Blender Molecular Visualization Tutorial V

CELLmicrocosmos Cell Modeling Project WS2013-14,
Björn Sommer, Bielefeld University, in part based on ePMV Tutorials.
Version 14.01.2014

Forum:
http://www.cellvisualization.org

Direct link to this forum entry:
http://www.cellmicrocosmos.org/Cmforum/viewtopic.php?f=21&t=737

Actual Version of Blender:
http://www.blender.org

Here, Blender 2.67b is used.

CELLmicrocosmos 1.1 CellExplorer/4.2 PathwayIntegration
http://cm4.cellmicrocosmos.org

Target

This tutorial describes how to work with the CellExplorer and how to import a cell model generated with the CellExplorer into Blender.

Abbreviation

RMB	Right Mouse Button
LMB	Left Mouse Button

CellExplorer

First make sure that you have installed the latest version of Java on your PC.

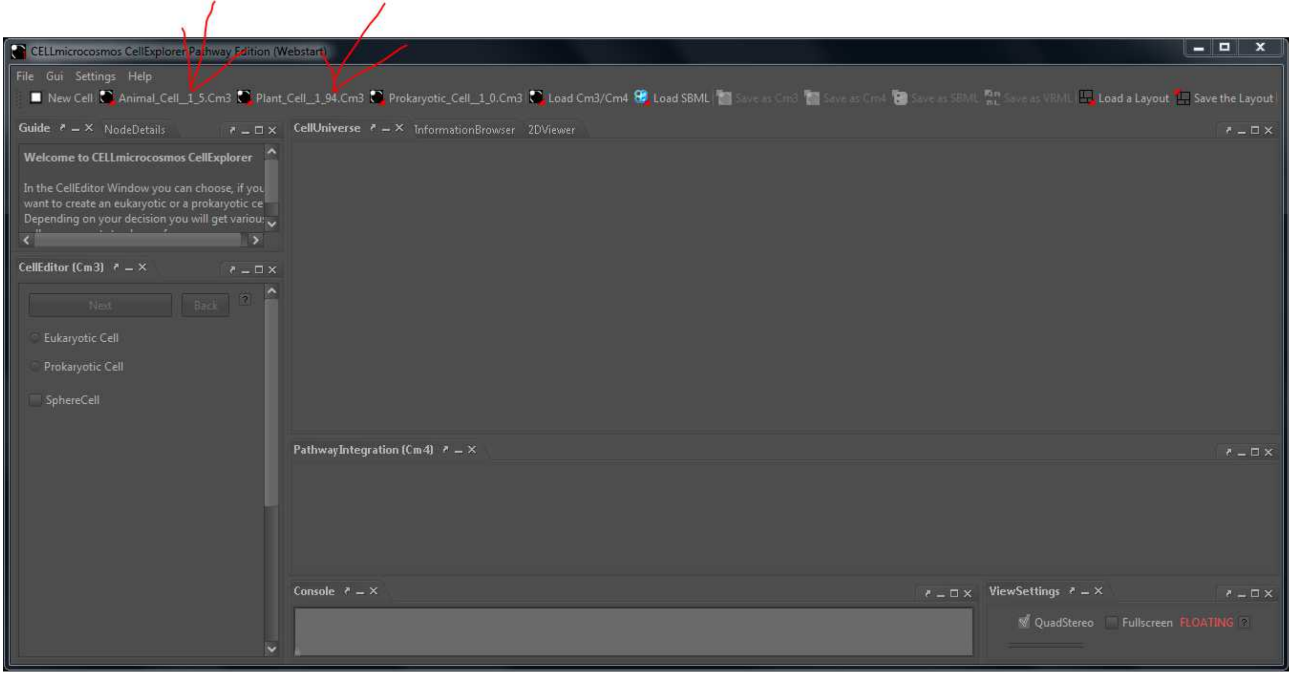
http://java.com

If you are using a 64 bit PC, make sure that you are also installing the 64 bit version of Java providing a much better performance than Java 32 bit! If you are using a Linux system, also the Open Java projects should work with the MembraneEditor, so you do not need the original Sun/Oracle Java.

