Home Exam BIOS13 Modelling Biological Systems

Dept. of Biology, Lund University, 2024-2025

Deadline: Tuesday, Jan 14th, 2025 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 14th, 2025 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. ANN and GA (5p)

1. You should now be familiar with the simplest artificial neural network, the single-layer perceptron consisting of one node with two inputs and a bias.

a) Explain why it cannot solve the logical operator XOR? (2p)

b) What will happen with the separation line if we remove the bias (or set it to 0)? (1p)

c) Give four differences between a binary (0 and 1) and a continuous (decimal numbers) genetic algorithm? (2p)

2. The dynamics of a spatially structured population (8p)
First consider a single population that follows the dynamics

$$\frac{dn_1}{dt} = (r_1 - kn_1^2)n_1,$$

where n_1 is population size, t is time, r_1 is the 'intrinsic growth rate' and k represents the strength of density dependence. All parameters are positive, i.e. larger than zero.

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

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

c) Write a script in R that plots $\frac{dn}{dt}$ as a function of n. Choose the parameter values yourself. (1p)

Now assume there is a second population of the same species that has the dynamics

$$\frac{dn_2}{dt} = (r_2 - kn_2^2)n_2.$$

Further assume that there is one-directional dispersal (one can think of drift down a stream or in a prevailing wind direction) from population 1 to population 2, such that a proportion m of population 1 disperses to population 2 per time unit. In other words, individuals disperse from population 1 to population 2 at a rate mn_1 per time unit.

d) Write down the new equations for the dynamics of n_1 and n_2, given the migration described above. (1p)

e) What is the new equilibrium of population 1? (1p)

f) Population 1 loses a lot of individuals through this one-directional dispersal. Above what value of m does population 1 go extinct? (1p)

g) Write an R script that simulates the coupled dynamics of n_1 and n_2 and plots them as functions of time. (2p)

3. Introgression (6p)

The process of 'foreign' genes entering, and becoming established in, a population is called introgression. For example, one can follow the introgression of genes across hybrid zones, where genes can travel from one population (or species) to another. A famous example is the finding that all humans with ancestors from outside Africa have a small proportion of Neanderthal genes, probably a result of hybridization and introgression that happened a long time ago. We shall now study the process of introgression, keeping things as simple as possible.

Consider a haploid population of n individuals (n is fixed). Each individual carries a genome of L genes. The genes can be of two types, the old type and the 'new' type. If we represent the old type with zeros and the new type with ones, an individual that carries some old and some new genes could be represented by a sequence like 0110 (for the case $L = 4$).

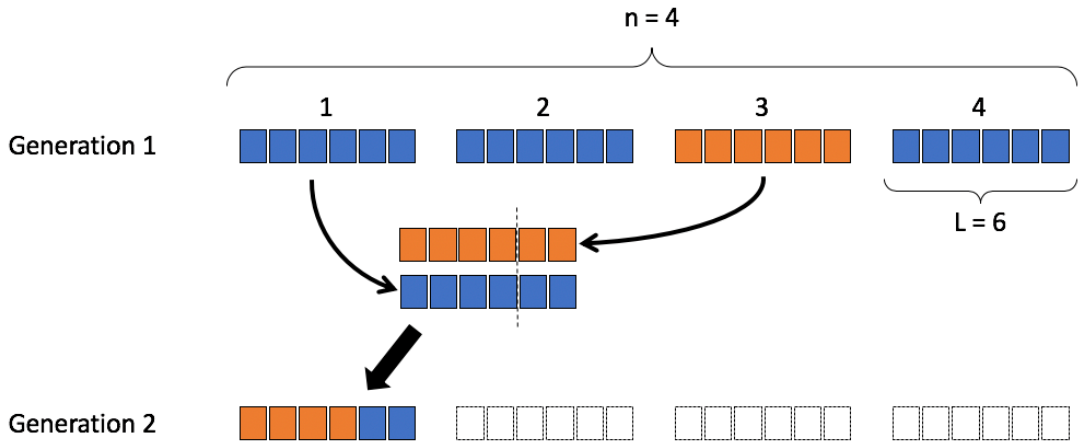
Each generation, the individuals mate randomly and the offspring is formed through recombination. More precisely (see figure):

Start the simulation (generation 1) with a single individual with a completely foreign genome (orange in the figure).

