

# VCell Tutorial

## BioModel with Multiple Applications

*Create a single biomodel of RAN nuclear transport then use different modeling strategies to solve simulations.*

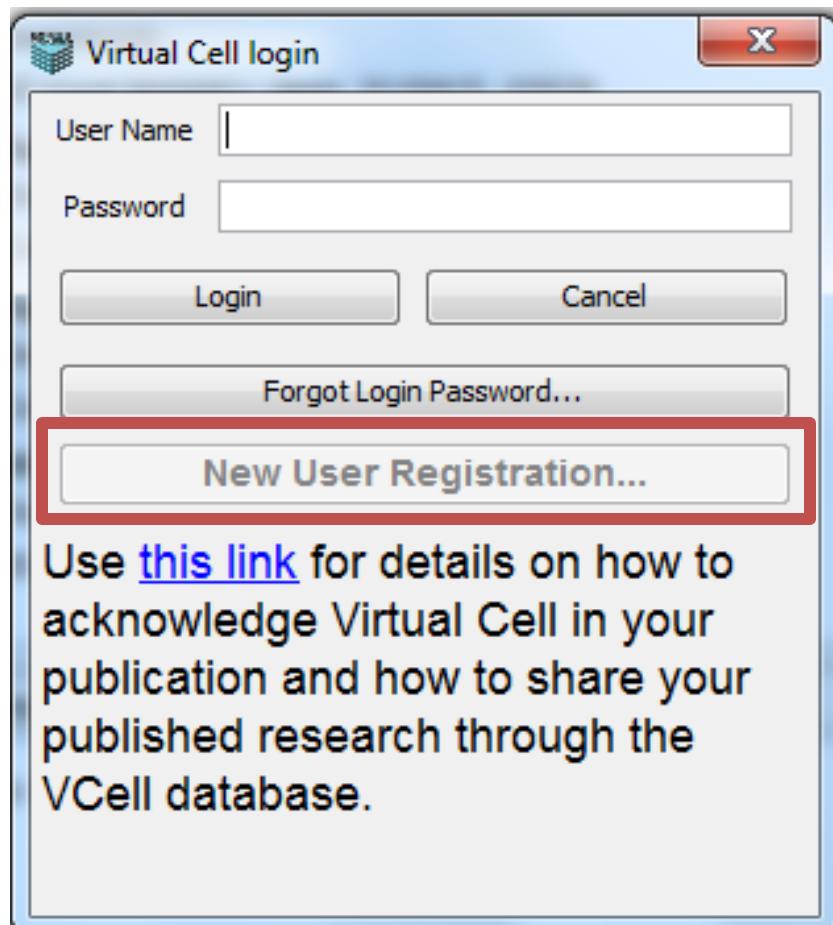
# In this tutorial...

- ▶ Create a Biomodel Physiology with species, reactions and fluxes
- ▶ Create a spatial deterministic application of the Physiology
- ▶ Import a fluorescence images into Vcell and segment a 3D image stack within VCell to create a geometry
- ▶ Create a simulation and specify solver, time, and computational mesh.
- ▶ Run the simulation, view results and create graphs

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- ▶ [Create a non-spatial deterministic application](#)
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- ▶ [Create a spatial stochastic application](#)

# First time opening VCell

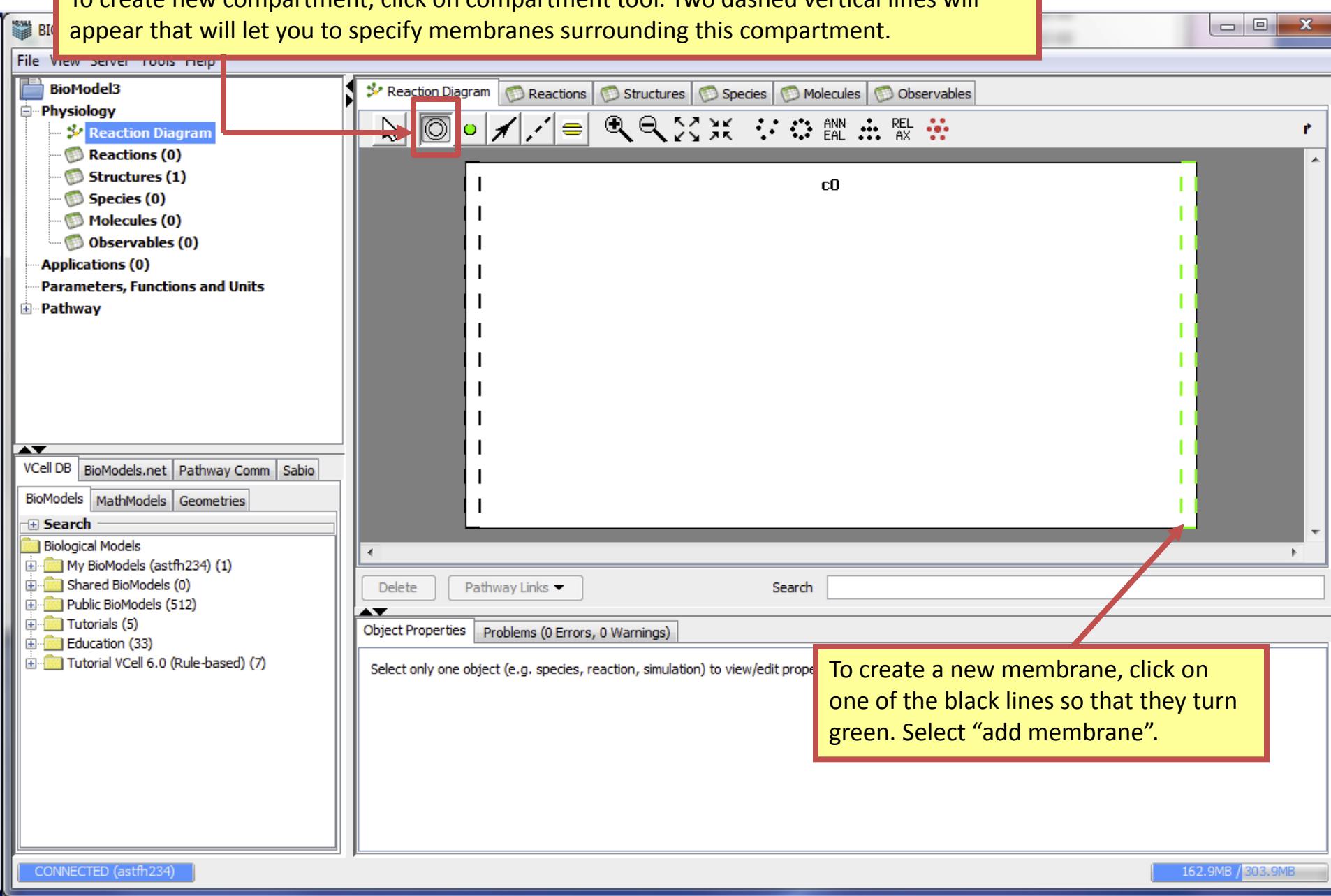


You need to register as a new user if you want to run simulations on VCell compute resources, or use the VCell database to store models that can be shared with collaborators.

To create a new VCell model, click “File” > “New” > “BioModel”

The screenshot shows the VCell software interface. At the top, there is a menu bar with File, View, Server, Tools, and Help. Below the menu is a toolbar with various icons for creating reaction diagrams, reactions, structures, species, molecules, and observables. A large central workspace is visible, currently showing a single node labeled "c0". On the left side, there is a tree view of the current BioModel3 project under Physiology, which includes Reaction Diagram, Reactions (0), Structures (1), Species (0), Molecules (0), and Observables (0). Below this, there are sections for Applications (0), Parameters, Functions and Units, and Pathway. At the bottom left, there is a sidebar with tabs for VCell DB, BioModels.net, Pathway Comm, and Sabio, with BioModels selected. The bottom right of the sidebar shows a search bar and a "Search" button. The bottom of the interface has a status bar with "CONNECTED (astfh234)" on the left and "161MB / 103.9MB" on the right.

To create new compartment, click on compartment tool. Two dashed vertical lines will appear that will let you to specify membranes surrounding this compartment.



To create a new membrane, click on one of the black lines so that they turn green. Select “add membrane”.

The screenshot shows the VCell 6.0 software interface for creating biological models. On the left, the 'BioModel3' tree view shows 'Reaction Diagram' selected. The main workspace displays a reaction diagram with two compartments:  $c_0$  (cytosol) and  $m_0$  (membrane). The membrane is defined by a green dashed line. A red arrow points from a yellow callout box to the dotted black lines within the membrane boundary. The bottom right of the callout box contains the following text:

To create a volumetric compartment within a membrane, click on the dotted black lines and select "add compartment".

At the bottom of the interface, there is a status bar with the text 'CONNECTED (astfh234)' and '178.4MB / 303.9MB'.

BIOMODEL: BioModel3 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel3  
Physiology  
Reaction Diagram (selected)  
Reactions (0)  
Structures (5)  
Species (0)  
Molecules (0)  
Observables (0)  
Applications (0)  
Parameters, Functions and Units  
Pathway

Reaction Diagram    Reactions    Structures    Species    Molecules    Observables

Reaction Diagram mode icon (highlighted with a red box and arrow)

Compartment and Membrane labels: c0, m0, c1, m1

To rearrange compartments and membranes, return to selection mode and drag them by their label.

Continue creating compartments and membranes until you have reached your desired model.

VCell DB BioModels.net Pathway Comm S  
BioModels MathModels Geometries

Search

Biological Models  
My BioModels (astfh234) (1)  
Shared BioModels (0)  
Public BioModels (512)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

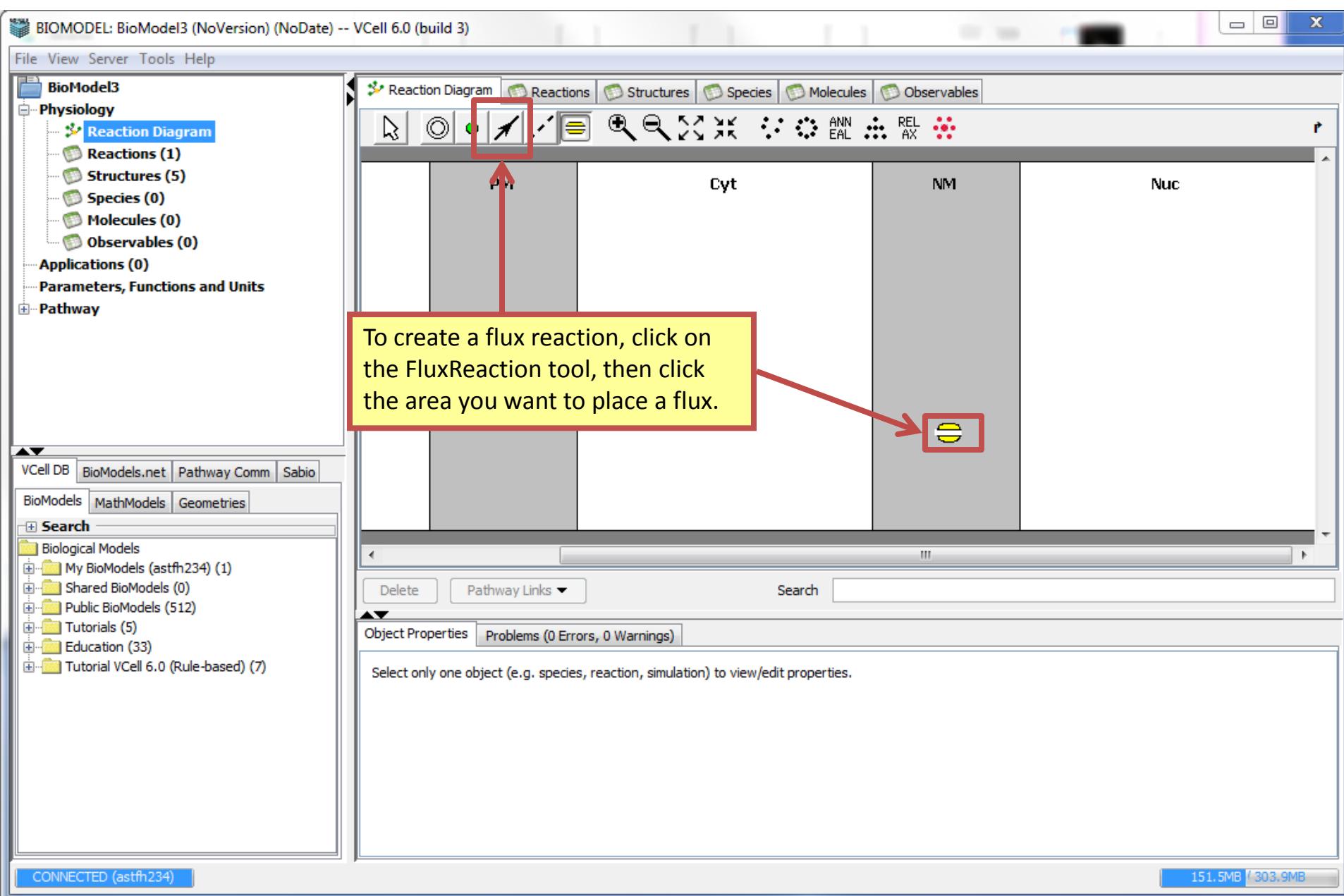
Structure Name: m1  
Size Variable Name: m1 [ $\mu\text{m}^2$ ]  
**Electrophysiology**  
Voltage Variable Name: Voltage\_m1 [mV]  
Positive (inside feature)  
Negative (outside feature)

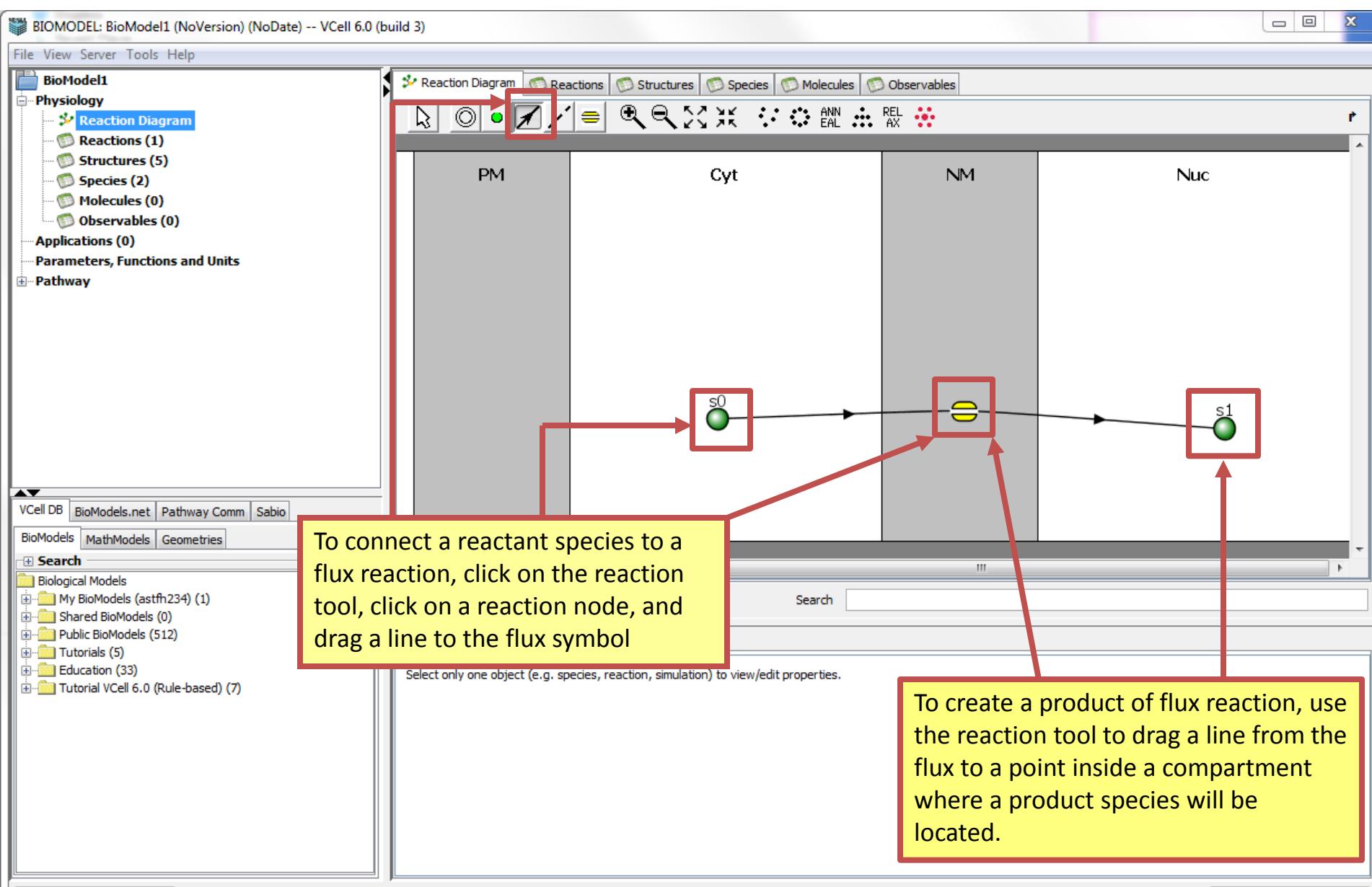
membrane voltage: "Voltage\_m1" = voltage(inside (+) compartment) - voltage(outside (-) compartment)  
inward currents: from compartment "outside (-) compartment" into compartment "inside (+) compartment"

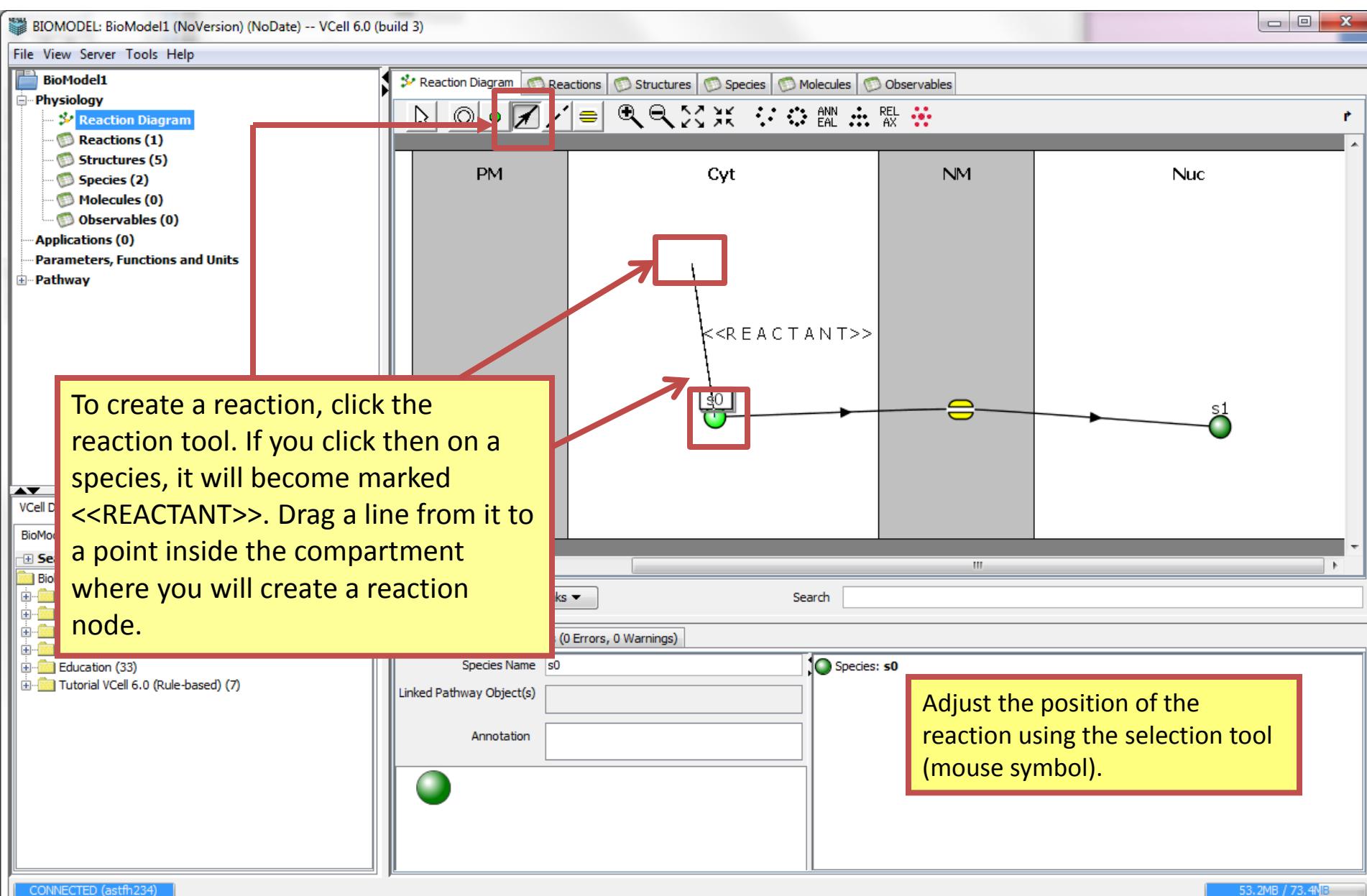
CONNECTED (astfh234) 107.1MB / 303.9MB

To name compartments and membranes, return to selection mode.

The screenshot shows the VCell 6.0 software interface. At the top, there is a menu bar with File, View, Server, Tools, and Help. Below the menu is a toolbar with various icons. On the left, there is a navigation pane with sections like BioModel3, Physiology, Applications (0), Parameters, Functions and Units, and Pathway. A red box highlights the 'Reaction Diagram' tab in the toolbar. Another red box highlights the 'EC' compartment label in the diagram area. A callout box with a red border contains the text: "To change the structure name you can double click on the label to change the name, or you can change the name under ‘Object Properties’". A red arrow points from this callout to the 'Object Properties' panel at the bottom. The 'Object Properties' panel has tabs for Object Properties and Problems (0 Errors, 0 Warnings). It displays fields for Structure Name (set to EC) and Size Variable Name (set to EC [ $\mu\text{m}^3$ ]). There is also an Annotation field which is empty. A red arrow points from the empty annotation field to another callout box with a red border containing the text: "To annotate compartments, type notes under ‘Object Properties’".







BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1  
Physiology  
Reaction Diagram (selected)  
Reactions (2)  
Structures (5)  
Species (2)  
Molecules (0)  
Observables (0)  
Applications (0)  
Parameters, Functions and Units  
Pathway

Reaction Diagram    Reactions    Structures    Species    Molecules    Observables

PM    Cyt    NM    Nuc

r0

s0

s1

Drop your mouse, and a reaction symbol will be created for you.

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

Biological Models  
My BioModels (astfh234) (1)  
Shared BioModels (0)  
Public BioModels (512)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Reaction Name r0  
Kinetic Type Mass Action [ $\mu\text{M}/\text{s}$ ] (recommended for stochastic application) Convert to [molecules. $\text{s}^{-1}$ ]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$K_f \cdot s_0$	$\mu\text{M} \cdot \text{s}^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	0.0	$\text{s}^{-1}$
Kr	reverse rate constant	<input type="checkbox"/>	0.0	$\mu\text{M} \cdot \text{s}^{-1}$
s0	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$

Annotation and Pathway Links

CONNECTED (astfh234) 54.7MB / 73.4MB

A screenshot of the VCell 6.0 software interface. The main window shows a reaction diagram with four compartments: PM, Cyt, NM, and Nuc. In the Cyt compartment, there is a reaction symbol (a rectangle with 'r0' inside) connected to a green species 's0'. An arrow from 's0' points to a green species 's1'. A red box highlights the reaction symbol 'r0'. A red arrow points from a text box containing the instruction 'Drop your mouse, and a reaction symbol will be created for you.' to the highlighted reaction symbol. The bottom half of the screen shows the 'Object Properties' panel for reaction 'r0', displaying its kinetic type as 'Mass Action [ $\mu\text{M}/\text{s}$ ] (recommended for stochastic application)' and its expression as ' $K_f \cdot s_0$ '. The 's0' species is listed as a variable with a concentration of 0.0. The 's1' species is also present in the list. The bottom status bar indicates 'CONNECTED (astfh234)' and memory usage of '54.7MB / 73.4MB'.

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1  
Physiology  
Reaction Diagram (selected)  
Reactions (2)  
Structures (5)  
Species (2)  
Molecules (0)  
Observables (0)  
Applications (0)  
Parameters, Functions and Units  
Pathway

To create a product species, use the reaction tool to drag from the reaction symbol to a point inside the compartment where your product species will be located.

Reaction Diagram | Reactions | Structures | Species | Molecules | Observables

PM Cyt NM Nuc

r0  
<<PRODUCT>>  
s0  
s1

BioModels | MathModels | Geometries

Search  
Biological Models  
My BioModels (astfh234) (1)  
Shared BioModels (0)  
Public BioModels (512)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Object Properties | Problems (0 Errors, 0 Warnings)

Reaction Name: r0  
Kinetic Type: Mass Action [ $\mu\text{M}/\text{s}$ ] (recommended for stochastic application) | Convert to [molecules. $\text{s}^{-1}$ ]  
Name Description Global Expression Units  
J reaction rate   $K_f \cdot s_0$   $\mu\text{M}\cdot\text{s}^{-1}$   
Kf forward rate constant  0.0  $\text{s}^{-1}$   
Kr reverse rate constant  0.0  $\mu\text{M}\cdot\text{s}^{-1}$   
s0 Species Concentration  Variable  $\mu\text{M}$

Annotation and Pathway Links

CONNECTED (astfh234) 62.2MB / 73.4MB

The screenshot shows the VCell 6.0 software interface for a biological model named 'BioModel1'. The main window displays a reaction diagram with four compartments: PM, Cyt, NM, and Nuc. A reaction 'r0' is shown with a green arrow pointing from a species 's0' in the Cyt compartment to a red box labeled '<<PRODUCT>>'. Another green arrow points from 's0' to a species 's1' in the Nuc compartment. The left sidebar shows the model structure with 'Reaction Diagram' selected. A yellow callout box contains the text: 'To create a product species, use the reaction tool to drag from the reaction symbol to a point inside the compartment where your product species will be located.' A red box highlights the reaction tool icon in the toolbar above the reaction diagram. The bottom right corner shows disk usage: '62.2MB / 73.4MB'.

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

Physiology

- Reaction Diagram (selected)
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (0)

Parameters, Functions and Units

Pathway

Reaction Diagram

Reactions Structures Species

PM Cyt NM Nuc

s2 s3  
s0 s1

To rearrange the position of species and reactions, click on selection mode and click on a species or reaction and drag the item to the desired location within a compartment.

Continue creating reactions and species until you have reached your desired model.

Search

Biological Models

- My BioModels (astfh234) (1)
- Shared BioModels (0)
- Public BioModels (512)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

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

To remove a species or reaction from your model, click on the species or reaction and click on either the "Delete" button or the backspace button on your keyboard.

CONNECTED (astfh234) 60.2MB / 73.4MB

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1  
Physiology  
Reaction Diagram (selected)  
Reactions (2)  
Structures (5)  
Species (4)  
Molecules (0)  
Observables (0)  
Applications (0)  
Parameters, Functions and Units  
Pathway

Reaction Diagram    Reactions    Structures    Species    Molecules    Observables

PM    Cyt    NM    Nuc

C\_Cyt    Ran\_Cyt    RanG\_Cyt    RanC\_Nuc

VCell DB BioModels.net Pathway Comm Sabio  
BioModels MathModels Geometries  
Search  
Biological Models  
My BioModels (astfh234) (1)  
Shared BioModels (0)  
Public BioModels (512)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Object Properties    Problems (0 Errors, 0 Warnings)  
Species Name: RanC\_Nuc  
Linked Pathway Object(s)  
Annotation

To rename species, click on a species and under "Object Properties" > "Species Name", type the desired name which is case-sensitive.

The screenshot shows the VCell 6.0 interface for a BioModel1. The left sidebar lists model components like Physiology, Reactions, and Species. The main area displays a reaction diagram with compartments PM, Cyt, NM, and Nuc. A cycle of species (C\_Cyt, Ran\_Cyt, RanG\_Cyt, RanC\_Nuc) is shown moving between Cyt and Nuc. A red box highlights the 'RanC\_Nuc' species in the Nuc compartment. A red arrow points from this highlighted species to the 'Species Name' field in the 'Object Properties' panel at the bottom. Another red box surrounds the 'Species Name' field, and a yellow callout box with black text provides instructions on how to rename it.

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

- Physiology
  - Reaction Diagram**
  - Reactions (2)
  - Structures (5)
  - Species (4)
  - Molecules (0)
  - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
  - My BioModels (astfh234) (1)
  - Shared BioModels (0)
  - Public BioModels (512)
  - Tutorials (5)
  - Education (33)
  - Tutorial VCell 6.0 (Rule-based) (7)

CONNECTED (astfh234) 61.5MB / 73.4MB

Reaction Diagram Reactions Structures Species Molecules Observables

To change the reaction rate of a flux reaction, click on the flux and under "Object Properties", in the "reaction rate" row and "Expression" column, type in the desired reaction rate.

Object Properties Problems (0 Errors, 0 Warnings)

Name	Description	Global	Expression	Units
J	reaction rate	<input checked="" type="checkbox"/>	Kflux*(RanC_Cyt-RanC_Nuc)	$\mu\text{M}\cdot\mu\text{m}\cdot\text{s}^{-1}$
I	inward current density	<input type="checkbox"/>	0.0	$\text{pA}\cdot\mu\text{m}^{-2}$
netValence	net charge valence	<input type="checkbox"/>	1.0	1
Kflux	user defined	<input type="checkbox"/>	0.0	$\mu\text{m}\cdot\text{s}^{-1}$

Annotation and Pathway Links

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

- Physiology
  - Reaction Diagram**
  - Reactions (2)
  - Structures (5)
  - Species (4)
  - Molecules (0)
  - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
  - My BioModels (astfh234) (1)
  - Shared BioModels (0)
  - Public BioModels (512)
  - Tutorials (5)
  - Education (33)
  - Tutorial VCell 6.0 (Rule-based) (7)

Reaction Diagram Reactions Structures Species Molecules Observables

To change the Kflux, click on the flux and under "Object Properties", in the "Kflux" row and "Expression" column, type in the desired value.

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$Kflux \cdot (RanC\_Cyt - RanC\_Nuc)$	$\mu\text{M} \cdot \mu\text{s}^{-1}$
I	inward current density	<input type="checkbox"/>	0.0	$\text{pA} \cdot \mu\text{m}^2$
netValence	net charge valence	<input type="checkbox"/>	1.0	1
Kflux	user defined	<input checked="" type="checkbox"/>	2.0	$\mu\text{M} \cdot \mu\text{s}^{-1}$
RanC_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
RanC_Nuc	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$

Annotation and Pathway Links

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

- Physiology
  - Reaction Diagram**
  - Reactions (2)
  - Structures (5)
  - Species (4)
  - Molecules (0)
  - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

Reaction Diagram

To change the forward rate constant of a reaction, click on a reaction and under “Object Properties”, in the “forward rate constant” row and “Expression” column, type in the desired value.

Object Prop

Reaction Name	r0			
Kinetic Type	Mass Action [ $\mu\text{M}/\text{s}$ ] (recommended for stochastic application)	Convert to [ $\text{molecules} \cdot \text{s}^{-1}$ ]		
Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot \text{RanC\_Cyt} - K_r \cdot \text{C\_Cyt} \cdot \text{Ran\_Cyt})$	$\mu\text{M} \cdot \text{s}^{-1}$
KF	forward rate constant	<input checked="" type="checkbox"/>	1.0	$\text{s}^{-1}$
Kr	reverse rate constant	<input type="checkbox"/>	0.0	$\text{s}^{-1} \cdot \mu\text{M}^{-1}$
RanC_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
C_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
Ran_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$

Annotation and Pathway Links

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

- Physiology
  - Reaction Diagram**
  - Reactions (2)
  - Structures (5)
  - Species (4)
  - Molecules (0)
  - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

Reaction Diagram

PM Cyt NM Nuc

C\_Cyt Ran\_Cyt

RanC\_Cyt RanC\_Nuc

To change the reverse rate constant of a reaction, click on a reaction and under "Object Properties", in the "reverse rate constant" row and "Expression" column, type in the desired value.

Object Properties

Reaction Name	Product	Kinetic Type	Convert to [molecules.s <sup>-1</sup> ]	
r0		Mass Action [ $\mu\text{M}/\text{s}$ ] (recommended for stochastic application)		
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot RanC\_Cyt - K_r \cdot C\_Cyt \cdot Ran\_Cyt)$	$\mu\text{M} \cdot \text{s}^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	1.0	$\text{s}^{-1}$
Kr	reverse rate constant	<input type="checkbox"/>	1000.0	$\text{s}^{-1} \cdot \mu\text{M}^{-1}$
RanC_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
C_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
Ran_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$

Annotation and Pathway Links

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

Physiology

- Reaction Diagram (selected)
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (0)

Parameters, Functions and Units

Pathway

Reactions Structures Species Molecules Observables

PM Cyt NM Nuc

s2 → s0 → s1

s0 → s3

Use the “Reactions”, “Structures”, “Species”, “Molecules” and “Observables” tabs to look up specific details of the physiology, which are useful when working with large and complicated models.

Search

Biological Models

- My BioModels (astfh234) (1)
- Shared BioModels (0)
- Public BioModels (512)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Delete Pathway Links Search

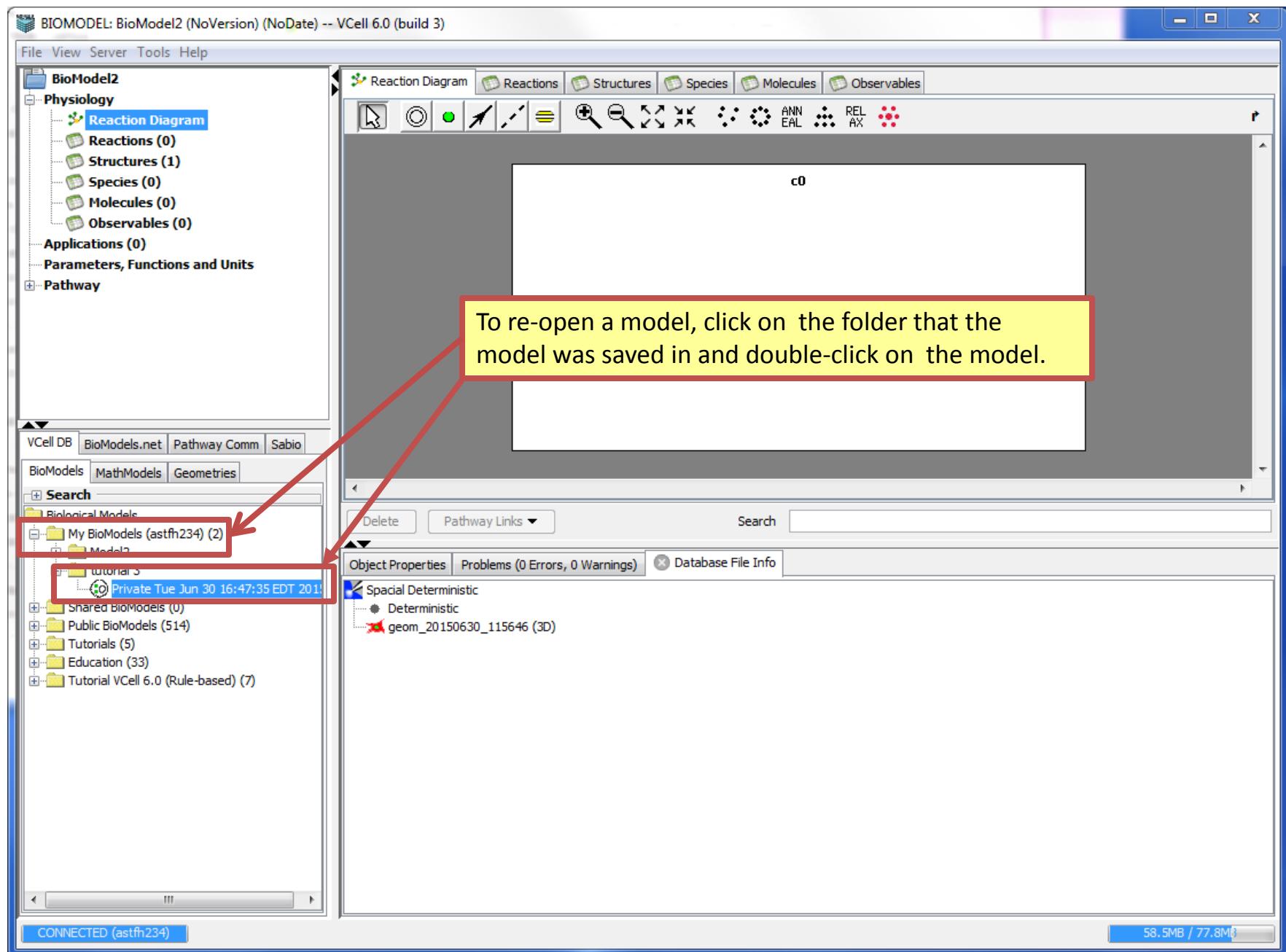
Object Properties Problems (0 Errors, 0 Warnings)

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

The physiology of your model is now complete.

CONNECTED (astfh234)

60.2MB / 73.4MB



To create a new deterministic model, click "Applications" > "Add New" > "Deterministic". To rename the application, double click on the label and type in a name.

