On the final evaluation

Instructions

Each student is assigned a final project on one of these topics (described in the presentations):
- chemotaxis
- neuroscience
- pattern formation

For the final evaluation, you should then submit your jupyter notebook and present your work in a final presentation.

The presentation should be given in English, last **15 minutes** (ideally, taking up to 2 extra minutes is acceptable), and be structured as follows:
1. give a brief **introduction** to the topic and the kind of problems that we would like to address,
2. explain the mathematical **model** used to describe the system under investigation,
3. present the **results** of the simulations (questions described below),
4. **discuss** your findings.

In addition to the presentation, you should **submit the relative jupyter notebook at least one day (24 hr) before your scheduled presentation**, so that the actual simulation code can also be evaluated and discussed after the presentation.

Evaluation scheme

The final grade is out of 100 points: 50 based on participation (engagement in class activities) and 50 based on the final project.

The final project will be evaluated as following (total: 50 points):

- Quality of the implementation of the model (15 points):
  - The code is well-organized, well-commented, and easy to understand (for example, you should organize your code into functions that are reused thoughout the code, without copying pieces of code over and over; the notebook should not include unused code)
  - The mathematical model is implemented correctly
  - The implementation is efficient, without performing operations that are not required, and uses numpy functionalities when appropriate
- Quality of the the presentation (15 points):
  The presentation gives a clear introduction and shows the student has a good understanding of the topic.
  The mathematical model is well explained, for example including its assumptions, limitations, range of applications, and meaning of the various parameters where appropriate.

Your results are appropriately discussed in reference to the topic. What is the meaning and the implications of your findings? How do they relate to the past literature and the theory on the topic?
The presentation is well-structured, it follows a logical argument, and contains clear and illustrative graphs (with labels etc.).

- Quality of the results and analysis (20 points):
4 tasks, each valued 5 points, are provided below for each project (described below).

Key tasks for the various topics (each 5 points)

Chemotaxis

- Implement regulatory network of sensing and adaptation, showing how the amount of active receptor changes upon a sudden change in ligand concentration (sensing), and also showing that the amount of active receptor should eventually go back to its equilibrium value before the signal (adaptation).
- Implement the full model of bacterial chemotaxis, showing that, given a non-uniform concentration of ligand, bacteria spend more time in regions with higher attractant concentration (you will need to make a histogram of the bacterial positions for this, for example using matplotlib.pyplot.hist). Give a clear explanation for why the mechanism actually works.
- Design a series of environemts with varying position-dependent ligand concentrations. For example, concentrations that are zero in half of the box, and non-zero somewhere else, of that grow linearly, or quadratically, with different slopes. Show that the bacterium can efficiently find food in all the various environments, regardless of the details of the environment (such property is called robustness).
- Evaluate the effect of cooperativity (the exponent in the relation between active receptor concentration and tumbling rate), or a mutation that affects the value of koff on the bacterium performance. Define a conveninent quantitative measure of bacterium performance, and show how this changes as a function of of cooperativity (between 1 to 20) and koff (for koff = 0.01, 0.1, 1, 10, 100).

Neuroscience

- Reproduce the behavior of different types of neurons as reported in the reference paper.
- Implement the mammalian cortex model from the same paper and try to reproduce the results about neuron synchronization (in order to reproduce the results, the model should be implemented as described in the paper, since it is very sensitive to minor details; in addition, it may be useful to slightly change the strength of the synaptic connections from the excitatory neurons compared to the value used in the paper). It is useful to plot, as a

function of time, the sum of the membrane potentials over all the neurons, or, as done in the paper, a 2d plot with time and neuron id indicating the neurons that fired (to do this, you can use the function imshow() from pyplot).

- Describe how the behavior (especially, synchronization) of the cortex changes as we increase or decrease the strength of the synapses (compared to the default parameters), or we change the proportion of inhibitory and excitatory neurons.
- Based on the implementation of the mammalian cortex, implement a model of two neurons connected by a synapse, which links the pre-synaptic neuron to the post-synaptic neuron. Tune the parameters of your model to show evidence that an action potential in the pre-synaptic neuron can propagate to the post-synaptic one if the synapsys is excitatory (note that compared to the cortex simulation, you may need change the synaptic strengths, the thalamic noise input, or other parameters).

Pattern formation

- Implement the Notch-Delta model for 2 neighboring cells in the absence of mutual inhibition, showing how the behavior changes as a function of the 2 cooperativities. What values allow for pattern formation?
- Implement the Notch-Delta model for 2 neighboring cells in the presence of mutual inhibition, showing how the behavior changes as a function of the 2 cooperativities. How do the results change compared to the case without co-operativity? Based on the literature, comment on the advantages and disadvantages of each model.
- Implement both models for a "tissue" of N cells aligned in one dimension, using periodic boundary conditions (cell N is neighboring with cell 1), and explore the formation of pattern starting from a uniform situation for various model parameters.
- One possible result of pattern formation via the Notch-Delta is the formation of "defects" consisting of neighboring cells with the same cell type. Explore how this situation may arise in a 1d tissue of cells and what parameters favor or disfavor the formation of such defects.

Extra tasks

Perfectly carrying out the tasks above correctly is sufficient for getting the full grade. However, the students are also encouraged to extend their models or to use them for extra tasks based on their own initiative. If relevant to the topic, valuable work in new directions may be rewarded with up to 5 extra points in the final evaluation. Here are a few directions in which you may want to extend your work:

- Chemotaxis: placing bacteria in a more complex environment (for example some kind of labyrinth as opposed to a square box), natural selection of bacteria with parameters that are optimal for chemotaxis.

- Neuroscience: implementation of spike-timing synaptic plasticity (STSP) for long-term potentiation and depression, neural network learning for pattern recognition.
- Pattern formation: cell differentiation in 2 dimentions, comparison with other types of pattern formation such as Turing patterns.