

VCell Tutorial

BioModel with Multiple Applications

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

Part 1: Spatial Deterministic Application using a
3D geometry derived from an image stack

The Multi-App Tutorial

- Part 1: Spatial Deterministic Application using a 3D geometry derived from an image stack

Create the Physiology for a simple Biomodel of RAN nuclear transport, create a 3D geometry directly from a z-stack of microscopy images, and run a deterministic spatial simulation.

- Part 2: Additional Applications

Compartmental stochastic application with data export; compartmental deterministic (ODE) application with parameter estimation parameters using external data; stochastic spatial application.

In Part 1 of 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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First time opening VCell

this link for details on how to acknowledge Virtual Cell in your publication and how to share your published research through the VCell database.'" data-bbox="71 242 501 881"/>

Virtual Cell login

User Name

Password

Login Cancel

Forgot Login Password...

New User Registration...

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

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 displays the VCell software interface. At the top left, the 'BioModel3' workspace is visible, containing a 'Physiology' folder with sub-items: 'Reaction Diagram', 'Reactions (0)', 'Structures (1)', 'Species (0)', 'Molecules (0)', and 'Observables (0)'. Below this are 'Applications (0)', 'Parameters, Functions and Units', and 'Pathway'. A search panel on the left shows 'BioModels', 'MathModels', and 'Geometries' tabs, with a search bar and a list of 'Biological Models' including 'My BioModels (astfh234) (1)', 'Shared BioModels (0)', 'Public BioModels (512)', 'Tutorials (5)', 'Education (33)', and 'Tutorial VCell 6.0 (Rule-based) (7)'. The main workspace features a 'Reaction Diagram' editor with a toolbar containing icons for selection, zoom, and editing. The diagram area is currently empty, showing only the text 'c0'. Below the editor is a 'Delete' button, a 'Pathway Links' dropdown, and a search input field. At the bottom, the 'Object Properties' panel shows 'Problems (0 Errors, 0 Warnings)' and 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 '16 MB / 103.9 MB'.

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

The screenshot shows a software interface for creating a compartment. On the left, a tree view shows the project structure under 'BioModel3' and 'Physiology'. The 'Reaction Diagram' tool is selected. The top toolbar contains various icons, with the compartment tool (a circle with a dot) highlighted by a red box and an arrow. The central workspace shows a compartment labeled 'c0' with two vertical dashed lines on its right side. A red arrow points from a callout box to one of these dashed lines. The bottom panel shows 'Object Properties' with a search bar and a status bar at the very bottom indicating 'CONNECTED (astfh234)' and '162.9MB / 303.9MB'.

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 software interface. On the left is a tree view for 'BioModel3' with categories like Physiology, Reactions (0), Structures (2), Species (0), Molecules (0), Observables (0), Applications (0), Parameters, Functions and Units, and Pathway. Below this is a search bar and a list of models. The main workspace shows a diagram with two compartments, 'c0' and 'm0', separated by a membrane. A red arrow points to a dotted black line on the right side of the membrane, which is highlighted with a green dashed box. A callout box with a yellow background and red border contains the text: 'To create a volumetric compartment within a membrane, click on the dotted black lines and select "add compartment"'. At the bottom, there is a status bar showing 'CONNECTED (astfh234)' and '178.4MB / 303.9MB'.

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

Multi-App tutorial part 1

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

The screenshot shows the BIOMODEL software interface. On the left is a tree view for 'BioModel3' containing 'Physiology' and its sub-items: 'Reaction Diagram', 'Reactions (0)', 'Structures (5)', 'Species (0)', 'Molecules (0)', 'Observables (0)', 'Applications (0)', 'Parameters, Functions and Units', and 'Pathway'. Below this is a search panel with 'Biological Models' and various folders like 'My BioModels (astfh234) (1)', 'Shared BioModels (0)', 'Public BioModels (512)', 'Tutorials (5)', 'Education (33)', and 'Tutorial VCell 6.0 (Rule-based) (7)'. The main workspace displays a compartment diagram with four compartments: 'c0' (white), 'm0' (grey), 'c1' (white), and 'm1' (grey). A red box highlights the selection tool in the toolbar, and another red box highlights the 'm1' compartment. A red arrow points from the selection tool to 'm1'. At the bottom, the 'Object Properties' panel for 'm1' is shown, with fields for 'Structure Name' (m1), 'Size Variable Name' (m1 [μm²]), and 'Voltage Variable Name' (Voltage_m1 [mV]). It also includes dropdowns for 'Positive (inside feature)' and 'Negative (outside feature)'. Below these are definitions for 'membrane voltage' and 'inward currents'. The status bar at the bottom shows 'CONNECTED (astfh234)' and '107.4MB / 303.9MB'.

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

To name compartments and membranes, return to selection mode.

The screenshot displays the BioModel3 software interface. On the left is a tree view of the model structure, including compartments like EC, PM, Cyt, and NM. The main workspace shows a diagram with these compartments. A red box highlights the selection tool icon in the toolbar. A second red box highlights the 'EC' compartment label in the diagram. The 'Object Properties' panel at the bottom is open, showing fields for 'Structure Name' (EC), 'Size Variable Name' (EC [μm³]), and an 'Annotation' field. A red arrow points from a text box to the 'Annotation' field. The status bar at the bottom indicates 'CONNECTED (astfh234)' and '146.3MB / 303.9MB'.

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".

To annotate compartments, type notes under "Object Properties".

The screenshot shows the VCell software interface. On the left is a tree view for 'BioModel3' with categories like Physiology, Reactions (1), Structures (5), Species (0), Molecules (0), and Observables (0). Below this is a search bar and a list of biological models. The main workspace is titled 'Reaction Diagram' and contains a cell diagram with compartments labeled 'Cyt', 'NM', and 'Nuc'. A toolbar at the top of the workspace includes icons for various tools, with the 'FluxReaction' tool (a red arrow) highlighted by a red box. A yellow callout box with a red border contains the text: 'To create a flux reaction, click on the FluxReaction tool, then click the area you want to place a flux.' An arrow from this box points to a yellow box with a red border containing a flux symbol (two horizontal lines with a vertical bar in the middle), which is placed on the 'NM' compartment. At the bottom of the interface, there is a status bar showing 'CONNECTED (astfh234)' and memory usage '151.5MB / 303.9MB'.

The screenshot shows the BIOMODEL software interface. The top-left pane displays a tree view of the model structure, including compartments (PM, Cyt, NM, Nuc) and various entities like Reactions, Structures, Species, Molecules, and Observables. The main workspace shows a reaction diagram with a flux reaction between species s_0 and s_1 . A red box highlights the reaction tool in the toolbar. Another red box highlights the flux symbol (a yellow circle with a horizontal line) on the reaction arrow. A third red box highlights the product species s_1 . A yellow callout box explains: "To connect a reactant species to a flux reaction, click on the reaction tool, click on a reaction node, and drag a line to the flux symbol". A second yellow callout box explains: "To create a product of flux reaction, use the reaction tool to drag a line from the flux to a point inside a compartment where a product species will be located." The bottom status bar shows "CONNECTED (astfh234)" and "58.3MB / 73.4MB".

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

File View Server Tools Help

BioModel1

- Physiology
 - Reaction Diagram
 - Reactions (1)
 - 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

<<REACTANT>>

s0 s1

Species Name: s0

Linked Pathway Object(s):

Annotation:

Species: s0

CONNECTED (astfh234)

53.2MB / 73.4MB

To create a reaction, click the reaction tool. If you click then on a species, it will become marked <<REACTANT>>. Drag a line from it to a point inside the compartment where you will create a reaction node.

Adjust the position of the reaction using the selection tool (mouse symbol).

The screenshot shows the BIOMODEL software interface. On the left is a tree view of the model structure. The main workspace displays a reaction diagram with species s_0 and s_1 and a reaction r_0 . A red box highlights the mouse cursor icon in the toolbar, and another red box highlights the reaction symbol r_0 in the diagram. A yellow callout box contains the text: "Drop your mouse, and a reaction symbol will be created for you." Below the diagram is a properties panel for the reaction r_0 , showing its name, kinetic type, and a table of parameters.

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

Object Properties Problems (0 Errors, 0 Warnings)

Reaction Name: r_0

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"/>	$K_f \cdot s_0$	$\mu\text{M}\cdot\text{s}^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	0.0	s^{-1}
Kr	reverse rate constant	<input type="checkbox"/>	0.0	$\mu\text{M}\cdot\text{s}^{-1}$
s_0	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

CONNECTED (astfh234) 54.7MB / 73.4MB

The screenshot shows the BIOMODEL software interface. The main workspace displays a reaction diagram with four compartments: PM, Cyt, NM, and Nuc. A reaction labeled 'r0' is located in the Cyt compartment. It shows a reactant species 's0' (green circle) and a product species 's1' (green circle). The reaction is represented by a red arrow pointing from 's0' to 's1', with a red box around the arrowhead. A yellow callout box with a red border 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." The callout box has two red arrows: one pointing to the reaction symbol in the toolbar and another pointing to the red box around the reaction arrowhead. The bottom panel shows the 'Object Properties' for the reaction 'r0', including its name, kinetic type (Mass Action), and a table of parameters.

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 [$\text{molecules}\cdot\text{s}^{-1}$]

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	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	μM

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

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.

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 (astfh234) 60.2MB / 73.4MB

The screenshot displays the BIOMODEL software interface. On the left is a navigation tree for 'BioModel1' with categories like Physiology, Applications, and Pathway. The main window shows a reaction diagram with compartments PM, Cyt, NM, and Nuc. A reaction network is visible, including species C_Cyt, Ran_Cyt, and RanC_Nuc. The 'Object Properties' panel at the bottom is open, showing the 'Species Name' field set to 'RanC_Nuc'. A yellow callout box with a red border contains the text: 'To rename species, click on a species and under "Object Properties" > "Species Name", type the desired name which is case-sensitive.' Red arrows point from this box to the 'RanC_Nuc' species in the diagram and to the 'Species Name' field in the properties panel.

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 software interface. On the left is a navigation pane with a tree view containing 'BioModel1', 'Physiology', 'Reaction Diagram', 'Reactions (2)', 'Structures (5)', 'Species (4)', 'Molecules (0)', 'Observables (0)', 'Applications (0)', 'Parameters, Functions and Units', and 'Pathway'. Below this is a search bar and a list of biological models. The main window displays a reaction diagram with compartments PM, Cyt, NM, and Nuc. A reaction 'flux0' is highlighted with a red box. Below the diagram is the 'Object Properties' panel for 'flux0', which includes fields for Reaction Name, Electrical Properties, Kinetic Type, and a table of parameters. A red box highlights the 'Expression' column in the table, containing the formula $Kflux * (RanC_Cyt - RanC_Nuc)$. A yellow text box with a red border provides instructions on how to change the reaction rate.

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.

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

The screenshot shows the BIOMODEL software interface. On the left is a navigation tree with 'BioModel1' expanded to 'Physiology' and 'Reaction Diagram' selected. Below this is a search bar and a list of models. The main window displays a reaction diagram with compartments PM, Cyt, NM, and Nuc. A reaction 'flux0' is highlighted with a red box. Below the diagram is a table of properties for 'flux0'.

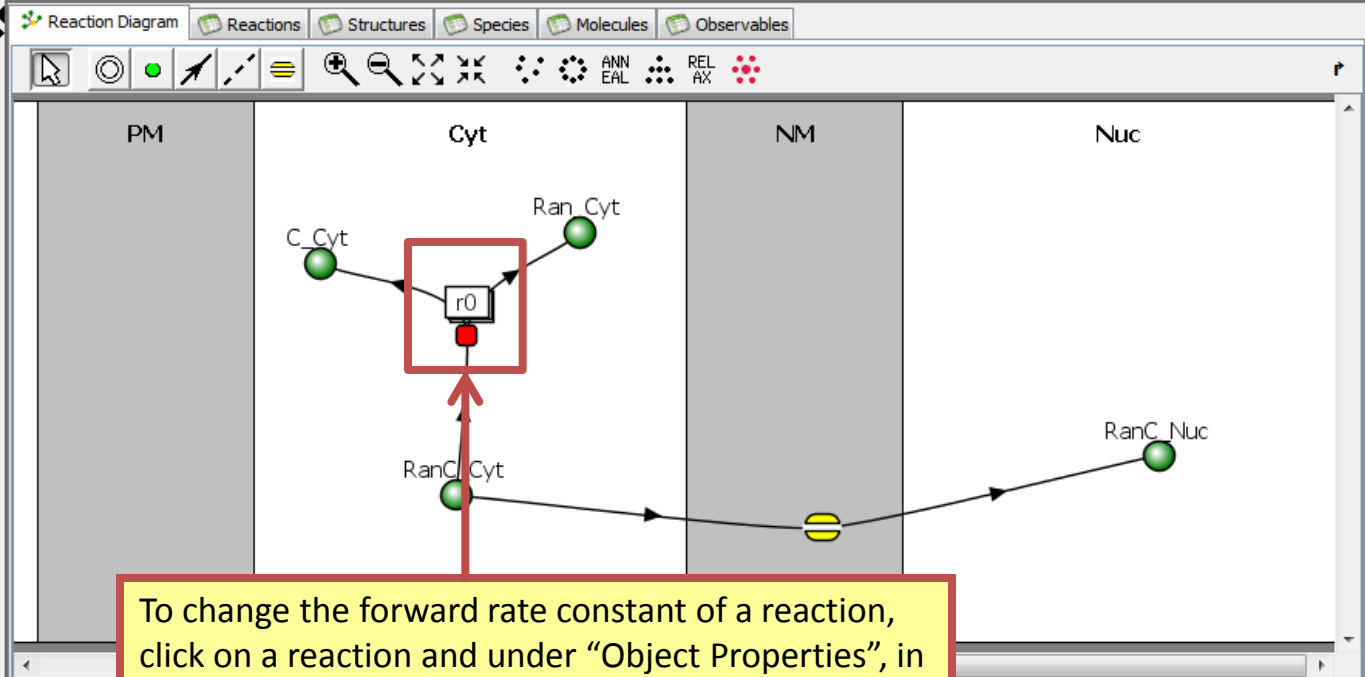
Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$Kflux \cdot (RanC_Cyt - RanC_Nuc)$	$\mu M \cdot \mu m \cdot s^{-1}$
I	inward current density	<input type="checkbox"/>	0.0	$pA \cdot \mu m^{-2}$
netValence	net charge valence	<input type="checkbox"/>	1.0	1
Kflux	user defined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

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

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



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.

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

Object Properties

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"/>	$(K_f \cdot \text{RanC_Cyt} - K_r \cdot \text{Cyt} \cdot \text{Ran_Cyt})$	$\mu\text{M}\cdot\text{s}^{-1}$
Kf	forward rate constant	<input type="checkbox"/>	1.0	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	μM
C_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
Ran_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

The screenshot shows the VCell software interface. On the left is a navigation tree with 'BioModel1' expanded to 'Physiology' and 'Reaction Diagram' selected. The main window displays a reaction diagram with compartments PM, Cyt, NM, and Nuc. A reaction 'r0' is highlighted in a red box, showing a transition from C_Cyt to Ran_Cyt. A red arrow points from a text box to the 'Kr' row in the 'Object Properties' table. The table has columns for Name, Description, Global, Expression, and Units.

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 type="checkbox"/>	1.0	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	μM
C_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
Ran_Cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

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.

1000.0

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

Reactions Structures Species Molecules Observables

PM Cyt NM Nuc

s2 s3 s0 s1

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

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

BIOMODEL: BioModel2 (NoVersion) (NoDate) -- VCell 6.0 (build 3)

File View Server Tools Help

BioModel2

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (1)
 - Species (0)
 - Molecules (0)
 - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

Reaction Diagram Reactions Structures Species Molecules Observables

c0

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

VCell 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 201...
- Shared BioModels (0)
- Public BioModels (514)
- Tutorials (5)
- Education (33)
- Tutorial VCell 6.0 (Rule-based) (7)

Delete Pathway Links Search

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

- Special Deterministic
 - Deterministic
 - geom_20150630_115646 (3D)

CONNECTED (astfh234) 58.5MB / 77.8MB

The screenshot shows the VCell software interface. On the left, a tree view shows the project structure under 'Tutorial', with 'Applications (0)' highlighted. At the bottom, the 'Add New' button is highlighted in the toolbar. A yellow callout box contains the following text:

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.

The main window displays a table with columns: Name, Math Type, and Annotation. The bottom status bar shows 'CONNECTED (tanyamiller1221)' and '356.5MB / 514.8MB'.

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.