BIOMODEL: Tutorial (Mon Jun 29 09:35:44 EDT 2015) -- VCell 5.3 (build 4)

File View Server Tools Help

Tutorial

Physiology

Reaction Diagram

Reactions (2)

Structures (5)

Species (4)

**Applications (0)**

Parameters and functions

Pathway

VCell DB BioModels.net Path...

BioModels MathModels Geometries

+ Search

Biological Models

My BioModels (tanyamiller1221)

Tutorial

BioModel2

Private Thu Jun 25 16:03:20 2015

Tutorial\_MultiApp

Shared BioModels (0)

Public BioModels (519)

Tutorials (5)

Education (33)

Add New ▾

Delete More Copy Actions Search

Object Properties Problems (0 Errors, 0 Warnings) Database File Info

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

CONNECTED (tanyamiller1221)

356.5MB / 514.9MB

VCell - The Virtual Cell

Health Center Web  Directory  
 Go

INTRO **USER GUIDE** PUBLISHED MODELS PUBLICATIONS EDUCATIONAL RESOURCES

## VCell User Guides

### User Guide

Release version now has online help from within the VCell interface. From the Help top menu select "Help" to open the guide.

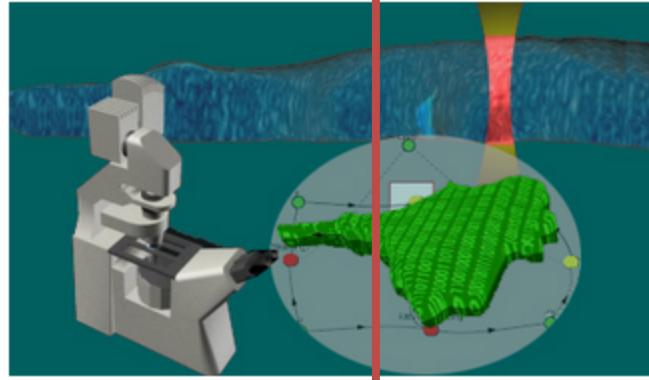
[Click here](#) for a Quick Start guide for Release.

[html version of VCell help program](#) (also available from Help menu of VCell software)

### Tutorials

The tutorials have been provided to work in conjunction with the users guide for the release version of Virtual Cell. The tutorials lead the user step by step through the construction of the BioModel, Application and Simulation. There are public versions of the BioModels, Applications and Simulations available in the Tutorial folder. Go to File Open BioModel Model Neighborhood Tutorial folder.

Tutorial Guides (pdf)
<a href="#">simple FRAP</a>
<a href="#">FRAP with binding</a>
<a href="#">PH-GFP Translocation</a>
<a href="#">Multiple Application of a Nuclear Transport Biomodel</a>
<a href="#">Using Pathway Commons</a>
Video Tutorials
<a href="#">VCell Education YouTube Channel</a>
<a href="#">VCell MultiApp Tutorial: Part 1. Creating Physiology</a>
<a href="#">VCell MultiApp Tutorial: Part 2. Creating Geometry (3D images for tutorial)</a>
<a href="#">VCell MultiApp Tutorial: Part 3. Deterministic Spatial Simulation</a>



Share your published VCell Models

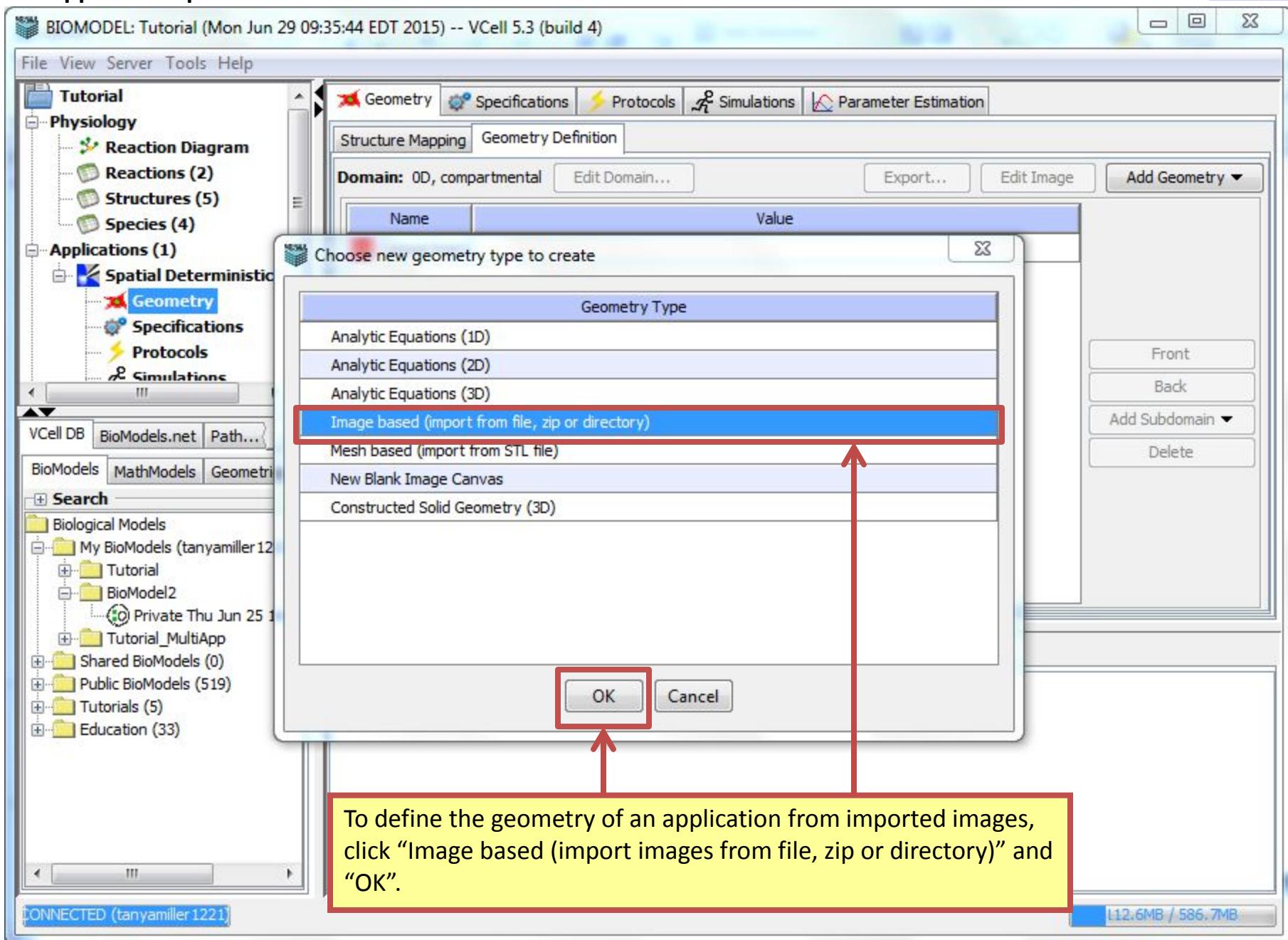
Modeling/Database Links

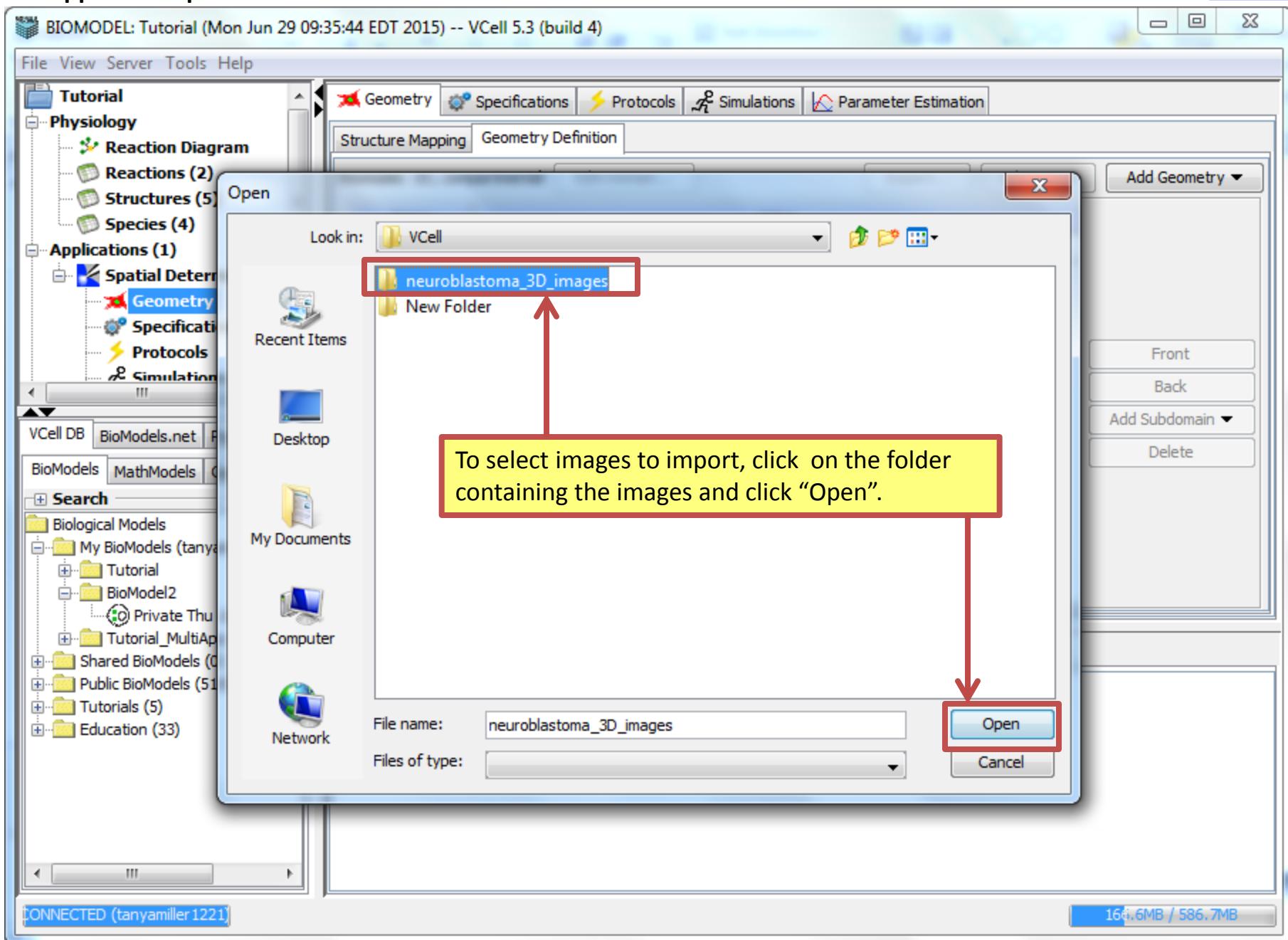
Software Support  
[vcell\\_support@uhc.edu](mailto:vcell_support@uhc.edu)  
VCell Discussion Forum

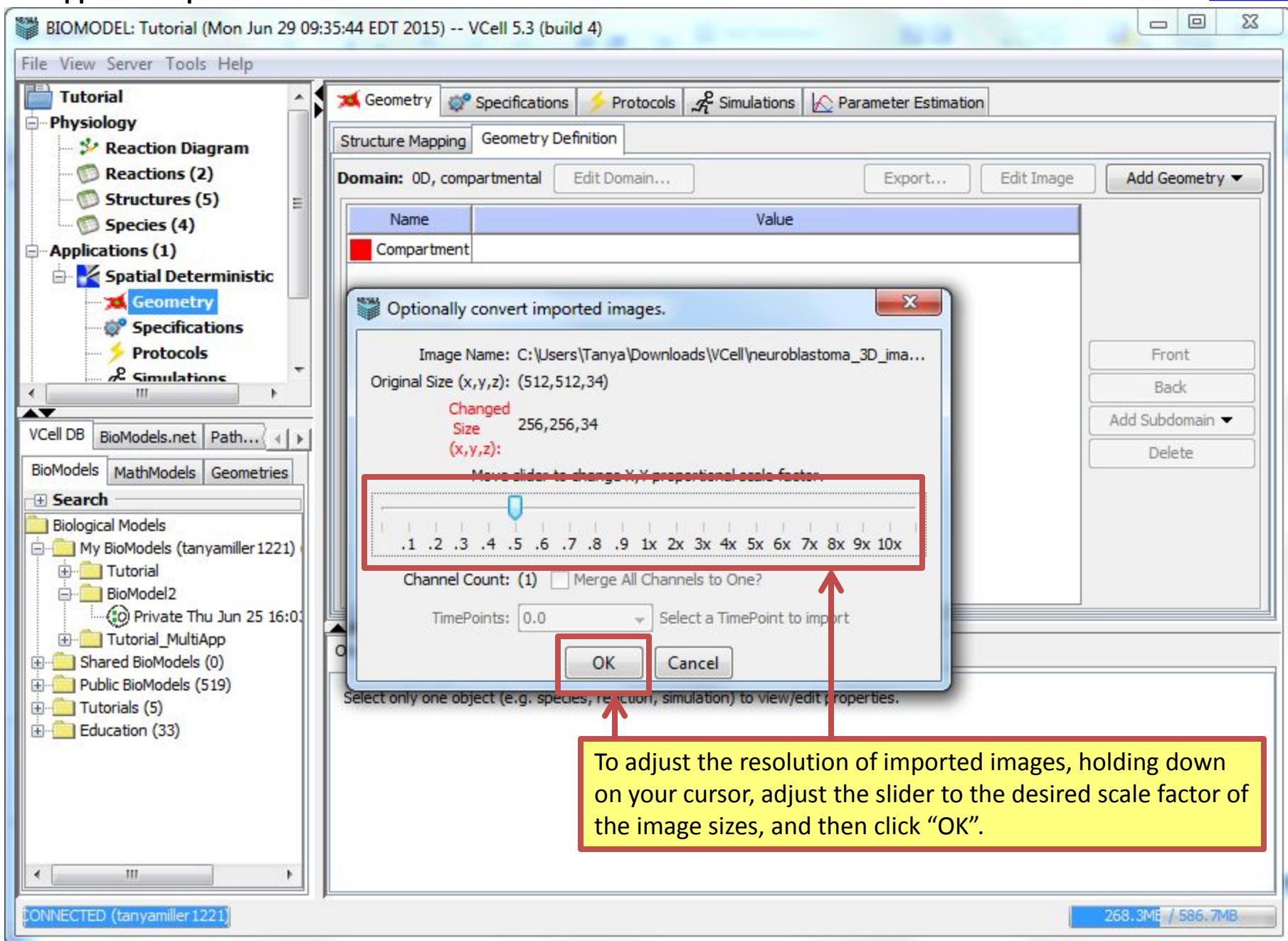
In this tutorial, example 3D neuroblastoma images will be used. These images are located on the VCell website ([vcell.org](http://vcell.org)) under “User Guide” > “Video Tutorials”. Click on “3D images for tutorial”, which will download the necessary 3D images, and then save and extract the files.

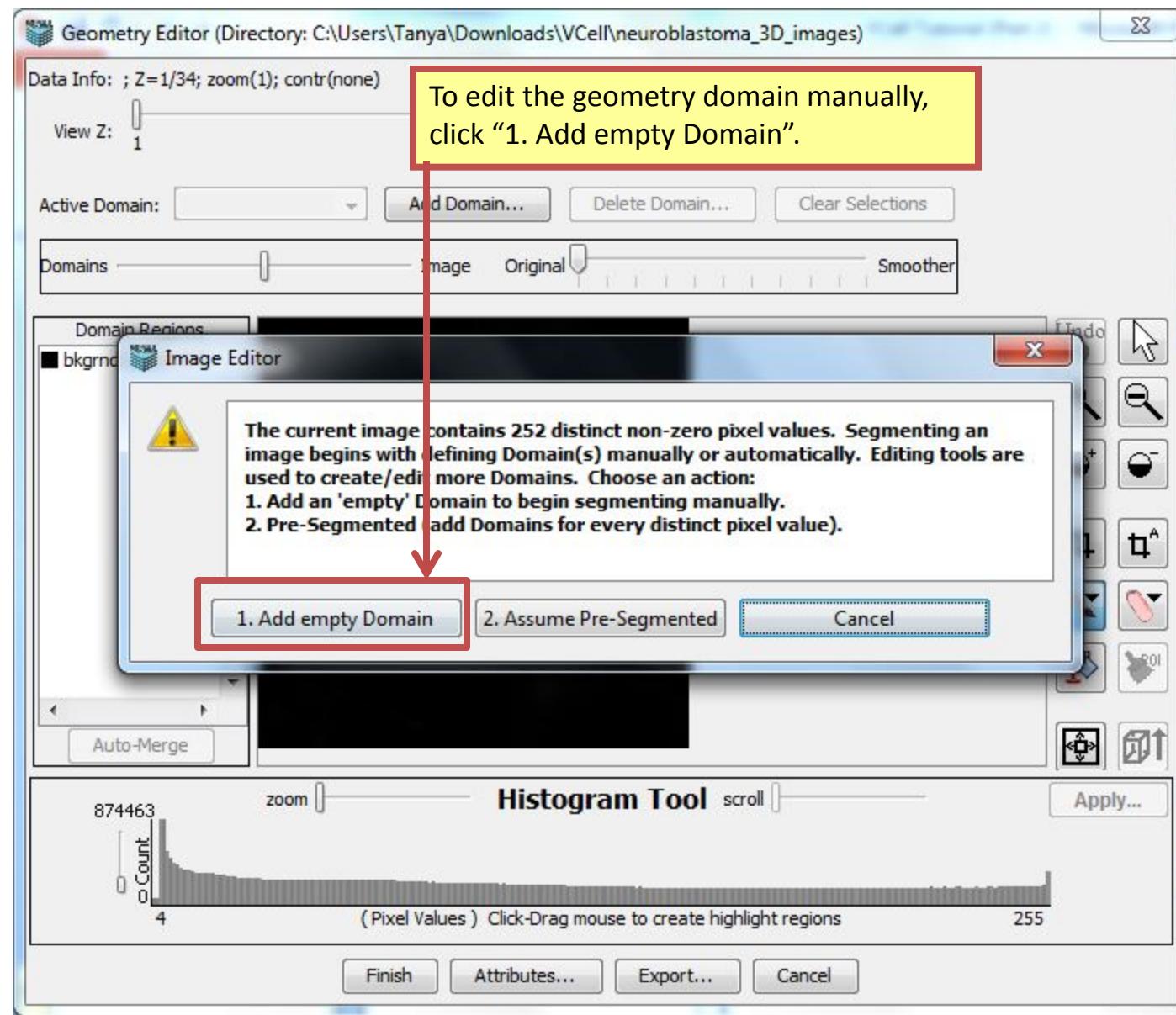
The screenshot shows the VCell 5.3 software interface. The title bar reads "BIOMODEL: Tutorial (Mon Jun 29 09:35:44 EDT 2015) -- VCell 5.3 (build 4)". The menu bar includes File, View, Server, Tools, and Help. On the left, a tree view shows "Tutorial", "Physiology" (with "Reaction Diagram", "Reactions (2)", "Structures (5)", "Species (4)" under it), and "Applications (1)" (with "Spatial Deterministic" containing "Geometry", "Specifications", "Protocols", and "Simulations"). Below this are tabs for "VCell DB", "BioModels.net", and "Path...". A "Search" panel lists "Biological Models" with categories like "My BioModels (tanyamiller1221)" containing "Tutorial" and "BioModel2", and other sections for "Shared BioModels (0)", "Public BioModels (519)", "Tutorials (5)", and "Education (33)". The main workspace has tabs for "Geometry", "Specifications", "Protocols", "Simulations", and "Parameter Estimation". The "Geometry" tab is active, showing "Structure Mapping" and "Geometry Definition". The "Geometry Definition" tab is selected, with a red box highlighting it. Below it, the text "Domain: 0D, compartmental" and "Edit Domain..." are visible. To the right, there's an "Export..." button, an "Edit Image..." button, and a "Add Geometry" dropdown menu with a red arrow pointing to it. A table titled "Geometry Definition" shows one row: "Compartments" with "Name" and "Value" columns. On the far right, buttons for "Front", "Back", "Add Subdomain", and "Delete" are available. At the bottom, tabs for "Object Properties", "Problems (0 Errors, 0 Warnings)", and "Database File Info" are shown, along with a message: "Select only one object (e.g. species, reaction, simulation) to view/edit properties." The status bar at the bottom indicates "CONNECTED (tanyamiller1221)" and "429.2MB / 514.9MB".

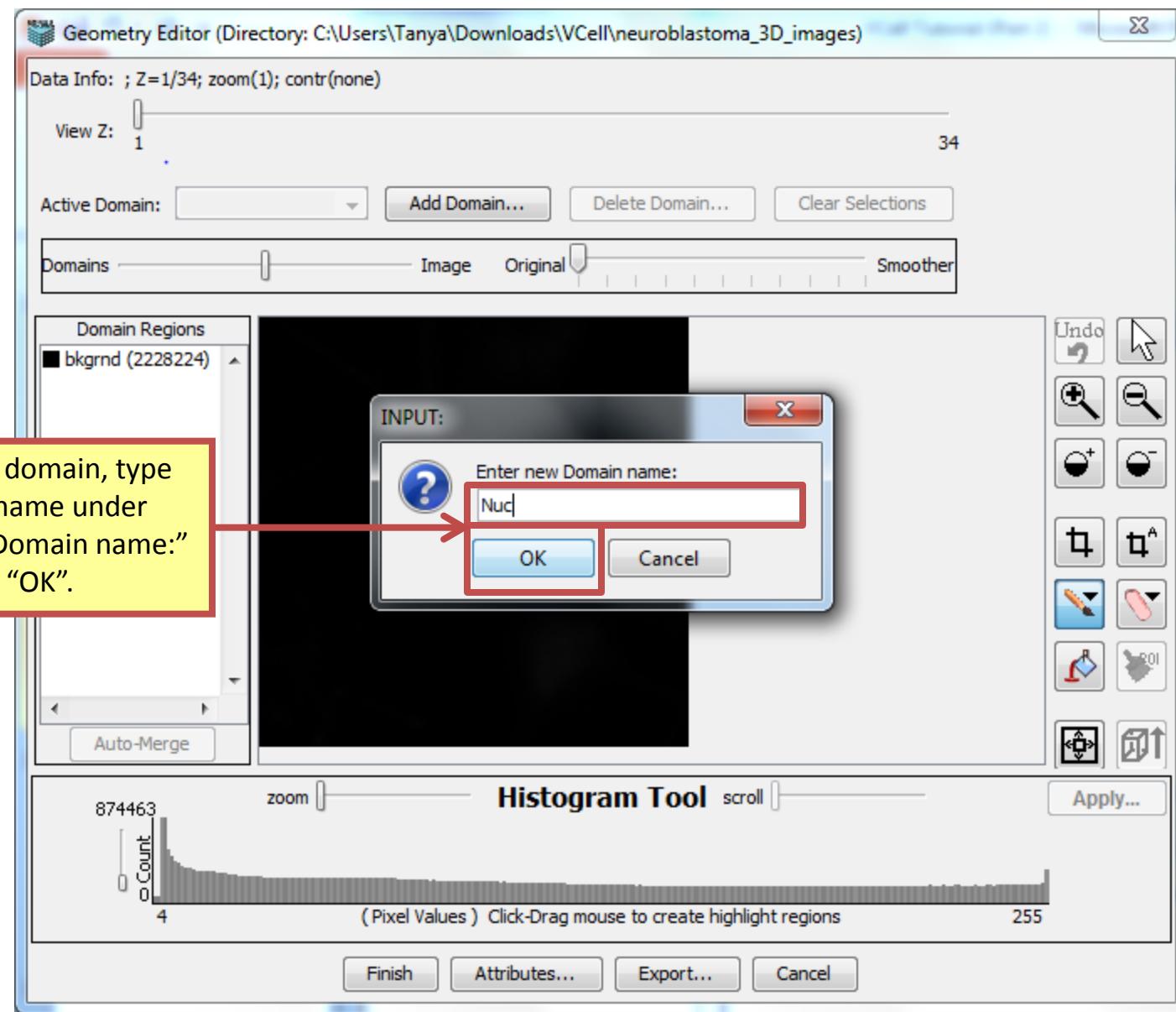
To define the geometry of an application, click “Geometry” > “Geometry Definition” > “Add Geometry” > “New”.

