



Computational Modeling of the Neurovascular Unit to Predict Microglia Mediated Effects on Blood-Brain Barrier Formation

Todd J. Zurlinden¹, Katherine S. Saili¹, Richard S. Spencer²,
Nancy C. Baker³, Thomas B. Knudsen¹

¹US EPA/ORD, National Center for Computational Toxicology (NCCT), Research Triangle Park, NC

²ARA, Research Triangle Park, NC

³Leidos, Research Triangle Park, NC

Teratology Society's 58th Annual Meeting
Graduate Student/Postdoctoral Fellow Platform Session

June 24, 2018

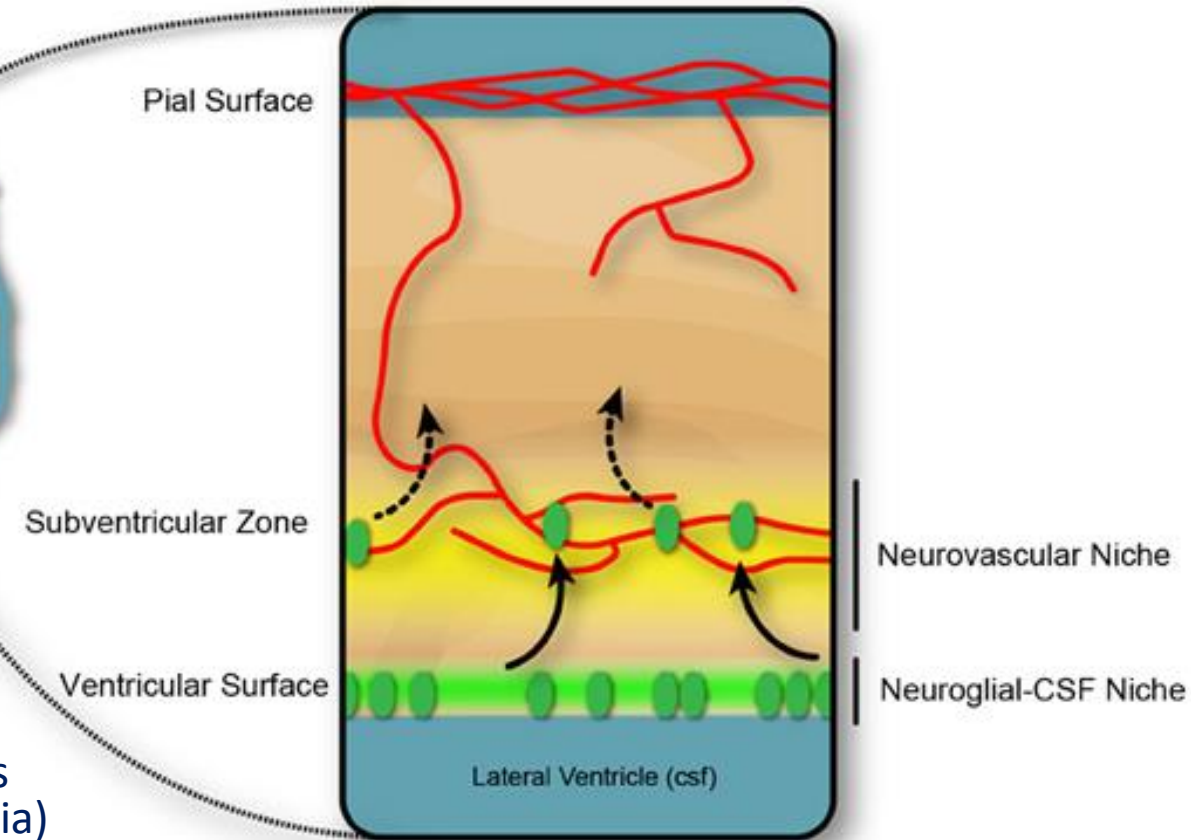
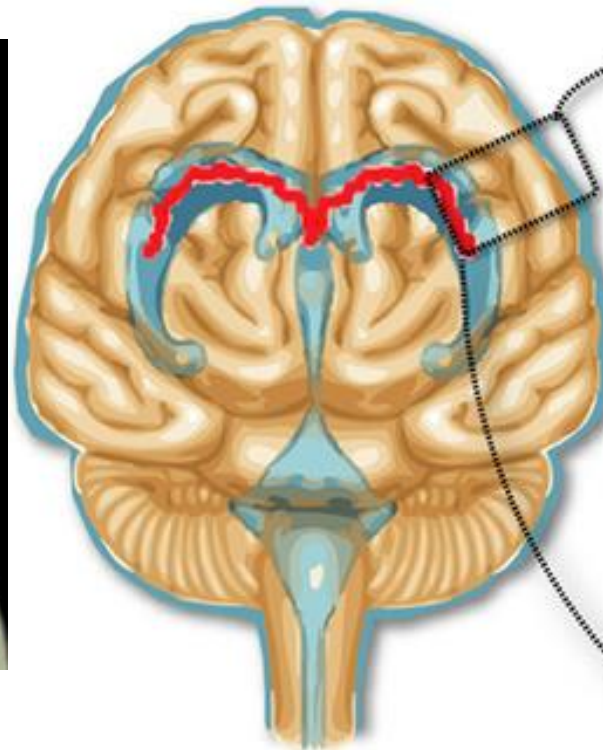
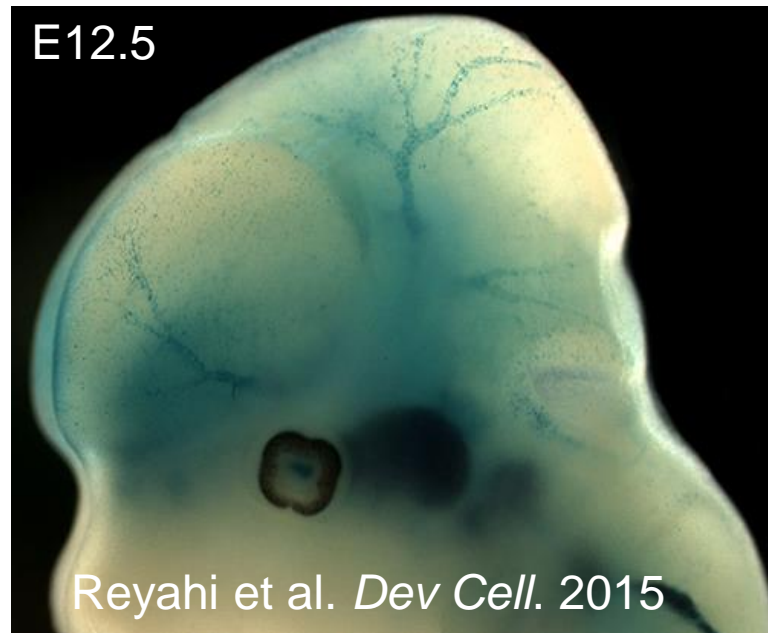
U.S. Environmental Protection Agency

Disclaimers

- The authors have no financial or other interests which pose a conflict of interest.
- This research was funded by the US EPA.
- Some of the data presented here were collected by Vala Sciences Inc. or ArunA Biomedical under contract to the US EPA.
- Some of the data presented here were collected by the University of Wisconsin – Madison H-MAP Center or Finnish Center for Alternative Methods (FICAM) under cooperative research agreements with the US EPA.
- The views expressed in this presentation do not reflect US EPA policy.

Computational neurovascular unit (cNVU) focus

Chemical signals from the neuroepithelium (eg, VEGF) initiate brain angiogenesis via sprouting from the PNVP.

