

Name _____
(please print clearly) first name last/family name

Bio 112 Survey #1: Evolution

Notes:

1. This is due in lecture TODAY (Monday 1/26).
2. You will receive full credit (10 points) for whatever you write in the space below; there is no need to consult outside sources when working out your answer. The more you write, the better I can teach the course.
3. This is intended to help me in setting up my lectures on evolution and as a warm-up for the material we will be dealing with in the next section of the course.
4. This is also intended to help me in evaluating the lectures and lab.

The Question:

Cheetahs (large African cats) are able to run faster than 60 miles per hour when chasing prey. How would you explain how the ability to run fast evolved in cheetahs, assuming their ancestors could only run 20 miles per hour?

Biology 112 Handout for Evolution 2

This handout contains:

- HMNH Lab Tips
- Sample Exam Answers
- Figures for this lecture

Bio 112 HMNH Lab Tips

1. There is no pre lab for this lab.
2. We will hand out free tickets to the HMNH on Friday.
3. You should read over the lab & be prepared (be sure to have notes on the phyla that are present at the HMNH- otherwise, 3 hours will not be enough time.
4. Your answers need not be long (1 to 3 sentences each), but they should be specific and concrete. Be sure to mention specific features, adaptations, etc..
5. You should bring a copy of Campbell to help you find the organisms in question (1).
6. You can go to the HMNH anytime it is open (mon - sat 9-5 & sun 1-5).
7. Your lab report will be due in your assigned lab section during the week of February 11.

Important Survey Quotes

The following were taken and adapted from your responses to the survey on Monday.

- 1) The slow ones had no girlfriends and were losers.

- 2) The food cheetahs eat now has more nutrients to make them stronger and run faster.

- 3) Because of evolution, which makes everything faster and better

- 4) Cheetahs realized that they could only run so fast at first. Realizing that faster limbs would help the chances of survival, cheetahs adapted, gaining the ability to run faster.

- 5) The cheetahs evolved to run 60 mph by running away from predators over generations. The training in running improved their speed.

- 6) The ability to run fast evolved out of necessity to survive. Cheetahs needed to develop the ability to run faster so that they could catch their prey. Animals who do not adapt as necessary for survival will eventually die off.

- 7) Those cheetahs which had this physical ability to run faster than average were better able to survive and reproduce. Over time, this heightened speed became a dominant trait.

- 8) Let's say cheetah's ancestors could run 20mph and let's also say that the cheetah's ancestors prey can also run 20mph. The ancestors do an OK job of catching the prey but one day a cat is born that can run 60mph. They are more effective hunters and thus are more likely to survive because of the mutation to run faster. Those faster cats reproduce to make other fast cats and soon the slow ancestors die out and there are only cheetahs left.

Sample Student Exam Answers

The following are sample student answers to the final exam question 1 from Spring 2007. The question was:

In the simplest evolutionary scenario, primitive pine trees produced only small amounts of pollen. Modern pines produce large quantities of pollen. Provide a plausible explanation for how modern pines make so much more pollen than primitive pine trees by a process of natural selection.

Full-credit answer:

(P) Initially, most pine trees produced small quantities of pollen. Very few randomly produced large quantities.

(G) The amount of pollen produced was genetically determined.

(A) The few tree that produced large quantities had a genetic advantage. More pollen leads to more chances of fertilizing a female and having more offspring.

(I) With each generation, there were more pine trees producing large quantities of pollen. Hence, modern pine trees produce large quantities of pollen.

For each of the answers below, determine which of the four components are present.

1. Pine trees started with primitive pine trees that produced small quantities of pollen and pine trees that produced large quantities of pollen. Pine trees that produced large quantities of pollen reproduced more, therefore more offsprings. Pine trees that produced small quantities of pollen have less offspring. Time goes on, pine trees that produced small quantities of pollen become less and less; pine trees that produced large quantities of pollen become more.
2. P – pre-existing variation caused pollen to be scarcely produced in pine trees. G – genetic variations caused pine trees to produce more pollen. A – advantageous in climate and environment, this it helped them in the long run. I – increase in population and pollen because of this.

