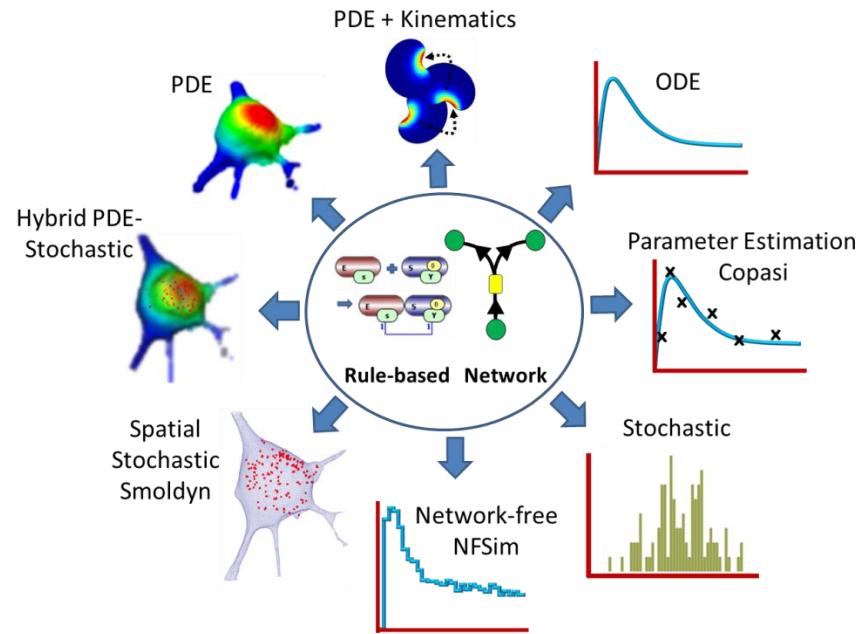


# VCell

A modeling environment for the simulation of cellular events. Download at [vcell.org](http://vcell.org).



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

# VCell BioModel using the Moving Boundary Solver

## Objective

Create a simple Biomodel of a fluorescence photobleaching (FRAP) experiment in a moving cell; learn how to specify kinematics in a VCell Biomodel and utilize the Moving Boundary solver.

## Goals

- Create a Biomodel Physiology that recreates a fluorescence photobleaching experiment and a spatial deterministic application of the Physiology using a 2D geometry created from analytic expressions for a simple circle
- Specify kinematics (i.e. velocities) of structures and the molecules contained within the structures
- Define initial conditions that vary in x and y using Boolean expressions.
- Create a simulation using the VCell Moving Boundary solver, specifying time course and computational mesh.
- Run the simulation, view and export results.

# Notes on the VCell Moving Boundary Solver

Moving Boundary Applications in VCell allow for PDE (spatial) simulations to occur within a geometry where the boundaries of compartments can change in shape and position within the overall computational space. There are some important things to keep in mind when you create this type of application.

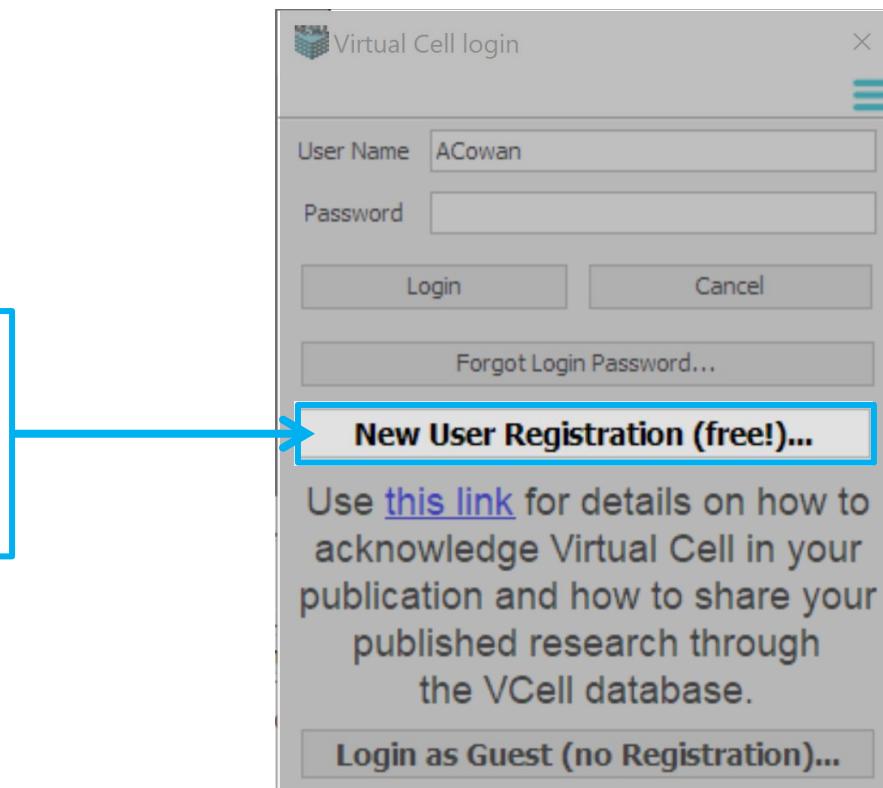
- The current implementation of the moving boundary solver only works with 2D geometries. We hope in the future to enable problems with 3D geometries.
- Creating an application with a moving boundary solver follows the same steps used for fixed domains, except that a velocity is assigned to points on the cell membrane (and optionally for species residing with the volume) by defining Kinematics for surface and volume objects as part of the description of the Geometry.
- Species will have both diffusion terms (which can be 0) and velocity terms defined by the kinematics. Because displacement terms will be different in different compartments, species in different compartments will not necessarily move together. This tutorial provides an example of different types of kinematics for membranes and volumes.
- Currently, VCell tools for analyzing spatial results are not available for results of moving boundary simulations, so it is necessary to export your results to other image processing software to analyze the results of simulations.

# Table of contents

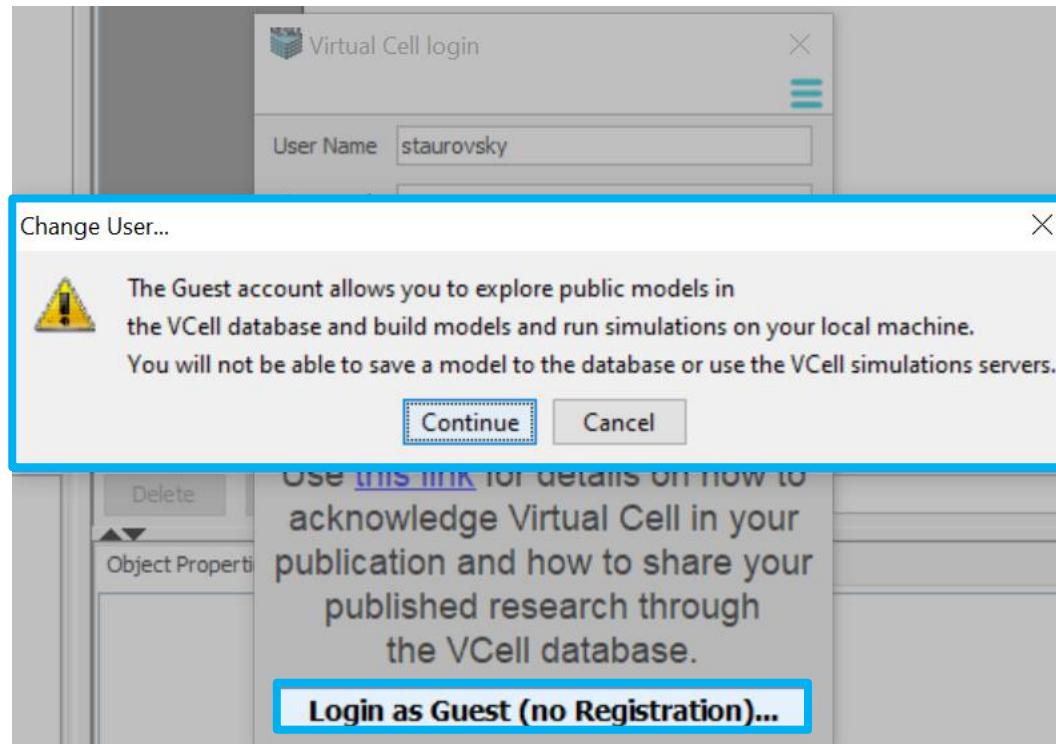
- ▶ [Opening VCell](#)
- ▶ [Using VCell Help](#)
- ▶ [Defining compartments](#)
- ▶ [Creating species](#)
- ▶ [Creating applications](#)
- ▶ [Creating a 2D geometry using algebraic expressions](#)
- ▶ [Editing computational domain size](#)
- ▶ [Mapping geometry to compartments](#)
- ▶ [Specifying kinematic processes.](#)
- ▶ [Specifying initial conditions](#)
- ▶ [Creating a simulation](#)
- ▶ [Using the Moving Boundary Solver](#)
- ▶ [Viewing simulation results](#)
- ▶ [Export simulation results as an NRRD or HDF5 file](#)
- ▶ [Export simulation results as a Quicktime movie](#)
- ▶ [Modify the model to see how volume species react to membrane changes](#)

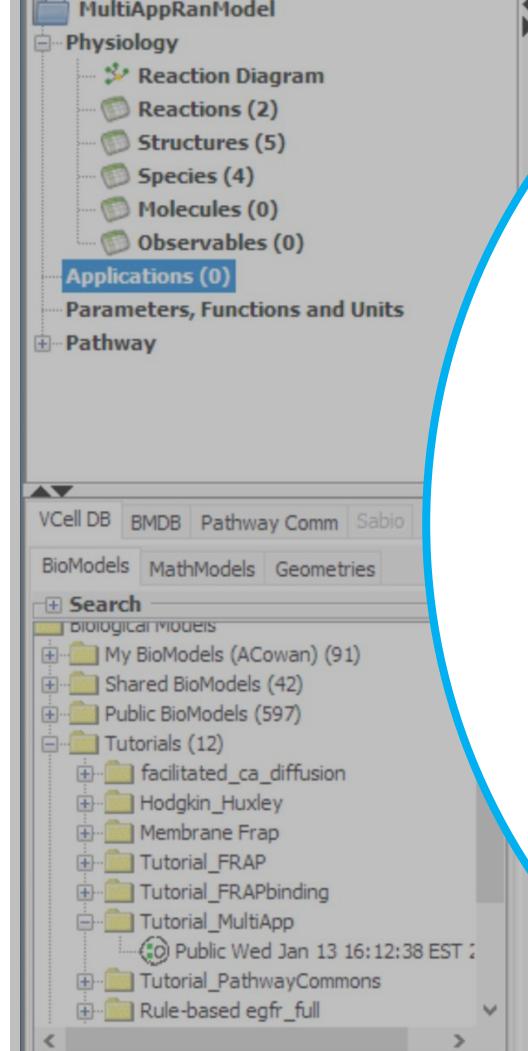
# Your first time opening VCell

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



# Your first time opening VCell Guest Login Option





## VCell BioModel Organization

### BioModel

Physiological representation of the model where the compartments, molecules, biochemical reactions and kinetic parameters are defined.

### Applications

There may be one or multiple applications within one BioModel. Here, simulation-dependent conditions are defined, such as initial conditions, simulation specific details, and changes in kinetic parameters.

### Simulations

Execution of BioModel Application with defined length of time, time step, resolution, solver and parameter overrides.

# The VCell Interface

File Account Window Tools Help

BioModel2

**Physiology**

- Reaction Diagram
- Reactions (0)
- Structures (1)
- Species (0)
- Molecules (0)
- Observables (0)

Applications (0)

Parameters, Functions, Units, etc.

Pathway

VCell DB BMDB Pathway Comm

BioModels MathModels Geometries

**Search**

Biological Models

- My BioModels (vcellguest) (0)
- Shared With Me (0)
- Tutorials (9)
- Public BioModels (869)
  - Published (184)
  - Curated (58)
  - Uncurated (627)

CONNECTED (vcellguest)

Reaction Diagram Reactions Structures Species Molecules Observables

Reaction Diagram

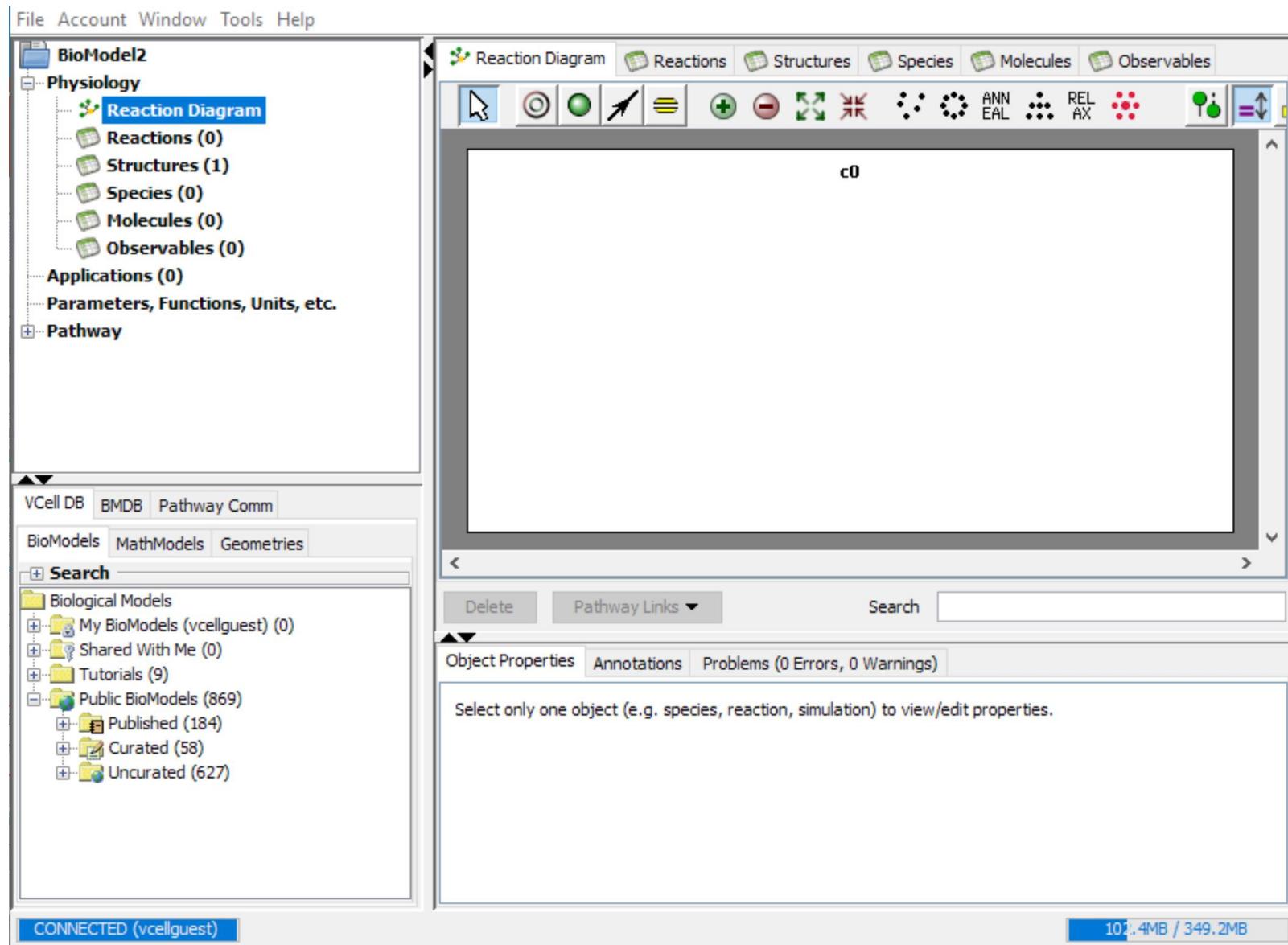
c0

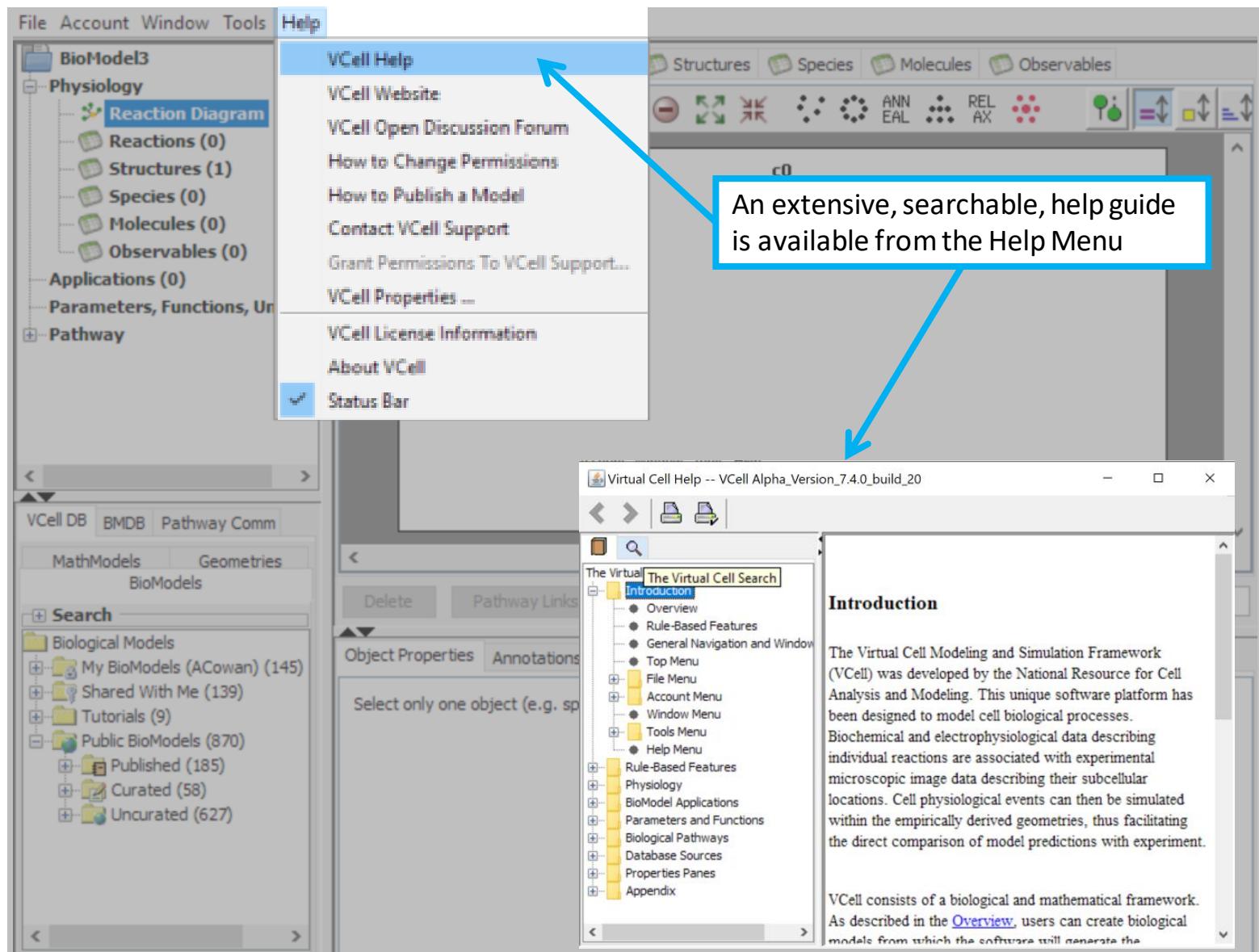
Delete Pathway Links Search

Object Properties Annotations Problems (0 Errors, 0 Warnings)

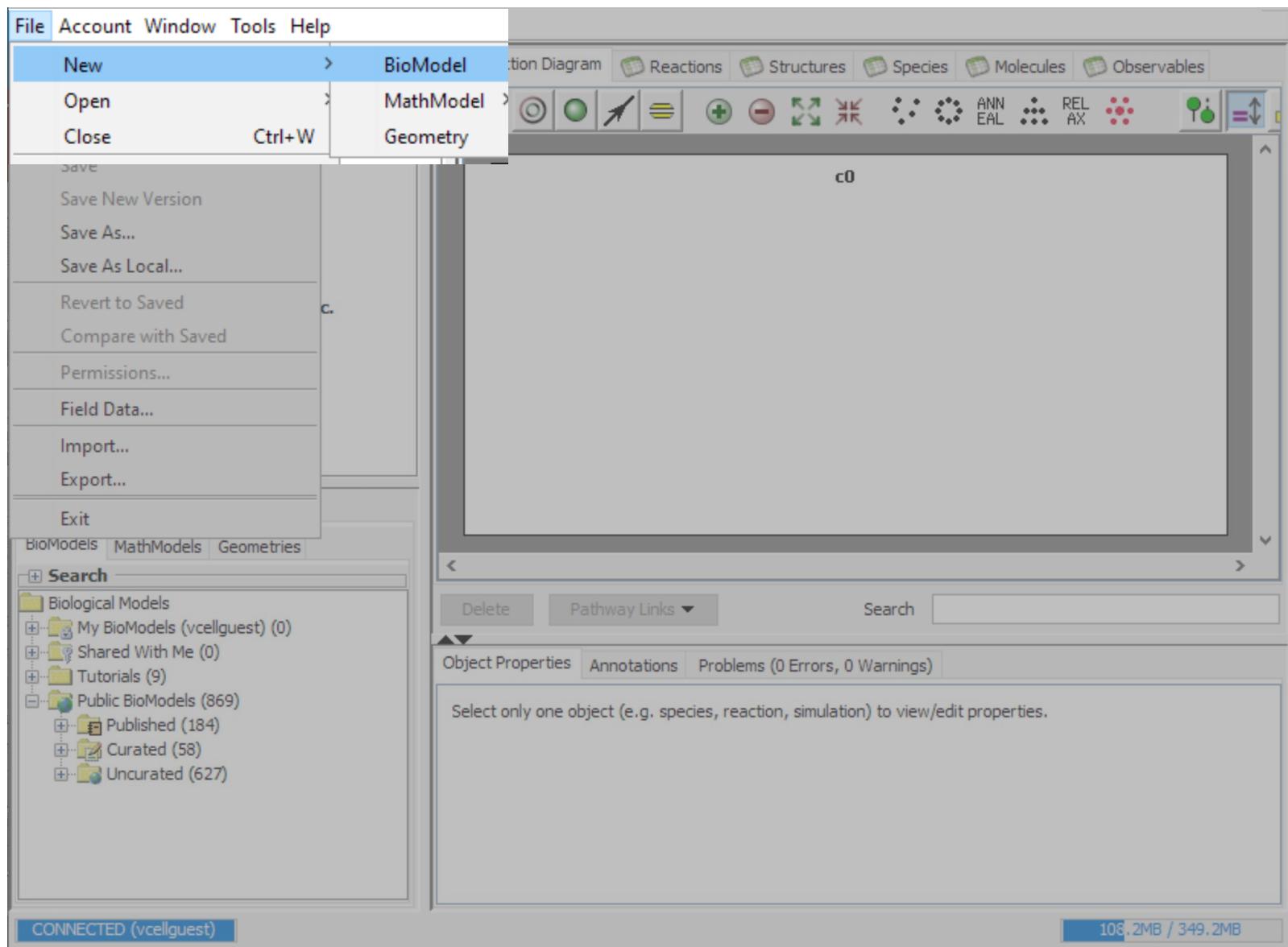
Select only one object (e.g. species, reaction, simulation) to view/edit properties.

