

### EXHIBITION SESSION, SEURAT PROGRESS MEETING, December 2015 - Brussels

# Developmental Systems Toxicology: computer simulation in a 'Virtual Embryo' prototype



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# Can a computer model of the developing embryo translate molecular and cellular disruptions into a prediction of dysmorphogenesis?

and if so ...

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

e.g., chemicals, doses, non-chemical stressors, mixtures, stages, sensitive subpopulations, ...

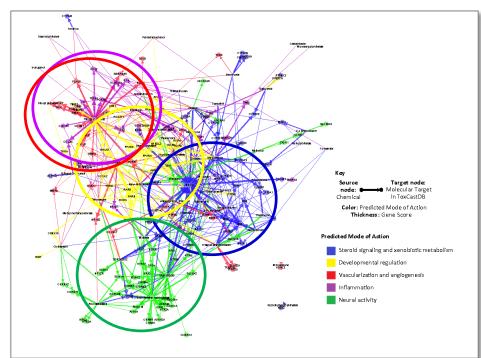


#### **Strategy**

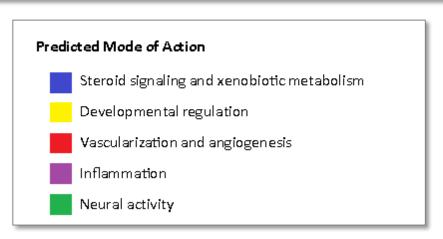
- Build spatially-explicit agent-based models (ABMs) of normal embryology that can simulate developmental systems dynamics.
- Seed computer models with 'big-data' profiles from ToxCast and set up complex and theoretical pathway-level scenarios.
- Run the computer models in parallel to simulate how molecularcellular dysfunctions could impact tissue structure and function.
- Compare computational outcomes with experimental results to reveal inconsistencies in our understanding of the system.
- Eventually can become part of an integrated testing strategy to address systems-level behaviors not easily studied experimentally.

### **Bipartite Network:** translates chemical-assay bioactivity profiles into predicted mode-of-action

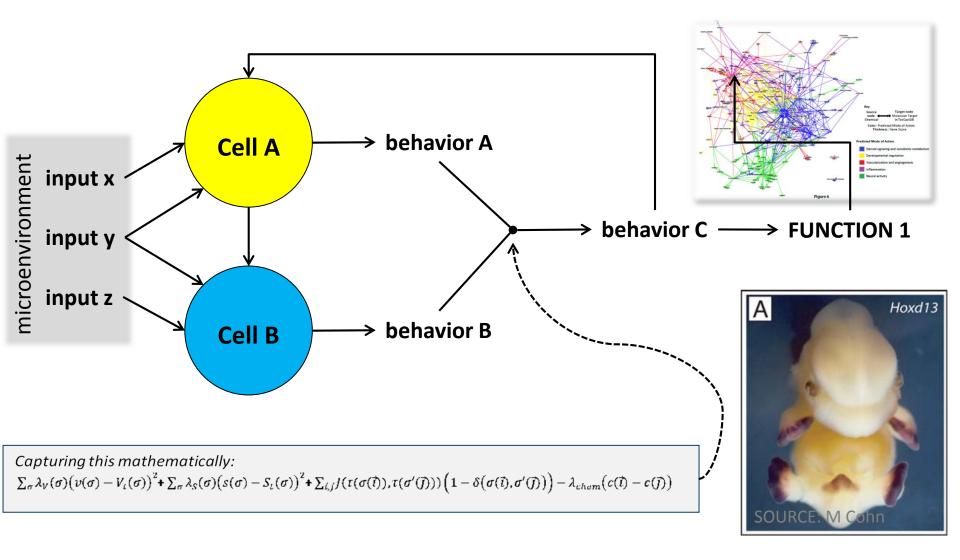
- Bipartite network for 54 ToxCast chemicals that produce male developmental toxicity.
- Functional annotation revealed 4-5 target biological processes (mode-ofaction) from ToxCast assays.



