Session 13: Intracellular with libRoadrunner (interactive demo)



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PhysiCell Project

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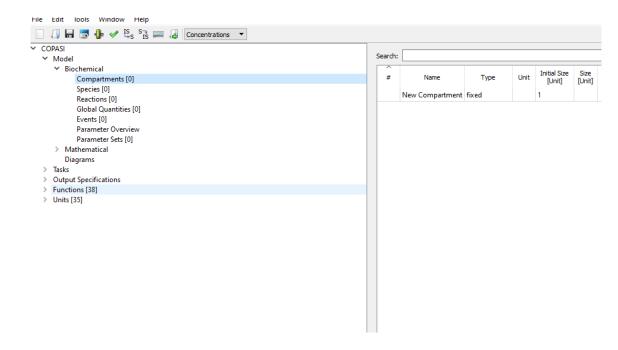


Agenda

- SBML Creation
- Adding Intracellular integrations
- Let's code together

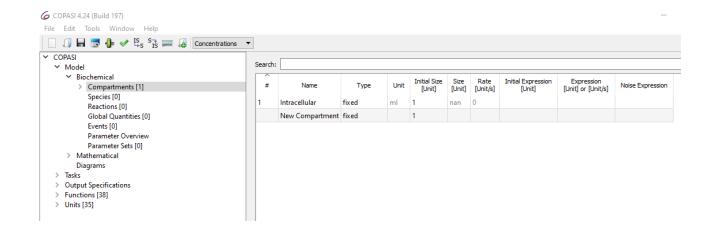
SBML Creation

- We need to create our SBML
- Let's start our Copasi



SBML Creation

- We will start with compartments
- Let's add "Intracellular" compartment
- Volume = 1.0



SBML Creation: Species

There will be 8 Species

#	Name	Compartment	Туре	Unit	Initial Concentration [Unit]	Concentration [Unit]	Rate [Unit/min]	Initial Expression [Unit]	Expression [Unit] or [Unit/min]	Noise Expression
1	Glucose	Intracellular	reactions	mmol/ml	100	nan	nan			
2	Oxygen	Intracellular	reactions	mmol/ml	100	nan	nan			
3	Energy	Intracellular	reactions	mmol/ml	450	nan	nan			
4	Lactate	Intracellular	reactions	mmol/ml	0	nan	nan			
5	apoptosis_rate	Intracellular	reactions	mmol/ml	0	nan	nan			
6	migration_speed	Intracellular	reactions	mmol/ml	0	nan	nan			
7	Lac_Secretion_Rate	Intracellular	reactions	mmol/ml	0	nan	nan			
8	Transition_Rate	Intracellular	reactions	mmol/ml	0	nan	nan			
	New Species	Intracellular	reactions	mmol/ml	1					

SBML Creation: Reactions

There will be three Reactions

#	Name	Reaction	Rate Law	Flux [mmol/min]	Noise Expression
1 A	erobic	Glucose + 6 * Oxygen -> 38 * Energy	Mass action (irreversible)	nan	
2 A	naerobic	Glucose -> 2 * Energy + Lactate	Mass action (irreversible)	nan	
3 Er	nergy_Usage	Energy ->	Mass action (irreversible)	nan	
N	ew Reaction				

SBML Creation : Global Quantities

There will be 6 Global Quantities

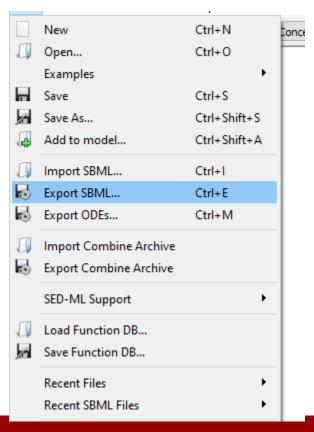
#	Name	Туре	Unit	Initial Value [Unit]	Transient Value [Unit]	Rate [Unit/min]	Initial Expression [Unit]	Expression [Unit] or [Unit/min]	Noise Expression
	k_aer	fixed	?	0.01	nan	0			
2	k_ane	fixed	?	0.00018	nan	0			
3	k_usage	fixed	?	0.0023	nan	0			
4	energy_move_thresh	fixed	?	440	nan	0			
5	energy_death_thresh	fixed	?	430	nan	0			
5	energy_prolif_thresh	fixed	?	445	nan	0			
	New Quantity	fixed		0					