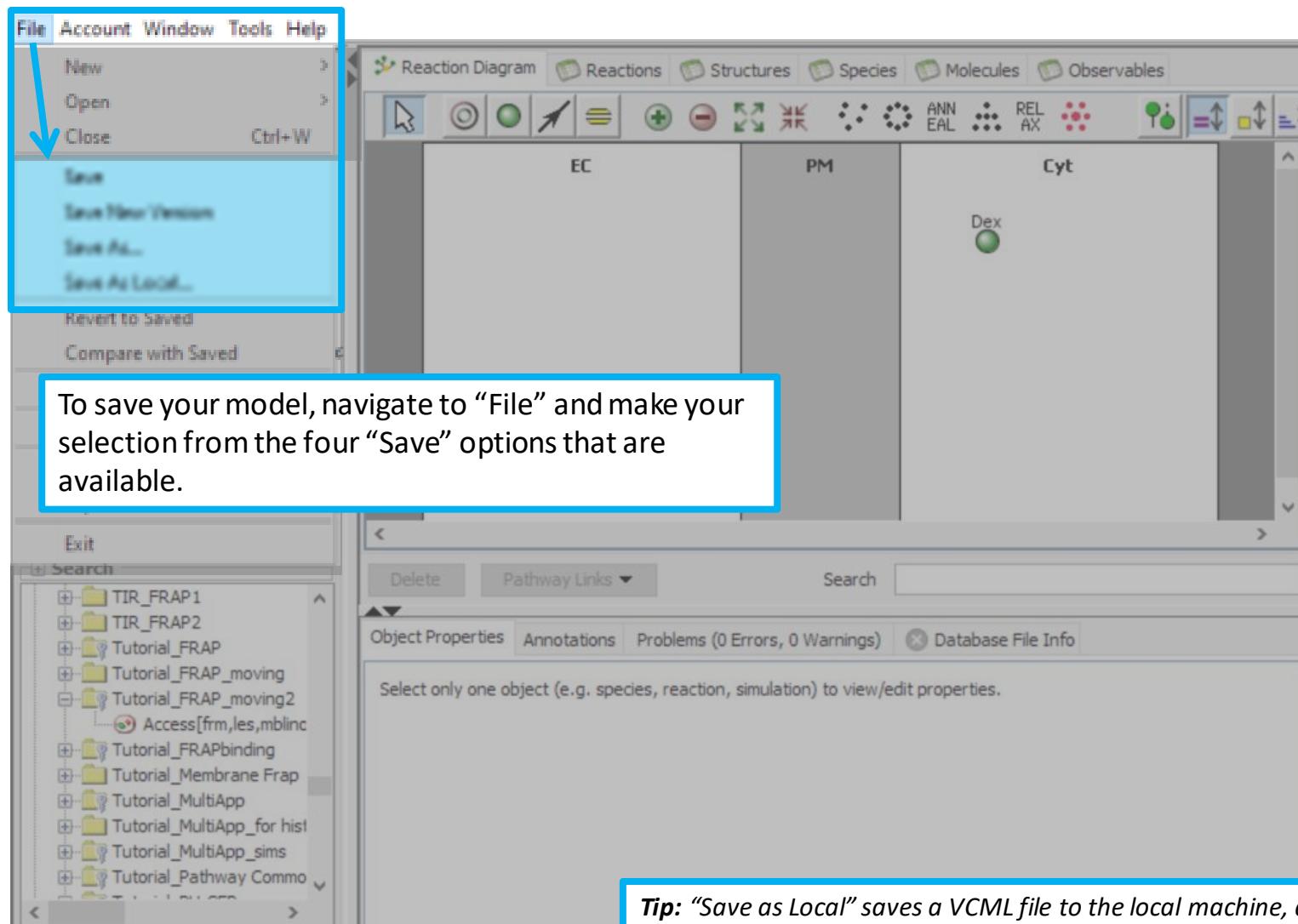
101.4MB / 349.2MB





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





The screenshot shows the VCell software interface. On the left, there is a navigation tree under the title "Tutorial\_FRAP\_moving2". The tree includes sections for Physiology (Reaction Diagram, Reactions 0, Structures 3, Species 1, Molecules 0, Observables 0), Applications (1) (d/dt FRAP), Parameters, Functions, Units, etc., and Pathway.

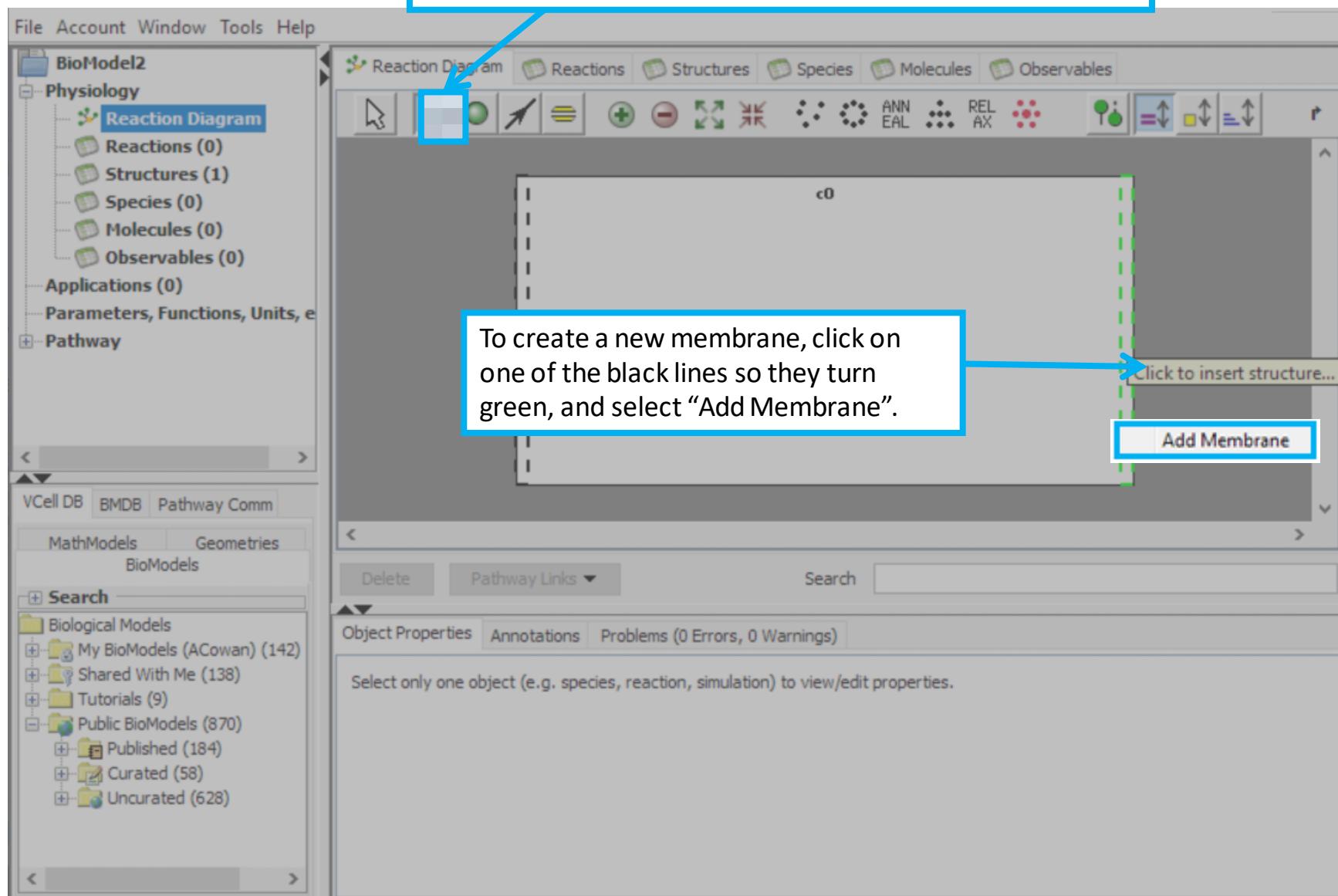
The main workspace is a "Reaction Diagram" tool. It features a grid with compartments labeled EC, PM, and Cyt. A green sphere representing the molecule "Dex" is located in the Cyt compartment. A toolbar above the diagram contains various icons for selection, zoom, and model manipulation.

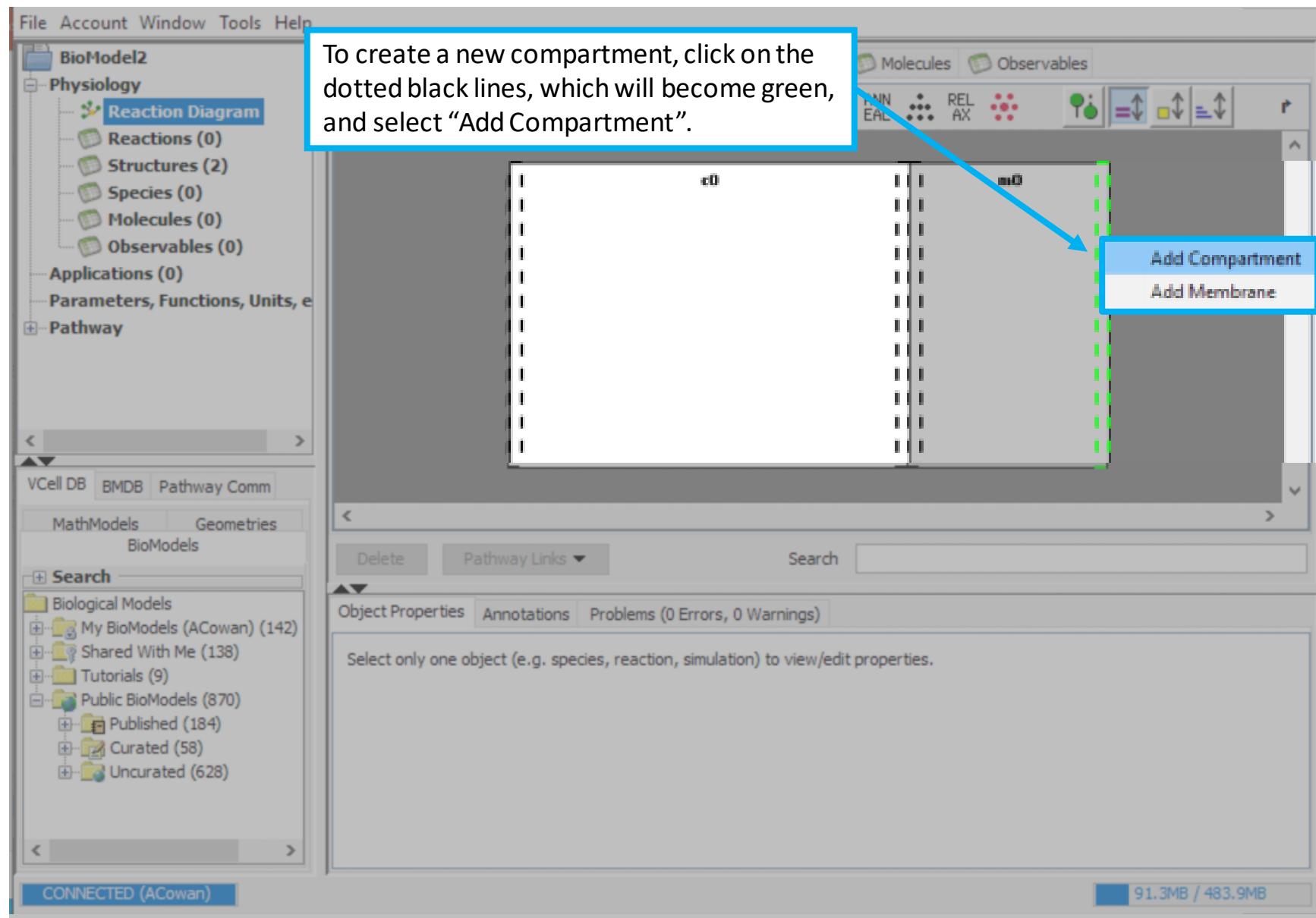
Below the main workspace is a "Database" window. It has tabs for VCell DB, BMD6, Pathway Comm, BioModels, MathModels, Geometries, and Search. The Search tab is active, showing a list of models: TIR\_FRAP1, TIR\_FRAP2, Tutorial\_FRAP, Tutorial\_FRAP\_moving, Tutorial\_FRAP\_moving2, Tutorial\_FRAPbinding, Tutorial\_Membrane Frap, Tutorial\_MultiApp, Tutorial\_MultiApp\_for\_hist, Tutorial\_MultiApp\_sims, Tutorial\_Pathway Comm, and Tutorial\_Pathway Comm2. The "Tutorial\_FRAP\_moving2" model is selected, highlighted with a blue border.

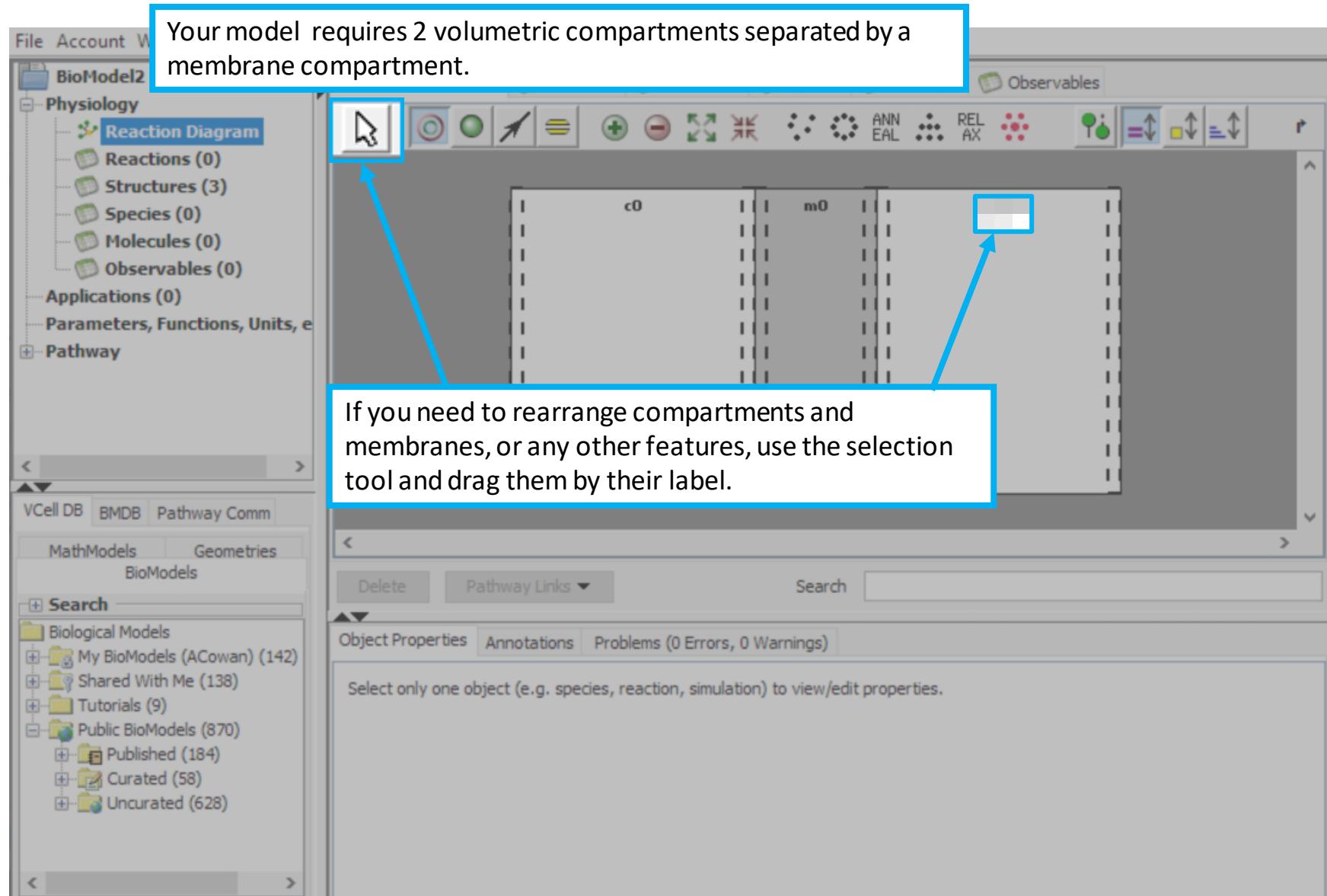
A blue arrow points from the "Tutorial\_FRAP\_moving2" entry in the database search results to the "Tutorial\_FRAP\_moving2" entry in the main workspace's reaction diagram. A callout box with a blue border contains the text: "To re-open a model, navigate to the folder that the model was saved in and double-click the model name."

