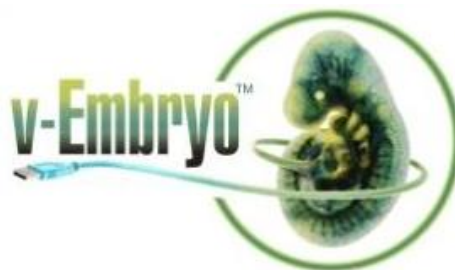


# Computational Modeling and Simulation of Developmental Toxicity



**Thomas B. Knudsen, PhD**  
Developmental Systems Biologist  
US EPA, National Center for Computational Toxicology  
Chemical Safety for Sustainability Research Program

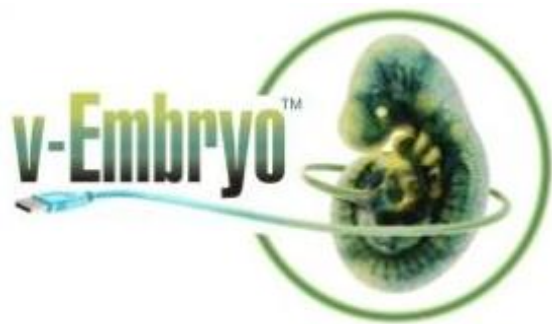
*DISCLAIMER: The views expressed in this presentation are  
those of the presenter and do not necessarily reflect the views  
or policies of the U.S. Environmental Protection Agency.*

# 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, ...*

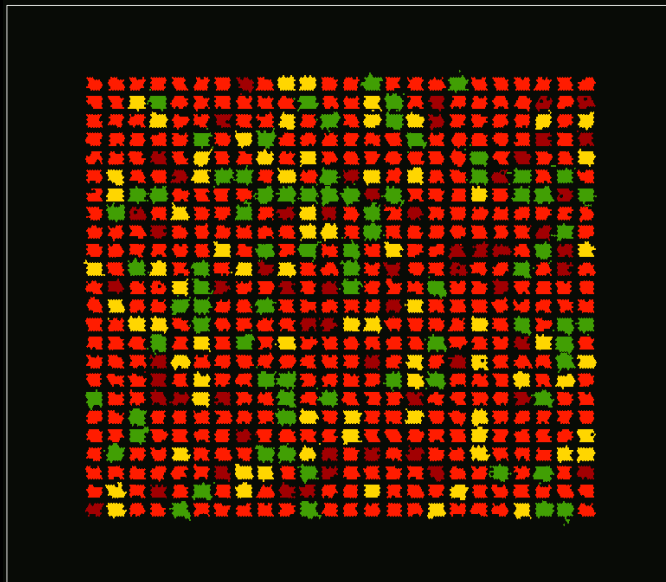


# Multicellular Agent-Based Models (ABMs)

- Computer models that recapitulate multiple signaling networks and coordinated cell behaviors.
- Running ABMs with real (*in vitro*) or synthetic (*in silico*) data is a heuristic to predict emergent responses following perturbation.
- Comparing simulated outcomes with reference experiments tells how well the ABM performs.
- Can use them to translate screening-level data from chemical-biology into predictive toxicology of a developmental hazard.

# Angiogenesis

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



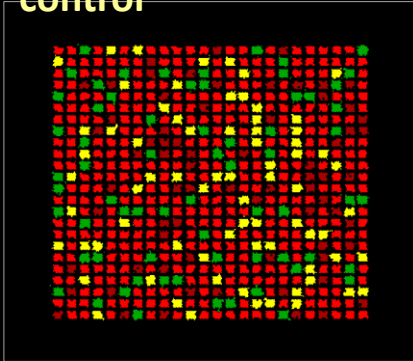
Endothelial Stalk  
Endothelial Tip  
Mural Cell  
Inflammatory Cell

- individual rules assigned to low-level 'agents' (cells)
- agents interact in a shared environment \*
- executing the biology leads to emergent features
- models run differently each time (stochastic)
- each run reveals one possible solution

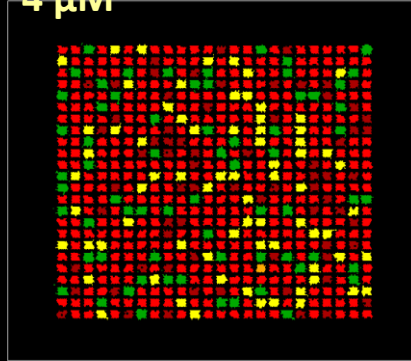
\* *CompuCell3D.org is an open-access environment for cell-oriented modeling developed at Indiana University by J Glazier and colleagues*

