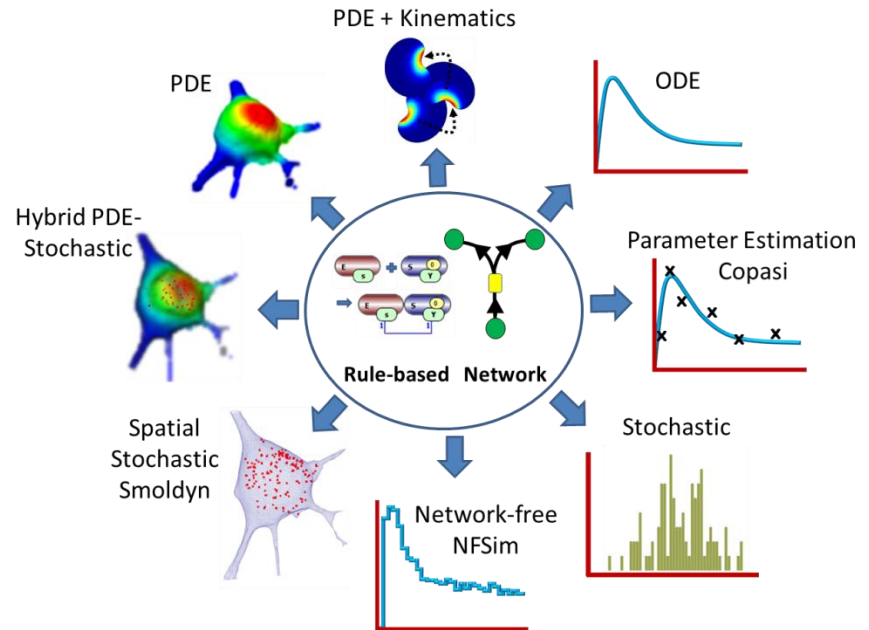


VCell

modeling environment for
mathematical simulation of
cellular events.

To run VCell go to:

vcell.org



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

VCell Tutorial

FRAP: Fluorescence Redistribution After Photo bleaching

Create a simple biomodel and spatial (PDE) application to simulate a photobleaching experiment and view the results.

In this tutorial...

- Gain a basic introduction to the Virtual Cell interface
- Create a very simple biomodel with species but no reactions
- Create a spatial deterministic (PDE) application of a model using analytic equations to create a simple geometry
- Define initial concentrations that are non-uniform using Boolean expressions
- View and analyze results of a spatial simulation

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)
 - Model 2
 - tutorial 3
 - Private Tue Jun 30 16:47:35 EDT 2018
 - 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

- Spatial Deterministic
 - Deterministic
 - geom_20150630_115646 (3D)

BioModel3

- 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

EC

Starting from a new model...

Choose the select tool and select the compartment. Type "EC" under Structure Name and "Extra Cellular" under Annotation

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BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (astfh234) (3)
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 - Tutorials (5)
 - Education (33)
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Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one structure to edit properties

Structure Name EC

Size Variable Name EC [μm^3]

Annotation Extra Cellular

BioModel3

- 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

The diagram shows a compartment labeled 'EC' with two vertical dotted black lines on the left and right sides. The right-side dotted line is highlighted with a green dashed border. A red arrow points from a yellow text box to the compartment tool icon (a circle with a dot) in the toolbar. Another red arrow points from the yellow text box to the green dashed border of the right-side dotted line.

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

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BioModels MathModels Geometries

Search

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

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

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

BioModel3

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

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Reaction Diagram Reactions Structures Species Molecules Observables

Click on the select tool.

Click on the label "m0".

PM

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one structure

Structure Name PM

Size Variable Name PM [μm^2]

Electrophysiology

Voltage Variable Name Voltage_PM [mV]

Positive (inside feature)

Negative (outside feature)

membrane voltage: "Voltage_PM" = voltage(inside (+) compartment) - voltage(outside (-) compartment)
inward currents: from compartment "outside (-) compartment" into compartment "inside (+) compartment"
Note: VCell reactions and fluxes specify inward currents (- to +) rather than conventional currents (+ to -).

Annotation

BioModel3

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

VCell DB | BioModels.net | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

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

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

EC | PM

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

Delete | Pathway Links | Search

Object Properties | Problems (0 Errors, 0 Warnings)

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

BioModel3

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (3)
 - Species (0)
 - Molecules (0)
 - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

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

EC | PM | **Cyt**

Click on the select tool and click on the newest compartment. Next to Structure Name type "Cyt" and next to Annotation type "Cytosol".

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BioModels | MathModels | Geometries

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 - My BioModels (astfh234) (3)
 - 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)

Select only one structure to edit properties

Structure Name	Cyt
Size Variable Name	Cyt [μm^3]
Annotation	Cytosol

BioModel3

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

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

Tools: [Select] [Erase] [Species] [Arrow] [Line] [Erase] [Zoom In] [Zoom Out] [Pan] [Zoom Reset] [Ann EAL] [REL AX]

EC | PM | Cyt

[s0]

Select the species tool.
Click on a point within the "Cyt" compartment and click to create a new species.

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BioModels | MathModels | Geometries

Search

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

Delete | Pathway Links | Search

Object Properties | Problems (0 Errors, 0 Warnings)

Species Name: s0

Linked Pathway Object(s):

Annotation:

Species: s0

BioModel3

- Physiology
 - Reaction Diagram**
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (0)
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Reaction Diagram Reactions Structures Species Molecules Observables

EC PM Cyt

Dex

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Species Name	Dex
Linked Pathway Object(s)	
Annotation	Dextran

Next to Species Name type "Dex" and next to Annotation type "Dextran".

