

PhysiCell Mini 1-Hour Course:

Introduction and a guided cancer model walk-through

<https://github.com/physicell-training/mini-one-hour>



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PhysiCell Curriculum

- **PhysiCell Mini 1-Hour Course (this course)**

- **Prerequisites:**

- Introduction from the Essentials Short Course
 - » Read in advance: <https://github.com/physicell-training/essentials/blob/main/README.md#introduction>
 - Basic knowledge of cell biology, concepts of mathematical functions

- **Software requirements:**

- Web browser access, OR installation of PhysiCell Studio

- **Curriculum:**

- **Brief introduction and walk-through example (this session)**

- **PhysiCell Essentials Short Course (this short course)**

- More extensive introduction to PhysiCell and hands-on model examples
 - Can be run entirely within a web browser (no software downloads or installations required)

- **Integration of Boolean Networks with PhysiBoSS**

- Learn how to integrate Boolean signaling networks into PhysiCell Models

- **Advanced PhysiCell Modeling**

- Learn about creating non-standard model components and visualization in C++
 - Learn about C++ extensions for ODE models, ECM fibers, and more.

- **PhysiCell for Developers**

- Learn about PhysiCell core C++ structure, and contributing to PhysiCell core and extensions



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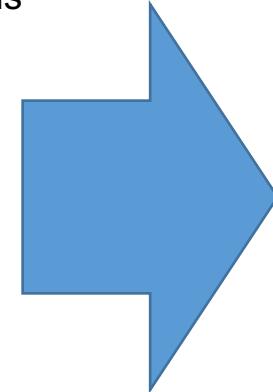
Session Goals

- Briefly introduce multicellular systems biology and agent-based models
- Introduce concepts of **signal-response** cell interactions
- Walk through basic cancer modeling example
- Prepare for deeper model development and exploration

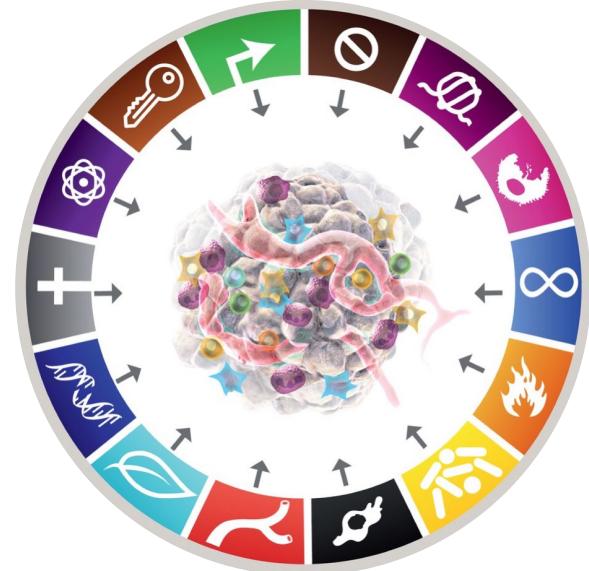


From single cells to tissue ecosystems

- Single-cell behaviors:
 - Growth
 - Division
 - Differentiation
 - Death
 - Consumption
 - Metabolism
 - Secretion
 - Signaling
 - Mutations
 - Variability
 - Damage response
 - Motility
- Cell-cell interactions:
 - Adhesion
 - Mechanics
 - Predation / Phagocytosis
 - Effector attack
 - Fusion
 - Contact communication
- Physical constraints:
 - Diffusion limits
 - Mechanical barriers



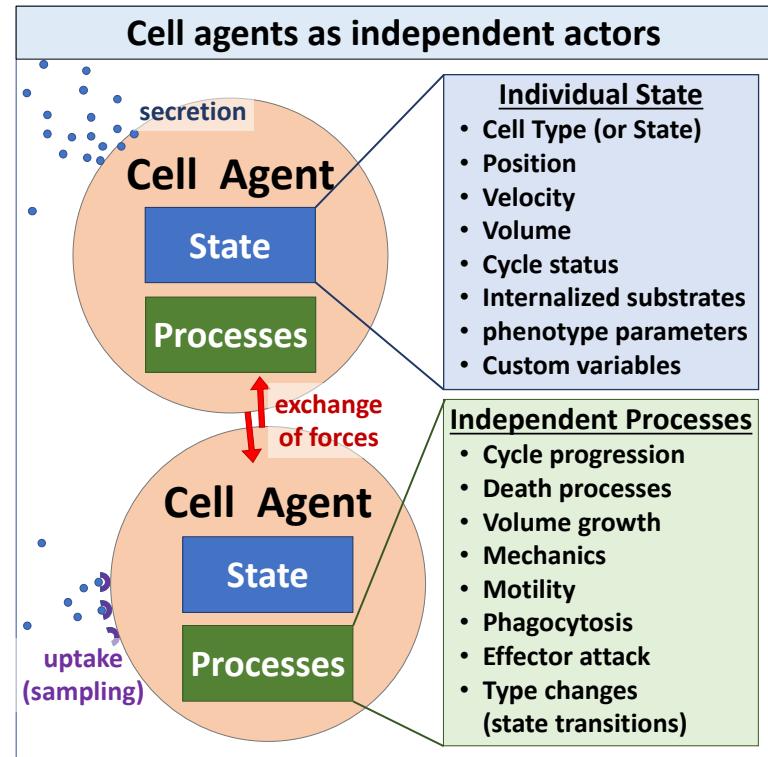
Multicellular tissue ecosystem



Source: Hanahan (2022)
DOI: [10.1158/2159-8290.CD-21-1059](https://doi.org/10.1158/2159-8290.CD-21-1059)

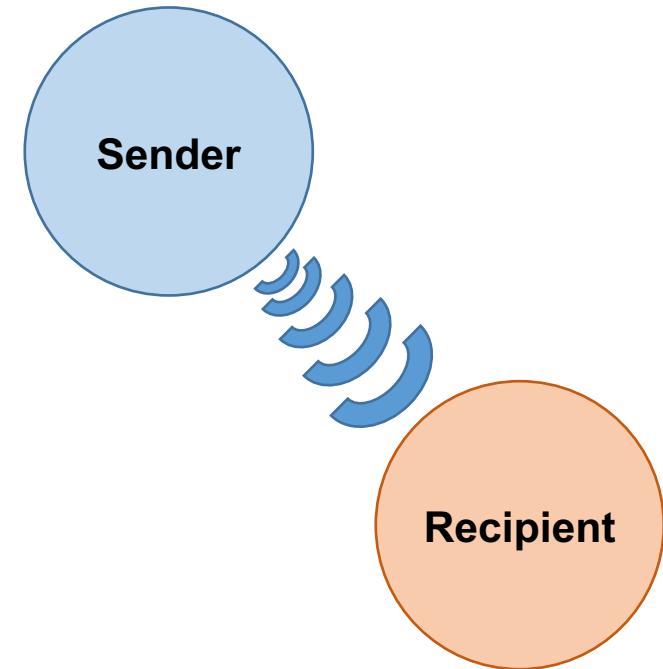
Agent-based models: overview

- Each cell is an **independent agent** with:
 - **Individual state**
 - Type
 - Position
 - Velocity
 - Phenotype parameters
 - Custom variables
 - **Independent processes**
 - Cycle and death processes
 - Volume growth
 - Mechanics and motility
 - Secretion and uptake / sampling
 - Phagocytosis, effector attack
 - State transitions (change of type)
 - Custom processes



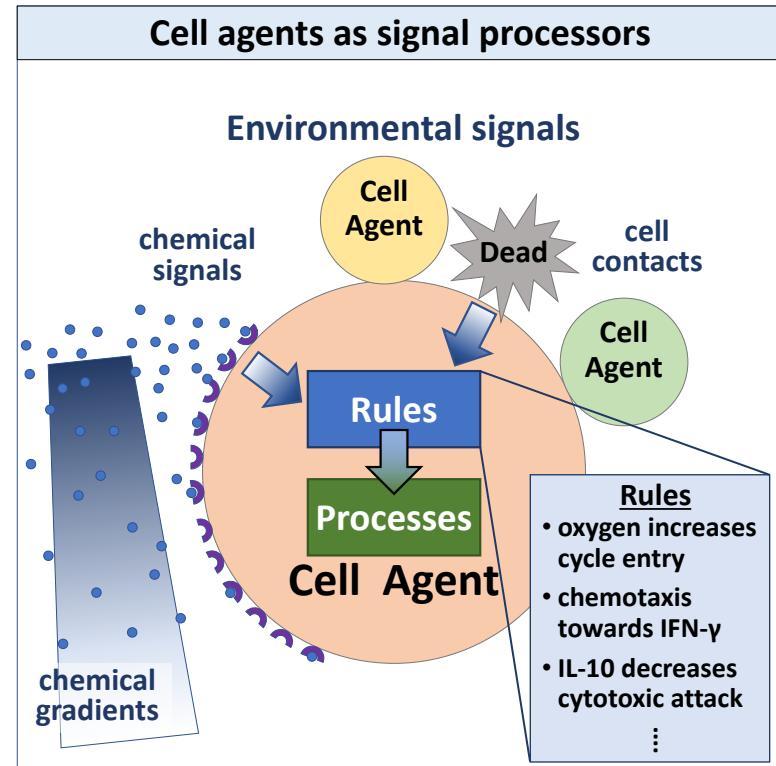
Signal-Response as a Conceptual Framing

- Much of the complexity of this system can be decomposed into pairwise interactions between a **sender** and a **recipient**
- A **signal** is a stimulus that can elicit a behavioral **response** in the recipient:
 - A macrophage (**sender**) secretes IL-6 (**signal**) that drives chemotaxis (**response**) in a CD8 T cell (**recipient**)
 - An epithelial cell (**sender**) exerts pressure (**signal**) that decreases cycle entry (**response**) in another epithelial cell (**recipient**)



