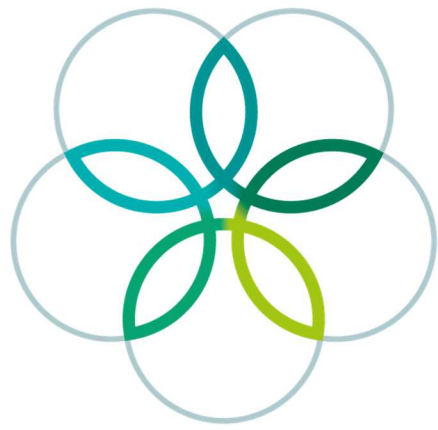
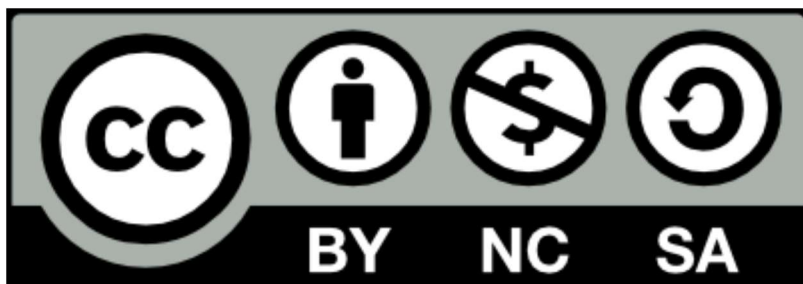


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IBO 2018, Tehran, Iran

Practical Exam "Evolution, Ecology & Behavior"

Student Code:



IBO 2018 Tehran, Iran

29th International Biology Olympiad
July 15-22, 2018

Practical Exam
Evolution, Ecology & Behavior

Total Points: **100**

Duration: **90 minutes**

General information

Total points: 100

Exam time: 90 minutes

Please check your student code in the box on the title page.

Use answer sheet, which is provided separately to answer all questions.

The answers written in the question paper **will not** be evaluated.

In order to use the yellow flag (the sign on your desk) just put it in the flag stand located on the left wall of your desk.

Please ensure that all the materials and equipments are available to you. If anything is missing, put your yellow flag in the flag stand no later than 15 minutes after the beginning of the exam. (Any complaints after 15 minutes will not be accepted)

In case of emergencies put your yellow flag in the flag stand.

We suggest you to read the entire protocol before starting the experiments which helps you with time management.

Stop answering and put down your pen immediately at the end of exam. Put the entire protocol with the answer sheet in the envelope. Our assistants will collect the envelopes.

Good luck

Write each indicated number in the cell next to it with your own handwriting.

1	
7	

PART A - INVESTIGATING A MODEL OF BIOLOGICAL DIVERSIFICATION

There are around 10 million different species of eukaryotes on this planet. Including prokaryotes would increase our estimate of the number of extant species on our planet drastically. Understanding why there is so much diversity on Earth has been one of the central questions in evolution and ecology. Rainey and Travisano (1998) attempted to answer certain aspects of this question in the lab. As their model organism, they used a prevalent aerobic bacterium, *Pseudomonas fluorescens*.

Starting from a monomorphic population of *P. fluorescens*, they allowed bacterial cells to grow in a static broth culture, i.e., a beaker that is not shaking. The morphology of the ancestral population could be described as “smooth”, referring to the smooth colonies it would form on a petri dish. It has been shown that two other morphologies are possible in *P. fluorescens*: wrinkly spreader and fuzzy spreader (**Figure 1**).



Figure 1: The three different morphologies of *P. fluorescens*: Smooth (SM), wrinkly spreader (WS), and fuzzy spreader (FS).

A bacterial lineage was established and evolved in the static environment for 7 days (in a beaker with 25ml of broth at 28 °C). After 7 days, Rainey and Travisano transferred a sample of bacterial cells from the first lineage -i.e., the lineage that evolved for 7 days in the static environment - and established the second lineage. They allowed the first and the second lineage to evolve for another 7 days, in static and shaking environments, respectively. (At the end of each day, a subsample from the current beaker was transferred to a new beaker with fresh media to keep the lineages evolving.) (**Figure 2**).