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

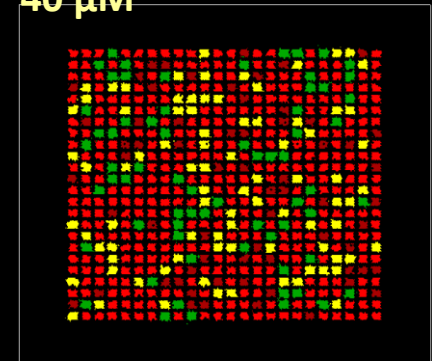
control



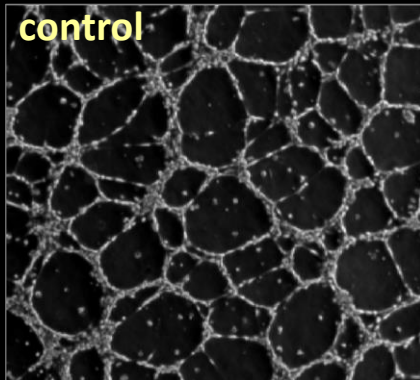
4  $\mu$ M



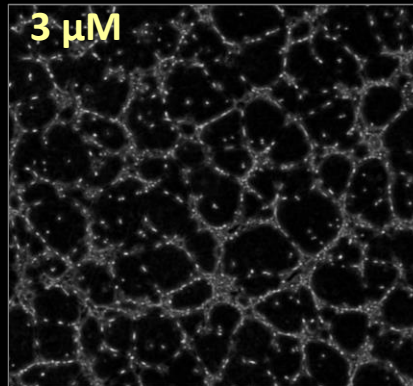
40  $\mu$ M



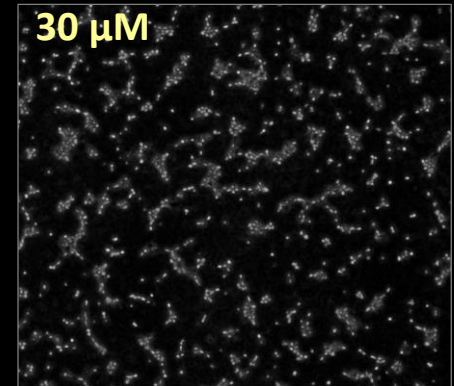
control



3  $\mu$ M



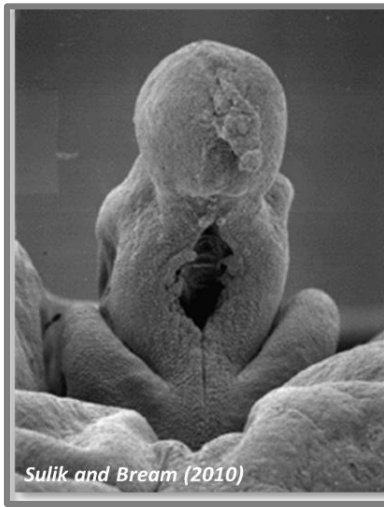
30  $\mu$ M



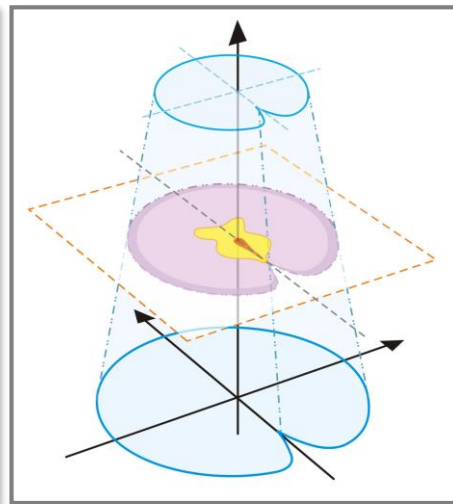


# Modeling Genital Tubercle Development

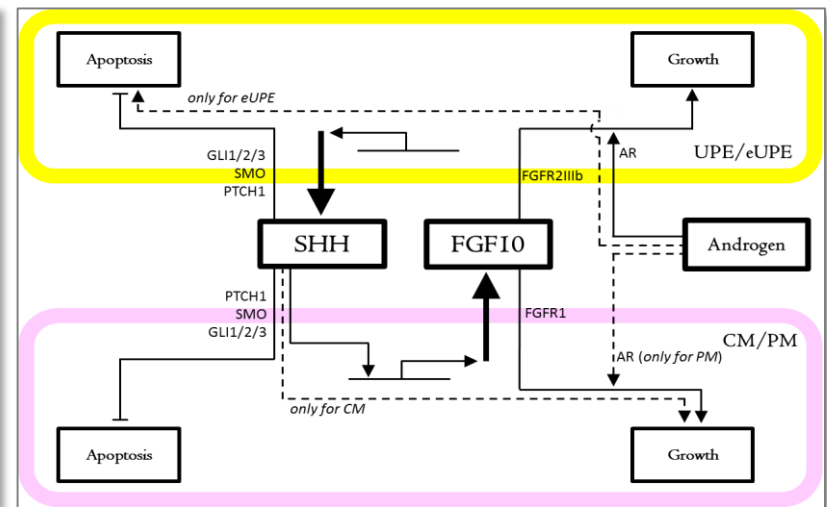
Embryonic GT



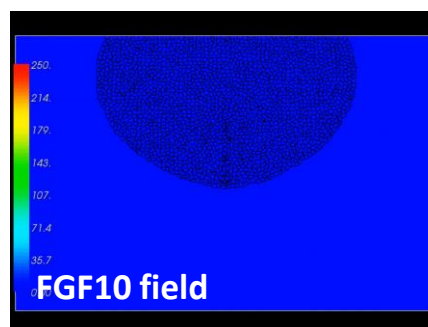
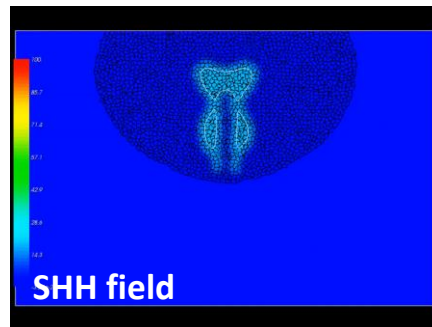
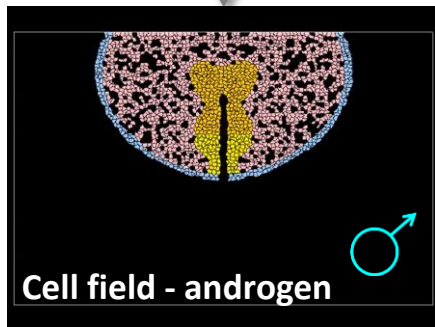
Abstracted GT



Control Network (mouse)



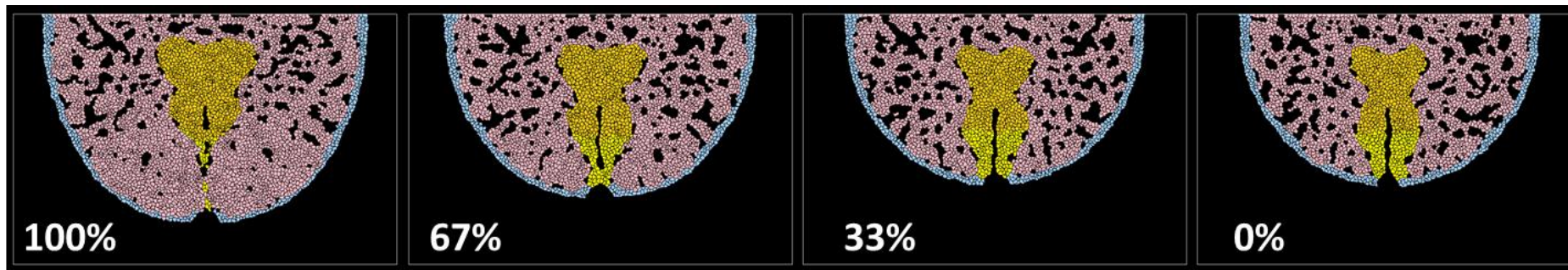
**ABM simulation for sexual dimorphism (MCS 4000 = GD13.5 – 17.5)**



- 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: complex process disrupted in 'hypospadias'

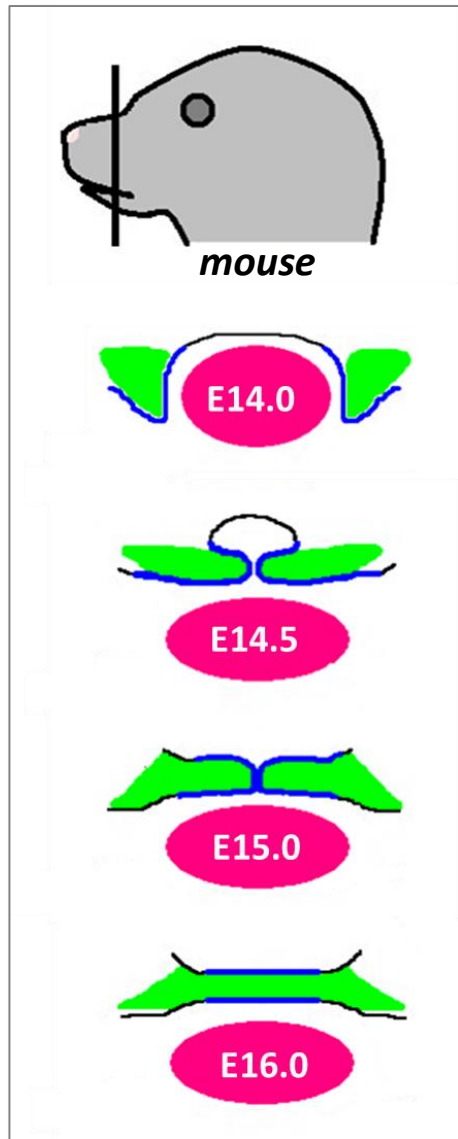
- Driven by urethral endoderm (contact, fusion apoptosis) and preputial mesenchyme (proliferation, condensation, migration).
- Disruption of SHH, FGF10, or AR signaling leads to urethral closure defects (e.g., hypospadias).



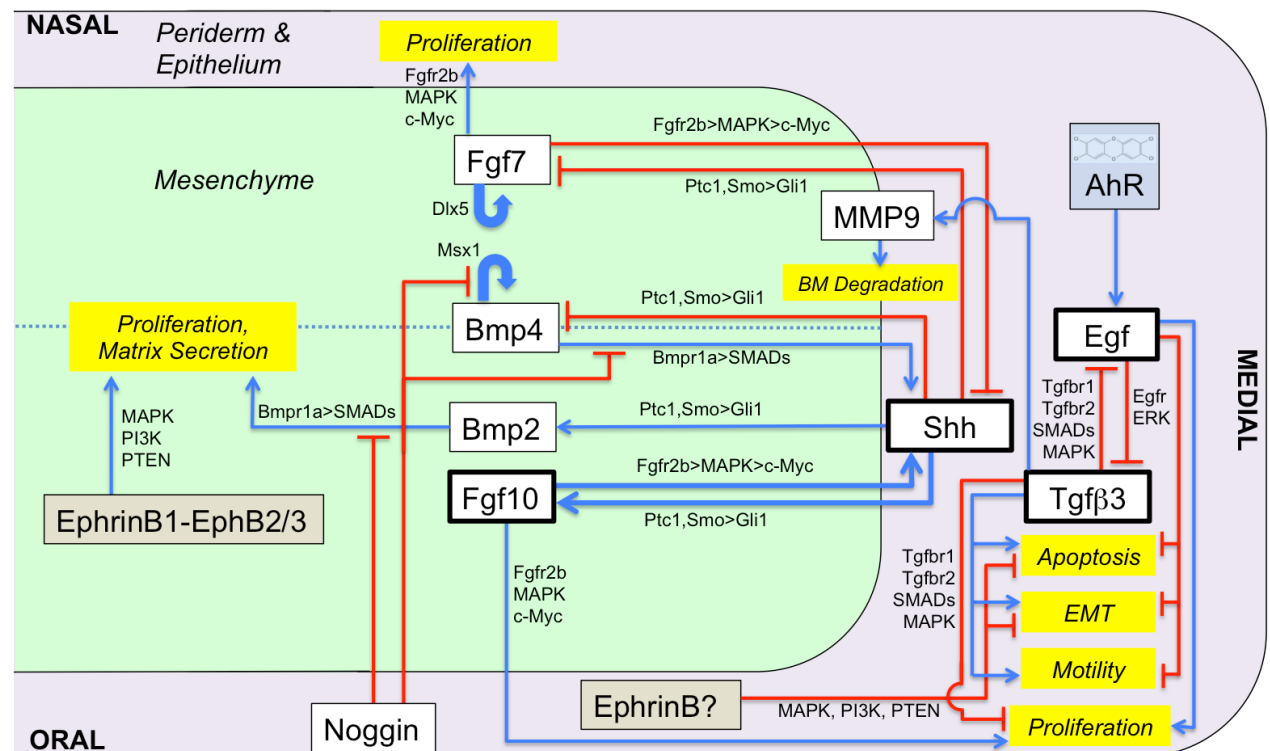
| <b>Androgenization</b><br>( <i>n</i> = 10 sims) | <b>Phenotype (MCS 4000)</b> |               |                | <b>Closure Index</b> |
|---|-----------------------------|---------------|----------------|----------------------|
|   | <u>Septation</u>            | <u>Fusion</u> | <u>Conden.</u> |                      |
| 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                 |