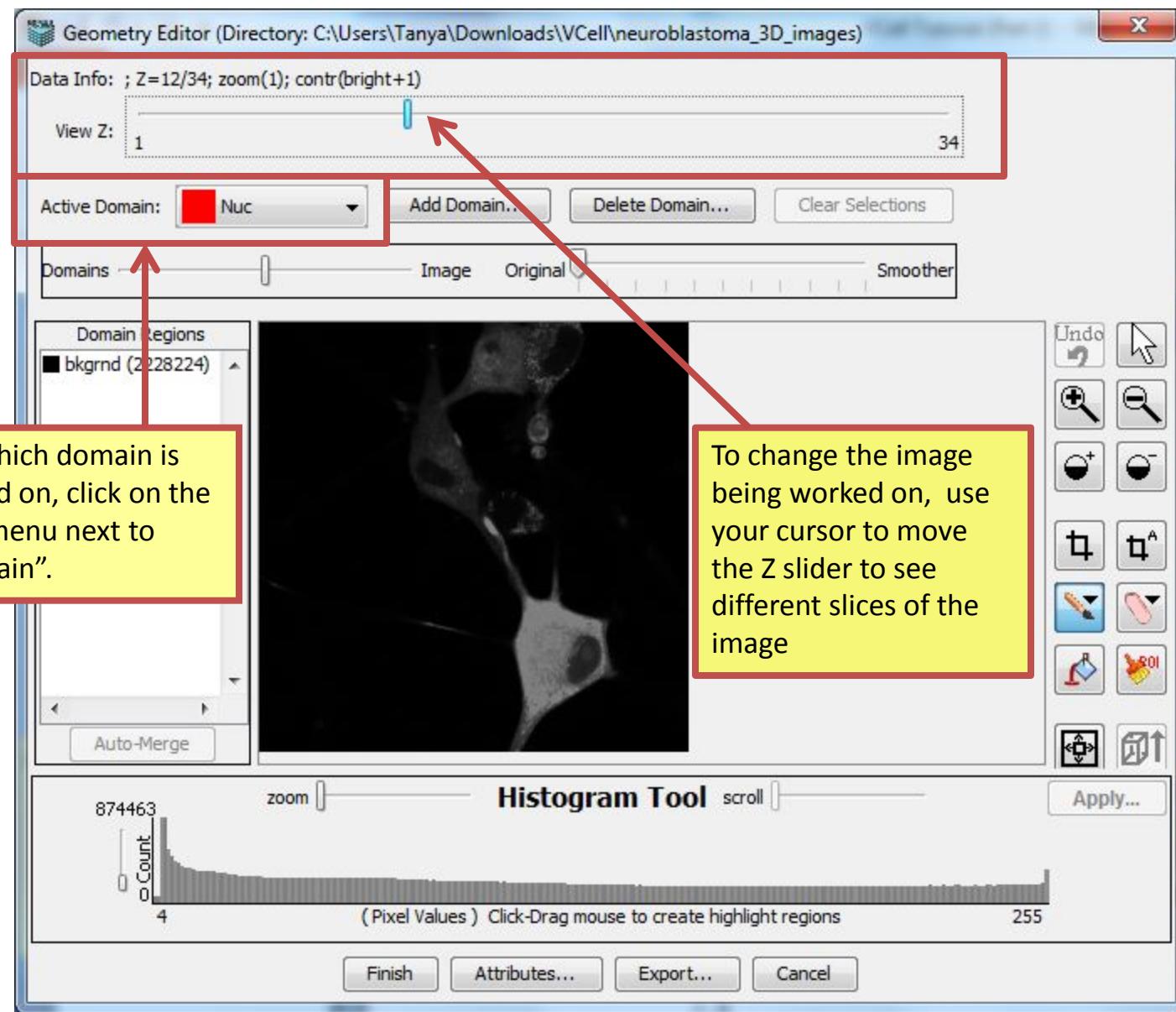


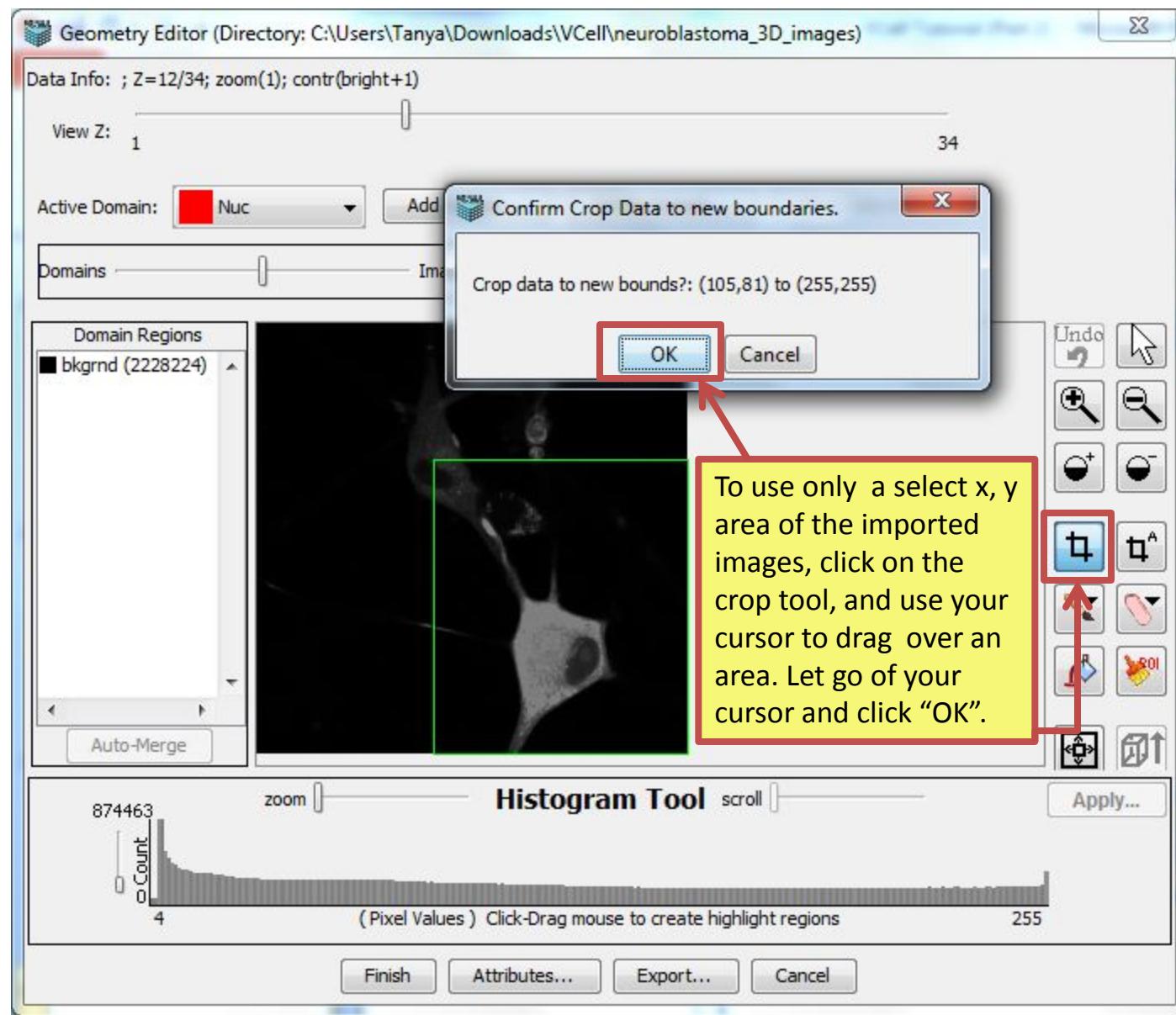


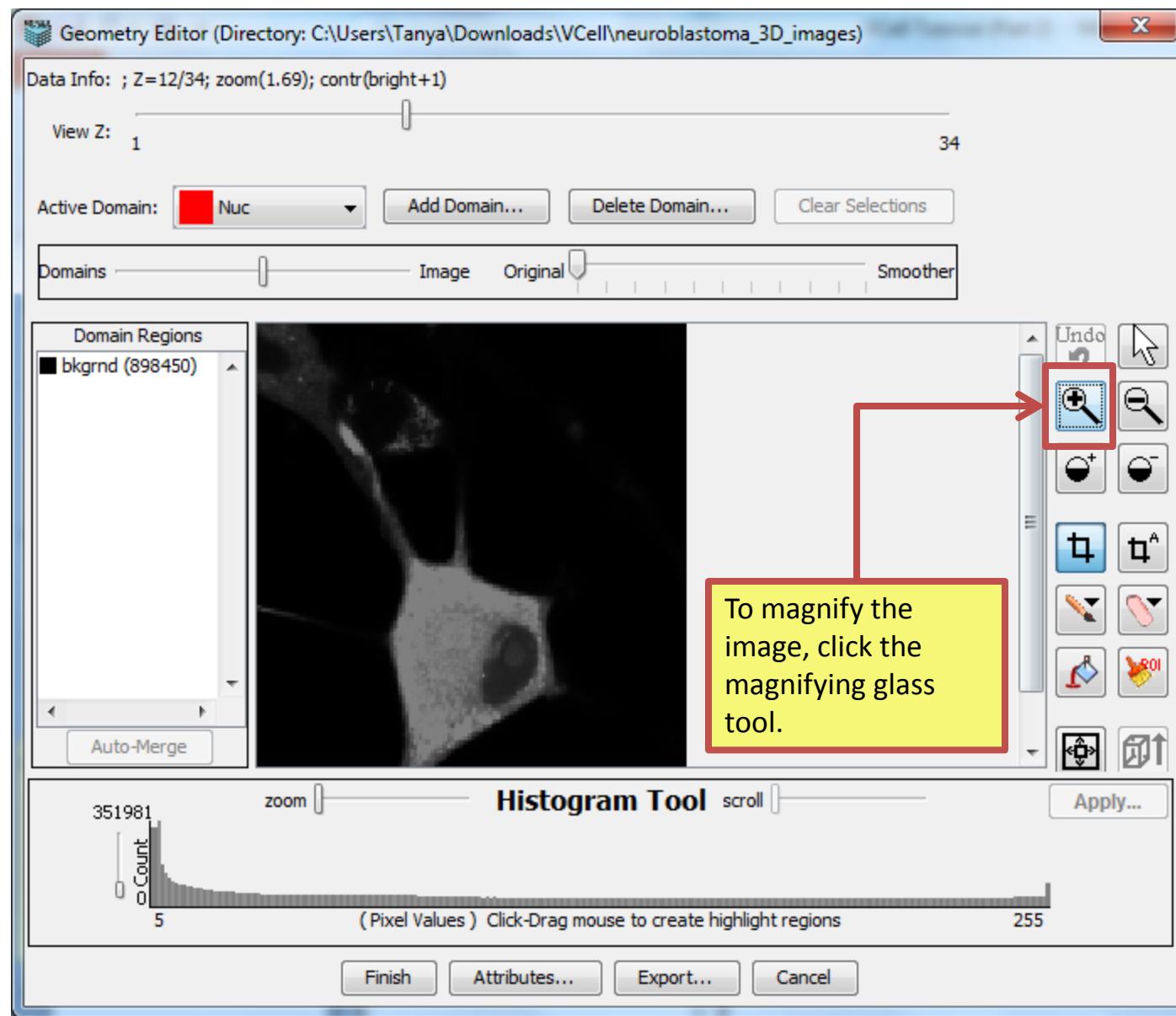


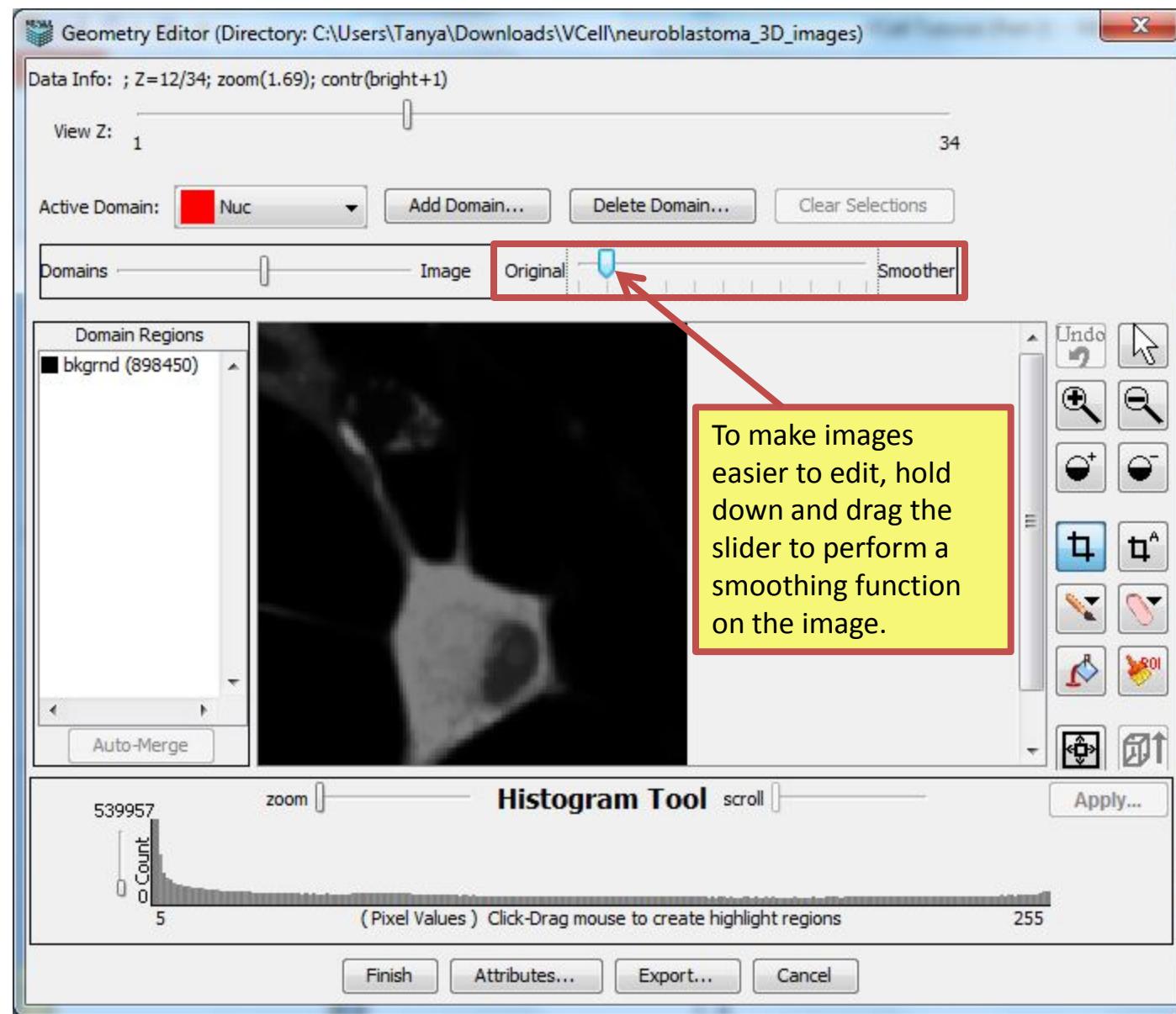


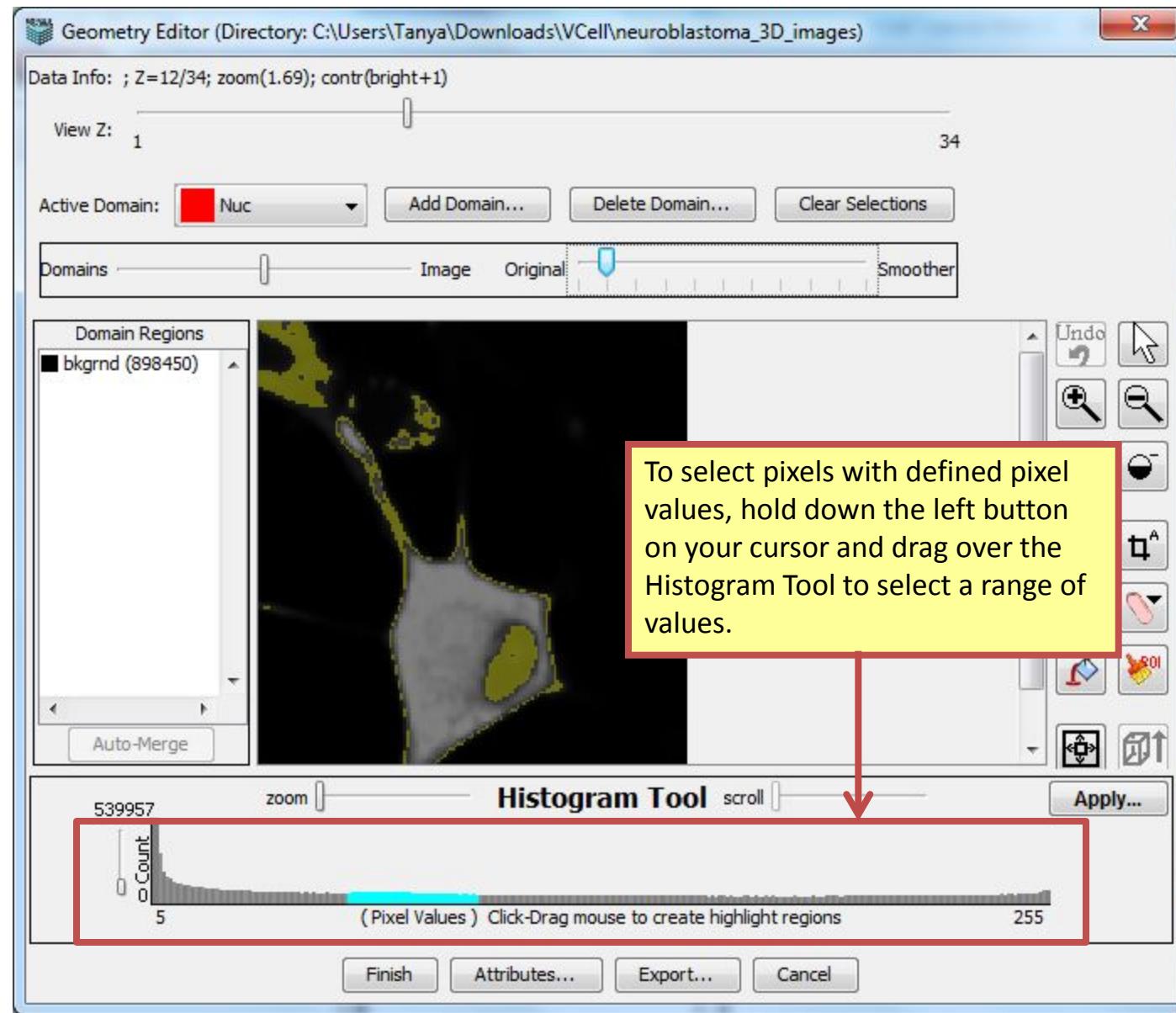


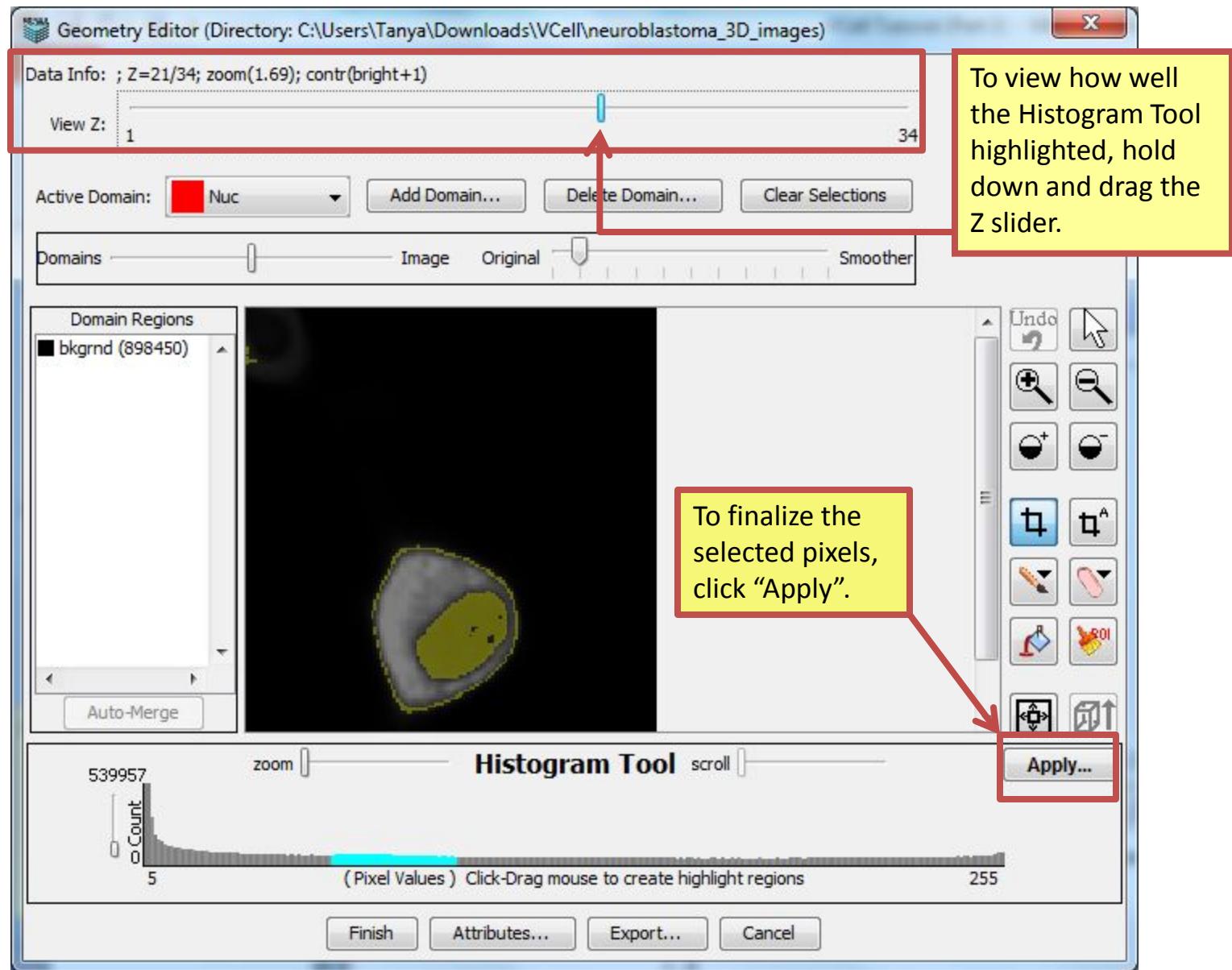


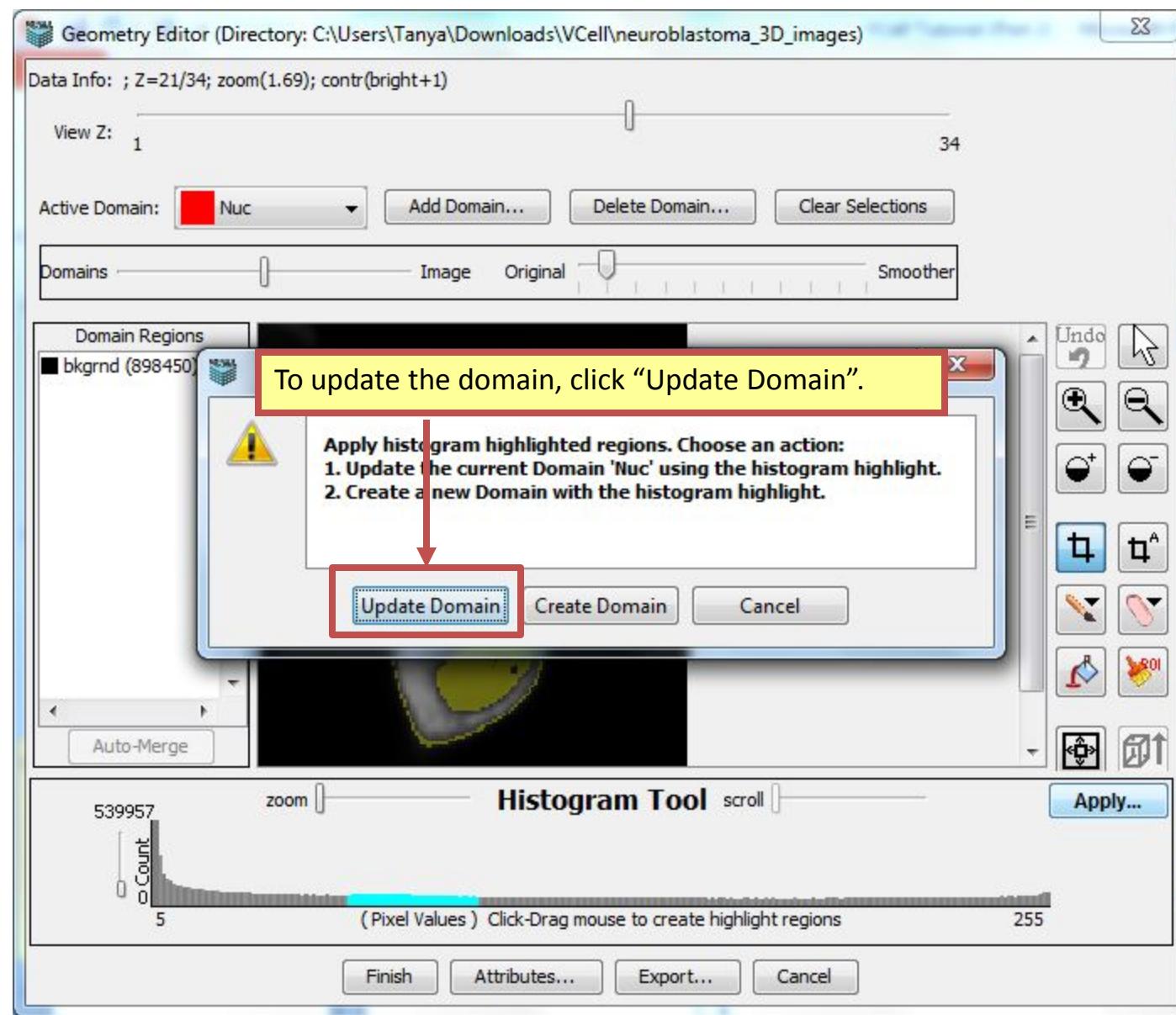


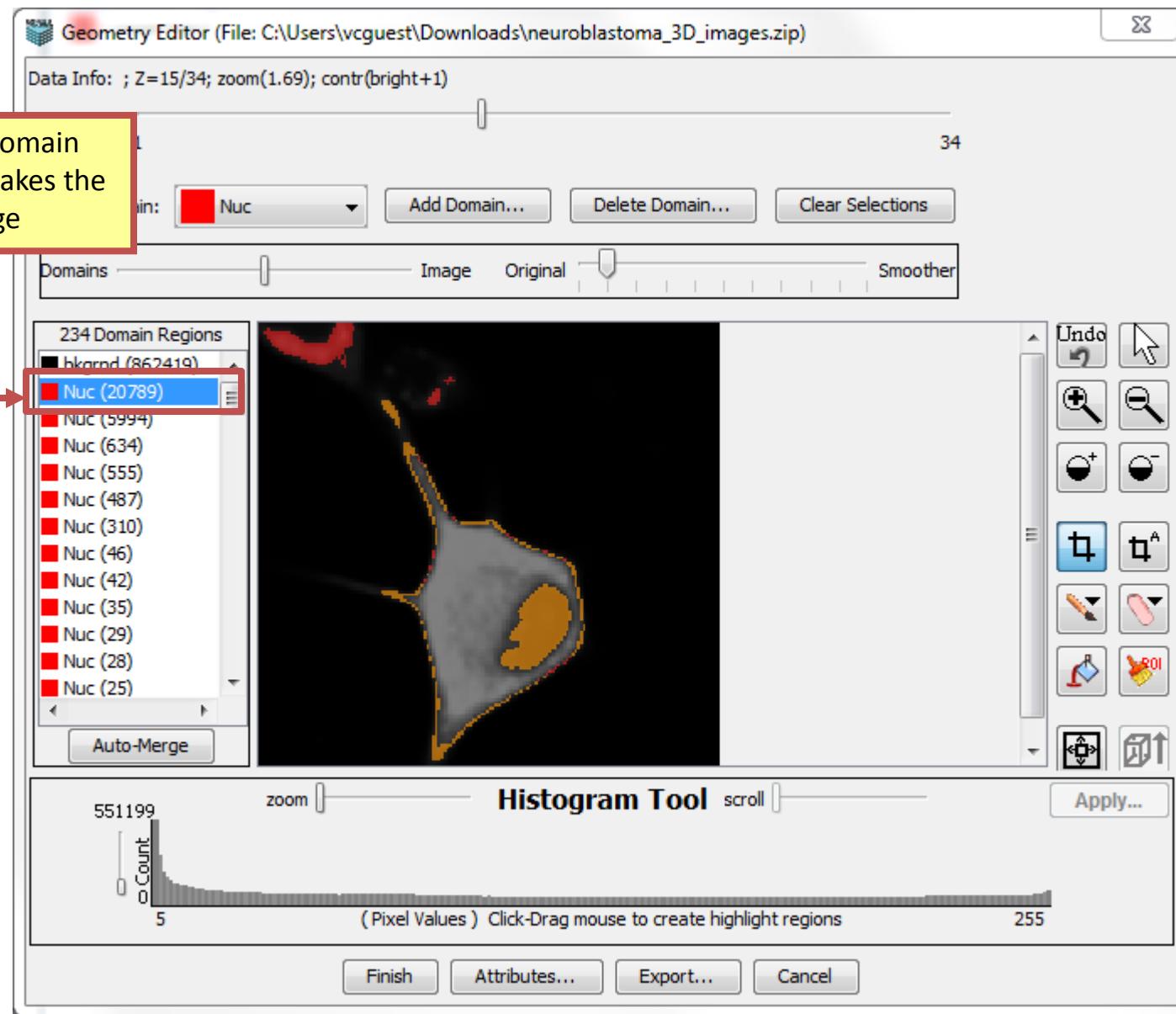


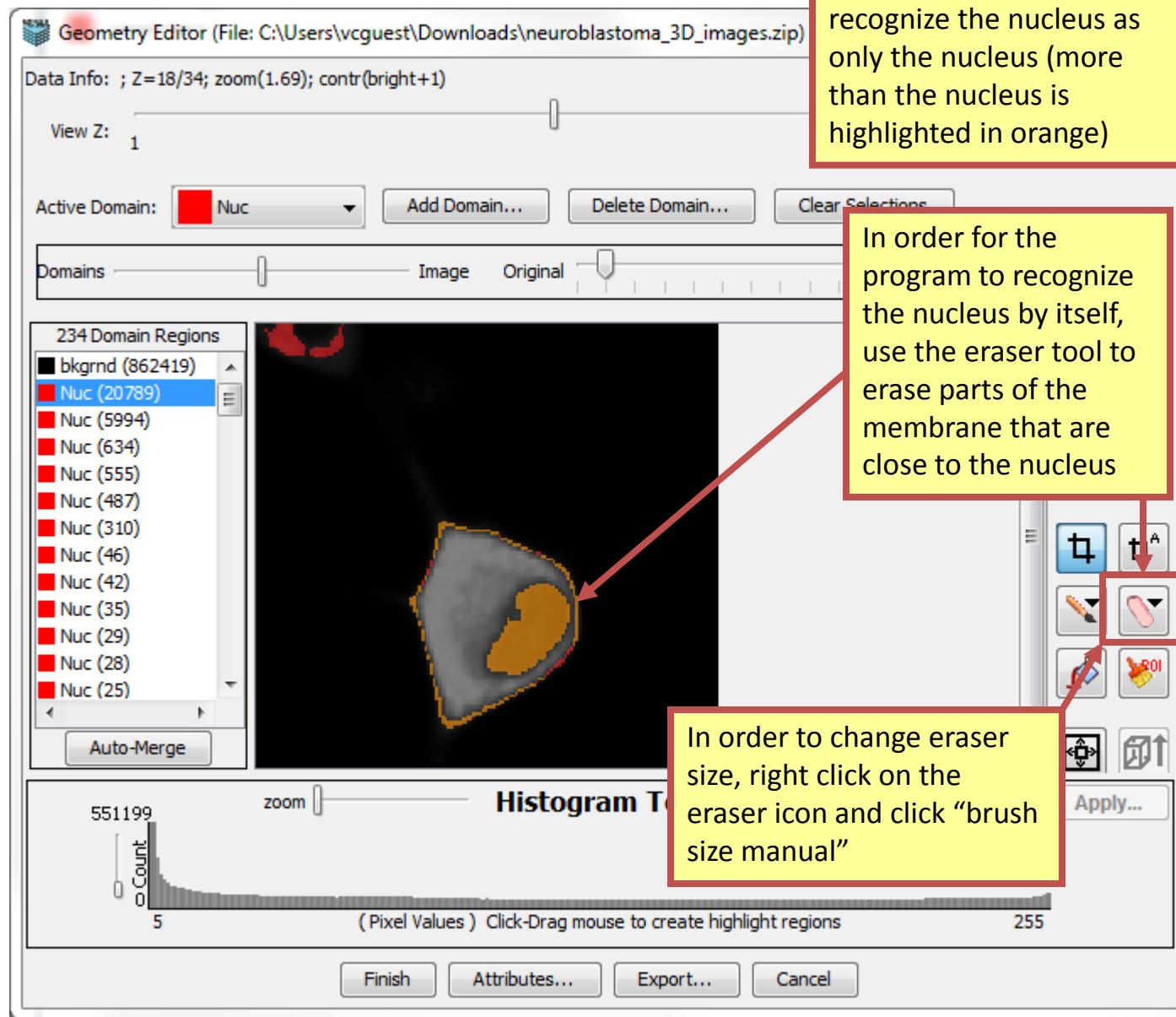


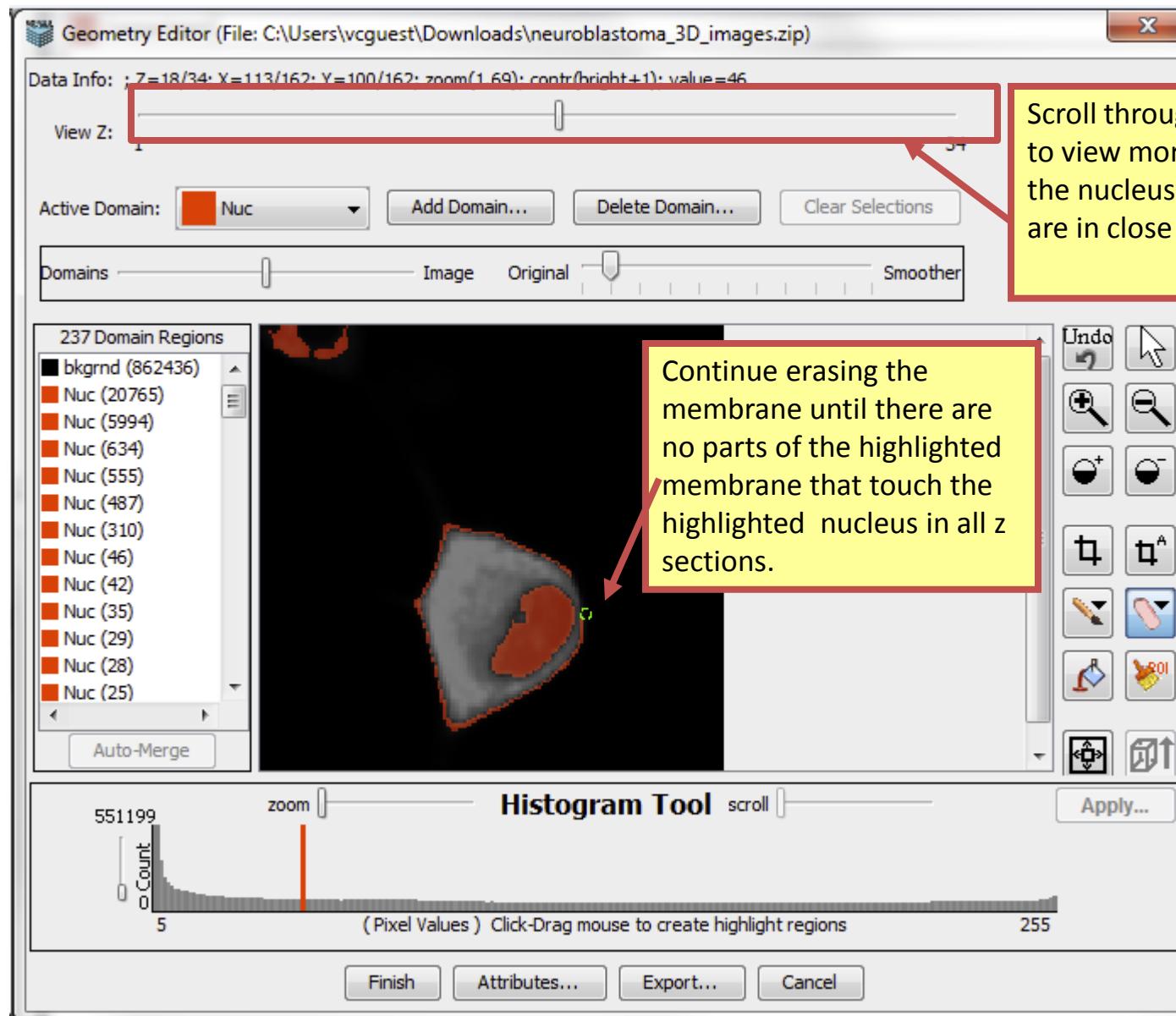






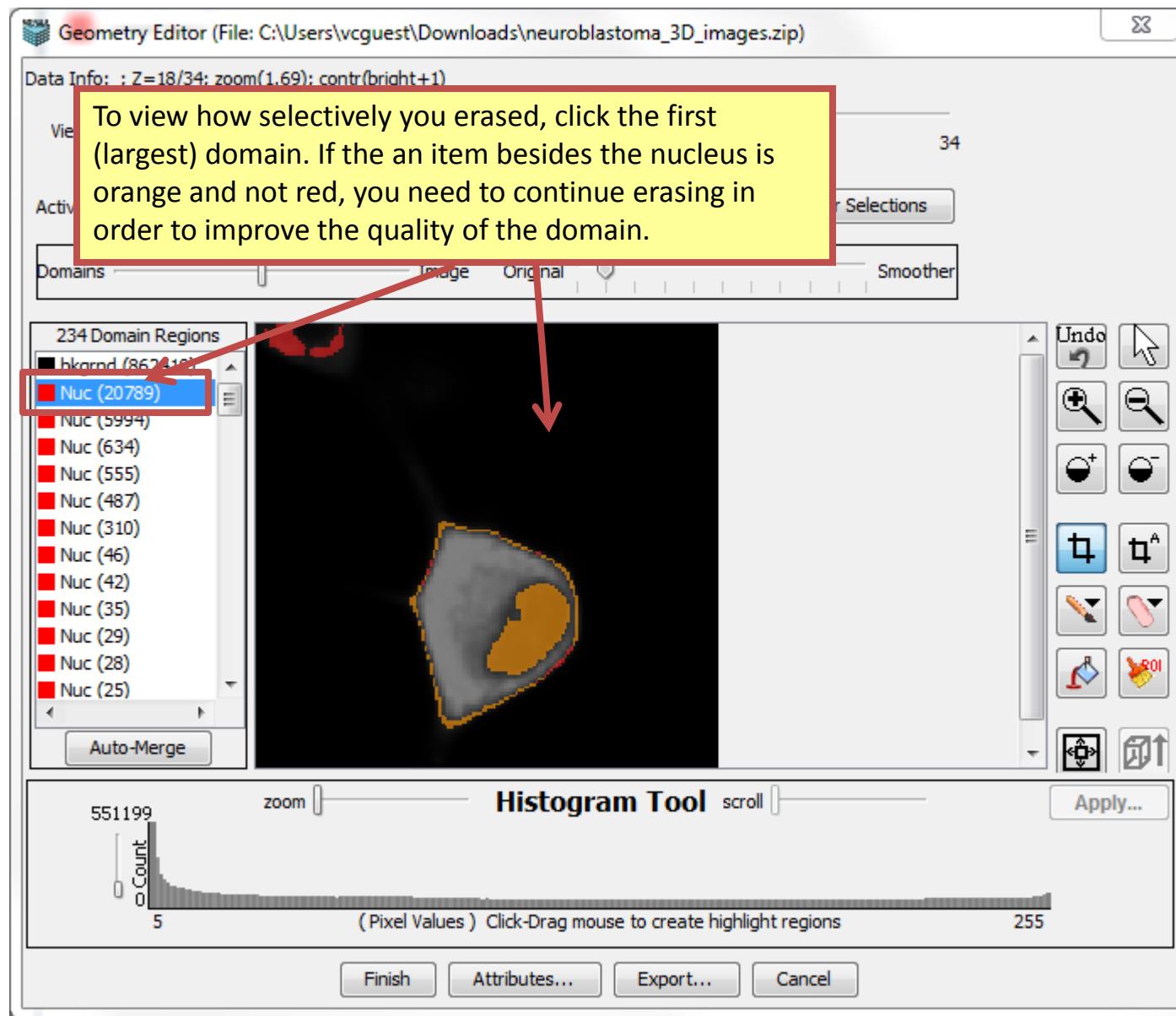


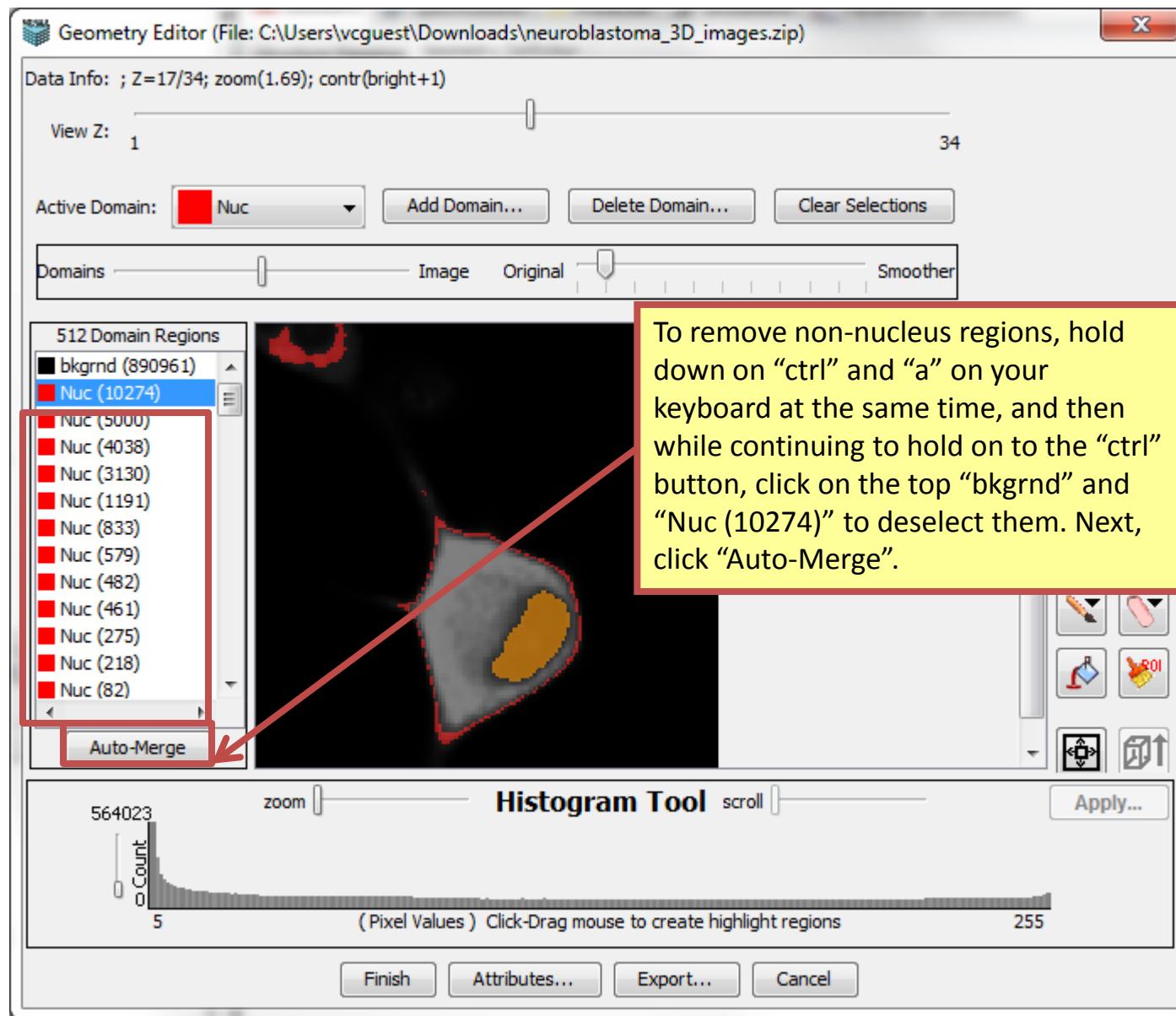


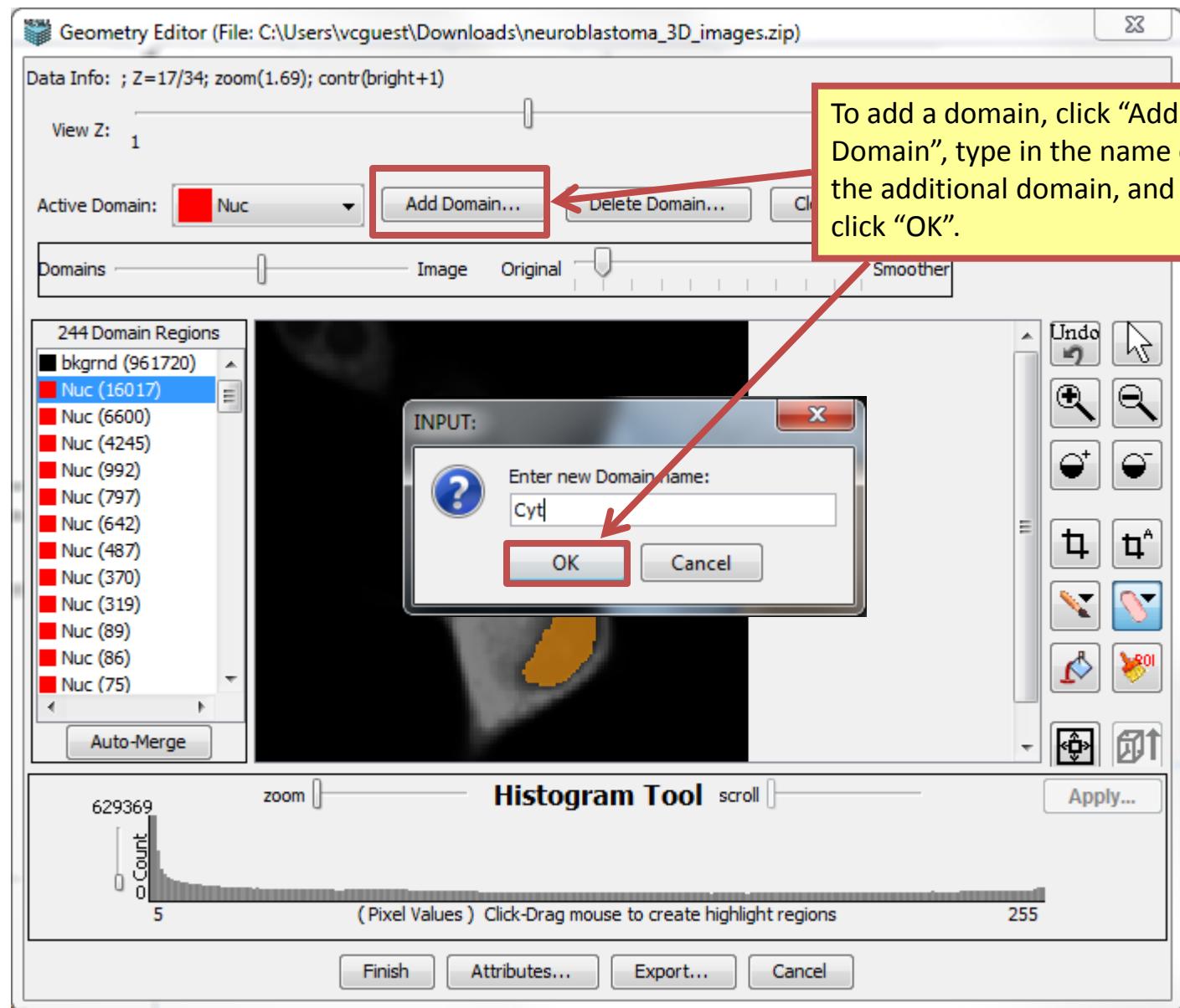


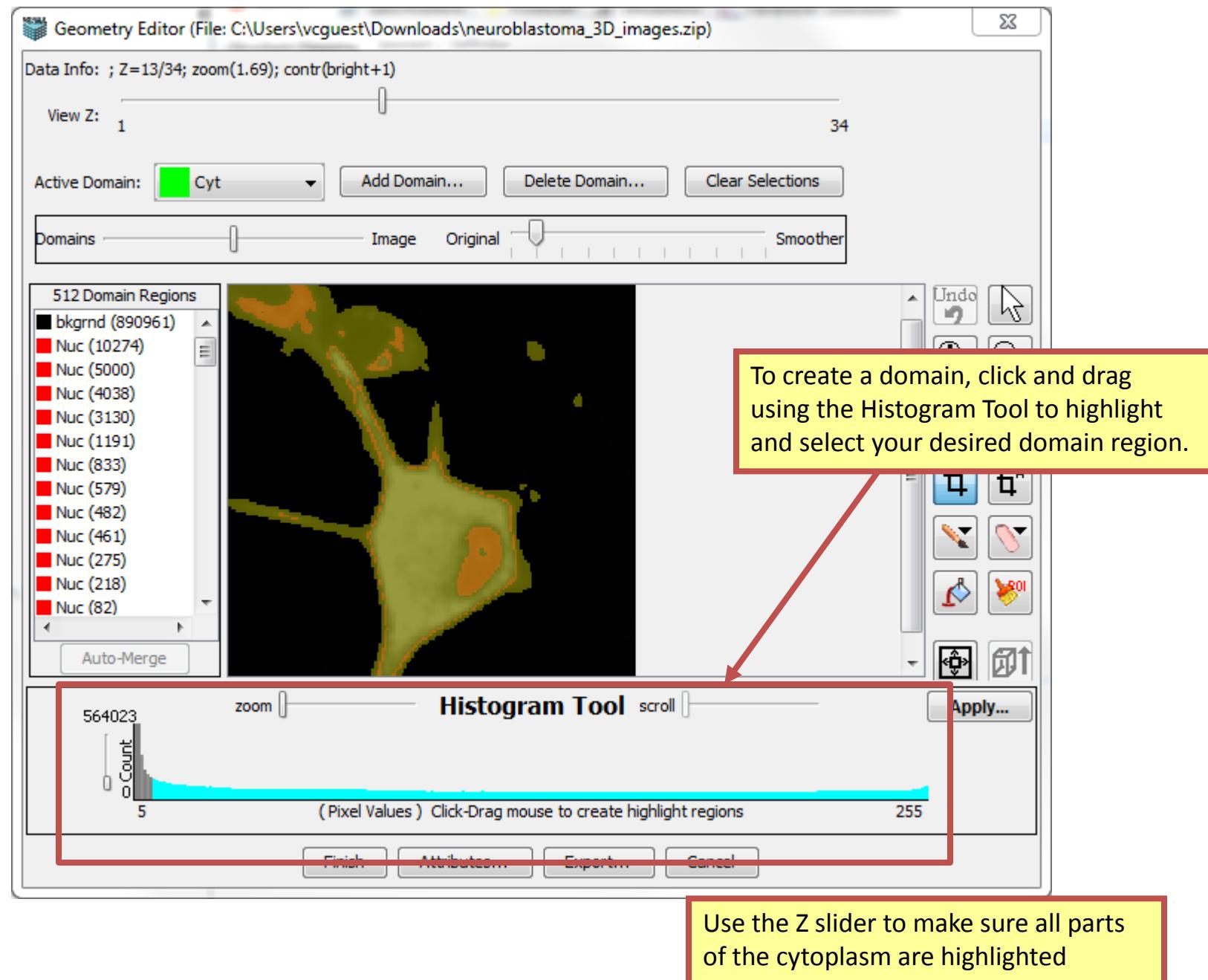
Scroll through the Z slider to view more slices in which the nucleus and membrane are in close proximity

