Slides, videos, links and more:
https://github.com/physicell-training/ws2021

Session 11: Intracellular Modeling

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PhysiCell Project

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What we have learned so far

- PhysiCell folder structure
- PhysiCell model domain
  - Different dts (diffusion_dt, mechanic_dt, phenotype_dt)
- Using GUI to create config file (XML)
- PhysiCell C++ functions

What we will learn

- Basics of Kinetic Modeling (ODE Model)
- How to integrate kinetic models to ABM
- How to control phenotype based on intracellular model
- Kinetic ODE solver (libRR) related functions
- How to save intracellular data
- How to make faster your simulation with losing convergence

Agenda:

- First Session
  - PhysiCell 1.9.0
  - Kinetic SBML
  - PhysiCell Integration
    - Model Design
    - Results
    - Convergence Tests
  - libRR Add-on
    - Functions
    - Phenotypic Changes
  - Sample Model
    - Description
    - Basic Domain Creation (If we can)

PhysiCell 1.9.0

- PhysiCell 1.9.0
  - Released: 12 July 2021
- Major new features
  - Includes three intracellular modeling approaches
    - Boolean Network => PhysiBoSS
    - Kinetic Modeling (ODEs) => libroadrunner
    - Flux Balance Analysis => PhysidFBA
  - New Intracellular Object in Phenotype
    - All intracellular packages basic generic functions with same syntax
      - Start(), Update(), get_parameter(), set_parameter(), …
    - Some special functions specific to packages
      - get_boolean_variable_value(PhysiBoSS) validate_SBML_species (ODE), …

3 Sample Projects

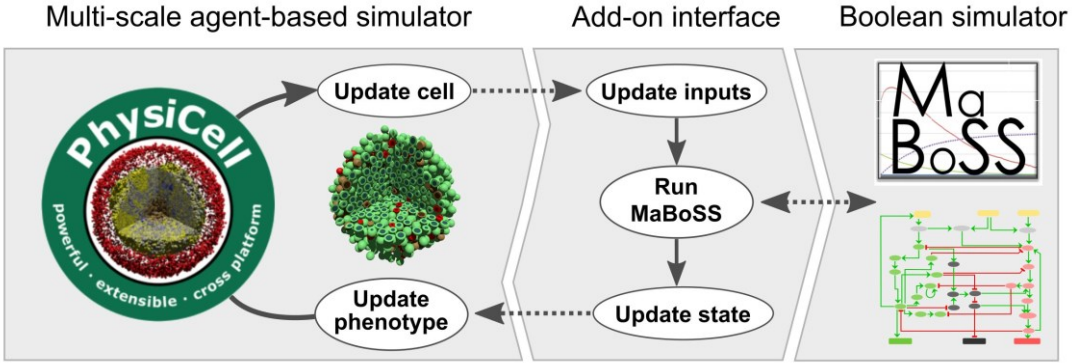
- PhysiBoSS
  - physiboss-cell-lines-sample
- Libroadrunner
  - ode-sample-project
- PhysidFBA
  - cancer-metabolism

Installation

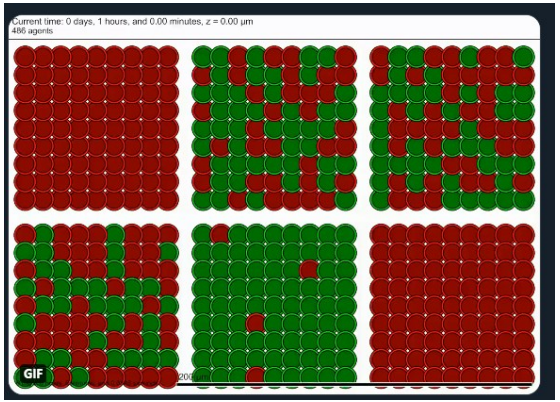
- Each add-on requires related solver
  - PhysiBoSS – MaBoSS
  - PhysidFBA – coin-clp
  - Libroadrunner – Libroadrunner (no surprise!)
- To install related solver, you need to populate sample-project, first
  - make ode-energy-sample
- Then, compile once.
  - make

PhysiBoSS

- Boolean Network
  - MaBoSS
- SysBioCurie & BSC

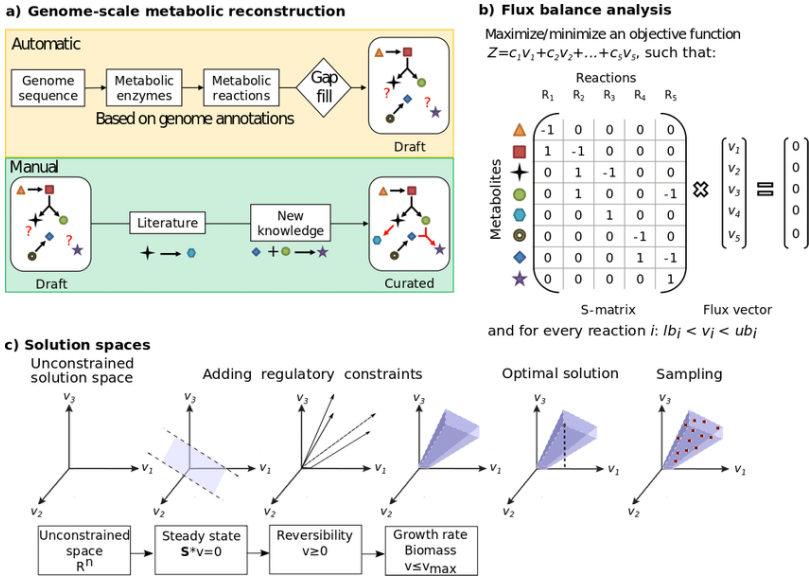


- https://github.com/gletort/PhysiBoSS
  - Fully integrated as “add-on” to PhysiCell
- We had an optional morning session
  - Please visit agenda for slides and video



PhysidFBA

- Aims to couple ABM and FBA.
- Miguel Ponce de Leon
- Approach will be explained in future slides.
- https://github.com/migp11/PhysiCelldFBA
  - Added alpha version as “add-on” to PhysiCell.



Heirendt et al, 2017

Libroadrunner

- Integrating intracellular kinetic models to individual agents.
- Individual phenotype changes according to molecular simulations
  - Intracellular values (Molecular Concentrations, Signal Transductions, i.e.)
    - Intracellular oxygen deficiency in cell leads to change necrosis rate.
    - Intracellular amino acids levels define the cellular growth / cycle rate.
- Opens new opportunities for PhysiCell syntax
  - Users can utilize SBML to model phenotypic behaviors.
  - Since molecular values can edit phenotypic parameters in SBML, PhysiCell interface is getting changed.
- LibRR is developed by
  - Herbert Sauro and Andy Somogyi
  - C++ API

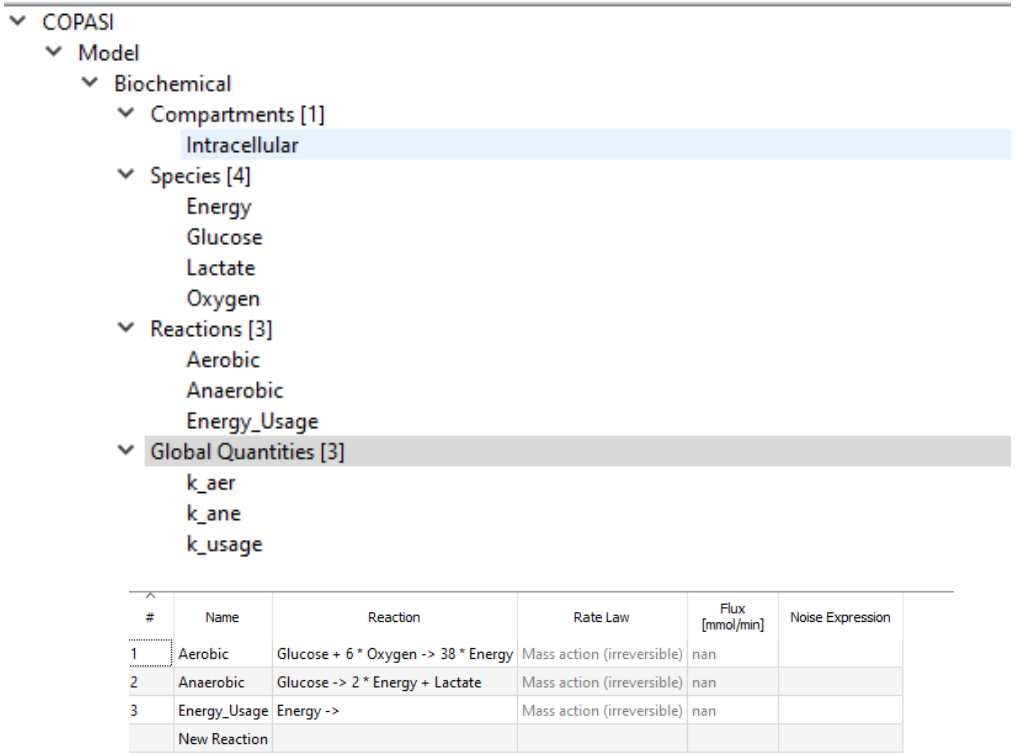
SBML

- Systems Biology Mark-up Language
- Reaction – Stoichiometry
- Kinetic – Pseudo Steady State
  - Kinetic – Ordinary Differential Equations
  - Pseudo Steady State – Optimization (Flux Balance Analysis)
- Hard to read for Human (xml file)
- Parsed according to some rules.

```
[...]
<species metaid="heme"
      id="heme"
      compartment="Comp01"
      initialConcentration="0">
   <annotation>
      <rdf:RDF xmlns:rdf="http://www.w3.org/1999/02/22-rdf-syntax-ns#"
               xmlns:bqbiol="http://biomodels.net/biology-qualifiers/">
         <rdf:Description rdf:about="#heme">
            <bqbiol:hasPart>
               <rdf:Bag>
                  <rdf:li rdf:resource="urn:miriam:uniprot:P69905" />
                  <rdf:li rdf:resource="urn:miriam:uniprot:P68871" />
                  <rdf:li rdf:resource="urn:miriam:obo.chebi:CHEBI%3A17627" />
               </rdf:Bag>
            </bqbiol:hasPart>
         </rdf:Description>
      </rdf:RDF>
   </annotation>
</species>
[...]
```

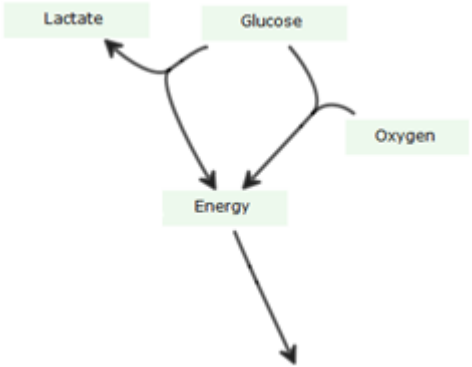
SBML

- Compartments
  - Volumetric Entities
- Species
  - Chemicals
- Reactions
  - Stoichiometric Relations
  - Boundaries (Lower and Upper) (FBA)
- Global Quantities
  - Parameters
  - Constants



