Home Exam BIOS13 Modelling Biological Systems

Dept. of Biology, Lund University, 2023-2024

Deadline: Tuesday, Jan 9th, 2024 at 16:00

Instructions (written exam)

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 embedded 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 on 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 9th, 2024 at 16:00**.

Instructions (oral exam)

Upload one PowerPoint presentation per question 2-4 and prepare to present it in a 10-minute oral presentation. Be prepared to present all three presentations (I will choose which one(s)) at the oral exam session.

The presentation should clearly describe the following:

1. The overarching scope of the problem (1-2 sentences). Put the exam problem in a broad context.
2. The specific scope of the problem (1-2 sentences). Why is these problems of particular interest for science?
3. Specific questions (essentially the questions posed in the exam)
4. General description of how you answered the questions (e.g. "*I solved question a. by solving equation 1 mathematically by rearranging…*" or "*I solved question b. by coding a simulation model that includes…* ").
5. Specific description of how you answered the questions (e.g. "*Specifically I used the chain rule and I implemented my simulation using a nested for-loop*"). Show equations and code if needed but illustrations for code structure is also good.
6. Clear results in equations and plots (mind notation, panel titles, axes, scales, etc)
7. Interpretation of results given your scope

Note: Put a **strong** emphasis on points 4 and 5 above as this is what is evaluated. At least 7 minutes should be devoted to these points. Also make sure that you stick to 10 minutes, I will interrupt you when time is up.

GOOD LUCK!

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Exam Questions

1. Describe shortly step-by-step how a genetic algorithm works according to Anders' lecture on this. You can chose to either describe a binary or a continuous GA. **(5p)**

2. Optimal fishing of an unstructured population (6p)

Consider a fish population that grows according to

$$\frac{dn}{dt} = rn\left(1 - \left(\frac{n}{K}\right)^2\right),$$

where *r* and *K* are positive constants.

a) What is the (non-trivial) equilibrium population size? (1p)

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

Now assume the population is harvested, such that a proportion *h* is harvested per time unit.

c) Add the harvesting to the population dynamic model! (1p)

d) Where is the new equilibrium population size? (1p)

e) At what harvest rate does the population go extinct? (1p)

f) At what harvest rate is the yield, i.e. the total number of harvested individuals, maximized? (1p)

3. The dynamics of an age-structured population (10p)

Consider a population consisting of juveniles (J) and adults (A). The juveniles mature to become adults at a rate g but also die at a rate μ_J. The adults reproduce at a rate b and die at a rate $\mu_0(1 + cA)$, where c is a positive constant representing density dependence of the mortality. The dynamics can be written

$$\begin{cases} \frac{dJ}{dt} = bA - gJ - \mu_J J \\ \frac{dA}{dt} = gJ - \mu_0(1 + cA)A \end{cases}$$

a) Where is the non-trivial equilibrium? (1p)

b) Calculate the Jacobian matrix of that equilibrium! (1p)

c) How would you use the Jacobian to evaluate the stability properties of the equilibrium (don't do it!)? (1p)

d) Write an R script that plots the isoclines of the system! (2p)
(Use if you wish the parameter values $b = 1,\ g = 0.5,\ \mu_J = 0.3,\ \mu_0 = 0.2,\ c = 0.01$)

e) Write another script that simulates the differential equations and plots the result in two ways: *i*) as A and J vs. time and *ii*) in the phase plane together with the isoclines. (2p)
(you may use the same parameter values as above, and an initial condition of your own choice)

f) Extend the model to include cannibalism, i.e. that adults feed on the juveniles (a common behaviour among many fish, reptiles, and other groups). Motivate all model extensions! Feel free to make extra assumptions, if necessary. The Lotka-Volterra predator-prey equations may be a source of inspiration. (3p)

4. The spread of a gene (7p)

The relative frequency p of a gene with fitness w in a population of size N has the approximate dynamics

$$p_{t+1} = \frac{w}{\overline{w}_t} p_t + \epsilon_t$$

where $\overline{w}_t$ is the population mean fitness at time t according to

$$\overline{w}_t = wp_t + 1 - p_t$$

and the random deviates ϵ_t are drawn from a Normal distribution with mean zero and the standard deviation

$$\sigma_t = \frac{1}{\bar{w}_t}\sqrt{\frac{w}{2N}p_t(1-p_t)}$$

It is assumed that the rest of the genes in the population have fitness equal to 1. The focal gene is thus at a fitness advantage if $w > 1$.

a) Ignoring the stochasticity (setting $\epsilon_t = 0$), show that $p^* = 0$ and $p^* = 1$ are the only equilibria of the system (assuming $w \neq 1$). (1p)

b) What are the stability criteria for $p^* = 0$? (1p)

c) Now taking the stochasticity into account again, write an R script that runs a simulation of p_t for 1000 generations and plots the resulting time series. The starting p-value should be 1/(2N), corresponding to a single mutant allele of a diploid individual.
Tip: Break the simulation as soon as p_t is equal to or below zero. Do the same thing as soon as p_t is at or above 1. The `break` command may be useful. (2p)

d) Write a *function* that takes N and w as input parameters, runs 1000 simulations like the one above and returns the probability of fixation, i.e. the probability that p reaches 1 within 1000 generations. (2p)

e) Write a script that uses the function in d) and plots the probability of fixation for a range of w-values from 0.9 to 1.1. Do the plot for $N = 20$ and $N = 200$. (You should be able to see that small populations are more likely to accumulate deleterious mutations than large ones.) (1p)