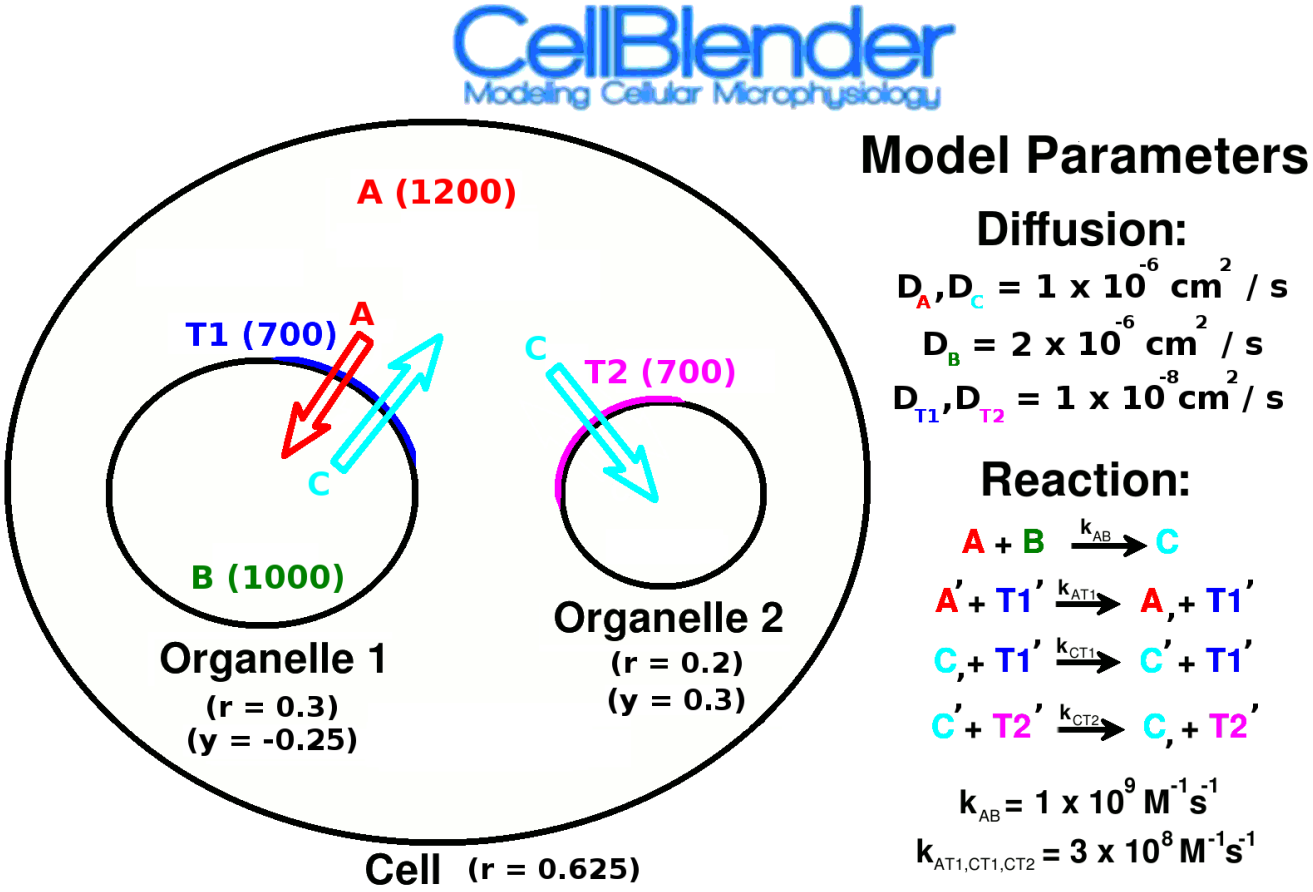
Organelle Model Tutorial

This tutorial builds a simple cell model consisting of a cell body, two internal organelles, and 5 species of molecules (two surface and 3 volume). The model is built up slowly and simulated at various points in the process to demonstrate particular biophysical principles and features of MCell and CellBlender.

This diagram gives an overall view of the final model and can be used to construct it without referring to the detailed instructions below.

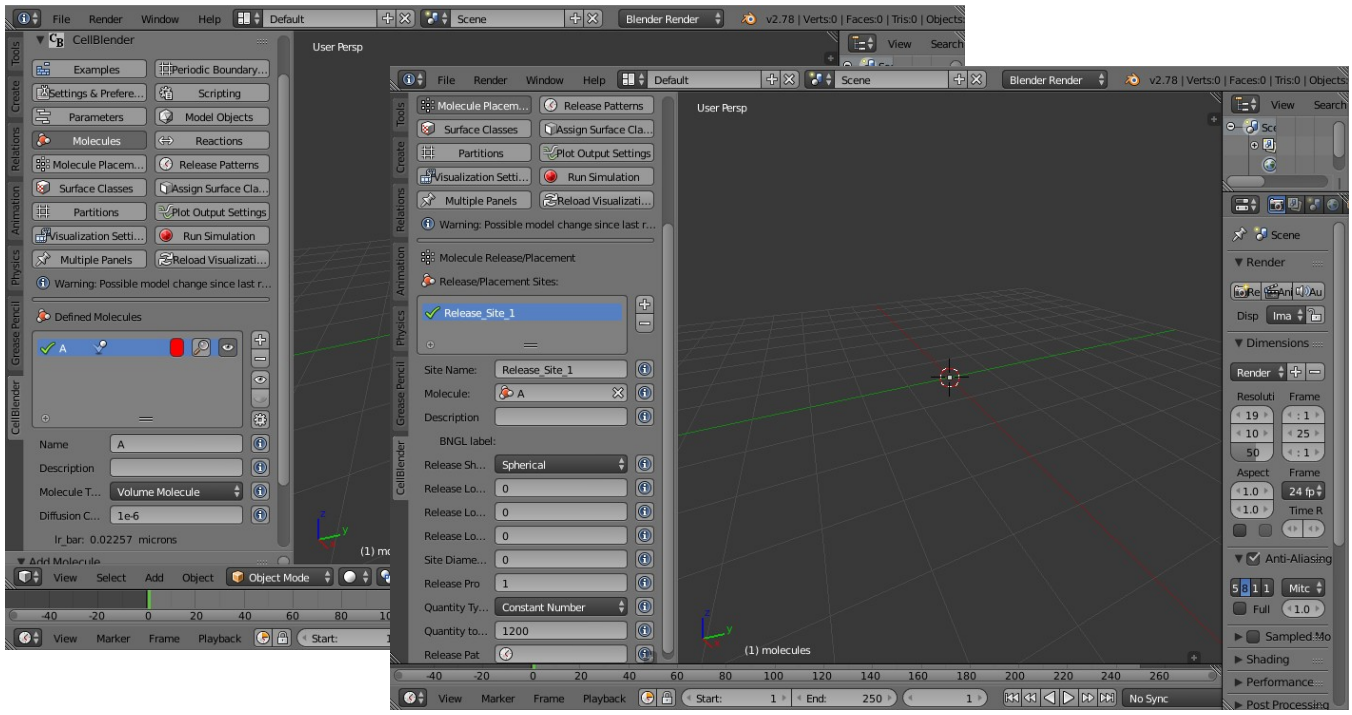


Detailed instructions

Begin with CellBlender initialized to an empty scene (no objects or molecules defined).