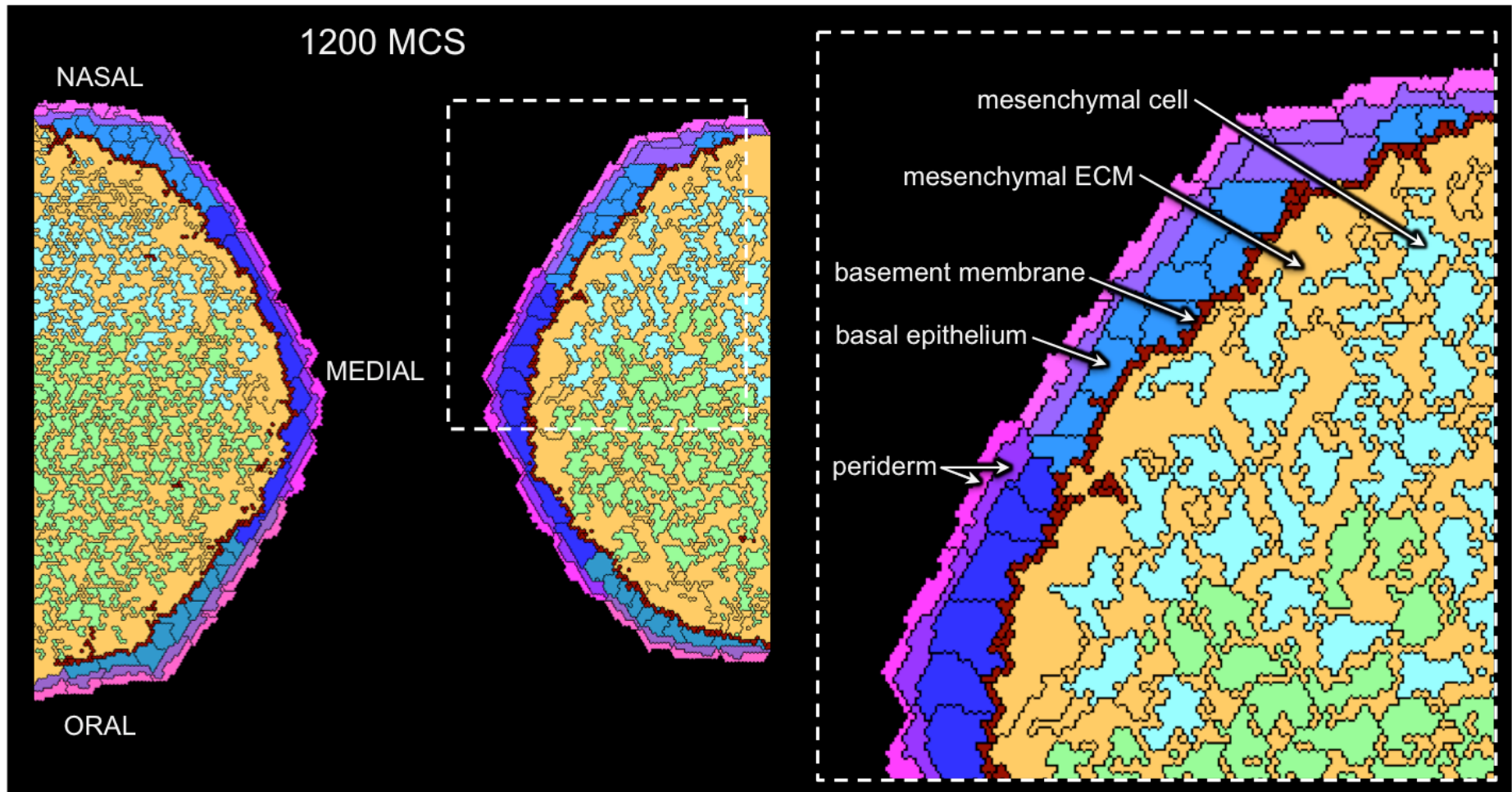
# Modeling Palatal Development

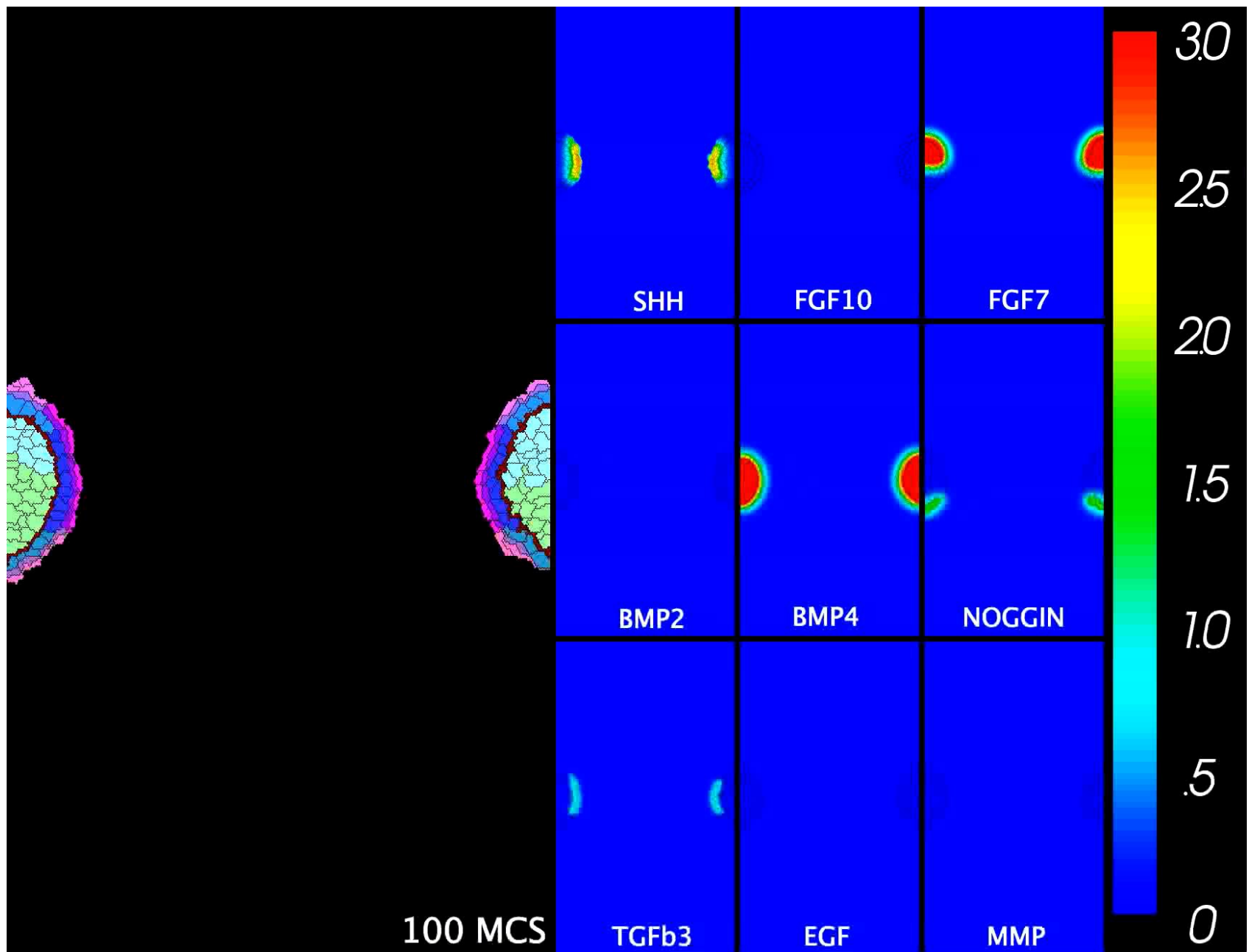


- E12.5 initial outgrowth of palatal shelves
- E13.5 expansion alongside the tongue
- E14.5 elevate, meet, and adhere at medial edge
- E15.5 fusion complete, mesenchymal confluence
- E16.5 osteogenic differentiation



