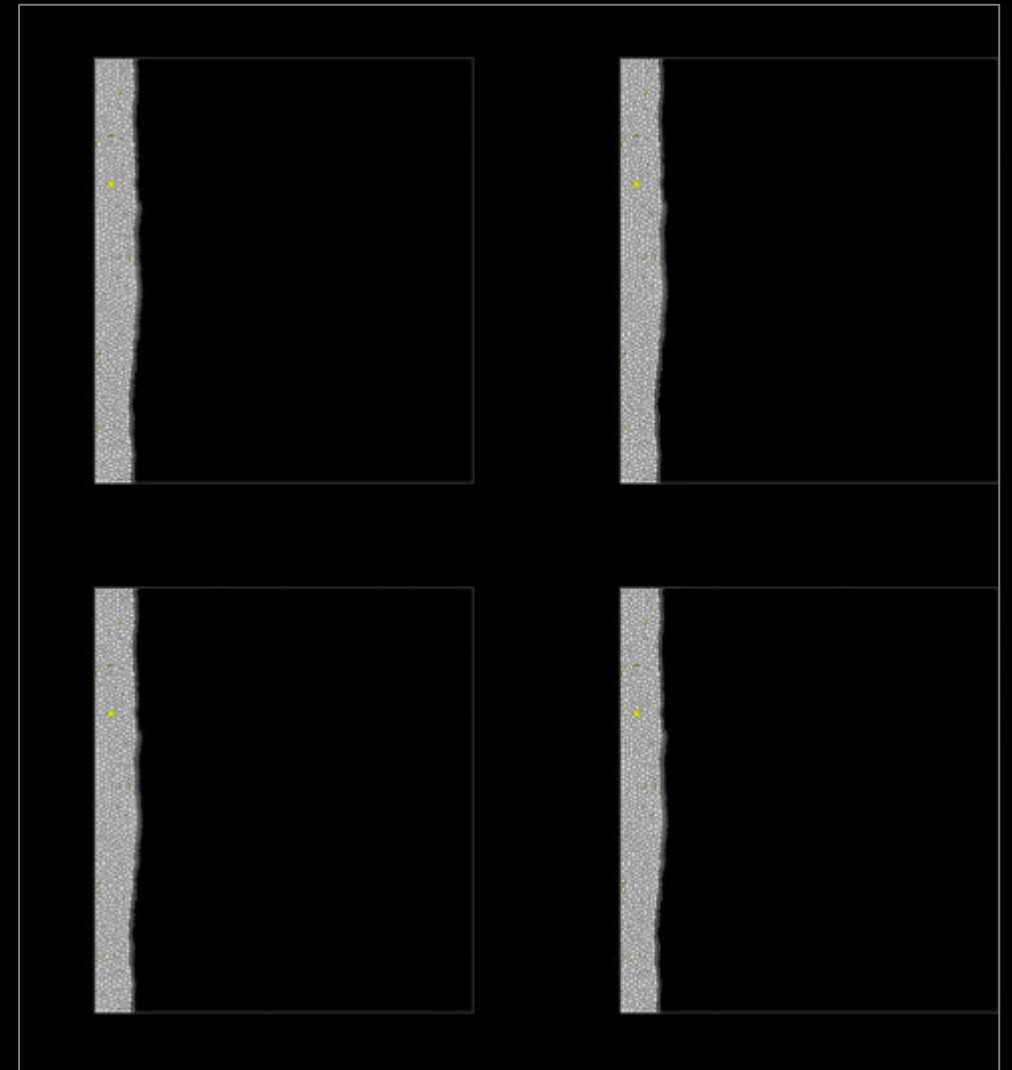
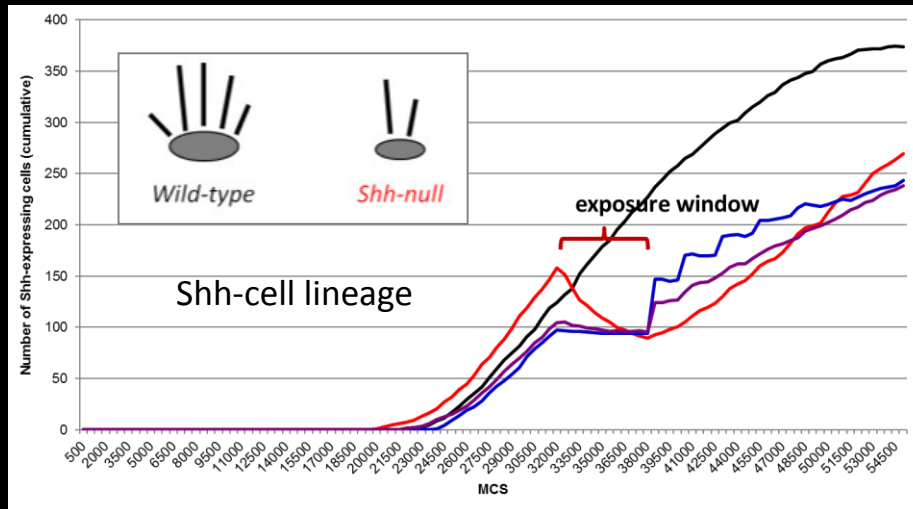
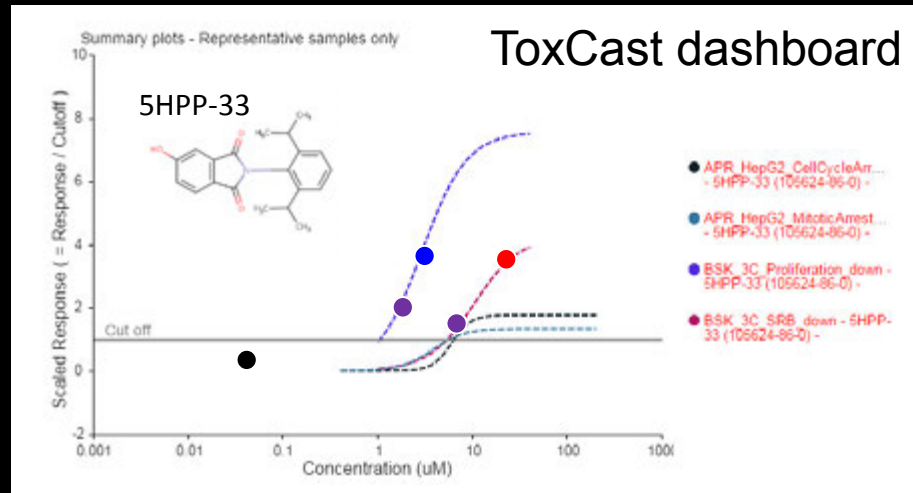


Limb-bud outgrowth



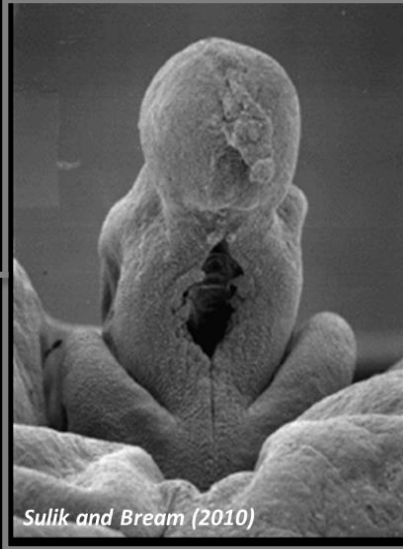
Knudsen et al. (in preparation)

