

CompuCellPlayer

Visualization is a crucial aspect of biological/biophysical modeling. This is especially true with respect to Cellular Potts Model (CPM). Traditionally researchers working on CPM modeling, in addition to writing their own CPM code had to develop visualization engines or use third party graphical packages for visualization post-processing. Both of these approaches are certainly require researchers to do extra work.

To streamline graphical operations related to CPM modeling we have developed special visualization tool - CompuCell Player - that hooks up directly to CompuCell libraries and allows both 2D and 3D real time visualization of the simulation lattice.

CompuCell Player has very intuitive graphical user interface that is very straightforward to use.

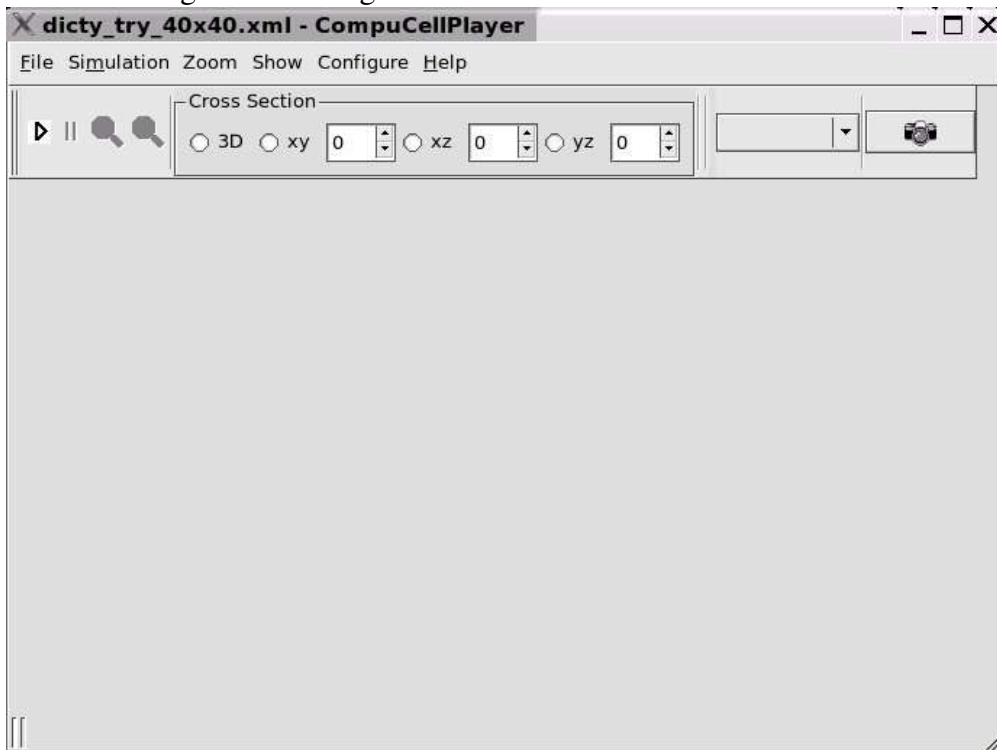
In this manual we will present major features of the CompuCell and save users some confusion or frustration.