Then, download and start the CellExplorer (incl. PathwayIntegration) from this website:

http://Cm4.CELLmicrocosmos.org/

After the program is started you should see something like this:

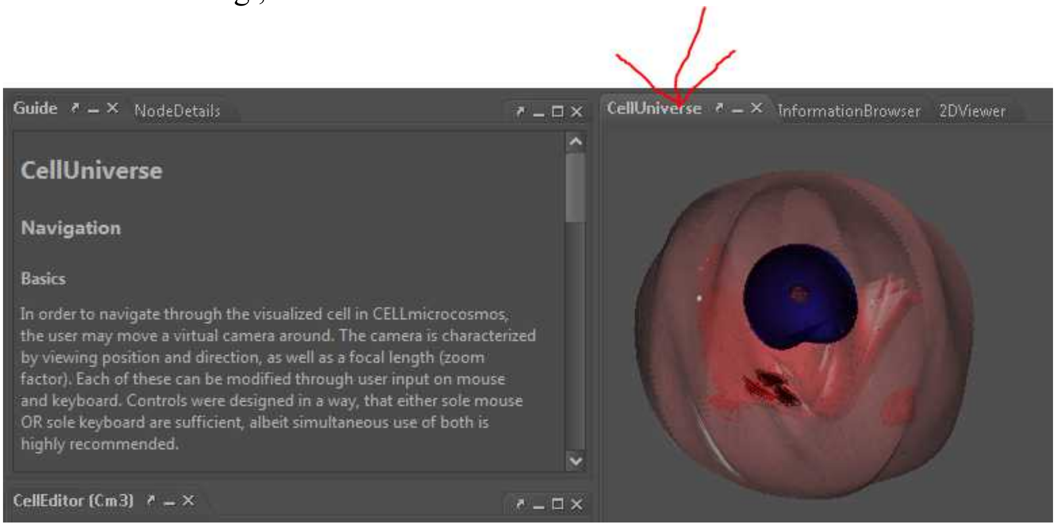


Welcome to CELLmicrocosmos CellExplorer

In the CellEditor Window you can choose, if you want to create an eukaryotic or a prokaryotic ce
Depending on your decision you will get variou

Click on the first file on the left side and the animal cell is loaded.

To get now information according the navigation etc., just click on the window for which you want to get more information. E.g., click on the Title "CellUniverse" at this



CellUniverse

Navigation

Basics

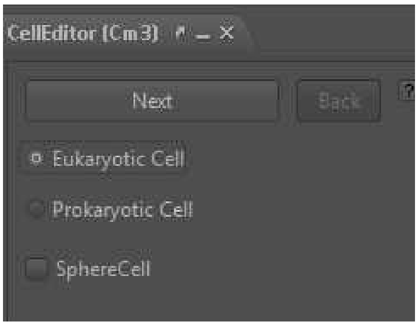
In order to navigate through the visualized cell in CELLmicrocosmos, the user may move a virtual camera around. The camera is characterized by viewing position and direction, as well as a focal length (zoom factor). Each of these can be modified through user input on mouse and keyboard. Controls were designed in a way, that either sole mouse OR sole keyboard are sufficient, albeit simultaneous use of both is highly recommended.

and have a look to the Guide showing all information about how to navigate through the CellUniverse.

You can also load the plant cell and navigate through this cell.

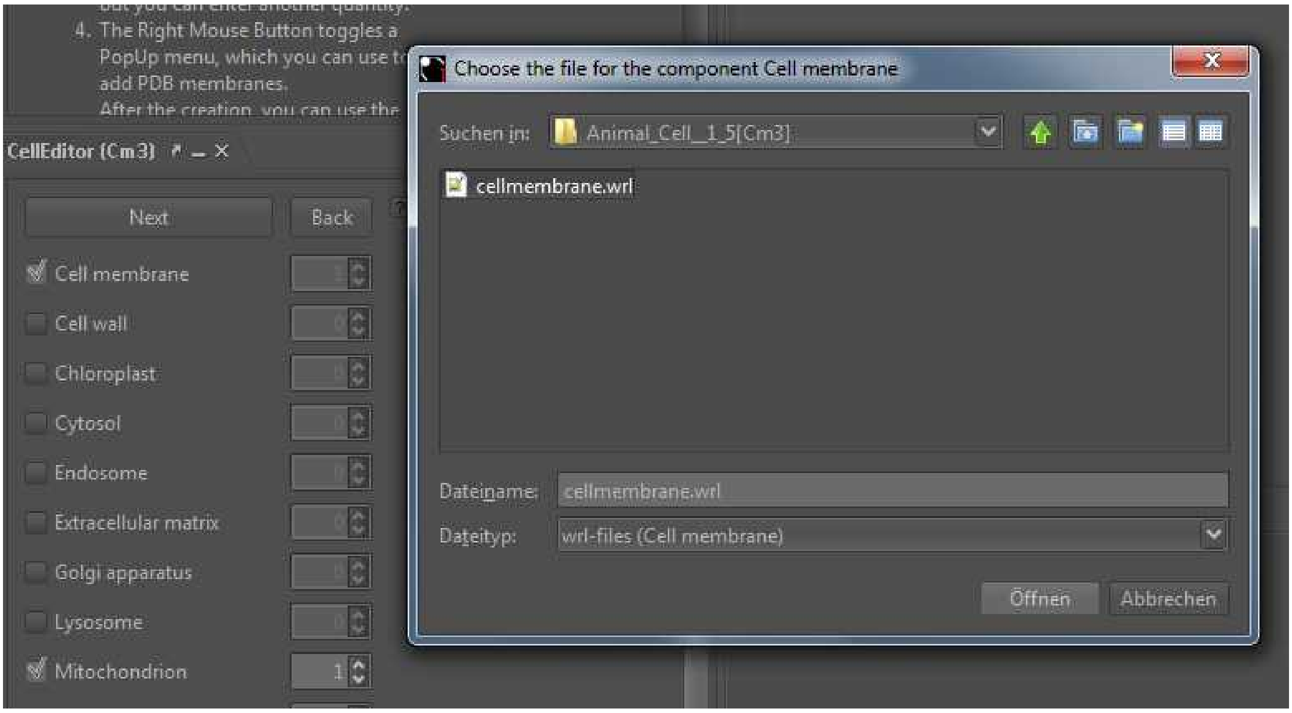
Now, click on the button ☐ New Cell. Click on the title “CellEditor” and read how to create a new cell.

Select “Eukaryotic Cell” and click “Next”:



● Eukaryotic Cell
○ Prokaryotic Cell
☐ SphereCell

Now, select “Cell membrane” and select a file containing a cellmembrane VRML97 file (.wrl):



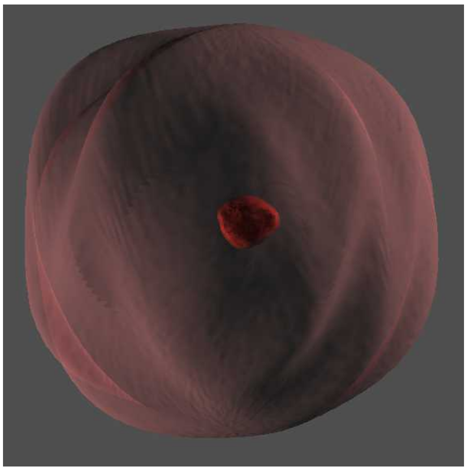
but you can enter another quantity.
4. The Right Mouse Button toggles a PopUp menu, which you can use t
add PDB membranes.
After the creation, you can use the

☑ Cell membrane 1
☐ Cell wall 0
☐ Chloroplast 0
☐ Cytosol 0
☐ Endosome 0
☐ Extracellular matrix 0
☐ Golgi apparatus 0
☐ Lysosome 0
☑ Mitochondrion 1

Suchen in: Animal_Cell_1_5[Cm3]
cellmembrane.wrl
Dateiname: cellmembrane.wrl
Dateityp: wrl-files (Cell membrane)

Click on “Mitochondrion” and choose now a mitochondrion file and then click “Next”.

A dialog appears asking if the PathwayIntegration should be activated. Click “No” and a cell environment is generated:



Both shapes are based on single VRML97 files. VRML97 or VRML 2.0 is a text-based format which defines three-dimensional objects. This file format contains color information, vertices and the definition of the edges between these vertices, transparency information, lighting, normals, etc. The VRML97 definition can be found here:

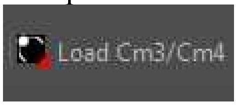
http://www.web3d.org/x3d/specifications/vrml/

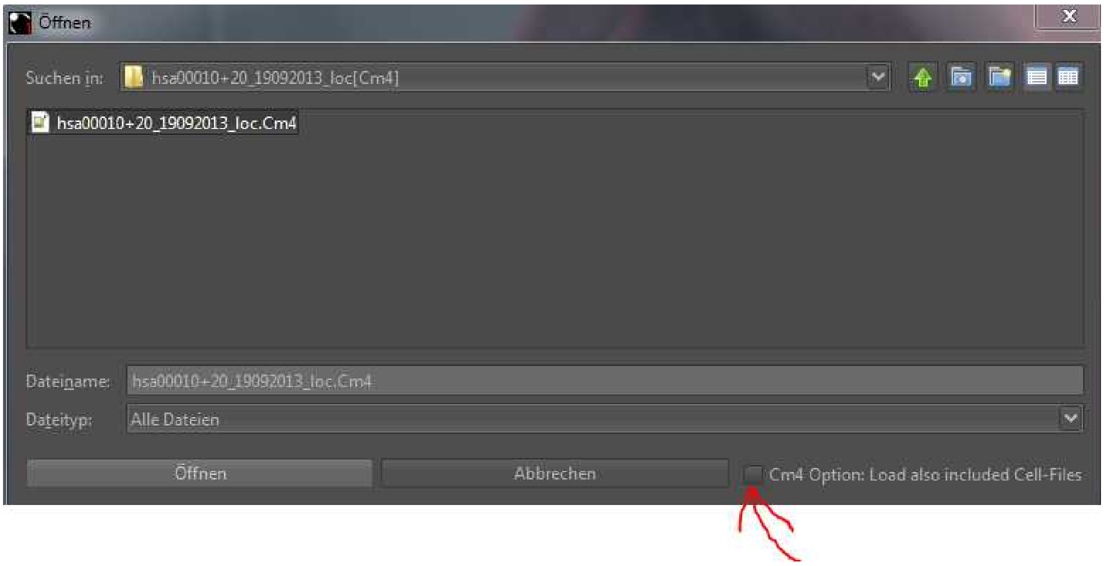
Now, we want to combine this simple cell model with a pathway. Now it is time that you download the following files from the forum:

http://www.cellmicrocosmos.org/Cmforum/viewtopic.php?f=21&t=737

the following two files:

- Blender_Tutorial_WS2013-14_5.zip
  - It contains the folder:
    - *io_scene_x3d/*
      - Place this file into the following Blender directory:
        - *C:\Program Files\Blender Foundation\Blender\2.67\scripts*
    - *vrml_export_266.py*
- hsa00010+20_19092013_loc[Cm4].zip

Unzip "hsa00010+20_19092013_loc[Cm4].zip" and click in the CellExplorer on the button , go to the folder "hsa00010+20_19092013_loc[Cm4]", deselect the "Cm4 option", as shown here:



Öffnen

Suchen in: hsa00010+20_19092013_loc[Cm4]

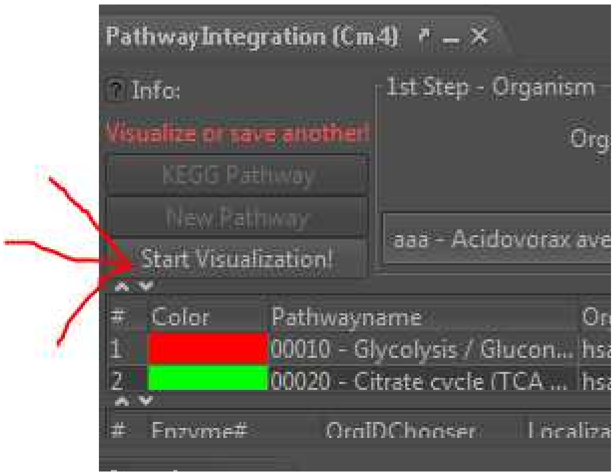
hsa00010+20_19092013_loc.Cm4

Dateiname: hsa00010+20_19092013_loc.Cm4

Dateityp: Alle Dateien

☐ Cm4 Option: Load also included Cell-Files

and then open the file “hsa00010+20_19092013_loc.Cm4”. The file is loaded and now just click on the “Start Visualization” button:



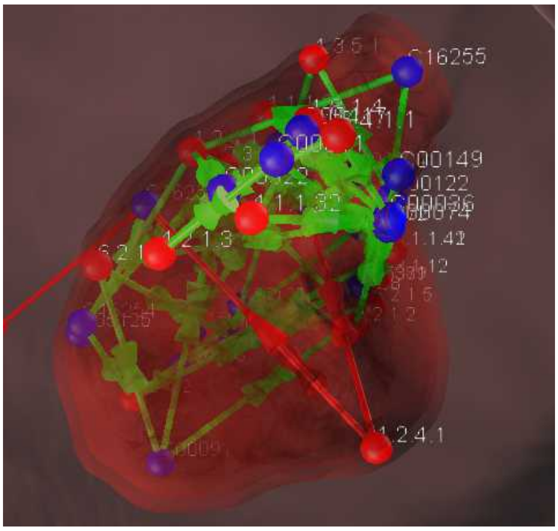
Visualize or save another!

aaa - Acidovorax ave

#	Color	Pathwayname	Or
1	🟥	00010 - Glycolysis / Glucon...	hs
2	🟩	00020 - Citrate cycle (TCA ...	hs

#	Enzyme#	OrgIDChooser	Localiza

The cell model is now combined with pathway.



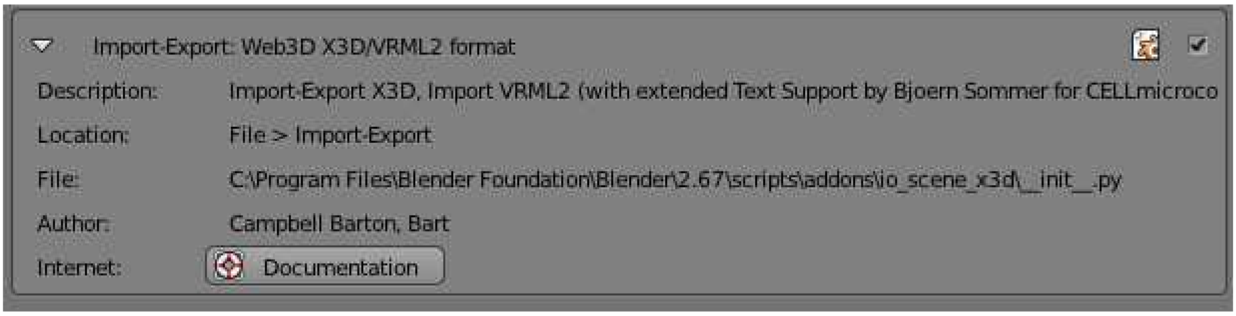
Now, export this cell model to a VRML file by clicking Save as VRML and saving the file.

