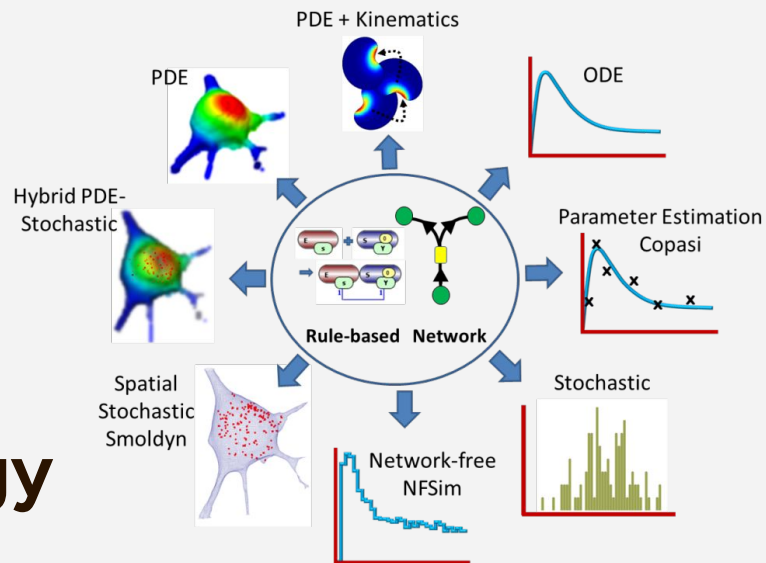


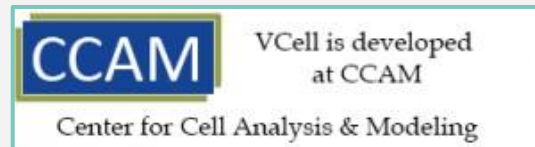
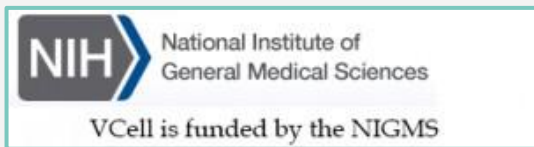


A modeling environment for the simulation of cellular events. Download at [vcell.org](http://vcell.org)  
Version 7.7 July 2025

## Defining Model Physiology



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



# Defining Model Physiology

## Objective:

Create a single Biomodel of Ran nuclear transport using Virtual Cell modeling and analysis software.

## Goals:

- Understand the basic functions of VCell software as it pertains to this tutorial.
- Create a Biomodel Physiology with species, reactions, and fluxes.

General familiarity with VCell software is recommended. Although this tutorial can be followed by a VCell novice, it is recommended that novice users first look through the VCell tutorials available at <http://vcell.org/support>

Model building can be matched to the BioModel **Tutorial\_MultiApp** in the [Tutorial folder](#) in the **VCell Database**.

# How to Save Your Model

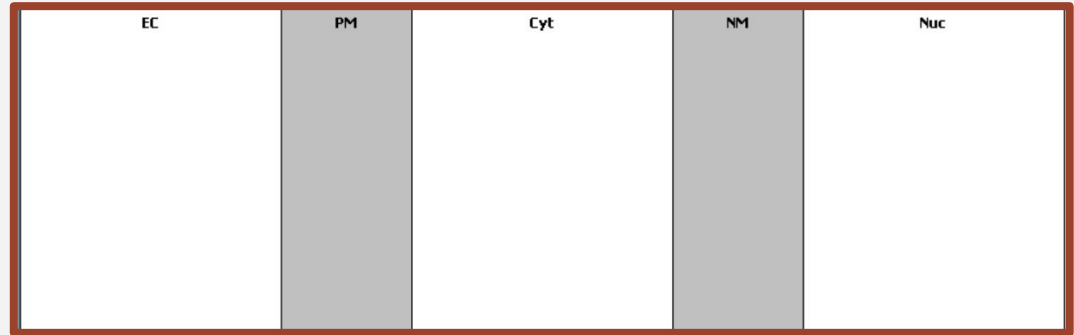
- **To save your model, go to the top left corner and click:**
  - **File → Save**
- If your model cannot be saved, check your errors in the bottom panel titled "Problems." Clicking on an error will lead you to the part of the model that may not let you save.
- If you can't save your model because of errors, you can save as local in the VCML format and reload into VCell later.

# Table of Contents

Click on a section title to go to that section.

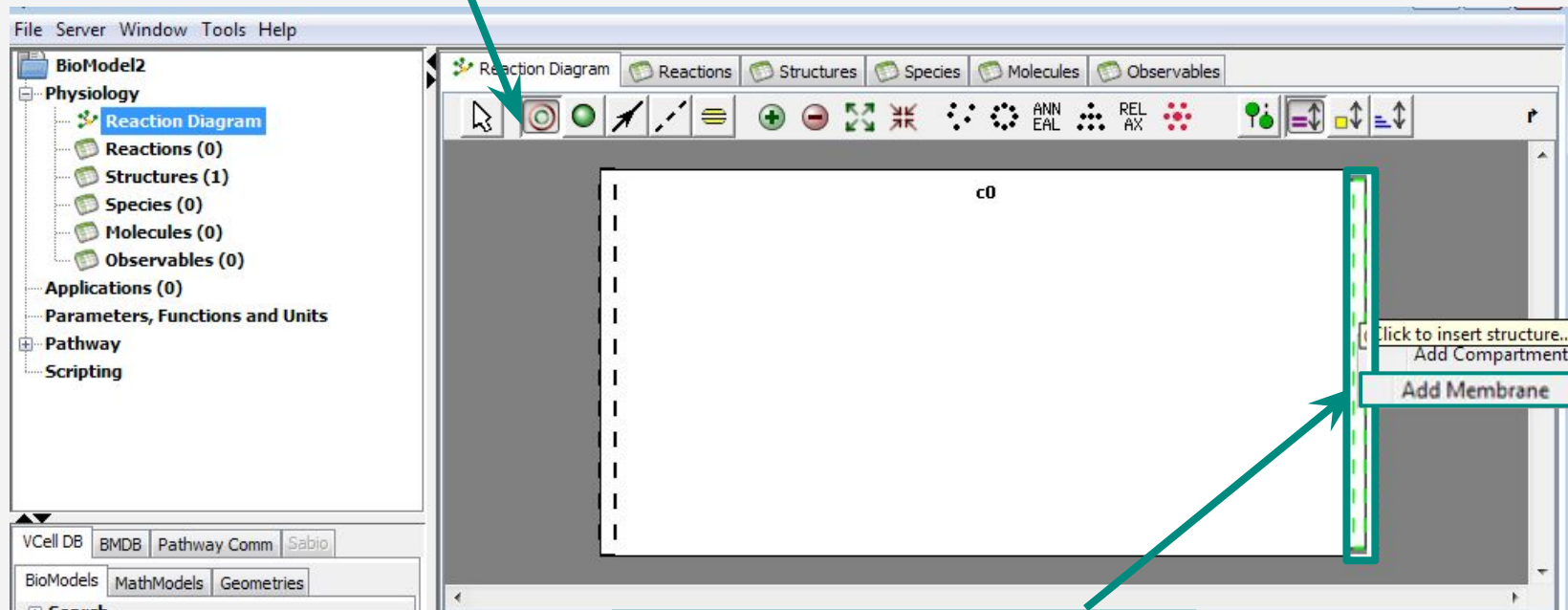
1. [Creating Compartments](#).....Slide 5
2. [Defining a Species](#).....Slide 12
3. [Making a Reaction Across a Membrane](#).....Slide 14
4. [Creating a Reaction in a Compartment](#).....Slide 18
5. [Defining Reaction Kinetics](#).....Slide 23