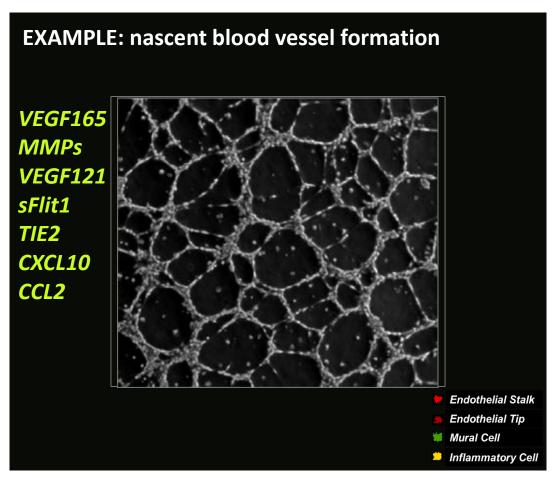
Leung MCK, Phuong J, Baker NC, Sipes NS, Klinefelter GR, Martin MT, McLaurin K, Setzer RW, Darney SP, Judson RS and Knudsen TB (2015) Systems Toxicology of Male Reproductive Development: Profiling 774 Chemicals for Molecular Targets and Adverse Outcomes. <a href="Env Hlth Persp">Env Hlth Persp</a> (accepted).



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



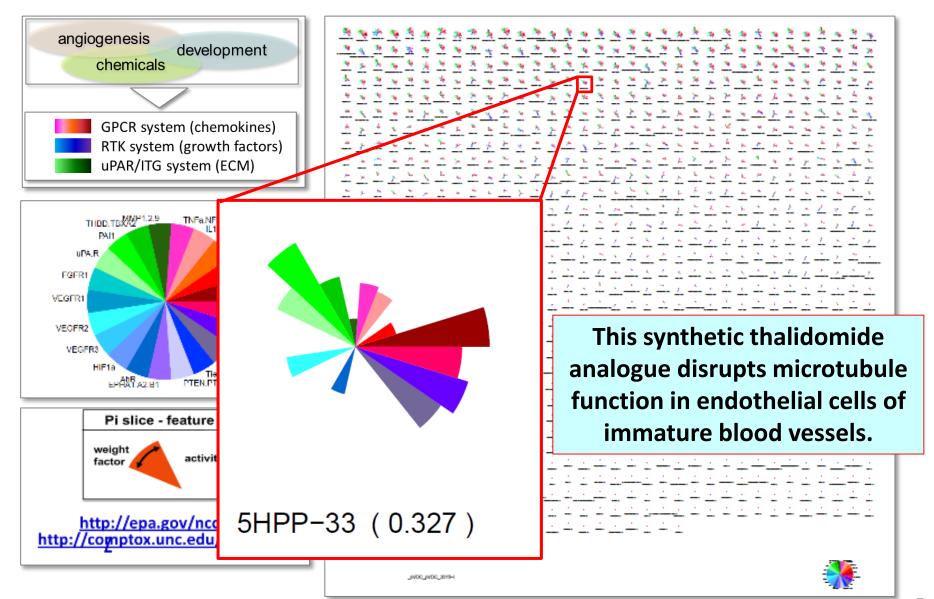
## **Cellular Agent-Based Models (ABMs):** use in multiscale modeling and dynamical simulation