#	Name	Reaction	Rate Law	Flux [mmol/min]	Noise Expression
1	Aerobic	Glucose + 6 * Oxygen -> 38 * Energy	Mass action (irreversible)	nan	
2	Anaerobic	Glucose -> 2 * Energy + Lactate	Mass action (irreversible)	nan	
3	Energy_Usage	Energy ->	Mass action (irreversible)	nan	
	New Reaction				

Kinetic Modeling



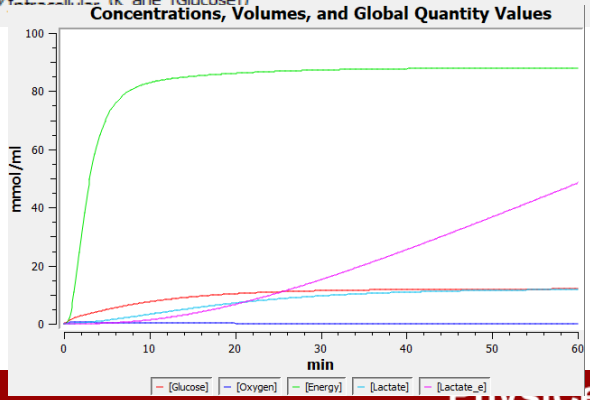
#	Name	Reaction
1	Aerobic	Glucose + 6 * Oxygen -> 38 * Energy
2	Anaerobic	Glucose -> 2 * Energy + Lactate
3	Energy_Usage	Energy ->
	New Reaction	

$$\frac{d([Glucose] \cdot V_{Intracellular})}{dt} = -V_{Intracellular} \cdot (k\_aer \cdot [Glucose] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen]) - V_{Intracellular} \cdot (k\_ane \cdot [Glucose])$$

$$\frac{d([Oxygen] \cdot V_{Intracellular})}{dt} = -6 \cdot V_{Intracellular} \cdot (k\_aer \cdot [Glucose] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen])$$

$$\frac{d([Energy] \cdot V_{Intracellular})}{dt} = +38 \cdot V_{Intracellular} \cdot (k\_aer \cdot [Glucose] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen] \cdot [Oxygen]) + 2 \cdot V_{Intracellular} \cdot (k\_ane \cdot [Glucose]) - V_{Intracellular} \cdot (k\_usage \cdot [Energy])$$

$$\frac{d([Lactate] \cdot V_{Intracellular})}{dt} = +V_{Intracellular} \cdot (k\_ane \cdot [Glucose])$$

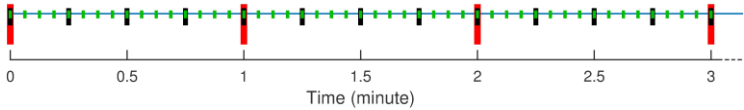


SBML

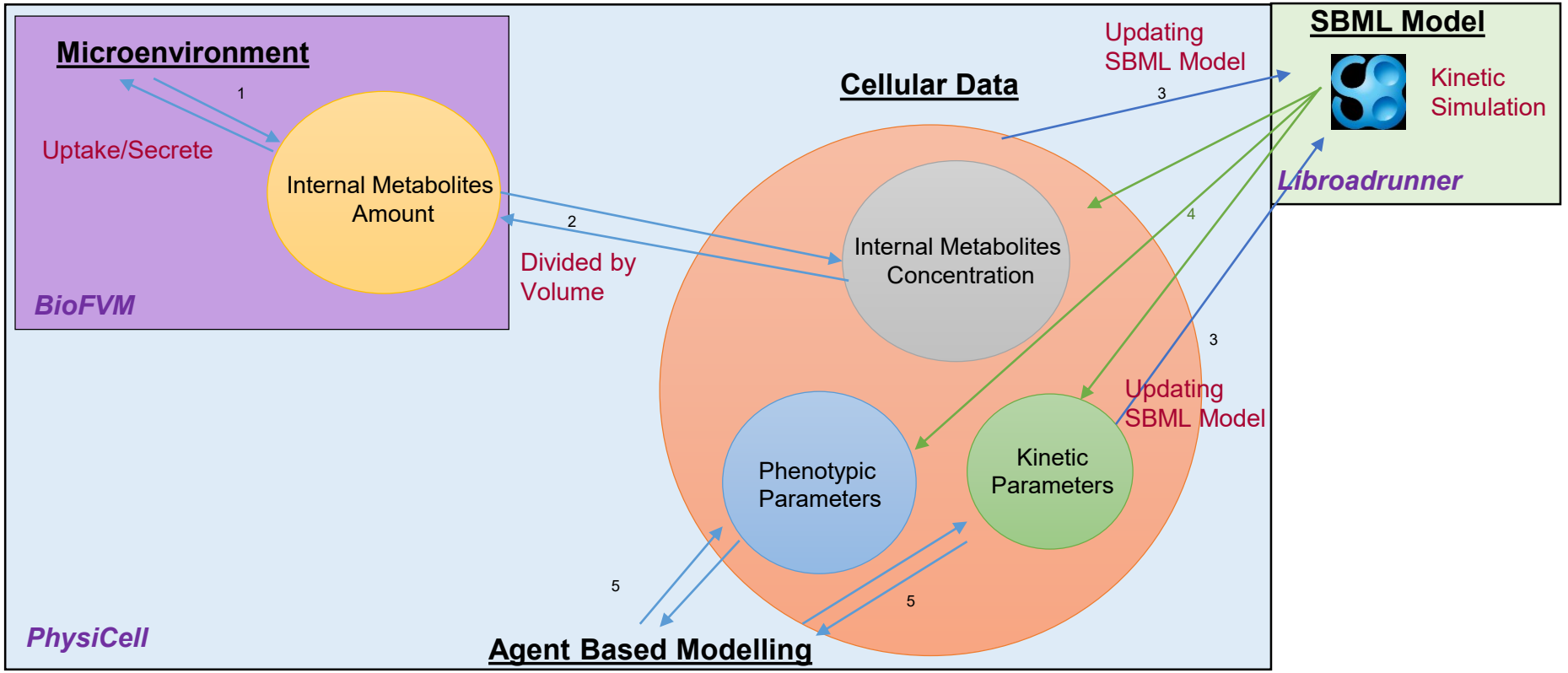
- General SBMLs have more than one compartment
  - Extracellular
  - Intracellular
  - Mitochondria (Sometimes)
  - Nucleus (?)
- And have two or more species for one substrate
  - Glucose[e] => extracellular
  - Glucose[i] => intracellular
- Transfer reaction between compartments
  - Glucose[e] = Glucose[i]

Assumptions

- **But …**
- PhysiCell has transfer reactions through
  - BioFVM
- So, we can support specific type of SBMLs
  - Only Intracellular (might have more than one compartment – Mitochondria, Nucleus)
- Well-Structured SBMLs
  - **Not all SBMLs are supported!!!**
    - **No External Compartment and Transfer Reactions in SBML!**
    - **Mapping is needed between SBML & PhysiCell**
  - Works on each diffusion_dt (0.01 min)
    - (as default for best convergence)



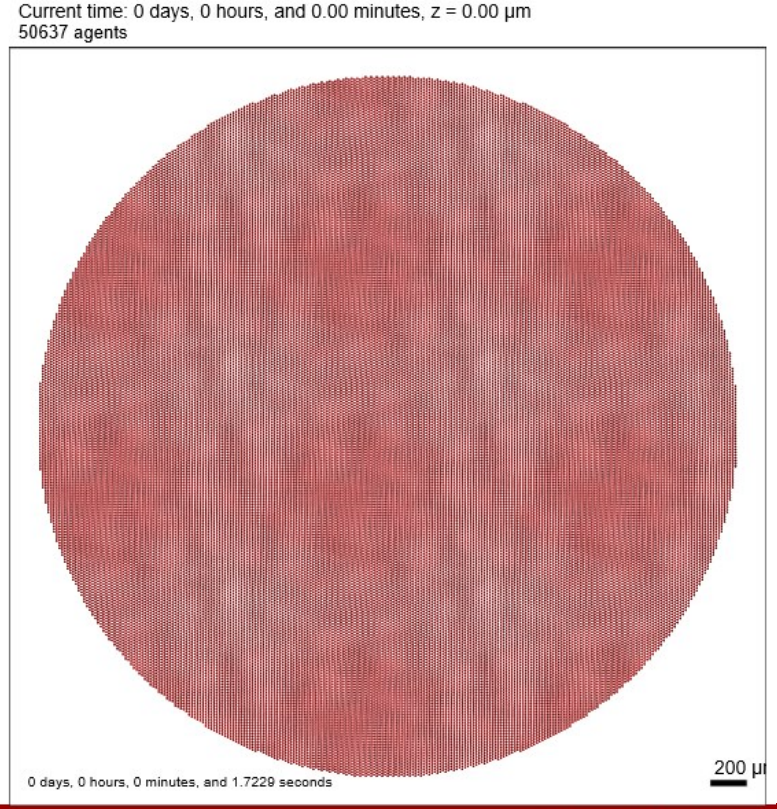
Integration Design



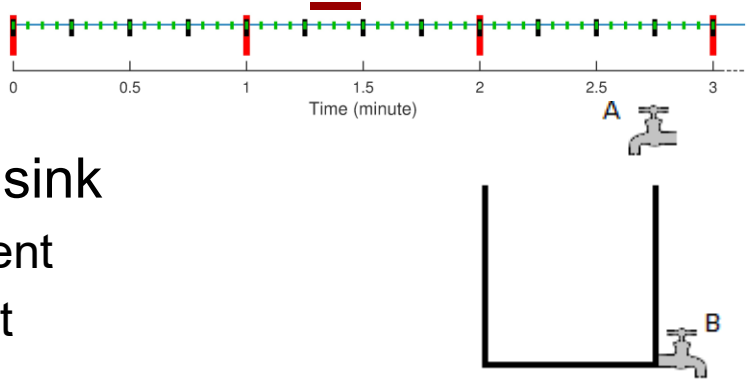
Performance Test

- More than 50,000 cells
- 4 substrate (internalization is on)
- 5 SBML species (4 reactions)
- 4000x4000x20 um dimensions (dx = 20 um)
- Personal PC
  - AMD 6 core 3.0 GHz, 16 GB RAM
  - 8-thread, OpenMP

	1 min output	60 min output
No SBML solver	11 secs	1 min 57 secs
SBML solver	20 secs	16 min 35 secs



How about intracellular_dt



- Default 0.01 min but…
- Imagine cell is like pool with source and sink
  - A = uptaking a chemical from microenvironment
  - B = secreting a chemical to microenvironment
- If diffusion_dt and intracellular_dt is same,
  - They are matching dt's so there is no convergence difference.
  - But it is slow!
- (Figure to be drawn during presentation)