Open the “Molecules” panel, and click the “+” button to define a molecule species. Change the name to “A” (no quotes in the actual name), and set the diffusion constant to “1e-6”.

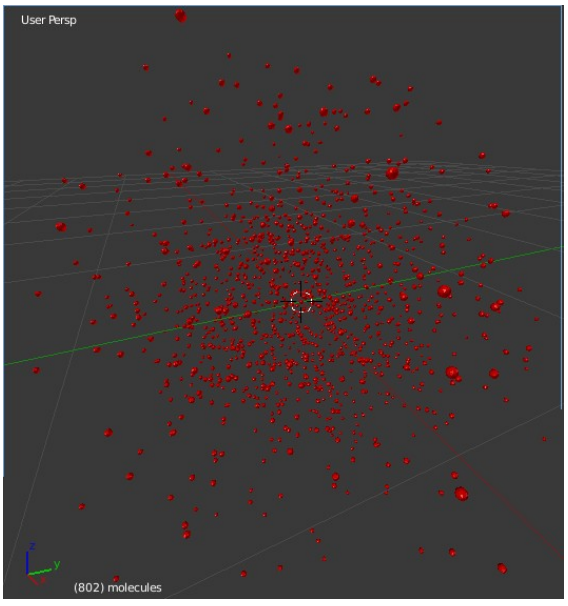
Open the “Molecule Placement” panel, and click the “+” button to define a molecule release/placement site. Click in the “Molecule” field (showing the molecule icon), and select the “A” molecule that was defined above. Set the “Quantity to Release” field to 1200.



Save the file from the top menu bar by clicking the “File” menu followed by the “Save as...” menu. This will bring up a file system navigation panel where you can change directory locations and create new folders. Find a place to store your project, and change the name from “untitled.blend” to something more appropriate (“organelle.blend” works fine). Then click the “Save as Blender File” button in the upper right corner.

Open the “Run Simulation” panel. Click the “Export & Run” button. You should see a “running man” icon and a process ID (PID) in the “Simulation Processes” box. Wait for the run to complete and show a green check mark (100% done).

Click the “Reload Visualization Data” button to show molecules, and press the “Play animation” button below the time line. As the animation is playing, you will want to zoom in with your mouse scroll wheel to get a better view of the molecules. Be sure to have the mouse in the 3D view window when scrolling (Blender is “hover sensistive”).

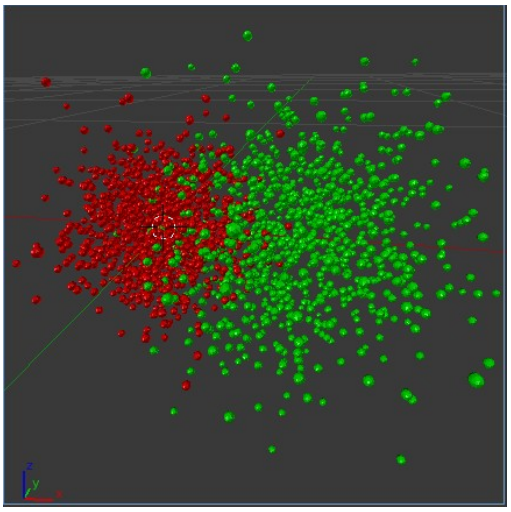


Click the pause button below the time line to stop the replay. You can click or click-and-drag in the time line to jump to any part of the simulation or scroll through it.

Blender has 2 primary viewing perspectives: Perspective and Orthographic. You can toggle between them with the “5” on the keypad (but not in the main keyboard) or with

the 3D view menu (View / View Persp/Ortho).

Define a second molecule species named “B” by clicking on the “Molecules” panel button. Click the “+” button to add a new species. Change its name to “B” and give it a diffusion constant of 2e-6 (a bit faster than the A molecules).



Release 1000 of these “B” molecules by opening the “Molecule Placement” panel. Click the “+” button to create a new release site. Select “B” in the “Molecule” field, and set “Quantity to Release” to 1000. In order to release at a different location, change the “Release Location X” field to 0.2.

Open the “Run Simulation” panel. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Scroll the time line to 0 and then step a few iterations to see the molecules released at different points. Play the simulation to observe that the “B” molecules are diffusing faster than the “A” molecules. Pause the animation when done viewing.

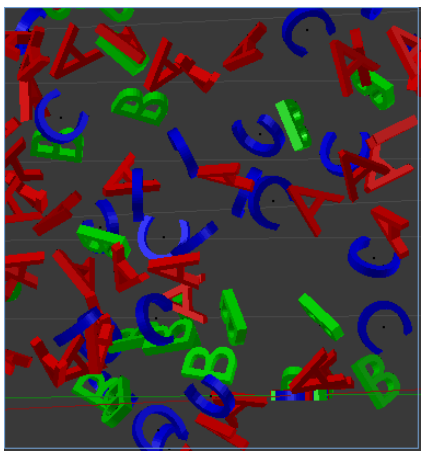
Define a third species named “C” by opening the “Molecules” panel and clicking the “+” button. Set the name to “C”, and set the diffusion constant to 1e-6.

Rather than releasing C molecules (as we have with A and B), we're going to define a reaction to create C molecules from A and B. The reaction will be “A + B → C”.

Open the Reactions panel and click the “+” button to define a new reaction. Click in the “Reactants” field and type “A + B” (without the quotes of course). Click in the “Products” field and type “C”. Click in the “Forward Rate” field, and type “1e9” to define the reaction rate.

Open the “Run Simulation” panel. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Scroll the time line to 0 and play the simulation to observe the creation of the blue “C” molecules where “A” and “B” react. Pause when done.

CellBlender can assign various visualization characteristics to different molecules to make them easier to see. These include color, size, glyph shape, and brightness.



Set the time line to a point near 500 iterations so you can see some of each molecule species. Open the “Molecules” panel again, and click on the “A” molecule. Below the “Diffusion Constant” field, you'll find a closed panel named “Display Options”. Click on it to open the closed panel. The “Shape” field will likely be defaulted to “Sphere_1”. Click on that button and choose “Cube”. All of the “A” molecules should appear as small cubes. For this model, let's use actual letters (“A”, “B”, “C”) for each molecule. Click on the same button (now showing “Cube”), and change it to “Letter”. The default letter will be “A” shown in the new selection below the “Letter” field. Next click on the “B” molecules in the “Defined Molecules”

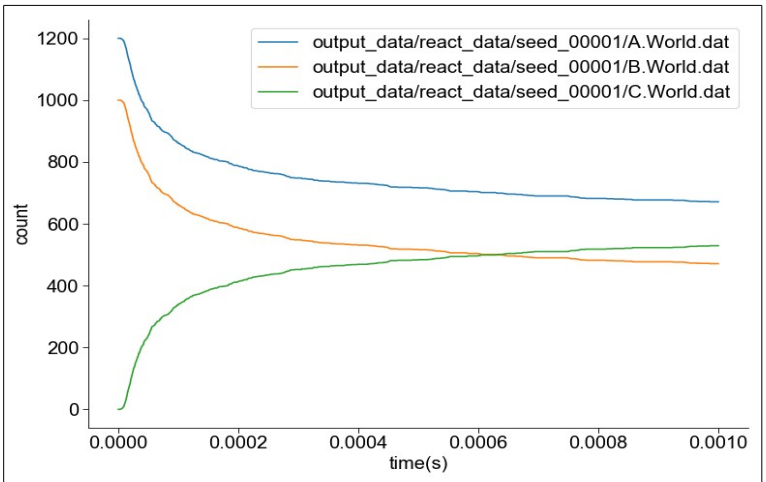
panel. Similarly click on its shape (“Sphere_1”) and change it to “Letter”. Click on the letter (“A”) and change it to “B”. Finally click on the “C” molecule in the “Defined Molecules” panel, and repeat the process to show a letter “C”.