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
 - Applications (0)**
- Parameters, Functions and Units
- Pathway
- Scripting

Name	Math Type	Annotation

Go to the Application workspace using the left menu tree. Select "New Application" and choose "Deterministic" from the dropdown menu.

VCell DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

▾

 ▾

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

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

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - Application0
- Parameters, Functions and Units
- Pathway
- Scripting

Name	Math Type	Annotation
FRAP	explicit network model, compartmenal, deter...	

Double click on the name box and rename the application as "FRAP". Press "Enter" on your keyboard to finalize.

VCeLL DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (ArundeeP2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

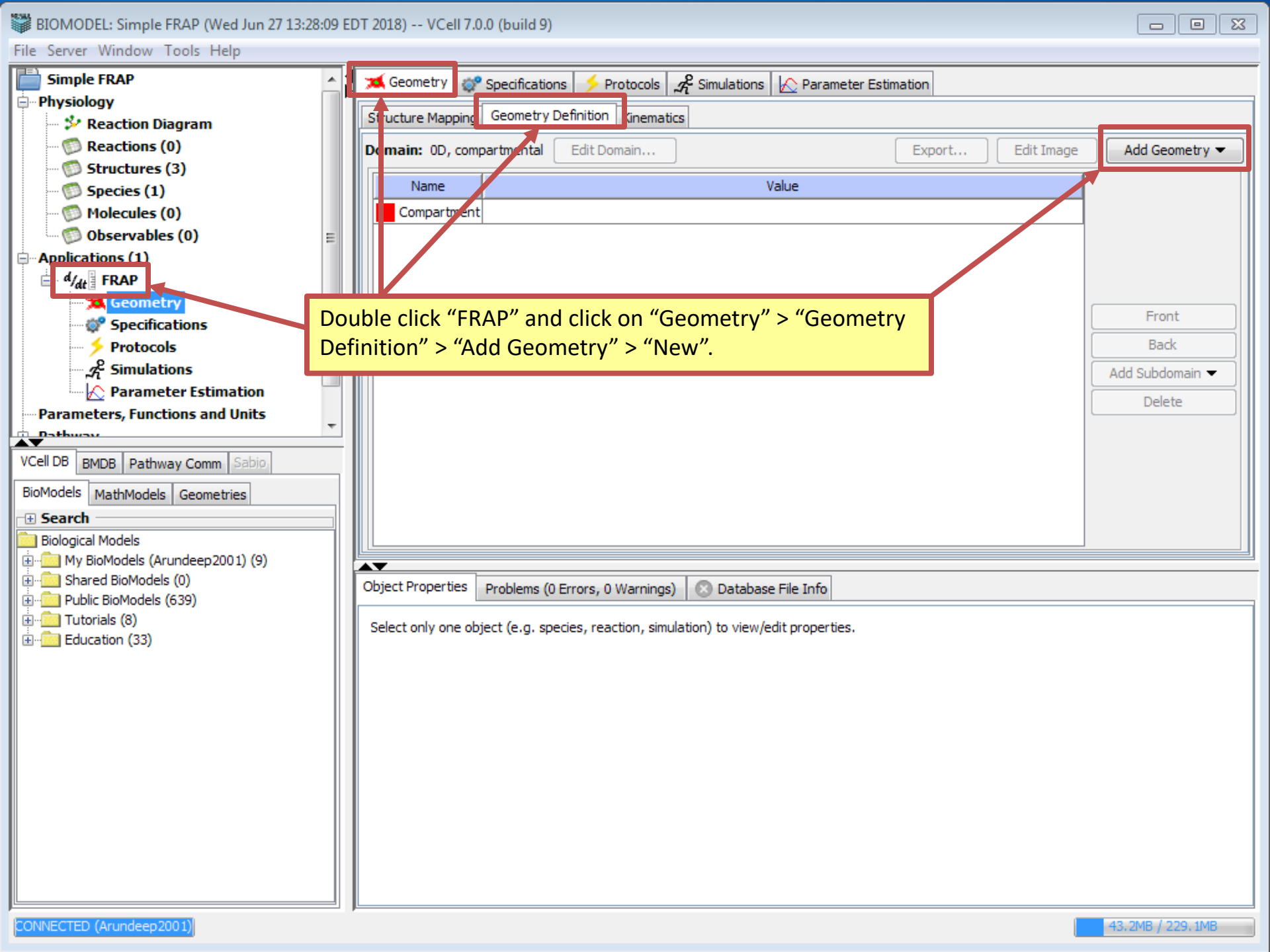
Object Properties | Problems (0 Errors, 0 Warnings) | Database File Info

Application Name: Application0

Annotation:

Summary

- Deterministic
- Compartmental
- math not generated



Double click "FRAP" and click on "Geometry" > "Geometry Definition" > "Add Geometry" > "New".

Name	Value
Compartment	

Buttons and options for geometry management:

- Front
- Back
- Add Subdomain ▼
- Delete

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
 - Parameter Estimation
- Parameters, Functions and Units
- Pathway

VCell DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

Geometry Specifications Protocols Simulations Parameter Estimation

Structure Mapping Geometry Definition Kinematics

Domain: OD, compartmental Edit Domain... Export... Edit Image Add Geometry ▾

Name	Value
Compartment	

Front
Back
Add Subdomain ▾
Delete

Choose new geometry type to

Click "Analytic Equations (2D)" > "OK".