How about intracellular_dt

- However, we can change intracellular_dt.
- Let's assume that we made it 1.00 min (100 times slower)
- How it will look like (Figure to be drawn during presentation)
- So much faster
  - You will see in the Demo

How it looks

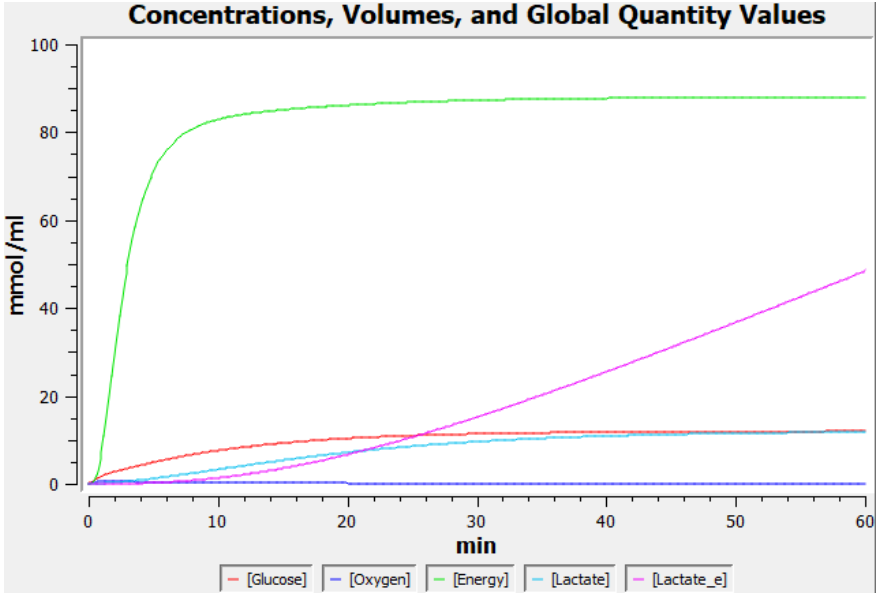
- Config File

```
<cell_definitions>
    <cell_definition name="default" ID="0">
        <phenotype>
            <cycle code="5" name="live">
                <!-- using higher than normal significant digits to match divisions in default code -->
                <transition_rates units="1/min">
                    <rate start_index="0" end_index="0" fixed_duration="false">0.0</rate>
                </transition_rates>
            </cycle>
            <death>
            <volume>
            <motility>
                <speed units="micron/min">0.0</speed>
                <persistence_time units="min">0.1</persistence_time>
                <migration_bias units="dimensionless">.9</migration_bias>
                <options>
                    <enabled>true</enabled>
                    <use_2D>true</use_2D>
                    <chemotaxis>
                        <enabled>false</enabled>
                        <substrate>oxygen</substrate>
                        <direction>1</direction>
                    </chemotaxis>
                </options>
            </motility>
            <secretion>
                
        </phenotype>
```

Some Results

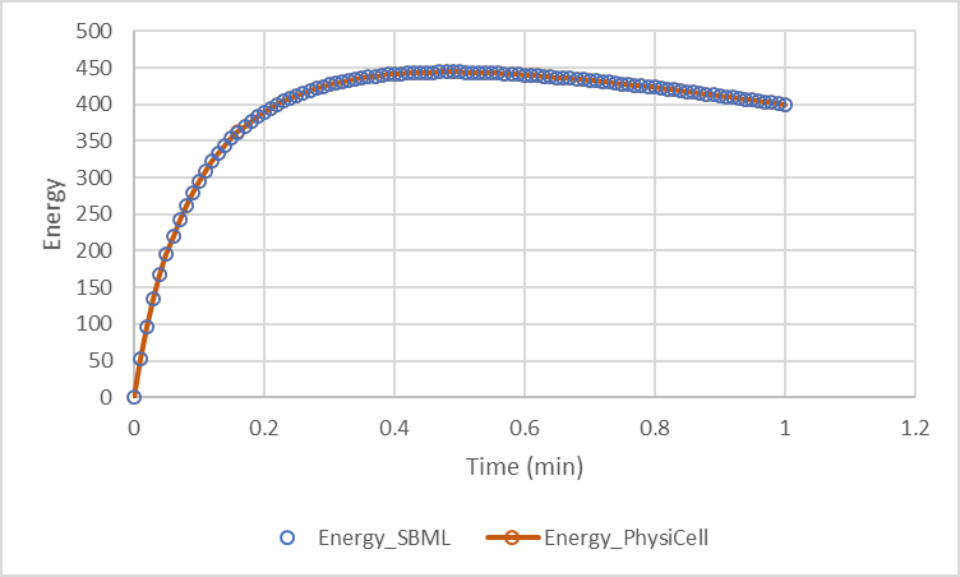
Model 0 - SBML Model

- 4 Species
  - Oxygen
  - Glucose
  - Lactate
  - Energy
- 3 Internal Reactions
  - ♦ Aerobic reaction
    - » Glucose + Oxygen -> Energy
  - ♦ Anaerobic reaction
    - » Glucose -> Energy + Lactate
  - ♦ Energy Usage
    - » Energy ->



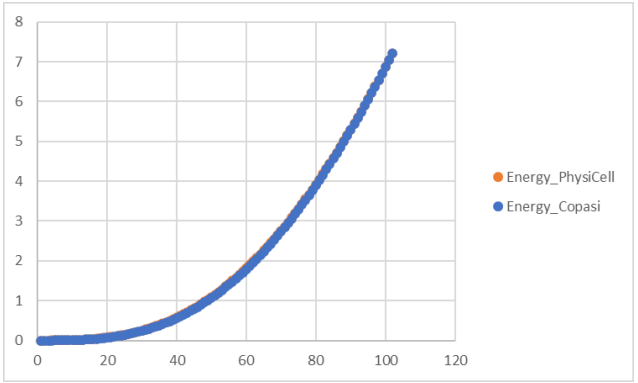
Model 0

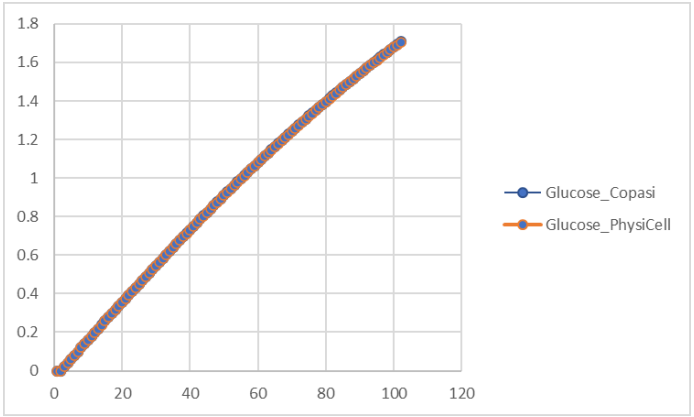
- Very Simple SBML toy model
- Both simulated in PhysiCell and Copasi
- No Transfer Reaction in SBML
- No Uptake Rate
- Only solving SBML



Model 1

- Uptake glucose, oxygen
- Produces Energy internally.

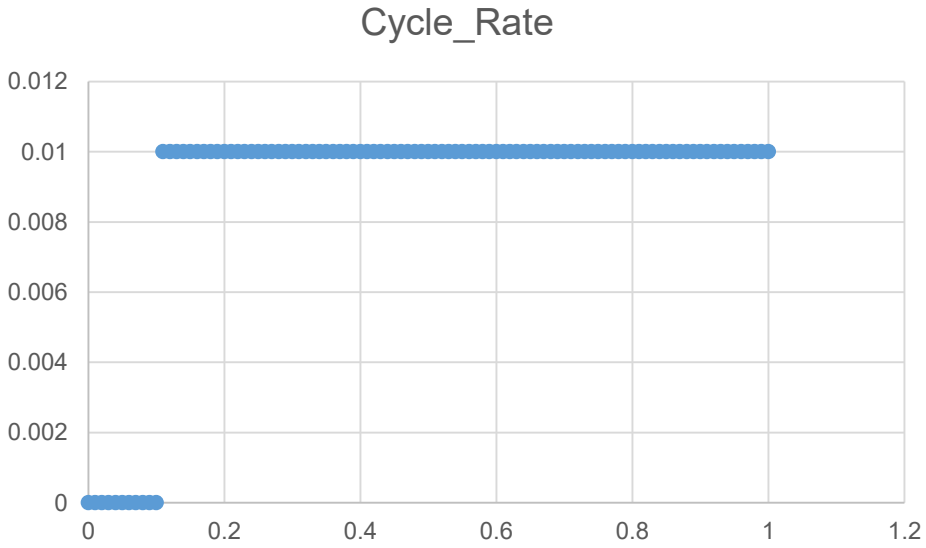




SBML Events

Cycle Rate

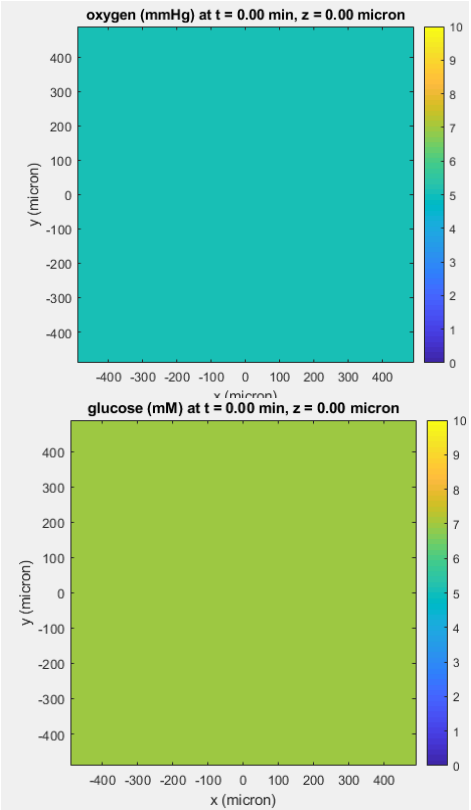
- If Energy level is smaller than 50 a.u.
  - Equals to zero 1/min
- If Energy level is greater than 50 a.u.
  - Equals to 0.01 1/min