# Modeling Palatal Development

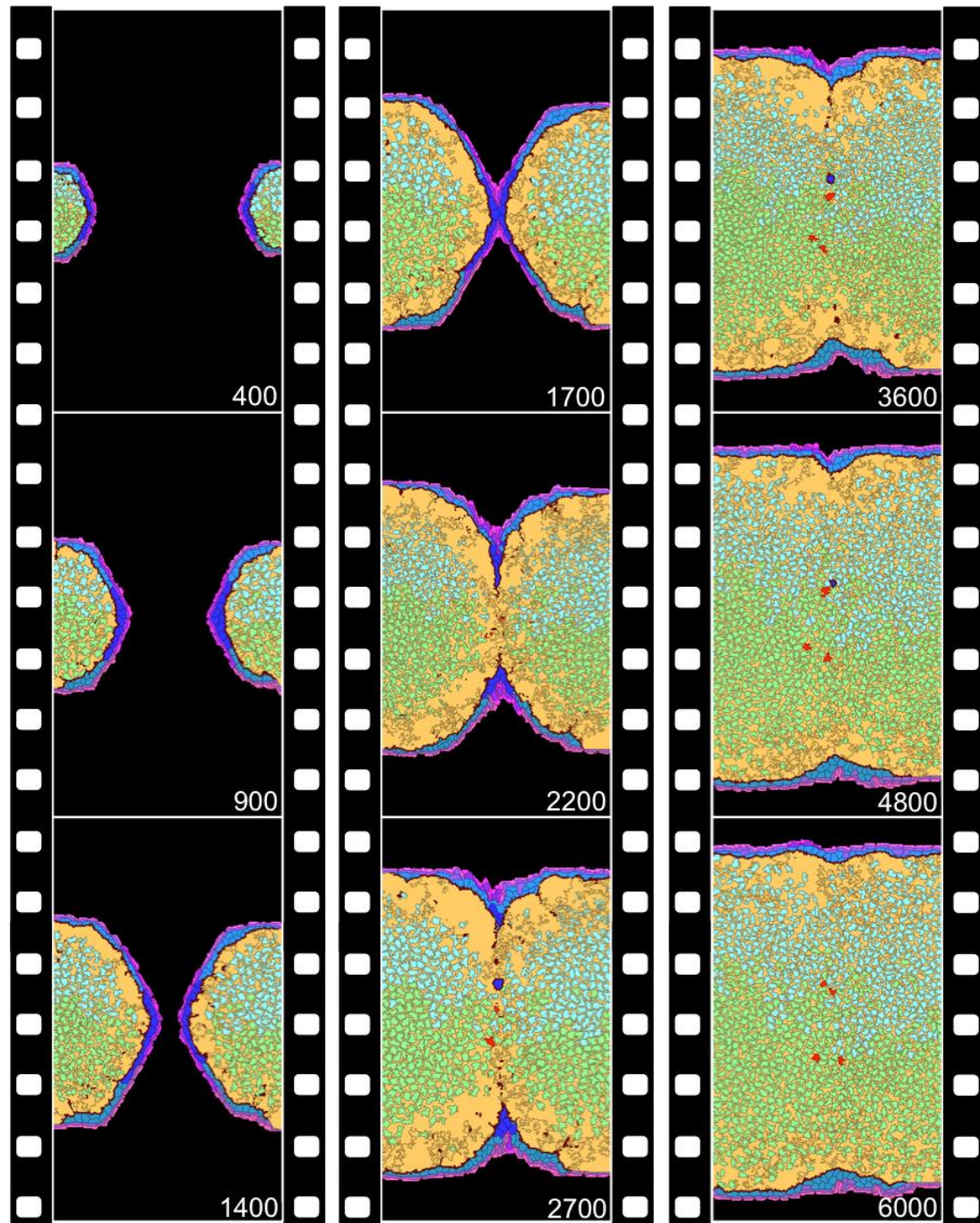
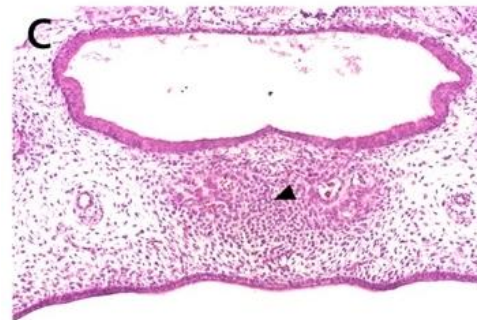
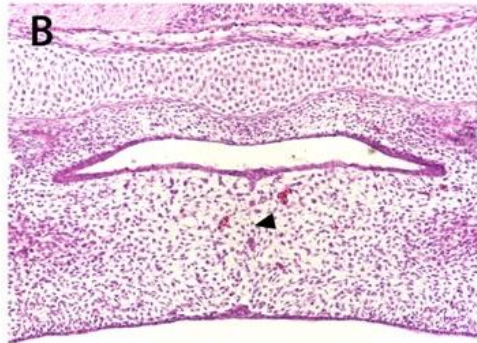
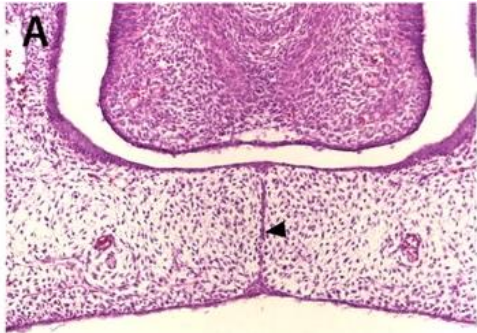