Startup screen

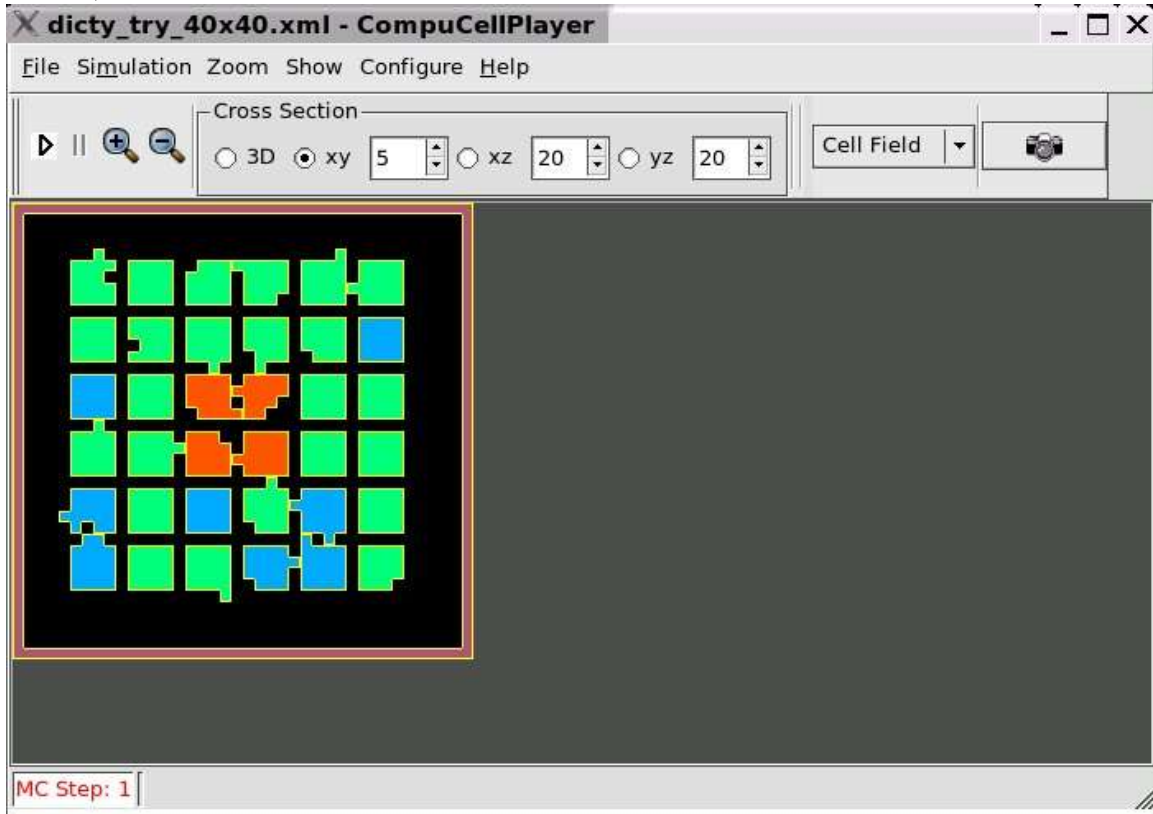
When you decide to use CompuCell through the CompuCell Player (which is strongly recommended) you need to go to CompuCell installation directory and type:

```
./run_CompuCellNew.sh
```

This will bring the following window:



This is Player's main window. We are pretty sure that looking at his window you probably know what you need to do in order to start running simulation. Yes, you need to go to File menu and choose open (or hit Ctrl-o). Once you are in the Open File dialog choose any file which contains an xml description of your simulation (it is a good habit to give such files extension xml because this is the extension that Player is looking for by default).



Once you picked your xml file. To start running simulation all you need to do is to click "Play" button on the toolbar. If everything is OK the simulation will start and you will be able to see a projection through the lattice on the screen. On the picture above we have just started simulation with an xml file called dicty_try_40x40.xml as displayed on the title bar.

Next to play button you can see Pause button which allows to pause simulation (execution of the simulation is temporarily halted) and examine the lattice. To restart simulation click Play button again and there you go – just like with your CD player.

That was simple. now let's get familiar with the rest of the toolbar:

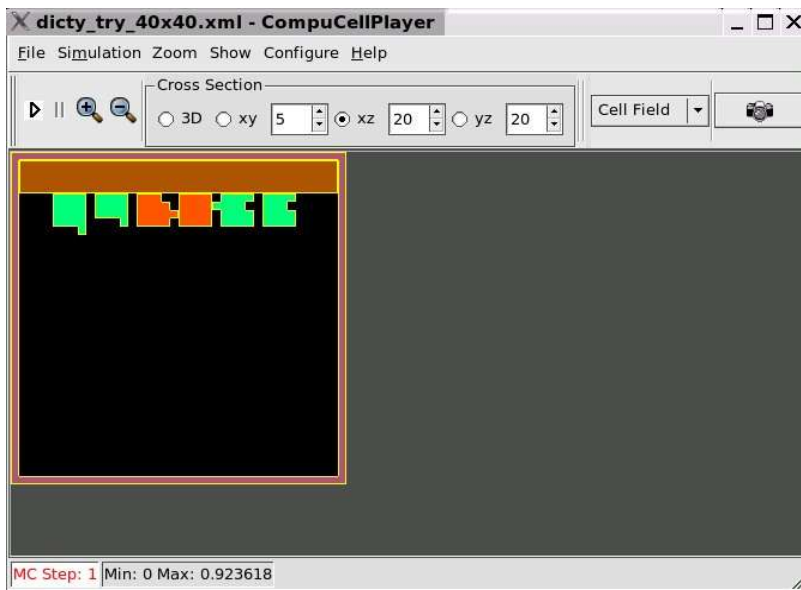


Next to Play and Pause buttons there are Zoom In and Zoom out buttons. The magnify/shrink image that Player is displaying.

