

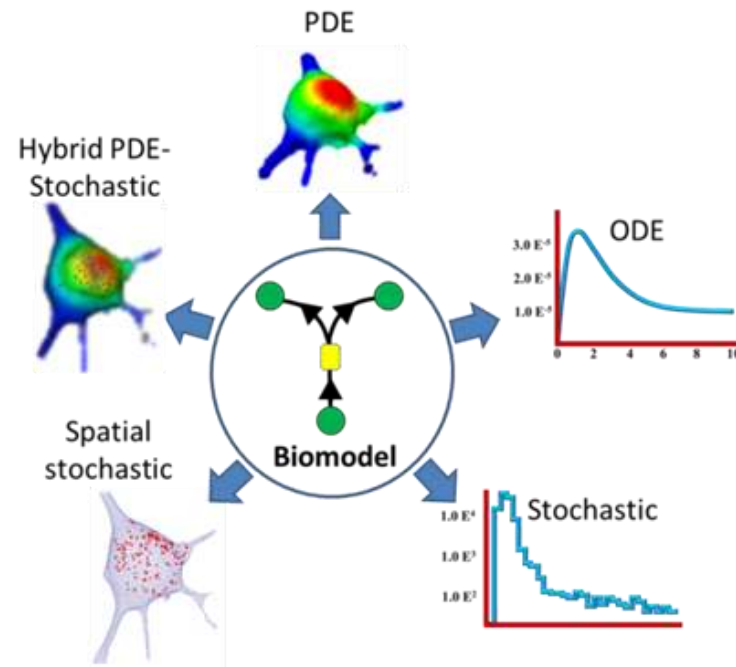
Virtual Cell Tutorials

VCell

modeling environment for
mathematical simulation of
cellular events.

To run VCell go to:

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

PH-GFP binding to PIP₂ and IP₃

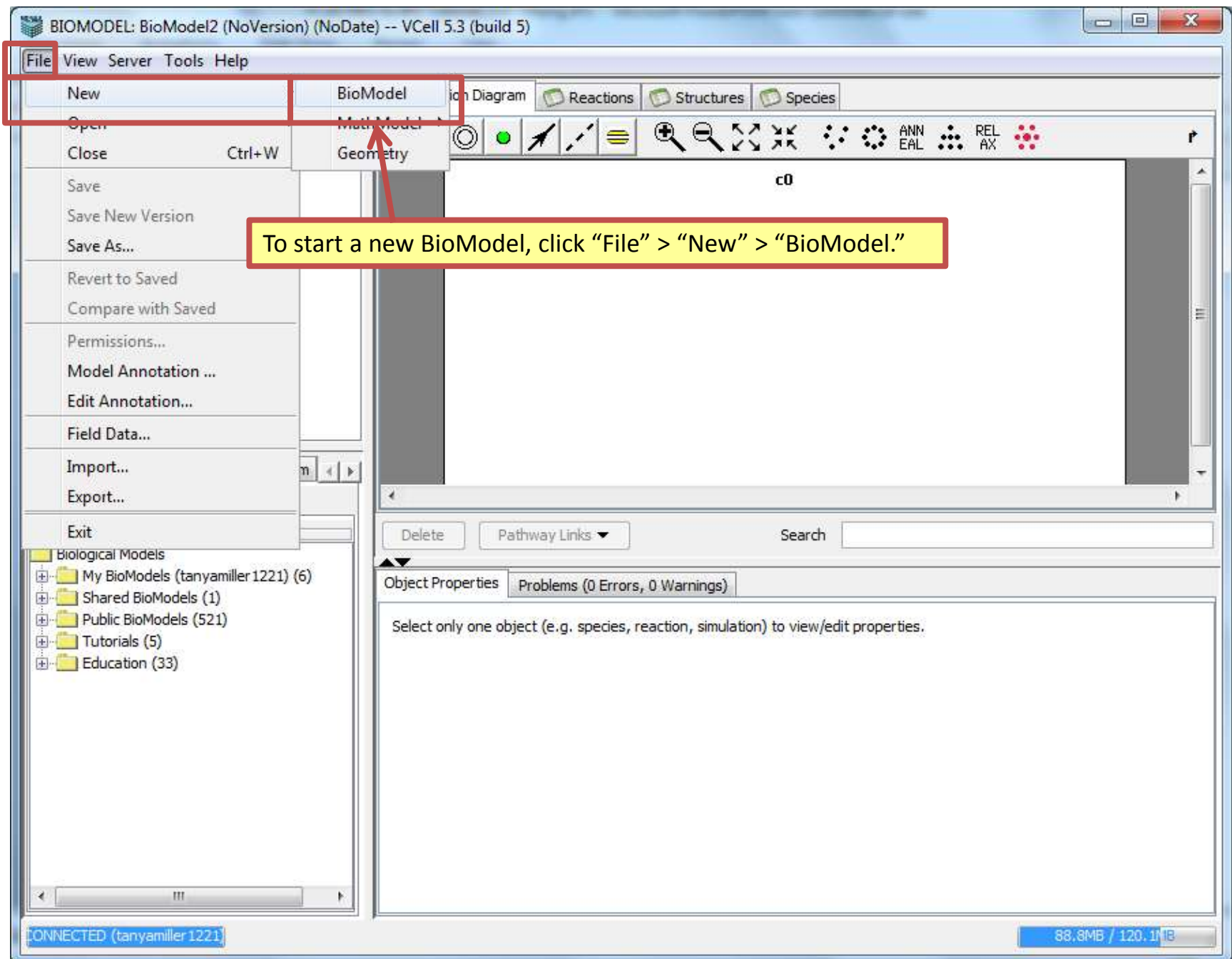
Create a biomodel and 3D spatial (PDE) application to simulate pleckstrin homology domain (PH-GFP) reporter of PIP₂ to IP₃ conversion.

In this tutorial...

- Create a biomodel with reactions involving membrane and volume species.
- Create a compartmental (ODE) application that uses events to include time-dependent triggers.
- Create a spatial deterministic (PDE) application of a model using analytic equations to create a 3D geometry
- Define initial concentrations that are non-uniform in space and create timed events in spatial models using Boolean expressions
- Create output functions for more complex analysis of simulation results, e.g. to sum all fluorescent species in a compartment.

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BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (1)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

VCell DB BioModels.net Pathway Comm

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (tanyamiller1221) (6)
 - Shared BioModels (1)
 - Public BioModels (521)
 - Tutorials (5)
 - Education (33)

Reaction Diagram Reactions Structures Species

Click on the compartment tool, and to the right of c0, right click on the dotted black lines so that they turn green and click "Add Membrane".

Object Properties Problems (0 Errors, 0 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 103MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (2)
 - Species (0)
- Applications (0)
- Parameters and Functions
- Pathway

VCell DB BioModels.net Pathway Comm

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (tanyamiller1221) (6)
 - Shared BioModels (1)
 - Public BioModels (521)
 - Tutorials (5)
 - Education (33)

Reaction Diagram Reactions Structures Species

Click on the compartment tool, and to the right of m0, right click on the dotted black lines so that they turn green and click "Add Compartment".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 45MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the black arrow icons to adjust your view of the diagram.

Continue creating compartments and membranes until from left to right your diagram reads "c0", "m0", "c1", "m1" and "c2".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221) 58.3MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the select tool.

Click on the label for "c0".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one structure to edit properties

Structure Name EC

Size Variable Name EC [μm³]

Annotation Extra Cellular

Next to Structure Name type "EC".

Next to Annotation type "Extra Cellular".

CONNECTED (tanyamiller1221)

66.2MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM c2

Click on the label for "m0".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

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 -).

CONNECTED (tanyamiller1221) 67.5MB / 18.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt

Click on the label for "c1".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Structure Name Cyt

Size Variable Name Cyt [μm^3]

Annotation Cytosol

Next to Structure Name type "Cyt".

Next to Annotation type "Cytosol".

CONNECTED (tanyamiller 1221)

72.5MB / 111.5MB

The screenshot shows the VCell 5.3 (build 5) interface. The main workspace displays a compartment diagram with two compartments, 'EC' and 'c2', separated by a vertical gray bar. A red box highlights this gray bar, and a yellow callout box with an arrow points to it, containing the text: "Click on the label for 'm1'".

Below the workspace, the 'Object Properties' panel is visible. It has tabs for 'Object Properties' and 'Problems (0 Errors, 0 Warnings)'. In the 'Object Properties' tab, the 'Structure Name' field is highlighted with a red box and contains the text 'NM'. A yellow callout box with an arrow points to this field, containing the text: "Next to Structure Name type 'NM' (which stands for Nuclear Membrane).".

Below the 'Structure Name' field, the 'Electrophysiology' section is visible. It includes fields for 'Voltage Variable Name' (set to 'Voltage_NM [mV]'), 'Positive (inside feature)', and 'Negative (outside feature)'. At the bottom of this section, there is explanatory text:

membrane voltage: "Voltage_NM" = 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 -).

The status bar at the bottom left shows "CONNECTED (tanyamiller1221)" and the bottom right shows "74.5MB / 118.5MB".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click on the label for "c2".

Nuc

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Structure Name Nuc

Size Variable Name Nuc [μm^3]

Annotation Nucleus

Next to Structure Name type "Nuc".

Next to Annotation type "Nucleus".

CONNECTED (tanyamiller1221)

77.1MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the species tool.

EC PM Cyt NM Nuc

s0 s1

Click any two points within the "PM" membrane to create two species.

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Species Name s1

Linked Pathway Object(s)

Annotation

CONNECTED (tanyamiller1221) 91MB / 118.5MB

The screenshot shows the VCell 5.3 software interface. At the top, the title bar reads 'BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)'. Below the title bar is a menu bar with 'File', 'View', 'Server', 'Tools', and 'Help'. A toolbar contains icons for 'Reaction Diagram' (selected), 'Reactions', 'Structures', and 'Species'. A red box highlights the 'Species' tool icon (a green circle with a white center), with a red arrow pointing to it and a yellow text box saying 'Click the species tool.'. The main workspace is divided into five vertical compartments: 'EC' (white), 'PM' (gray), 'Cyt' (white), 'NM' (gray), and 'Nuc' (white). In the 'PM' compartment, two species are shown: 's0' (a green circle) and 's1' (a red circle). Red boxes highlight each species, with red arrows pointing to them from a yellow text box at the bottom that says 'Click any two points within the "PM" membrane to create two species.'. Below the workspace is a toolbar with 'Delete', 'Pathway Links', and a 'Search' field. At the bottom, there is a panel for 'Object Properties' with tabs for 'Object Properties' and 'Problems (0 Errors, 0 Warnings)'. The 'Object Properties' tab is active, showing fields for 'Species Name' (s1), 'Linked Pathway Object(s)', and 'Annotation'. The status bar at the very bottom shows 'CONNECTED (tanyamiller1221)' and a memory usage indicator '91MB / 118.5MB'.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

s0 s1 s2 s3 s4 s5

Click any four points within the "Cyt" membrane to create four species.

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Species Name s5

Linked Pathway Object(s)

Annotation

CONNECTED (tanyamiller1221)

95.4MB / 118.5MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the select tool.

Click on "s0".

Next to Species Name type "PIP2_PM".

Species Name PIP2_PM

Linked Pathway Object(s)

Annotation

DISCONNECTED

51MB 115.9MB

The screenshot shows the VCell 5.3 (build 5) interface. The main workspace displays a compartment diagram with five compartments: EC, PM, Cyt, NM, and Nuc. The PM compartment is highlighted in grey. Inside the PM compartment, a species 's1' is represented by a green circle. A red box around 's1' has an arrow pointing to it from a yellow box containing the text 'Click on "s1".'.

Below the workspace is the 'Object Properties' panel. The 'Species Name' field contains the text 'PIP2_PHGFP_PM'. A red box around this field has an arrow pointing to it from a yellow box containing the text 'Next to Species Name type "PIP2_PHGFP_PM".'.

The bottom of the interface shows a 'DISCONNECTED' status bar on the left and a memory usage bar on the right indicating '57MB / 115.9MB'.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

Click on "s2".

PIP₂ PM IP₃ Cyt s3 s4 s5

IP₃_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Species Name IP₃_Cyt

Next to Species Name type "IP₃_Cyt".

Linked Pathway Object(s)

Annotation

DISCONNECTED 62.1MB / 115.9MB

The screenshot shows the VCell 5.3 (build 5) interface. The main workspace displays a compartment diagram with five compartments: EC, PM, Cyt, NM, and Nuc. The PM compartment is shaded gray. A reaction is shown between the PM and Cyt compartments, involving species PIP2_PM, IP3_PM, and IP3_Cyt. The species IP3_Cyt is highlighted with a red box, and a yellow callout box with the text "Click on 's3'." points to it. Below the workspace, the Object Properties panel is visible. The Species Name field is highlighted with a red box, and a yellow callout box with the text "Next to Species Name type 'IP3_PHGFP_PM'." points to it. The Species Name field currently contains "IP3_PHGFP_Cyt".

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

PIP2_PM IP3_PM IP3_Cyt s5

Click on "s3".

IP3_PHGFP_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Species Name IP3_PHGFP_Cyt

Next to Species Name type "IP3_PHGFP_PM".

Linked Pathway Object(s)

Annotation

DISCONNECTED 63.4MB / 115.9MB

The screenshot displays the VCell 5.3 (build 5) interface. The main workspace is divided into compartments: EC, PM, Cyt, NM, and Nuc. A reaction is shown in the Cyt compartment, involving the conversion of PIP₂ to IP₃. A yellow callout box with the text "Click on 's4'." points to a green circle labeled "s4" in the reaction diagram.

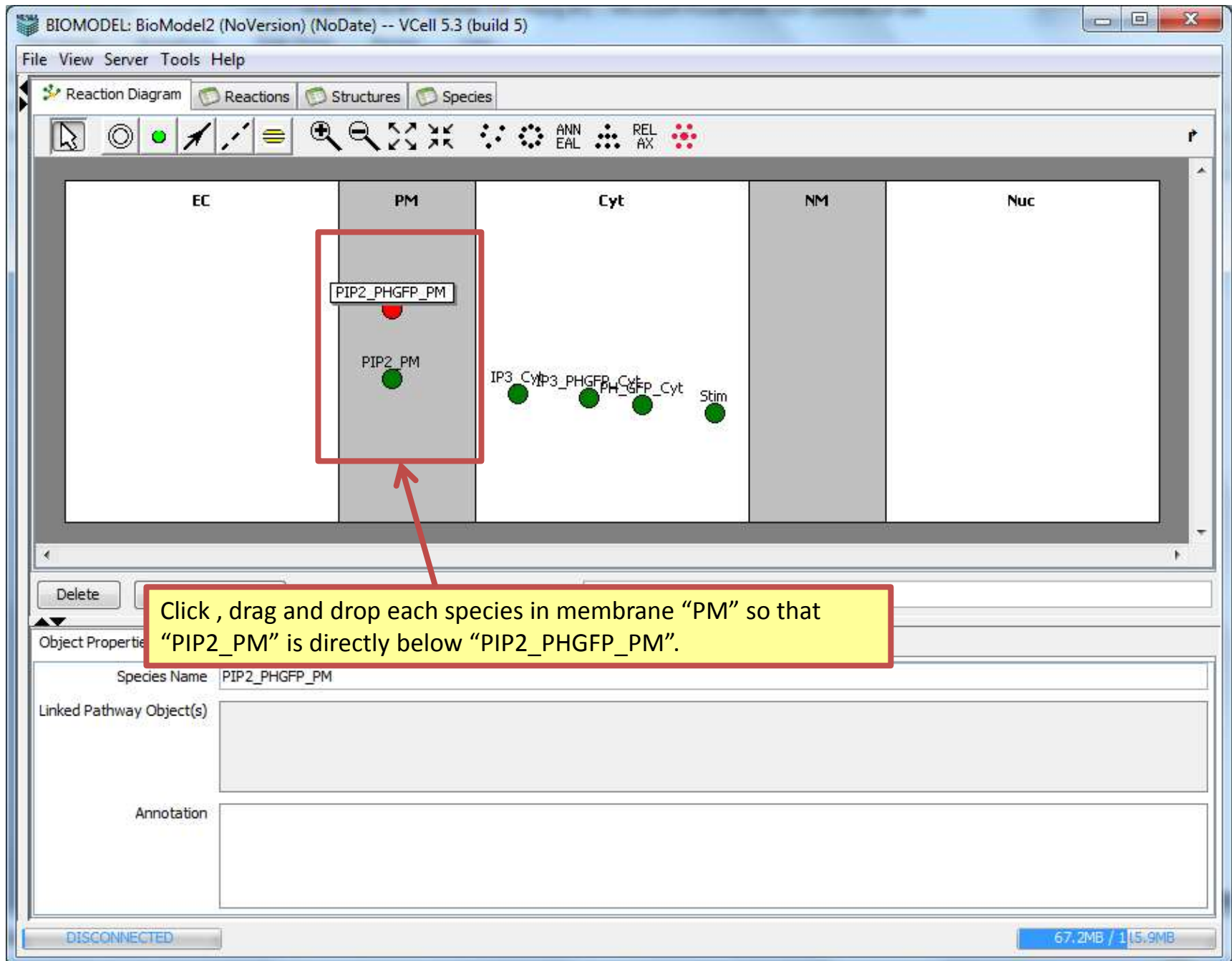
Below the workspace, the "Object Properties" panel is visible. A yellow callout box with the text "Next to Species Name type 'PH_GFP_Cyt'." points to the "Species Name" field, which contains the text "PH_GFP_Cyt".