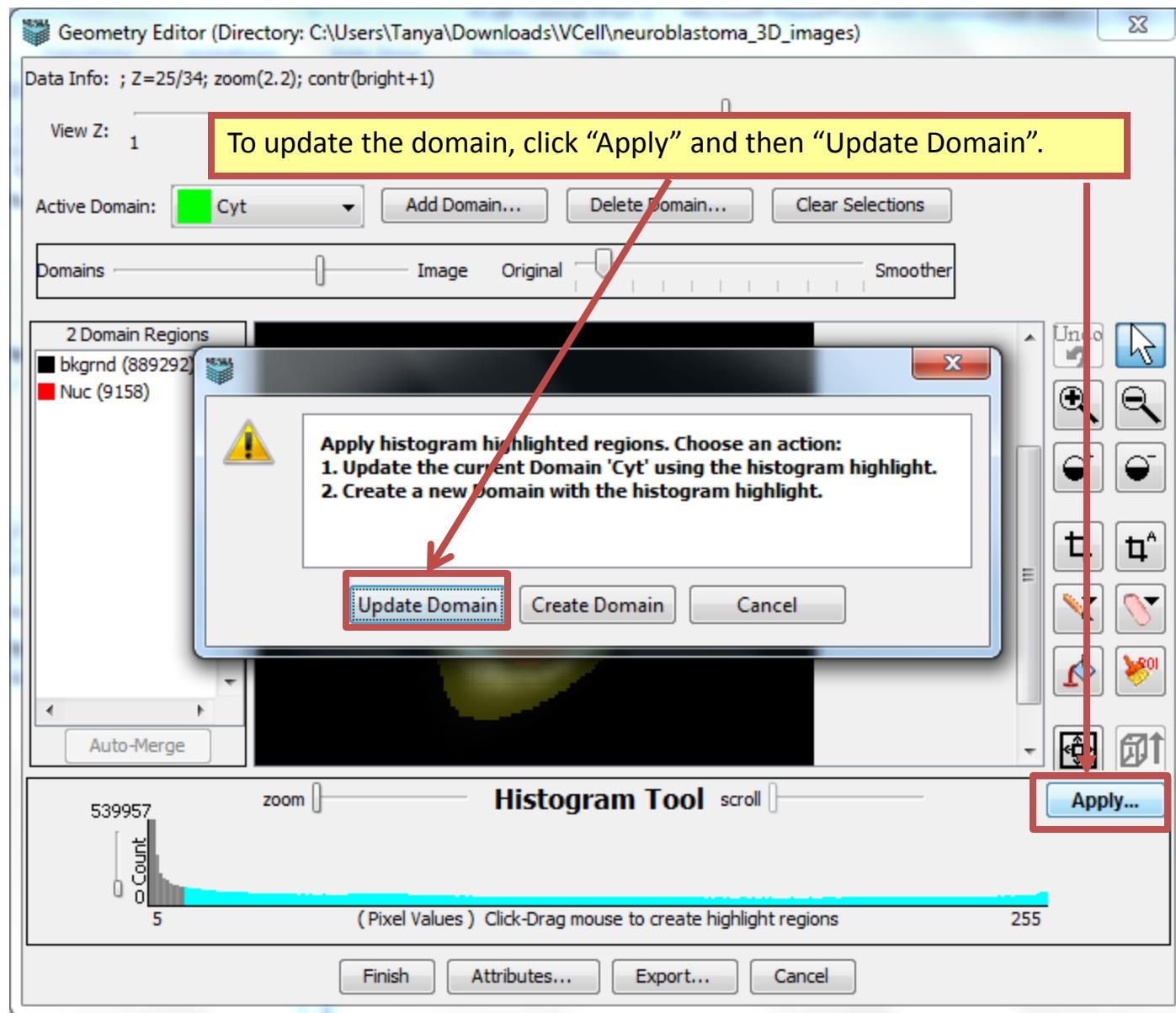
Continue erasing the membrane until there are no parts of the highlighted membrane that touch the highlighted nucleus in all z sections.

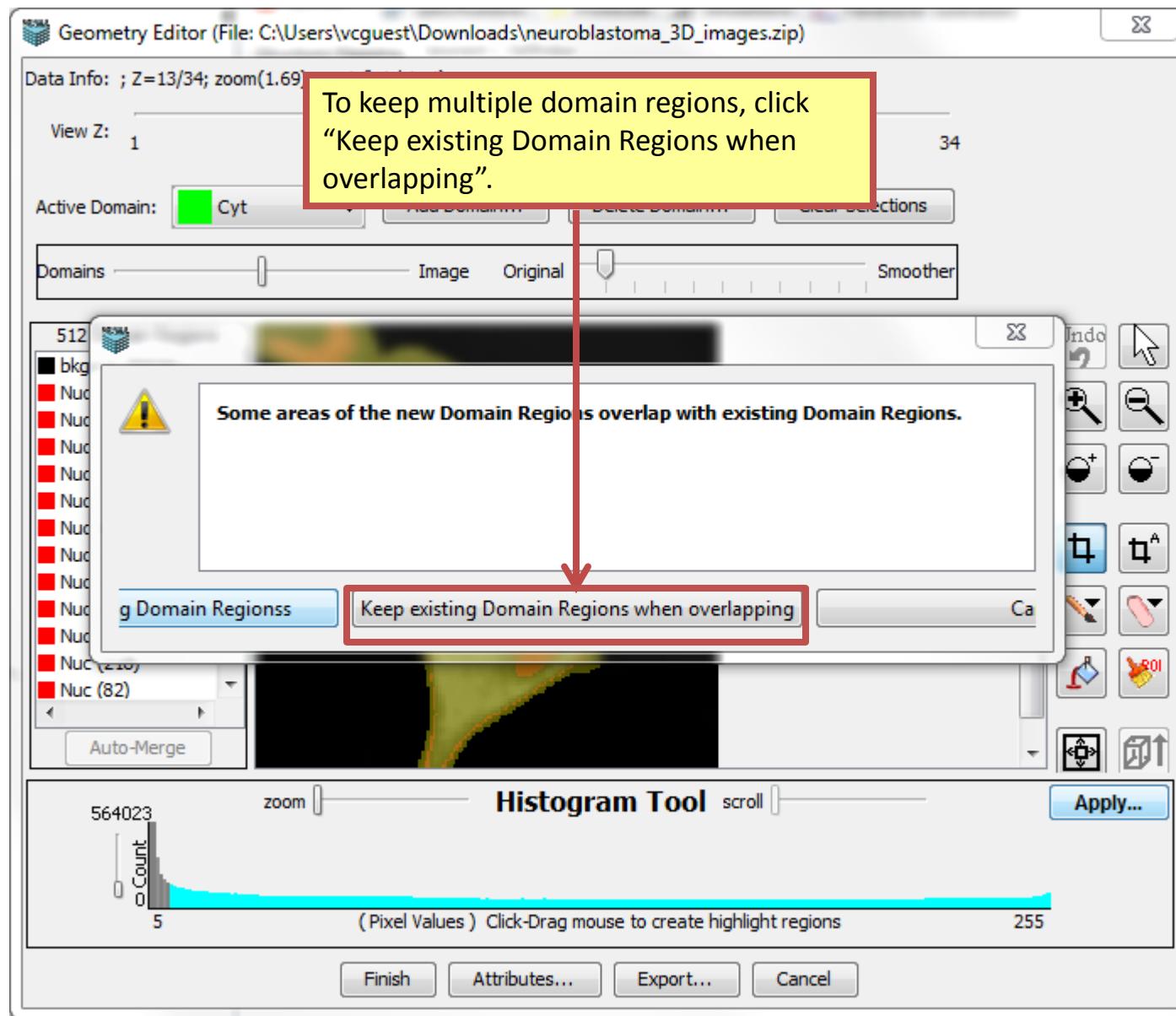


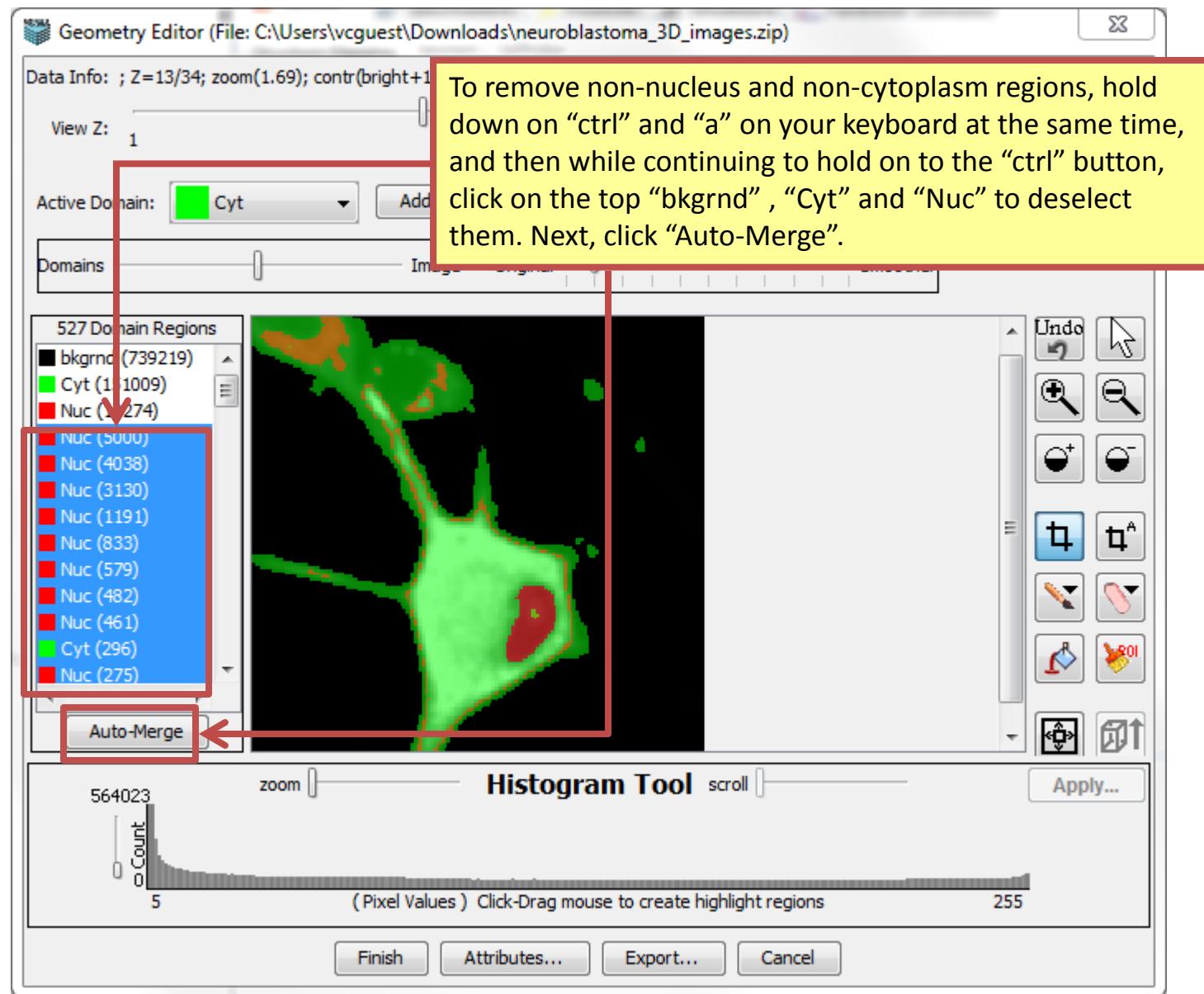


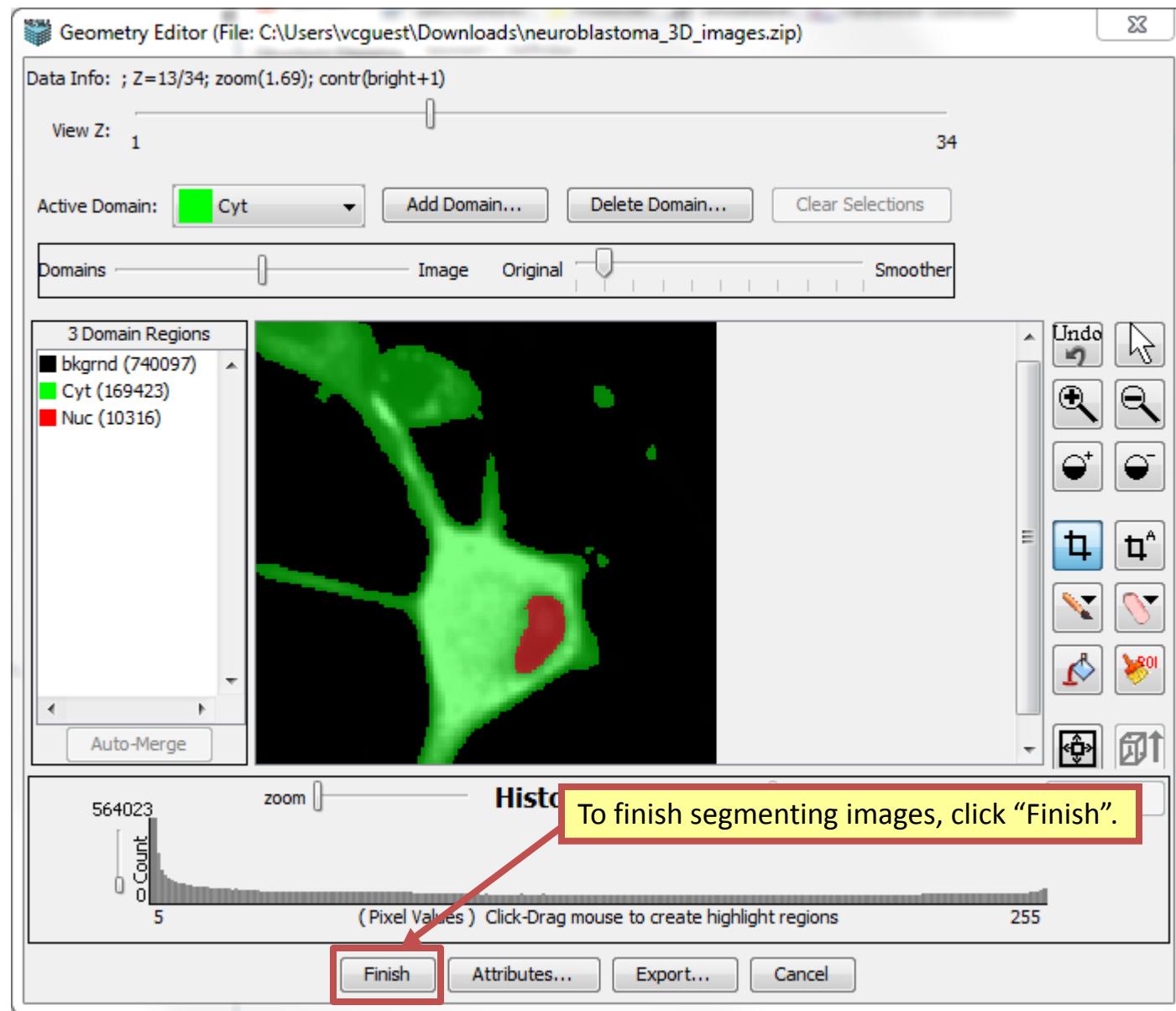


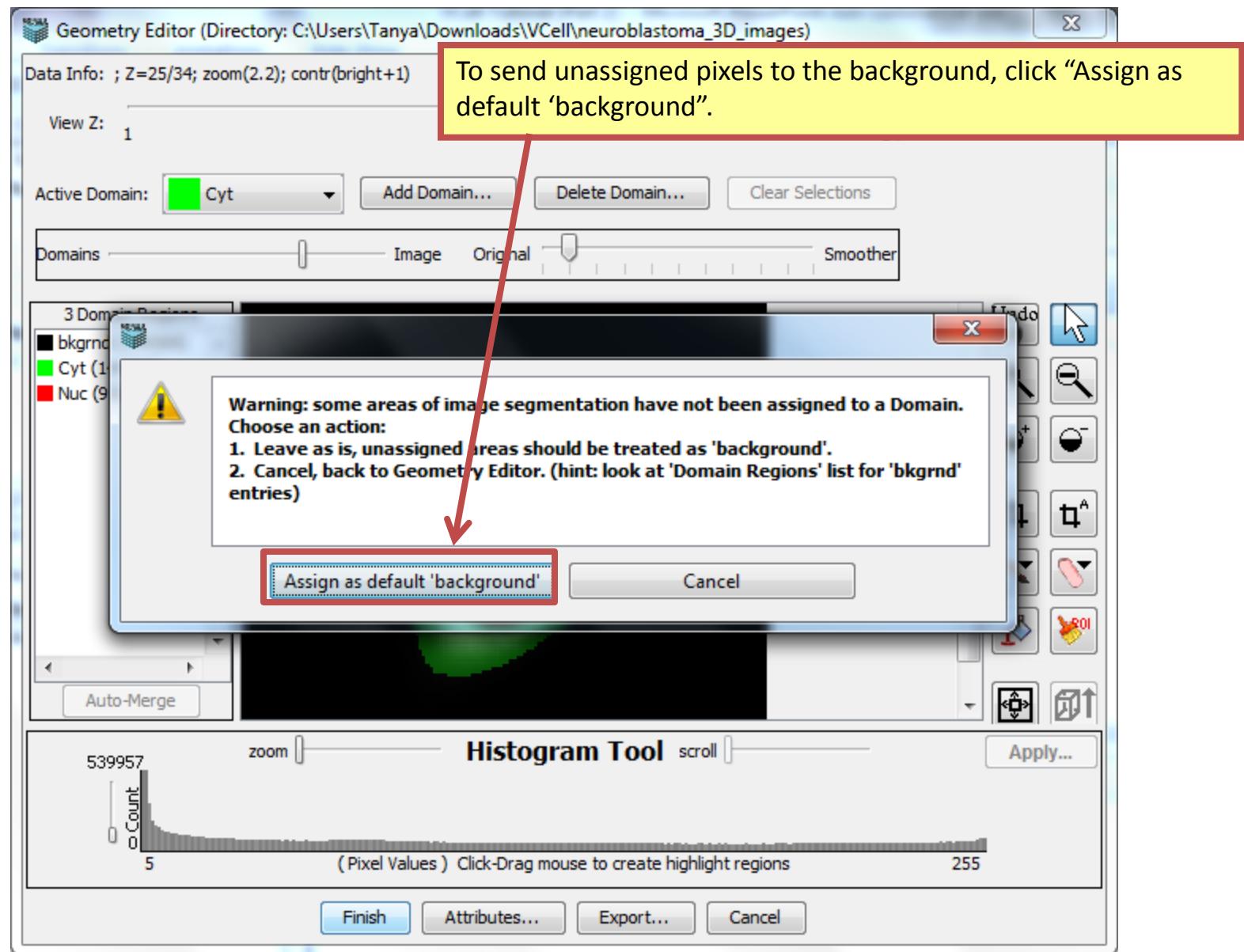


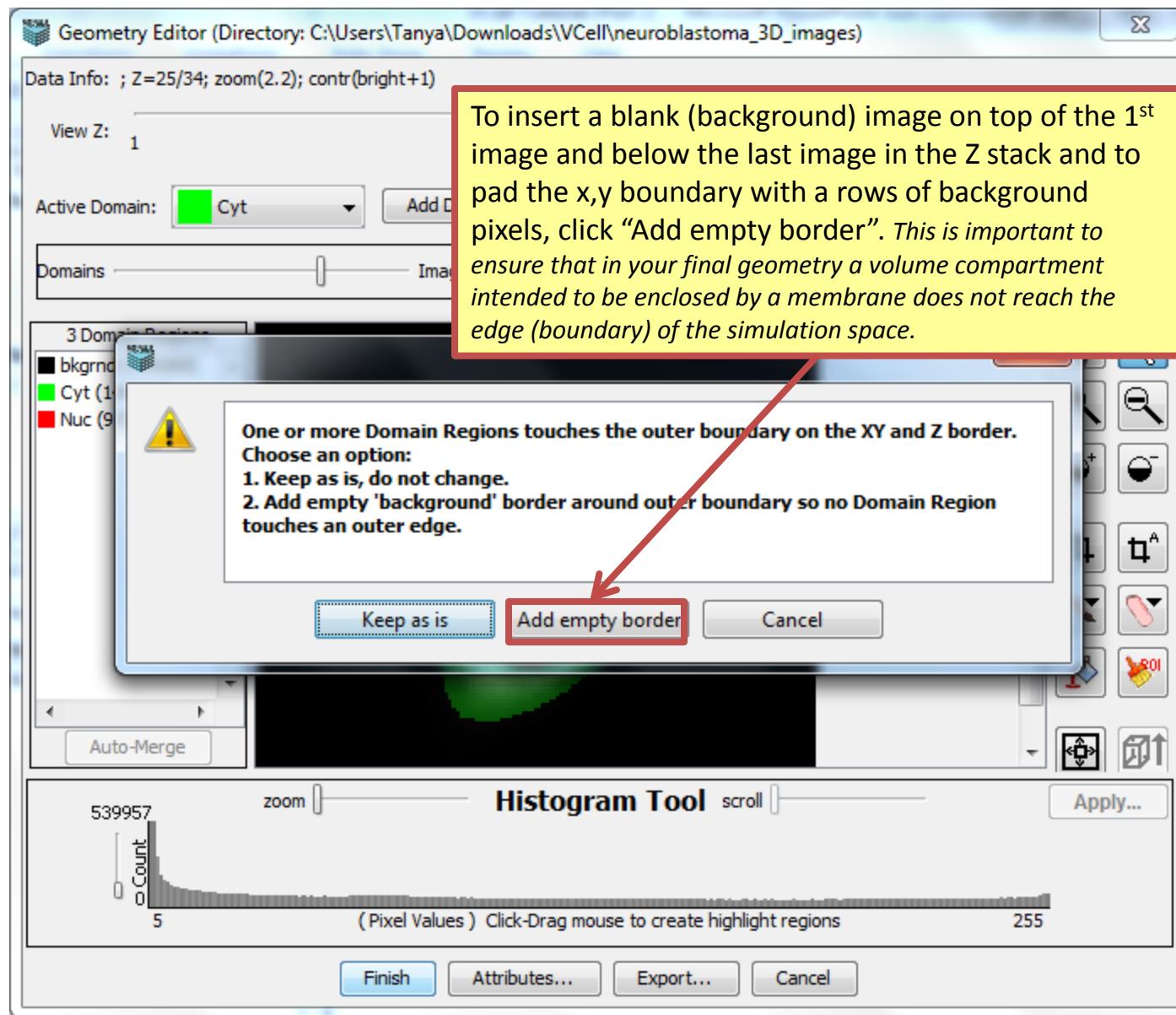












BIOMODEL: Tutorial (Mon Jun 29 09:35:44 EDT 2015) -- VCell 5.3 (build 4)

File View Server Tools Help

Tutorial  
Physiology  
Reaction Diagram  
Reactions (2)  
Structures (5)  
Species (4)  
Applications (1)  
Spatial Deterministic  
Geometry  
Specifications  
Protocols  
Simulations

Structure Mapping Geometry Definition

Domain: 3D, size=(62841.3,84404.8,9.00000E-7), origin=(0,0,0) Export... Edit Image Replace Geometry ▾

Name	Value
background	
Nuc	
Cyt	

Front  
Back  
Add Subdomain ▾  
Delete

Slice View Surface View Geometric Region Details

Reset View

Opacity: 100, 75, 50, 25, 0

Object Properties Problems (0 Errors, 10 Warnings) Database File Info

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

DISCONNECTED 150.4MB / 355.5MB

To view the surfaces in 3-D, click “Surface View”.

# Multi-App tutorial part 1

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

**Physiology**

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

**Applications (1)**

- $\frac{d}{dt}$  Spacial Deterministic
  - Geometry
  - Specifications
  - Protocols
  - Simulations

Parameters, Functions and Units

Pathway

VCCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

+ Search

Biological Models

- My BioModels (astfh234) (1)
- Shared BioModels (0)
- Public BioModels (512)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

Domain: 3D, size=(72330.5,76864.2,9.00000E-7), origin=(0,0,0) Edit Domain...

Export... Edit Image Replace Geometry ▾

Name	Value
background	
Nuc	
Cyt	

Front Back Add Subdomain ▾ Delete

Slice View Surface View Geometric Region

Reset View

Opacity 100  
75  
50  
25  
0

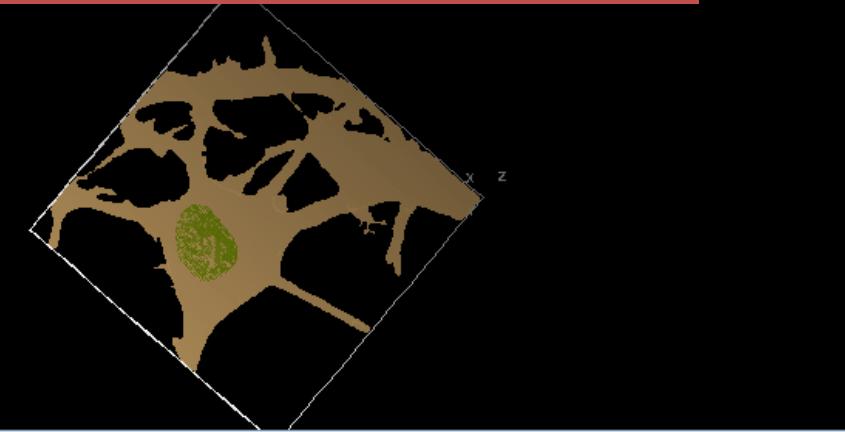
To edit the 3-D dimensions, click "Edit Domain".

Object Properties Problems (0 Errors, 10 Warnings)

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

CONNECTED (astfh234)

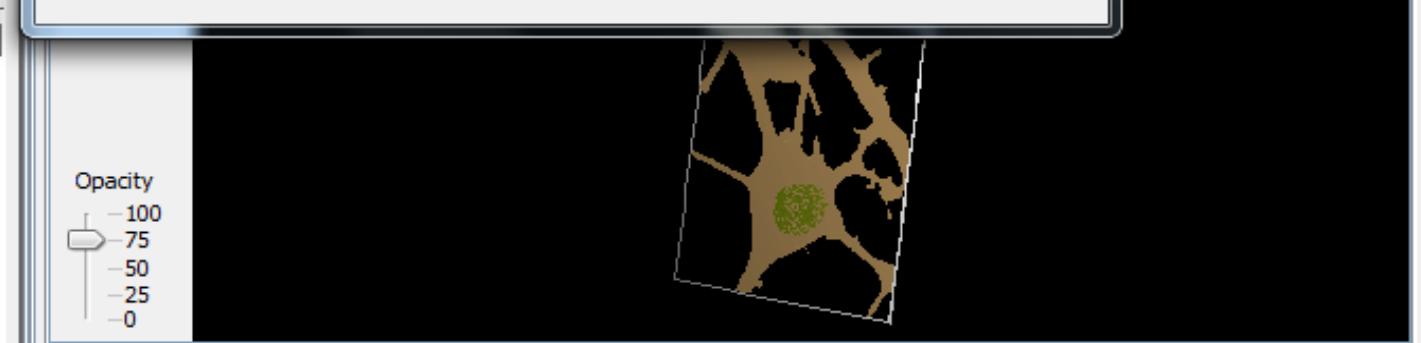
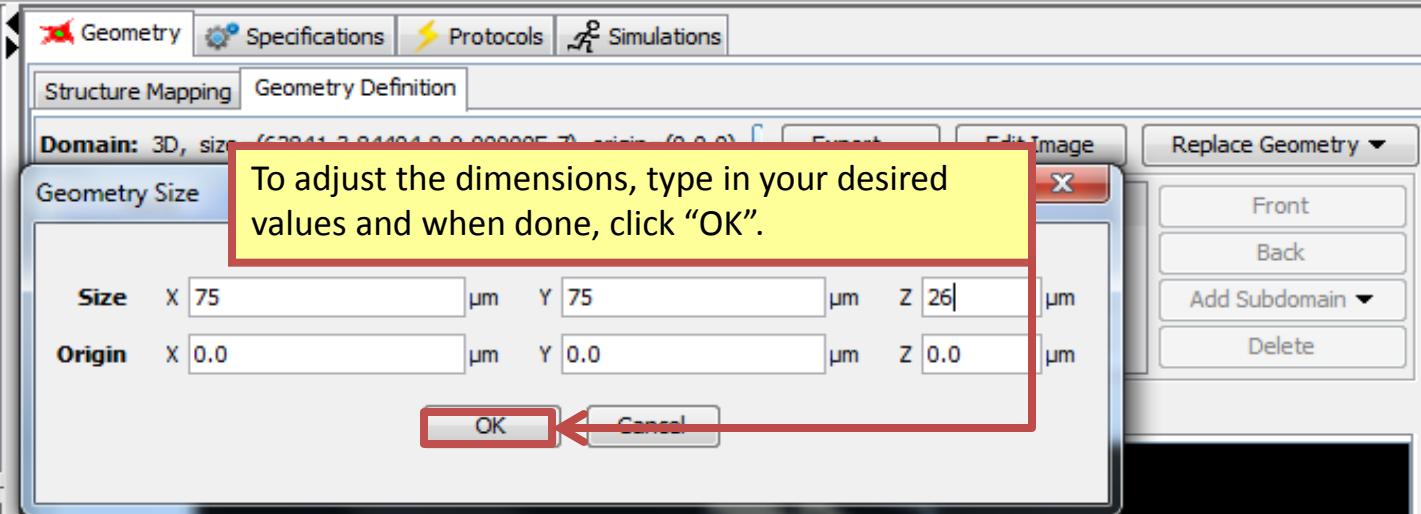
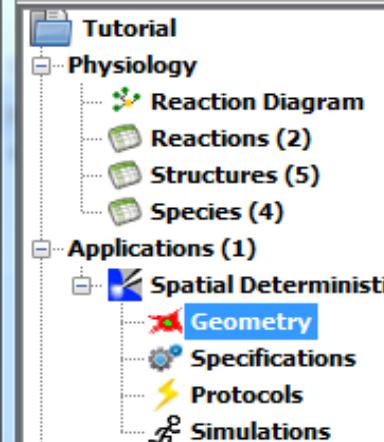
184MB / 281.2MB



## Multi-App tutorial part 1

BIOMODEL: Tutorial (Mon Jun 29 09:35:44 EDT 2015) -- VCell 5.3 (build 4)

File View Server Tools Help



Object Properties Problems (0 Errors, 10 Warnings) Database File Info

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

DISCONNECTED

268.1MB / 330.8MB

## Multi-App tutorial part 1

BIOMODEL: BioModel1 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel1

- Physiology
  - Reaction Diagram
  - Reactions (2)
  - Structures (5)
  - Species (4)
  - Molecules (0)
  - Observables (0)
- Applications (1)
  - d/dt Spacial Deterministic
    - Geometry
    - Specifications
    - Protocols
    - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

+ Search

- Biological Models
  - My BioModels (astfh234) (1)
  - Shared BioModels (0)
  - Public BioModels (512)
  - Tutorials (5)
  - Education (33)
  - Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

Domain: 3D, size=(75.0,75.0,26.0), origin=(0.0,0.0,0.0) Edit Domain... Export... Edit Image Replace Geometry ▾

Name	Value
background	
Nuc	
Cyt	

To adjust opacity of the cytoplasm to better see the nucleus, drag the slider with your cursor.

Slice View Surface View Geometric Region Details

Reset View

Opacity

100  
75  
50  
25  
0

The geometry of your model is now complete.

Object Properties Problems (0 Errors, 10 Warnings)

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

CONNECTED (astfh234) 200.9MB / 303.9MB

To link physiology to geometry, click "Structure Mapping" and use the line tool to drag your cursor from a structure to its corresponding subdomain.

BIOMODEL: tutorial 3 (Tue Jun 30 16:47:35 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

tutorial 3

Physiology

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (1)

- d/dt Spacial Deterministic
- Geometry
- Specifications
- Protocols
- Simulations

Parameters, Functions and Units

Pathway

VCel DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

Biological Models

- My BioModels (astfh234) (2)
  - Model2
  - tutorial 3
    - Private Tue Jun 30 16:47:35 EDT 2015
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

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

Physiology (structures)

EC Cyt Nuc PM NM

Geometry (subdomains)

- background
- Nuc
- Cyt
- Cyt\_background\_membrane
- Cyt\_Nuc\_membrane

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+	Z-	Z+
EC	background	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Cyt	Cyt	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Nuc	Nuc	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
PM	Cyt_background_me...	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
NM	Cyt_Nuc_membrane	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux

CONNECTED (astfh234) 58.1MB / 77.8MB

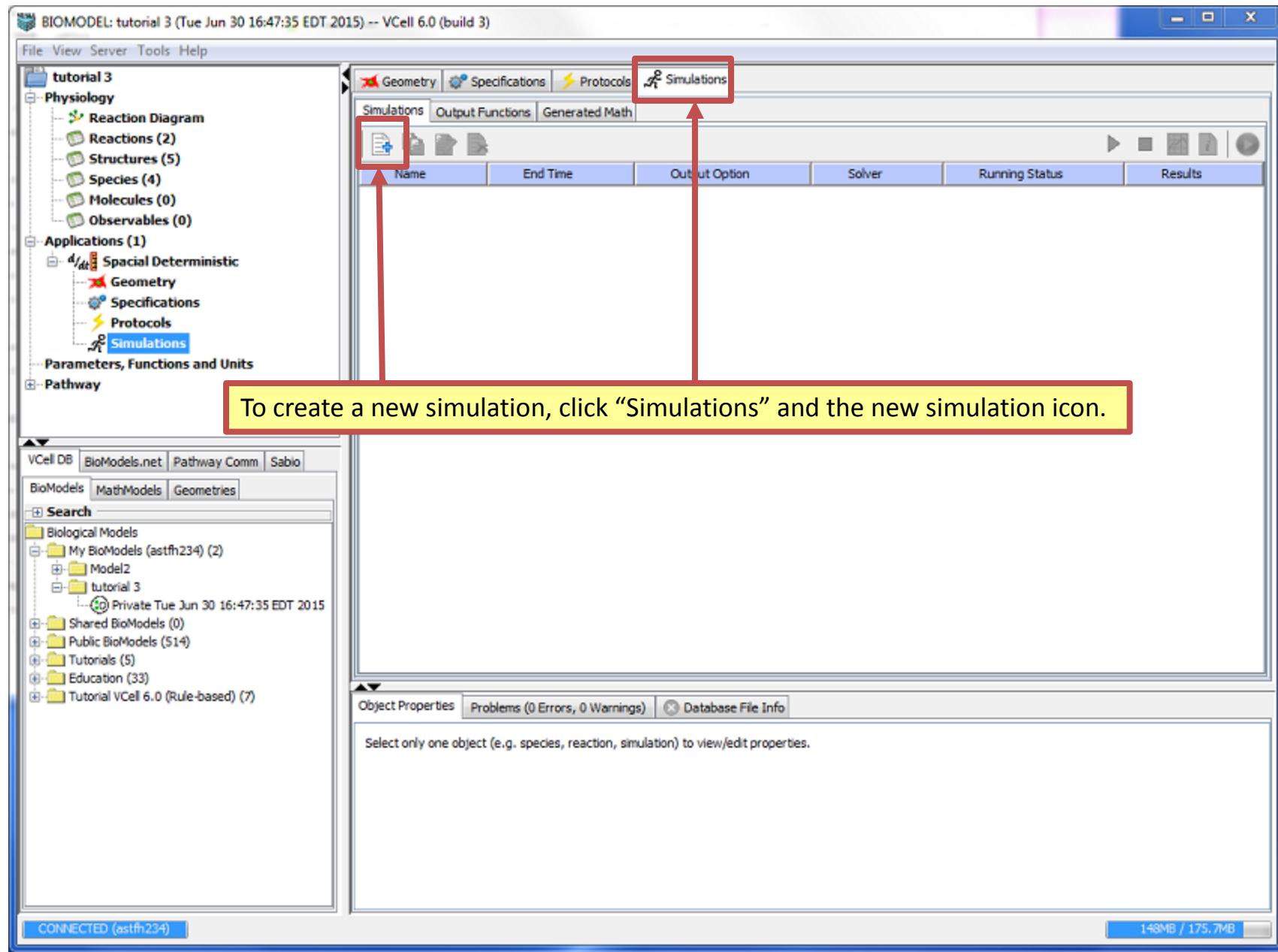
To change the concentration of a species, click “Specifications” and type in a value under the “Initial Condition” column.