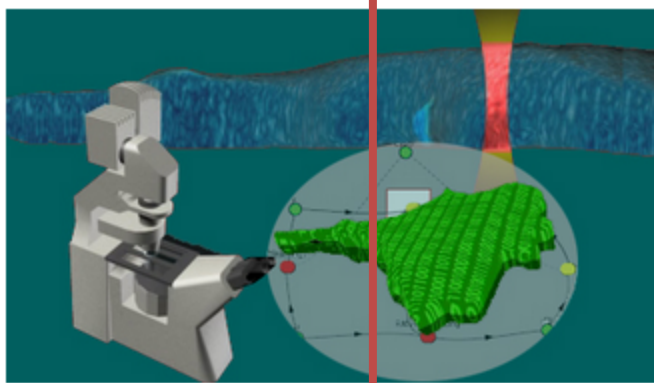
[Click here](#) for a Quick Start guide for Release.

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



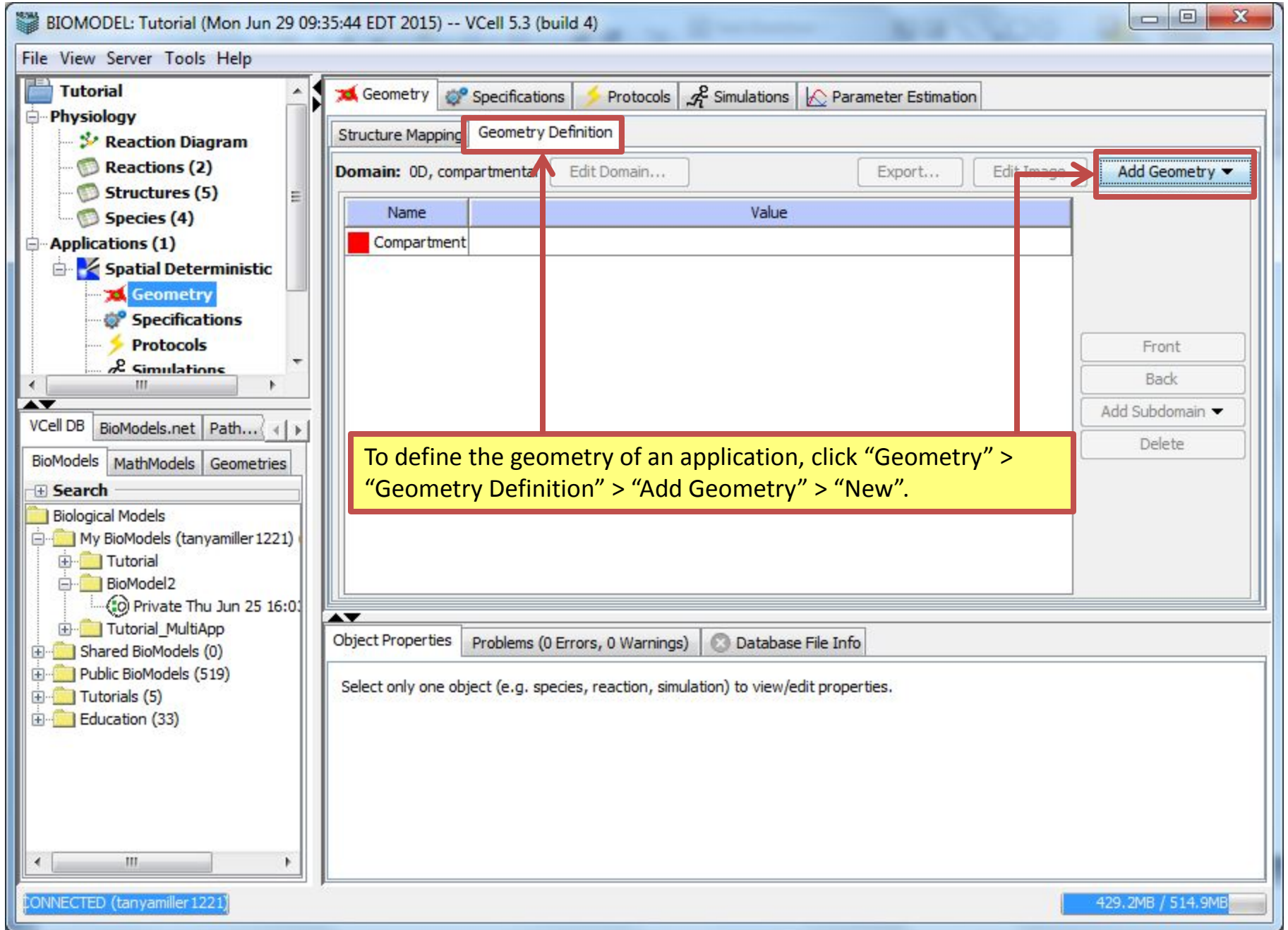
Share your published VCell Models

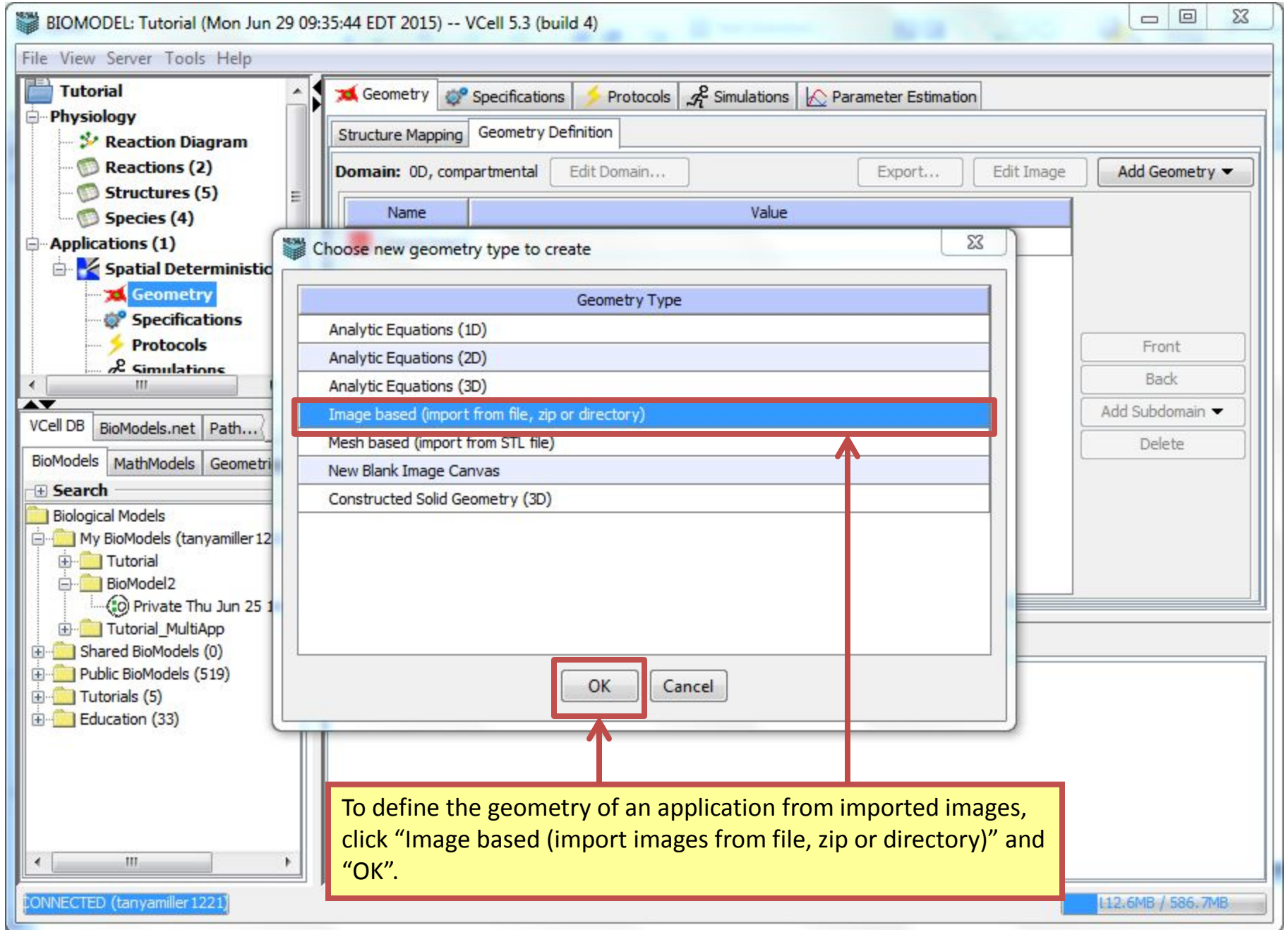
Modeling/Database Links

Software Support
vcell_support@uchc.edu
[VCell Discussion Forum](#)

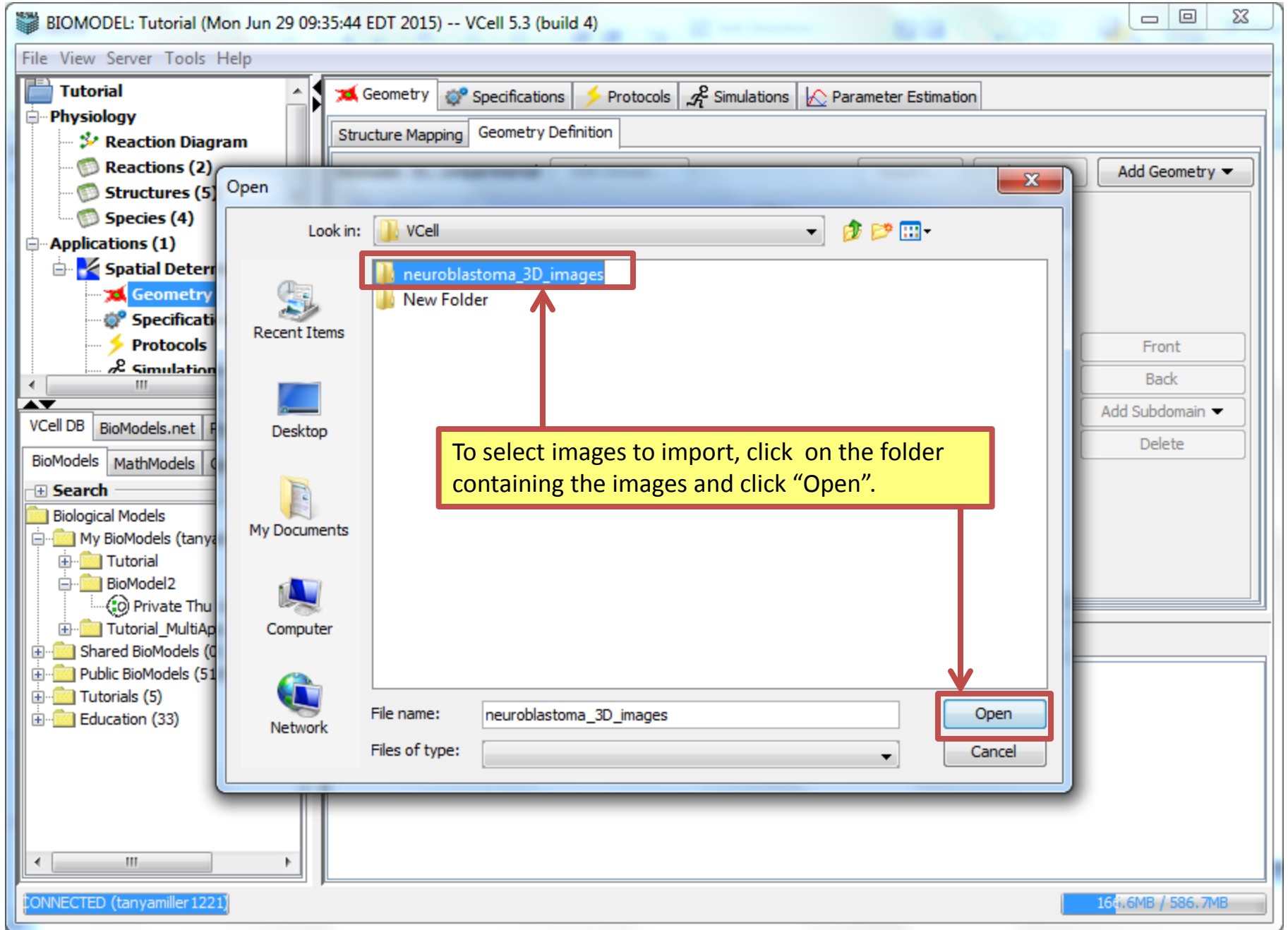
In this tutorial, example 3D neuroblastoma images will be used. These images are located on the VCell website (vcell.org) under "User Guide" > "Video Tutorials". Click on "3D images for tutorial", which will download the necessary 3D images, and then save and extract the files.

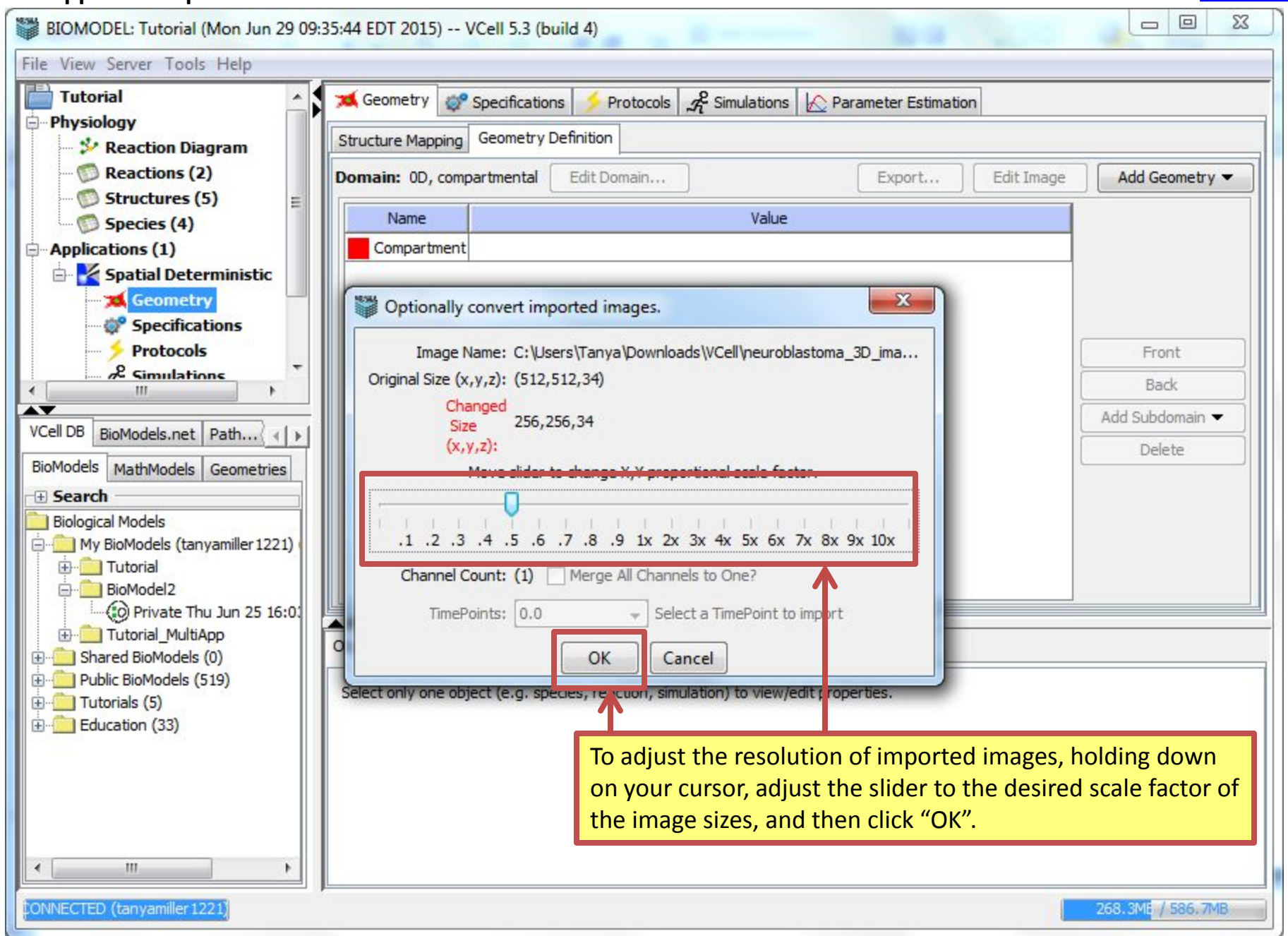
[3D images](#)