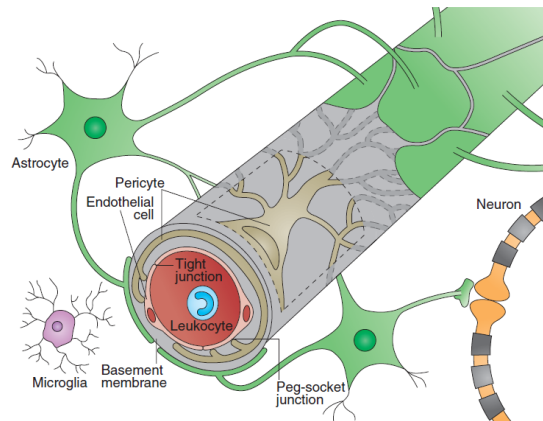
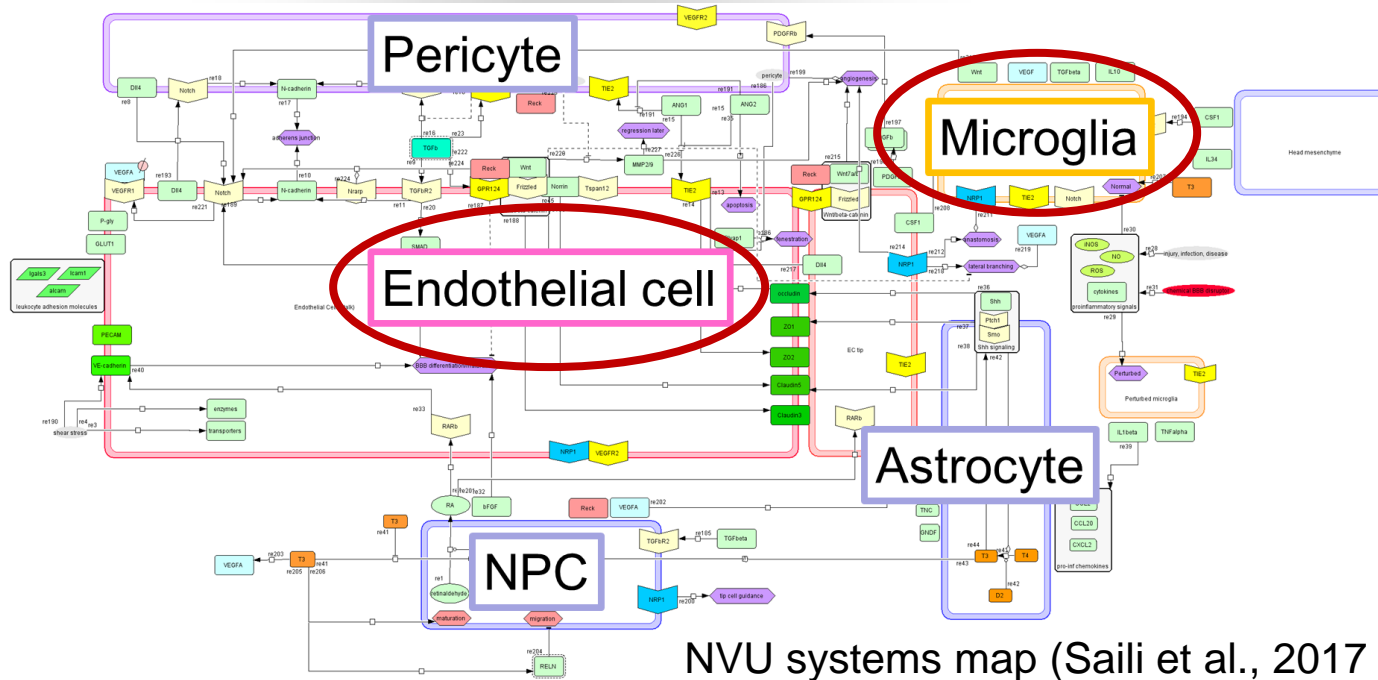


Neurovascular unit (NVU): The functional interface that develops between vascular (endothelial, pericytes) and neural (neurons, glia) compartments of the embryo-fetus.

Hypothesis: Chemical disruption of NVU development adversely impacts blood-brain-barrier (BBB) formation leading to abnormal brain development and function.

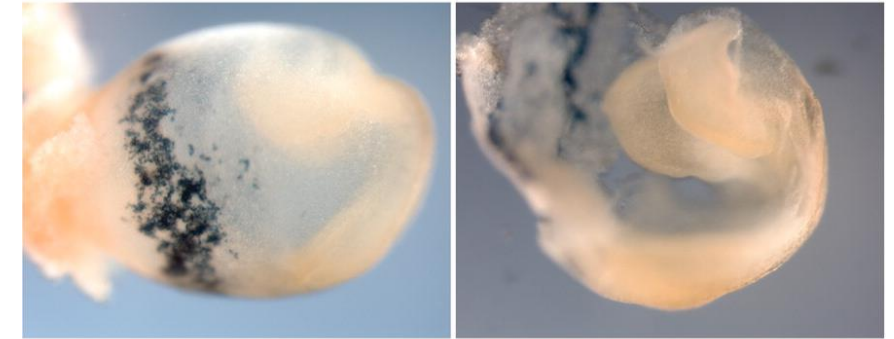
Stolp wt al., *Front. Integr. Neurosci.* 2013

Cell-Cell interactions of the NVU

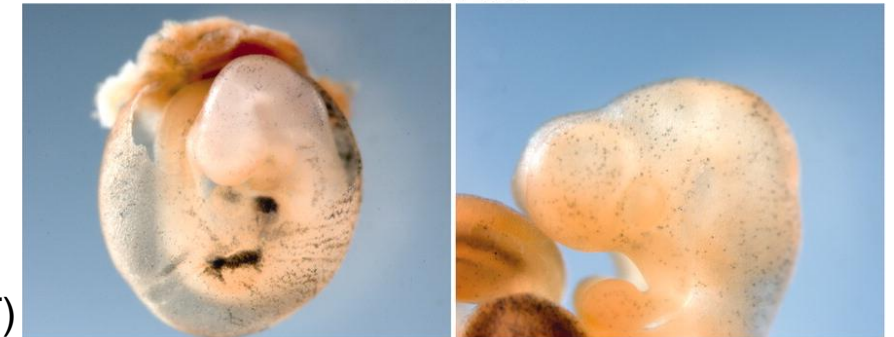


- Microglia, resident macrophages of the brain.
- During development...
 - Orchestrate neurovascular ramifications, surveillance of local injury where hyperactivation can invoke an adverse neuroinflammatory response
 - Are they mediators of developmental toxicity?

