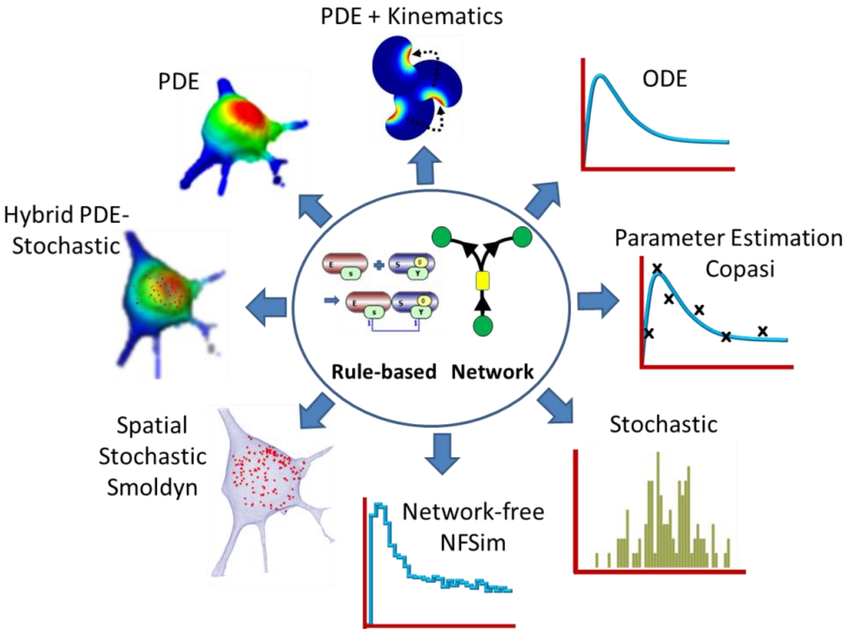
VCell

A modeling environment for the simulation of cellular events. Download at vcell.org.



Virtual Cell is developed by the Center for Cell Analysis and Modeling at the University of Connecticut Health Center. It is funded as a Biomedical Technology Research Resource by the National Institute of General Medical Sciences (NIGMS)

VCell Tutorial

FRAP: Fluorescence Redistribution After Photobleaching

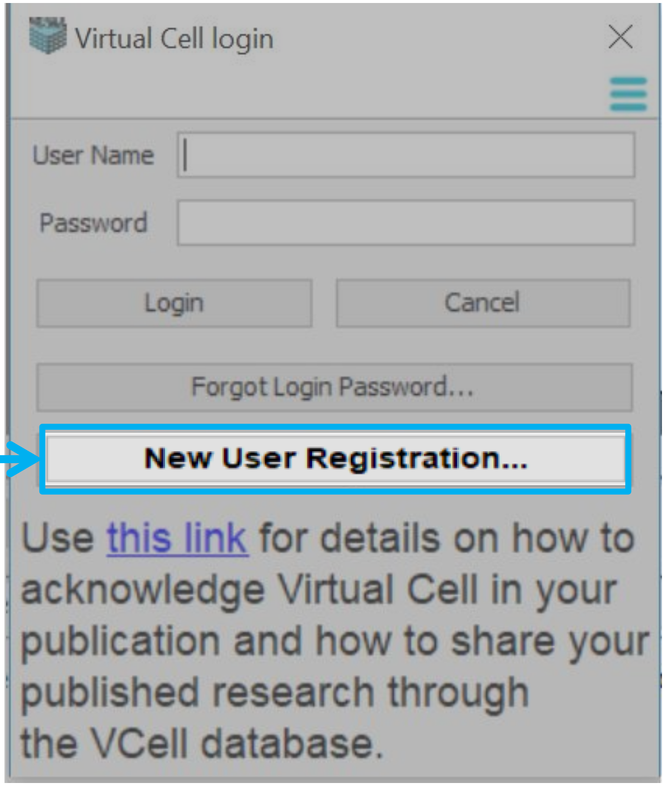
Objective: Create a simple biomodel and spatial (PDE) application to simulate a photobleaching experiment and view the results.

In this tutorial you will:

- Gain a basic introduction to the Virtual Cell interface
- Create a very simple biomodel with species but no reactions
- Create a spatial deterministic (PDE) application of a model using analytic equations to create a simple geometry
- Use Boolean expressions to define initial concentrations that are non-uniform
- View and analyze results of a spatial simulation

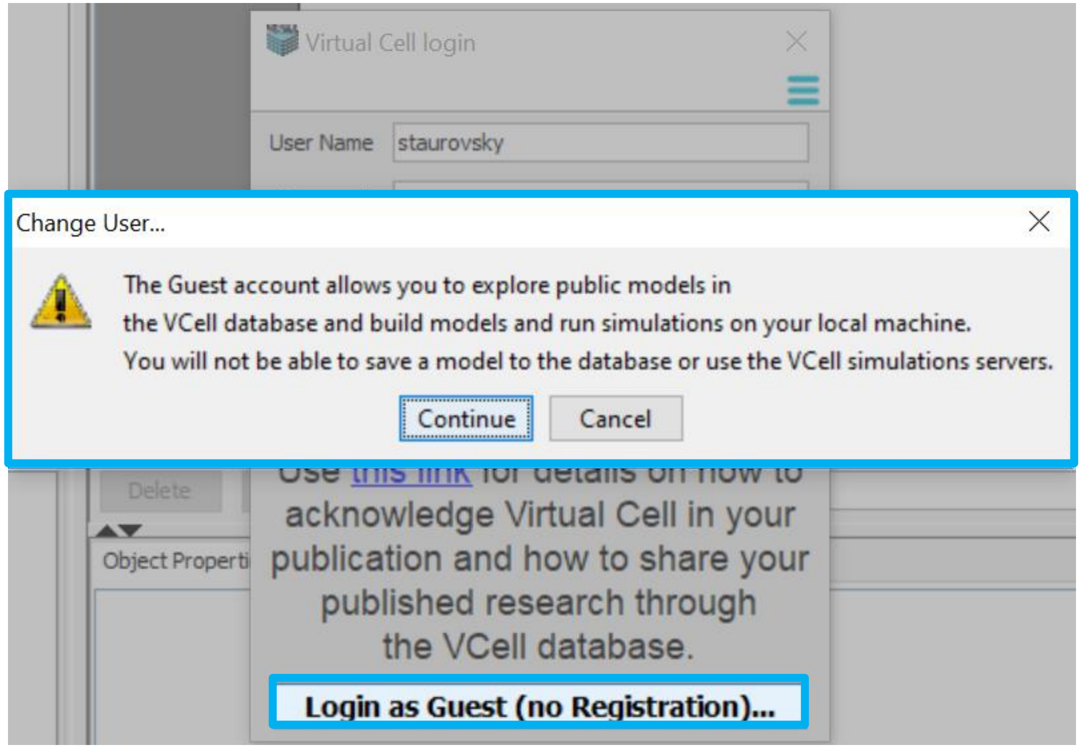
Your first time opening VCell

You need to register as a New User if you want to run simulations on the VCell compute resources, or use the VCell database to store models that can be shared with collaborators.



Use this link for details on how to acknowledge Virtual Cell in your publication and how to share your published research through the VCell database.

Your first time opening VCell
Guest Login Option

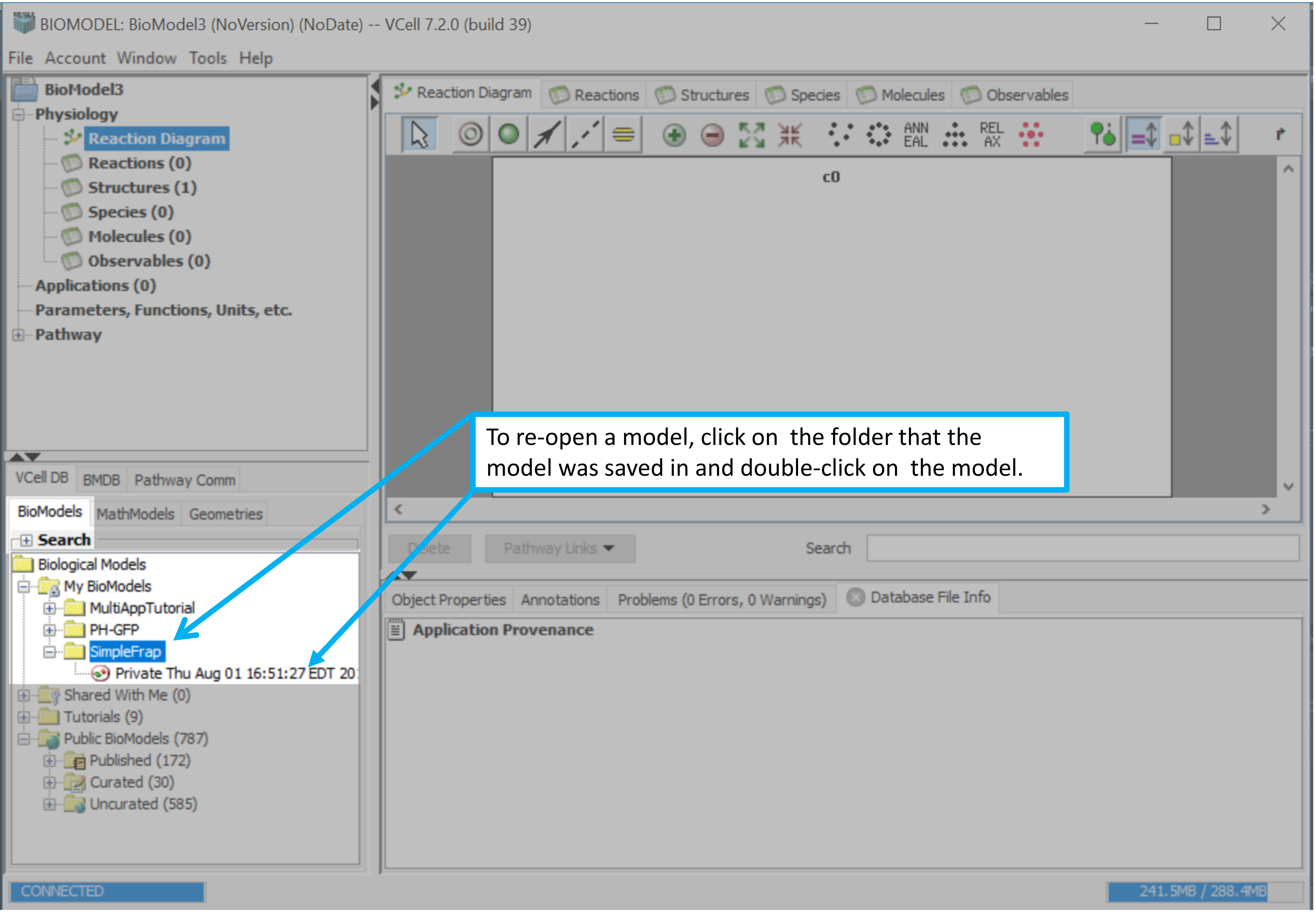


User Name: staurovsky

Change User...

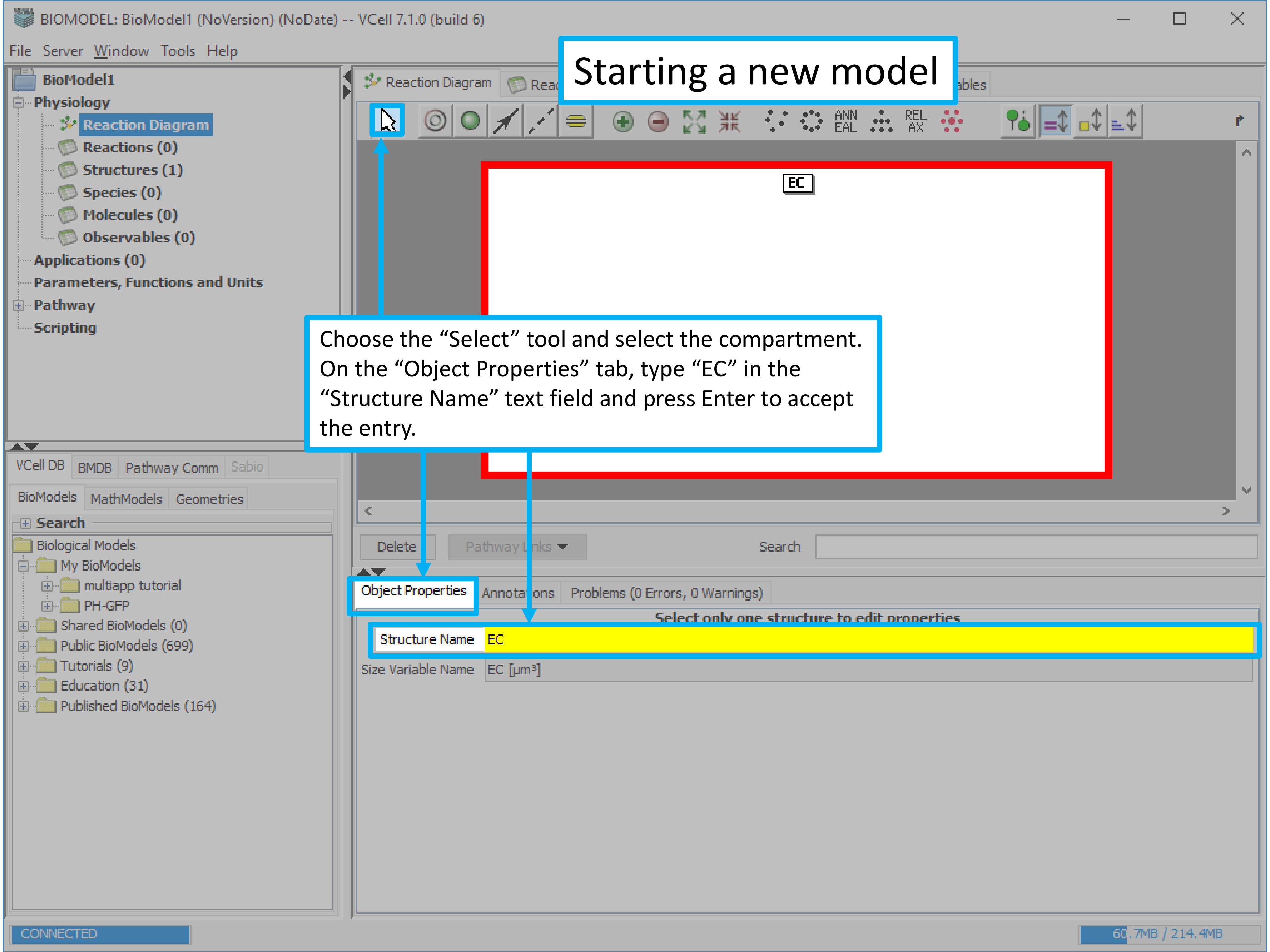
The Guest account allows you to explore public models in the VCell database and build models and run simulations on your local machine. You will not be able to save a model to the database or use the VCell simulations servers.

Use this link for details on how to acknowledge Virtual Cell in your publication and how to share your published research through the VCell database.



To re-open a model, click on the folder that the model was saved in and double-click on the model.

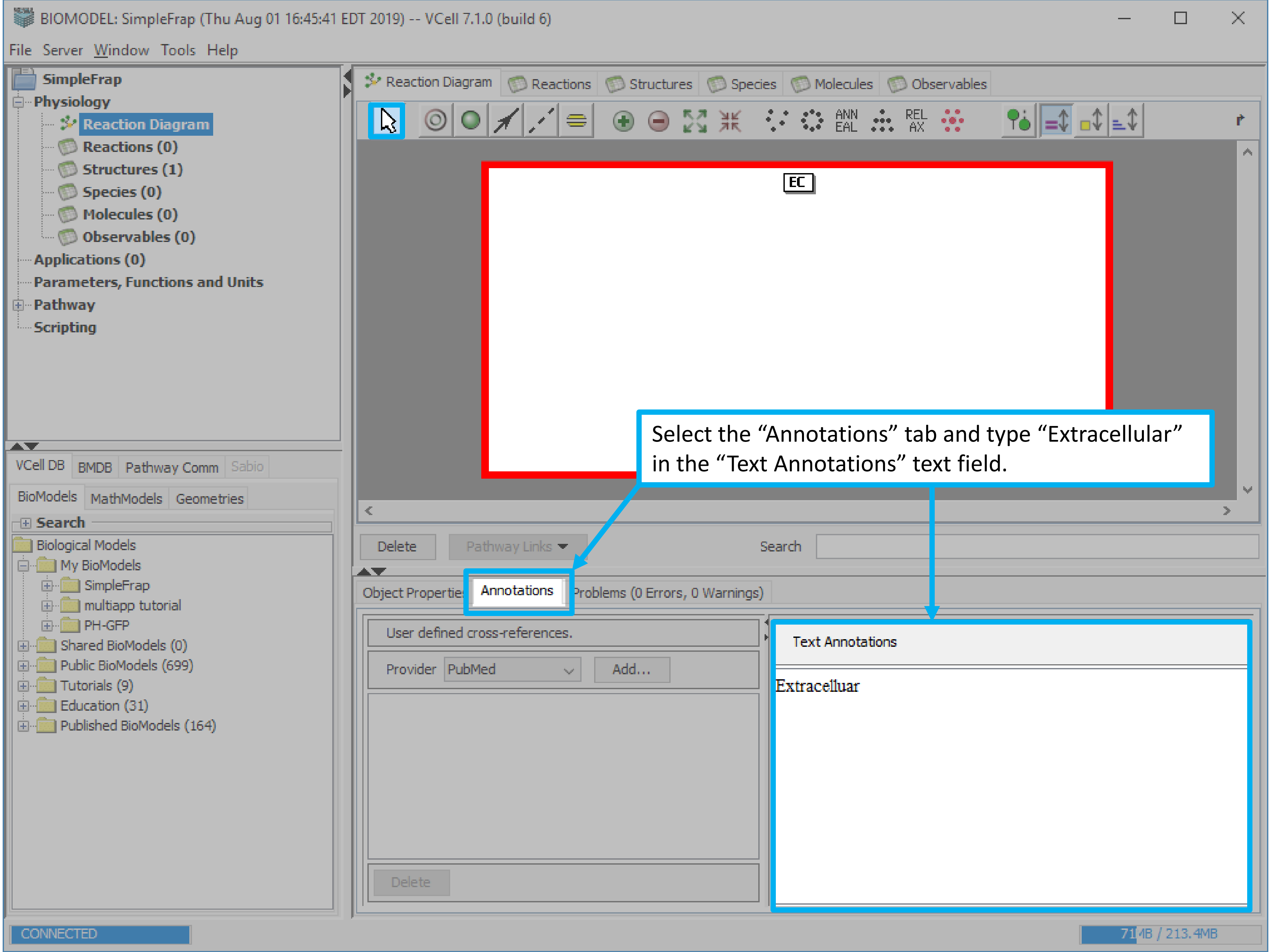
Starting a new model



Choose the “Select” tool and select the compartment. On the “Object Properties” tab, type “EC” in the “Structure Name” text field and press Enter to accept the entry.