Teratogenesis *in silico*

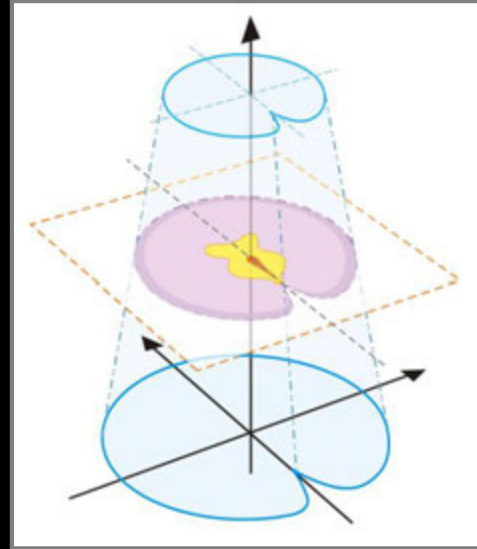


Genital Tubercle (GT) differentiation

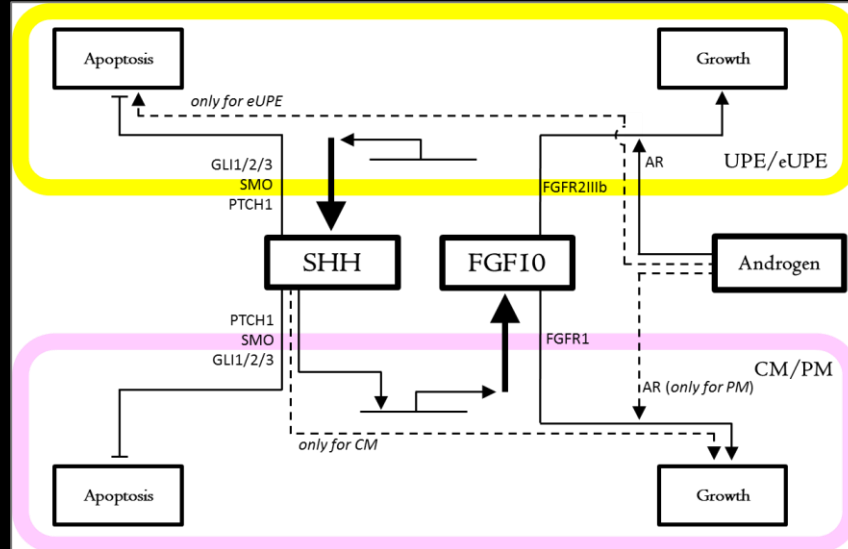
Embryonic GT



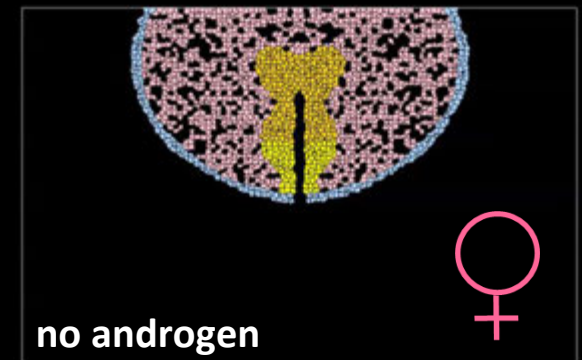
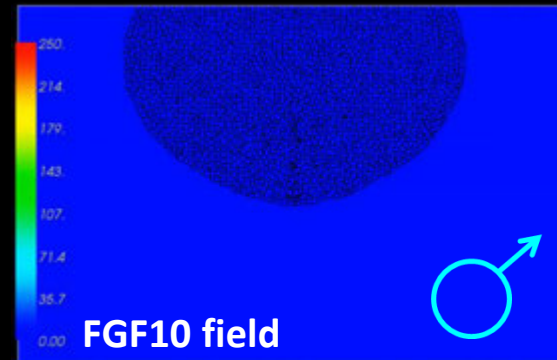
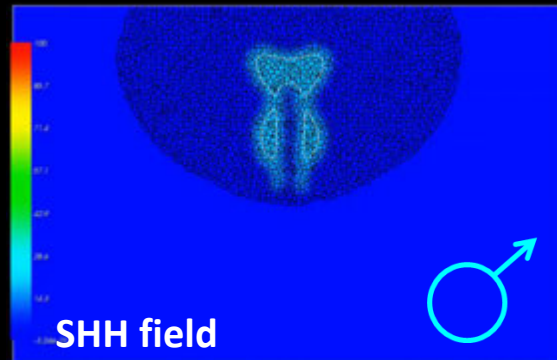
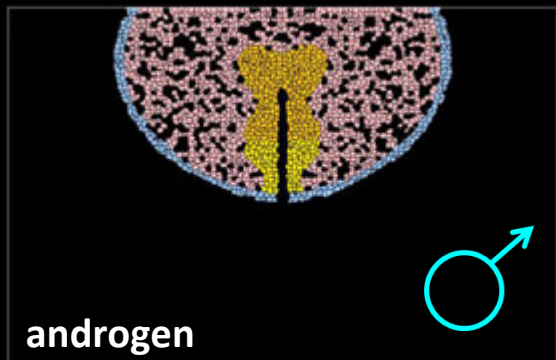
Abstracted GT



Control Network (mouse)

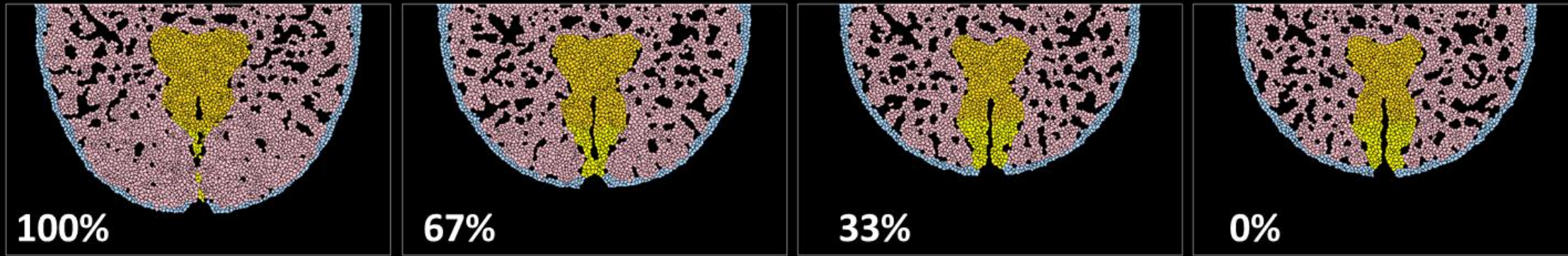


ABM simulation for sexual dimorphism (mouse GD13.5 – 17.5)

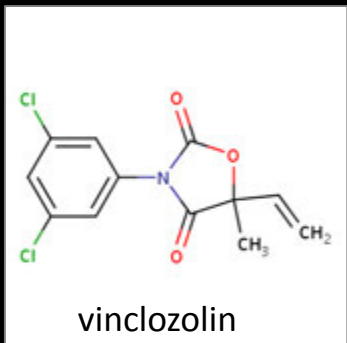


Urethral Closure: complex process disrupted in 'hypospadias'

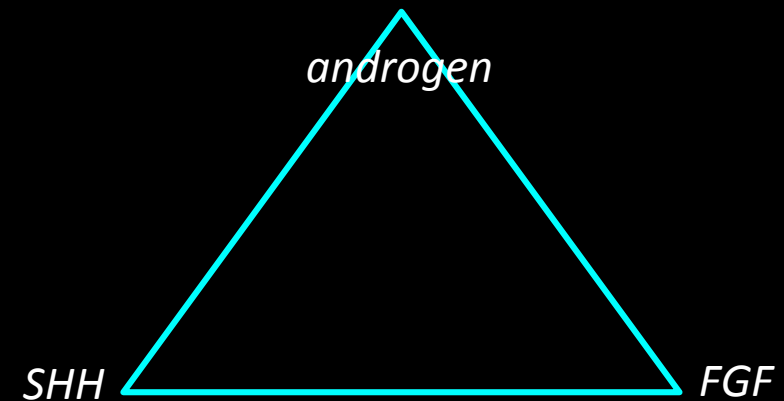
Driven by urethral endoderm (contact, fusion apoptosis) and androgen-dependent effects on preputial mesenchyme (proliferation, condensation, migration) via FGFR2-IIIb.



