https://github.com/physicell-training/ws2023

# Advanced Session 7: Intracellular with libRoadrunner (interactive demo)



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Markon PhysiCell

# PhysiCell Project

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# Logistics

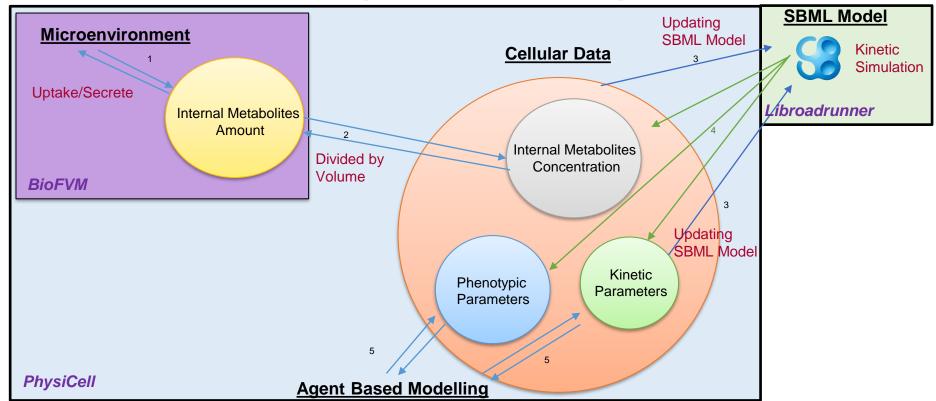
- This is an interactive demo session
- You can stop me during the presentation if you have any question
- Due to limited time SBML-creation will not be covered.
  - Please follow previous years tutorial
  - https://youtu.be/IMtG44cJejM?t=1691
- In this session we will be using PhysiCell studio to create config file.
- Rest of it will be on coding including running
- It is a slightly simple model than "ode-energy-sample" model
  - No cycling

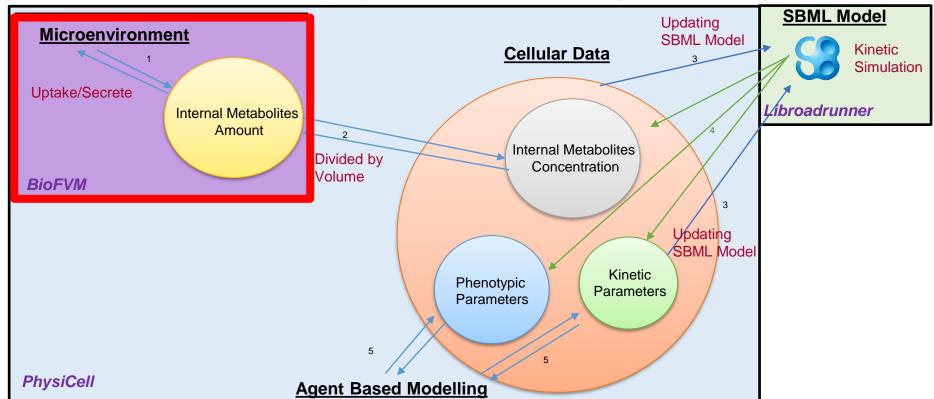
# Agenda:

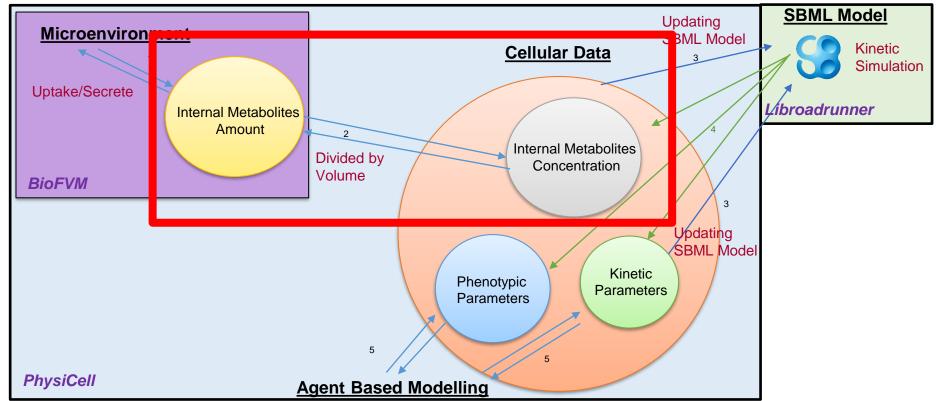
- Previous Session
  - Integration
  - Tokens
- Model Description
- SBML Model
  - Copasi Exploration
- SBML Integration in PhysiCell
- Simulation & Analysis