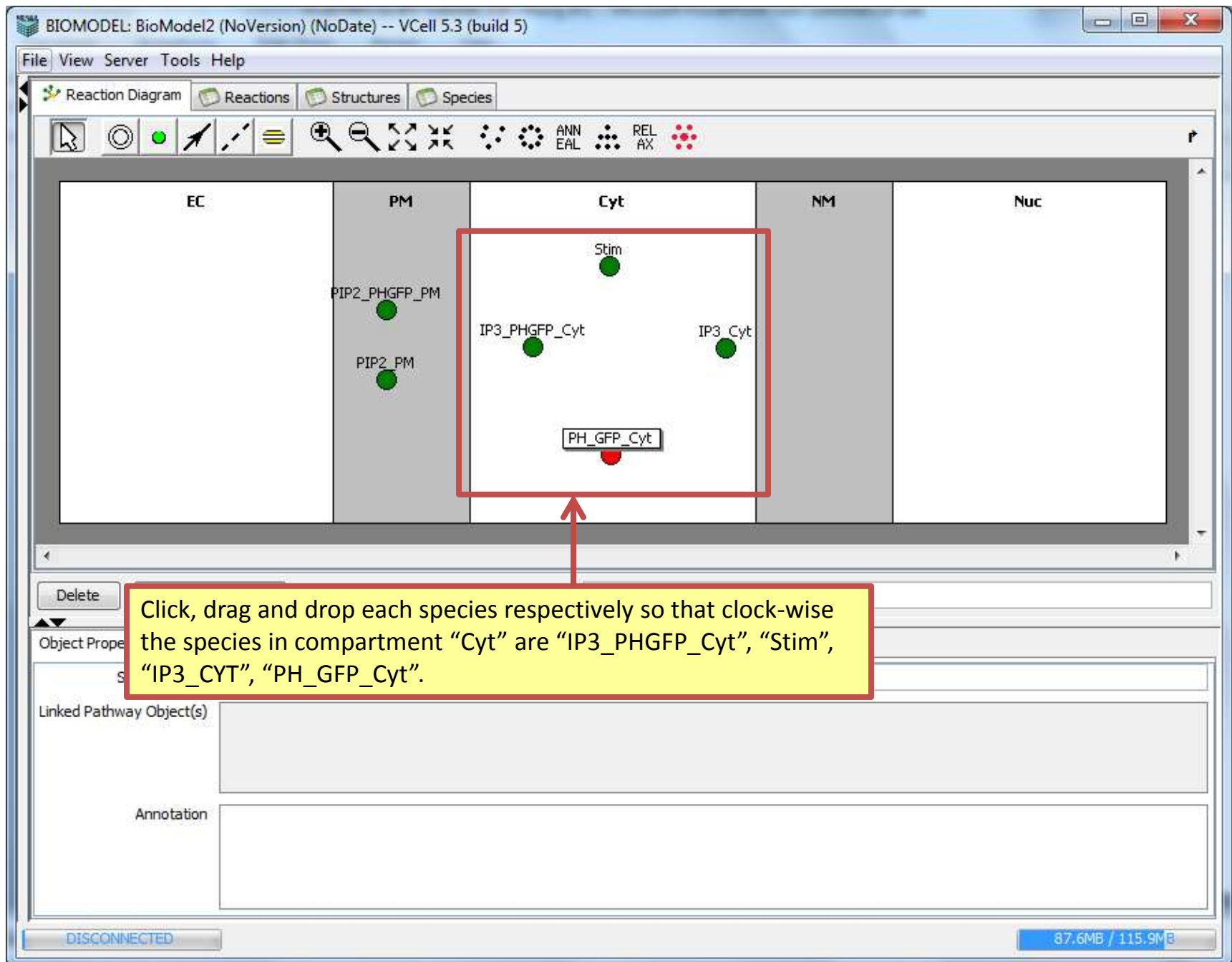
The status bar at the bottom indicates "DISCONNECTED" and shows memory usage: "66.5MB / 15.9MB".

The screenshot displays the VCell 5.3 (build 5) interface. The main workspace is divided into five compartments: EC, PM, Cyt, NM, and Nuc. A biochemical pathway is shown, starting with PIP₂ in the PM compartment, which is converted to IP₃ and DAG in the Cyt compartment. A red box highlights a 'Stim' species in the Cyt compartment, with a yellow callout box pointing to it that says "Click on 's5'".

Below the main workspace is the 'Object Properties' panel. It contains a 'Species Name' field with the text 'Stim' entered. A yellow callout box points to this field with the text "Next to Species Name type 'Stim'". The panel also includes a 'Linked Pathway Object(s)' section and an 'Annotation' field.

At the bottom of the window, there is a status bar showing 'DISCONNECTED' and memory usage '70.8MB / 115.9MB'.





BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the RX connection tool.

Click on "PIP2_PM" and drag your cursor, which will create a line marked <<REACTANT>>. Drop your cursor on "PIP2_PHGFP_PM" which will create a reaction node called "r0".

Object Properties Problems (0 Errors, 0 Warnings)

Reaction Name: r0

Electrical Properties: ☒ include molecular flux ☐ include electric current (into inside structure "undefined")

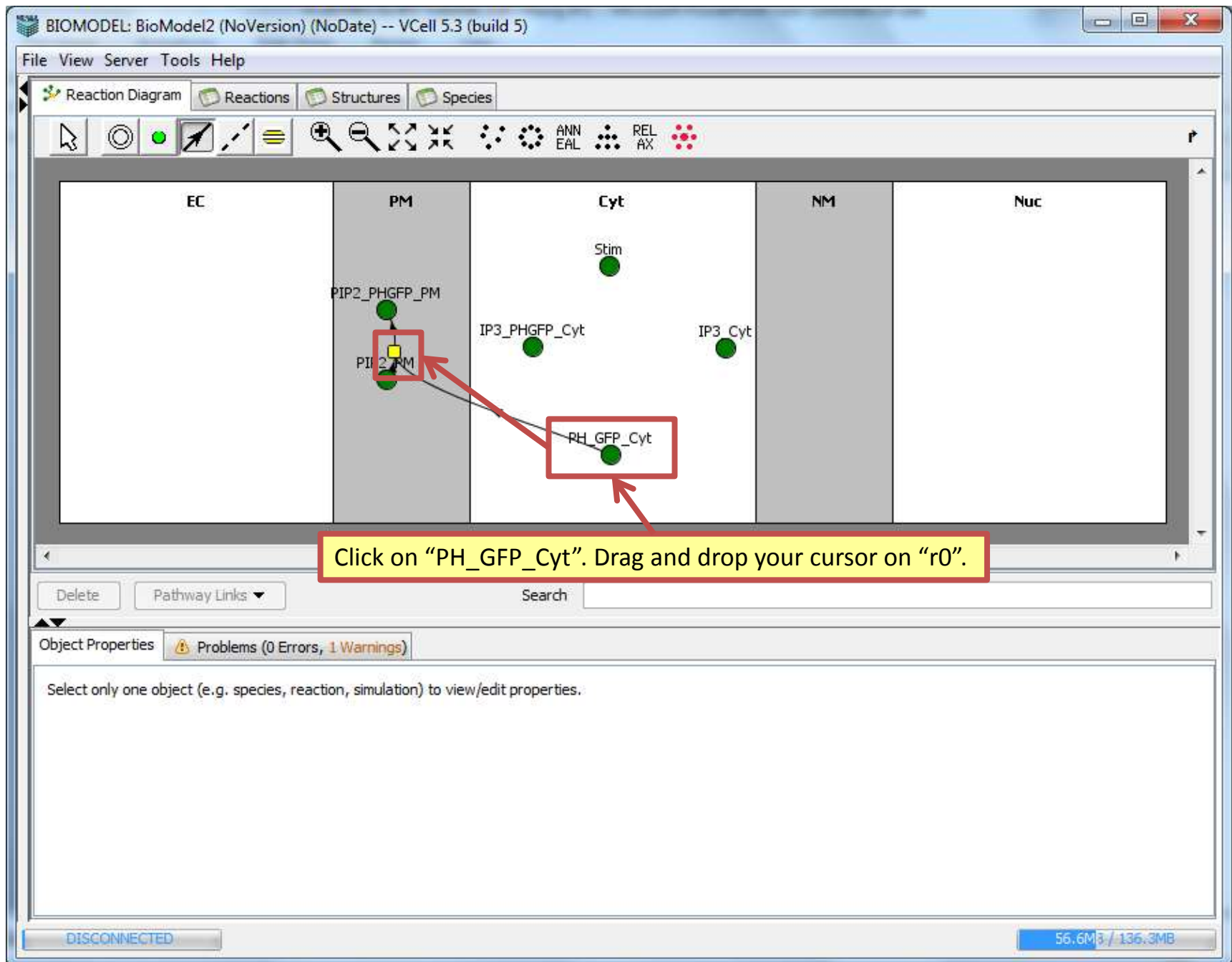
Kinetic Type: Mass Action [molecules/(μm² s)] Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot \text{PIP2_PM} - K_r \cdot \text{PIP2_PHGFP_PM})$	molecules.μm ⁻² .s ⁻¹
I	inward current density	<input type="checkbox"/>	0.0	pA.μm ⁻²
netValence	net charge valence	<input type="checkbox"/>	1.0	1
k _f	forward rate constant	<input type="checkbox"/>	0.0	s ⁻¹

Annotation and Pathway Links

DISCONNECTED

49.5 MB / 136.3 MB



BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click on “IP3_Cyt” and drag your cursor, which will create a line marked <<REACTANT>>. Drop your cursor on “IP3_PHGFP_PM” which will create a reaction node called “r1”.

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name r1

Kinetic Type Mass Action [μM/s] (recommended for stochastic application) Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	(Kf · IP3_Cyt - Kr · IP3_PHGFP_Cyt)	μM.s ⁻¹
Kf	forward rate constant	<input type="checkbox"/>	0.0	s ⁻¹
Kr	reverse rate constant	<input type="checkbox"/>	0.0	s ⁻¹
IP3_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
IP3_PHGFP_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

+ Annotation and Pathway Links

DISCONNECTED 76.4MB / 136.3MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram

Reactions

Structures

Species

ANN EAL REL AX

EC

PM

Cyt

NM

Nuc

```
graph TD
    PIP2_PM[PIP2_PM] --> PIP2_PHGFP_PM[PIP2_PHGFP_PM]
    PIP2_PHGFP_PM --> IP3_Cyt[IP3_Cyt]
    IP3_Cyt --> IP3_PHGFP_Cyt[IP3_PHGFP_Cyt]
    IP3_PHGFP_Cyt --> r1[r1]
    r1 --> PH_GFP_Cyt[PH_GFP_Cyt]
    PH_GFP_Cyt --> IP3_Cyt
```

Delete

Pathway Links ▾

Object Properties

Problems (0 Errors, 1 Warnings)

Reaction Name

r1

Kinetic Type

Mass Action [μM/s] (recommended for stochastic application)

Convert to [molecules.s⁻¹]

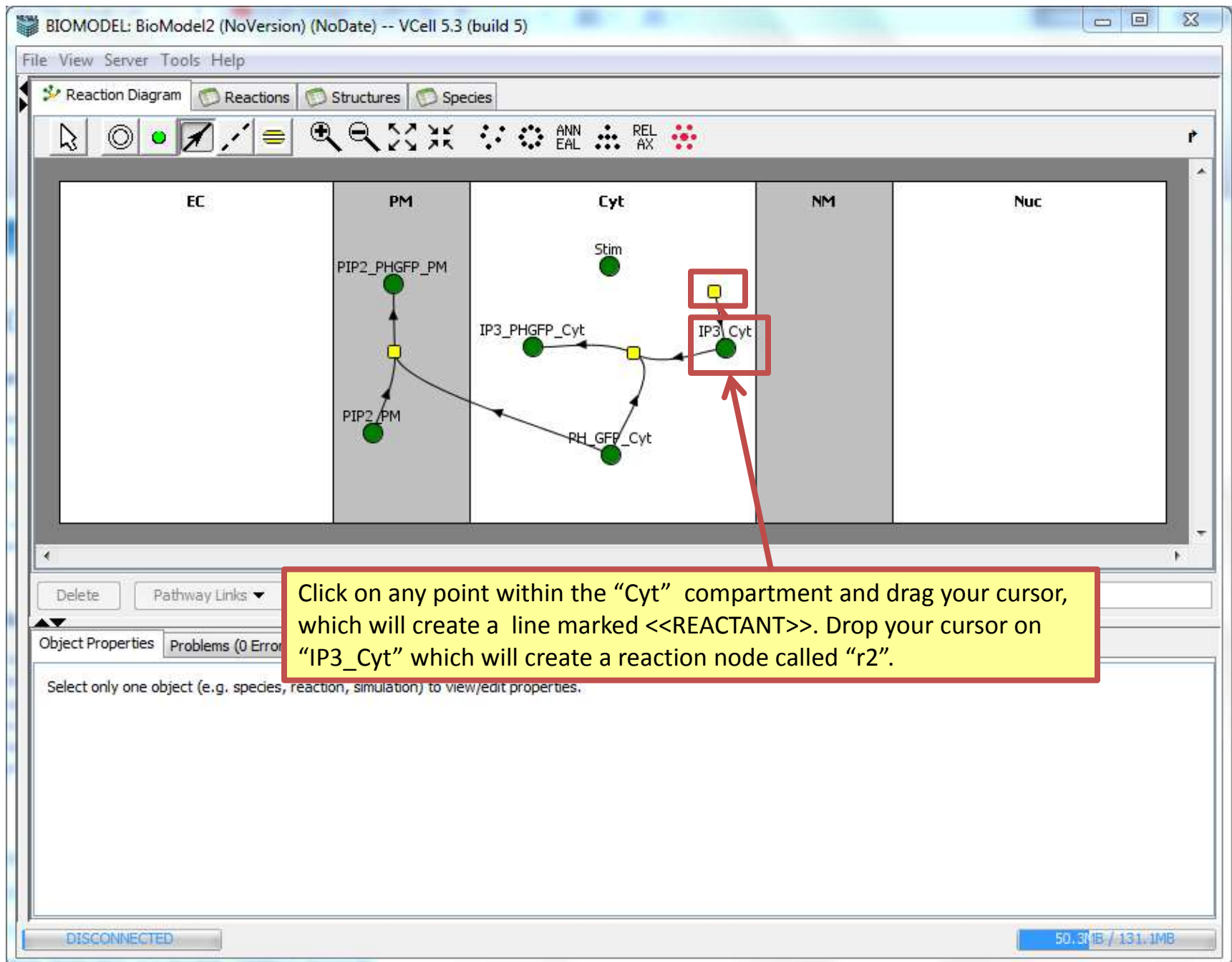
Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot IP3_Cyt \cdot PH_GFP_Cyt - K_r \cdot IP3_PHGFP_Cyt)$	μM.s ⁻¹
Kf	forward rate constant	<input type="checkbox"/>	0.0	s ⁻¹ .μM ⁻¹
Kr	reverse rate constant	<input type="checkbox"/>	0.0	s ⁻¹
IP3_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
IP3_PHGFP_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

DISCONNECTED

85.3MB / 138.3MB

Click on "PH_GFP_Cyt". Drag and drop your cursor on "r1".



BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the catalyst tool.

Click on "Stim" and drag your cursor, which will create a line marked <<CATALYST>>. Drop your cursor on "r2".

EC PM Cyt NM Nuc

PIP2_PHGFP_PM

Stim

P_Cyt

IP3_Cyt

RH_GFP_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

DISCONNECTED 55.3MB / 131.1MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click the select tool.

Click "r0".

Next to Reaction Name type "PIP2_PH".

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name PIP2_PH

Electrical Properties ☒ include molecular flux ☐ include electric current (into inside structure "undefined")

Kinetic Type Mass Action [molecules/($\mu\text{m}^2 \text{ s}$)] Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot \text{PIP2_PM} \cdot \text{PH_GFP_Cyt} - K_r \cdot \text{PIP2_PHGFP_PM})$	molecules. $\mu\text{m}^{-2} \cdot \text{s}^{-1}$
I	inward current density	<input type="checkbox"/>	0.0	pA. μm^{-2}
netValence	net charge valence	<input type="checkbox"/>	1.0	1
kf	forward rate constant	<input type="checkbox"/>	0.0	$\text{s}^{-1} \cdot \mu\text{M}^{-1}$

+ Annotation and Pathway Links

DISCONNECTED

54.5MB / 141MB

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

Stim

PIP2_PHGFP_PM

PIP2_PH

PIP2/PM

IP3_PHGFP_Cyt

IP3 Cyt

RH_GFP_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name PIP2_PH

Kinetic Type Mass Action [molecules/($\mu\text{M} \cdot \text{s}$)] Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
net/valence	net charge valence	<input type="checkbox"/>	1	1
Kf	forward rate constant	<input type="checkbox"/>	0.12	s ⁻¹ μM^{-1}
Kr	reverse rate constant	<input type="checkbox"/>	(Kf*KdPIP2PH)	s ⁻¹

PIP2/PM Species Concentration 1/1 Variable molecules μM^{-2}

Annotation and Pathway Links

Type ".12" for the forward rate constant expression. Press "Enter" on your keyboard to finalize.

Type in "(Kf*KdPIP2PH)" for the reverse rate constant expression. Press "Enter" on your keyboard to finalize.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

PIP2_PHGFP_PM

PIP2_PH

PIP2/PM

IP3_PHGFP_Cyt

IP3_Cyt

PH_GFP_Cyt

Stim

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name PIP2_PH

Electrical Properties ☒ include molecular flux

Kinetic Type Mass Action [molecules/($\mu\text{m}^2 \text{s}$)]

Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
Kr	reverse rate constant	<input type="checkbox"/>	K_r $K_d\text{PIP2PH}$	s ⁻¹
KdPIP2PH	user defined	<input checked="" type="checkbox"/>	2	μM
PIP2/PM	Species Concentration	<input checked="" type="checkbox"/>	Variable	molecules. μm^{-2}
PIP2_PHGFP_PM	Species Concentration	<input type="checkbox"/>	Variable	molecules. μm^{-2}

Annotation and Pathway Links

DISCONNECTED

62.9MB / 135.8MB

Type in "2" for the expression of "KdPIP2PH". Press "Enter" on your keyboard to finalize.

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

Click "r1".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name IP3PH

Next to Reaction Name type "IP3PH".

Kinetic Type Mass Action [μM/s] (recommended for stochastic application) Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
Kf	forward rate constant	<input type="checkbox"/>	0.0	s ⁻¹ .μM ⁻¹
Kr	reverse rate constant	<input type="checkbox"/>	0.0	s ⁻¹
IP3_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
IP3_PHGFP_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
PH_GFP_Cyt	Species Concentration	<input checked="" type="checkbox"/>	2	μM

+ Annotation and Pathway Links

DISCONNECTED

78.3MB / 15.8MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

PIP2_PHGFP_PM

Stim

IP3_PHGFP_Cyt

IP3PH

IP3_Cyt

PIP2/PM

PH_GFP_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name

Kinetic Type

Type "10" for the forward rate constant expression. Press "Enter" on your keyboard to finalize.

Name	Description	Global	Expression	Units
1	reaction rate	<input type="checkbox"/>	$k_f \cdot \text{IP3_Cyt} \cdot \text{PH_GFP_Cyt} - k_r \cdot \text{IP3_PHGFP_Cyt}$	$\mu\text{M} \cdot \text{s}^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	10.0	$\text{s}^{-1} \cdot \mu\text{M}^{-1}$
Kr	reverse rate constant	<input type="checkbox"/>	$(K_f \cdot K_d \text{IP3PH})$	s^{-1}
IP3_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
PH_GFP_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

Type in "(Kf*KdIP3PH)" for the reverse rate constant expression. Press "Enter" on your keyboard to finalize.

