Virtual Cell Image-Based Geometry (VCell 7.7, July 2025)

Table of Contents:

1. Initializing the Geometry	Page 2
2. Importing the Image Stack	Page 2
3. <u>Creating a New Domain</u>	Page 2
4. <u>Cropping the Image</u>	Page 2
5. <u>Smoothing the Image</u>	Page 3
6. <u>Domain Selection</u>	Page 3
7. <u>Updating Domain</u>	Page 3
8. <u>Manual Editing (Erasing)</u>	Page 3
9. Filling in Nucleus Domain Gaps	Page 4
10. <u>Merging Regions</u>	Page 4
11. Adding the Cytoplasm Domain	Page 4
12. <u>Finalizing Cytoplasm Domain</u>	Page 4
13. <u>Completing Geometry Setup</u>	Page 5
14. <u>Defining the Size of the Image</u>	Page 5
15. Acknowledgements	Page 6

1. Initializing the Geometry:

Open VCell and open an application. Navigate Geometry \rightarrow Geometry Definition to create a new geometry by clicking New \rightarrow Image Based. You will then be prompted to select a file from your computer.

	Structure Mapping Geometry Definition	Kinematics		
3D, size=(74.24	,74.24,26.0), origin=(0.0,0.0,0.0) Export	Edit Image	Replace Ge	ometry
Name	Value		Front	New
ec cvtosol			Back	Open fr
Nucleus			Add Subdomai	n 🕶
			Delete	

2. Importing the Image Stack:

Use your own images or download them from <u>https://vcell.org/support</u>.

The image can be scaled up or down in the next screen.

Tutorial Guides (pdf) for VCell Moving Boundaries Multiple Application of a Nuclear Transport (Neuroblastoma Stack for Tutorist) (CSV File) (ver 7.2) Rule-Based Modeling (single compartment) EGFR model (ver 6.1) Rule-Based Modeling (multiple compartment) swith transport and anchoring) Ran model (ver 6.1) simple FRAP (ver 7.2) FRAP with blinding (ver 7.2) PH-GFP Translocation (ver 7.2) Using Pathway Commons (ver 6.0) VCell Video Tutorials

3. Creating a New Domain:

Each pixel in the gray-scale image has an intensity from 0 (black) to 255 (white). VCell informs you that there are 253 intensities, so it may define 253 domains based on the intensity. Choose option **2**. **Assume Pre-Segmented** if this is what you prefer. If you want to define domains yourself, choose **1. Add Empty Domain**, and name it (e.g. "Nuc" for nucleus).



Data Info: : Z=15/34 3.81818E-7/9.00000E-7: zoom(1); contr(bright+1)

View Z: 1

4. Cropping the Image: Navigate through the image slices using the Z slider and adjust the zoom

- Crop unnecessary parts of the image using the **cropping tool**.



5. Smoothing the Image:

Apply the averaging filter to smooth the image. The intensities of the pixels in each 9x9 box are averaged together to replace the original pixel values of the center pixel.

Original

6. Domain Selection:

- The **histogram** at the bottom shows the pixels in the 3D image ordered by intensities.

- Using the histogram tool, select pixels with intensities most closely resembling the nucleus.

Note that it cannot be perfect, as many pixels have the same intensities elsewhere in the image. You can edit the selection later.

- View selections across different slices using the Z slider.

7. Updating Domain:

Click Apply and then Update Domain to finalize the initial selections.

8. Manual Editing (Erasing):

- Your selection usually generates a disjoint set of regions (65 in this case). The regions are ordered by size, from largest to smallest. The number in parentheses is the number of pixels in this region.

- Click on the largest region of interest to retain (highlighted as the largest Nuc domain). It will become orange.

- Using the **eraser tool**, **V** erase irrelevant orange pixels across ALL slices, carefully distinguishing and removing regions not belonging to the nucleus. You can change the size of the eraser by right-clicking the icon.

- Ensure accuracy by frequently zooming out and navigating the Z slider. Make sure to keep selecting the largest Nuc domain region as you erase.

255 Export... Import stl... Cancel







255





Smoother

9. Filling in Nucleus Domain Gaps:

- Use the brush/paint tool $\boxed{8}$ to fill in gaps within the nucleus.
- Adjust tool size by right-clicking for more precise editing.

10. Merging Regions:

- Select smaller regions (everything besides the largest Nuc domain) and click **Automerge**. Automerging joins smaller regions to the largest adjacent regions.

- It is advised to automerge in sections, selecting regions starting from the smallest and ending with the largest, ensuring that the regions join the proper domain.

- Check accuracy often by revisiting the slices again with the Z slider.

11. Adding the Cytoplasm Domain:

After the nucleus is defined, the rest of the cell will be

set as the cytosol. This step is similar to adding the nucleus domain.

- Click **Add Domain** and name it "Cyt".

- Use histogram selection to identify pixels that comprise the cytoplasm, confirm by clicking **Apply**, and click **Update Domain.**

766015

1 0 0

- Choose the option **Keep existing domain regions when overlapping** to maintain the integrity of the nucleus domain.

zoom

Histogram Tool scroll

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

12. Finalizing Cytoplasm Domain:

- Auto-merge smaller regions, preserving the cytoplasmic region with the most pixels.

- Verify accuracy through slice-by-slice examination.









Ap



14 Domain Regions

Nuc (48913)



Auto-Merge

13. Completing Geometry Setup:

- Click **Finish**, then select **Assign as default background**.

- Select **Add empty border** to guarantee that cytoplasm and nucleus do not touch the borders of the simulation volume.

766015	zoom	Hi	stogram T	00 scroll		Apply
gener						
• ō	(1	Pixel Values) Click	-Drag mouse to c	reate highlight region	s	255
	Finisko	Attributes	Export	Import stl	Cancel	

14. Defining the Size of the Image:

The Z-stack may not have the information about the height of each image plane. The x and y coordinates may

need to be scaled as well. Click Edit Domain and adjust the size. Set X and Y to 100.0 um and Z to 26.0 um.

Size	Х	100.0	μm	Y	100.0	μm	Z	26	μm
Origin	х	0.0	μm	Y	0.0	μm	z	0.0	μm

Edit Imag

Acknowledgements

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