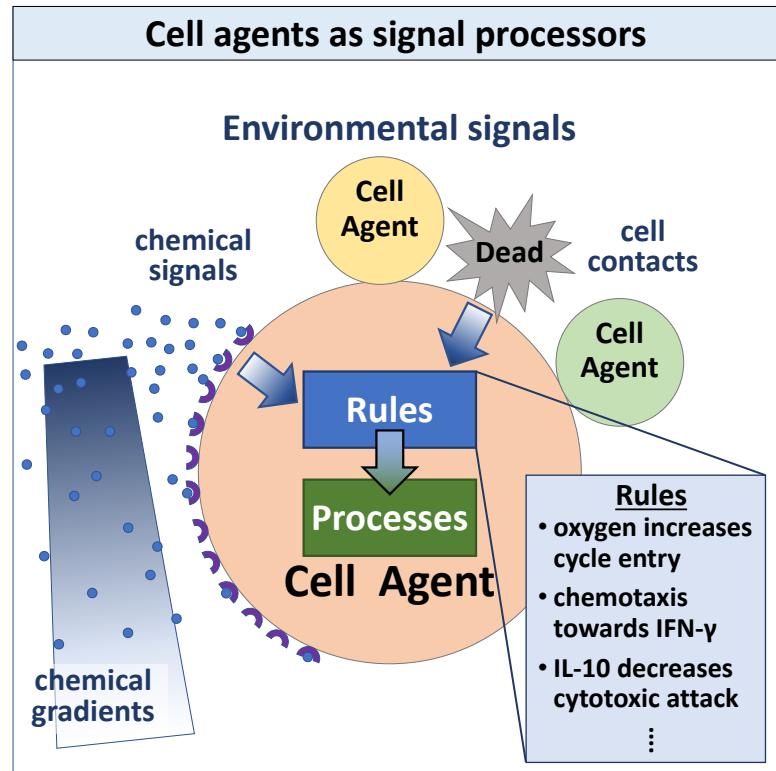
Cell agents are signal processors

- Cells interact through chemical and physical **signals** (or stimuli)
 - Secreted chemical signals & gradients
 - ECM properties
 - Contact with a live or dead cell
 - ...
- Signals drive changes in **behavior**
 - Increased or decreased rates of cycling or death
 - Changes in motility, secretion, phagocytosis, ...
- Signal-behavior relationships are **agent rules**



Our computable model grammar

- A "dictionary" of signals (stimuli)
- A "dictionary" of reference behaviors
- A grammar to connect signals to behavioral responses
- Map grammar statements onto mathematics and code



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A dictionary of signals

- A dictionary of signals that can be used as inputs for hypothesis statements
- **Diffusible chemical substrates**
 - extracellular and intracellular concentrations
 - extracellular gradients
- **Cell mechanics / physics**
 - Cell pressure
 - Cell volume
- **Contact**
 - Number of contacts with each cell type
 - # of contacts with live and dead cells
 - Contact with basement membrane
- **Attack and damage interactions**
 - Accumulated damage
 - Cumulative attack time
 - Attack status
 - Am I attacking?
 - How much damage have I delivered?
- **Live / dead status**
 - Dead, apoptotic, necrotic
- **Global information**
 - Current simulation time (for event timing)
- **Custom symbols**

Each symbol uniquely maps to a mathematical quantity at a cell's position



A dictionary of behaviors

- Based on years of modeling, we created a "dictionary" of standardized behaviors ***and well-defined reference models***
 - **Cycling**
 - Exit rates from each cycle phase
 - Asymmetric division
 - **Death**
 - Apoptotic and necrotic death rates
 - **Transport**
 - Secretion, uptake, and export rates
 - **Migration and chemotaxis**
 - Migration speed, bias, persistence time
 - Chemotactic sensitivities (to each diffusible factor)
 - **Mechanics and Adhesion**
 - Adhesion and repulsion potential coefficients
 - Adhesion affinities (to each cell type)
 - Elastic adhesion constant, maximum number of adhesions
 - Rate of forming and breaking elastic adhesions
 - **Transition / Type change / Transformation**
 - Rate of transforming (to each cell type)
 - **Fusion**
 - Rate of fusing (combining with) each cell type
 - **Phagocytosis (or ingestion / predation)**
 - Rate of ingesting dead cells
 - Apoptotic & Necrotic rates can differ!
 - Rate of ingesting live cells (one rate for each type)
 - **Effector Attack**
 - Rate of initiating attacks on live cells (one for each type),
 - Immunogenicity (one for each cell type)
 - Duration of attacks, rate of causing damage during attack
 - **Damage and Repair**
 - Damage rate (e.g., via doxorubicin)
 - Repair rate
 - **Custom symbols**

These give a dictionary of behavioral parameters that can be modulated in models.



Hypothesis statements

- For [cell type T], [S] increases / decreases [B] **[optional arguments]**
 - **Cell type T** is as cell type defined in the simulation model
 - **S** is a signal in our signal dictionary
 - **B** is a behavioral parameter in our behavior dictionary
- **Examples:**
 - For M0 macrophages, necrotic cell debris increases transformation to M1 macrophages
 - For malignant epithelial cells, doxorubicin increases apoptosis
 - Radioisotope edition:
 - For malignant epithelial cells, internalized radioisotope increases alpha particle secretion (release)
 - For malignant epithelial cells, alpha particles increase damage rate
 - For malignant epithelial cells, damage increases apoptosis



Using a response function

- If signal S increases / decreases behavior B
 - Vary behavioral parameter p with base value p_0 and maximal response value p_M

$$p(s) = p_0 + (p_M - p_0)R(s) = (1 - R(s)) \cdot p_0 + R(s) \cdot p_M$$

- We generally use **Hill response functions**:

$$R(s) = \frac{s^h}{s_{\text{half}}^h + s^h} = \frac{\left(\frac{s}{s_{\text{half}}}\right)^h}{1 + \left(\frac{s}{s_{\text{half}}}\right)^h} \quad \text{if } s \geq 0, \quad \text{and } H(s) = 0 \text{ if } s < 0.$$



PhysiCell Studio (on Galaxy)

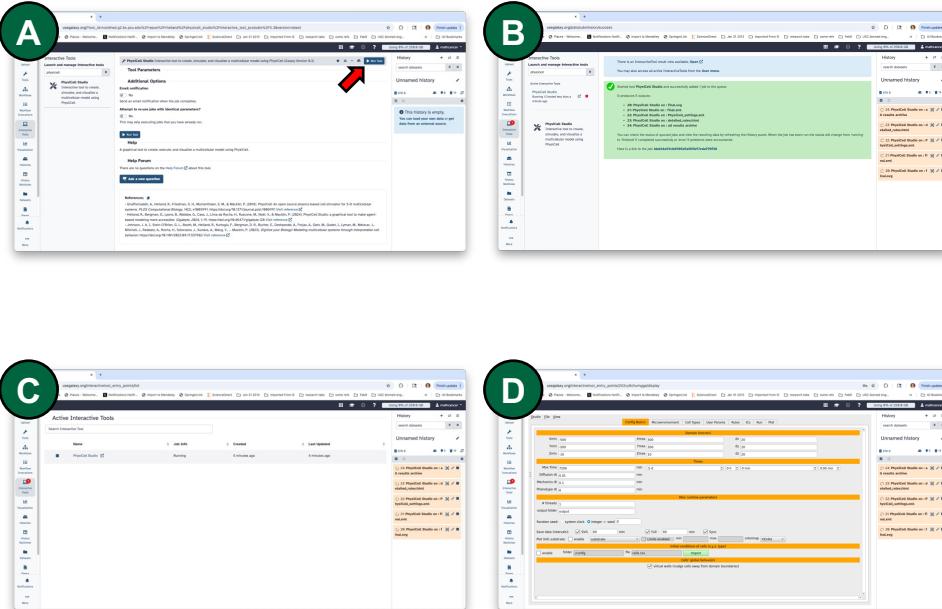


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Starting PhysiCell Studio on Galaxy

1. Start at UseGalaxy.org
 - Visit <https://usegalaxy.org>
 - If new: Create and validate an account.
 - Sign in with your account
2. Find PhysiCell Studio
 - Click the "all tools" or "interactive tools" search bar on the left
 - Search for "PhysiCell" to find **PhysiCell Studio** as an interactive tool
3. Run (activate) PhysiCell Studio
 - Click the blue "Run Tool" button  at the top (See A.)
 - Wait for studio to activate (watch for ① on the left side). (See B.)
4. Open the running studio for use
 - Click on "interactive tools" on the left menu.
 - Click once more to collapse the menu. (See C.)
 - When PhysiCell Studio appears in the active list, click to interact. (See D.)
 - Optionally, click the three dots on left and choose **remote rescaling**
5. Further notes and documentation:
 - <https://physicell-studio.readthedocs.io/en/latest/galaxy.html>