01

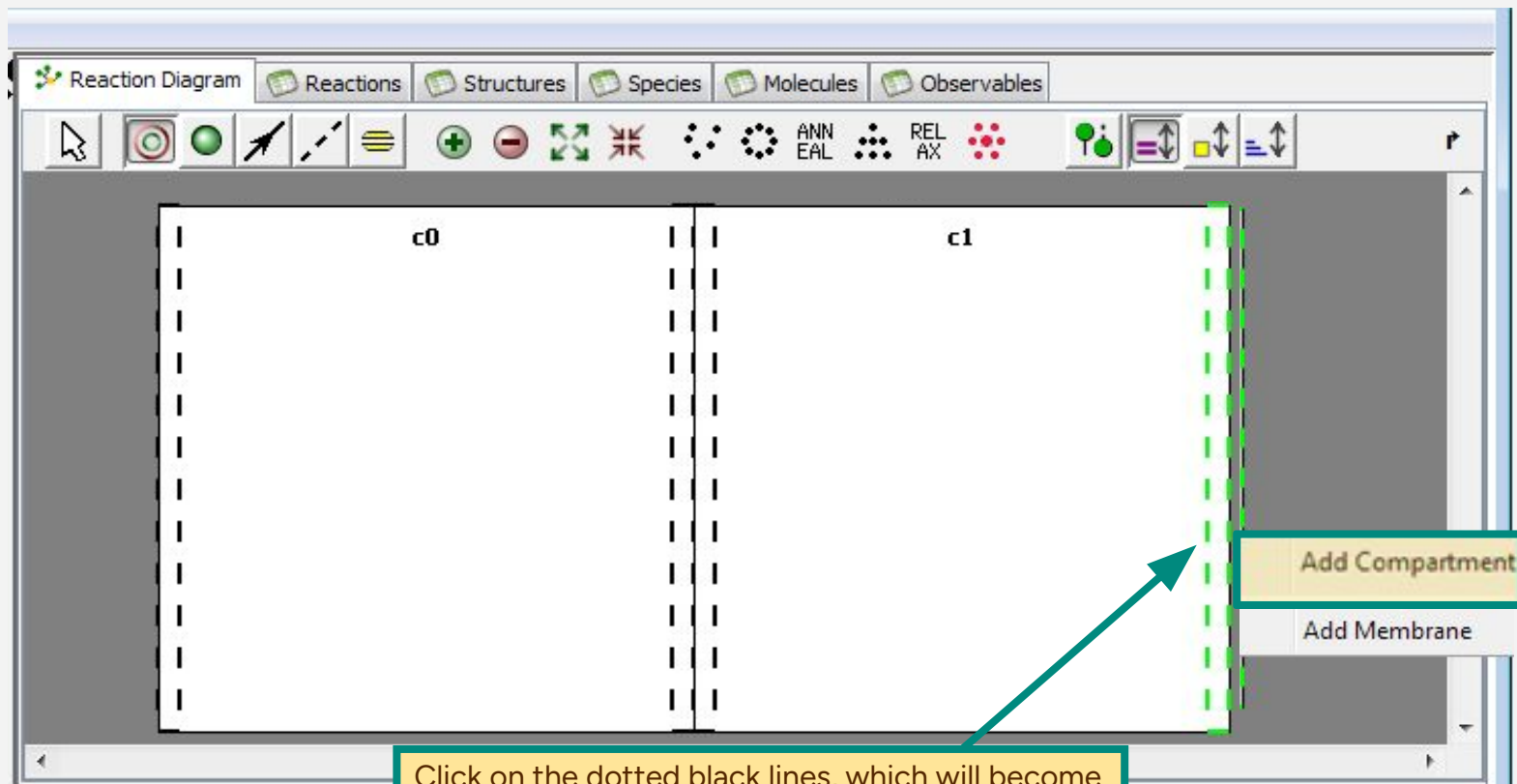


# Creating Compartments

Start with creating a volumetric compartment by selecting the **Structure Tool**.

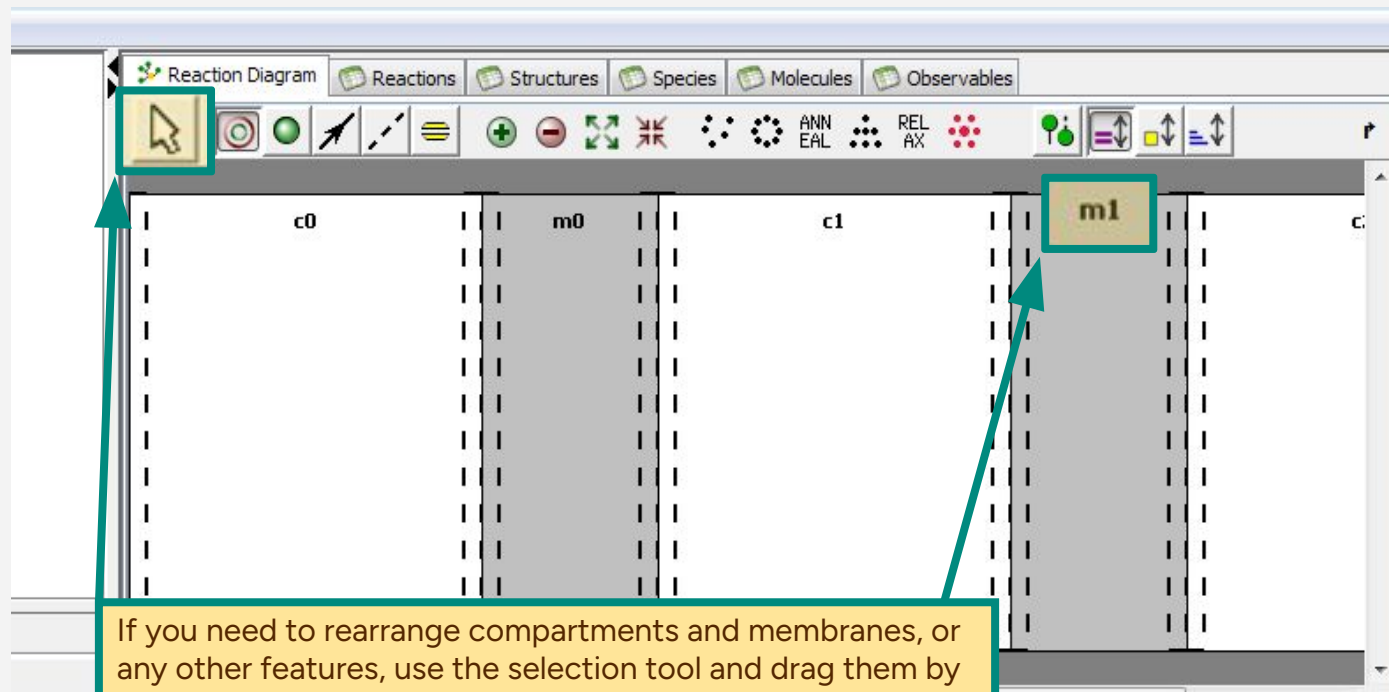


Click on one of the black lines so they turn green, and select **Add Membrane** to make a new membrane.