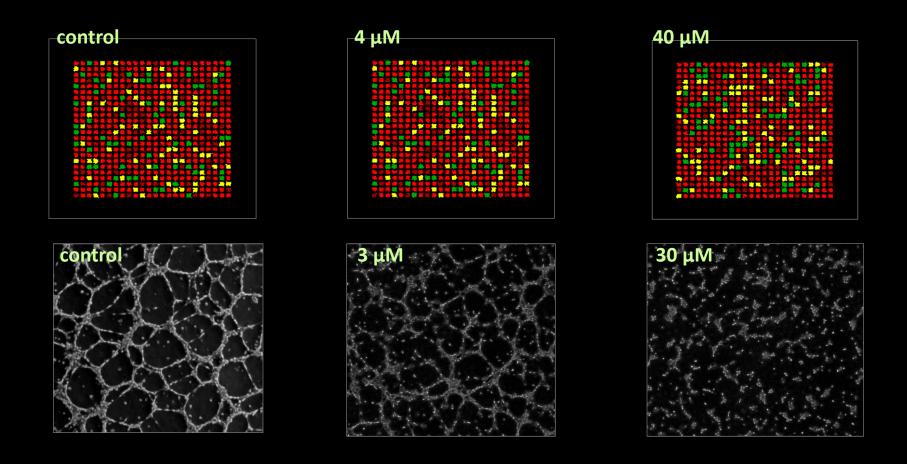
- individual rules are assigned to low-level 'agents' (here = cells)
- agents then interact in a shared environment (CompuCell3D\*)
- running the simulation executes this biology (emergence)
- models run differently each time (stochastic)
- each run reveals one possible solution (outcome)

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

#### **ToxCast:** chemicals sorted by predicted vascular disruption (pVDCs)

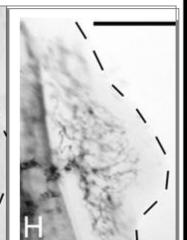


### 5HPP-33 concentration response predicted in silico from ToxCast and demonstrated in vitro with a human endothelial cell assay



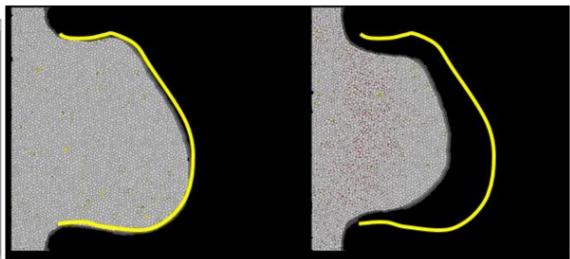
#### 'Virtual Embryo' prototype of early limb-bud outgrowth

Thalidomide disrupts immature blood vessels *Therapontos et al. (2009)* 



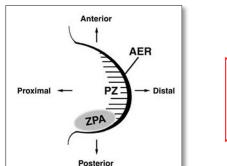
normal



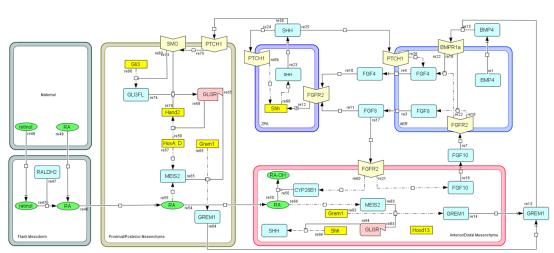


This occurs as the organizing centers are established

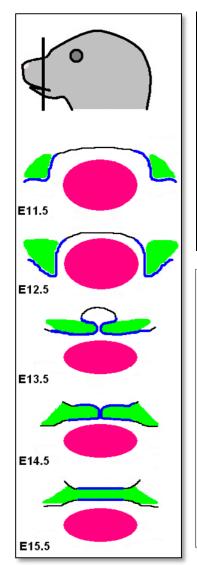
Dewoskin et al. (in preparation)

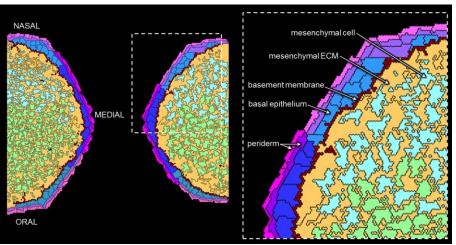


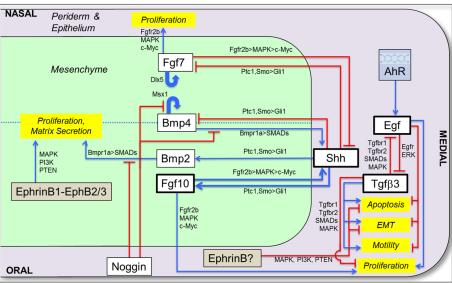


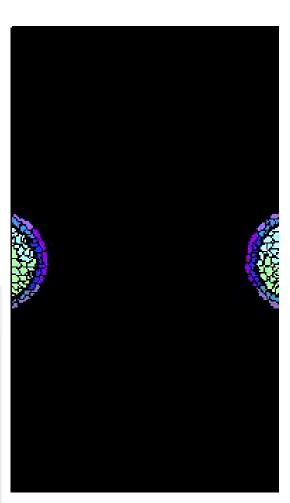


## Palatal Closure: ABM can probe quantitative relationships during Medial Edge Epithelium (MEE) fusion and seam breakdown.