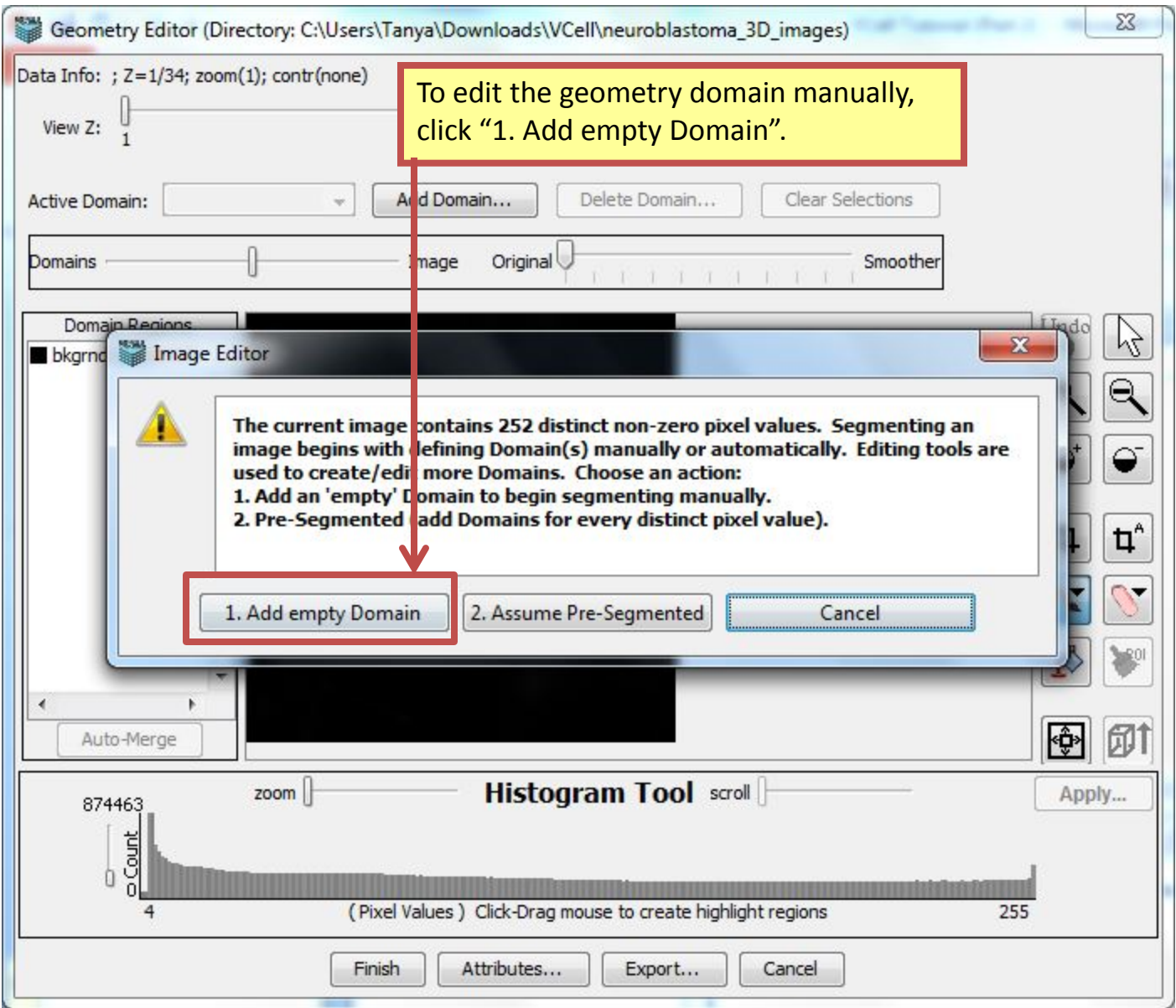


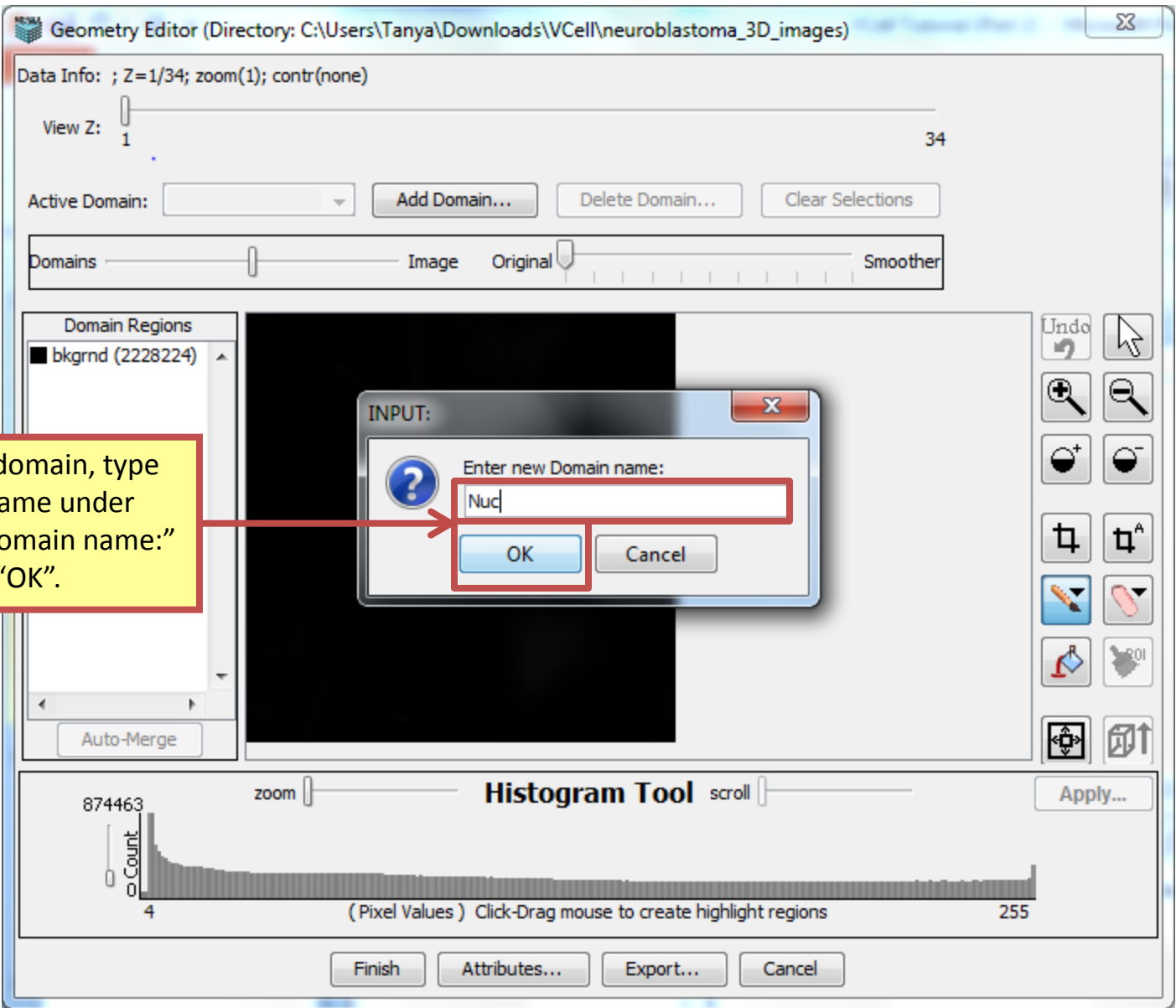
To define the geometry of an application from imported images, click "Image based (import images from file, zip or directory)" and "OK".



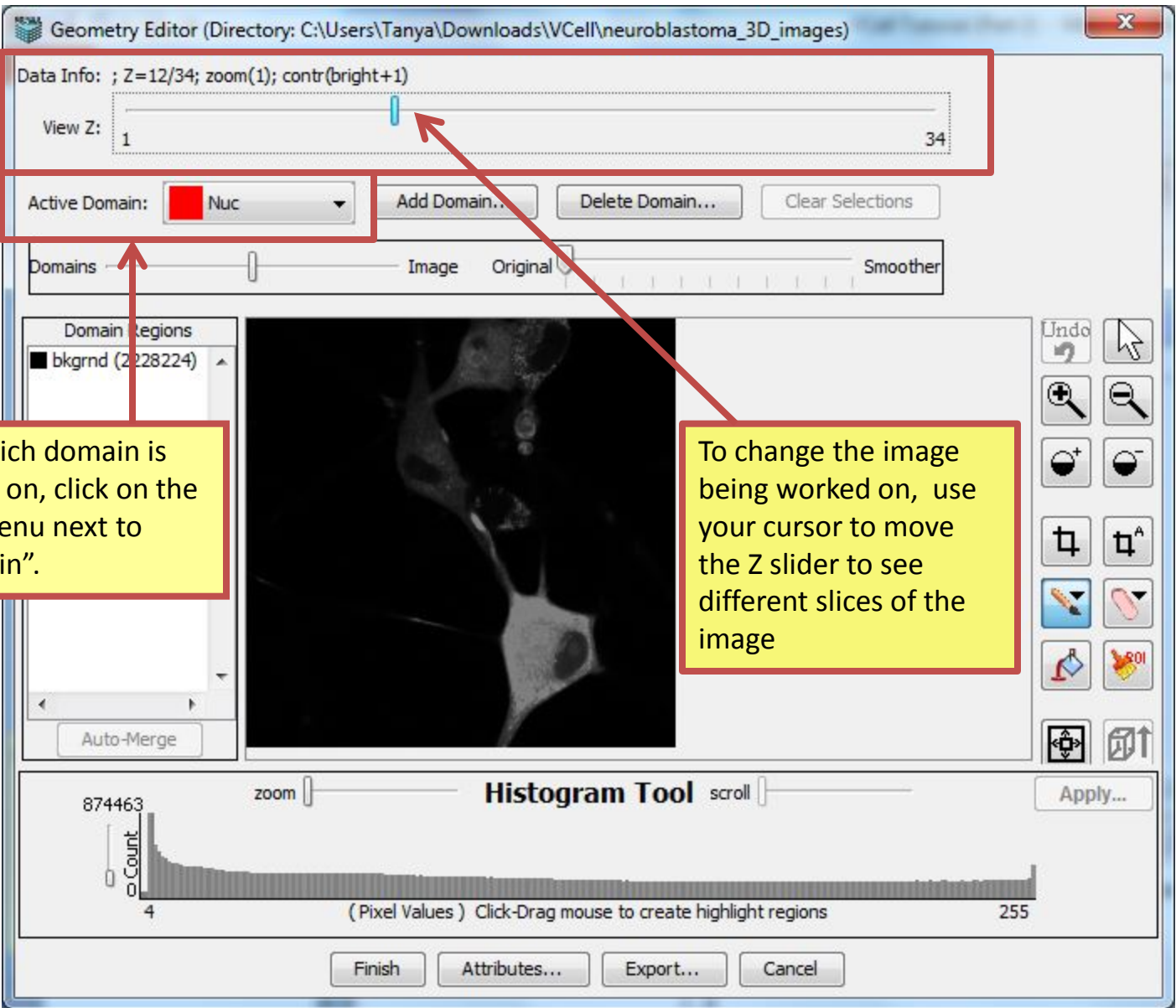


To adjust the resolution of imported images, holding down on your cursor, adjust the slider to the desired scale factor of the image sizes, and then click "OK".

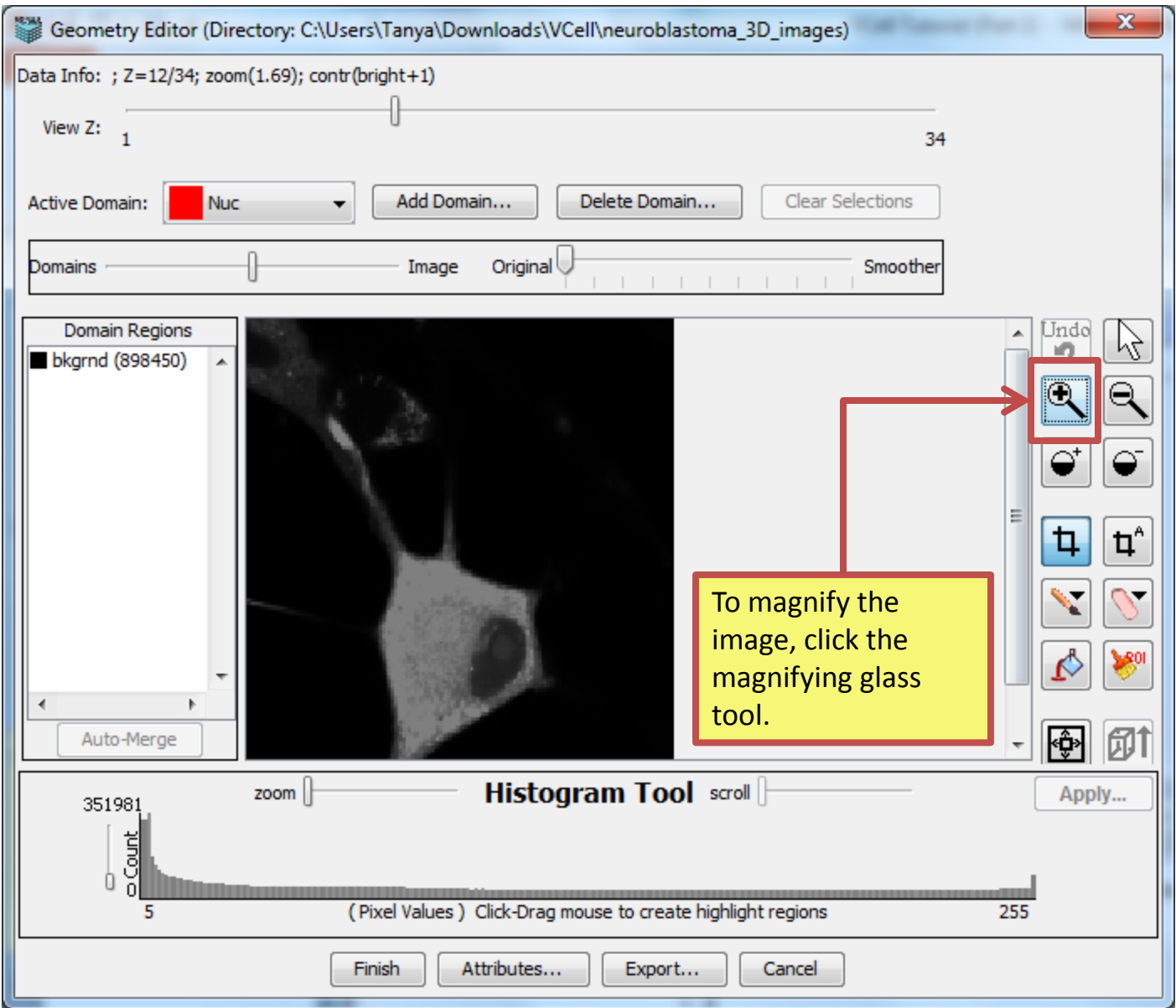


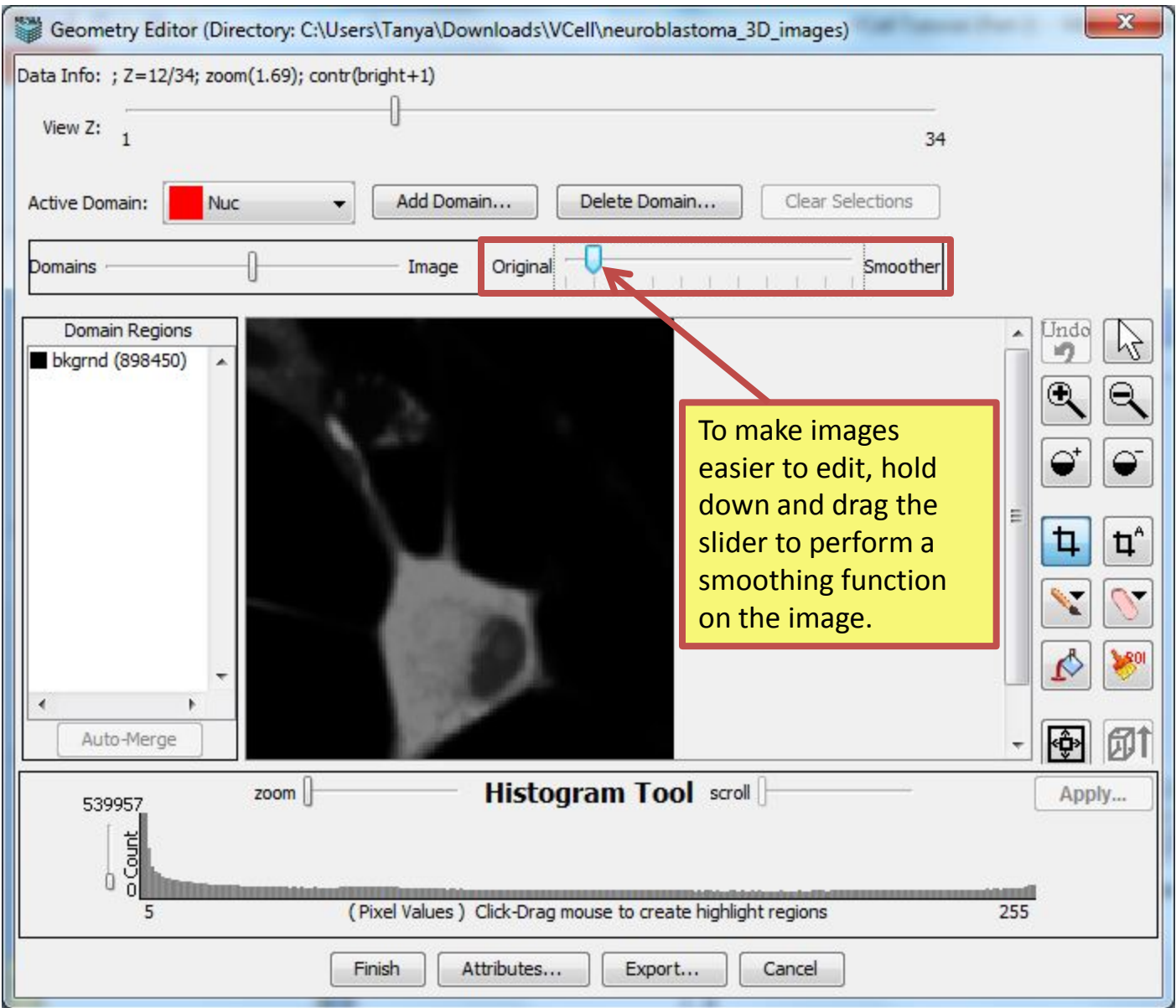


To name the domain, type the domain name under "Enter new Domain name:" and the click "OK".