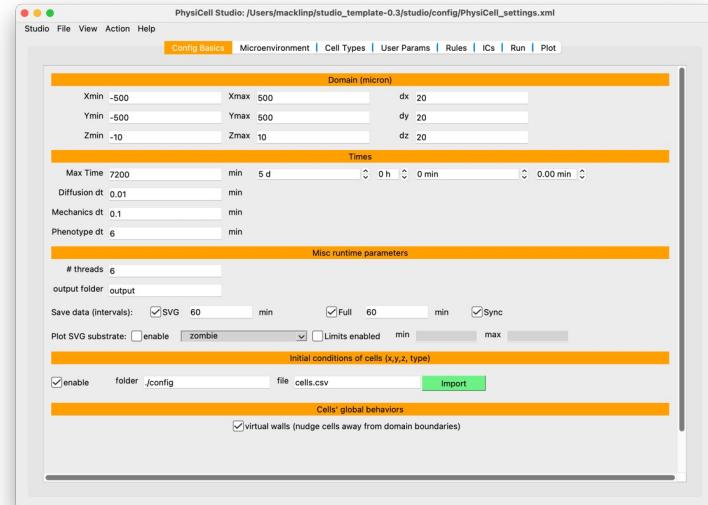
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PhysiCell Studio: Overview

A graphical user interface (GUI) application to make it easier to build and explore PhysiCell models

- Config basics:** Domain size, simulation duration, output
- Microenvironment:** Diffusing substrates, boundary conditions
- Cell types:** Define cell types and their base phenotypes
- User params:** Model-specific parameters
- Rules:** Hypothesis-based cell behaviors
- ICs:** Initial cell positions
- Run:** Use this to start executing the model
- Plot:** Plot cells and diffusible substrates



Galaxy: [[Click here](#)]

NanoHub backup: <https://nanohub.org/tools/pcstudio>

Galaxy: [[Click here](#)]



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Key Modeling steps

1. Plan the modeling problem.

- What are the important things we want to learn?
- What cell types are important?
 - What are their key behaviors?
 - What diffusible factors drive their behaviors?
 - Any other important interactions?
- Can we estimate parameters (at least to order of magnitude)?
- Can we build the model sequentially? (Add components one at a time?)

2. Set up diffusing factors.

3. Set up cell types.

4. Add rules.

5. Simulate and assess.

6. Iterate and improve.



Iterative modeling example

- In this session, we'll iteratively build a simple tumor model, bit-by-bit:
 1. **Growing tumor with oxygen consumption**
 2. Add a mechanofeedback on cycling
 3. Add oxygen-driven cycling
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 5. Add a chemotherapy



Initial tumor and oxygen consumption



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Growing tumor with oxygen: 1

- First, we add oxygen in the **Microenvironment** tab
- We use the **diffusion length scale** from physics / applied mathematics:
 - Penetration into a tissue is competition between effects:
 - Diffusion (D) increases spread
 - Uptake (U) and decay (λ) tend to halt spread

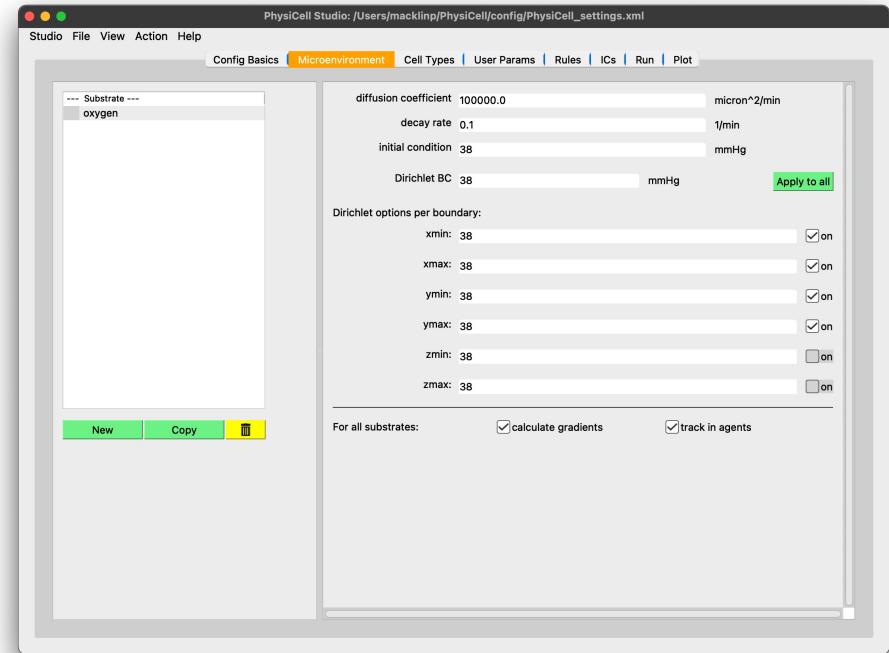
$$L = \sqrt{\frac{D}{U + \lambda}}$$

- Literature for oxygen:
 - $D \sim 10^5 \frac{\mu\text{m}^2}{\text{min}}$
 - $L \sim 100 \mu\text{m}$ in dense tissues
 - We'll assume L is tenfold larger in cell-free tissue, so $\lambda \sim 0.1 \text{ min}^{-1}$
 - In physioxic tissues, $\text{pO}_2 \sim 5\% = 38 \text{ mmHg}$



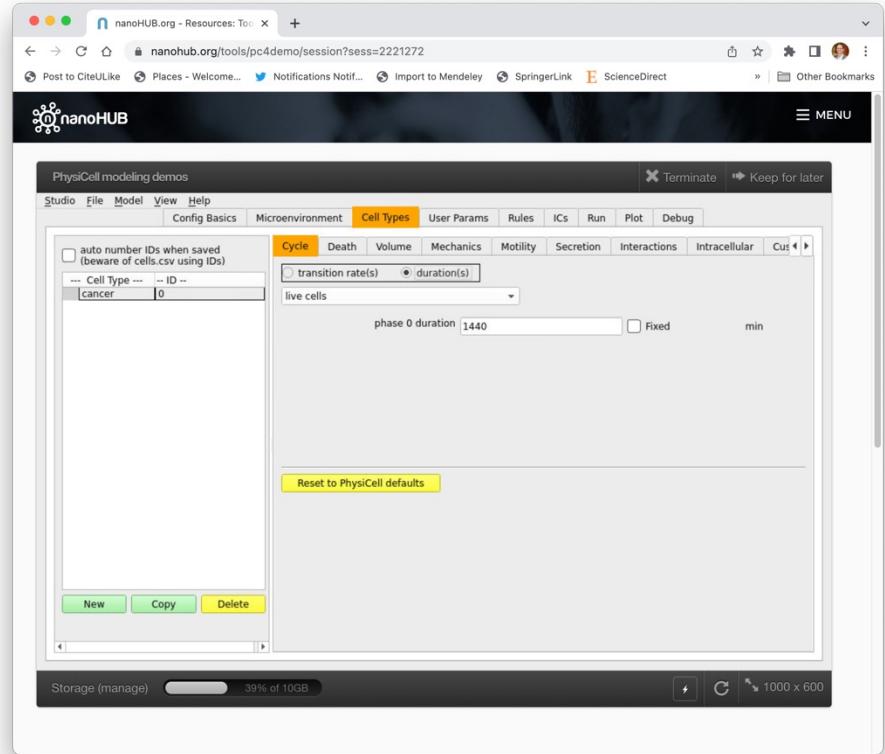
Growing tumor with oxygen: 2

- Go to **Microenvironment** tab
 - double-click **substrate**
 - rename it to **oxygen**
 - set the **decay rate** to 0.1
 - set the **initial condition** to 38 mmHg
 - set the **boundary condition** to 38 mmHg
 - Hint: use the **apply to all** button
 - Make sure they enabled on X and Y



