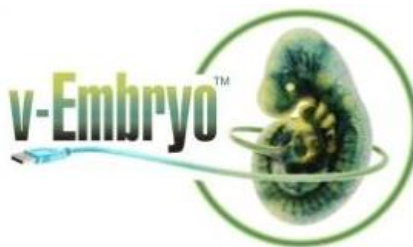


# Computer Simulation of Embryonic Systems

*What can a virtual embryo teach us about developmental toxicity?*



**Thomas B. Knudsen, PhD**  
**Developmental Systems Biologist**  
**National Center for Computational Toxicology**  
**US EPA, Research Triangle Park, NC 27711**  
[knudsen.thomas@epa.gov](mailto:knudsen.thomas@epa.gov)

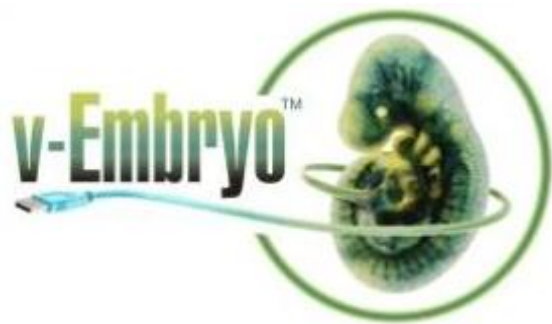
***DISCLAIMER: The views expressed in this presentation are  
those of the presenter and do not necessarily reflect the  
views or policies of the U.S. Environmental Protection Agency.***

# Anatomical homeostasis in a self-regulating multicellular system



*SOURCE: Tim Otter, – with permission*

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



**Can a computer model of the developing embryo translate cellular disruptions into a prediction of dysmorphogenesis?**

*and if so ...*

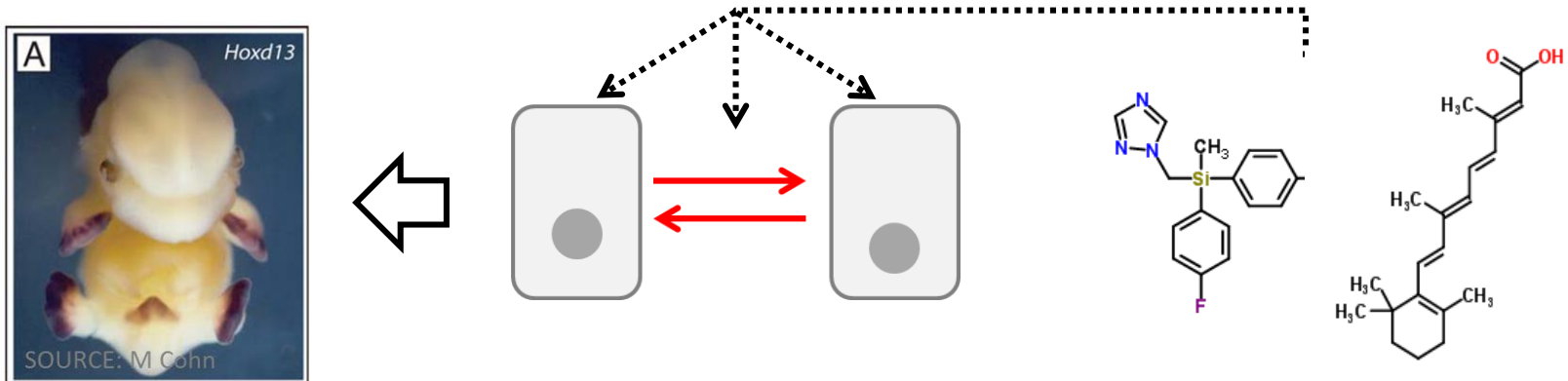
How might such models be used with high-performance computing **analytically** (to understand) and **theoretically** (to predict) adverse developmental outcomes for different exposure scenarios?

*e.g., chemicals, non-chemical stressors, drugs, mixtures, lifestages, ...*



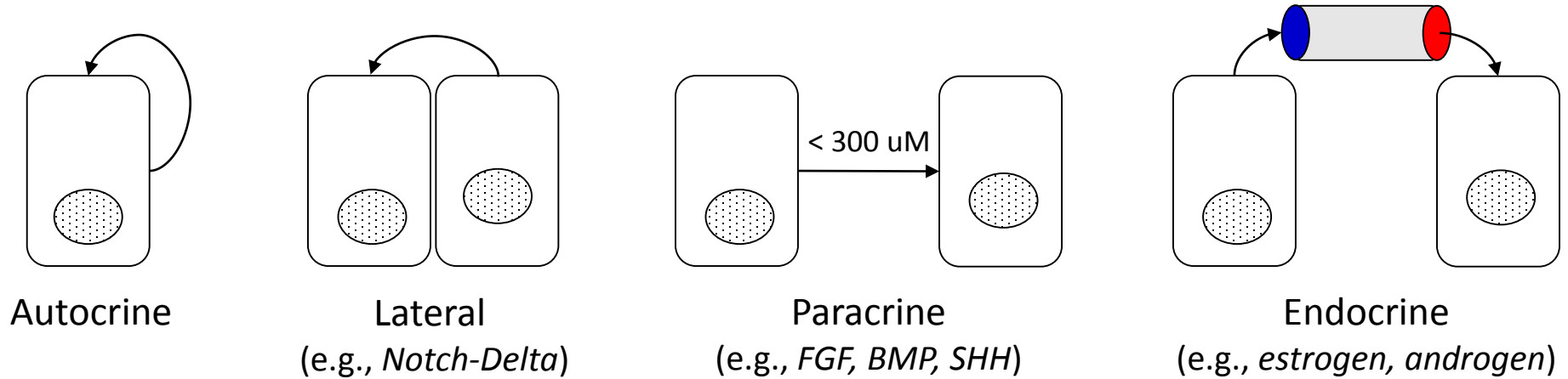
# Organizing Principles

1. In patterning the embryo, genetic signals setup spatial information that cells then translate into a coordinated biological response.
2. A hallmark of multicellular organization is the ability of cells to interact with one another via well-conserved signaling pathways.
3. Just as 'the Cell' is the fundamental unit of biology, so too should it be the computational unit ('Agent') for modeling embryogenesis.



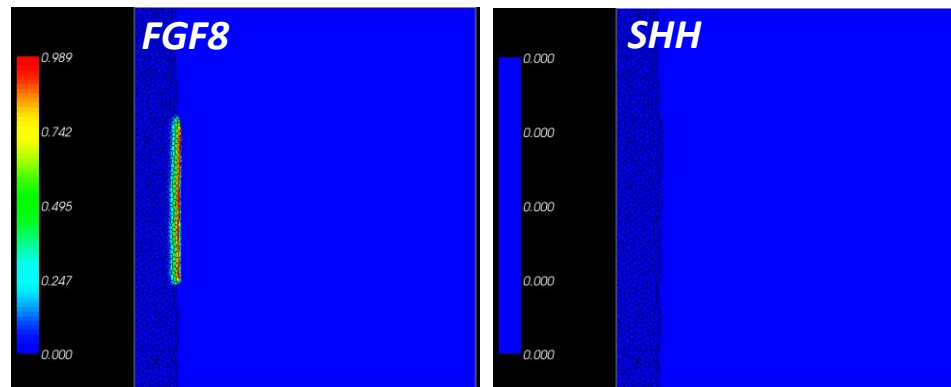
# Cell Signaling Domains

- Kinematics: range of activity varies by distance and geometry.



- Dynamics: spatial relationships in a developing system vary over time and space.

This complexity can be captured in a 'virtual tissue'.



# Cellular Agent-Based Models (ABMs)

- Built from the known biology of an embryological system and structured to recapitulate key cell signals and responses.
- Running the models with real (*in vitro*) or synthetic (*in silico*) data can be used to predict emergent responses to perturbation.
- Simulated outcomes can be validated against experimental phenotypes to assess model performance and analyze sensitivity.
- Models can help translate screening-level data from chemical-biology into predictive toxicology of a developmental hazard.

# Predictive Toxicology & Human Development



- Evaluating and assessing impacts to development is an Agency priority – *EPA's Children's Environmental Health (CEH) Research Roadmap*.
- Too many chemicals (~80K) to test each by traditional animal-based methods (cost, time, 3Rs).
- Profile the 'human exposure universe' of chemicals *in vitro* with high-throughput (HTS) assays (ToxCast/Tox21).
- ToxCast >1060 chemicals evaluated in over 600 assays; >27M data points and ~1.7M concentration response curves.

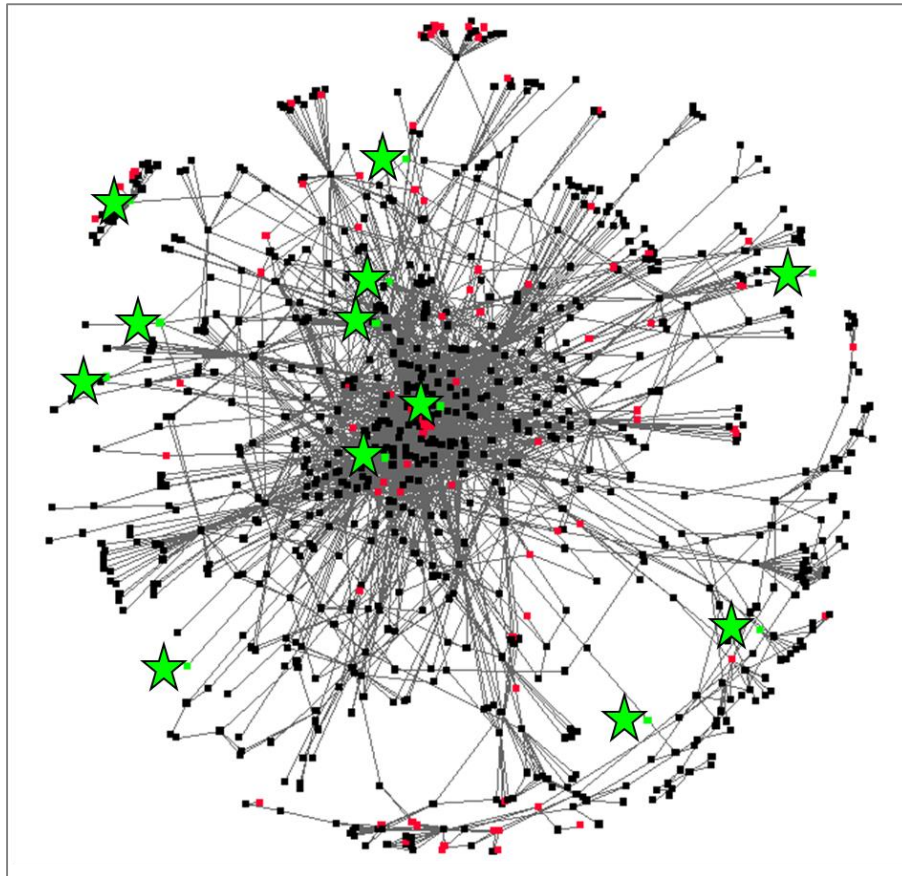
<http://actor.epa.gov/dashboard/>



## 1. ToxCast Predictive Signature: *developmental toxicity*

## univariate DevTox features

★ **angiogenesis**

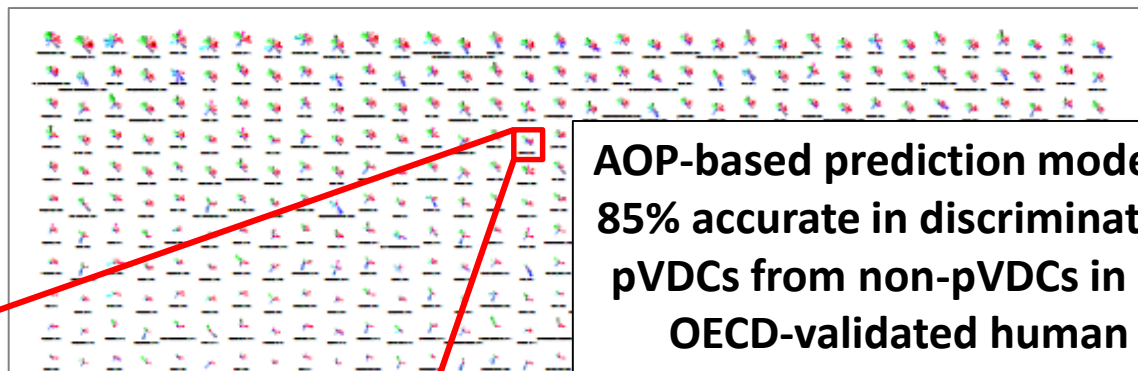
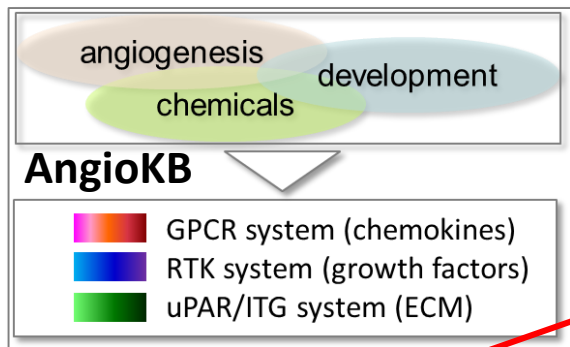