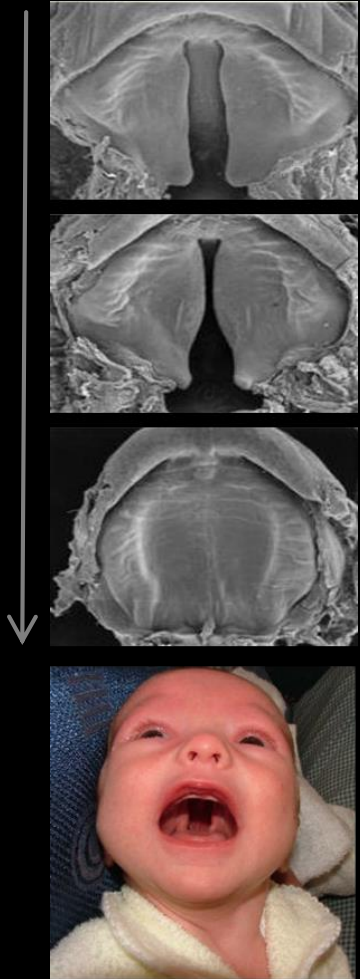
Leung et al. (2016) *Reproductive Toxicology*



Androgenization (n = 10 sims)	
	<u>Closure Index</u>
100%	0.80
67%	0.57
33%	0.13
0%	0.07

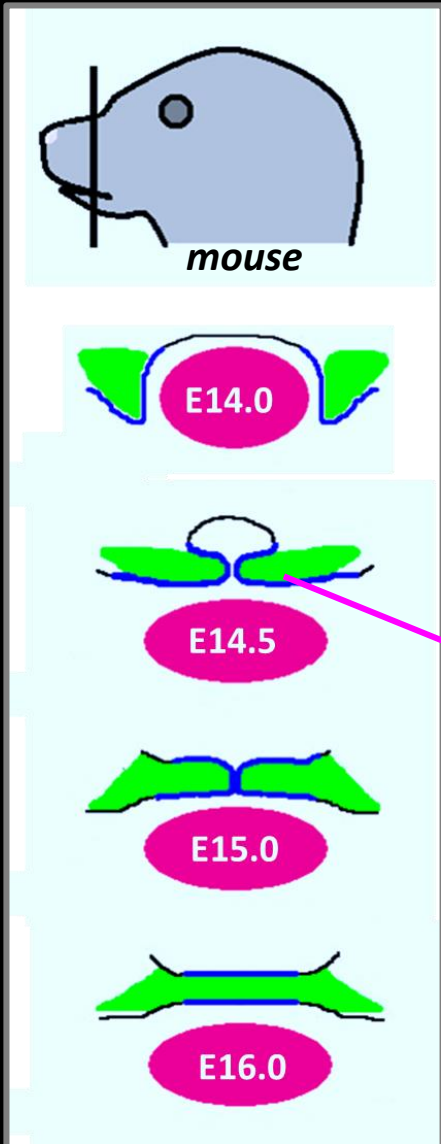


Cleft Palate

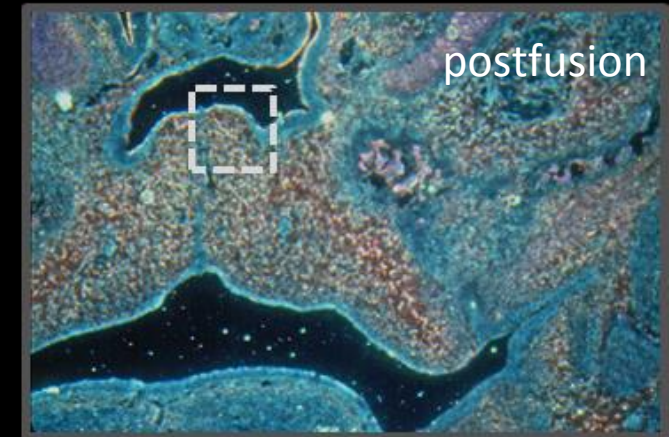
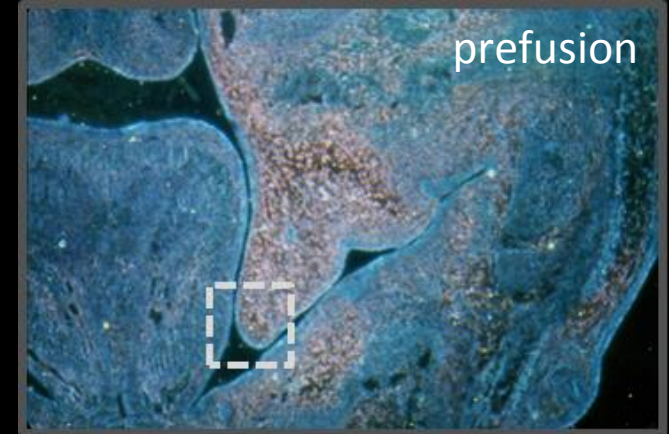
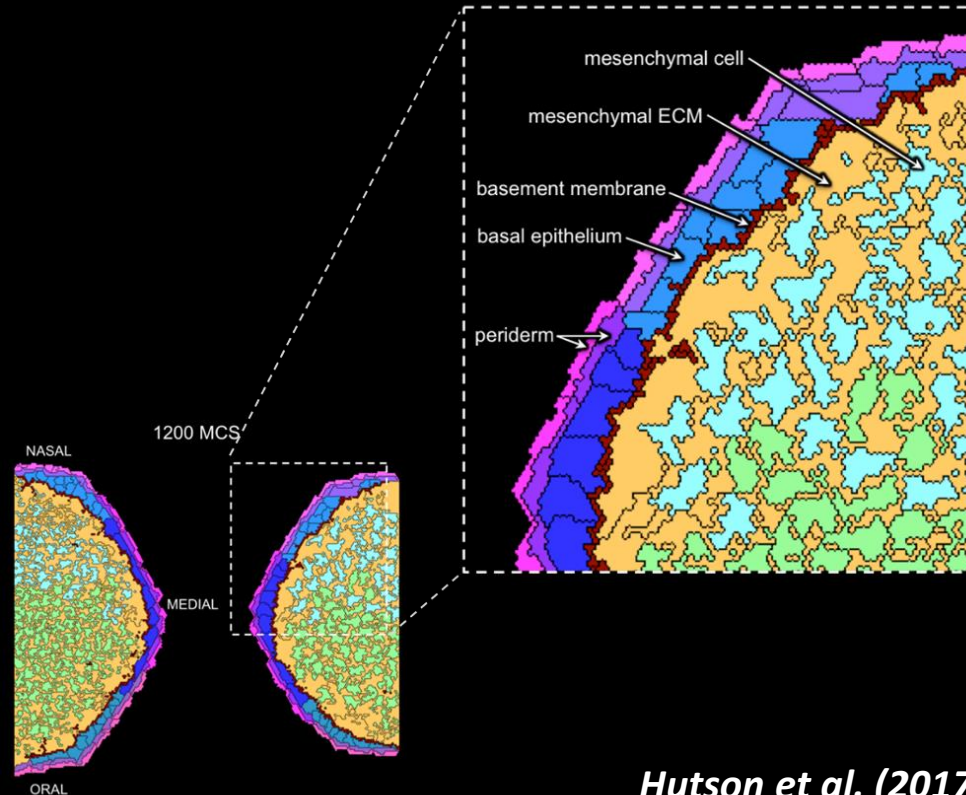


- ▶ Most prevalent craniofacial birth defect (annually ~7000 newborns in the USA and ~200,000 worldwide).
- ▶ Etiology is multifactorial: interaction of genetic, environmental, and lifestyle factors.
- ▶ Vulnerable period encompasses outgrowth of right-left palatal process in the oral cavity of the 1st trimester embryo.
- ▶ Local disruption of epithelial-mesenchymal interaction impairs outgrowth and fusion of the palatal processes.