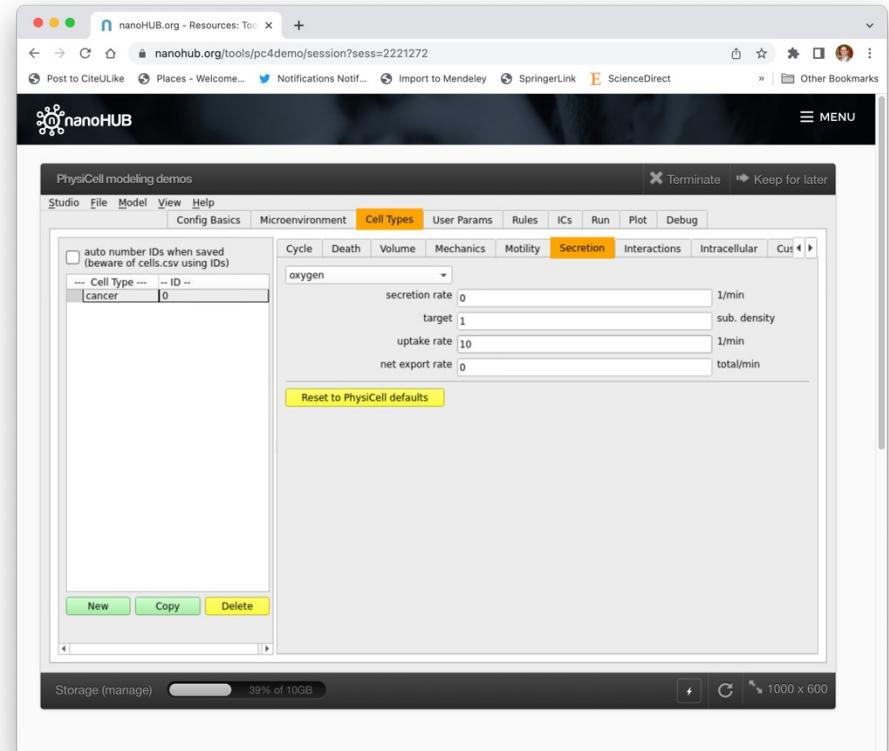
Setting up cancer cells: 1

- Set the name
 - Go to **Cell Types** tab
 - double-click **default**
 - rename it to **cancer**
- Set cycling to ~24 hour cycle
 - Go to **cycle**
 - Choose the simpler **live cells** model
 - Use the **duration** representation
 - Set mean duration to 1440 min = 24 h



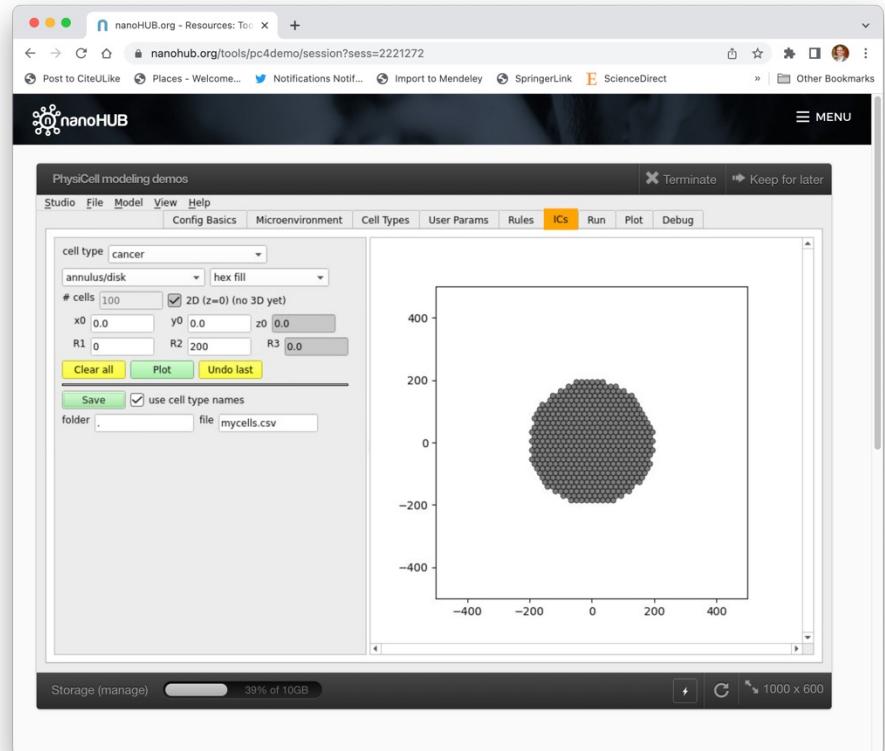
Setting up cancer cells: 2

- Set up oxygen consumption
 - Go to **secretion**
 - Choose **oxygen** from the drop-down
 - Set **uptake** to 10
 - Chosen for a 100 micron length scale



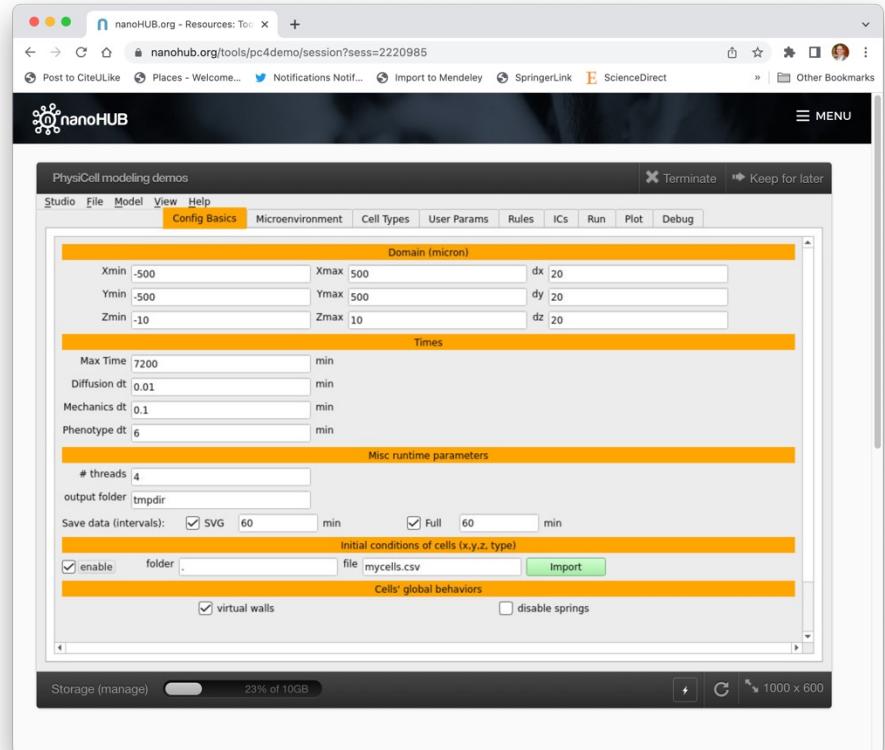
Set up an initial state: 1

- We want a packed 400 micron circle of cancer cells
 - Go to the **ICs** tab
 - Choose **cancer** cell type
 - Choose **annulus/disk**
 - Choose **hex fill**
 - Choose min radius (R1) = 0
 - Choose max radius (R2) = 200
 - Click **plot**
 - Click **save**



Set up an initial state: 2

- Make sure PhysiCell uses the initial list of cells
 - Go to **config basics**
 - Browse to **initial conditions of cells**
 - Set the **enabled** box
- Set to **4 threads** for faster runs.



Set up an initial state: 3

- Make sure PhysiCell doesn't randomly place other cells
 - Go to **User Params** tab
 - Go to the **number_of_cells** variable
 - Set the value to **0**

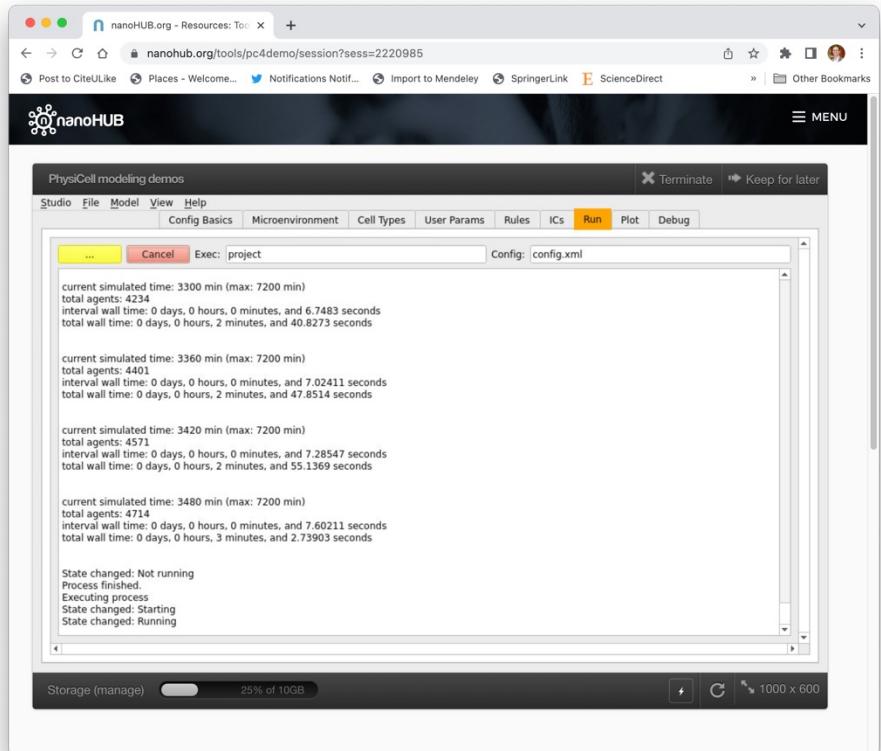
The screenshot shows a web browser window for nanoHUB.org. The URL is nanohub.org/tools/pc4demo/session?sess=2220985. The page title is "PhysiCell modeling demos". The "User Params" tab is selected in the navigation bar. A table lists parameters with their types, values, units, and descriptions. The "number_of_cells" parameter is highlighted with a yellow border, showing its value is 0. A note at the top of the table says "(Note: validation check performed at Save or Run)".