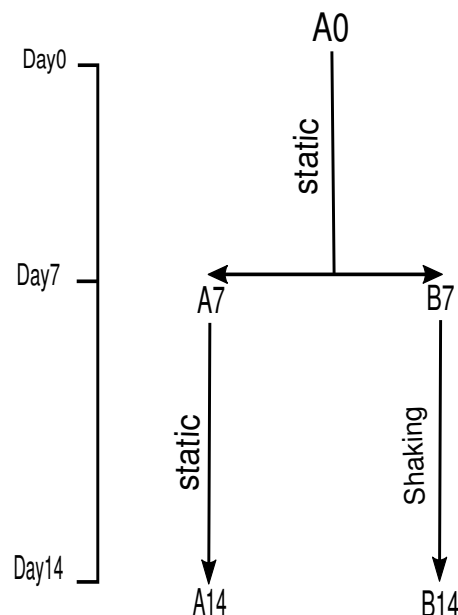


Figure 2: The schematic representation of the experiment conducted by Rainey and Travisano

Here, you will play the parts of Rainey and Travisano and try to make sense of the results observed by them. You are given plates from an experiment done in the exact same fashion as the one carried out by Rainey and Travisano. The plates are created by sampling from evolving populations at different stages (as shown in **Figure 2**).

Change in the phenotypic diversity

Count the number of different morphs you see on each plate (Assume each plate is representative of its original population). For each plate, you can calculate the level of heterogeneity (H) using this formula:

$$H = 1 - \sum_{i=0}^n (f_i)^2$$

where f_i is the frequency of morph i on the petri dish and n is the number of morphs present on the petri dish.

A-1) Based on the observed results on plates, fill the table 1 in the answer sheet. (Correct to two digits after decimal point).

Plate	SM (Count)	WS (Count)	FS (Count)	SM (Freq)	WS (Freq)	FS (Freq)	H
A0							
A7							
B7							
A14							
B14							

A-2) Based on the data obtained, indicate if each of the following statements is true or false with a “✓” in the answer sheet.

- a) It is more likely that diversity is due to phenotypic plasticity rather than mutations.
- b) Static environment provides more ecological niches, which increases diversity.
- c) The observed diversity results from mutations that existed in the ancestral population.
- d) Larger subsamples result in higher heterogeneity.
- e) Using bacteria is preferable for conducting this experiment due to short generation time and large population size.

A-3) Assuming that there are only three bacterial morphs, calculate maximum achievable heterogeneity:

PART B

Investigating a model of population evolution

One of the main models for studying population genetics is the Wright-Fisher model (named after two of the founding fathers of the modern evolutionary theory, R. A. Fisher and Sewall Wright).

In its simplest form, the model assumes a population with a fixed number of haploid individuals. Individuals are asexual and simply make copies of themselves to reproduce. In order to create the next generation, one individual is randomly selected from the current generation and contributes one offspring to the next generation. This process is repeated until the next generation reaches the same size as the current one. Note that some individuals can be picked as parents for the next generation more than once by chance alone. After this step, the next generation replaces the current generation. This entire process is repeated to create future generations sequentially one at a time.

If all the individuals in a population have the same fitness, then it is equally likely for each one to be picked as a parent, but if their fitness differ, then sampling process is weighted so that the fitter individuals are more likely to be picked.

On your laptop, there is an application which shows the expected results from a Wright-Fisher model (On your desktop, go to \IBO2018\Task2 and double-click on "WF_model.py" and wait for the application to start). There are 4 variables you can play with. The sliders allow you to change the values for each variable. After you have chosen the desired values for each parameter, simply click on <Simulate> to see how heterogeneity (H) changes over time in the Wright-Fisher model, given the chosen parameters. (See the formal definition of H in **Part A**)