For each individual of the next generation:

i. choose two parents randomly from the parent generation
ii. pair up their genomes and choose a random point of gene crossover (dashed line in figure).
iii. put the recombined offspring in the next generation
iv. repeat until the new population is full

The new population then replaces the old one and the whole procedure repeats. There is no selection for or against the new genes.

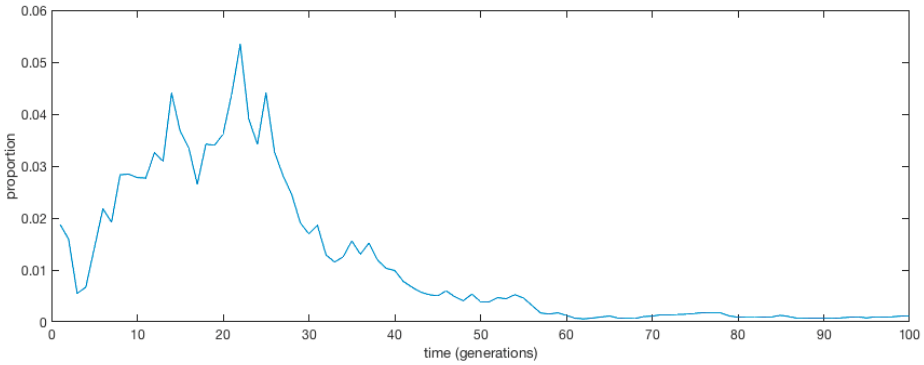


a) If you would write a program to simulate this process, what would be an appropriate representation of the population, describing the current 'system state'? (1p)

b) Write a *function* in *R* that takes two parent genomes as input and returns a single recombined offspring genome, following the procedure of recombination described above. (2p)

c) Write a script in R that uses the above function and simulates the population for 100 generations. For your own convenience, write it such that you can easily change the population size n and the genome size L. (2p)

d) Revise the script to calculate the proportion of new genes in the population for each generation. Plot the result as a proportion over time (example figure below). You may notice that quite often there is no introgression, i.e. the new type disappears from the population. Use $L = 100$ and $n = 100$. (1p)



e) *Extra (no points!)*: After a long time, say 1000 generations, most new genes (out of the original L) have either gone extinct or come to fixation. The population now has a mixed genome of old and new genes (like non-African humans). Add a few lines to your script to also plot the frequency of new genes at each locus of the final population. You may find short sequences of introgressed genes spread out over the genome, but usually they occur together, side-by-side. Can you think of why? (0p)

4. The dynamics of a chemical reaction (4p)

A mixture has two chemical compounds, X and Y. Two units of X can combine and form a single unit of Y. The compound Y is, however, unstable and spontaneously disintegrates into two units of X. The chemical reactions can be written

$$2X \leftrightarrow Y$$

The dynamics of the corresponding concentrations, denoted x and y, respectively, follow

$$\begin{cases} \frac{dx}{dt} = -2kx^2 + 2\mu y \\ \frac{dy}{dt} = kx^2 - \mu y \end{cases},$$

where k and μ are positive constants.

a) Show that the system has a whole suite of equilibrium states (which depend on the initial conditions, i.e. x(0) and y(0)) (1p)

b) Write an R script that plots the possible equilibria in the xy phase plane. (1p) (Any positive values of k and μ will do)

c) Write another script that simulates the differential equations above, using a few different initial conditions, and plots the result in two ways: *i*) as x and y vs. time and *ii*) in the phase plane together with the solution in b). (2p)