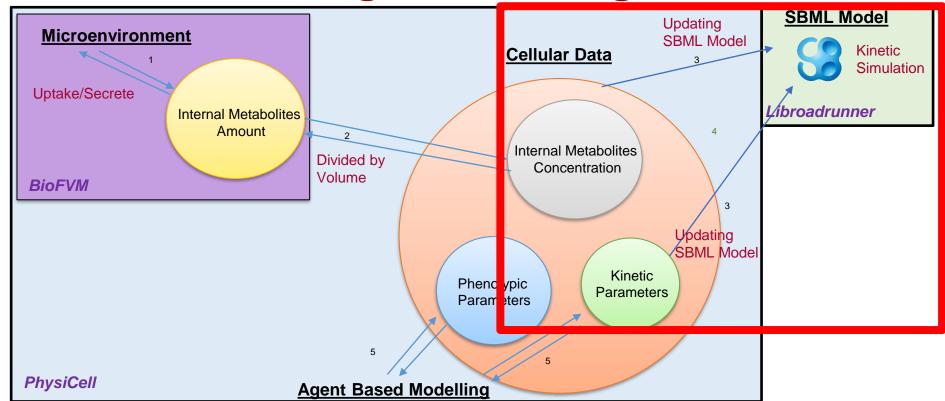
# Agenda:

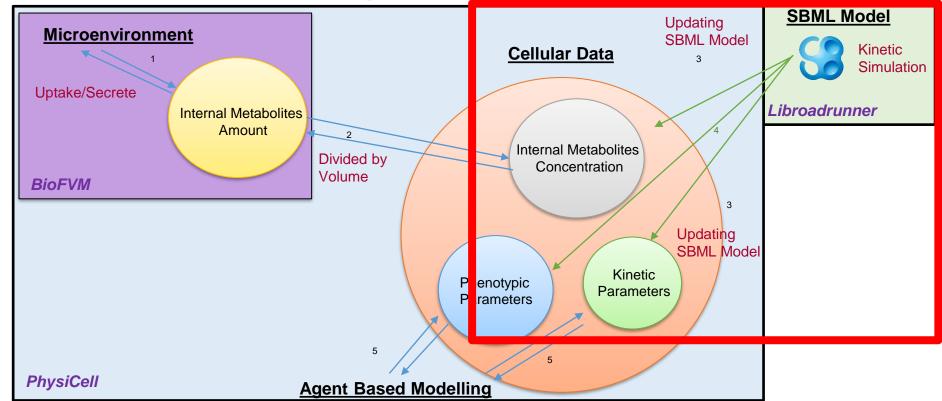
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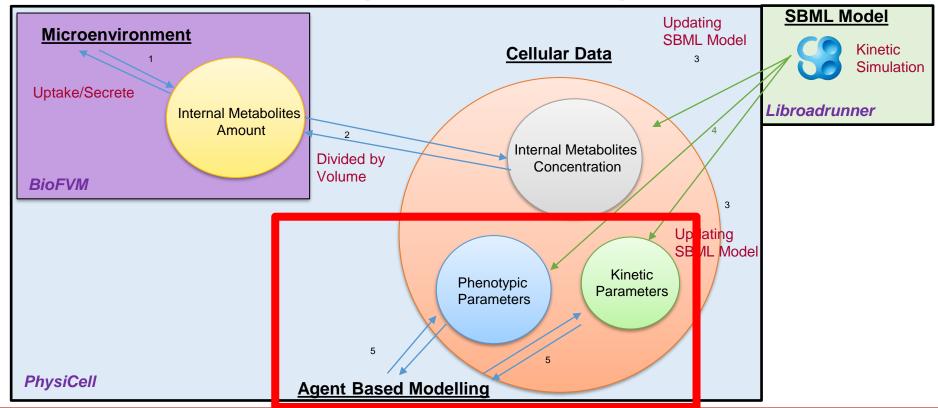