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

Stim

PIP2_PHGFP_PM

PIP2/PM

IP3_PHGFP_Cyt

IP3PH

IP3 Cyt

PH_GFP_Cyt

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name IP3PH

Kinetic Type Mass Action [uM/s] (recommended for stochastic application) Convert to [molecules.s⁻¹]

Type in ".1" for the expression of "KdIP3PH". Press "Enter" on your keyboard to finalize.

				Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot IP3_Cyt \cdot PH_GFP_Cyt - K_r \cdot IP3_PHGFP_Cyt)$	$\mu M.s^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	10.0	$s^{-1}.\mu M^{-1}$
Kr	reverse rate constant	<input type="checkbox"/>	$K_f / KdIP3PH$	s^{-1}
KdIP3PH	user defined	<input type="checkbox"/>	.1	μM
IP3 Cyt	Species Concentration	<input checked="" type="checkbox"/>	variable	μM

Annotation and Pathway Links

CONNECTED (tanyamiller1221)

70.7MB / 13.7MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

Stim

PIP2_PHGFP_PM

IP3_PHGFP_Cyt

IP3 Cyt

PI3 r2

PI3 PHGFP_Cyt

Click "r2".

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name r2

Kinetic Type General [μM/s] Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
r2	reaction rate	<input type="checkbox"/>	0.0	μM.s ⁻¹

Click the drop down menu next to Kinetic Type. Click "General [μM/s]".

Annotation and Pathway Links

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82.3MB / 123.7MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

PIP2_PHGFP_PM

Stim

IP3_Cyt

IP3_PHGFP_Cyt

PIP2/PM

PH_GFP_Cyt

r2

Type "Ksynth*Stim" for the reaction rate expression. The reaction is case-sensitive. Press "Enter" on your keyboard to finalize.

Reaction Name r2

Kinetic Type General [μM/s]

Convert to [molecules.s⁻¹]

Name	Description	Global	Expression	Units
r2	reaction rate	<input type="checkbox"/>	Ksynth*Stim	μM.s ⁻¹

Annotation and Pathway Links

CONNECTED (tanyamiller1221)

87.9MB / 123.7MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

Reaction Diagram Reactions Structures Species

EC PM Cyt NM Nuc

PIP2_PHGFP_PM

PIP2/PM

IP3_PHGFP_Cyt

PH_GFP_Cyt

Stim

IP3_Cyt

r2

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name: r2

Kinetic

Type "1.0" for the expression of "Ksynth". Press "Enter" on your keyboard to finalize.

Name	Description	Global	Expression	Units
1	reaction rate	<input type="checkbox"/>	Ksynth * Stim	$\mu\text{M.s}^{-1}$
Ksynth	user defined	<input type="checkbox"/>	1.0	s^{-1}
Stim	Species Concentration	<input checked="" type="checkbox"/>	variable	μM

Annotation and Pathway Links

CONNECTED (tanyamiller1221)

46.4 MB / 126.9 MB

File View Server Tools Help

PIP2Tutorial2

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 - Reactions (3)
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- Applications (0)
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VCell DB BioModels.net Pathway Comm

BioModels MathModels Geometries

+ Search

- Biological Models
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Click the right black arrow icon.

Reaction Diagram

EC PM Cyt NM

Stim

IP3_PHGFP_Cyt

IP3_Cyt

PIH_GFP_Cyt

PIP2_PHGFP_PM

PIP2_PM

r2

Delete Pathway Links Search

Object Properties Problems (0 Errors, 1 Warnings)

Reaction Name r2

Kinetic Type General $\mu\text{M/s}$ Convert to $[\text{molecules.s}^{-1}]$

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$k_{\text{synth}} \cdot \text{Stim}$	$\mu\text{M.s}^{-1}$
k _{synth}	user defined	<input type="checkbox"/>	1.0	s^{-1}
Stim	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

+ Annotation and Pathway Links

CONNECTED (tanyamiller1221)

59.7MB / 126.9MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

PIP2Tutorial2

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Click "Applications"> "Add New" > "Deterministic".

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Name	Math Type	Annotation
------	-----------	------------

Add New Delete More Copy Actions Search

Deterministic

Stochastic

Items (0 Errors, 1 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

CONNECTED (tanyamiller1221)

70.1MB / 126.9MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

PIP2Tutorial2

- Physiology
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 - Reactions (3)
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- Applications (1)**
 - Application0
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BioModels MathModels Geometries

Search

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Name	Math Type	Annotation
Steady State	compartmental deterministic	

Double click "Application0" under the Name column. Type in "Steady State". Press "Enter" on your keyboard to finalize.

Add New Delete More Copy Actions Search

Object Properties Problems (0 Errors, 1 Warnings)

Application Name Application0

Annotation

Summary

- Deterministic
- Compartmental
- math not generated

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55.9MB / 120.1MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

PIP2Tutorial2

Click "Specifications" > "Species".

Applications (1)

- Steady State
- Geometry
- Specifications**
- Protocols
- Simulations
- Parameter Estimation

Parameters and Functions

Pathway

VCell DB BioModels.net Pathway Comm

BioModels MathModels Geometries

Search

- Biological Models
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Geometry Specifications Protocols Simulations Parameter Estimation

Species Reactions

Species	Structure	Clamped	Initial Condition
IP3_Cyt	Cyt	<input type="checkbox"/>	0.1
IP3_PHGFP_Cyt	Cyt	<input type="checkbox"/>	0.0
PH_GFP_Cyt	Cyt	<input type="checkbox"/>	1.0
Stim	Cyt	<input type="checkbox"/>	0.0
PIP2_PM	PM	<input type="checkbox"/>	120000.0
PIP2_PHGFP_PM	PM	<input type="checkbox"/>	0.0

Click "IP3_Cyt" and type in ".1" for its initial condition.
Click "PH_GFP_Cyt" and type in "1.0" for its initial condition.
Click "PIP2_PM" and type in "120,000" for its initial condition.
Press "Enter" after each input to finalize.

Search

Object Properties Problems (0 Errors, 1 Warnings)

Description	Parameter	Expression	Units
initial concentration for PH_GFP_Cyt	initConc	0.0	μM

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55.1ME / 123.2MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical **Events** Rate Rules

Search **Add New** Delete Selected

Name	Trigger	Delay	Event Assignment Vars
(add new here)			

Click "Protocols" > "Events" > "Add New".

Object Properties Problems (0 Errors, 1 Warnings)

Select only one object (e.g. species, reaction, simulation) to view/edit properties.

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BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

PIP2Tutorial2

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Search

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search

Name	Trigger	Delay	Event Assignment Vars
Act	0.0	None	None
Add new here			

Double click "event0" and type in "Act" (Activation). Press "Enter" on your keyboard to finalize.

Object Properties Problems (0 Errors, 1 Warnings)

Trigger

Delay **seconds** ☒ Use Values at Trigger Time

Event Assignments:

Variable	Expression	Units
----------	------------	-------

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91.4MB / 123.2MB

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File View Server Tools Help

PIP2Tutorial2

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+ Search

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search Add New Delete Selected

Name	Trigger	Delay	Event Assignment Vars
Act	(t > 5.0)	None	None
(add new here)			

Object Properties Problems (0 Errors, 1 Warnings)

Trigger

Delay

seconds ☒ Use Values at Trigger Time

Event Assignments:

Variable	Expression	Units
Add Variable Delete Variable		

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57.2MB 117.4MB

Type in "(t>5)" for the trigger.

Click "Add Variable".

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File View Server Tools Help

PIP2Tutorial2

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search Add New Delete Selected

Name	Trigger	Delay	Event Assignment Vars
Act	(t>5)		
(add new here)			

Click the drop down menu next to "Event Assignment Variable Name" and click "Stim".

Add Event Assignment

Event Assignment Variable Name Stim

Event Assignment Expression 1

OK Cancel

Type "1" for the event assignment expression.

Click "OK".

Object Properties Problems (0 Errors, 1 Warnings)

Trigger (t>5)

Delay

seconds ☒ Use Values at Trigger Time

Event Assignments:

Add Variable Delete Variable

Variable	Expression	Units
----------	------------	-------

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65.3MB / 117.4MB

File View Server Tools Help

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+ Search

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search **Click "Add New".** **Add New** Delete Selected

Name	Trigger	Delay	Event Assignment Vars
Act	$(t > 5.0)$	None	Stim
(add new here)			

Object Properties Problems (0 Errors, 1 Warnings)

Trigger

Delay seconds ☒ Use Values at Trigger Time

Event Assignments:

Variable	Expression	Units
Stim	1.0	μM

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78.7MB / 117.1MB

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BioModels MathModels Geometries

Search

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search

Name	Trigger	Delay	Event Assignment Vars
Act	$(t > 5.0)$	None	Stim
Inact	0.0	None	None
(add new here)			

Double click "event0" and type in "Inact" (Inactivation). Press "Enter" on your keyboard to finalize.

Object Properties Problems (0 Errors, 1 Warnings)

Trigger 0.0

Delay **seconds** ☒ Use Values at Trigger Time

Event Assignments:

Variable	Expression	Units
----------	------------	-------

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BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

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+ Search

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Geometry Specifications Protocols Simulations Parameter Estimation

Electrical Events Rate Rules

Search Add New Delete Selected

Name	Trigger	Delay	Event Assignment Vars
Act	$(t > 5.0)$	None	Stim
Inact	$(t > 6.0)$	None	None
(add new here)			

Object Properties Problems (0 Errors, 1 Warnings)

Trigger $(t > 6)$

Delay

seconds ☒ Use Values at Trigger Time

Event Assignments:

Variable	Expression	Units
----------	------------	-------

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Type in "(t>6)" for the trigger.

Click "Add Variable".

File View Server Tools Help

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VCell DB

BioModels MathModels Geometries

+ Search

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Electrical Events Rate Rules

Search Add New Delete Selected

Name	Event Assignment Vars
Act	Stim
Ina	None
(add new here)	

Click the drop down menu next to "Event Assignment Variable Name" and click "Stim".

Add Event Assignment

Event Assignment Variable Name

Event Assignment Expression

OK Cancel

Leave "0.0" as the event assignment expression.

Click "OK".

Object Properties Protocols (Settings)

Trigger

Delay

seconds ☒ Use Values at Trigger Time

Event Assignments:

Add Variable Delete Variable

Variable	Expression	Units
----------	------------	-------

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75MB / 119MB

BIOMODEL: Tutorial_PH-GFP (Tue Jul 28 11:33:04 EDT 2015) -- VCell 5.3 (build 9)

File View Server Tools Help

Tutorial_PH-GFP

- Physiology
 - Reaction Diagram
 - Reactions (3)
 - Structures (5)
 - Species (6)
- Applications (2)
 - sphere
 - steady state
- Parameters and Functions
- Pathway

Geometry

Structure Mapping

Click "Geometry" > "Structure Mapping".

Physiology (structures)

Geometry (subd

Cyt

Nuc

EC

NM

Compartment

In the Size column for "Cyt", "Nuc", "EC", "NM" and "PM" type in "489.794", "33.389", "476.817", "49.8" and "501.804" respectively. Press "Enter" on your keyboard to finalize.

Volume and Surface Calculator >>

Structure	Size	Surface : Volume	Volume : Volume
Cyt	489.794 [μm^3]		0.523183
Nuc	33.389 [μm^3]		0.06381897
EC	476.817 [μm^3]		
NM	49.8 [μm^2]	1.4915092	
PM	501.804 [μm^2]	0.95913667	

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84.6MB / 147.8MB

BIOMODEL: PIP2Tutorial2 (Fri Jul 10 10:09:58 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

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VCell DB BioModels.net Pathway Comm

BioModels MathModels Geometries

Search

- Biological Models
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 - Education (33)

Simulations

Click "Simulations" > new simulation icon.

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	1.0	keep every 1 sample	Combined IDA/CVODE	not saved	no

Object Properties Problems (0 Errors, 1 Warnings)

Annotation:

Settings:

max timestep	output	rel tol	abs tol	Sensitivity Analysis
1.0s	keep every 1 sample, at most 1000	1.0E-9	1.0E-9	no

Mesh Refinement: Finest Level Mesh:

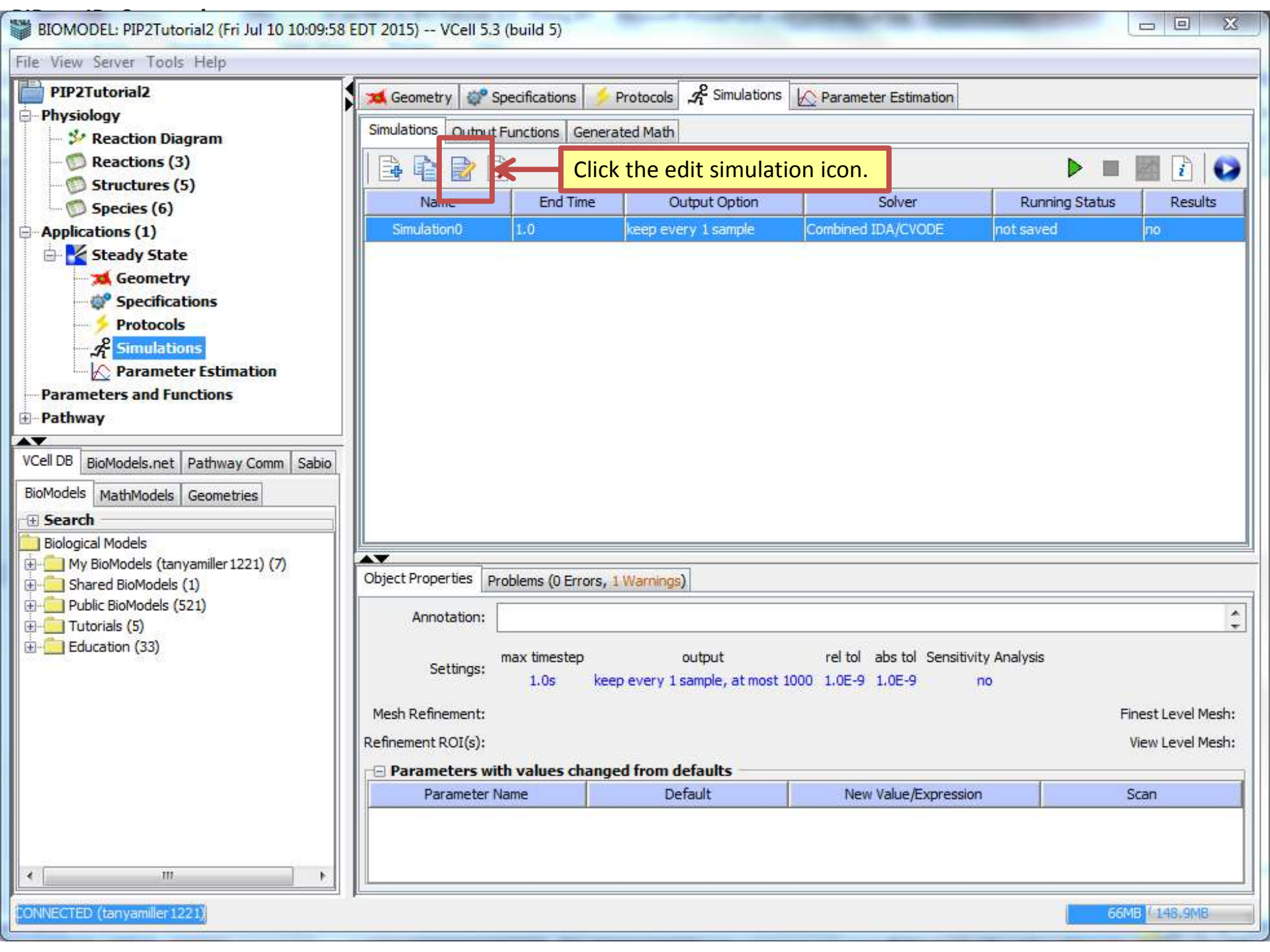
Refinement ROI(s): View Level Mesh:

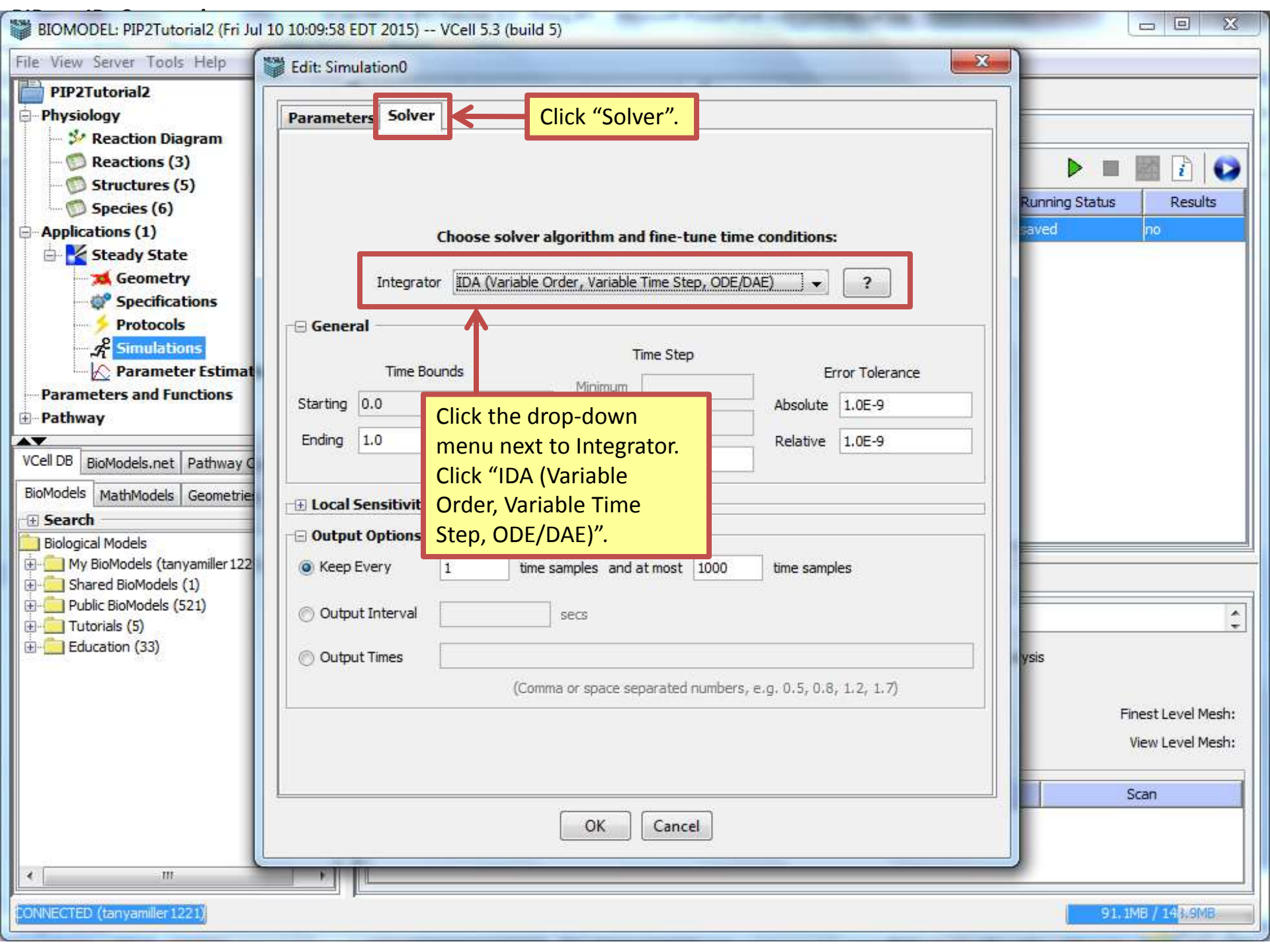
☐ **Parameters with values changed from defaults**