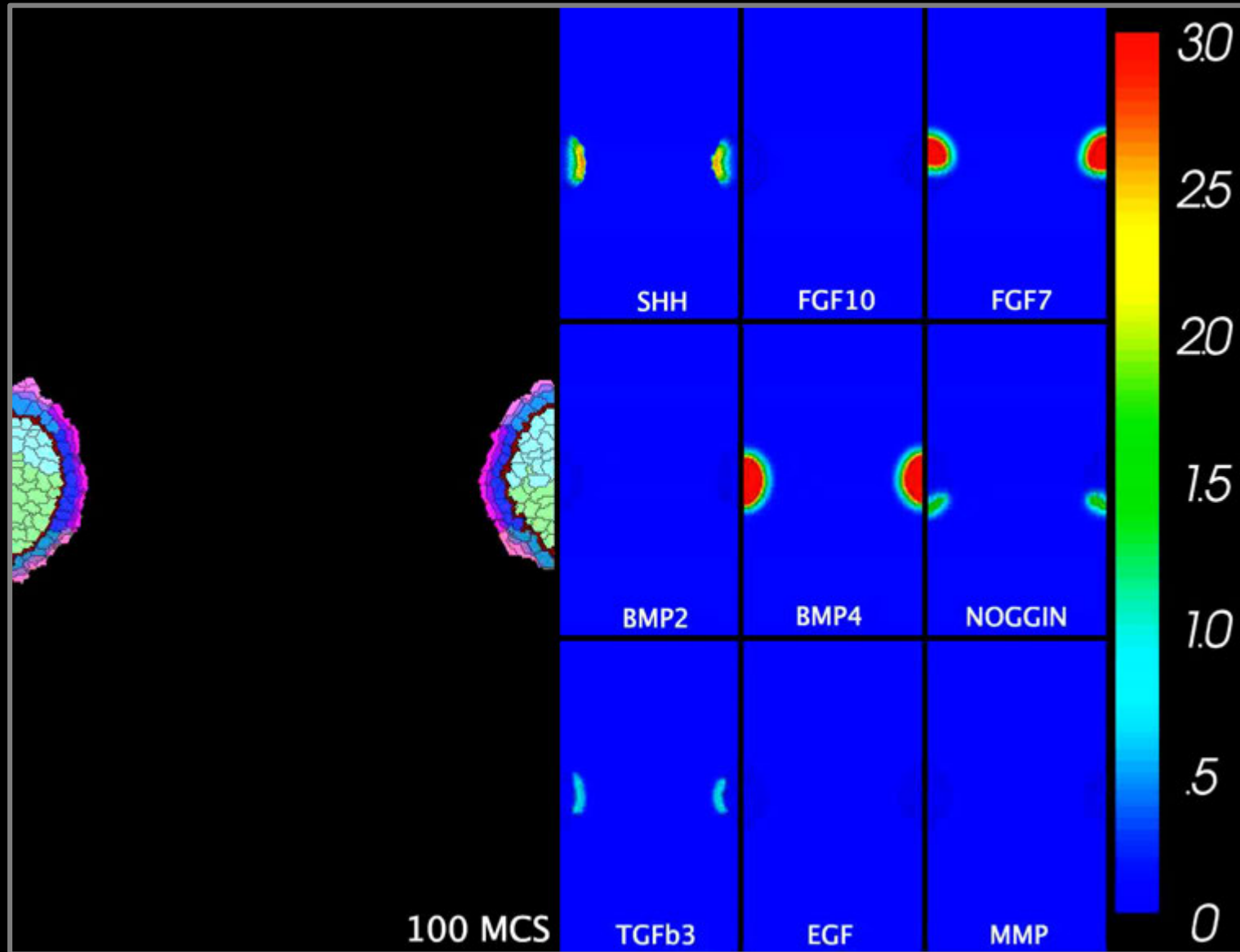
Modeling Palatal Development



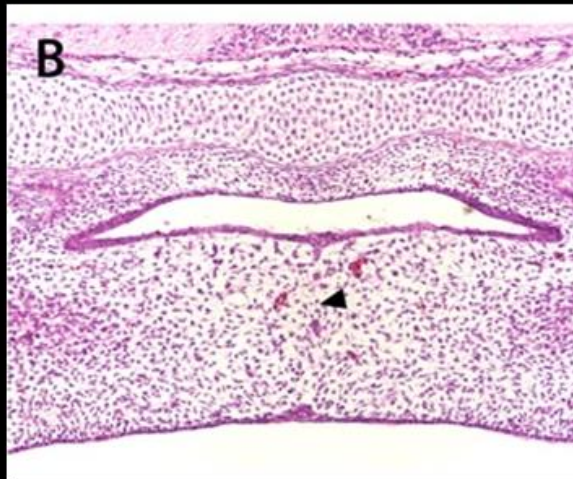
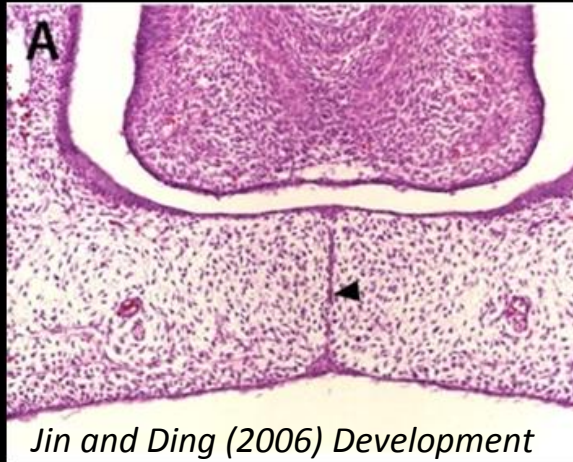
- E12.5 initial outgrowth of palatal shelves
- E13.5 expansion alongside the tongue
- E14.5 elevate, meet, and adhere at medial edge
- E15.5 fusion complete, mesenchymal confluence
- E16.5 osteogenic differentiation



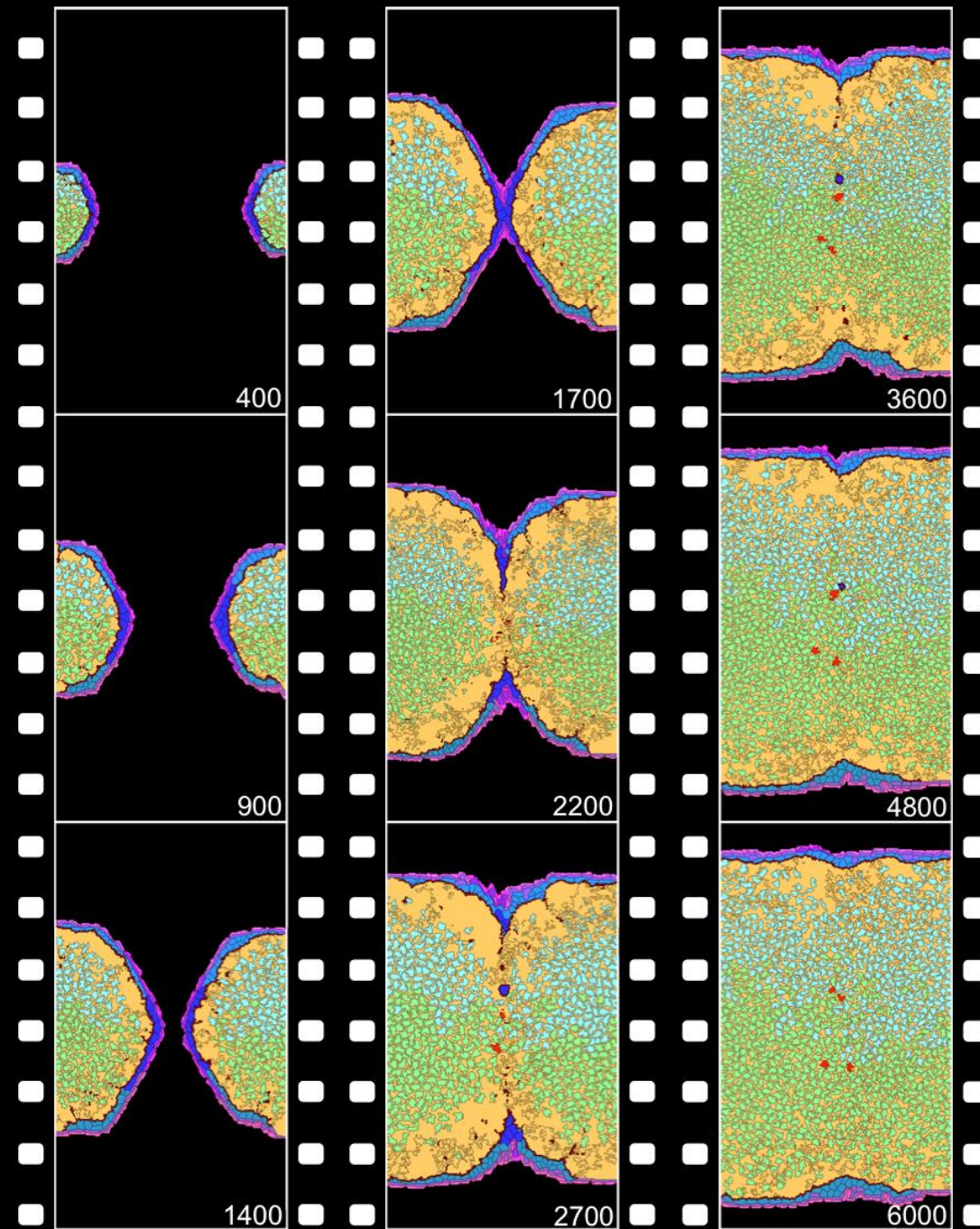
Spatially-dynamic ABMS for palate development