**SBML-Phenotypic Parameters** 

PhysiCell Phenotype Parameter	First letter	phenotype_token	example
Phase Transition Rate	С	ctr_*_*	ctr_ <mark>0_1</mark>
Death Rate	d	da,dn	da,dn
Persistence Time	m	mpt	mpt
Migration Speed	m	mms	mms
Migration Bias	m	mmb	mmb
Uptake rate	S	sur_*	sur_oxygen
Secretion rate	S	ssr_*	ssr_glucose
Saturation density	S	ssd_*	ssd_oxygen
Export rate	S	ser_*	ser_lactate
Target solid cytoplasmic	V	vtsc	vtsc
Target solid nuclear	V	vtsn	vtsn
Target fluid fraction	V	vff	∨ff



PhysiCell Project
PhysiCell.org

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# LibRoadRunner Interactive Demo

#### SBML Model

- Three Substrates
  - Oxygen, Glucose, Lactate
  - Energy is created with two reactions
    - ♦ Glucose + Oxygen -> 38 \* Energy (Aerobic)
    - ♦ Glucose -> 4 \* Energy + Lactate (Anaerobic)
  - Energy consumes
    - ♦ Energy -> (Energy\_Usage)
- Phenotypic Tokens
  - migration speed, apoptosis\_rate, lac\_Secretion\_Rate

Please be aware this is a toy model to show libRR capability. Parameters are not scientifically estimated.

### **Model Rules**

- Initial Energy = 450
- If Energy > 445
  - Yellow
- If Energy < 440</li>
  - Motile
- If Energy < 430
  - Die

#### **Generic Workflow**

- Create (we will browse) SBML on Copasi
- Create the model domain in the PhysiCell Studio
  - Config Basics
  - Microenvironment
  - Cell parameters
- Integrate SBML to PhysiCell model

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# **SBML Exploration**

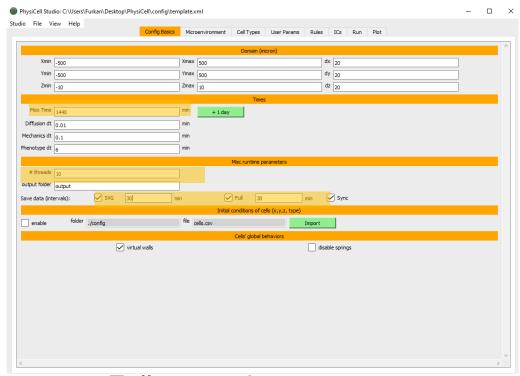


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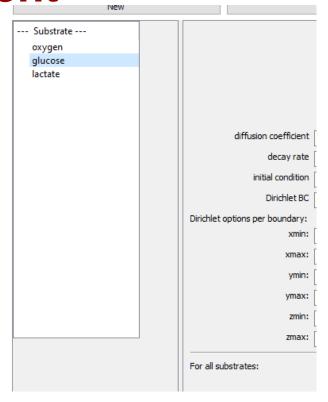
# **Config Basics**

- Domain size
  - X=[-500,500]
  - Y=[-500,500]
  - Z=[-10,10]
  - dx,dy,dz = 20
  - Use\_2D = true
- Max-time = 1440 min
- Thread = your choice
- Save data : SVG = 30 min,

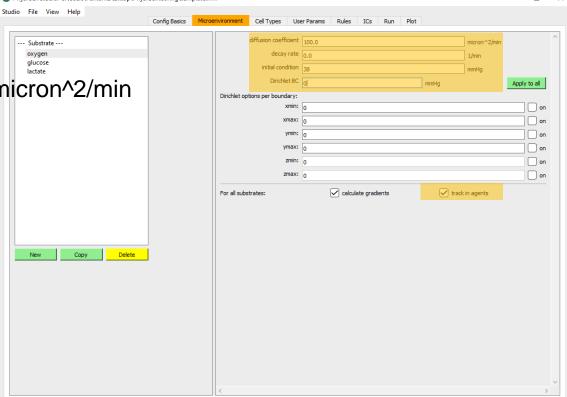


Full = 30 min

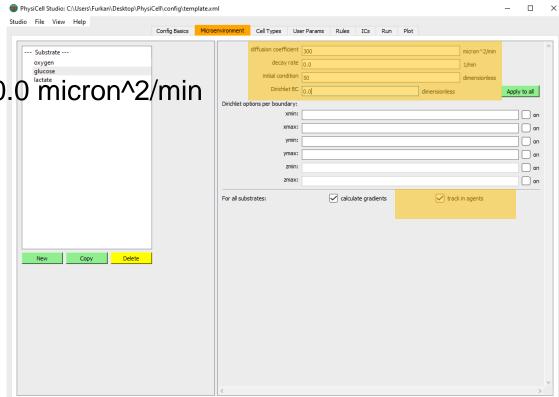
- Microenvironment Tab
- Let's add "oxygen", "glucose", "lactate"