Geometry Type

- Analytic Equations (1D)
- Analytic Equations (2D)**
- Analytic Equations (3D)
- Image based (import from file, zip or directory)
- Mesh based (import from STL file)
- New Blank Image Canvas
- Constructed Solid Geometry (3D)
- Import from Fiji/Imagej
- Import from Blender

OK Cancel

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry**
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

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
EC	1.0

Front | Back | Add Subdomain ▾ | Delete

Slice View | Surface View

Info

Double click on "Subdomain0" and type in "EC". Press "Enter" on your keyboard to finalize the name.

Object Properties | Problems (0 Errors, 4 Warnings) | Database File Info

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

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry**
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

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
EC	1.0

Front
Back
Add Subdomain ▾
Delete

Slice View Surface View Geometric Region Details

Info

Click "Add Subdomain" > "Analytic".

Object Properties Problems (0 Errors, 4 Warnings) Database File Info

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

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations

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	
EC	1.0

Click the drop down menu next to "Select Subdomain Shape:" and click "Circle".

Define New Subdomain Shape

Select Subdomain Shape: Circle

Center Point (x,y)
0,0

Radius
10

Analytic Expression
 $x^2 + y^2 < 10.0^2$

Copy Expression

Help New Subdomain Cancel

Type in "10" for the radius.

Click "Add New Subdomain".

VCell DB BMDB Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway
- Scripting

VCell DB BMDB Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

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 2.0 2.0 $(x) + (y) < (10.0)$
EC	1.0

Front Back Add Subdomain ▾

Slice View Surface View Geom

Info

Double click on the name box of the new subdomain and type in "Cyt". Press "Enter" on your keyboard to finalize the name.

Object Properties Problems (0 Errors, 6 Warnings) Database File Info

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

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry**
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

Geometry Specifications Protocols Simulations

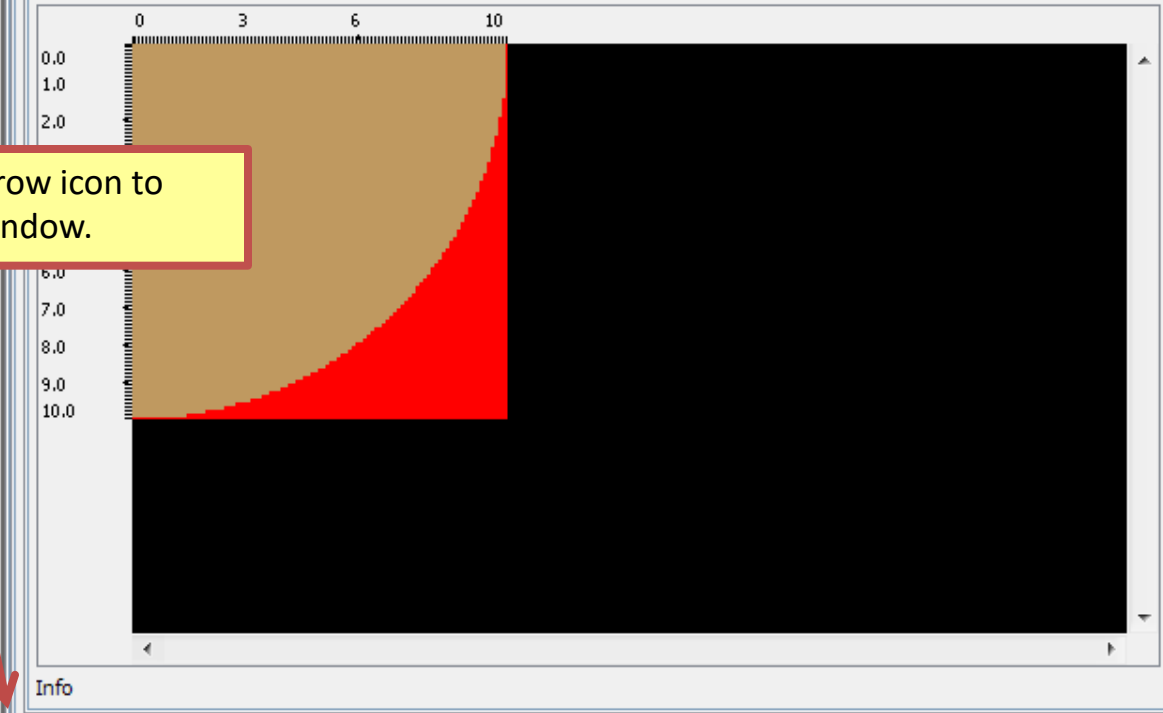
Structure Mapping Geometry Definition Kinematics

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

Name	Value
Cyt	2.0 2.0 2.0 $((x) + (y)) < (10.0)$
EC	1.0

Front
Back
Add Subdomain ▾
Delete

Slice View Surface View Geometric Region Details



Navigation icons: arrow, magnifying glass, hand

Click the black down arrow icon to adjust the Slice View window.

Info
A small black down arrow icon in a red box.

