

Home Exam BIOS13 Modelling Biological Systems

Dept. of Biology, Lund University, 2022-2023

Deadline: Tuesday Jan 10, 2023 at 16:00

Instructions

Solve the problems on your own, without discussing with your classmates. Needless to say, working in groups or copying text from elsewhere will be cheating and thus render repercussions. Cross-referencing of answers will be done within the class but also to exam answers from previous years and the internet. Email me questions if you need clarifications or have other issues. I will respond to the whole group.

The exam is set up as four separate assignments, corresponding to the four (main) questions found below, numbered 1-4. Prepare your answers as one main document per question (in total 4). Use Word or pdf format and all text should be written in a text editor. Scanned or photographed hand-written equations or illustrations are allowed, *as long as they are easy to read and properly imbedded in the total answer.*

Please paste the required R code in the answer document, with the code in the word/pdf-document it is easier for me to comment the code. In addition, make sure to provide the code as separate R-files (you can submit several files to the same assignment). Do make sure it is obvious which code belongs to which (sub-)question! Also, do make sure that I can run the scripts, code that does not run will not be considered! Test them yourselves by clearing the workspace and using source:

```
> rm(list=ls())  
> source('my_script_1.R')
```

Any code that solves the task at hand is fine with me. It is perfectly allowed to use modified scripts from exercises or lectures. *However*, make sure to remove bits of code that do not contribute to the solution of the problem at hand. Otherwise, I may get the impression you do not know what you are doing and will grade accordingly.

Present the necessary steps of all calculations, at least briefly. Even an incorrect answer can give you points if the equations were put up correctly.

If a problem depends on the answer of a previous problem, and you failed to solve the previous problem, at least describe how you would proceed *if* you had the answer.

Submit your answers at the very latest on **Tuesday Jan 10, 2023 at 16:00.**

GOOD LUCK!

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1. Genetic Algorithms (GA) and Artificial Neural Networks (ANN)

- a) Describe how you step by step would construct a binary genetic algorithm for a complex problem (4p).
- b) Why does a single layer perceptron need a bias? (1p)

2. Protein production (6p)

Assume a cell produces a particular protein at a fixed rate a . The protein leaks out of the cell membrane at a rate depending on the protein concentration within the cell. The dynamics of the protein concentration in the cell can thus be written

$$\frac{dP}{dt} = a - bP$$

where P is protein concentration and b is a 'leaking rate'.

a) What is the equilibrium protein concentration in the cell? (1p)

b) Show (mathematically) that it is a stable equilibrium. (1p)

Assume further that the cell also produces *another* protein, Q , which catalyzes the breakdown of P . The production of Q is stimulated by the concentration of P . One can think of Q as a way to regulate the concentration of P . The combined dynamics of P and Q can now be written

$$\begin{cases} \frac{dP}{dt} = a - bP - cPQ \\ \frac{dQ}{dt} = rP - bQ \end{cases}$$

where it is assumed that Q has the same leaking rate b as P .

c) Calculate the equilibrium (P^*, Q^*) . (1p)

d) Trajectories of the protein dynamics can be visualized in the system *phase space* (or phase plane). What are the coordinate axes of this phase space? (1p)

e) Write an R script that

- i)* plots the isoclines in the phase space of the system above (1p)
- ii)* simulates the dynamics and plots the resulting trajectory in the same phase space. (1p)

3. Bumble bee colony growth (5p)

Bumble bees have colonies that start with a single queen in spring. She produces workers, that, as they mature, help produce new workers. At some point, a switching time t_s , the colony switches to produce new queens (and drones) instead. Queen production continues until the end of the season (at time T). The new queens mate and then hibernate until next spring, when they form new colonies.

The growth of the worker population (W) before the switching time can be formulated as