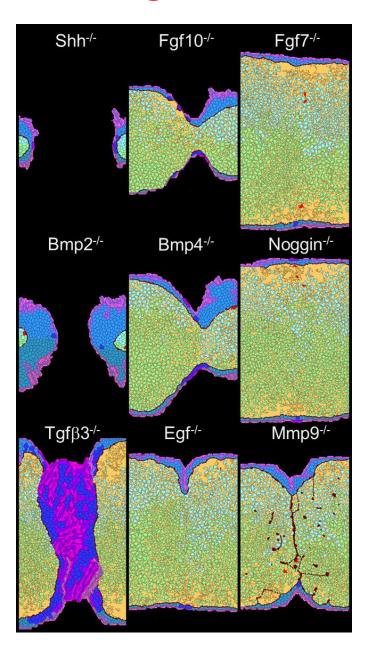




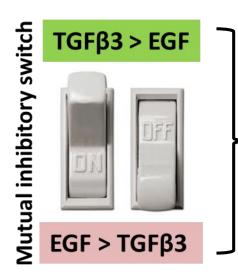


Hutson et al. (in preparation)

#### **Hacking the Control Network**

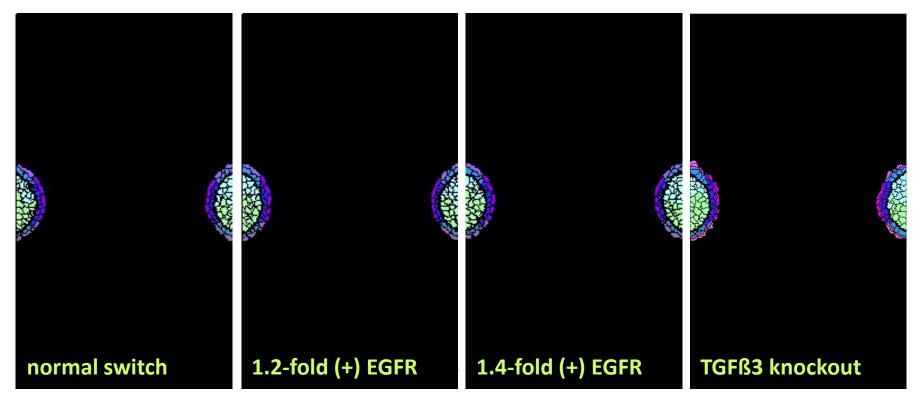


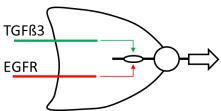
- in silico knockouts of elements in the underlying signaling network
- predicted impacts on MEE contact and seam breakdown (critical events)



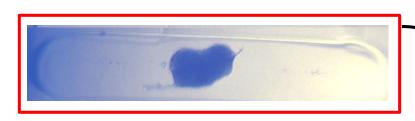
primary biological switch for MEE seam breakdown

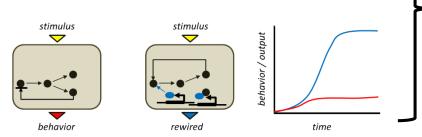
$$k_{EGF} = 15 + \text{Random}[0,1] - 12 \frac{[Tgfb3]^4}{[Tgfb3]^4 + AC_{50}^4} + k_{EGF-AhR}$$





| TGFß3 | EGFR | СР |
|-------|------|----|
| 1.0   | 1.0  | 0  |
| 0     | 1.0  | 1  |
| 1.0   | 1.2  | 0  |
| 1.0   | 1.4  | 1  |
| 1.0   | 1.5  | 1  |