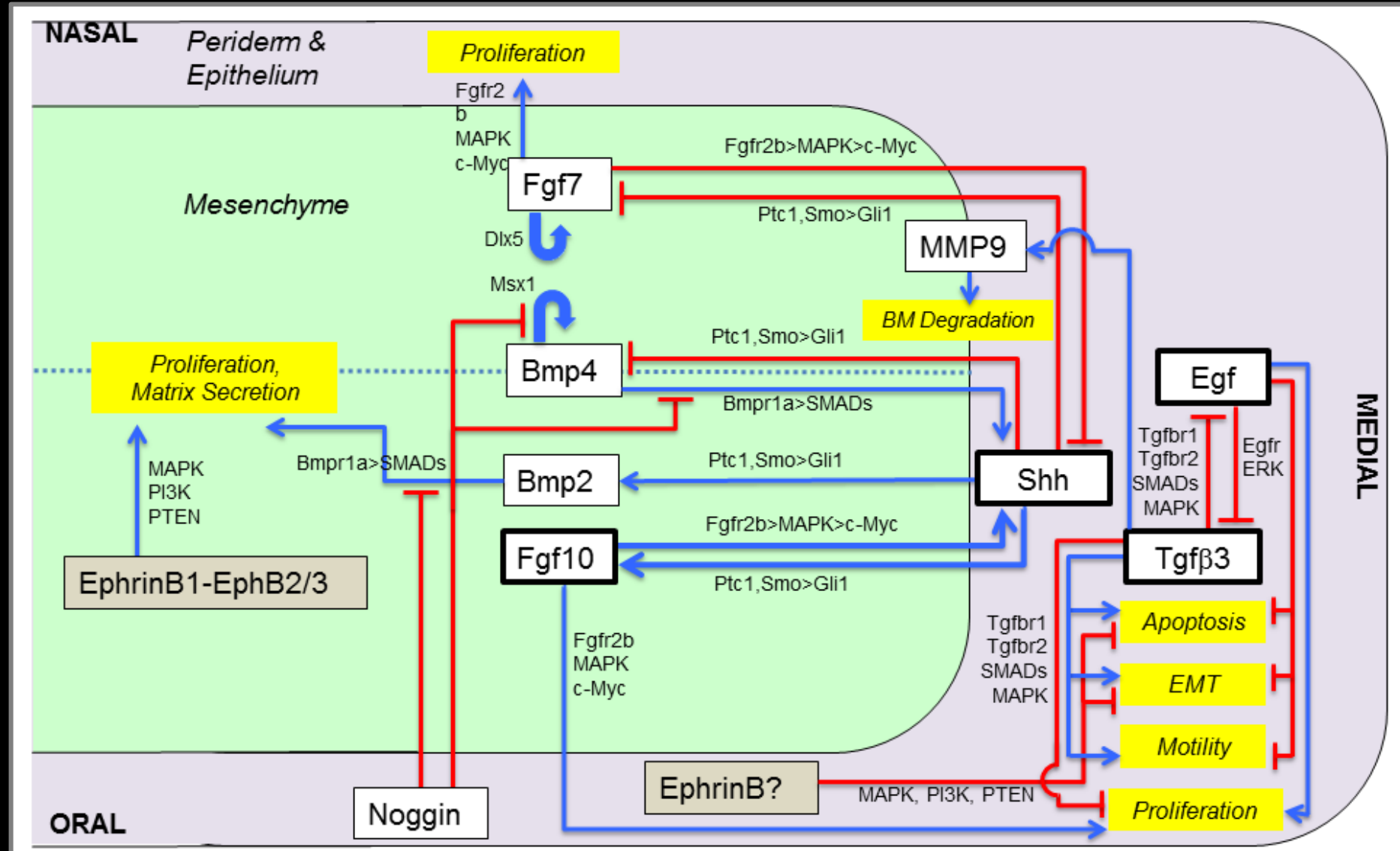
Morphogenetic fusion



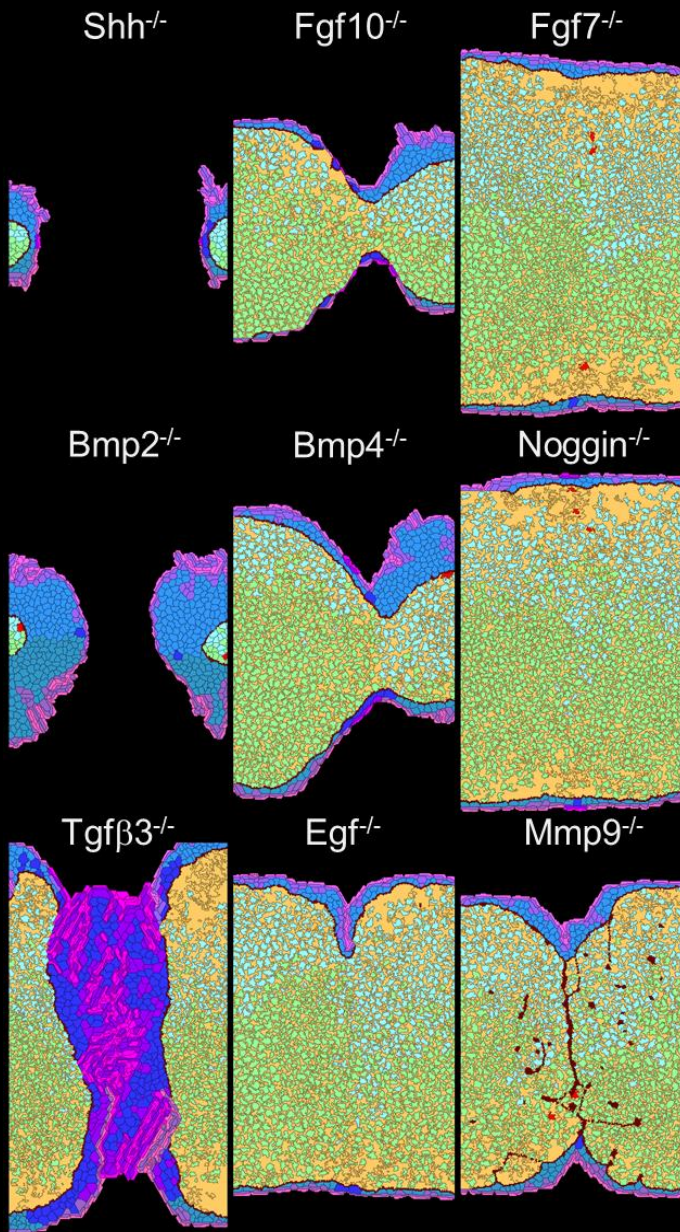
*MES breakdown is
programmed genetically to
coincide with MEE apposition*



Control network



Hacking the Control Network: *in silico* knockouts → ‘Cybermorphs’



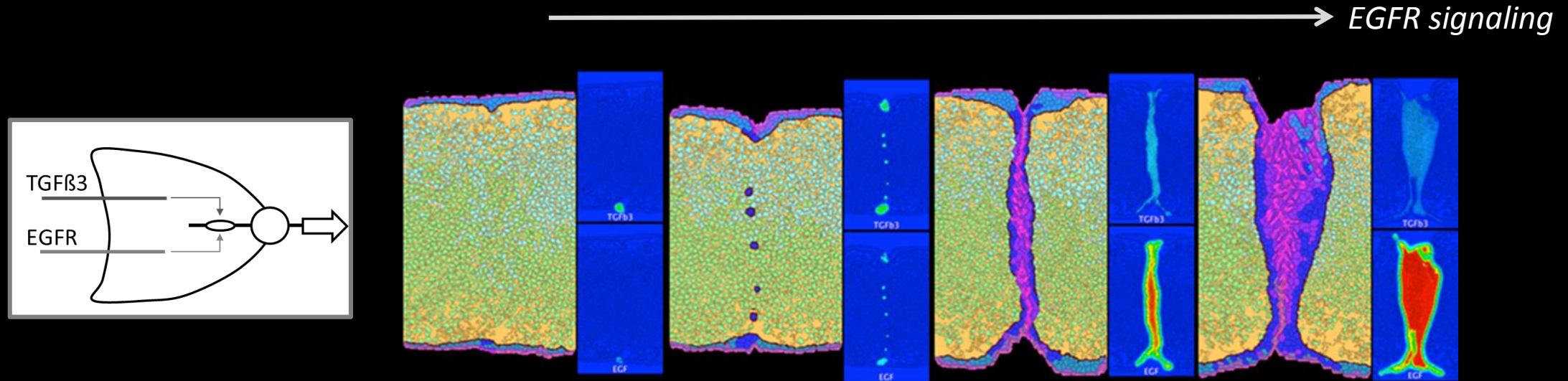
Signals driving outgrowth to apposition and MEE contact (MCS 200-2000)

- SHH from the MEE drives mesenchymal proliferation and ECM production via FGFs/BMPs.
- Positive and negative feedback loops modulate epithelial-mesenchymal signaling cell-by-cell and interaction-by-interaction.