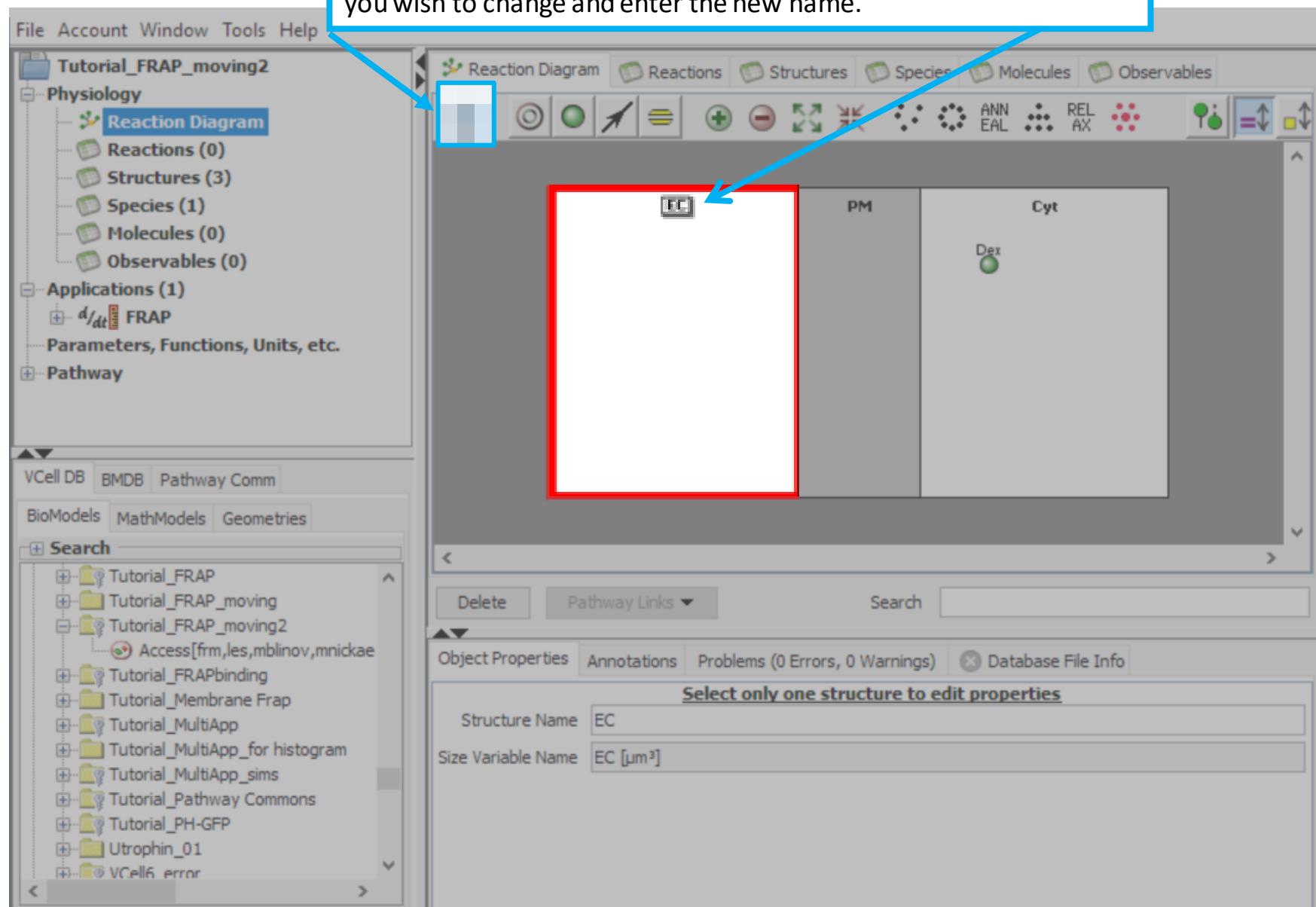
In the bottom right corner of the Database window, there is a detailed view of the selected model. It shows "Object Properties", "Annotations", "Problems (0 Errors, 0 Warnings)", and "Database File Info". Under "Database File Info", it lists "biomodel-216053715" and "ACowan" (last modified "Wed Sep 22 11:38:37 E"). Below this, under "Model Provenance", it states: "cloned from 'Tutorial\_FRAP\_moving2' owned by user mblinov", "cloned from 'Tutorial\_FRAP\_moving2' owned by user ACowan", "cloned from 'Tutorial\_FRAP\_moving' owned by user schaff", and "cloned from 'Tutorial\_FRAP' owned by user tutorial". A second callout box with a blue border contains the tip: "Tip: When click on a model in the database window, Annotations about the model appear in the properties pane here."

To create the components to your model, start with creating a volumetric compartment by selecting the Structure Tool. This will automatically create your first compartment.









File Account Window Tools Help

Tutorial\_FRAP\_moving2

Physiology

- Reaction Diagram (selected)
- Reactions (0)
- Structures (3)
- Species (1)
- Molecules (0)
- Observables (0)

Applications (1)

- d/dt FRAP

Parameters, Functions, Units, etc.

Pathway

VCell DB BMDB Pathway Comm

BioModels MathModels Geometries

Search

- Tutorial\_FRAP
- Tutorial\_FRAP\_moving
- Tutorial\_FRAP\_moving2
  - Access[frm,les,mblinov,mnickae]
- Tutorial\_FRAPbinding
- Tutorial\_Membrane Frap
- Tutorial\_MultiApp
- Tutorial\_MultiApp\_for histogram
- Tutorial\_MultiApp\_sims
- Tutorial\_Pathway Commons
- Tutorial\_PH-GFP
- Utrrophin\_01
- VCell6\_error

Reaction Diagram    Reactions    Structures    Species    Molecules    Observables

EC    PM    Cyt

You can also change the Structure Name on the Object Properties tab.  
You can annotate compartments and rename species here as well.

Delete Pathway Links Search

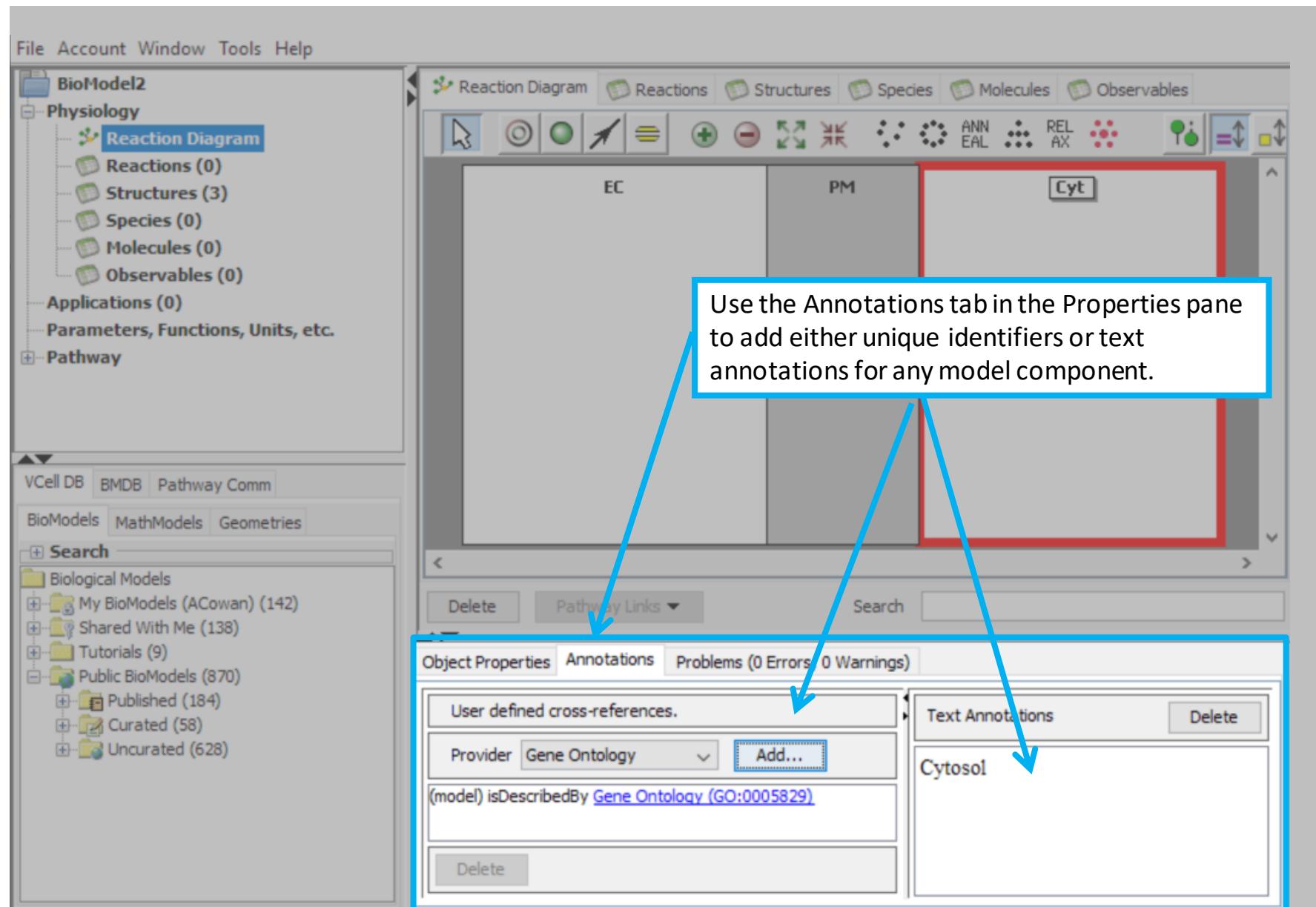
Object Properties Annotations Problems (0 Errors, 0 Warnings) Database File Info

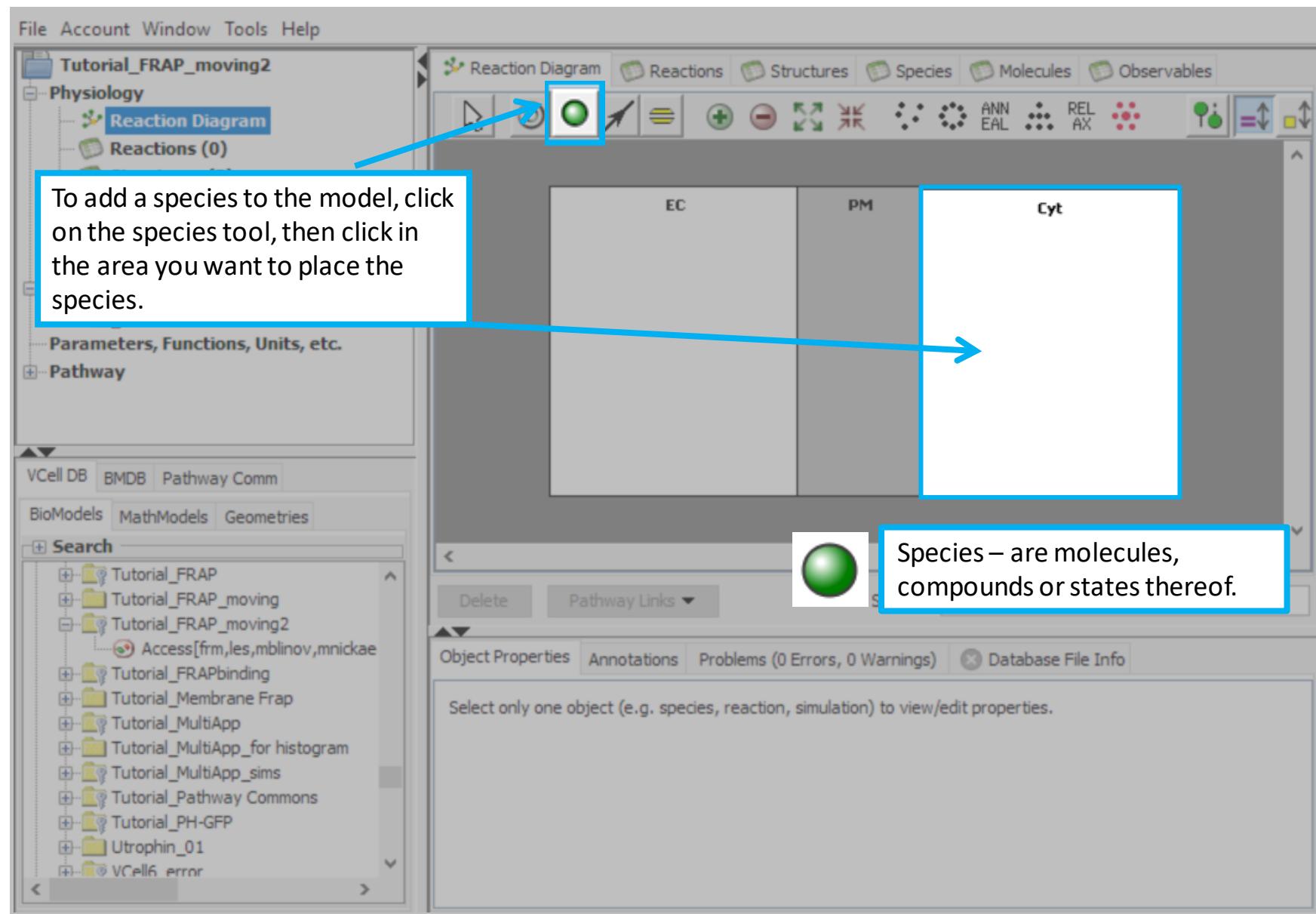
Select only one structure to edit properties

Structure Name: EC

Size Variable Name: EC [ $\mu\text{m}^3$ ]

The volume compartments in this tutorial are EC and Cyt, separated by a membrane, PM





This screenshot shows the VCell software interface for a "Tutorial\_FRAP\_moving2" project. The left sidebar displays a tree view of the model components under "Physiology". A blue box highlights the following text:

This tutorial uses only a single diffusing species ("Dex" for fluorescently labelled dextran) that will be photobleached in a moving cell.

Look at other tutorials to see how to create reactions among species.

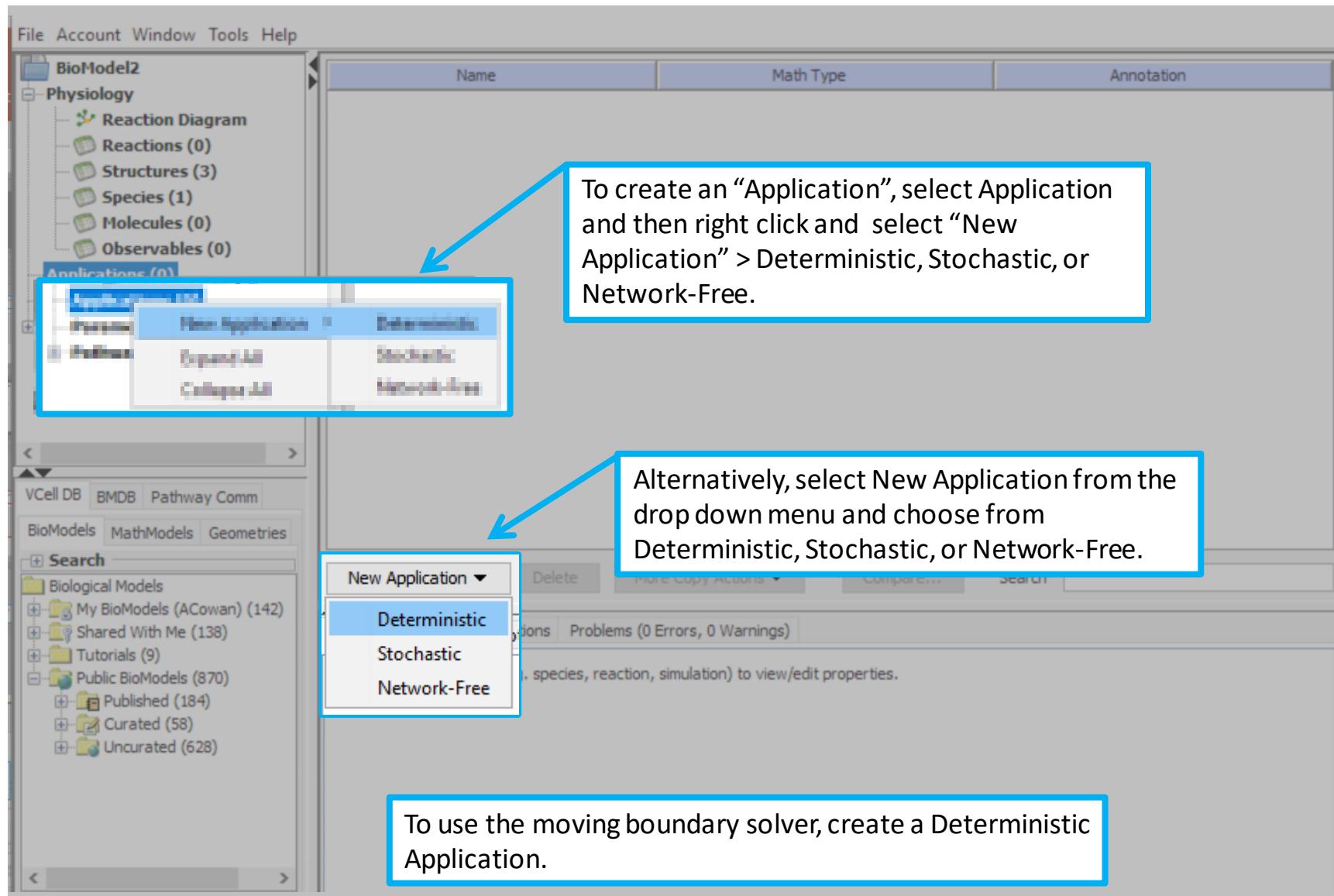
The main workspace shows a reaction diagram with three compartments: PM (Plasma Membrane), PM, and Cyt (Cytosol). A green sphere representing the species "Dex" is located in the Cyt compartment. The toolbar above the workspace contains various icons for selection, zoom, and simulation controls.

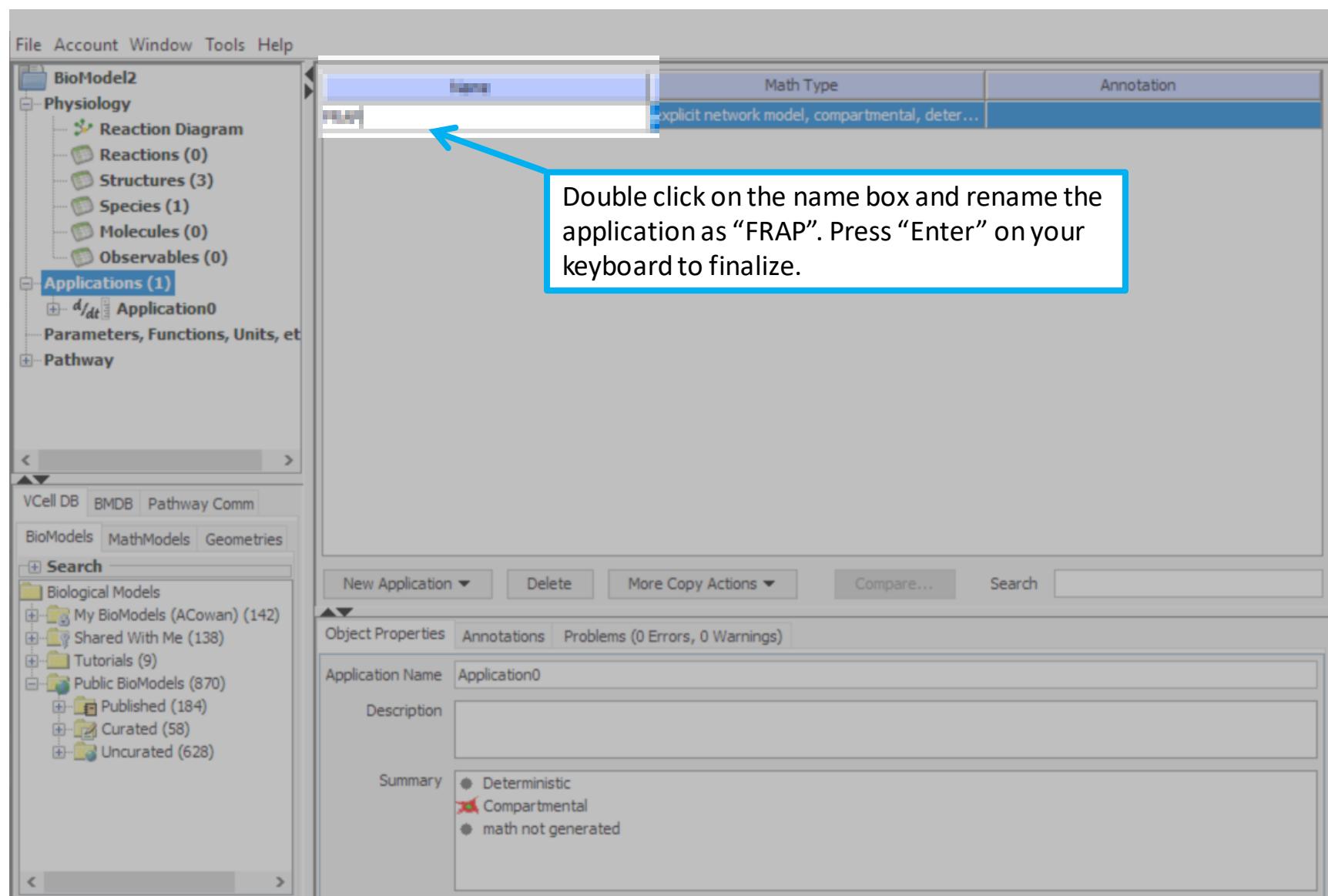
The bottom left pane shows a search results list with items like "Tutorial\_FRAP", "Tutorial\_FRAP\_moving", and "Tutorial\_FRAP\_moving2". The bottom right pane shows the properties of the selected species "Dex", with the "Species Name" field set to "Dex".