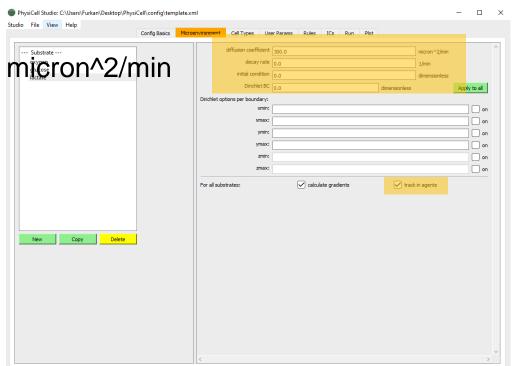
- Oxygen
- Diffusion Coefficient = 100.0 micron^2/min
- Decay Rate = 0.0 1/min
- Initial condition = 38.0 mmHg
- Dirichlet = OFF
- Track in agents = ON



- Glucose
- Diffusion Coefficient = 300.0 micron^2/min
- Decay Rate = 0.0 1/min
- Initial condition = 50.0 a.u
- Dirichlet = OFF
- Track in agents = ON



- Lactate
- Diffusion Coefficient = 300.0 micron^2/min
- Decay Rate = 0.0 1/min
- Initial condition = 0.0 mmHg
- Dirichlet = OFF
- Track in agents = ON

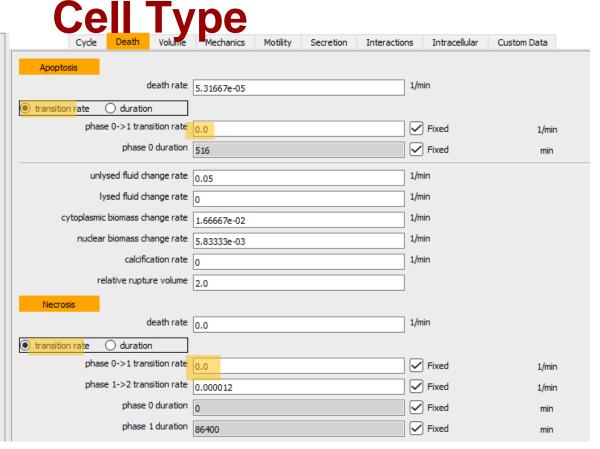


# **Cell Type**

- Only one type of cell in the name of "default"
- Cycle
  - Live Cells
  - Transition rate(s)
  - **0.0**

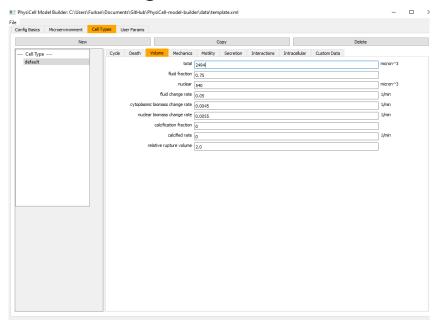


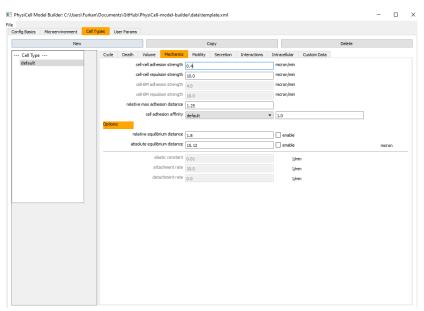
#### No Death



# **Cell Type**

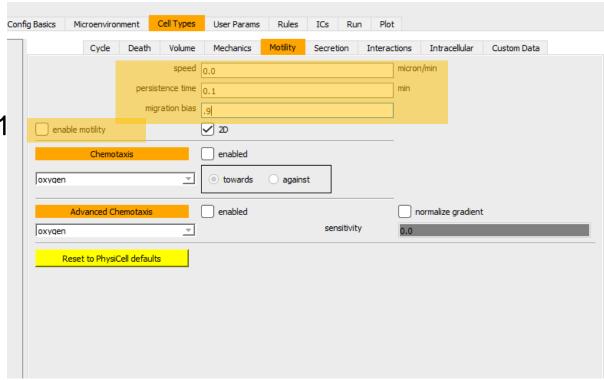
No change in the Volume and Mechanics Tab





