

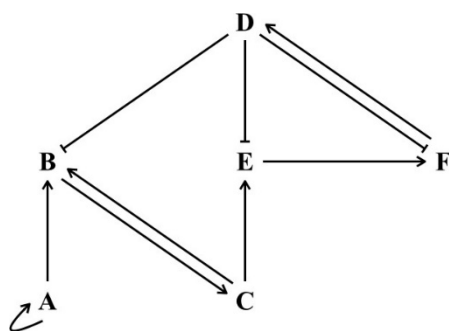
10 Project 10

- Deadline: 12.01.2020, 23:59
- All files need to be available through your GIT repository, in the directory “Project 10”.
- You can work in teams up to 3 people. Please state in the report the group member names.
- If your code is in python, I must be able to run your code within a Google Colab notebook. If your code is not in Python or R, you must provide a manual how to compile and run it on a Linux machine.

We will use the “The CoLoMoTo Interactive Notebook” by Naldi et al. (<https://colomoto.github.io/colomoto-docker/>) to model and simulate complex biological systems.

10.1 Modeling and Simulation of a simple boolean network

(1a) Implement and simulate the following 6 gene network (as a boolean network):



* A line with an arrowhead means activation while a flat stands for an inhibition, e.g. **A** activates **B** and **D** inhibits **B**.

* Enumerate the initial states in the following way: convert the binary levels of the genes into an integer where **A** is the least and **F** the most significant bit. A state where **A=1, B=0, C=1, D=1, E=0** and **F=0** would translate into $1+4+8 = 13$.

* Use a synchronous update schema.

(1b) Determine the attractors and the corresponding basins of attraction.

(1c) Interpret the results.

10.2 Modeling and Simulation the quorum sensing of *Vibrio fischeri*

Implement, simulate and analyze the quorum sensing of *Vibrio fischeri*. Use the information given in the lecture slides or other resources you might find.

10.3 Deliverables

Your need to upload all source codes and a report to your GIT repository.

- The report should be about 600-1200 words in length (this is roughly 1-2 pages, depending on your layout).
- The report must be delivered in PDF format using the BMC template (including the abstract as defined in project 5).
- The following sections must be present (you can add more if needed):
 - Toy Model
 - Implementation and Simulation
 - (1) Describe briefly how the model was implemented and
 - (2) the simulation was performed.
 - (3) Visualize the implementation using GINsim.
 - (4) Perform simulations starting from states 1, 4, 21 and 33. List the individual sequences that you get.
 - Attractors & Fixpoints
 - (1) Analyse, how many attractors exist. List the found periodic orbits with their respective lengths and basins of attraction.
 - (2) Give the relative coverages of the state space by the basins of attraction. Important: Make sure to consider all possible initial states.
 - (3) Compute and list up to three the fixpoints of the network and
 - (4) visualize one using GINsim.
 - Interpretation
 - (1) Briefly describe / characterize the attractors in terms of the active genes. Which are the special genes and what are their respective effects on the behavior of the network?
 - (2) Explain what is determining the period of the orbits.
 - (3) Compare the two shorter orbits which each other. Which gene is responsible for the difference?
 - Quorum Sensing Model
 - Background and Description of the model
 - Describe briefly the biological background of the model.
 - Implementation and Simulation
 - (1) Describe briefly how the model was implemented and
 - (2) the simulation was performed.
 - (3) Visualize the implementation using GINsim.
 - Attractors & Fixpoints
 - (1) Analyse, how many attractors exist. List the found periodic orbits with their respective lengths and basins of attraction.
 - (2) Give the relative coverages of the state space by the basins of attraction. Important: Make sure to consider all possible initial states.
 - (3) Compute and list up to three the fixpoints of the network and
 - (4) visualize one using GINsim.
 - Interpretation
 - (1) Briefly describe / characterize the attractors in terms of the active genes. Which are the special genes and what are their respective effects on the behavior of the network?
 - (2) Explain what is determining the period of the orbits.