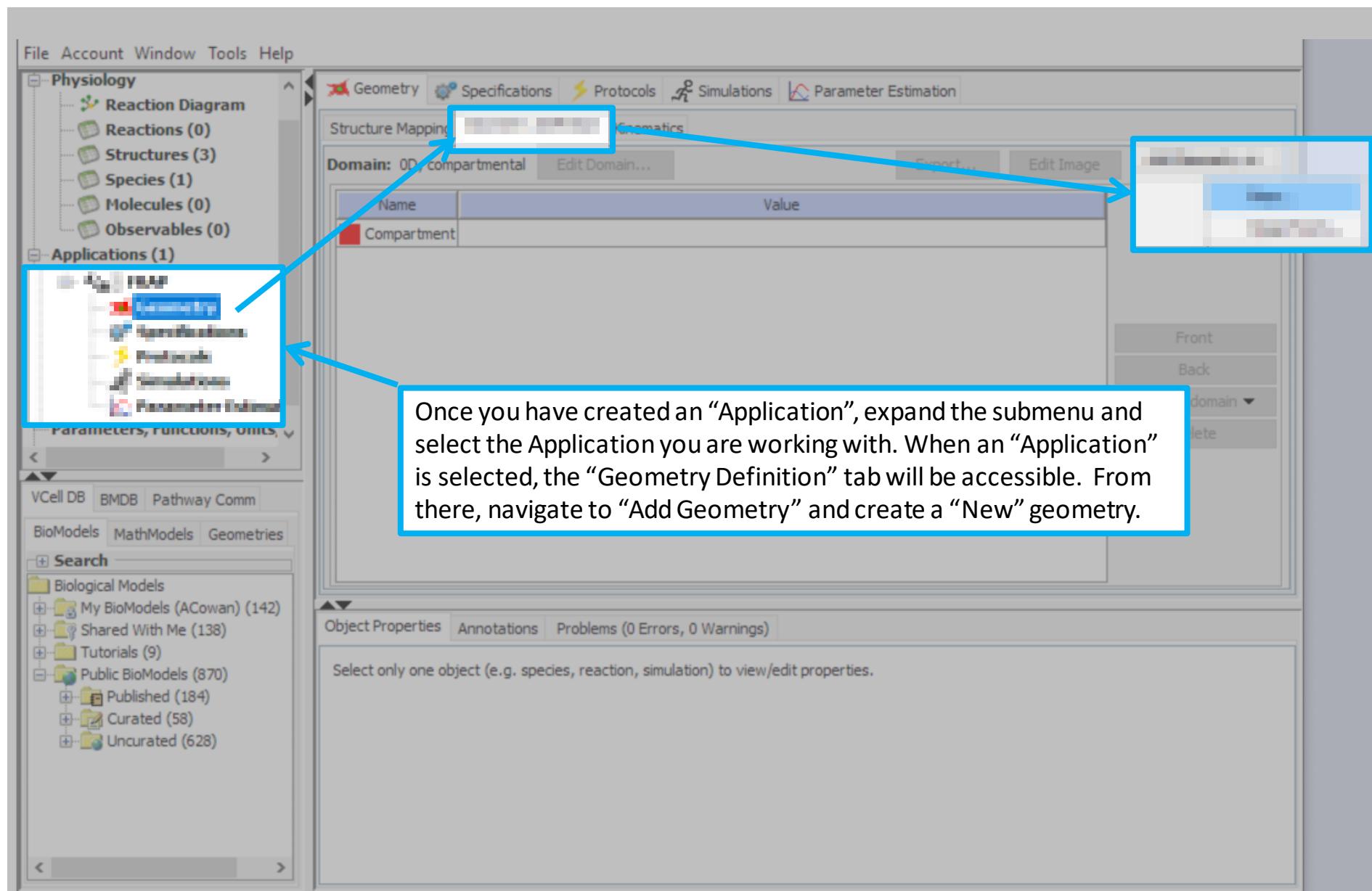
The screenshot shows the BioModeler software interface. On the left, there's a navigation panel with a tree view of a model named "BioModel2". Under "Physiology", "Reaction Diagram" is selected. Below it are sections for Reactions (0), Structures (3), Species (1), Molecules (0), and Observables (0). There are also sections for Applications (0) and Pathways. At the bottom of this panel are links to VCell DB, BMDB, and Pathway Community. A "Search" section lists categories like Biological Models, My BioModels (ACowan) (142), Shared With Me (138), Tutorials (9), and Public BioModels (870).  
The main workspace is a "Reaction Diagram" window. It features a toolbar at the top with icons for selection, zoom, and various tools. Below the toolbar is a compartment grid divided into three columns: EC, PM, and Cyt. In the Cyt compartment, there is a green sphere representing a species named "Dex".  
At the bottom of the screen, there's a "Pathway Links" dropdown menu, a search bar, and tabs for Object Properties, Annotations, and Problems (0 Errors, 0 Warnings). The "Object Properties" tab shows the "Species Name" field set to "Dex" and a "Linked Pathway Object(s)" list.

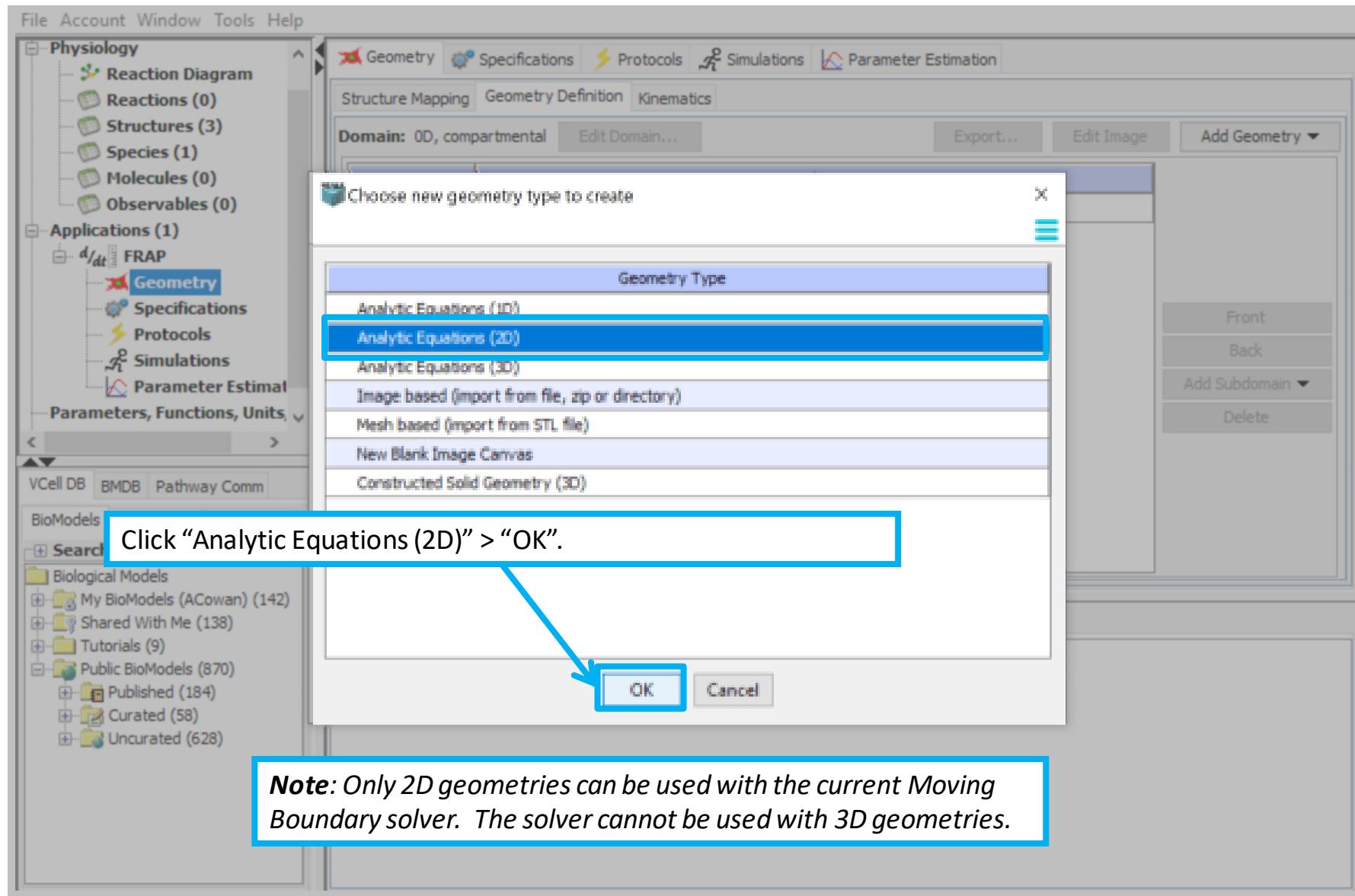
To remove a species or reaction from your model, select the species or reaction and click on either the “Delete” button or the backspace button on your keyboard.

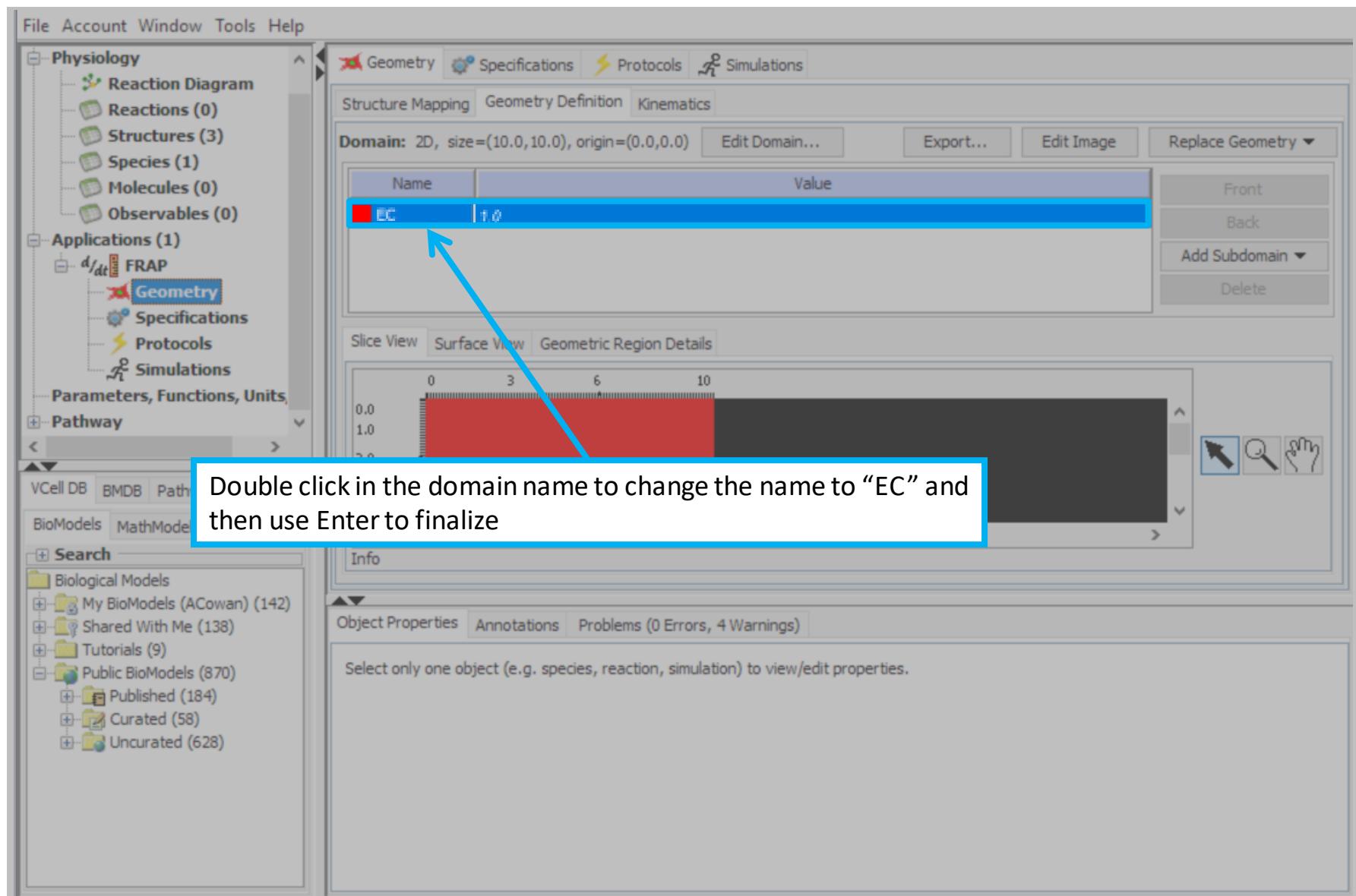
Note that you cannot move species, reactions, or fluxes from one compartment to another. You must delete a species, flux, or reaction from one compartment and then create it in another compartment.











Double click in the domain name to change the name to “EC” and then use Enter to finalize

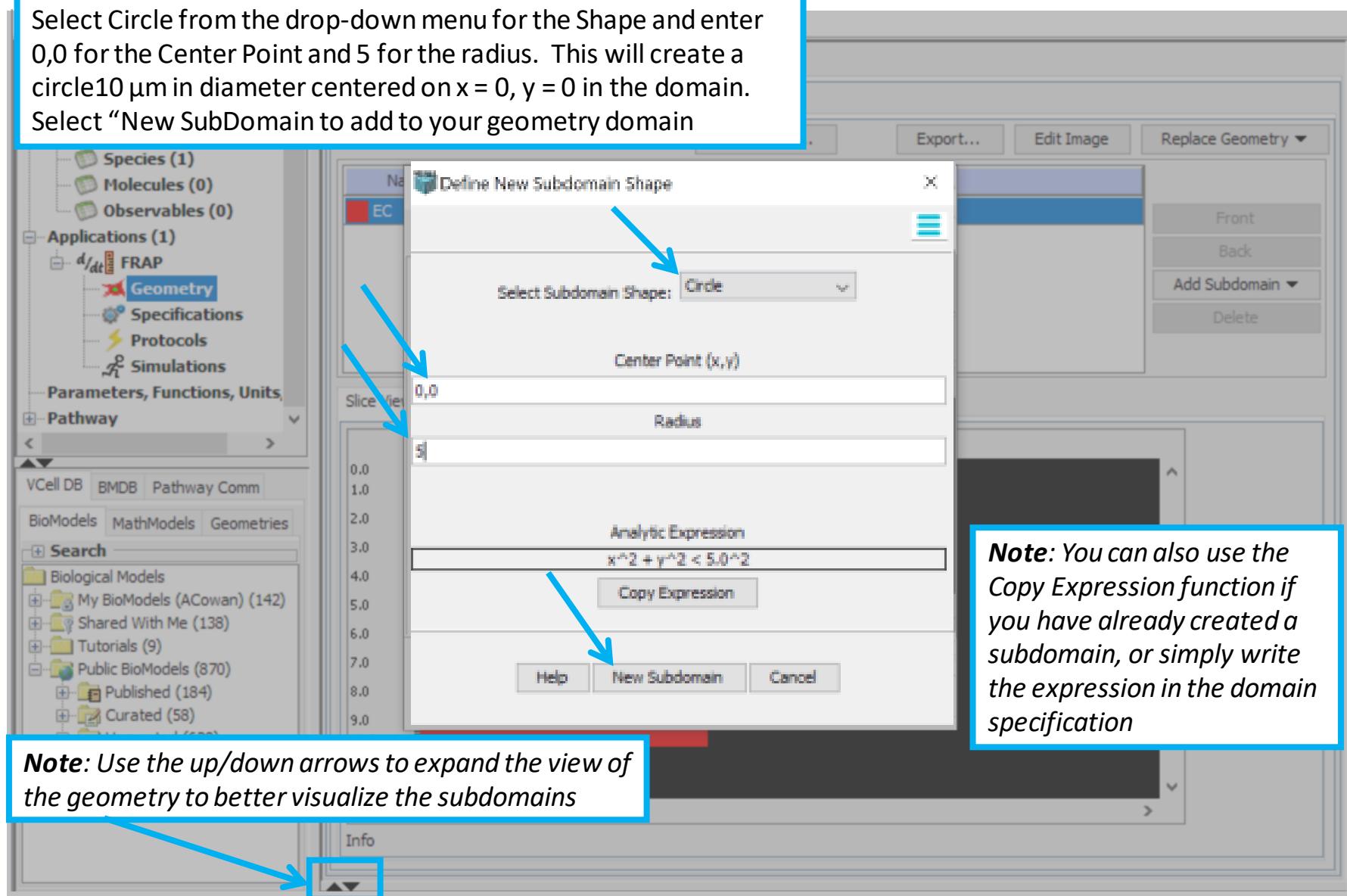
The screenshot shows the VCell software interface. On the left is a navigation tree with sections like Physiology, Applications (1), and Pathway. The main area is the Geometry panel, which includes tabs for Structure Mapping, Geometry Definition, and Kinematics. Under Geometry Definition, there's a table for domains. One row in the table has "Name" as "EC" and "Value" as "1.0". A blue callout box with the text "Double click in the domain name to change the name to “EC” and then use Enter to finalize" is positioned over this row. A blue arrow points from the text in the callout box to the "EC" entry in the table. The bottom right of the Geometry panel contains icons for Front, Back, Add Subdomain, and Delete. The bottom right corner of the window has icons for Info, Object Properties, Annotations, and Problems (0 Errors, 4 Warnings). The bottom status bar says "Select only one object (e.g. species, reaction, simulation) to view/edit properties."

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

- File Account Window Tools Help**: Standard application menu.
- Project Tree (left):**
  - Physiology**:
    - Reaction Diagram
    - Reactions (0)
    - Structures (3)
    - Species (1)
    - Molecules (0)
    - Observables (0)
  - Applications (1)**:
    - d/dt FRAP
    - Geometry** (selected)
    - Specifications
    - Protocols
    - Simulations
  - Parameters, Functions, Units**
  - Pathway**- Toolbar (top center):** Geometry, Specifications, Protocols, Simulations.
- Domain Definition Panel:** Shows a 2D domain of size (10.0, 10.0) centered at (0.0, 0.0). It includes buttons for Edit Domain..., Export..., Edit Image, and Replace Geometry.
- Table View (Domain Data):** A table with columns Name and Value. One row is shown: EC with value 1.0.
- Context Menu (highlighted by a blue arrow):** A dropdown menu with options: Add Subdomain, Analytic... (selected), and Constructed Solid Geometry.
- View Options (bottom left):** Slice View, Surface View, Geometric Region Details.
- Figure View (bottom center):** A 2D plot showing a red rectangular region from x=0 to x=10 and y=2.0 to y=3.0, adjacent to a dark gray region.
- Search Panel (bottom left):** Includes BioModels, MathModels, Geometries, and a search bar.
- Object Properties Panel (bottom right):** Displays a message: "Select only one object (e.g. species, reaction, simulation) to view/edit properties."

A blue callout box points to the "Analytic..." option in the context menu, with the text: "Select ‘Add Subdomain’ > ‘Analytic’".

Select Circle from the drop-down menu for the Shape and enter 0,0 for the Center Point and 5 for the radius. This will create a circle 10 µm in diameter centered on x = 0, y = 0 in the domain. Select "New SubDomain to add to your geometry domain



File Account Window Tools Help

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition Kinematics

Domain: 2D, size=(10.0,10.0), origin=(0.0,0.0) Edit Domain... Export... Edit Image Replace Geometry ▾

Name	Value
Cyt	$2.0 \leq (x^2 + y^2) \leq 4.0$
EC	1.0

Front Back Add Subdomain ▾ Delete

Double click the Name for the new domain and rename as “Cyt”.  
Use Enter to finalize the new name.