Name	Type	Value	Units	Desc
1 random_seed	int	0	dimensionless	
2 number_of_cells	int	0	none	number of cells per each cell type
3	double			
4	double			
5	double			
6	double			
7	double			
8	double			
9	double			
10	double			
11	double			
12	double			
13	double			



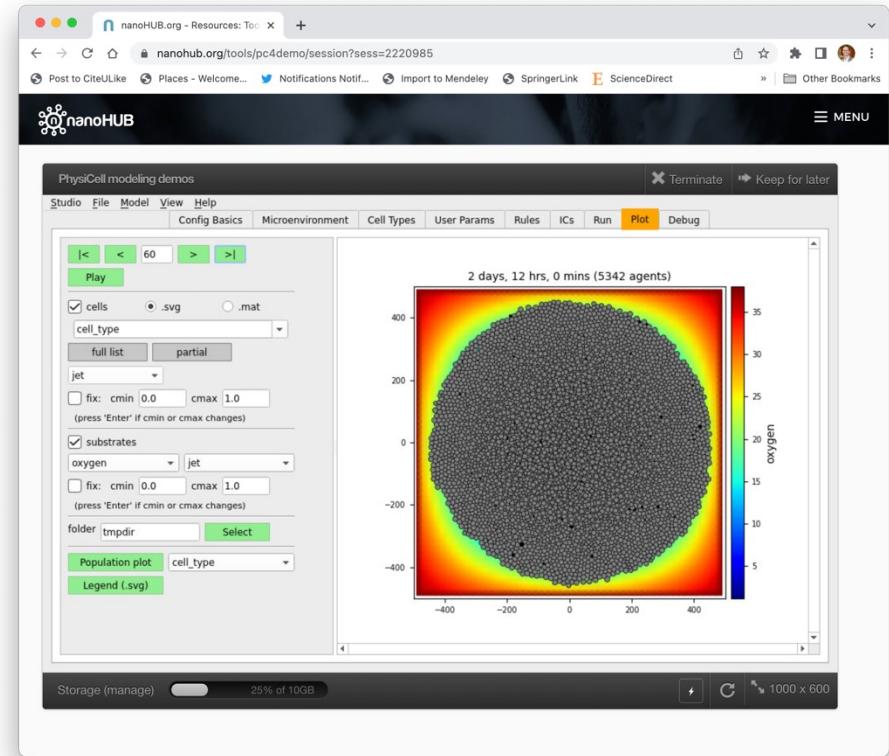
Run the model!

- Go to the **Run** tab
- Click the **run simulation** button
 - Click **cancel** if you ever need to interrupt it



View and explore the simulation

- Go to the **Plot** tab
- To navigate times:
 - Click |< to go to the beginning
 - Click >| to go forward by one frame
 - Click <| to go back by one frame
 - Click >| to go to the last frame
- Click **cells** to toggle cell plots on or off
 - For now, use **SVG** coloring
 - We'll show how to change cell coloring soon
- Click **substrates** to toggle plots of diffusible substrates
 - Choose the field from the first drop-down
 - Choose the color map from the second



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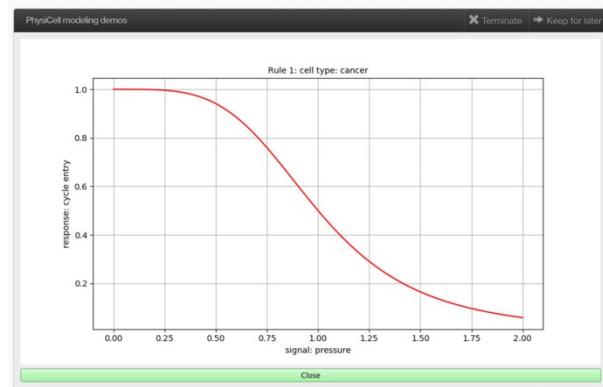
Let's improve the biology

- Notice a **non-physical behavior**
 - All cells proliferate regardless of available space.
 - Non-physical (physically impossible) overlap of cells
- Non-physical behaviors (or a failure to match reality) leads us to conclude that either:
 - Our hypotheses are wrong, OR
 - We are missing a hypothesis
- We'll add a new hypothesis:
 - mechanical pressure (compression) reduces cell cycling



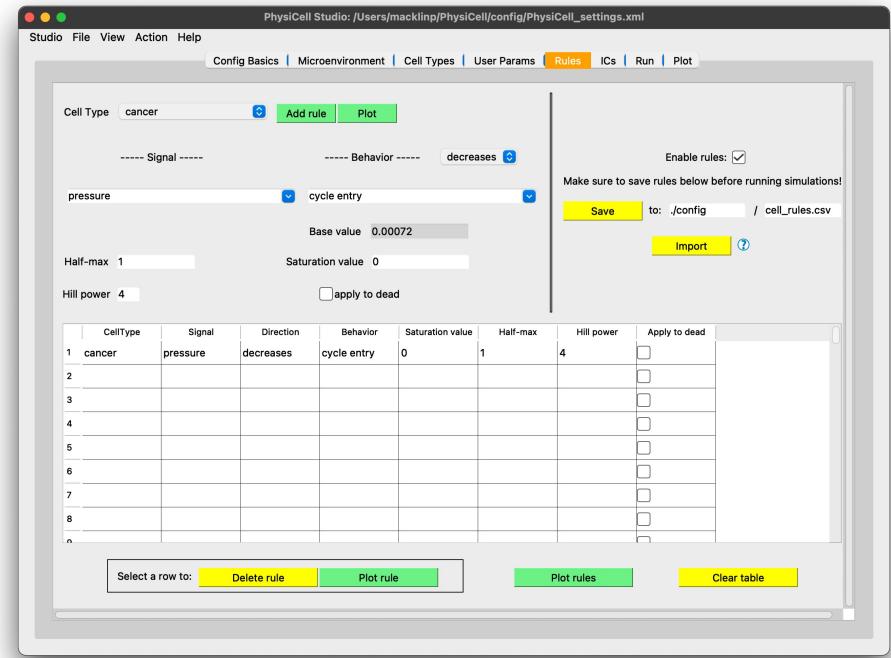
Our mathematics

- Rule: **pressure** decreases **cycle entry**
- Mathematical form of pressure:
 - Based on potentials
 - Nondimensionalized to 1 for 3D confluent tissues
 - Nondimensionalized to 0.5 for 2D confluent tissues
- We'll suppose cancer cells can accept some compression
 - Use a **half-max** of 1:
 - Once pressure hits 1.0, cycling is already halved
 - Use a **saturation value** of 0:
 - As pressure increases, cycling goes to 0
 - Use a strong **Hill parameter** of 4
 - Spreads the response over pressures from 0 to 2



Add the rule: 1

- Go to the **rules** tab
 - Select **cancer** cell
 - Choose **pressure** as the signal
 - Choose **cycle entry** as the behavior
 - Choose **decreases** as the response
 - Choose **0** as the saturation value of the behavior
 - Choose **4** as the Hill power
 - Choose **1** as the half-max
 - Then, click **add rule**
 - Click **save** on the right.



Add the rule: 2

- Make sure we use the rule
 - At the bottom, use a name **rules.csv**
 - Click the **save** button
 - Click the **enable** checkbox
- Run the model as before

The screenshot shows the nanoHUB.org interface for PhysiCell modeling. The 'Rules' tab is active. A table defines rules for 'cancer' cells:

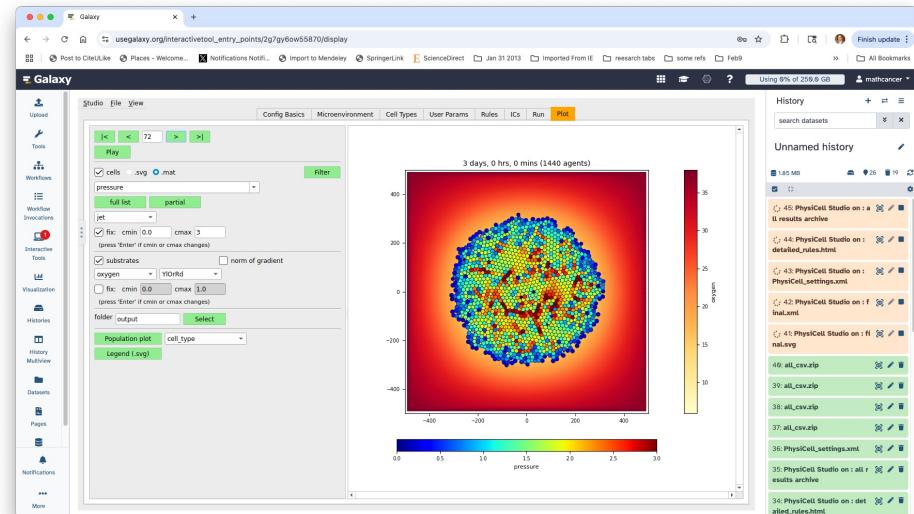
Cell Type	Signal	Direction	Behavior	saturation value	Half-max	Hill power	Apply to dead
1 cancer	pressure	decreases	cycle entry	0	1	4	<input type="checkbox"/>
2							<input type="checkbox"/>
3							<input type="checkbox"/>
4							<input type="checkbox"/>
5							<input type="checkbox"/>
6							<input type="checkbox"/>

At the bottom, there are buttons for 'Import', 'Save', 'Clear table', and a file input field set to 'rules.csv'. The 'enable' checkbox is checked.