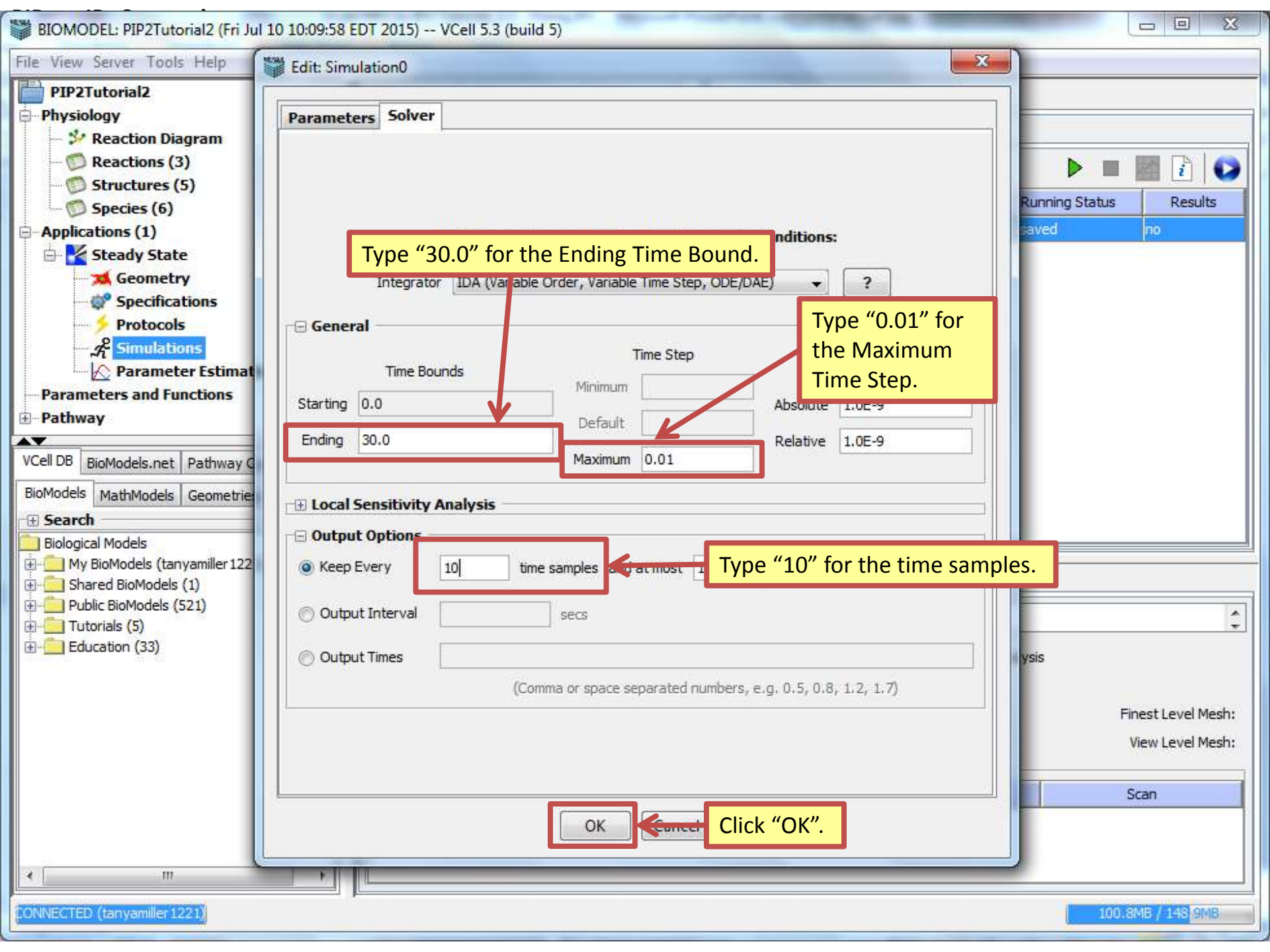
Parameter Name	Default	New Value/Expression	Scan
----------------	---------	----------------------	------

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46.6MB / 113.2MB







Type "30.0" for the Ending Time Bound.

Type "0.01" for the Maximum Time Step.

Type "10" for the time samples.

Click "OK".

BIOMODEL: PIP2Tutorial2 (Mon Jul 13 09:56:40 EDT 2015) -- VCell 5.3 (build 5)

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PIP2Tutorial2

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BioModels MathModels Geometries

Search

- Biological Models
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Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	30.0	keep every 10 samples	IDA	completed	yes

Click "Simulation0" > green play icon.

Object Properties Problems (0 Errors, 1 Warnings)

Annotation:

Settings:

max timestep	output	rel tol	abs tol	Sensitivity Analysis
0.01s	keep every 10 samples, at most 1000	1.0E-9	1.0E-9	no

Mesh Refinement:

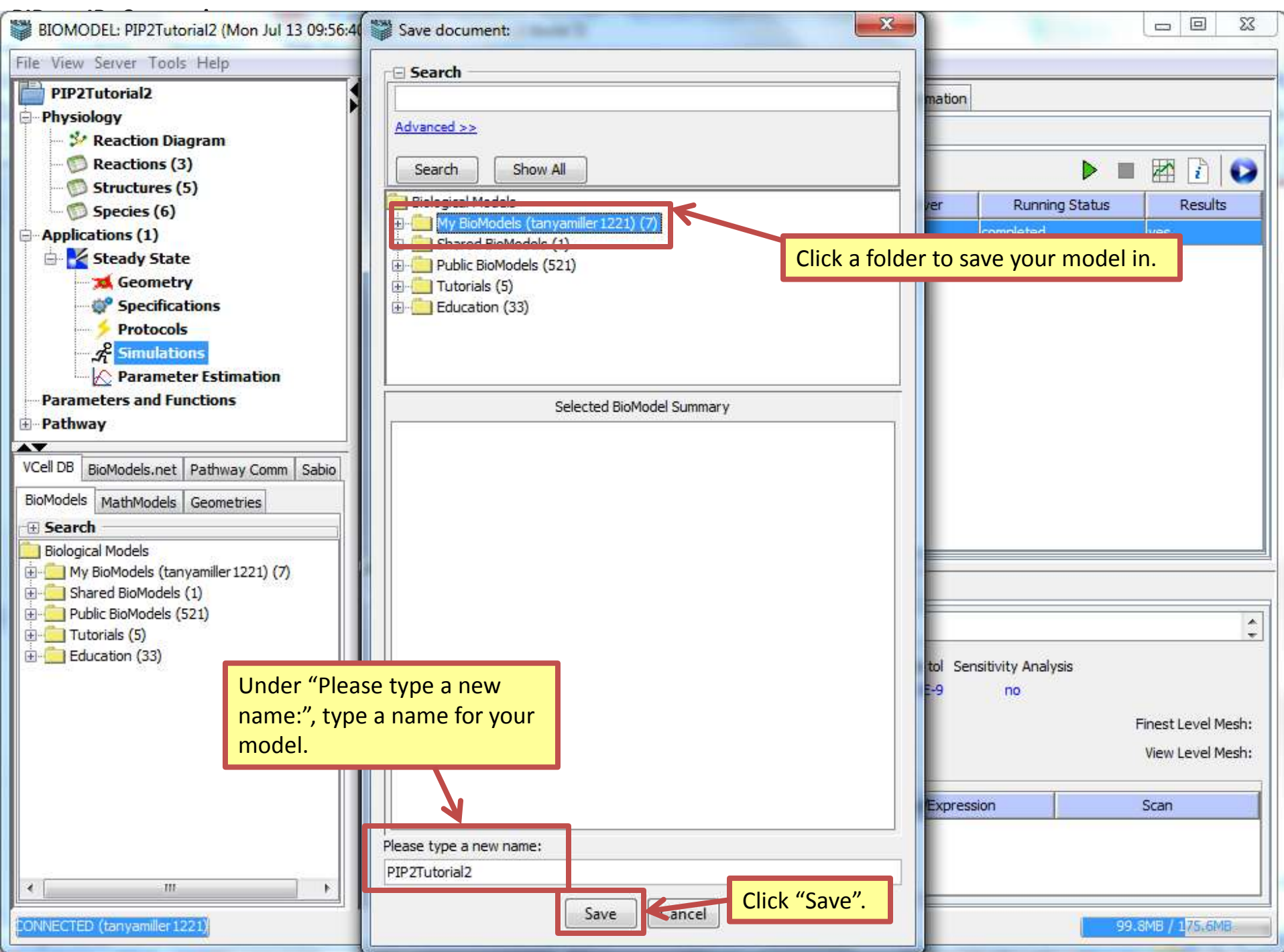
Refinement ROI(s):

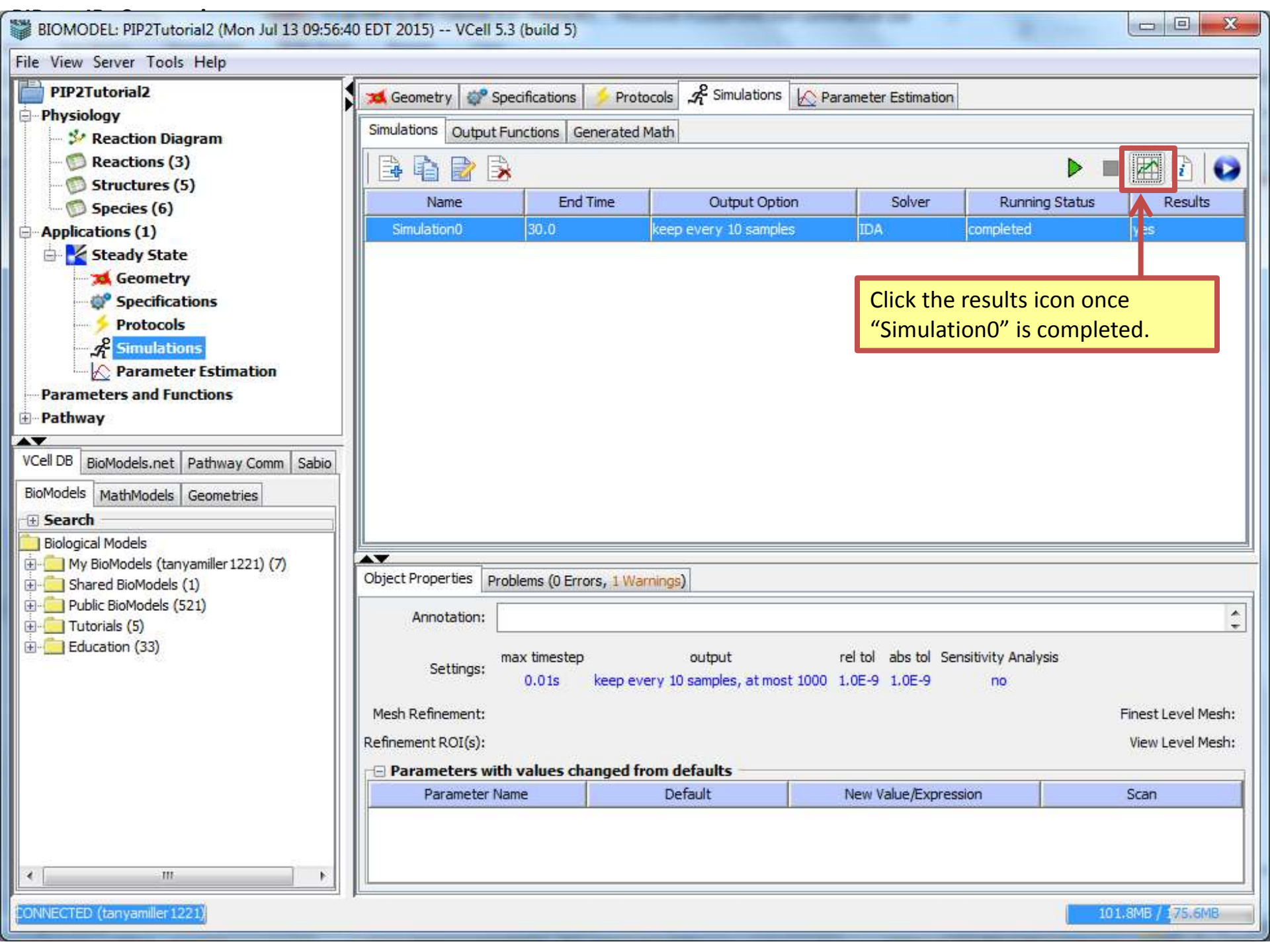
Parameters with values changed from defaults

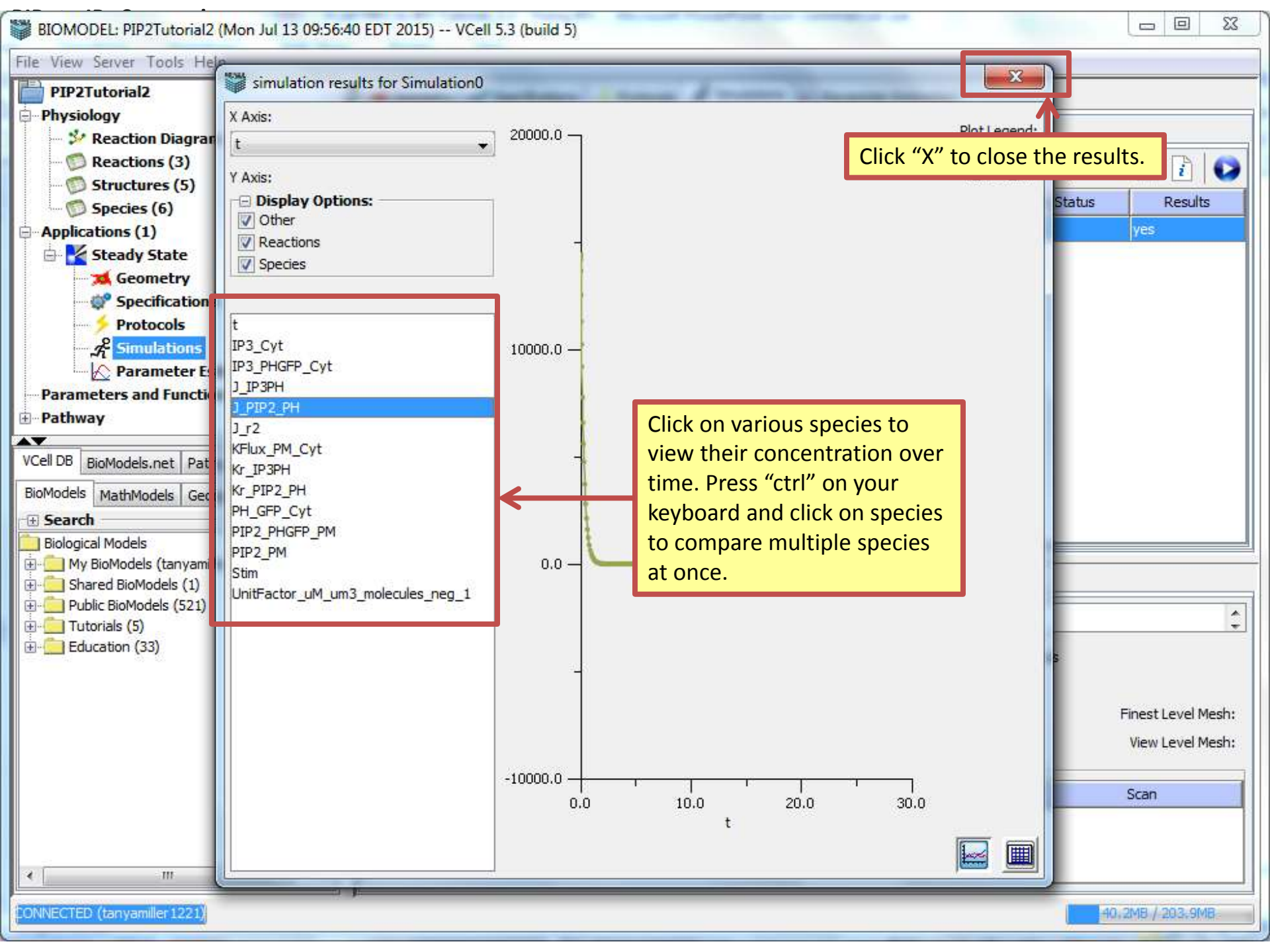
Parameter Name	Default	New Value/Expression	Scan
----------------	---------	----------------------	------