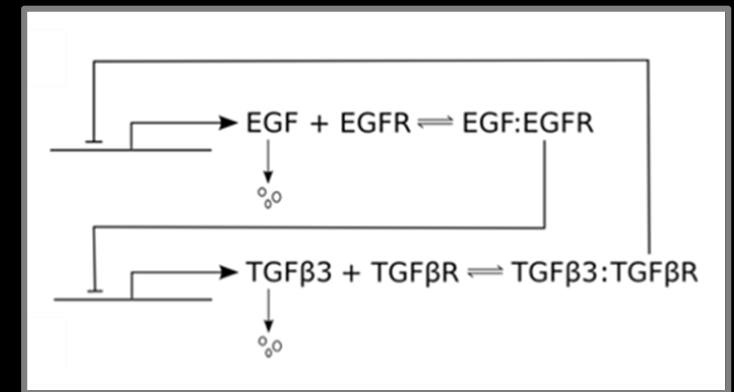
Signals driving MES breakdown (MCS 2000-3000)

- TGFβ3 triggers MEE cells to undergo apoptosis (PCD), epithelial-mesenchymal transition (EMT), and migration (retraction).
- EGF has the opposite effect, maintaining MEE cell growth, proliferation, and survival.

Messin' with the switch: system fragility and fault tolerance

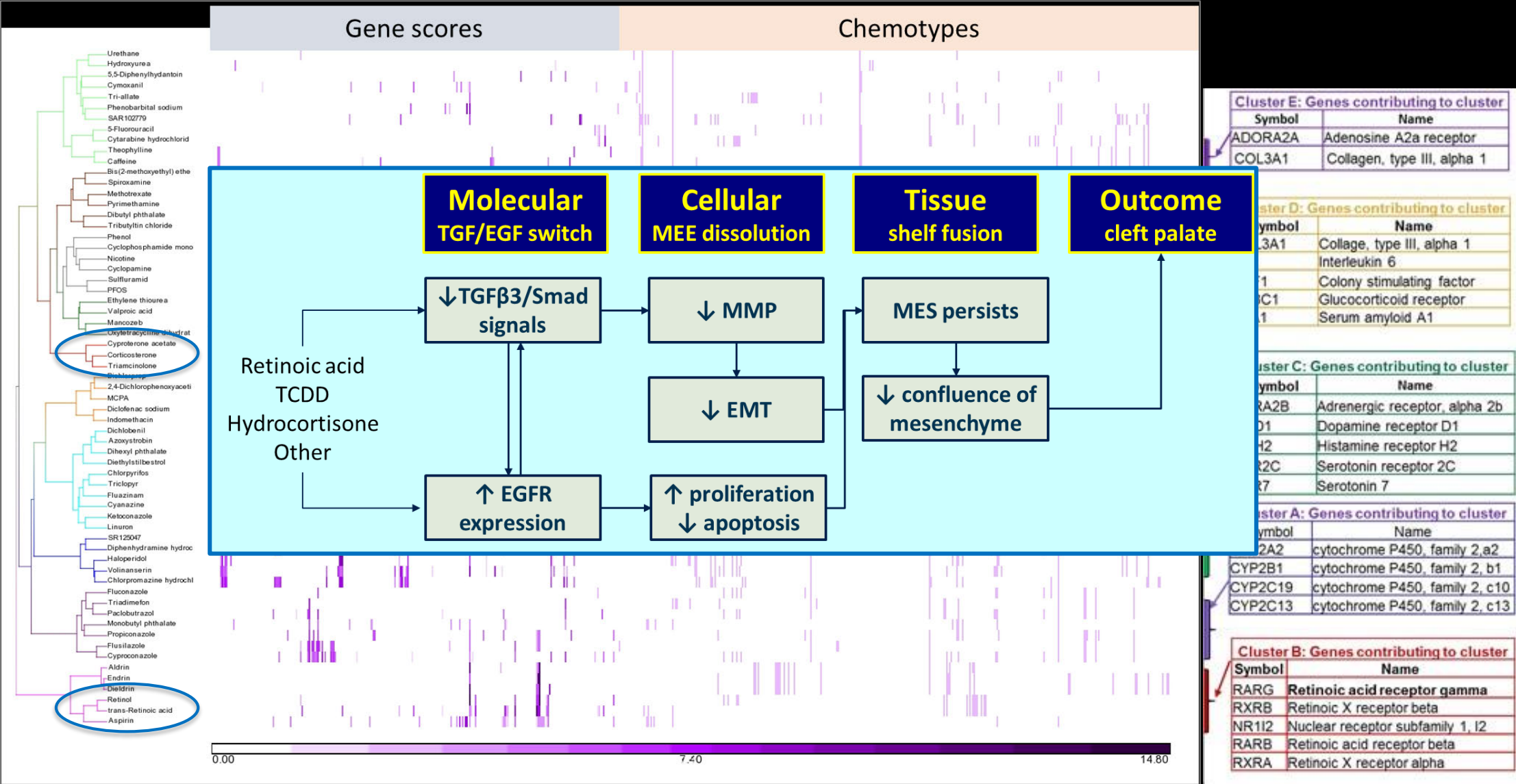


- A mutual inhibitory gene regulatory circuit exhibits switch-like behavior in the MEE.
- $EGFR$ expression normally wanes several hours prior to MEE apposition to flip the switch to the $TGF\beta 3$ state.
- Several cleft palate teratogens are known to maintain $EGFR$ expression (Retinoic acid, Hydrocortisone, TCDD) [Abbott 2010]).



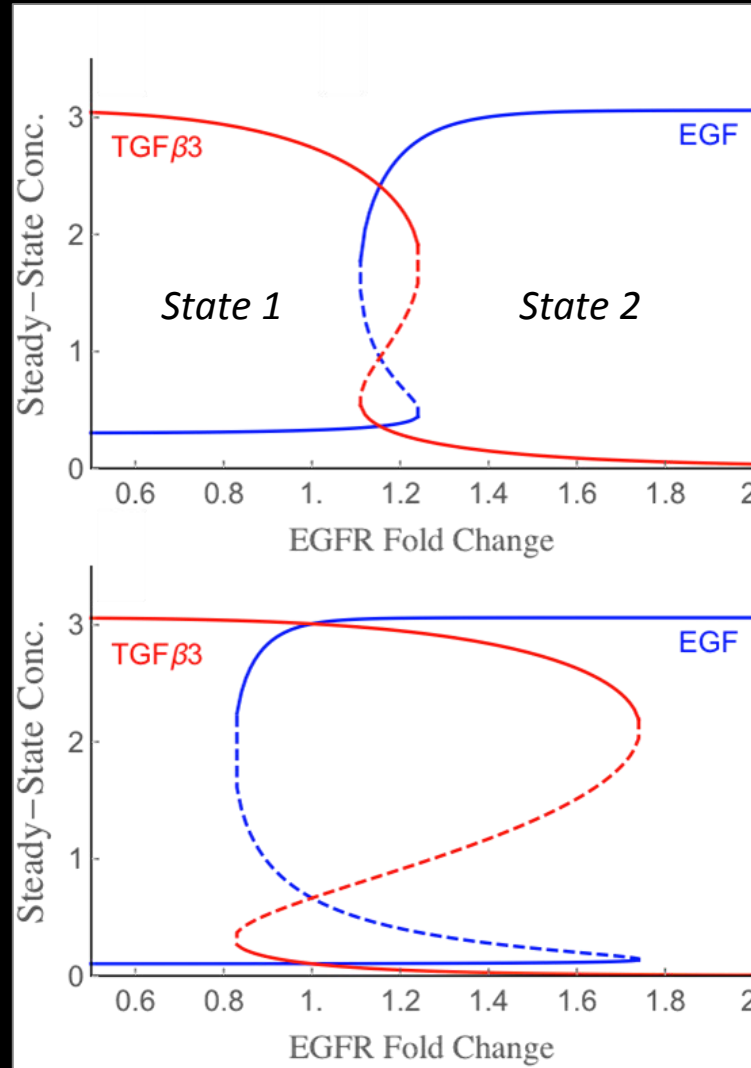
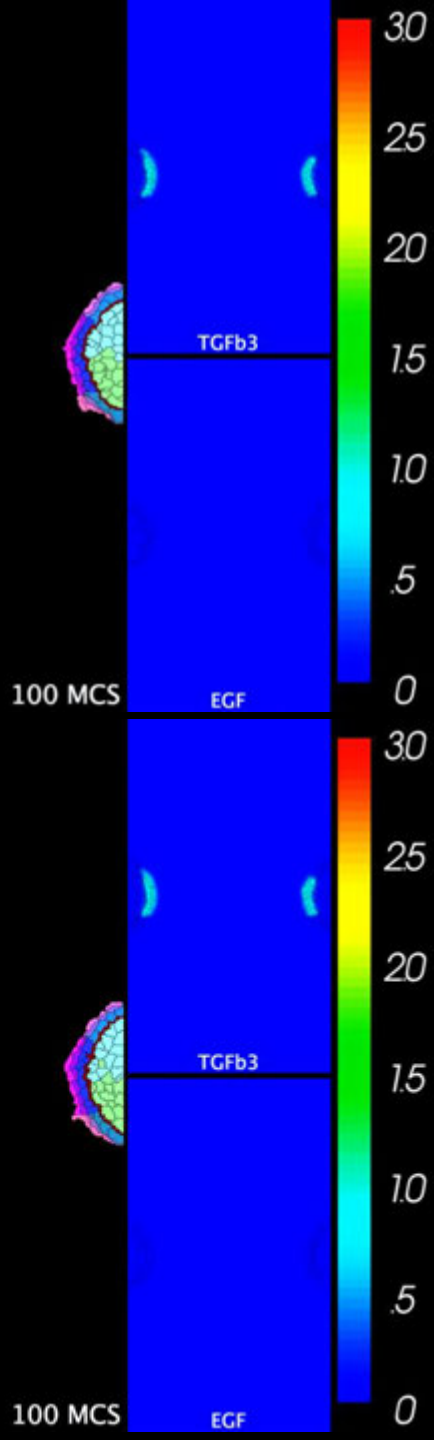
63 cleft palate (animal) teratogens in ToxCast