The “C” molecules will play an important role in our model, so let's make it a brighter color (maybe “Cyan” for “C”). Click in the color patch (likely blue), and then click in the color chooser near the top (the light blue or “cyan” region). To make them even brighter, click the “Brightness” / “Emit” field and change the number to 2.0. That should make them very bright. Press the play button (below the time line) to watch the animation. Pause when done.

We would like to plot the number of molecules to observe the quantitative results of the reaction (A+B→C). Open the “Plot Output Settings” panel. Click the “+” button once to define a new plot item. Click in the “Molecule” field (shows a molecule icon), and select “A”. The plot item should show a green check mark and display “Count A in World”. Add a second plot item with the “+” button, and change its molecule to “B”. Add a third item (“+”) and change its molecule to “C”.

Open the “Run Simulation” panel. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. The molecules should be in the same locations (although their random orientation may differ).

Open the “Plot Output Settings” panel again. There are a number of display controls on that panel. For now, just change the “One Page, Multiple Plots” button to be “One Page, One Plot”. Then click the “Plot” button. Depending on the plotters installed in your system, you should see a plot that looks like the figure to the right. It shows the initial release of 1200 A molecules, 1000 B molecules, and 0 C molecules. There is a very short period where no reactions take place (because the molecules are released a small distance from each other. But as the molecules meet, they react and create C molecules. Leave the window open. Next, we will add a surface to enclose these molecules. That surface will become the “cell body” for our simulation.



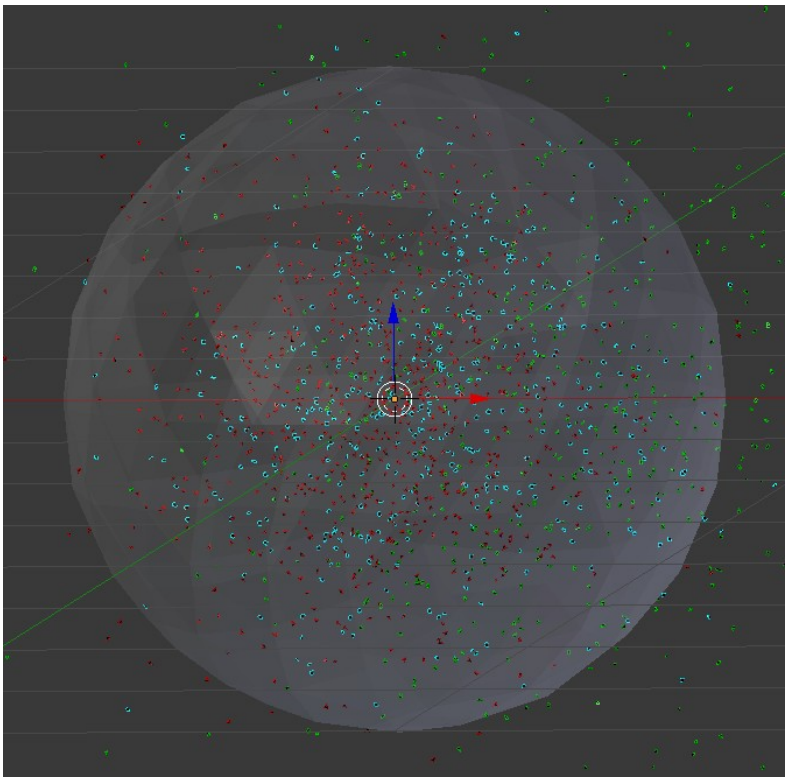
Plot output for: A+B → C (unbounded)

Return to the main Blender window and open the “Model Objects” panel. Click on the second button from the left (hovering over it will show it as “Snap the 3D Cursor to the Center”). Then click the 4th button from the left (hovering will show it as “Construct and Icosphere mesh”). Depending on your zoom, you will see a large object obscuring much of the 3D view window. Don't click on anything else yet because there are certain options that are only available in this state. Rather than clicking, just hover over the 3D view window and roll the scroll wheel so you can see the entire icosphere. Below the “Model Objects” panel, you will find a panel named “Add Ico Sphere”. Depending on your screen size, it may be only partly showing. Hover over the top border of that panel (just above the “Add Ico Sphere” text”) and the cursor should become a double headed arrow (up and down). That indicates that you can drag the dividing line between the two panels. Drag it (usually upward) so you can at least see the “Size” field and its default value (usually 1.0). Then click in the “Subdivisions” field and change the default value (usually 2) to 3. The icosphere should appear a bit smoother. Next click in the “Size”

field, and change the value to 0.625. The icosphere should shrink appropriately.

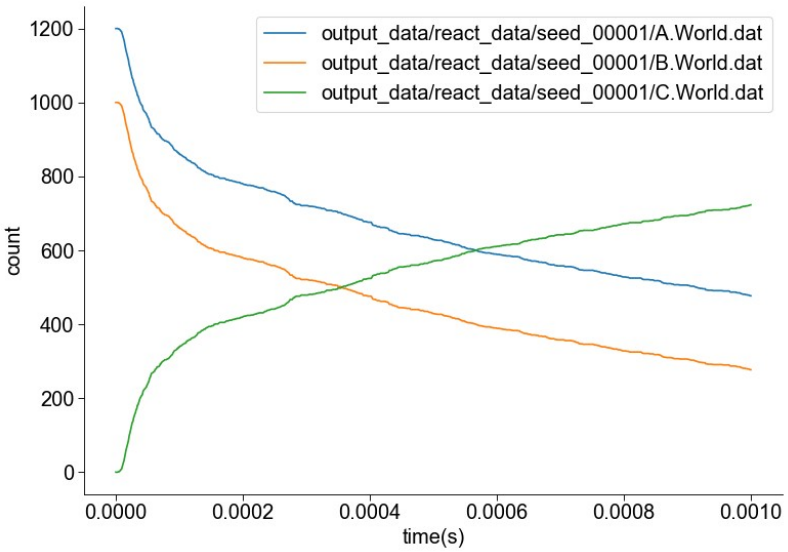
At this point, the Icosphere object exists in Blender … but not in CellBlender. Before importing it into CellBlender, click in the “Active Object” field (near the top of the “Model Objects” panel), and change the name from “Icosphere” to “cell”. It's best to set the proper names of objects before including them in a CellBlender model. Notice that the newly named “cell” object should still be surrounded with an orange outline. This means that it is the actively selected object. You'll also see its name “cell” in the lower left corner of the 3D view window. CellBlender will add the currently selected objects when the “+” button is clicked in the “Model Objects” panel. Since the “cell” is currently selected, click the “+” button and its name and characteristics should appear in the model objects panel.