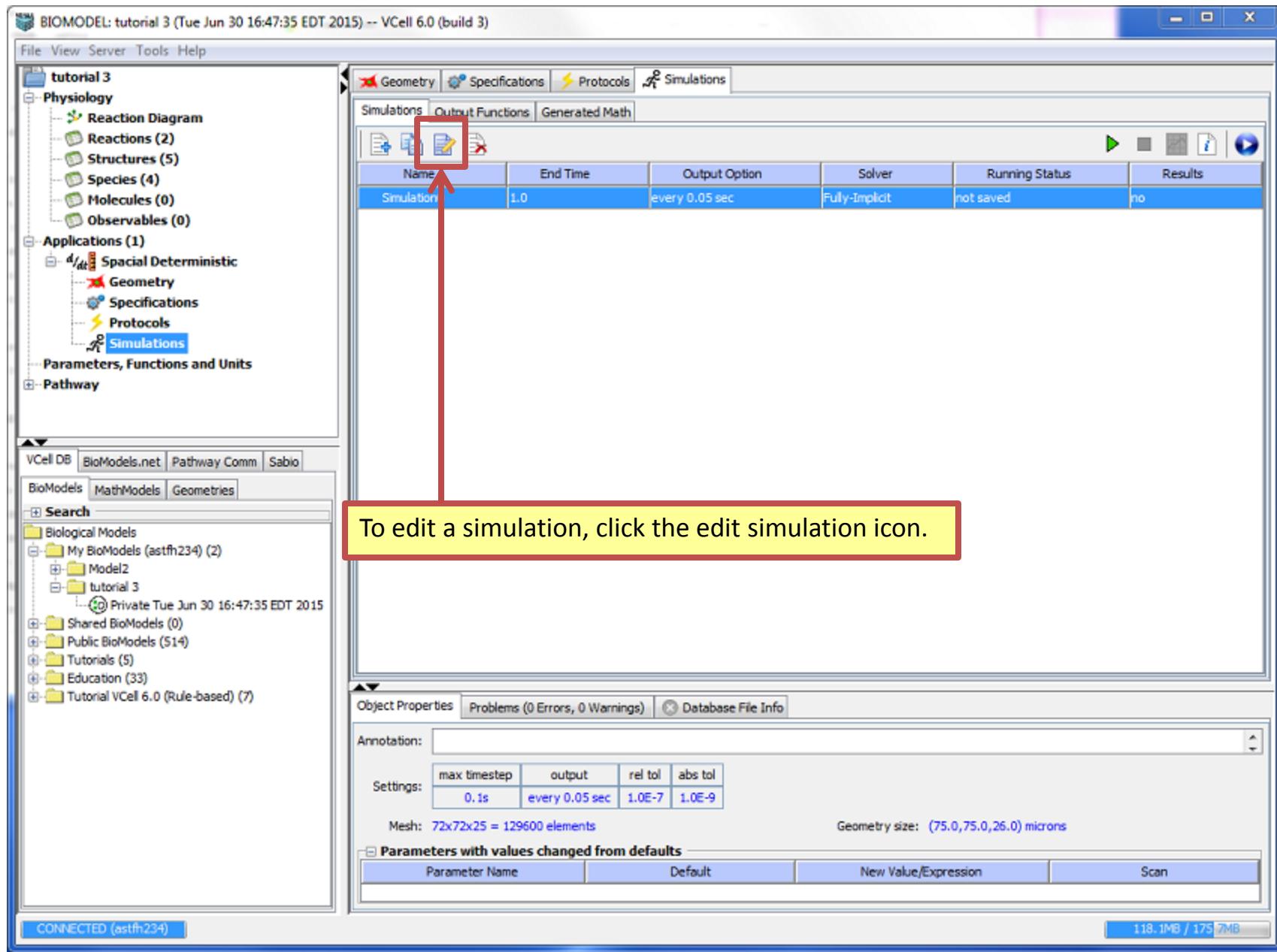
Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant
RanC_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0
C_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0
Ran_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0
RanC_Nuc	Nuc	<input type="checkbox"/>	0.00045	<input type="checkbox"/>	10.0

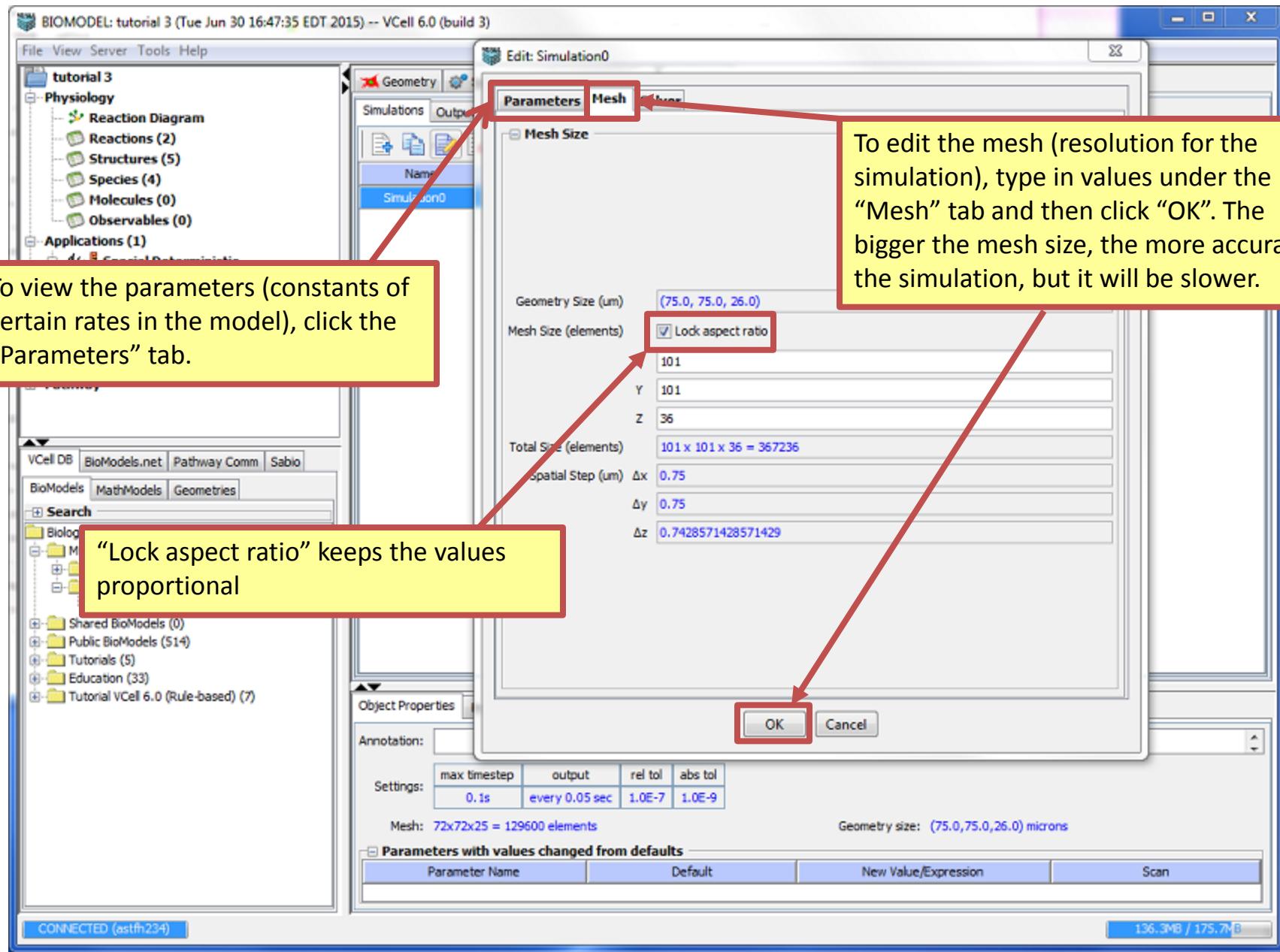
Object Properties    Problems (0 Errors, 0 Warnings)    Database File Info

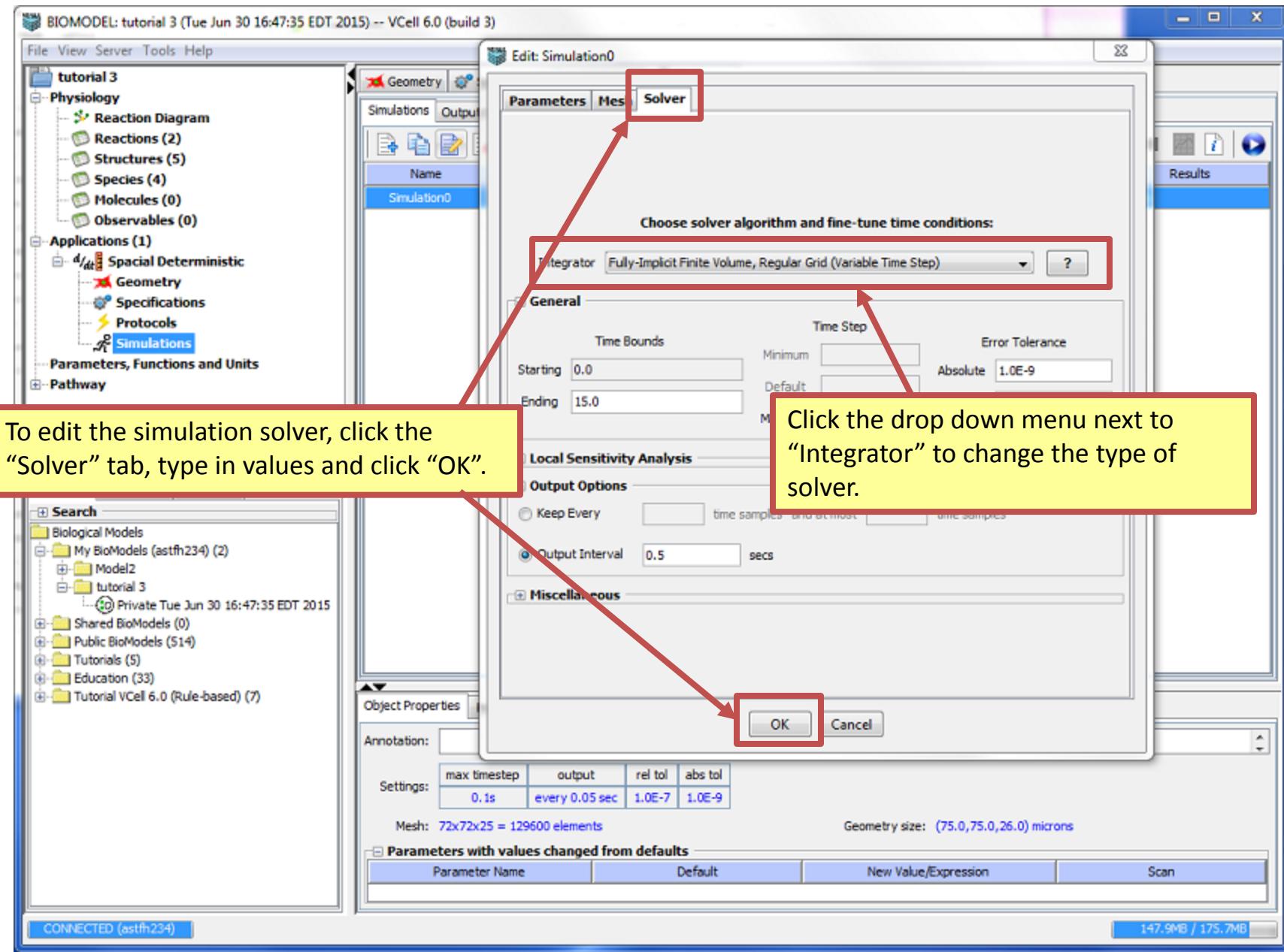
Description	Parameter	Expression	Units
initial concentration for RanC_Nuc	initConc	4.5E-4	µM
diffusion constant for RanC_Nuc	diff	10.0	µm².s⁻¹
Boundary Condition X- for RanC_Nuc	BC_Xm	<zero flux>	µM.µm.s⁻¹
Boundary Condition X+ for RanC_Nuc	BC_Xp	<zero flux>	µM.µm.s⁻¹
Boundary Condition Y- for RanC_Nuc	BC_Ym	<zero flux>	µM.µm.s⁻¹
Boundary Condition Y+ for RanC_Nuc	BC_Yp	<zero flux>	µM.µm.s⁻¹
Boundary Condition Z- for RanC_Nuc	BC_Zm	<zero flux>	µM.µm.s⁻¹

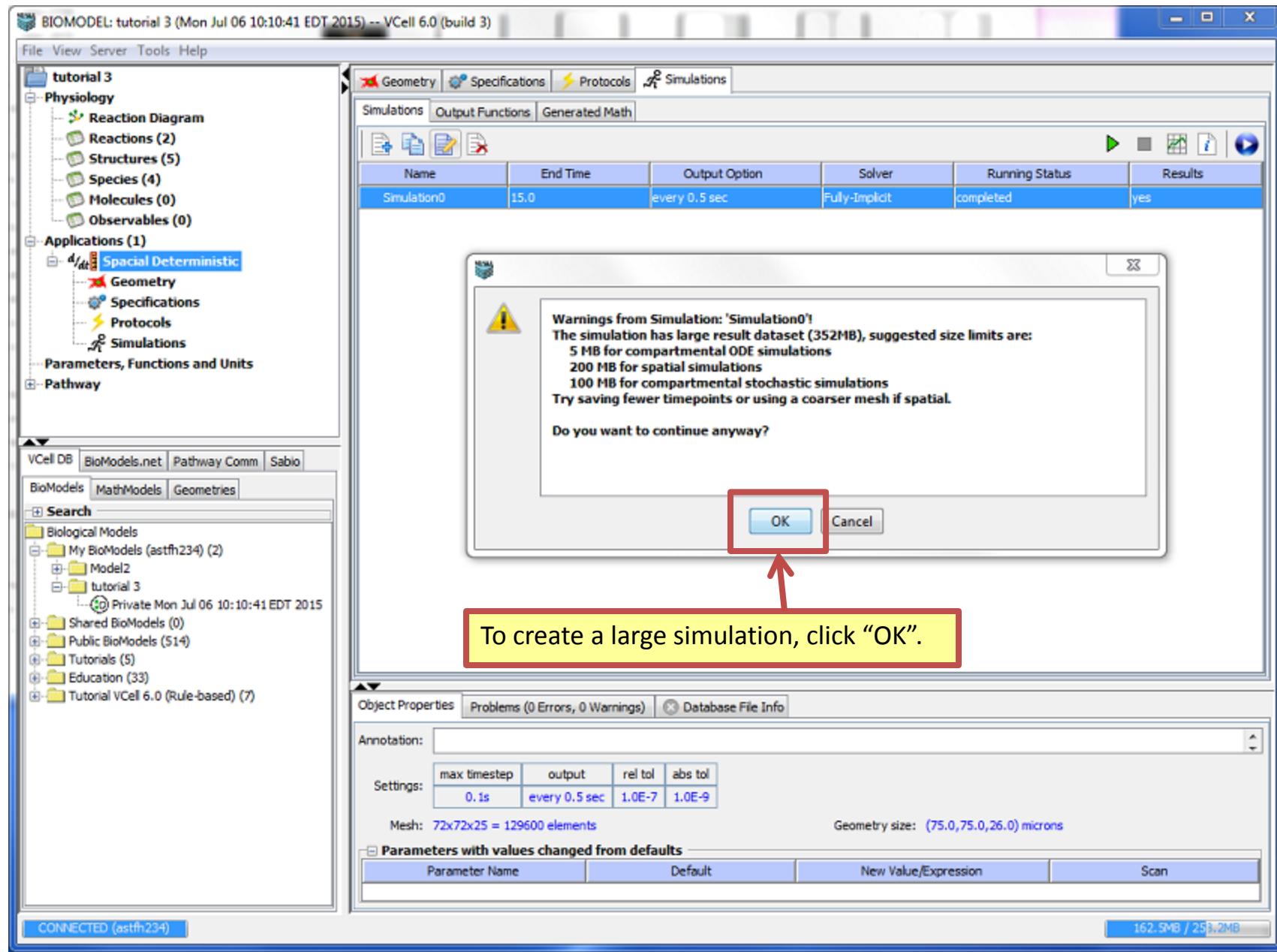
CONNECTED (astfh234)    134MB / 175.7MB

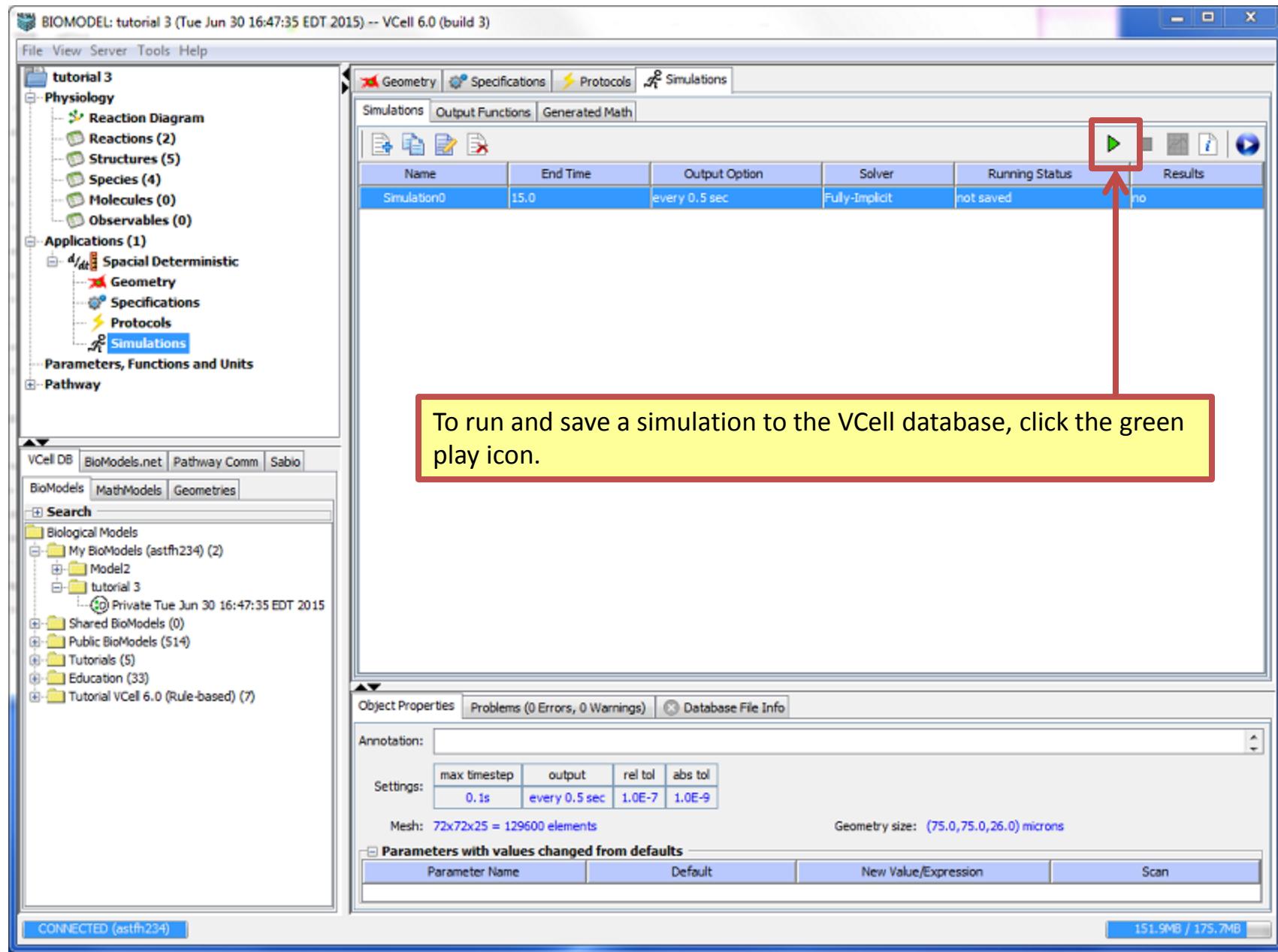






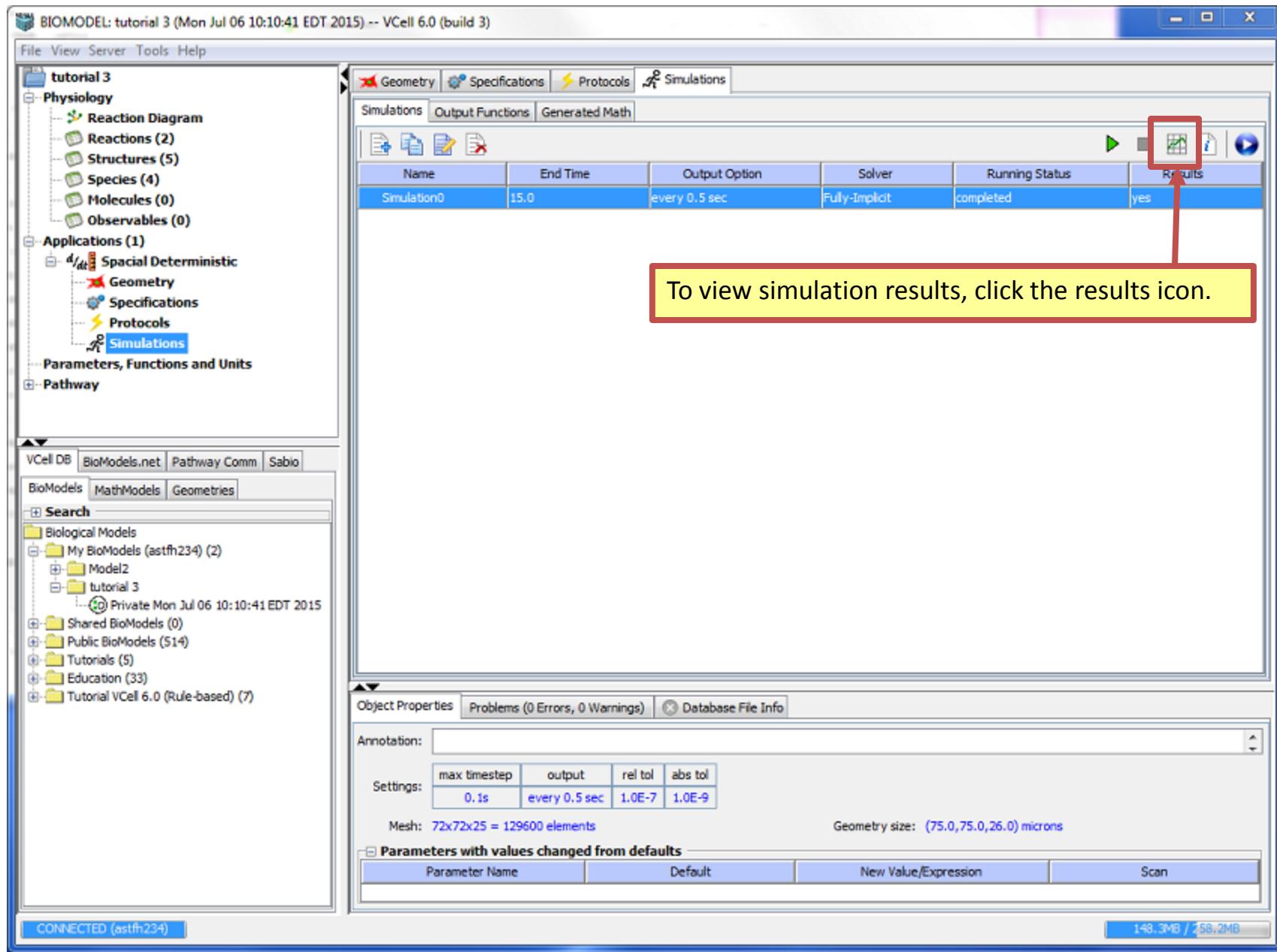


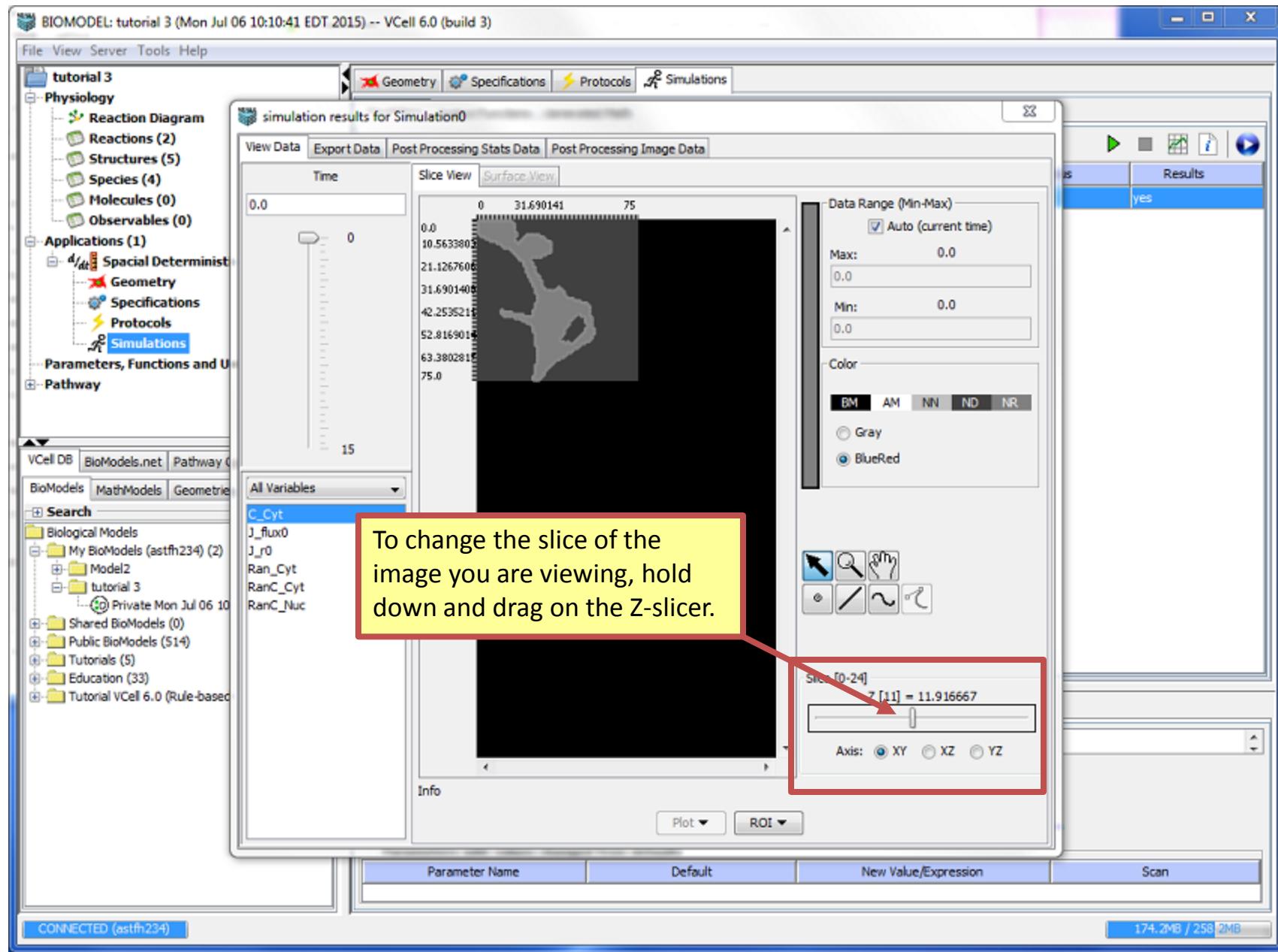


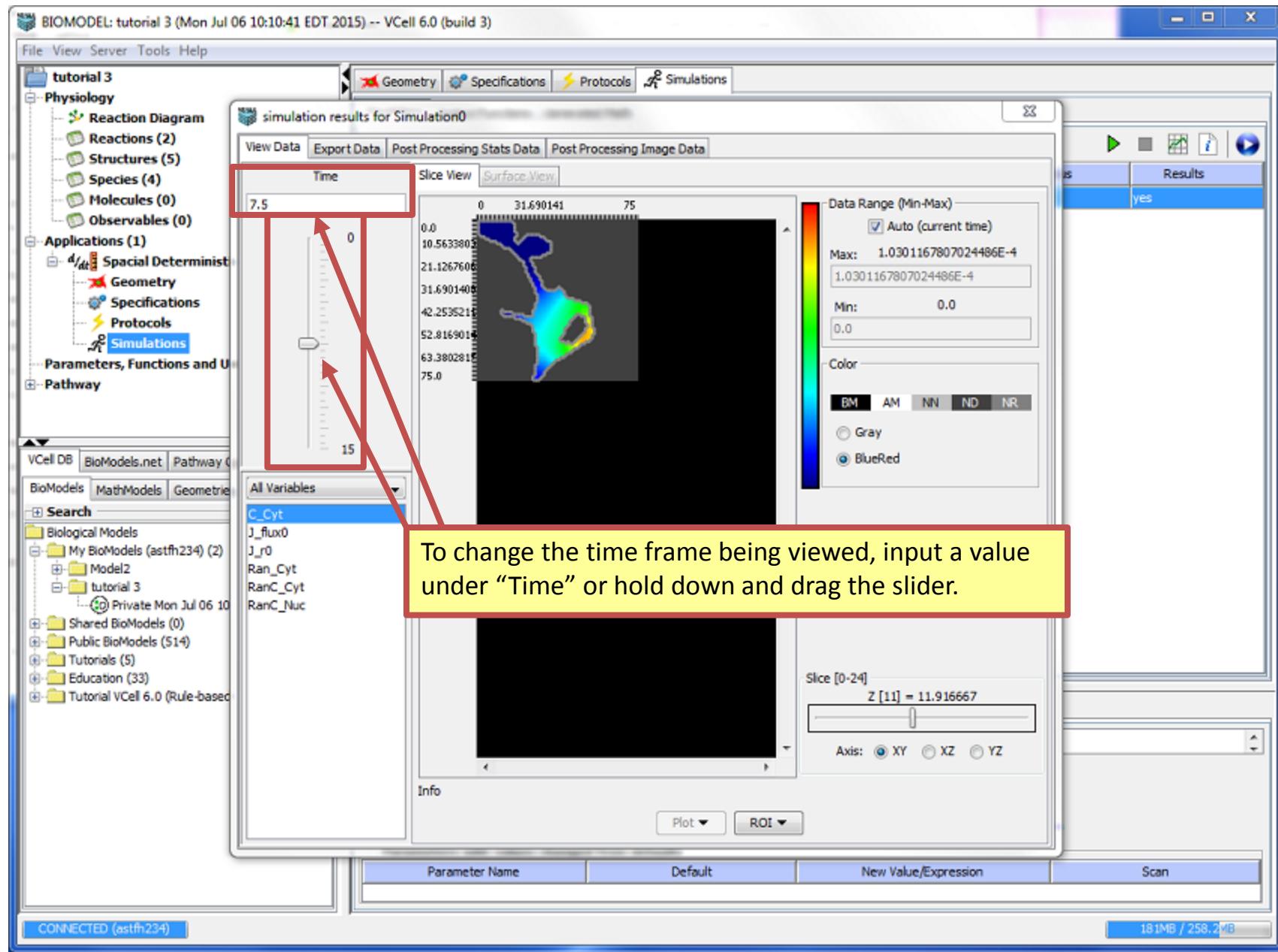


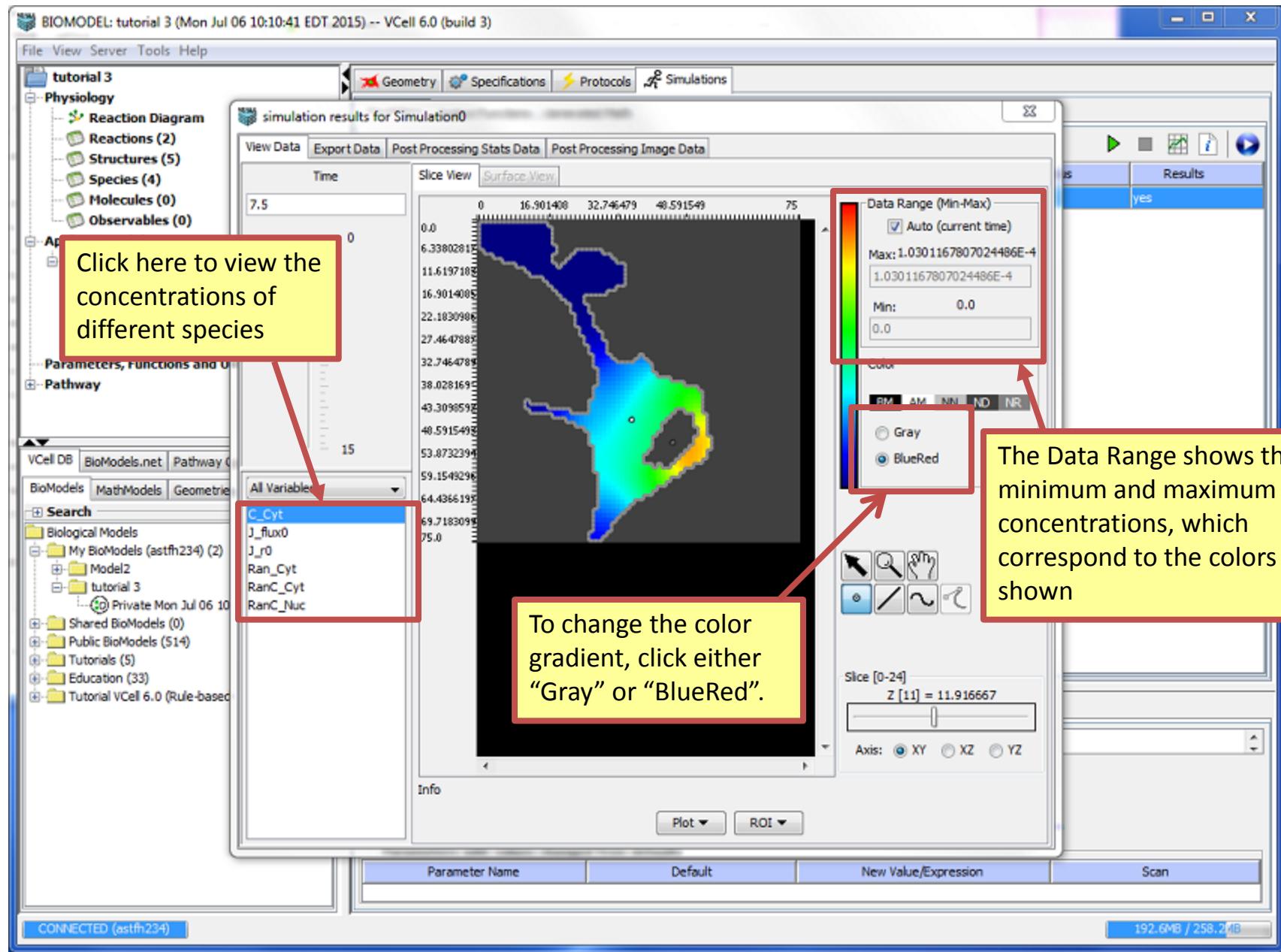
The screenshot shows the VCell 6.0 software interface. In the top left, the title bar reads "BIOMODEL: tutorial 3 (Mon Jul 06 10:10:41 EDT 2015) -- VCell 6.0 (build 3)". The menu bar includes File, View, Server, Tools, and Help. On the left, a tree view shows the project structure: "tutorial 3" expanded to show "Physiology" (Reaction Diagram, Reactions 2, Structures 5, Species 4, Molecules 0, Observables 0), "Applications (1)" (d/dt Spacial Deterministic, Geometry, Specifications, Protocols, Simulations selected), "Parameters, Functions and Units", and "Pathway". Below this is the "VCell DB" section with tabs for BioModels, MathModels, Geometries, and a "Search" panel showing "Biological Models" with "My BioModels (astfh234) (2)" expanded to "Model2" and "tutorial 3" (with a timestamp). The main workspace is titled "Simulations" and contains tabs for Simulations, Output Functions, and Generated Math. A table lists "Simulation0" with columns: Name, End Time, Output Option, Solver, and Running Status (showing "53.3%"). A red box highlights the "Running Status" column, and a red arrow points from it to a callout box containing the text: "To view the status of the simulation, look under the ‘Running Status’ column." At the bottom, tabs for Object Properties, Problems (0 Errors, 0 Warnings), and Database File Info are shown, along with a message: "Select only one object (e.g. species, reaction, simulation) to view/edit properties." The status bar at the bottom indicates "CONNECTED (astfh234)" and "138.8MB / 258.2MB".