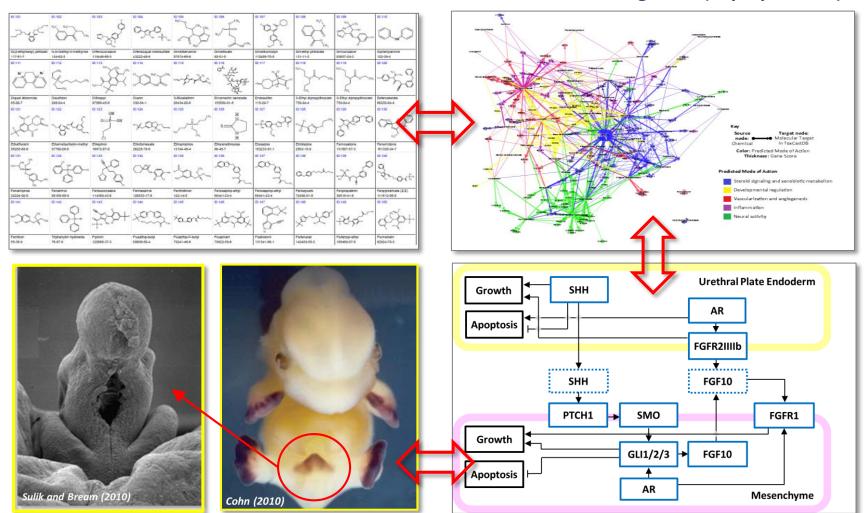


Validate with fusion-competent human iPSC-microsystems and rewire switching

## How do chemical-bioactivity <u>bipartite networks</u> interact with <u>control networks</u> in disrupting development?

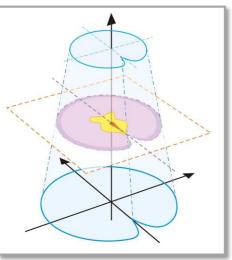
#### EXAMPLE: hypospadias, a urethral closure defect

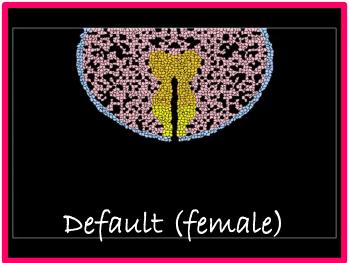
Leung et al. (in preparation)



#### **Cell ABM for Genital Tubercle (GT) development**



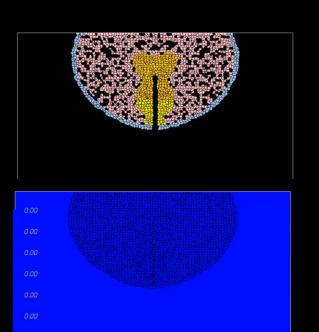




Embryonic GT - Abstraction

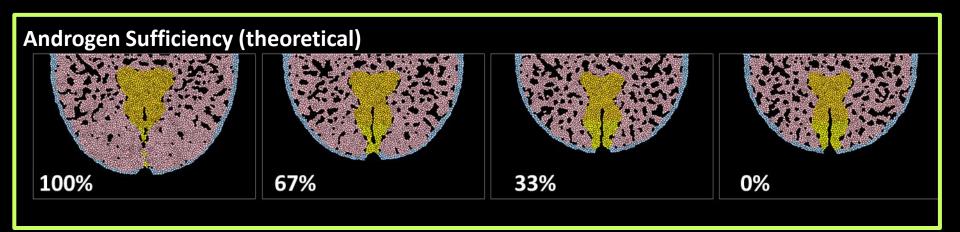
Androgen production by fetal testis triggers sexual dimorphism of the GT into male or female phenotypes.