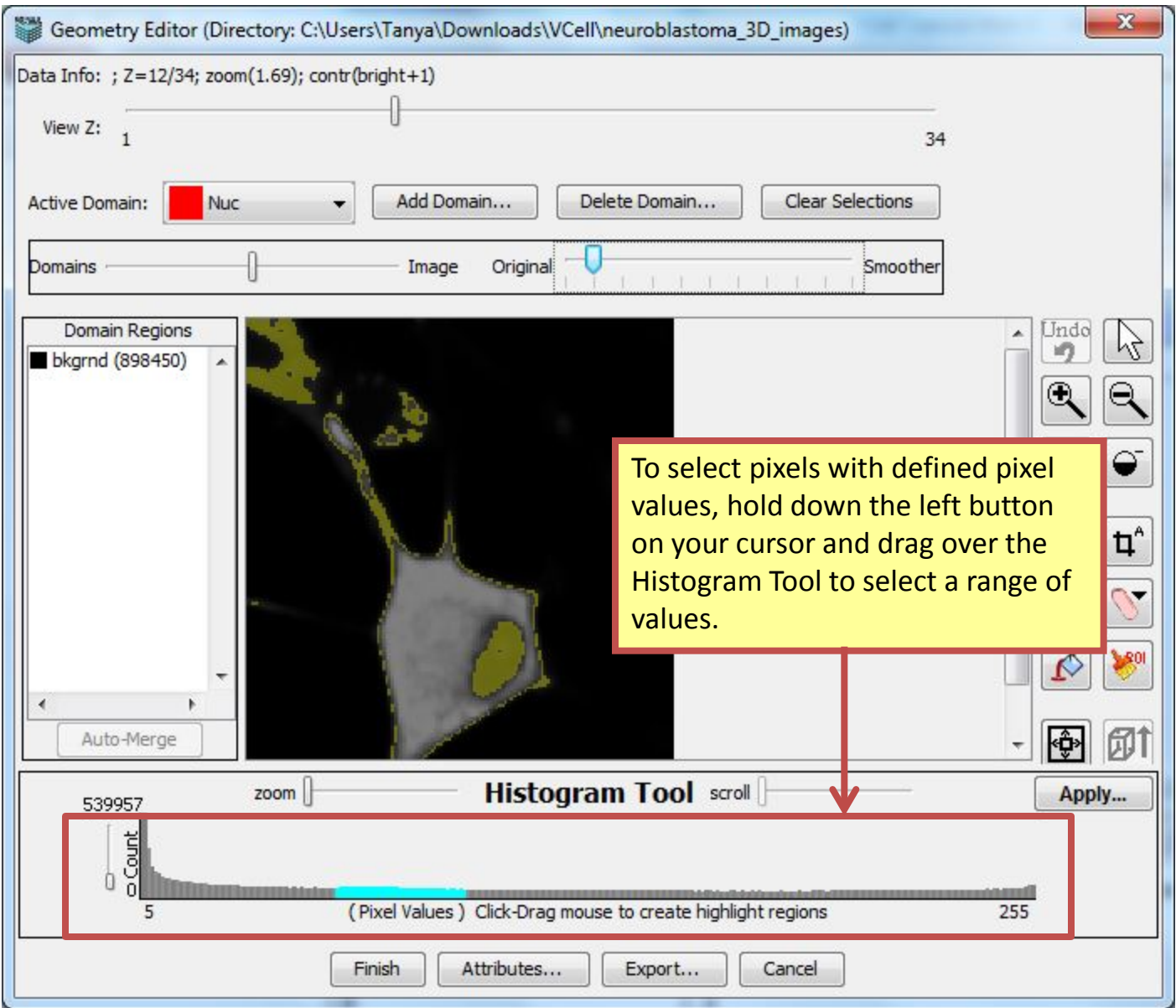


The screenshot shows the Geometry Editor interface. At the top, the title bar reads "Geometry Editor (Directory: C:\Users\Tanya\Downloads\VCell\neuroblastoma_3D_images)". Below the title bar, the "Data Info" section shows parameters: "; Z=12/34; zoom(1); contr(bright+1)". A "View Z" slider is set to 1, with a range from 1 to 34. The "Active Domain" is set to "Nuc" with a red square icon. A "Domains" slider is visible below. On the left, the "Domain Regions" list contains "bkgnd (2228224)". The main window displays a grayscale image of a cell with a green rectangular crop box. A "Confirm Crop Data" dialog box is open in the center, asking "Crop data to new bounds?: (105,81) to (255,255)". The "OK" button in this dialog is highlighted with a red box. A yellow text box with a red border contains the instruction: "To use only a select x, y area of the imported images, click on the crop tool, and use your cursor to drag over an area. Let go of your cursor and click 'OK'". A red arrow points from this text box to the crop tool icon (a blue square with a white crop symbol) in the right-hand toolbar. At the bottom, the "Histogram Tool" is visible, showing a histogram with a peak at 874463 and a range from 4 to 255. The histogram is labeled "(Pixel Values) Click-Drag mouse to create highlight regions". At the very bottom, there are buttons for "Finish", "Attributes...", "Export...", and "Cancel".

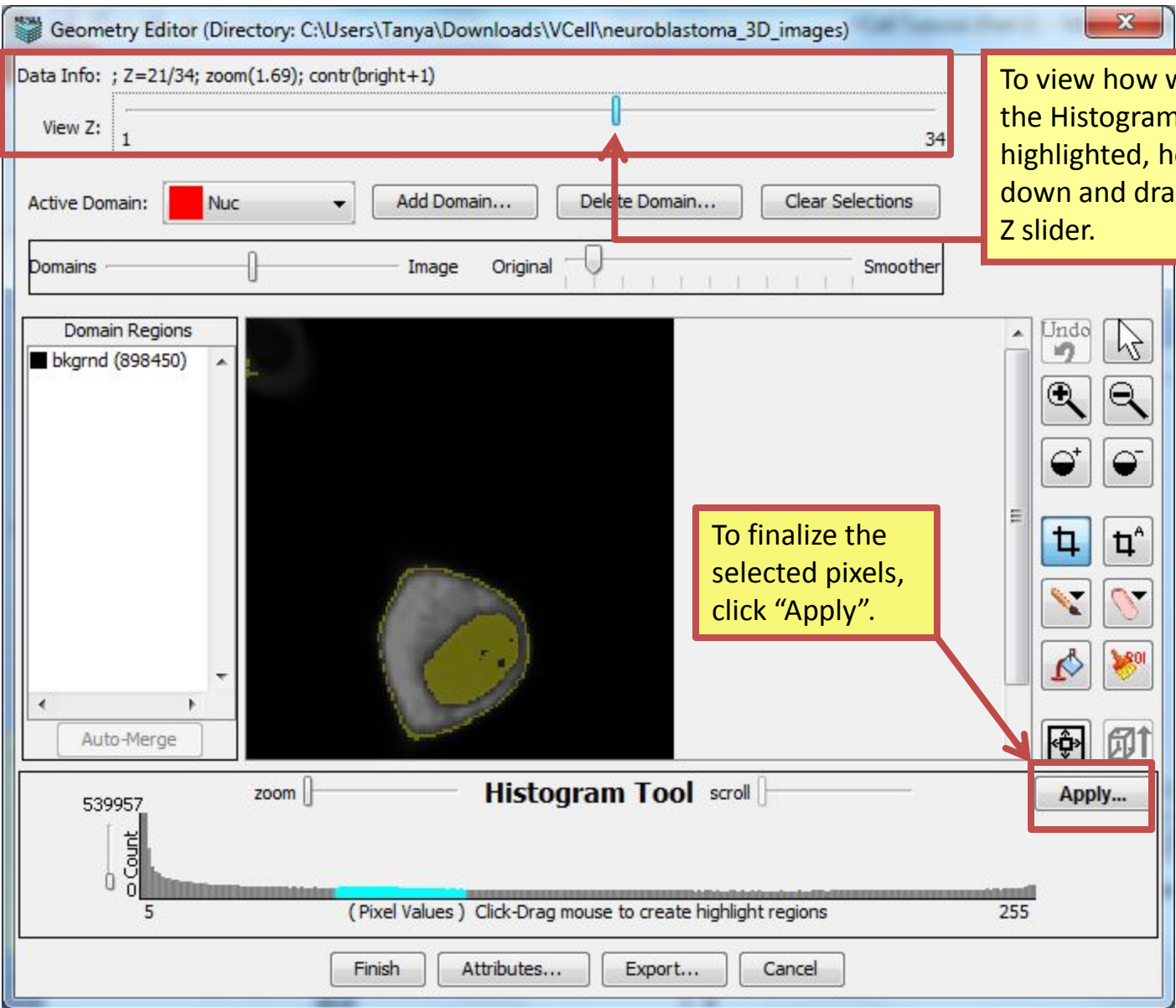




To make images easier to edit, hold down and drag the slider to perform a smoothing function on the image.



To select pixels with defined pixel values, hold down the left button on your cursor and drag over the Histogram Tool to select a range of values.



To view how well the Histogram Tool highlighted, hold down and drag the Z slider.

To finalize the selected pixels, click "Apply".

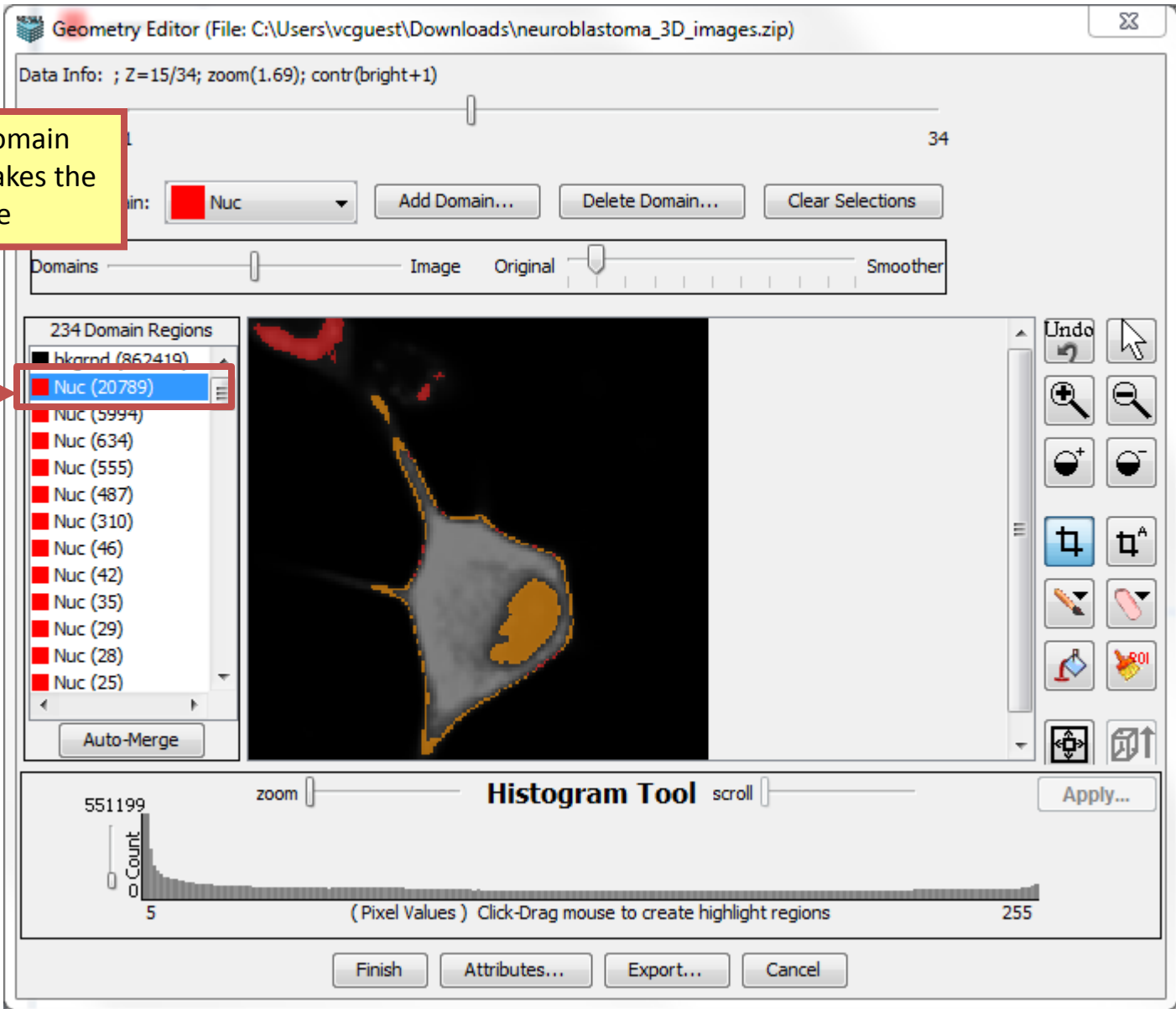
Apply...

The screenshot displays the Geometry Editor application window. The title bar reads "Geometry Editor (Directory: C:\Users\Tanya\Downloads\VCe\neuroblastoma_3D_images)". The main interface includes a "Data Info" section with parameters: "; Z=21/34; zoom(1.69); contr(bright+1)". Below this is a "View Z" slider ranging from 1 to 34. The "Active Domain" is set to "Nuc", with buttons for "Add Domain...", "Delete Domain...", and "Clear Selections". A "Domains" slider is positioned between "Image" and "Smoother".

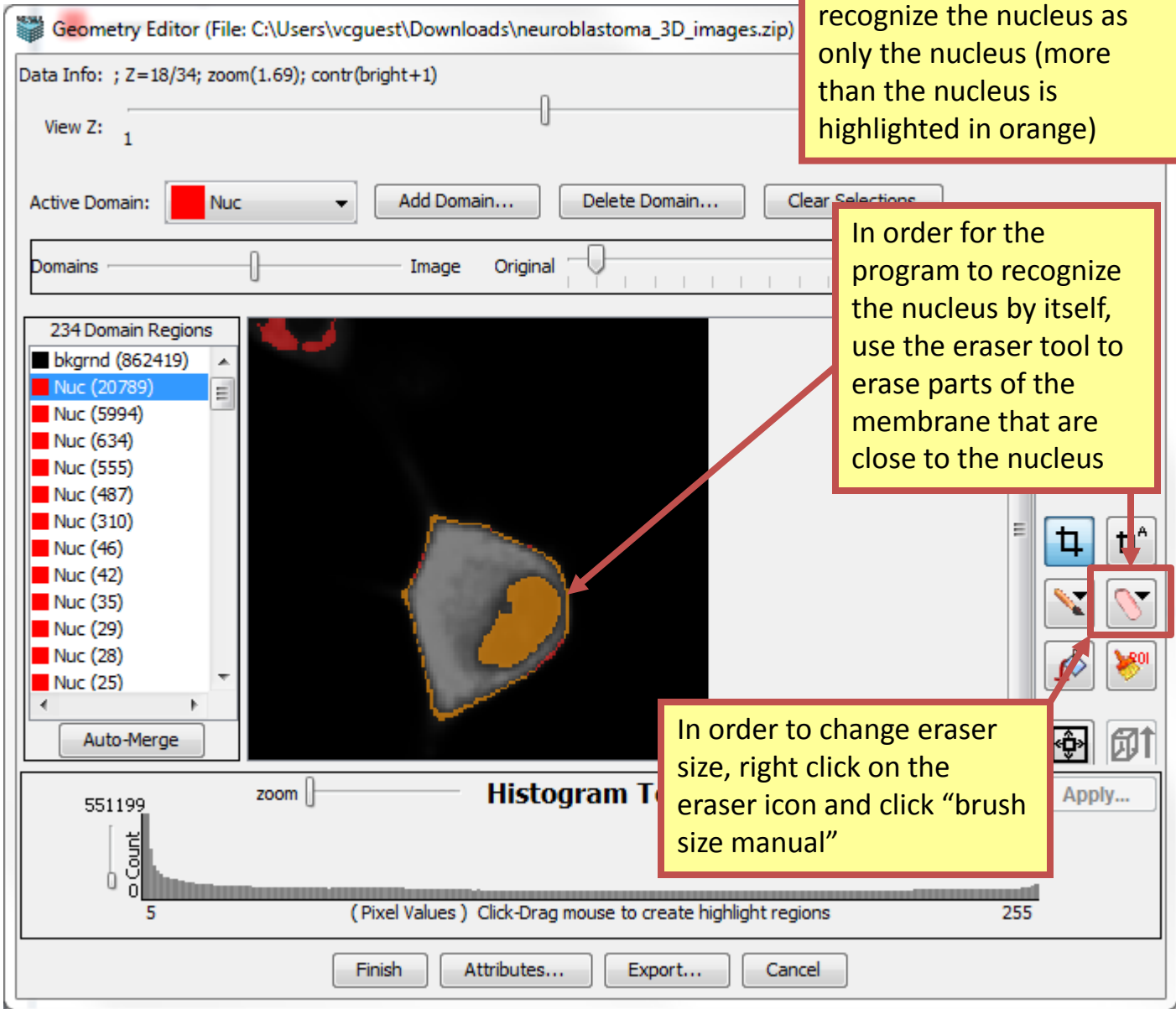
A "Domain Regions" panel on the left shows a list with "bkgnd (898450)". A central 3D visualization shows a cell structure with a highlighted region. A "Histogram Tool" is active at the bottom, showing a histogram of pixel values from 5 to 255. A red highlight is visible on the histogram, and the "Apply..." button is highlighted. The histogram is labeled "Histogram Tool" and "scroll".