SBML Creation: Events

6 Events to create

#	Name	Trigger Expression	Delayed	Delay Expression	Assignment Target	Assignment Expression
1	die	[Energy] It Values[energy_death_thresh]	Assignment	0	apoptosis_rate	8.99999999999999e+99
2	do_not_move	[Energy] gt Values[energy_move_thresh]	Assignment	0	migration_speed	0
3	move	[Energy] It Values[energy_move_thresh]	Assignment	0	migration_speed	10
4	Lac_Sec	[Lactate] gt 0.01	Assignment	0	Lac_Secretion_Rate	0.0001
5	divide	[Energy] gt Values[energy_prolif_thresh]	Assignment	0	Transition_Rate	0.00016666660000000001
6	do_not_divide	[Energy] It Values[energy_prolif_thresh]	Assignment	0	Transition_Rate	0
	New Event					

SBML Creation: Save



Agenda

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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>
```

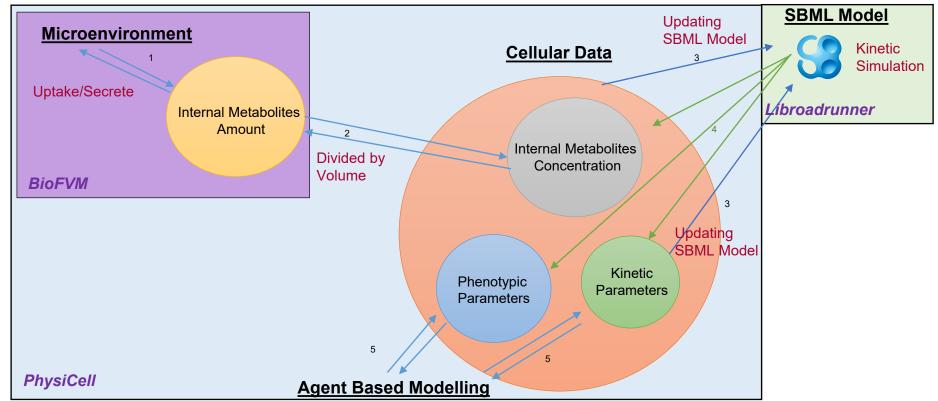
```
</cell interactions>
    <cell transformations>
     <transformation rates>
          <transformation rate name="default" units="1/min">0.0</transformation rate>
          </transformation rates>
     </cell transformations>
  <intracellular type="roadrunner">
              <sbml filename>./config/Toy 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>
    </phenotype>
  <custom data>
   <intra oxy conserved="false" description="" units="dimensionless">0.0</intra oxy>
   <intra glu conserved="false" description="" units="a.u">0.0</intra glu>
   <intra lac conserved="false" description="" units="a.u">0.0</intra lac>
    <intra energy conserved="false" description="" units="a.u">0.0</intra energy>
  </custom data>
</cell definition>
```

Let's edit custom module

Setup_tissue()