E8.25-E8.5

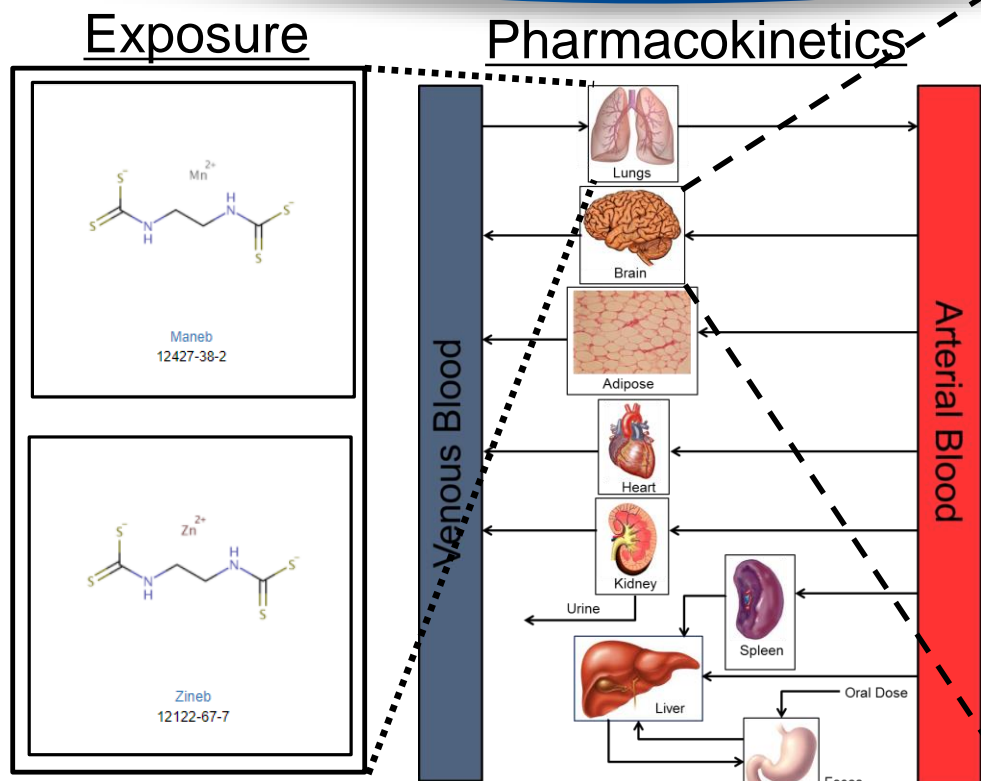


E9.25-E9.5



Ginhoux et al., *Science*, 2010

Computational source-to-outcome framework

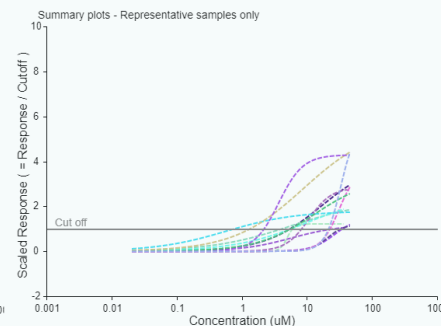
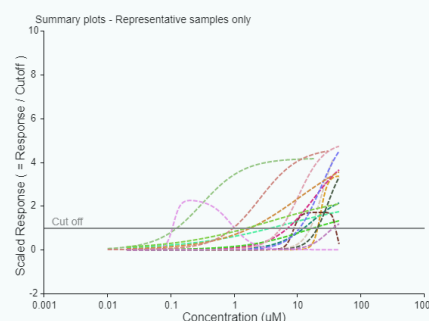


Translation

In vitro assays

~600 Cell & biochemical assays

~1,000 Chemicals



Pharmacodynamics

- Apoptosis
- Blood-brain barrier integrity
- Cell growth
- Dysmorphogenesis
- Endothelial cell migration

Utilize screening techniques to predict a concentration-dependent disruption of neurovascular development.

In vitro: Characterize chemical effects on cell-based phenotypes.

In silico: Use mechanistic information to translate HTS data into cell/tissue predictions.

Cell Agent-Based Modeling

- **Agent-Based Modeling and Simulation (ABMS):** a heuristic approach to reconstruct tissue dynamics using knowledge of biochemistry and cell-by-cell interactions.
 - Program each *agent* (cell) to follow specific rules
 - Interactions of agents gives rise to *emergent features* (phenotypic outcomes)
 - Qualify emergent feature with experimentally derived phenotypes (tissue level morphology)
 - Make toxicodynamic predictions by integrating biological knowledge & high throughput data
- **CompuCell3D*:** open source modeling environment
 - Rules (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.
 - Methodology applied to past systems: vasculogenesis, genital tubercle, palate fusion, etc.