Now click the “+” button in the “Model Objects” panel. Depending on your screen size, it may be helpful to drag the border (just above the “Model Objects Include” line) down to show more of the upper panel. Click the “cell Object Options” line to show some of the options for this new object. A number of controls should appear. Click the “Add a Material” button. The default material is white and opaque. To make it semi-transparent, click both the “Object Transparent” and the “Material Transparent” check boxes. When they are both checked, an “Alpha” control will appear. Click on the “Alpha” control and change the number to 0.1. The sphere should become semi-transparent. If you play the animation, you'll notice that the molecules go right through the sphere. That's because the simulation hasn't been run since we added the sphere.



Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Now all of the molecules should be inside the sphere. Play the simulation again and watch it run a few times. Pause when done.

Open the “Plot Output Settings” panel again, and click the “Plot” button. The plot should be similar (A and B decreasing, and C increasing), but the rates will be different. In particular, more C molecules will be produced because the A and B molecules have been confined to remain in closer proximity to each other.



Our original simulations were done without any objects present. So molecules could only be released at coordinates without

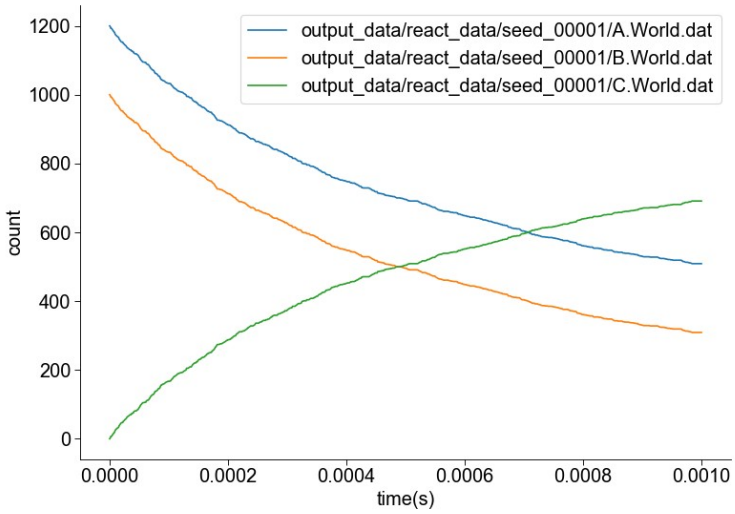
reference to any objects. But now that we've defined a cell, we can release our molecules uniformly inside that structure.

Open the “Molecule Placement” panel again. There should be 2 release sites (typically named “Release_Site_1” and “Release_Site_2”). Click on the first release site. Observe that it is releasing molecule “A” in a “Spherical” Release Shape at (0,0,0). Change the “Spherical” selector to show “Object/Region”. The release site will show an error (“Object name error”) because releasing in an object requires an object name. Click in the “Object/Region” field and type “cell” (without the quotes of course) followed with the Enter key. The error message should be replaced with a green check mark indicating that the name “cell” is a recognized object. Repeat for Release_Site_2 (select it, change “Spherical” to “Object/Region”, and enter the name “cell”).

Before running, set the time line near 10 (drag to left or use the “VCR” controls). Note that the molecules are clustered near their initial release points.

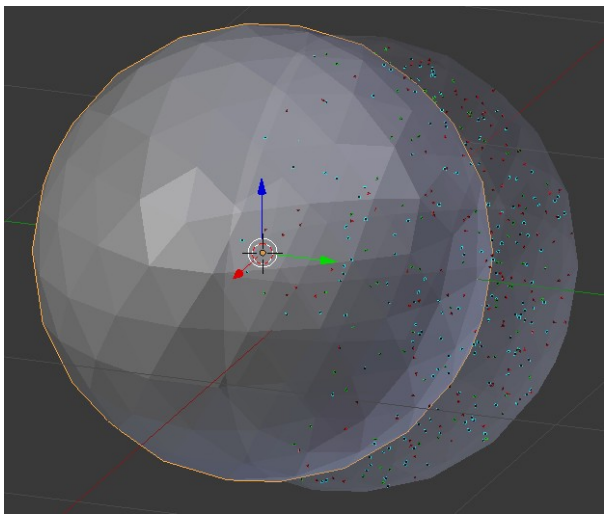
Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Now the molecules will be uniformly distributed throughout the sphere from the very first iteration. This is the effect of releasing within (or sometimes “on”) an object.

Open the “Plot Output Settings” panel again, and click the “Plot” button. Observe the differences from the previous plots. First, there is no “flat” section of the curve. The molecules start out well mixed, so there's no initial travel time before they can react. Also notice that the curves are smooth and approximate the theoretical results for well-mixed reactions.



The next steps will add the two organelles from the original diagram (above). The process will be similar to the one we used to add the original “cell” object. But we will use the 3D cursor to determine the initial locations of our objects BEFORE we create them.

Open the “Model Objects” panel again. Click the far left button near the top of the Model Objects panel (hovering over it shows “Show/Hide 3D Cursor Location”). That will show the location of the 3D Cursor. It should be (0.0 0.0 0.0). If not, then click the second button to center the cursor. Then click in the “Y” field and set the “Y” location to “-0.25”. You should see the 3D cursor (alternating red and white ring) move in the negative “y” direction. The 3D cursor has many uses, and one of them is to define the default location for newly created objects. We want our first organelle to be at (0,-.25,0) so that's where we've set the 3D Cursor.

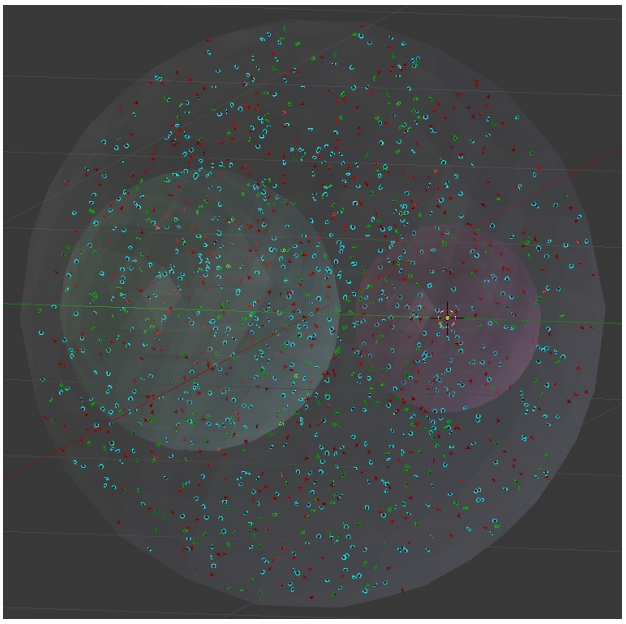


Create the actual object by clicking the “Construct an Icosphere mesh” button (4th from the left). The new

object will be the same size as the last one created (Blender remembers the last settings). The “Add Ico Sphere” panel will be directly below the “Model Objects” panel, and you may again need to drag it upward to see the settings for “Subdivisions” and “Size”. The “Subdivisions” should still be 3, but the “Size” will likely still be 0.625. Change the “Size” to 0.3 (note that for Icospheres, the “Size” is the radius and not the diameter). This should place the new icosphere fully within the outer cell.