```
// 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:custom:intra glu" , parameters.doubles("initial internal glucose"));
  set single behavior( pCell , "custom:custom:intra lac" , parameters.doubles("initial internal lactate"));
  set single behavior( pCell , "custom:custom:intra energy" , parameters.doubles("initial energy" ));
// set the internalized values
double cell volume = get single signal( pCell , "volume");
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;
(*all cells)[i]->phenotype.intracellular->set parameter value("Energy", get single signal( pCell ,
"custom:intra energy"));
```

Integration Design



Update Intracellular

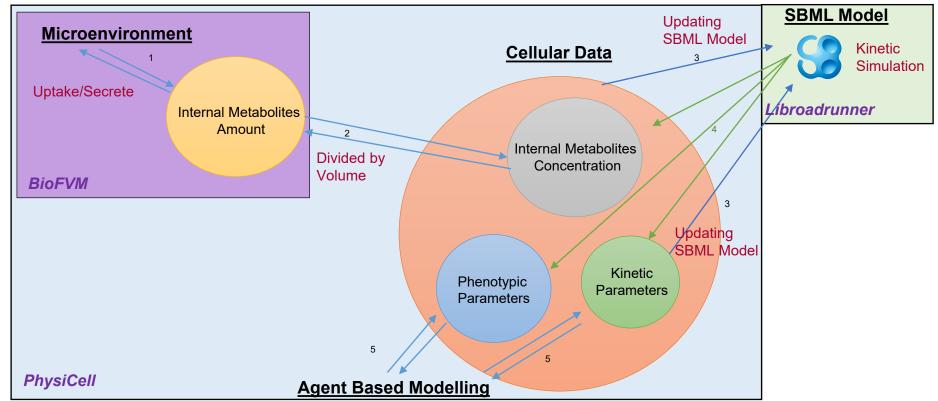
Let's start changing update_intracellular()

For loop for all cells

```
#pragma omp parallel for
for( int i=0; i < (*all_cells).size(); i++ )
{
    if( (*all_cells)[i]->is_out_of_domain == false )
    {
      }
}
```

Let's start filling

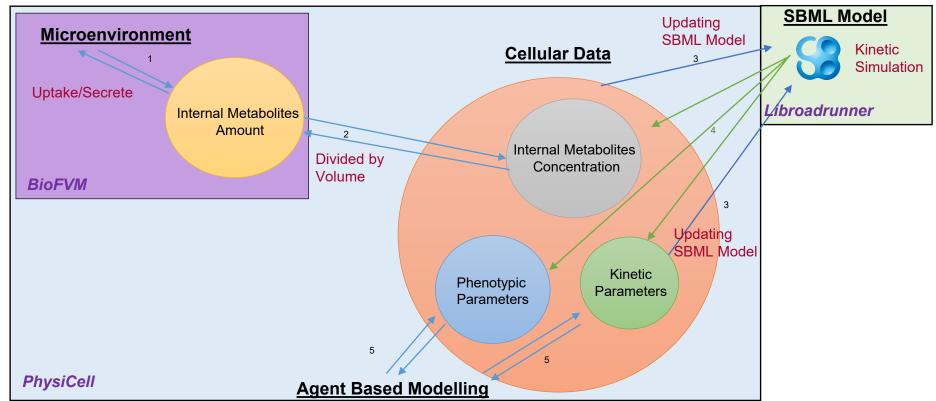
Integration Design



Update SBML

```
if( (*all cells)[i]->is out of domain == false )
// Cell Volume
double cell volume = (*all cells)[i]->phenotype.volume.total;
// Intracellular Concentrations
double oxy val int = (*all cells)[i]-
>phenotype.molecular.internalized total substrates[oxygen substrate index]/cell volume;
double glu val int = (*all cells)[i]-
>phenotype.molecular.internalized total substrates[glucose substrate index]/cell volume;
double lac val int = (*all cells)[i]-
>phenotype.molecular.internalized_total_substrates[lactate_substrate_index]/cell_volume;
// 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);
```

Integration Design

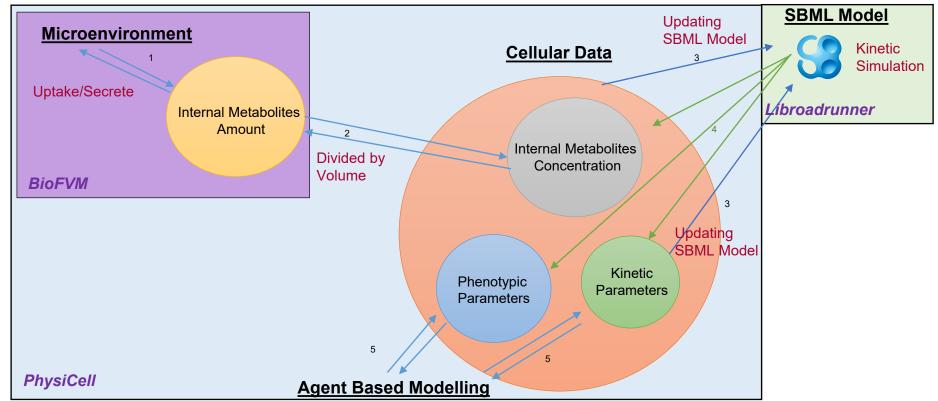


SBML Simulation

