Cellular Potts model assignments

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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.

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.