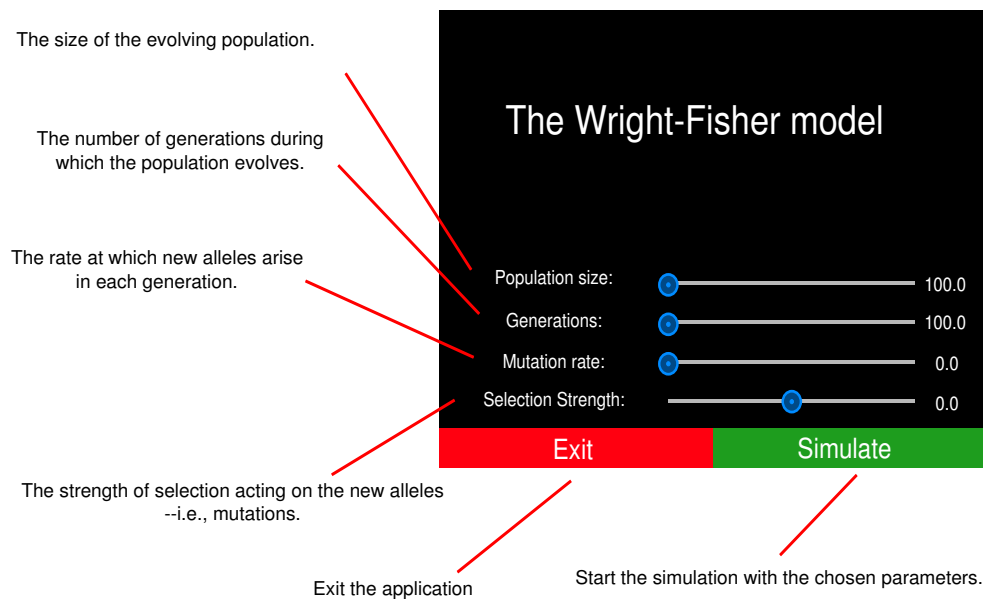


Figure 3: *The interface of the Wright-Fisher model app.*

Using this application, answer the following questions (Keep in mind that the behavior of the model is purely a function of the given parameters).

B-1) indicate if each of the following statements is true or false with a “✓” in the answer sheet.

- A) Increasing the number of generations alters heterogeneity at equilibrium.
- B) Shrinking population size **does not** increase heterogeneity at equilibrium in any parameter set.
- C) Decreasing population size accelerates achieving equilibrium heterogeneity.
- D) Increasing mutation rate accelerates achieving equilibrium heterogeneity
- E) When there is no mutation, increasing selection strength decreases heterogeneity at equilibrium.

B-2) Indicate with a “✓” in the answer sheet which of the following equations about equilibrium heterogeneity best fit with simulation results. (N is population size and u is mutation rate.)

A)
$$H = \frac{4Nu}{1+4Nu}$$

B)
$$H = e^{-4Nu}$$

C)
$$H = \frac{2N}{N+4u}$$

D)
$$H = 1 - \frac{1}{2N}$$

E)
$$H = \frac{1-e^{-2Nu}}{1-e^{-2N}}$$

PART C

*Investigating the feeding behavior in *Drosophila melanogaster* larva*

There are two forms of fruit flies' larva: active rovers and sedentary sitters. Active rovers maneuver through the medium in search for food, while sedentary sitters do not. It seems that these foraging strategies is genetically determined.

In a series of videos on your laptop (IBO2018\Task3), you can see the different types of larva in a population for five consecutive generations (Gen1 to Gen5).

C-1) Using the film from the fruit flies larva, complete the table below (Use the same method as part A to calculate H ; Correct to two digits after decimal point).

Note: For a larva to be counted as a sitter, its **whole body** should **stay in or touch the boundary** of a food patch (two **dark grey circles** in the footage correspond to two food patches) for the entirety of a movie clip.

No. of generation	Sitters (count)	Active rovers (count)	Sitters (freq)	active rovers (freq)	H
1					
2					
3					
4					
5					

C-2) Based on the results indicate if each of the following statements is true or false with a "✓" in the answer sheet.

A) The fruit fly larva foraging behavior follows the optimal foraging theory, which means in each generation the best feeding strategy will be chosen according to the environmental factors.

B) The fruit fly larva foraging behavior follows conditional strategy, which is a mechanism that gives individuals the ability to alter their behavior, in this case foraging behavior between sitter and rover.

C) The results are consistent with negative frequency-dependent selection.

D) Assuming negative frequency-dependent selection is acting on the foraging strategies, none of the strategies can go to fixation in a population.

We can predict the change in the size of population over time by either considering the population itself, or taking into the effect of biological interactions, such as competition, on the population dynamics. Below two models are introduced which represent these two approaches when considering the way a population changes over time.

I: discontinuous model of logistic growth:

$$N_{t+1} = N_t + rN_t \left(1 - \frac{N_t}{K}\right)$$

N_t : population size in generation t .
 r : intrinsic per capita rate of population growth.
 K : carrying capacity.

Note: This model is applicable for both active rovers and sitters.

II: discontinuous model of competition for sitters and active rovers (S, R):

$$S_{t+1} = S_t + r_S S_t \left(1 - \frac{S_t + \alpha_{SR} R_t}{K_S}\right)$$

$$R_{t+1} = R_t + r_R R_t \left(1 - \frac{R_t + \alpha_{RS} S_t}{K_R}\right)$$

S_t : population size of sitters in generation t .
 R_t : population size of rovers in generation t .
 r_S : intrinsic per capita rate of population growth of sitters.
 r_R : intrinsic per capita rate of population growth of rovers.
 K_S : carrying capacity for sitters.
 K_R : carrying capacity for rovers.
 α_{RS} : effect exerted by sitters on rovers through competition on population growth.
 α_{SR} : effect exerted by rovers on sitters through competition on population growth.

C-3-1) Complete the table below based on model I and model II. Parameters of model are as follow (Correct to two digits after decimal point):

Model I:

r	3
K	500

Model II:

r_S	3	r_R	2
k_S	500	k_R	500
α_{SR}	0.1	α_{RS}	0.1

	Model I	Model II	Model II
No. of generation	Sitter (count)	Sitter (count)	Rover (count)
0	184.00	184.00	262.00
1			
2	427.79	343.22	408.41
3			
4	196.94	120.45	381.17
5			
6	371.71	539.93	368.38
7			
8	34.89	571.68	459.81
9			
10	424.04	459.64	522.19
11			
12	182.86	516.81	497.54
13			
14	432.68	589.09	510.47
15			

We have conducted a more extensive study to investigate the long-term change in the frequency of feeding strategies in *D. melanogaster* larva. The result of this study are shown in the table below.

C-3-2) Calculate frequencies of feeding strategies predicted by model I and model II and fill the table below (For model I, since we have rovers in the population in addition to the sitters, to calculate the frequency of the sitters divide the number of sitter by $2 \times K$); Correct to two digits after decimal point).

	Result of our study	Prediction of model I	Prediction of model II	Prediction of model II
No. of generation	Sitter	Sitters	Sitter	Active rover
0	0.41			
1	0.54			
2	0.61			
3	0.62			
4	0.91			
5	0.32			
6	0.68			
7	0.63			
8	0.46			
9	0.27			
10	0.84			
11	0.67			
12	0.47			
13	0.39			
14	0.42			
15	0.54			

C-3-3) Models I and II need some Initial values in order to make predictions; which of the following initial values, is the best? (Indicate with a “✓” in the answer sheet.)

- A) sitter: 289, active rover: 212
- B) sitter: 205, active rover: 295
- C) sitter: 523, active rover: 300
- D) sitter: 307, active rover: 514

Pearson correlation:

Pearson correlation is a mathematical function to estimate the correlation between two sets of data (x_1, \dots, x_n and y_1, \dots, y_n). Correlation coefficient is calculated as follows:

$$\text{correlation coefficient} = \frac{\sum_{i=0}^n (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=0}^n (x_i - \bar{x})^2} \sqrt{\sum_{i=0}^n (y_i - \bar{y})^2}}$$

n = the sample size

x_i = the individual sample points for sample x

y_i = the individual sample points for sample y

$$\bar{x} = \frac{1}{n} \sum_{i=0}^n x_i \quad \bar{y} = \frac{1}{n} \sum_{i=0}^n y_i$$

C-4) Calculate correlation coefficient (r) for the desired correlations and fill in the table below.

Sample x	Observed sitters (frequency)	Observed sitters (frequency)
Sample y	Sitters predicted by model I (frequency)	Sitters predicted by model II (frequency)
Correlation coefficient		

C-5) Indicate each of the following statements is true or false with a “✓” in the answer sheet.

- A) The logistic model I explains the observed changes in frequencies given the parameters.
- B) Your calculations show that including competition in our model significantly increased the fit between model and our observation.
- C) We need to explore the parameter space to establish the ability of these models to explain our observation.
- D) The correlation estimates suggest that the change in the frequencies of sitters and rovers is not due to competition.