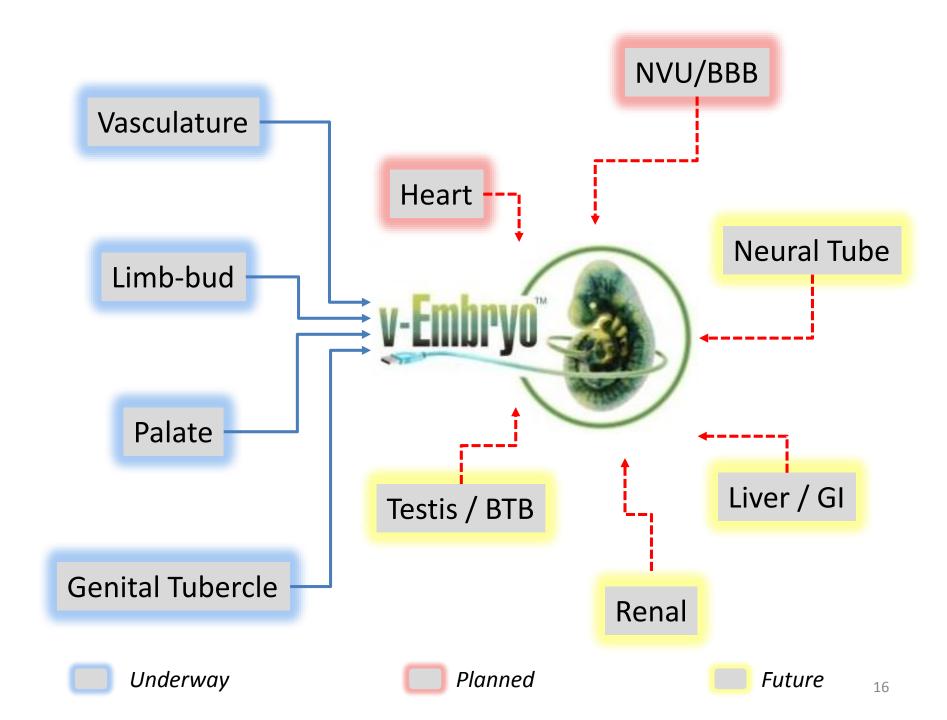




Apoptosis

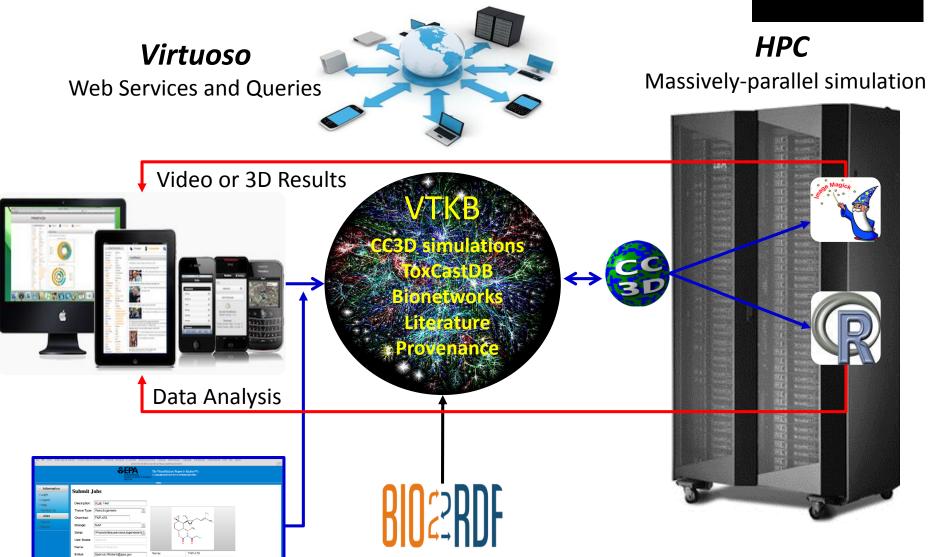
- Endodermal apoptosis & Mesenchymal (preputial) proliferation drives closure and centralization of the urethral rudiment.
- Disruption of SHH, FGF10, or AR signaling leads to closure defect (hypospadias).





### **Virtual Tissues Laboratory System**





#### **Special Thanks**

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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



**National Center for Computational Toxicology**