Now, we want to import the exported VRML file to Blender. For this purpose, make sure that you have substituted the folder io_scene_x3d in the Blender\2.67\scripts folder with the one downloaded from the forum website. This version support the import of text from VRML to Blender.

Now, start Blender. Go to

File → User Preferences

and make sure that the Web 3D X3D/VRML2 exporter/importer is activated here:



Import-Export: Web3D X3D/VRML2 format ☑

Description: Import-Export X3D, Import VRML2 (with extended Text Support by Bjoern Sommer for CELLmicroco

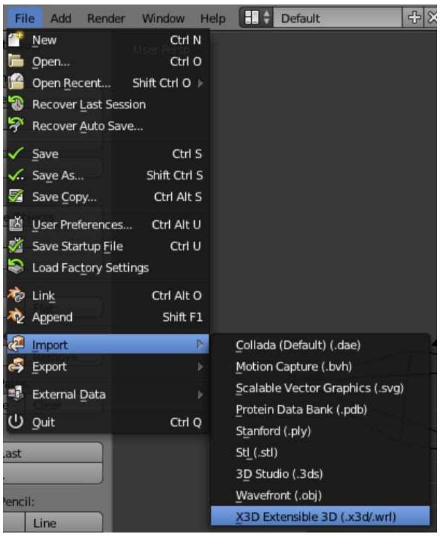
Location: File > Import-Export

File: C:\Program Files\Blender Foundation\Blender\2.67\scripts\addons\io_scene_x3d__init__.py