VCell DB BMDB Pathway Comm

BioModels MathModels Geometries

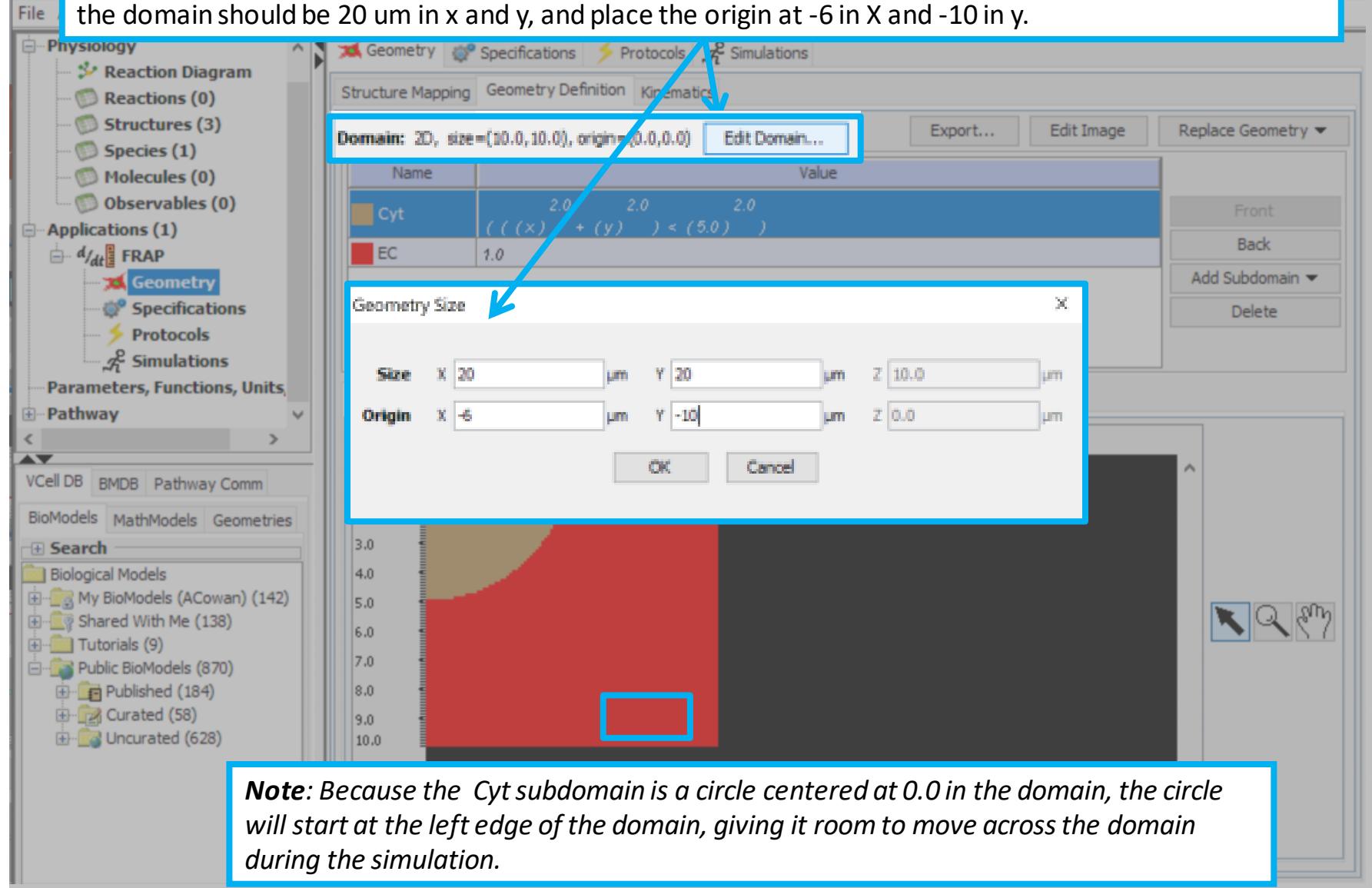
+ Search

Biological Models

- My BioModels (ACowan) (142)
- Shared With Me (138)
- Tutorials (9)
- Public BioModels (870)
  - Published (184)
  - Curated (58)
  - Uncurated (628)

You will notice that the new Subdomain (shown in brown) is not centered and takes up most of the entire computational domain (defined by default as a 10μm square). You will next use the Edit Domain function to adjust the size of the computational domain.

Select “Edit Domain” to adjust the overall size of the computational domain. For this tutorial, the extent of the domain should be 20 um in x and y, and place the origin at -6 in X and -10 in y.



**Note:** Because the Cyt subdomain is a circle centered at 0.0 in the domain, the circle will start at the left edge of the domain, giving it room to move across the domain during the simulation.

The geometry now defines a circular “Cyt” domain at the left boundary of a square “EC” domain. Next we will define the motion of the subdomain within the geometry.

The screenshot shows the VCell software interface. The top menu bar includes File, Account, Window, Tools, and Help. A navigation sidebar on the left lists Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables), Applications (FRAP), and a selected Geometry entry. The main workspace is divided into several panels: a Geometry panel with tabs for Structure Mapping, Geometry Definition (selected), and Kinematics; a 2D plot area showing a red square domain with a yellow circular subdomain (labeled "Cyt") centered on the left boundary; and a Pathway panel on the left containing tabs for VCell DB, BMDB, Pathway Comm, and links to BioModels, MathModels, and Geometries. A search bar and a tree view of biological models are also present in the Pathway panel.

Geometry Definition tab is selected.

Domain: 2D, size=(20.0,20.0), origin=(-6.0,-10.0)

Name	Value
Cyt	$( ( (x) + (y) ) < (5.0) )$
EC	1.0

Front, Back, Add Subdomain, Delete buttons are visible on the right.

2D Plot Area:

- Y-axis: -10.0 to 10.0
- X-axis: -6 to 14
- A red square domain is centered at (-6, -10).
- A yellow circle (labeled "Cyt") is centered on the left boundary of the red square at approximately (-6, -8.5).

Select the “Kinematics” Tab in the Geometry workspace

File Account Window Tools Help

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition Kinematics

Spatial Objects

Name	Description	Quantities
vobj_EC0	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1_EC0	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size

New Delete Selected

Spatial Process

Search New Delete Selected

Name	Description	Spatial Objects (and Quantities)

Object Properties Annotations Problems (0 Errors, 6 Warnings)

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

The screenshot shows the VCell software interface with the following components:

- Left Sidebar:** Contains sections for Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables), Applications (FRAP, Geometry, Specifications, Protocols, Simulations), Parameters, Functions, Units, Pathway, VCell DB, BioModels, MathModels, Geometries, and a Search section.
- Main Window (Top):** Titled "Geometry". It has tabs for Structure Mapping, Geometry Definition, and Kinematics. Below is a "Spatial Objects" table:

Name	Description	Quantities
vobj_EC0	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1 EC0	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size

- Main Window (Bottom):** Titled "Spatial Process". It has a table and a "New" dropdown menu:
  - New ▾
  - new Point Location
  - new Point Kinematics
  - new Surface Kinematics** (highlighted with a blue arrow)
  - new Volume Kinematics

A callout box with a blue border and a blue arrow points from the text "In the Spatial Process window, select ‘New’>‘new Surface Kinematics.’" to the "new Surface Kinematics" option in the dropdown menu.

In the bottom right of the main window, there is a message: "Select only one object (e.g. species, reaction, simulation) to view/edit properties."

File Account Window Tools Help

Physiology

- Reaction Diagram
- Reactions (0)
- Structures (3)
- Species (1)
- Molecules (0)
- Observables (0)

Applications (1)

- $d/dt$  FRAP
- Geometry
- Specifications

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition Kinematics

Spatial Objects

Name	Description	Quantities
vobj_EC0	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1_EC0	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size

Click on the Spatial Process to select that process

Parameters, Functions, Units, Pathway

VCell DB BMDB Pathway Comm

BioModels MathModels Geometries

Search

Biological Models

- Curated (58)
- Uncurated (628)

Spatial Process

Name	Description	Spatial Objects (and Quantities)
sproc_0	Membrane Kinematics	sobj_Cyt1_EC0 (vel)

Write in an expression to define the velocity in x and y. For this example, x is a constant velocity of 4  $\mu\text{m}/\text{s}$ . Velocity in y is described as a sine function that varies with time ( $5*\sin(10*t)$ )  $\mu\text{m}/\text{s}$ , so the object will move up and down as well as to the right during the simulation.

Description	Parameter	Expression	Units
surface velocity (x coord)	velocityX	4.0	$\mu\text{m}\cdot\text{s}^{-1}$
surface velocity (y coord)	velocityY	$5.0*\sin(10*t)$	$\mu\text{m}\cdot\text{s}^{-1}$

In the Spatial Process window, select “New”>“new Volume Kinematics.”

The screenshot shows the VCell software interface. On the left is a navigation tree with sections like Physiology, Applications (1), Parameters, Functions, Units, and Pathway. Below the tree are links for VCell DB, BMDB, Pathway Comm, BioModels, MathModels, Geometries, and a Search bar. The main workspace has tabs for Geometry, Specifications, Protocols, and Simulations. The Geometry tab is active, showing the Spatial Objects window with a table of objects like vobj\_E0 and vobj\_Cut1. The Spatial Process window is also open, showing a table with a single row for sproc\_0. A context menu is open over the Spatial Objects table, with the 'new Volume Kinematics' option highlighted. The bottom section shows the Object Properties, Annotations, and Problems tabs, along with a table of parameters for surface velocity.

Name	Description	Spatial Obj
sproc_0	Membrane Kinematics	sobj_Cut1_E0 (v)

Description	Parameter	Expression	Units
surface velocity (x coord)	velocityX	4.0	$\mu\text{m.s}^{-1}$
surface velocity (y coord)	velocityY	5.0 * sin(10 * t)	$\mu\text{m.s}^{-1}$

The software by default will create volume spatial processes in the order of volumes shown in the top spatial volume table. Continue to create new processes until you create a process for the volume object you want; in this case, the vobj\_Cyt1 (cytosol). Select the process you do not want, and “Delete Selected”

Name	Description	Spatial Obj
sproc_0	Membrane Kinematics	sobj_Cyt1_ECO
vproc_0	Volume Kinematics	vobj_ECO (vel)
vproc_1	Volume Kinematics	vobj_Cyt1 (vel)

Description	Parameter	Expression	Units
internal velocity (x coord)	velocityX	0.0	$\mu\text{m} \cdot \text{s}^{-1}$
internal velocity (y coord)	velocityY	0.0	$\mu\text{m} \cdot \text{s}^{-1}$

When a new Spatial Process for a volume object is created, an error is created associated with the Spatial Object because it has not been enabled to have an Interior Velocity. You must go back and select that Spatial Object.

The screenshot shows the VCell software interface with several windows open:

- Spatial Objects Tab:** Shows a list of spatial objects:

Name	Description	Quantities
vobj_EC0	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1_EC0	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size
- Spatial Process Tab:** Shows a list of spatial processes:

Name	Description	Spatial Objects (and Quantities)
sproc_0	Membrane Kinematics	sobj_Cyt1_EC0 (vel)
vproc_1	Volume Kinematics	vobj_Cyt1 (vel)
- Object Properties Window:** Shows the properties for a selected spatial object (vobj\_Cyt1). The "Interior Velocity" checkbox is checked, highlighted with a blue border.

Spatial Quantity Name	Description	Enabled	Units
vobj_Cyt1_centroidX	Volume Centroid (x component)	<input type="checkbox"/>	μm
vobj_Cyt1_centroidY	Volume Centroid (y component)	<input type="checkbox"/>	μm
vobj_Cyt1_velX	Interior Velocity (x component)	<input type="checkbox"/>	μm <sup>3</sup>
vobj_Cyt1_velY	Interior Velocity (y component)	<input type="checkbox"/>	μm <sup>3</sup>
vobj_Cyt1_size	Volume Region Size	<input checked="" type="checkbox"/>	μm <sup>3</sup>

File Account Window Tools Help

Tutorial\_FRAP\_moving2

Geometry Specifications Protocols Simulations

Structure Mapping Geometry Definition Kinematics

Physiology

- Reaction Diagram
- Reactions (0)
- Structures (3)
- Species (1)
- Molecules (0)
- Observables (0)

Applications (1)

- d/dt FRAP
- Geometry
- Specifications

Spatial Objects

Name	Description	Quantities
vobj_ECO	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1_ECO	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size

Click on the Volume Process to select that process.

Search New Delete Selected

Name	Description	Spatial Objects (and Quantities)
sproc_0	Membrane Kinematics	sobj_Cyt1_ECO (vel)
vproc_1	Volume Kinematics	vobj_Cyt1 (vel)

VCell DB BMDB Pathway Comm

MathModels Geometries BioModels

Search

In this example the cytosol will move with the membrane, so the same functions are used to describe the x and y velocities

Description	Parameter	Expression	Units
internal velocity (x coord)	velocityX	4.0	$\mu\text{m}\cdot\text{s}^{-1}$
internal velocity (y coord)	velocityY	$5.0 \cdot \sin(10.0 \cdot t)$	$\mu\text{m}\cdot\text{s}^{-1}$

Access[Arundeep2]

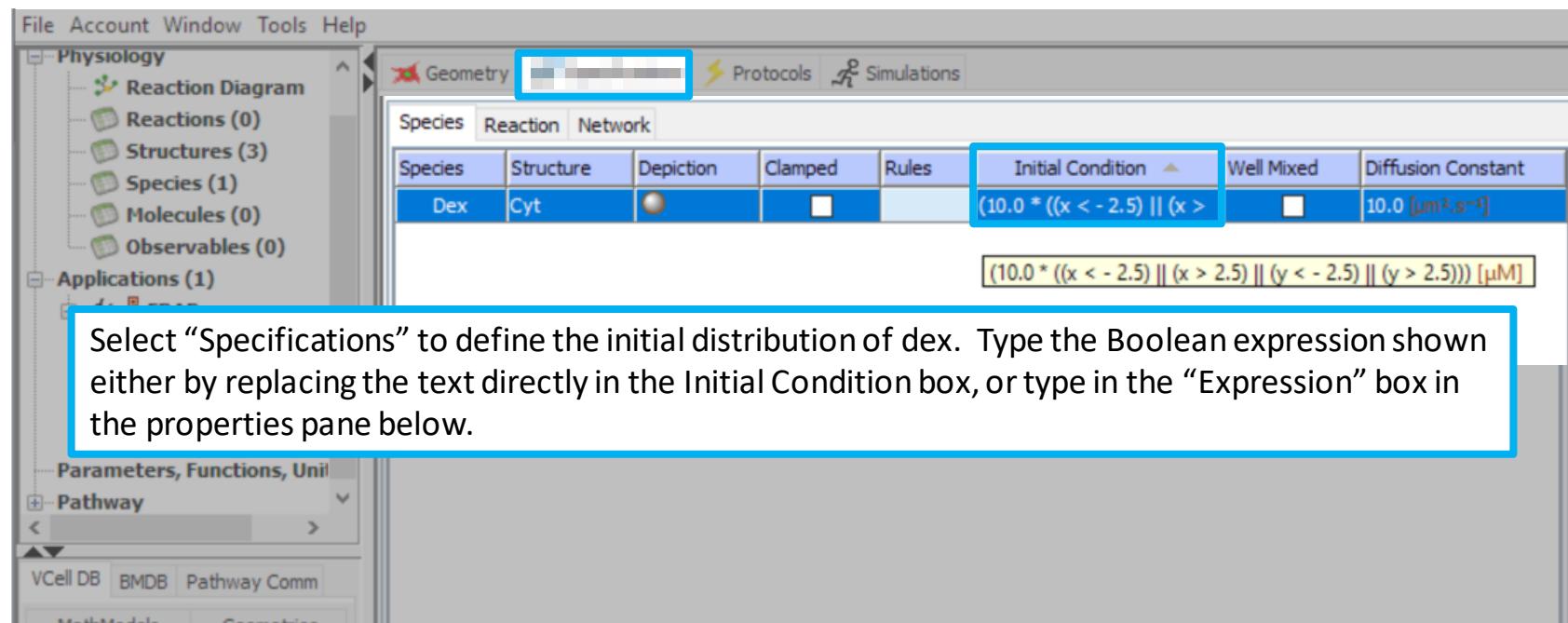
- Tutorial\_FRAPbinding
- Tutorial\_Membrane Fra
- Tutorial\_MultiApp
- Tutorial\_MultiApp\_for h
- Tutorial\_MultiApp\_sims
- Tutorial\_Pathway Comm
- Tutorial\_PH-GFP
- Utrrophin\_01

On the Geometry tab > Structure Mapping tab, use the line tool to link the physiology to the geometry. You must select the line tool each time and drag your cursor from a structure to its corresponding subdomain.

The screenshot shows the VCell software interface with a blue border around the central workspace. On the left, there is a navigation tree under 'Physiology' and 'Applications'. In the center, the 'Structure Mapping' tab is active, displaying a diagram of a cell with compartments: EC (Endoplasmic Reticulum), Cyt (Cytosol), and PM (Plasma Membrane). To the right of the diagram is a legend for 'Geometry (subdomains)' with three entries: Cyt (brown square), EC (red square), and Cyt\_EC\_membrane (a red square overlapping a brown circle). A dashed blue arrow points from the 'EC' entry in the mapping table below to the 'EC' compartment in the diagram. Below the diagram is a note: 'Membrane boundary conditions are chosen alphabetically among the adjacent subdomains.' At the bottom, there is a table mapping structures to subdomains:

Structure	Subdomain	Size Ratio	X-	X+	Y-	Y+
EC	EC	1 [ 1 ]	Flux	Flux	Flux	Flux
Cyt	Cyt	1 [ 1 ]	Flux	Flux	Flux	Flux
PM	Cyt_EC_membrane	1 [ 1 ]	from Cyt	from Cyt	from Cyt	from Cyt

At the bottom of the workspace, there are tabs for 'Object Properties', 'Annotations', and 'Problems (0 Errors, 0 Warnings)'. A message at the bottom of the workspace says: 'Select only one object (e.g. species, reaction, simulation) to view/edit properties.'



Select “Specifications” to define the initial distribution of dex. Type the Boolean expression shown either by replacing the text directly in the Initial Condition box, or type in the “Expression” box in the properties pane below.

**Note:** A Boolean expression evaluates as 1.0 when true and 0 when false. The expression defines the concentration of dex as 10  $\mu\text{M}$  when  $x$  is less than -2.5 OR greater than 2.5, OR when  $y$  is less than -2.5 OR when  $y$  is greater than 2.5; otherwise, the value is 0.

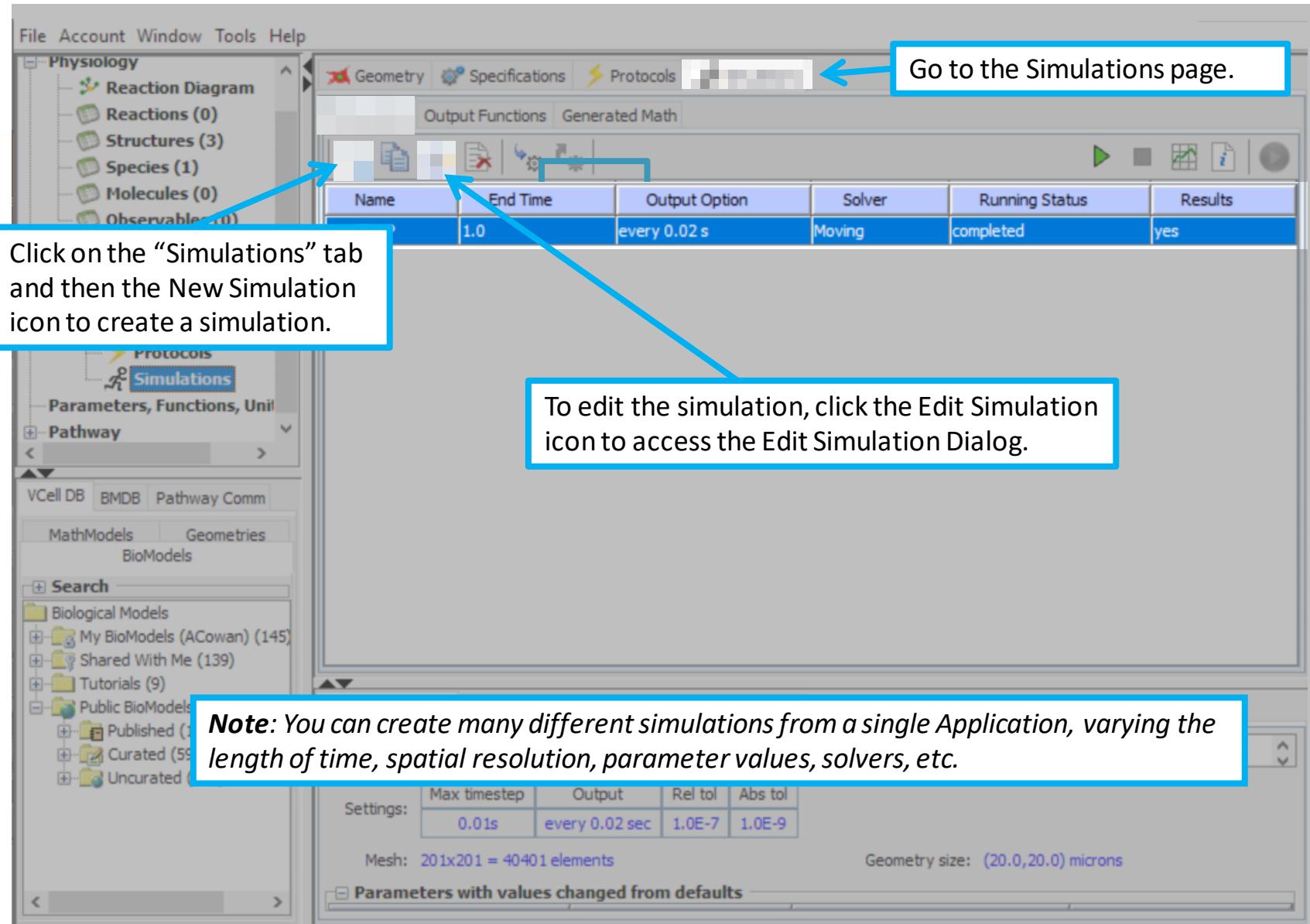
Description	Parameter	Expression	Units
initial concentration for Dex	initConc	$10.0 \cdot ( (x < -2.5) \parallel (x > 2.5) \parallel (y < -2.5) \parallel (y > 2.5) )$	$\mu\text{M}$
diffusion constant for Dex	diff	10.0	$\mu\text{m}^2\text{s}^{-1}$
Boundary Condition X- for Dex	BC_Xm	<zero flux>	$\mu\text{M}\mu\text{m.s}^{-1}$
Boundary Condition X+ for Dex	BC_Xp	<zero flux>	$\mu\text{M}\mu\text{m.s}^{-1}$

The screenshot shows the VCell software interface. On the left, the **Physiology** panel is open, displaying categories like Reaction Diagram, Reactions (0), Structures (3), etc. The **Species** tab is selected in the main window. A table lists species: Dex (Cyt). The **Diffusion Constant** column shows the value **10.0 [μm² s⁻¹]**. A blue arrow points from this value to a callout box containing the text: **Use the default value of 10.0 μm²/s for the Diffusion Constant for Dex**.