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry**
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB | BMDB | Pathway Comm | Sabio

BioModels | MathModels | Geometries

Search

- Biological Models
 - My BioModels (Arundeeep2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

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	$((x) + (y)) < (10.0)$
EC	1.0

Front | Back | Add Subdomain ▾ | Delete

Slice View | Surface View | Geometric Region Details

Info

Click "Edit Domain"

Simple FRAP

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

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BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (ArundeeP2001) (9)
 - Shared BioModels (0)
 - Public BioModels (639)
 - Tutorials (8)
 - Education (33)

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 2.0 2.0 $((x) + (y) < (10.0))$
EC	1.0

Front
Back
Add Subdomain ▾
Delete

Geometry Size

Size X 22 μm Y 22 μm Z 10.0 μm
Origin X -11 μm Y -11 μm Z 0.0 μm

OK Cancel

Click "OK".

Info

In the "Size" row, type in "22" for X and Y.
In the "Origin" row, type in "-11" for X and Y.

Click "OK".

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specificat
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Geometry Specifications Protocols Simulations

Structu

Domain

Name	Value
Cyt	$(((x) + (y)) < (10.0))$
EC	1.0

Replace Geometry ▾

Front

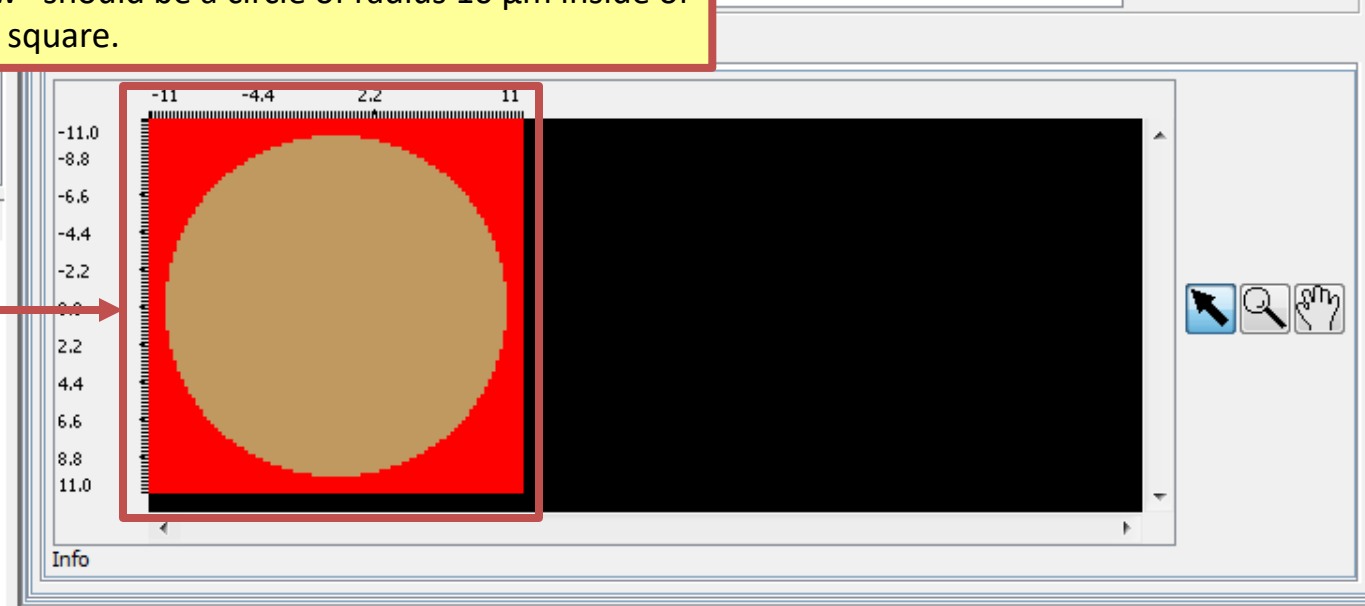
Back

Add Subdomain ▾

Delete

Click "Front" or "Back" to rearrange the geometry order. The order determines which subdomain a point in space belongs to; the front layer "hides" layers below.

Your "Slice View" should be a circle of radius 10 μm inside of an 22 X 22 μm square.



Object Properties Problems (0 Errors, 6 Warnings)

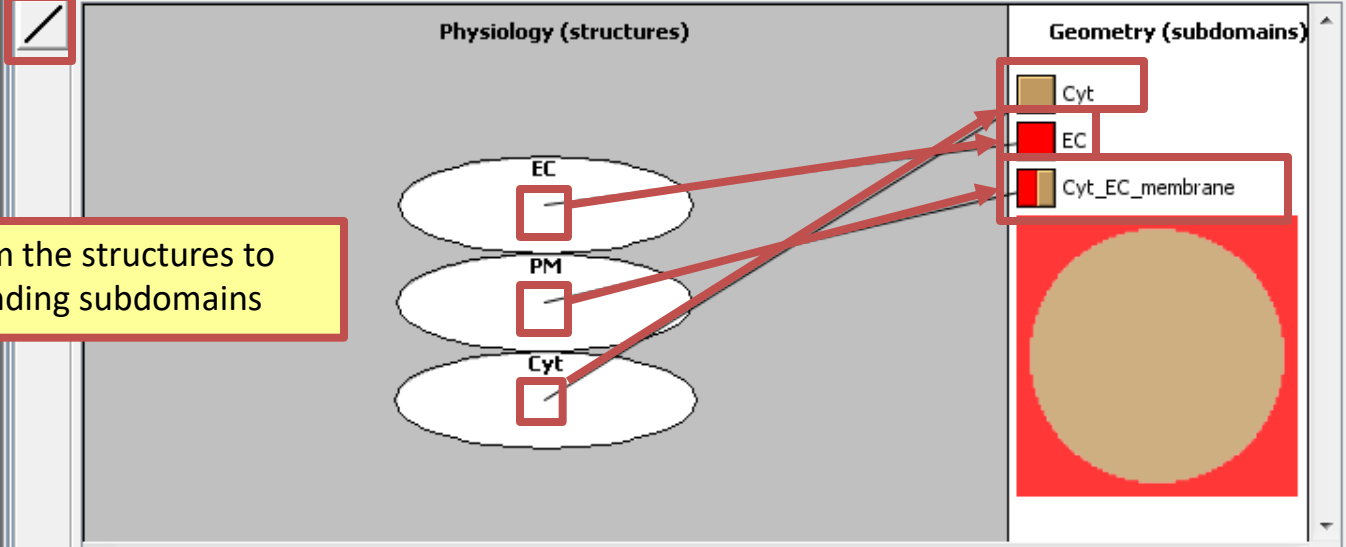
Select only one object (e.g. species, reaction, simulation) to view/edit properties.