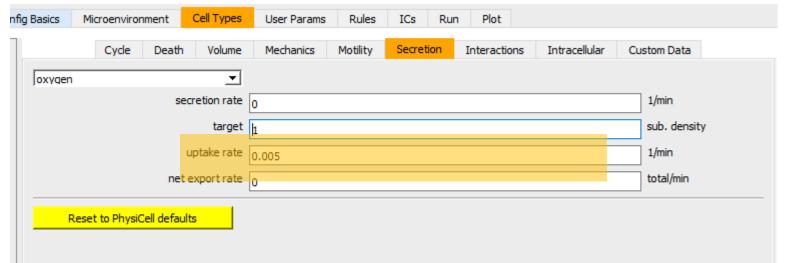
# **Cell Type**

- Motility
- Speed = 0.0
- Persistence Time = 0.1
- Migration Bias = 0.9
- Enable-motility
- 2D = Yes



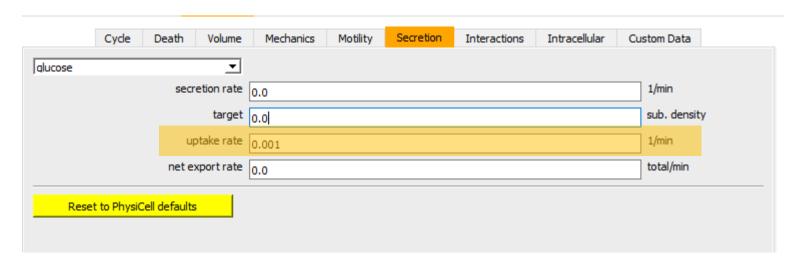
# **Cell Type: Secretion**

- Oxygen Tab
- Uptake rate = 0.005



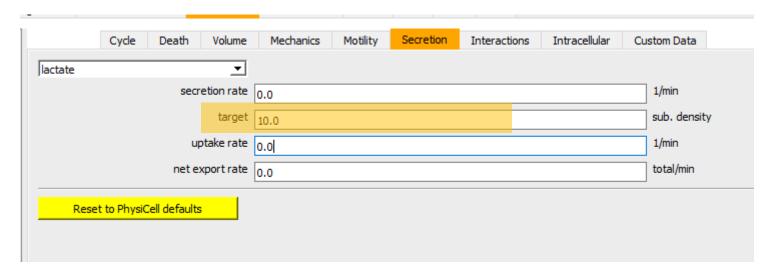
# **Cell Type: Secretion**

- Glucose Tab
- Uptake rate = 0.001



# **Cell Type: Secretion**

- Lactate Tab
- Secretion Target = 10.0



# **Cell Type**

#### No Interactions

Cycle	Death	Volume	Mechanics	Motility	Secretion	Interactions	Intracellular	Custom Data
				dead ph	agocytosis rate	: ol		1/min
!	live phagocy	ytosis rate	default		_	0		1/min
	a	ttack rate	default		_	0		1/min
					damage rate	1		1/min
	f	usion rate	default		_	0		1/min
	transform	ation rate	default			0		1/min

#### **Cell Custom Data**

- We need to create intracellular data to save the data
- intra\_oxy = 0.0
- intra\_glu = 0.0
- intra\_lac = 0.0
- intra\_energy = 0.0

	Cycle	Death	Volume	Mechanics	Motility	Secretion	Inte
Sear	rch for Name						
	Name		Value	Conser	ve	Units	
1	intra_oxy	0.0			din	nensionless	
2	intra_glu	0.0					
3	intra_lac	0.0					
4	intra_energy	0.0					
5		0.0					
6		0.0					
7		0.0					

### **User Params**

- initial\_internal\_oxygen (double) = 0.8
- initial\_internal\_glucose (double) = 15
- initial\_internal\_lactate (double) = 0.0
- initial\_energy (double) =450

	Name	Туре	Value	Units	Desc
1	random_seed	int •	0	dimensionless	
2	ial_internal_oxygen	double 🔻	0.8	none	(for each cell type)
3	ial_internal_glucose	double 🔻	15		
4	tial_internal_lactate	double •	0.0		
5	initial_energy	double 🔻	450	I	
6		double 🔻			
7		double 🔻			