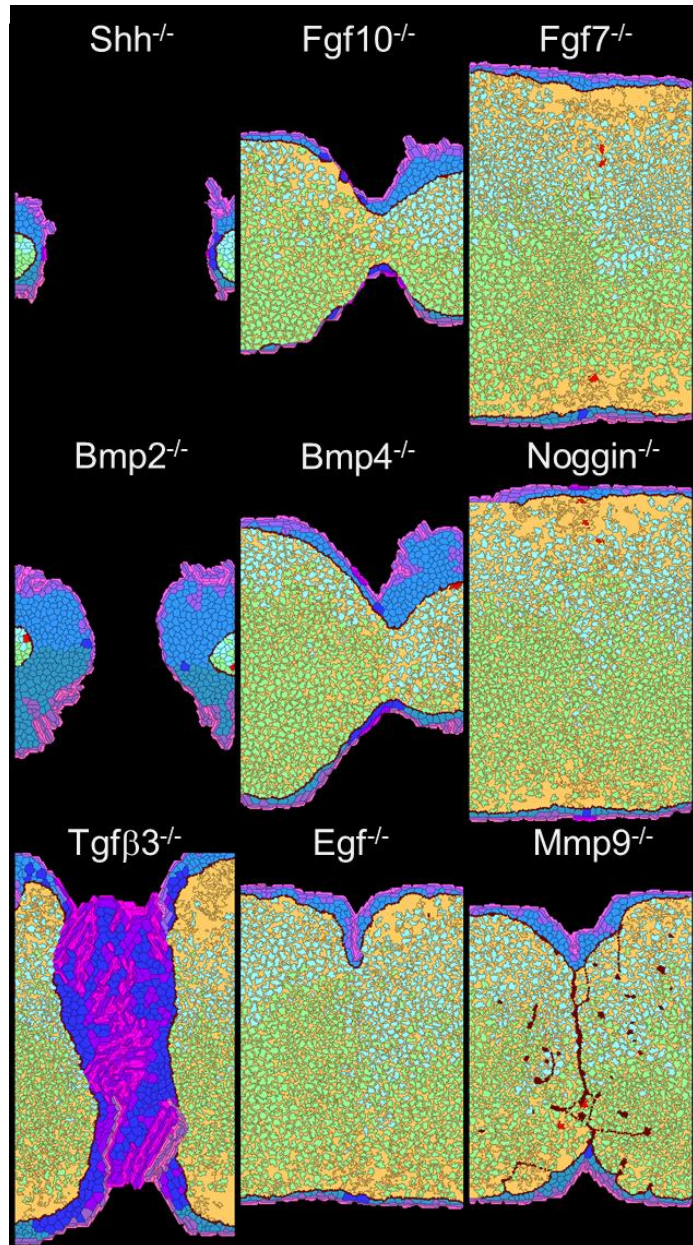
# ABM for Fusion

*Jin and Ding (2006) Development*





# Hacking the Control Network: *in silico* knockouts



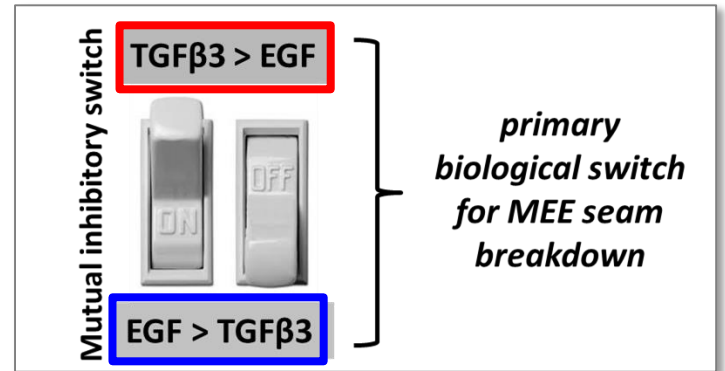
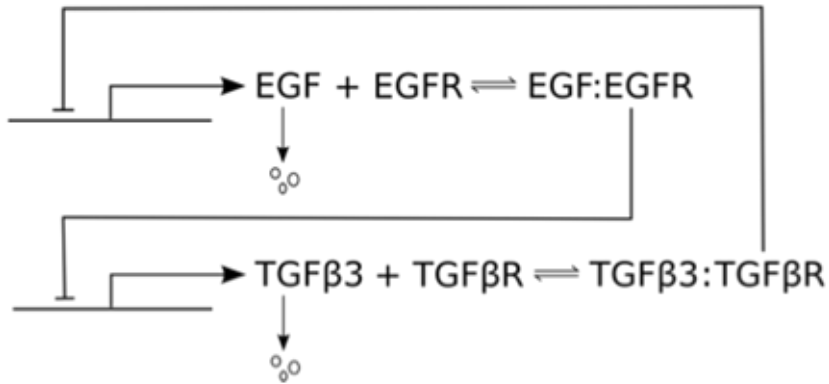
## Outgrowth to MEE contact (MCS 200-2000)

- SHH emanating from MEE is the primary driver of mesenchymal proliferation and ECM production.
- FGF10, BMP2, BMP4 are main effectors in the mesenchyme and feedback onto the epithelium.
- FGF7, Noggin are negative effectors in the mesenchyme, and feedback onto epithelium.

## MES breakdown (MCS 2000-3000)

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

# TGF-EGF switch as a molecular target

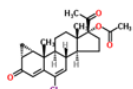


- MEE expression of **TGFβ3** peaks just before adhesion, whereas **EGFR** expression drops (e.g., switch is flipped).
- Several teratogens ↑EGFR expression, induce MEE proliferation, and disrupt fusion (e.g., switch not flipped): Retinoic acid, Hydrocortisone, TCDD [Abbott 2010].



# ToxCast profiling of 63 cleft palate teratogens

Cyproterone acetate



Chemical

Cleft palate

Gene score NR3C1  
(glucocorticoid  
receptor)

Triamcinolone

Cyproterone acetate

1

4.74

Chemical

Cleft palate

Gene score RARG  
(retinoic acid  
receptor gamma)

Aldrin



Endrin



Aldrin

1

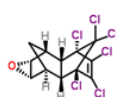
11.6

Endrin

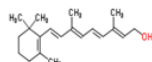
1

11.9

Dieldrin



Retinol



Dieldrin

1

12.0

Retinol

1

13.5

Trans-retinoic acid

1

8.2

Tributyltin chloride

1

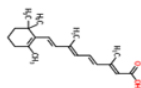
8.6

Bromuconazole

0

10.8

Trans-retinoic acid



Paclobutrazol  
Monobutyl phthalate  
Propiconazole  
Flusilazole

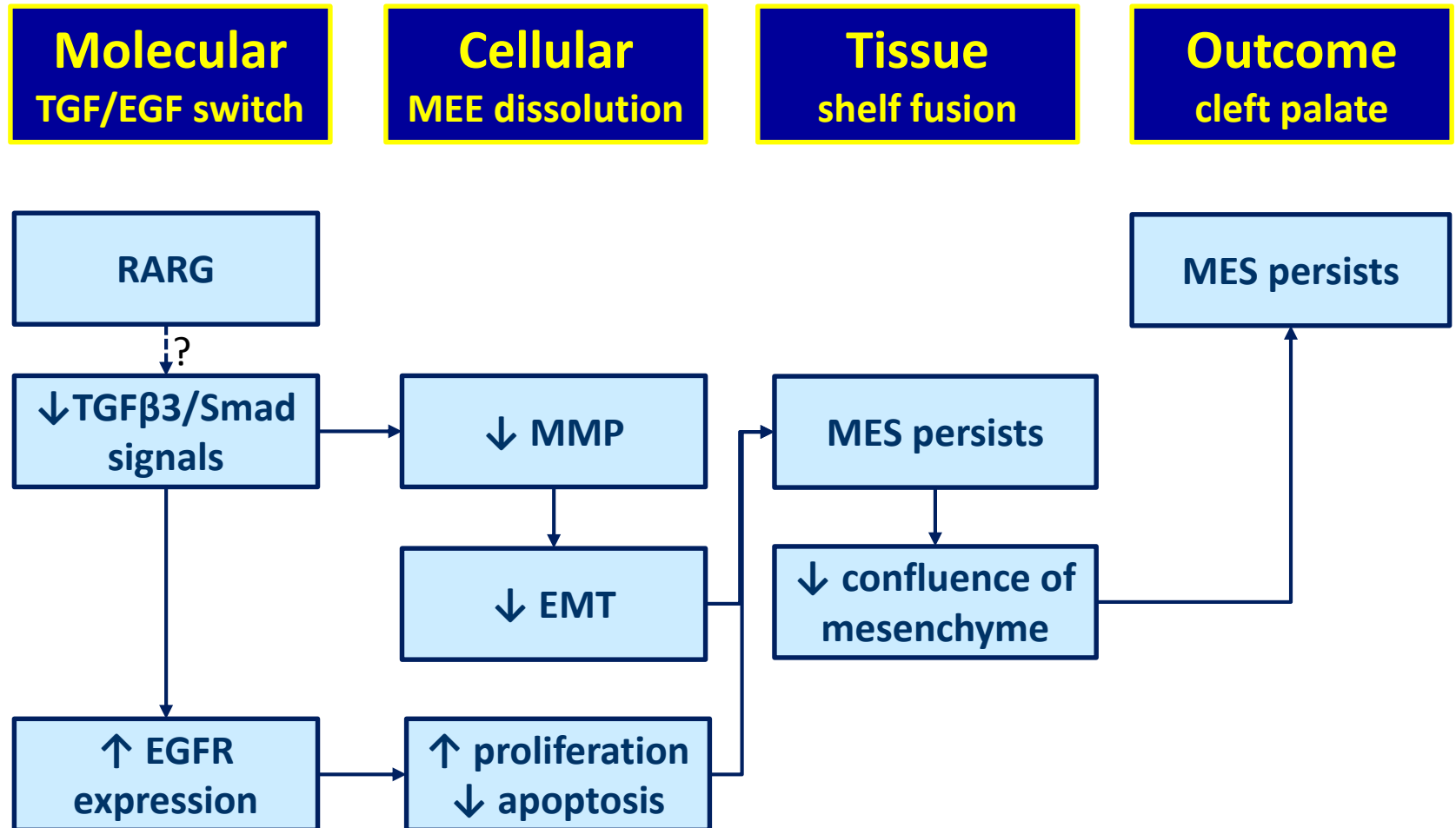
Aldrin  
Endrin  
Dieldrin  
Retinol  
trans-Retinoic acid  
Aspirin