**136 of 1065 ToxCast chemicals tested  
(12.8%) were positive in an embryonic  
stem cell assay predicting  
teratogenicity in a human system**

[illegible]

*Knudsen et al (2016) in preparation*

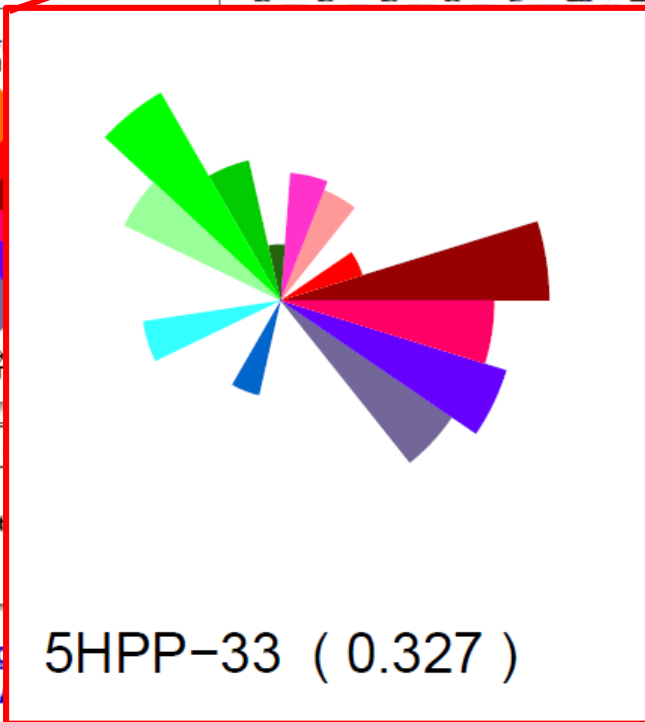
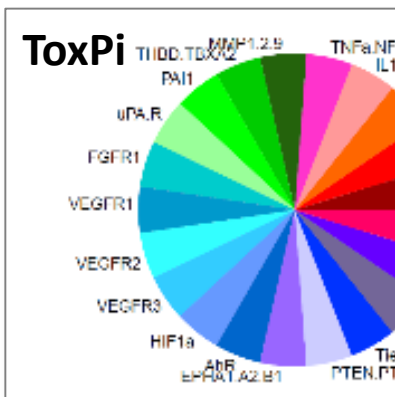
# pVDCs: chemicals sorted for potential vascular disruption (pVDCs)



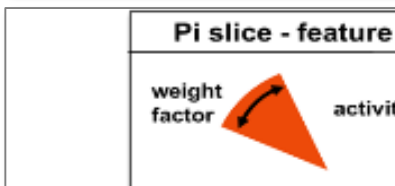
**AOP-based prediction model is 85% accurate in discriminating pVDCs from non-pVDCs in an OECD-validated human complex angiogenesis assay.**



*T Heinonen*



**This synthetic thalidomide analogue disrupts microtubule function in endothelial cells of immature blood vessels.**

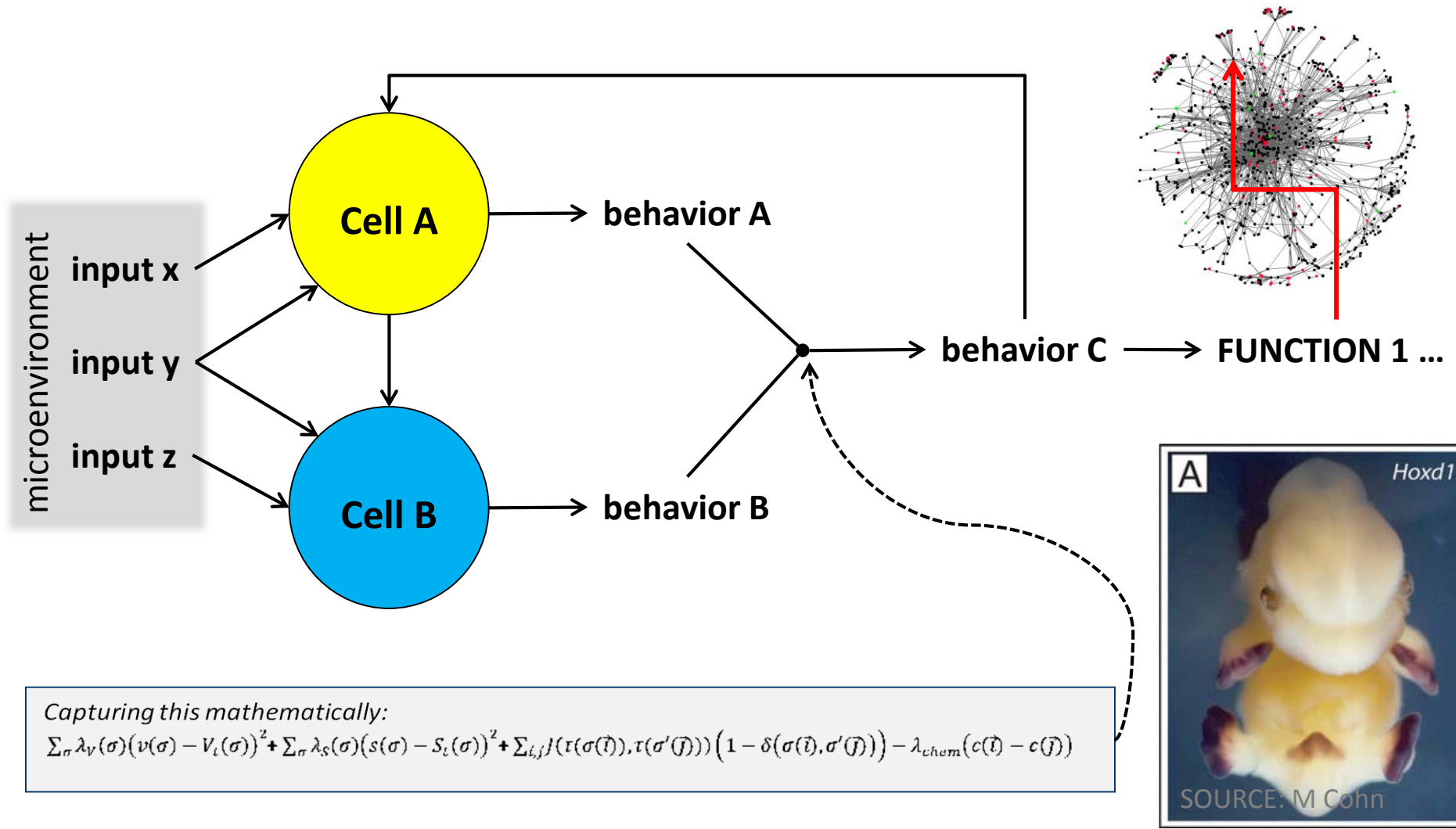


<http://epa.gov/nce>  
<http://comptox.unc.edu>

AVDC\_pVDC\_2015-1



# Cellular Response Network (CRN): how cellular systems translate spatial information into higher-order function



# Cellular Agent-Based Models (ABMs)

OPEN ACCESS Freely available online

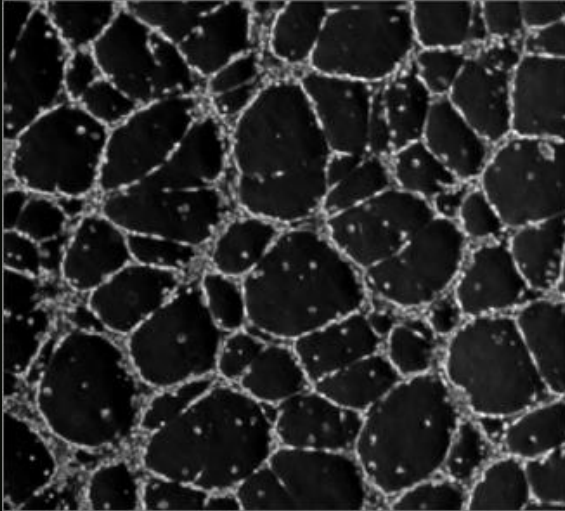
PLOS COMPUTATIONAL BIOLOGY

## A Computational Model Predicting Disruption of Blood Vessel Development

Nicole Kleinstreuer<sup>1</sup>, David Dix<sup>1</sup>, Michael Rountree<sup>1</sup>, Nancy Baker<sup>2</sup>, Nisha Sipes<sup>1</sup>, David Reif<sup>1</sup>, Richard Spencer<sup>2</sup>, Thomas Knudsen<sup>1\*</sup>

<sup>1</sup>National Center for Computational Toxicology, Office of Research and Development, U.S. Environmental Protection Agency, Research Triangle Park, North Carolina, United States of America, <sup>2</sup>Lockheed Martin, Research Triangle Park, North Carolina, United States of America

**VEGF165**  
**MMPs**  
**VEGF121**  
**sFlit1**  
**TIE2**  
**CXCL10**  
**CCL2**

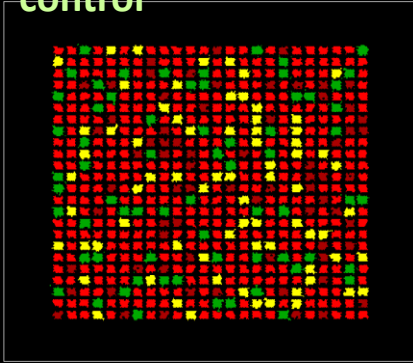


Endothelial Stalk  
Endothelial Tip  
Mural Cell  
Inflammatory Cell

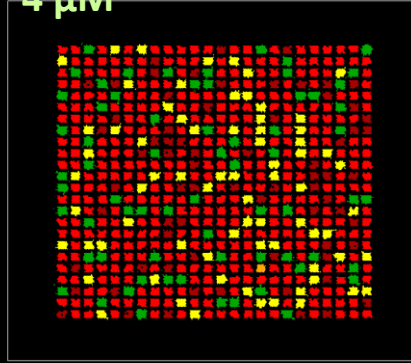
- individual rules are assigned to low-level 'agents' (here = cells)
- agents then interact in a shared environment (CompuCell3D\*)
- running the simulation executes this biology (emergence)
- models run differently each time (stochastic)
- each run reveals one possible solution (outcome)

# 5HPP-33 concentration response predicted *in silico* from ToxCast and demonstrated *in vitro* with a human endothelial cell assay