Next to Zoom In and Zoom out buttons you can see group of buttons used to view different projections through the lattice or switch to 3D visualization.

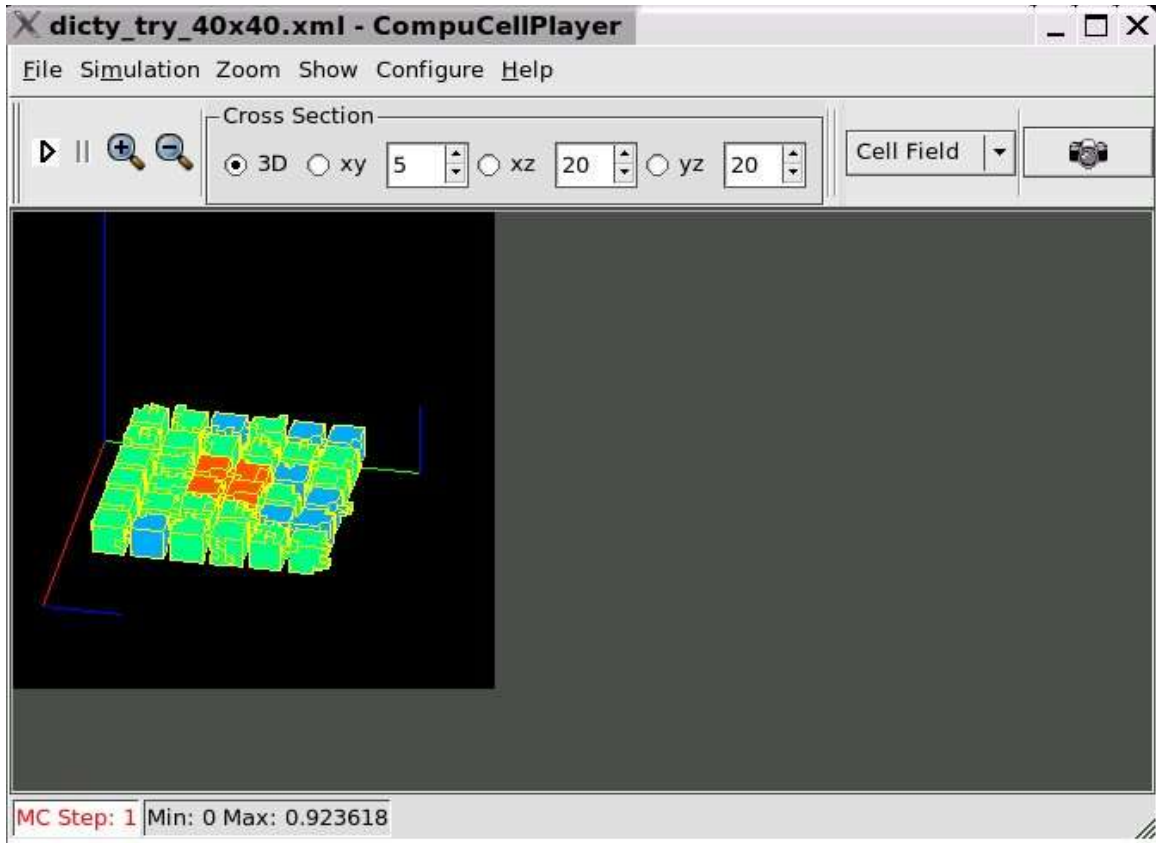
Viewing lattice projections

We can “slice” the lattice using radio buttons named “xy”, “xz”, “yz”. For example if you choose “xy” button then you are looking at the “xy” plane of the lattice. The value of “z” coordinate is given by the value of the scroll box next to “xy” button. On the picture above this value is 5. Below we show another projection - “xz” - it is view of the lattice “sliced” by the plane parallel to “xz” plane with $y=20$. We hope you get an idea how projection buttons work.

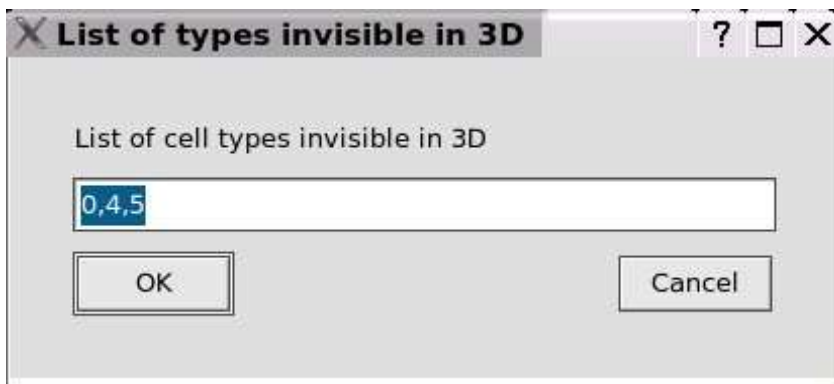


3D viewing

Looking at 2D projections is a great debugging tool and gives you a lot of insight into what is going on in the simulation. nevertheless it is useful to see “big picture” of the simulation by looking at the 3D view. It's easy – click “3D” radio button and you get the following:



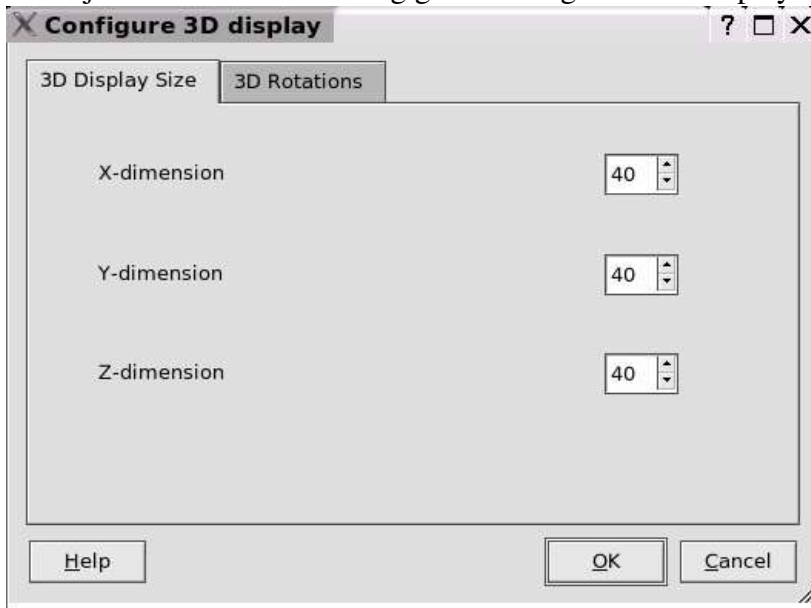
Not bad, and how easy... Now, 3D viewing is expensive computationally expensive. For that reason it is useful to visualize only necessary parts of the simulation. By this I mean that you make unimportant cells 3D invisible. In the simulation shown above cells we made certain cell types invisible in 3D mode. For example , above we had layer of frozen cells around the lattice, we had ground cells and we had medium. All those cells were not too useful from the point of view of our simulation. That's why we have made them invisible. To do that you need to go to Configure->Cell Types invisible in 3D... and you get the following dialog:



You specify these cell type numbers that you want to be invisible in 3D. you should almost always make Medium (type number 0) invisible. To separate types you use comas.

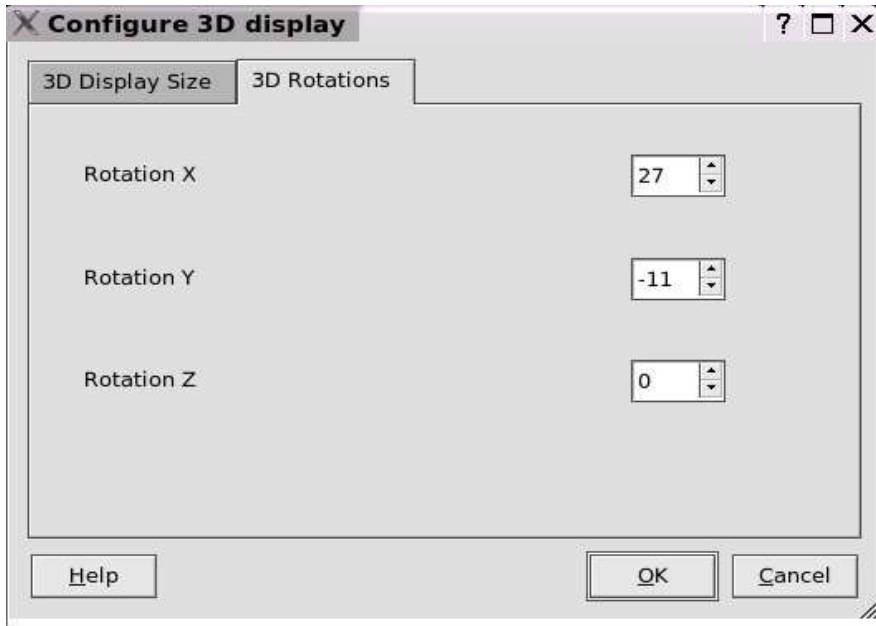
It is important to “turn off” unwanted cell types prior to switching to 3D view because on slower machines 3D rendering may take a while and GUI may become less responsive.

While we talk about 3D viewing it is useful to go over 3D configuration dialog. This is where you can specify basic settings for 3D rendering and determine the orientation of the object. To access the dialog go to Configure->3D Display Configuration:



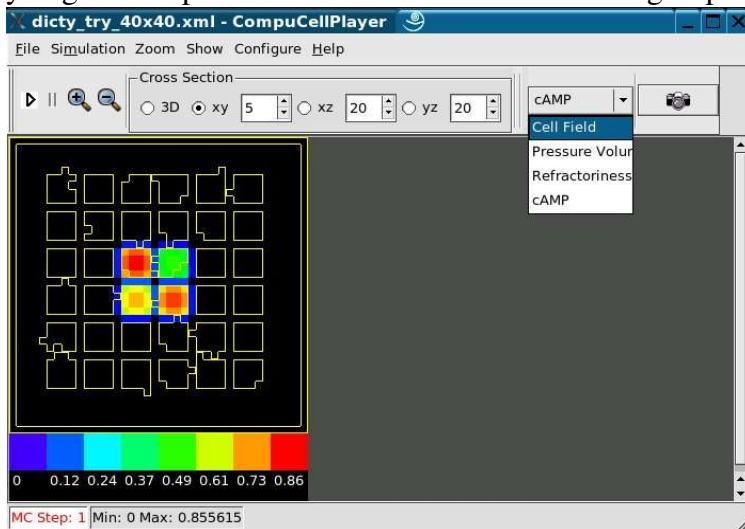
Above you specify the size of the 3D viewing area in such a way that if you increase it your object becomes smaller and occupies less lattice. It might be a little bit unintuitive to use, so the best way is to try. To protect users from entering some absurd numbers, in one step you can at most double the values displayed in this dialog.

If you click “Rotation” tab on the above dialog you will be able to rotate the object. Values displayed are in degrees and correspond to rotations around x,y, and z axes.



Plot Types

In CompuCell you can visualize not only cells but also different physical quantities that appear in given simulation. On the pictures above we were visualizing cells only, but if you go to the pull down list next to Cross Section group of buttons :



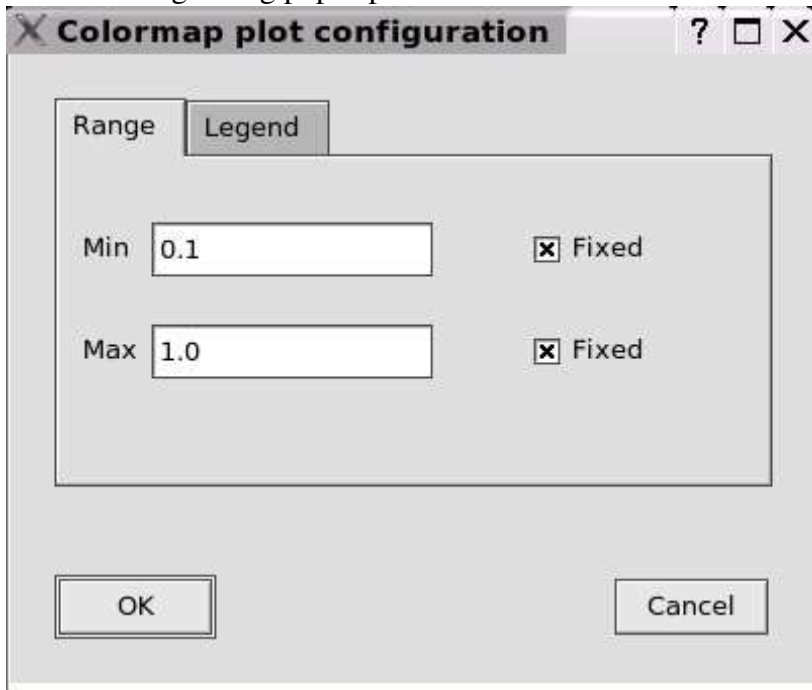
You can see a list of plot choices associated with current simulation that Player can display. So let us choose cAMP. This will be a plot cAMP concentration. Whenever in CompuCell3D you define concentration field the concentration plot can be viewed in the Player. You just need to select it from the pull down list.

Above we have chosen to view cAMP concentration profile.

Concentration Profile Configuration

Once you switch to concentration you may want to tune display parameters so that you see what you want to see not what the Player wants you to see. To change settings of concentration profile visualization (or any scalar field visualization) go to Configure->Colormap plot ...

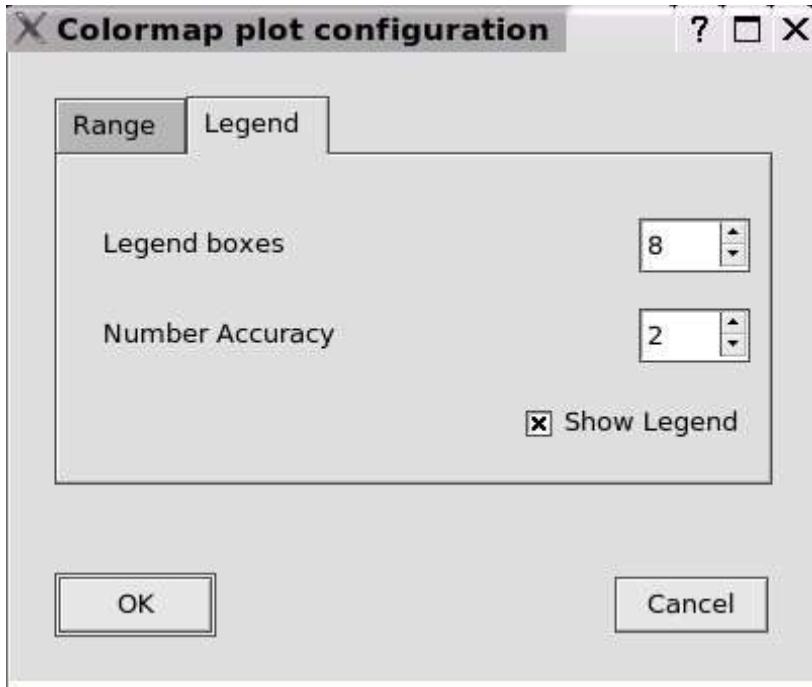
The following dialog pops up



Here you may tell the Player that the highest/lowest value of the concentration field so that they will be colored in red (if greater or equal to highest value chosen – here 1.0) or black (if equal or less than lowest value chosen – 0.1 in our case). Everything in between will range from blue to red. Do not forget to click “Fixed” check boxes for this feature to work.

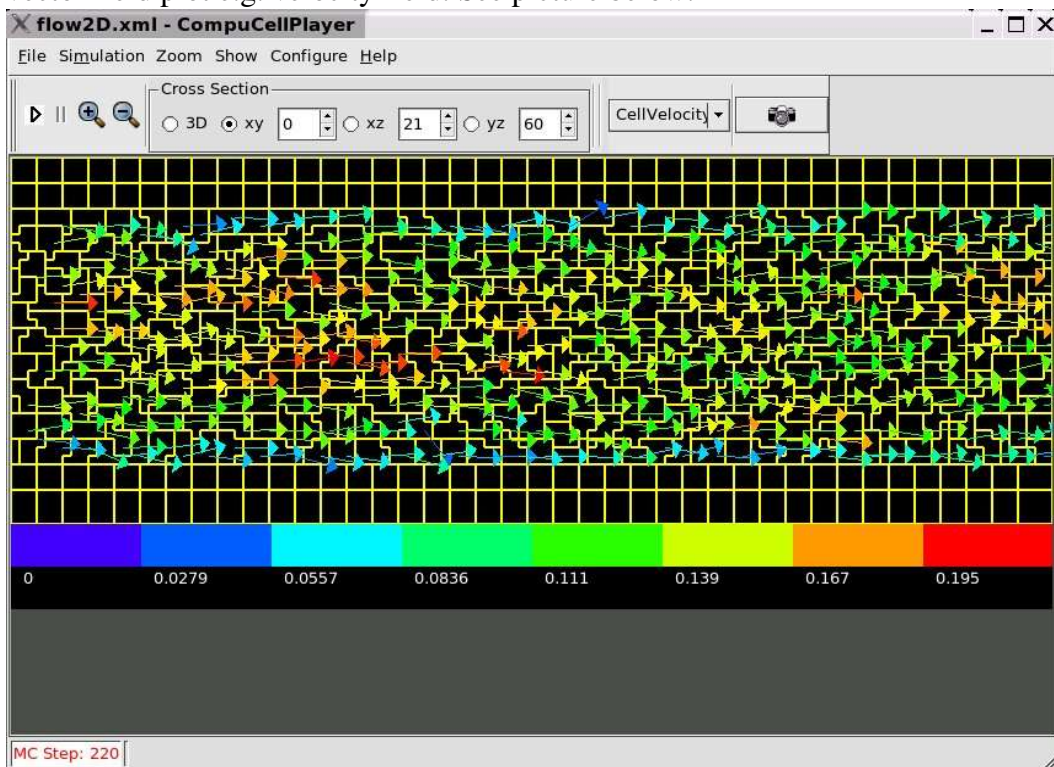
If you do not click “Fixed” check box the Player will automatically choose highest lowest values of the concentration based on a given concentration profile.

Now, let's click “Legend” tab in the same dialog:



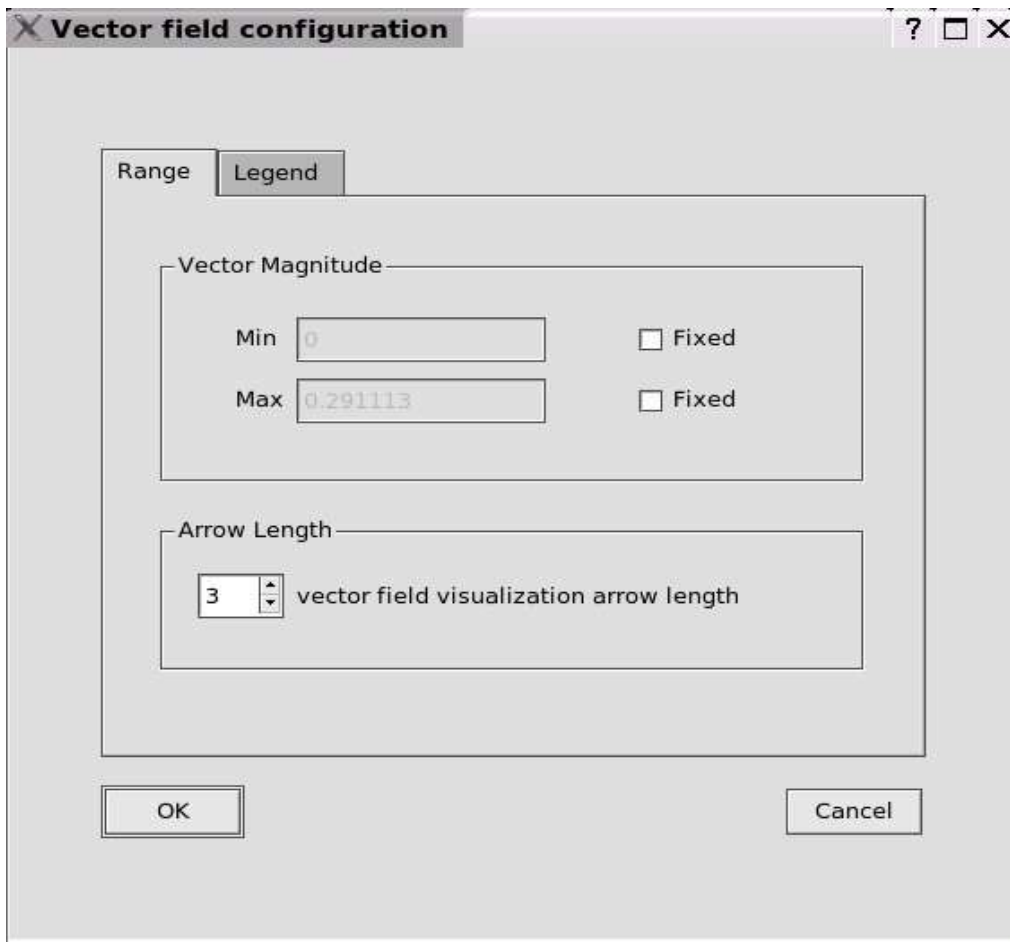
Here you tell the Player whether you want legend to be displayed , how many color boxes legend should have, and how many decimal points the legend numbers should have. Very easy , and also very handy.

While we talk about plot configuration let's take a look at different type of plot, namely vector field plot e.g. velocity field. See picture below.