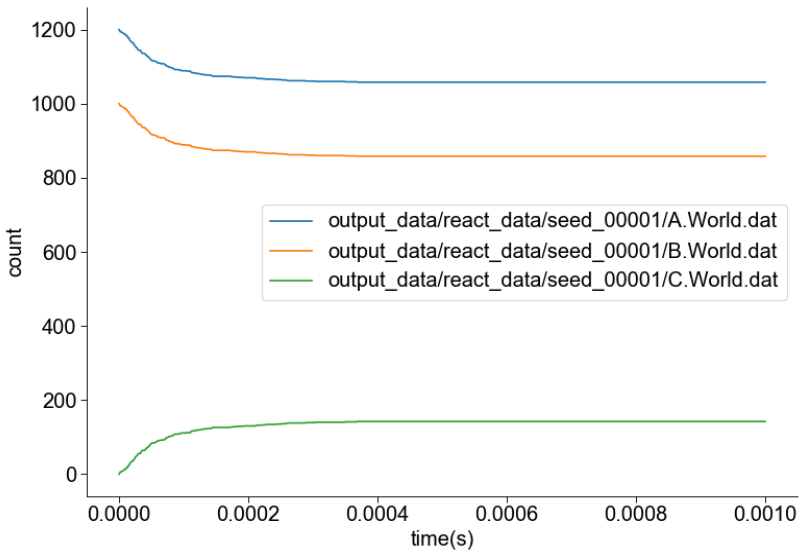
Before adding the new Icosphere to the CellBlender model, rename it to “organelle_1” by clicking in the “Active Object” box that should currently show “Icosphere”. Type the name “organelle_1” which should also show up in the lower left corner of the 3D view window.

Now it's time to add the new object to the CellBlender model. Remember that Blender objects are NOT part of a CellBlender model until they've been added. In the “Model Objects” panel, click the “+” button to add the new organelle_1 to the object list. The default color wheel is displayed when an object doesn't actually have a material (it shows as default gray). Click that button once and the material should turn white. Click again to bring up the color chooser and choose a light pastel color near the center (maybe a very light green). The panel below the object list should show “organelle_1 Object Options”. As before, check the “Object Transparent” and “Material Transparent” boxes and set the “Alpha” field to 0.2.



Let's repeat this process for organelle_2 with a radius of 0.2 and a center at y=0.3. Briefly, set the cursor values to (0, 0.3, 0). Note that the 3D cursor has moved. Click the Icosphere button to add the object at that location. Change the “Size” field from 0.3 (previous value) to 0.2 (new value). The “Subdivisions” should still be 3. Change the name from default of “Icosphere” to “organelle_2”. Click “+” to add the Blender object to the CellBlender model. Click the material (color wheel) and select a light pastel (maybe a light red). Set both the Object and Material to be transparent with an “Alpha” of 0.2.
Now we can begin to place our molecules in separate compartments within the model. We can do this by changing the molecule placement settings.

Open the “Molecule Placement” panel and click on the second release site (“Release_Site_2”). That shows releasing of molecule “B” inside Object/Region of “cell”. Change the “Object/Region” from “cell” to “organelle_1”. Then open the “Run Simulation” panel and click “Export & Run”. Wait for the simulation to complete and then click “Reload Visualization Data”. Play the animation again and note the high concentration of “B” molecules inside “organelle_1” and none anywhere else.



Open the “Plot Output Settings” panel and click the “Plot” button.

Notice the very different behavior of the system. What's happening?

When MCell releases molecules within an object, the molecules are released uniformly throughout the entire interior of that object – *including the interiors of any enclosed objects*. Since the “A” molecules were released inside the entire “cell”, that means that some percentage of them were also released within both organelles. But ALL of the “B” molecules were released inside “organelle_1”. So the large number of “B” molecules inside “organelle_1” were able to react with the much smaller number of “A” molecules inside “organelle_1” until all of those “A” molecules were exhausted. At that point, no further reactions could take place and the graphs reflect that result.

Rather than releasing the “A” molecules throughout the entire “cell”, we want to release them only in the parts of the “cell” that are outside of “organelle_1” and “organelle_2”. We can do that with MCell's solid geometry operations. Specifically, we can subtract the volumes of the organelles from the volume of the cell in the release specification.

Open the “Molecule Placement” panel, and click on the first release site (“Release_Site_1”). That should be releasing “A” molecules inside of Object/Region “cell”. Change the “cell” field to be:

“cell[ALL] – organelle_1[ALL] – organelle_2[ALL]”

The “ALL” value is an MCell keyword specifying the entire object. Be careful if cutting and pasting from this document because the “minus” signs in this document may not be the normal ASCII “minus” sign. If you get an error, re-type the minus signs (and possibly the entire expression) by hand.

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Notice that there are no “C” molecules at all. The “A” molecules remain outside of both organelles, and the “B” molecules remain stuck inside “organelle_1”. A plot would show no change in the counts of any species because there are no reactions.

The next step will be the creation of a transporter to bring “A” molecules from the outside of organelle_1 to the inside of organelle_1 where they can react with the “B” molecules to create “C” molecules inside organelle_1. These transporter molecules (“T1”) will be placed on the surface of organelle_1.

Open the “Molecules” panel and click the “+” button to create a new species. Change the name to “T1”. Change the “Molecule Type” from “Volume Molecule” to “Surface Molecule”. Note that the symbol for surface molecules is different from the symbol for volume molecules in the “Defined Molecules” panel. Set the “Diffusion Constant” to “1e-8”. Change the “Shape” to “Receptor”, and change its color to a dark blue.

Open the “Molecule Placement” panel, and click “+” to add another release site. Select molecule “T1” and note that the “Release Shape” automatically becomes “Object/Region”. This is because surface molecules must be released on a surface. Set the “Object/Region” field to “organelle_1”, and change the “Quantity to Release” field to “700”.

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Notice the dark blue “T1” transporters on the surface of organelle_1. Rewind and play the animation to see that they are moving fairly slowly

(diffusion constant of 1e-8) on the surface. Zoom in to see that they're all oriented in the same direction relative to the surface. This is the default release behavior. Note that nothing else has changed because we haven't defined a transport reaction yet. Pause the animation.