Cell-signaling network

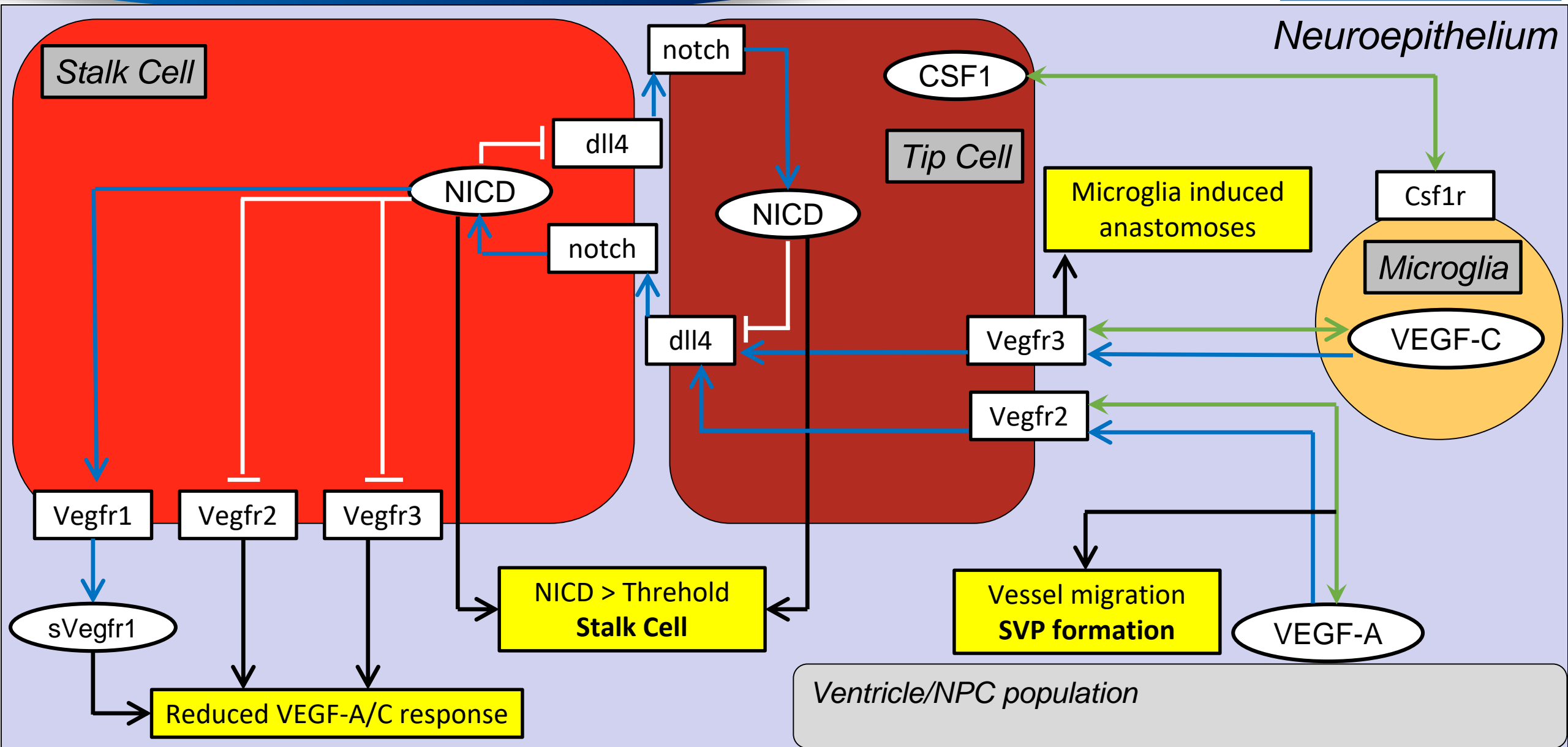
Cell type

Ligand

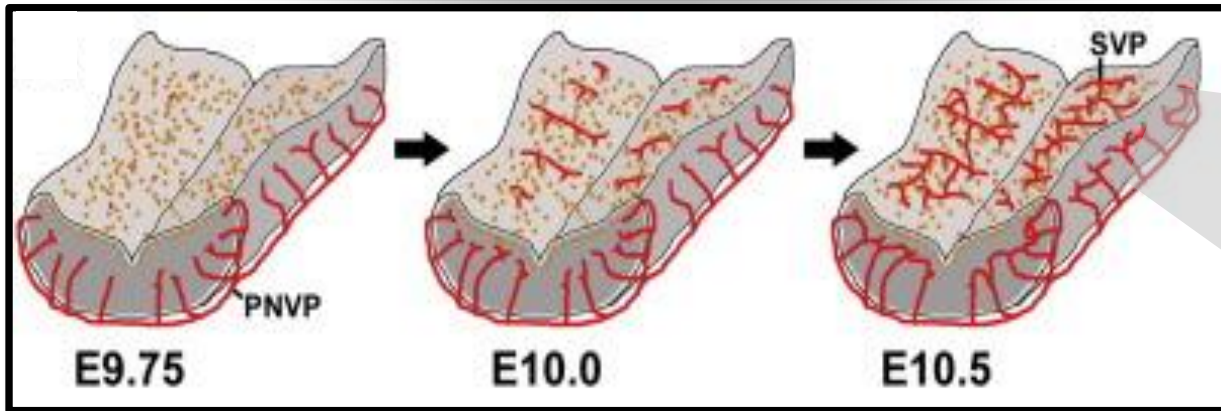
Chemotaxis
Agonist
Antagonist

Phenotype

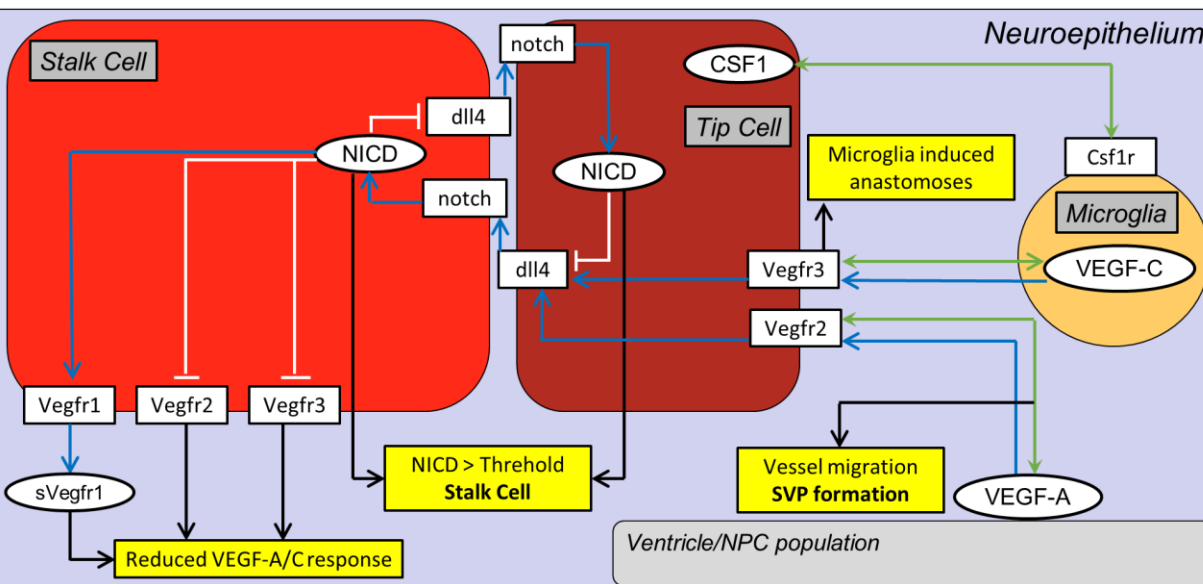
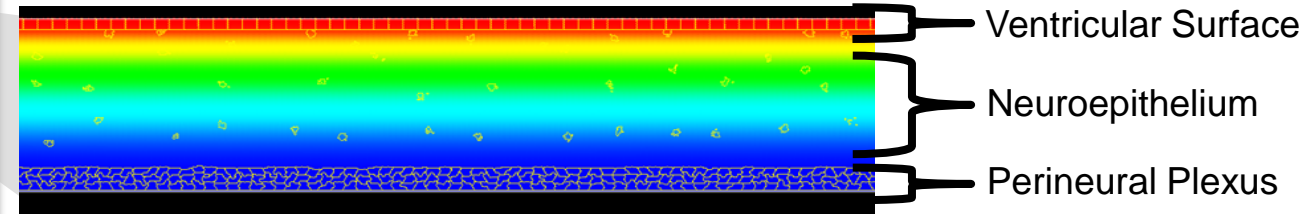
Receptor



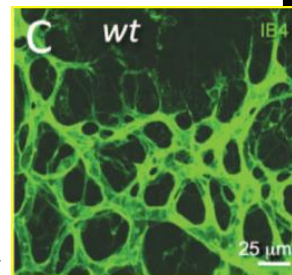
Modeling Brain Angiogenesis



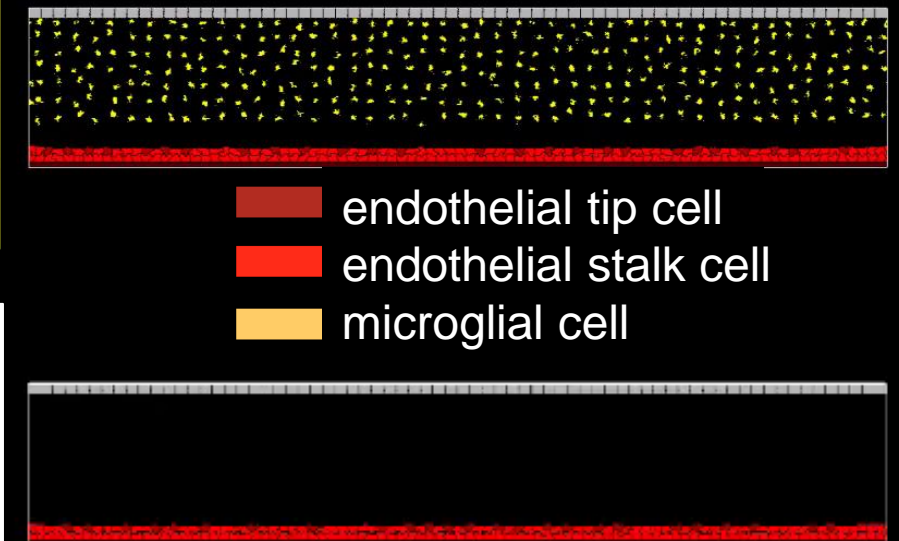
VEGF-A gradient: NPCs in the subventricular zone



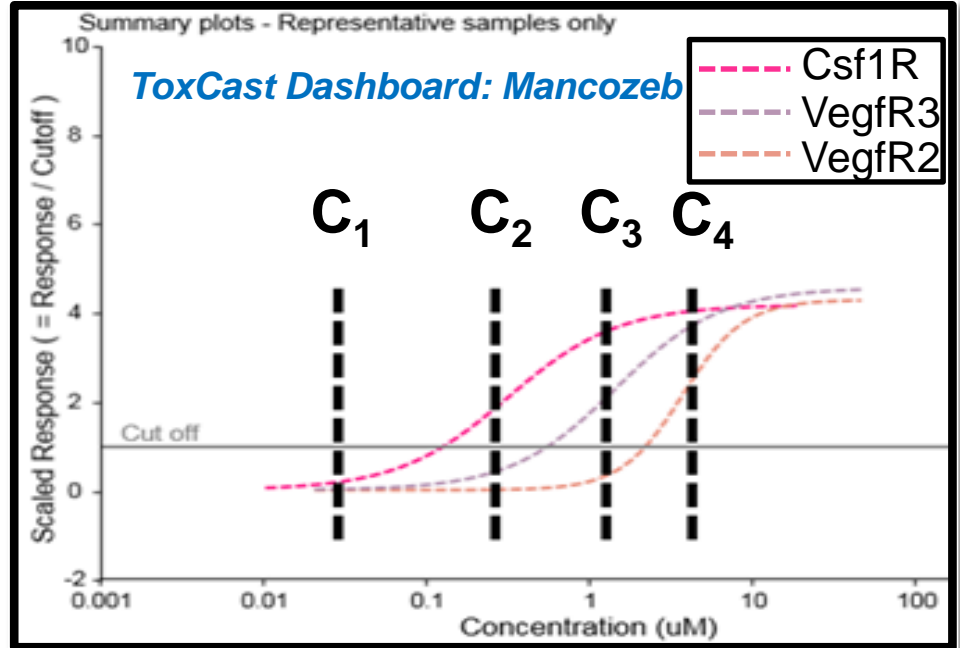
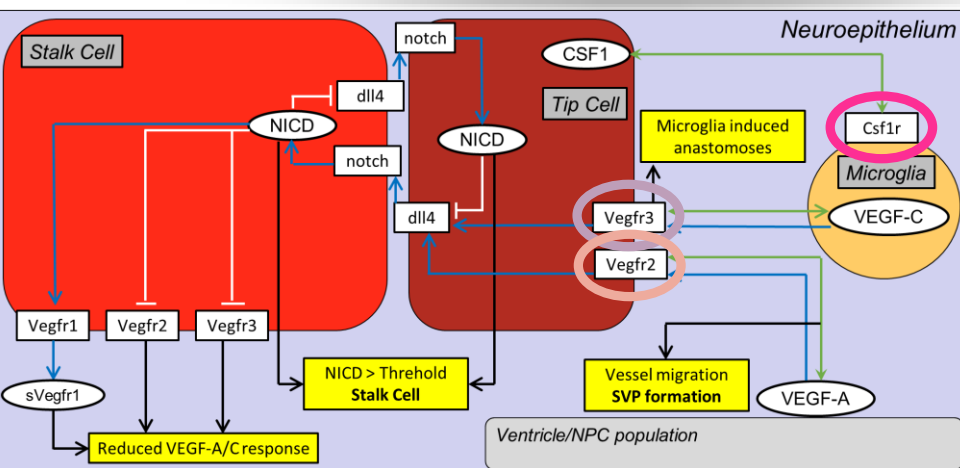
Rymo et al. (2011) PLoS One