Evolution of the Equidae (horse-like animals)

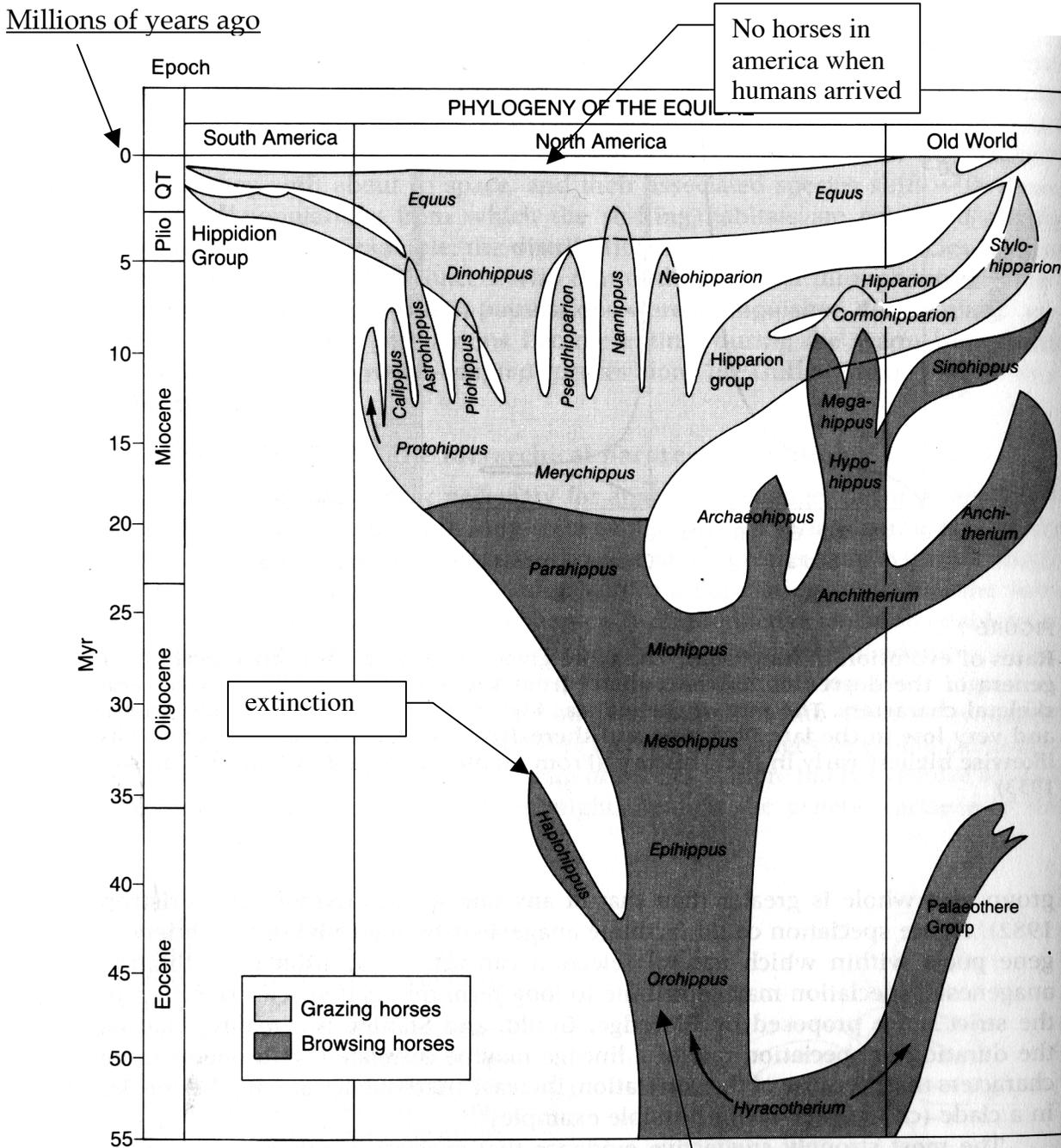
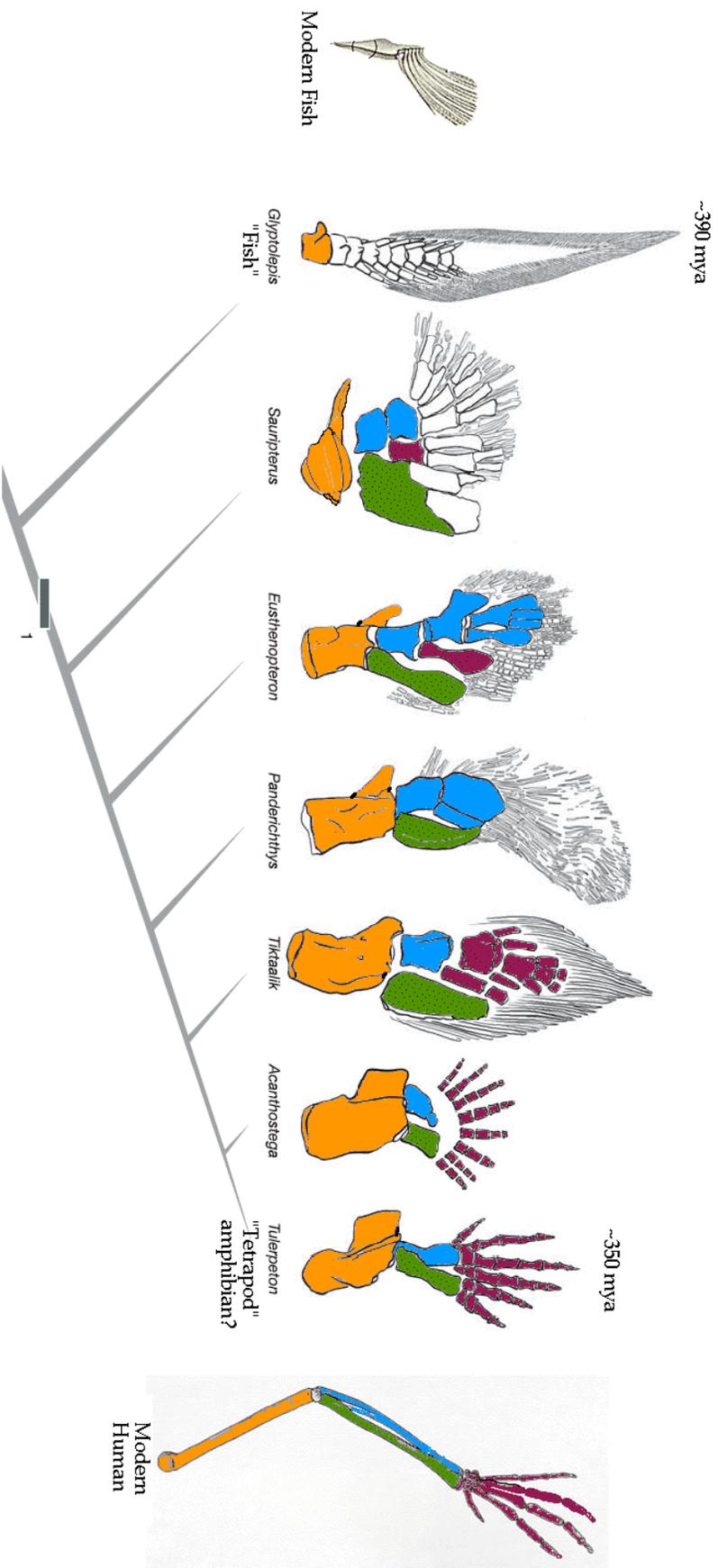