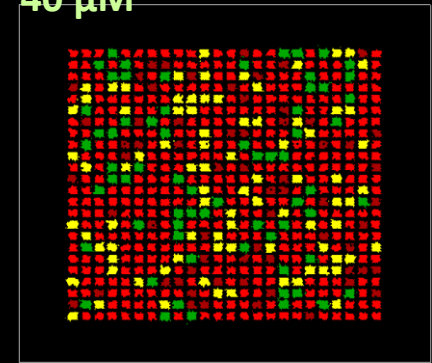
control



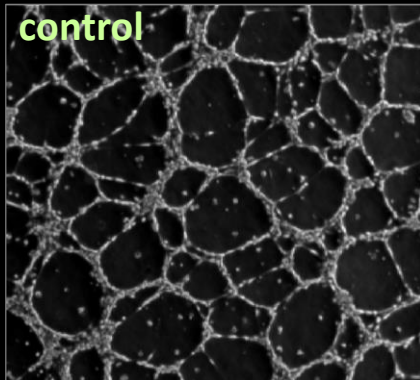
4  $\mu\text{M}$



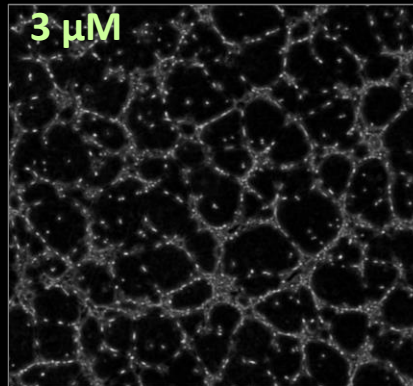
40  $\mu\text{M}$



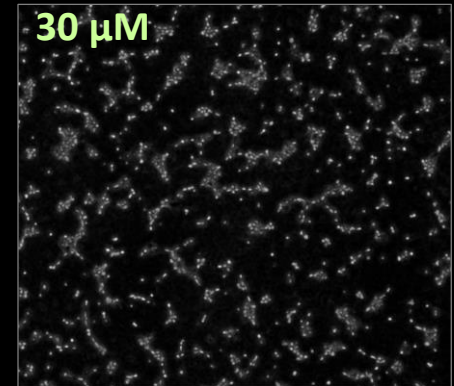
control



3  $\mu\text{M}$



30  $\mu\text{M}$



# 2. Limb Development

Stage 16  
GD9

Stage 18  
GD10

Stage 19  
GD12

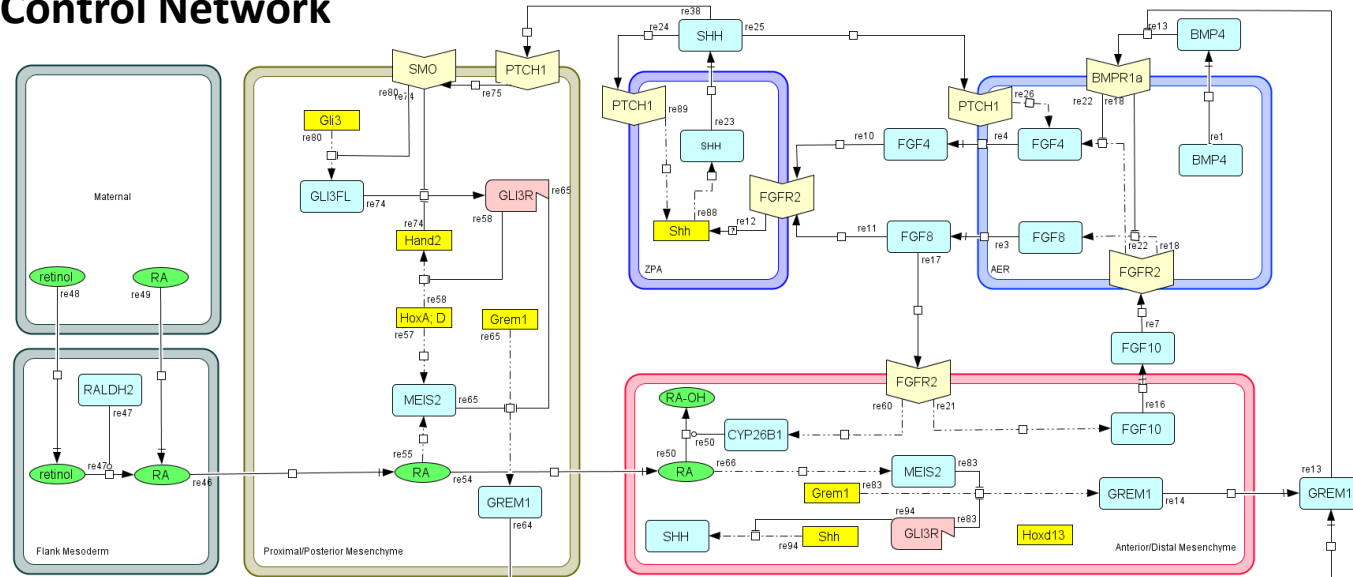
Stage 20  
GD12.5

Stage 21  
GD13



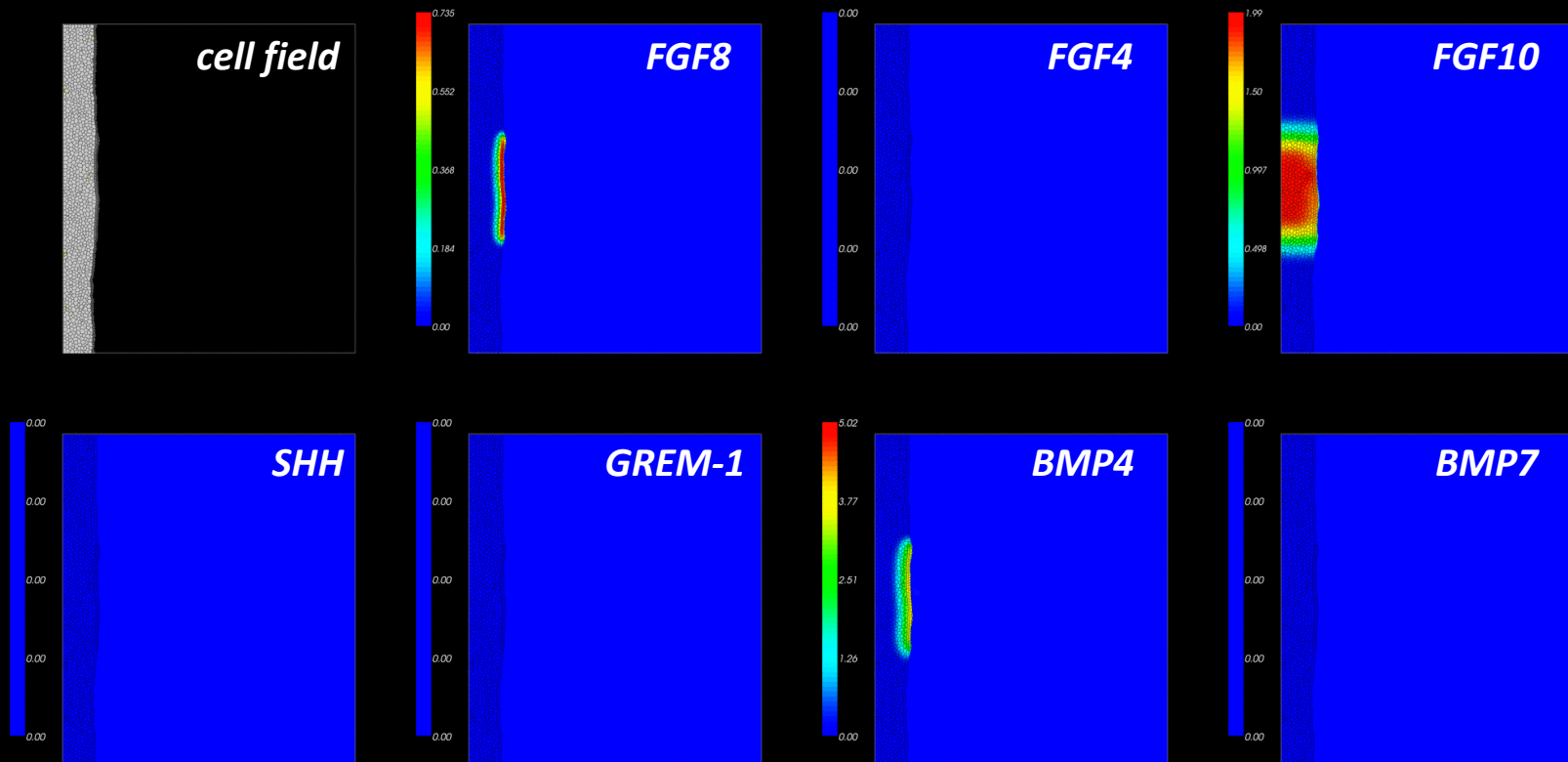
*Boehm et al. (2011) Development 138*

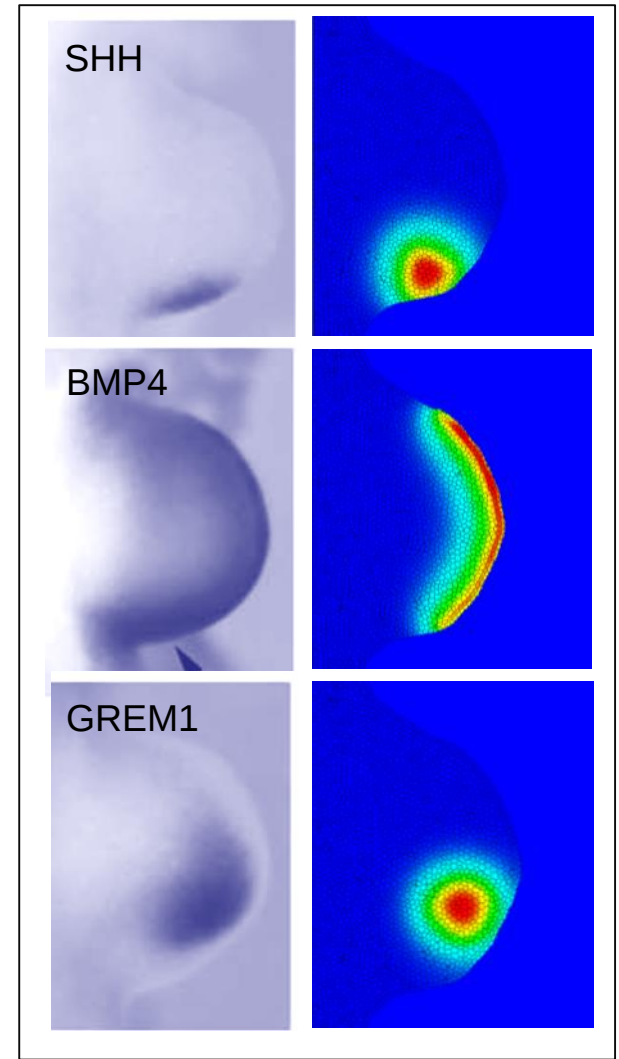
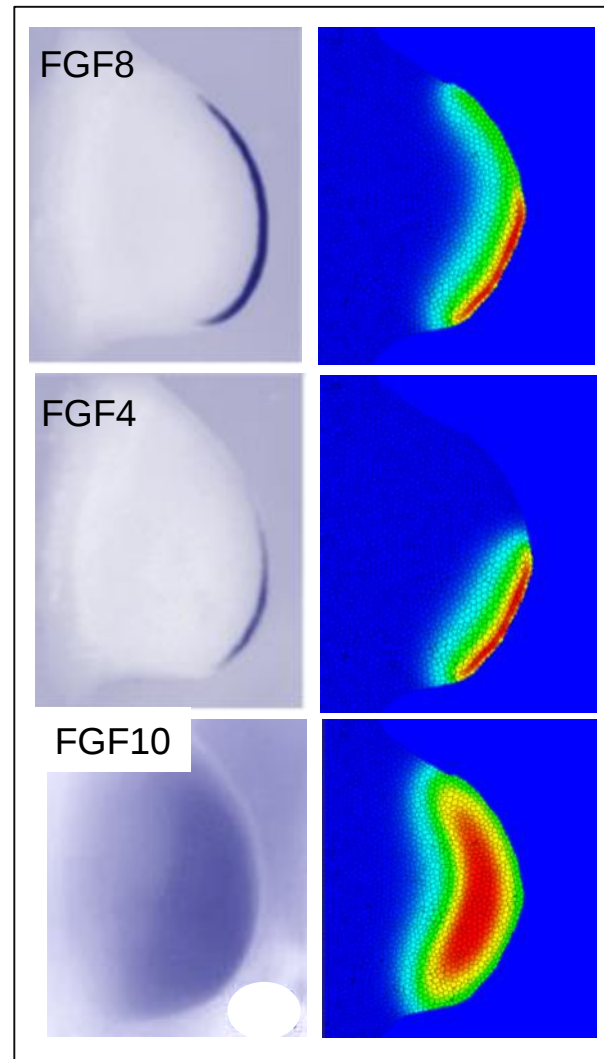
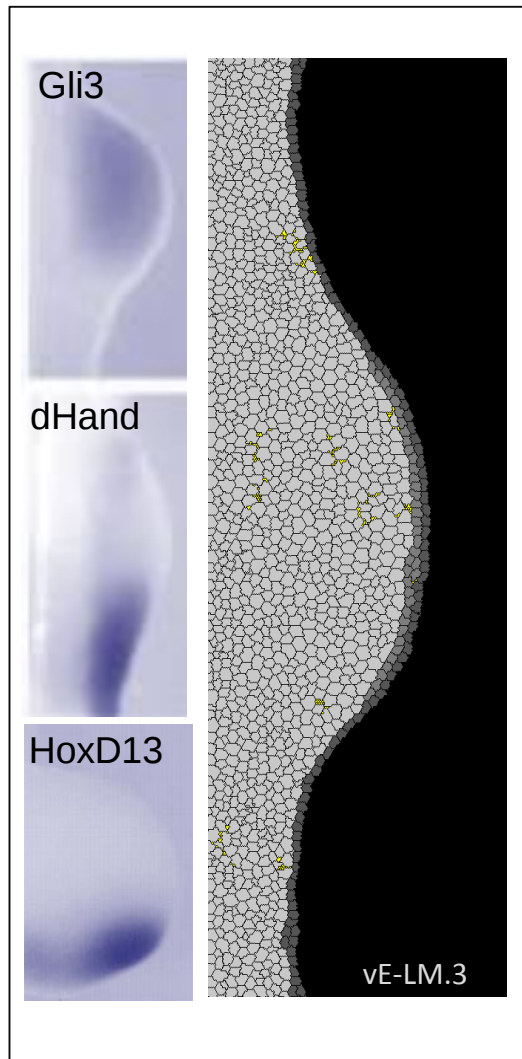
## Control Network