Visualization

- Now, let's color cells by their color
 - Go to **Plot**, then **cells**
 - Choose **mat** instead of **SVG**
 - Choose **pressure** from the drop-down.
 - I suggest a **jet** coloring
 - I suggest fixing the range 0 to 3.
- Options:
 - Click **full list** to see a list of all possible variables we can use to color the cells
 - Choose color maps and ranges, etc.
- Observe:
 - With this feedback, there's much less cycling.
 - Pressure tends to be higher in the center



Oxygen-based cycling



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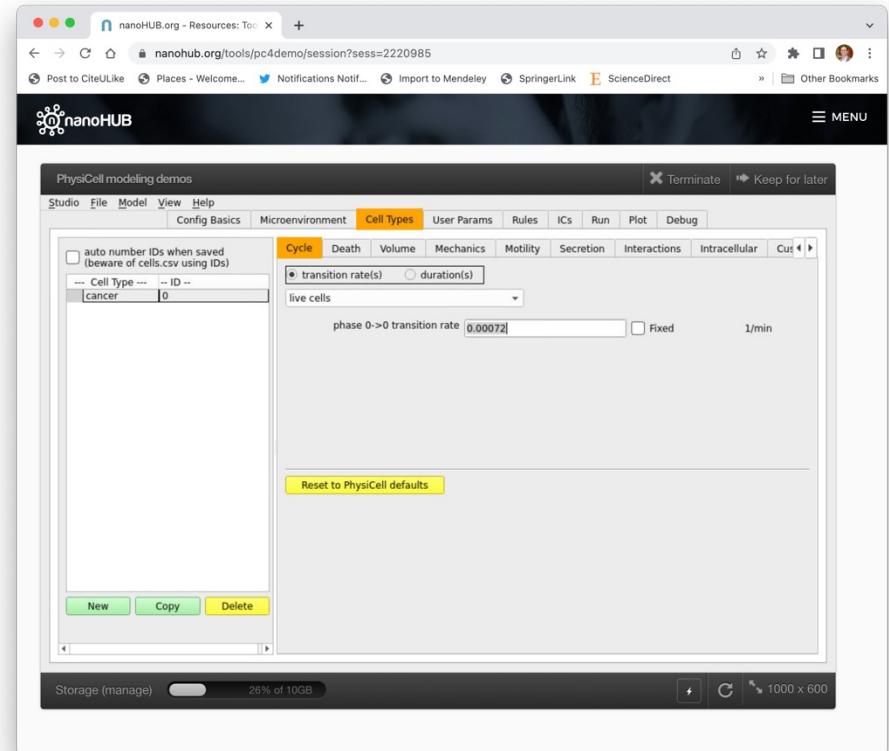
Iterative modeling example

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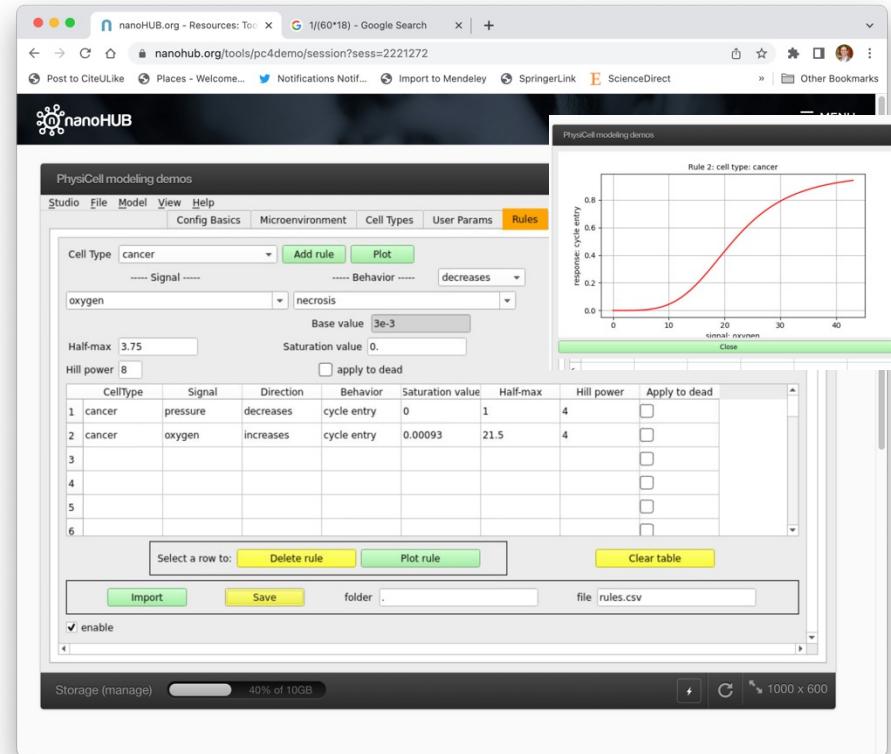
Oxygen-based cycling setup: 1

- We'll suppose cycle entry increases with oxygen availability
 - This is a sort of proxy for cell energy
- We'll need to modify our base phenotype:
 - Phenotype is the **base behavior** in the absence of other signals
 - No cycling in the absence of oxygen
 - So, we need to set base cycle rate = 0
- Go to **cell types**
 - Choose **cancer**
 - Go to the **cycle** sub-tab
 - View it as a **transition rate**
 - Set the rate to 0



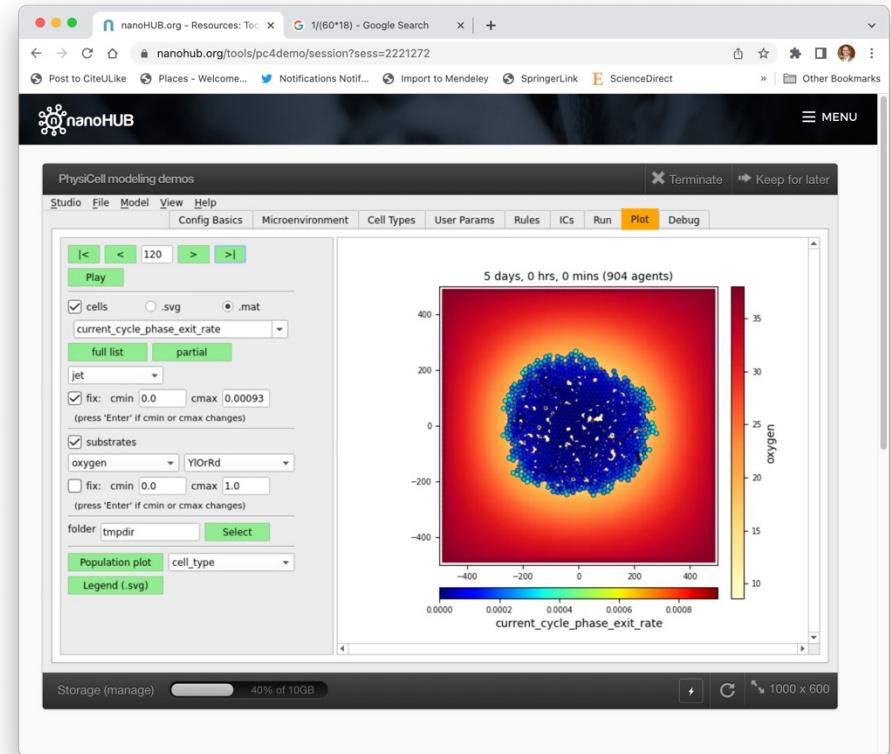
Oxygen-based cycling setup: 2

- Go to the **rules** tab
 - Select **cancer** cell
 - Choose **oxygen** as the signal
 - Choose **cycle entry** as the behavior
 - Choose **increases** as the response
 - Choose **0.00093** as the saturation value of the behavior
 - This sets a max cycle time of around 18 hours
 - Choose **21.5 mmHg** as the half-max
 - Choose **4** as the Hill power
 - Then, click **add rule**
- Make sure to click the **save** button!