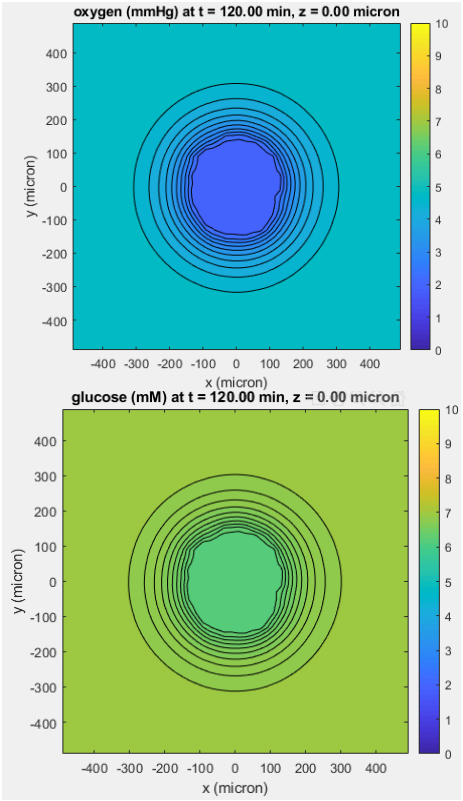


Model 2

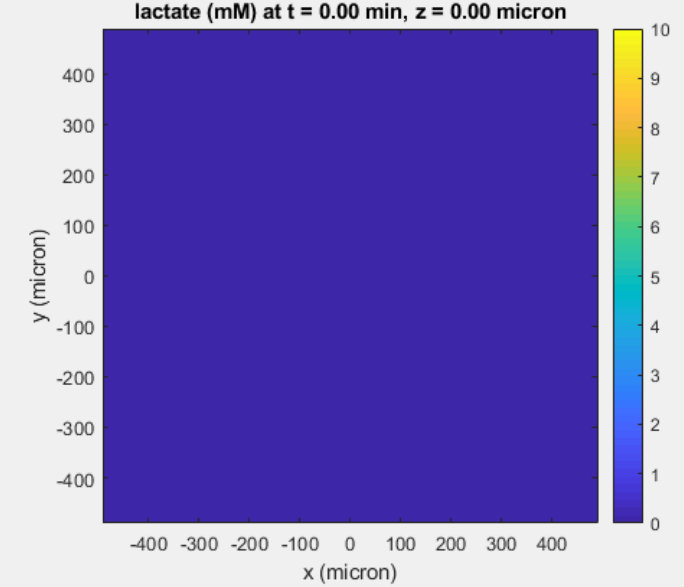
- Phenotypic changes according to SBML species
- Organoid (2D) seeding.
- Lactate Secretion Rate increases
  - Lactate Concentration
- If oxygen level is less than threshold
  - Cells increase their migration speed
- If Energy level is less than threshold
  - Cells go apoptosis

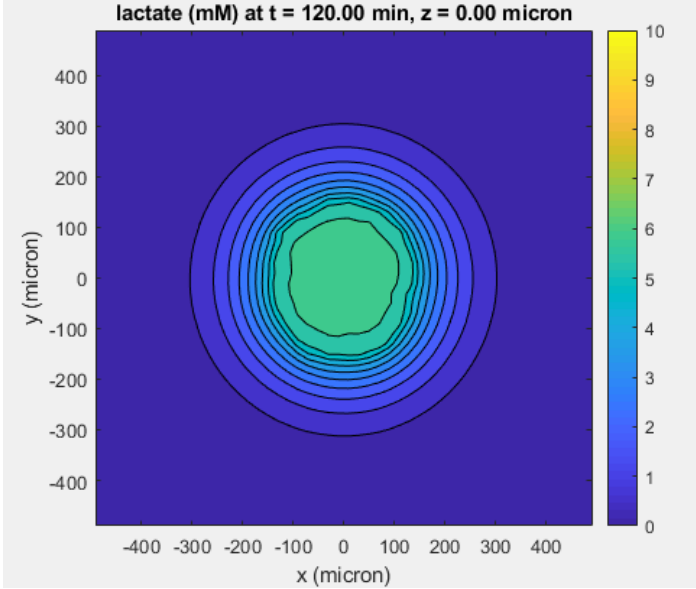
Microenvironment Results

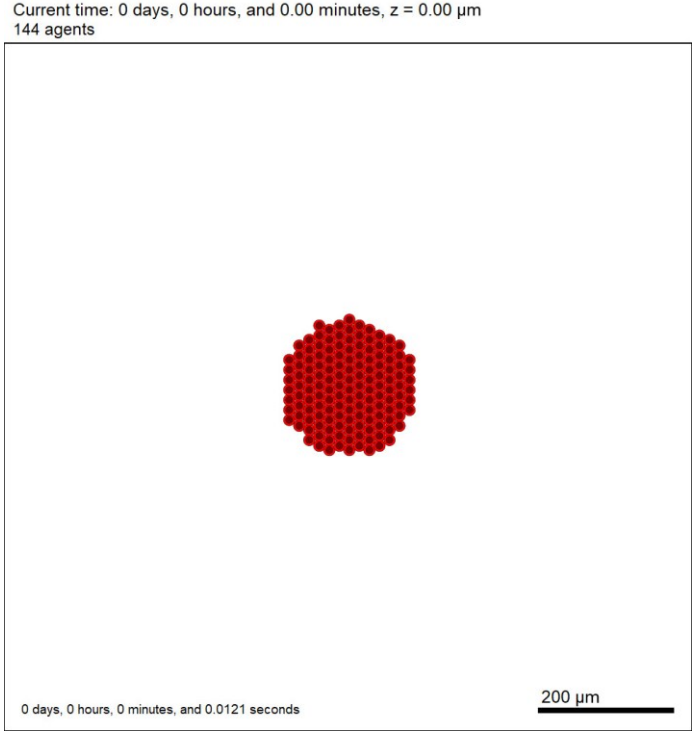




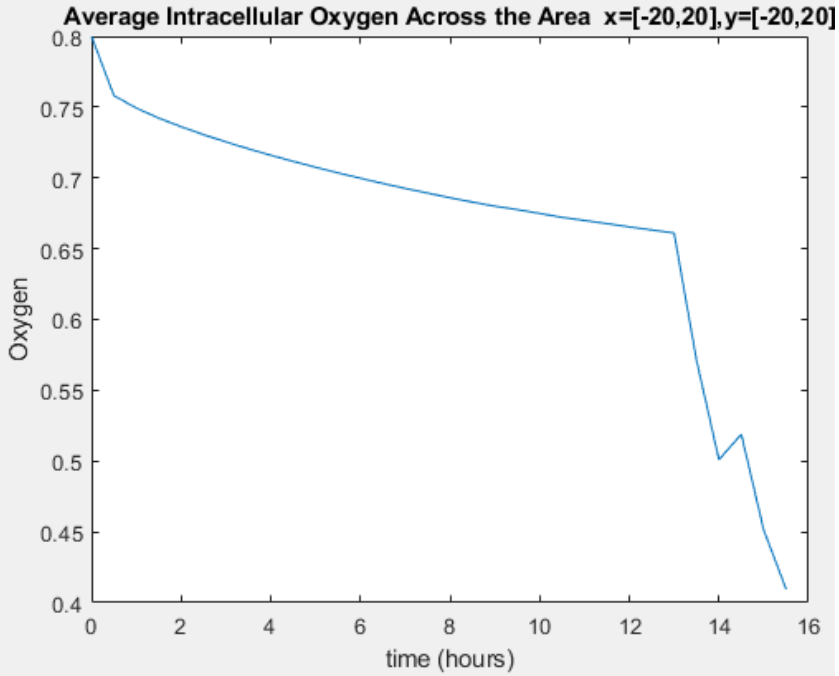
Lactate Secretion

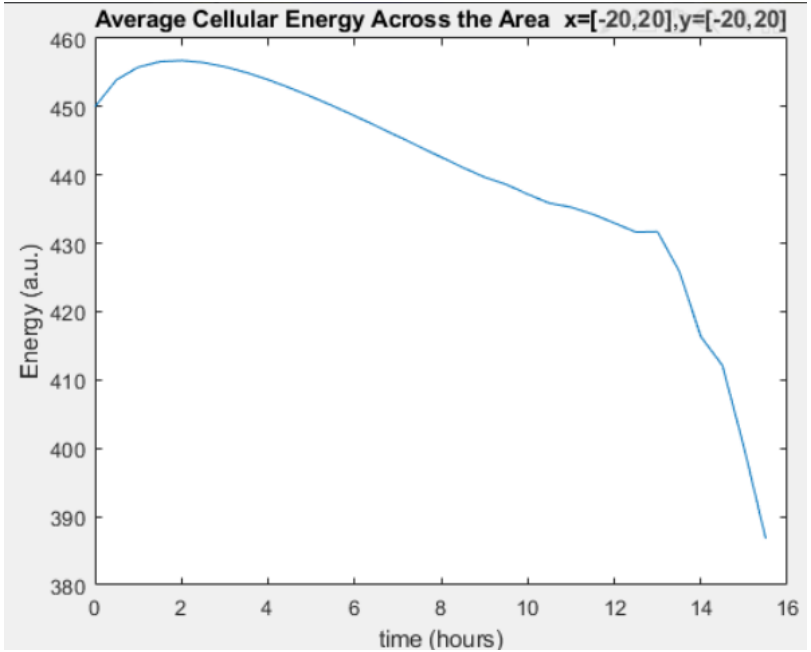





Current time: 0 days, 0 hours, and 0.00 minutes, z = 0.00 μm
144 agents
0 days, 0 hours, 0 minutes, and 0.0121 seconds
200 μm

Intracellular





How it looks

- Config File

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<cell_definitions>
    <cell_definition name="default" ID="0">
        <phenotype>
            <cycle code="5" name="live">
                <!-- using higher than normal significant digits to match divisions in default code -->
                <transition_rates units="1/min">
                    <rate start_index="0" end_index="0" fixed_duration="false">0.0</rate>
                </transition_rates>
            </cycle>
            <death>
            <volume>
            <motility>
                <speed units="micron/min">0.0</speed>
                <persistence_time units="min">0.1</persistence_time>
                <migration_bias units="dimensionless">.9</migration_bias>
                <options>
                    <enabled>true</enabled>
                    <use_2D>true</use_2D>
                    <chemotaxis>
                        <enabled>false</enabled>
                        <substrate>oxygen</substrate>
                        <direction>1</direction>
                    </chemotaxis>
                </options>
            </motility>
            <secretion>
                