*Dewoskin – NCCT, unpublished*

# Spatial dynamics: patterning early limb outgrowth

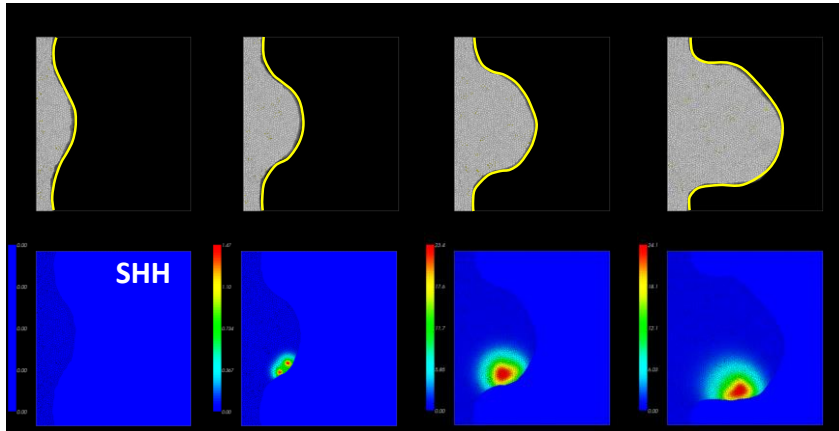




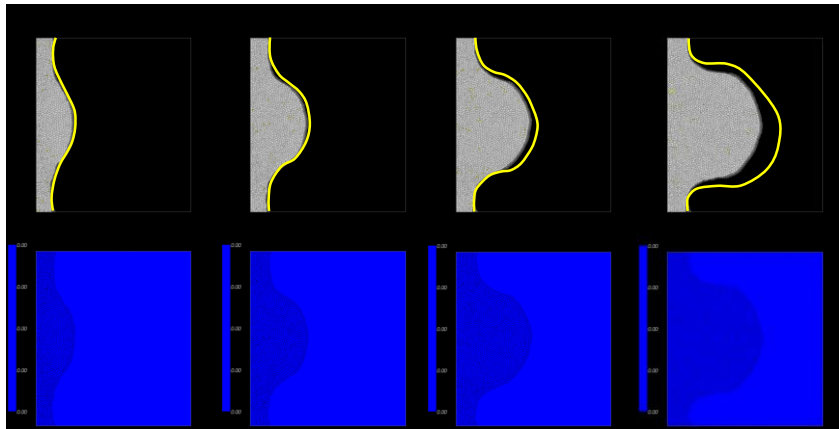
*ISH (mouse literature) vs ABM*

**Failability:** exposures may disrupt signaling domains directly

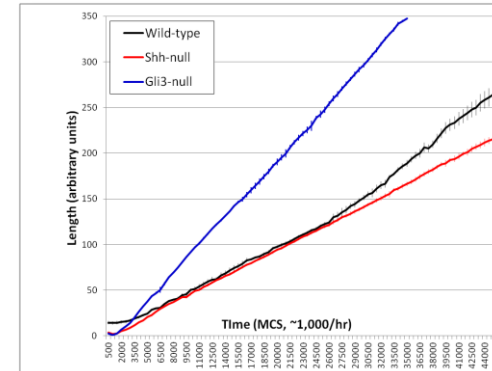
*Wild-type*



*Shh-null*



**Rate of outgrowth (n=5)**



**Predicted impact of SHH disruption on limb outgrowth**

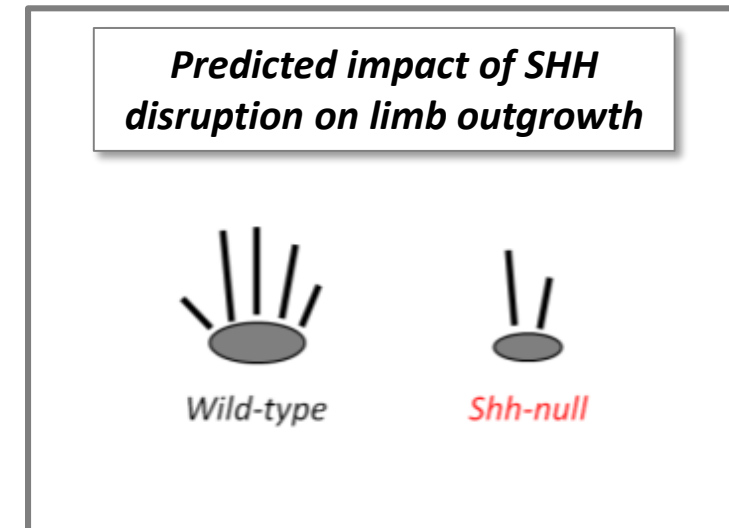
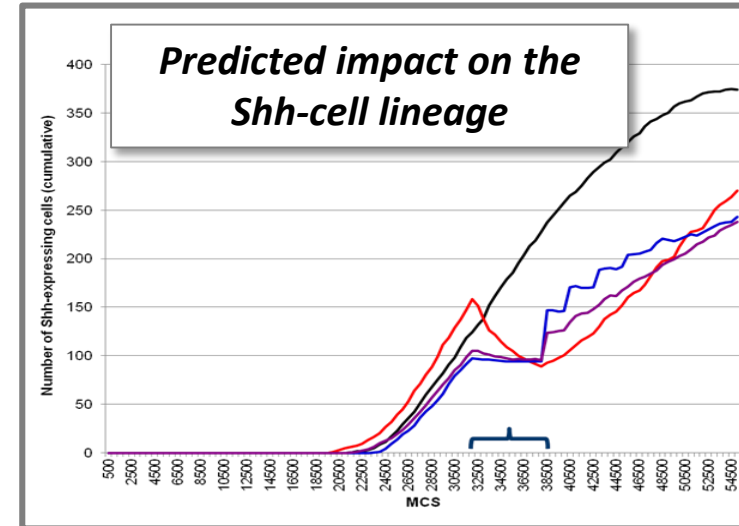
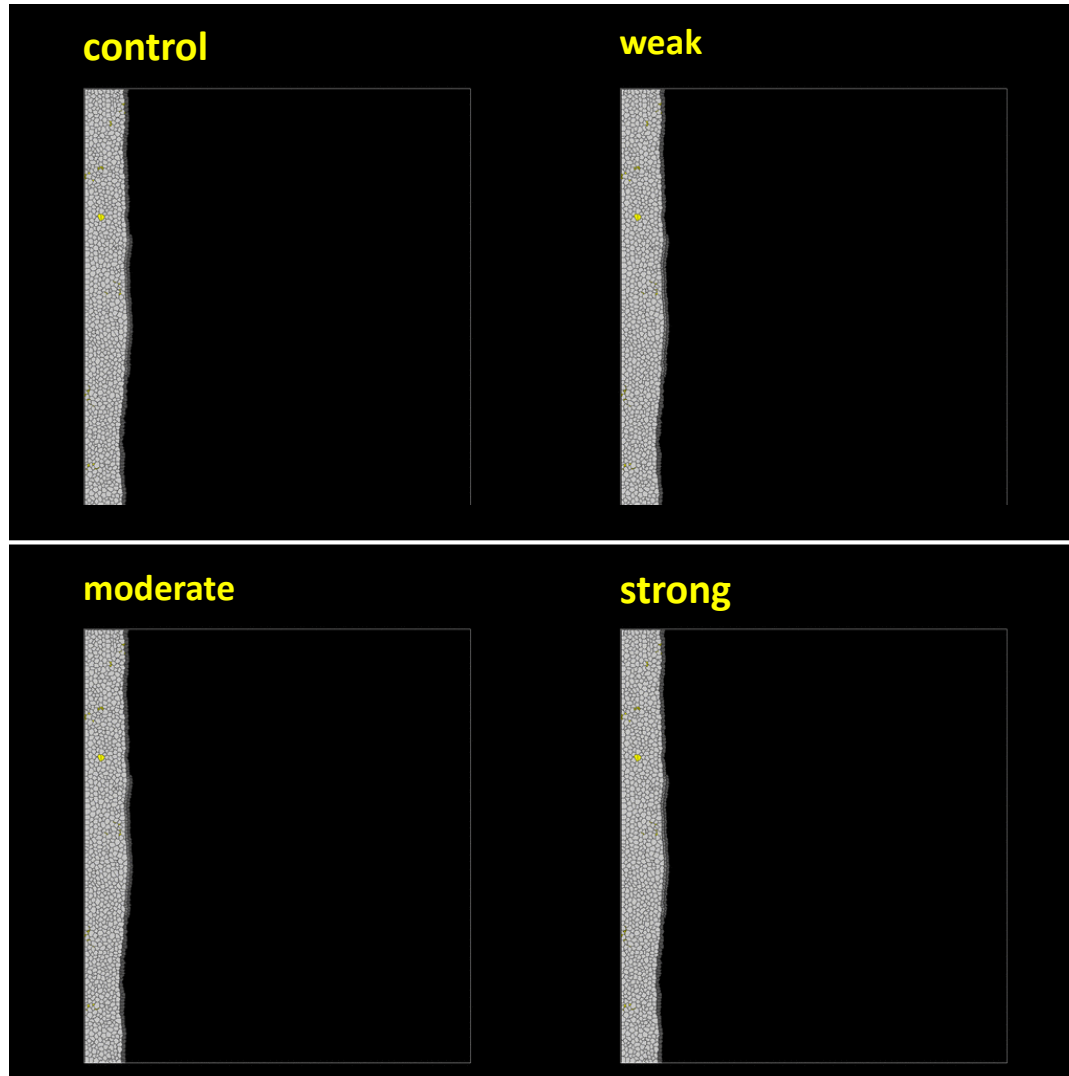


*Wild-type*

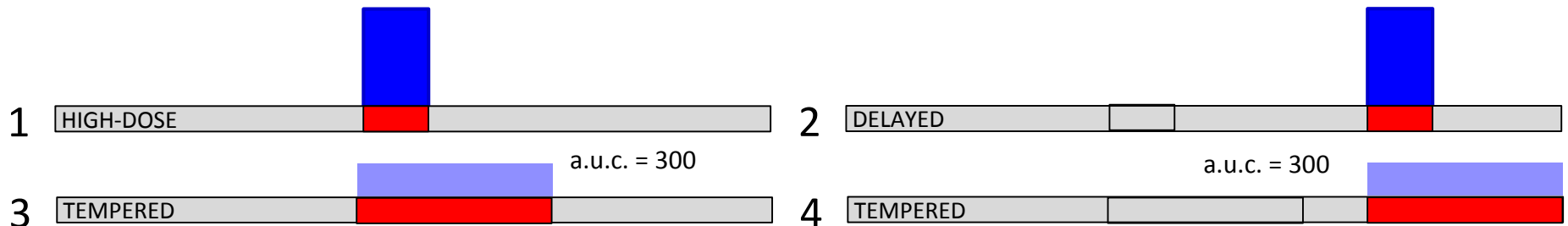
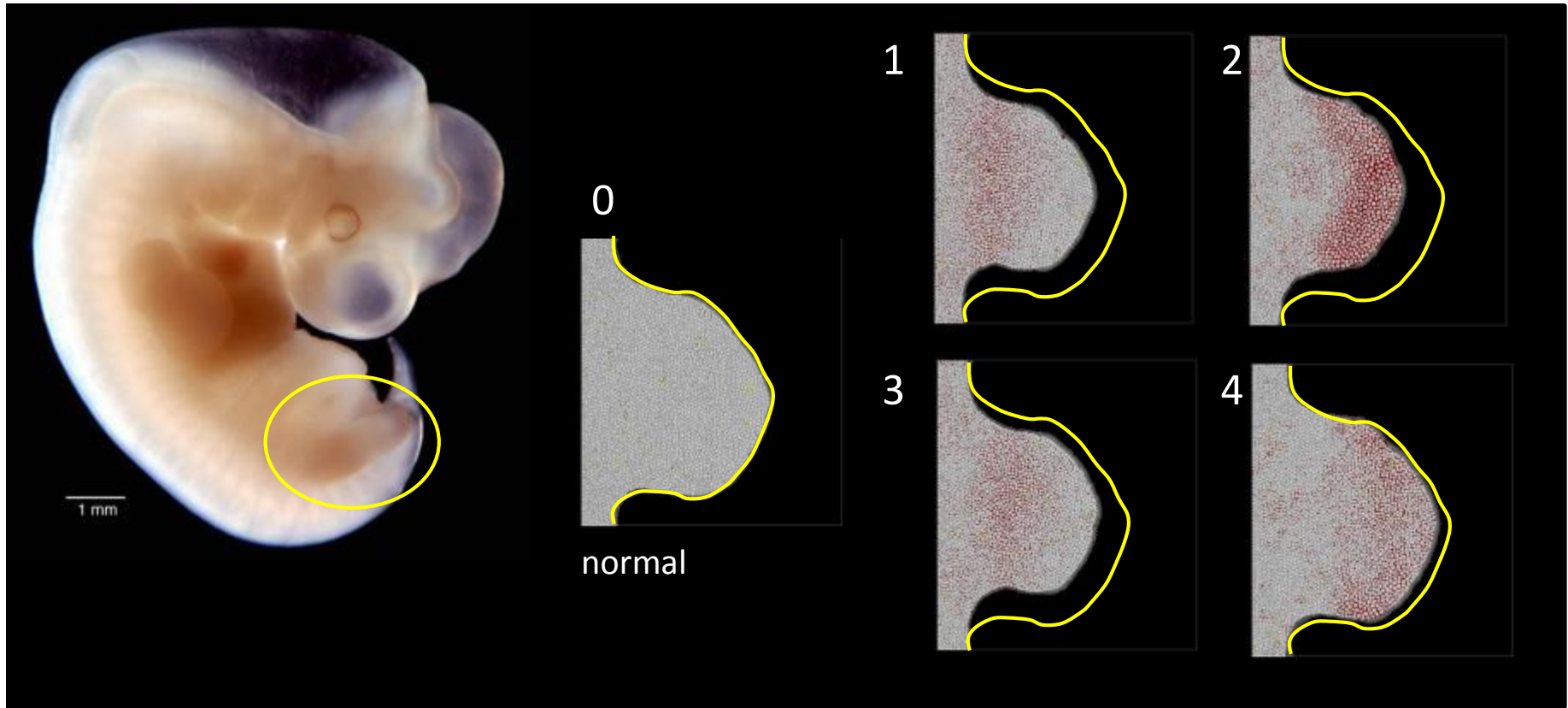