0.00

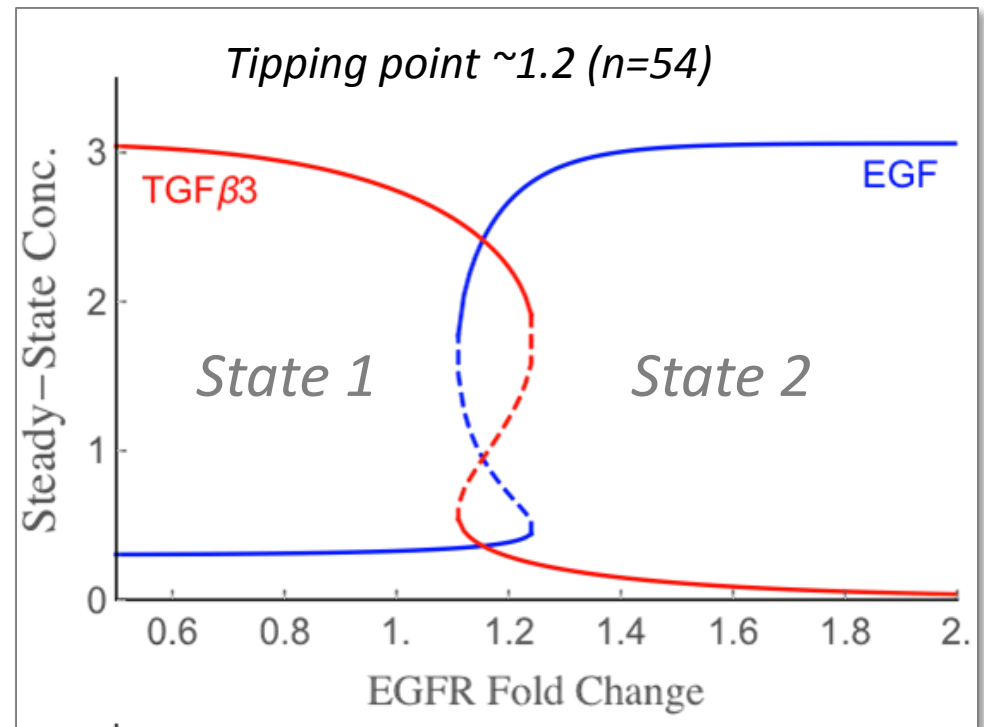
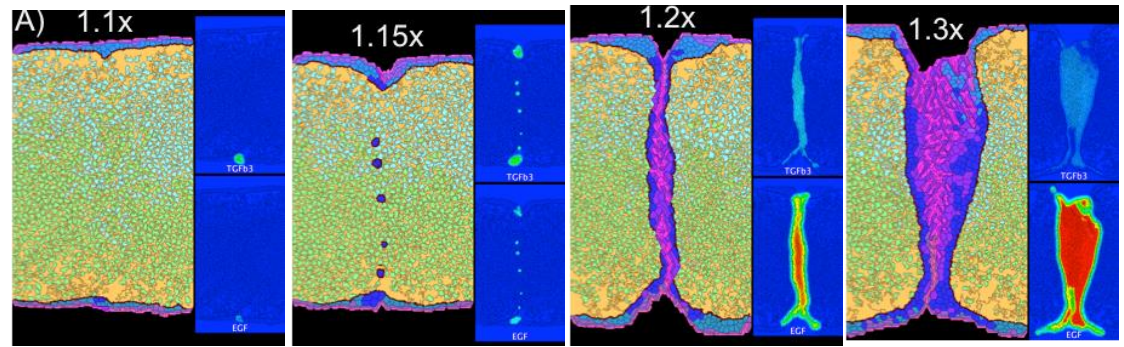
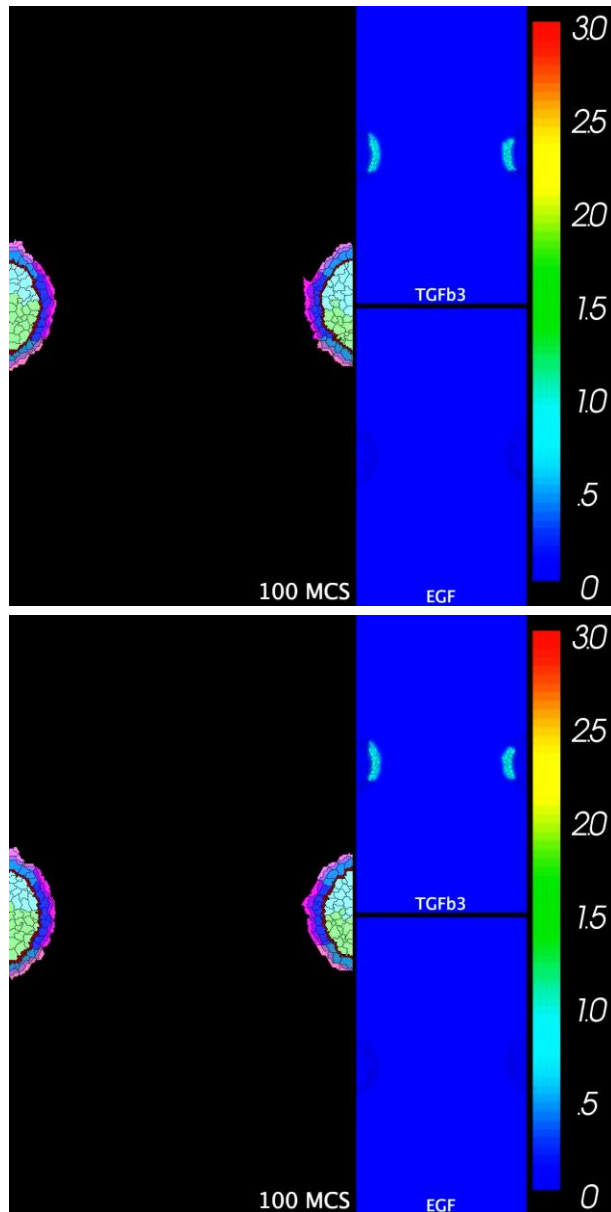
7.40