Baker et al. (in preparation)

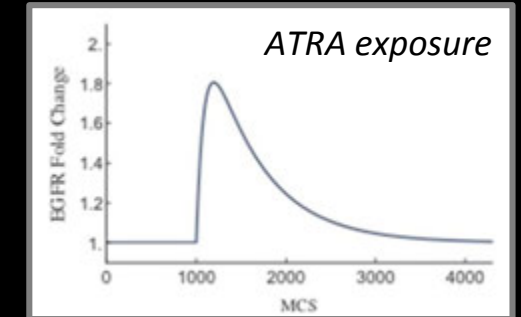


Dissecting circuit dynamics *in silico*:

two scenarios for differential teratogenicity

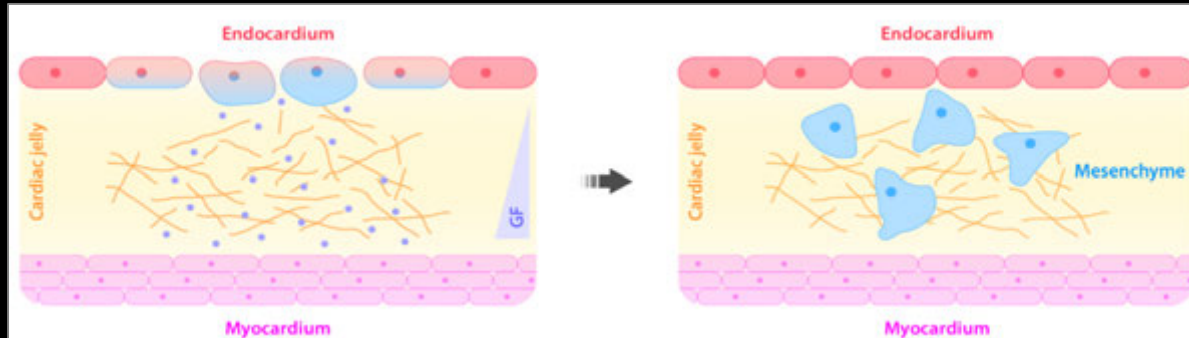
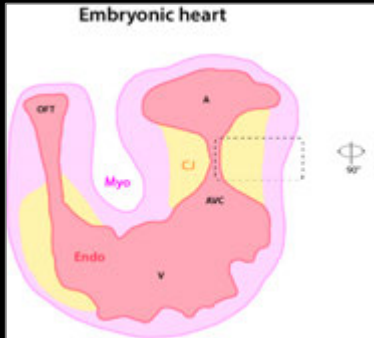


*tipping point >1.8x (n=24)
(reversible)*



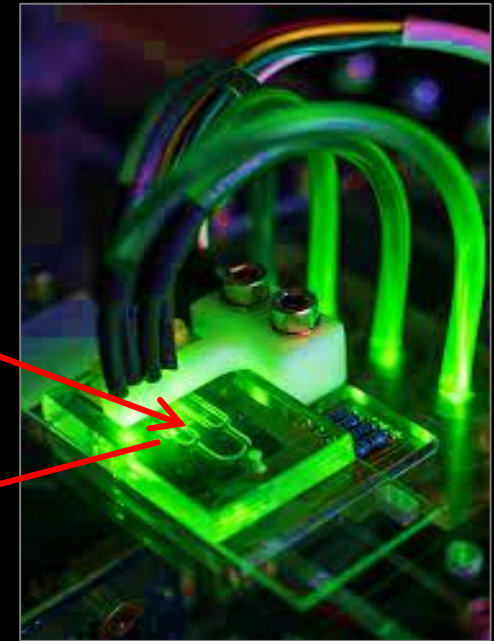
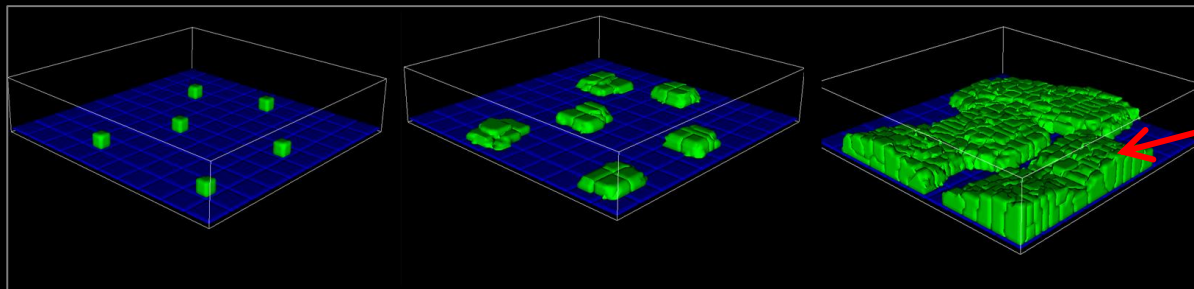
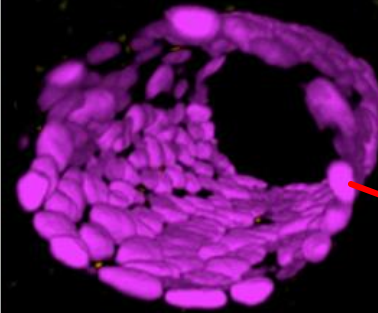
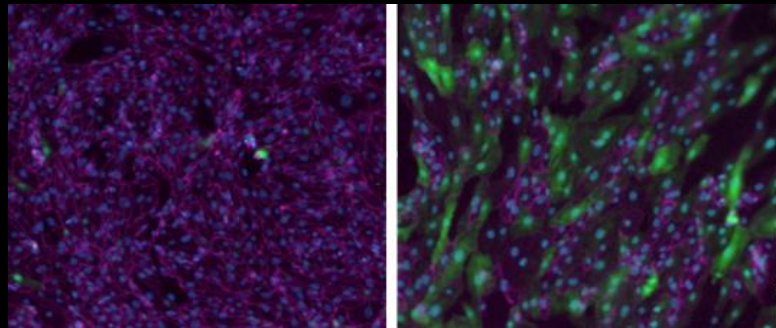
*tipping point ~1.5x (n=16)
(not reversible)*

Epithelial-Mesenchymal Transition: delay or disruption underlies some congenital malformations (e.g., valvulo-septal heart defects) ...