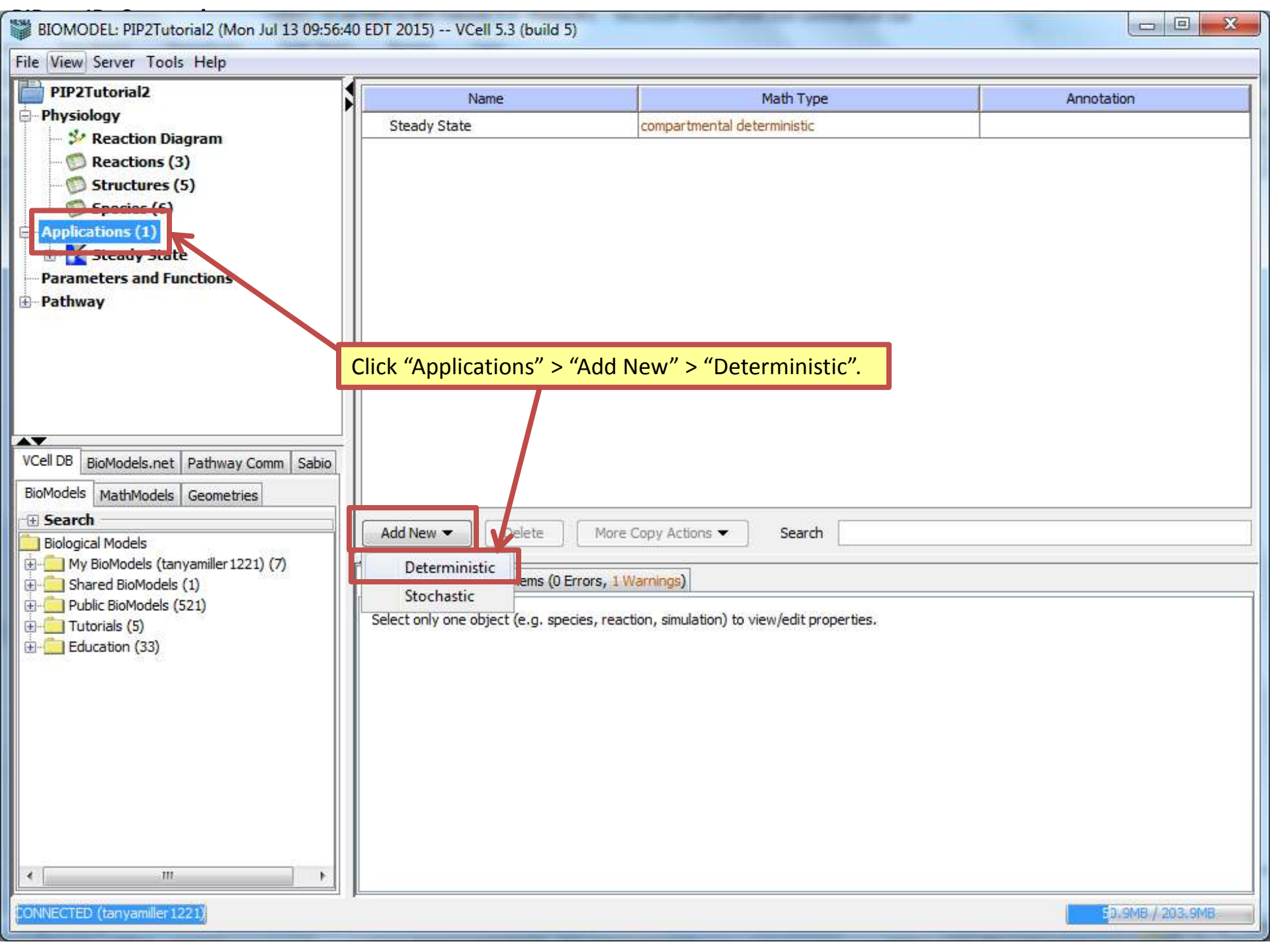
CONNECTED (tanyamiller1221)

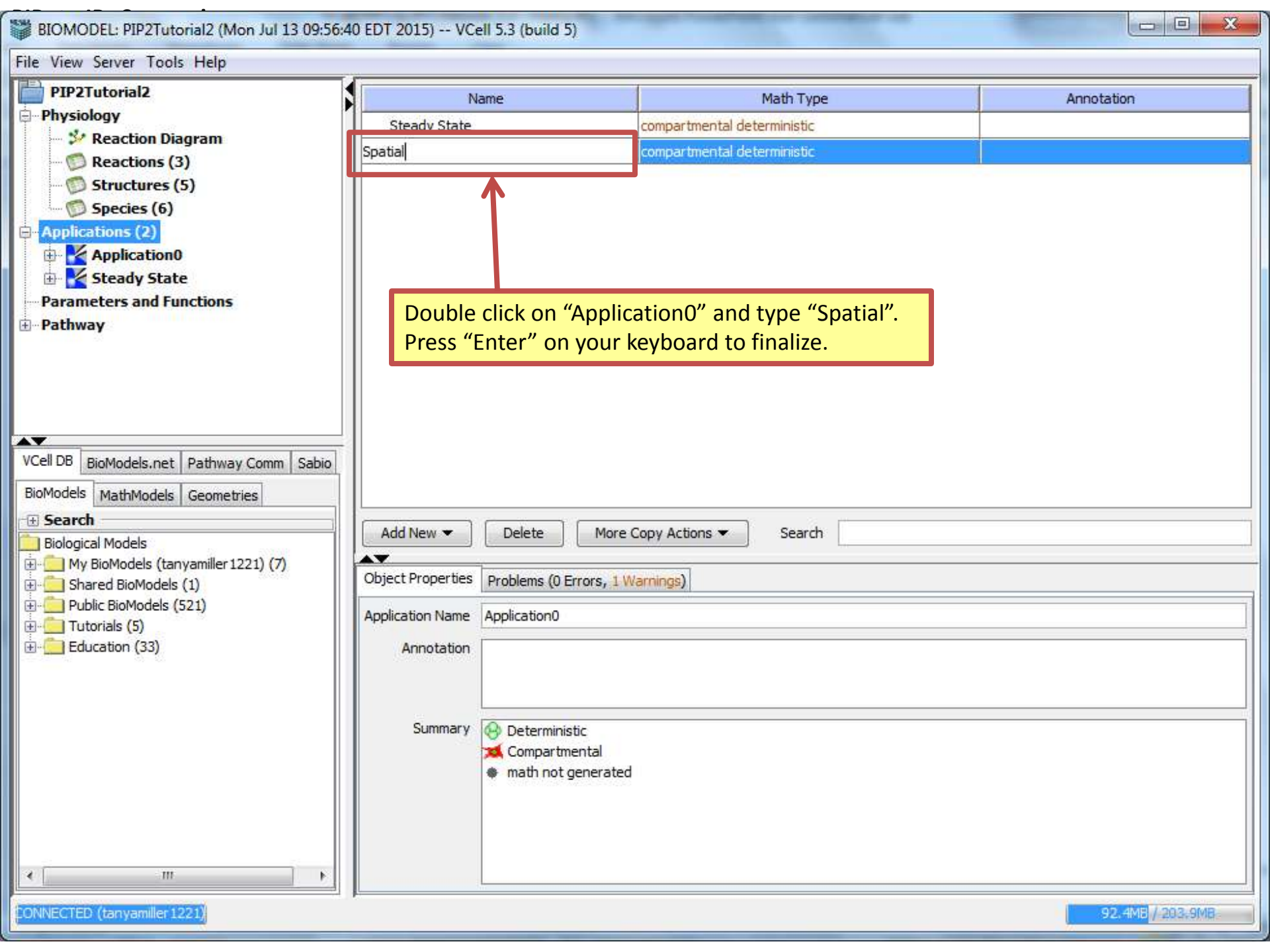
4.1MB / 175.6MB











PIP2Tutorial2

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- Applications (2)**
 - Application0
 - Steady State
- Parameters and Functions
- Pathway

Name	Math Type	Annotation
Steady State	compartmental deterministic	
Spatial	compartmental deterministic	

Double click on "Application0" and type "Spatial". Press "Enter" on your keyboard to finalize.

Search

- Biological Models
 - My BioModels (tanyamiller1221) (7)
 - Shared BioModels (1)
 - Public BioModels (521)
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Add New Delete More Copy Actions Search

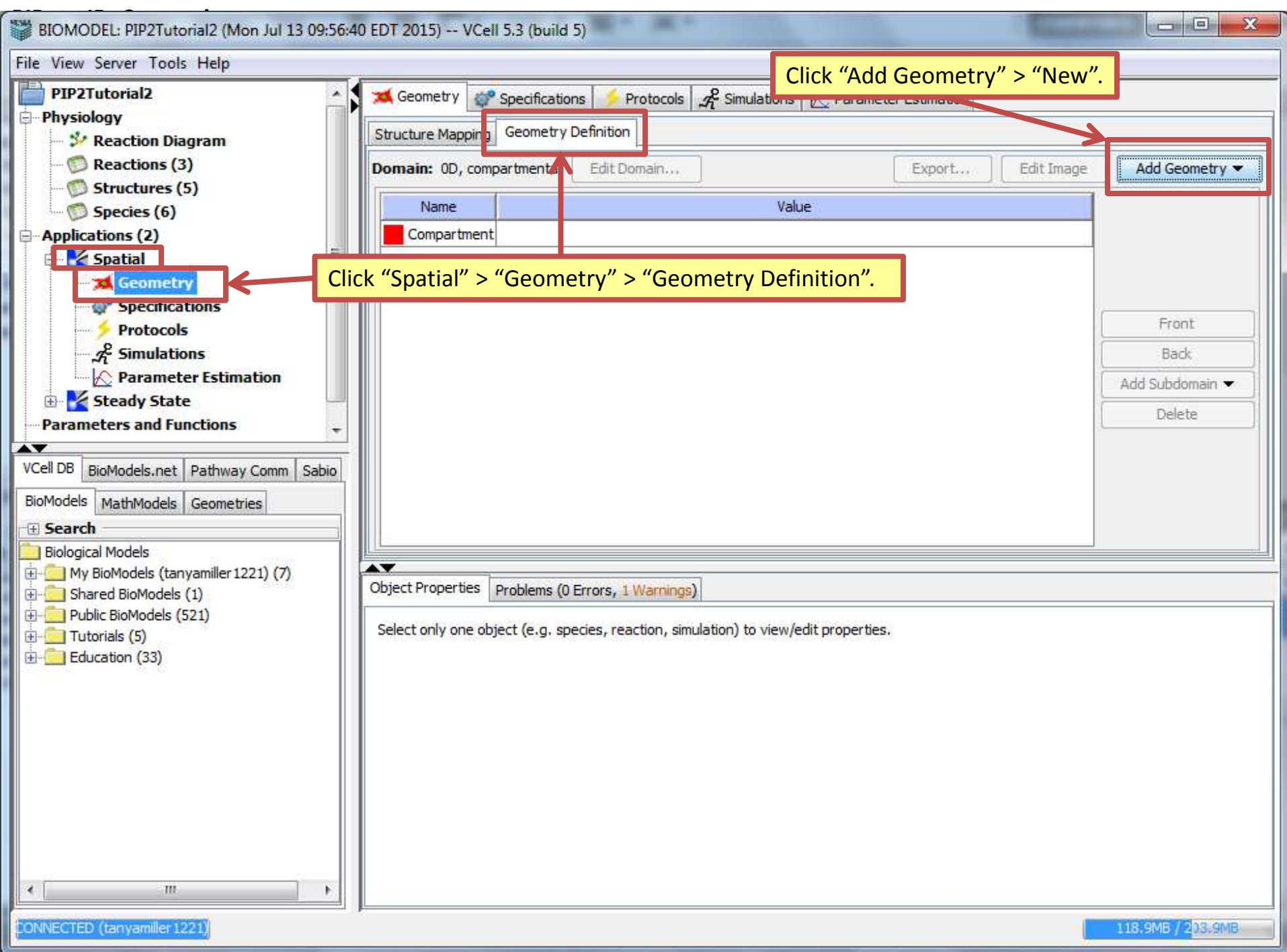
Object Properties Problems (0 Errors, 1 Warnings)