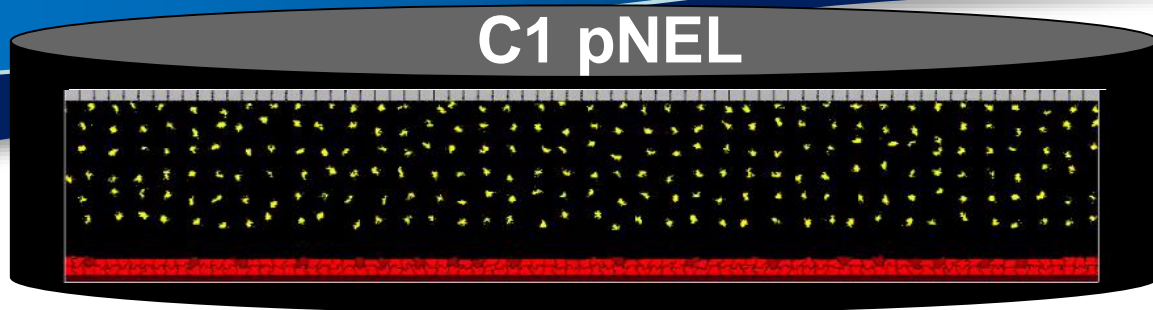
Cell agent Based model of microglia-endothelial interaction



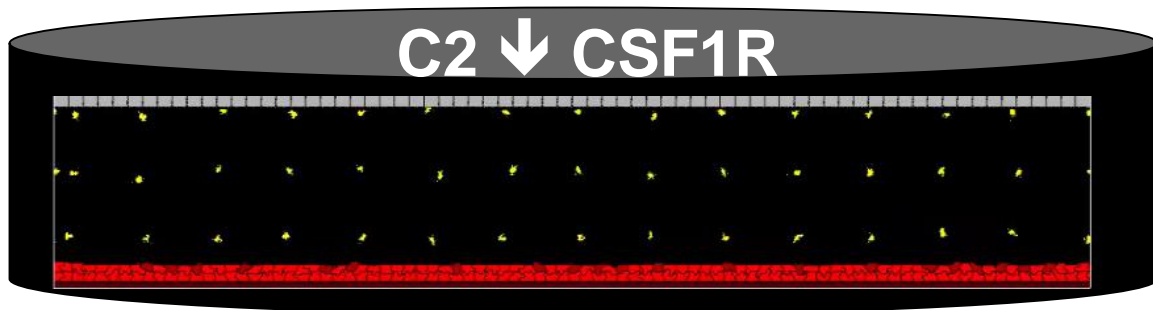
Translating HTS Data - Mancozeb



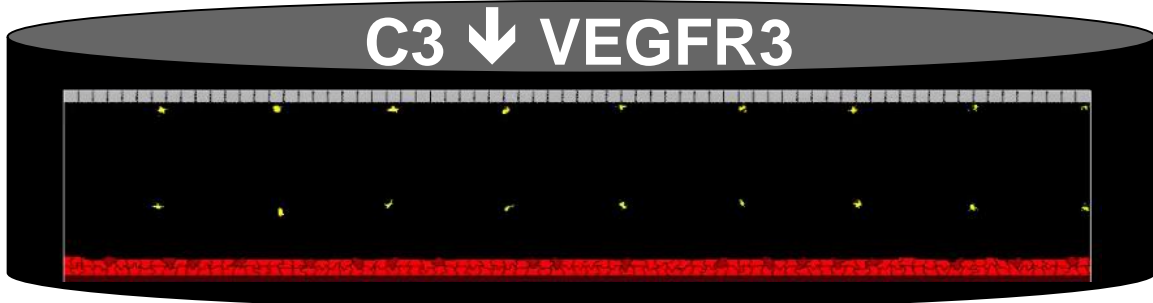
0.03 μ M
No significant
reduction in any
receptor



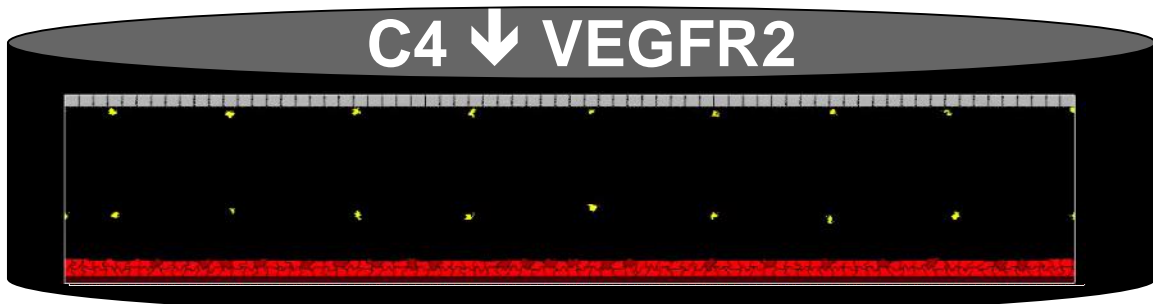
0.3 μ M
50% \downarrow CSF1R



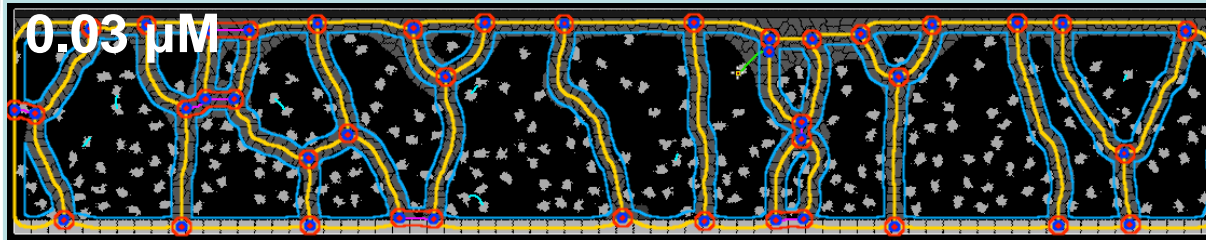
2 μ M
50% \downarrow VEGFR3
80% \downarrow CSF1R



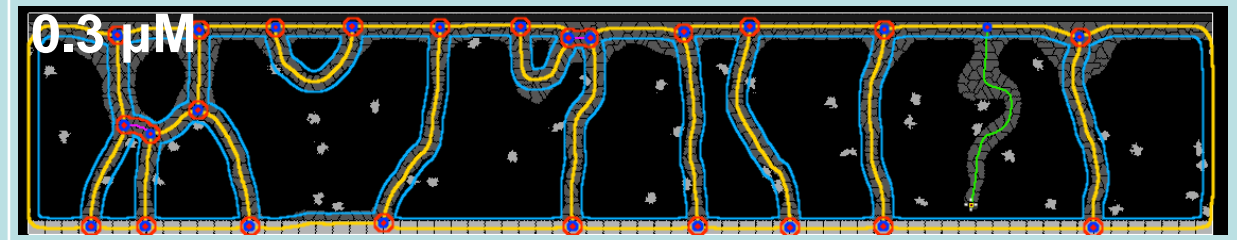
7 μ M
50% \downarrow VEGFR3
85% \downarrow VEGFR2
95% \downarrow CSF1R