### Save

Let's check is it right

## Let's add intracellular attribute at config

```
<intracellular type="roadrunner">
<sbml filename>./config/Toy Metabolic Model.xml</sbml filename>
            <intracellular dt>0.01</intracellular dt>
            <map PC substrate="oxygen" sbml species="Oxygen"></map >
            <map PC_substrate="lactate" sbml_species="Lactate"></map >
            <map PC substrate="glucose" sbml species="Glucose"></map >
            <map PC phenotype="da" sbml species="apoptosis rate"></map>
            <map PC phenotype="mms"</pre>
sbml species="migration speed"></map>
            <map PC_phenotype="ssr lactate"</pre>
sbml species="Lac Secretion Rate"></map>
</intracellular>
```

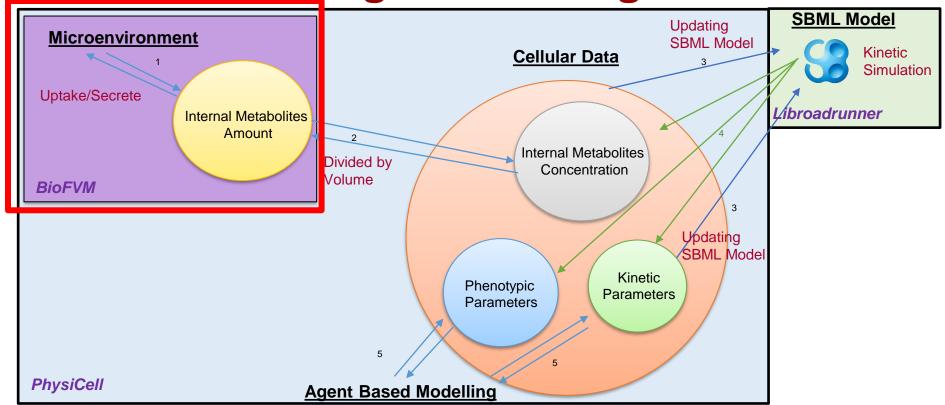
# Reproducing

- We will remove intracellular-related parts
- And build one-by-one
- At custom.cpp
  - setup\_tissue():
    - ♦ Remove lines between #174-198
  - update\_intracellular():
    - ♦ Remove anything in if loop #216-245
      - » Beware line numbers might shift after first removal

