Cellular Potts model assignments

November 2020

1 Cell sorting

In this assignment you will work with the Morpheus example **CellSorting_2D.xml**. As discussed in class, it reproduces the original cellular Potts model formulation from reference [2]. The goal here is to run a parameter sweep with Morpheus that displays a variety of cell sorting configurations depending of the contact energies of the two cell types, as shown in reference [1]. For that, we can define the surface tension between two different cell types τ_1, τ_2 as:

$$\gamma_{\tau_1,\tau_2} = J_{\tau_1,\tau_2} + \frac{J_{\tau_1,\tau_1} + J_{\tau_2,\tau_2}}{2}, \tag{1}$$

which enable us to determine whether contact energies favor homotypic ($\gamma_{\tau_1,\tau_2} > 0$) or heterotypic ($\gamma_{\tau_1,\tau_2} < 0$) cell bonds. For instance, if we use the subindex m for the medium and y and r for yellow and red cells respectively, the following cell sorting configurations should be obtained depending on the specified surface tensions:

- Simple cell sorting ($\gamma_{y,r} > 0$, $\gamma_{y,m} = \gamma_{r,m} > 0$)
- Engulfment of red cells by yellow cells ($\gamma_{y,r} > 0$, $\gamma_{r,m} > \gamma_{y,m} > 0$)
- Mosaic cell ordering ($\gamma_{y,r} < 0$, $\gamma_{r,m} > 0$, $\gamma_{y,m} > 0$)
- Engulfment of yellow cells by red cells ($\gamma_{y,r} > 0$,$\gamma_{y,m} > \gamma_{r,m} > 0$)

(A) Design a parameter sweep for two of the contact energies to reproduce all those patterns and possible transitions between them. When the sweep is finished, display all the results together using the table plot functionality of Morpheus in the ParamSweep section. Tips: Use the same initial conditions for 100 cells used in CellSorting_2D.xml: 50 cells of each type distributed at random in a circle at the center of the lattice. You might want to increase the parameter Temperature slightly to facilitate cell patterning in shorter times.

(B) Generate a surface plot showing how the boundary length between red and yellow cells at the end of the simulations changes for the different

combinations of contact energies that you have investigated in the parameter sweep. Tips: The length of the boundary between both cell types is defined in CellSorting_2D.xml as 'boundary' and it is stored in the file 'logger.csv' for each time point. You have to modify the Jupyter notebook for the toggle switch analysis used in class to read the results of the parameter sweep done above. Note that the 'sweep_data.csv' should have three columns in this case. The first one called 'Folder' contains the name of the folder where each simulation results are stored. The other two columns, called 'P1' and 'P2', contain the values of the two contact energies used in each case.

2 Tumor growth

In this assignment you have to improve the simple tissue growth model that we built in the class (see file **tumor_growth.xml**). In that model we coupled a simple ODE model for the cell cycle to a classical cellular Potts model with only one cell type and we added a cell division plugin. If you let the simulation to run long enough, it would fill the entire lattice with cells. At that point, there is no space for cells to grow to their target area after each cell division but they would continue dividing and becoming smaller and smaller.

(A) Your task is to correct that behaviour in the model by allowing cells to divide only when they are 90% of their target size. For that you shall modify the cell division condition using the operator '&&'. The symbol for cell size counted in lattice nodes is 'cell.volume'.

(B) Can you think in other possible changes to this simple model that would make it more realistic to model tumor growth?

3 Networks

Open and run the Morpheus example **CPM_Game_of_Life.xml**. This model corresponds to the classical cellular Potts model from reference [2] plus a couple of simple extra mechanisms/rules. As specified in the model description, cells divide if they have less than three neighbors and die if they have more than six neighbors.

(A) Try to identify in the appropriate model section where those mechanisms are encoded.

(B) Run a parameter sweep modifying the number of neighbors needed for cell division and/or cell death and observe how the generated structures depend on them.

References

[1] James A Glazier and François Graner. Simulation of the differential adhesion driven rearrangement of biological cells. *Physical Review E*, 47(3):2128, 1993.

[2] François Graner and James A Glazier. Simulation of biological cell sorting using a two-dimensional extended potts model. *Physical review letters*, 69(13):2013, 1992.