$$\frac{dW}{dt} = rW$$

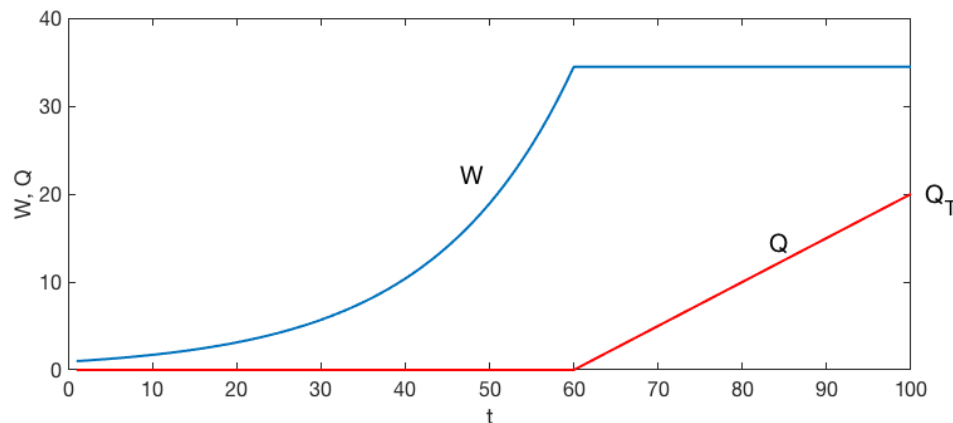
where r is a positive constant ($r > 0$).

a) Assuming the colony starts with a single worker at $t = 0$, what is the number of workers at the switching time t_s ? (1p)

After the switching time, the number of workers is assumed to remain constant (assume they don't die). The production of queens (Q) depends on the number of workers, following

$$\frac{dQ}{dt} = cW$$

where c is another positive constant. Queen production is thus constant until the end of the season, and the total number of queens in the colony grows linearly with time (following a straight line). An example season is depicted below (using $t_s = 60$, $T = 100$).



b) What is the number of queens at the end of the season, Q_T ? Express it as a function of the switching time t_s and the parameters r , c and T . (1p)

c) Colony fitness can be assessed by the number of new queens it can produce. Calculate the optimal switching time that maximizes Q_T , i.e. that maximizes the number of queens at the end of the season. (1p)

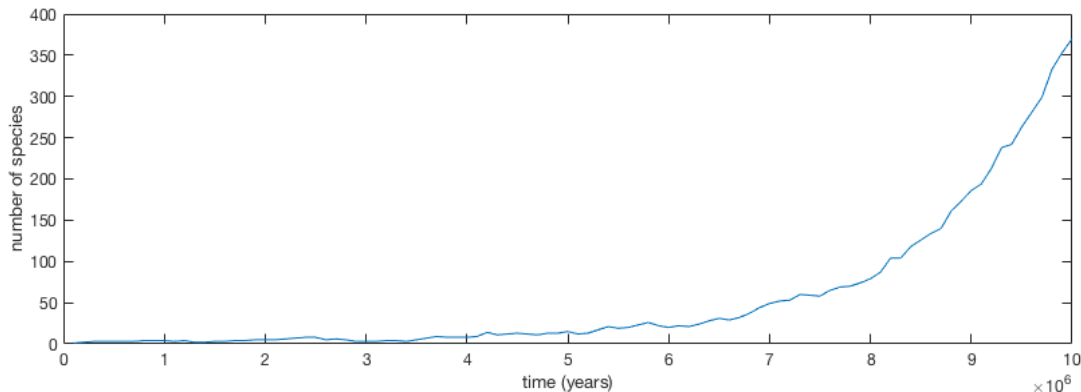
d) Extend the model to include worker and queen mortality. Motivate (briefly) your model extension. (1p)

e) Write a script in R that simulates colony growth (following your extended model in *d*)) and produces a plot similar to the one above. (1p)

4. Phylogenesis (4p)

The number of species within a lineage increases with speciation events and decreases with extinction events. For simplicity, assume a species goes extinct with probability P_E within a period of 100,000 years. *If it does not go extinct*, it may speciate (and become two species) with probability P_S during the same time period.

a) Write an R *function* that simulates the number of species N over a period of 10 million years, plots the number of species over time, and *returns* the number of species present after 10 million years. The function should take the extinction probability P_E and speciation probability P_S as input parameters. (2p)



b) Write a script that uses the function above to simulate the evolutionary process above 1000 times and plot a histogram of the number of species after 10 million years. Use $P_E = 0.1$, $P_S = 0.2$.

For this task, it is advisable to turn off the plotting of species over time.

Tip: The R-function `hist(v)` makes a histogram of the data in vector `v`.

(1p)

c) It can be assumed that closely related species compete with each other to some extent, and that niche space is limited. Modify (somehow) the function in *a)* such that the probability of speciation is *density dependent*, i.e. assume P_S declines with the number of species. Motivate (briefly) your model choice. (1p)