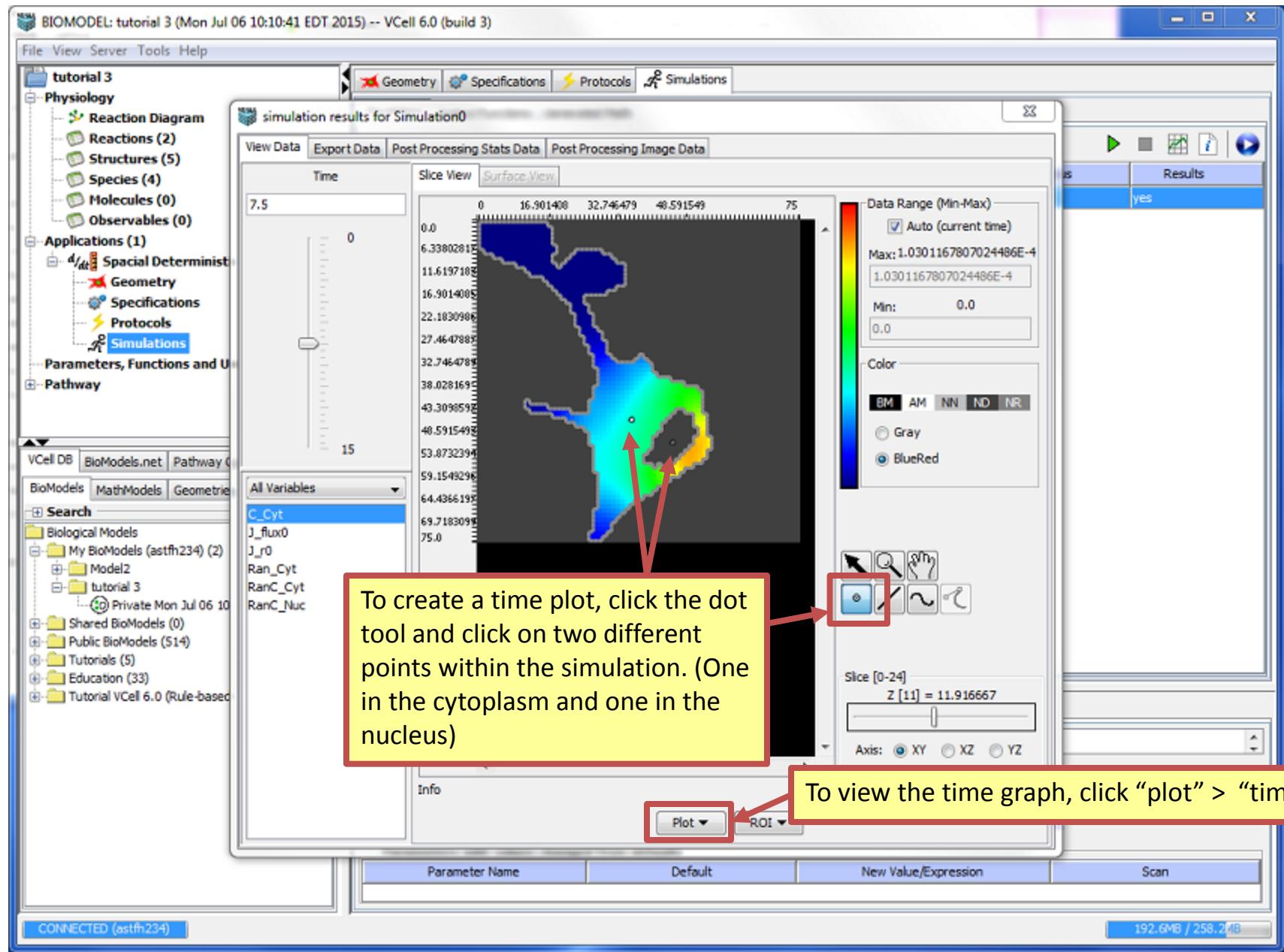
To view the status of the simulation, look under the “Running Status” column.

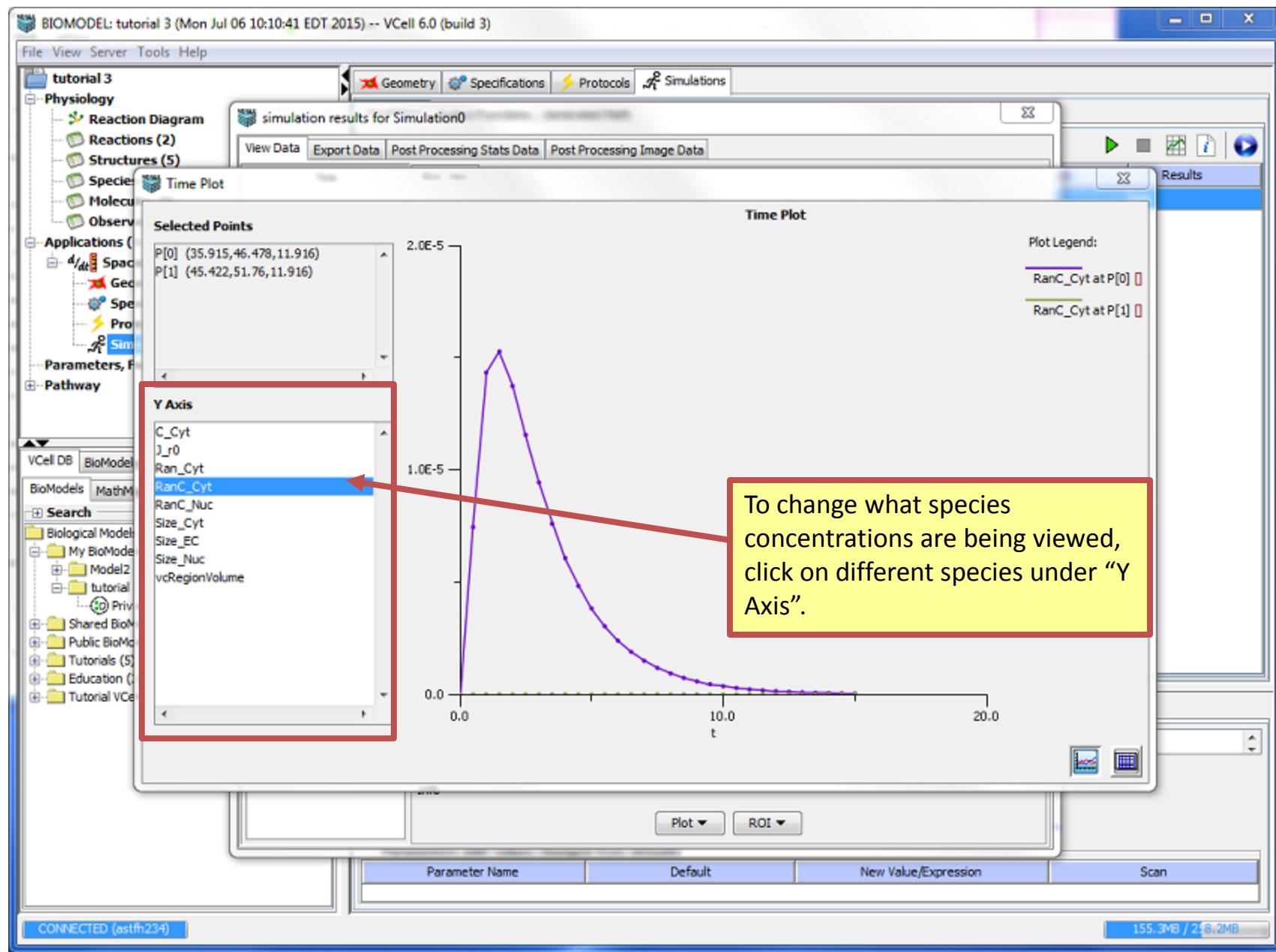


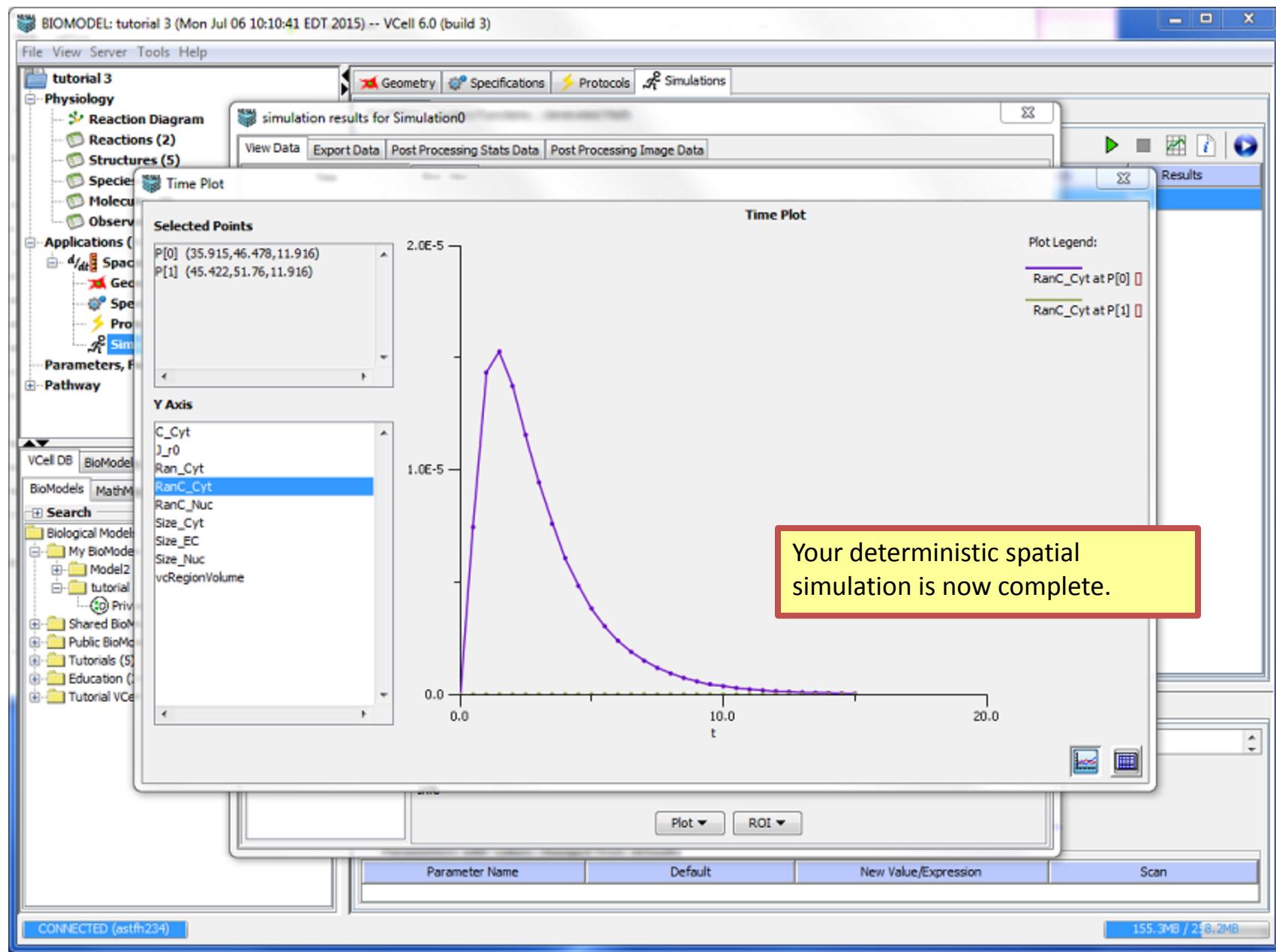


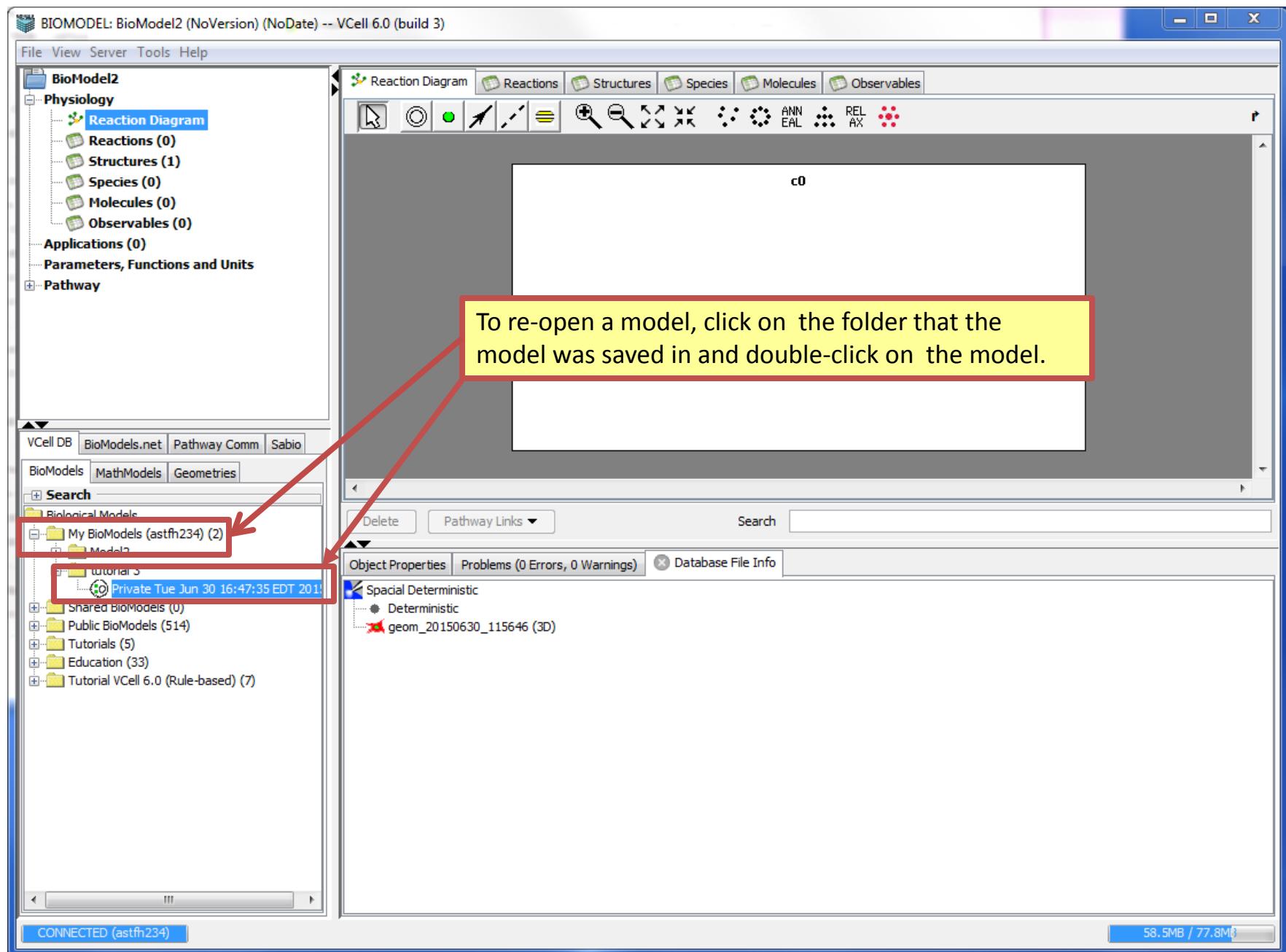












The screenshot shows the VCell 6.0 software interface. In the top left, the title bar reads "BIOMODEL: tutorial 3 (Mon Jul 06 11:08:43 EDT 2015) -- VCell 6.0 (build 3)". The menu bar includes File, View, Server, Tools, and Help. The left sidebar displays a project tree with "tutorial 3" expanded, showing "Physiology" with "Reaction Diagram" (1), "Reactions (2)", "Structures (5)", "Species (4)", "Molecules (0)", and "Observables (0)". Below this is an "Applications (1)" section with "Spatial Deterministic" selected, highlighted by a red box and a red arrow pointing to a callout box. Other items in this section include "Parameters, functions and units" and "Pathway". The main workspace has tabs for Geometry, Specifications, Protocols, and Simulations, with "Simulations" active. The "Simulations" tab shows a table with one row:

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	15.0	every 0.5 sec	Fully-Implicit	completed	yes

A yellow callout box contains the text: "We have finished the first application and now need to create a new one. In order to create a non-spatial stochastic copy of an application, right click on an application and click “Copy As” > “Non-Spatial” > “Stochastic”."

The bottom left pane shows the "VCell DB" with tabs for BioModels.net, Pathway Comm, and Sabio. Under "BioModels", there is a "Search" section and a list of models: "My BioModels (astfh234) (2)" containing "Model2" (with two private versions) and "tutorial 3" (with one private version); "Shared BioModels (0)", "Public BioModels (514)", "Tutorials (5)", "Education (33)", and "Tutorial VCell 6.0 (Rule-based) (7)". The bottom right pane shows "Object Properties", "Problems (0 Errors, 0 Warnings)", and "Database File Info". A message in this pane says: "Select only one object (e.g. species, reaction, simulation) to view/edit properties." The status bar at the bottom indicates "CONNECTED (astfh234)" and "253.8MB / 375.5MB".

The screenshot shows the VCell 6.0 software interface. In the center, a modal dialog box titled "Warning:" displays the message: "Simulations are not copied because new application is of different type." An "OK" button is at the bottom of the dialog. A red callout box with the text "Click 'OK'." points to the "OK" button. The background of the main window shows a project tree on the left and a "Simulations" tab in the center.

BIOMODEL: tutorial 3 (Mon Jul 06 11:08:43 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

tutorial 3

Physiology

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (2)

- Copy of Spacial Deterministic
- Spacial Deterministic

Parameters, Functions and Units

Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

Biological Models

- My BioModels (astfh234) (2)
  - Model2
    - Private Mon Jun 29 12:52:37 EDT 2015
    - Private Mon Jun 29 12:20:43 EDT 2015
  - tutorial 3
    - Private Mon Jul 06 11:08:43 EDT 2015
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Object Properties Problems (0 Errors, 0 Warnings) Database File Info

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

CONNECTED (astfh234)

319.7MB / 375.5MB

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

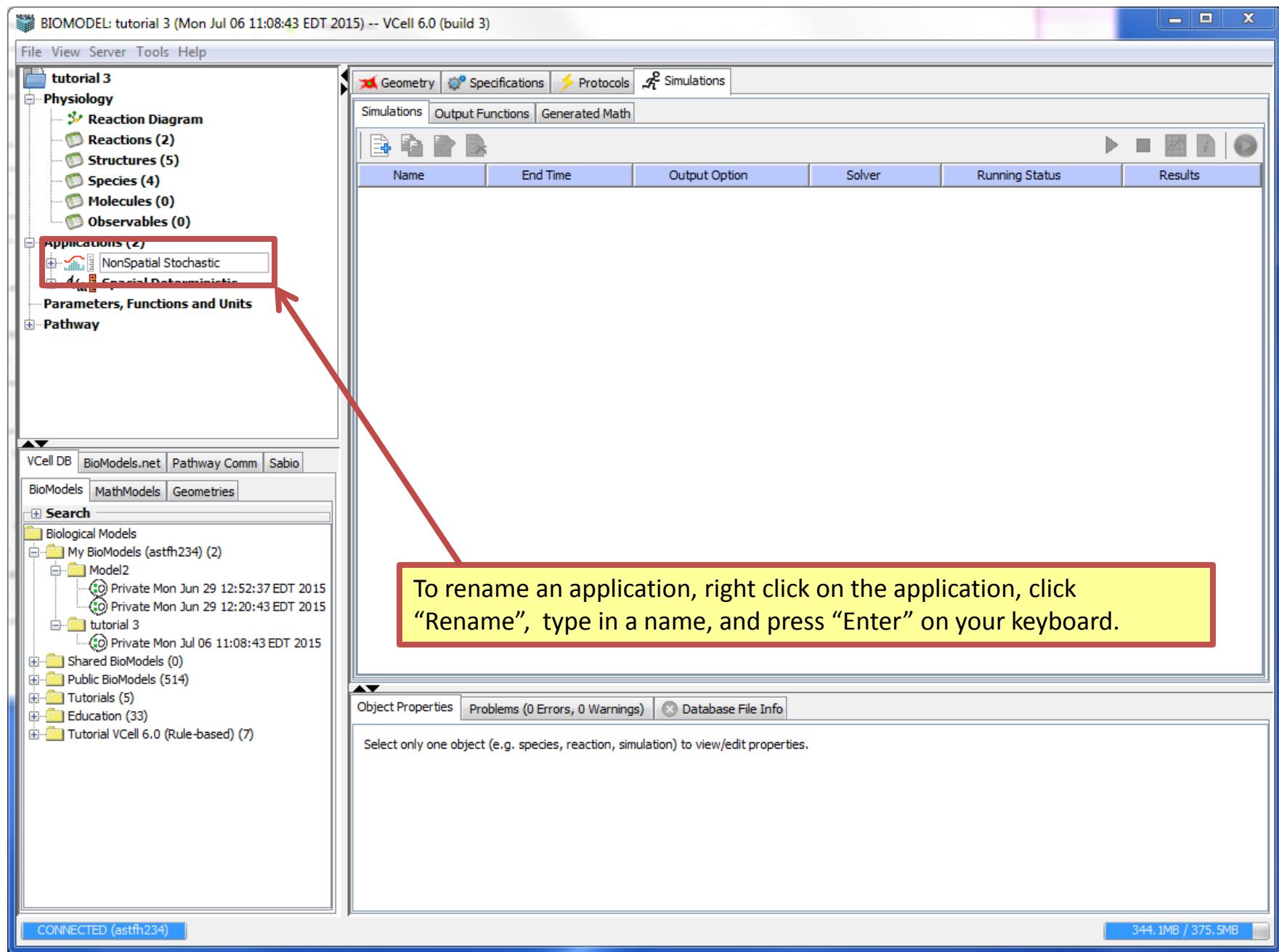
Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	15.0	every 0.5 sec	Fully-Implicit	completed	yes

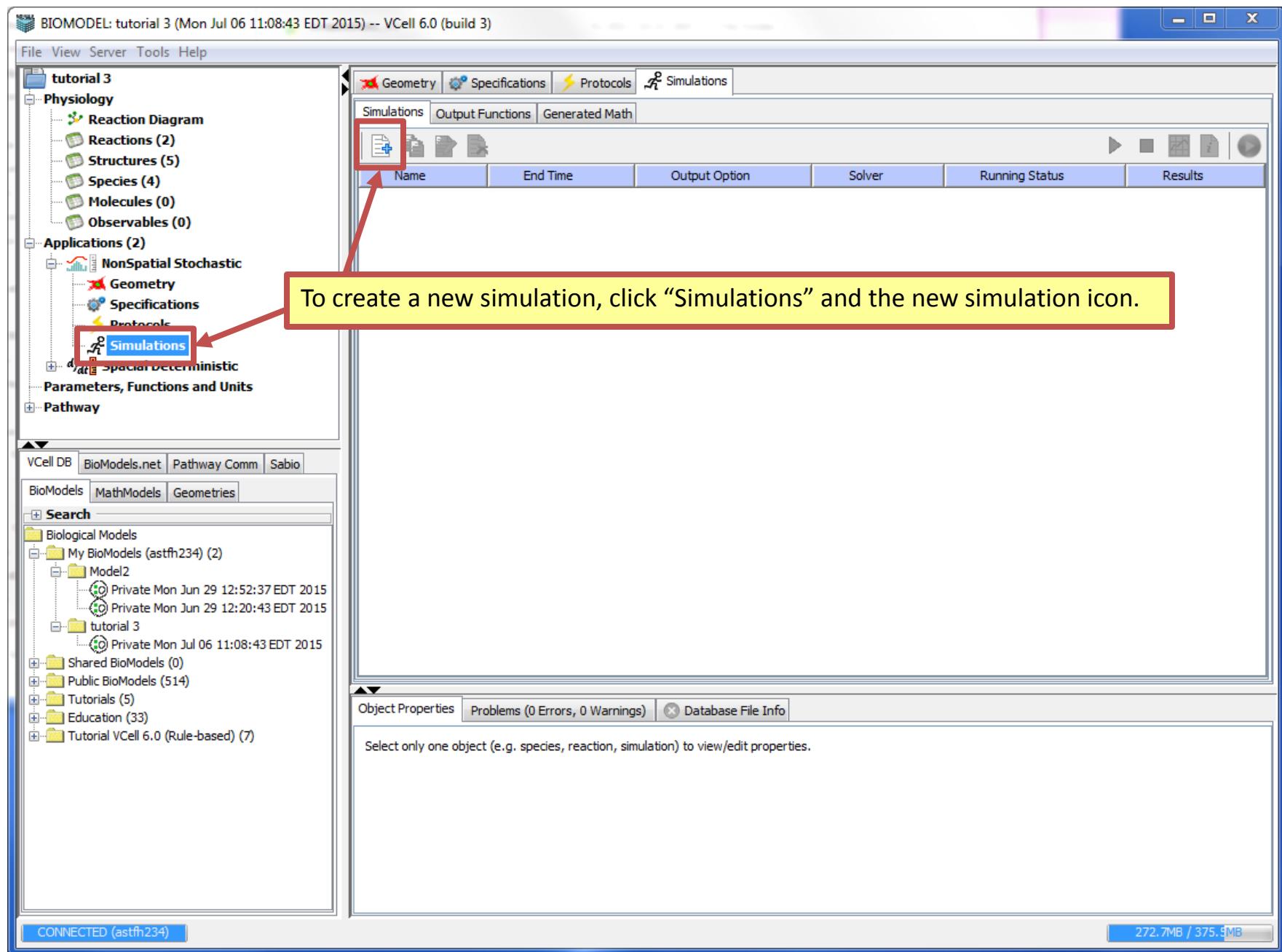
Warning:

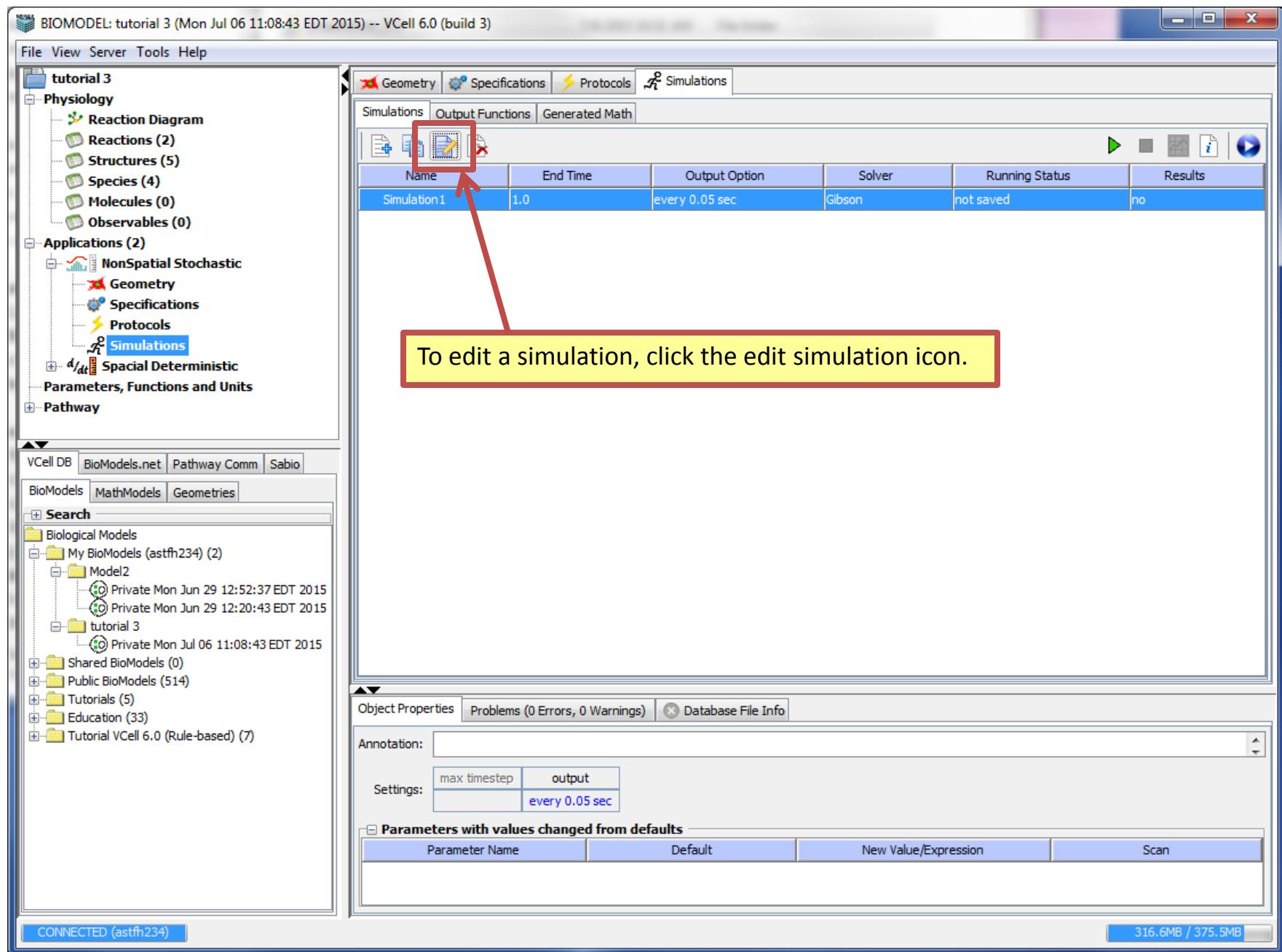
Simulations are not copied because new application is of different type.

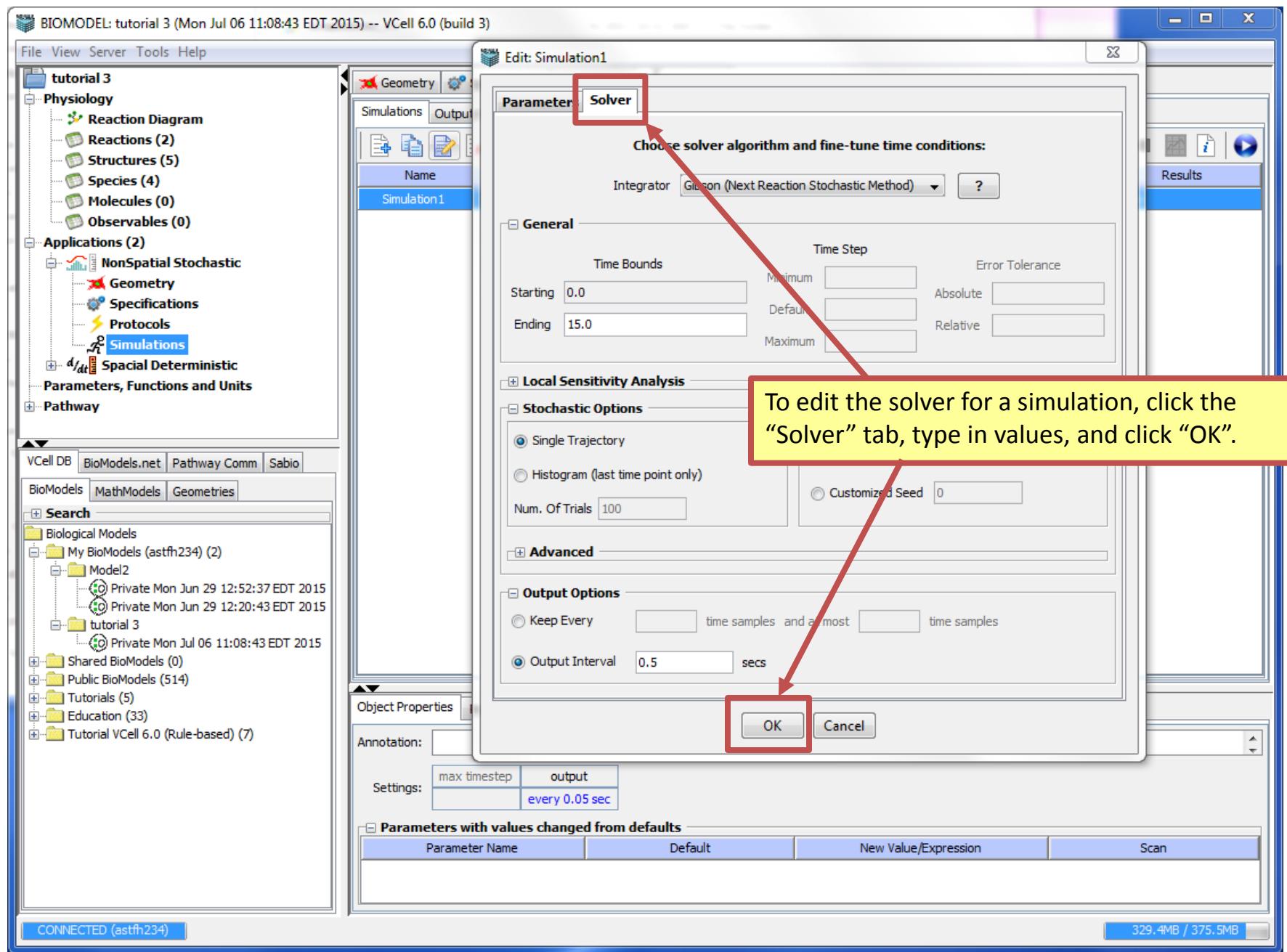
OK

Click "OK".









The screenshot shows the VCell 6.0 software interface. On the left, there's a tree view of a model named "tutorial 3". Under "Physiology", it lists "Reaction Diagram", "Reactions (2)", "Structures (5)", "Species (4)", "Molecules (0)", and "Observables (0)". Under "Applications (2)", it lists "NonSpatial Stochastic" (with "Geometry", "Specifications", "Protocols", and "Simulations" sub-options) and "Spatial Deterministic". Below these are "Parameters, Functions and Units" and "Pathway".

The main workspace is titled "BIOMODEL: tutorial 3 (Mon Jul 06 11:50:10 EDT 2015) -- VCell 6.0 (build 3)". It features tabs for "Geometry", "Specifications", "Protocols", and "Simulations". The "Simulations" tab is active, showing a table with one row:

Name	End Time	Output Option	Solver	Running Status	Results
Simulation1	15.0	every 0.5 sec	Gibson	completed	yes

A red box highlights the green play button icon in the "Running Status" column, and another red arrow points from a yellow callout box to this icon. The callout box contains the text: "To run a simulation, click the green play icon and wait until the Running Status is 'completed'."

At the bottom left, there's a "Search" panel for "Biological Models" with sections for "My BioModels", "Shared BioModels", "Public BioModels", "Tutorials", "Education", and "Tutorial VCell 6.0 (Rule-based)".

At the bottom right, there are tabs for "Object Properties", "Problems (0 Errors, 0 Warnings)", and "Database File Info". The "Object Properties" tab shows settings for "max timestep" (set to "output every 0.5 sec").

At the very bottom, status bars show "CONNECTED (astfh234)" on the left and "267MB / 401,3MB" on the right.

The screenshot shows the VCell 6.0 software interface. On the left, there's a tree view of a model named "tutorial 3". Under "Physiology", there are sections for Reaction Diagram, Reactions (2), Structures (5), Species (4), Molecules (0), and Observables (0). Under "Applications (2)", there are NonSpatial Stochastic (with Geometry, Specifications, Protocols, Simulations) and Spacial Deterministic (with d/dt). Other sections include Parameters, Functions and Units and Pathway. Below this is a "VCell DB" section with tabs for BioModels.net, Pathway Comm, and Sabio. The BioModels tab is selected, showing a search bar and a list of biological models, including "My BioModels (astfh234)" which contains "Model2" and "tutorial 3". "Model2" has two entries: "Private Mon Jun 29 12:52:37 EDT 2015" and "Private Mon Jun 29 12:20:43 EDT 2015". "tutorial 3" has one entry: "Private Mon Jul 06 11:50:10 EDT 2015". The main workspace on the right is titled "Simulations" and contains tabs for Simulations, Output Functions, and Generated Math. It lists a single simulation named "Simulation1" with parameters: End Time = 15.0, Output Option = every 0.5 sec, Solver = Gibson, Running Status = completed, and Results = yes. A red arrow points from a callout box to the "Results" icon in the toolbar above the table. The bottom of the interface shows tabs for Object Properties, Problems (0 Errors, 0 Warnings), and Database File Info. The "Object Properties" tab is active, showing settings for max timestep (output) and output every 0.5 sec. A table at the bottom lists parameters with values changed from defaults, but it is currently empty.

To view simulation results, click the simulation and click the results icon.