FIGURE 8

The phylogeny of the horse family, Equidae, as currently understood. Note that the grazing habit evolved in the Miocene, in only one of the lineages extant at that time. (From MacFadden 1985)

Width indicates number of species of each group (diversity not population).

Evolution of Vertebrate Limbs



Biology 112 Handout for Evolution 3

This handout contains:

- today's iClicker Question

Bio 112 iClicker Question #0 - after lecture

Given the following individuals with the following genotypes:

<u>Genotype</u>	<u>Number</u>	<u># of A alleles</u>	<u># of a alleles</u>
AA	10		
Aa	10		
aa	80		
	Total:		

What are the frequencies of the A and a alleles in this population?

- A) frequency of A = $\frac{20}{100}$ and frequency of a = $\frac{90}{100}$
- B) frequency of A = $\frac{20}{200}$ and frequency of a = $\frac{90}{200}$
- C) frequency of A = $\frac{20}{110}$ and frequency of a = $\frac{90}{110}$
- D) frequency of A = $\frac{30}{200}$ and frequency of a = $\frac{170}{200}$
- E) None of the above.

Beaming in your answers

1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
3. Transmit your answer as follows:
 - a. Press the button corresponding to the answer you've selected (A thru E).
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Bio 112 Handout for Evolution 4

This handout contains:

- Today's iClicker Question
- Figures for today's lecture

iClicker Question #1 - after lecture

Which of the following statements are false:

- A. If the genotype frequencies of a population in nature match those expected at HWE, the population is at HWE.
- B. After one generation where all 5 conditions for HWE are met, the population will be at HWE.
- C. If a small sample of a starting population that was at HWE founds a new population, that new population will always be at HWE.
- D. More than one is false.
- E. All are true.

Beaming in your answers

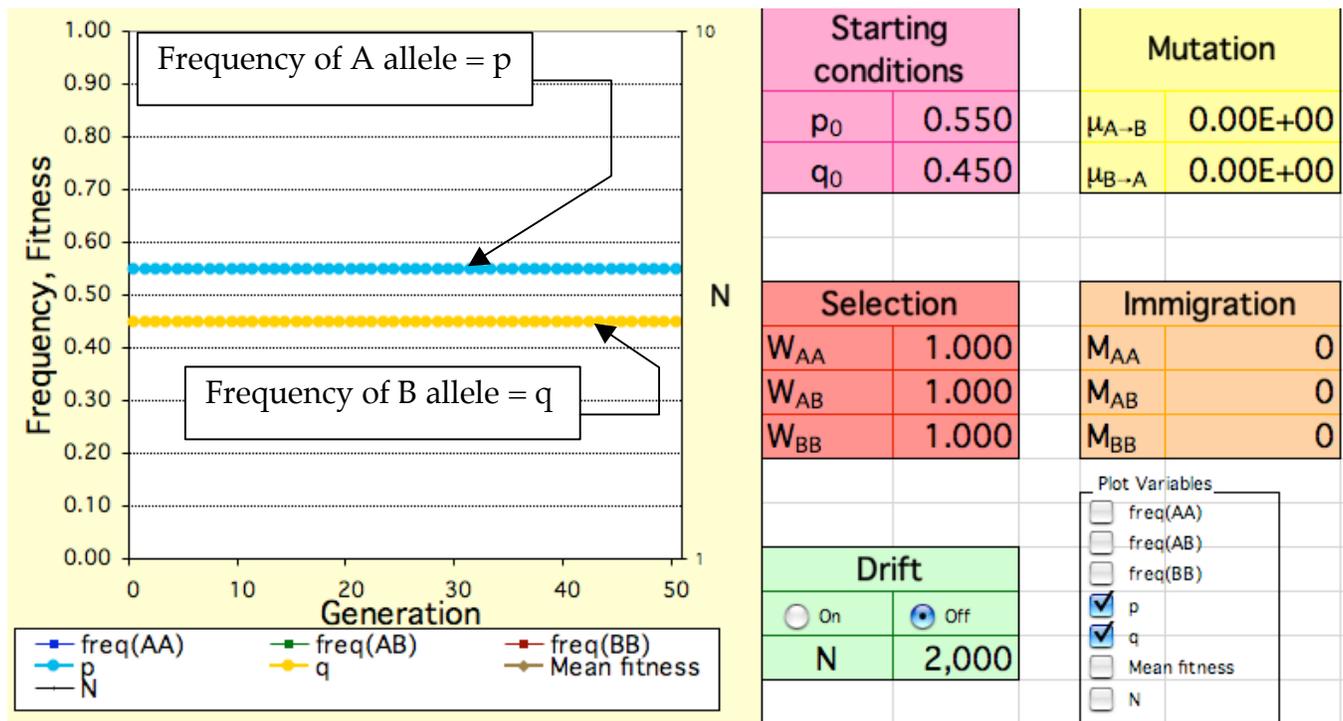
1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
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Hardy-Weinberg Simulations

Deme 1.0 is a Microsoft Excel spreadsheet available on the course website.

The simplest case:

- large population (Drift OFF)
- no mutation (rates = 0)
- no migration (immigration = 0)
- random mating
- no selection (all fitnesses = 1)



Since all 5 HWE conditions hold, the population is at HWE “forever”
 - allele frequencies stay the SAME in all generations

Uses of HWE (1): Human Genetic Traits

Example: attached/detached earlobes (model for genetic disease)



Attached
Earlobe



Unattached
Earlobe

Are your earlobes attached or unattached? A person with attached ear lobes will have the lowest point of the ear lobe attached to the face. A person with unattached ear lobes will not have the lowest point of the ear lobe attached to the face.