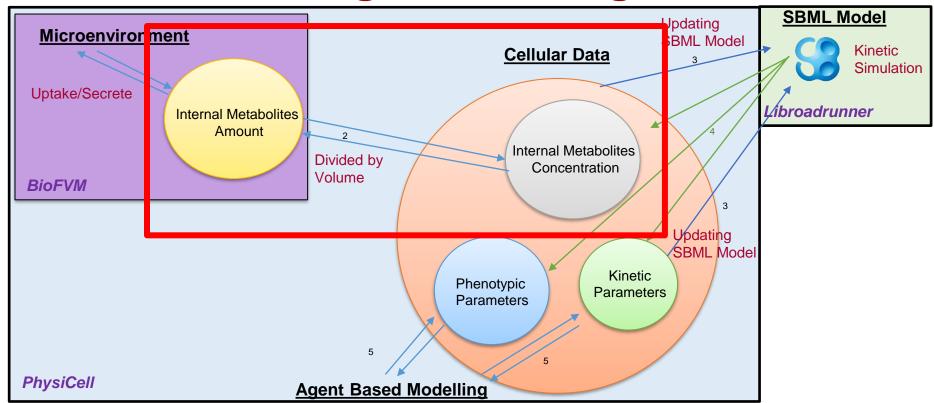
```
----- GROUND_ZERO.zip -----
```

## setup\_tissue(): after cell seeding

```
// let's set initial intracellular custom data according to config specifications
set single behavior (pCell, "custom:intra oxy", parameters.doubles ("initial internal oxygen"));
set single behavior( pCell , "custom:intra glu" , parameters.doubles("initial internal glucose"));
set single behavior(pCell, "custom:intra lac", parameters.doubles("initial internal lactate"));
set single behavior( pCell , "custom:intra energy" , parameters.doubles("initial energy"));
double cell volume = pCell->phenotype.volume.total;
// set the internalized values
set single behavior( pCell , "custom:intra oxy" , parameters.doubles("initial internal oxygen"));
pCell->phenotype.molecular.internalized total substrates[oxygen substrate index] = get single signal( pCell,
"custom:intra oxy") * cell volume;
pCell->phenotype.molecular.internalized total substrates[glucose substrate index] = get single signal( pCell,
"custom:intra glu") * cell volume;
pCell->phenotype.molecular.internalized total substrates[lactate substrate index] = get single signal( pCell,
"custom:intra lac") * cell volume;
pCell->phenotype.intracellular->start();
pCell->phenotype.intracellular->set parameter value("Energy",get single signal( pCell, "custom:intra energy"));
```



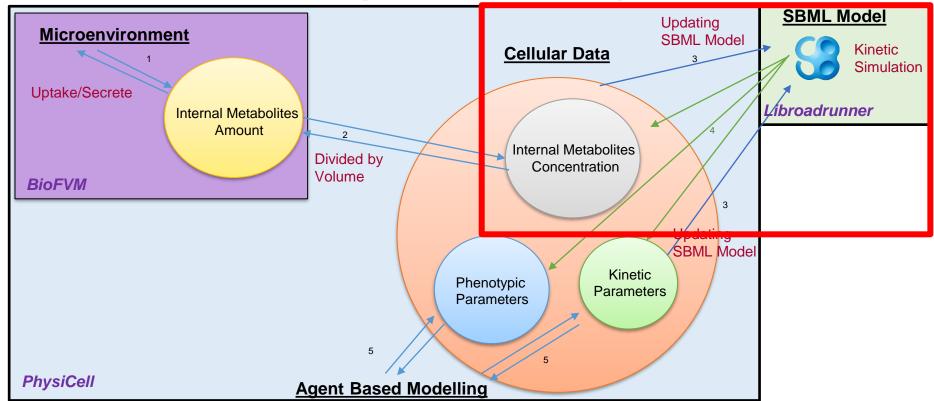






```
// Cell Volume
double cell_volume = (*all_cells)[i]->phenotype.volume.total;

// Get Intracellular Concentrations
double oxy_val_int = get_single_signal((*all_cells)[i], "intracellular oxygen");
double glu_val_int = get_single_signal((*all_cells)[i], "intracellular glucose");
double lac_val_int = get_single_signal((*all_cells)[i], "intracellular lactate");
```

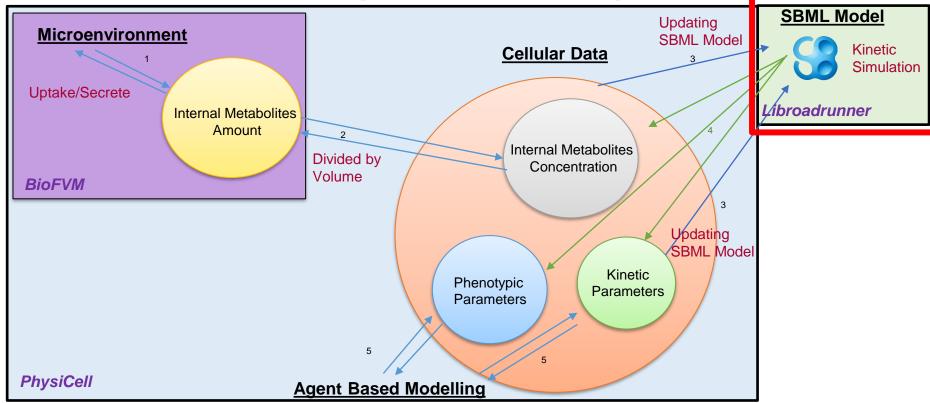


```
// Update SBML

(*all_cells)[i]->phenotype.intracellular->set_parameter_value("Oxygen",oxy_val_int);

(*all_cells)[i]->phenotype.intracellular->set_parameter_value("Glucose",glu_val_int);

(*all_cells)[i]->phenotype.intracellular->set_parameter_value("Lactate",lac_val_int);
```