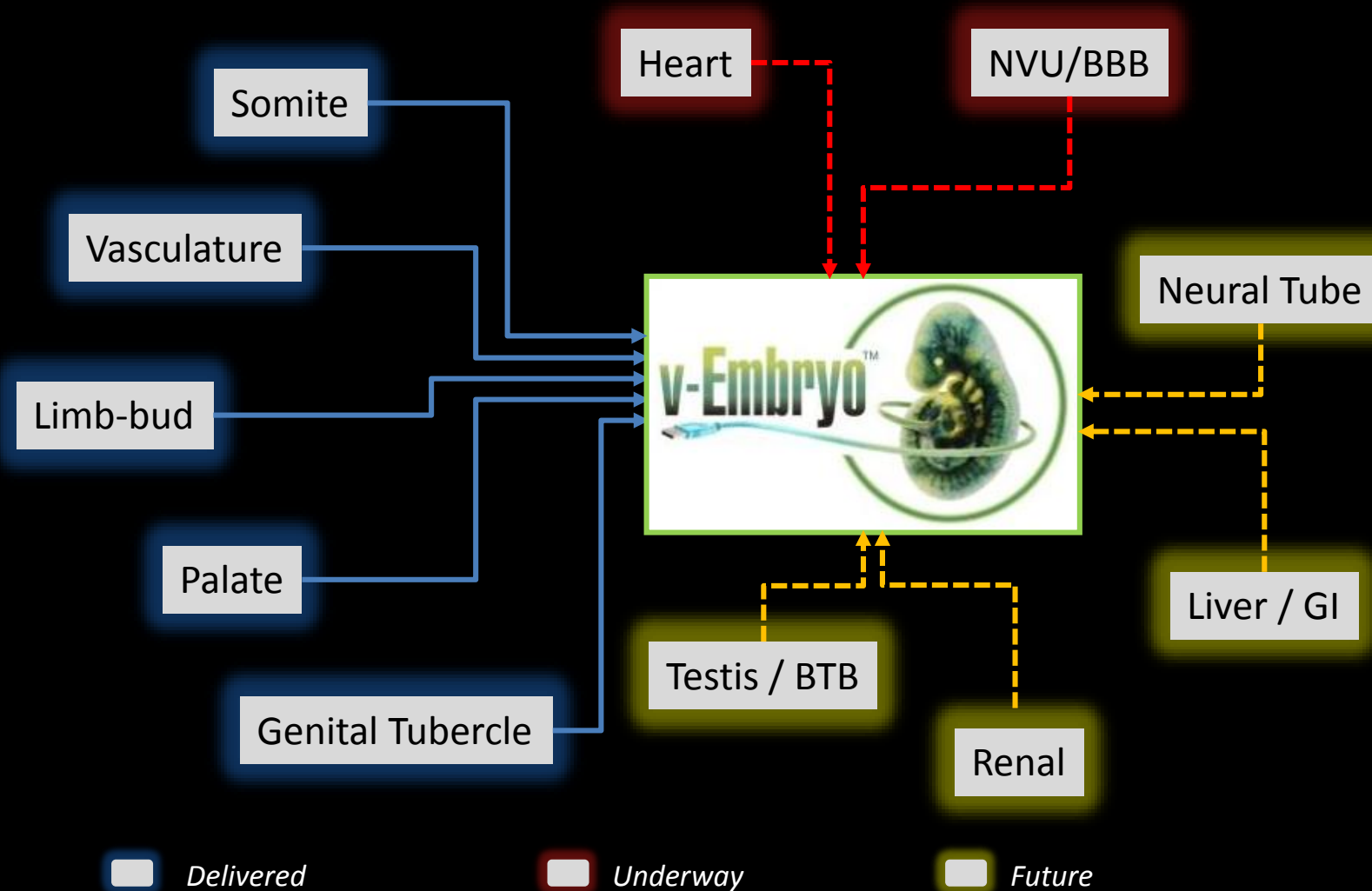


... but endocardial EMT does not occur in a static environment; need to “go with the flow”.

TGF-beta
Wnt
FGF
Chemokine/Cytokine
Integrin
Angiogenesis
Cadherin
GPCR
Notch
PDGF



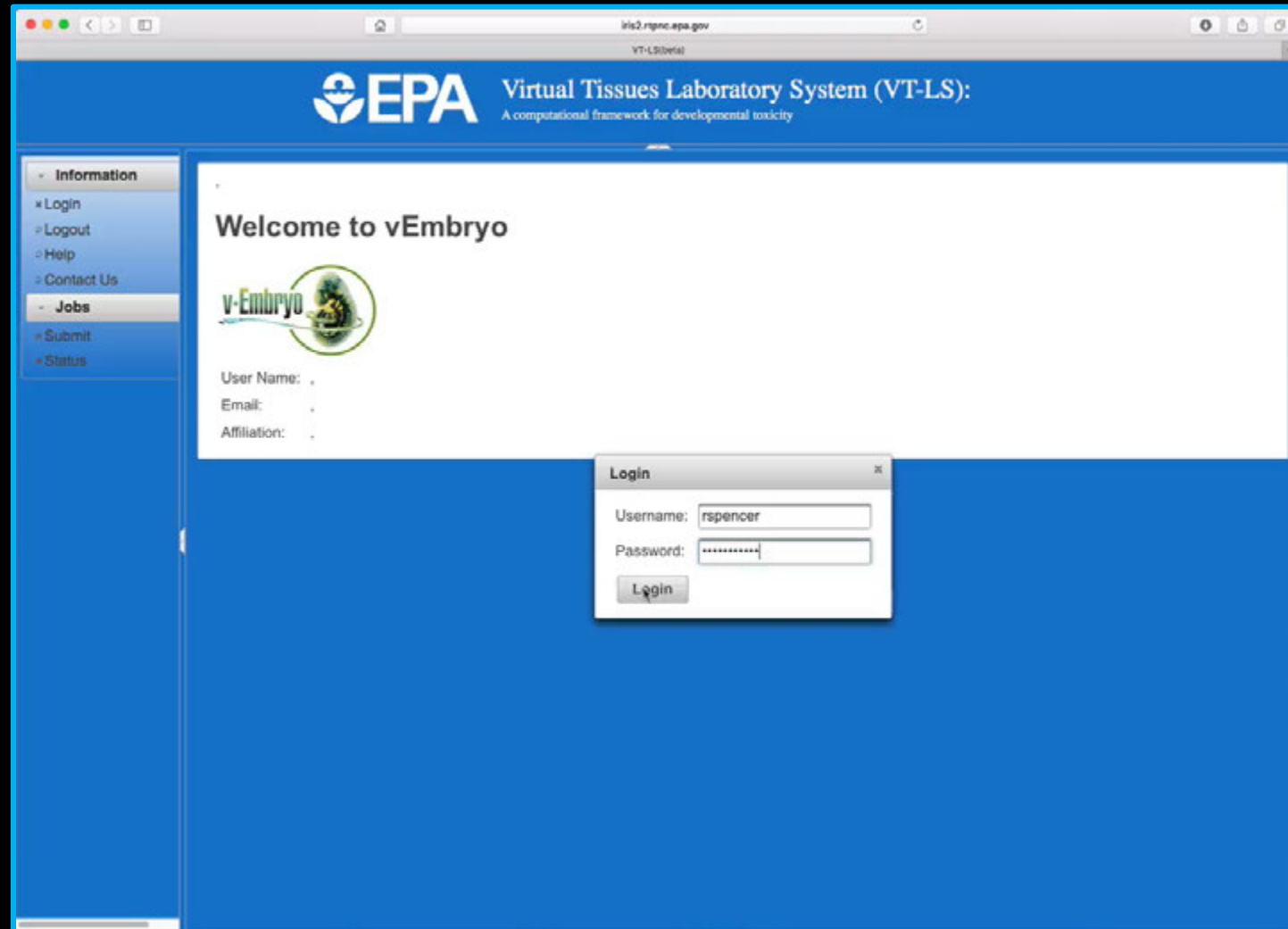
Toward a 'Virtual Embryo'



- Hester et al. (2011) PLoS Comp Bio; Dias et al (2014) Science
- Kleinstreuer et al. (2013) PLoS Comp Bio.
- Ahir et al. (MS in preparation).
- Hutson et al. (2017) Chem Res Toxicol.

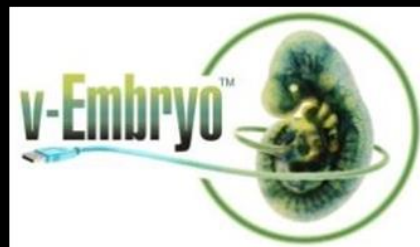
- Leung et al. (2016) Reprod Toxicol.
- Zurlinden/Saili et al. (FY17 product).
- Hunter et al. (FY18 product).
- Your name here.

Virtual Tissue Laboratory System (VTLS)



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- Imran Shah - NCCT
- Alex Tseutaki – HS intern



http://www2.epa.gov/sites/production/files/2015-08/documents/virtual_tissue_models_fact_sheet_final.pdf