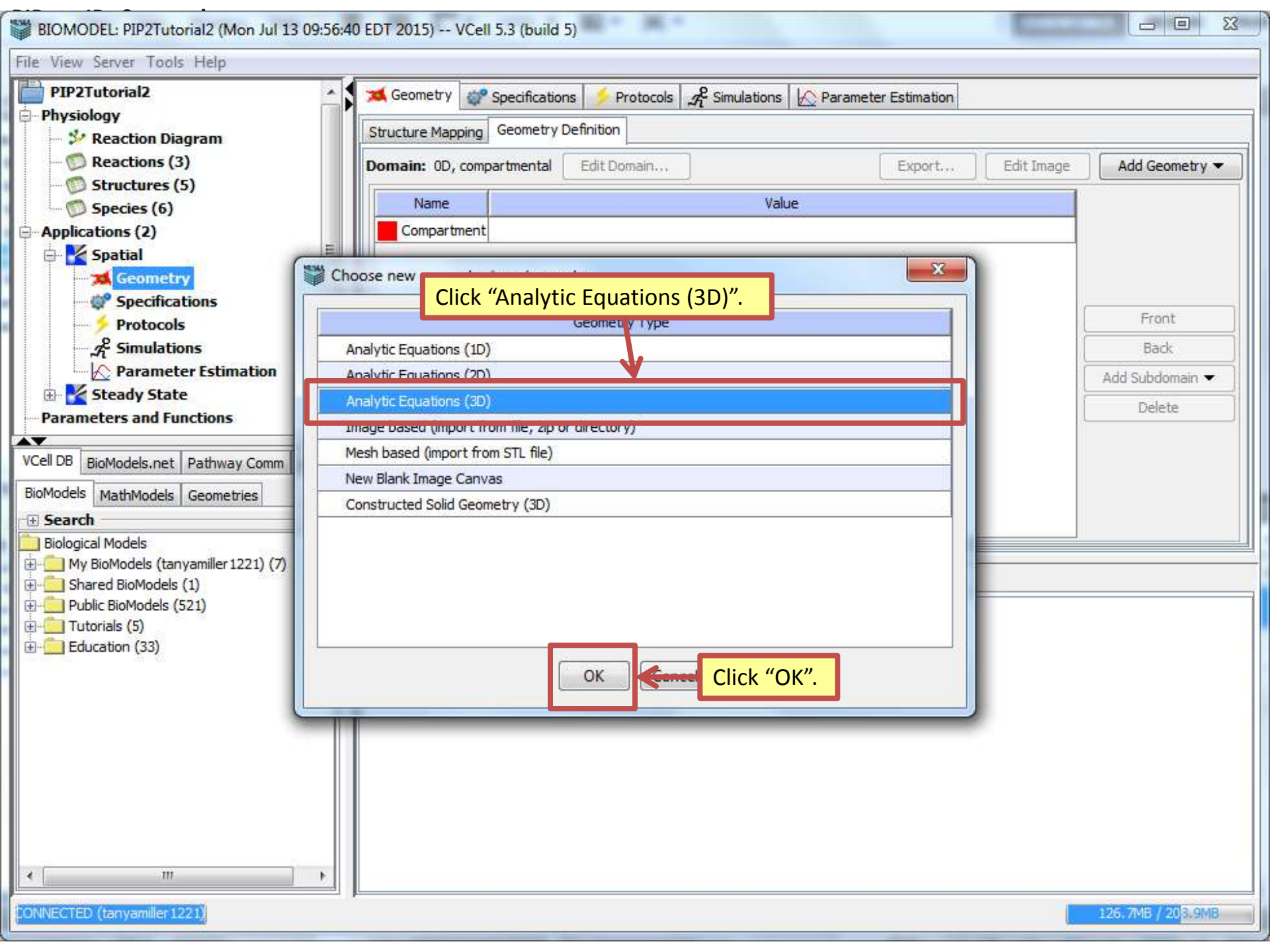
Application Name Application0

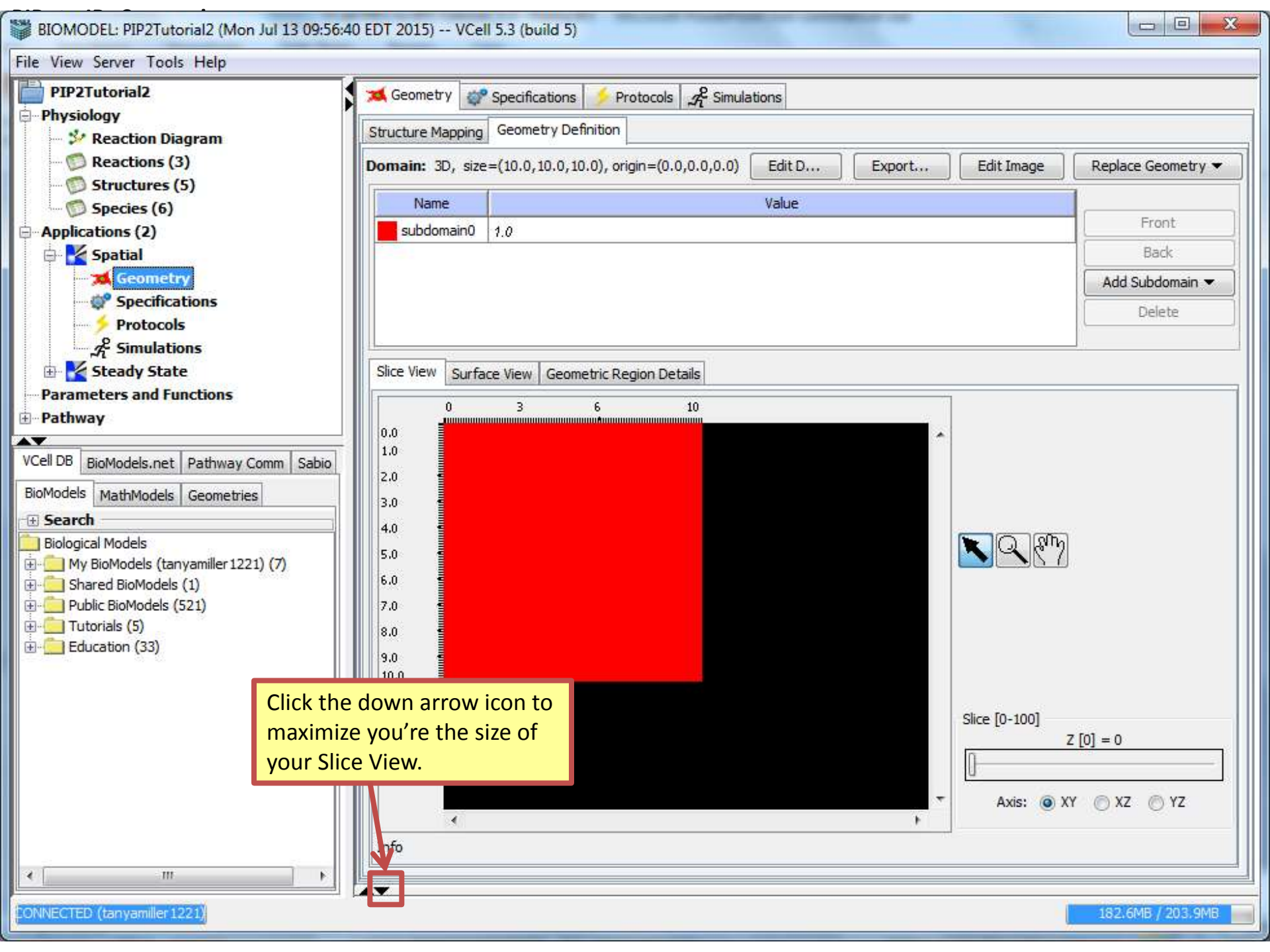
Annotation

Summary

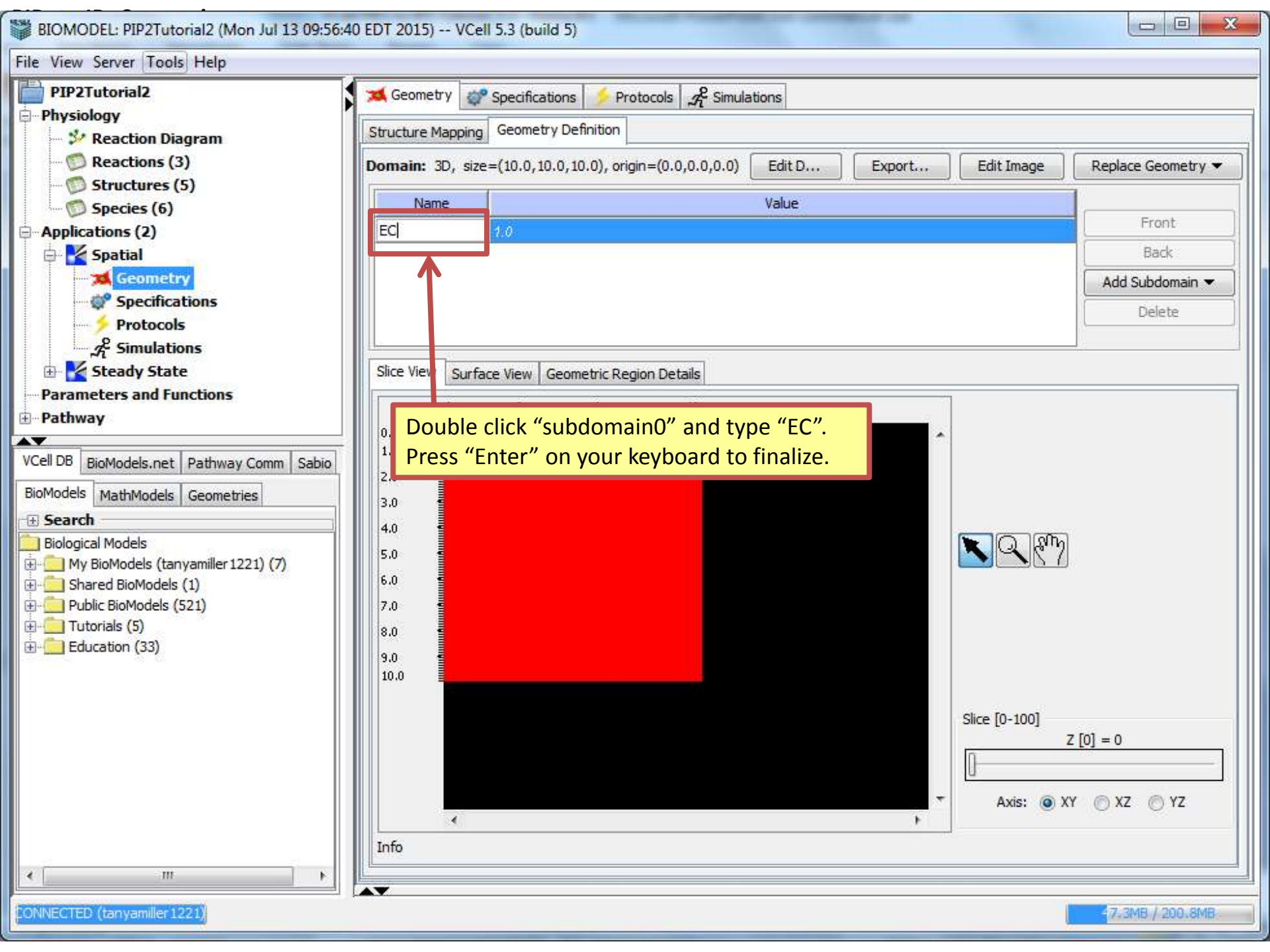
- Deterministic
- Compartmental
- math not generated

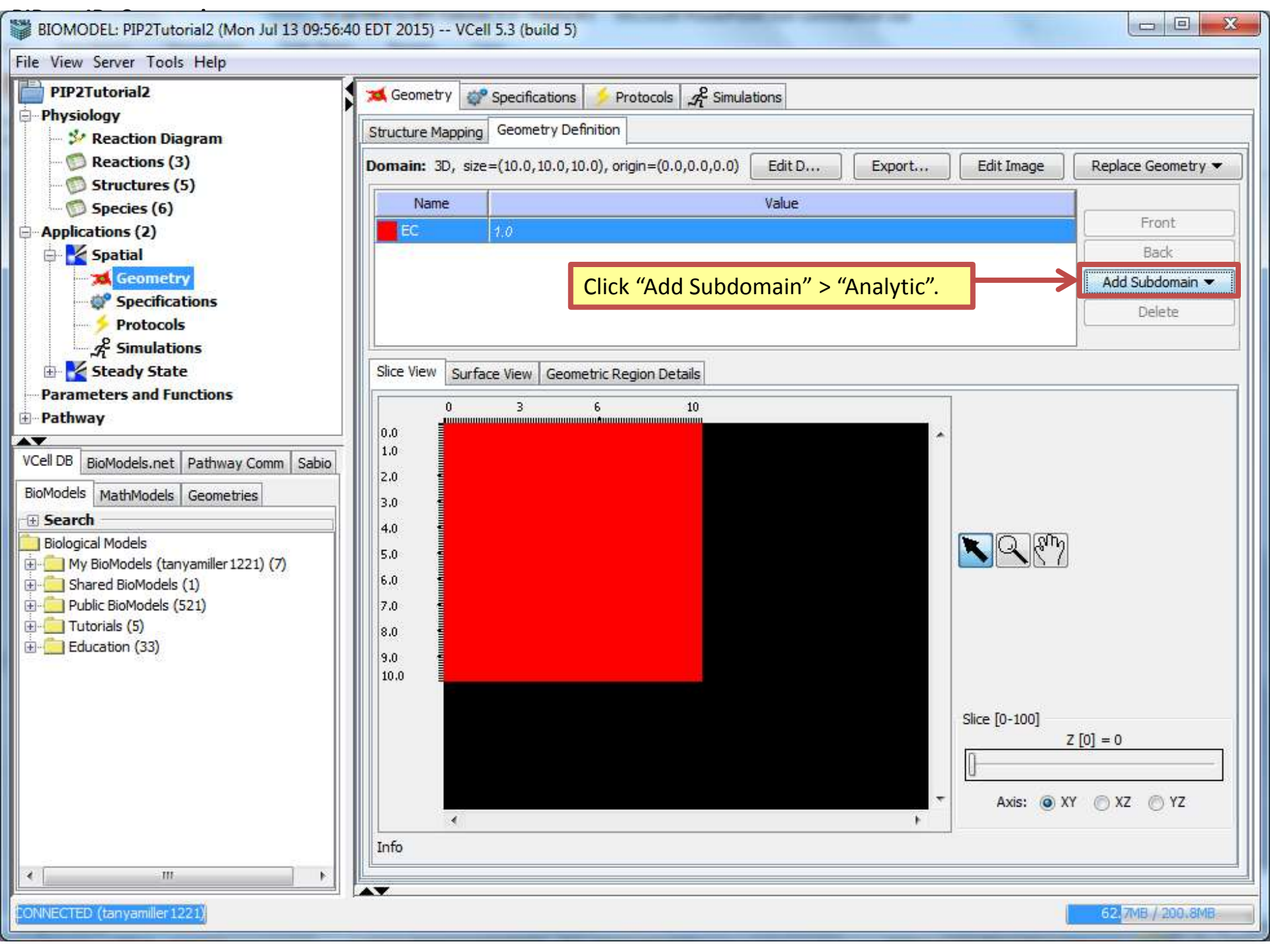


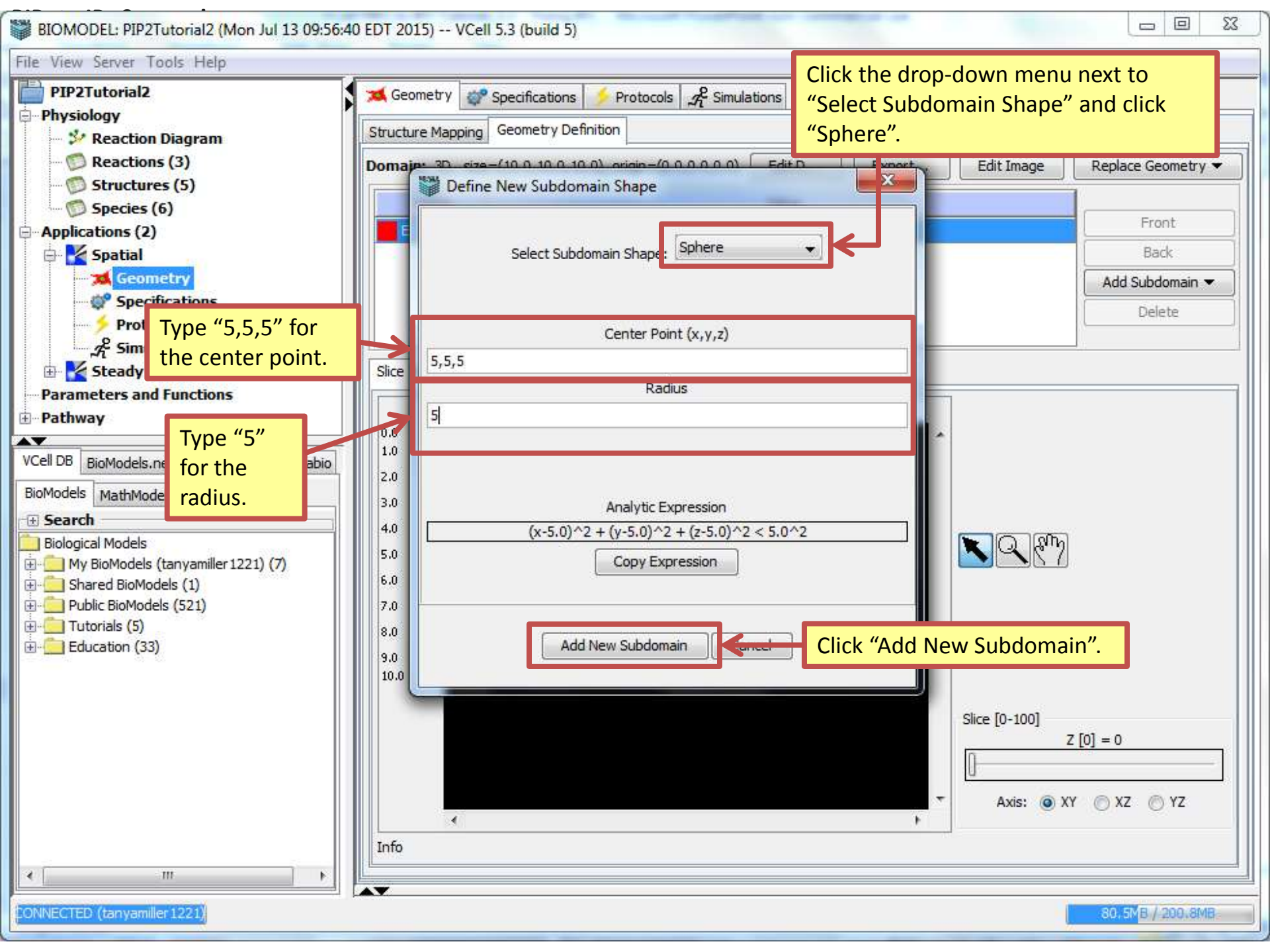




Click the down arrow icon to maximize you're the size of your Slice View.







BIOMODEL: PIP2Tutorial2 (Mon Jul 13 09:56:40 EDT 2015) -- VCell 5.3 (build 5)

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Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

Domain: 3D, size=(10.0,10.0,10.0), origin=(0.0,0.0,0.0) Edit D... Export... Edit Image Replace Geometry ▾

Name	Value
Cyt	$(((x - 5.0))^2 + ((y - 5.0))^2 + ((z - 5.0))^2) < (5.0)^2$
subdomain0	1.0

Front Back Add Subdomain ▾ Delete

Double click "subdomain0" and type "Cyt". Press "Enter" on your keyboard to finalize.