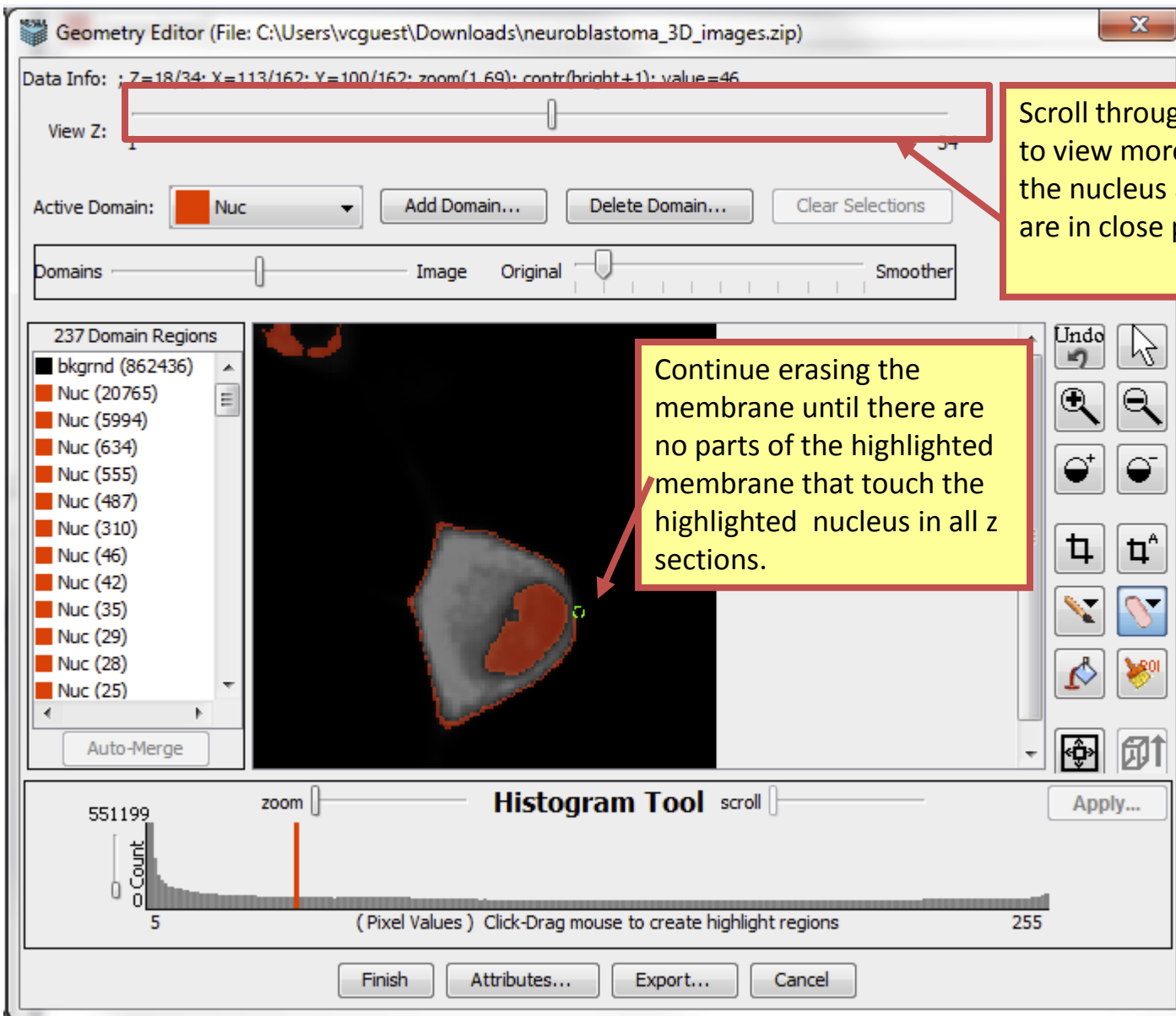
A dialog box is overlaid on the center of the screen. It has a yellow header with the text "To update the domain, click 'Update Domain'." The main text of the dialog reads: "Apply histogram highlighted regions. Choose an action: 1. Update the current Domain 'Nuc' using the histogram highlight. 2. Create a new Domain with the histogram highlight." The "Update Domain" button is highlighted with a red dashed border, and a red arrow points from the instruction text to this button. Other buttons in the dialog include "Create Domain" and "Cancel".

At the bottom of the application window, there are buttons for "Finish", "Attributes...", "Export...", and "Cancel".



Click on the domain region that makes the nucleus orange





Geometry Editor (File: C:\Users\vcgquest\Downloads\neuroblastoma_3D_images.zip)

Data Info: : Z=18/34; zoom(1.69); contr(bright+1)

View: 34

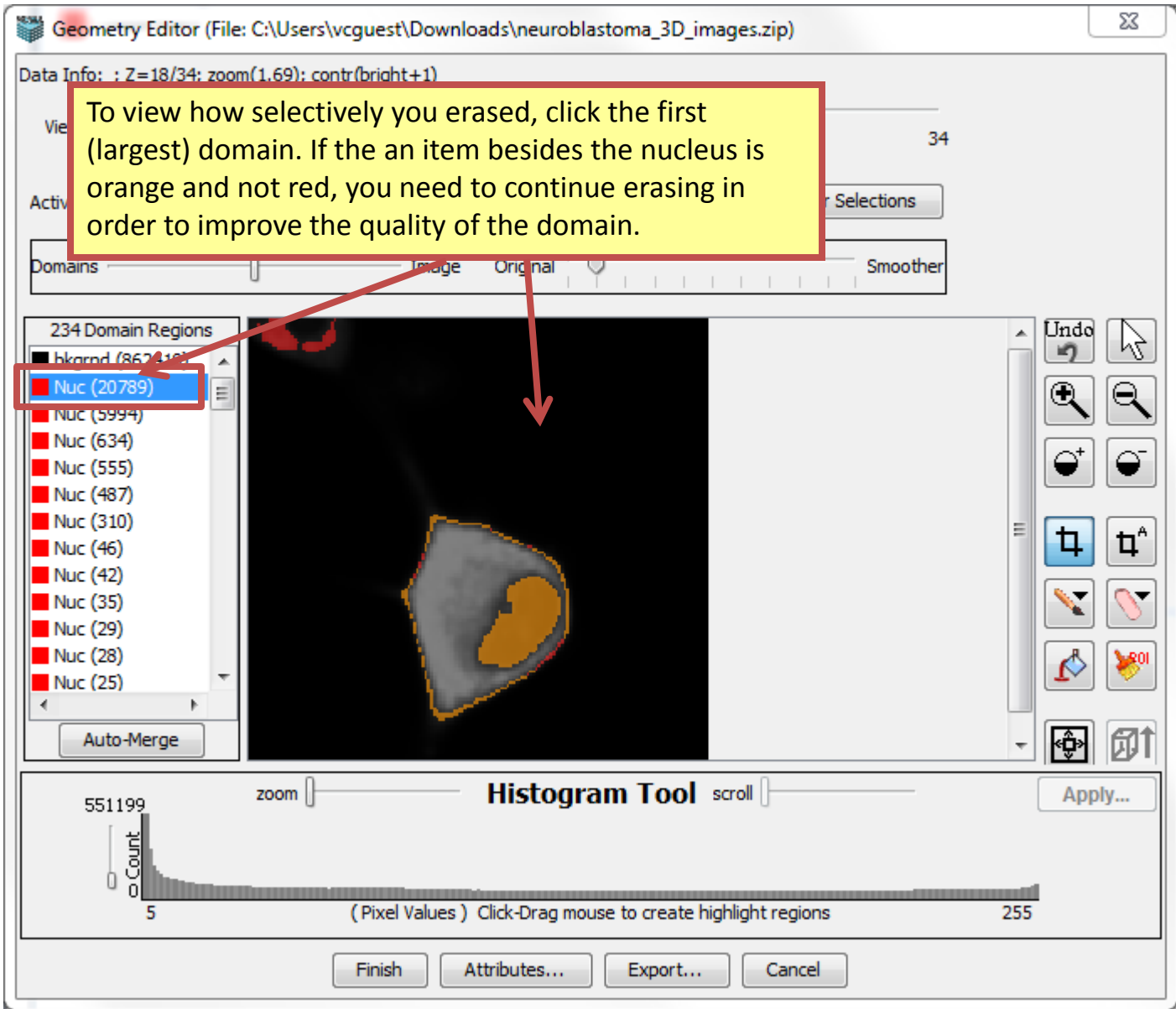
Active: Selections

Domains: Image Original Smoother

234 Domain Regions

- bkgrnd (862418)
- Nuc (20789)**
- Nuc (5994)
- Nuc (634)
- Nuc (555)
- Nuc (487)
- Nuc (310)
- Nuc (46)
- Nuc (42)
- Nuc (35)
- Nuc (29)
- Nuc (28)
- Nuc (25)

Auto-Merge



Undo

Zoom in Zoom out

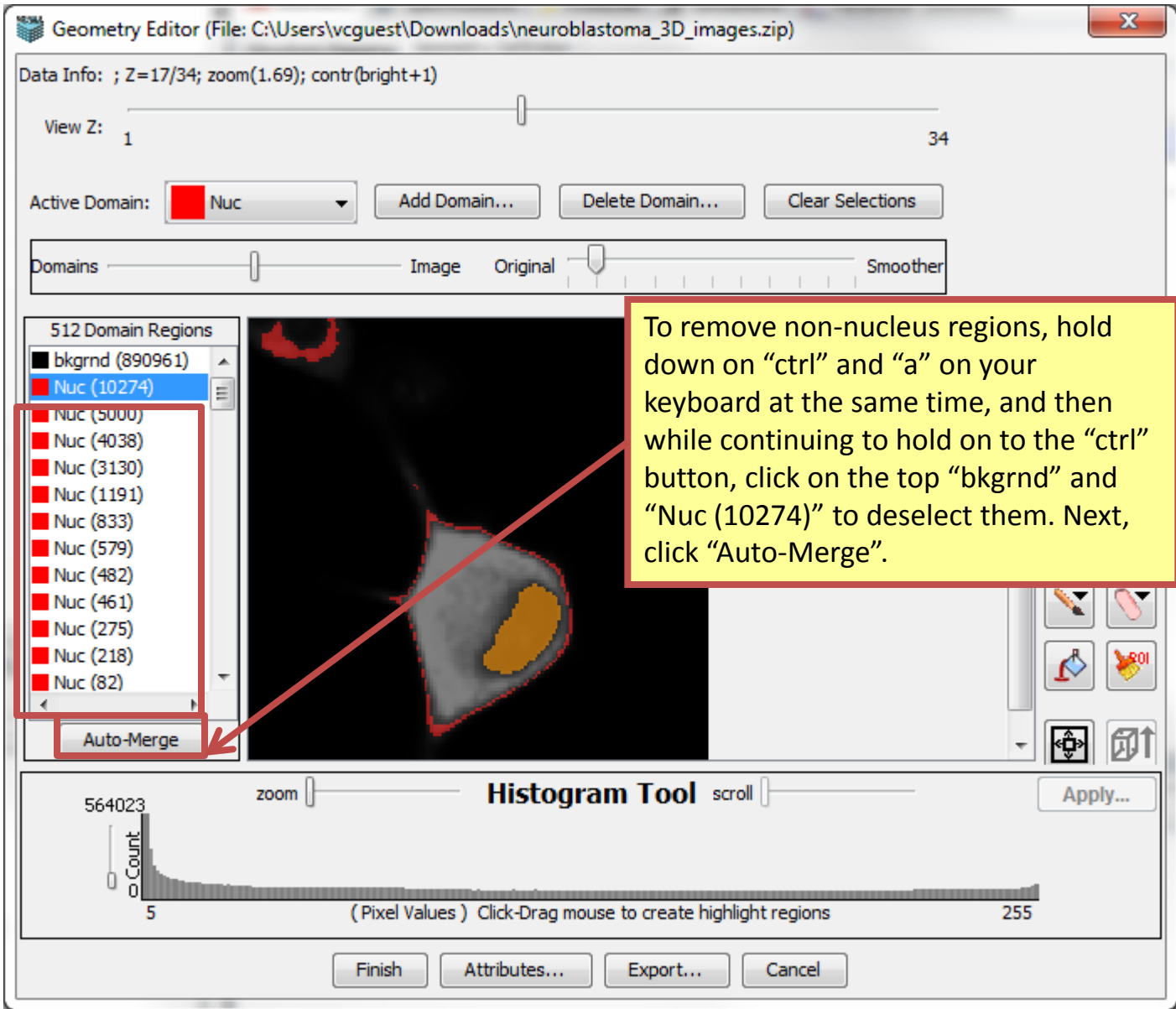
Fit to window

Tools

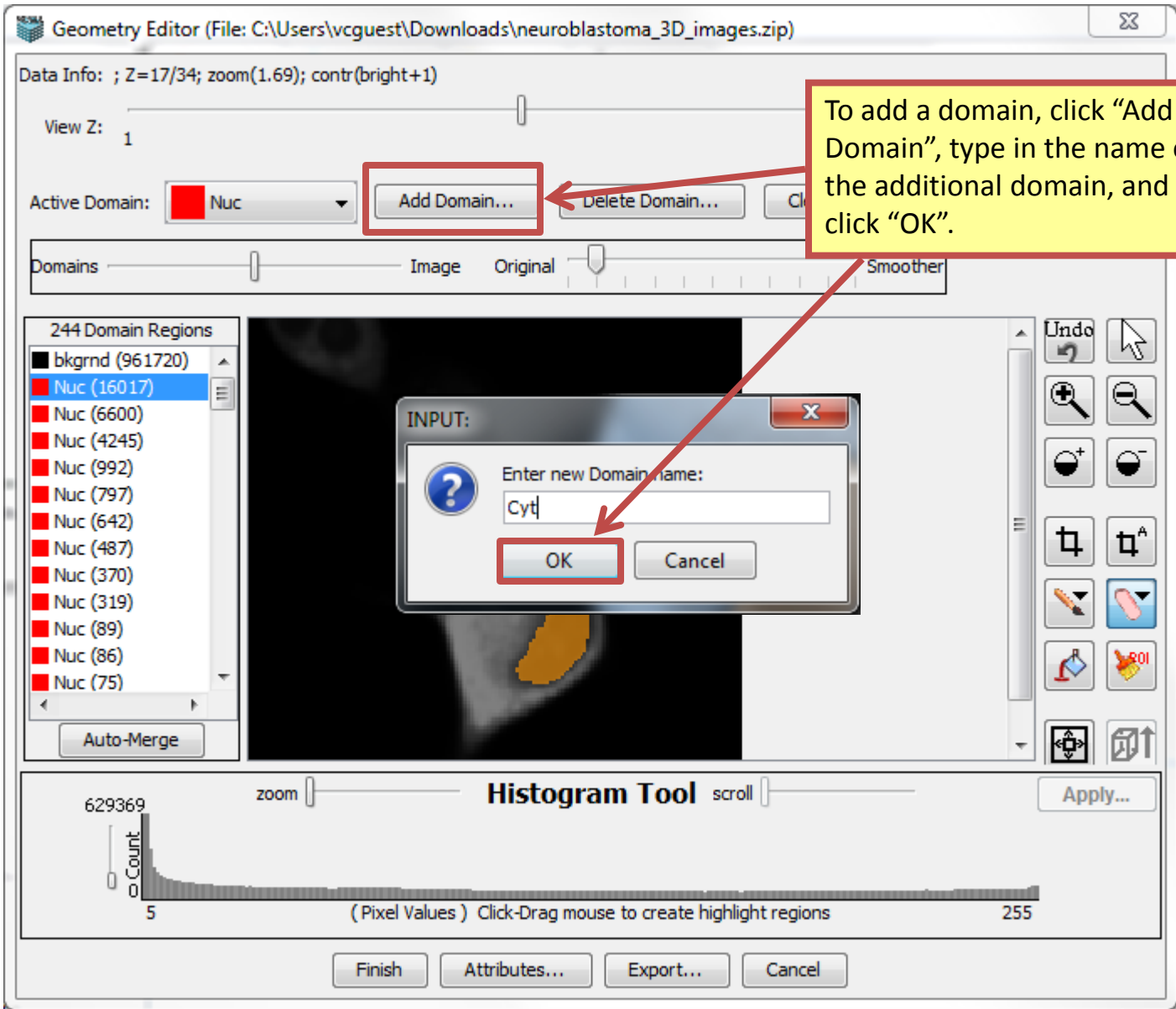
551199 zoom scroll Apply...