Run and Visualize

- Let's color cells by cycling:
 - Go to **cells** and select **mat**
 - Use the **full list** drop-down to get more options
 - Use **current_cycle_phase_exit_rate**
 - Set the range from 0 to 0.00093
- This says how quickly cells are trying to exit the current cycle phase
 - (In this case, phase 0: "live")
 - Notice greatest cycling along the outer periphery



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Adding invasive cells (EMT and MET)



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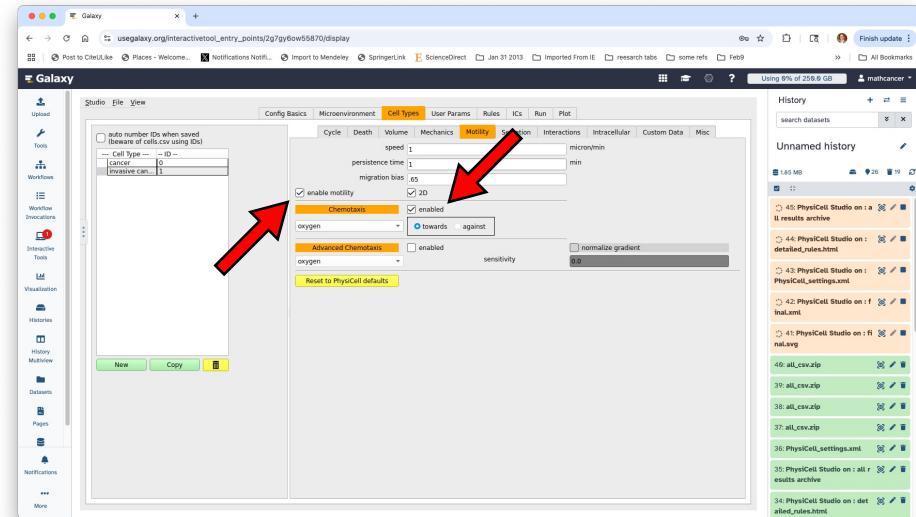
Iterative modeling example

- In this session, we'll iteratively build a simple tumor model, bit-by-bit:
 1. Growing tumor with oxygen consumption
 2. Add a mechanofeedback on cycling
 3. Add oxygen-driven cycling
 4. **Add an oxygen-based switching to/from an invasive phenotype (EMT and MET)**
 5. Add a chemotherapy



Invasive cells: 1

- First, we add a new cell type
 - Go to the **Cell types** tab
 - Select on **cancer**
 - Choose **copy**
 - Double-click and rename to **invasive cancer**
- Enable migration
 - Go to **motility**
 - Set **migration speed** to 1
 - Set **migration bias** to 0.65
 - Enable **migration**
 - Enable **chemotaxis**
 - Use **towards oxygen**



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Invasive cells: 2

- Now, make invasive cells less adhesive
 - Go to **mechanics**
 - Set **cell-cell adhesion strength** to **0**
- And make cancer cells switch to invasive cancer cells in low O₂:
 - Go to **interactions**
 - Select **cancer** cells
 - Set the **transformation rate to invasive cancer** to **0.01**
 - (100 minute mean waiting time)

The screenshot shows the 'Mechanics' tab of the PhysiCell Studio configuration interface. Under the 'cancer' cell type, the 'cell-cell adhesion strength' is set to 0.0. Other parameters like 'cell adhesion affinity' and 'attachment rate' are also visible.

The screenshot shows the 'Interactions' tab of the PhysiCell Studio configuration interface. Under the 'cancer' cell type, the 'transformation rate to invasive cancer' is set to 0.01. Other parameters like 'attack rate' and 'attack damage rate' are also visible.



Invasive cells: 3

- For cancer cells, oxygen prevents transition to the invasive type:
 - Go to rules
 - Select **cancer** cell
 - Choose **oxygen** as the signal
 - Choose **transform to invasive cancer** as the behavior
 - Choose **decreases** as the response
 - Choose **0** as the saturation value of the behavior
 - Choose **5** as the Hill power
 - Choose **7.5** as the half-max
 - Then, click **add rule**

CellType	Signal	Direction	Behavior	Saturation value	Half-max	Hill power	Apply to dead	
1	cancer	pressure	decreases	cycle entry	0	1	4	<input type="checkbox"/>
2	cancer	oxygen	increases	cycle entry	0.00093	21.5	4	<input type="checkbox"/>
3	cancer	oxygen	decreases	transform to invasive cancer	0	7.5	5	<input type="checkbox"/>
4								<input type="checkbox"/>
5								<input type="checkbox"/>
6								<input type="checkbox"/>
7								<input type="checkbox"/>
8								<input type="checkbox"/>
9								<input type="checkbox"/>
10								<input type="checkbox"/>

▪ Then, click **add rule**



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Invasive cells: 4

- For invasive cancer cells, oxygen increases transition to the non-invasive invasive type:
 - Go to rules
 - Select **invasive cancer** cell
 - Choose **oxygen** as the signal
 - Choose **transform to invasive cancer** as the behavior
 - Chose **increases** as the response
 - Choose **0.01** as the saturation value of the behavior
 - Choose **5** as the Hill power
 - Choose **7.5** as the half-max
 - Then, click **add rule**
 - Don't forget to **save**

CellType	Signal	Direction	Behavior	saturation value	Half-max	Hill power	Apply to dead	
1	cancer	pressure	decreases	cycle entry	0	1	4	<input type="checkbox"/>
2	cancer	oxygen	increases	cycle entry	0.00093	21.5	4	<input type="checkbox"/>
3	cancer	oxygen	decreases	transform to invasive cancer	0	7.5	5	<input type="checkbox"/>
4	invasive cancer	oxygen	increases	transform to cancer	0.01	7.5	5	<input type="checkbox"/>
5								<input type="checkbox"/>
6								<input type="checkbox"/>
7								<input type="checkbox"/>
8								<input type="checkbox"/>
9								<input type="checkbox"/>
10								<input type="checkbox"/>



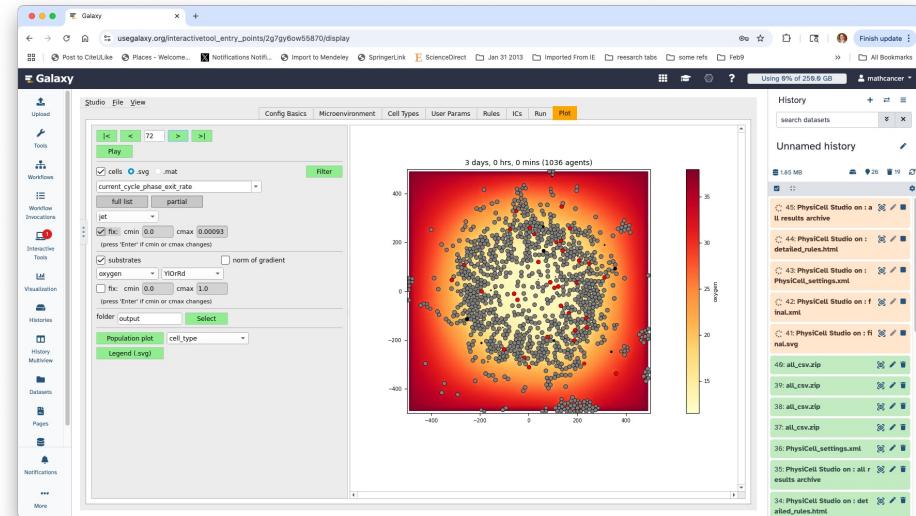
Run and Visualize

- Now, let's color cells by their color

- Go to **Plot**, then **cells**
- Choose **SVG**

- Observe:**

- Invasive cells (red) stream out of low oxygen regions
- Once they reach higher oxygen, they stop and switch back
- These escaped cells nucleate new tumors



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Adding chemotherapy



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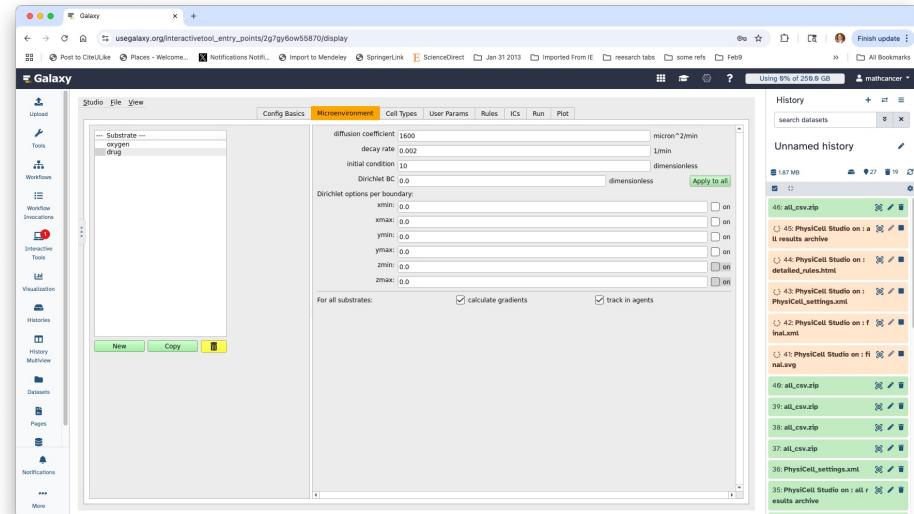
Iterative modeling example

- In the last session, we iteratively built a simple tumor model, bit-by-bit:
 1. Growing tumor with oxygen consumption
 2. Add a mechanofeedback on cycling
 3. Add oxygen-driven cycling
 4. Add an oxygen-based switching to/from an invasive phenotype (EMT and MET)
 - 5. Add a chemotherapy**