```
// SBML Simulation
(*all_cells)[i]->phenotype.intracellular->update();

// Phenotype Simulation
(*all_cells)[i]->phenotype.intracellular->update_phenotype_parameters((*all_cells)[i] ->phenotype);
...
```

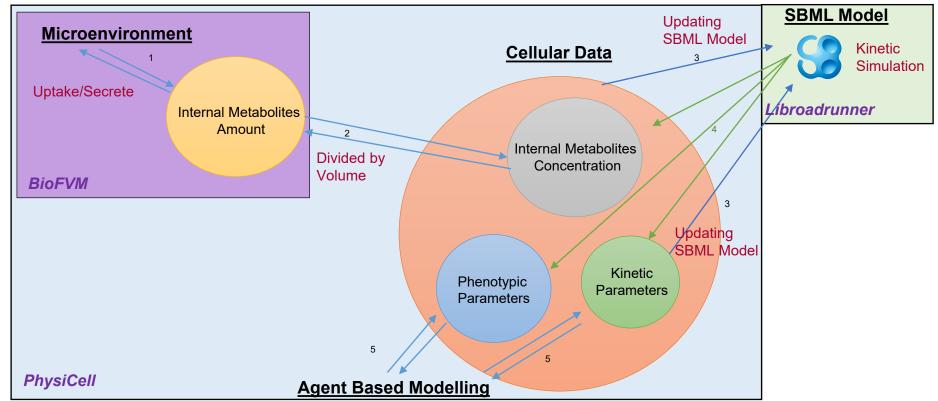
Integration Design

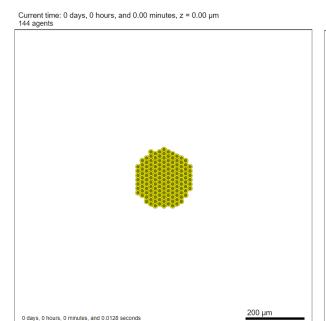


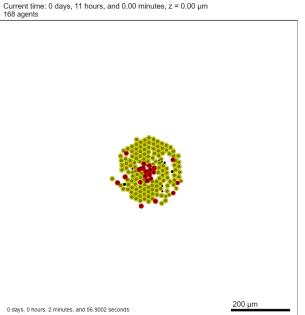
Update PhysiCell

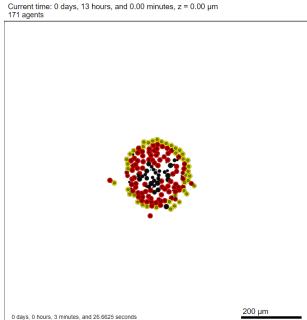
```
// Internalized Chemical Update After SBML Simulation
(*all cells)[i]->phenotype.molecular.internalized_total_substrates[oxygen_substrate_index] = (*all_cells)[i]->phenotype.intracellular-
>get parameter value("Oxygen") * cell volume;
(*all cells)[i]->phenotype.molecular.internalized total substrates[glucose 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
(*all cells)[i]->custom data[i Oxy i] = (*all cells)[i]->phenotype.intracellular->get parameter value("Oxygen");
(*all cells)[i]->custom data[i Glu i] = (*all cells)[i]->phenotype.intracellular->get parameter value("Glucose");
(*all_cells)[i]->custom_data[i_Lac_i] = (*all_cells)[i]->phenotype.intracellular->get parameter value("Lactate");
(*all_cells)[i]->custom_data[energy_vi] = (*all_cells)[i]->phenotype.intracellular->get_parameter_value("Energy");
```

Integration Design









Different Intracellular_dt

- Let's change intracellular_dt
- Demo

Up next

- End of live sessions for today.
- Two async sessions left
- Let's meet at the Hackathon for the first Team Time

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