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry**
 - Specificatio
 - Protocols
 - Simulation
- Parameters, Function
- Pathway

Drag a line from the structures to their corresponding subdomains

Under Geometry > Structure mapping, select the line tool.



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

VCeLl DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Object Properties Problems (0 Errors, 2 Warnings)

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

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

Geometr Specifications Protocols Simulations

Species Reaction Network

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant
Dex	Cyt	<input type="checkbox"/>	$y < -5.0 \parallel (y > 5.0))$	<input type="checkbox"/>	10.0

Click "Specifications" > "Species".

Double click on the "Initial Condition" box for Dex and type in "(10.0*((x<-5.0) || (x>5.0) || (y<-5.0) || (y>5.0)))". Press "Enter" on your keyboard to finalize. This Boolean expression for the initial concentration evaluates to 10 μM everywhere except from x = -5 to 5 and from y = -5 to 5, where the expression evaluates to 0.

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Search

Object Properties Problems (0 Errors, 0 Warnings)

Description	Parameter	Expression	Units
initial concentration for Dex	initConc	$10.0 \cdot ((x < -5.0) \parallel (x > 5.0) \parallel (y < -5.0) \parallel (y > 5.0))$	μM
diffusion constant for Dex	diff	10.0	μM ² .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
Boundary Condition Y- for Dex	BC_Ym	<zero flux>	μM.μm.s ⁻¹

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications**
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Geometry Specifications Protocols Simulations

Species Reaction Network

Species	Structure	Clamped	Initial Condition	Well Mixed	Diffusion Constant
Dex	Cyt	<input type="checkbox"/>	(10.0 * ((x < -5.0) ...	<input type="checkbox"/>	20

Search

Type in "20" under "Diffusion Constant".
Press "Enter" on your keyboard to finalize.

Object Properties Problems (0 Errors, 0 Warnings)

Description	Parameter	Expression	Units
initial concentration for Dex	initConc	$10.0 \cdot ((x < -5.0) \parallel (x > 5.0) \parallel (y < -5.0) \parallel (y > 5.0))$	μM
diffusion constant for Dex	diff	10.0	$\mu\text{M}^2 \cdot \text{s}^{-1}$
Boundary Condition X- for Dex	BC_Xm	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition X+ for Dex	BC_Xp	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$
Boundary Condition Y- for Dex	BC_Ym	<zero flux>	$\mu\text{M} \cdot \mu\text{m} \cdot \text{s}^{-1}$

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations**
- Parameters, Functions and Units
- Pathway

Geometry Specifications Protocols **Simulations**

Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
------	----------	---------------	--------	----------------	---------

Click "Simulations" and the new simulation icon.

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Object Properties Problems (0 Errors, 0 Warnings)

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

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
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- Parameters, Functions and Units
- Pathway

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

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

Double click on "Simulation0" and type in "FRAP". Press "Enter" on your keyboard to finalize.

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Object Properties Problems (0 Errors, 0 Warnings)

Annotation:

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

Mesh: 101x101 = 10201 elements Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
FRAP	0	every 0.05 sec	Fully-Implicit	not saved	no

Click the edit simulation icon.

Object Properties Problems (0 Errors, 0 Warnings)

Annotation:

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

Mesh: 101x101 = 10201 elements

Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Edit: FRAP

Parameters **Mesh** ← Click "Mesh".

Mesh Size

Geometry Size (um) (22.0, 22.0)

Mesh Size (elements)

- Lock aspect ratio
- X 51
- Y 51

Total Size (elements) 51 x 51 = 2601

Spatial Step (um) Δx 0.44

Δy 0.44

OK Cancel

Leave "Lock aspect ratio" checked.
Type in "51" for X "Mesh Size".

Results

no

Mesh: 101x101 = 10201 elements Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults

File Server Window Tools Help

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geomet
 - Specific
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Edit: FRAP

Parameters Mesh **Solver**

Choose solver algorithm and fine-tune time conditions:

Integrator Fully-Implicit Finite Volume, Regular Grid 0 (variable Time Step)

Time Bounds

Starting	0.0	Minimum		Error Tolerance	
Ending	3.0	Default		Absolute	1.0E-9
		Maximum	0.01	Relative	1.0E-7

Local Sensitivity Analysis

Output Options

Keep Every [] time samples and at most [] time samples

Output Interval 0.05 secs

Miscellaneous

OK Cancel

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

Mesh: 51x51 = 2601 elements

Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults

Type "3.0" for the Ending Time Bound.