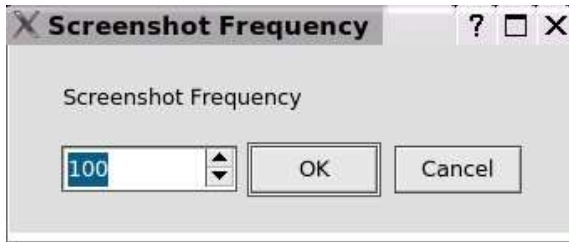
This is an example of vector field visualization. Every cell has a velocity which is represented by an arrow and the color encodes the magnitude. The orientation and magnitude of the vector field visualization are calculated by taking projection of vector quantity onto the

As far as magnitude, similar rules apply as in the case of concentration profile plots. Let's look at the configuration of this kind of plot. Go to Configure->Vector Field plot This is what you get:



This works analogously to concentration plot configuration. The only difference is that you can specify the length of the vector arrow drawn on the screen. The legend tab has analogous content to concentration plot profile.

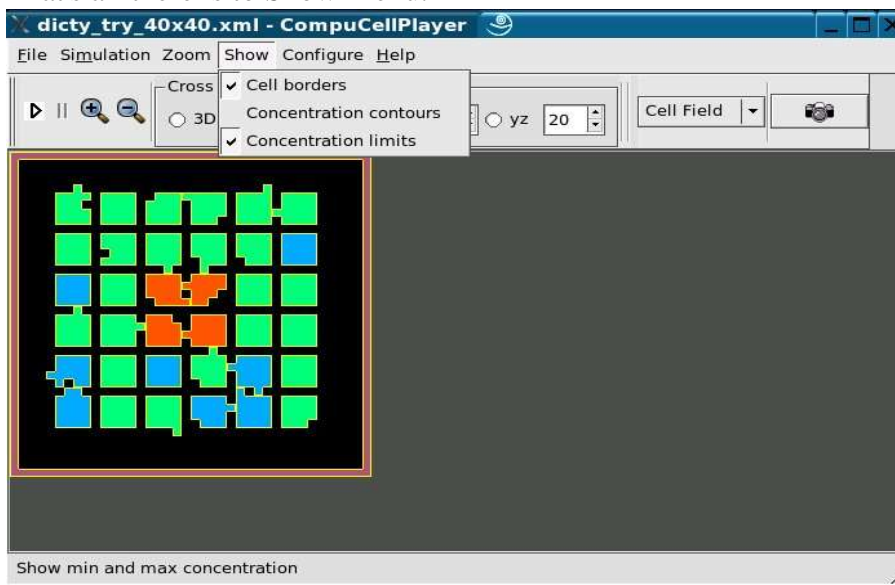
While we talk about Configure menu options, let's check the following dialog – Configure->Screenshot Frequency...



Here you specify how often you want the Player to save screenshots of your simulation. In this example it is every 100 MCS. Notice that by default the Player stores a *.png (PNG-Portable Network Graphics) image of what is currently on the screen. Now, you may want to store other screens as well in the single simulation run. To do that, change the view to the desired view, and hit camera button on the toolbar. This will cause that the view you have just chosen will be stored regardless what is currently displayed on the screen. For efficiency reasons we have decided to limit a number of these additional screenshots to 20, however this can be changed upon request. Make sure you do not press camera button twice on the same configuration. This will close the simulation.

Show Menu

This menu is really simple. It allows you to choose what to display. Checked Concentration limits item means that on the lower information bar you will be able to see max/min concentration value. Concentration contours work in the concentration profiling – they add contour lines to the plot. Cell borders activates the display of the cell borders. That's all there is to Show Menu.



Running CompuCell on cluster.

While GUI front end is fun to play with and very informative, at some point in your research you will want to run CompuCell3D on cluster and will require that screenshots of many views are taken. Can you do it with CompuCell Player? Yes, CompuCell Player

can be run in the so called “silent” mode where no GUI is displayed but screenshots are taken. So how do you do this. Well, first you need to tell the Player what screenshots you want to take while running in the silent mode. The way to accomplish it is to start the simulation with regular GUI approach. You may hit Pause button, and then change view to the one that you wish to save, hit camera button , and go to next view, hit camera button and when you are done, go to File->Save Screenshot Description ... and enter the name you want to give to the file that contains screenshot description. Do not worry too much the Player writes this file based on your selection of views. All you have to do is to supply the name of the file.

Once your file has been stored, to start the simulation in the silent mode (without GUI but with screenshots) you type the following:

```
./run_CompuCellNew_silent --xml=<name of xml simulation description file>  
--screenshot=<name of the screenshot description file that you have just saved>
```

Quite simple