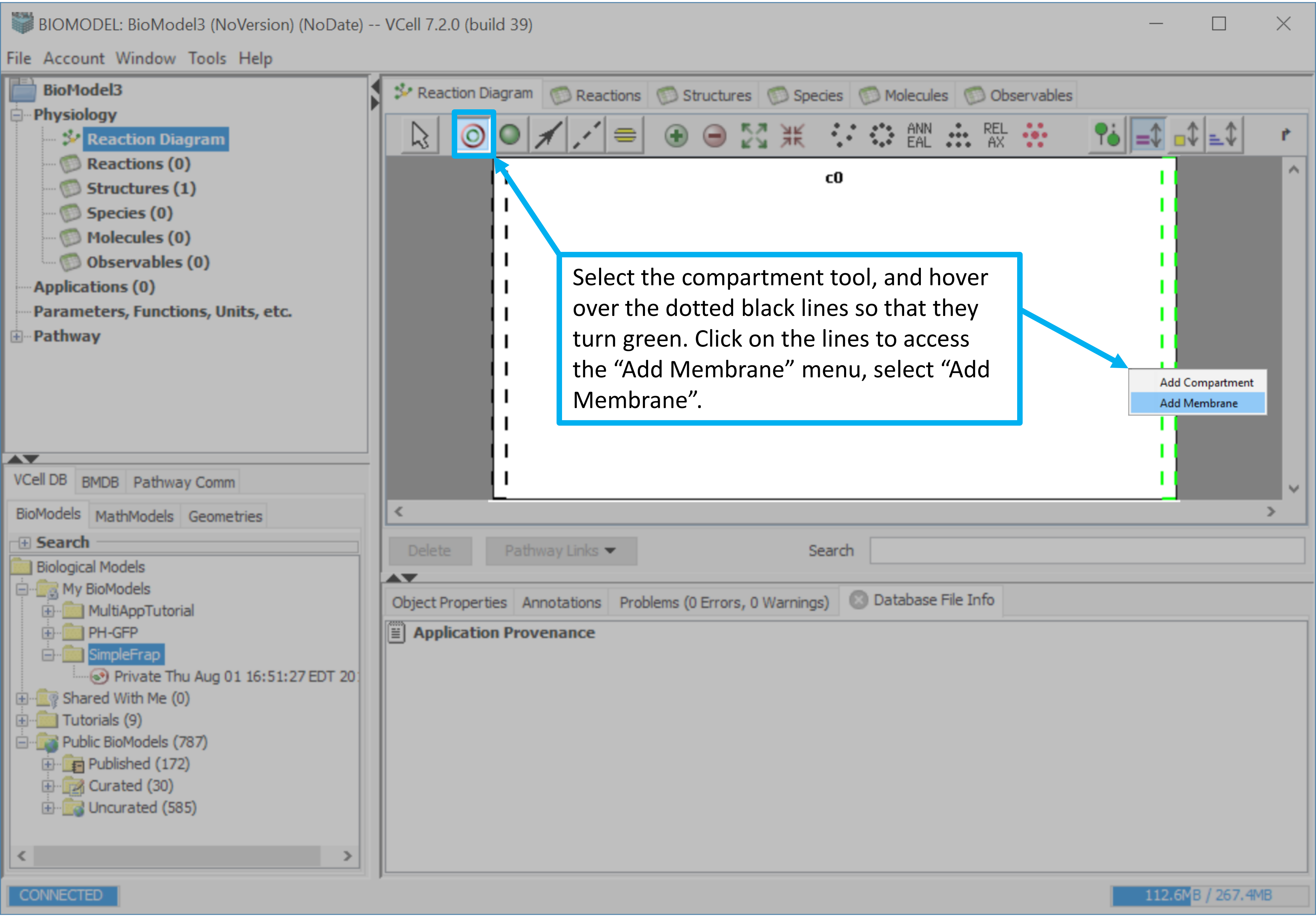
Structure Name: EC

Size Variable Name: EC [µm³]

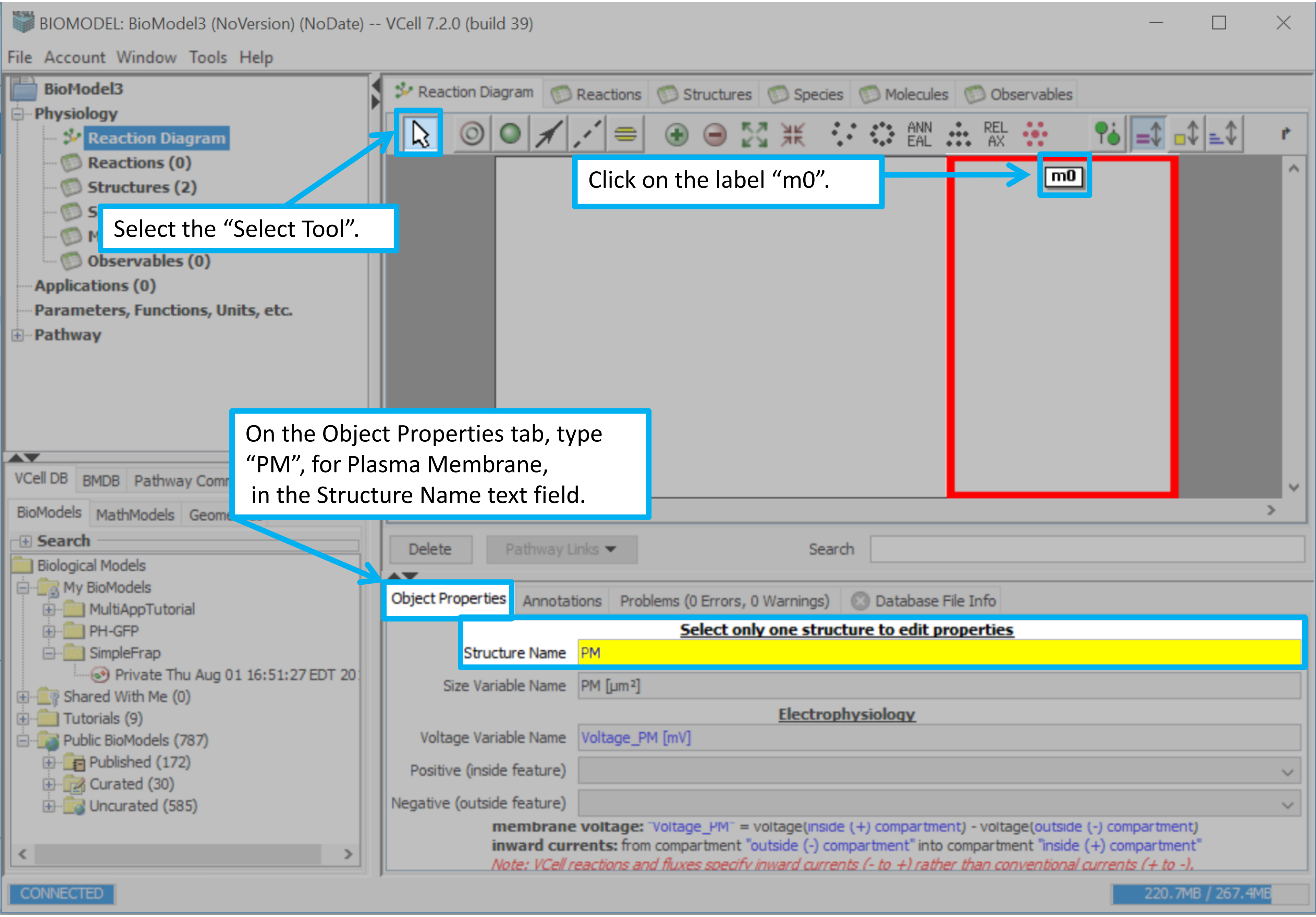


Select the “Annotations” tab and type “Extracellular” in the “Text Annotations” text field.

Text Annotations: Extracelluar



Select the compartment tool, and hover over the dotted black lines so that they turn green. Click on the lines to access the “Add Membrane” menu, select “Add Membrane”.



Select the “Select Tool”.

Click on the label “m0”.

On the Object Properties tab, type “PM”, for Plasma Membrane, in the Structure Name text field.

Select only one structure to edit properties

Structure Name: PM

Size Variable Name: PM [µm²]

Electrophysiology

Voltage Variable Name: Voltage_PM [mV]

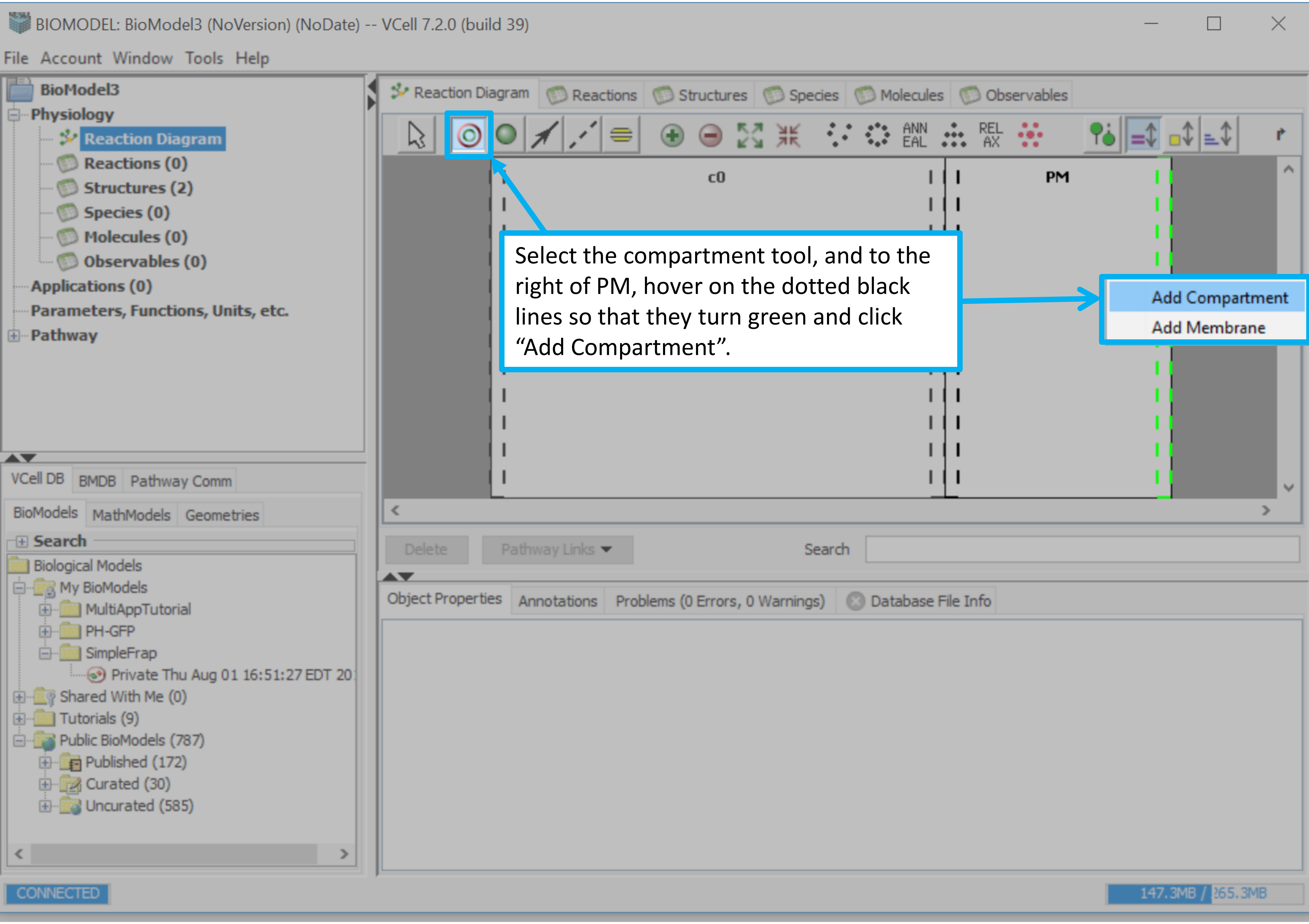
Positive (inside feature):

Negative (outside feature):

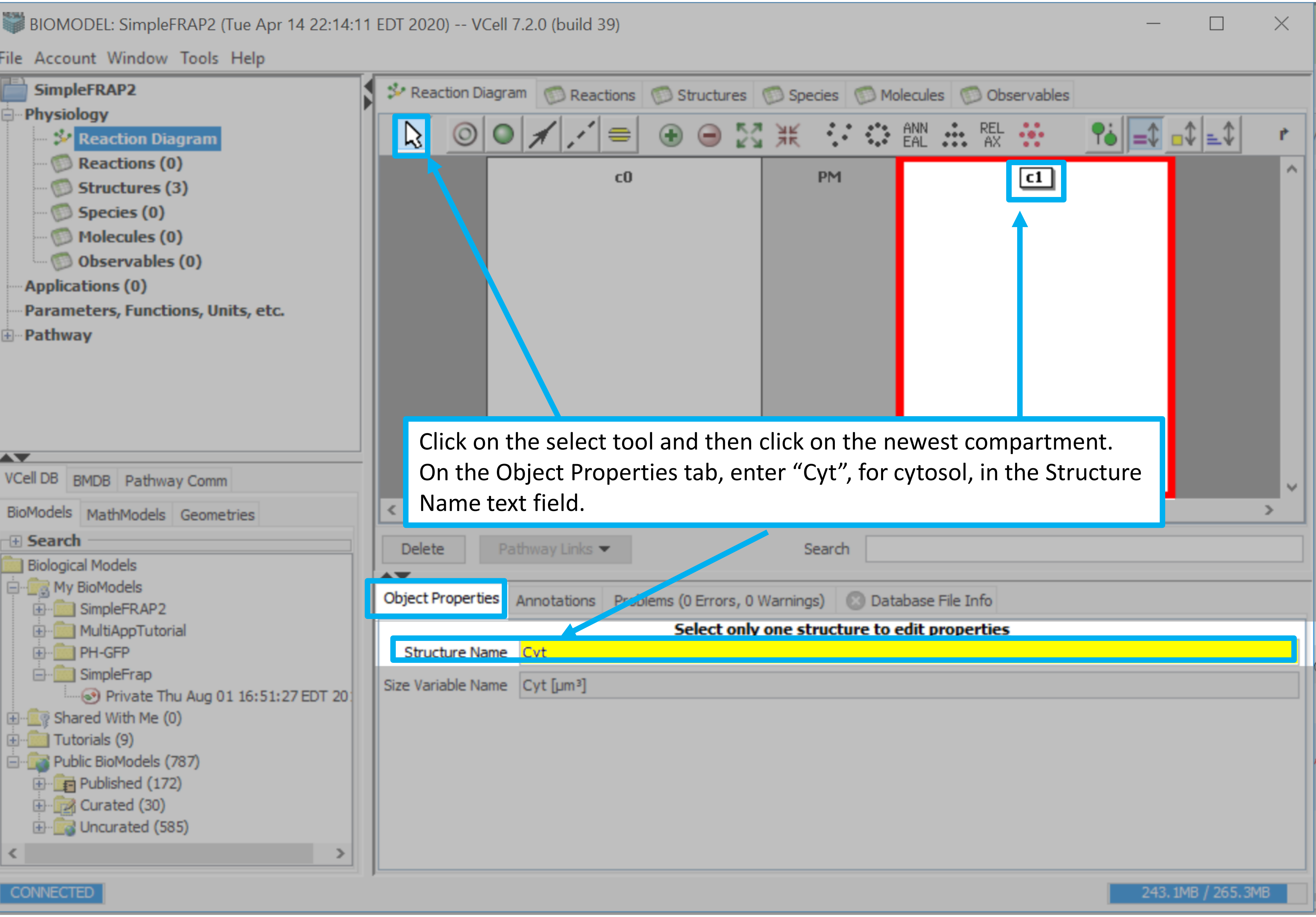
membrane voltage: "Voltage_PM" = voltage(inside (+) compartment) - voltage(outside (-) compartment)

inward currents: from compartment "outside (-) compartment" into compartment "inside (+) compartment"

Note: VCell reactions and fluxes specify inward currents (- to +) rather than conventional currents (+ to -).



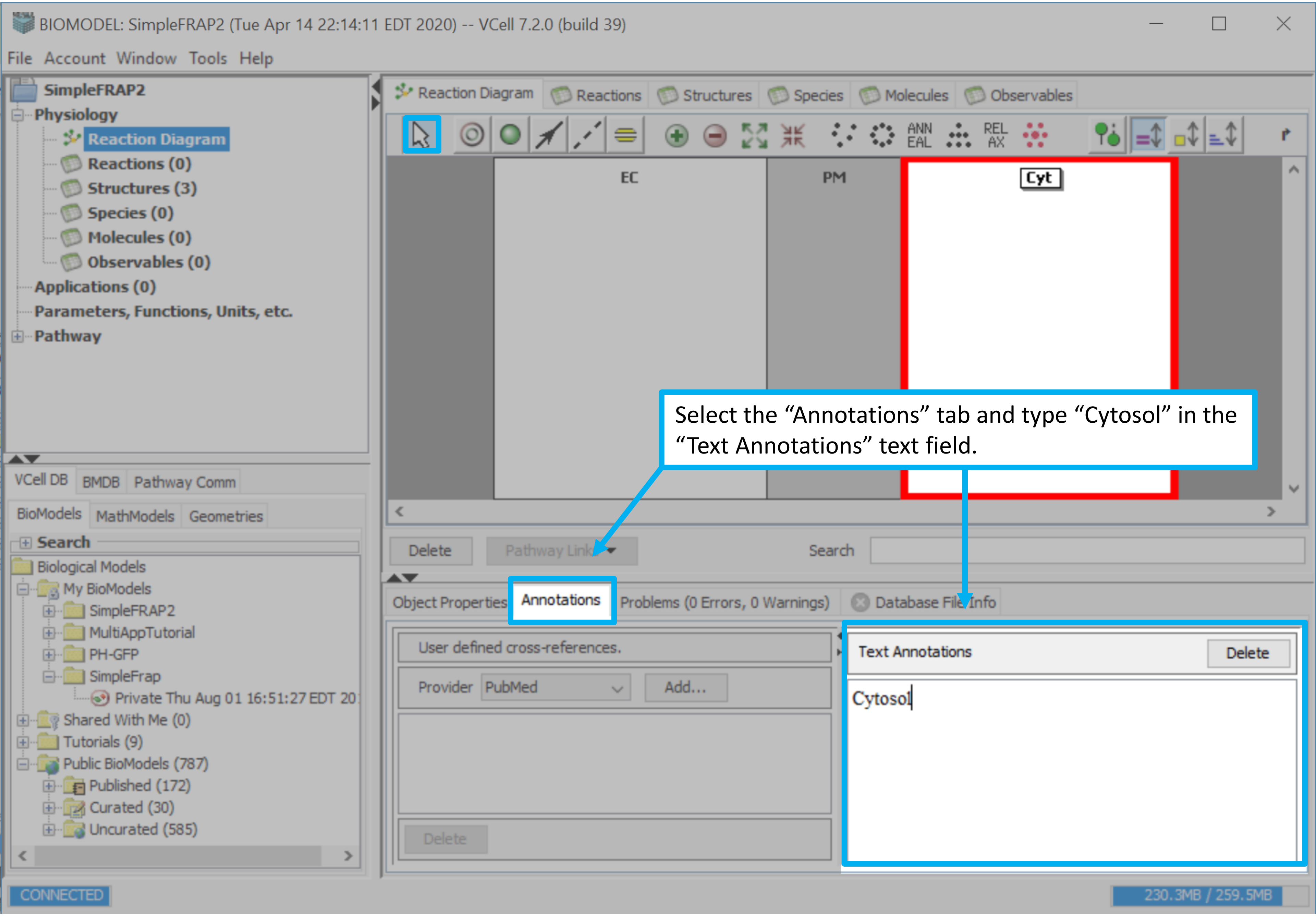
Select the compartment tool, and to the right of PM, hover on the dotted black lines so that they turn green and click “Add Compartment”.



Structure Name: Cyt

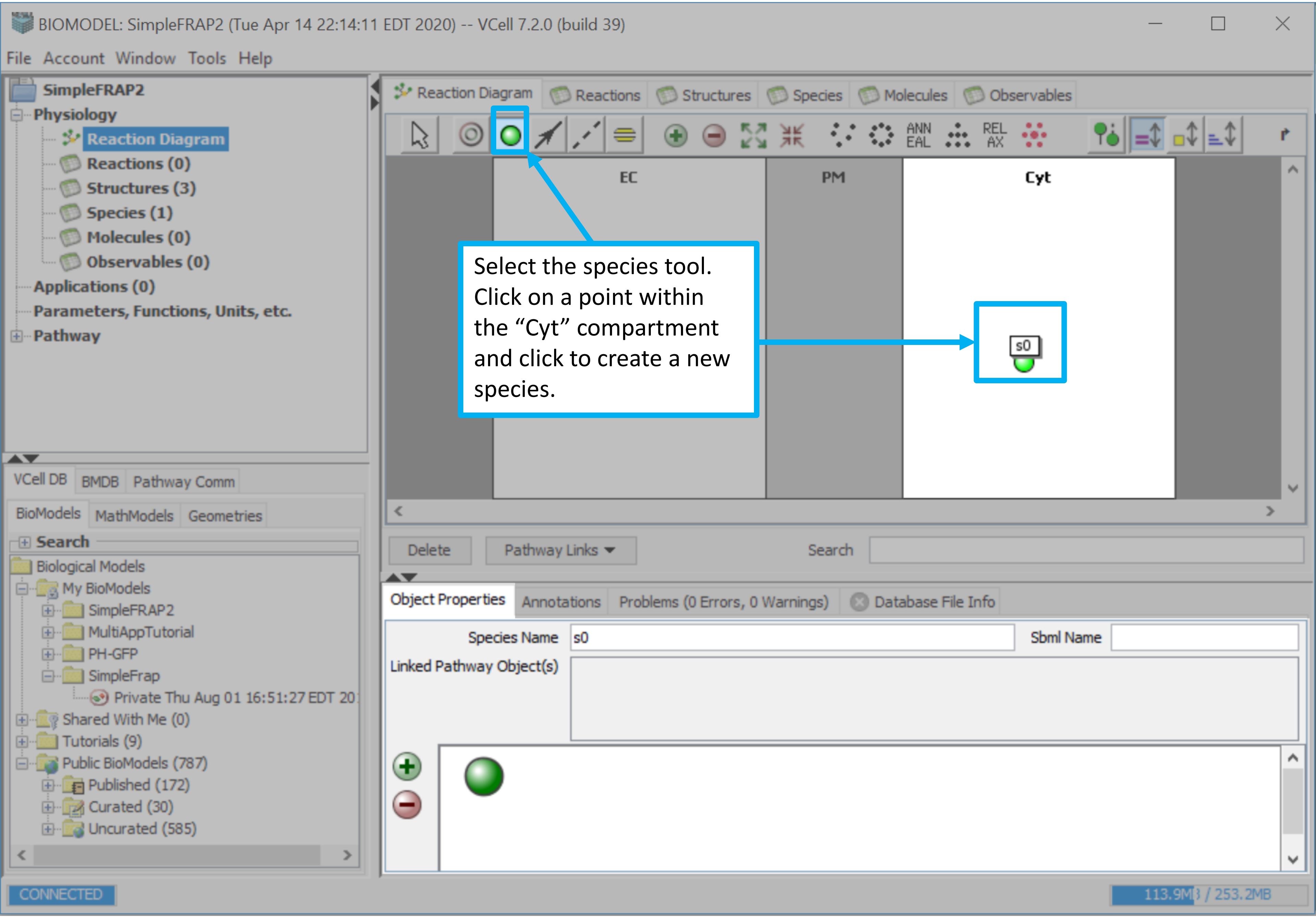
Size Variable Name: Cyt [µm³]

Click on the select tool and then click on the newest compartment. On the Object Properties tab, enter “Cyt”, for cytosol, in the Structure Name text field.