Click "Solver".

Type in ".01" for the Maximum Time Step.

Type "0.05" for the Output Interval.

Click "OK".

BioModel3

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

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

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
FRAP	3.0	every 0.05 sec	Fully-Implicit	not saved	no

Press the green play button to run the simulation

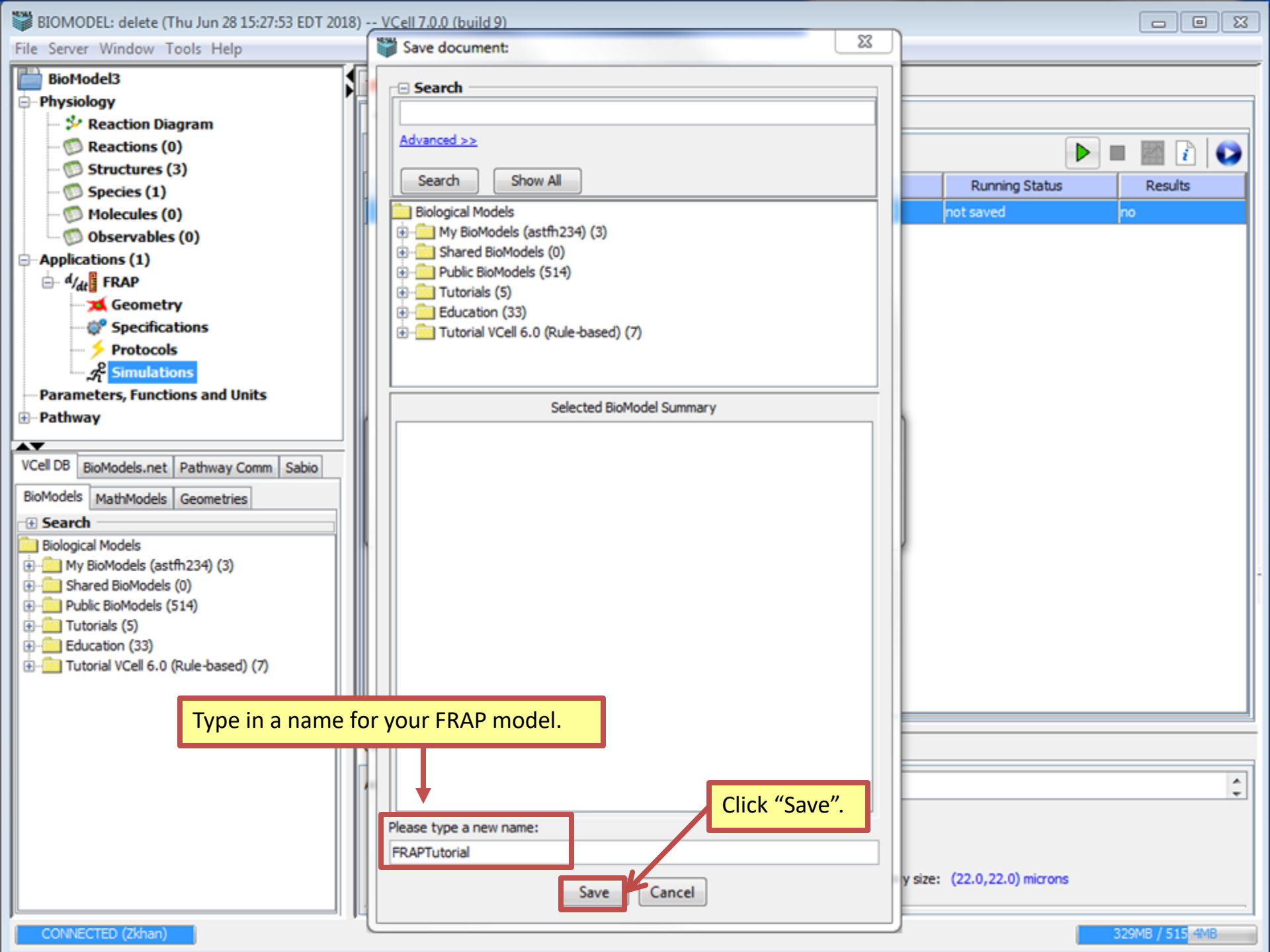
Object Properties Problems (0 Errors, 0 Warnings)

Annotation:

Settings:	max timestep	output	rel tol	abs tol
	0.01s	every 0.05 sec	1.0E-7	1.0E-9

Mesh: 51x51 = 2601 elements Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults



Type in a name for your FRAP model.

Please type a new name:
FRAPTutorial

Click "Save".

Save Cancel

Running Status	Results
not saved	no

FRAPTutorial

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (astfh234) (4)
 - Shared BioModels (0)
 - Public BioModels (514)
 - Tutorials (5)
 - Education (33)
 - Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Name	End Time	Output Option	Solver	Running Status	Results
FRAP	3.0	every 0.05 sec	Fully-Implicit	completed	yes

Under "Running Status" you can view the status of the simulation. You can view the results as soon as there are time points saved to the database.