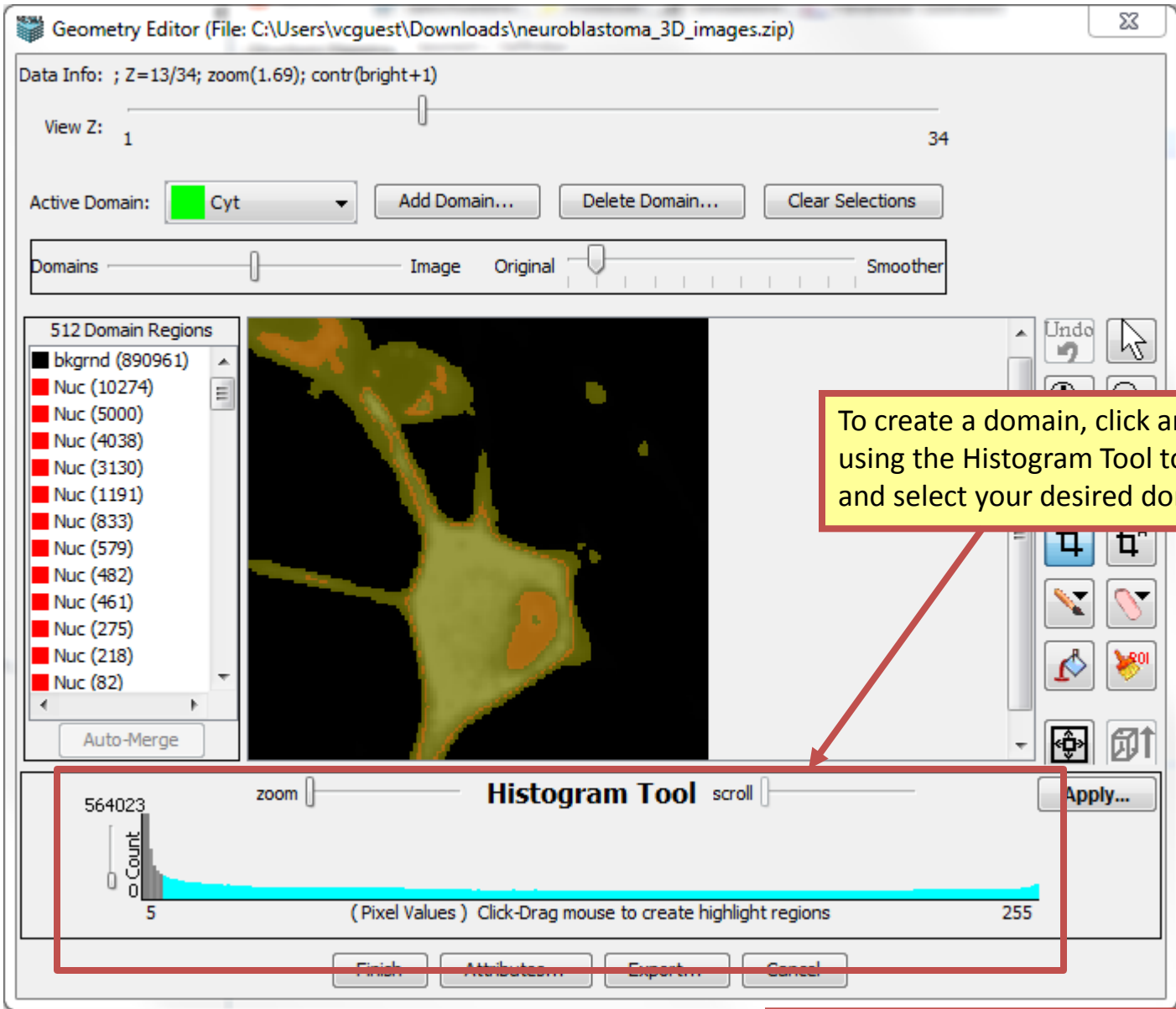
o Count (Pixel Values) Click-Drag mouse to create highlight regions 255

Finish Attributes... Export... Cancel



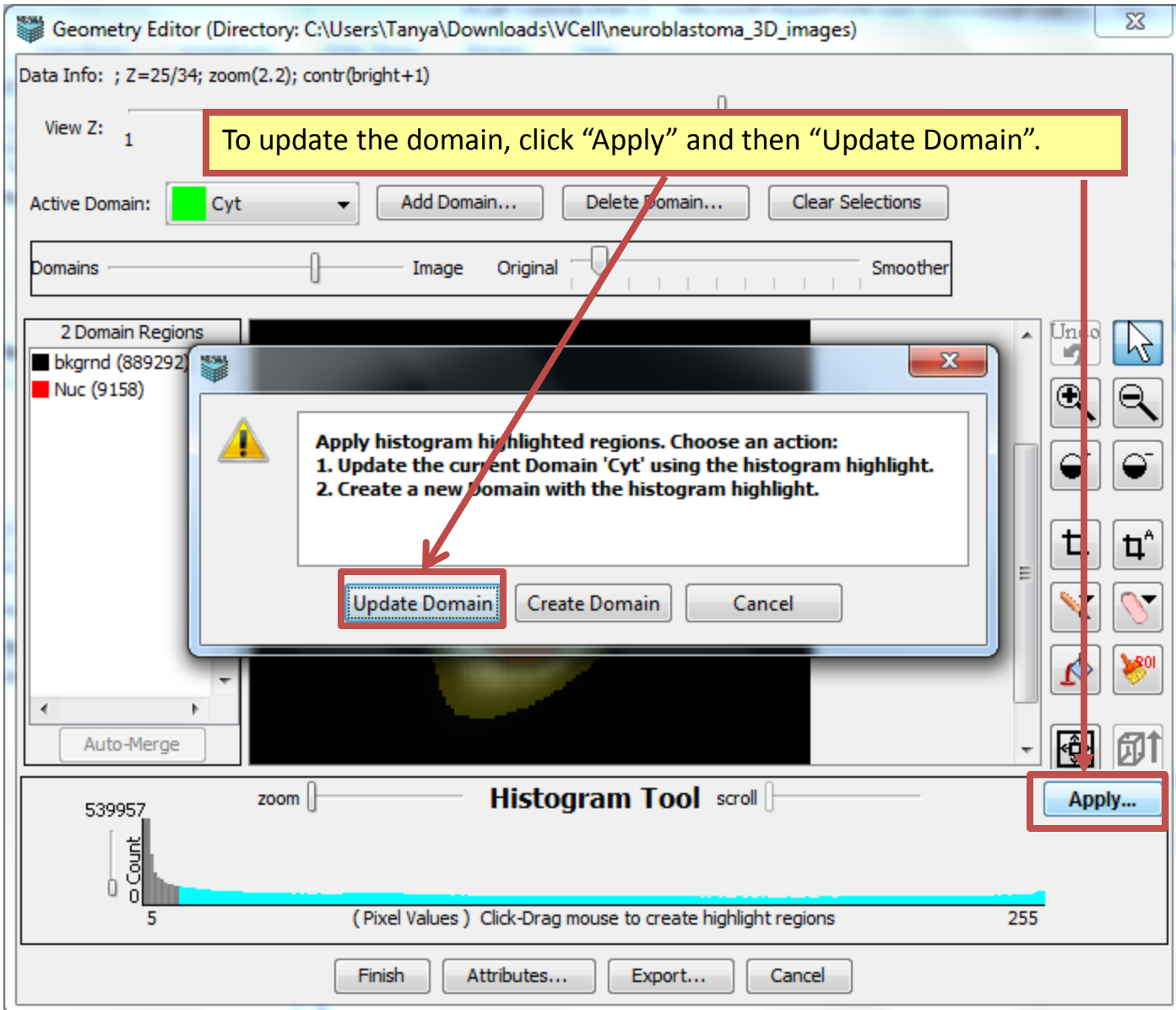
To remove non-nucleus regions, hold down on "ctrl" and "a" on your keyboard at the same time, and then while continuing to hold on to the "ctrl" button, click on the top "bkgrnd" and "Nuc (10274)" to deselect them. Next, click "Auto-Merge".



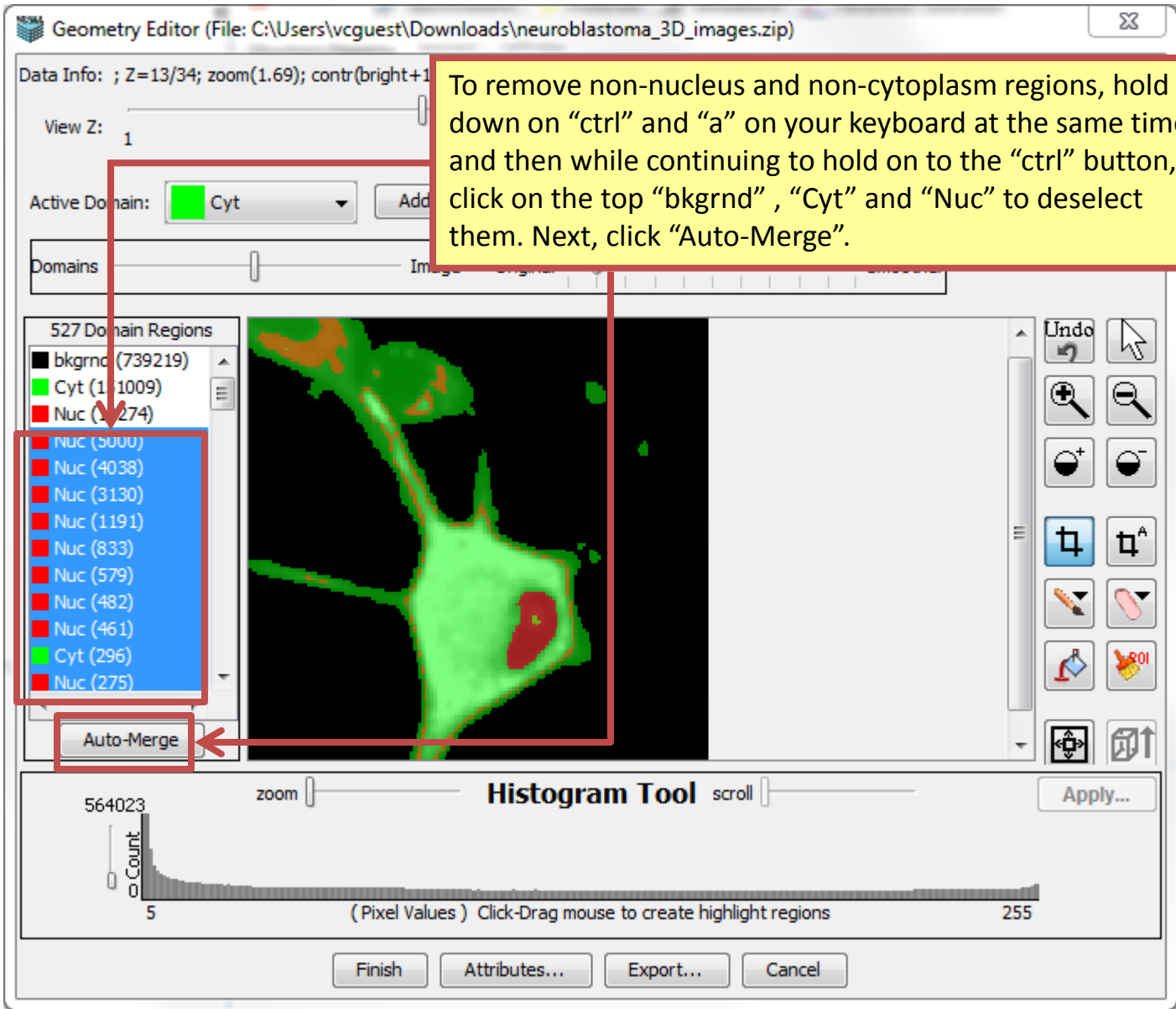


To create a domain, click and drag using the Histogram Tool to highlight and select your desired domain region.

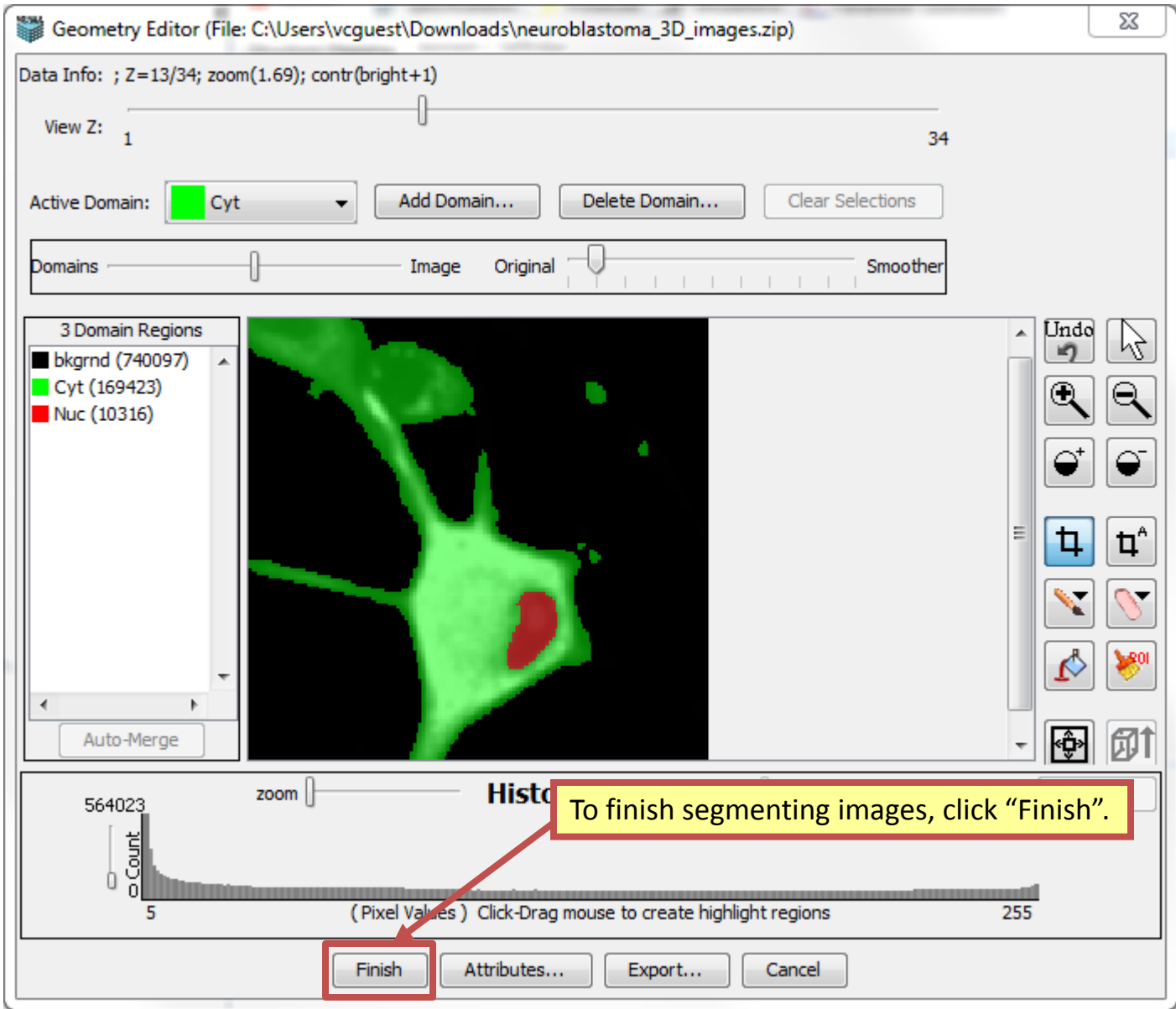
Use the Z slider to make sure all parts of the cytoplasm are highlighted

