Outstanding Issues Regarding the Gastrulation Paper

1 June, 2007

"Contact Following" or "Cell Orientation": Bakhtier used the term "contact following" for cell orientation interaction. This term is rarely used in the biological literature, but does have some basis. Perhaps the term "polarization interaction" is better?

Problems: This feature has not fully been implemented into CC3D. We did have one past version which implemented what we have been calling "cell orientation". However, in later versions it either did not exist or does not completely work.

Resolution: Maciek says he can have a working prototype simulation by next week. Ariel has given him the necessary files for the simulation:

1) PIF file for the initial configuration of the blastodisk with AP, AO, Sickle, and Streak Tip cells.
2) XML configuration file specifying contact energies, volume and surface parameters, diffusion/secretion/decay parameters and a single cell orientation parameter which takes the place of a chemotaxis parameter. Other cell orientation parameters, such as how much neighboring cell orientations co-influence each other, are not specified in the XML file. They are specified in the simulation specific python file.
3) Simulation specific python script which calls the cell orientation and cell velocity steppables. This is also where we specify orientation interaction parameters, frequency of polarization interaction and frequency of velocity calculation updates.
4) Steppable definitions python file. This contains the definition of the python steppables. When I left off, it was possible to display the velocity vector field in the CC3D player, but still necessary to use gnuplot to graph the orientation vectors. A few other things still also needed to be specified here unless we fixed them.

As soon as the prototype simulation is runnable again, Ariel can start generating data. It will be beneficial to also get CC3D running on bigred for doing parameter sweeps, but work can continue before this happens.

Note: The "polarization" or "orientation" algorithm is as follows:

1) Each cell has a polarization vector that has both direction and magnitude.
2) At each MCS all cell polarizations are updated as follows. Using the notation:

   $\mathbf{p}_k$: the polarization vector of the k^{th} cell

   $\mathbf{r}_{m,k}$: the vector between cells k and m

   $\overline{\mathbf{r}}_k$: the location of the center of mass of the k^{th} cell

   $C(\overline{\mathbf{r}}_k)$: the concentration of the chemical field C at the point $\overline{\mathbf{r}}_k$

   d, g : cell specific parameters

a : model specific parameter
t : Monte Carlo steps

$$\mathbf{p}_m(t+1) = g_m \mathbf{p}_m(t) + \sum_{k \in \{\text{neighbors}\}} g_k \frac{\mathbf{p}_k(t)}{\left|\mathbf{r}_{m,k}(t)\right|^a} + d_k \nabla C(\bar{\mathbf{r}}_k)$$

Bakhtier used $a = 1$. With $a = 2$, the polarization interaction terms look like a Laplacian, and can be thought of as secretion and diffusion of polarization. In viscous flow, the N-S equations can always be reduced to a diffusion of vorticity. Thus $a = 2$ causes polarization act almost identically to fluid viscosity.

3) The velocity-dependent Hamiltonian has an energy term

$$H_{\text{polarization}} = \sum_{k \in \{\text{cells}\}} l_k \mathbf{p}_k(t) \times \mathbf{v}_k(t)$$

where $\mathbf{v}_k(t)$ is the velocity of the center of mass of the k^{th} cell at time t. How the velocity is actually calculated is one of the choices that must be made.

Parameter sweeps: These are mostly for our benefit currently. We only plan do refer to individual results or general types of results in the paper. However, we want to be able to confidently state that "our model works over a wide range of parameters". I have done a number of these already. However, things keep changing—compucell3d, parameter ranges—and some parameter ranges never got run. A complete set of sweeps apropos to the paper would be nice.

Problems: We no longer have access to the odin cluster. Abbas has tried to run compucell3d on bigred, but it does not work.

Resolution: Abbas shows Benji and Ariel what he has tried in order to get compucell3d to run on bigred. Benji and Ariel will talk to the bigred administrators to explain what we need and why. If this doesn't work, go to McRobbie.

Two Sickle simulations: These should reproduce the experiment in which two streaks growing 90^o apart should avoid colliding.

Problems: Now a long time ago, but I was having a hard time getting the two streaks to really avoid each other as in the experiment. I'm not sure why. At the time I thought it had something to do with how fast the signal was diffusing. The parameter sweeps I was doing at the time showed that streak repulsion required finely tuned parameters.

Resolution: Conduct new parameter sweeps with a current version of CC3D and current parameter values. If the desired result does not occur, discuss with James and Kees.