Object Properties Problems (0 Errors, 0 Warnings)

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

FRAPTutorial

- Physiology
 - Reaction Diagram
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulations
- Parameters, Functions and Units
- Pathway

VCell DB BioModels.net Pathway Comm Sabio

BioModels MathModels Geometries

Search

- Biological Models
 - My BioModels (astfh234) (4)
 - Shared BioModels (0)
 - Public BioModels (514)
 - Tutorials (5)
 - Education (33)
 - Tutorial VCell 6.0 (Rule-based) (7)

Geometry Specifications Protocols Simulations

Simulations Output Functions Generated Math

Click the results icon.

Name	End Time	Output Option	Solver	Running Status	Results
FRAP	3.0	every 0.05 sec	Fully-Implicit	completed	yes

Object Properties Problems (0 Errors, 0 Warnings)

Annotation:

Settings:	max timestep	output	rel tol	abs tol
	0.01s	every 0.05 sec	1.0E-7	1.0E-9

Mesh: 51x51 = 2601 elements Geometry size: (22.0,22.0) microns

Parameters with values changed from defaults

Tutorial_FRAP

- Physiology
 - Reaction Diagrams
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulation
- Parameters, Functions
- Pathway
- Scripting

Results for Simulation FRAP

View Data | Export Data | Post Processing

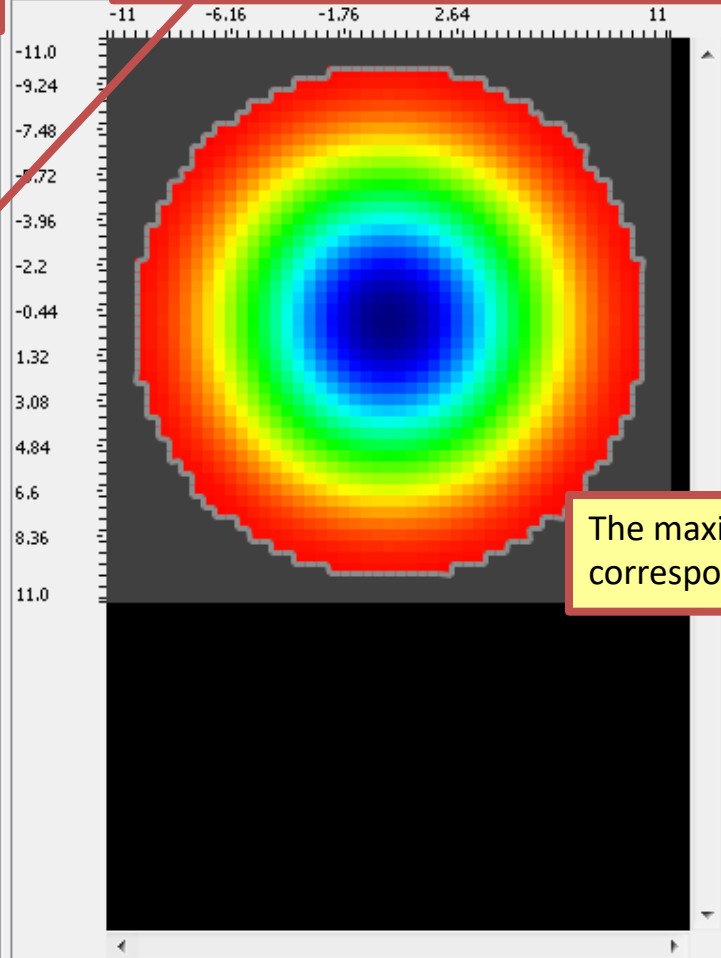
Time: 1.2

Slider: 0 to 3

All Variables

- Dex
- Dex_init_uM
- sobj_Cyt1_EC0_size
- vobj_Cyt1_size
- vobj_EC0_size

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



Data Range (Min-Max)

Auto range

at time all times

Max: 6.848905627991789
6.848905627991789

Min: 6.4356996097316355
6.4356996097316355

Color

BM AM NN ND NR

Gray

BlueRed

The maximum and minimum values correspond to the colors shown

Results

yes

Scan

Tutorial_FRAP

- Physiology
 - Reaction Diagrams
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulation
- Parameters, Functions
- Pathway
- Scripting

VCell DB | BMDB | Pathway

BioModels | MathModels

Search

- Biological Models
 - My BioModels (Zkhan)
 - Shared BioModels (1)
 - Public BioModels (6)
 - Tutorials (8)
 - Education (33)

Results for Simulation FRAP

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

Time: 1.2

Slice View

Data Range (Min-Max)

Auto range

at time all times

Max: 6.848905627991789

6.848905627991789

Min: 6.4356996097316355

6.4356996097316355

Color

BM AM NN ND NR

Gray

BlueRed

Info

Plot | ROI

Select the line tool, click on a point within the data and click on another point. A line will form and connect the two points.

Click "Plot" > "Spatial".

Results

yes

Scan

Tutorial_FRAP

- Physiology
 - Reaction Diagrams
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulation
- Parameters, Functions
- Pathway
- Scripting

VCell DB | BMDB | Pathway

BioModels | MathModels

Search

- Biological Models
 - My BioModels (Zkhan)
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 - Tutorials (8)
 - Education (33)

Results for Simulation FRAP

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

Time | Slice View

1.2 | 0 | 3

Spatial Plot: 'Dex' [Tutorial_FRAP::FRAP]:[FRAP]:ps=0

Values along curve

Plot Legend: Dex [µM]

6.848905627991789

6.848905627991789

AM NN ND NR

Gray

BlueRed

Info

Plot ROI

Click "X" to close.

Click the spreadsheet icon to open a spreadsheet of the graph.