<u>allele</u>	<u>contribution to phenotype</u>	<u>frequency</u>
E	unattached earlobe (dominant)	p
e	attached earlobe (recessive)	q

<u>Genotype</u>	<u>Phenotype</u>
EE	unattached
Ee	unattached
ee	attached

Q: How many people in class are carriers for the attached allele?

Assume that this trait is at HWE.

Bio 112: Hardy-Weinberg Equilibrium Examples

General Info

- Allele frequencies: the frequency of each allele (R or r, for example) in the gene pool. The symbols p and q are used to represent these frequencies.
- Genotype frequencies: the frequency of each genotype (RR, Rr, rr for example) in the population. These are always equal to the number of individuals with a particular genotype divided by the total population size. They are sometimes equal to p^2 , $2pq$, and q^2 - only when the population is at HWE.

For a particular pair of allele frequencies ($p = 0.2$ and $q = 0.8$ for example), there are many possible sets of genotype frequencies that have the same allele frequencies (actually, infinitely many). This is illustrated by the 4 example populations below; all 4 of these populations have the same allele frequencies. However, given a pair of allele frequencies, there is only one set of these genotype frequencies that are at HWE. This is illustrated by the last two populations shown below; in addition to having the same allele frequencies as the other populations, their genotype frequencies match the predictions of HWE - that the frequency of RR = p^2 (0.04 in this example), the frequency of Rr = $2pq$ (0.32 in this example), and the frequency of rr = q^2 (0.64 in this example).

Population 1

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	0	0	0	0
Rr	40	0.40	40	40
rr	60	0.60	0	120
		<u>totals</u>	40	160

Allele frequencies

Freq. of R = $p = 40/200 = 0.2$

Freq. of r = $q = 160/200 = 0.8$

Genotype frequencies

Freq. of RR = 0, not 0.04

Freq. of Rr = 0.4, not 0.32

Freq. of rr = 0.6, not 0.64

NOT AT HWE

Population 2

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	400	0.20	800	0
Rr	0	0.00	0	0
rr	1600	0.80	0	3200
		<u>totals</u>	800	3200

Allele frequencies

Freq. of R = $p = 800/4000 = 0.2$

Freq. of r = $q = 3200/4000 = 0.8$

Genotype frequencies

Freq. of RR = 0.2, not 0.04

Freq. of Rr = 0.0, not 0.32

Freq. of rr = 0.8, not 0.64

NOT AT HWE

Population 3

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	4	0.04	8	0
Rr	32	0.32	32	32
rr	64	0.64	0	128
		<u>totals</u>	40	160

Allele frequencies

Freq. of R = $p = 40/200 = 0.2$

Freq. of r = $q = 160/200 = 0.8$

Genotype frequencies

Freq. of RR = 0.04

Freq. of Rr = 0.32

Freq. of rr = 0.64

AT HWE

Population 4

<u>Genotype</u>	<u>#</u>	<u>Genotype frequency</u>	<u>#R's contributed to gene pool</u>	<u>#r's contributed to gene pool</u>
RR	12	0.04	24	0
Rr	96	0.32	96	96
rr	192	0.64	0	384
		<u>totals</u>	120	480

Allele frequencies

Freq. of R = $p = 120/600 = 0.2$

Freq. of r = $q = 480/600 = 0.8$

Genotype frequencies

Freq. of RR = 0.04

Freq. of Rr = 0.32

Freq. of rr = 0.64

AT HWE

Bio 112 Handout for Evolution 5

This handout contains:

- Today's iClicker Questions
- Handouts for today's lecture

iClicker Question #2A - before lecture

Which of the following scenarios describe an event involving selection (fitness depends on genotype) and not founder or bottleneck effects (fitness is a matter of chance)?