        </phenotype>
```

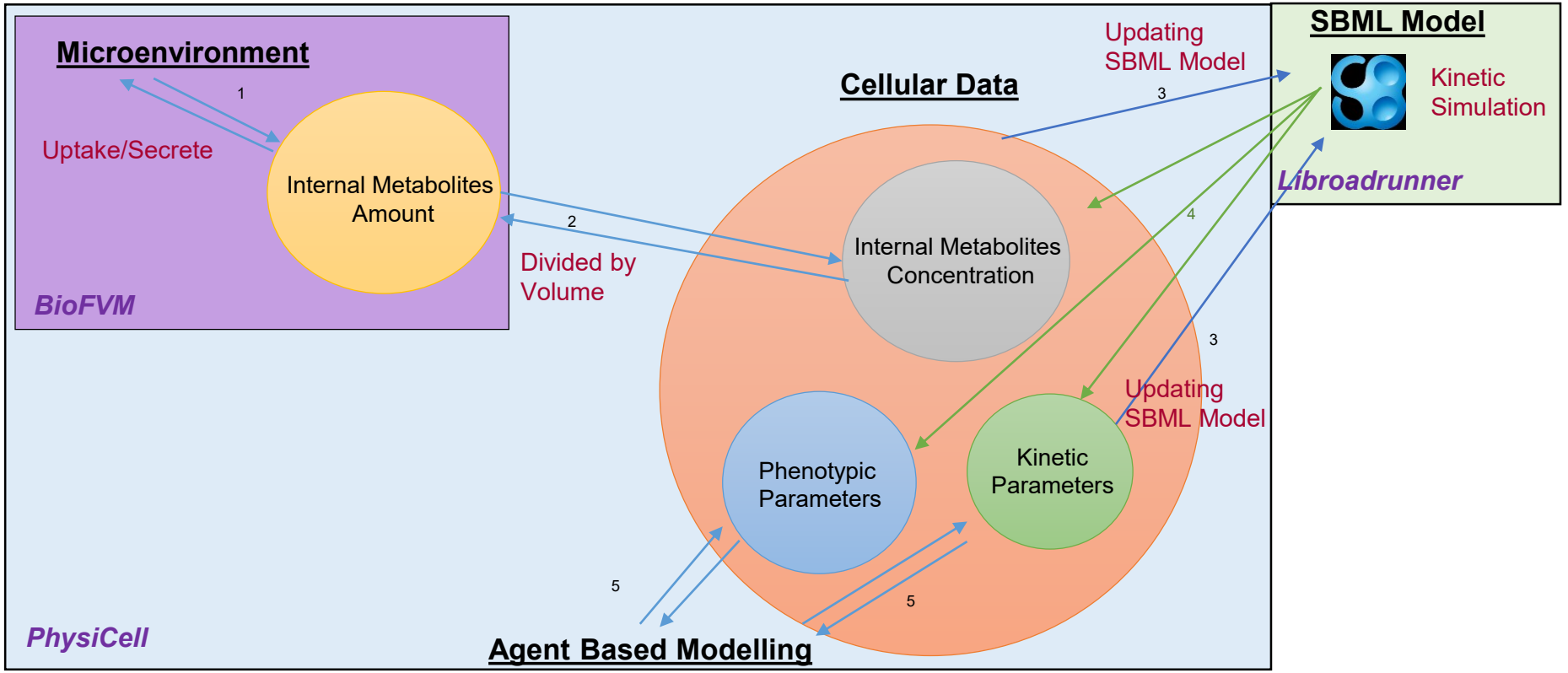
SBML-Phenotypic Parameters

PhysiCell Phenotype Parameter	First letter	phenotype_token	example
Phase Transition Rate	c	ctr_*_*	ctr_0_1
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	vff

Libroadrunner Addon

- Same format for intracellular addons. (PhysiFBA, PhysiBoSS)
- Libroadrunner
  - **start()** = start intracellular in cell (it should be used after seeding and is called after proliferation)
  - **Initialize_SBML()** = to read SBML (users will not use)
  - **get_values()** = to get value from SBML
  - **set_values()** = to set value in SBML
  - **update()** = to simulate SBML
  - **get_state()** = to get the name of SBML
  - **update_phenotypic_parameters()** = to update phenotype according to given tokens
  - **validate_tokens()** = to validate given token
  - **validate_species()** = to validate SBML species

Integration Design

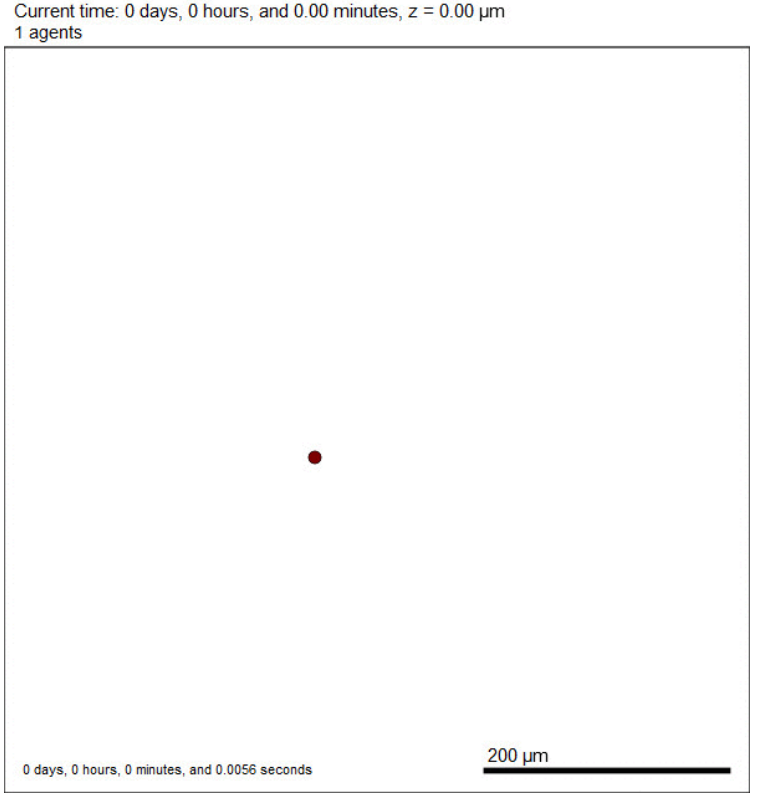


Migration Speed

Cell Definition

```
<motility>
    <persistence_time units="min">0.1</persistence_time>
    <migration_bias units="dimensionless">.9</migration_bias>
    <options>
```

```
<intracellular type="roadrunner">
    <sbml_filename>./config/Toy_oxy_mms_tr_01.xml</sbml_filename>
    <map PC_substrate="oxygen" sbml_species="Oxy"></map >
    <map PC_custom data="PC_Test_CD" sbml_species="death_rate"></map>
</intracellular>
```



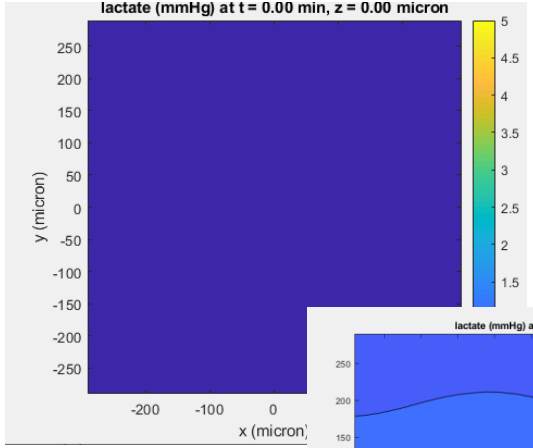
Chemokine Distribution

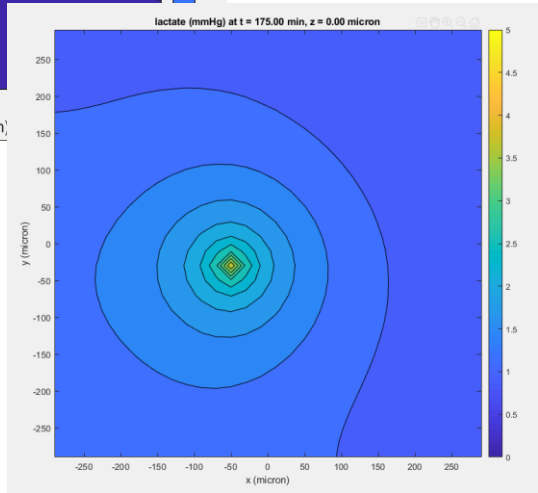
Cell Definition

```
        <secretion_target units="substrate density">10</secretion_target>
        <uptake_rate units="1/min">0.0</uptake_rate>
        <net_export_rate units="total substrate/min">0</net_export_rate>
    </substrate>
```

```
<intracellular type="roadrunner">
    <sbml_filename>./config/Toy_oxy_mms_tr_01.xml</sbml_filename>
    <map PC_substrate="oxygen" sbml_species="Oxy"></map >