Species	Structure	Depiction	Clamped	Rules	Initial Condition	Well Mixed	Diffusion Constant
Dex	Cyt				(10.0 * ((x < -2.5)    (x > 2.5)))		10.0 [μm² s⁻¹]

Below the table, the **Object Properties** panel shows the following parameters:

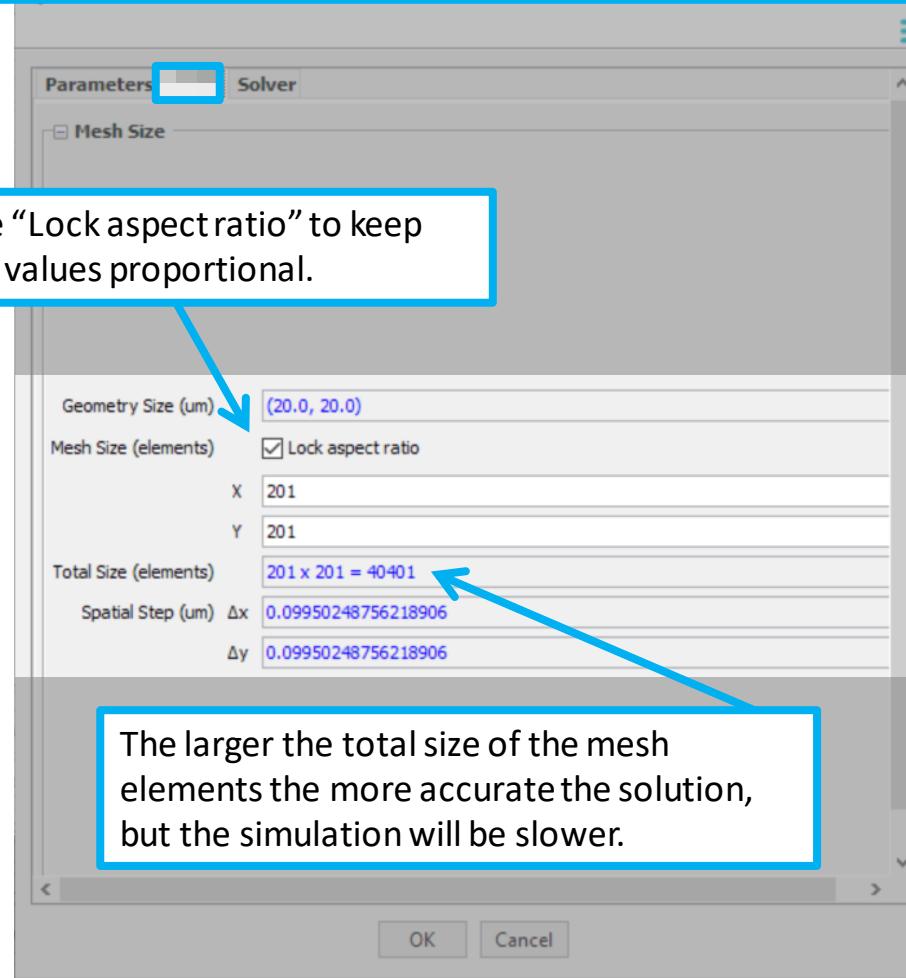
Description	Parameter	Expression	Units
initial concentration for Dex	initConc	$10.0 \cdot ((x < -2.5)    (x > 2.5))$	μM
diffusion constant for Dex	diff	10.0	μm².s⁻¹
Boundary Condition X- for Dex	BC_Xm	<zero flux>	μM.μm.s⁻¹
Boundary Condition X+ for Dex	BC_Xp	<zero flux>	μM.μm.s⁻¹



The Edit Simulation Dialog has 3 tabs. The Parameters Tab is used to adjust parameters for each simulation, or to scan multiple parameters. Use the Default settings for this tutorial

Parameter Name	Default	New Value/Expression	Scan
AreaPerUnitArea_PM	1.0		<input type="checkbox"/>
Dex_diffusionRate	10.0		<input type="checkbox"/>
KMOLE	0.001660538783162726		<input type="checkbox"/>
K_millivolts_per_volt	1000.0		<input type="checkbox"/>
Voltage_PM	0.0		<input type="checkbox"/>
VolumePerUnitVolume_Cyt	1.0		<input type="checkbox"/>
VolumePerUnitVolume_EC	1.0		<input type="checkbox"/>
_F_	96485.3321		<input type="checkbox"/>
_F_nmol_	9.64853321E-5		<input type="checkbox"/>
_K_GHK_	1.0E-9		<input type="checkbox"/>
_N_pmol_	6.02214179E11		<input type="checkbox"/>
_PI_	3.141592653589793		<input type="checkbox"/>
_R_	8314.46261815		<input type="checkbox"/>
_T_	300.0		<input type="checkbox"/>
sproc_0.velocityX	4.0		<input type="checkbox"/>
vproc_1.velocityX	4.0		<input type="checkbox"/>

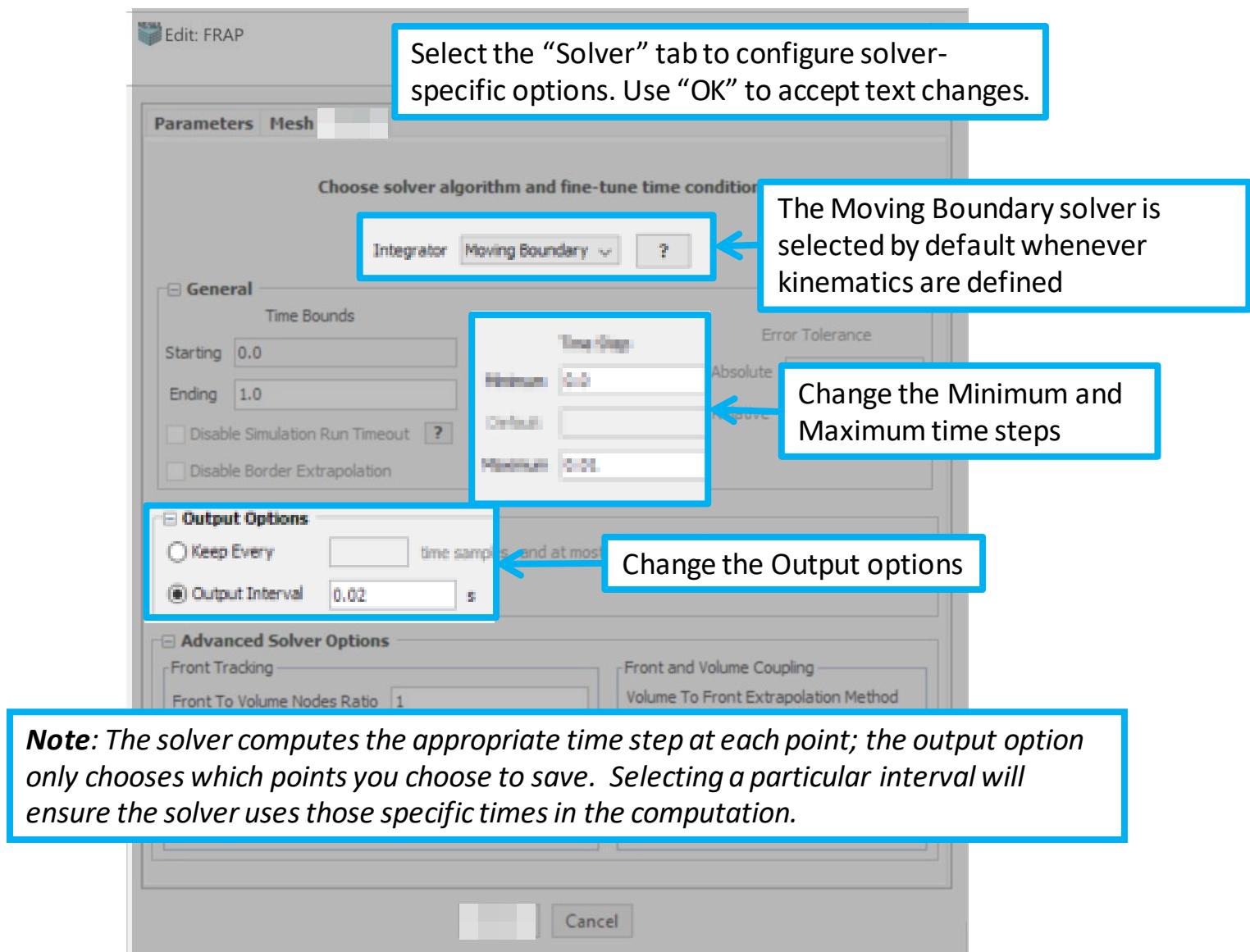
Select the “Mesh” tab to edit the mesh resolution for the simulation in the X and Y planes. Select “OK” to accept any changes.

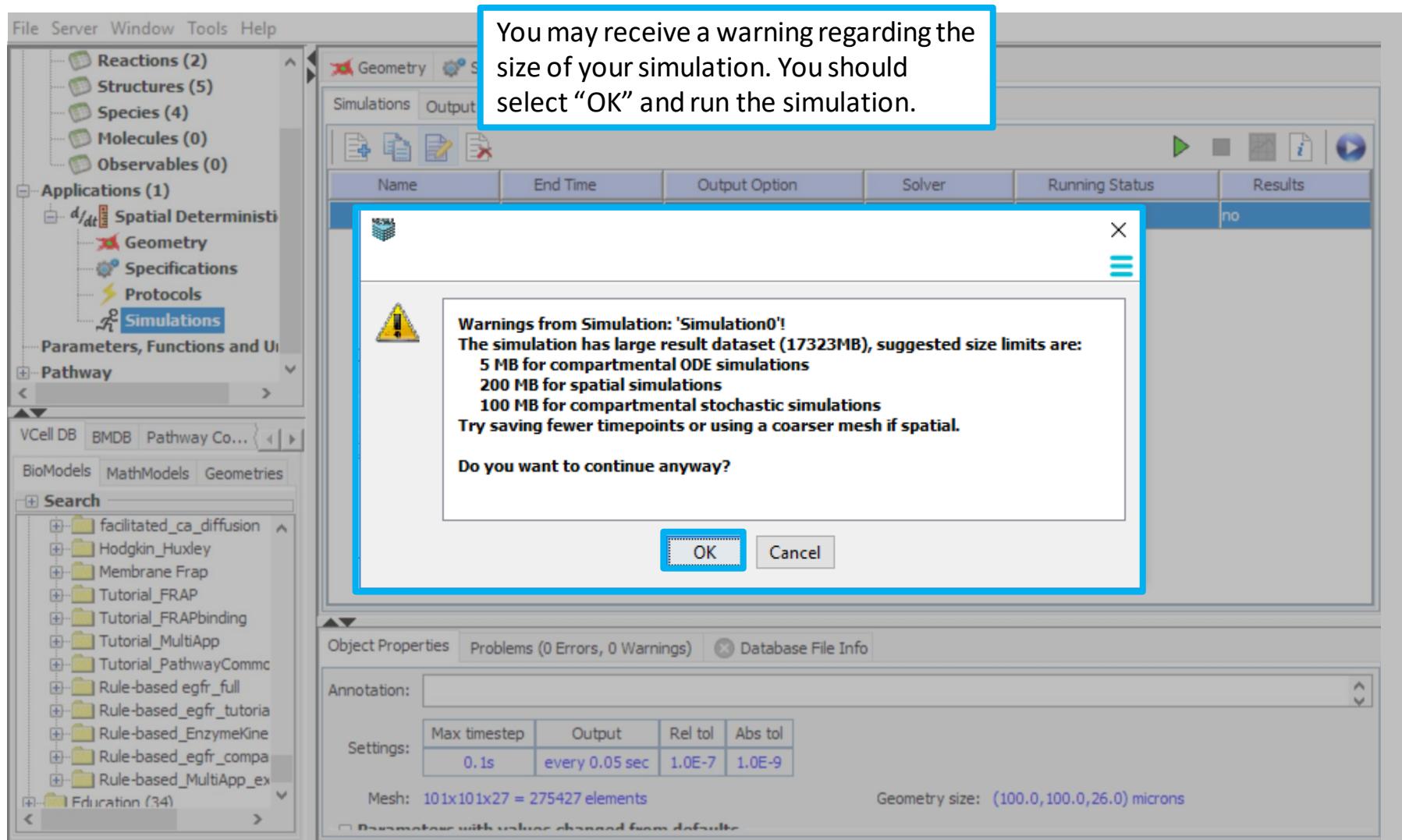


Use “Lock aspect ratio” to keep the values proportional.

The larger the total size of the mesh elements the more accurate the solution, but the simulation will be slower.

**Note:** Use the smaller mesh size values shown here for the tutorial, or the simulation will take a long time to run.





Select the simulation you want to run, then click the green “run” arrow to save the model to the database and run the simulation on the remote servers at VCell. Your simulation results will be saved in the database.

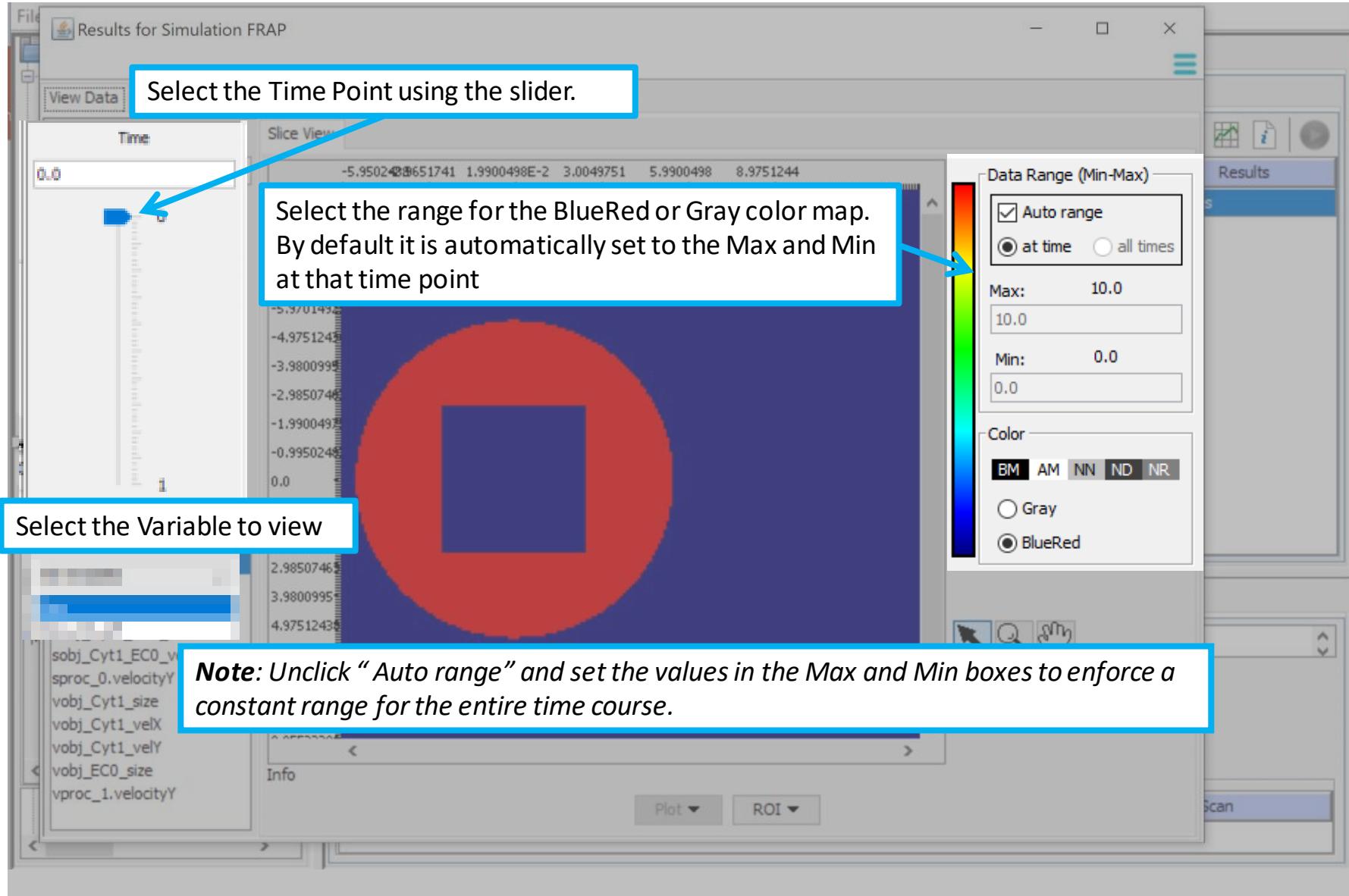
The screenshot shows the VCell software interface. On the left, there's a navigation tree with sections like Physiology, Applications (FRAP), and Pathway. Below the tree are tabs for VCell DB, BMDB, and Pathway, with MathModels and Geometries selected. A search panel on the left lists categories such as Biological Models, My BioModels (ACowan) (145), Shared With Me (139), Tutorials (9), Public BioModels (870), Published (184), Curated (59), and Uncurated (627). The main workspace has tabs for Geometry, Specifications, Protocols, and Simulations. The Simulations tab is active, showing a table with one row for 'FRAP'. The table columns are Name, End Time, Output Option, Solver, Running Status, and a checkbox labeled 'Run and Save Simulation'. A green play button icon is located to the right of the 'Run and Save Simulation' checkbox. At the bottom of the workspace, there's an 'Object Properties' panel showing an annotation field with 'cloned from 'FRAP' owned by user mblinov' and a settings table with Max timestep (0.01s), Output (every 0.02 sec), Rel tol (1.0E-7), and Abs tol (1.0E-9). Below that, it says Mesh: 201x201 = 40401 elements and Geometry size: (20.0,20.0) microns. A section titled 'Parameters with values changed from defaults' is also visible.

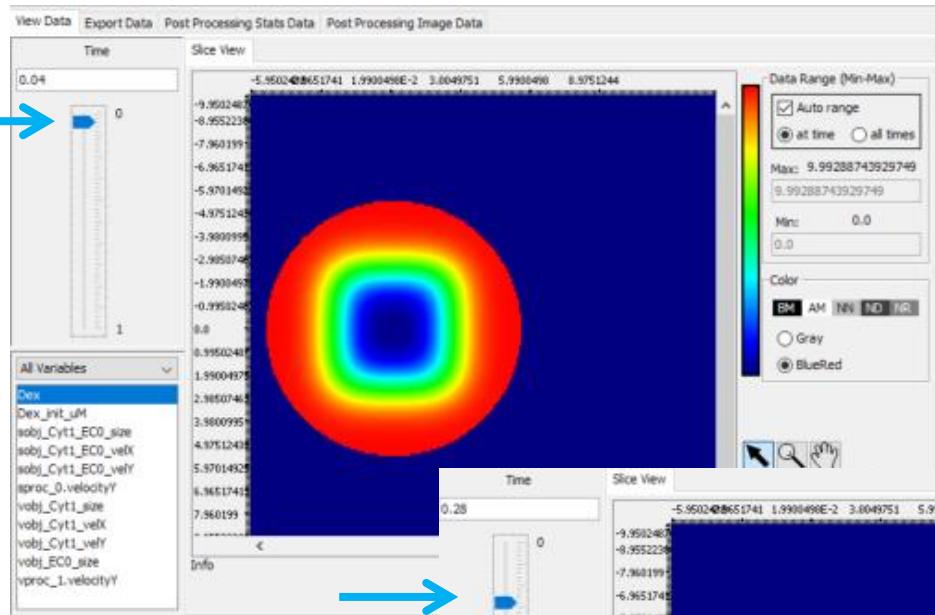
The screenshot shows the VCell software interface. On the left, there's a navigation tree under 'Physiology' and 'Applications'. The main area has tabs for 'Geometry', 'Specifications', 'Protocols', and 'Simulations'. The 'Simulations' tab is active, showing a table with one row for 'FRAP'. The table columns are 'Name', 'End Time', 'Output Option', 'Solver', 'Running Status', and 'Results'. The 'Results' column for 'FRAP' contains 'yes'. A blue arrow points from this 'yes' text to a 'View Results' button in the top right of the simulation table. Another blue box highlights the 'Results' column header. In the bottom right, there's a note: 'Note: You can view results any time the Results tab says "yes", even before the simulation is 100% complete.' Other visible sections include 'Parameters, Functions, Units' and 'Search'.