Cytosol

Select the “Annotations” tab and type “Cytosol” in the “Text Annotations” text field.



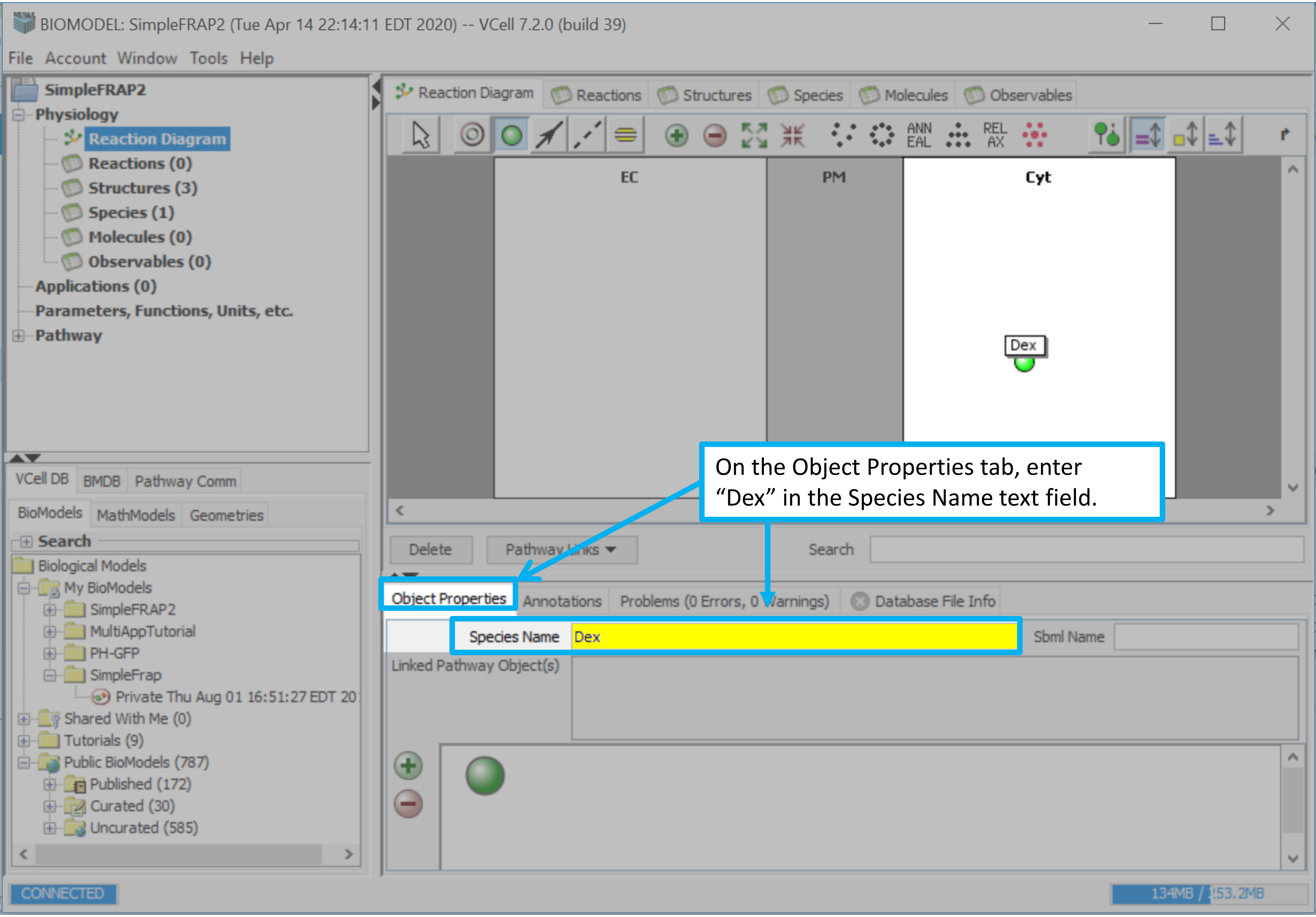
BIOMODEL: SimpleFRAP2 (Tue Apr 14 22:14:11 EDT 2020) -- VCell 7.2.0 (build 39)

Select the species tool. Click on a point within the “Cyt” compartment and click to create a new species.

Species Name: s0

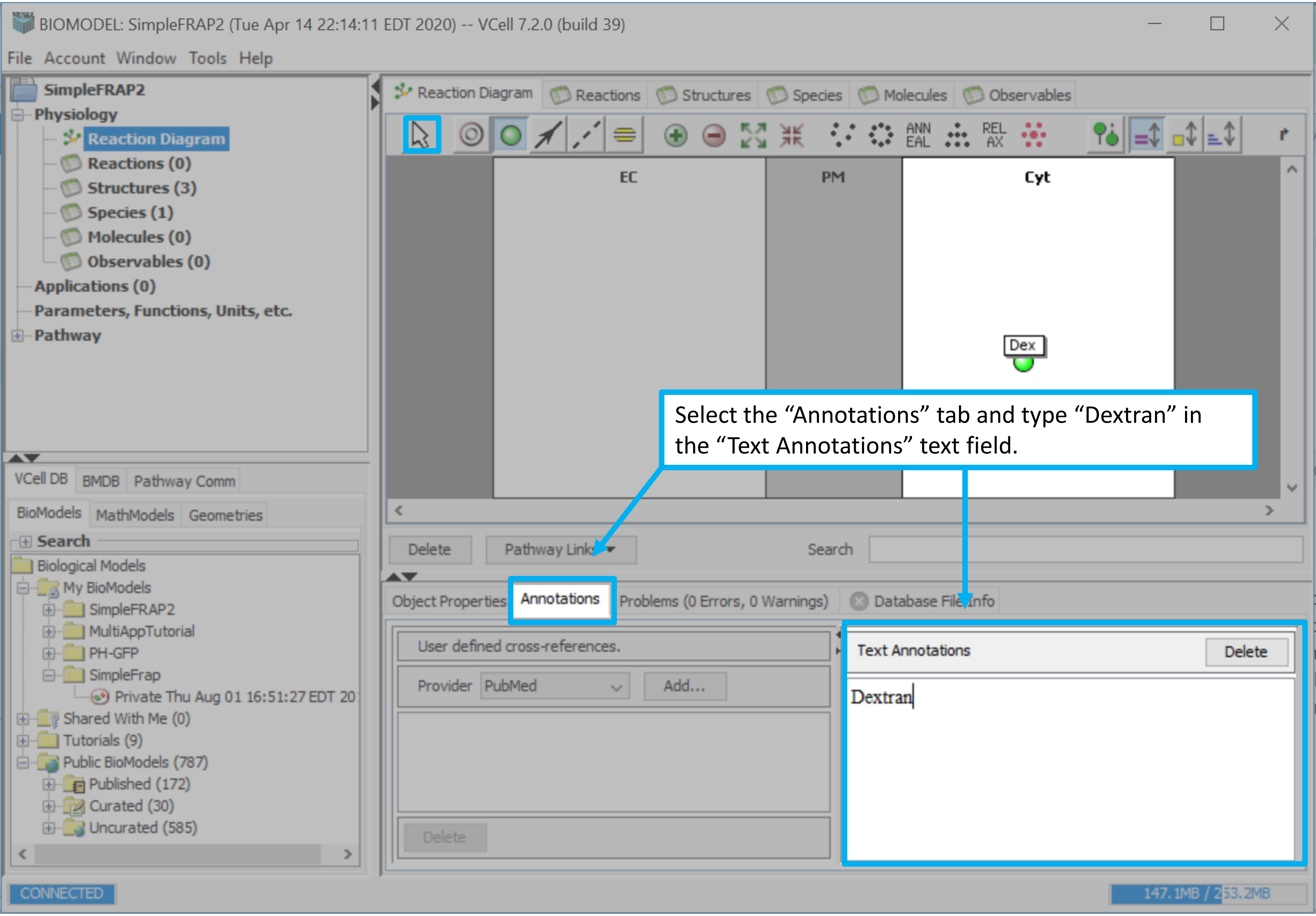
Sbml Name:

Linked Pathway Object(s):



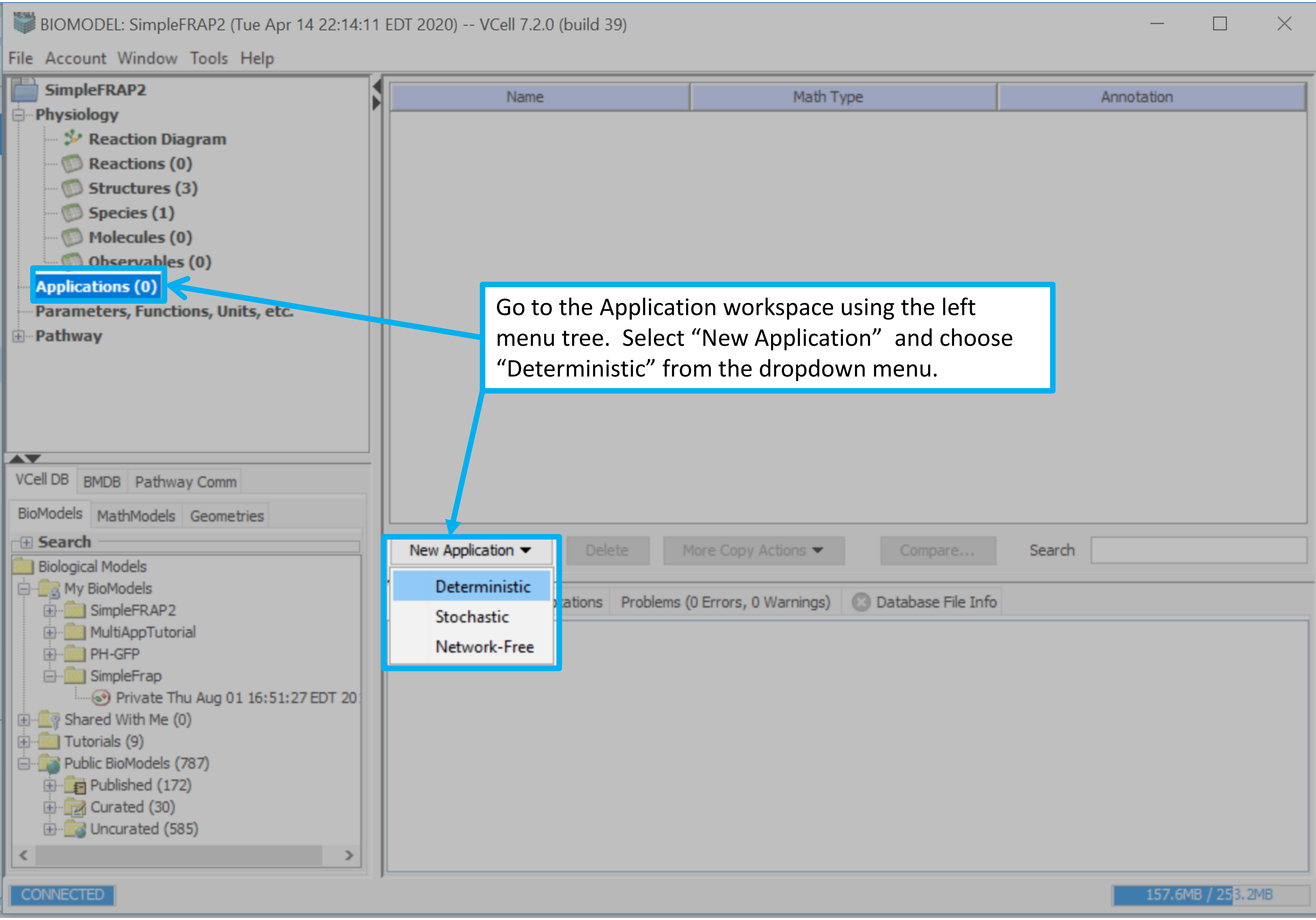
Species Name: Dex

On the Object Properties tab, enter “Dex” in the Species Name text field.

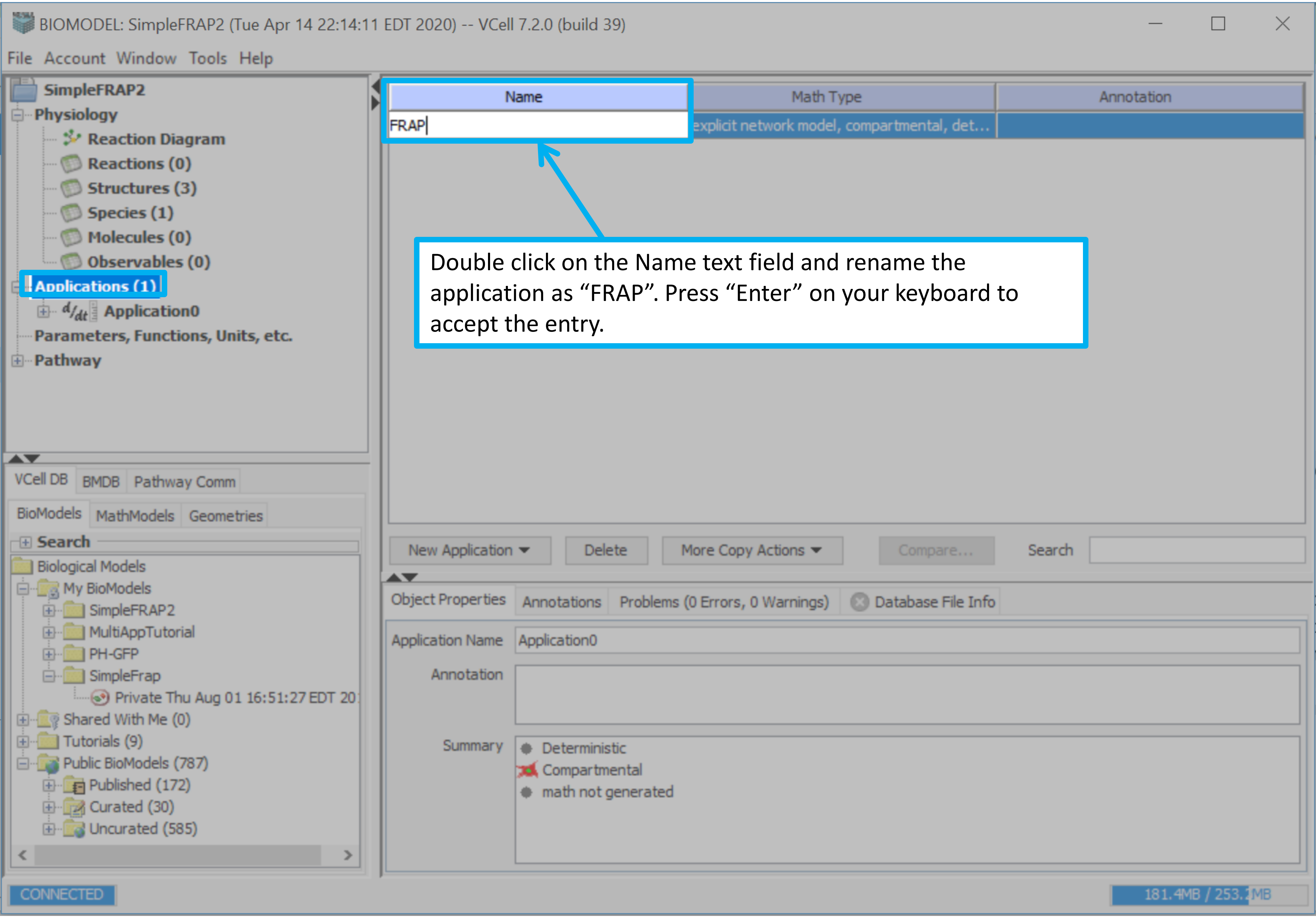


Dextran

Select the “Annotations” tab and type “Dextran” in the “Text Annotations” text field.



Go to the Application workspace using the left menu tree. Select "New Application" and choose "Deterministic" from the dropdown menu.



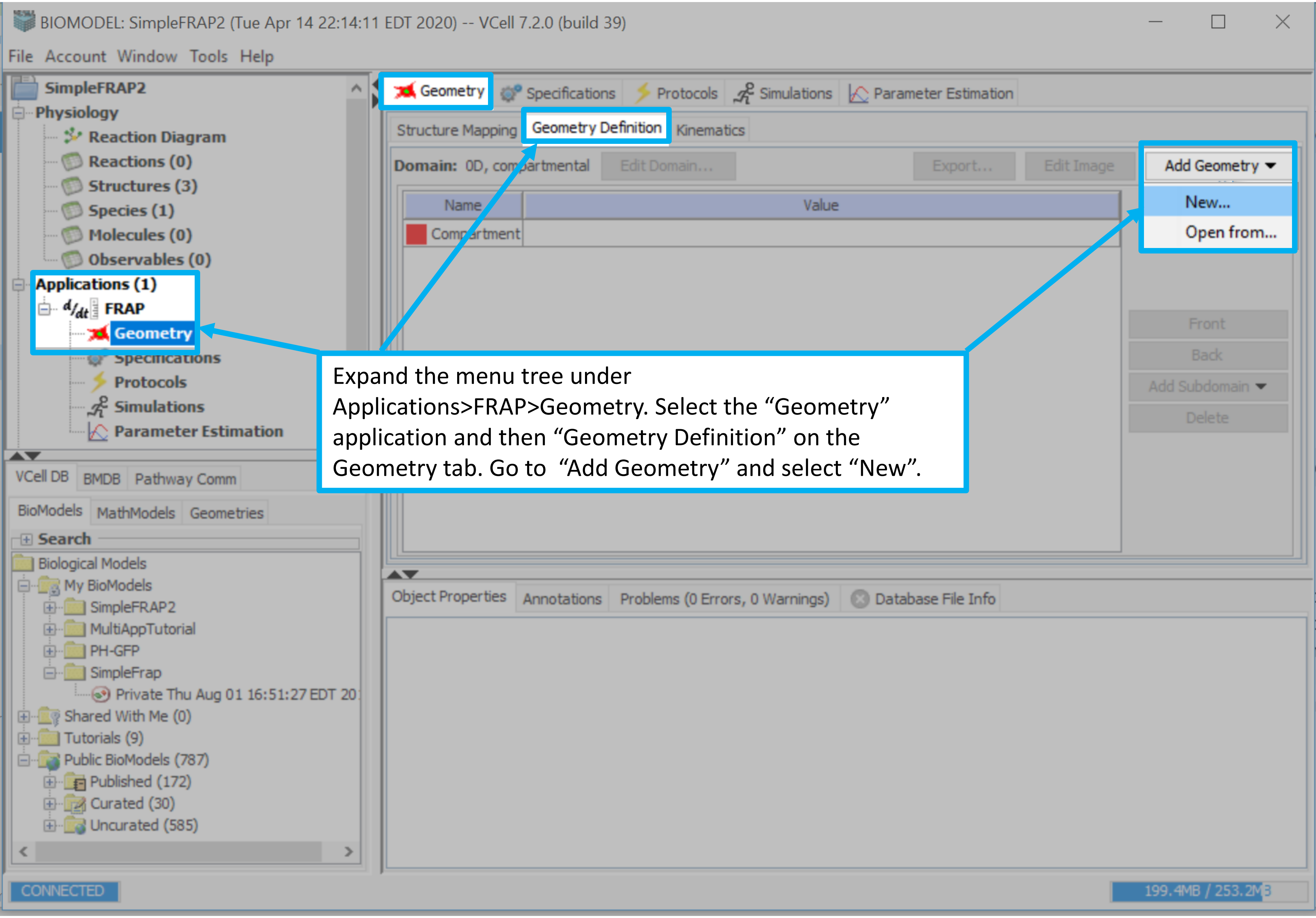
Name	Math Type	Annotation
FRAP	explicit network model, compartmental, det...	

Application Name: Application0

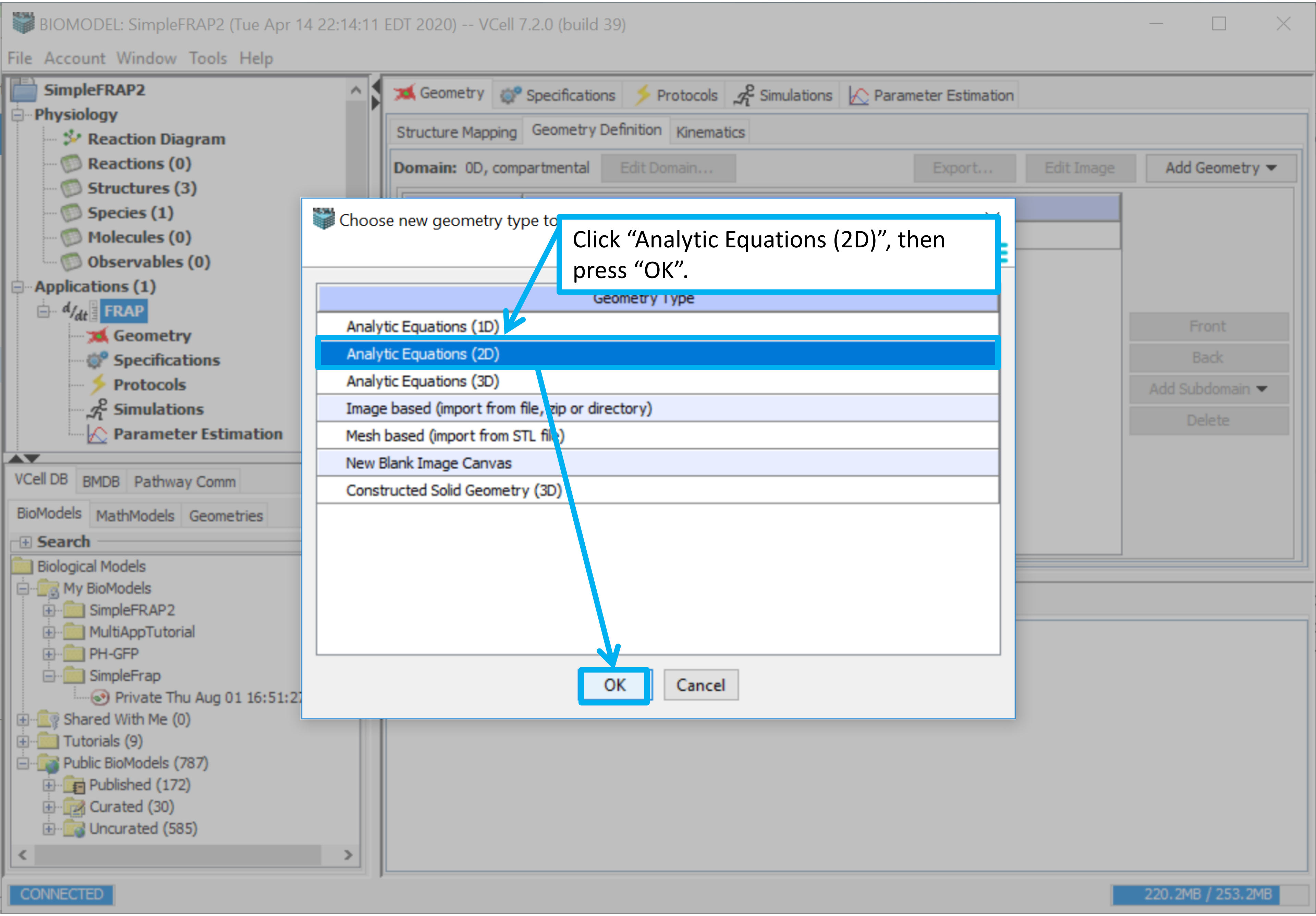
Annotation:

Summary:
- Deterministic
- Compartmental
- math not generated

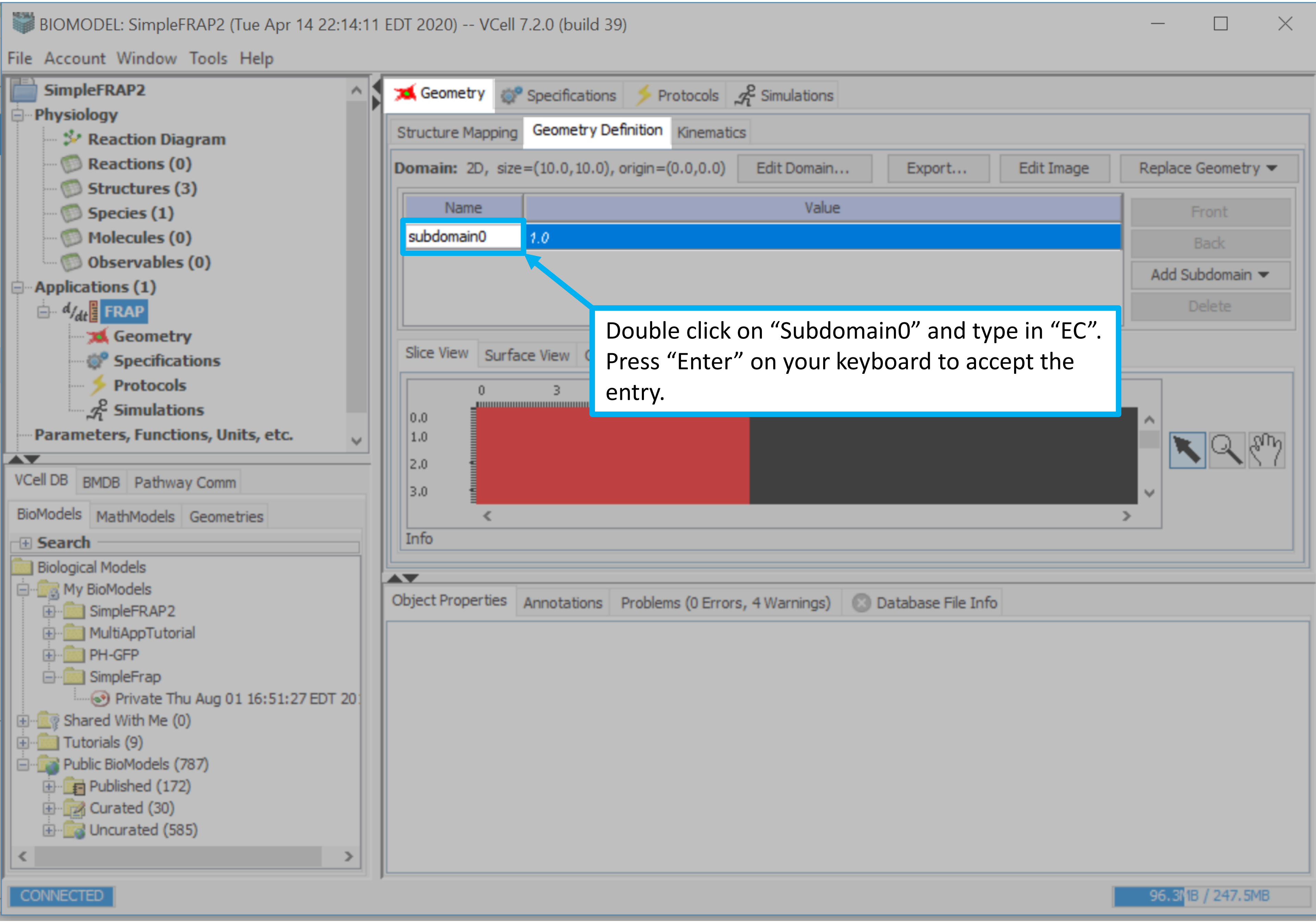
Double click on the Name text field and rename the application as “FRAP”. Press “Enter” on your keyboard to accept the entry.



Expand the menu tree under Applications>FRAP>Geometry. Select the "Geometry" application and then "Geometry Definition" on the Geometry tab. Go to "Add Geometry" and select "New".



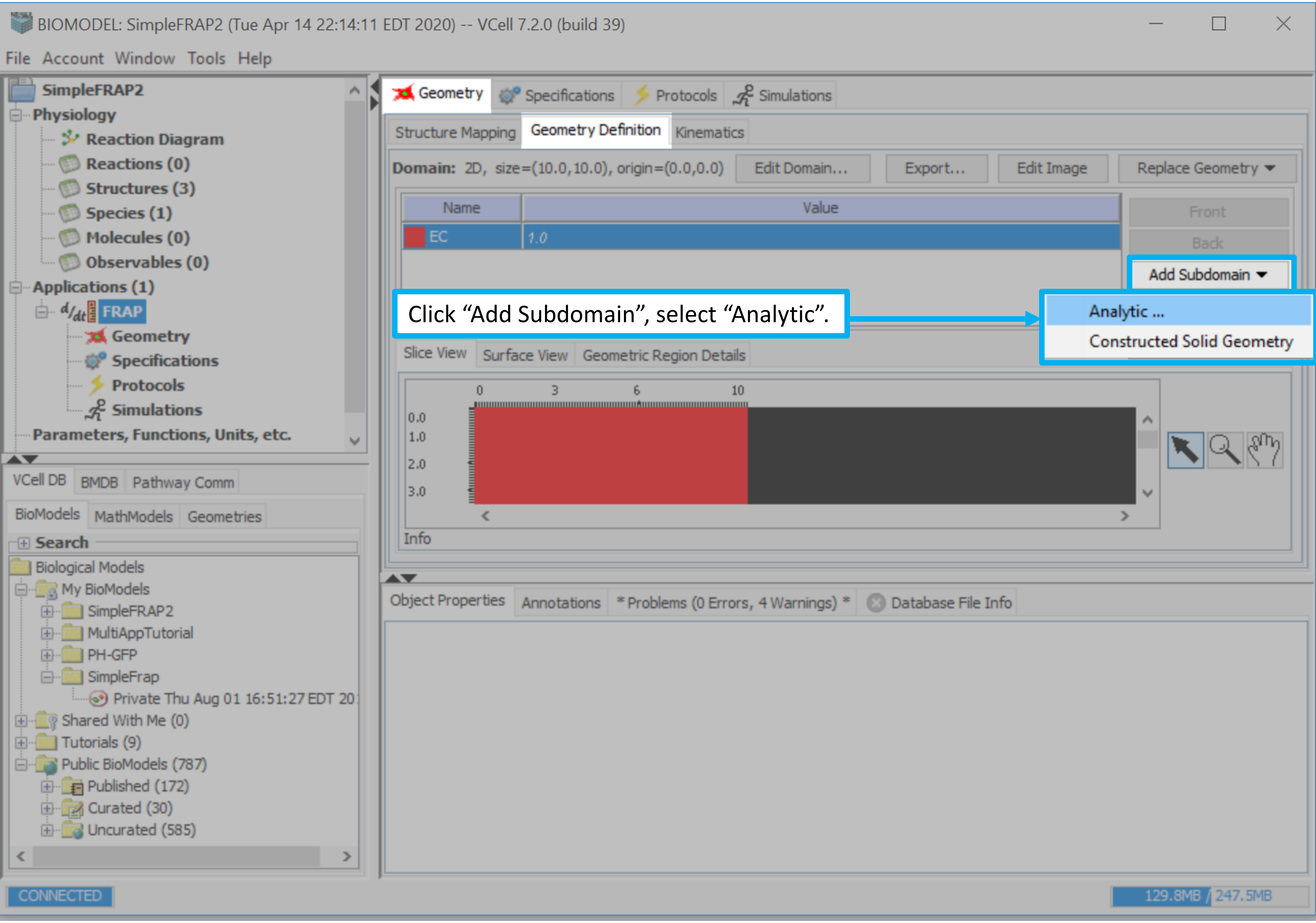
Click “Analytic Equations (2D)”, then press “OK”.



Domain: 2D, size=(10.0,10.0), origin=(0.0,0.0)

Name	Value
subdomain0	1.0

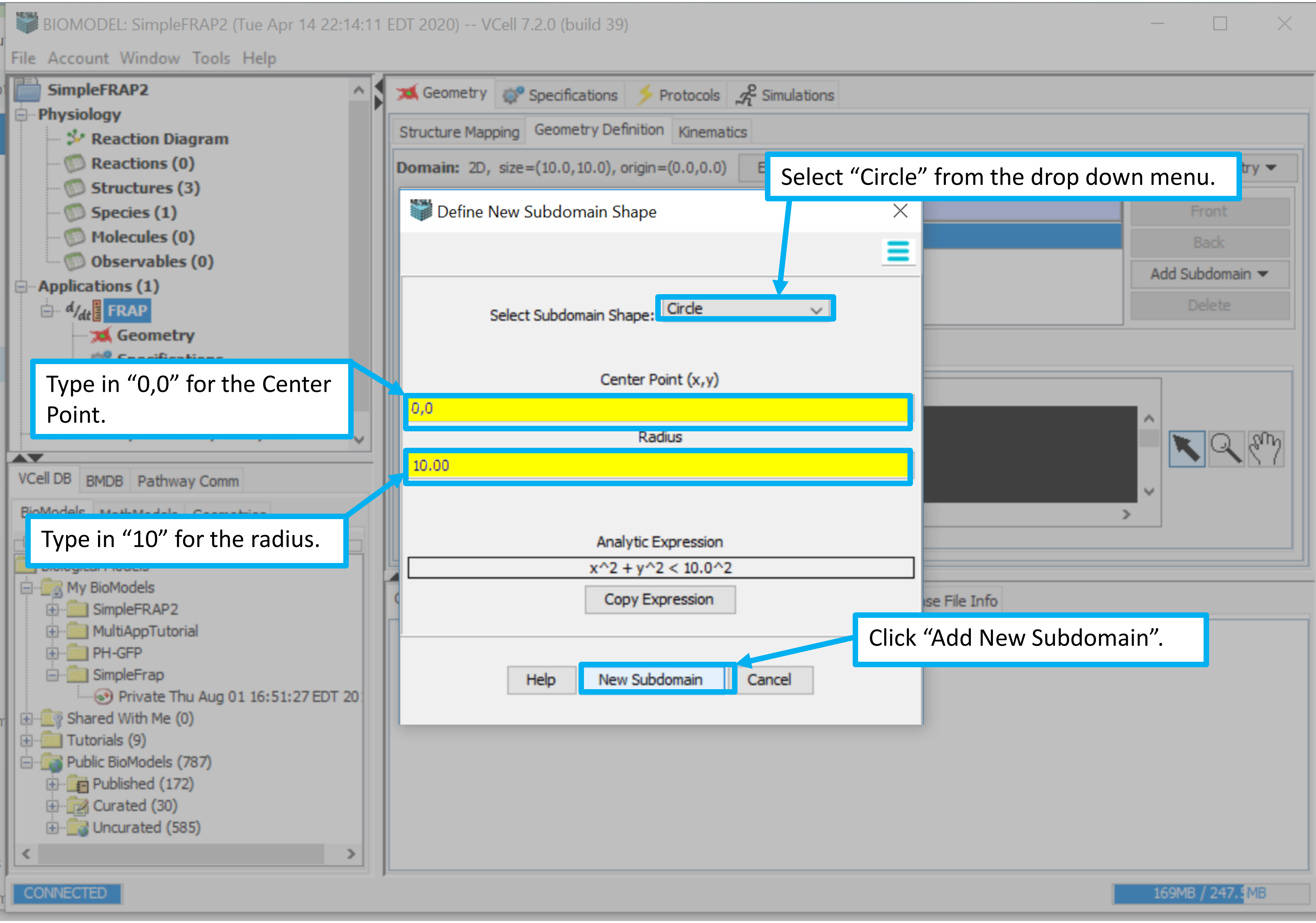
Double click on “Subdomain0” and type in “EC”. Press “Enter” on your keyboard to accept the entry.



Domain: 2D, size=(10.0,10.0), origin=(0.0,0.0)

Name	Value
🟥 EC	1.0

Click “Add Subdomain”, select “Analytic”.



Domain: 2D, size=(10.0,10.0), origin=(0.0,0.0)

Define New Subdomain Shape

Select Subdomain Shape: Circle

Center Point (x,y): 0,0

Radius: 10.00

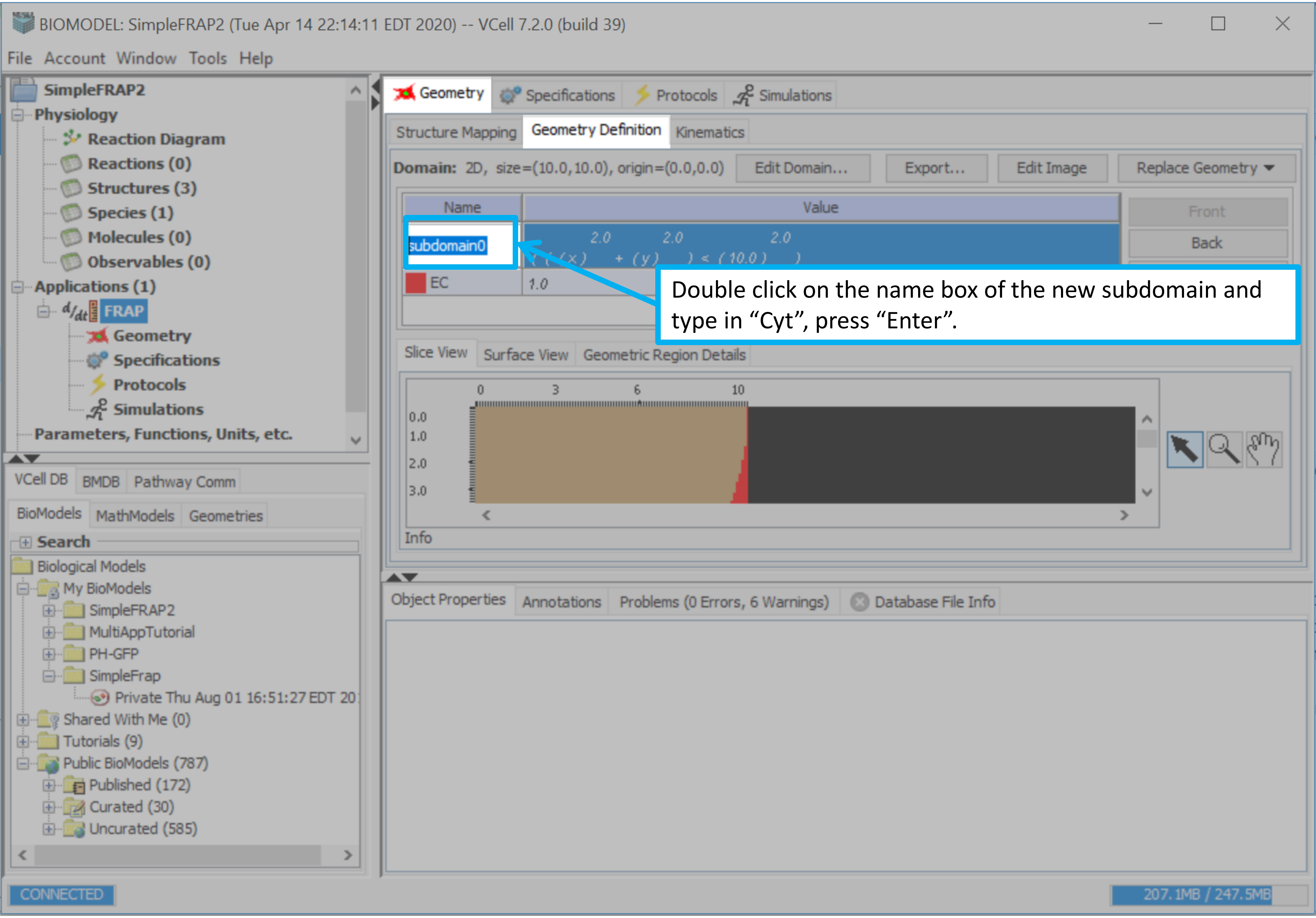
Analytic Expression: x^2 + y^2 < 10.0^2

Select "Circle" from the drop down menu.

Type in "0,0" for the Center Point.

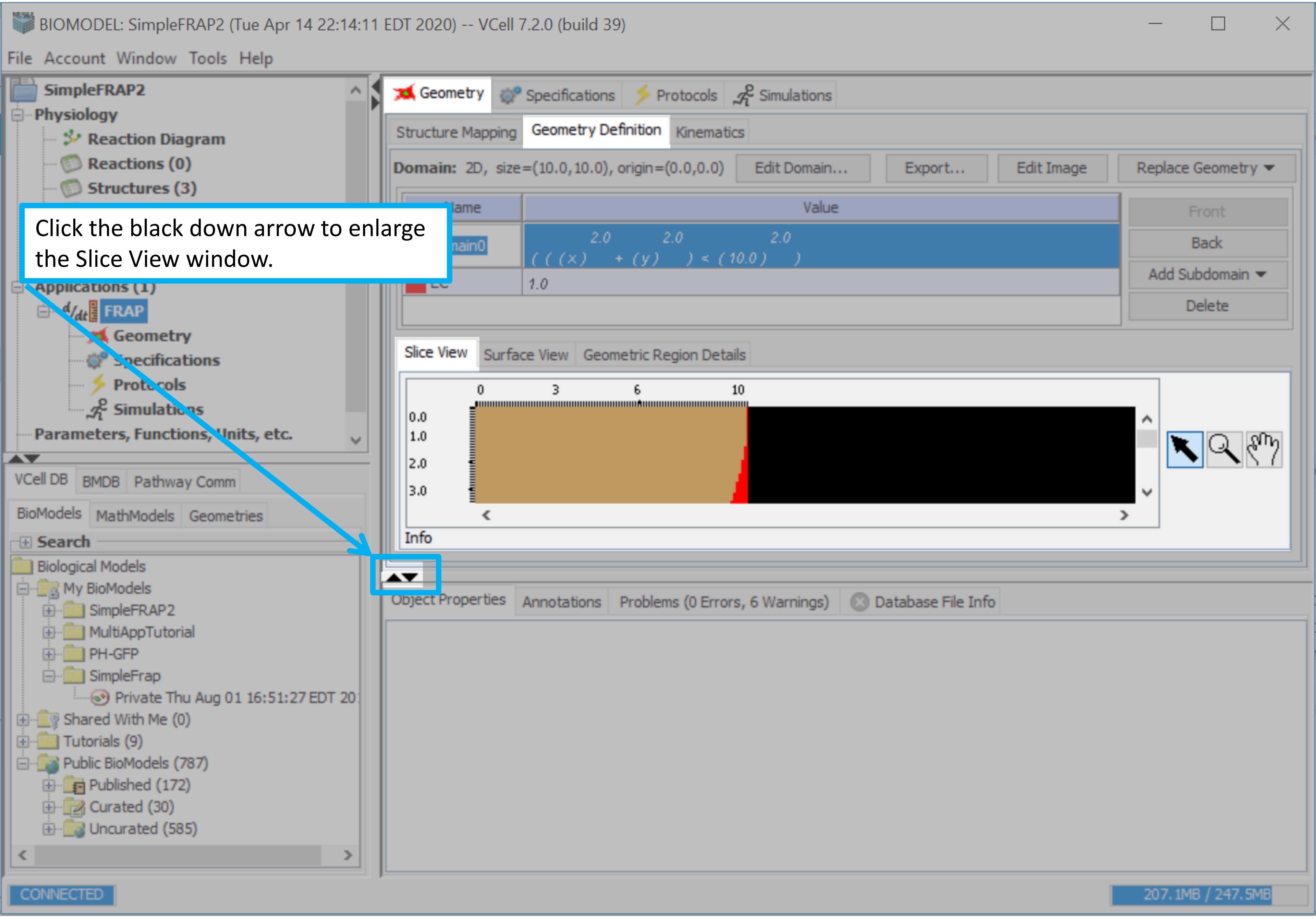
Type in "10" for the radius.

Click "Add New Subdomain".

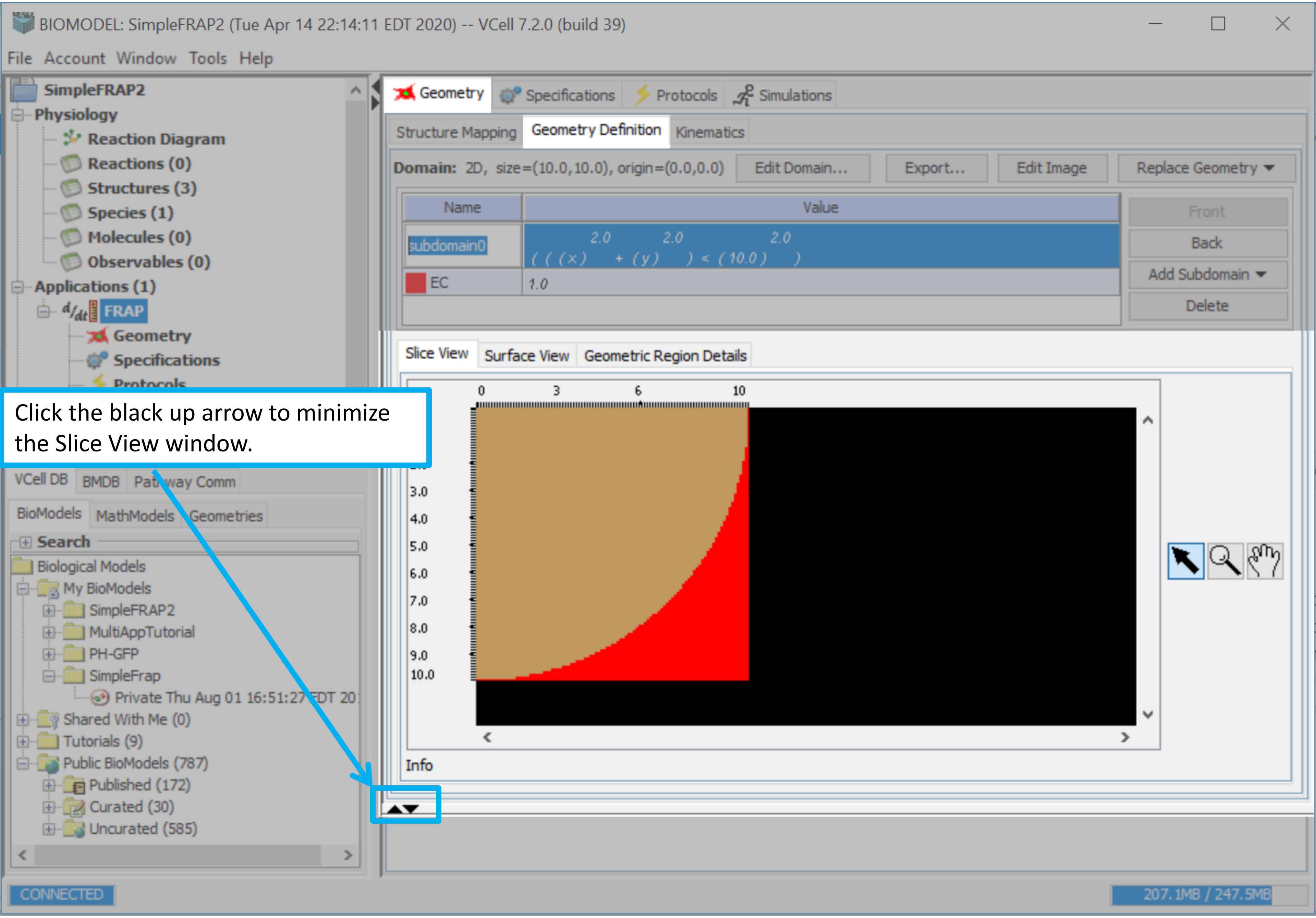


Name	Value
subdomain0	$((x)^{2.0} + (y)^{2.0}) < (10.0)^{2.0}$
EC	1.0

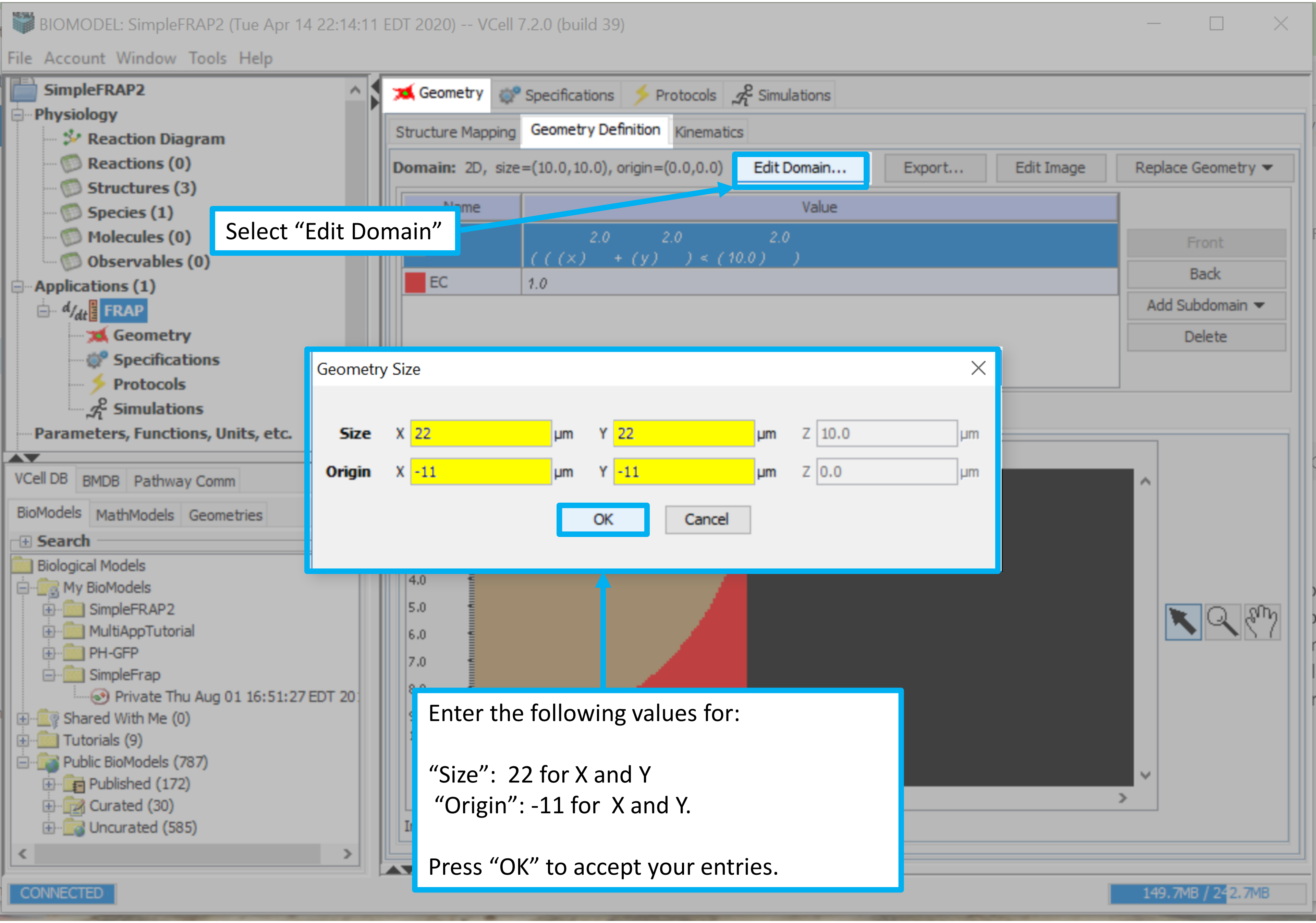
Double click on the name box of the new subdomain and type in “Cyt”, press “Enter”.



Click the black down arrow to enlarge the Slice View window.



Click the black up arrow to minimize the Slice View window.



Select “Edit Domain”

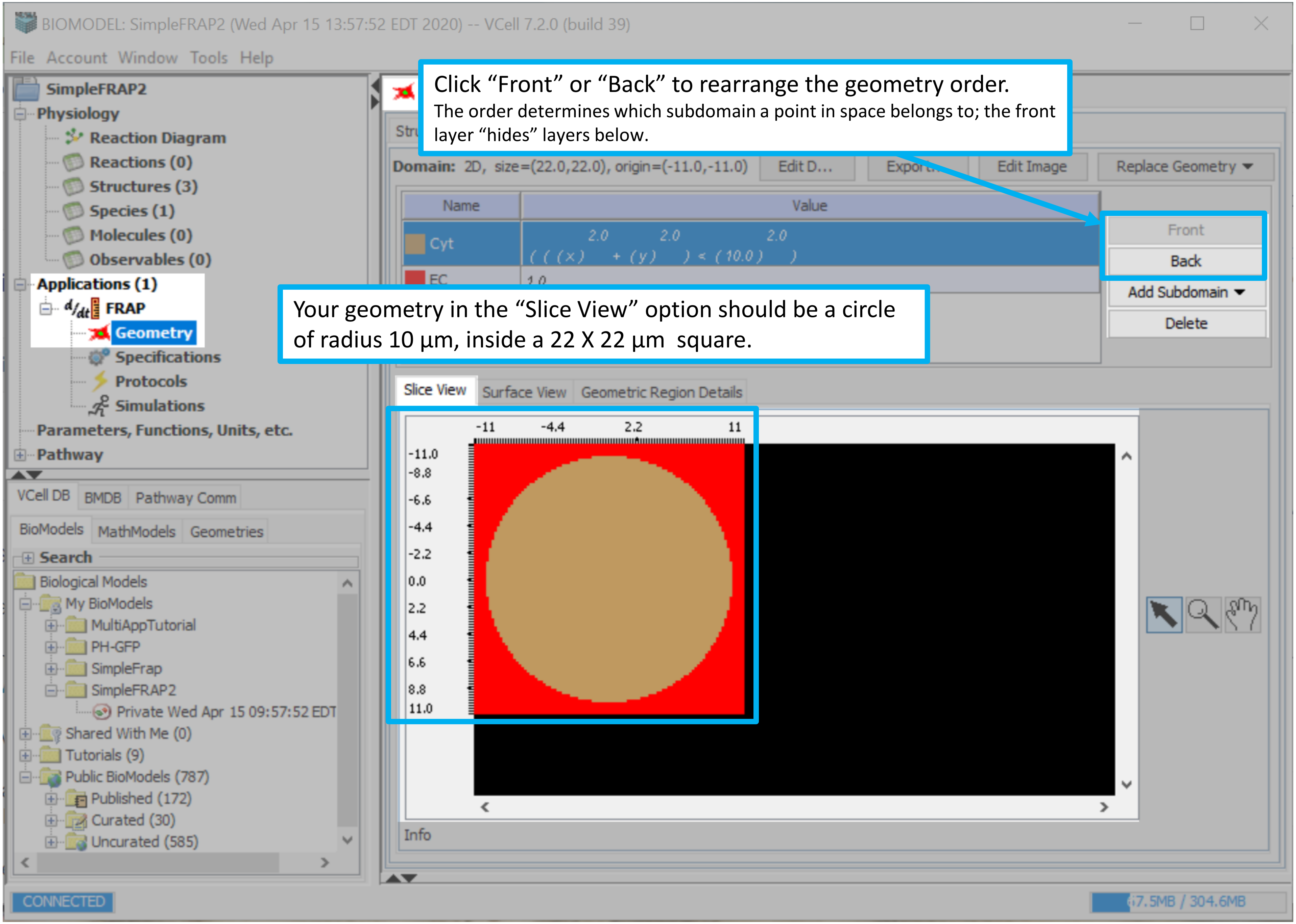
Geometry Size

Size	X	22	µm	Y	22	µm	Z	10.0 µm
Origin	X	-11	µm	Y	-11	µm	Z	0.0 µm

Enter the following values for:

“Size”: 22 for X and Y
“Origin”: -11 for X and Y.

Press “OK” to accept your entries.



Click “Front” or “Back” to rearrange the geometry order.

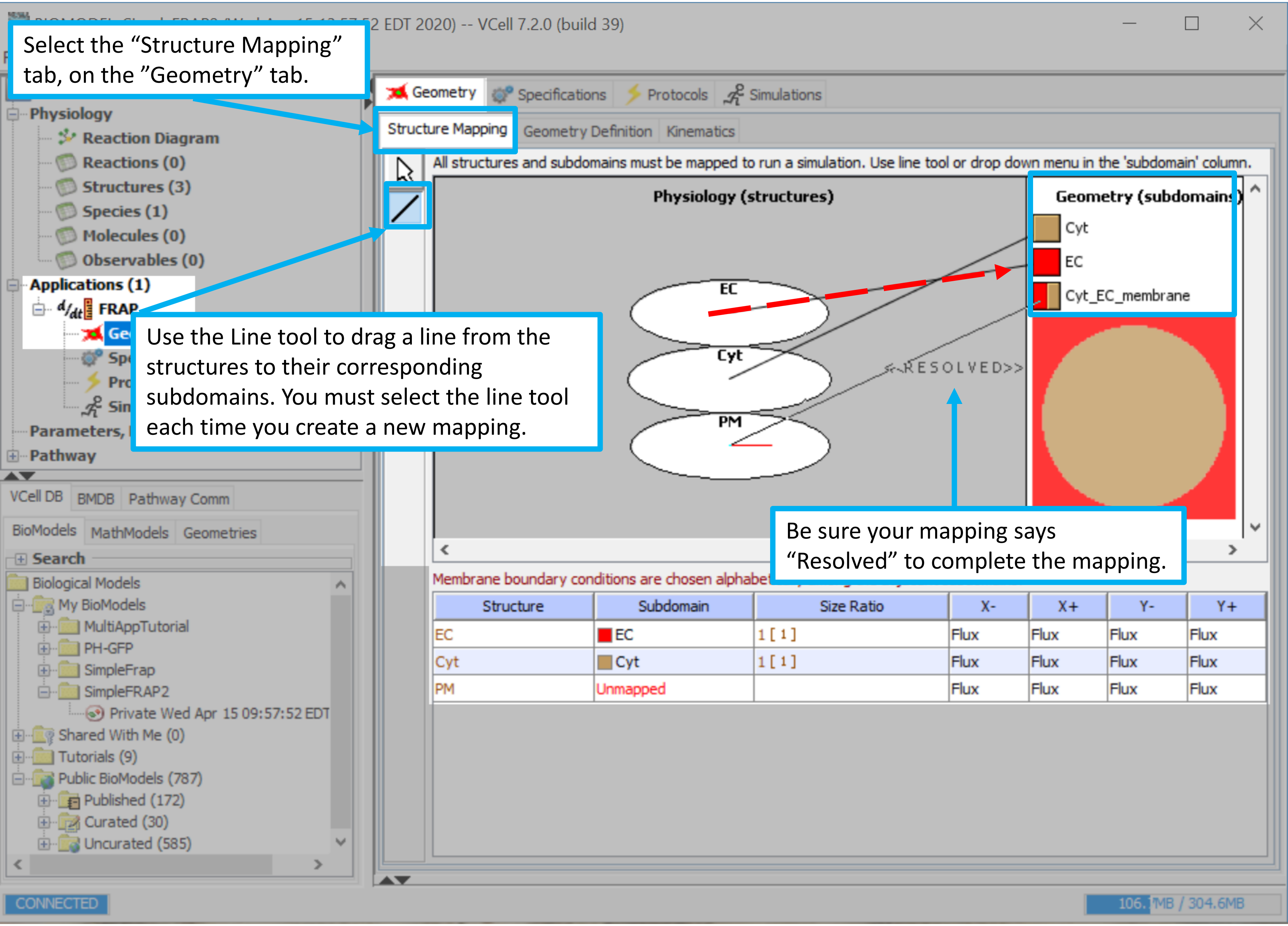
The order determines which subdomain a point in space belongs to; the front layer “hides” layers below.

Your geometry in the “Slice View” option should be a circle of radius 10 µm, inside a 22 X 22 µm square.

BIOMODEL: SimpleFRAP2 (Wed Apr 15 13:57:52 EDT 2020) -- VCell 7.2.0 (build 39)

Domain: 2D, size=(22.0,22.0), origin=(-11.0,-11.0)

Name	Value
🟫 Cyt	$((x)^{2.0} + (y)^{2.0}) < (10.0)^{2.0}$
🟥 EC	1.0



Select the “Structure Mapping” tab, on the ”Geometry” tab.

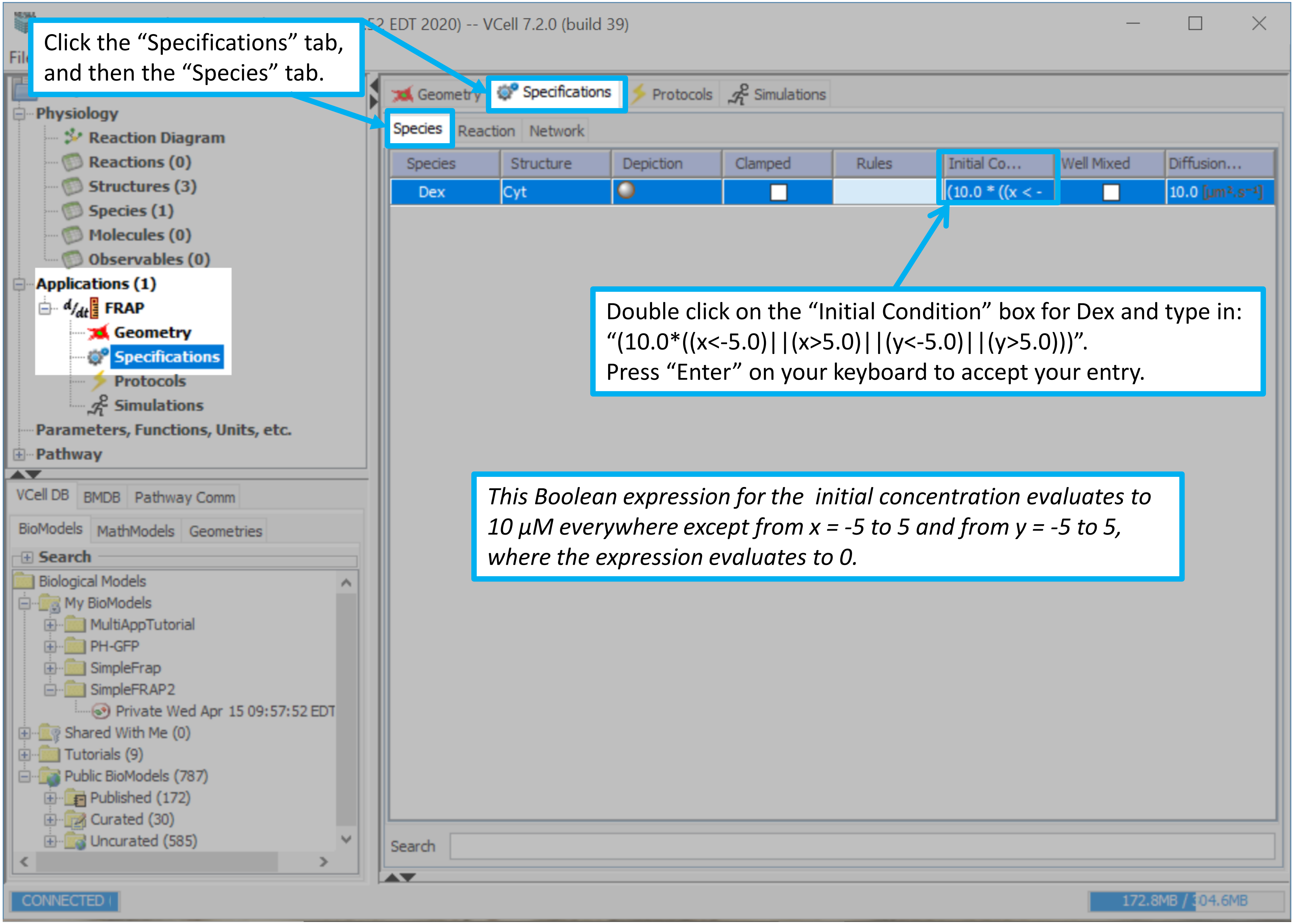
Use the Line tool to drag a line from the structures to their corresponding subdomains. You must select the line tool each time you create a new mapping.

Be sure your mapping says “Resolved” to complete the mapping.

All structures and subdomains must be mapped to run a simulation. Use line tool or drop down menu in the 'subdomain' column.

Membrane boundary conditions are chosen alphabet

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+
EC	🟥 EC	1 [1]	Flux	Flux	Flux	Flux
Cyt	🟫 Cyt	1 [1]	Flux	Flux	Flux	Flux
PM	Unmapped		Flux	Flux	Flux	Flux

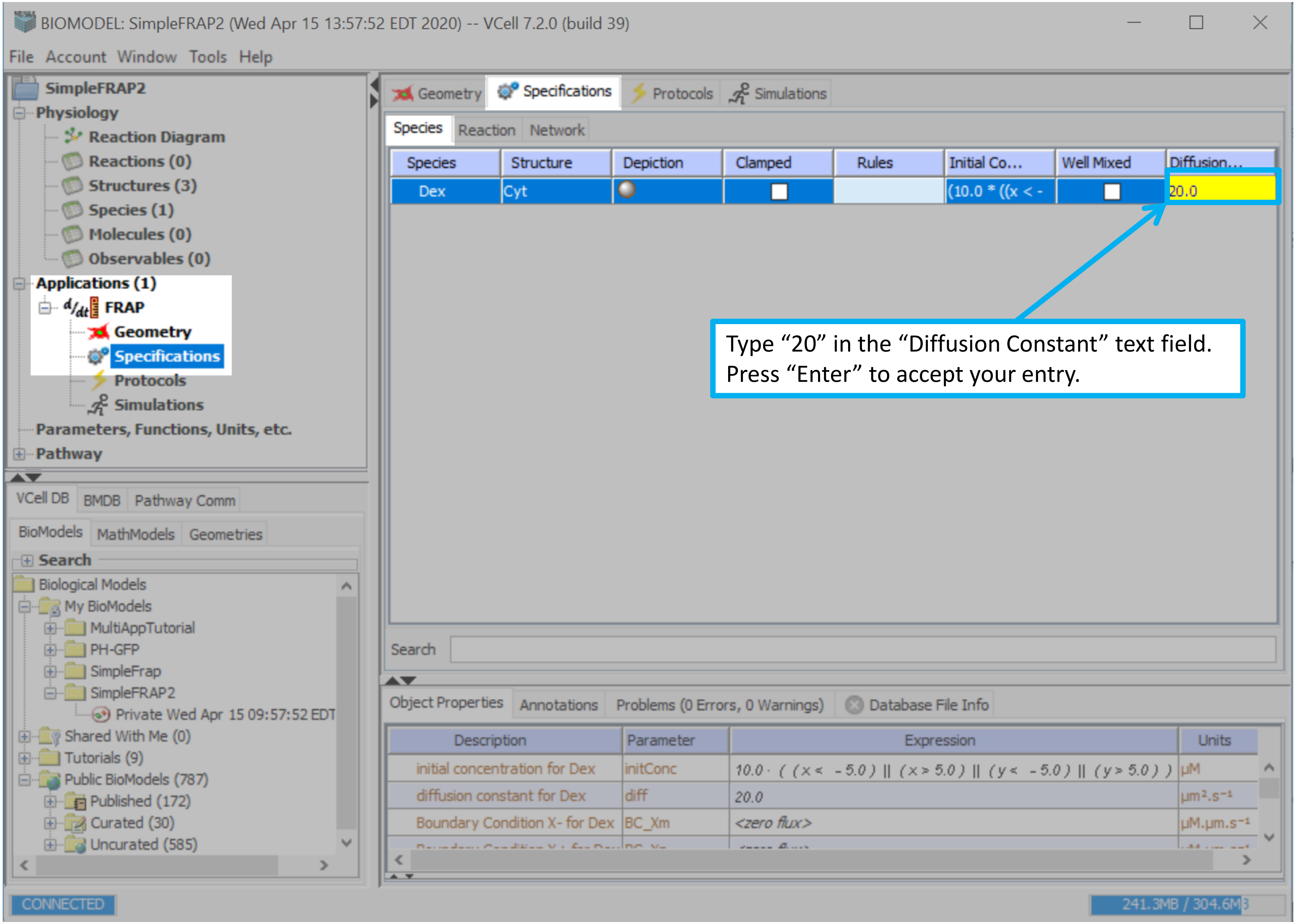


Species	Structure	Depiction	Clamped	Rules	Initial Co...	Well Mixed	Diffusion...
Dex	Cyt	●	☐		(10.0 * ((x < -	☐	10.0 [µm².s⁻¹]

Click the "Specifications" tab, and then the "Species" tab.

Double click on the "Initial Condition" box for Dex and type in: "(10.0*((x<-5.0)||(x>5.0)||(y<-5.0)||(y>5.0)))".
Press "Enter" on your keyboard to accept your entry.

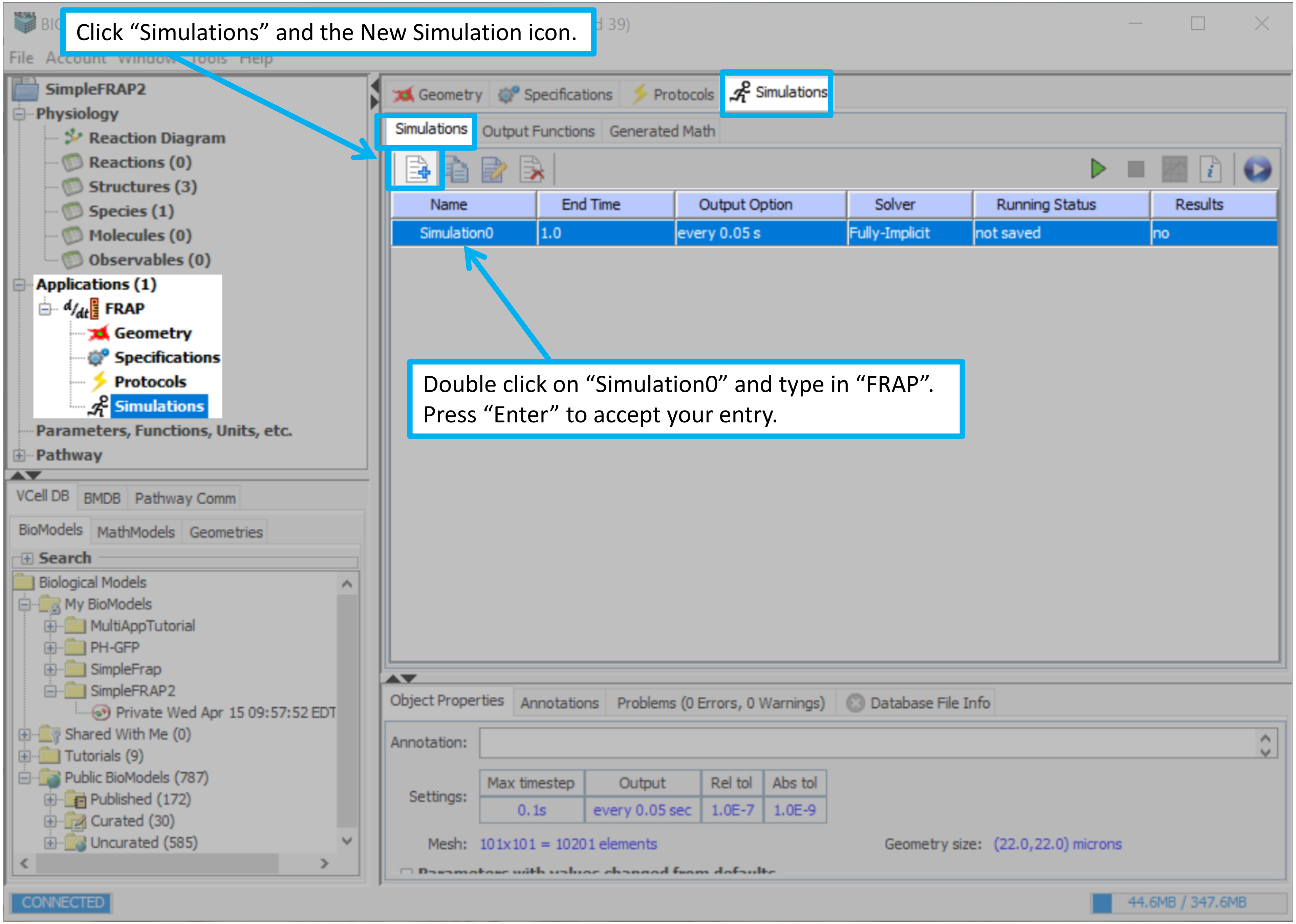
This Boolean expression for the initial concentration evaluates to 10 µM everywhere except from x = -5 to 5 and from y = -5 to 5, where the expression evaluates to 0.



Species	Structure	Depiction	Clamped	Rules	Initial Co...	Well Mixed	Diffusion...
Dex	Cyt	●	☐		(10.0 * ((x < -	☐	20.0

Description	Parameter	Expression	Units
initial concentration for Dex	initConc	10.0 · ((x < -5.0) || (x > 5.0) || (y < -5.0) || (y > 5.0))	μM
diffusion constant for Dex	diff	20.0	μm².s⁻¹
Boundary Condition X- for Dex	BC_Xm	<zero flux>	μM.μm.s⁻¹

Type “20” in the “Diffusion Constant” text field. Press “Enter” to accept your entry.



Click "Simulations" and the New Simulation icon.

Double click on "Simulation0" and type in "FRAP". Press "Enter" to accept your entry.

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	1.0	every 0.05 s	Fully-Implicit	not saved	no

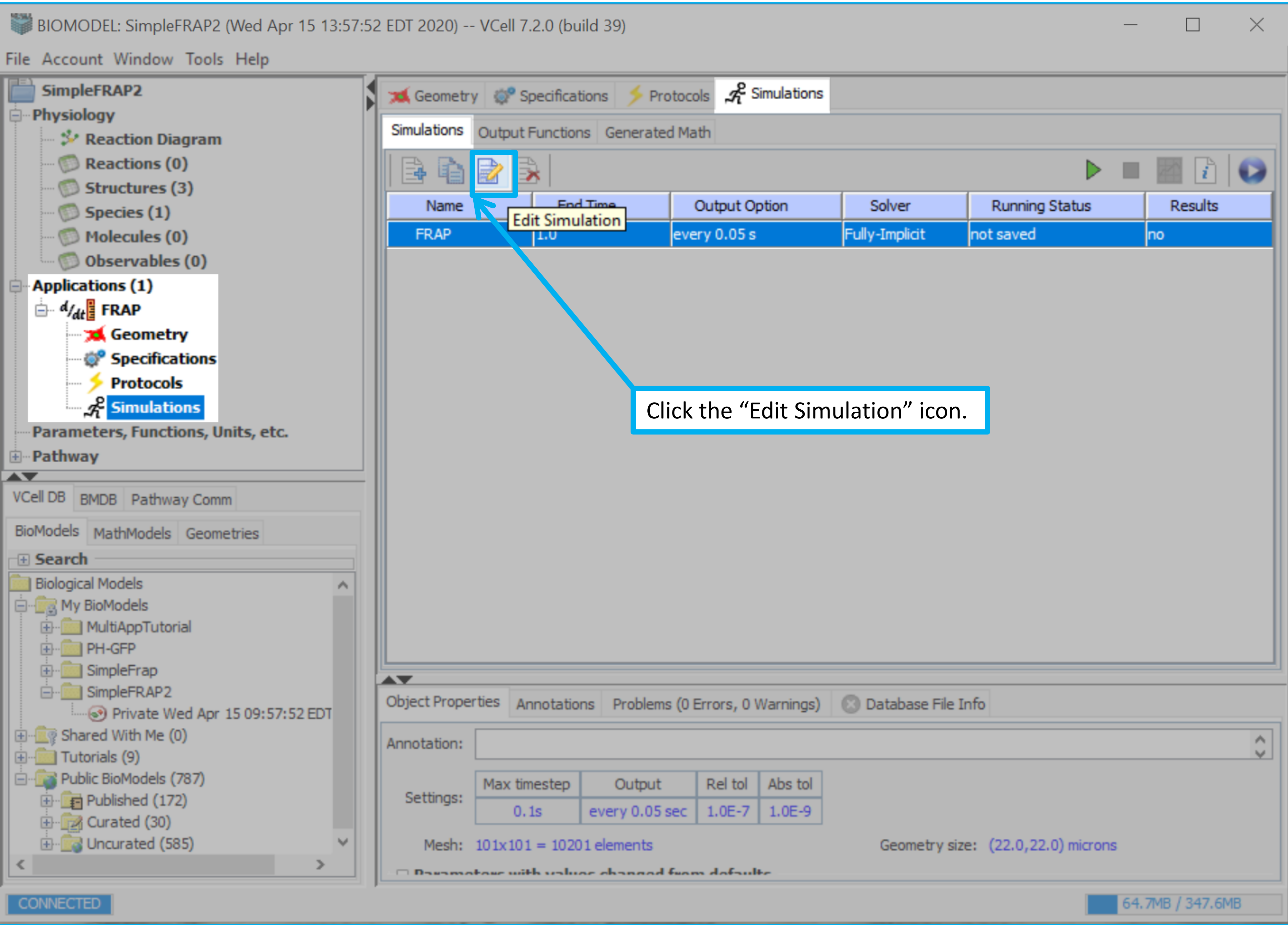
Annotation:

Settings:

Max timestep	Output	Rel tol	Abs tol
0.1s	every 0.05 sec	1.0E-7	1.0E-9

Mesh: 101x101 = 10201 elements

Geometry size: (22.0,22.0) microns



BIOMODEL: SimpleFRAP2 (Wed Apr 15 13:57:52 EDT 2020) -- VCell 7.2.0 (build 39)

Name	End Time	Output Option	Solver	Running Status	Results
FRAP	1.0	every 0.05 s	Fully-Implicit	not saved	no

Annotation:

Settings:

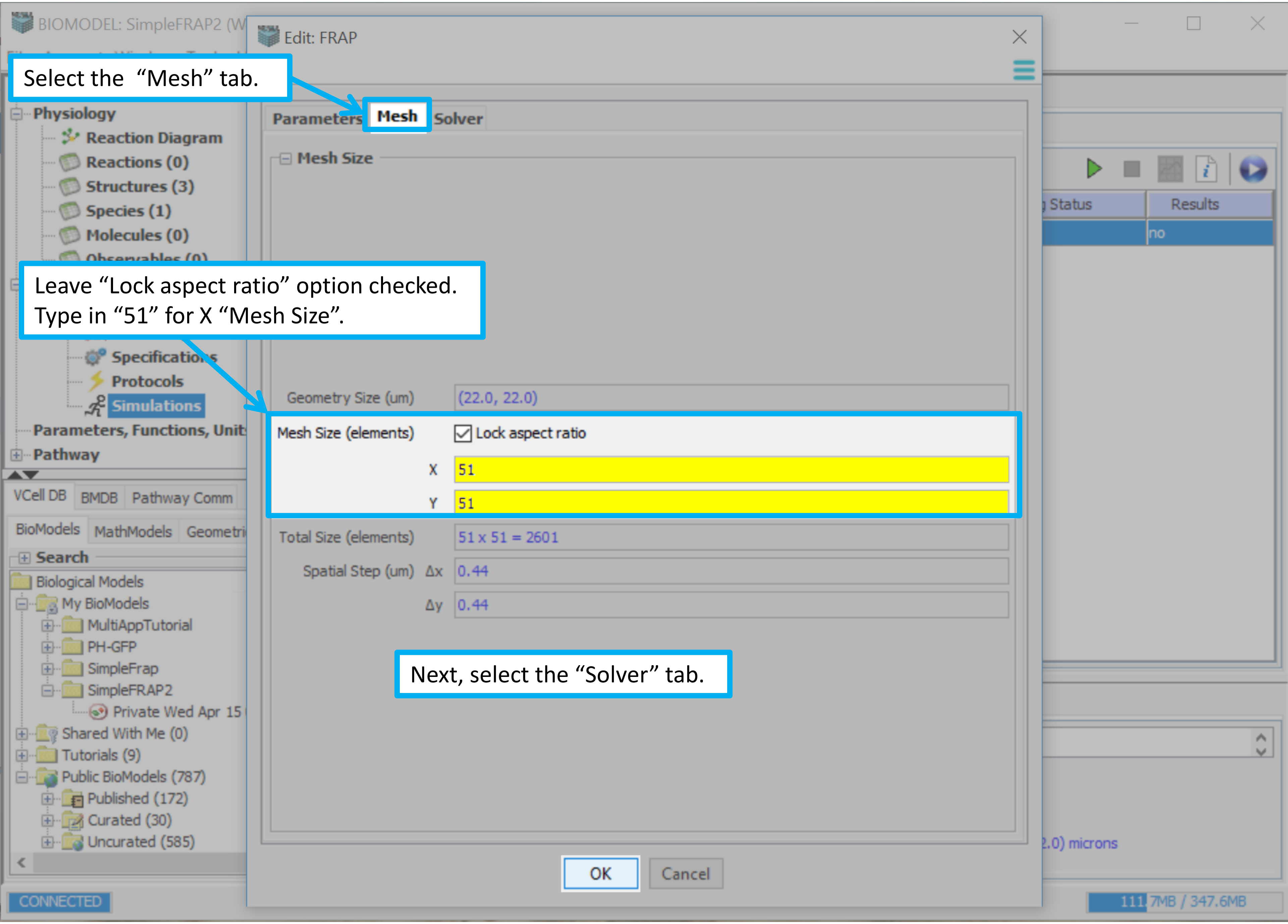
Max timestep	Output	Rel tol	Abs tol
0.1s	every 0.05 sec	1.0E-7	1.0E-9

Mesh: 101x101 = 10201 elements

Geometry size: (22.0,22.0) microns

☐ Parameters with values changed from defaults

Click the “Edit Simulation” icon.



Select the "Mesh" tab.

Leave "Lock aspect ratio" option checked.
Type in "51" for X "Mesh Size".