Open the Reactions panel and click the “+” button to define a new reaction. Click in the “Reactants” field and type:

A' + T1'

(with the single quotes). This says that the reactants are “A” volume molecules approaching from the “top side” and reacting with the “top side” of the “T1” surface molecules. Click in the “Products” field and type:

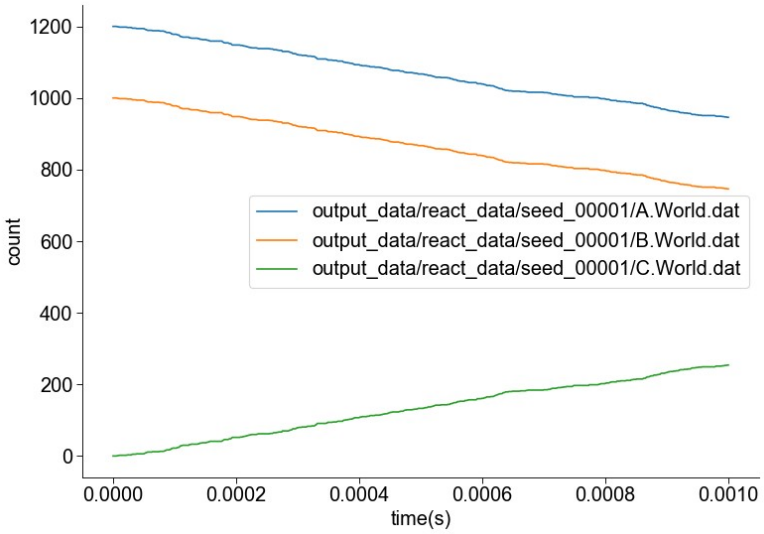
A, + T1'

(again with the single quotes). Click in the “Forward Rate” field, and type “3e8” to define the reaction rate. Notice that the entire reaction shows up in the list as:

A' + T1' → A, + T1'

The only thing different between the left and right sides is the change of the single quote (often called a “tick”) to a comma on the “A” molecule. This indicates (in this case) that the “A” molecule is transported from the top to the bottom side of T1 (i.e. across the membrane from the outside to the inside).

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Notice that the animation starts out with no “C” molecules, but that they are created inside of organelle_1 as the “A” molecules are transported inside to react with the “B” molecules.



Open the “Plot Output Settings” panel and click the “Plot” button. The rate of reactions is now limited by the transport process.
Now we're going to write a reaction to transport the “C” molecules from inside the organelle to outside the organelle. We'll used similar tick marks and commas to express the sides of the surface.

Open the Reactions panel and click the “+” button to define another new reaction. Click in the “Reactants” field and type “ C, + T1' ” (with the single quotes, but without the double quotes). Click in the “Products” field and type “ C' + T1' ” (again with the single quotes, but without the double quotes). Click in the “Forward Rate” field, and again type “3e8” to define the reaction rate. Notice that the entire reaction shows up in the list as:

C, + T1' → C' + T1'

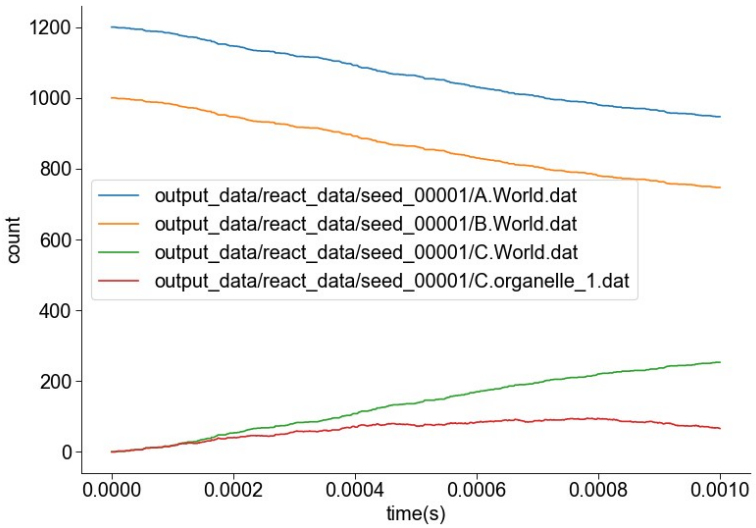
The only thing different between the left and right sides is the change of the comma (on “C”) to a single quote (“tick”) on “C”. This indicates (in this case) that the “C” molecule is moved from the inside to the outside.

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. Notice again that there are no “C” molecules at the start of the simulation. But as “A” molecules are transported inside “organelle_1”, they can react with the “B” molecules inside “organelle_1” to produce “C” molecules. The new transport reaction then uses the same “T1” transporters to move the “C” molecules back out of the organelle.

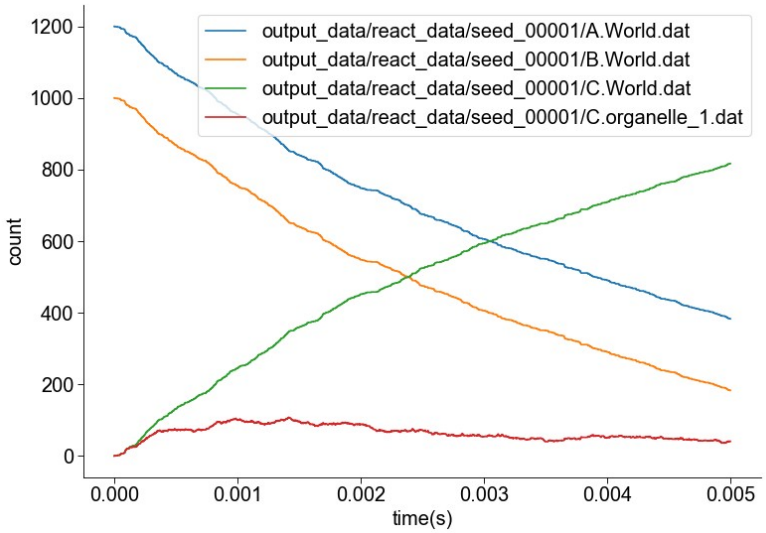
The plots of this simulation would be the same as the previous since we've only moved the “C” molecules without changing their overall population in the entire simulation. We can, however, count just the number of “C” molecules in “organelle_1” to get a better understanding of the dynamics.

Open the “Plot Output Settings” panel and click the “+” button to create a new plot item. Choose the “C” molecule, but this time select “Object” directly below the “Molecule” field. This will bring up an object selector. Choose “organelle_1” for the “Object” field.

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete. There's no need to reload the visualization data since we haven't changed the simulation. But we have added a new plot item. Open the “Plot Output Settings” panel and click the “Plot” button to see the plot. The count of “C” molecules in “organelle_1” starts out at zero, but grows as more “A” molecules enter to react with “B” molecules. Over time, this levels out.



We're starting to get to the point where we want to see more simulation time. But more time will take longer, so this is a good time to add “partitions” to the model. Partitions provide a way of making simulations more efficient by subdividing the work. Open the “Partitions” panel and click the “Include Partitions” button. This will set up the default partitioning from -1 to 1 in all dimensions. We can make this more efficient by clicking the “Automatically Generate Boundaries” button. You'll notice that the ranges of the partition will be set to include the geometry in the model (in this case -0.625 to 0.625).