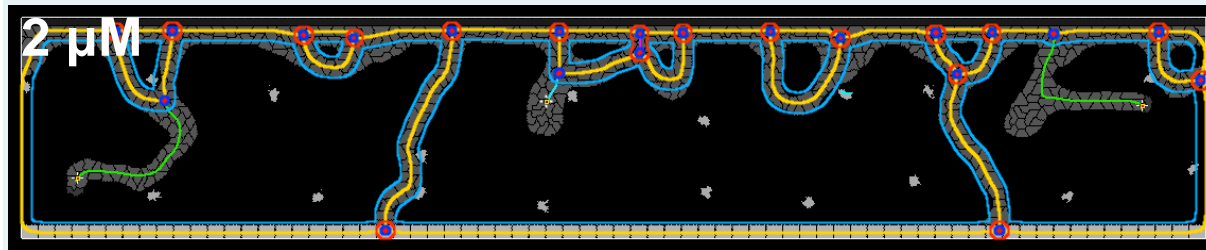
Vascular Quantitation - Mancozeb



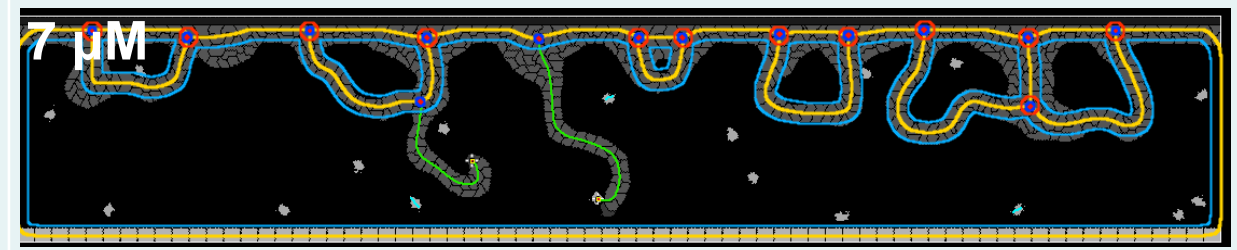
Predicted NEL (pNEL): No changes to vasculature



Predicted LEL (pLEL): Reduced tortuosity

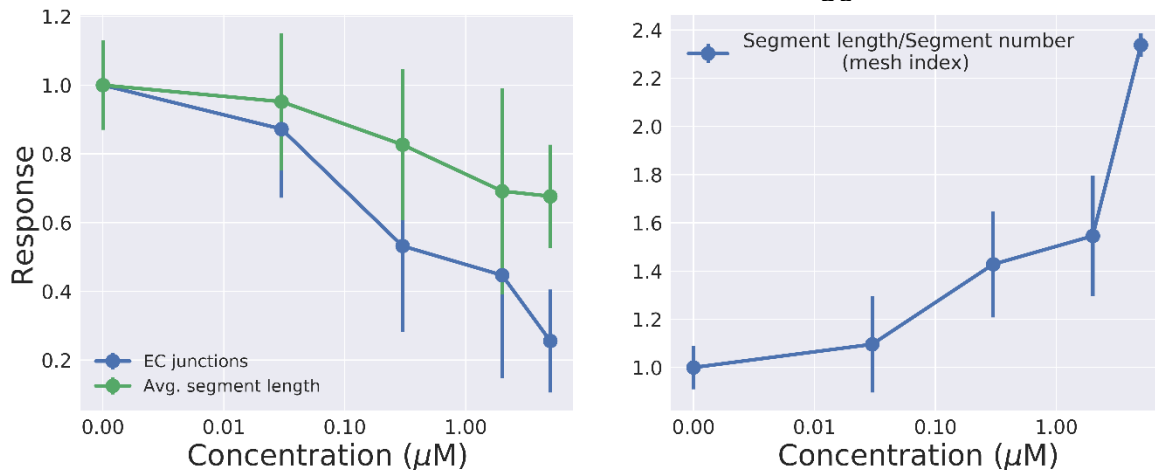


Reduction in overall vascular area



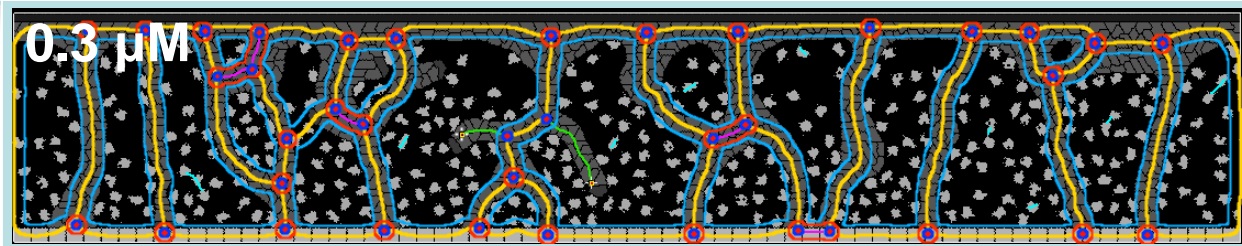
Hypo-vascular angiodyspasia

Mancozeb conc-response: $AC_{50} \sim 0.5\mu\text{M}$

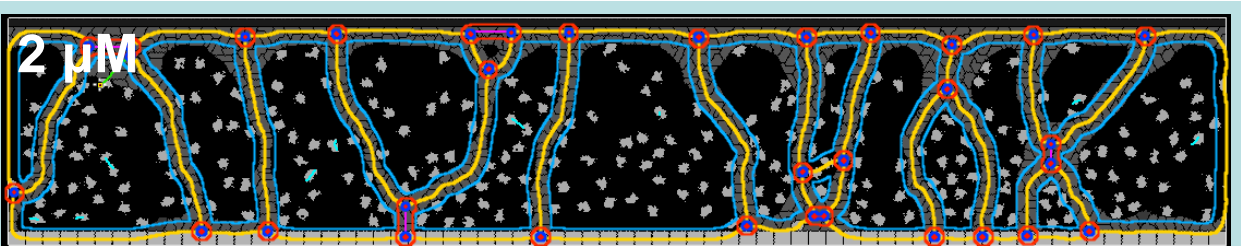


- Quantitate multiple vascular network endpoints in concentration response.
- Running multiple simulations allows us to account for stochastic variability.

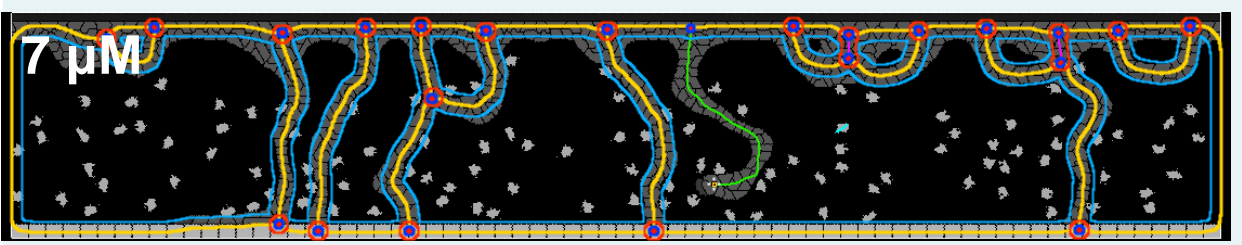
Vascular Quantitation – Oxytetracycline dihydrate



