

Core bioinformatics

Systems Biology

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As I explained to correctly handle and work with EmbryoMaker and Network_maker you can read the manuals in:

<http://www.biocenter.helsinki.fi/salazar/software.html> (see documentation section):

In brief:

-Network_maker allows to modify the parameters

-EmbryoMaker generates (runs the model) the values of the variables of the model based on the initial conditions and the parameters.

Each file has a part specifying the parameters and a part specifying the variables.

The initial conditions are just one such file that has the value of the variables at iteration 0. This is usually a flat epithelium with some cells expressing gene 1.

EmbryoMaker generates, based on this initial conditions file, the files for subsequent iterations (you decide which of those iterations to see in the screen and which to save).

What you have to do first:

1. Run Network_maker in a terminal giving the initial conditions file (e.g. original_initial_conditions.dat) to it as input (e.g. “./Network_maker ini2.dat”).

-The network included by default in the initial conditions file will show up.

-You can modify it at wish.

-Once modified save it in a file. This file will then include the initial conditions (e.g. a flat epithelium) and the new parameters (network). You could name each modified file with a different name (e.g. “modified_initial_conditions1.dat” or “network1.dat”) etc...

-Notice that any new added gene has by default zero diffusion rate and zero degradation rate. You probably want to modify that in some cases.

-Notice that you may want to add growth factor genes and that for that you have to “modify gene properties” and give to a gene the “kindof” property a value of 4.

2. Run the modified initial conditions with EmbryoMaker (e.g. “./EMaker modified_initial_conditions1.dat”) and see which are the results over iterations. You can save the results at a given iteration from EmbryoMaker in the same way you saved the initial conditions (again

the file will be in a folder in the output folder and it would include the parameters and variables so that this file could be used as the “initial conditions” for another simulation).

Remarks:

- Genes affect node and cell properties only where they are expressed.
- You can not change the initial conditions as such (only the parameters).
- So if you want to affect node or cell properties in a part of the embryo you have to first make that a gene is expressed in that part and you can only do that by modifying the gene network in such a way that gene interaction dynamics lead to a gene to be expressed in that region. This is only possible if some of the genes are growth factors that diffuse in space and/or if you have some genes repressing others (and it requires some thinking).
- The growth factor received by diffusion from a source (e.g. a cell) decreases exponentially with the distance to that source (so if you want to see the concentration of a diffusible molecule it is better to use arrows rather than colors in EmbryoMaker). Notice also that diffusion is a slow process so it would take many iterations to be visible by you.
- Notice also that transcription happens only in nodes that are nuclei (you can see from the EmbryoMaker menu options which nodes are nucleus and which ones are not) so if you want to activate a growth factor secretion ensure that there is a gene in the initial conditions that is expressed in some nucleus and make a connection between it and your growth factor.

Exercises:

You have to make one of the following:

1. You take any of the initial conditions provided in ini2.dat and explore its genotype phenotype map. This is you have to identify the model parameters that affect the obtained morphology and depict how changes in those affect it. Thus, you do not have to modify the network topology but some of the values of the connections in it (either in the interactions between genes or in the regulation of node or cell properties by genes). You should send me:
 - The file with this pattern (as saved from EmbryoMaker).
 - A screen capture of each of the final morphologies you have obtained for each of the relevant parameters values you have tried (all the screen captures in a table; at least 16 of them).
 - A text describing reasoning why the parameters you change the morphology in the observed way.
2. As in 1 but you chose which final morphology to produce from the model. It should be much more complex than the initial conditions and more complex than the morphology this initial conditions would produce if you would not have changed. You have to reason why the produced morphology is more complex than the initial conditions and what it means to be complex in this context for you.

YOU SHOULD SEND THE EXERCISES TO ME BEFORE the 5th of december (either by email or through the master's webpage).