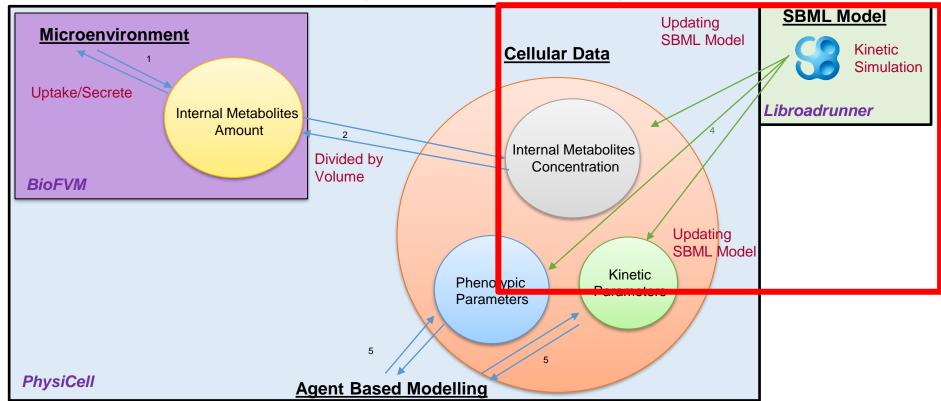


```
// SBML Simulation

(*all_cells)[i]->phenotype.intracellular->update();

// Phenotype Simulation

(*all_cells)[i]->phenotype.intracellular->update_phenotype_parameters((*all_cells)[i]
```



```
// Internalized Chemical Update After SBML Simulation
(*all cells)[i]->phenotype.molecular.internalized total substrates[oxygen substrate index] =
(*all cells)[i]->phenotype.intracellular->get parameter value("Oxygen") * cell volume;
(*all cells)[i]->phenotype.molecular.internalized total substrates[glucose substrate index] =
(*all cells)[i]->phenotype.intracellular->get parameter value("Glucose") * cell volume;
(*all cells)[i]->phenotype.molecular.internalized total substrates[lactate substrate index] =
(*all cells)[i]->phenotype.intracellular->get parameter value("Lactate") * cell volume;
//Save custom data
set single behavior( (*all cells)[i] , "custom:intra oxy" , (*all cells)[i]->phenotype.intra
>get parameter value("Oxygen") );
set single behavior( (*all cells)[i] , "custom:intra glu" , (*all cells)[i]->phenotype.intra
>get parameter value("Glucose") );
set single behavior( (*all cells)[i] , "custom:intra lac" , (*all cells)[i]->phenotype.intra
>get parameter value("Lactate") );
set single behavior( (*all cells)[i] , "custom:intra energy" , (*all cells)[i]->phenotype.int
```



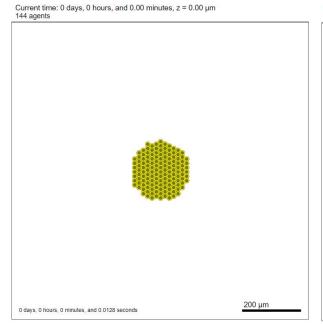
>get parameter value("Energy") );

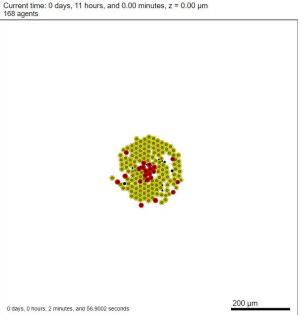
### Let's Simulate

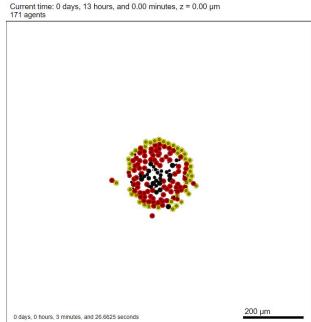
I will use beta/plot\_cells.py and beta/plot\_data for analysis

```
(base) C:\Users\Furkan\Desktop\PhysiCell>python beta/plot_data.py
```

```
----- Final_Model.zip ------
```







### If time allows

Let's change dt\_intracellular to 6 min

Do you see any differences?

## **Up next**

- End of live sessions for today.
- One lecture is left tomorrow at 11:05am (ET)
- Let's meet at the Hackathon for the Team Time

# Funding Acknowledgements











#### **PhysiCell Development:**

- Breast Cancer Research Foundation
- Jayne Koskinas Ted Giovanis Foundation for Health and Policy
- National Cancer Institute (U01CA232137)
- National Science Foundation (1720625, 1818187)

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- NIH Common Fund (3OT2OD026671-01S4)