Name	End Time	Output Option	Solver	Running Status	Results
Simulation1	15.0	every 0.5 sec	Gibson	completed	yes

Annotation: \_\_\_\_\_

Settings:

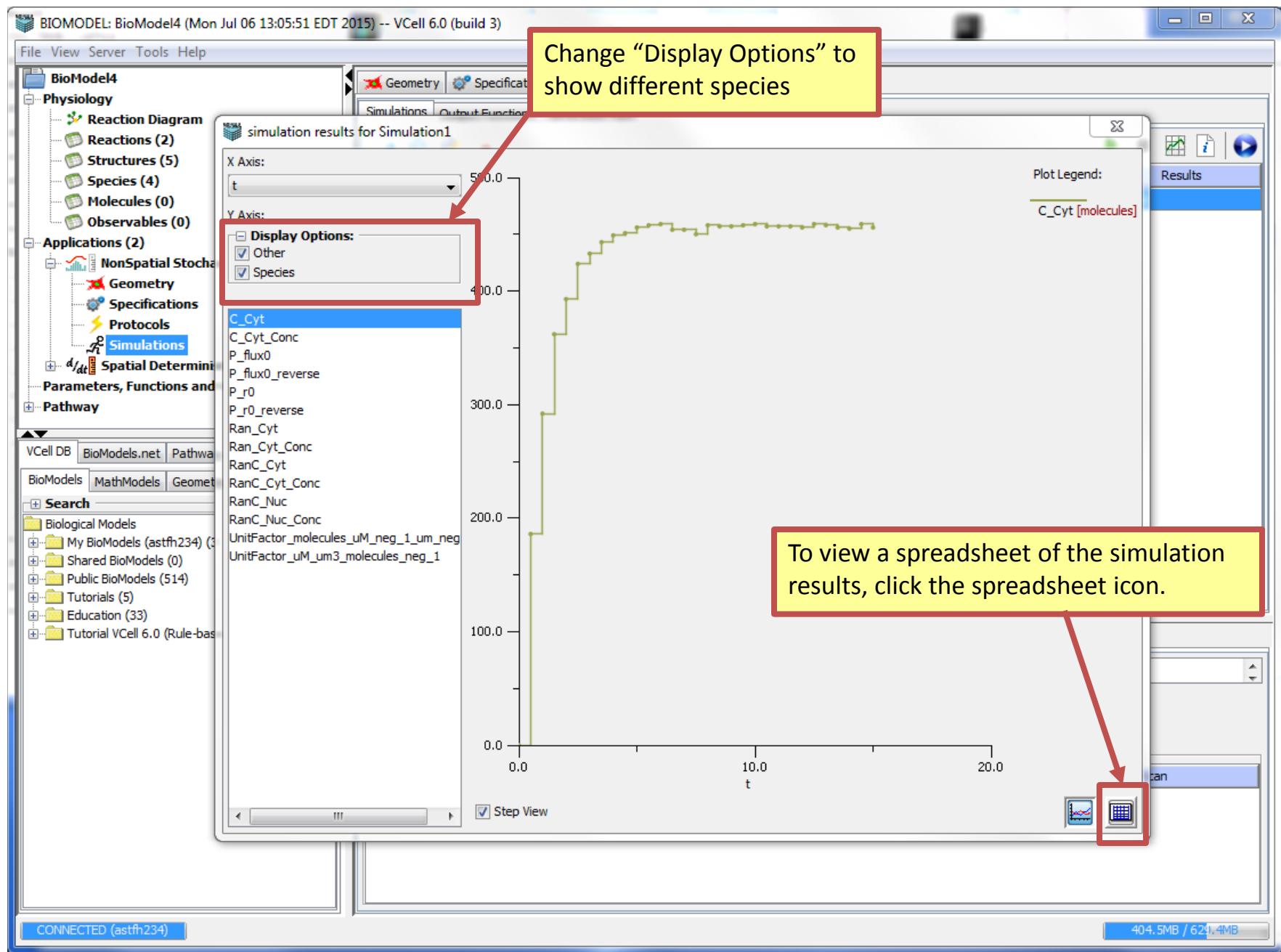
max timestep	output
	every 0.5 sec

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan

CONNECTED (astfh234)

267MB / 401,3MB



BIMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4  
Physiology  
Reaction Diagram Reactions (2)  
Structures (5)  
Species (4)  
Molecules (0)  
Observables (0)  
Applications (2)  
NonSpatial Stochastic  
Geometry  
Specifications  
Protocols  
Simulations  
 $\frac{d}{dt}$  Spatial Deterministic  
Parameters, Functions and Pathway

X Axis: t  
Y Axis:  
Display Options: Other Species

simulation results for Simulation1

t	RanC_Cyt_Conc
0	0
0.5	1.7138629E-5
1	1.0735896E-5
1.5	6.4674071E-6
2	4.7858813E-6
2.5	2.5222888E-6
3	2.2635925E-6
3.5	1.4875036E-6
4	1.3581555E-6
4.5	1.1641333E-6
5	8.4076293E-7
5.5	
6	
6.5	
7	
7.5	1.2934814E-6
8	7.7608886E-7
8.5	7.7608886E-7
9	8.4076293E-7
9.5	7.1141479E-7
10	6.4674071E-7
10.5	8.4076293E-7
11	7.1141479E-7
11.5	8.4076293E-7
12	8.4076293E-7
12.5	7.1141479E-7
13	7.7608886E-7

To copy a spreadsheet, right click on a cell and click "Copy All".

VCell DB BioModels.net Pathways  
BioModels MathModels Geometries  
Search  
Biological Models  
My BioModels (astfh234) (3)  
Shared BioModels (0)  
Public BioModels (514)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based)

CONNECTED (astfh234) 453.9MB / 629.4MB

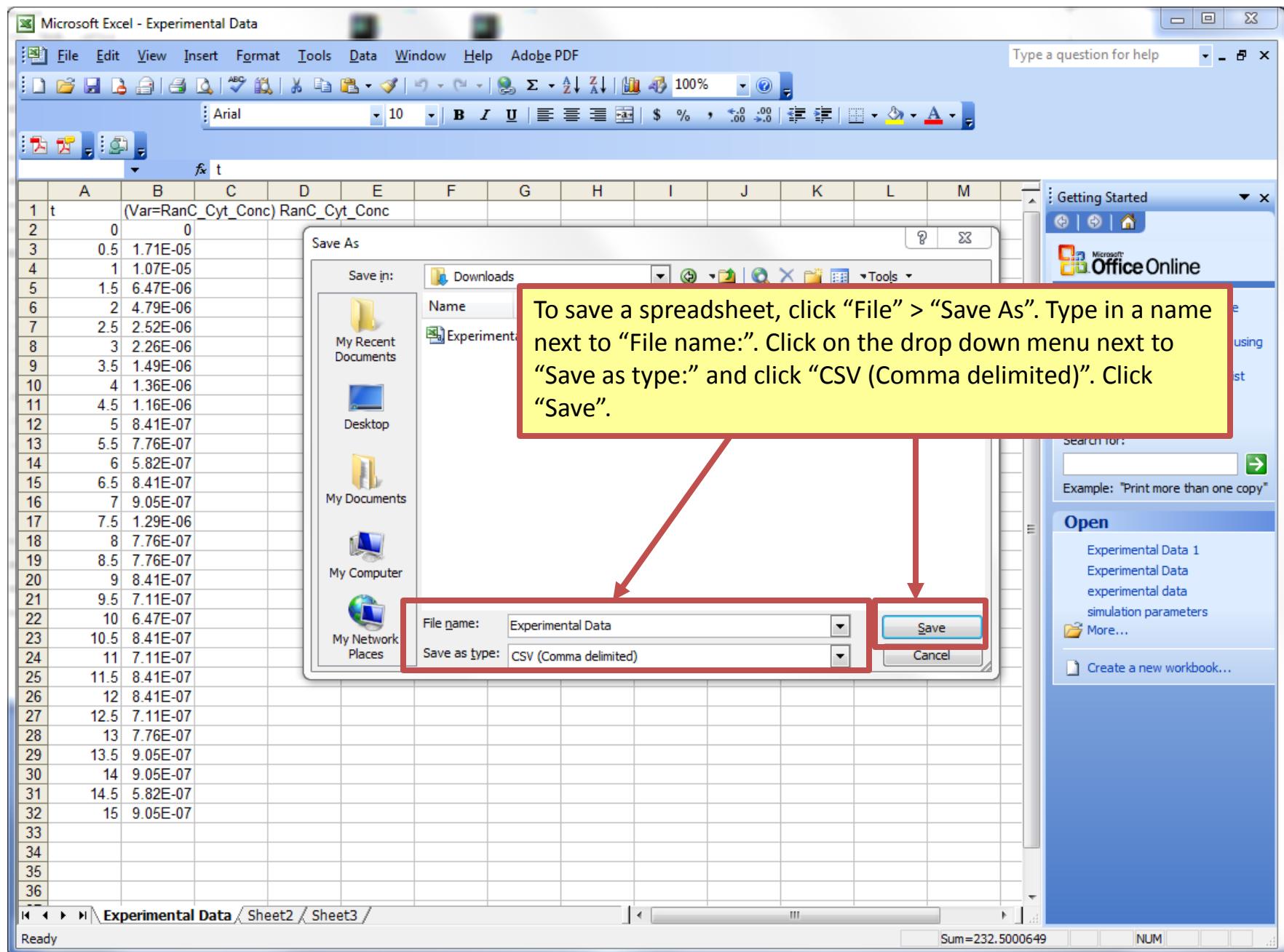
To paste a spreadsheet, open spreadsheet software, click on an empty cell, and paste

The screenshot shows a Microsoft Excel window titled "Microsoft Excel - Book1". The ribbon menu includes File, Edit, View, Insert, Format, Tools, Data, Window, Help, and Adobe PDF. The main area displays a table with columns A through M. Column A contains time values from 1 to 36. Column B contains the formula "(Var=RanC\_Cyt\_Conc)" and the value "RanC\_Cyt\_Conc". The rest of the cells in the table are empty. A yellow callout box with a red border is positioned over the first few rows of the table, containing the text "To paste a spreadsheet, open spreadsheet software, click on an empty cell, and paste". To the right of the main window is the "Getting Started" ribbon, which includes sections for "Office Online" (with links to connect to Microsoft Office Online, get news about Excel, and automatically update from the web), a search bar, and a "Create a new workbook..." button.

	A	B	C	D	E	F	G	H	I	J	K	L	M
1	t	(Var=RanC_Cyt_Conc)	RanC_Cyt_Conc										
2		0	0										
3		0.5	1.71E-05										
4		1	1.07E-05										
5		1.5	6.47E-06										
6		2	4.79E-06										
7		2.5	2.52E-06										
8		3	2.26E-06										
9		3.5	1.49E-06										
10		4	1.36E-06										
11		4.5	1.16E-06										
12		5	8.41E-07										
13		5.5	7.76E-07										
14		6	5.82E-07										
15		6.5	8.41E-07										
16		7	9.05E-07										
17		7.5	1.29E-06										
18		8	7.76E-07										
19		8.5	7.76E-07										
20		9	8.41E-07										
21		9.5	7.11E-07										
22		10	6.47E-07										
23		10.5	8.41E-07										
24		11	7.11E-07										
25		11.5	8.41E-07										
26		12	8.41E-07										
27		12.5	7.11E-07										
28		13	7.76E-07										
29		13.5	9.05E-07										
30		14	9.05E-07										
31		14.5	5.82E-07										
32		15	9.05E-07										
33													
34													
35													
36													

Sheet1 Sheet2 Sheet3

Ready Sum=232.5000649 NUM



Microsoft Excel - Experimental Data

The selected file type does not support workbooks that contain multiple sheets.

- To save only the active sheet, click OK.
- To save all sheets, save them individually using a different file name for each, or choose a file type that supports multiple sheets.

OK Cancel

Click "OK"

Experimental Data / Sheet2 / Sheet3 /

Ready Sum=232.5000649 NUM

Getting Started

Microsoft Office Online

- Connect to Microsoft Office Online
- Get the latest news about using Excel
- Automatically update this list from the web

More...

Search for:

Example: "Print more than one copy"

Open

- Experimental Data 1
- Experimental Data
- experimental data
- simulation parameters
- More...

Create a new workbook...

t	(Var=RanC_Cyt_Conc)	RanC_Cyt_Conc
1	0	0
2	0.5	1.71E-05
3	1	1.07E-05
4	1.5	6.47E-06
5	2	4.79E-06
6	2.5	2.52E-06
7	3	2.26E-06
8	3.5	1.49E-06
9	4	1.36E-06
10	4.5	1.16E-06
11	5	8.41E-07
12	5.5	7.76E-07
13	6	5.82E-07
14	6.5	8.41E-07
15	7	9.05E-07
16	7.5	1.29E-06
17	8	7.76E-07
18	8.5	7.76E-07
19	9	8.41E-07
20	9.5	7.11E-07
21	10	6.47E-07
22	10.5	8.41E-07
23	11	7.11E-07
24	11.5	8.41E-07
25	12	8.41E-07
26	12.5	7.11E-07
27	13	7.76E-07
28	13.5	9.05E-07
29	14	9.05E-07
30	14.5	5.82E-07
31	15	9.05E-07
32		
33		
34		
35		
36		

Microsoft Excel - Experimental Data

File Edit View Insert Format Tools Data Window Help Adobe PDF

Type a question for help

Getting Started

Microsoft Office Online

- Connect to Microsoft Office Online
- Get the latest news about using Excel
- Automatically update this list from the web

Experimental Data 1  
Experimental Data  
experimental data  
simulation parameters  
More...

Create a new workbook...

Experimental Data.csv may contain features that are not compatible with CSV (Comma delimited). Do you want to keep the workbook in this format?

- To keep this format, which leaves out any incompatible features, click Yes.
- To preserve the features, click No. Then save a copy in the latest Excel format.
- To see what might be lost, click Help.

Yes      No      Help

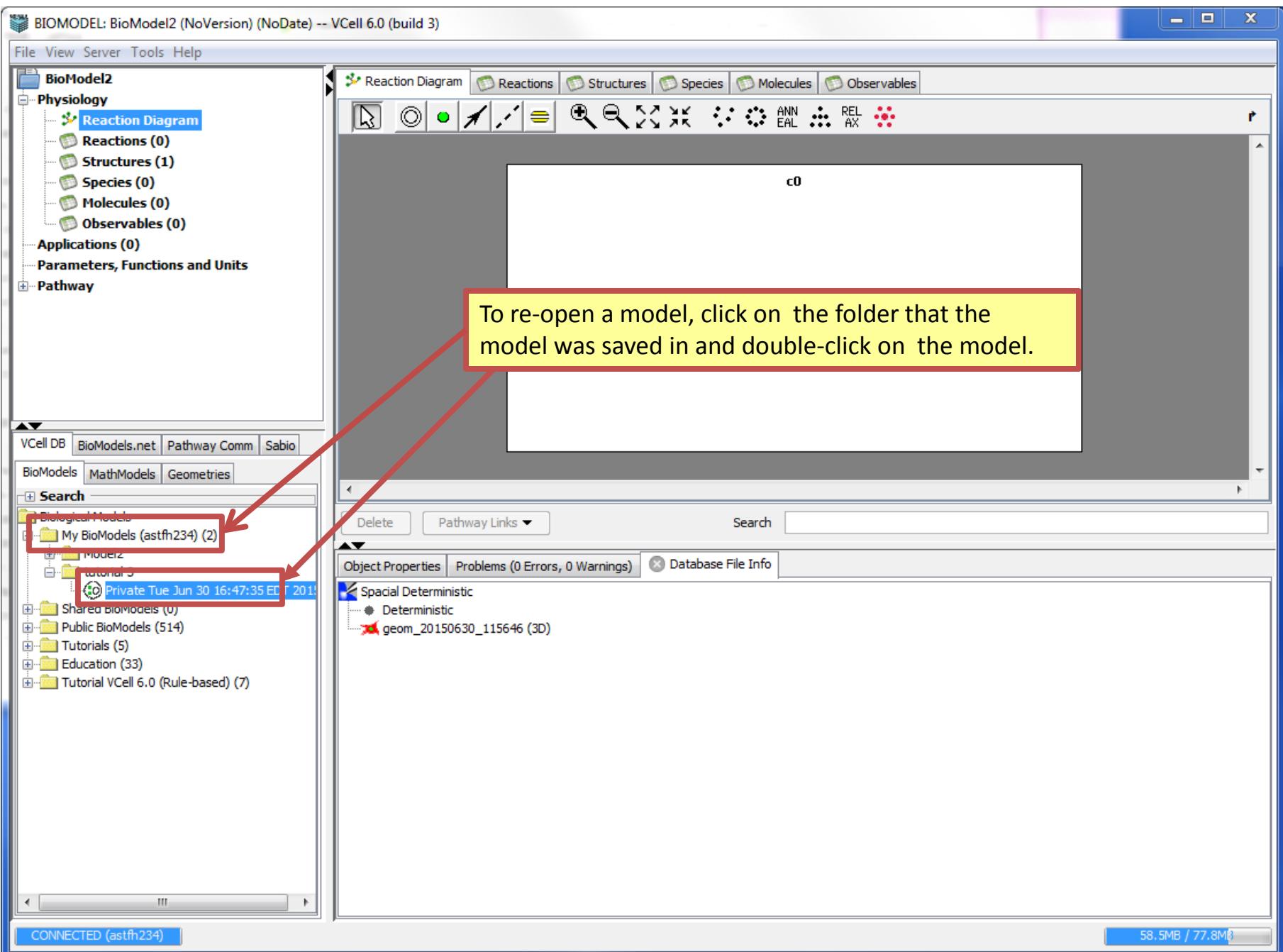
Click "Yes".

This application is now complete.

t	(Var=RanC_Cyt_Conc)	RanC_Cyt_Conc
0	0	
0.5	1.71E-05	
1	1.07E-05	
1.5	6.47E-06	
2	4.79E-06	
2.5	2.52E-06	
3	2.26E-06	
3.5	1.49E-06	
4	1.36E-06	
4.5	1.16E-06	
5	8.41E-07	
5.5	7.76E-07	
6	5.82E-07	
6.5	8.41E-07	
7	9.05E-07	
7.5	1.29E-06	
8	7.76E-07	
8.5	7.76E-07	
9	8.41E-07	
9.5	7.11E-07	
10	6.47E-07	
10.5	8.41E-07	
11	7.11E-07	
11.5	8.41E-07	
12	8.41E-07	
12.5	7.11E-07	
13	7.76E-07	
13.5	9.05E-07	
14	9.05E-07	
14.5	5.82E-07	
15	9.05E-07	
33		
34		
35		
36		

Experimental Data / Sheet2 / Sheet3 /

Ready      Sum=232.5000649      NUM

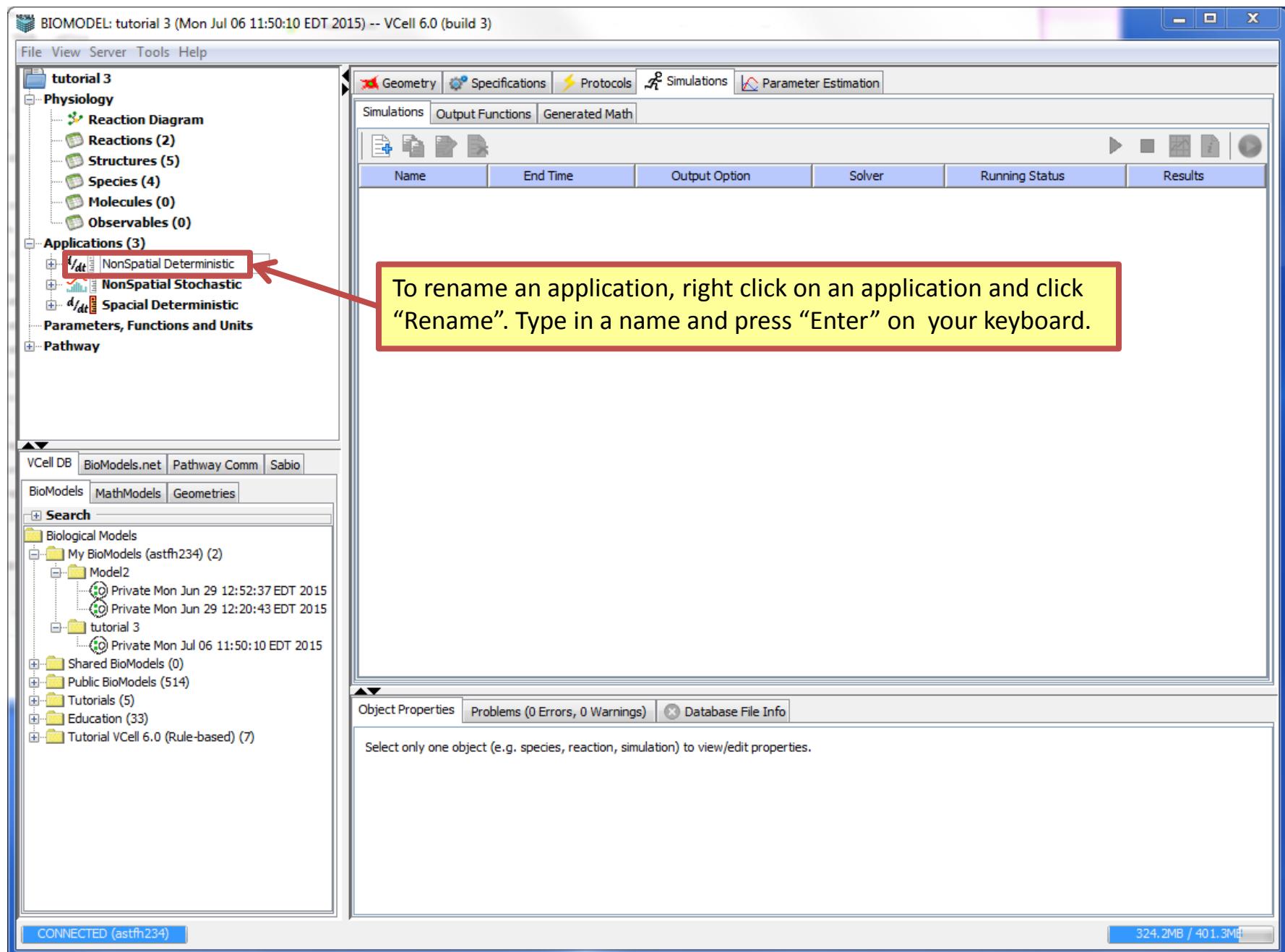


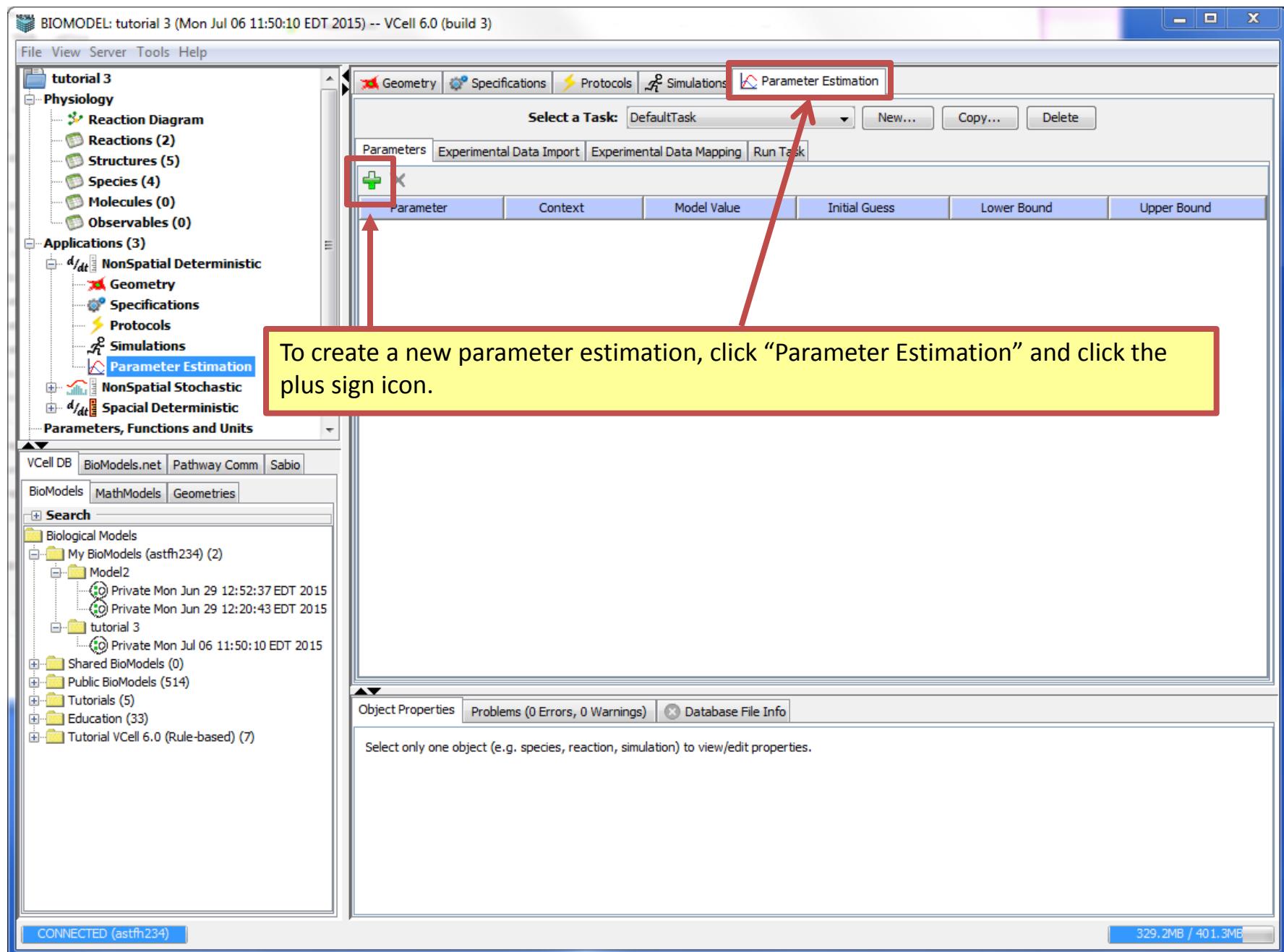
The screenshot shows the VCell 6.0 application window. The title bar reads "BIOMODEL: tutorial 3 (Mon Jul 06 11:50:10 EDT 2015) -- VCell 6.0 (build 3)". The menu bar includes File, View, Server, Tools, and Help. The toolbar has icons for Geometry, Specifications, Protocols, and Simulations. The main interface is divided into several panes:

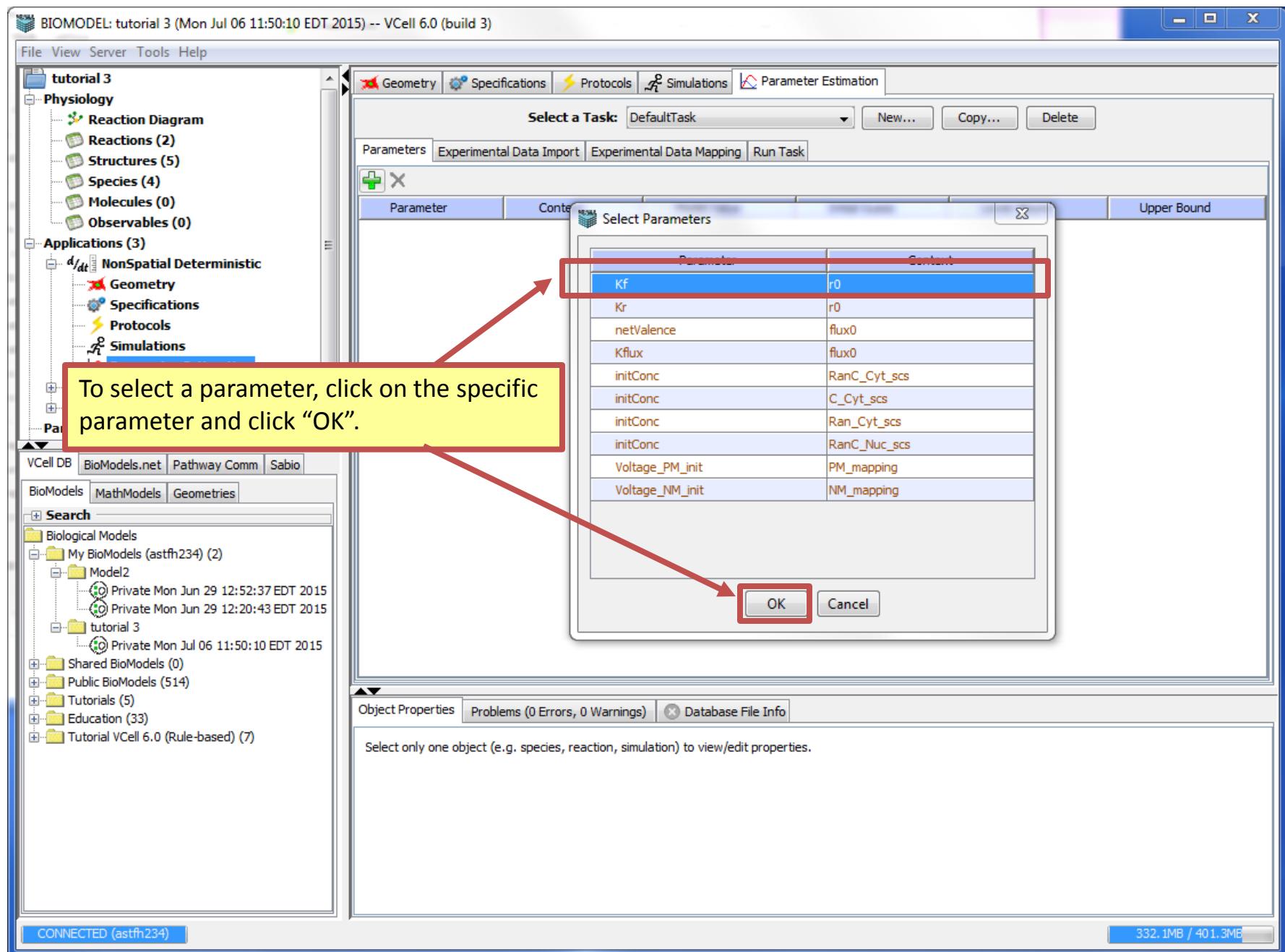
- Left pane (Tree View):** Shows a tree structure under "tutorial 3".
  - Physiology:** Reaction Diagram, Reactions (2), Structures (5), Species (4), Molecules (0), Observables (0).
  - Applications (2):** NonSpatial Stochastic, Spacial Deterministic (highlighted with a red box and arrow).
  - Parameters, Functions and Units
  - Pathway
- Top right pane (Simulations Tab):** Shows tabs for Simulations, Output Functions, and Generated Math. A yellow callout box contains the following text:

To create a non-spatial deterministic copy of an application, right click on an application and click “Copy As” > “Non-Spatial” > “Deterministic”.
- Bottom left pane (Database):** Includes tabs for VCell DB, BioModels.net, Pathway Comm, and Sabio. Under "BioModels", it lists My BioModels (astfh234) (2), Shared BioModels (0), Public BioModels (514), Tutorials (5), Education (33), and Tutorial VCell 6.0 (Rule-based) (7). A search bar is also present.
- Bottom right pane (Object Properties):** Displays "Object Properties", "Problems (0 Errors, 0 Warnings)", and "Database File Info". A message at the bottom says "Select only one object (e.g. species, reaction, simulation) to view/edit properties."

At the bottom of the window, status bars indicate "CONNECTED (astfh234)" and "246.6MB / 401.3MB".







BIMODEL: tutorial 3 (Mon Jul 06 11:50:10 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

**Physiology**

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

**Applications (3)**

- $\frac{d}{dt}$  NonSpatial Deterministic
  - Geometry
  - Specifications
  - Protocols
  - Simulations
  - Parameter Estimation
- $\frac{d}{dt}$  NonSpatial Stochastic
- $\frac{d}{dt}$  Spacial Deterministic

Parameters, Functions and Units

Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

+ Search

Biological Models

- My BioModels (astfh234) (2)
  - Model2
    - Private Mon Jun 29 12:52:37 EDT 2015
    - Private Mon Jun 29 12:20:43 EDT 2015
  - tutorial 3
    - Private Mon Jul 06 11:50:10 EDT 2015
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations Parameter Estimation

Select a Task: DefaultTask New... Copy... Delete

Parameters Experimental Data Import Experimental Data Mapping Run Task

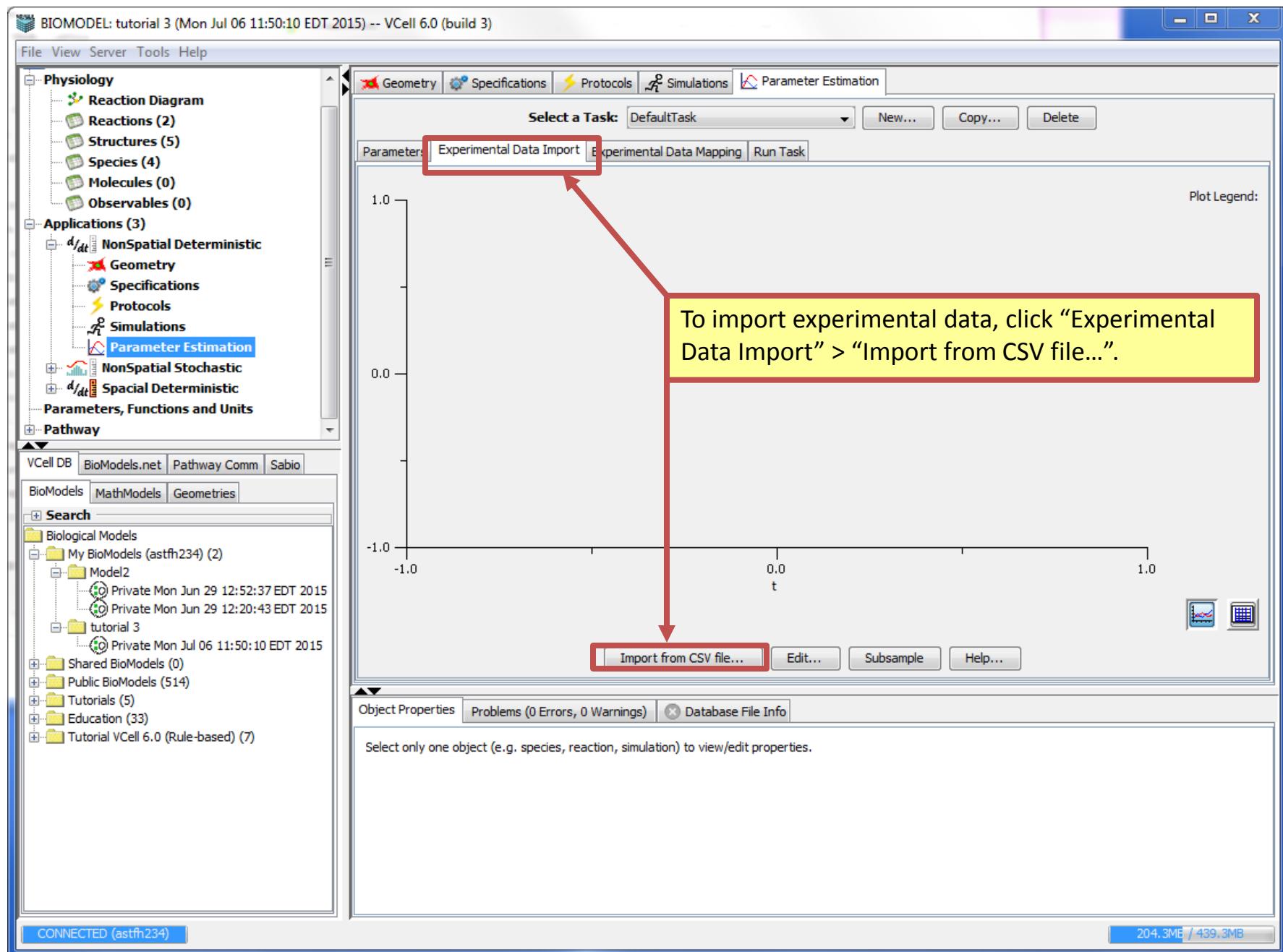
Parameter	Context	Model Value	Initial Guess	Lower Bound	Upper Bound
Kf	r0		1	1	0.1 10
Kr	r0	1000		1000	100 10000

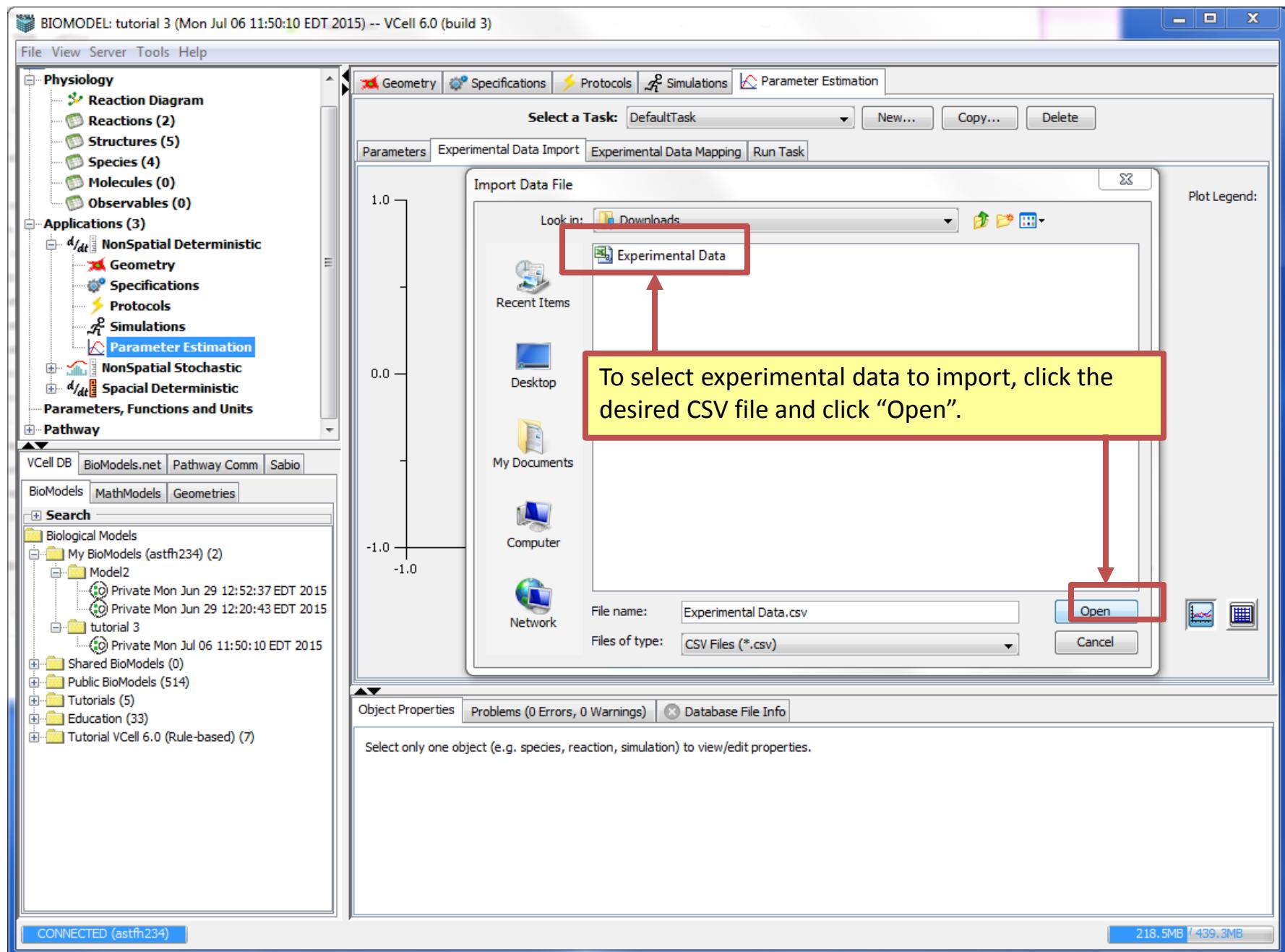
Continue adding parameters until you have reached your desired amount.