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

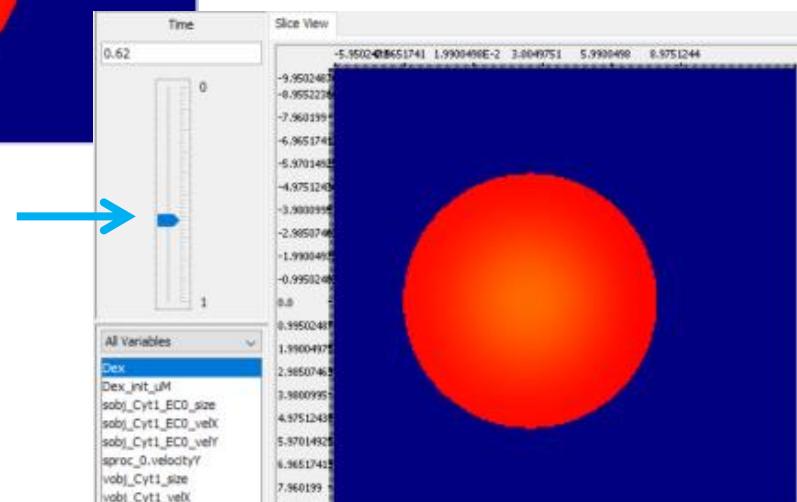
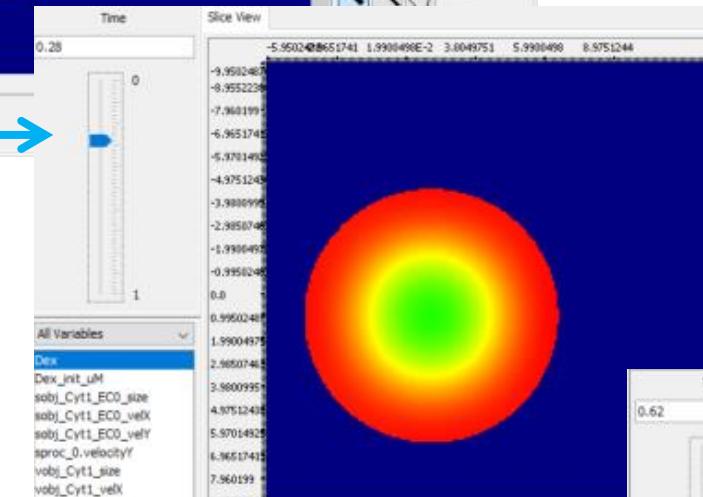
Use the “View Results” button to see the simulation results.

**Note:** You can view results any time the Results tab says “yes”, even before the simulation is 100% complete.





**Note:** The data Range (Min-Max) had Auto range selected for these images, so the color scale is different at each time point.



The screenshot shows the 'Post Processing' tab in the VCell software. At the top, there are tabs for 'View Data', 'Post Processing Stats Data', and 'Post Processing Image Data'. Below these, a section titled 'Specify data to be exported' contains a dropdown menu with various file formats. The 'HDF5 files (\*.hdf5)' option is selected and highlighted with a blue arrow. Other options include 'Comma delimited ASCII files (\*.csv)', 'QuickTime movie files (\*.mov)', 'GIF89a image files (\*.gif)', 'Animated GIF files (\*.gif)', 'JPEG image files (\*.jpg)', 'Nearly raw raster data (\*.nrrd)', and 'UCD (\*.ucd)'. To the right of the dropdown is a 'Start Export ...' button. Below the dropdown, there is a section titled 'Define Export Time interval:' with two input fields: '0.0' and '0.16'. At the bottom, a table titled 'Export jobs' lists three completed export jobs:

Job ID	Format	Export Progress	Completed ?	File Location	Simulation
6218096477	MOV	Complete	<input checked="" type="checkbox"/>	<a href="http://vcell.org/export/6218096477.MOV">http://vcell.org/export/6218096477.MOV</a>	SimID_217607372_0
3276680485		Export failed!	<input type="checkbox"/>		SimID_217607372_0
6441339100	NRRD	Complete	<input checked="" type="checkbox"/>	<a href="http://vcell.org/export/6441339100.zip">http://vcell.org/export/6441339100.zip</a>	SimID_217607372_0

To export as HDF5 files:

Select the Species to export (there is only one in this model).  
Select the Time Interval to Export

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

-Specify data to be exported

Export Format: HDF5 files (\*.hdf5)

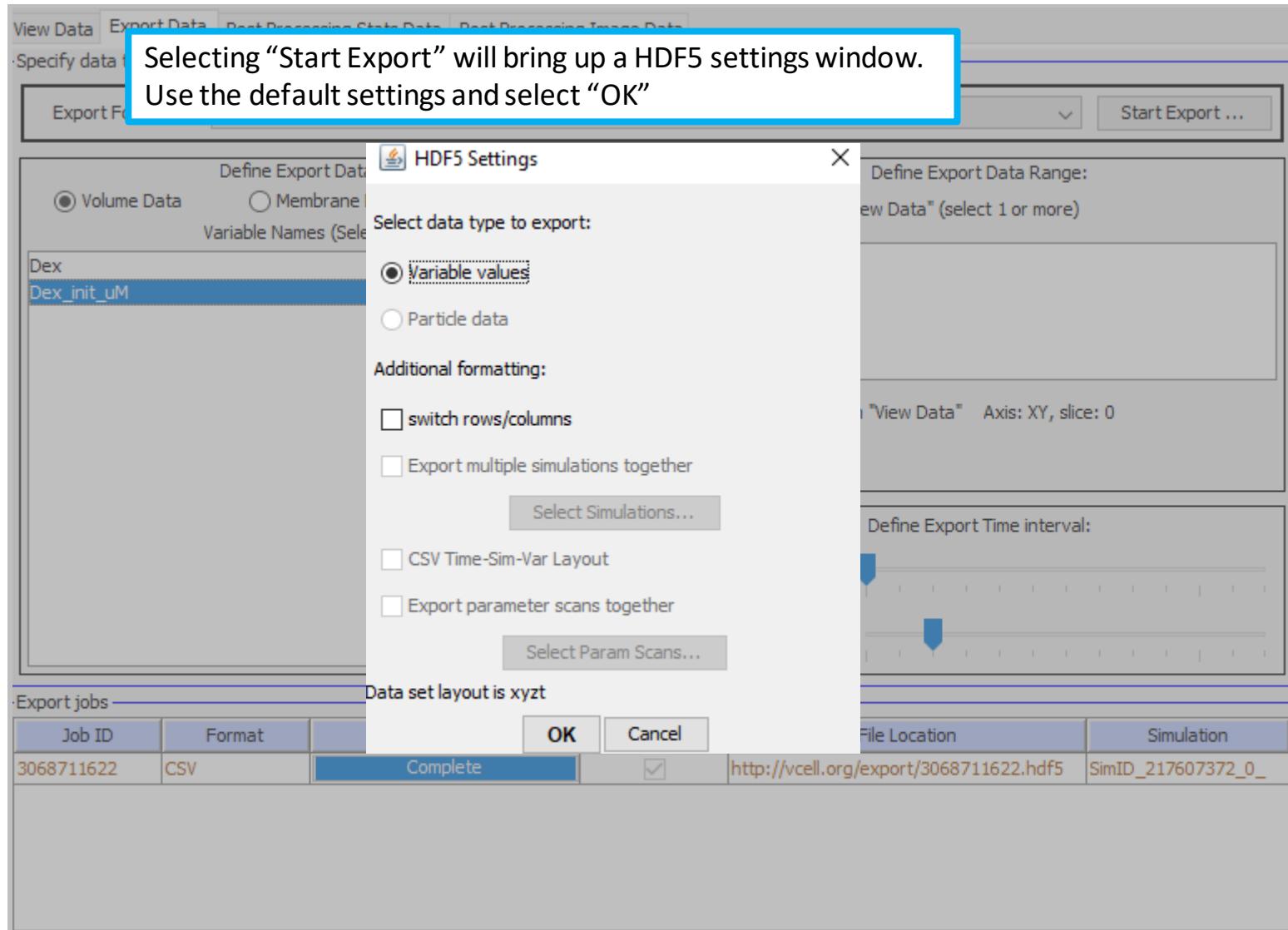
Define Export Data Variables:  
 Volume Data  Membrane Data  Vol/Membr Data  
Variable Names (Select 1 or more)  
Dex  
Dex\_init\_uM

Define Export Data Range:  
 User ROI from "View Data" (select 1 or more)  
 Current Slice from "View Data" Axis: XY, slice: 0  
 Full

Define Export Time interval:  
0.0 0.15

Export jobs

Job ID	Format	Export Progress	Completed ?	File Location	Simulation
3068711622	CSV	Complete	<input checked="" type="checkbox"/>	<a href="http://vcell.org/export/3068711622.hdf5">http://vcell.org/export/3068711622.hdf5</a>	SimID_217607372_0_



To export as HDF5 files:

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

Specify data to be exported

Export Format: Nearly raw raster data (\*.nrrd) Start Export ...

Define Export Data Variables:

Volume Data  Membrane Data  Vol/Membr Data

Variable Names (Select 1 or more)

Dex  
Dex\_rn\_U/M

Select the Species to export (there is only one in this model).  
Select the Time Interval to Export

Current Slice from View Data Axis: XY, slice: 0

Full

Define Export Time Interval:

0.0 0.15

Export jobs

Job ID	Format	Export Progress	Completed ?	File Location	Simulation
6218096477	MOV	Complete	<input checked="" type="checkbox"/>	<a href="http://vcell.org/export/6218096477.MOV">http://vcell.org/export/6218096477.MOV</a>	SimID_217607372_0_
3276680485		Export failed!	<input type="checkbox"/>		SimID_217607372_0_
6441339100	NRRD	Complete	<input checked="" type="checkbox"/>	<a href="http://vcell.org/export/6441339100.zip">http://vcell.org/export/6441339100.zip</a>	SimID_217607372_0_

The screenshot shows the software interface for the Moving Boundary Solver. At the top, there is a menu bar with tabs: View Data, Export Data, Post Processing Stats Data, and Post Processing Image Data. The Export Data tab is currently selected. Below the menu, there is a section titled "Specify data to be exported". A dropdown menu labeled "Export Format" is open, showing "Nearly raw raster data (\*.nrrd)" as the selected option. A blue arrow points from this dropdown to a callout box containing the following text:

Click "Start Export" and an additional dialog box appears with NRRD specific options. Use the selections shown here, there press "OK"

Below the export format dropdown, there is a "Raster Settings" dialog box. This dialog has two sections: "Select export format" and "Additional formatting". Under "Select export format", the "NRRD (\*.nrrd)" option is selected, while "Planes by Time" and "Planes by Variable" are unselected. Under "Additional formatting", the "Separate header files" checkbox is unselected. A blue arrow points from this dialog to another callout box containing the following text:

Export jobs are saved to the server; when the job is complete you are prompted to save a local file.

At the bottom left, there is a table titled "Export jobs" showing three entries:

Job ID	Format	Export Progress	Completed ?	Link
6218096477	MOV	Complete	<input checked="" type="checkbox"/>	<a href="http://">http://</a>
3276680485		Export failed!	<input type="checkbox"/>	
6441339100	NRRD	Complete	<input checked="" type="checkbox"/>	<a href="http://">http://</a>

A blue arrow points from the bottom right of the "Export jobs" table to a "Save exported dataset..." dialog box. This dialog shows a file selection interface with "Recent Items" and "This PC" sections. The "File name" field contains "SimID\_217607372\_0\_\_exported.zip" and the "Files of type" dropdown is set to "ZIP Files (\*.zp)". A blue arrow points from this dialog to a callout box containing the following text:

Save exported dataset...

Save in: Simulation Exports

Recent Items

Desktop

Documents

This PC

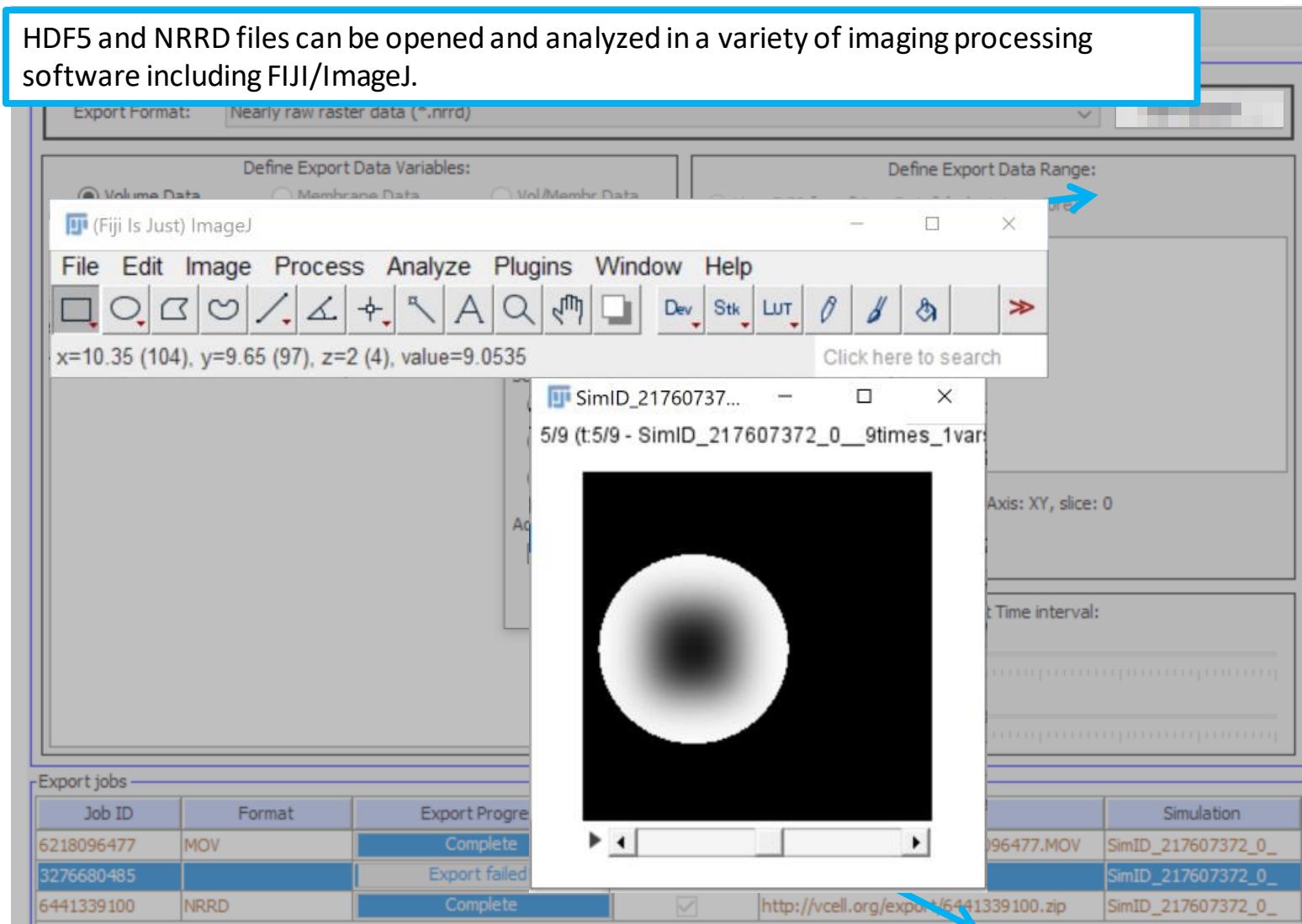
Network

File name: SimID\_217607372\_0\_\_exported.zip

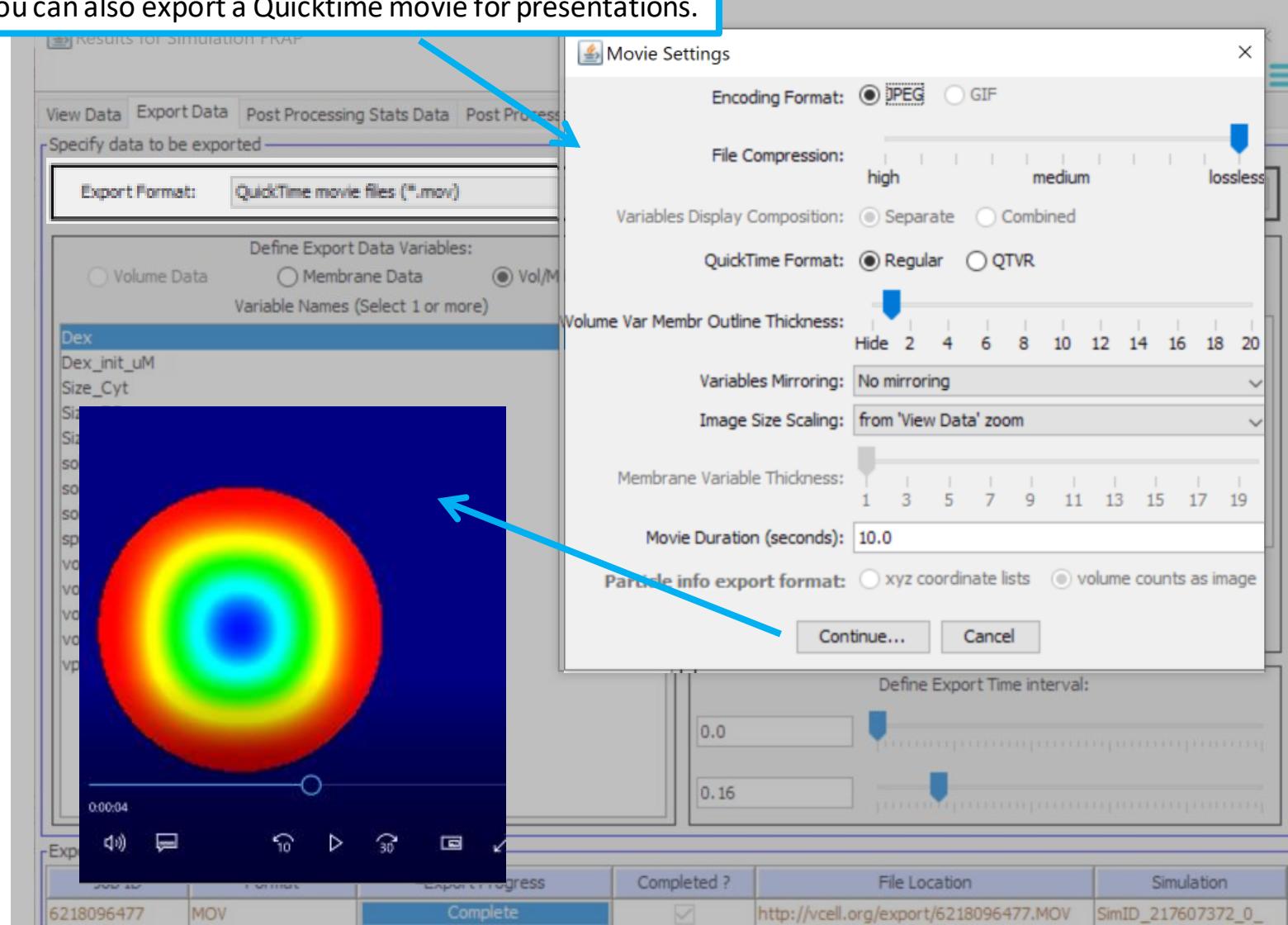
Files of type: ZIP Files (\*.zp)

Save Cancel

HDF5 and NRRD files can be opened and analyzed in a variety of imaging processing software including FIJI/ImageJ.



You can also export a Quicktime movie for presentations.