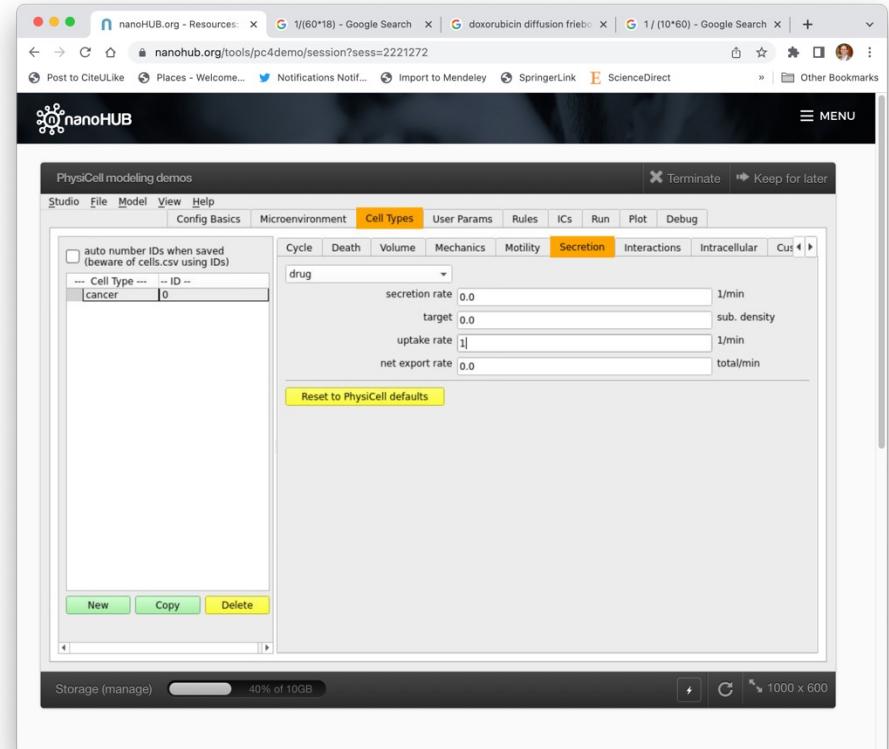
Cytotoxic drug: 1

- First, we add a diffusible drug (e.g., to doxorubicin)
 - Go to the **microenvironment** tab
 - Click on **new**
 - Double-click and rename to **drug**
 - Set diffusion to **1600**
 - Set decay (removal) to **0.002**
 - Most doxorubicin eliminated from tissue by 30 hours. Call this 3 half lives.
 - Set the initial condition to **10**
 - A single initial bolus of drug
 - Make sure the Dirichlet conditions have a (zero) value, but not enabled.



Cytotoxic drug: 2

- Now, we use a cell uptake
 - Go to **cell types**
 - Select **cancer** cells
 - Go to **secretion**
 - Select **drug**
 - Set uptake to 1
 - Use this to give a 40 micron length scale
- Repeat this for invasive cancer



Cytotoxic drug: 3

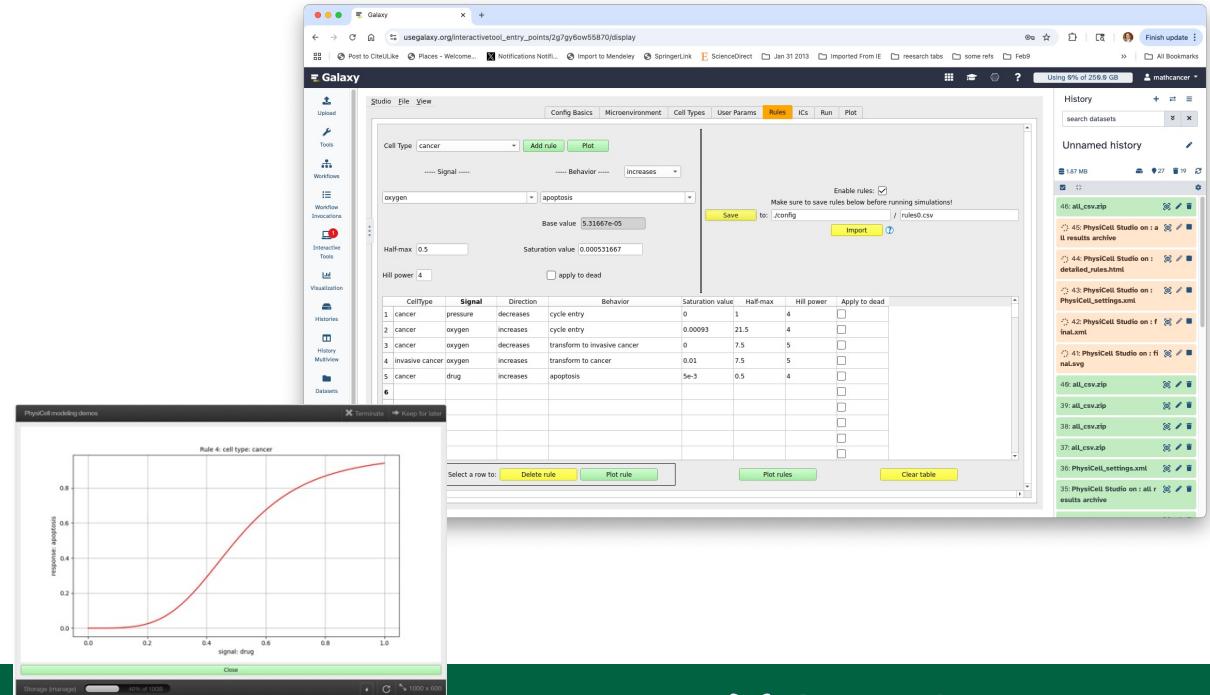
- Now, we add a cytotoxic response

- Go to **rules**
- Add a new rule

- cell type: cancer
- signal: drug
- response: increases
- behavior: apoptosis
- half-max: 0.5
- Hill power: 4
- saturation value: 5e-3
 - » 100x increase over base death
- Click on **add rule**

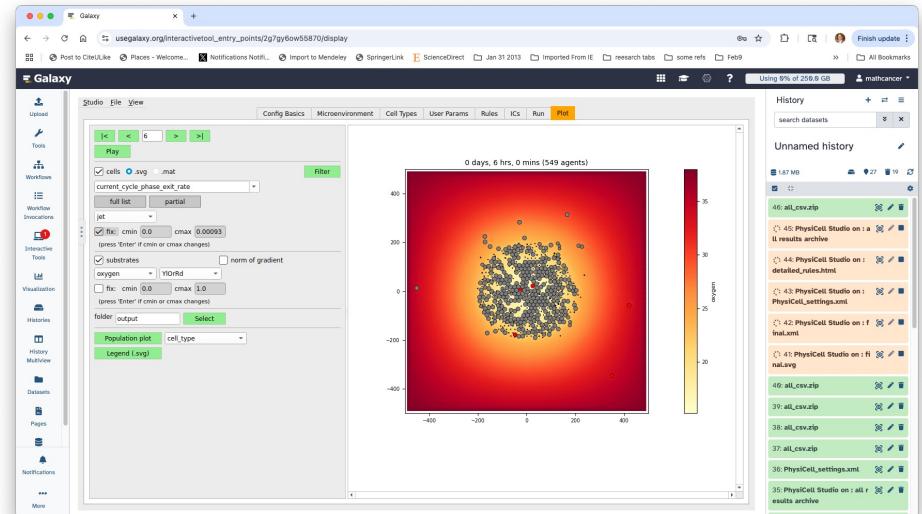
- No effect on invasive cells

- Make sure to click save!**



Run and Visualize

- Let's color cells by standard again:
 - Go to **cells** and select **SVG**
 - Apoptotic cells are black
- **Observe:**
 - Lots of death at first
 - Steep drug gradient
 - Drug quickly removed due to fast drug uptake
 - Tumor recovers
- Better modeling in future:
 - Time-varying boundary conditions



Acknowledgements

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 - **Randy Heiland** : major development of PhysiCell Studio and ports to NanoHub and Galaxy. PhysiCell core developer.
 - **Heber Rocha** : model grammar development, stability analyses on HPC, and more! PhysiCell core developer
 - **Elmar Bucher** Data loading in Python, visualization , ...
 - **Aneequa Sundus** : Training apps, model development, ...
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- **Johns Hopkins (selected)**
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 - **Atul Deshpande** : uncertainty analysis, model selection
 - **Jeanette Johnson** : immunology, simulation model development
- **University of Maryland**
 - **Elana Fertig** : Co-leadership, immune model development, CoGAPS and spatial transcriptomics
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- **Oregon Health & Science University (selected)**
 - **Lisa Coussens** : cancer immunology
 - **Laura Heiser** : cancer immunology, modeling
 - **Joe Gray** : cancer biology & physics
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 - (Heiser, Macklin, Gilkes, Ewald PIs on several awards)



Resources and Thank you!

Cell paper with the modeling language
and spatial transcriptomics:

DOI: [10.1016/j.cell.2025.06.048](https://doi.org/10.1016/j.cell.2025.06.048)



PhysiCell Essentials virtual course

Build your first tumor-immune model in
just a few hours without code.

<https://physicell.org/Training.html>



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PhysiCell Curriculum: Next Steps

Other Virtual Training:

<https://physicell.org/Training.html>

- **PhysiCell Essentials**

- More extensive introduction to PhysiCell and hands-on model examples
- Can be run entirely within a web browser (no software downloads or installations required)

- **Integration of Boolean Networks with PhysiBoSS**

- Learn how to integrate Boolean signaling networks into PhysiCell Models

- **Advanced PhysiCell Modeling**

- Learn about creating non-standard model components and visualization in C++
- Learn about C++ extensions for ODE models, ECM fibers, and more.

- **PhysiCell for Developers**

- Learn about PhysiCell core C++ structure, and contributing to PhysiCell core and extensions

