Mathematical Biology: from Individual Cell Behavior to Biological Growth and Form

Please write a short report (one or two pages) on the questions and hand them in by next week (10/9/2014) by e-mail to merks@cwi.nl. Subject line: "HOMEWORK TURING".

Lab Session 1: Turing Patterns

$$\frac{\partial A}{\partial t} = c_A \frac{A^2}{I} - \mu A + D_A \nabla^2 A + \rho_A$$
$$\frac{\partial I}{\partial t} = c_I A^2 - \nu I + D_I \nabla^2 I + \rho_I$$

1. Try to rewrite the above system to the form treated in the lecture by rescaling A, H, x and t. Which terms are new, compared to the 'standard' GM-model?
2. Find the stationary, homogeneous solutions to the simplified system in terms of the new parameters.
3. Linearize the system around the nontrivial (nonzero) solution and write the result system in 'matrix form'.
4. Derive a (set of) condition(s) for the occurrence of a Turing pattern. Give an explicit formula for the critical wave number.
5. Check your findings numerically: for a chosen set of initial values, vary the diffusion coefficient and see if a Turing pattern emerges at the right value, with the right wave number. For an extra check, take δ close to zero to see if you obtain the same formulas as derived in the lecture.

   Download the software from the course website, at http://biomodel.project.cwi.nl/education.

   Unpack: type "tar xzf VirtualLeaf0v1.01-Turing.tgz" in a Terminal.

   Type "cd VirtualLeaf-v1.0.1/bin" to go to the right folder, and type "./VirtualLeaf" to start the program.

   To inspect or change the diffusion rate of the diffusion coefficient, choose "Option->Edit Parameters". Look for D (it's under 'Auxin transport and PIN1 dynamics' - for reasons that will become clear later during the course). Change the first (activator) and second (inhibitor) values in this comma-separated list. To reset to initial values, choose "Edit -> Reset Chemicals and Transporters". To make snapshots for your report, choose "File -> Snapshot". "File ->Export Cell Data" will export and Excel sheet with the chemical concentrations in each of the cells for further analysis (optional).

   Start the simulation by pressing "CTRL-S" and observe what happens. What kind of equilibrium do you see? Why? Is this what you would expect given the parameter values? What could be the problem? (Hint: Inspect the values in the grid sites by hovering over them with your mouse pointer. Then check the "Edit" drop-down menu.)

   Do the numerical results match your analysis?

Read more on Turing patterns and reaction-diffusion equations? See, e.g., http://www.eb.tuebingen.mpg.de/departments/former-departments/h-meinhardt/primary.html