Let's create a second Application to change the parameters for both the kinematics and diffusion coefficient and see how that affects the spatial distribution of the fluorescent probe

The screenshot shows the VCell application interface. On the left, the navigation window displays a tree structure with 'Tutorial\_MovingBoundary' selected. Under 'Tutorial\_MovingBoundary', there are sections for 'Physiology' (including 'Reaction Diagram' and 'Reactions (0)'), 'Observables (0)', and 'Applications (1)'. The 'Applications (1)' section contains one item, 'FRAP'. A context menu is open over the 'FRAP' application, with the 'Copy' option highlighted. A blue arrow points from the text in the callout box to the 'Copy' option in the menu.

Right click on the FRAP application from the navigation window and select "Copy" to copy the original FRAP application.

File Account Window Tools Help

Tutorial\_MovingBoundary

Geometry Specifications Protocols

Simulations Output Functions Generated Math

Applications (1)

FRAP

Parameters Pathway

VCell DB BMDB

MathModels Geometries

BioModels

Search

- Hodgkin\_Huxley
- Membrane Frap
- Rule-based\_egfr\_
- Rule-based\_EGFR
- Rule-based\_egfr\_
- Rule-based\_Ran\_
- Tutorial\_FRAP
- Tutorial\_FRAPbind
- Tutorial\_MovingBc

Geometry Specifications Protocols

Simulations Output Functions Generated Math

FRAP

cloned from 'FRAP' owned by user ACowan

cloned from 'FRAP' owned by user mblinov

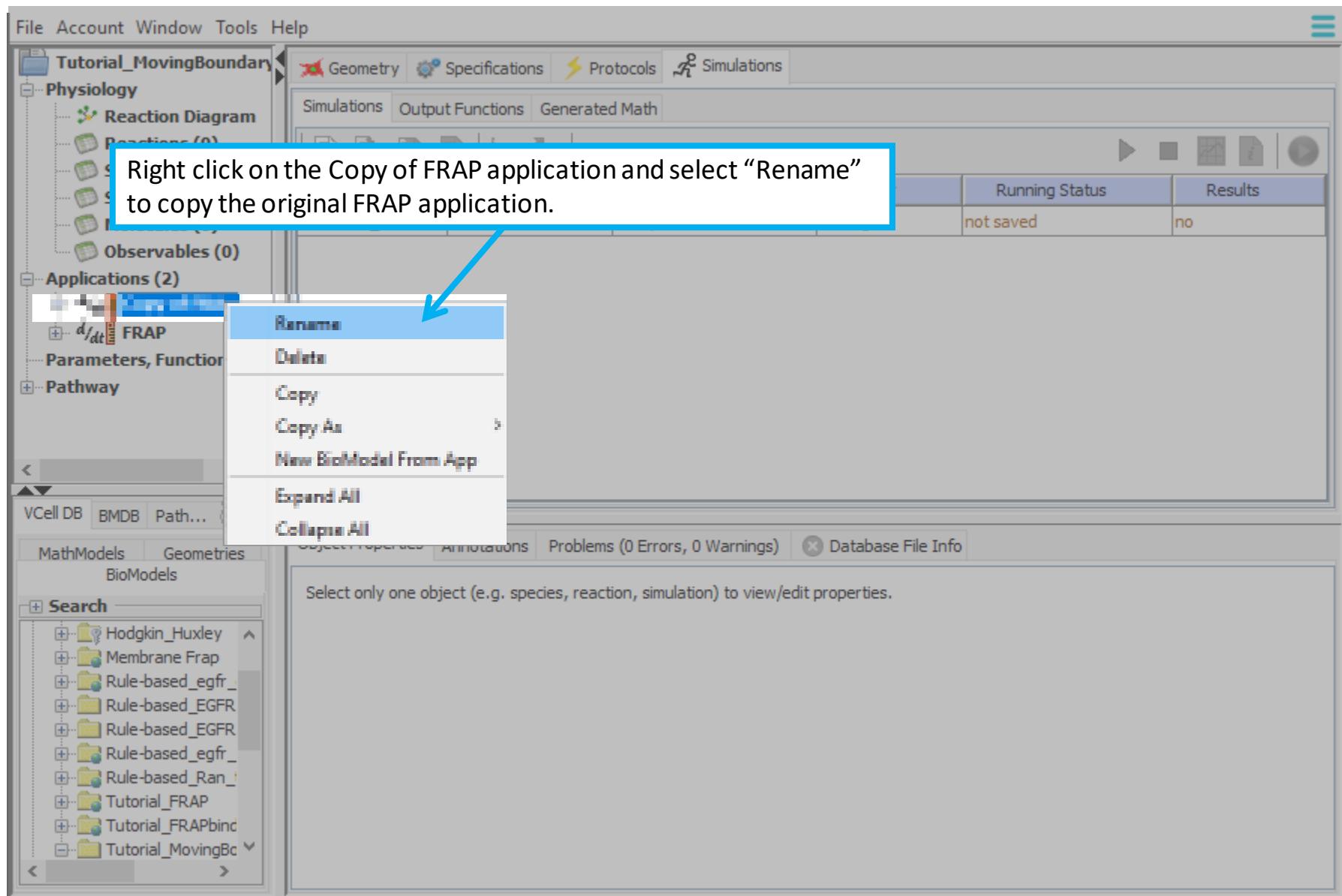
cloned from 'FRAP' owned by user ACowan

Deterministic

FRAP\_geometry1094988791 (2D)

math generated

FRAP



We can call the new Application “Modified FRAP”. You need to use the enter key to accept the new name.

The screenshot shows the VCell application interface. On the left, there's a tree view of models and applications. A blue arrow points from the text box above to the 'FRAP' entry in the 'Applications' list. The main workspace shows a simulation setup for 'FRAP\_1' with parameters: 1.0, every 0.02 s, Moving, and not saved. The bottom panel displays object properties and a search bar.

File Account Window Tools Help

Tutorial\_MovingBoundary

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Molecules (0) Observables (0)

Applications (2)

$d/dt$  FRAP

Parameters, Functions, Units Pathway

VCell DB BMDB Path... MathModels Geometries BioModels

Search

- Hodgkin\_Huxley
- Membrane Frap
- Rule-based\_egfr\_
- Rule-based\_EGFR
- Rule-based\_EGFR
- Rule-based\_egfr\_
- Rule-based\_Ran\_
- Tutorial\_FRAP
- Tutorial\_FRAPbind
- Tutorial\_MovingBc

FRAP\_1 1.0 every 0.02 s Moving not saved no

Solver Running Status Results

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

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

Return to the Geometry > Kinematics tab

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

- Top Menu:** File, Account, Window, Tools, Help.
- Left Sidebar:** Tutorial\_MovingBound, Physiology (Reaction Diagram, Reactions (0), Molecules (0), Observables (0)), Applications (2) (FRAP, Modified FRAP, Geometry, Specifications, Protocols, Simulations).
- Central Area:**
  - Specifications:** Structure Mapping, Geometry Definition (highlighted by a blue box).
    - Spatial Objects:** A table with columns Name, Description, and Quantities.

Name	Description	Quantities
vobj_ECO	Volume Object for EC[0]	centroid, vel, size
vobj_Cyt1	Volume Object for Cyt[1]	centroid, vel, size
sobj_Cyt1_ECO	Surface Object between Cyt[1] and EC[0]	normal, vel, distance, direction, size
    - Spatial Process:** A table with columns Name, Description, and Spatial Objects (and Quantities). (This section is mostly empty in the screenshot.)
  - Bottom Panel:** Object Properties (highlighted by a blue box).
    - Checkboxes: Surface Velocity (checked), Distance to Surface (Distance Map) (unchecked), Direction to Surface (unchecked), Surface Size (checked).
    - Table: Spatial Quantity Name, Description, Enabled, Units.

Spatial Quantity Name	Description	Enabled	Units
sobj_Cyt1_ECO_normalX	Surface Normal (x component)	<input checked="" type="checkbox"/>	1
sobj_Cyt1_ECO_normalY	Surface Normal (y component)	<input checked="" type="checkbox"/>	1
sobj_Cyt1_ECO_size	Surface Size	<input checked="" type="checkbox"/>	μm <sup>2</sup>

Select the Spatial Process for the surface object `sobj_Cyt1_EC0` so the surface velocity properties appear in the bottom window.

Change the expression for the surface velocity for x to  $( - 5.0 * \text{sobj\_Cyt1\_EC0\_normalX} * \sin((20.0 * t)) ) + 4.0$ . Change the expression for the surface velocity for y to  $( - 5.0 * \text{sobj\_Cyt1\_EC0\_normalY} * \sin((20.0 * t)) )$

The expression for the surface velocity will move the normal to the surface in both x and y, thus causing the membrane to contract and expand; overall x will have a constant velocity of 4  $\mu\text{m/s}$ .

The screenshot shows the VCell software interface. The top menu bar includes File, Account, Window, Tools, Help, Specifications, Protocols, and Simulations. On the left, a tree view shows a project named "Tutorial\_MovingBound" with branches for Physiology (Reaction Diagram, Reactions, Structures, Species, Molecules, Observables) and Applications (2). The main workspace has tabs for Structure Mapping, Geometry Definition, and Spatial Objects. The Spatial Objects table lists a single entry: vobj\_EC0, Volume Object for EC[0], with Quantities centroid, vel, size. Below this is the Spatial Process table, which lists two entries: sproc\_0 (Membrane Kinematics) associated with sobj\_Cyt1\_EC0 (vel), and vproc\_1 (Volume Kinematics) associated with vobj\_Cyt1 (vel). A blue arrow points from the "Name" column of the Spatial Process table to the "Name" column of the Spatial Objects table. Another blue arrow points from the "Expression" column of the Spatial Process table to the "velocityX" row in the table below. The bottom table shows two rows: "surface velocity (x coord)" with Parameter velocityX and Expression  $( - 5.0 * \text{sobj\_Cyt1\_EC0\_normalX} * \sin((20.0 * t)) ) + 4.0$ , and "surface velocity (y coord)" with Parameter velocityY and Expression  $- 5.0 * \text{sobj\_Cyt1\_EC0\_normalY} * \sin((20.0 * t))$ . The Units for both are  $\mu\text{m.s}^{-1}$ .

Description	Parameter	Expression	Units
surface velocity (x coord)	velocityX	$( - 5.0 * \text{sobj\_Cyt1\_EC0\_normalX} * \sin((20.0 * t)) ) + 4.0$	$\mu\text{m.s}^{-1}$
surface velocity (y coord)	velocityY	$- 5.0 * \text{sobj\_Cyt1\_EC0\_normalY} * \sin((20.0 * t))$	$\mu\text{m.s}^{-1}$

File Account Window Tools Help

Application

- d/dt FRAP
- Geometry
- Specifications
- Protocols
- Simulations
- d/dt Modified FRAP

Parameters, Functions, Unit: v

VCell DB BMDB Pathway Comm

MathModels Geometries BioModels

Search

- Membrane Frap
- Rule-based\_egfr\_comp
- Rule-based\_EGFR\_sing
- Rule-based\_EGFR\_spat
- Rule-based\_egfr\_tutor
- Rule-based\_Ran\_trans
- Tutorial\_FRAP
- Tutorial\_FRAPbinding
- Tutorial\_MovingBounda
- Private Tue Sep 06
- Tutorial\_MultiApp
- Tutorial\_PathwayComm

Go to the Specifications tab and change the Diffusion Constant to 1.0. Double click in the box to edit.

Species	Structure	Depiction	Clamped	Rules	Initial Condition	Well Mixed	Diffusion Constant
Dex	Cyt	●	□		(10.0 * ((x < - 2.5)    (x > 2.5))	□	1.0

For this demonstration, the diffusion constant is for a large, slowly diffusing species. The simulation results will show what happens to a slowly diffusing volume species when the membrane contracts rapidly.

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

Description	Parameter	Expression	Units
initial concentration for Dex	initConc	$10.0 \cdot ( (x < - 2.5)    (x > 2.5)    (y < - 2.5)    (y > 2.5) )$	μM
diffusion constant for Dex	diff	1.0	μm <sup>2</sup> .s <sup>-1</sup>
Boundary Condition X- for Dex	BC_Xm	<zero flux>	μM.μm.s <sup>-1</sup>

The screenshot shows the VCell software interface. On the left, there's a tree view of a project named "Physiology" containing "Reaction Diagram", "Reactions (0)", "Structures (3)", "Species (1)", "Molecules (0)", and "Observables (0)". Below this is an "Applications (2)" section with "d/dt FRAP" and "d/dt Modified FRAP". The main workspace has tabs for "Geometry", "Specifications", and "Protocols". The "Simulations" tab is active, showing a table with one row:

Name	End Time	Output Option	Solver	Running Status	Results
FRAP_1	1.0	every 0.02 s	Moving	never ran	no

A blue arrow points from the "FRAP\_1" row to the green arrow icon in the toolbar above the table. A tooltip box with a blue border contains the text: "Go to the Simulations tab. The simulation will have been copied along with the application, but not run. There is no need to edit the simulation parameters, and you can simply run by selecting the green arrow to run remotely on VCell servers."

Below the simulations table, there's an "Object Properties" panel with tabs for "Annotations", "Problems (0 Errors, 0 Warnings)", and "Database File Info". The "Annotations" tab shows "cloned from 'FRAP' owned by user ACowan". The "Settings" tab shows the following table:

Max timestep	Output	Rel tol	Abs tol
0.01s	every 0.02 sec	1.0E-7	1.0E-9

At the bottom, it says "Mesh: 201x201 = 40401 elements" and "Geometry size: (20.0,20.0) microns".

The screenshot shows the VCell software interface with the 'Simulations' tab selected. A tooltip box highlights the 'Results' column in the simulation table, which contains the value 'yes'. A blue arrow points from the tooltip to the 'Graph' icon in the toolbar above the table.

Once Running Status indicates there are results, select the simulation and use the graph icon button to open the results viewer

Name	End Time	Output Option	Solver	Running Status	Results
FRAP_1	1.0	every 0.02 s	Moving	completed	yes

Annotation: cloned from 'FRAP' owned by user ACowan

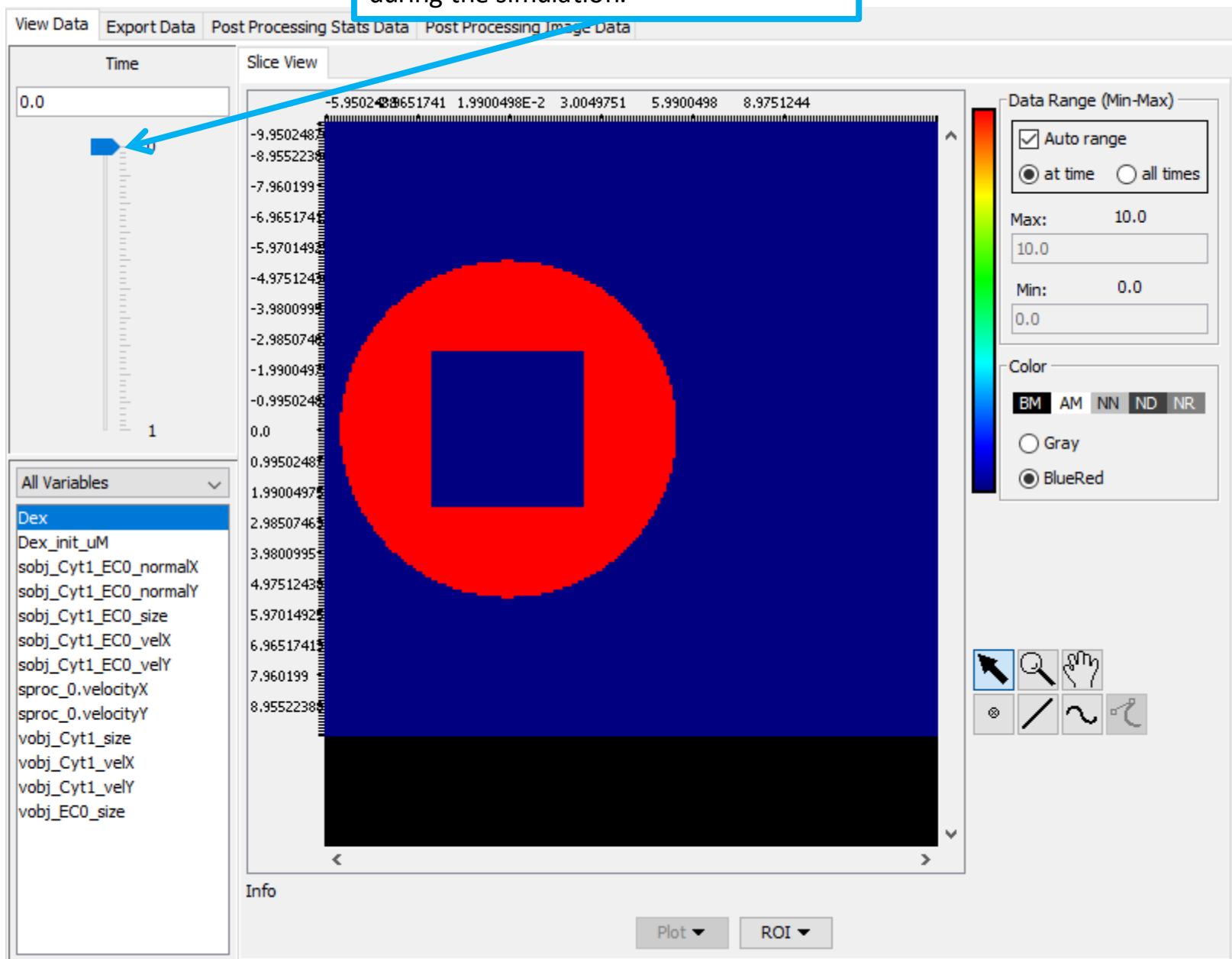
Settings:

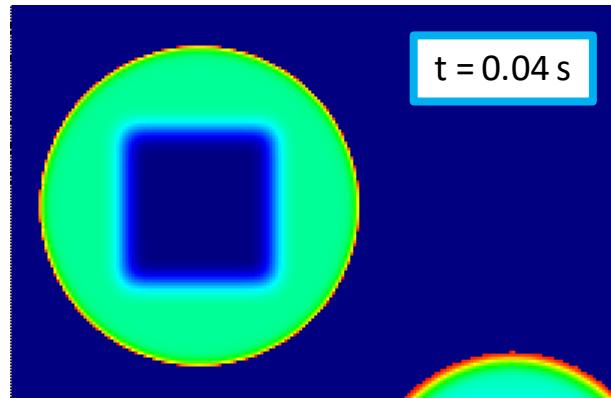
Max timestep	Output	Rel tol	Abs tol
0.01s	every 0.02 sec	1.0E-7	1.0E-9

Mesh: 201x201 = 40401 elements

Geometry size: (20.0,20.0) microns

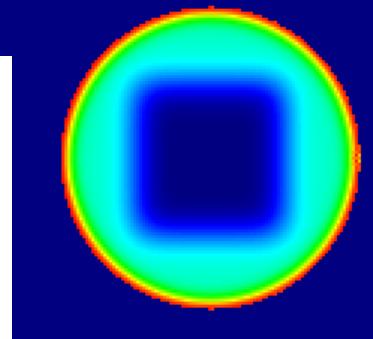
Use the Time slider to see what happens during the simulation.





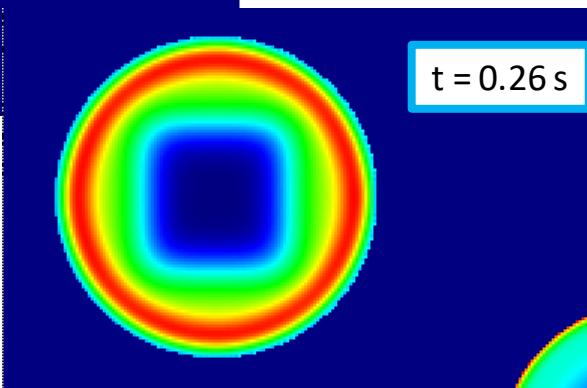
$t = 0.04$  s

*The velocity of the membrane contraction is sufficiently fast that the volume species becomes concentrated under the membrane before the concentration gradient can be dispersed by diffusion. When the membrane expands, there is a low concentration of dex under the membrane as it diffuses into the newly created volume.*

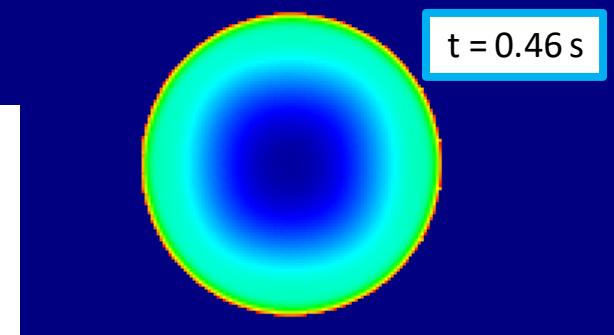


$t = 0.16$  s

*Note that autorange is selected for each image.*



$t = 0.26$  s



$t = 0.46$  s