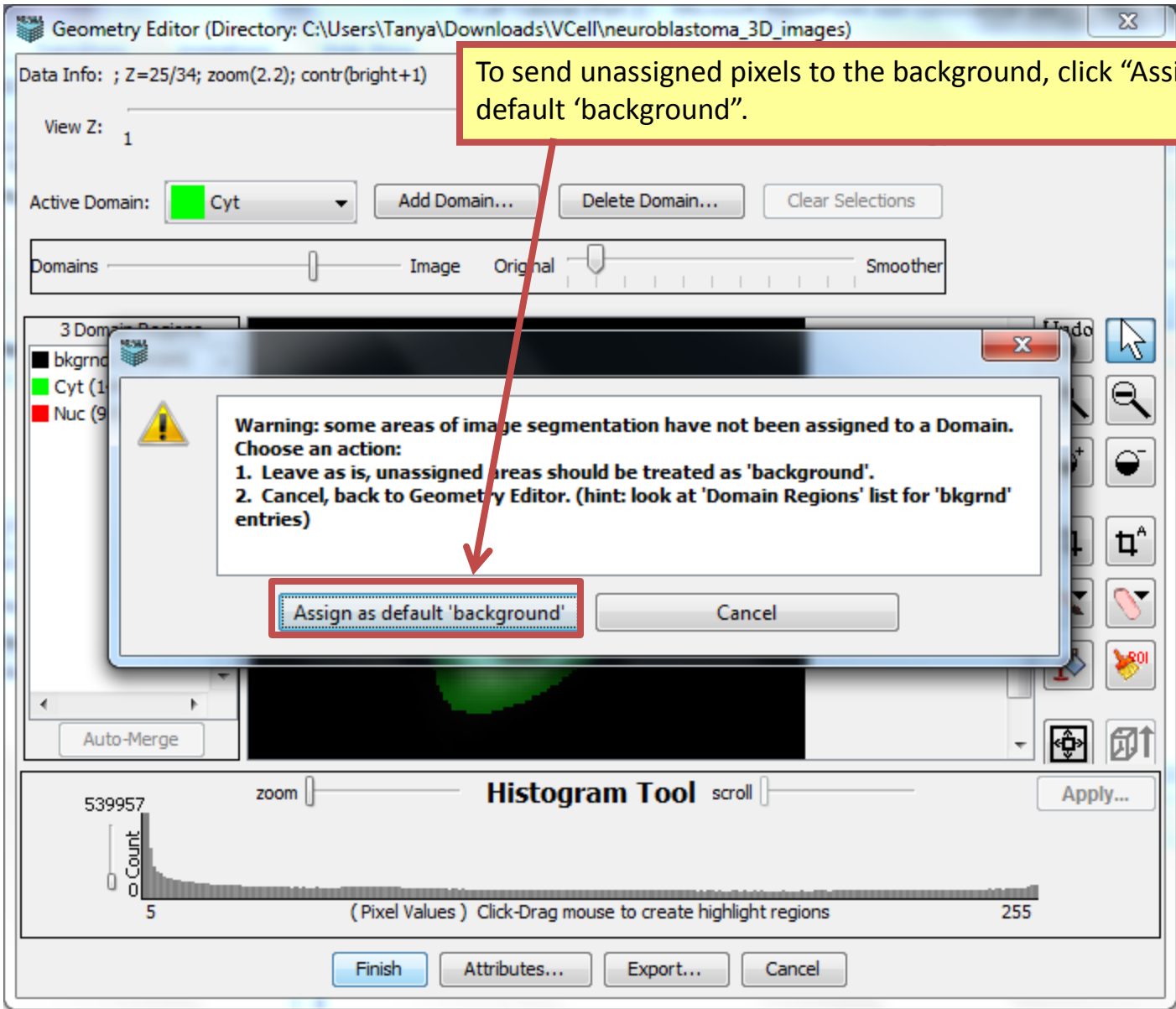


The screenshot shows the Geometry Editor interface. At the top, the title bar reads "Geometry Editor (File: C:\Users\vcgquest\Downloads\neuroblastoma_3D_images.zip)". Below the title bar, the "Data Info" section shows "Z=13/34; zoom(1.69)". The "View Z" is set to 1. The "Active Domain" is "Cyt", represented by a green square. A yellow callout box with a red border contains the text: "To keep multiple domain regions, click 'Keep existing Domain Regions when overlapping'". Below this, there are buttons for "Add Domain...", "Delete Domain...", and "Clear Selections". A "Domains" slider is visible, with "Image", "Original", and "Smoother" options. A central warning dialog box is open, displaying a yellow warning icon and the text: "Some areas of the new Domain Regions overlap with existing Domain Regions." The dialog has three buttons: "g Domain Regions", "Keep existing Domain Regions when overlapping" (which is highlighted with a red box), and "Ca". Below the dialog, a "Histogram Tool" is visible, showing a histogram with a cyan bar. The histogram has a y-axis labeled "Count" with a value of 564023 and an x-axis labeled "(Pixel Values)" with values 5 and 255. At the bottom of the window are buttons for "Finish", "Attributes...", "Export...", and "Cancel".



To remove non-nucleus and non-cytoplasm regions, hold down on "ctrl" and "a" on your keyboard at the same time, and then while continuing to hold on to the "ctrl" button, click on the top "bkgrnd", "Cyt" and "Nuc" to deselect them. Next, click "Auto-Merge".





The screenshot shows the Geometry Editor interface. At the top, the title bar reads "Geometry Editor (Directory: C:\Users\Tanya\Downloads\VCell\neuroblastoma_3D_images)". Below the title bar, the "Data Info" section shows "Z=25/34; zoom(2.2); contr(bright+1)". The "View Z" is set to 1. The "Active Domain" is "Cyt" (green). A "Domains" slider is visible. A central window displays a 3D visualization of a cell with a green cytoplasmic domain. A warning dialog box is open, with a red arrow pointing to the "Add empty border" button. The dialog text reads: "One or more Domain Regions touches the outer boundary on the XY and Z border. Choose an option: 1. Keep as is, do not change. 2. Add empty 'background' border around outer boundary so no Domain Region touches an outer edge." The "Add empty border" button is highlighted with a red box. Below the dialog is a "Histogram Tool" showing a histogram of pixel values from 5 to 255, with a peak count of 539957. The histogram has a "zoom" slider and an "Apply..." button. At the bottom of the window are buttons for "Finish", "Attributes...", "Export...", and "Cancel".

Data Info : Z=25/34; zoom(2.2); contr(bright+1)

View Z: 1

Active Domain: Cyt

Domains

3 Domain Regions

- bkgrnd
- Cyt (1)
- Nuc (9)

Auto-Merge

Warning Dialog:

One or more Domain Regions touches the outer boundary on the XY and Z border. Choose an option:

- Keep as is, do not change.
- Add empty 'background' border around outer boundary so no Domain Region touches an outer edge.

Buttons: Keep as is, Add empty border, Cancel

Histogram Tool

Count: 539957

zoom

scroll

Apply...

(Pixel Values) Click-Drag mouse to create highlight regions

5 255

Buttons: Finish, Attributes..., Export..., Cancel

To insert a blank (background) image on top of the 1st image and below the last image in the Z stack and to pad the x,y boundary with a rows of background pixels, click "Add empty border". This is important to ensure that in your final geometry a volume compartment intended to be enclosed by a membrane does not reach the edge (boundary) of the simulation space.

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

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

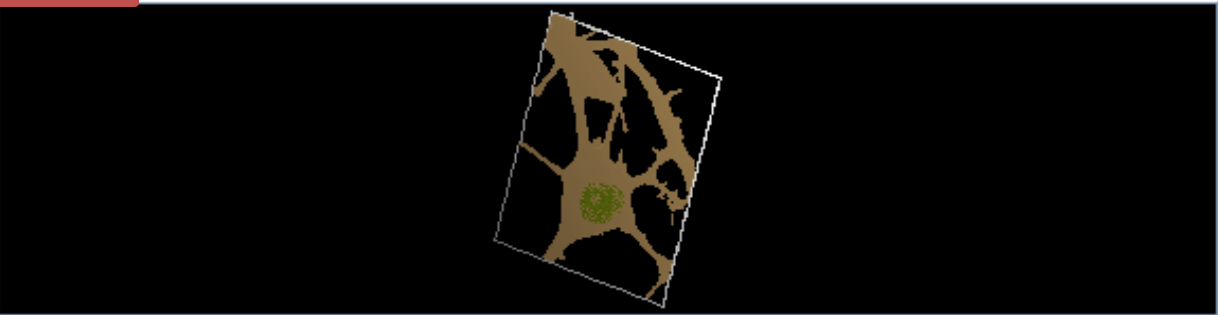
Domain: 3D, size=(62841.3,84404.8,9.00000E-7), origin=(0,0,0) Export... Edit Image Replace Geometry

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)
 - Spacial Deterministic
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

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

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

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition

Domain: 3D, size (62841.2 84484.8 0.0 000005 7) origin (0.0 0.0)

Geometry Size

To adjust the dimensions, type in your desired values and when done, click "OK".

Size	X	75	μm	Y	75	μm	Z	26	μm
Origin	X	0.0	μm	Y	0.0	μm	Z	0.0	μm

OK Cancel

Replace Geometry

Front

Back

Add Subdomain

Delete

VCell DB BioModels.net Path...

BioModels MathModels Geometries

Search

disconnected

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

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)
 - Spacial Deterministic
 - Geometry**
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

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

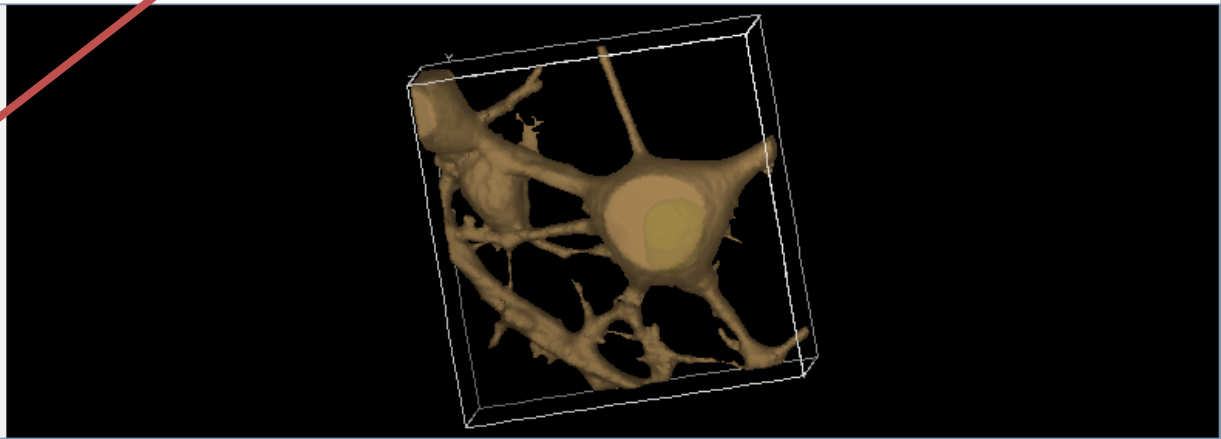
100

75

50

25

0



Object Properties Problems (0 Errors, 10 Warnings)

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

The geometry of your model is now complete.

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)
 - Spatial Deterministic
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

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)

Geometry (subdomains)

EC
Cyt
Nuc
PM
NM

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

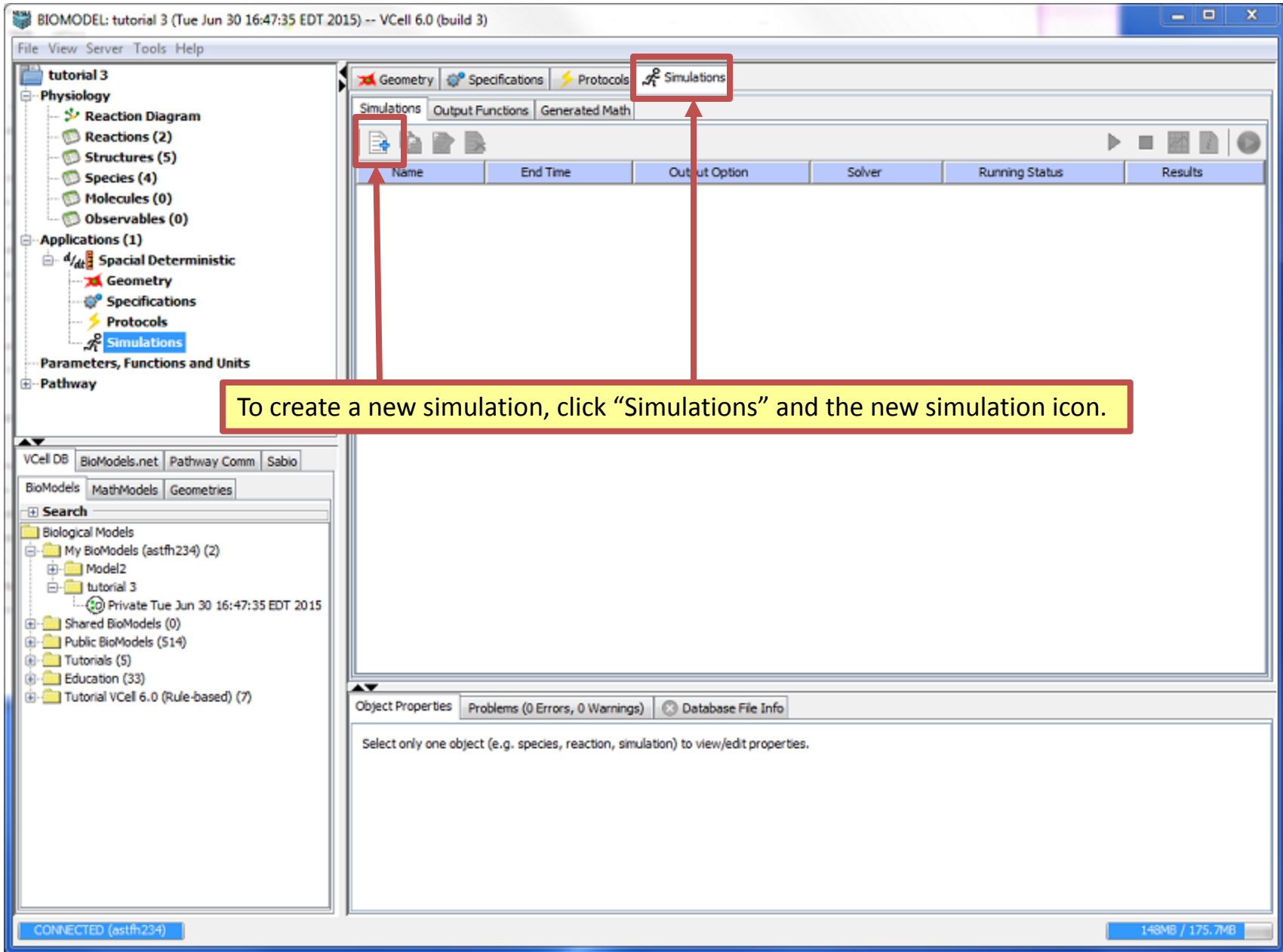
CONNECTED (astfh234) 58.1MB / 77.8MB

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

The screenshot shows the VCell 6.0 interface. The left sidebar contains a tree view for 'tutorial 3' with categories like Physiology, Applications, and Pathway. The 'Specifications' tab is active, displaying a table of species properties. The 'Initial Condition' for 'RanC_Nuc' is highlighted with a red box and a red arrow pointing to a yellow callout box. The callout box contains the text: '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

Description	Parameter	Expression	Units
initial concentration for RanC_Nuc	initConc	4.5E-4	μM
diffusion constant for RanC_Nuc	diff	10.0	$\mu\text{M}^2 \cdot \text{s}^{-1}$
Boundary Condition X- for RanC_Nuc	BC_Xm	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition X+ for RanC_Nuc	BC_Xp	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition Y- for RanC_Nuc	BC_Ym	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition Y+ for RanC_Nuc	BC_Yp	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition Z- for RanC_Nuc	BC_Zm	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$



To create a new simulation, click "Simulations" and the new simulation icon.