Predicted NEL (pNEL): No changes to vasculature



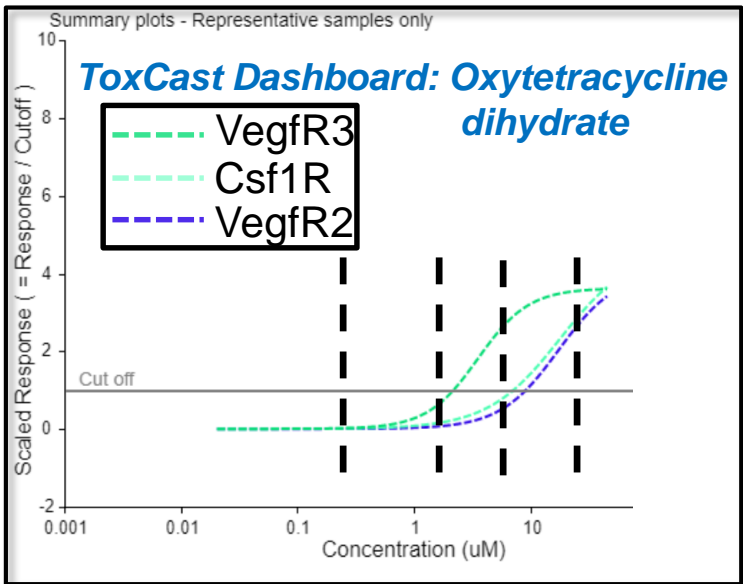
Predicted LEL (pLEL): Reduced vascular area



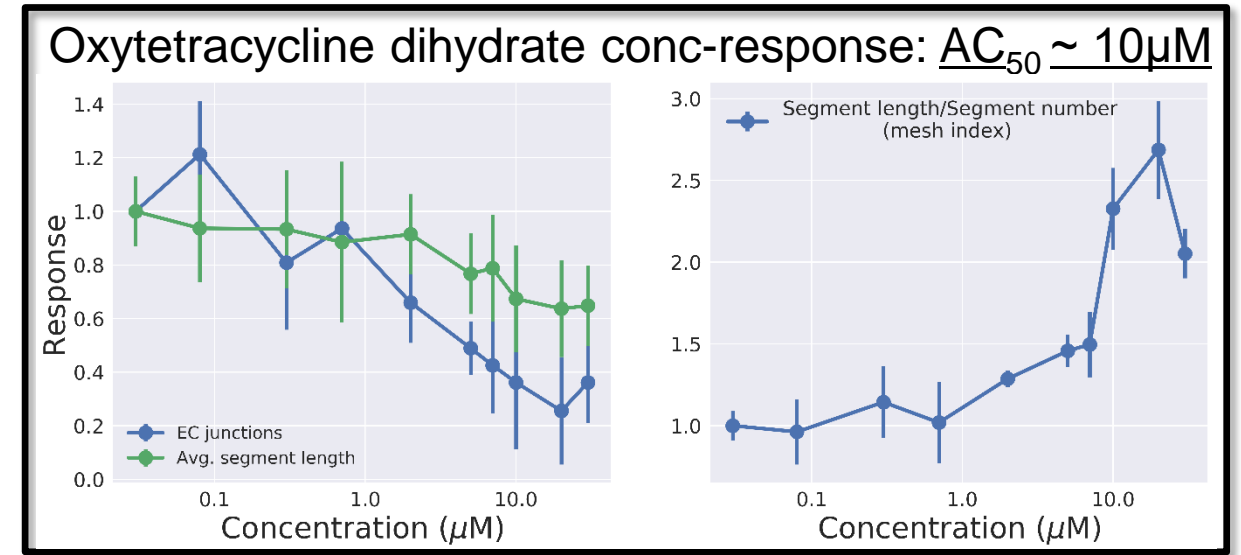
Reduced branching and anastomoses



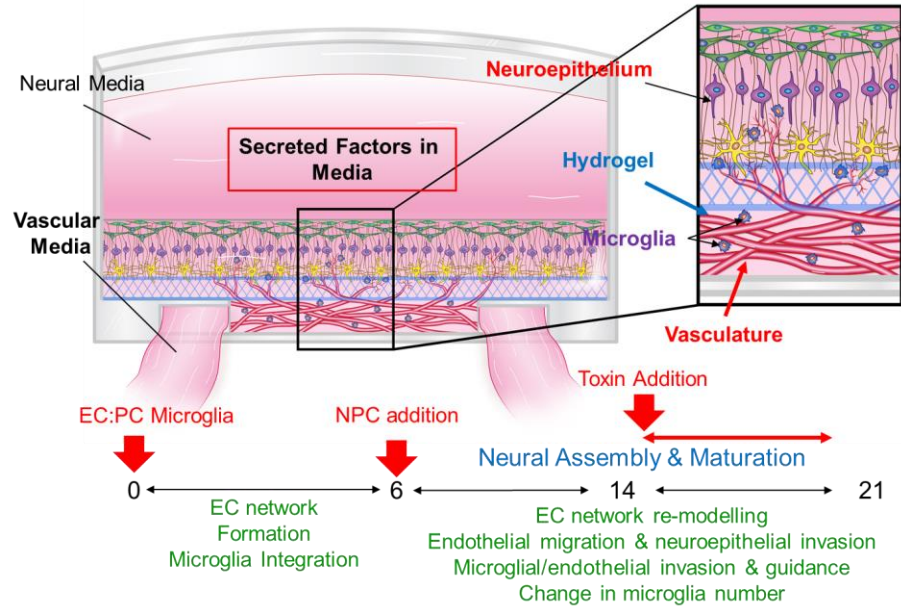
Hypo-vascular angiodysplasia



VEGFR3 serves as the more sensitive angiogenesis endpoint for oxytetracycline dihydrate exposure

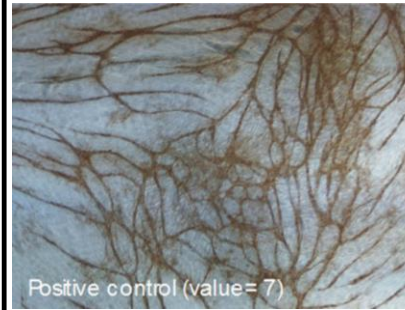
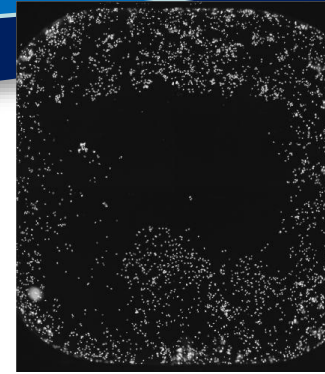


Experimental comparison

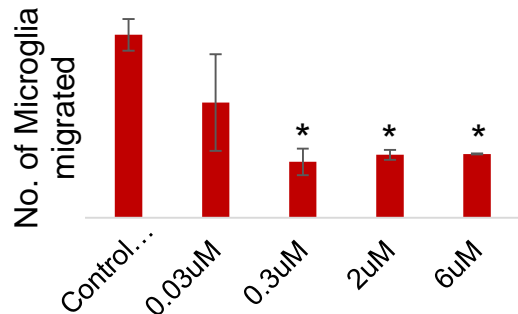


NVU OCM

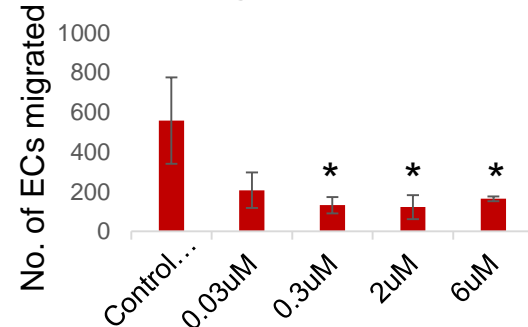
- Pilot study using mancozeb concentrations tested *in silico*
- In vitro*: ~0.3 μM
- In silico*: ~0.5 μM