0.0 1.0 2.0 3.0 4.0 5.0 6.0 7.0 8.0 9.0 10.0

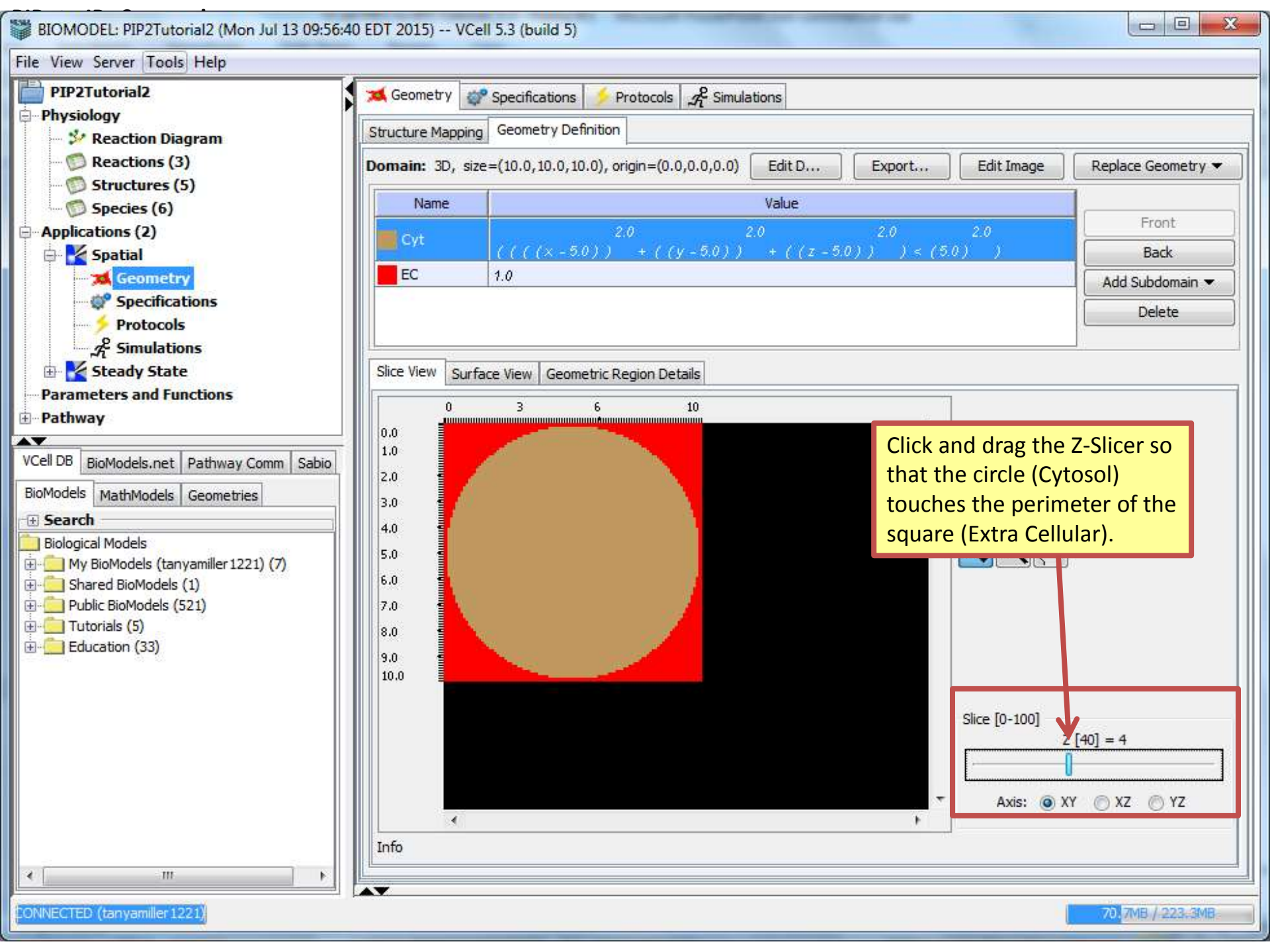
Info

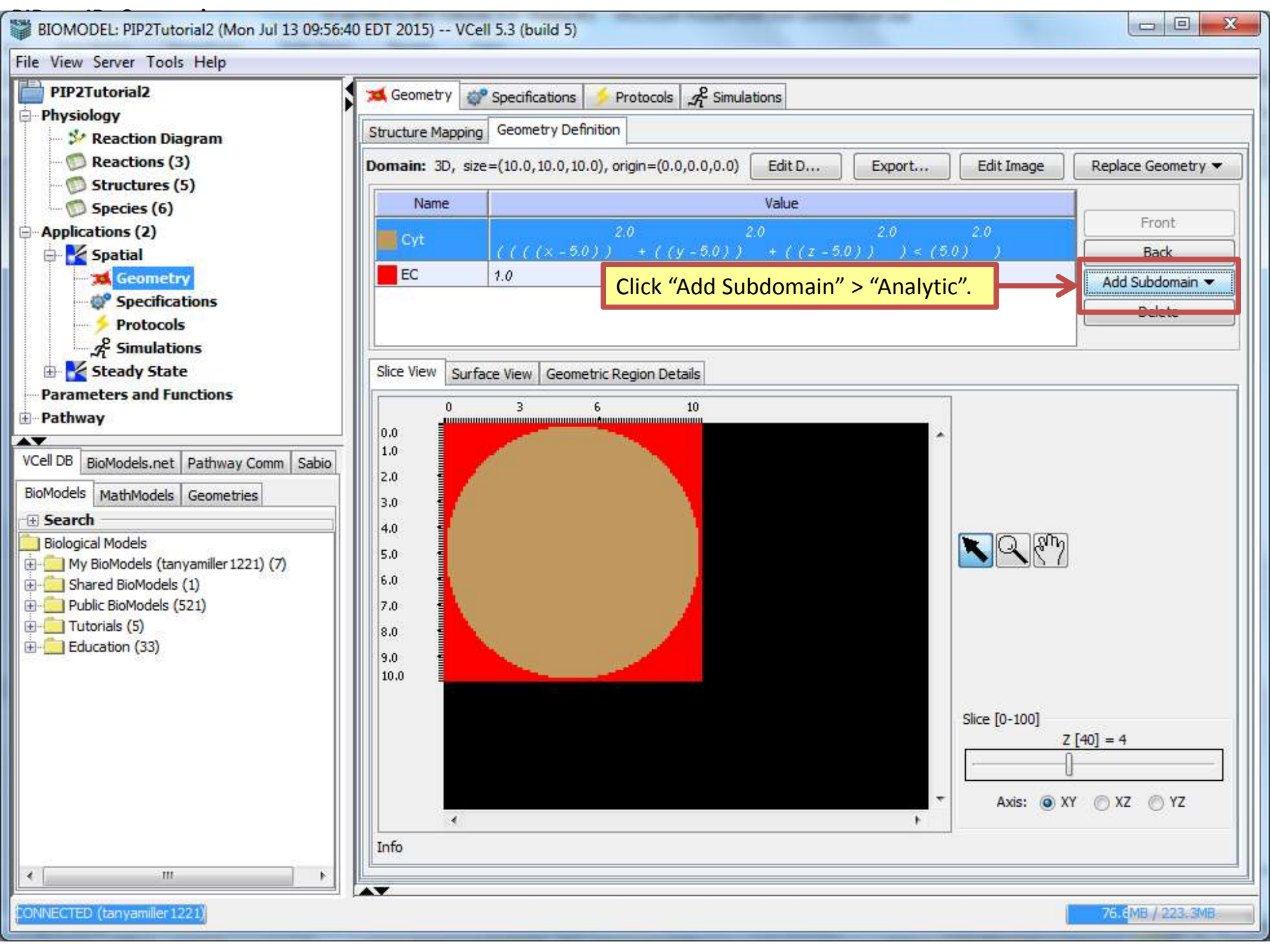
Slice [0-100] Z [0] = 0

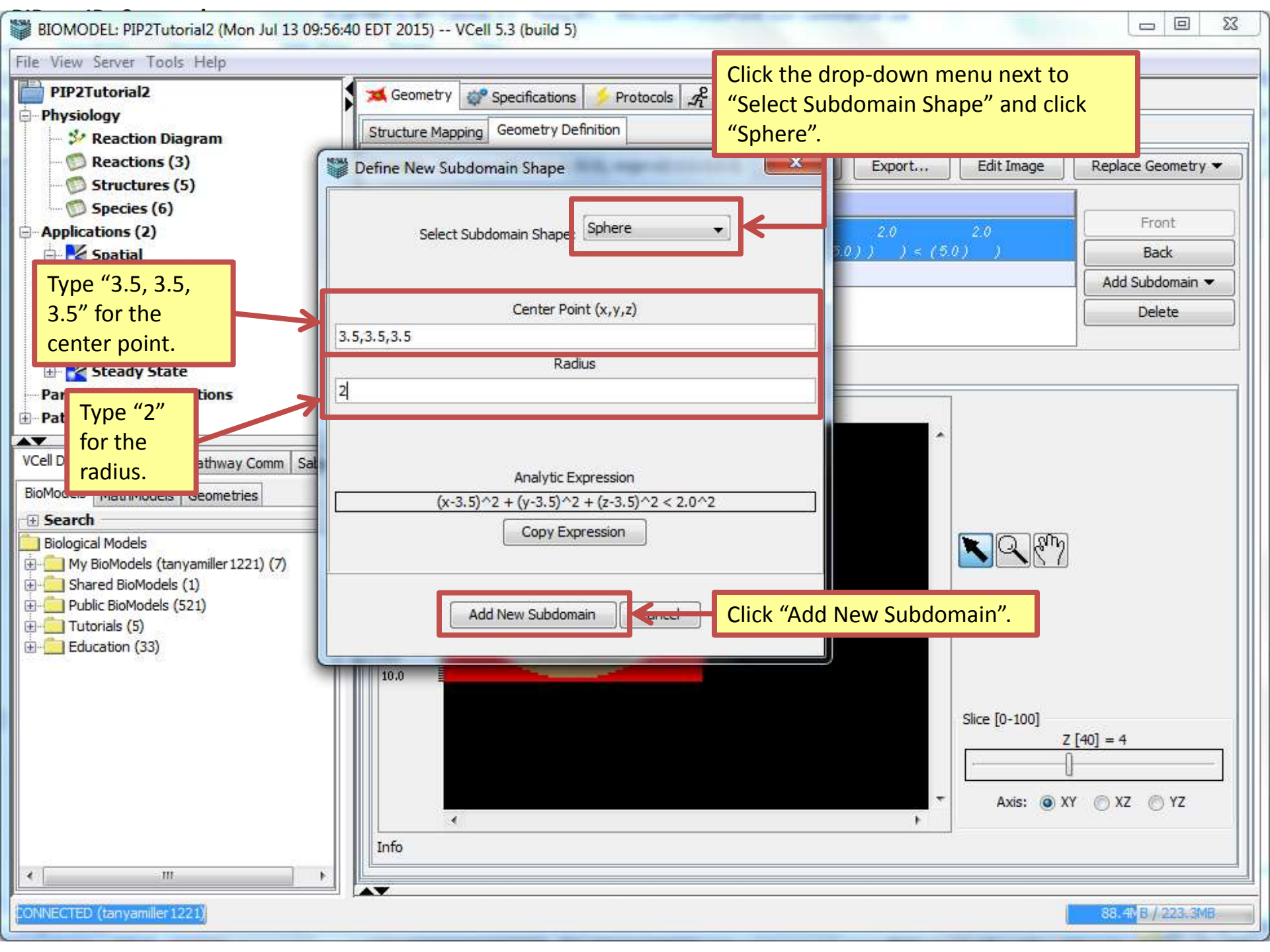
Axis: ☒ XY ☐ XZ ☐ YZ

CONNECTED (tanyamiller1221)

182.1MB / 200.8MB







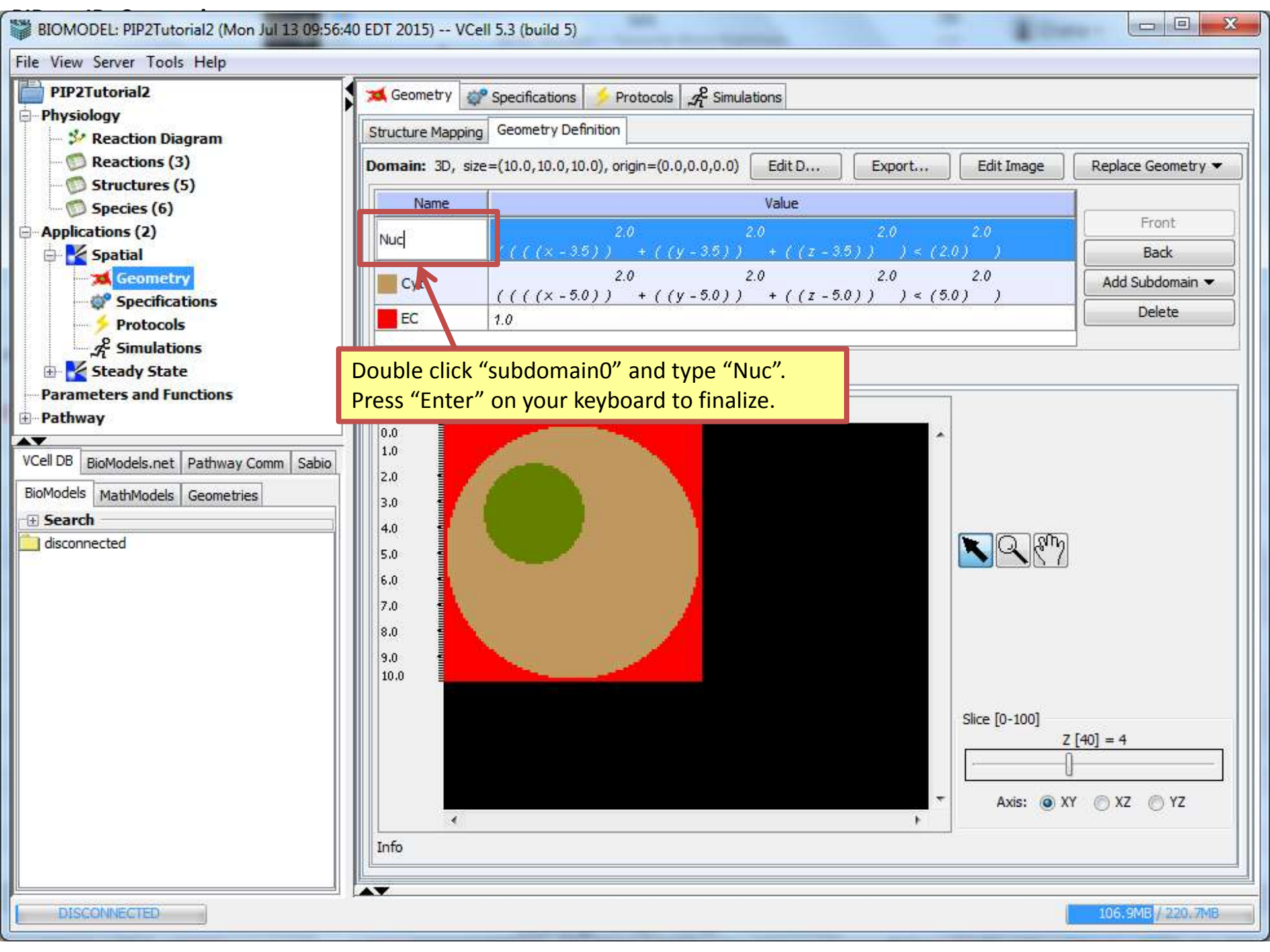
Click the drop-down menu next to "Select Subdomain Shape" and click "Sphere".

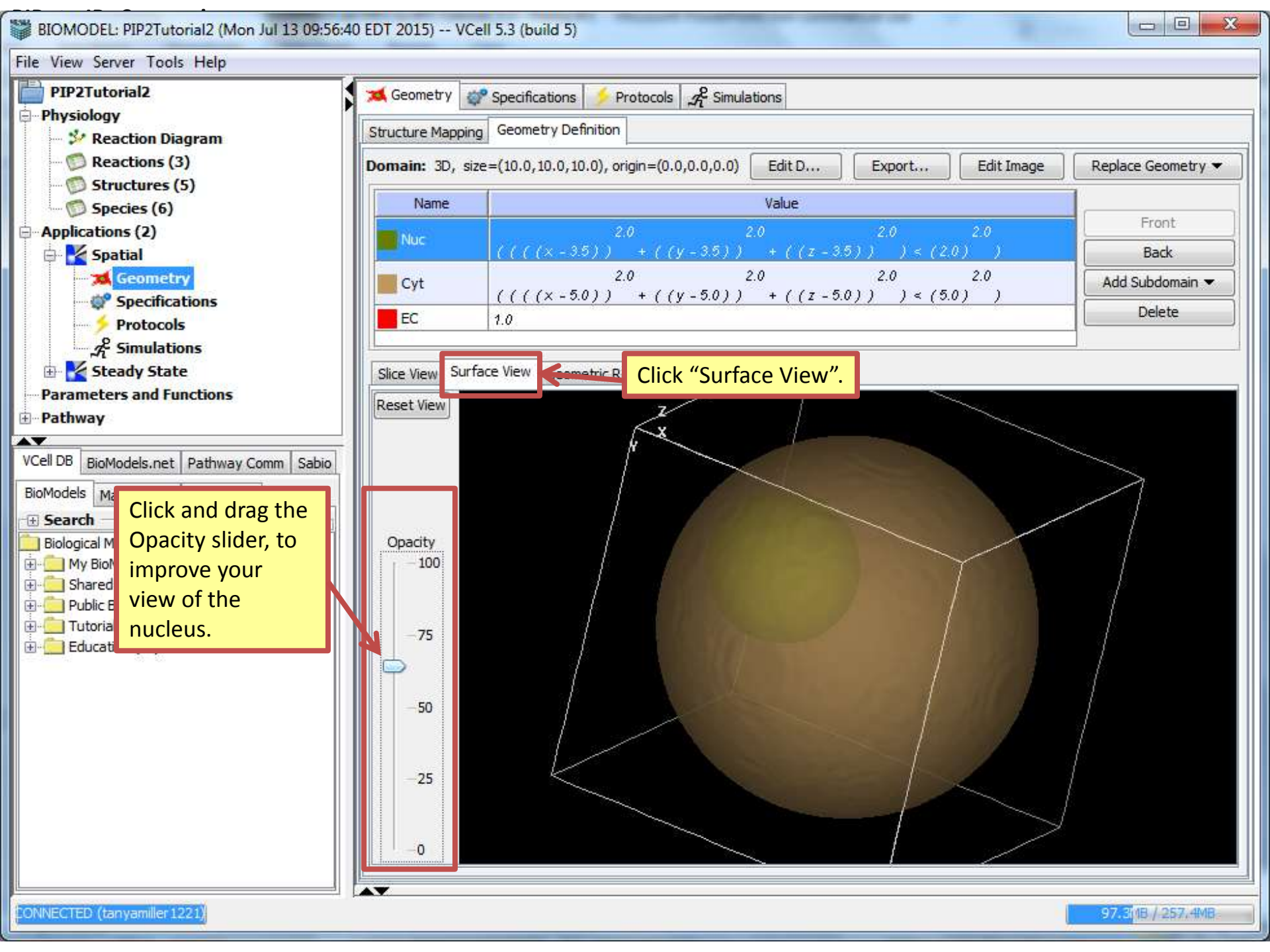
Type "3.5, 3.5, 3.5" for the center point.

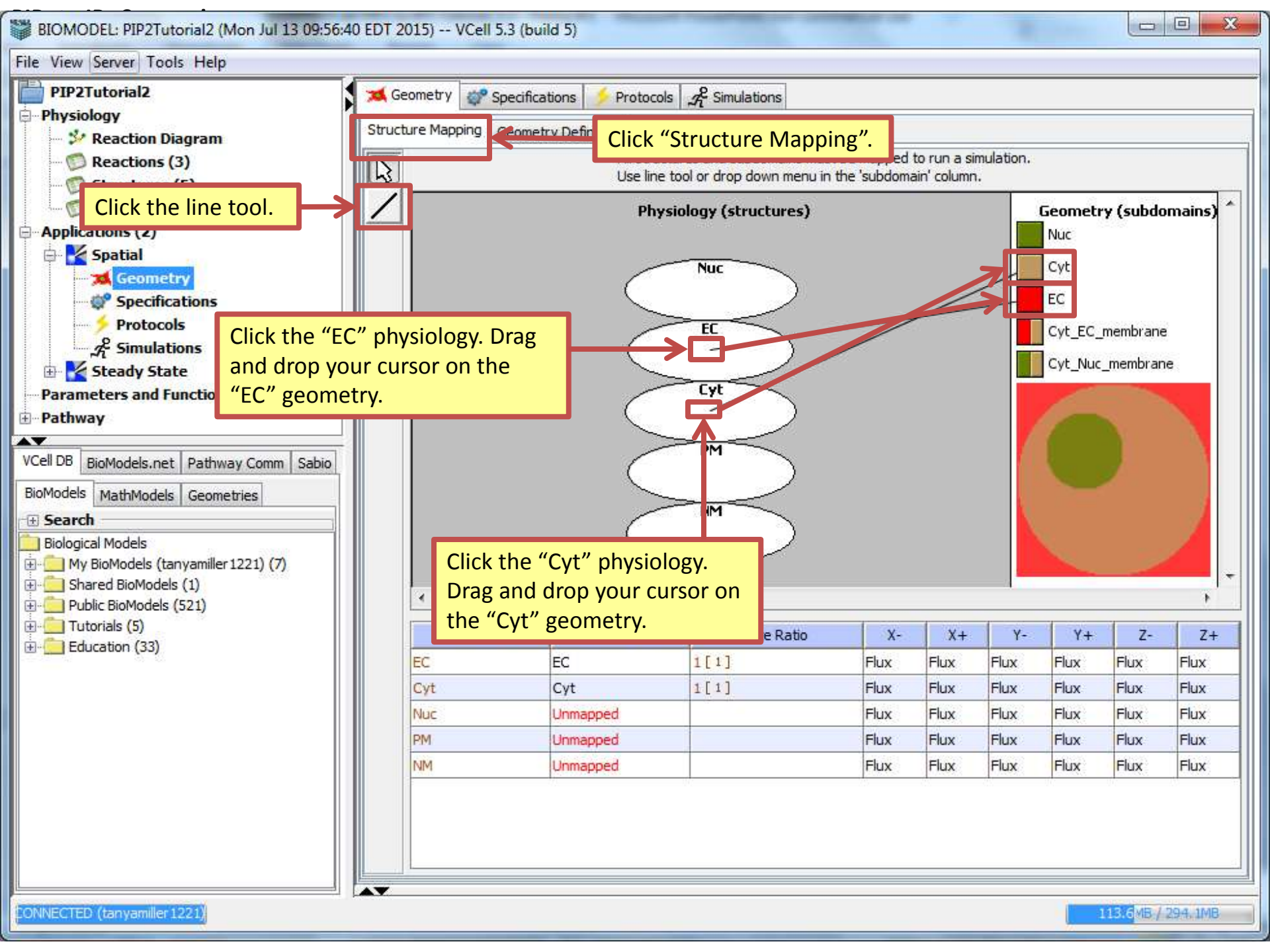
Type "2" for the radius.