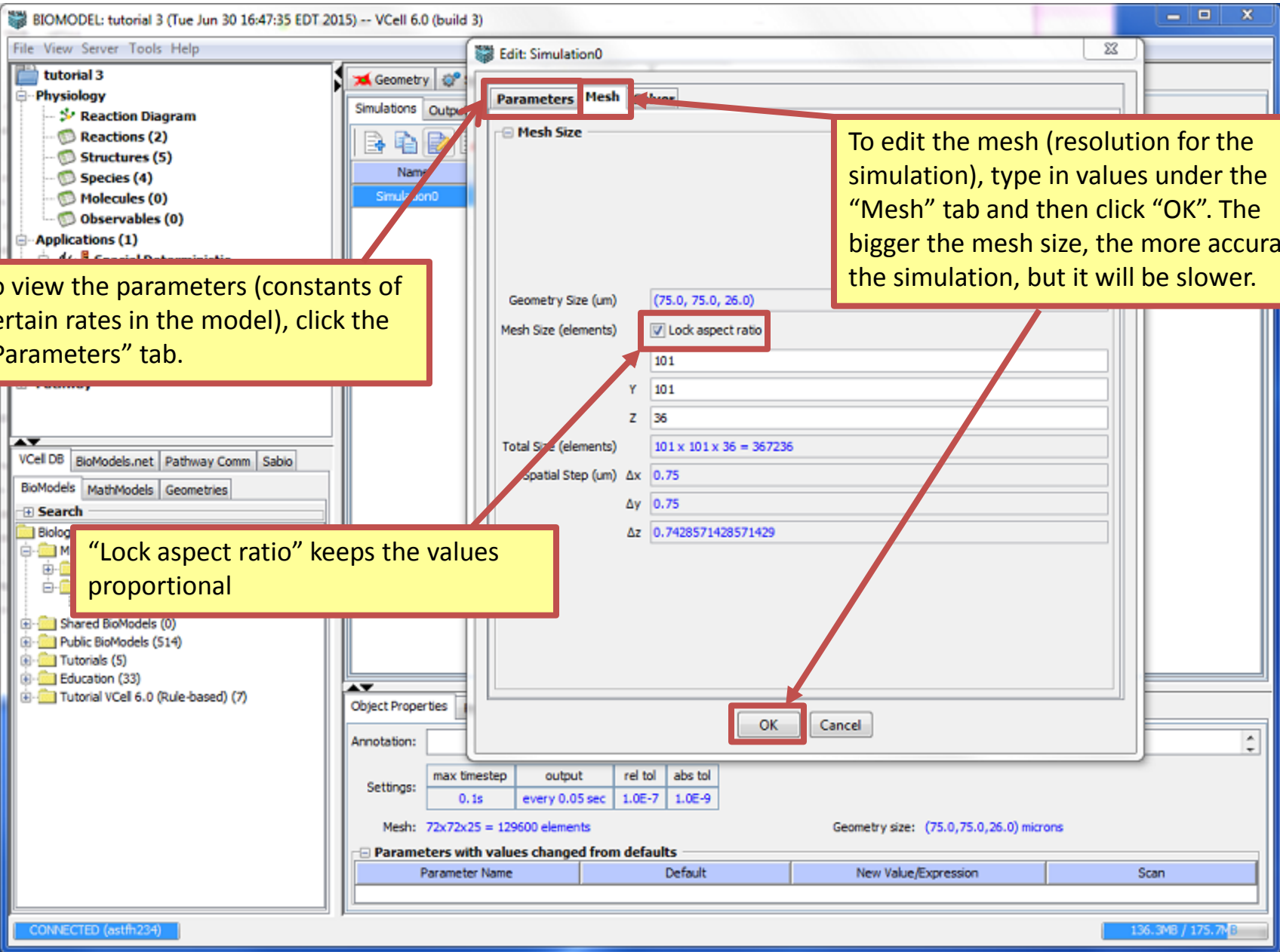
The screenshot shows the VCell software interface. On the left is a tree view of the model structure, including 'Physiology' (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables) and 'Applications' (Spatial Deterministic, Geometry, Specifications, Protocols, Simulations). The 'Simulations' sub-tab is selected. The main window displays a table of simulation settings:

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

A red box highlights the 'edit simulation' icon (a document with a pencil) in the toolbar above the table. A red arrow points from this icon to a yellow callout box containing the text: "To edit a simulation, click the edit simulation icon." Below the table, the 'Object Properties' panel shows simulation settings:

max timestep	output	rel tol	abs tol
0.1s	every 0.05 sec	1.0E-7	1.0E-9

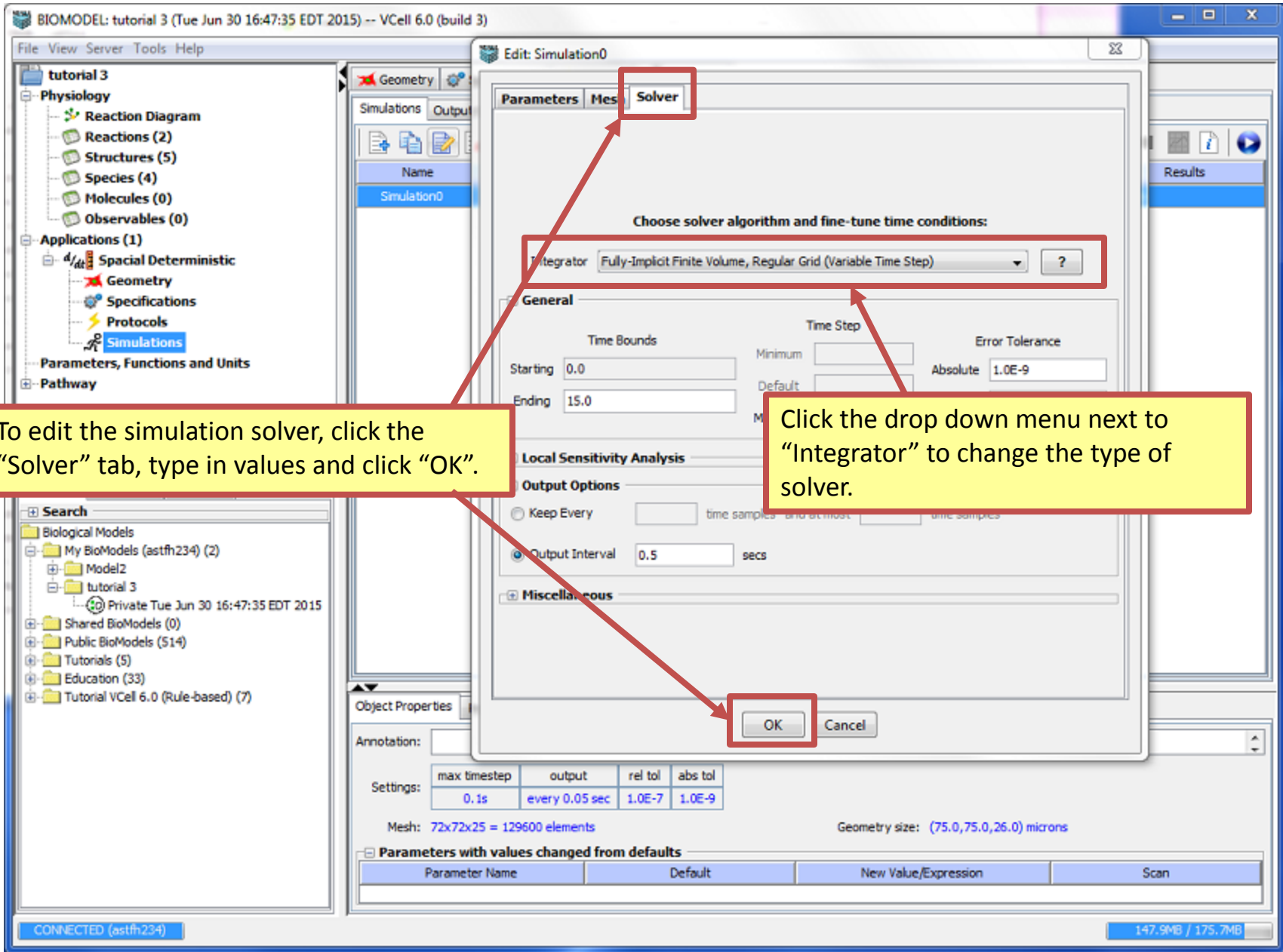
Additional information includes: Mesh: 72x72x25 = 129600 elements; Geometry size: (75.0,75.0,26.0) microns. A table at the bottom lists parameters with values changed from defaults.



To view the parameters (constants of certain rates in the model), click the "Parameters" tab.

To edit the mesh (resolution for the simulation), type in values under the "Mesh" tab and then click "OK". The bigger the mesh size, the more accurate the simulation, but it will be slower.

"Lock aspect ratio" keeps the values proportional



To edit the simulation solver, click the "Solver" tab, type in values and click "OK".

Click the drop down menu next to "Integrator" to change the type of solver.

Settings:

max timestep	output	rel tol	abs tol
0.1s	every 0.05 sec	1.0E-7	1.0E-9

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
----------------	---------	----------------------	------

BIOMODEL: tutorial 3 (Mon Jul 06 10:10:41 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

Geometry Specifications Protocols Simulations

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

Warnings from Simulation: 'Simulation0'1
The simulation has large result dataset (352MB), suggested size limits are:
5 MB for compartmental ODE simulations
200 MB for spatial simulations
100 MB for compartmental stochastic simulations
Try saving fewer timepoints or using a coarser mesh if spatial.
Do you want to continue anyway?

OK Cancel

To create a large simulation, click "OK".

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

Annotation:

max timestep	output	rel tol	abs tol
0.1s	every 0.5 sec	1.0E-7	1.0E-9

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
----------------	---------	----------------------	------

CONNECTED (astfh234) 162.5MB / 258.2MB

The screenshot shows the VCell software interface. On the left is a tree view of the model structure. The main window displays a table of simulations. A red box highlights a green play button icon in the top right of the simulation table, with a red arrow pointing to it. A yellow text box with a red border contains the instruction: "To run and save a simulation to the VCell database, click the green play icon." Below the simulation table are sections for "Object Properties" and "Settings".

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	15.0	every 0.5 sec	Fully-Implicit	not saved	no

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

Annotation: [text box]

Settings:

max timestep	output	rel tol	abs tol
0.1s	every 0.5 sec	1.0E-7	1.0E-9

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

CONNECTED (astfh234) 151.9MB / 175.7MB

The screenshot shows the VCell 6.0 interface. On the left is a tree view for 'tutorial 3' containing 'Physiology' (Reaction Diagram, Reactions (2), Structures (5), Species (4), Molecules (0), Observables (0)) and 'Applications (1)' (Spatial Deterministic, Geometry, Specifications, Protocols, Simulations). Below this is a 'VCell DB' section with 'BioModels' and 'MathModels' tabs, and a search tree showing 'Biological Models' and 'Tutorial VCell 6.0 (Rule-based) (7)'. The main window 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 red box highlights the 'Running Status' column, which shows '53.3%' for 'Simulation0'. A red arrow points from this box to a yellow text box. The bottom status bar shows 'CONNECTED (astfh234)' and '138.8MB / 258.2MB'.

Name	End Time	Output Option	Solver	Running Status	Results
Simulation0	15.0	every 0.5 sec	Fully-Implicit	53.3%	yes

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

The screenshot displays the VCell software interface. On the left, a tree view shows the project structure for 'tutorial 3', including Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables) and Applications (Spatial Deterministic, Geometry, Specifications, Protocols, Simulations). The 'Simulations' tab is active in the main window, showing a table with the following data:

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

A red box highlights the 'Results' icon in the table header, with a red arrow pointing to a yellow callout box containing the text: "To view simulation results, click the results icon." Below the table, the 'Object Properties' panel shows simulation settings: max timestep (0.1s), output (every 0.5 sec), rel tol (1.0E-7), and abs tol (1.0E-9). The mesh size is 72x72x25 = 129600 elements, and the geometry size is (75.0, 75.0, 26.0) microns. A table at the bottom lists parameters with values changed from defaults.

CONNECTED (astfh234) 148.3MB / 258.2MB

simulation results for Simulation0

View Data | Export Data | Post Processing Stats Data | Post Processing Image Data

Time: 0.0 | 15

Surface View

Data Range (Min-Max):
 Auto (current time)
Max: 0.0
Min: 0.0

Color:
BM AM NN ND NR
 Gray
 BlueRed

All Variables:
C_Cyt
J_flux0
J_r0
Ran_Cyt
RanC_Cyt
RanC_Nuc

Slice: [0-24] 7 [11] = 11.91667

Axis: XY XZ YZ

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

CONNECTED (astfh234) 174.2MB / 258MB

simulation results for Simulation0

Time: 7.5

Data Range (Min-Max):
Max: 1.0301167807024486E-4
Min: 0.0

Color: BlueRed

Slice [0-24]: Z [11] = 11.916667

Parameter Name	Default	New Value/Expression	Scan
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CONNECTED (astfh234) 181MB / 258.2MB

To change the time frame being viewed, input a value under "Time" or hold down and drag the slider.

The screenshot shows the VCell software interface. The main window displays simulation results for Simulation0 in a Surface View. A color gradient map is shown, with a legend on the right indicating the data range (Min-Max) and color options (Gray or BlueRed). The legend shows a maximum value of 1.0301167807024486E-4 and a minimum of 0.0. The color gradient is currently set to BlueRed. A callout box points to the 'Data Range (Min-Max)' legend, stating: "The Data Range shows the minimum and maximum concentrations, which correspond to the colors shown". Another callout box points to the 'All Variable' dropdown menu, which lists variables such as C_Cyt, J_flux0, J_r0, Ran_Cyt, RanC_Cyt, and RanC_Nuc. A third callout box points to the 'Gray' and 'BlueRed' radio buttons, stating: "To change the color gradient, click either 'Gray' or 'BlueRed'". A fourth callout box points to the 'C_Cyt' variable in the dropdown menu, stating: "Click here to view the concentrations of different species". The interface also shows a 'Slice View' and 'Surface View' tab, a 'Time' slider, and a 'Results' panel on the right.

BIOMODEL: tutorial 3 (Mon Jul 06 10:10:41 EDT 2015) -- VCell 6.0 (build 3)

File View Server Tools Help

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simulation results for Simulation0

View Data Export Data Post Processing Stats Data Post Processing Image Data

Time 7.5 15

Slice View Surface View

0 16.901408 32.746479 48.591549 75

0.0 6.33802817 11.6197189 16.9014085 22.1830906 27.4647889 32.7464789 38.028161 43.3096516 48.5915499 53.8732394 59.1548296 64.4366199 69.7183099 75.0

Data Range (Min-Max)

Auto (current time)

Max: 1.0301167807024486E-4

1.0301167807024486E-4

Min: 0.0

0.0

Color

BM AM NN ND NR

Gray

BlueRed

Plot

ROI

Parameter Name Default New Value/Expression Scan

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To create a time plot, click the dot tool and click on two different points within the simulation. (One in the cytoplasm and one in the nucleus)

To view the time graph, click "plot" > "time".

The screenshot shows the VCell software interface. The main window displays a 'Time Plot' for 'simulation results for Simulation0'. The plot shows a purple curve representing the concentration of 'RanC_Cyt' over time 't'. The Y-axis ranges from 0.0 to 2.0E-5, and the X-axis ranges from 0.0 to 20.0. A red box highlights the 'Y Axis' list, which includes species like C_Cyt, I_r0, Ran_Cyt, RanC_Cyt, RanC_Nuc, Size_Cyt, Size_EC, Size_Nuc, and vcRegionVolume. A yellow callout box with a red arrow pointing to 'RanC_Cyt' in the list contains the text: 'To change what species concentrations are being viewed, click on different species under "Y Axis".'

Parameter Name	Default	New Value/Expression	Scan

CONNECTED (astfh234) 155.3MB / 2.6.2MB

The screenshot shows the VCell software interface. The main window displays a 'Time Plot' for 'RanC_Cyt' at two different points, P[0] and P[1]. The Y-axis represents concentration, ranging from 0.0 to 2.0E-5. The X-axis represents time (t), ranging from 0.0 to 20.0. The plot shows a sharp peak in concentration around t=2, followed by a gradual decay. A yellow callout box with a red border contains the text: 'Your deterministic spatial simulation is now complete.'

Selected Points

Point	X	Y	Z
P[0]	35.915	46.478	11.916
P[1]	45.422	51.76	11.916

Y Axis

- C_Cyt
- I_r0
- Ran_Cyt
- RanC_Cyt
- RanC_Nuc
- Size_Cyt
- Size_EC
- Size_Nuc
- vcRegionVolume

Plot Legend:

- RanC_Cyt at P[0]
- RanC_Cyt at P[1]

Parameter Name	Default	New Value/Expression	Scan

CONNECTED (astfh234) 155.3MB / 2.6.2MB

Next: VCell Tutorial
BioModel with Multiple Applications

Part 2 Compartmental Applications and
Parameter Estimation