*Shh-null*

# Failability: exposures may disrupt signaling domains indirectly

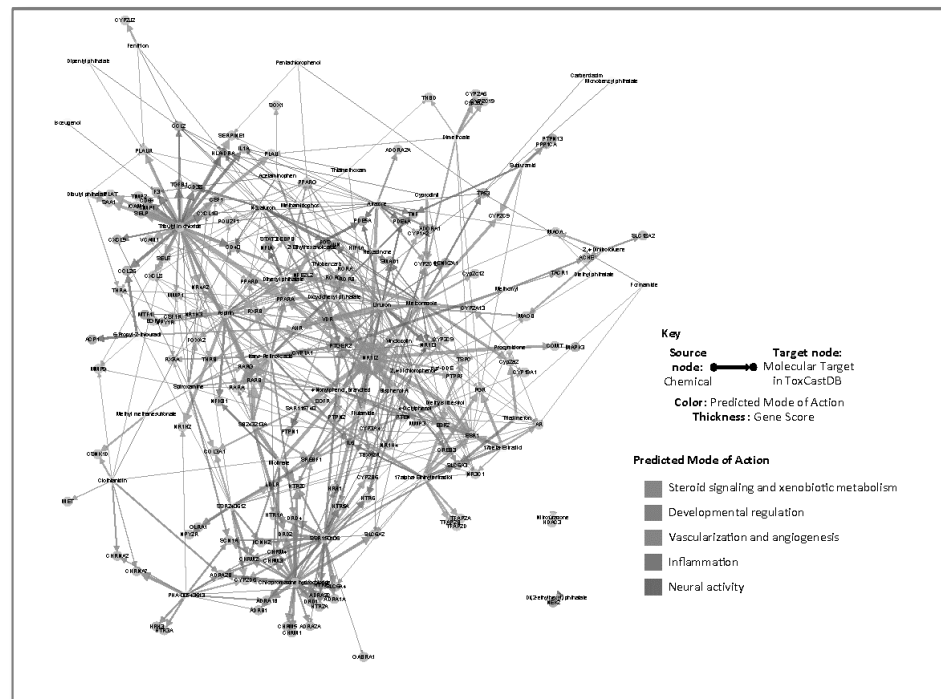


# 'What-if'? simulating different exposure scenarios



### 3. Chemical-Target Bipartite Network: translates ToxCast bioactivity profiles into predicted mode-of-action for an AOP

- BPN for 54 ToxCast chemicals that produce male developmental toxicity.
- Functional annotation revealed 4-5 target biological processes.



**ehp** ENVIRONMENTAL HEALTH PERSPECTIVES

*Leung et al. (2016)*

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RESEARCH ARTICLE ADVANCE PUBLICATION

Environ Health Perspect, DOI:10.1289/ehp.1510385

**Systems Toxicology of Male Reproductive Development: Profiling 774 Chemicals for Molecular Targets and Adverse Outcomes**

Maxwell C.K. Leung<sup>1,2</sup>, Jimmy Phuong<sup>2</sup>, Nancy C. Baker<sup>3</sup>, Nisha S. Sipes<sup>1,2</sup>, Gary R. Klinefelter<sup>4</sup>, Matthew T. Martin<sup>2</sup>, Keith W. McLaurin<sup>1,2</sup>, R. Woodrow Setzer<sup>2</sup>, Sally Perreault Darney<sup>4</sup>, Richard S. Judson<sup>2</sup>, and Thomas B. Knudsen<sup>2</sup>

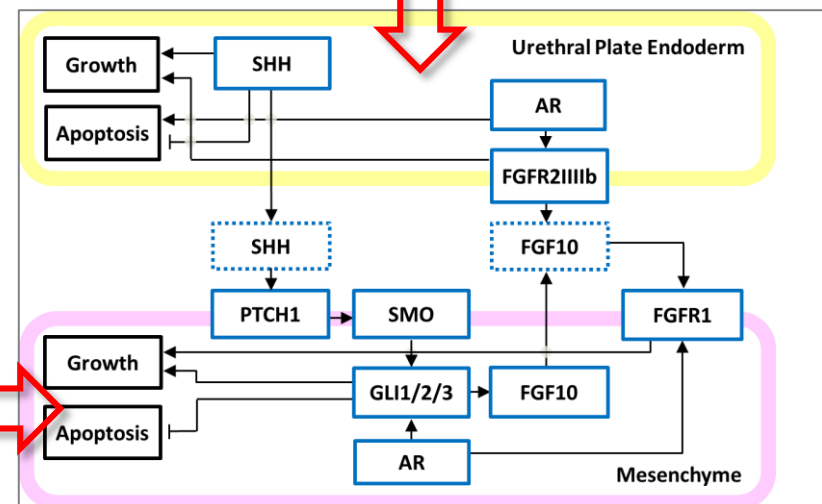
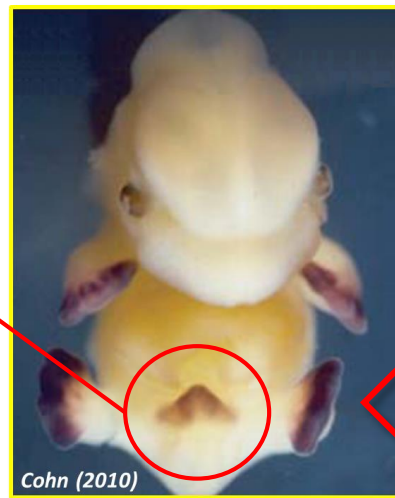
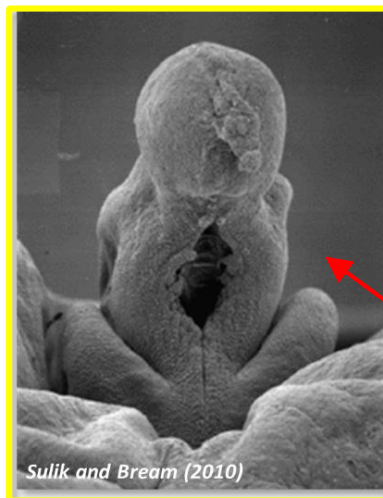
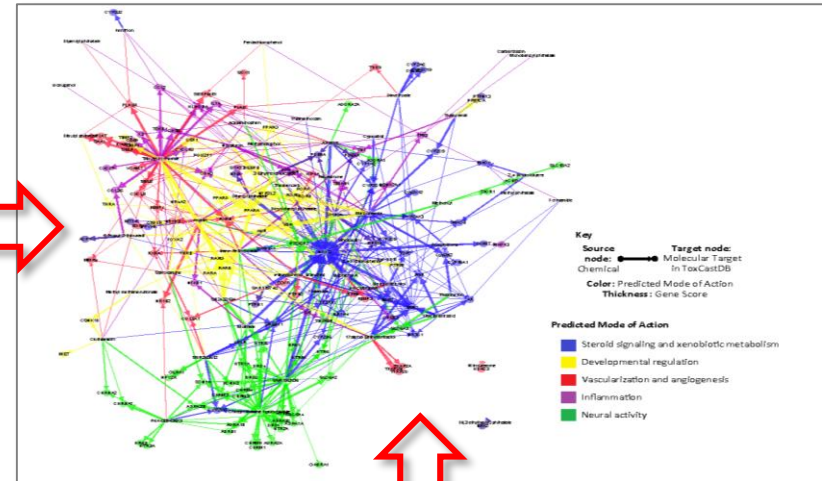
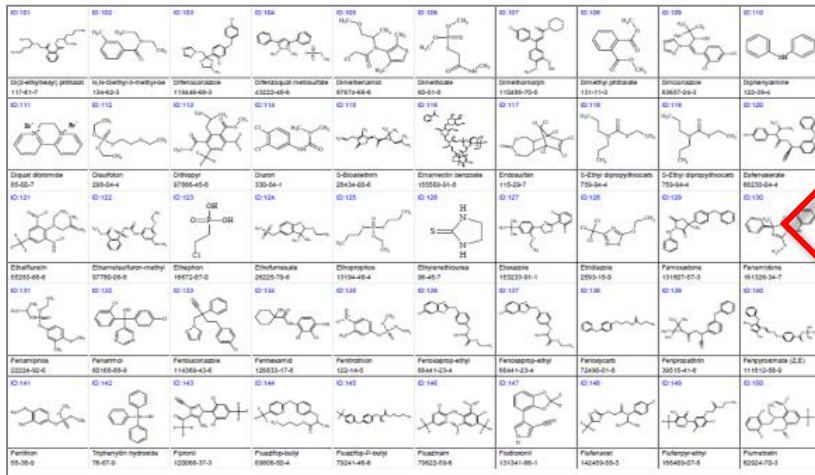
Author Affiliations open

PDF Version (5.1 MB)

# How do chemical-bioactivity bipartite networks interact with control networks in disrupting development?

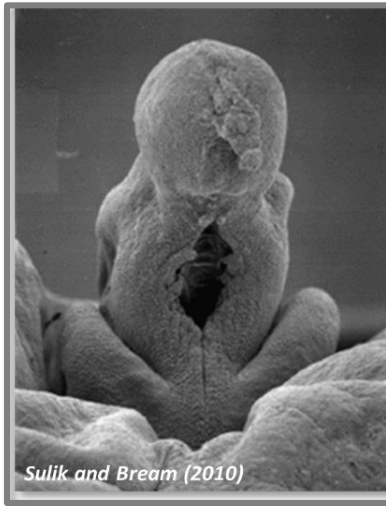
**EXAMPLE: hypospadias, a urethral closure defect**

*Leung et al. (in preparation)*

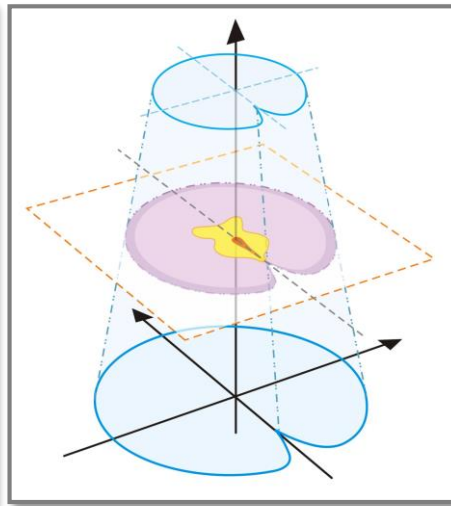


# Genital Tubercle (GT) development

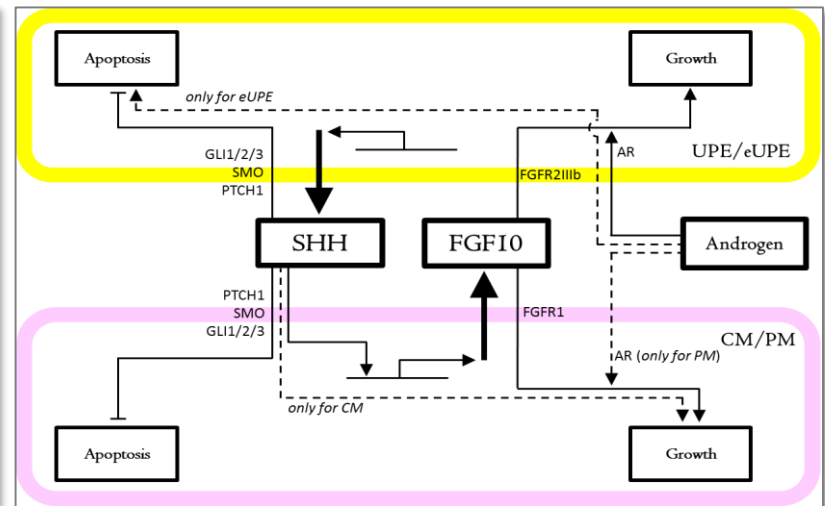
Embryonic GT



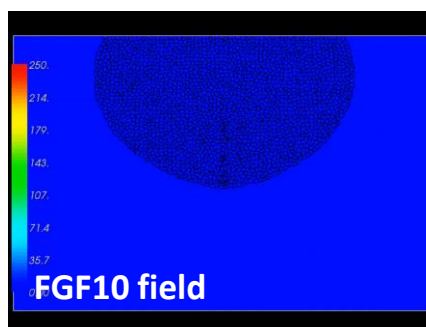
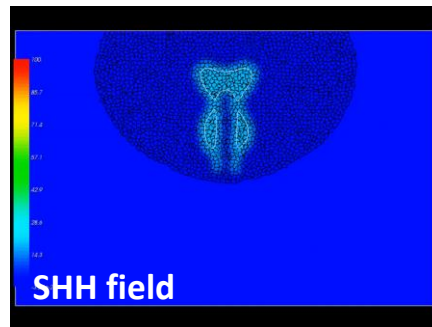
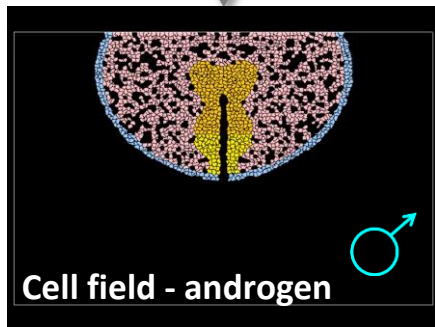
Abstracted GT



Control Network (mouse)



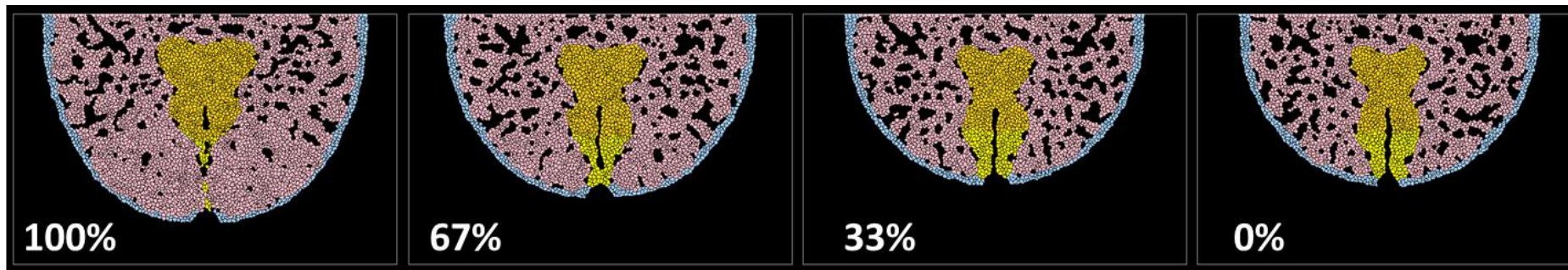
**ABM simulation for sexual dimorphism (MCS 4000 = GD13.5 – 17.5)**



- sexually indifferent at MCS 0 (GD13.5)
- androgen production by fetal testis introduced at MCS 2000 (GD15.5)
- sexual dimorphism evaluated at MCS 4000 (GD17.5)

# Urethral Closure

- Driven by urethral endoderm (contact, fusion apoptosis) and preputial mesenchyme (proliferation, condensation, migration).
- Disruption of SHH, FGF10, or AR signaling leads to urethral closure defects (e.g., hypospadias).



| <b>Androgenization</b> | <b>Phenotype (MCS 4000)</b> |               |                |                      |
|------------------------|-----------------------------|---------------|----------------|----------------------|
| <i>(n = 10 sims)</i>   | <u>Septation</u>            | <u>Fusion</u> | <u>Conden.</u> | <u>Closure Index</u> |
| 100%                   | 6/10                        | 8/10          | 10/10          | 0.80                 |
| 67%                    | 2/10                        | 5/10          | 10/10          | 0.57                 |
| 33%                    | 0/10                        | 4/10          | 0/10           | 0.13                 |
| 0%                     | 0/10                        | 2/10          | 0/10           | 0.07                 |

# Programmed Fusion of Opposing Surfaces

- Disruption is a key event in AOPs for many human birth defects: NTDs, coloboma, cleft palate, valvuloseptal defects, hypospadias, gastroschisis, ...
- Emergent property orchestrated by CRNs: EMT, apoptosis, epithelial cell adhesion / migration / intercalation are recurring themes.

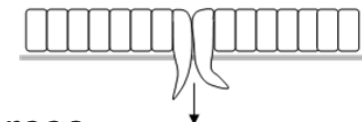
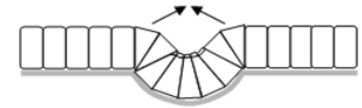
## Cellular primitives

- growth (proliferation)
- programmed cell death (apoptosis)
- genetic signals and responses
- differentiation
- cell adhesion
- shape (geometry)
- motility (cell migration)
- ECM (remodeling)

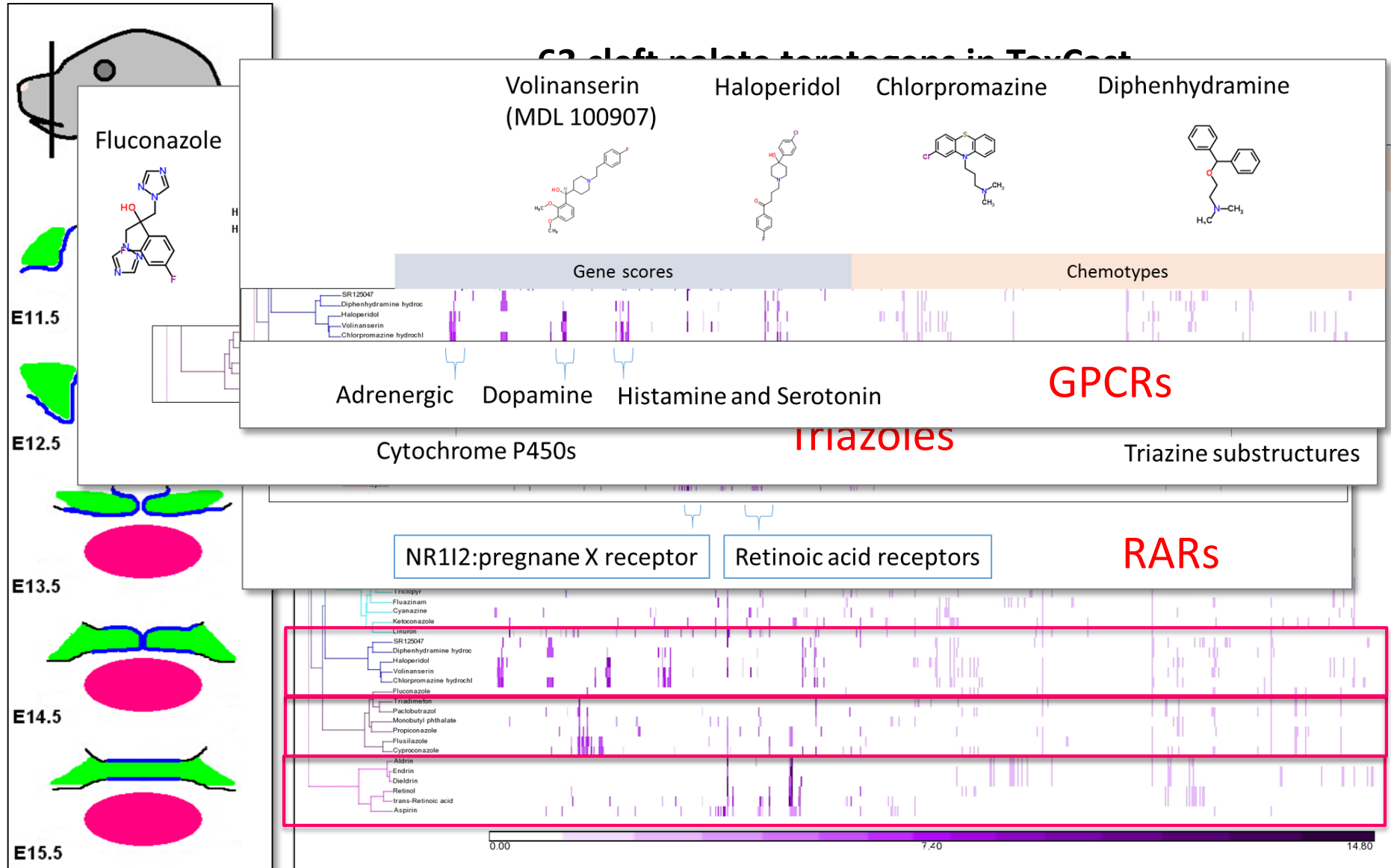


## Tissue movements

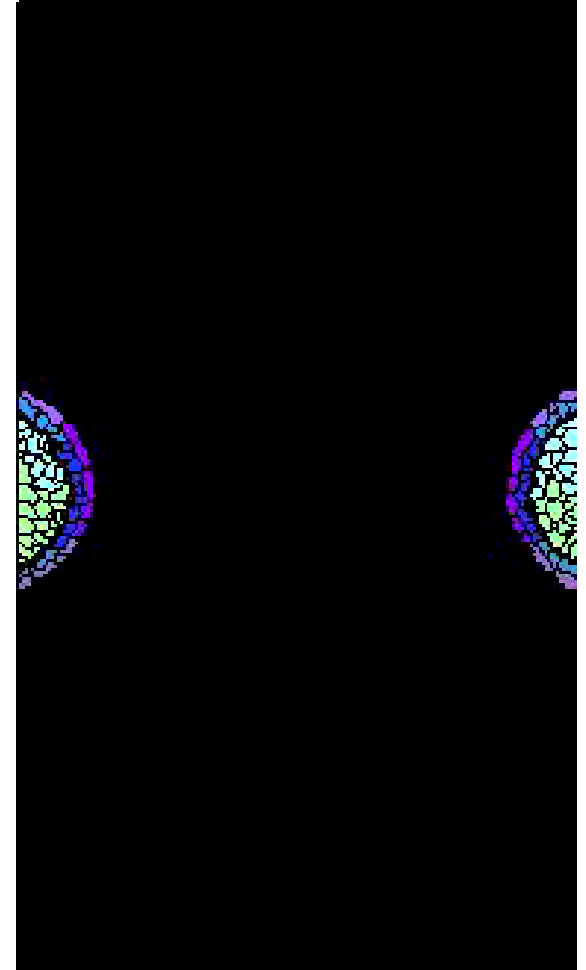
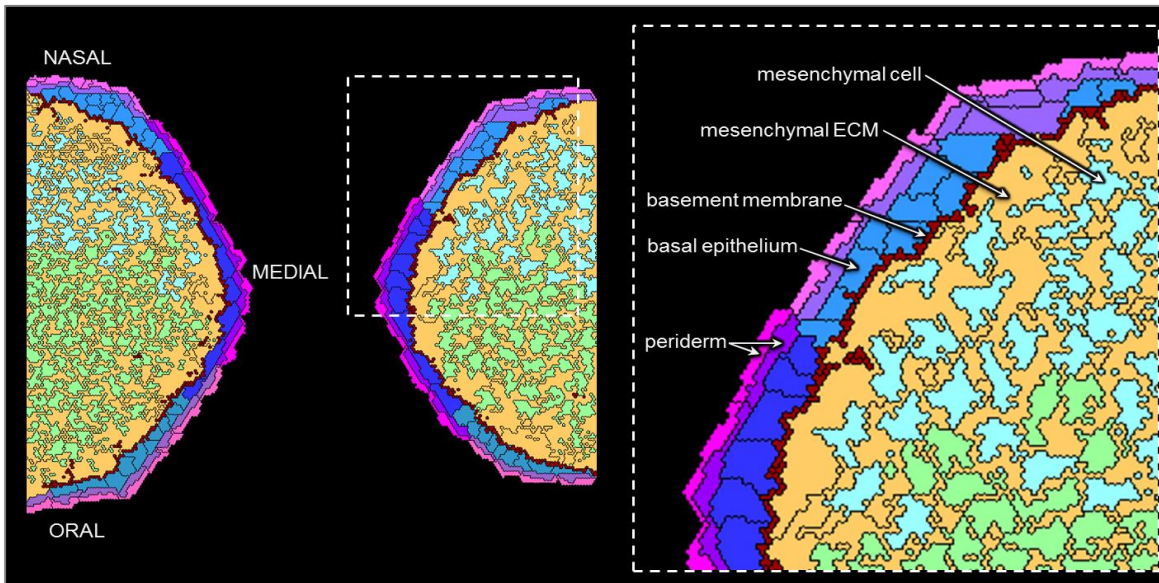
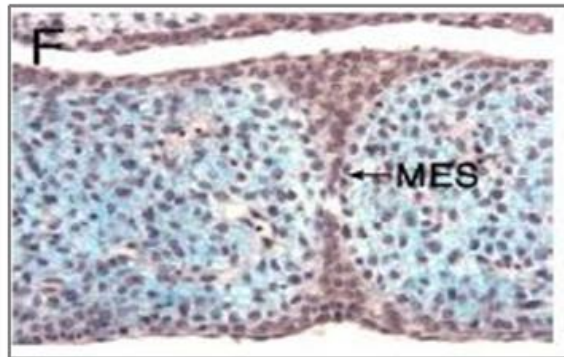
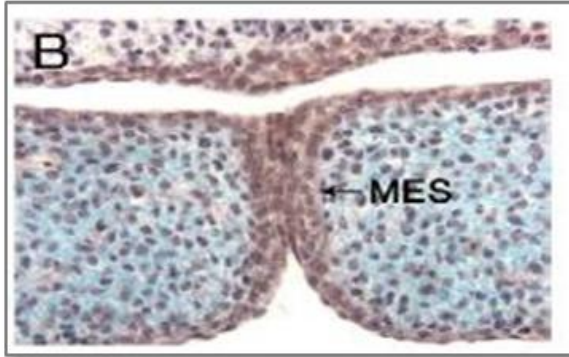
- folding
- epiboly
- convergent extension
- branching morphogenesis
- cell condensation
- cell sorting
- trans-differentiation (EMT)
- cavitation
- involution
- tractional forces
- ...



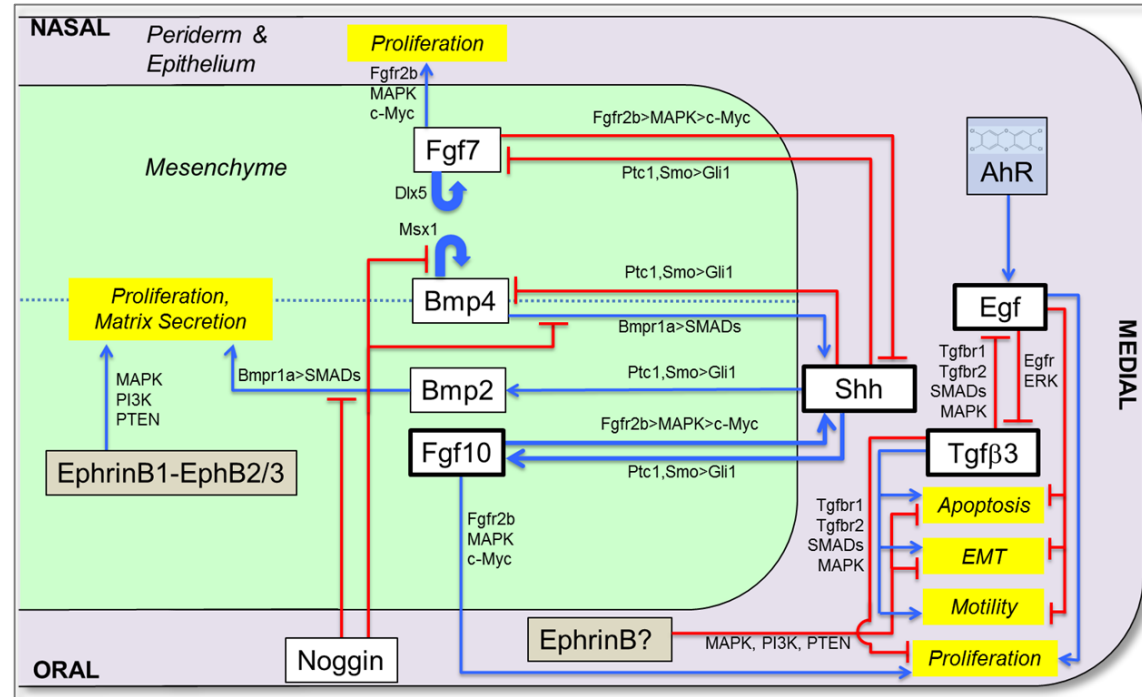
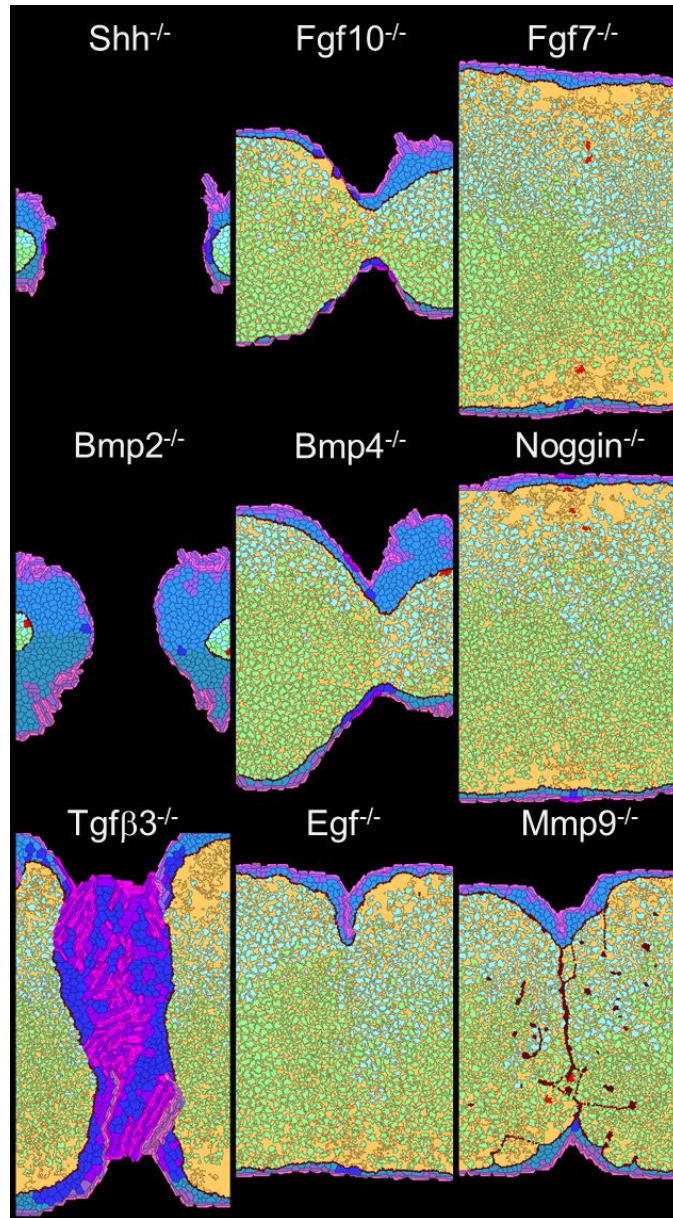
# 4. Palatal Closure: complex process disrupted in 'cleft palate'.



# Palatal Closure: ABM recapitulating cellular dynamics of Medial Edge Epithelium (MEE) contact and seam (MES) breakdown.

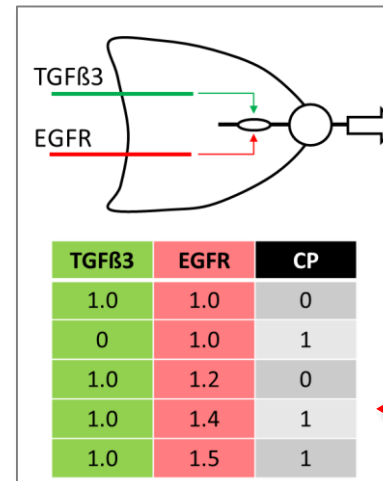
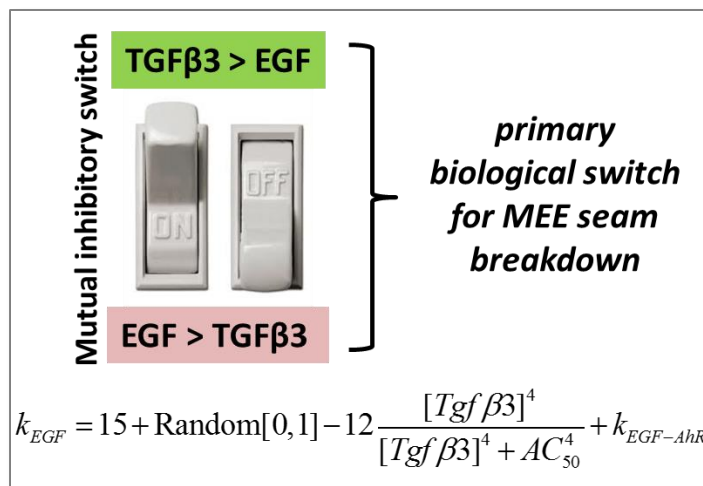
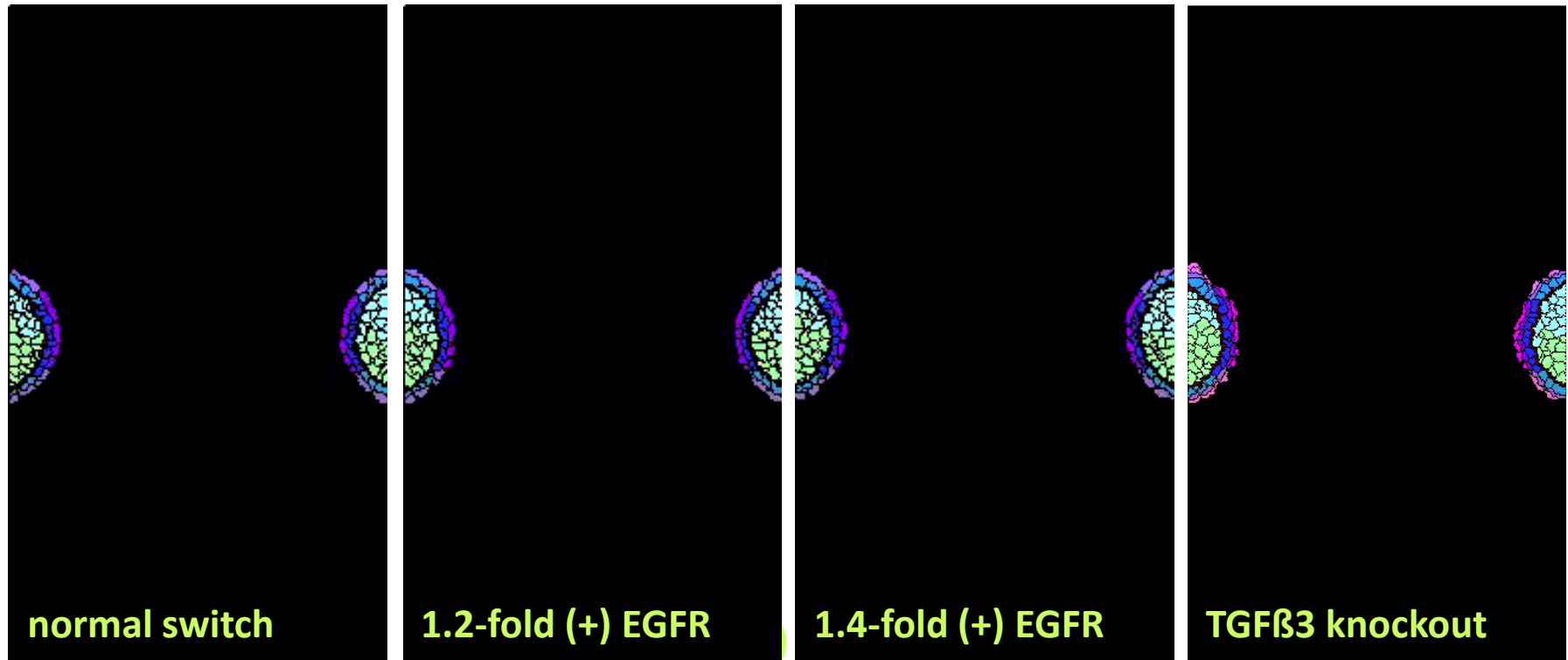


# Hacking the Control Network



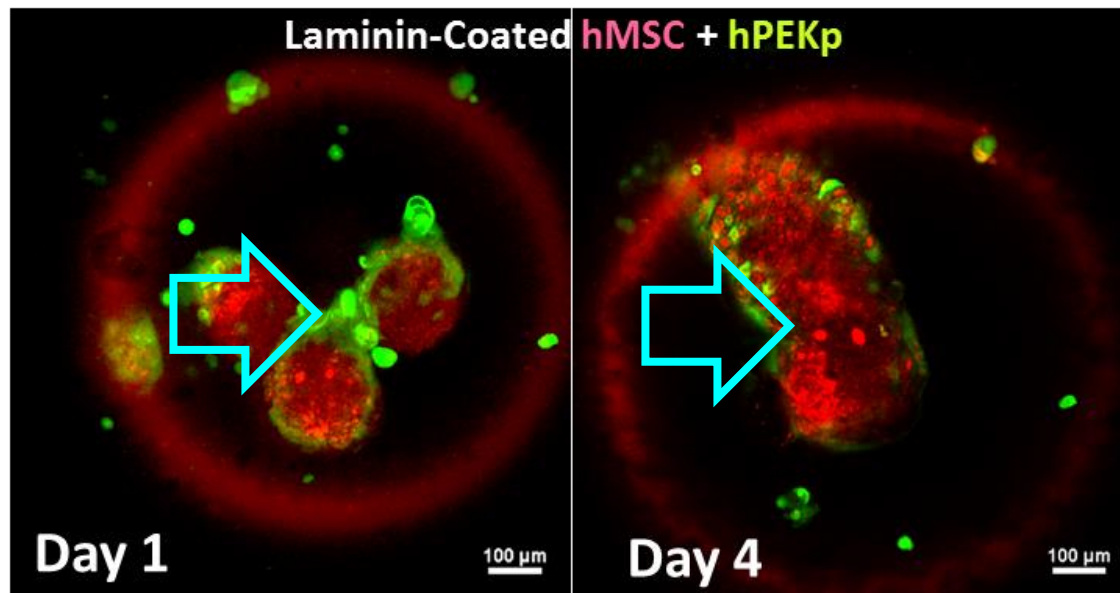
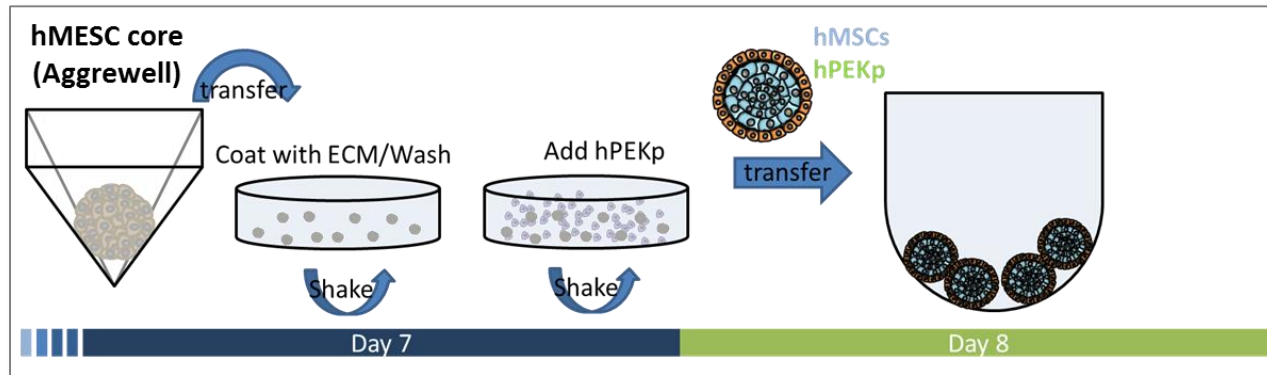
- *in silico* knockouts of elements in the underlying signaling network
- predicted impacts on MEE contact and seam breakdown (critical events)

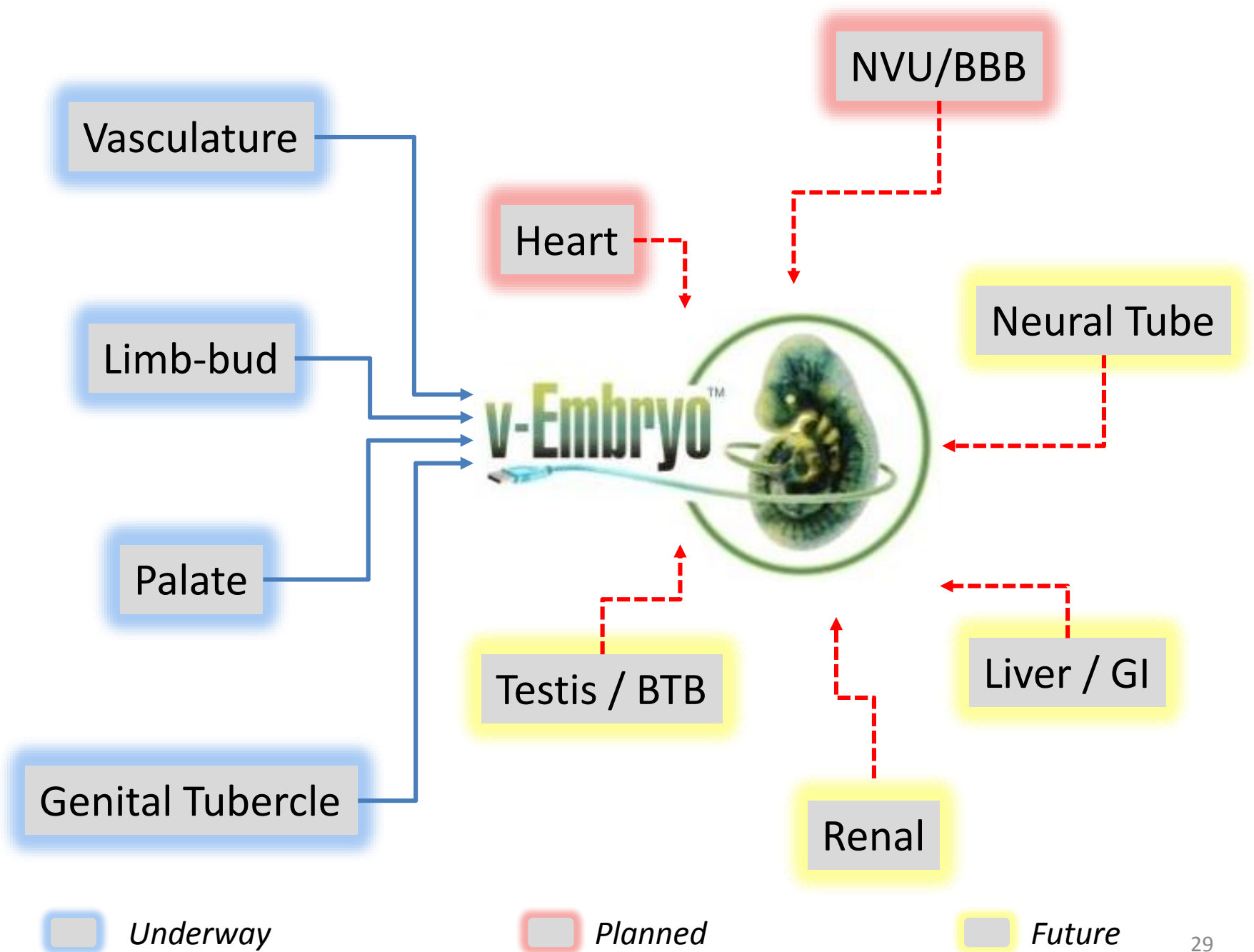
# MES Differentiation: TGFβ3/EGF switching



**Predicted imbalance disrupting the timing of MES differentiation**

# **Fusion-Competent hMSC Spheroids:** engineering a HTS human MES breakdown assay from pluripotent human cell lines





# Virtual Tissues Laboratory System



**Virtuoso**

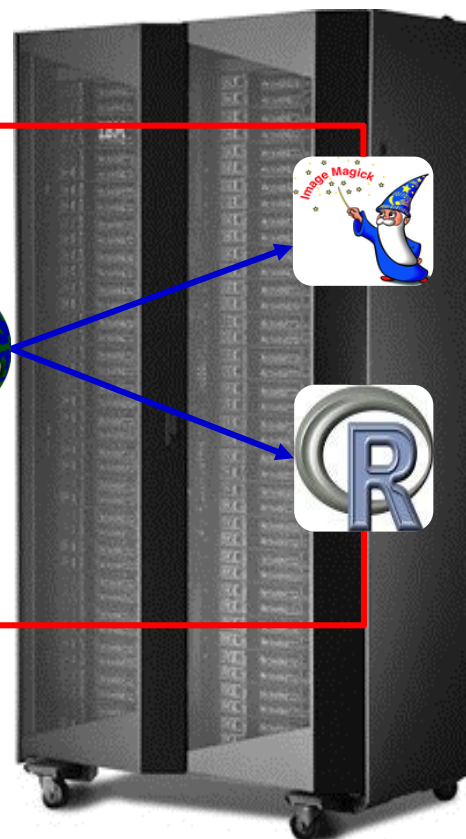
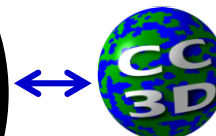
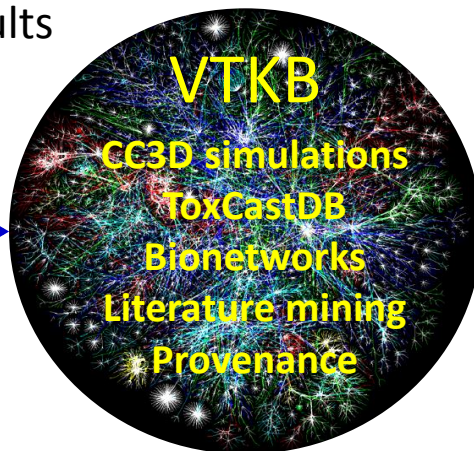
Web Services and Queries



VIRTUAL TISSUES  
LABORATORY SYSTEM

**HPC**

Massively-parallel simulation



BIO2RDF

# Special Thanks

- Richard Judson – NCCT
- Imran Shah – NCCT
- Barbara Abbott – NHEERL / TAD
- Sid Hunter – NHEERL / ISTD
- Dustin Kapraun – NCCT (ORISE)
- Eric Watt – NCCT (ORISE)
- Max Leung – NCCT (ORISE)
- Jill Franzosa – NCCT (ORISE)
- Nicole Kleinstreuer – NCCT (now NIEHS/NTP)
- Nisha Sipes – NCCT (now NIEHS/NTP)
- Richard Spencer – Lockheed Martin / EMVL
- Nancy Baker – Lockheed Martin / NCCT
- Rob DeWoskin – EPA / NCEA
- Tamara Tal – NHEERL / ISTD
- Monica Linnenbrink – NCCT / CSS
- Christina Baghdikian – NCCT / CSS
- Ed Carney† – Dow Chemical Company
- T Heinonen – U Tampere / FICAM
- E Berg – DiscoverX – BioSeek
- A Seifert – U Kentucky
- L Egnash – Stemina Biomarker Discovery
- M Bondesson – U Houston / STAR
- J Glazier – Indiana U / STAR
- Shane Hutson – Vanderbilt U / STAR
- William Murphy – U Wisconsin / STAR
- William Daly – U Wisconsin / STAR
- John Wikswø – Vanderbilt U / STAR



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## science in ACTION

INNOVATIVE RESEARCH FOR A SUSTAINABLE FUTURE

Virtual Tissue Models: Predicting How Chemicals Impact Human Development

[http://www2.epa.gov/sites/production/files/2015-08/documents/virtual\\_tissue\\_models\\_fact\\_sheet\\_final.pdf](http://www2.epa.gov/sites/production/files/2015-08/documents/virtual_tissue_models_fact_sheet_final.pdf)



**National Center for Computational Toxicology**