Geometry Size (um) (22.0, 22.0)

Mesh Size (elements) ☑ Lock aspect ratio

X 51

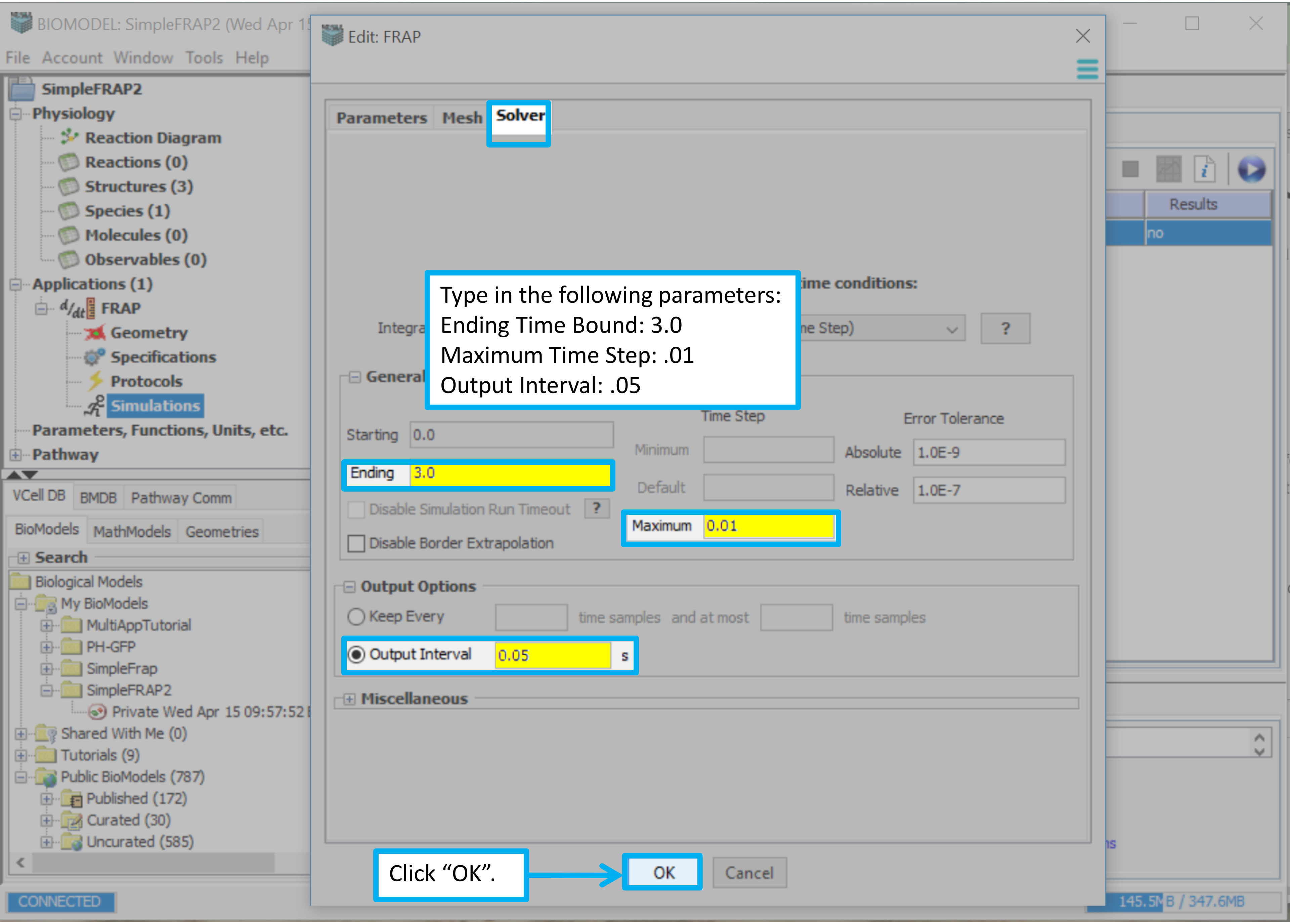
Y 51

Total Size (elements) 51 x 51 = 2601

Spatial Step (um) Δx 0.44

Δy 0.44

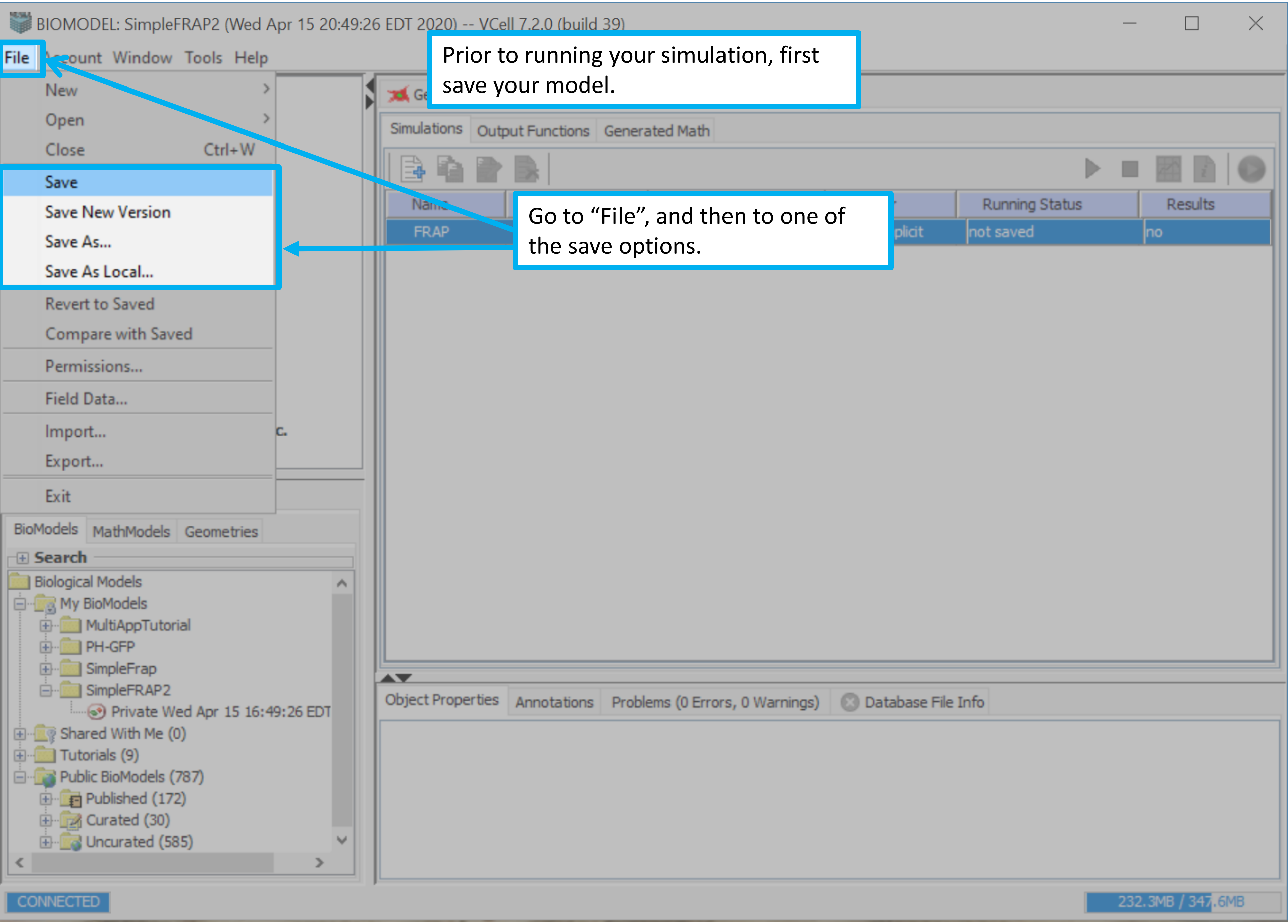
Next, select the "Solver" tab.



Type in the following parameters:
Ending Time Bound: 3.0
Maximum Time Step: .01
Output Interval: .05

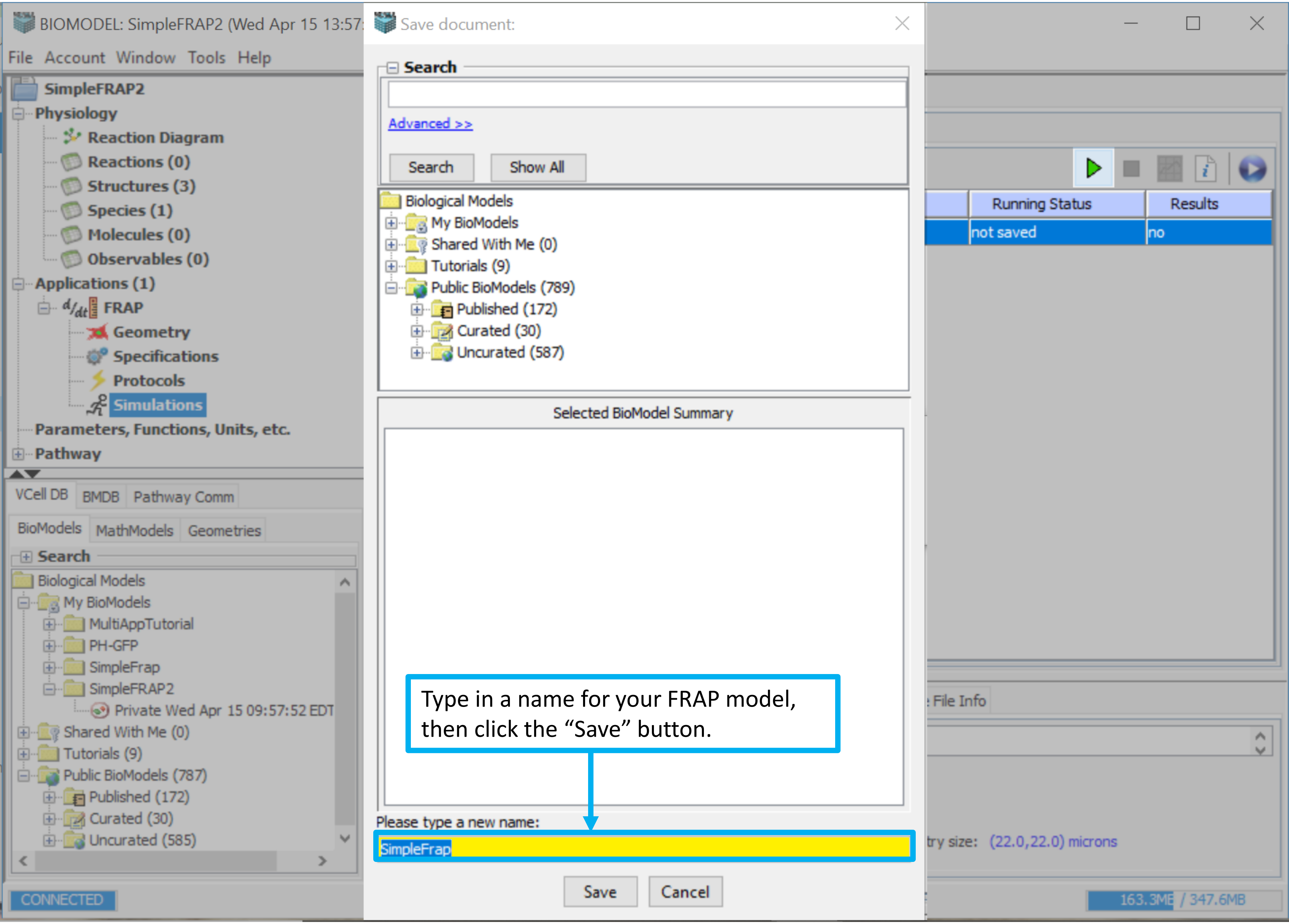
Starting: 0.0
Ending: 3.0
Minimum:
Default:
Maximum: 0.01
Absolute: 1.0E-9
Relative: 1.0E-7
● Output Interval: 0.05 s

Click “OK”.



Prior to running your simulation, first save your model.

Go to “File”, and then to one of the save options.

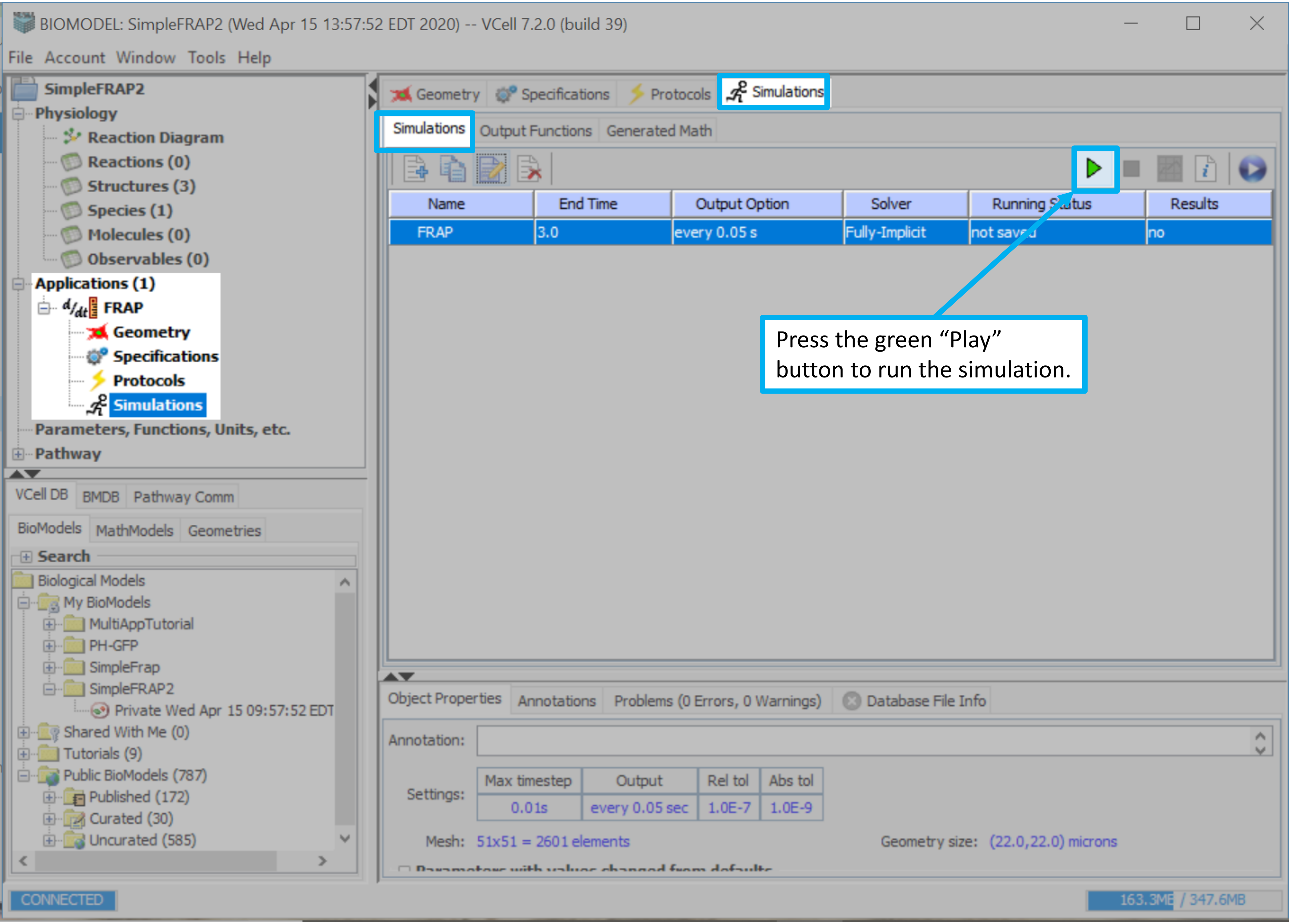


Please type a new name: SimpleFrap

not saved | no

try size: (22.0,22.0) microns

Type in a name for your FRAP model, then click the “Save” button.



Name	End Time	Output Option	Solver	Running Status	Results
FRAP	3.0	every 0.05 s	Fully-Implicit	not saved	no

Annotation:

Settings:

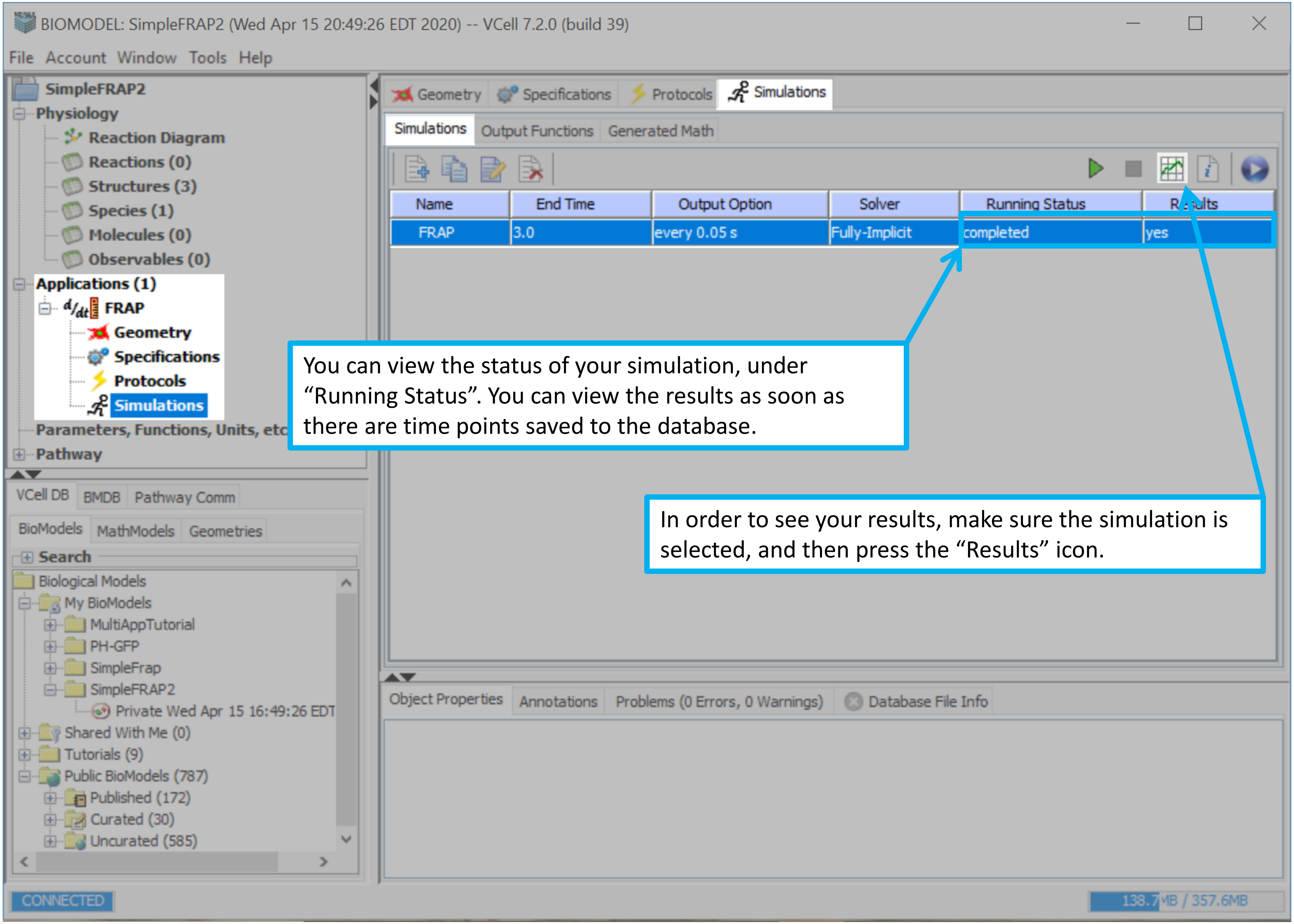
Max timestep	Output	Rel tol	Abs tol
0.01s	every 0.05 sec	1.0E-7	1.0E-9

Mesh: 51x51 = 2601 elements

Geometry size: (22.0,22.0) microns

☐ Parameters with values changed from defaults

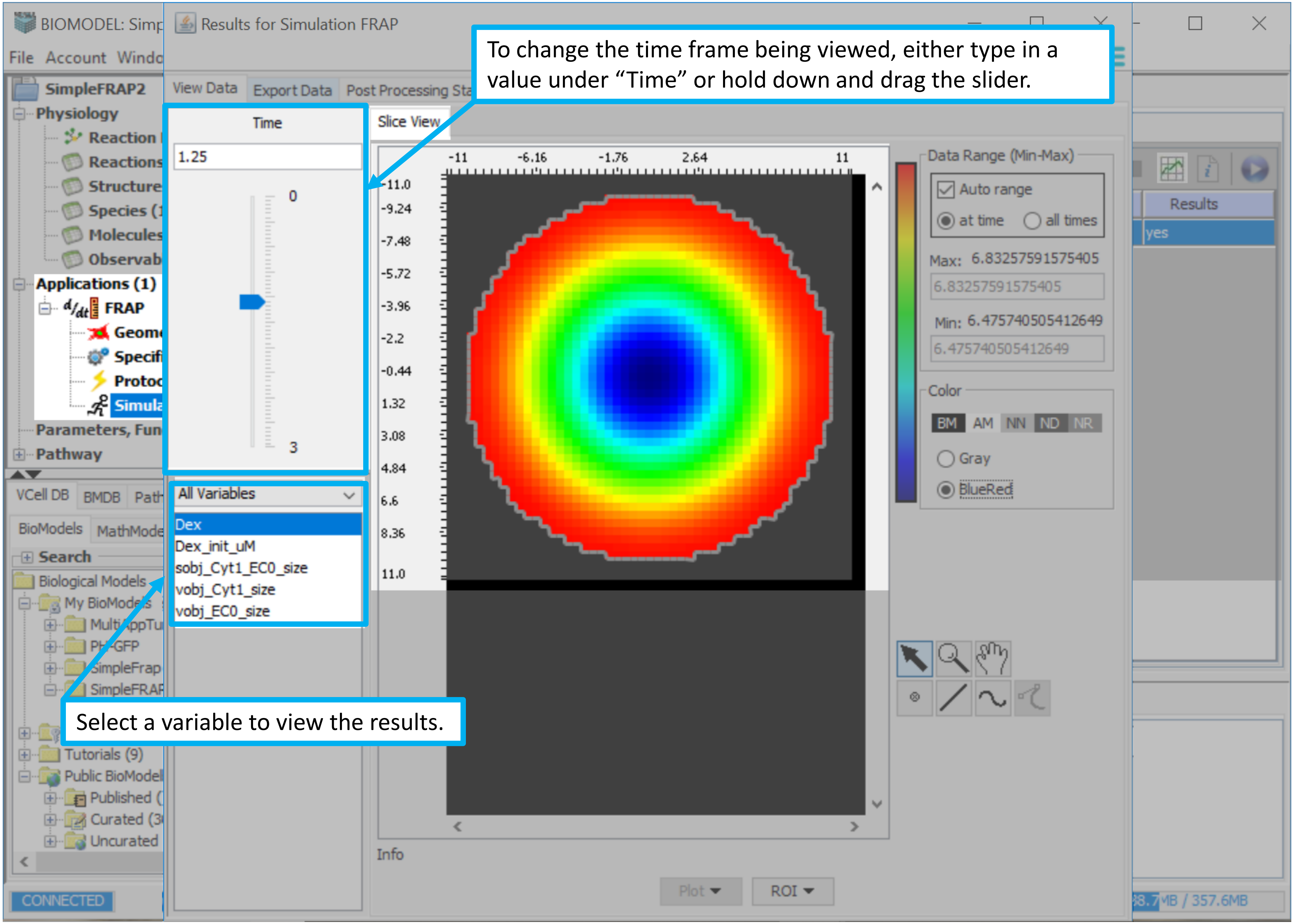
Press the green “Play” button to run the simulation.