</intracellular>
```





Wrong Tokens

```
<intracellular type="roadrunner">
    <sbml_filename>./config/Toy_oxy_mms_tr_01.xml</sbml_filename>
    <map PC_substrate="oxygen" sbml_species="Oxy"></map >
    <map PC_custom_data="PC_Test_CD" sbml_species="death_rate"></map>
    <map PC_phenotype="ctr00" sbml_species="transition_rate_0_1"></map>
    <map PC_phenotype="ssr1" sbml_species="secretion_rate_Lactate"></map>
</intracellular>
```

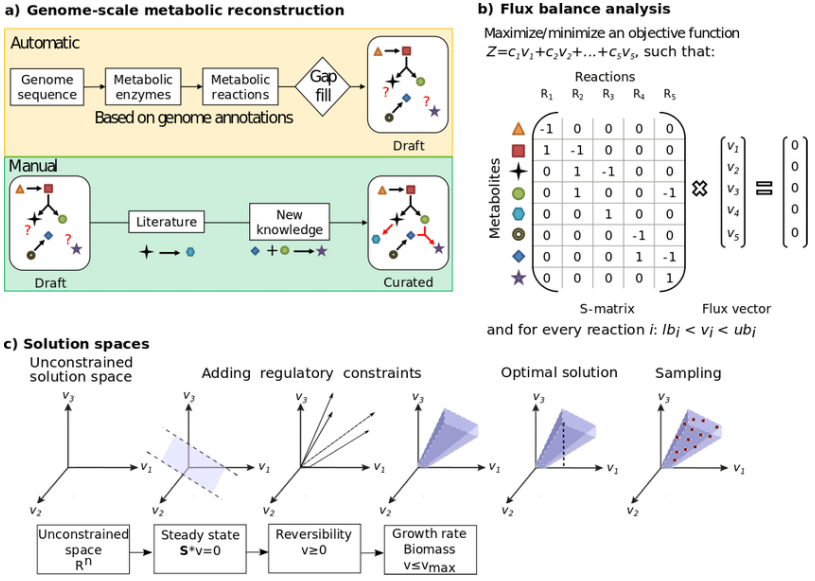
```
PS C:\Users\Furkan\Documents\GitHub\PhysiCell-SBML-trials\PhysiCell_intracellular_Phenotype>
```

Code walk

- Let's do code walk together…

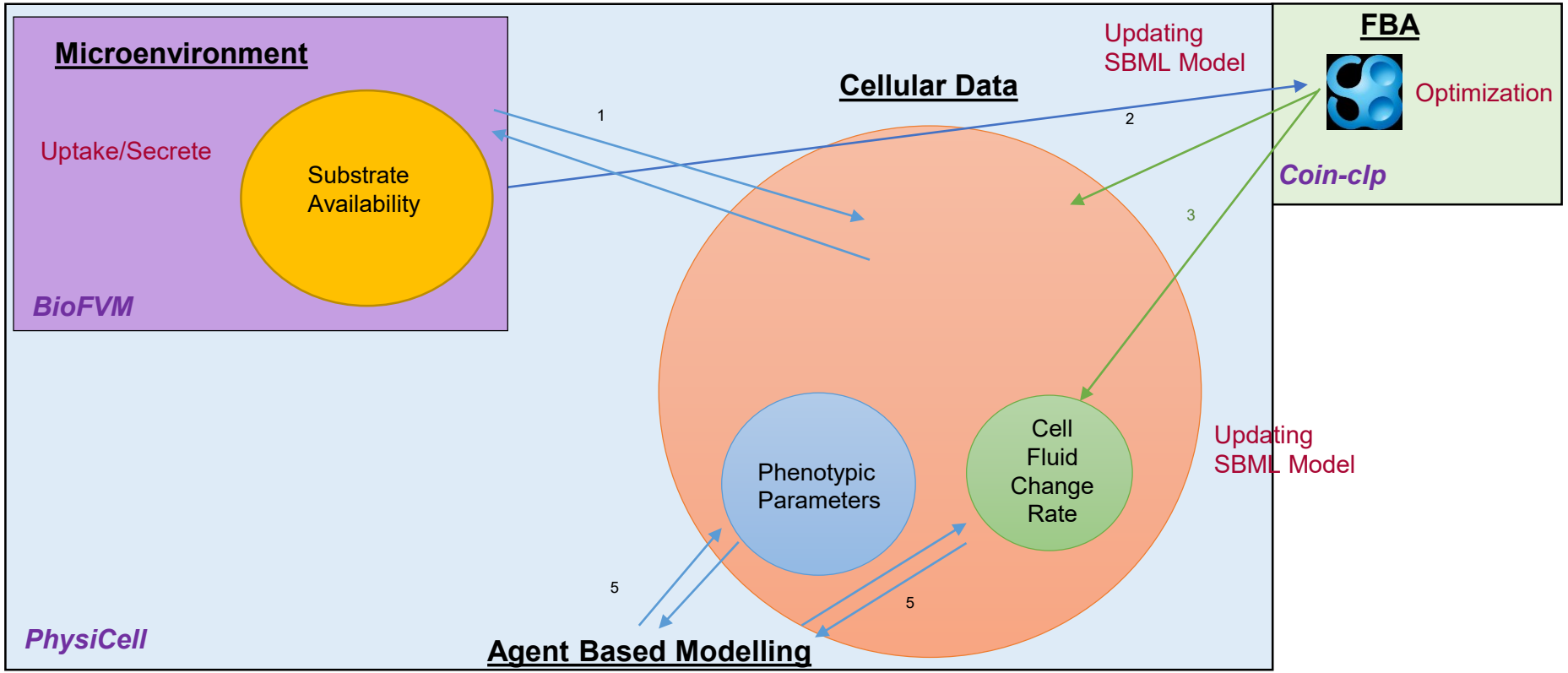
PhysidFBA

Flux Balance Analysis



Heirendt et al, 2017

Integration Design



PhysidFBA

- FBA is like taking a photo
- dFBA is like stop-motion video.
- dFBA simulates intracellular model
  - Finds optimal biomass creation flux
  - This value is used for volume calculation (growth of cell)
  - If cell is greater than the volume threshold
    - Divide
    - Arrest function

LibRoadRunner Interactive Demo

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, Transition_Rate

Model Rules

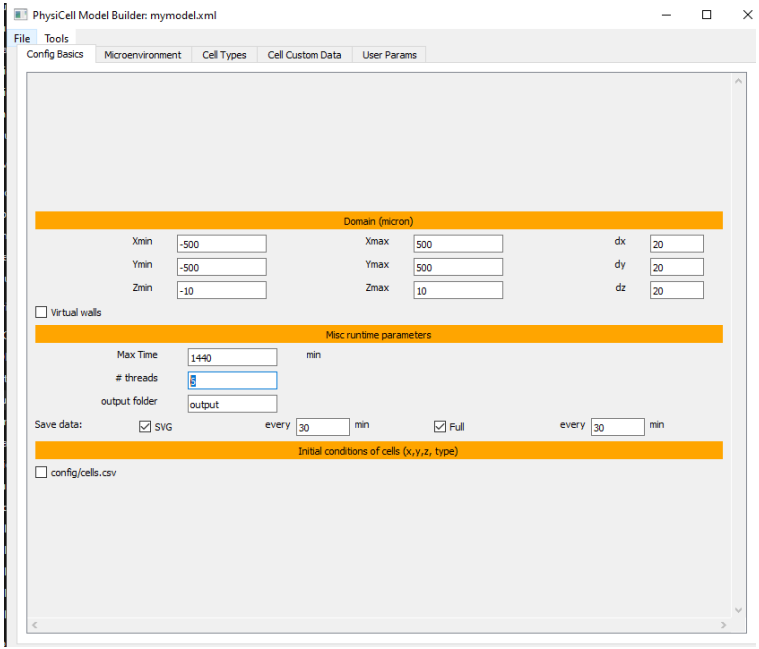
- Initial Energy = 450
- If Energy > 445
  - Cycle
- If Energy < 445
  - Don’t Cycle
- If Energy < 440
  - Move
- If Energy < 430
  - Die

Populate together

- **PhysiCell folder**
- make clean
- make data-cleanup
- make reset
- make list-projects
- make ode-energy-sample
- make

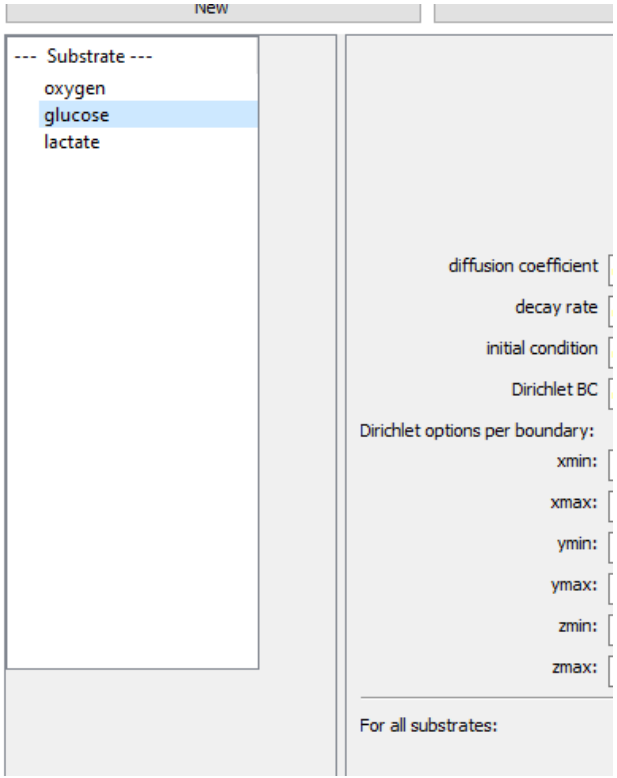
Demo Model

- 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



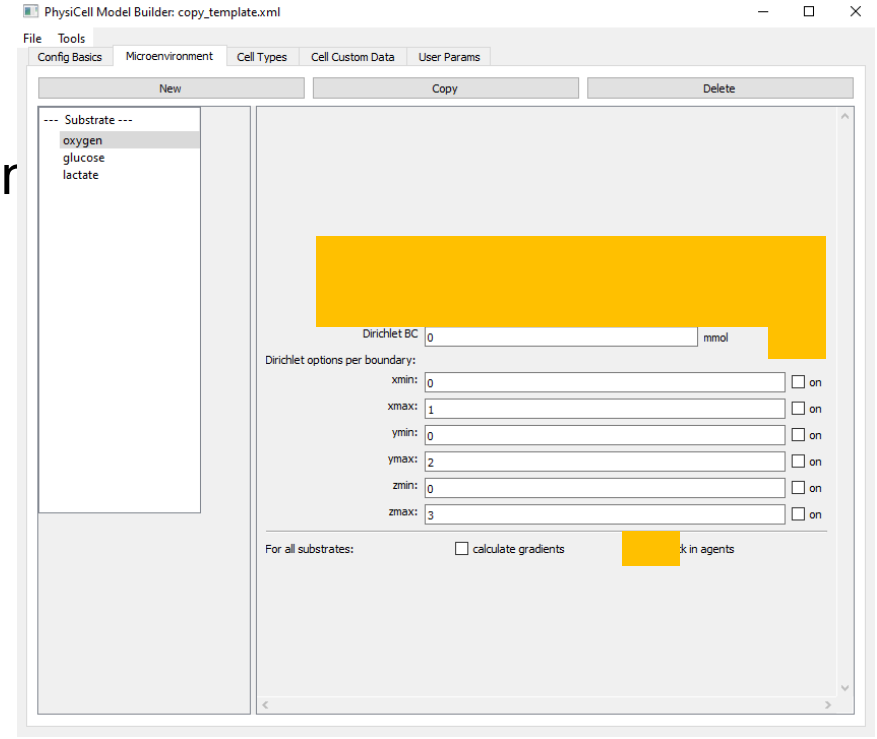
Demo Model

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



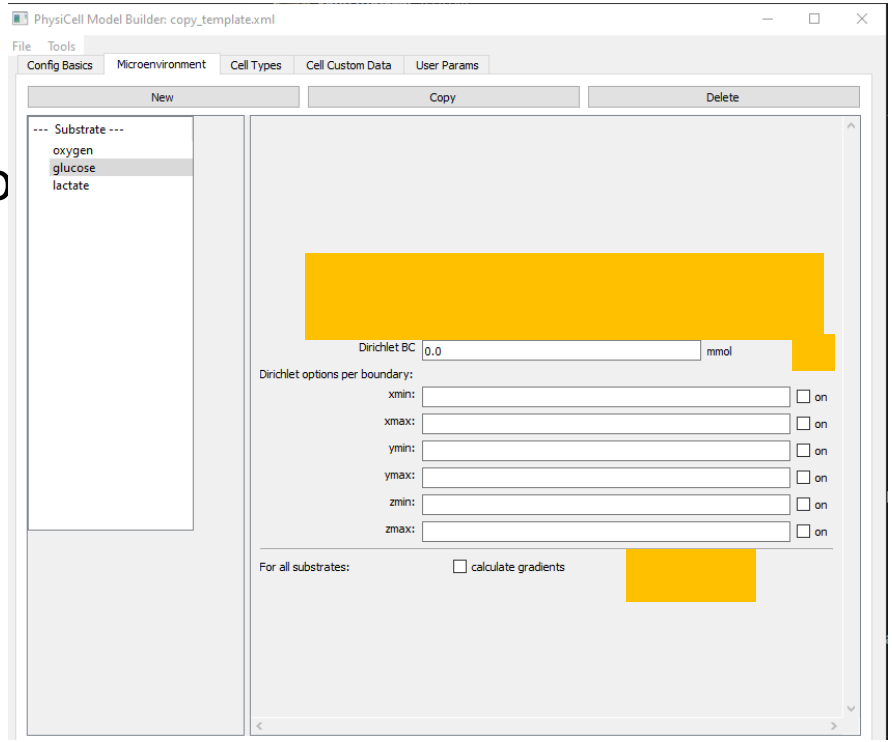
Demo Model

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



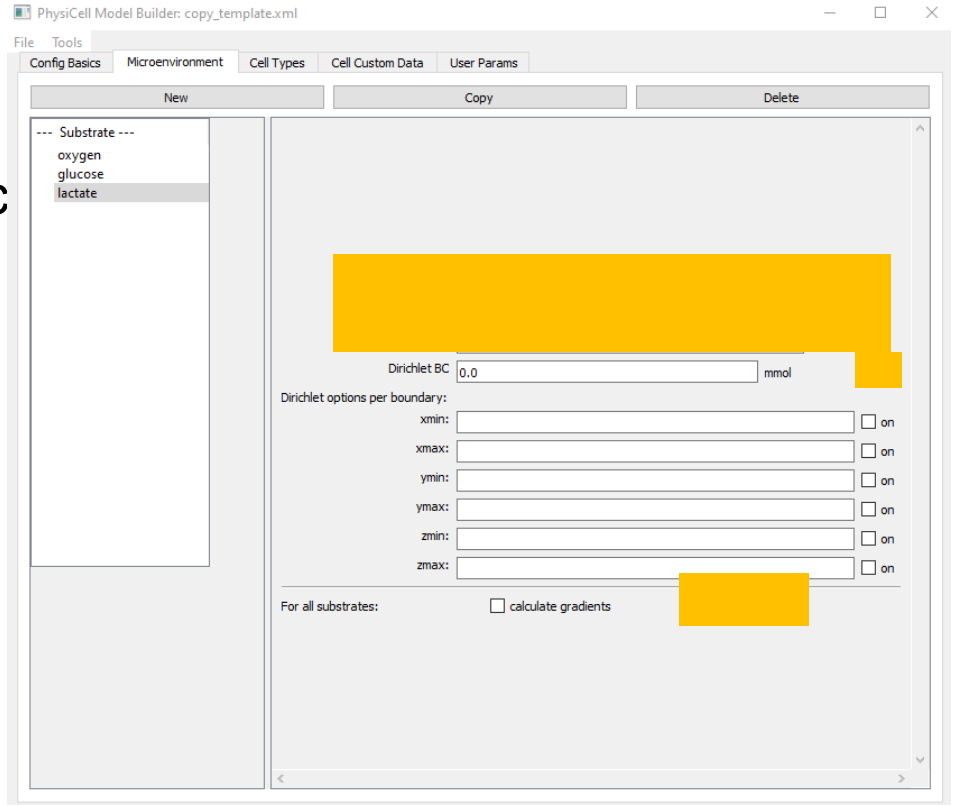
Demo Model

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



Demo Model

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

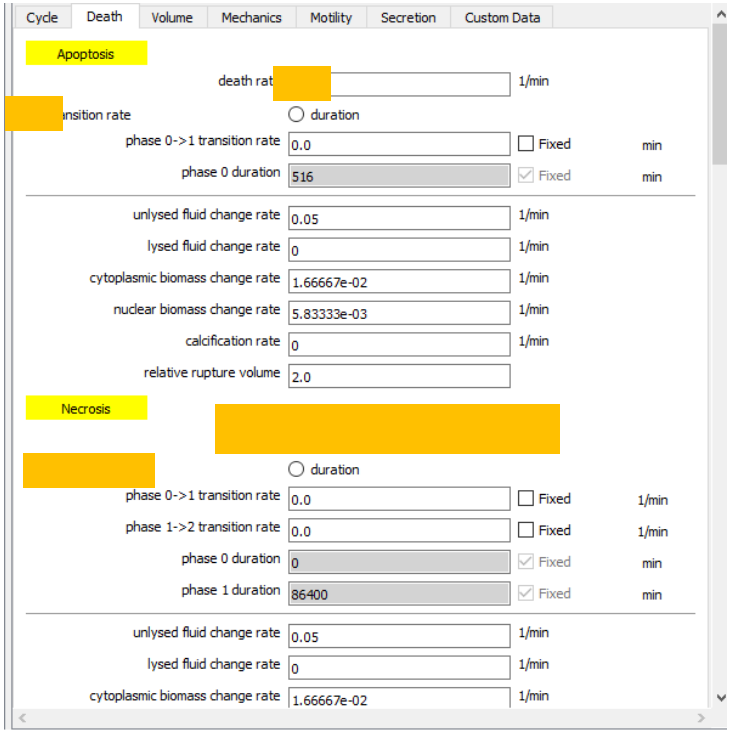


Cell Type

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

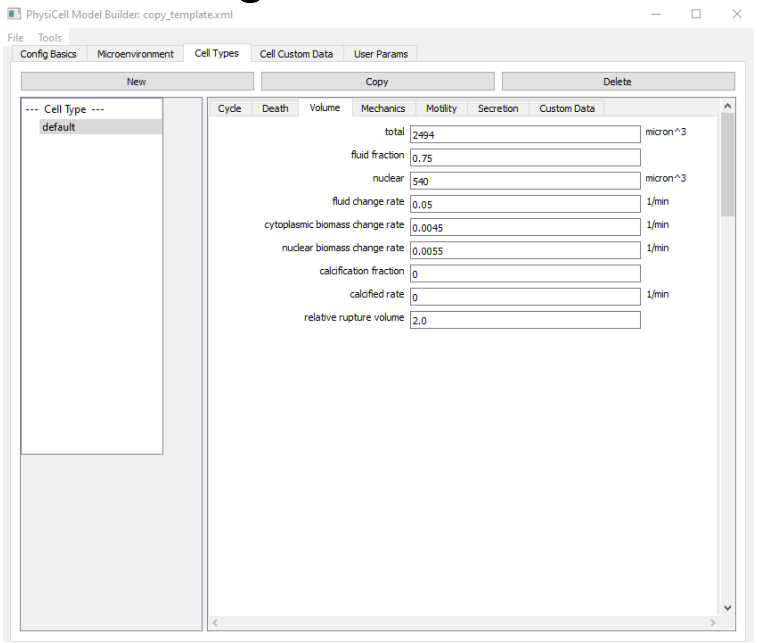
Cell Type

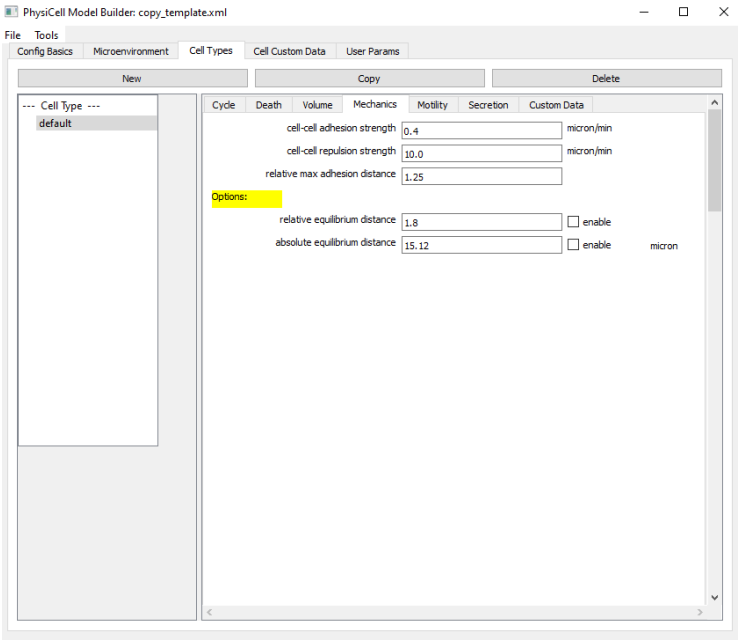
- No Death



Cell Type

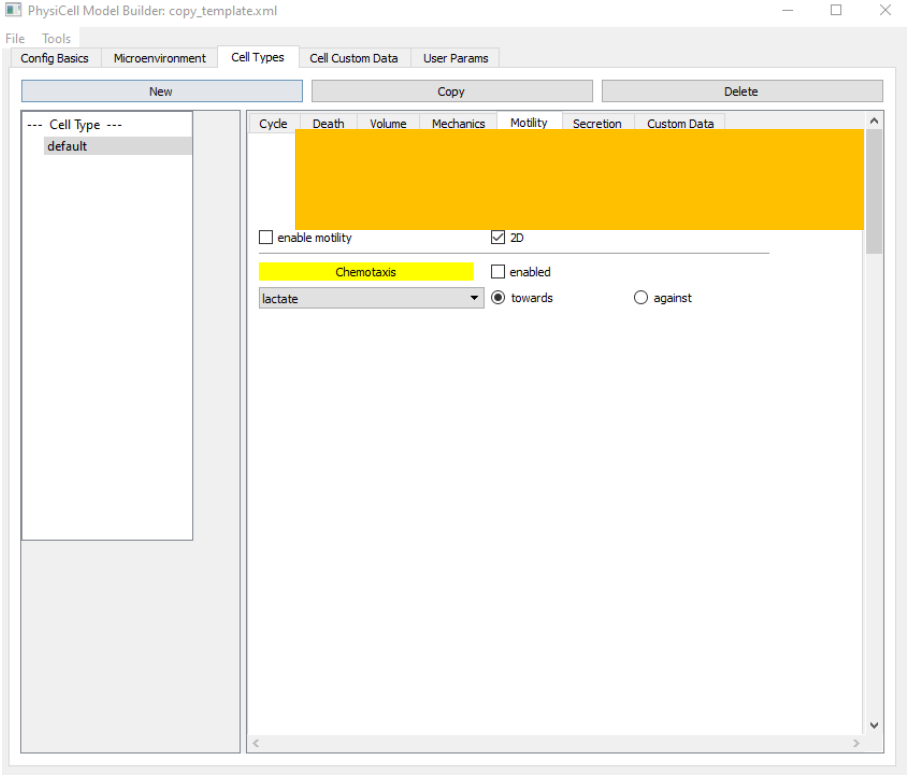
- No change in the Volume and Mechanics Tab





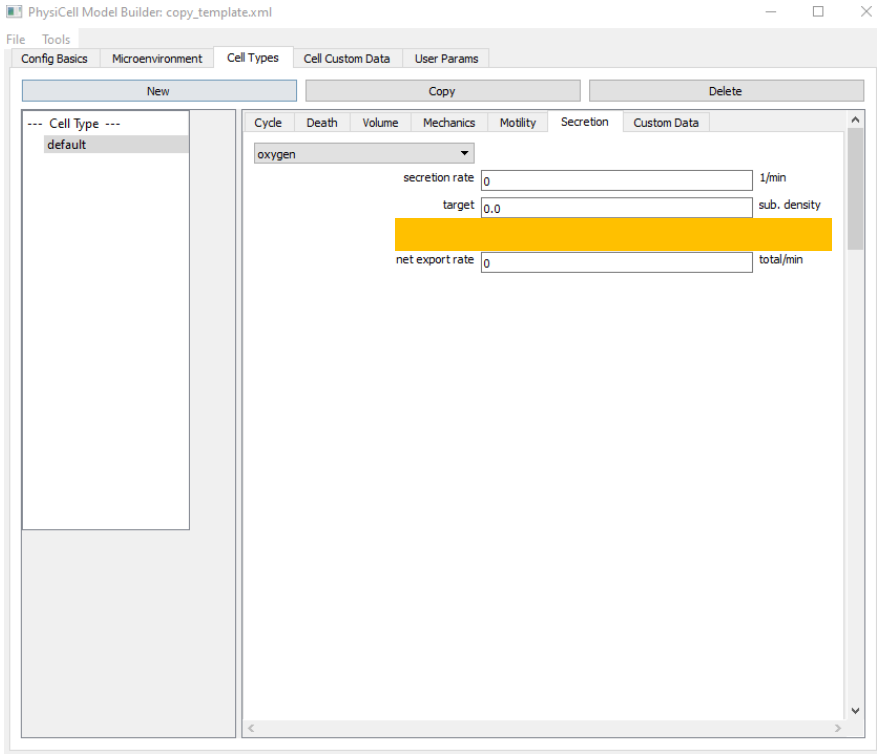
Cell Type

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



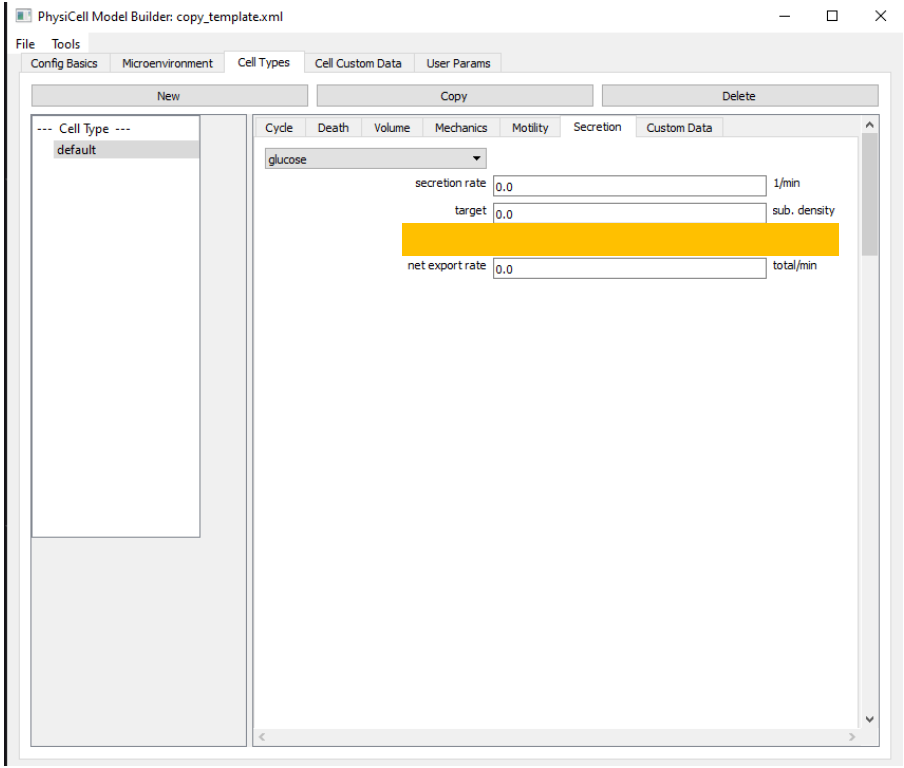
Cell Type : Secretion

- Oxygen Tab
- Uptake rate = 0.005



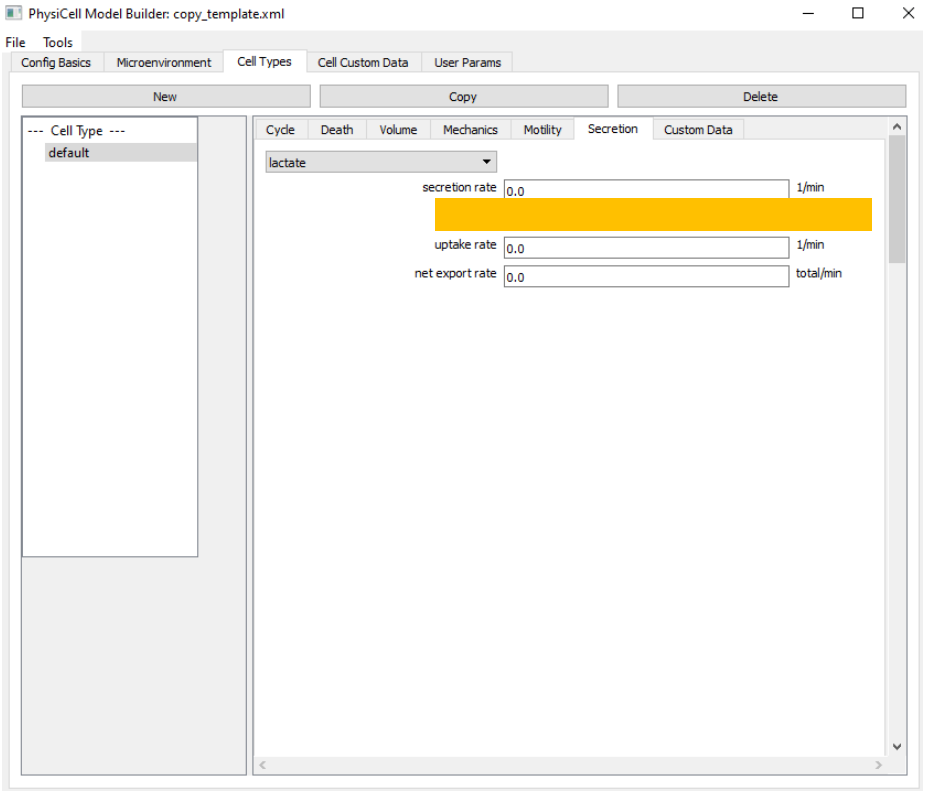
Cell Type : Secretion

- Glucose Tab
- Uptake rate = 0.001



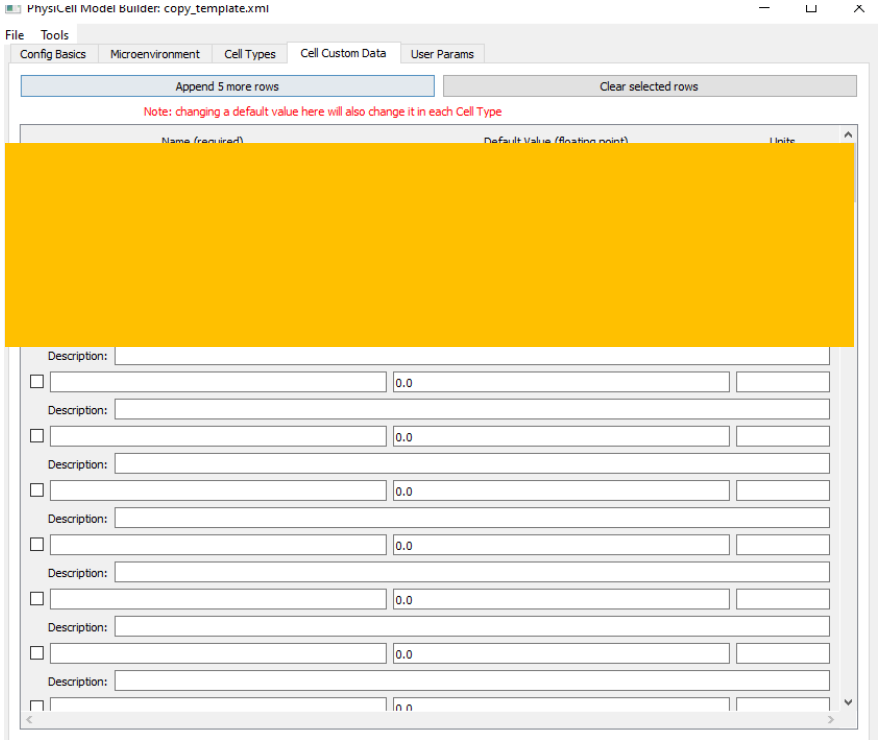
Cell Type : Secretion

- Lactate Tab
- Secretion Target = 10.0



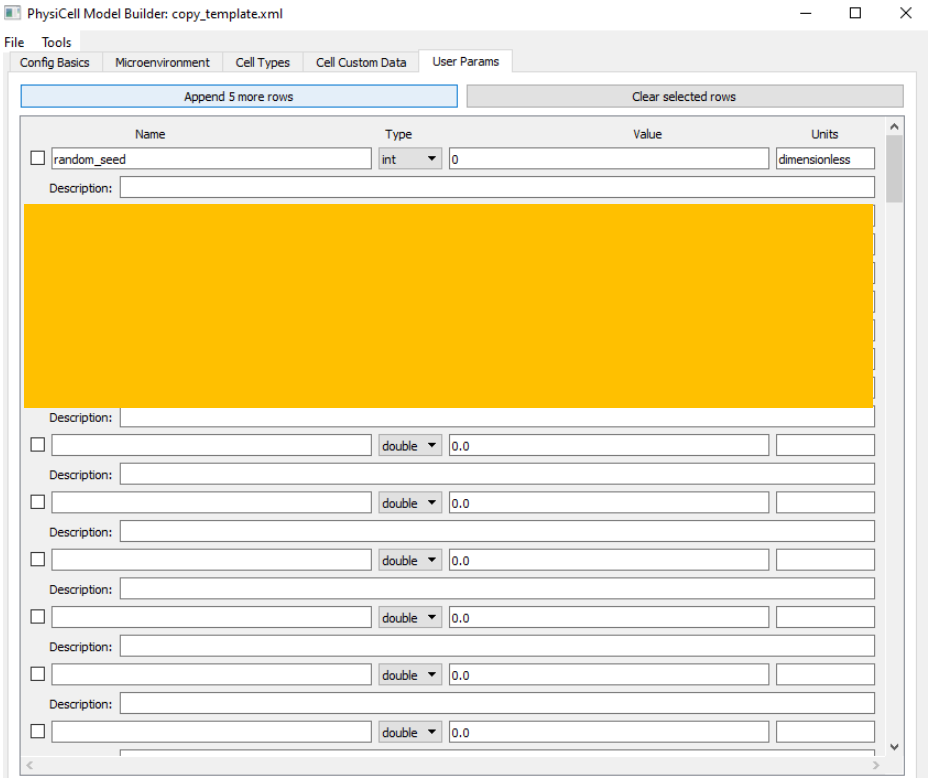
Cell Custom Data

- 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



User Params

- initial_internal_oxygen (double) = 0.8
- initial_internal_glucose (double) = 15
- initial_internal_lactate (double) = 0.0
- initial_energy (double) =450



Save

- Let’s look is it right.
- In my case, it did not put cell custom data
- I went to custom data in cell types tab
- And just make them 0.0
- Saved again.
- It worked!

Let's Add Intracellular Attribute

```
<intracellular type="roadrunner">

        <sbml_filename>./config/Toy_Metabolic_Model.xml</sbml_filename>
            <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" sbml_species="migration_speed"></map>
            <map PC_phenotype="ssr_lactate" sbml_species="Lac_Secretion_Rate"></map>
            <map PC_phenotype="ctr_0_0" sbml_species="Transition_Rate"></map>
</intracellular>
```

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PhysiCell Development:

- Breast Cancer Research Foundation
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- National Science Foundation (1720625)

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