

Practicum Core Bioinformatics

Systems Biology

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1. Chose a partner (the exercise is made in pairs).
2. Choose a gene network. This network should have:
 - 5 genes
 - At least two interactions per gene
 - Each gene should receive at least one positive connection from some other generate
3. Choose a function. The function should be of the form:
 - $\partial g_i / \partial t = f(g_1, g_2, g_3, g_4, g_5) ::$ is a function of some of the other genes
 - f should be continuous and derivable
 - For example:

$$\partial g_i / \partial t = \Phi(\sum w_{ij} g_j) / (\Phi(\sum w_{ij} g_j) + K_i) - m_i g_i$$

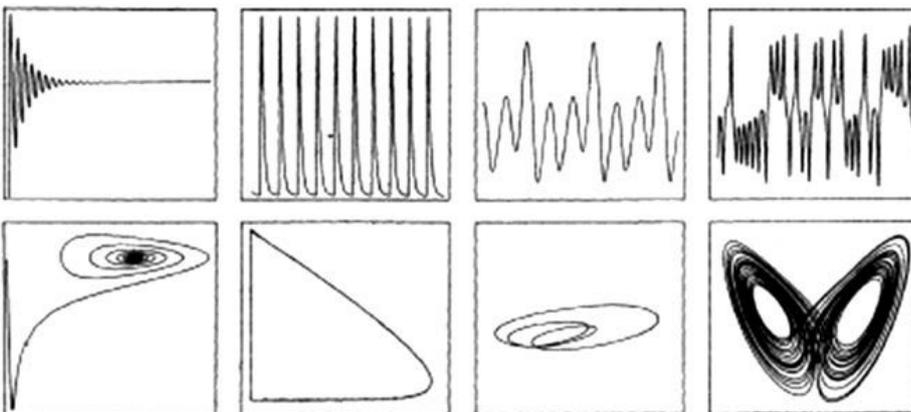
-Where Φ is the Heaviside function that is:

$$\Phi(x) = 0 \text{ if } x < 0$$

$$\Phi(x) = x \text{ if } x > 0$$

- w_{ij} are parameters: the weight of any gene interaction w_{ij} can be negatively
 - K_i and m_i are parameters for each generate

4. Calculate the concentration of each gene over time until equilibrium with your own code.
5. The code can only use control instructions and basic mathematical operations: +, -, *, / and transcendental functions. This means you cannot use already made functions to calculate differential equations or alike. The code should be written in either of these languages: perl, python, C, C++, fortran, fortran90, R, matlab, mathematica, basic.
6. Find the most interesting type of attractor in your network. Different attractors may be possible depending on the initial condition and parameter values and gene network you chose. Your grades will depend on the type of attractor you find. 7 points for fixed points, 8,5 for limit cycle (periodic dynamics), 9 for torus and 10 points for a strange attractor (chaotic dynamics).



Fixed point

Limit cycle

Torus

Strange

8. Send some plot proving the kind of attractor you found (for example gene concentration vs time)
9. Send the code
10. Code and plots should be send in a single pdf file. The name of the pdf should include the NIU of the two students.