Object Properties Problems (0 Errors, 0 Warnings) Database File Info

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

CONNECTED (astfh234) 251.8MB / 439.3MB

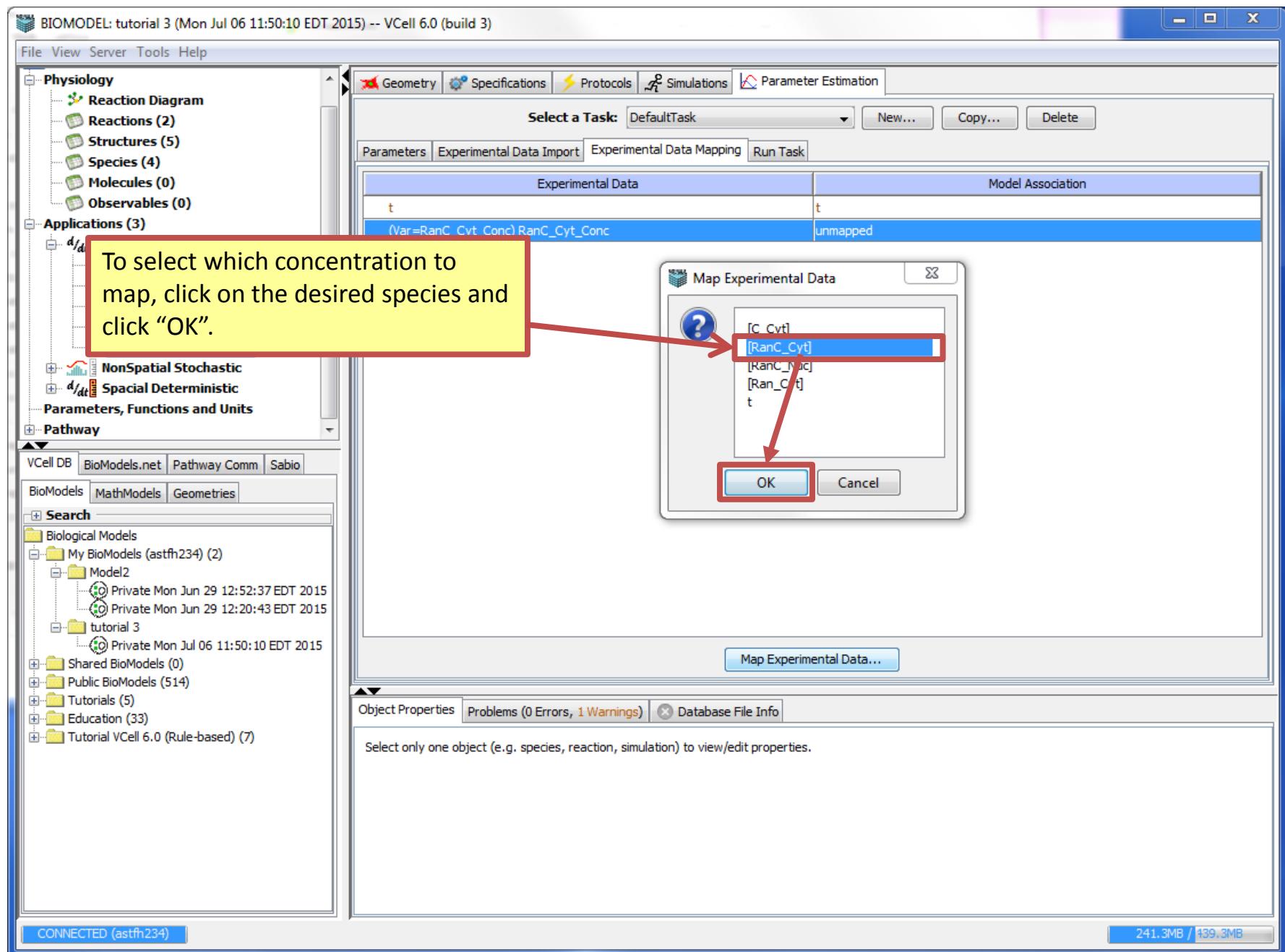




To map a concentration, click “Experimental Data Mapping” > an unmapped concentration > “Map Experimental Data...”

The screenshot shows the VCell 6.0 interface with the following details:

- Title Bar:** BIOMODEL: tutorial 3 (Mon Jul 06 11:50:10 EDT 2015) -- VCell 6.0 (build 3)
- Menu Bar:** File View Server Tools Help
- Left Sidebar:** Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables), Applications (NonSpatial Deterministic, NonSpatial Stochastic, Spatial Deterministic), Parameters, Functions and Pathway.
- Bottom Left:** VCell DB, BioModels.net, Pathway Comm, Sabio. Submenu under BioModels shows: My BioModels (astfh234) (2), Model2, tutorial 3, Shared BioModels (0), Public BioModels (514), Tutorials (5), Education (33), Tutorial VCell 6.0 (Rule-based) (7).
- Central Area:** Task bar with tabs: Geometry, Specifications, Protocols, Simulations, Parameter Estimation. The "Experimental Data Mapping" tab is highlighted with a red border. Below it is a table titled "Experimental Data" with columns "Experimental Data" and "Model Association". A row is selected, showing "t" in both columns. Another row is highlighted with a blue background, showing "(Var=RanC\_Cyt\_Conc) RanC\_Cyt\_Conc" in the first column and "unmapped" in the second column.
- Bottom Right:** Object Properties, Problems (0 Errors, 1 Warnings), Database File Info. A message says: "Select only one object (e.g. species, reaction, simulation) to view/edit properties."
- Bottom Status Bar:** CONNECTED (astfh234), 236.9MB / 439.3MB



The screenshot shows the BIOMODEL: tutorial 3 interface in VCell 6.0. The main window title is "BIOMODEL: tutorial 3 (Mon Jul 06 11:50:10 EDT 2015) -- VCell 6.0 (build 3)". The left sidebar contains a tree view of model components under "Physiology" and "Applications". The "Parameter Estimation" node under Applications is selected. The top menu bar includes File, View, Server, Tools, and Help. The toolbar has tabs for Geometry, Specifications, Protocols, Simulations, and Parameter Estimation. The main workspace is titled "Select a Task: DefaultTask". It features a "Supported COPASI Methods" section with a dropdown set to "Evolutionary Programming" and a table of parameters:

Parameter	Value
Number of Generations	200
Population Size	20
Random Number Generator	1
Seed	0

A red arrow points from the "Run Task" button in the toolbar to a yellow callout box containing the text: "To solve for parameter estimations, click “Run Task”> “Solve by Copasi”.". Another red arrow points from the "Solve by Copasi" button in the bottom right of the workspace to the same callout box. The workspace also includes sections for "Parameters", "Experimental Data Import", "Experimental Data Mapping", and "Solution". The bottom status bar shows "CONNECTED (astfh234)" and memory usage "251.4MB / 439.3MB".

To solve for parameter estimations, click “Run Task”> “Solve by Copasi”.

Number of Runs: 1

Solve by Copasi | Copasi Methods Help

See COPASI for additional parameter estimation options and model analysis features

Object Properties | Problems (0 Errors, 0 Warnings) | Database File Info

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

251.4MB / 439.3MB

BIOMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4  
Physiology  
Reaction Diagram  
Reactions (2)  
Structures (5)  
Species (4)  
Molecules (0)  
Observables (0)  
Applications (3)  
d/dt NonSpatial Deterministic  
Geometry  
Specifications  
Protocols  
Simulations  
Parameter Estimation  
NonSpatial Stochastic  
d/dt Spatial Deterministic  
Parameters Functions and Units

VCell DB BioModels.net Pathway Comm Sabio  
BioModels MathModels Geometries  
Search  
Biological Models  
My BioModels (astfh234) (3)  
Shared BioModels (0)  
Public BioModels (514)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Parameter Estimation  
Supported COPASI Methods  
Evolutionary Programming  
Parameter Value  
Number of Generations 200  
Population Size 20  
Random Number Generator 1  
Seed 0  
Number of Runs: 1  
Solve by Copasi Copasi Methods Help  
See COPASI for additional parameter estimation options and model analysis features

Object Properties Problems (0 Errors, 0 Warnings)  
Select only one object (e.g. species, reaction, simulation) to view/edit properties.

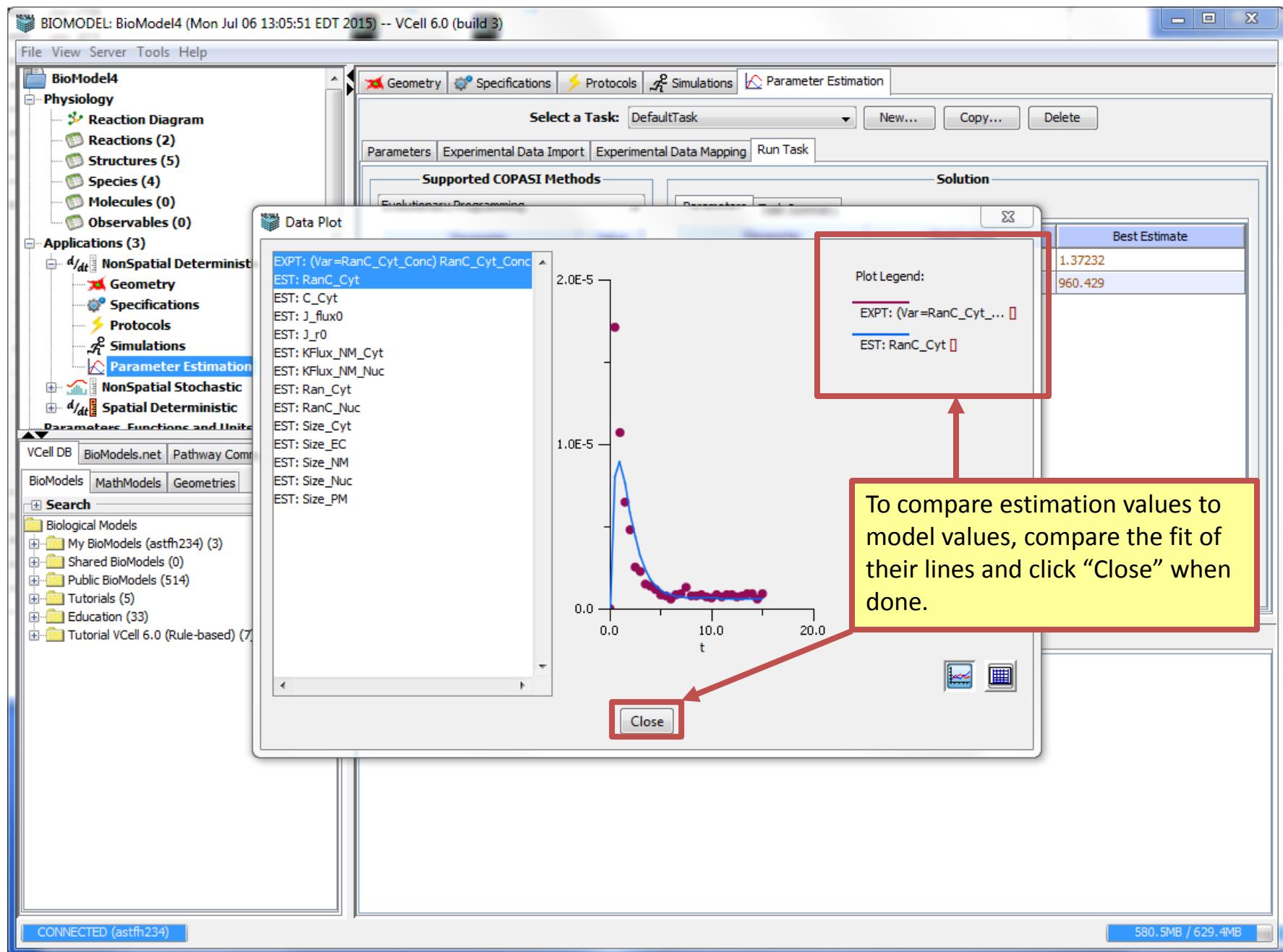
Plot Create New Simulation from Solution...

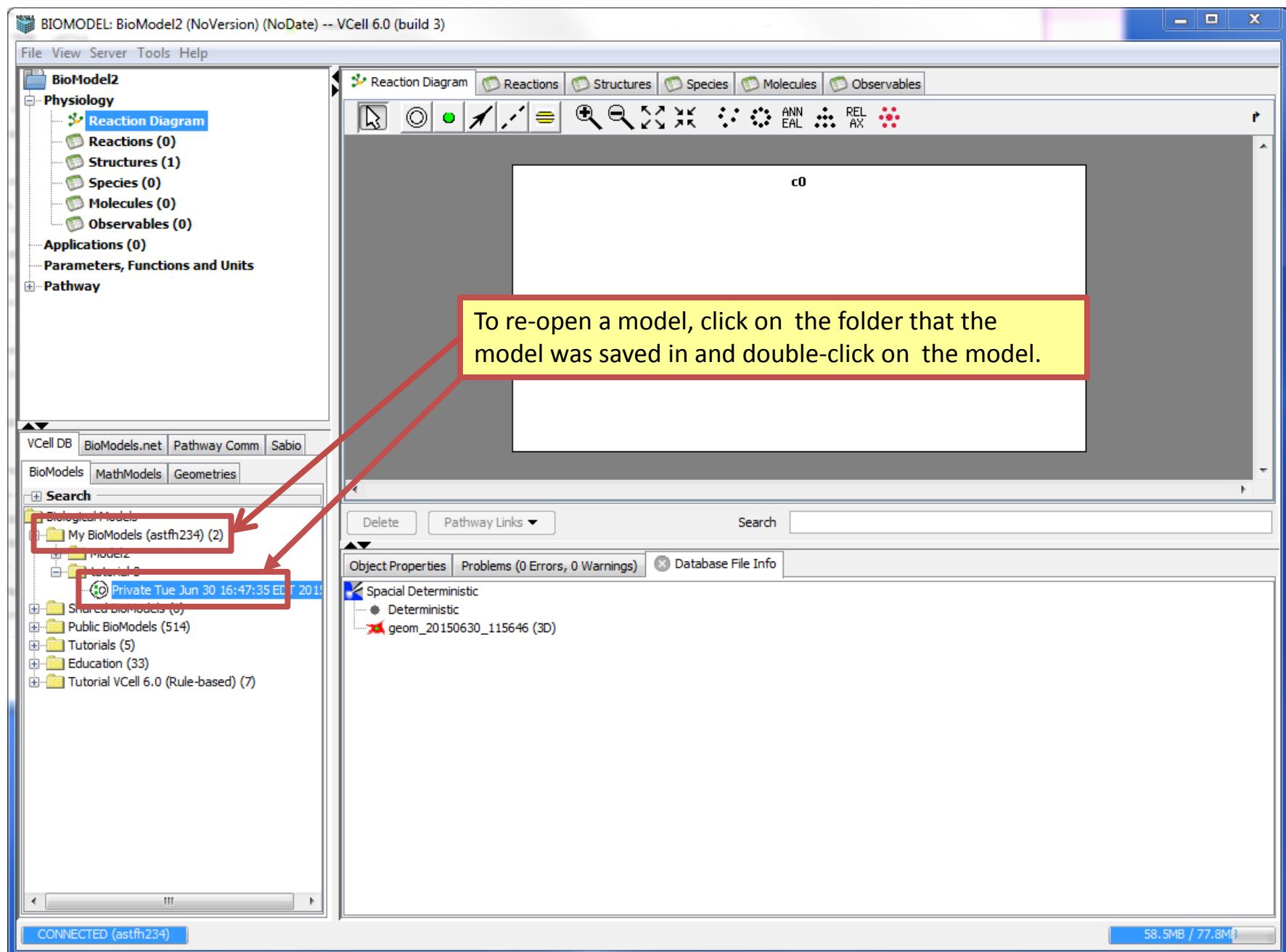
Notice how accurate the estimate is in relation to the model value

Parameter	Model Value	Best Estimate
Kf	1	1.37232
Kr	1000	960.429

To plot estimation values versus model values, click "Plot".

CONNECTED (astfh234) 571.8MB / 629.4MB





BIMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4  
Physiology  
Reaction Diagram  
Reactions (2)  
Structures (5)  
Species (4)  
Molecules (0)  
Observables (0)  
Applications (3)  
 $\frac{d}{dt}$  NonSpatial Deterministic  
 $\frac{d}{dt}$  NonSpatial Stochastic  
 $\frac{d}{dt}$  Spatial Deterministic  
Parameters, Functions and Units  
Pathway

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

All structures and subdomains must be mapped to run a simulation.

To create a spatial stochastic copy an application, right click on an application and click “Copy As” > “Spatial” > “Stochastic”.

Geometry (subdomains)

- background
- Nuc
- Cyt
- Cyt\_background\_membrane
- Cyt\_Nuc\_membrane

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+	Z-	Z+
EC	background	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Cyt	Cyt	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Nuc	Nuc	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
PM	Cyt_background_me...	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

Biological Models  
My BioModels (astfh234) (3)  
Shared BioModels (0)  
Public BioModels (514)  
Tutorials (5)  
Education (33)  
Tutorial VCell 6.0 (Rule-based) (7)

Object Properties Problems (0 Errors, 0 Warnings)

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

CONNECTED (astfh234)

466.5MB / 629.4MB

BIMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4  
Physiology  
Reaction Diagram  
Reactions (2)  
Structures (5)  
Species (4)  
Molecules (0)  
Observables (0)  
Applications (4)  
Spatial Stochastic  
NonSpatial Deterministic  
NonSpatial Stochastic  
Spatial Deterministic  
Parameters, Functions and Units  
Pathway

Geometry Specifications Protocols Simulations

Right click the application and press “Rename” to type in a new name. Press “Enter” on your keyboard.

EC Cyt Nuc PM NM

Geometry (subdomains)

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+	Z-	Z+
EC	background	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Cyt	Cyt	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
Nuc	Nuc	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux
PM	Cyt_background_me...	1 [ 1 ]	Flux	Flux	Flux	Flux	Flux	Flux

Object Properties Problems (0 Errors, 0 Warnings)

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

CONNECTED (astfh234) 609.6MB / 629.4MB

The screenshot shows the VCell 6.0 interface for BioModel4. The main window has tabs for Geometry, Specifications, Protocols, and Simulations. The Specifications tab is selected, showing a table of species and their initial conditions. A red box highlights the 'Initial Condition' column, and another red box highlights the radio button for 'Number of Particles'. A yellow callout box contains the text: "To work with number of particles instead of concentration (for stochastic models only), double click your new application and click ‘Specifications’ > ‘Number of Particles’".

BIOMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4

Physiology

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (4)

- Spatial Stochastic
  - Geometry
  - Specifications
  - Protocols
  - Simulations
- NonSpatial Deterministic
- NonSpatial Stochastic
- Spatial Deterministic

Parameters Functions and Units

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

Biological Models

- My BioModels (astfh234) (3)
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Object Properties Problems (0 Errors, 0 Warnings)

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

CONNECTED (astfh234)

365.5MB / 795.8MB

To work with number of particles instead of concentration (for stochastic models only), double click your new application and click “Specifications” > “Number of Particles”.

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant	Force Continuous
RanC_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
C_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
Ran_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
RanC_Nuc	Nuc	<input type="checkbox"/>	471.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>

The screenshot shows the VCell 6.0 interface for BioModel4. On the left, the navigation pane includes sections for BioModel4, Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables), Applications (Spatial Stochastic, NonSpatial Deterministic, NonSpatial Stochastic, Spatial Deterministic), and Database links (VCell DB, BioModels.net, Pathway Comm, Sabio). Below these are tabs for BioModels, MathModels, and Geometries, along with a search bar.

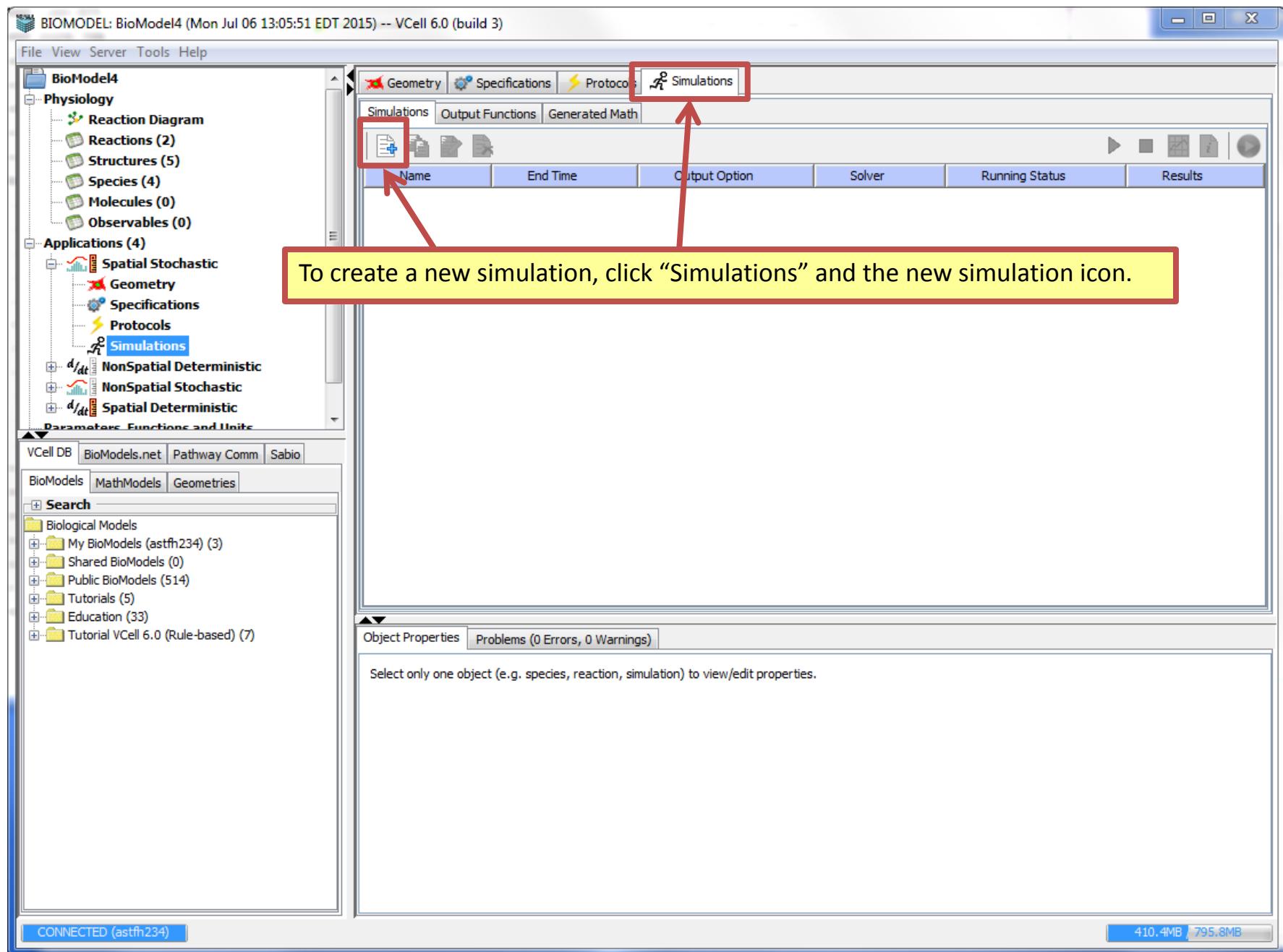
The main workspace displays a table under the "Species" tab. The table has columns for Species, Structure, Clamped, Initial Condition, Well Mixed, Diffusion Constant, and Force Continuous. A red box highlights the "Initial Condition" column for the species "RanC\_Nuc", which is set to "1000". An arrow points from a yellow callout box below the table to this highlighted cell.

**To change the number of particles of a species, type in a value under the “Initial Condition” column.**

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant	Force Continuous
RanC_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
C_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
Ran_Cyt	Cyt	<input type="checkbox"/>	0.0	<input type="checkbox"/>	10.0	<input type="checkbox"/>
RanC_Nuc	Nuc	<input checked="" type="checkbox"/>	1000	<input type="checkbox"/>	10.0	<input type="checkbox"/>

At the bottom, the "Object Properties" tab is active, showing parameters for RanC\_Nuc, such as initial count (initCount), diffusion constant (diff), and boundary conditions (BC\_Xm, BC\_Xp, BC\_Ym, BC\_Yp, BC\_Zm, BC\_Zp) and velocities (Vel\_X, Vel\_Y).

Bottom status bar: CONNECTED (astfh234) / 400MB / 795.8MB



The screenshot shows the VCell 6.0 software interface. On the left, there's a navigation tree under 'BioModel4' with sections like 'Physiology' (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables), 'Applications' (Spatial Stochastic, Geometry, Specifications, Protocols, Simulations), and 'd/dt' (NonSpatial Deterministic, NonSpatial Stochastic, Spatial Deterministic). Below this is a search bar and a list of biological models. The main workspace has tabs for 'Geometry', 'Specifications', 'Protocols', and 'Simulations'. The 'Simulations' tab is active, showing a table with columns: Name, End Time, Output Option, Solver, Running Status, and Results. A row for 'Simulation 1' is selected, and a red arrow points from a tooltip to the edit icon (pencil) in the first column of the table. A yellow callout box contains the text: 'To edit a simulation, click the simulation and click on the edit simulation icon.' At the bottom, there's an 'Object Properties' panel showing settings like timestep (1.0E-4s), output (every 0.05 sec), and mesh information (72x72x25 = 129600 elements). The 'Parameters with values changed from defaults' section is empty. The status bar at the bottom indicates 'CONNECTED (astfh234)' and memory usage '435.2MB / 795.8MB'.

To edit a simulation, click the simulation and click on the edit simulation icon.

Name	End Time	Output Option	Solver	Running Status	Results
Simulation 1	1.0	every 0.05 sec	Smoldyn	not saved	no

Annotation: \_\_\_\_\_

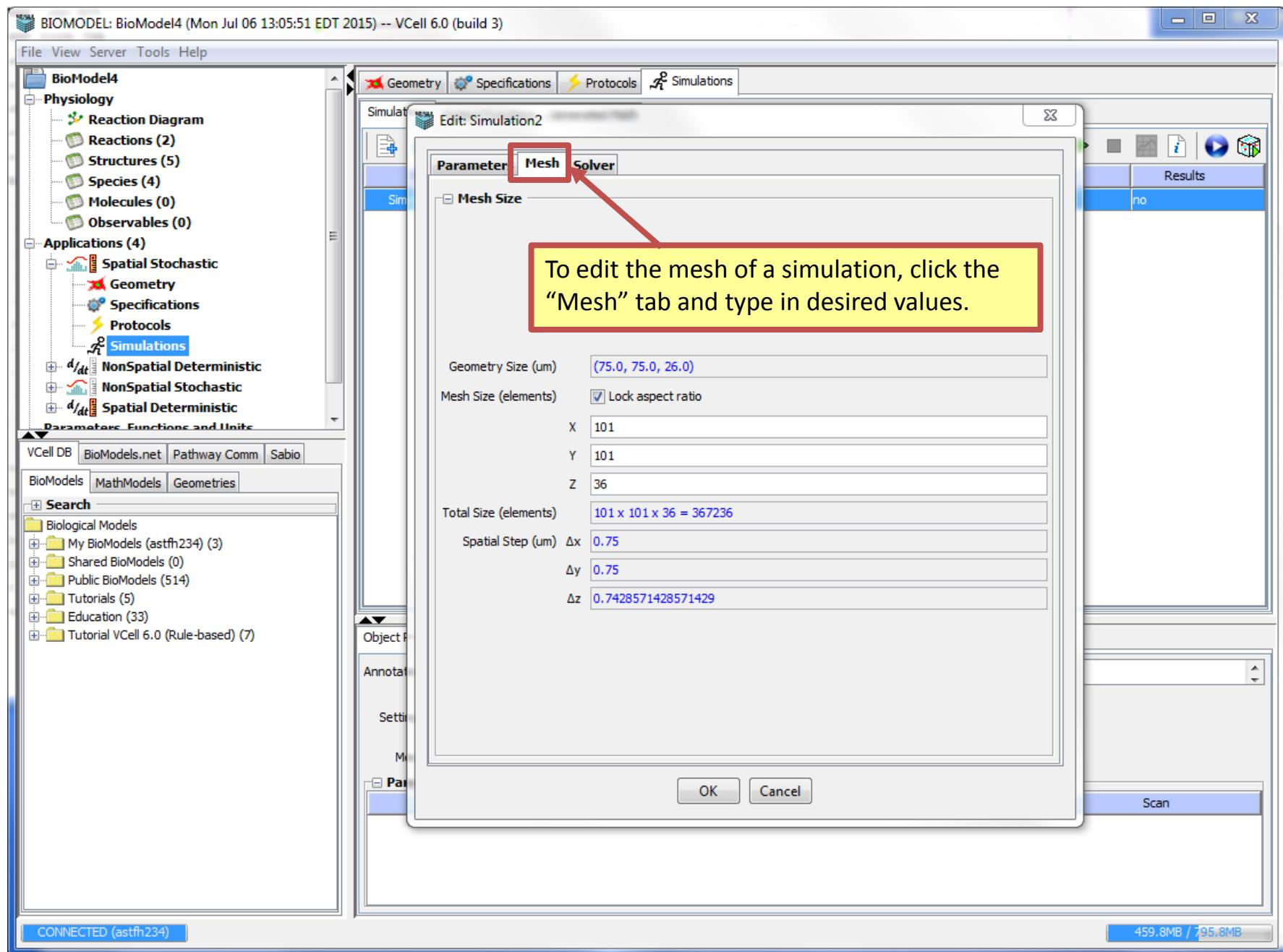
Settings:

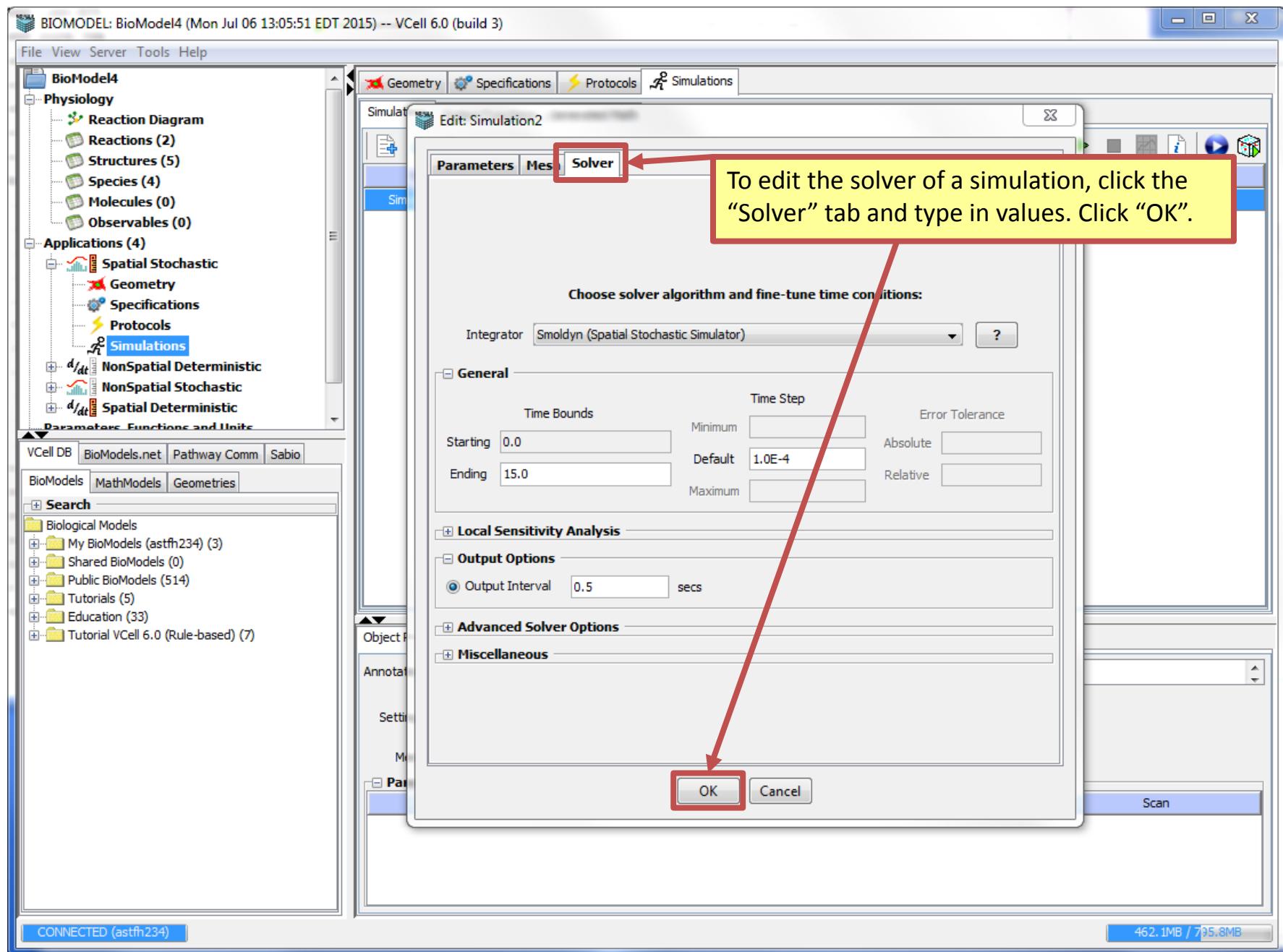
timestep	output	rel tol	abs tol
1.0E-4s	every 0.05 sec		

Mesh: 72x72x25 = 129600 elements      Geometry size: (75.0, 75.0, 26.0) microns

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan





The screenshot shows the VCell 6.0 software interface for BioModel4. The main window has a title bar "BIOMODEL: BioModel4 (Mon Jul 06 13:05:51 EDT 2015) -- VCell 6.0 (build 3)". The menu bar includes File, View, Server, Tools, and Help. On the left, there's a tree view of the model structure under "BioModel4" and "Physiology". The "Simulations" tab is selected in the top navigation bar. A table lists a single simulation entry:

Name	End Time	Output Option	Solver	Running Status	Results
Simulation2	15.0	every 0.5 sec	Smoldyn	not saved	no

A red arrow points from a yellow callout box to the green play icon in the toolbar above the table. The callout box contains the text: "To run and save a simulation, click the green play icon." At the bottom of the interface, there are tabs for "Object Properties" and "Problems (0 Errors, 0 Warnings)". The "Object Properties" tab shows settings like timestep (1.0E-4s), output (every 0.5 sec), and mesh information (101x101x36 = 367236 elements). The "Parameters with values changed from defaults" section is empty.

Bottom status bar: CONNECTED (astfh234) | 493.4MB / 795.8MB

BIOMODEL: BioModel4 (Mon Jul 06 13:48:44 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel4

Physiology

- Reaction Diagram
- Reactions (2)
- Structures (5)
- Species (4)
- Molecules (0)
- Observables (0)

Applications (4)

- NonSpatial Deterministic
- NonSpatial Stochastic
- Spatial Deterministic
- Spatial Stochastic
  - Geometry
  - Specifications
  - Protocols
  - Simulations

Parameters Functions and Units

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

+ Search

Biological Models

- My BioModels (astfh234) (3)
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Name End Time Output Option Solver Running Status Results

Simulation2	15.0	every 0.5 sec	Smoldyn	completed	yes
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To view simulation results, click the simulation and click the results icon.

Annotation:

Settings: timestep output rel tol abs tol  
1.0E-4s every 0.5 sec

Mesh: 101x101x36 = 367236 elements Geometry size: (75.0, 75.0, 26.0) microns

Parameters with values changed from defaults

Parameter Name	Default	New Value/Expression	Scan

CONNECTED (astfh234) 493.9MB / 8 0.9MB