Open the “Run Simulation” panel again. But change the “Iterations” from “1000” to “5000”. Click the “Export & Run” button. Wait for the simulation to

complete and then click the “Reload Visualization Data” button. You'll notice that the time line (which previously ran from 0 to 1000) now runs from 0 to 5000. As you scroll further to the right, you'll notice lots of “C” molecules being transported out of “organelle_1” into the cell's interior. Open the “Plot Output Settings” panel and click the “Plot” button to see the plot. The count of “C” molecules in the world continues to rise. But the count of C molecules in “organelle_1” does indeed seem to be limited as the “C” molecules are transpoted (one way) out of “organelle_1”. Eventually, the supply of “A” and “B” molecules is depleted and the production of “C” molecules in organelle_1 drops off.

Now we're going to turn our attention to “organelle_2”. Our plan is to simulate sequestering of “C” molecules into “organelle_2”. We could actually use the same “T1” transporters turned upside down (known as “Top Back”) which will cause them to transport “C” molecules from outside to inside. Since there are no “A” molecules inside organelle_2, that part of the “T1” functionality wouldn't come into play. However, that would be a bad design if we didn't intend for that pathway to exist. Future changes to the model might end up bringing “A” molecules into “organelle_2” by some other means, and then our “T1” transporters would be bringing them back out. The better design calls for a new transporter that we'll call “T2” to bring “C” molecules into “organelle_2”.

Open the “Molecules” panel and click the “+” button to create a new species. Change the name to “T2”. Change the “Molecule Type” from “Volume Molecule” to “Surface Molecule”. Again, note the different symbols for volume and surface molecules in the list. Set the “Diffusion Constant” to “1e-8”. Change the “Shape” to “Cone”, and change its color to a dark red..

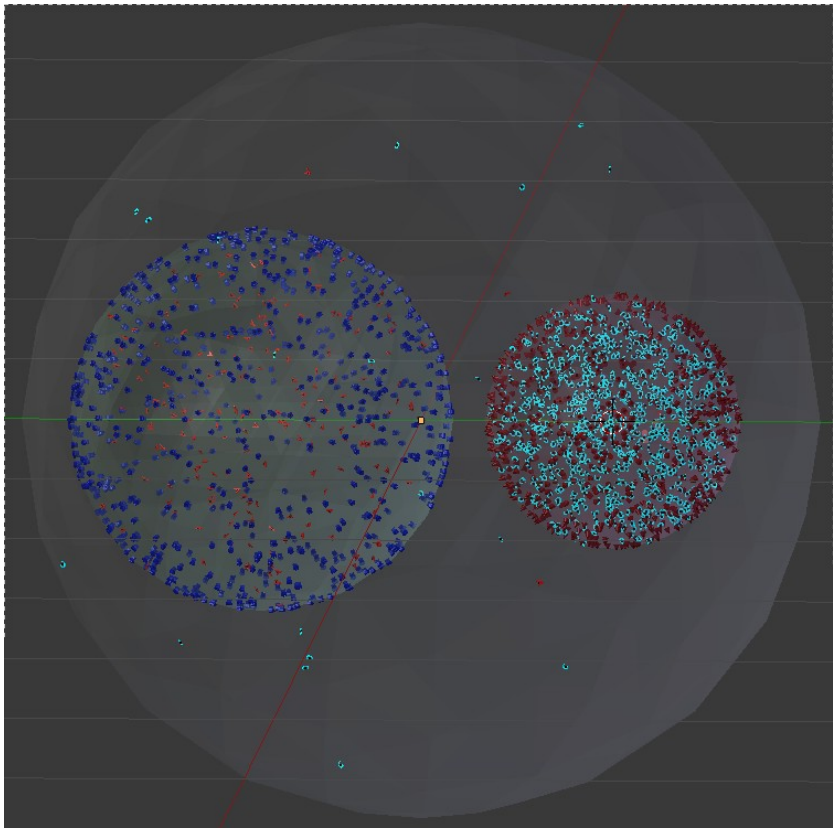
Open the “Molecule Placement” panel, and click “+” to add another release site. Select molecule “T2” and the “Release Shape” automatically becomes “Object/Region”. Set the “Object/Region” field to “organelle_2”, and change the “Quantity to Release” field to “700”.

Open the “Run Simulation” panel again. Click the “Export & Run” button. Wait for the simulation to complete and then click the “Reload Visualization Data” button. You should see some dark red cones on the outside of “organelle_2”. They don't have any function yet, so the rest of the simulation will be the same.

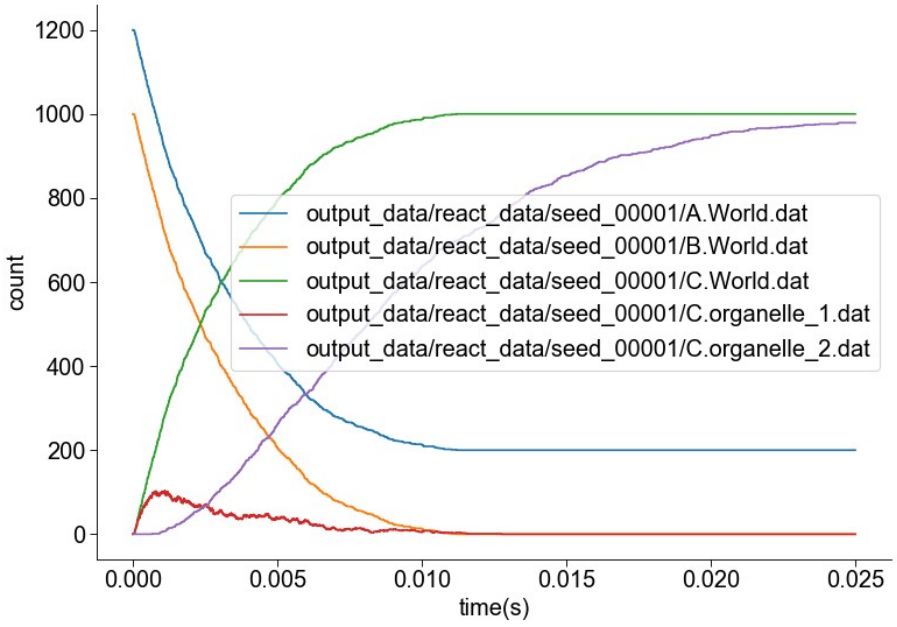
Now it's time for the final reaction. Our new “T2” transporters need to bring “C” molecules from the outside to the inside. Open the “Reactions” panel and click “+” to add a new reaction. Set the “Reactants” to “ C' + T2' ” and set the “Products” to “ C, + T2' ”. The only thing changing from the reactants to the products is the change of “C'” to “C,”. This moves “C” molecules from the outside of “organelle_2” to the inside of “organelle_2”. Set the “Forward Rate” to 3e8.

Before running, let's add a plot item to count the “C” molecules in “organelle_2”. Open the “Plot Output Settings” panel and click the “+” button to create a new plot item. Choose the “C” molecule, and again select “Object” directly below the “Molecule” field. This will bring up an object selector. Choose “organelle_2” for the “Object” field this time. The plot line should read “Count C in/on organelle_2”.