14.80

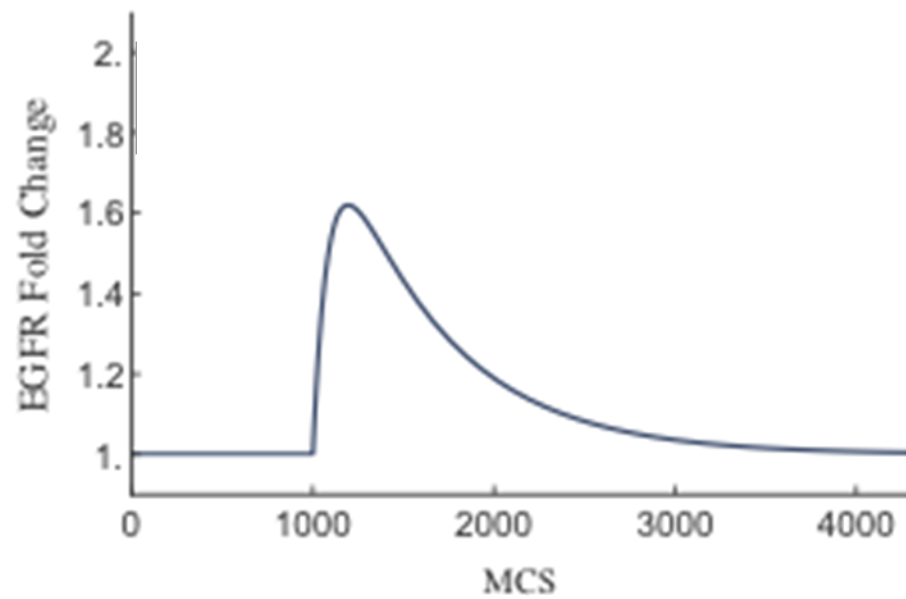
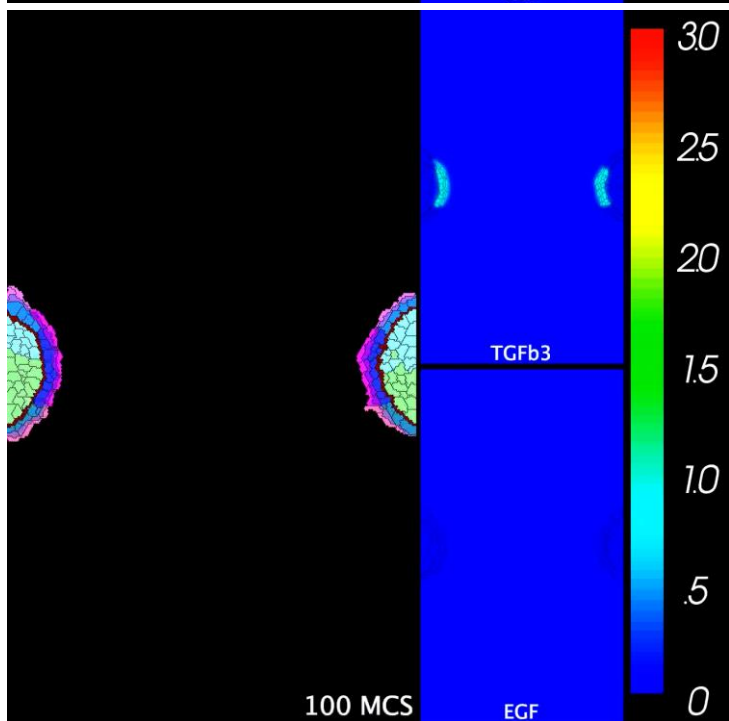
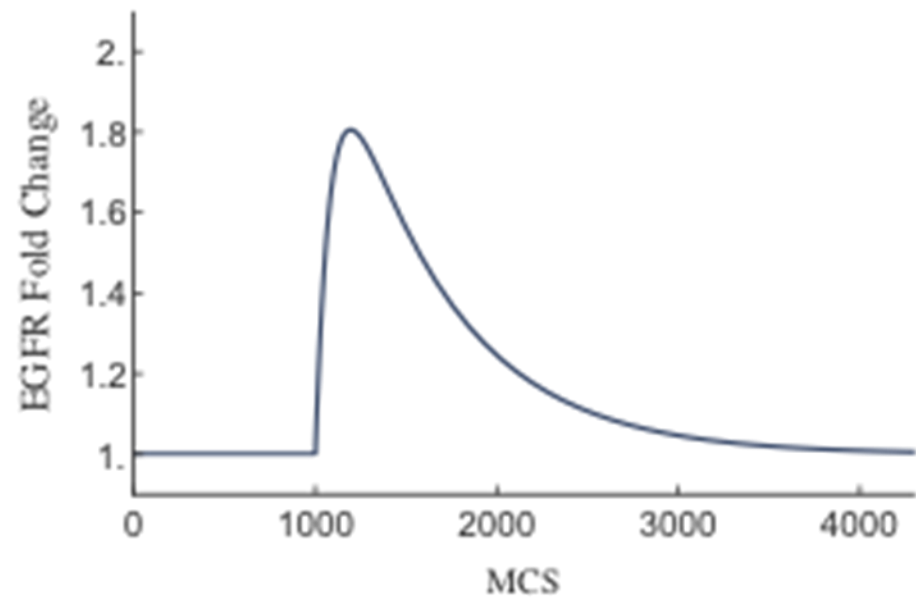
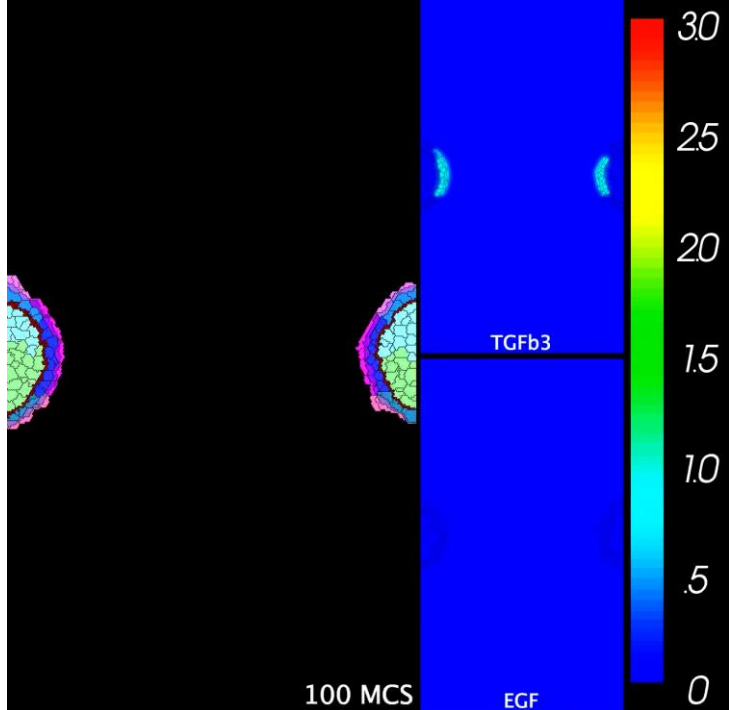
# Putative AOP for Retinoic acid *(one of several!)*



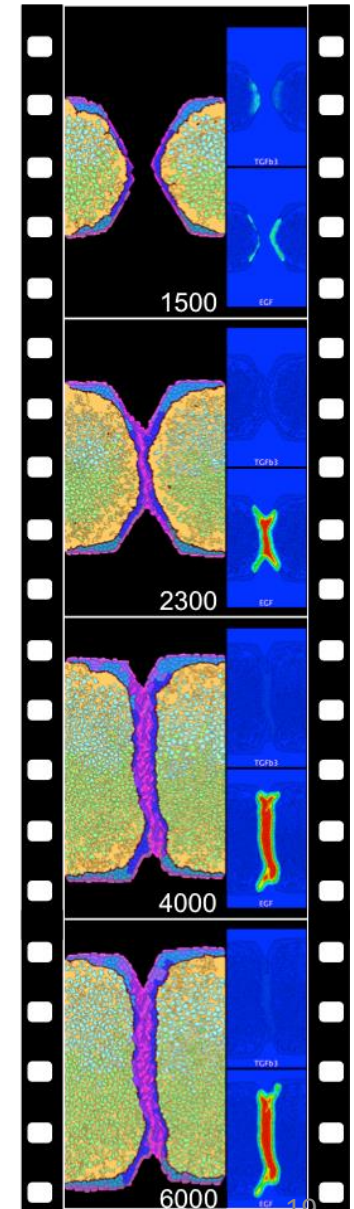
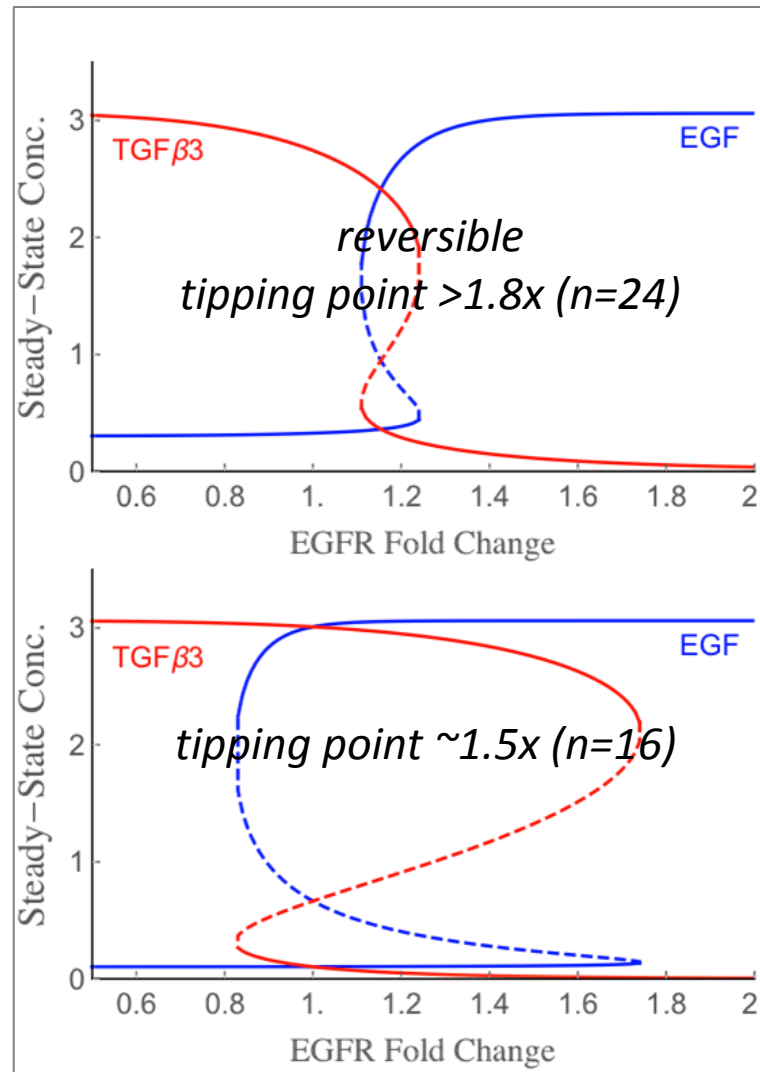
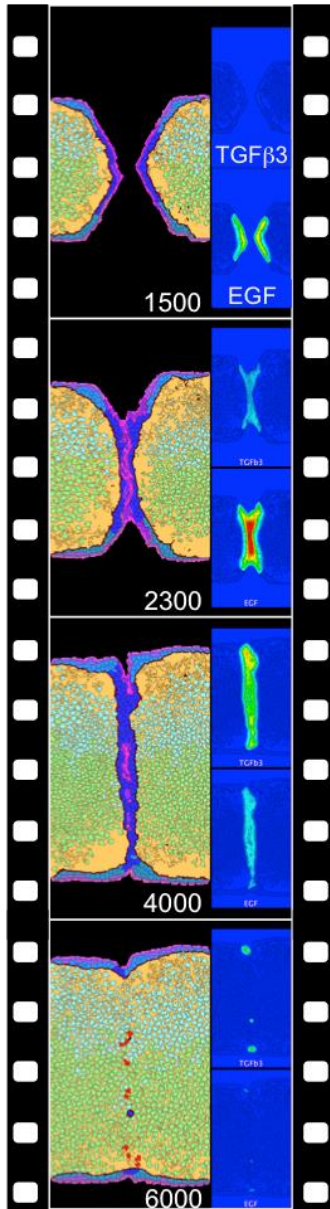
# TGF-EGF circuit dynamics