Tutorial_FRAP

- Physiology
 - Reaction Diagrams
 - Reactions (0)
 - Structures (3)
 - Species (1)
 - Molecules (0)
 - Observables (0)
- Applications (1)
 - FRAP
 - Geometry
 - Specifications
 - Protocols
 - Simulation
- Parameters, Functions
- Pathway
- Scripting

VCell DB | BMDB | Pathway

BioModels | MathModels

Search

- Biological Models
 - My BioModels (Zkhan)
 - Shared BioModels (6)
 - Public BioModels (6)
 - Tutorials (8)
 - Education (33)

Results for Simulation FRAP

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

Time: 1.2

Slice View

Data Range (Min-Max)

- Auto range
- at time all times
- Max: 6.848905627991789
- 6.848905627991789
- Min: 6.4356996097316355
- 6.4356996097316355

Color

- BM AM NN ND NR
- Gray
- BlueRed

Info

Plot ROI

Select the dot tool and click on a point within the data and click on another point.

Click "Plot" > "Time".

Results

yes

Scan

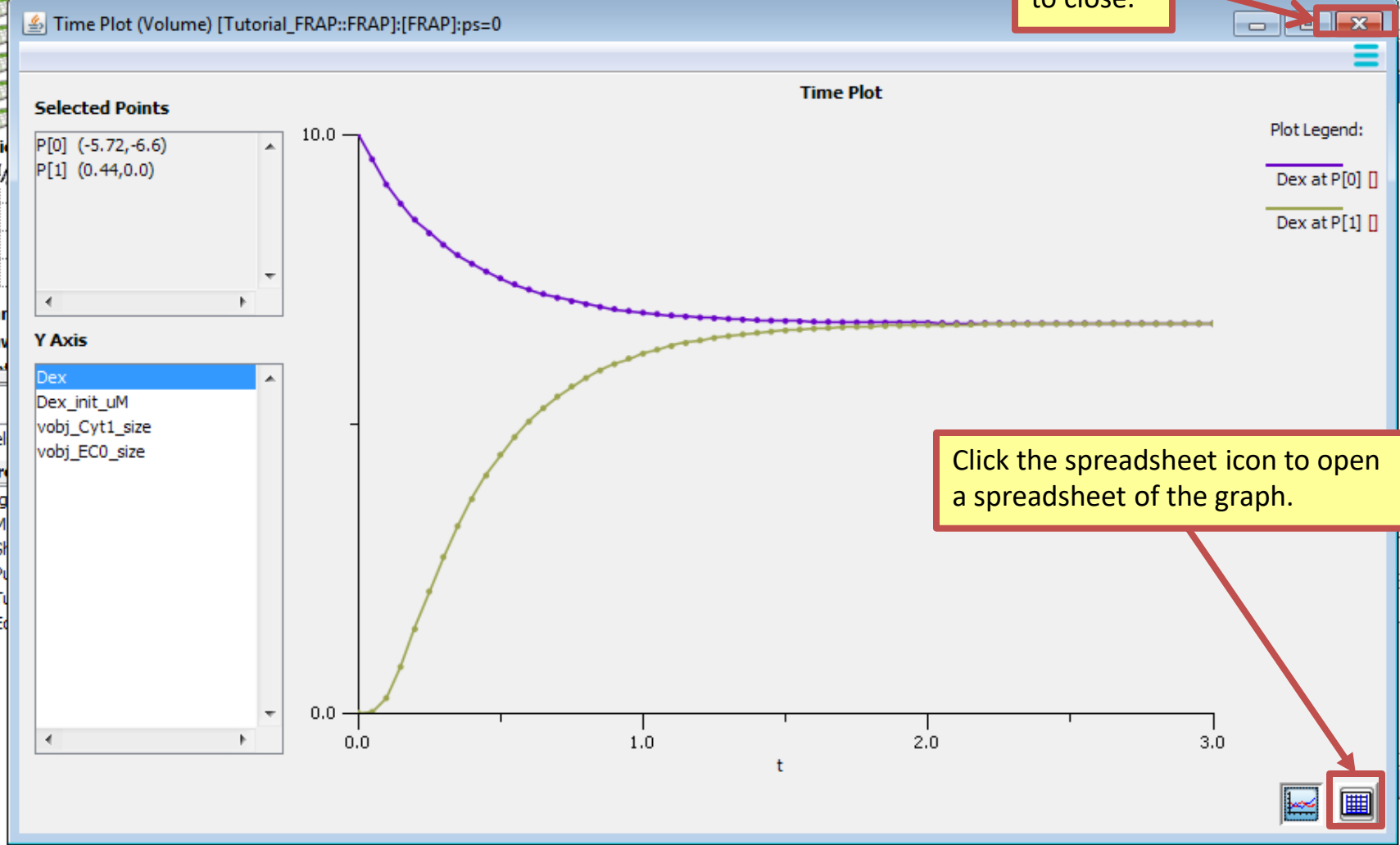
Tutorial_FRAP

- Physiology
- Reaction Diagram
- Applic
- Param
- Pathw
- Scen
- VCell DB
- BioModel
- Search
- Biolog
- M
- St
- Pu
- Tu
- Ec

Results for Simulation FRAP

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

Click "X" to close.



Click the spreadsheet icon to open a spreadsheet of the graph.

Acknowledgements

The following students worked on this tutorial:

Arundeeep Singh (2018) – Sport and Medical Sciences Academy

Zaiba Khan (2018) – East Windsor High School

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