Name	End Time	Output Option	Solver	Running Status	Results
FRAP	3.0	every 0.05 s	Fully-Implicit	completed	yes

You can view the status of your simulation, under "Running Status". You can view the results as soon as there are time points saved to the database.

In order to see your results, make sure the simulation is selected, and then press the "Results" icon.



Time: 1.25

All Variables
- Dex
- Dex_init_uM
- sobj_Cyt1_EC0_size
- vobj_Cyt1_size
- vobj_EC0_size

Data Range (Min-Max)

☑ Auto range

● at time ○ all times

Max: 6.83257591575405

Min: 6.475740505412649

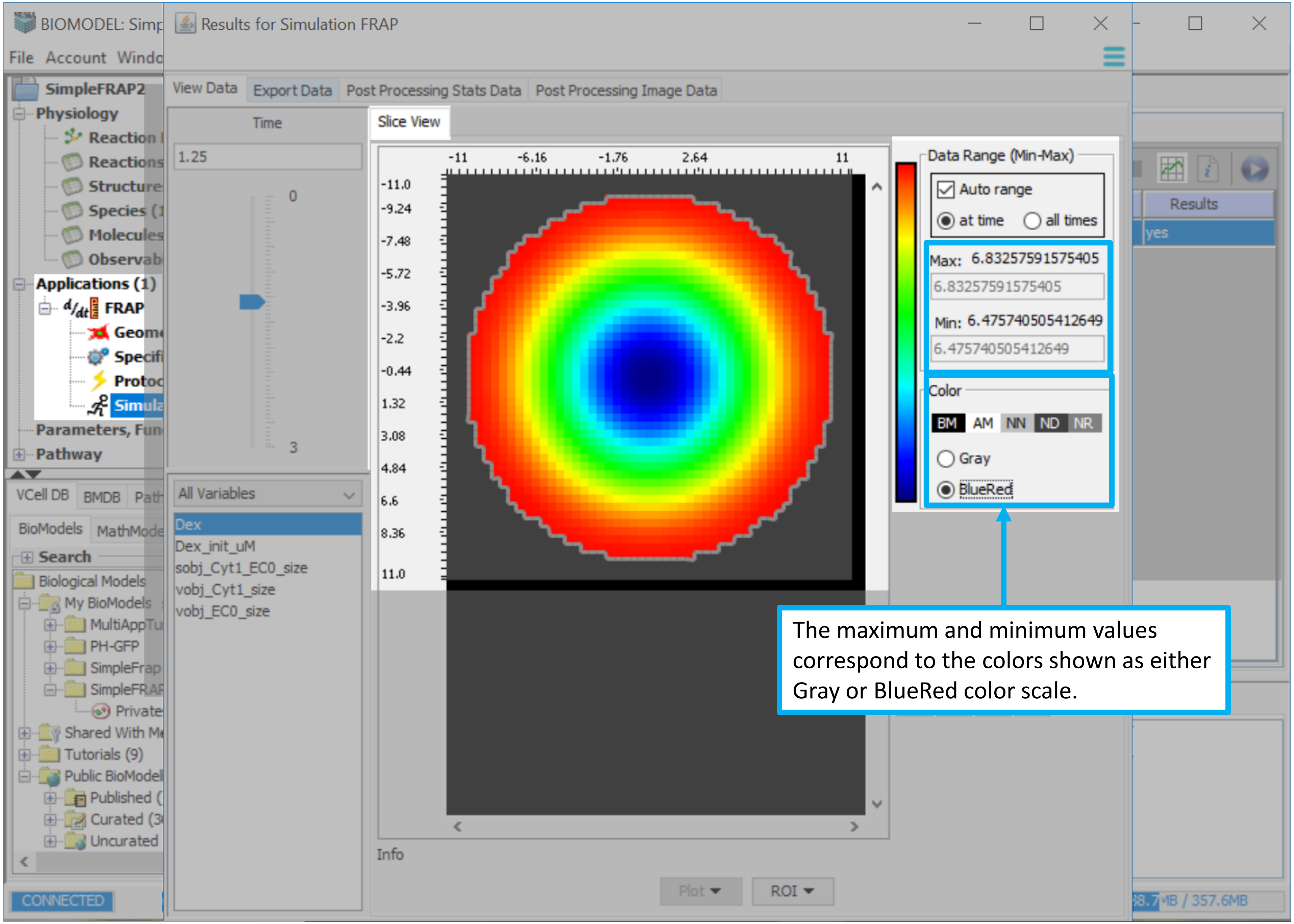
Color

○ Gray

● BlueRed

To change the time frame being viewed, either type in a value under “Time” or hold down and drag the slider.

Select a variable to view the results.



Time: 1.25

☑ Auto range

● at time ○ all times

Max: 6.83257591575405

6.83257591575405

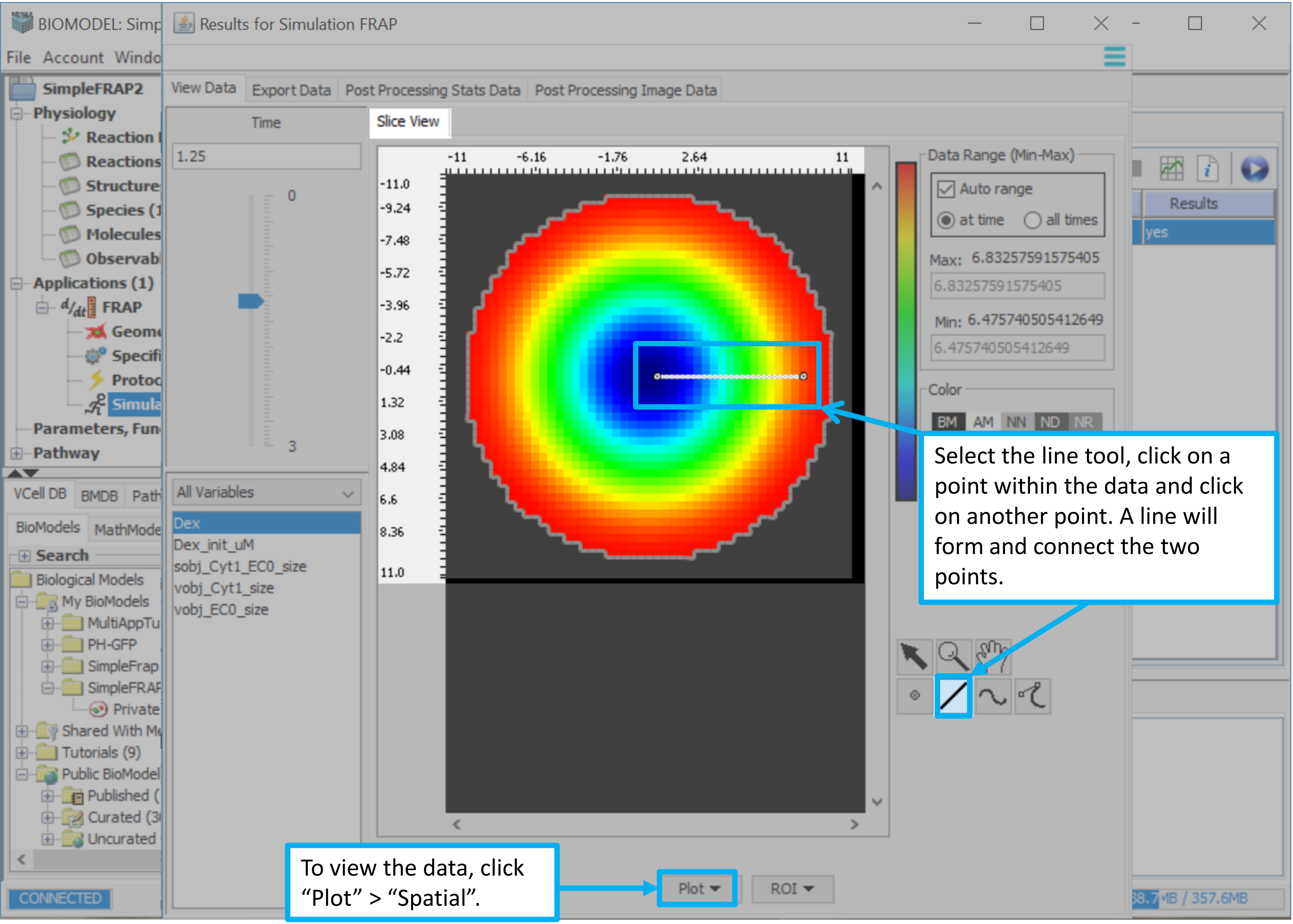
Min: 6.475740505412649

6.475740505412649

○ Gray

● BlueRed

The maximum and minimum values correspond to the colors shown as either Gray or BlueRed color scale.



Time: 1.25

☑ Auto range

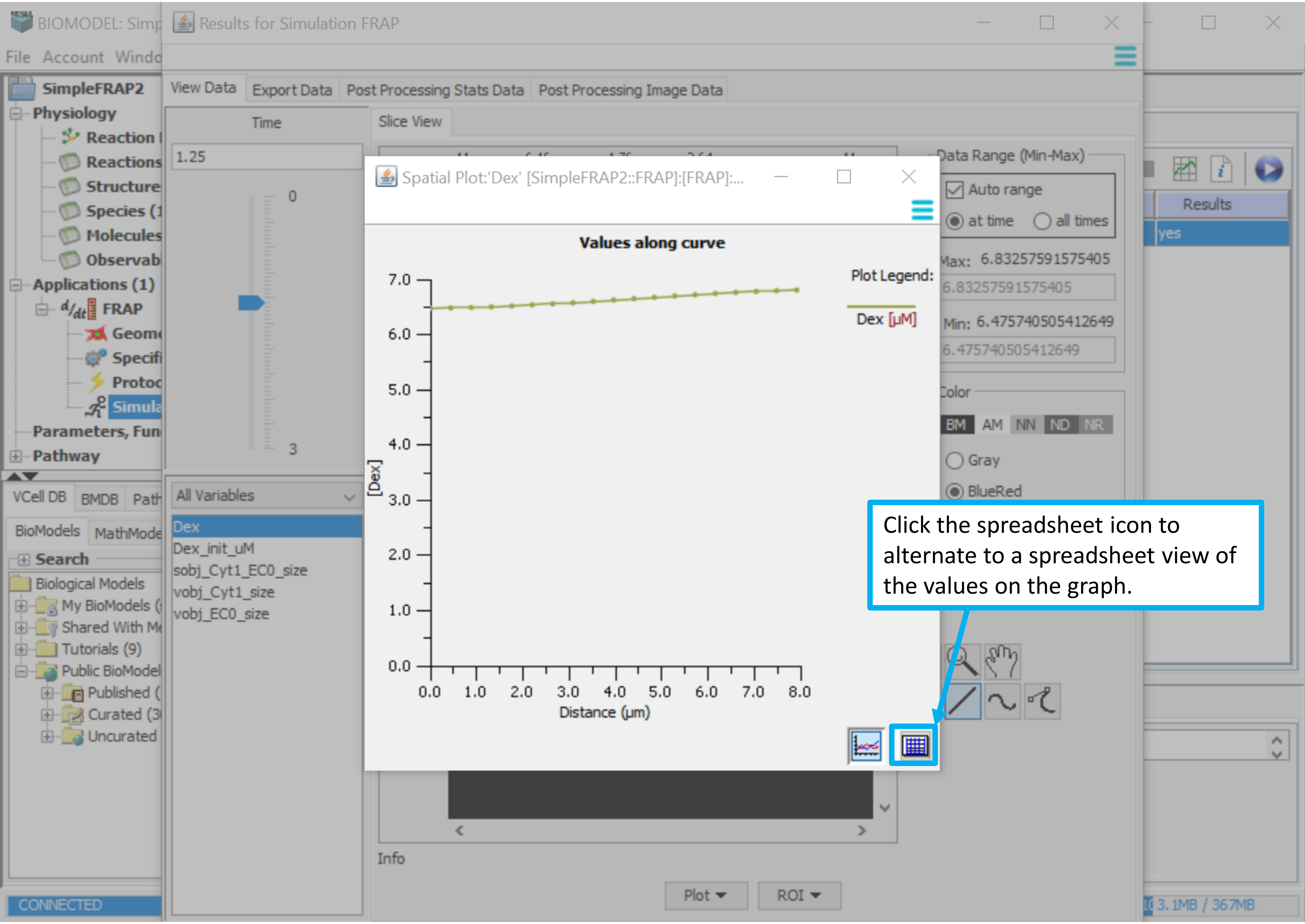
● at time ○ all times

Max: 6.83257591575405

Min: 6.475740505412649

Select the line tool, click on a point within the data and click on another point. A line will form and connect the two points.

To view the data, click “Plot” > “Spatial”.



Time: 1.25

☑ Auto range

● at time ○ all times

Max: 6.83257591575405

6.83257591575405

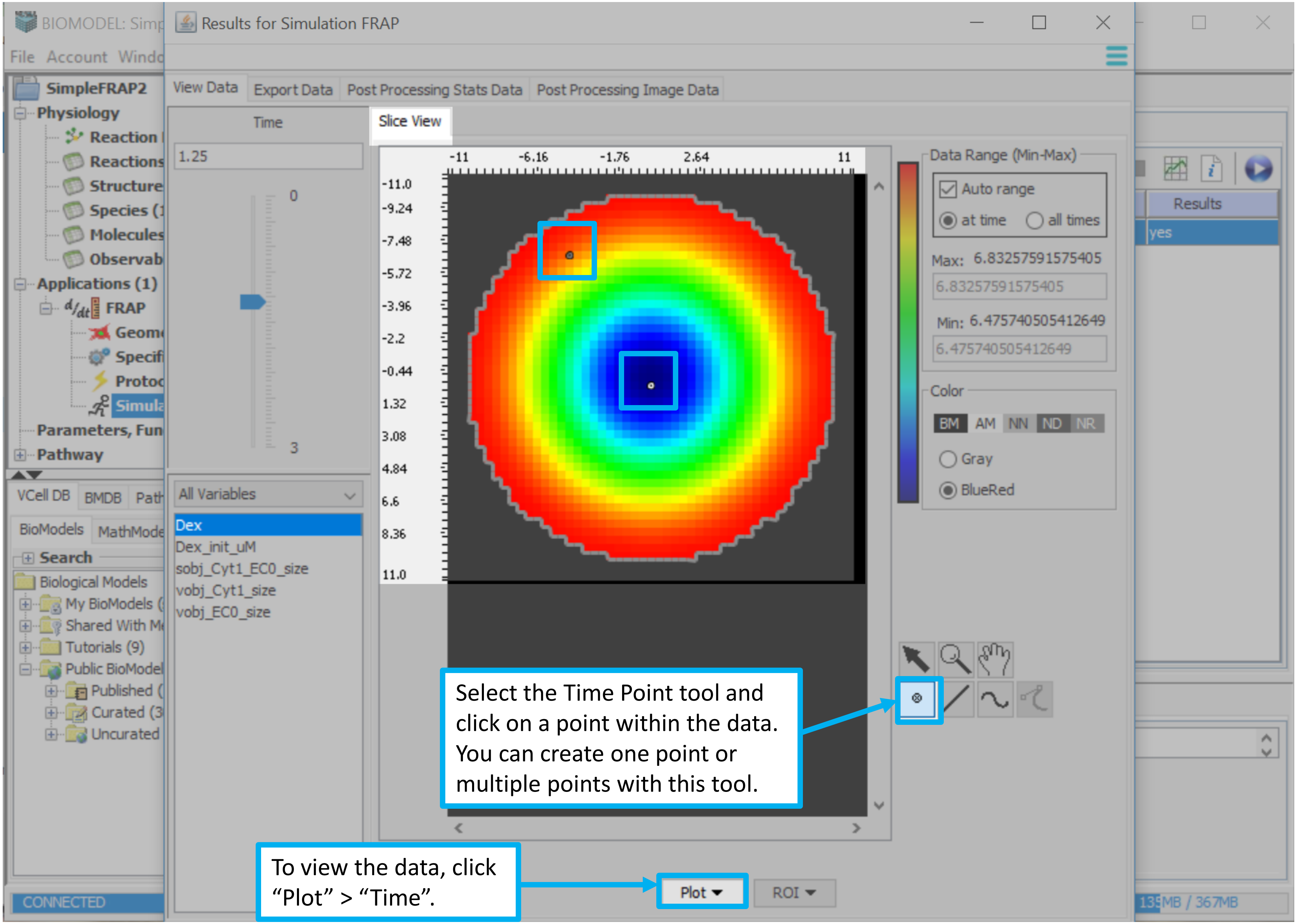
Min: 6.475740505412649

6.475740505412649

○ Gray

● BlueRed

Click the spreadsheet icon to alternate to a spreadsheet view of the values on the graph.



Time: 1.25

☑ Auto range

● at time ○ all times

Max: 6.83257591575405

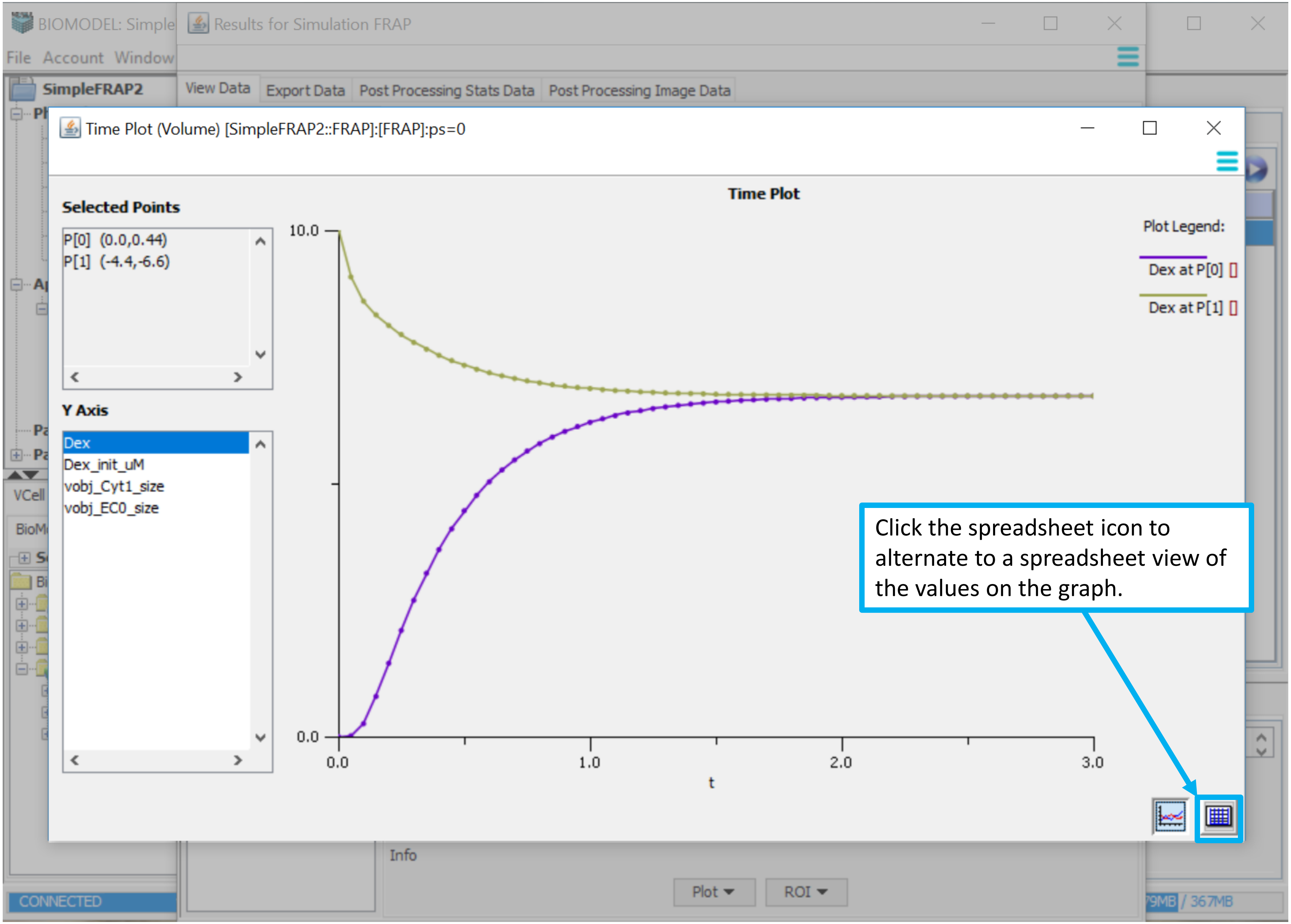
Min: 6.475740505412649

○ Gray

● BlueRed

Select the Time Point tool and click on a point within the data. You can create one point or multiple points with this tool.

To view the data, click “Plot” > “Time”.



Click the spreadsheet icon to alternate to a spreadsheet view of the values on the graph.