Microglia migration



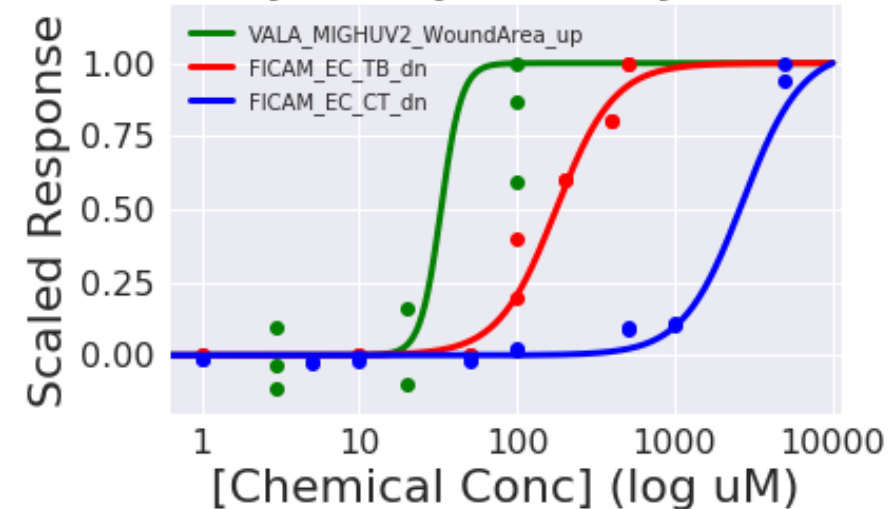
Endothelial cells migration



Cell-based assays

- Endothelial cell tubulogenesis and migration assays
- In vitro*: ~30 μM
- In silico*: ~10 μM
- No microglia *in vitro*

Oxytetracycline dihydrate

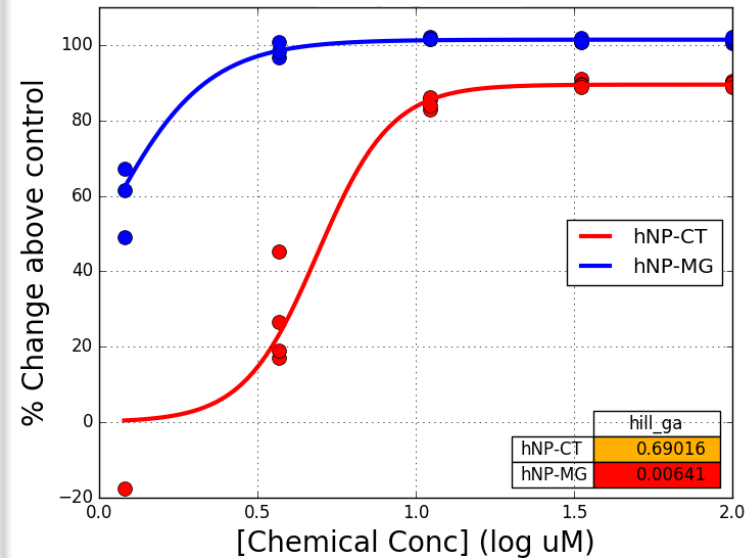


VALA Sciences, FICAM

W. Daly, G. Kaushik, UW Madison

NVU cell-based assays

Cell-based Assays

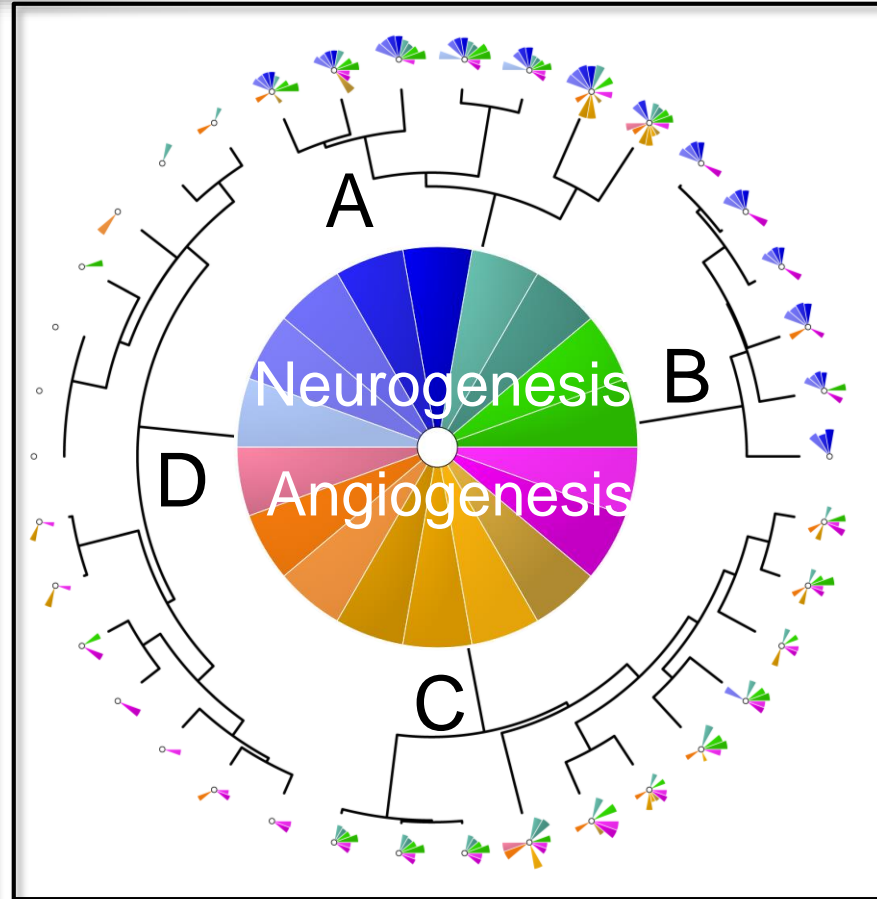


ArunA: Migration/Proliferation
hNP/hNC/hNN cells

VALA: Migration/Proliferation
HUVEC cells

FICAM: Tubulogenesis/Proliferation
HUVEC cells

Process data



Cluster through ToxPi

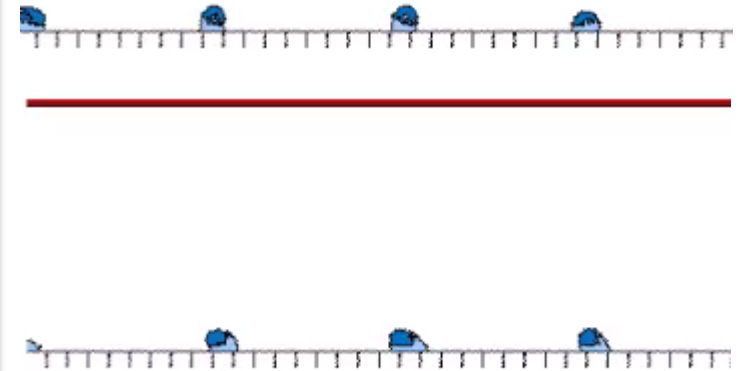


Define in literature

Towards a functional cNVU model

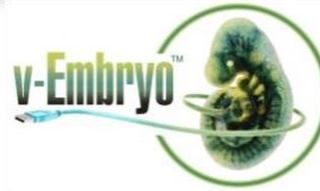
- Biological pathway perturbations
 - Predict NVU phenotypes from literature fingerprint and cell-agent based model
 - ‘Cybermorphs’ for investigating single pathway knockouts
 - Continuum response following chemical exposure and resulting receptor inhibition
- Neurogenesis submodel
 - Differentiation/migration to neurons and astrocytes
 - Utilize intracellular signaling pathways (cell/centrosome cycle)
 - Endothelial network interacting with neural network (3D)
- Phenotype quantitation
 - Microglia abundance, vessel branch points, network complexity (cortical angiogenesis)
 - Neuron proliferation/differentiation (neurogenesis)
 - Barrier permeation for chemical distribution to neural compartment (barriergenesis)

Neuroprogenitor Differentiation



Acknowledgements

- Tom Knudsen (mentor, NCCT)
- Kate Saili (NCCT)
- Sid Hunter (NHEERL-ISTD)
- Andrew Schwab (NHEERL-ISTD)
- Nancy Baker (Leidos)
- Richard Spencer (ARA-EMVL)
- Florent Ginhoux (A*STAR)
- Aymeric Silvan (A*STAR)
- Bill Daly (H-MAP, Wisc)
- Eric Nguyen (H-MAP, Wisc)
- Virtual Tissues Modeling Group





Thank You

Questions?