- A. Tusk length in elephants is inherited. Some elephants have shorter tusks and some have longer tusks. Hunters prefer to kill elephants with long tusks. Over time, hunting results in a population of elephants with shorter tusks on average.
- B. Color in a species of bird is inherited. There is an island with blue and red birds. Originally, the majority of the population was red with a few blue birds. A hurricane floods the island and kills all but 10 birds; 2 red birds and 8 blue birds. The birds re-populate the island. The resulting population is now mostly blue.
- C. Another island has palm trees on it. The mountain in the center of the island shades one side of the island for most of the day. The trees in the shade are shorter than the trees in the sunny parts of the island.
- D. more than one of the above
- E. none of the above.

iClicker Question #2B - after lecture

In 1848 in England, a species of moth was mostly light in color; this allowed it to blend in with light-colored trees. Over the next 50 years, the trees became darker due to soot from factories. In 1898, those same moths were mostly dark. Which of the following explanations for the increase in frequency of dark moths **do not** involve selection?

- A. The soot from the factories is more toxic to light moths than dark moths.
- B. The climate in England was cooling over that time period, and dark moths are more cold-tolerant than light moths.
- C. Many dark moths flew in to England from France, where the population is mostly dark.
- D. All of these involve selection.
- E. None of these involve selection.

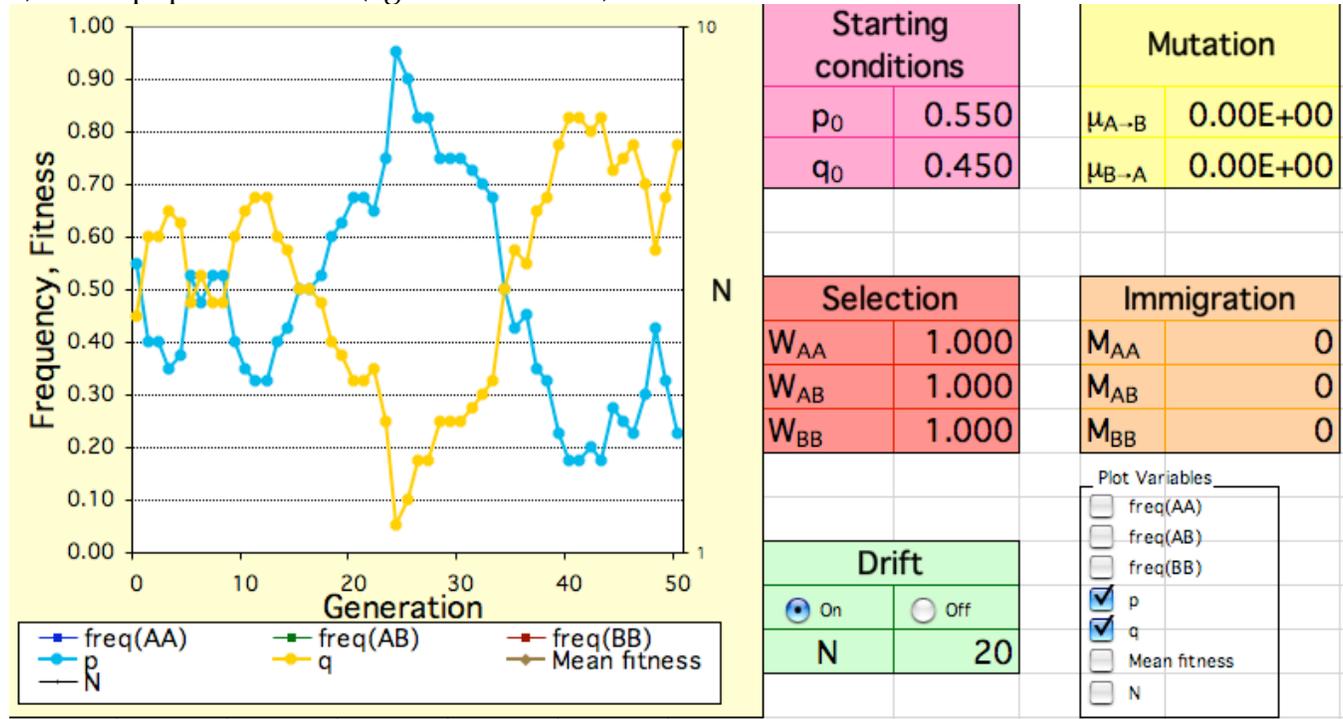
Beaming in your answers

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Population Genetics Simulations II

Violations of the Hardy-Weinberg Assumptions:

a) Small population size ("genetic DRIFT")



e) Natural Selection:

- for example “Industrial Melanism” in the Peppered Moth in England

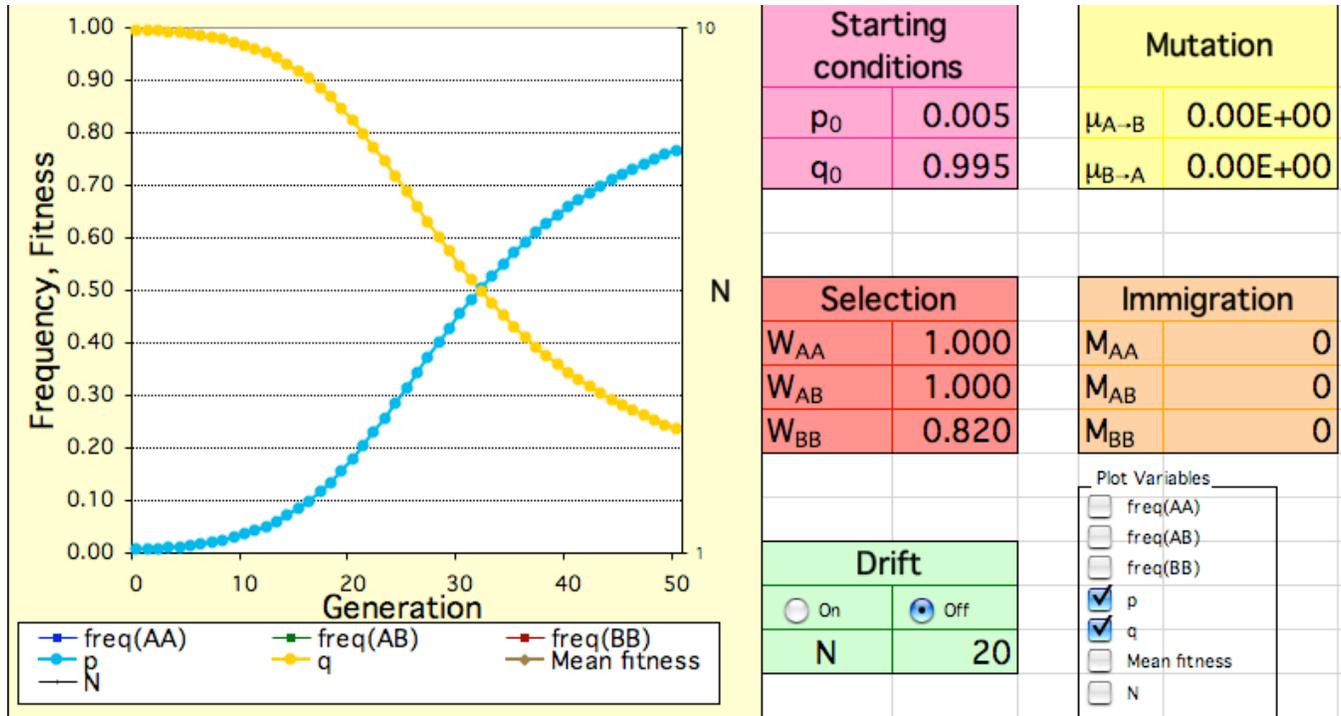
color controlled by one gene with two alleles

allele	contribution to phenotype	frequency	Genotype	Phenotype
A	dark body (dominant)	p	AA	dark
B	light body (recessive)	q	AB	dark
			BB	light

Data:	Year	% of moths that are DARK	% of moths that are LIGHT	freq (A) (p)	freq (B) (q)
	1848	1%	99%	0.005	0.995
	1898	95%	5%	0.776	0.224

- In 1848, the trees had clean light bark ⇒ dark moths eaten ⇒ moths mostly light
- Industrial revolution ⇒ coal burning ⇒ soot accumulates on trees ⇒ trees have dark bark ⇒ light moths eaten ⇒ moths mostly dark.

Can simulate in Deme:



Bio 112 Handout for Evolution 6

This handout contains:

- Today's iClicker Questions
- Handouts for today's lecture
- Information on Diversity of Life Survey
- Population Genetics Practice Problems and Solutions

iClicker Question #3A - before lecture

Which of the following statements is/are **true**?