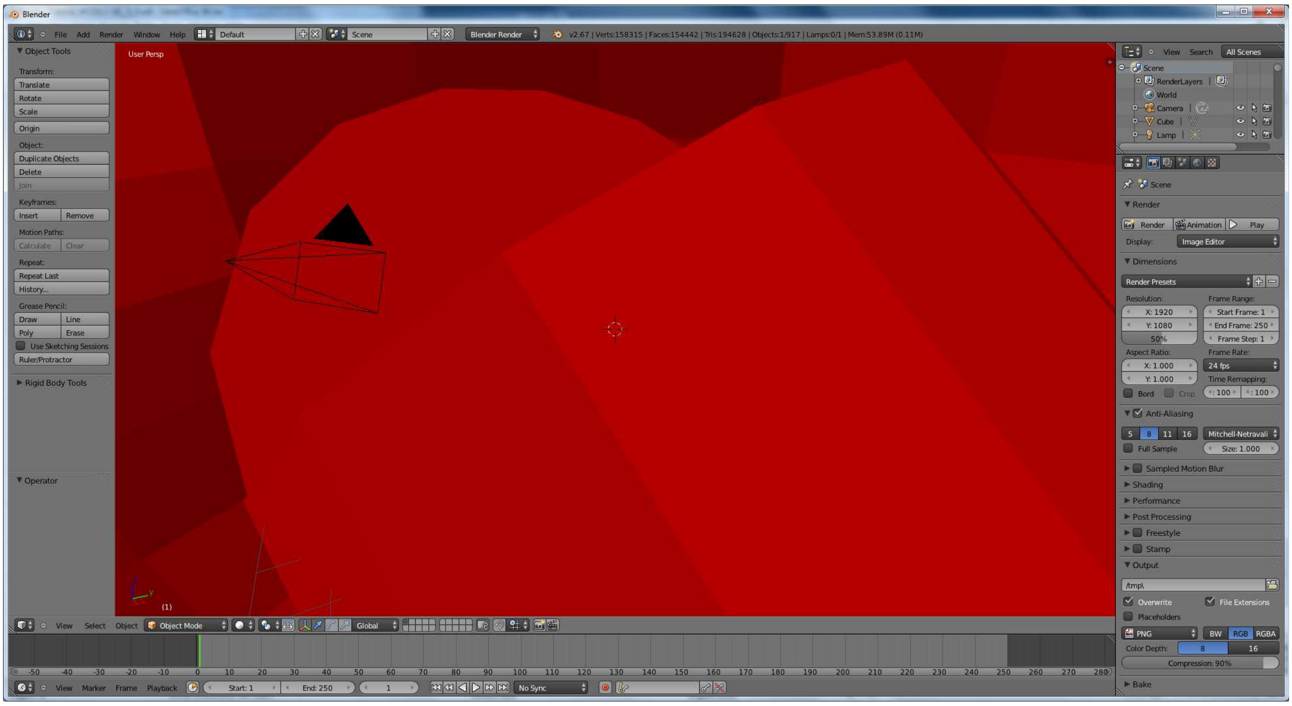
Author: Campbell Barton, Bart

Note: this plugin supports only the import of VRML files. If you want to export VRML files, use the file “vrml_export_266.py”, activate it just like the importer and find it in the Files → Export dialog. This exporter can also be used to prepare shapes for cell components for the CellExplorer.

Now, import the .wrl file by using:



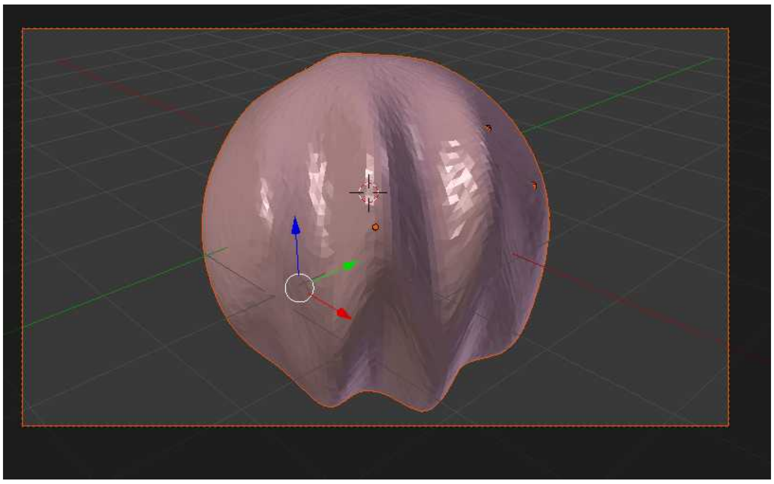
After the file is important, you will see something like this:



Obviously, the 3D model is much too huge.

Select the whole model with *A* and then use now a combination of scaling (with *S*) and grabbing (with *G*) to decrease the size and to change the position of the cell model. Combine these two modes with restricting the movement to a single axis, e.g. by pressing *Z* afterwards. Always make sure that the cell model does not disappear from the view port and move it towards the center of the membrane by looking from the top or from the side. A good trick to take the line into account which appears during pressing *S*. This line indicates the direction and the position of the rpugh center of all shapes.

In the end, the cell model should be located in the center:



You know how to handle this model from the previous tutorials. One last hint should be given. If you look to the Outliner, you will see a lot of different shapes. The problem is now that it is not easy to identify the correct cell component in the Outliner. Just select now the visible cell components and give them names. But how to do this?

Just change to “Selected” mode in the Outliner and click the cell membrane and change the name of the shape with a name like “ShapeIndexedFaceSet” to “Cell Membrane”:

Deactivate the eye symbol and hide the cell membrane. Select the mitochondrion component and change then its name.

Now, you can filter objects in the Outliner. Go back to “All Scenes” and use the search field to search for a cell component name.