As the sequence of reactions grows, we will need to simulate for longer periods to see all of the effects. For this model, open the “Run Simulation” panel and change the “Iterations” field from 5,000 to 25,000. Click the “Export & Run” button. Wait for the simulation to complete (it will take quite a bit longer) and then click the “Reload Visualization Data” button. The time line will now show the new range from 0 to 25,000. Click in the time line out near 25,000 to see the final accumulation of “C” in organelle_2. At this point all of the “B” molecules have been consumed in the production of “C” molecules. There are about 200 excess “A” molecules remaining because we started with 1200 of “A” and only 1000 of “B”. Most of these excess “A” molecules end up trapped in “organelle_1” with no means to exit. Nearly all of the “C” molecules (979 out of 1000) end up inside “organelle_2” as planned.

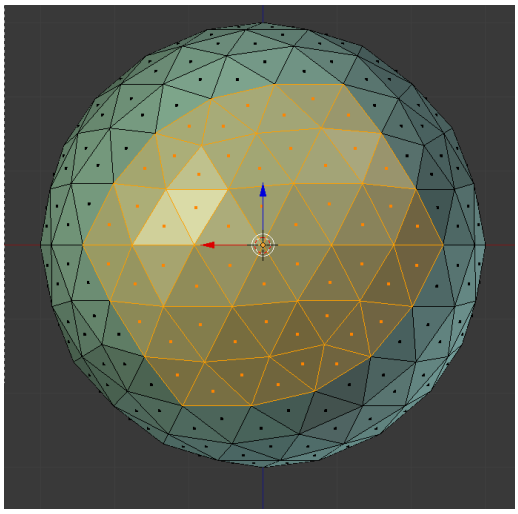


The plot at this point shows the constant difference of 200 between “A” and “B”. It shows the rapidly increasing production of “C” inside “organelle_1” when “B” molecules are plentiful followed by a gradual decline until the “B” molecules are exhausted. It shows the total growth of “C” and the delayed accumulation of C inside “organelle_2”.



Up to this point, all of our surface molecule releases have involved entire objects. MCell and CellBlender also support releasing surface molecules on “Regions” of an object. Regions are created by tagging certain faces of an object with a region label. Attributes (known as “Surface Classes”) can then be associated with these tagged regions. Creating surface regions can be difficult to describe, and it benefits from a number of Blender manipulation techniques (rotating, zooming, and hiding) that are difficult to describe in a tutorial. The following instructions won't attempt to describe all of those manipulations in detail, but will provide all of the steps with the assumption that the manipulations are done properly.

Start with “organelle_1” by hiding all other objects and molecules. View from the positive “y” axis (“View Back”). Select “organelle_1” and enter “Edit” mode and then “Face Select” mode. Unselect all faces, and only select a subset of those facing the positive “y” axis (toward “organelle_2”).



Open the “Model Objects” panel, and select “organelle_1” from the list. Click the “+” button down below in the “Defined Surface Regions for organelle_1” subpanel. Name the region any appropriate name (“toward_2” in this case). Click the “Assign” button to assign all of the selected faces to the “toward_2” region. Return to “Object Mode” and show hidden objects (Alt-H).

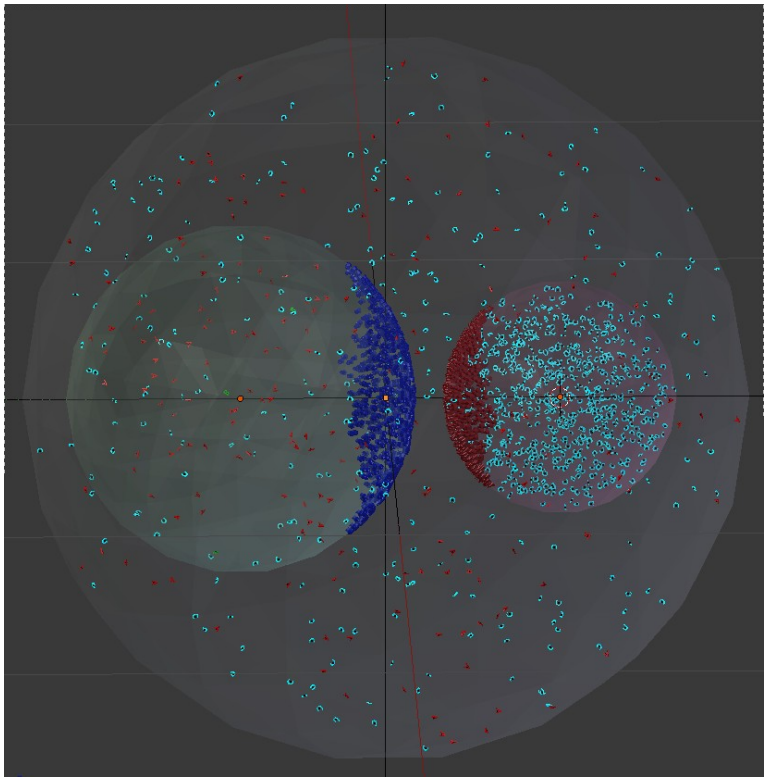
Repeat the procedure for “organelle_2” by hiding all other objects and molecules. View from the negative “y” axis (“View Front”). Select “organelle_2” and enter “Edit” mode and then “Face Select” mode. Unselect all faces, and only select a subset of those facing the negative “y” axis (toward “organelle_1”).

Open the “Model Objects” panel, and select “organelle_2” from the list. Click the “+” button down below in the “Defined Surface Regions for organelle_2” subpanel. Name the region any appropriate name (“toward_1” in this case). Click the “Assign” button to assign all of the selected faces to the “toward_1” region. Return to “Object Mode” and show hidden objects (Alt-H).

Open the “Molecule Release” panel and change the release site for “T1” from “organelle_1” to “organelle_1[toward_2]”. Similarly change the release site for “T2” from “organelle_2” to “organelle_2[toward_1]”.

In order to keep the surface molecules within the desired regions, we could slow down their diffusion rates via their diffusion constants (even setting them to zero). A better method involves the use of “Surface Classes”. Open the “Surface Classes” panel, and click the “+” to add a new surface class. Name the class “reflect_surf_mols”. Add a “Property” to this class by clicking the “+” button by the “reflect_surf_mols Properties” subpanel. Set the “Molecules” field to “All Surface Molecules”. Set the “Orientation” field to “Ignore”. Set the “Type” field to “Reflective”. This defines a surface class that will reflect all molecules that reach its borders.

Open the “Assign Surface Classes” panel, and click the “+” button to make the first assignment. Choose the “Surface Class Name” of “reflect_surf_mols”. Choose the object “Organelle_1”. Select a “Specified Region” and choose “toward_2”. Click the “+” button again to make the second assignment. Choose the “Surface Class Name” of “reflect_surf_mols”. Choose the object “Organelle_2”. Select a “Specified Region” and choose “toward_1”.
Open the “Run Simulation” panel again, and click the “Export & Run” button. Wait for the simulation to complete (it might take a few minutes) and then click the “Reload Visualization Data” button. You will get a similar result (shown here at 15,000 iterations):



You can plot the results and compare them to the earlier plots without regions: