MODELING BIOLOGICAL SYSTEMS

INSTRUCTIONS TP-TD3

General reminders for reports

- Provide answers to all questions, no matter the form. You can write an answer directly, detail a mathematical solution, provide a diagram, a graph or a code. All of this must appear in your report.
- If the question concerns programming, or requires you to code something for the answer, please include your code to any answer you might provide. Your code needs to be a "standalone" in your report, *i.e.* all the code provided can be exported with an easy *copy and paste*, and it should run as it is. Do not forget to include any library you would use, or any variable you might have created earlier. You do not have to give every library for each question, but it needs to be presented at least once if it was used in your code.
- Please pay particular attention to the way your different elements stand out : **rewrite the question number** at the beginning of your answer ; make your code, formula and text **distinguishable from each other**, etc...
- **Make sure the resolution of your graphs and diagrams is sufficient** to retrieve the information. And be careful not to crop your code by mistake neither.
- Always add a legend to figures (with x-axis and y-axis titles) and tables, and analyze their content in your answer.
- Upload your work **with a PDF format**, and add the code you programmed.
- If you see that some of your results are incoherent, for example if the mathematical solution and the graphical solution you provided do not show the same results (or do not fit at all!), **say it**. **Always explain when you can see an error**, even if you are unable to solve it, and provide hypothesis as to where the mistake could be.

The answers to the following exercises are to be written in a report to be uploaded on *DeVinci-Online Brightspace* (TD4 - Tutorial 4 Report). **The deadline is November 27, 2022 (23:59).**

I - Exercice 1

The *Ricker model* (Ricker 1954) is a population dynamic model that is often used in fishery management. It can be expressed by the following equation:

$$N_{t+1} = N_t e^{r(1-\frac{N_t}{k})}$$

Where :

- *r* is the growth rate,
- k is the carrying capacity of the environment

Questions :

A. Use the graphical method to get some first insights into the behavior of this model. (You can use R or Python to plot the function, diagonal and lines)

B. What are the equilibria of this model?

C. Determine the stability of the equilibria.

D. Use R to create and plot the model, and corroborate graphically your results of equilibria and stability (explain the examples you present, and how they prove your findings).

E. How does this model compare to the *logistic model*?

II - Exercice 2

During our class, the simple *natural selection model* assumed that there is only a single, closed population in which the dynamics take place. One extension of this model that relaxes this assumption might assume that there is a continuous migration from another population consisting of only *B type* individuals (*A type* being implicit). This new extended model can be described by the recursion equation:

$$p_{t+1} = m + (1 - m)\frac{(1 + s)p_t}{1 + sp_t}$$

Questions :

A. Provide an intuitive explanation for this equation and the new parameter m.

B. What are the equilibria of this model?

C. Determine the stability of the equilibria.

D. Use the graphical method to gain additional insights into your model and compare the plot with your analytical results.

E. How does migration impact the dynamics compared to the simpler, one population model?

III - Exercice 3 (facultative in the report)

The polymerase chain reaction (PCR) is a powerful and very widely used molecular method to amplify DNA fragments.
Here is how it basically works, to amplify a DNA fragment you need:

- The double helix DNA strands to replicate, your "template" DNA, from which you are going to target a specific sequence, usually between 0,1 and 10 kilo base pair (kbp) long
- An enzyme, the DNA polymerase (hence the name)
- Primers. A primer is a short single strand of DNA, able to bind to DNA strand
- Nucleotides
- A buffer solution, to create a viable environment
- Bivalent cations, like magnesium ions

A cycle of PCR takes 3 successive phases:

- (Phase 1) *Denaturation*: the solution is heated to above 90°C, in order to break the hydrogen bonds between the two strands of DNA
- (Phase 2) *Annealing*: at a lower temperature, primers are going to bind to the DNA strands. Primers match specific sequences of DNA and are used to start the process. You need one primer per DNA strand
- (Phase 3) *Extension*: the polymerase uses the available nucleotides to create complementary DNA strand for each of the original strands. This create more strands of identical DNA The cycle is repeated several times, usually about 40, to create a large number of copies.

This cycle is then repeated several times, usually about 40, to create a large number of copies.

For this exercise, it is asked to develop a model that predicts the number of DNA fragments after each round of amplification, for each of these situations :

A. Assume that there is always an excess of primers and nucleotides present in the solution, and that all DNA fragments are copied in each round of replication.

B. Assume that there is always an excess of primers and nucleotides present in the solution, but that now a certain fraction of DNA fragments fails to replicate in each round.

C. Assume that all DNA fragments can be replicated in principle but that now primers are no longer present in excess. (There might be enough primers for the first few rounds but not for later rounds.) Nucleotides are still always present in excess.

D. Finally, assume that all DNA fragments can be replicated in principle and that primers are always present in excess, but that the number of free nucleotides in the solution can become limiting. To keep the model simple, just assume that a certain fixed number of nucleotides is required to replicate one DNA molecule, but do not distinguish between different types of nucleotides. Note that this model version is more challenging than the others in that it will probably require more than one variable!

Useful links for the last exercise :

- in English :
https://www.britannica.com/science/polymerase-chain-reaction

- in French :
https://www.gnis-pedagogie.org/sujet/coeur-adn/