Click on the dotted black lines, which will become green, and select **"Add Compartment"** to create a new compartment.

This model requires 3 compartments separated by 2 membranes. Continue creating two additional compartments that are separated by a membrane.

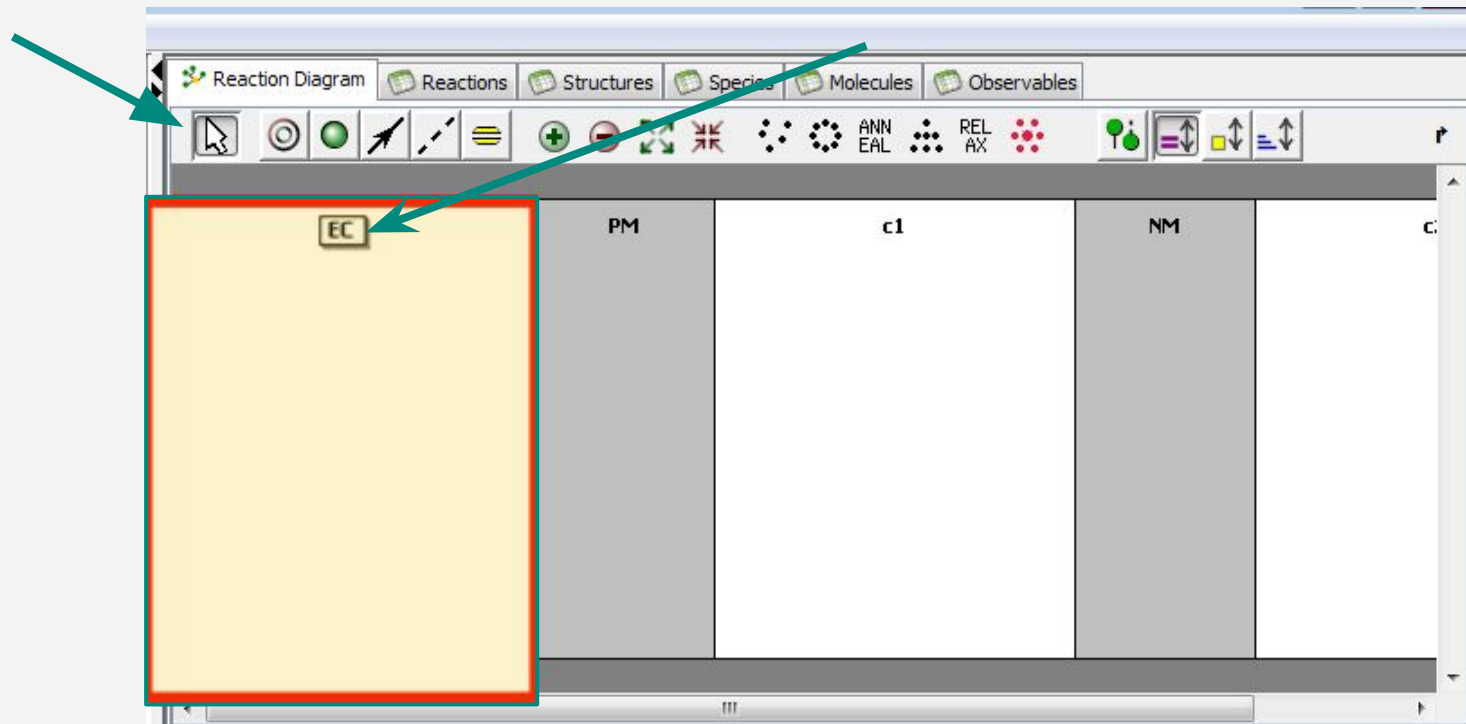


If you need to rearrange compartments and membranes, or any other features, use the selection tool and drag them by their label.

**TIP:** add compartments and membranes in numerical order (e.g. c0, c1, c2).



Use the **selection tool** to name compartments and membranes. The area will turn red upon selection. Double click the structure name you wish to change and enter the new name.



Reaction Diagram Reactions Structures Species Molecules Observables

EC PM c1 NM c

You can also change the Structure Name on the **Object Properties** tab.

You can type any text to be saved with the model (known as annotations).

Delete Pathway Links Search

Object Properties Problems (0 Errors, 0 Warnings)

Select only one structure to edit properties

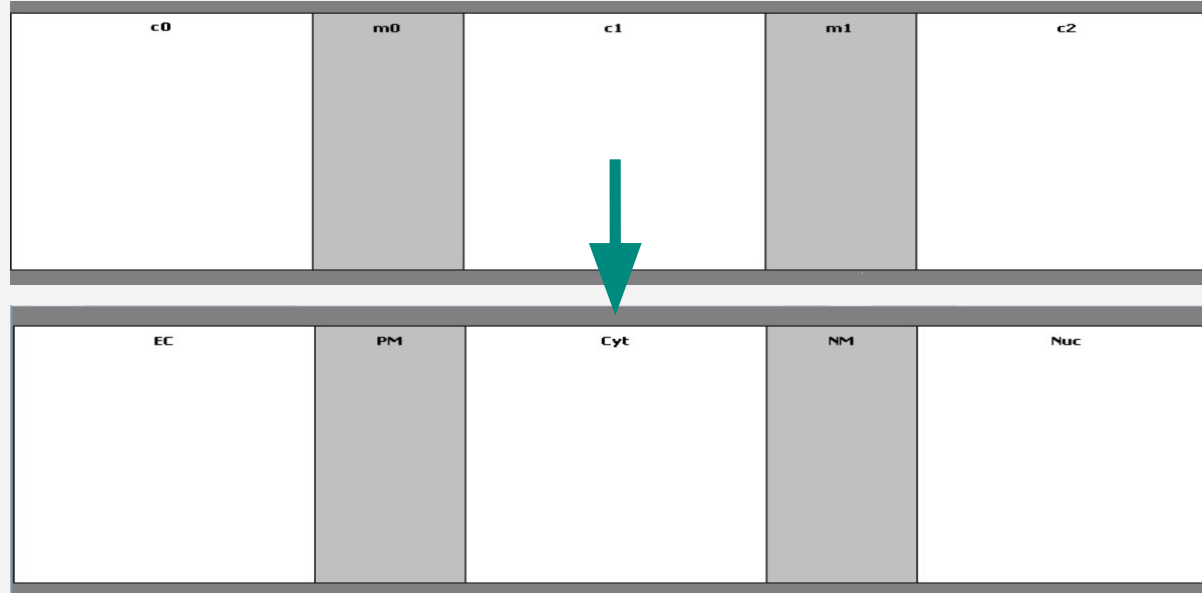
Structure Name EC

Size Variable Name EC [μm³]

Annotation

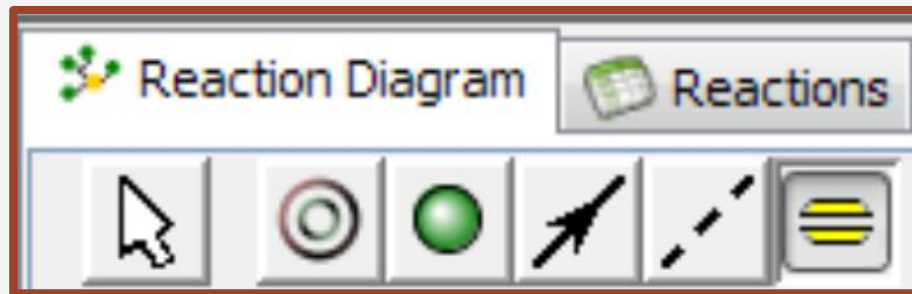
**To be consistent with the next tutorials and the MultiApp\_Tutorial model, please rename the compartments and membranes to the following:**

- C0 -> EC (Extracellular)
- M0 -> PM (Plasma Membrane)
- C1 -> Cyt (Cytosol)
- M1 -> NM (Nuclear Membrane)
- C2 -> Nuc (Nucleus)



02

# Defining a Species

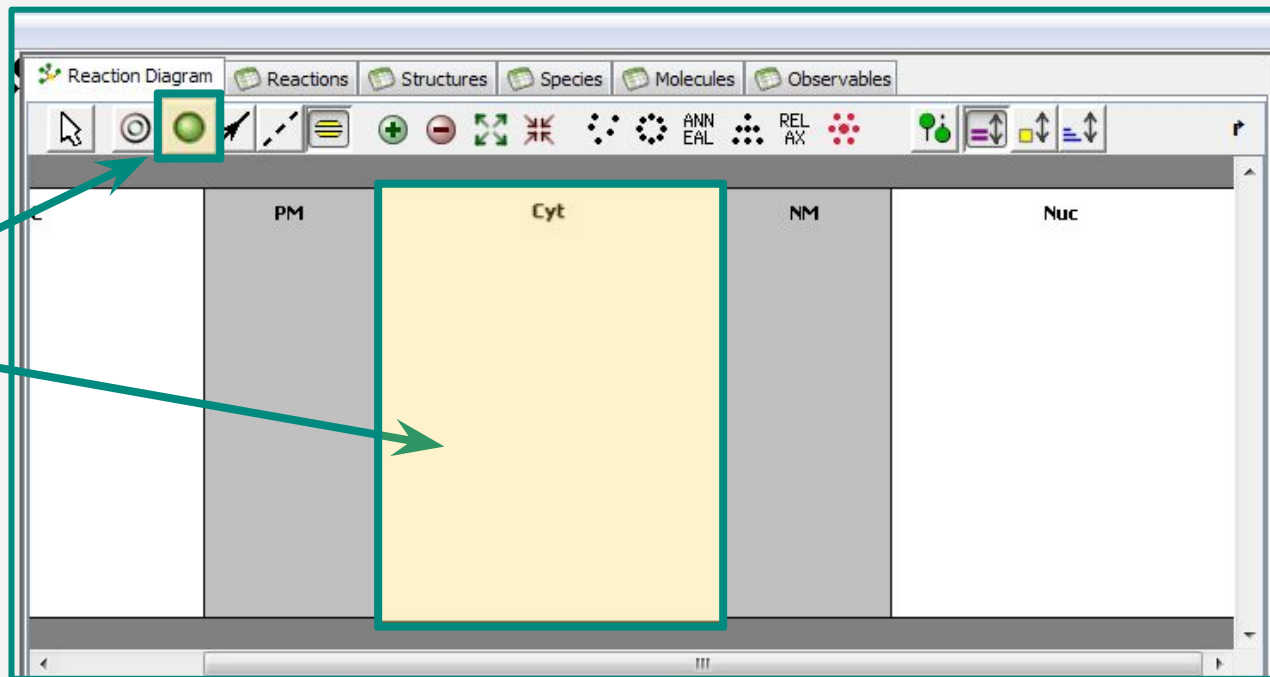


**Chemical Species** - A pool of chemically identical molecular entities that serve as variables in the model.

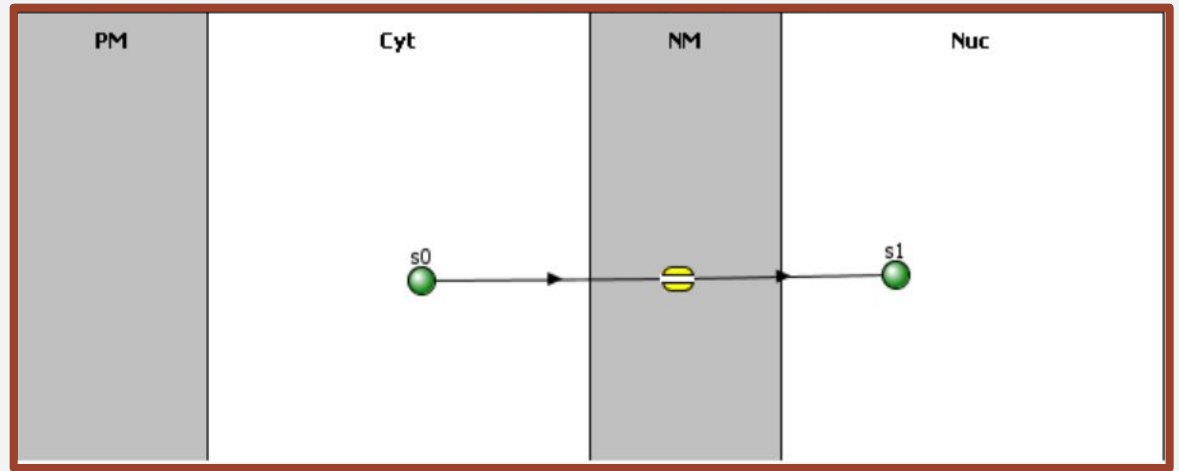


**TIP:** Always save your model as soon as possible; begin saving after adding your first species and structures.

To create a species, click on the **species** tool and click in the area you want to place the species.

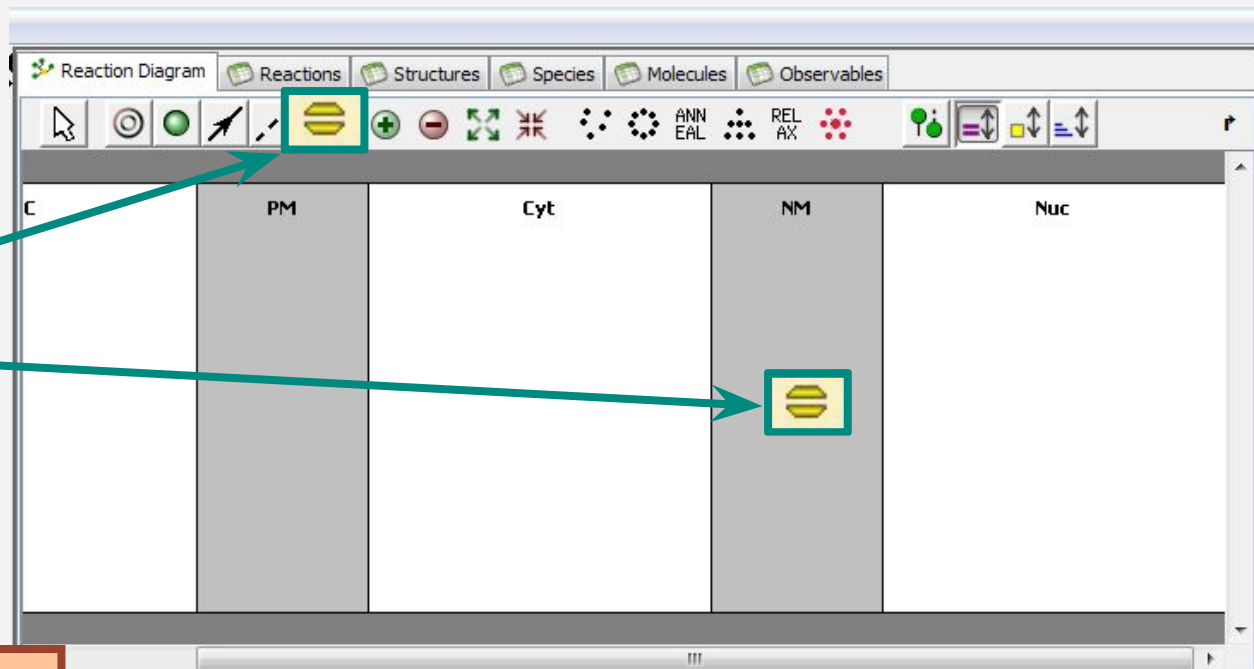


03

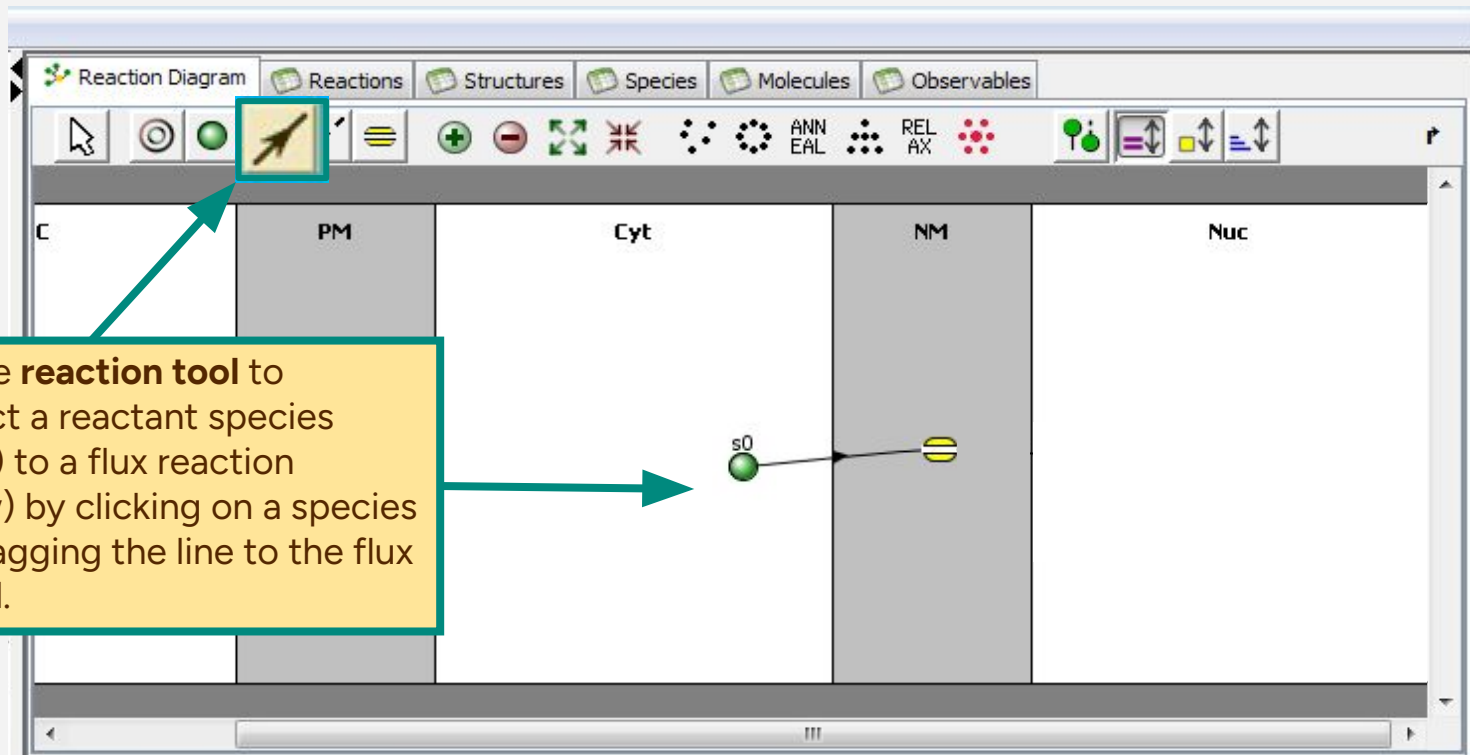


# Making a Reaction Across a Membrane

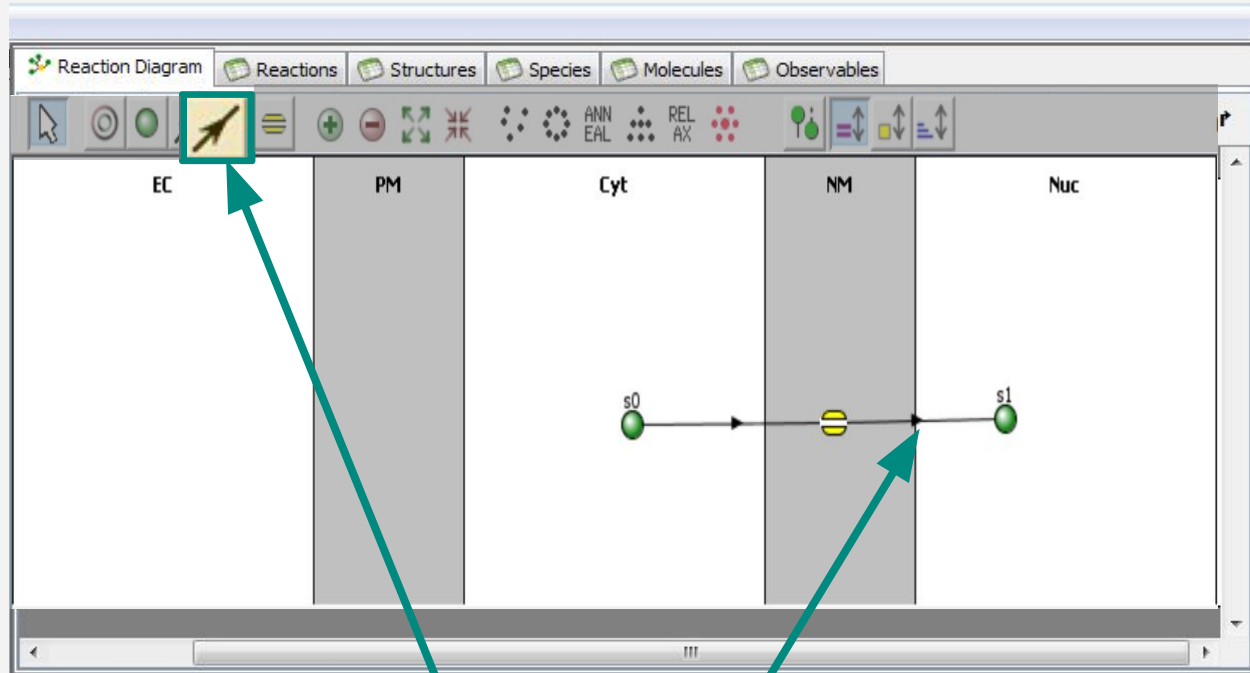
Click on the **FluxReaction** tool, then click in the area where you want to place the flux (NM). Fluxes can be placed in membranes only.



**Flux:** The rate at which a substance, energy, or property passes through a surface.

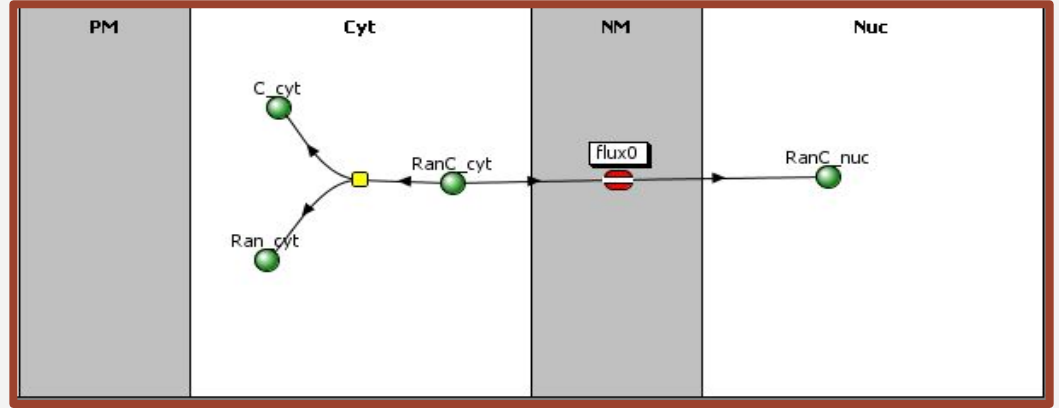






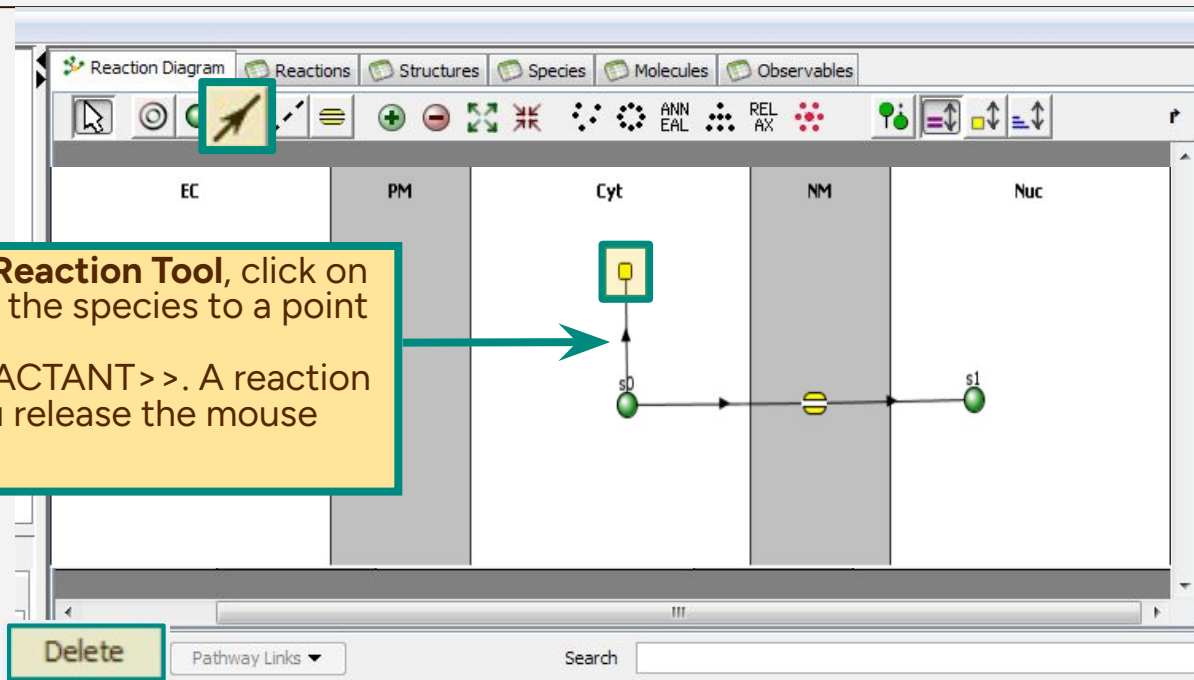
To create a product of a flux reaction, use the **reaction tool** to drag a line from the flux to a point inside the compartment where a product species will be made.

04



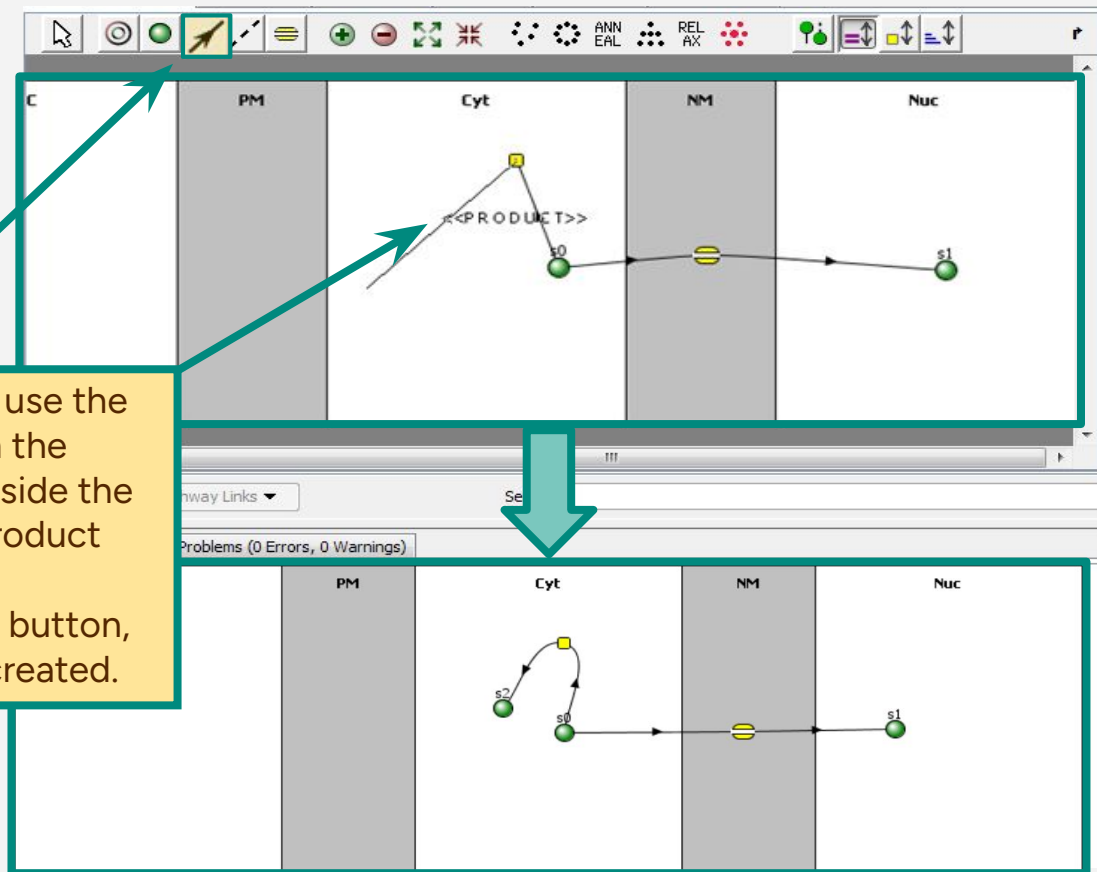
# Creating a Reaction in a Compartment

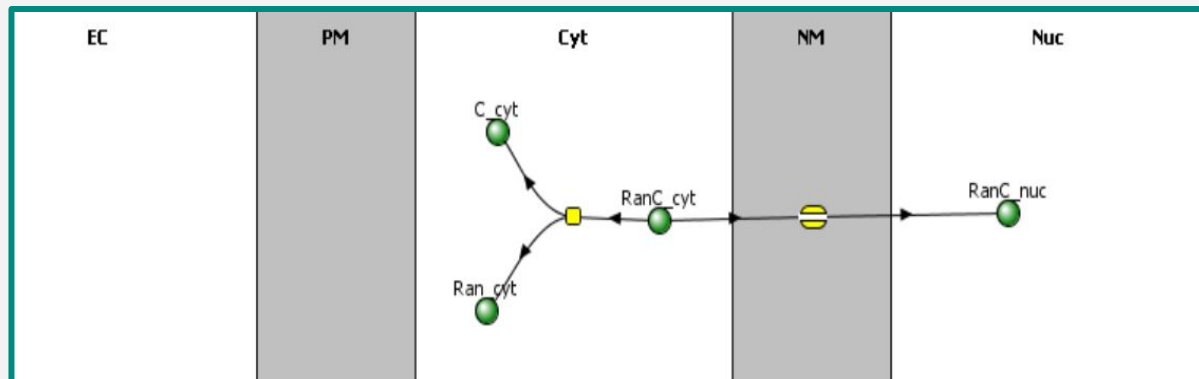
To create a reaction with the **Reaction Tool**, click on a species and drag a line from the species to a point inside the compartment. The active line will read <<REACTANT>>. A reaction node will be created once you release the mouse button.



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

To create a product species, use the **Reaction Tool** and drag from the reaction symbol to a point inside the compartment where your product species will be located. Once you release the mouse button, the product species will be created.





Continue adding components to your model and naming them until you have the following objects as described in the table below.

**NOTE:** you can't 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.

Name	Description	Location
RanC_nuc	Ran-Cargo Complex	Nucleus
	Flux Reaction Node	Nuclear Membrane
RanC_cyt	Ran-Cargo Complex	Cytoplasm
	Reaction Node	Cytoplasm
C-cyt	Cargo	Cytoplasm
Ran_cyt	Ran- GTPase	Cytoplasm

If you need to rename a component, select it, and on the **Object Properties** tab, use the component's name text field to supply the new name.

The screenshot shows a compartmental model diagram with compartments EC, PM, Cyt, NM, and Nuc. In the Cyt compartment, C\_cyt and Ran\_cyt are connected to a yellow node. This node is connected to a green node labeled 'RanC\_nuc' in the NM compartment. A red arrow points from the 'RanC\_nuc' node to the 'Object Properties' tab at the bottom. The 'Object Properties' tab is active, showing 'Species Name' as 'RanC\_nuc'.

The screenshot shows the same compartmental model diagram. In the NM compartment, a red node labeled 'flux0' is connected to the 'RanC\_nuc' node. A red arrow points from the 'flux0' node to the 'Object Properties' tab at the bottom. The 'Object Properties' tab is active, showing 'Reaction Name' as 'flux0'.

05

Reaction Name

Electrical Properties ☒ include molecular flux ☐ include electric current (into inside structure "undefined")

Reversible ☒ Kinetic Type

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$k_{fl} \cdot (RanC_{cyt} - RanC_{nuc})$	$\mu\text{M}\cdot\mu\text{m}\cdot\text{s}^{-1}$
I	inward current density	<input type="checkbox"/>	0.0	$\text{pA}\cdot\mu\text{m}^{-2}$
netValence	net charge valence	<input type="checkbox"/>	1.0	1
kfl	user defined	<input type="checkbox"/>	0.0	$\mu\text{m}\cdot\text{s}^{-1}$
RanC_cyt	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$
RanC_nuc	Species Concentration	<input checked="" type="checkbox"/>	Variable	$\mu\text{M}$

# Defining Reaction Kinetics

To define the reaction rate,  
select the **flux icon**, and in the  
**Object Properties** tab, double  
click the **Expression** column  
and type:  
**kfl \* (RanC\_cyt - RanC\_nuc).**

The screenshot displays a compartmental model diagram and its corresponding 'Object Properties' window. The diagram shows compartments Cyt (Cytosol) and Nuc (Nucleus) with species C\_cyt, RanC\_cyt, and RanC\_nuc. A reaction arrow labeled 'flux0' connects RanC\_cyt to RanC\_nuc. The 'Object Properties' window is open for 'flux0', showing the 'Expression' column with the formula '(kfl \* (RanC\_cyt - RanC\_nuc))'.

**Object Properties**

Reaction Name: flux0

Electrical Properties: ☒ include molecular flux ☐ include electric current (into inside structure "undefined")

Reversible: ☒ Kinetic Type: General Flux Density ( $\mu\text{M}\cdot\mu\text{m}/\text{s}$ )

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



With the flux icon still selected, on the **Object Properties** tab locate the defined parameter **K<sub>fl</sub>**. Double click and type **2.0** in the **Expression** column.

File Server Window Tools Help

BioModel2

Physiology

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

Reactions and Units

Way Comm Sabio

Geometries

Biological Models

- My BioModels (Arundeepp2001) (9)
- Shared BioModels (0)
- Public BioModels (539)
- Tutorials (8)
- Education (33)

Reaction Diagram

Reactions Structures Species Molecules Observables

PM Cyt NM Nuc

C<sub>cyt</sub> RanC<sub>cyt</sub> Flux0 RanC<sub>nuc</sub>

Delete Pathway Links Search

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

Reaction Name flux0

Electrical Properties ☒ include molecular flux ☐ include electric current (into inside structure "undefined")

Reversible ☒ Kinetic Type General Flux Density (μM-μm/s) Convert to [molecules.s<sup>-1</sup>]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$k_{fl} \cdot (RanC_{cyt} - RanC_{nuc})$	μM.μm.s <sup>-1</sup>
I	inward current density	<input type="checkbox"/>	0.0	pA.μm <sup>-2</sup>
netValence	net charge valence	<input type="checkbox"/>	1.0	1
k <sub>fl</sub>	user defined	<input checked="" type="checkbox"/>	2.0	μm.s <sup>-1</sup>
RanC <sub>cyt</sub>	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
RanC <sub>nuc</sub>	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

Linked Pathway Object(s):

To define the forward rate constant, Kf, select the reaction node. In the **Object Properties** tab, locate the **forward rate constant** parameter, double click the Expression column, and type in **1.0**.

File Server Window Tools Help

BioModel2

Physiology

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

Reaction Diagram

Reactions Structures Species Molecules Observables

PM Cyt NM Nuc

C<sub>cyt</sub> Ran<sub>cyt</sub> RanC<sub>cyt</sub> RanC<sub>nuc</sub>

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

Reaction Name: r0

Reversible: ☒ Kinetic Type: Mass Action [μM/s] (recommended for stochastic application) Convert to [molecules.s<sup>-1</sup>]

Name	Description	Global	Expression	Units
J	reaction rate	<input type="checkbox"/>	$(K_f \cdot \text{RanC}_{\text{cyt}} - K_r \cdot \text{Ran}_{\text{cyt}} \cdot \text{C}_{\text{cyt}})$	μM.s <sup>-1</sup>
Kf	forward rate constant	<input checked="" type="checkbox"/>	1.0	s <sup>-1</sup>
Kr	reverse rate constant	<input type="checkbox"/>	0.0	s <sup>-1</sup> .μM <sup>-1</sup>
RanC <sub>cyt</sub>	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
Ran <sub>cyt</sub>	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM
C <sub>cyt</sub>	Species Concentration	<input checked="" type="checkbox"/>	Variable	μM

Annotation and Pathway Links

Linked Pathway Object(s):

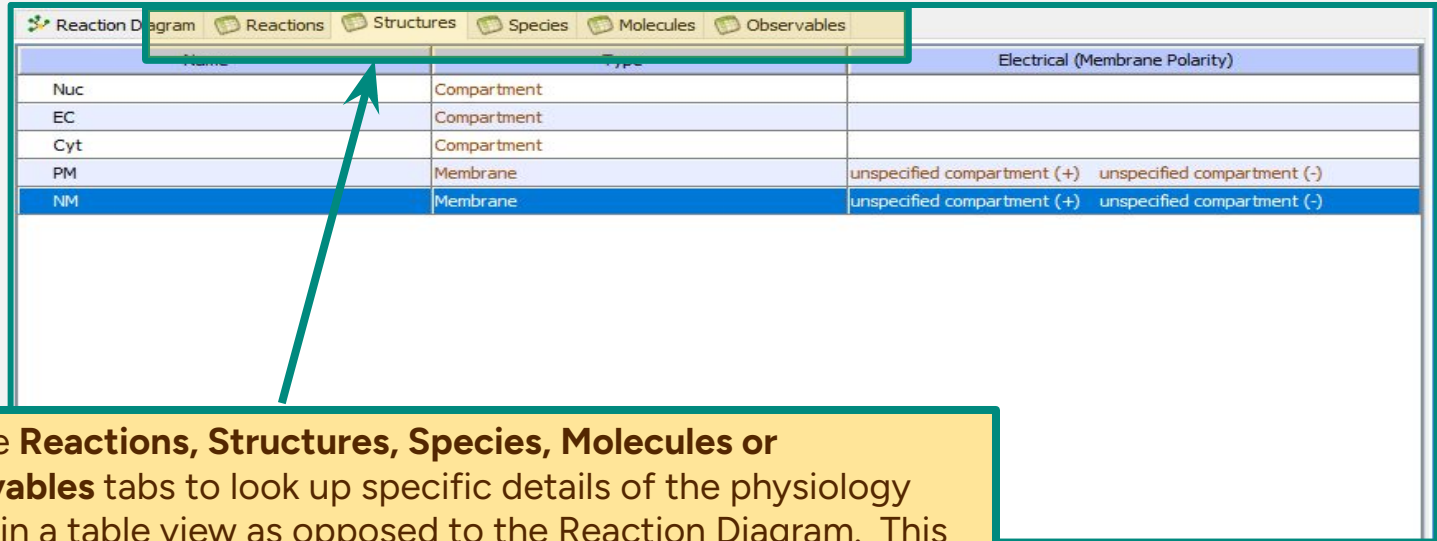
With the reaction node still selected, define the reverse rate constant, Kr. On the **Object Properties** tab, find Kr, double click the **Expression** column, and type in **1000.0**.

The screenshot displays the BioModel2 software interface. On the left, a tree view shows the project structure under 'BioModel2', with 'Physiology' expanded and 'Reaction Diagram' selected. The main workspace shows a reaction diagram with compartments PM, Cyt, NM, and Nuc. A reaction node 'r0' is highlighted in the Cyt compartment, with a teal box and arrow pointing to its 'Object Properties' tab.

The 'Object Properties' tab for reaction 'r0' is shown below. It includes fields for 'Reaction Name' (r0), 'Reversible' (checked), and 'Kinetic Type' (Mass Action [μM/s]). A table lists the reaction parameters:

Name	Description	Global	Expression	Units
Kf	forward rate constant	<input type="checkbox"/>	1.0	s <sup>-1</sup>
Kr	reverse rate constant	<input type="checkbox"/>	1000.0	s <sup>-1</sup> μM <sup>-1</sup>

The 'Expression' column for Kr is highlighted in blue. Below the table, the species 'C\_cyt' is listed with its concentration in μM. The 'Annotation and Pathway Links' section at the bottom is also visible.



Name	Type	Electrical (Membrane Polarity)	
Nuc	Compartment		
EC	Compartment		
Cyt	Compartment		
PM	Membrane	unspecified compartment (+)	unspecified compartment (-)
NM	Membrane	unspecified compartment (+)	unspecified compartment (-)

Use the **Reactions, Structures, Species, Molecules or Observables** tabs to look up specific details of the physiology shown in a table view as opposed to the Reaction Diagram. This is useful when working with large and complicated models.

**Tip:** If someone shares a model with you, click **Account-> Reconnect** to refresh your device's connection to the database.

# Acknowledgments

This tutorial was prepared by Sreekirthana Kolla (East Granby High School) and Justine Laureano (East Hartford High School) under the guidance of Dr. Michael L. Blinov, Associate Professor, Center for Cell Analysis and Modeling. The students were funded by the Department of Health Career Opportunity Programs; the Aetna Foundation; Connecticut State Legislative Fund; John and Valerie Rowe Health Professions Scholars Program; The Hartford; the University of Connecticut Foundation; the Friends of the Department of Health Career Opportunity Programs; and UConn Health.