# Acute Exposure

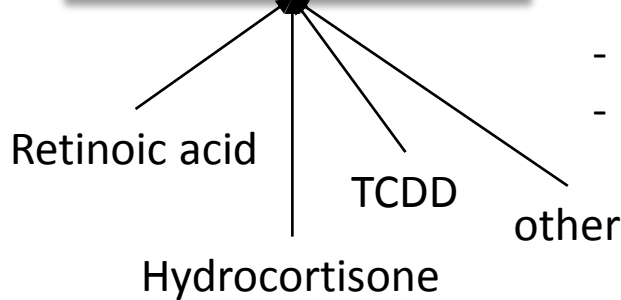
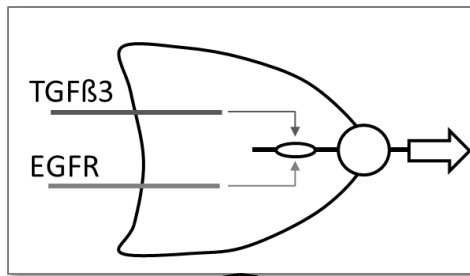


# Impact of the bifurcation zone (acute exposure)



# TGF-EGF switch (predicted impact)

## Molecular TGF/EGF switch



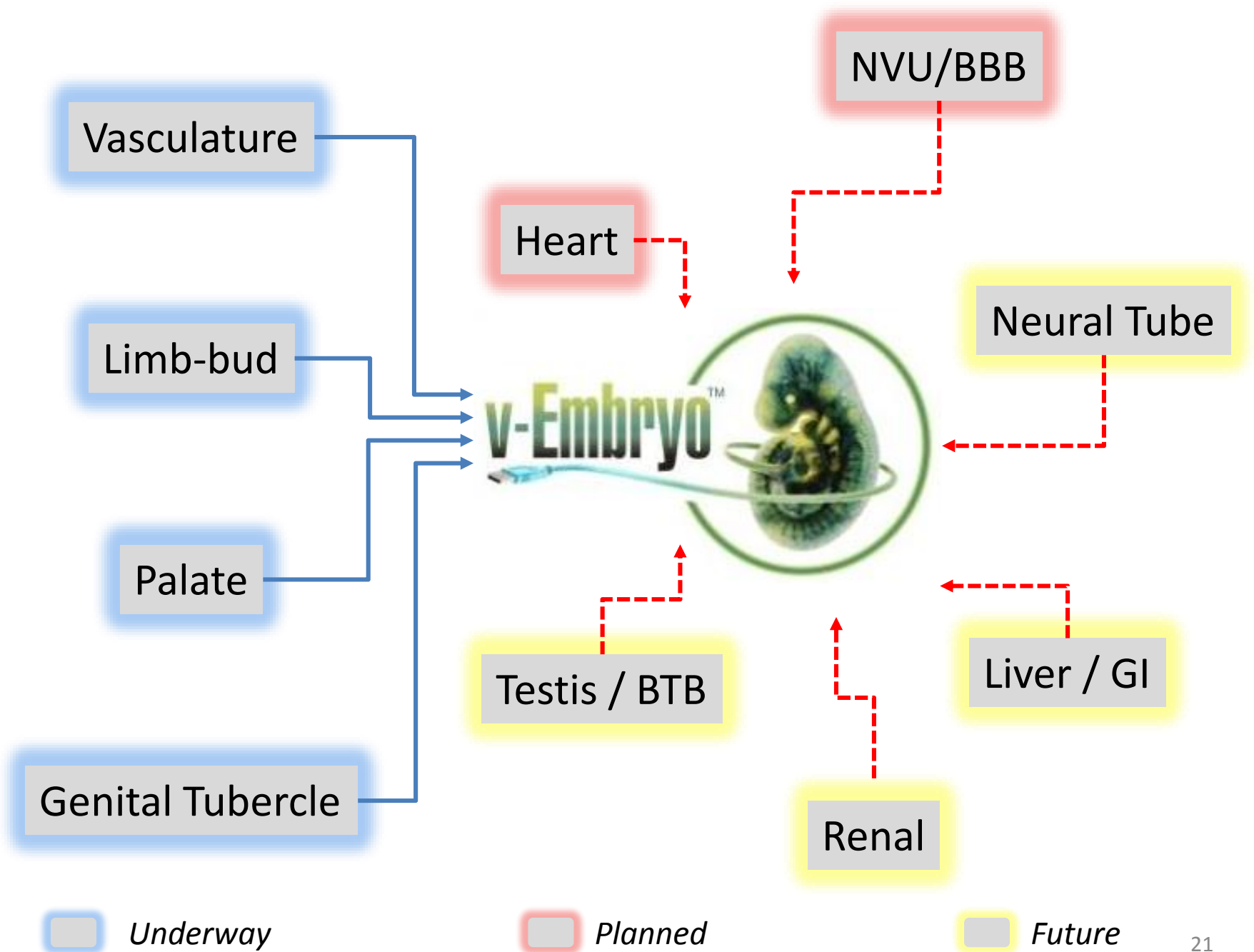
## Chronic exposure scenario

- low hysteresis system tips at  $\sim 1.2\times$  EGFR (n=54)
- high hysteresis system tips at  $\sim 1.2\times$  EGFR (n=32)
- width of bifurcation zone does not seem to matter

## Acute exposure scenario

- low hysteresis system tips at  $>1.8\times$  EGFR (n=24)
- high hysteresis system tips at  $\sim 1.5\times$  EGFR (n=16)
- more canalization with a narrow bifurcation zone





# Special Thanks

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- W Murphy – U Wisconsin / STAR
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- D Belair – NHEERL / TAD
- Sid Hunter – NHEERL / ISTD
- Max Leung – NCCT (now U Pittsburgh)
- Jill Franzosa – NCCT (ORISE)
- Nicole Kleinstreuer – NCCT (now NIEHS/NTP)
- Nisha Sipes – NCCT (now NIEHS/NTP)
- Richard Spencer – Leidos / EMVL
- Nancy Baker – Leidos / NCCT
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- B Cai – Vala Sciences
- D Rines – Vala Sciences
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- J Glazier – Indiana U / STAR
- Shane Hutson – Vanderbilt U / STAR
- K Saili – NCCT
- T Zurlinden - NCCT



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**National Center for Computational Toxicology**