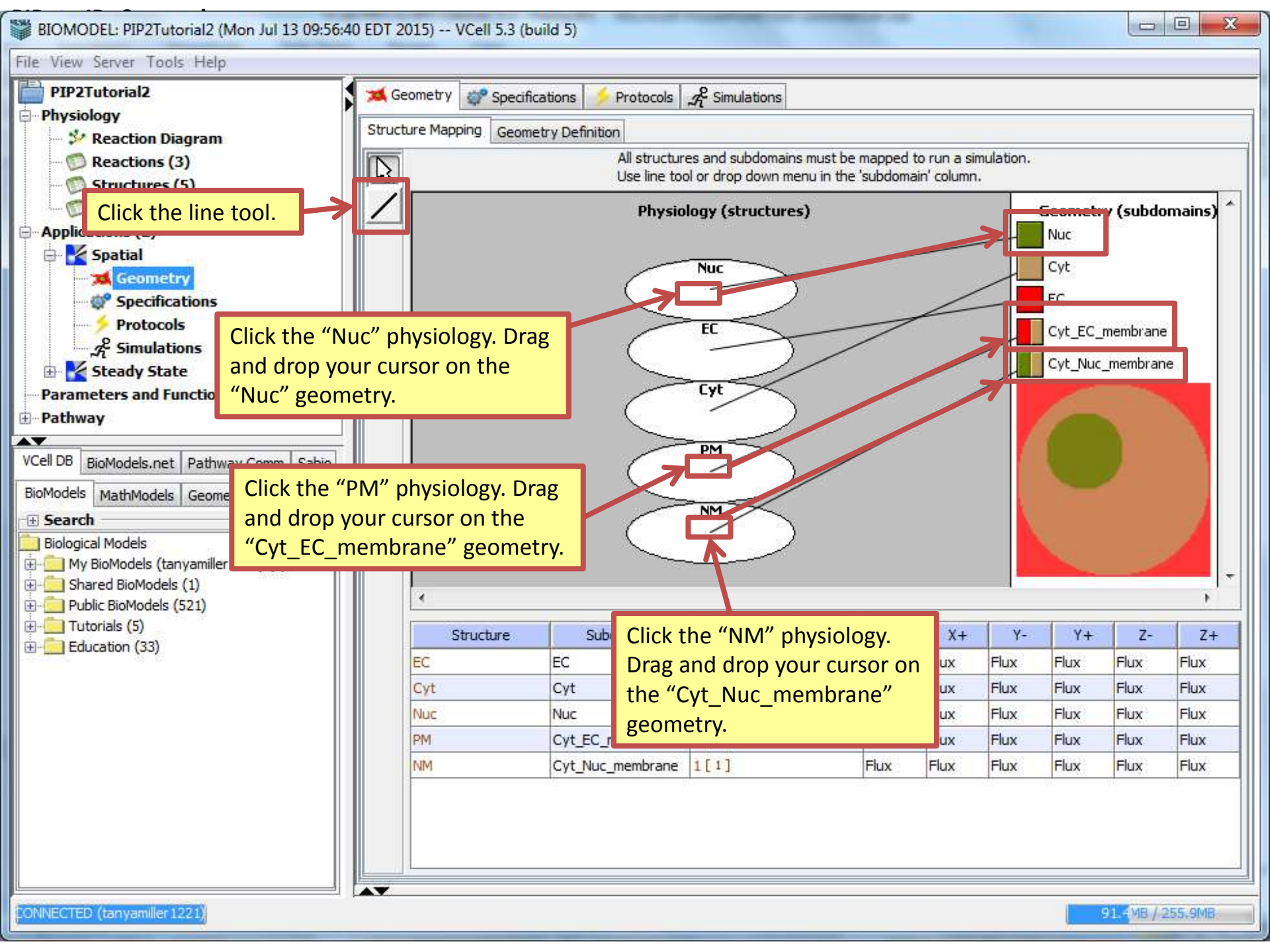
Add New Subdomain

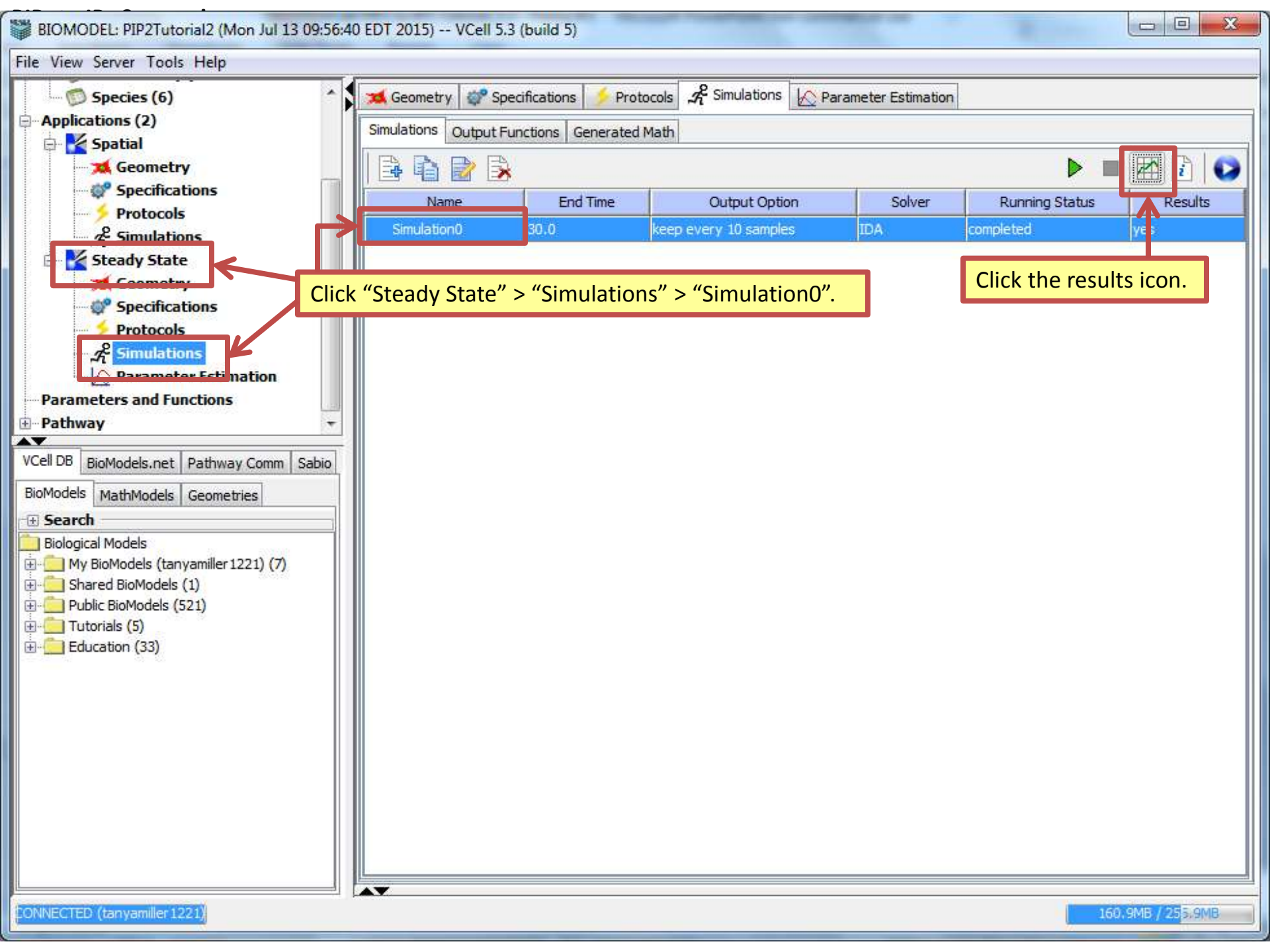
Click "Add New Subdomain".











t	J_PIP2_PH
0	14400
3.5555555E-11	14400
3.6408888E-8	14399.998
2.7962026E-5	14398.188
4.0078904E-4	14374.066
2.9509258E-3	14210.703
1.2147152E-2	13644.176
3.2074478E-2	12524.441
5.6983636E-2	11297.26
8.1892794E-2	10224.504
0.10929287	9188.9046
0.15412935	7753.8929
0.19896584	
0.24380232	
0.28863881	4761.6047
0.35948045	3710.5595
0.44018613	2802.4269
0.5208918	2121.5952
0.60159747	1608.5789
0.68230314	1220.6807
0.78037371	873.34233
0.88037371	620.62075
0.98037371	440.61779
1.0803737	312.2762
1.1803737	220.71848
1.2803737	155.3928
1.3803737	108.79501

Click the spreadsheet icon.



BIOMODEL: PIP2Tutorial2 (Mon Jul 13 09:56:40 EDT 2015) -- VCell 5.3 (build 5)

FileViewServerToolsHelp

Species (6)

Applications (2)

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Results for Simulation Simulation0

X Axis:

t

Y Axis:

t

IP3_Cyt

IP3_PHGFP_Cyt

J_IP3PH

J_PIP2_PH

J_r2

KFlux_PM_Cyt

Kr_IP3PH

K_PIP2_PH

PH_GFP_Cyt

PIP2_PHGFP_PM

PIP2_PM

Stim

UnitFactor_uM_um3_molecules_neg_1

Display Options:

Other

Reactions

Species

t	IP3_Cyt	IP3_PHGFP_Cyt	PH_GFP_Cyt	PIP2_PHGFP_PM	PIP2_PM
0	0.1	0	1	0	120000
3.555555...	0.1	3.555542...	1	5.119999...	120000
3.640888...	9.999996...	3.640887...	0.99999985	5.242879...	120000
2.796202...	9.997204...	2.795650...	0.99988425	0.40262785	119999.6
4.007890...	9.960034...	3.996561...	0.99834309	5.7661628	119994.23
2.950925...	9.710957...	2.890425...	0.98790544	42.213096	119957.79
1.214715...	8.882529...	1.117470...	0.95170038	170.26662	119829.73
3.207447...	0.07401758	0.02598242	0.88009177	430.77355	119569.23
3.98363...	0.0600449	0.0399551	0.80150686	727.10572	119272.89
8.189229...					
0.10929287					
0.15412935					
0.19896584					
0.24380232					
0.28863881					
0.35948045	1.296767...	8.703232...	0.31085585	2761.4759	117238.52
0.44018613	1.034762...	8.965237...	0.25131838	3022.5172	116977.48
0.5208918	8.609333...	9.139066...	0.20654021	3219.9117	116780.09
0.60159747	7.392310...	9.260768...	0.17271427	3369.4666	116630.53
0.68230314	6.500423...	9.349957...	0.14708709	3482.9104	116517.09
0.78037371	5.694584...	9.430541...	0.12409991	3584.6411	116415.36
0.88037371	5.074678...	9.492532...	0.10734864	3658.6247	116341.38
0.98037371	4.586986...	9.541301...	9.540189...	3711.1795	116288.82
1.0803737	4.188422...	9.581157...	8.687393...	3748.4635	116251.54
1.1803737	3.852283...	9.614771...	8.078314...	3774.8562	116225.14
1.2803737	3.561494...	9.643850...	7.643199...	3793.4783	116206.52
1.3803737	3.304844...	9.669515...	7.332374...	3806.5566	116193.44

Graph

Table

Status

Results

yes

Simultaneously hold down on "ctrl" on your keyboard and click "IP3_Cyt", "IP3_PHGFP_Cyt", "PH_GFP_Cyt", "PIP2_PHGFP_PM", and "PIP2_PM".

CONNECTED (tanyamiller 1221)

207.9MB / 255.9MB

BIOMODEL: PIP2Tutorial2 (Mon Jul 13 09:56:40 EDT 2015) -- VCell 5.3 (build 5)

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Education (33)

Results for Simulation Simulation0

X Axis: t
Y Axis: t

Display Options:
☒ Other
☒ Reactions
☒ Species

t	IP3_Cyt	IP3_PHGF...	PH_GFP_Cyt	PIP2_PHG...	PIP2_PM
4.7803737	3.460930...	9.965390...	6.580628...	3827.4643	116172.54
4.8803737	3.240506...	9.967594...	6.580968...	3827.3476	116172.65
4.9803737	3.034110...	9.969658...	6.581287...	3827.2383	116172.76
5	2.995171...	9.970048...	0.06581348	3827.2177	116172.78
5	2.995171...	9.970048...	0.06581348	3827.2177	116172.78
5.0000001	2.995811...	9.970048...	0.06581348	3827.2177	116172.78
5.0000656	3.650713...	9.970049...	6.581348...	3827.2176	116172.78
5.00577	6.057473...	9.971255...	6.580277...	3827.2114	116172.79
5.0372429	3.708399...	0.10015895	6.537946...	3827.1033	116172.9
5.1169743					5.05
5.200902					2.71
5.2848298					7.62
5.3687575					0.08
5.4687575					5.74
5.5687575					9.29
5.6687575					8.72
5.7687575					2.34
5.8687575					8.83
5.9687575					7.25
6	0.8722564	0.2277436	1.691728...	3464.2248	116535.78
6	0.8722564	0.2277436	1.691728...	3464.2248	116535.78
6.0000001	0.87225638	0.22774362	1.691728...	3464.2247	116535.78
6.0000864	0.87224365	0.22775635	1.691574...	3464.1734	116535.83
6.0076003	0.87113997	0.22886003	1.678722...	3459.701	116540.3
6.0426996	0.86609908	0.23390092	1.631191...	3438.7618	116561.24
6.1016697	0.85794309	0.24205691	1.582719...	3403.5789	116596.42
6.1651719	0.84944757	0.25055243	1.554283...	3365.92	116634.08

Scroll down the spreadsheet and find where t = 5. Simultaneously hold down on "ctrl" on your keyboard and click the cells for "IP3_Cyt", "IP3_PHGFP_Cyt", "PH_GFP_Cyt", "PIP2_PHGFP_PM", and "PIP2_PM" where t = 5. Right click "Copy Cell"

CONNECTED (tanyamiller 1221)

153.8MB / 248.8MB

BIOMODEL: PIP2Tutorial2 (Mon Jul 13 09:56:40 EDT 2015) -- VCell 5.3 (build 5)

File View Server Tools Help

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Click "Spatial" > "Specifications".

Click the first "Initial Condition" cell.
Right click "Paste All".

Geometry Specifications Protocols Simulations

Species Reactions

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant
IP3_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0
IP3_PHGFP_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	
PH_GFP_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	
Stim	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	
PIP2_PM	PM	<input type="checkbox"/>	0.0	<input type="checkbox"/>	

Copy
Copy All
Paste
Paste All
Specify Column Value for Selected Row(s)
Clamped
Initial Condition
Well Mixed
Diffusion Constant

VCCell DB BioModels.net Pathway Comm Sabio

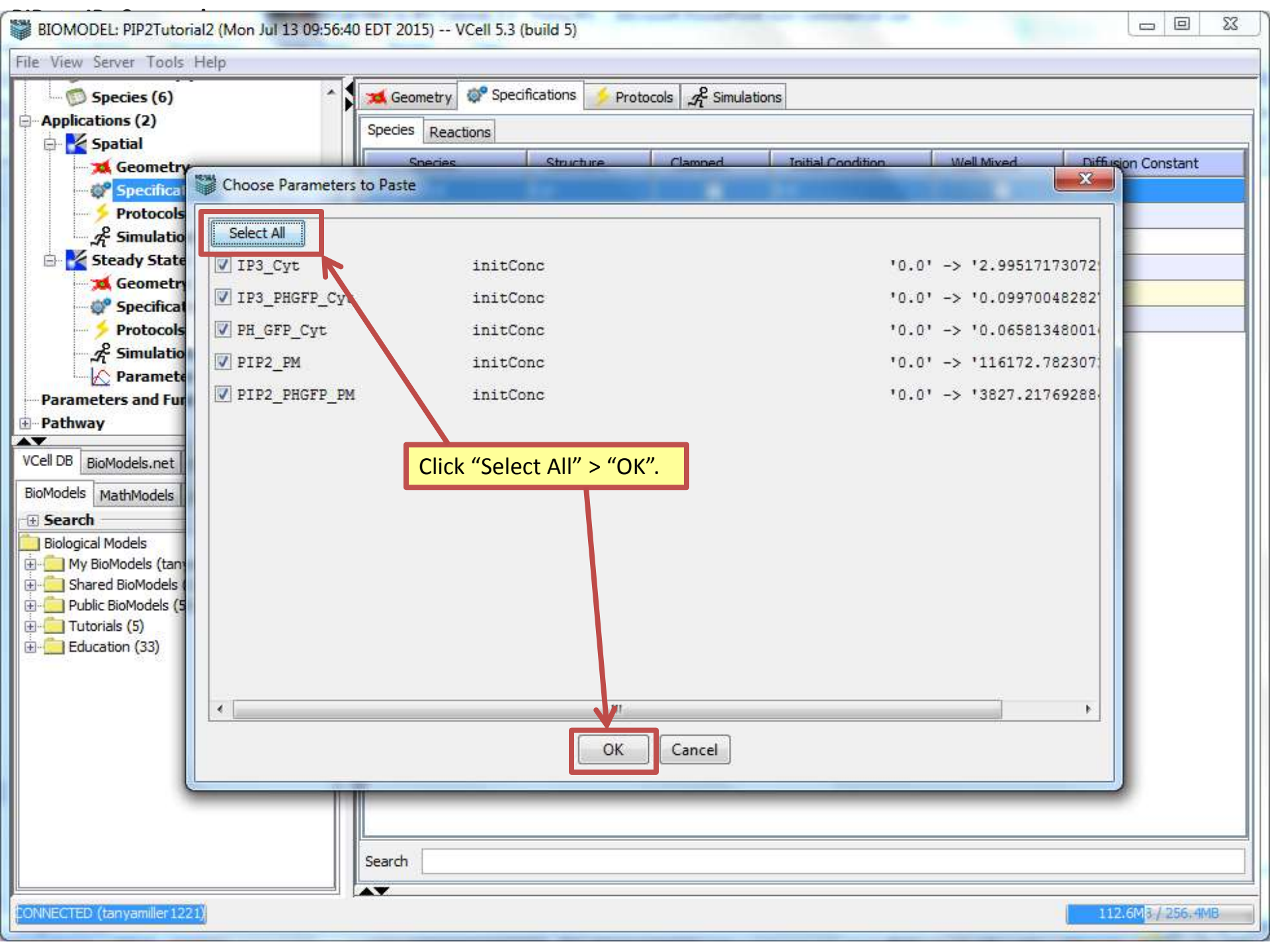
BioModels MathModels Geometries

Search

Biological Models
My BioModels (tanyamiller1221) (7)
Shared BioModels (1)
Public BioModels (521)
Tutorials (5)
Education (33)

CONNECTED (tanyamiller1221)

106.3M / 240.1MB



Click "Species" to rearrange the order of the species.

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant
Stim	Cyt	<input checked="" type="checkbox"/>	0.0	<input checked="" type="checkbox"/>	
PIP2_PM	PM	<input type="checkbox"/>	116172.78230711578	<input type="checkbox"/>	0.1
PIP2_PHGFP_PM	PM	<input type="checkbox"/>	3827.2176928842186	<input type="checkbox"/>	0.1
PH_GFP_Cyt	Cyt	<input type="checkbox"/>	0.06581348001685475	<input type="checkbox"/>	10.0
IP3_PHGFP_Cyt	Cyt	<input type="checkbox"/>	0.09970048282702804	<input type="checkbox"/>	10.0
IP3_Cyt	Cyt	<input type="checkbox"/>	2.9951717307295144...	<input type="checkbox"/>	10.0

Check off "Clamped" for "Stim".