- A. Evolution only happened in the past; it is not happening now.
- B. Humans are not evolving any more.
- C. A disadvantageous allele will always be removed from the population.
- D. Organisms which are more physically fit will always have more offspring.
- E. None of the above are true.

iClicker Question #3B - after lecture

Which of the following is/are **not** examples of sexual selection?

- A. Semen (the fluid produced by males to carry sperm) produced by some species coagulates in the female's reproductive tract forming a plug that prevents further matings.
- B. Semen produced by fruit flies contains chemicals that reduce the female's interest in subsequent matings.
- C. Semen produced by some insects contains proteins that stimulate increased egg production in females.
- D. Male giraffes use their long necks in combat to determine which will mate with a female.
- E. All of the above.

Beaming in your answers

1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
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Evolution Examples (3): Sickle-cell anemia

Trait controlled by one gene with two alleles:

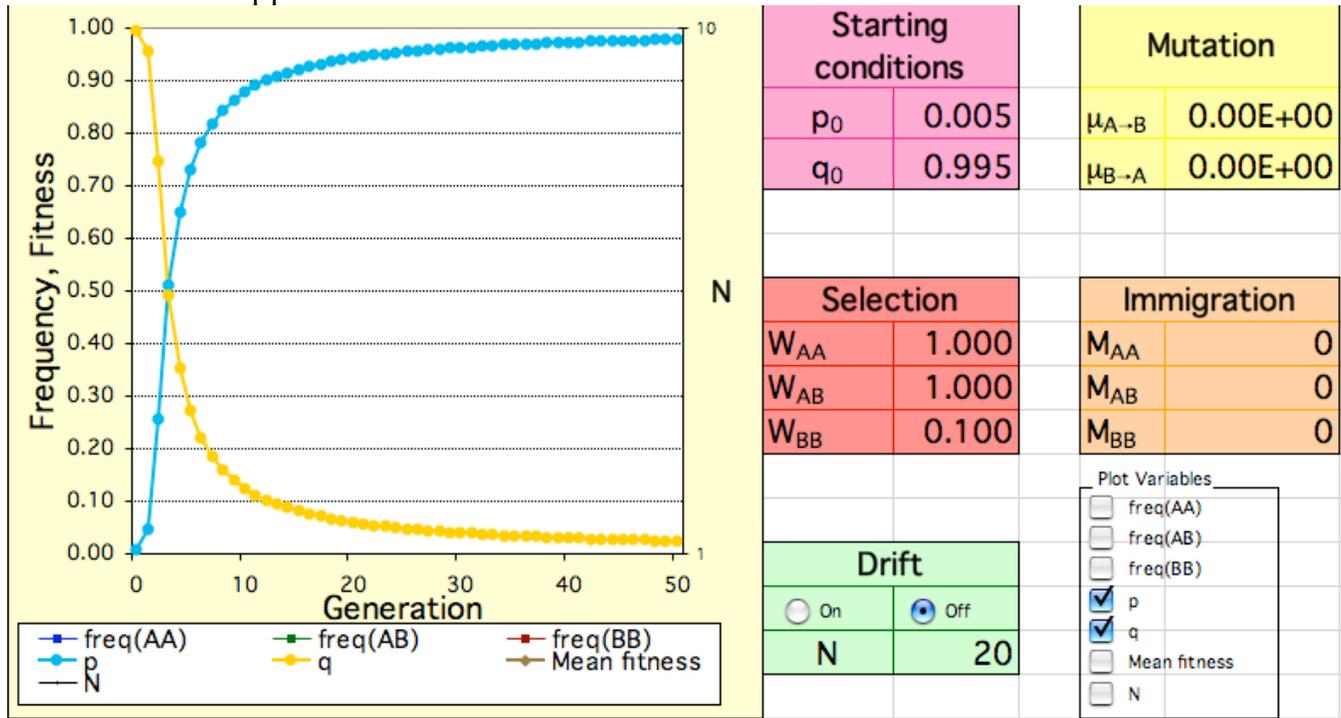
allele contribution to phenotype frequency

A normal blood (dominant) p

B sickle-cell anemia (recessive) q

- BB individuals have sickle-cell anemia and greatly reduced fitness.

- What should happen to the B allele?



However, in areas with high incidence of Malaria (severe and often fatal parasitic infection of red blood cells), the frequency of B (q) is high (0.2) and constant (Campbell fig 23.17). In areas without Malaria, the sickle-cell allele is virtually unknown.

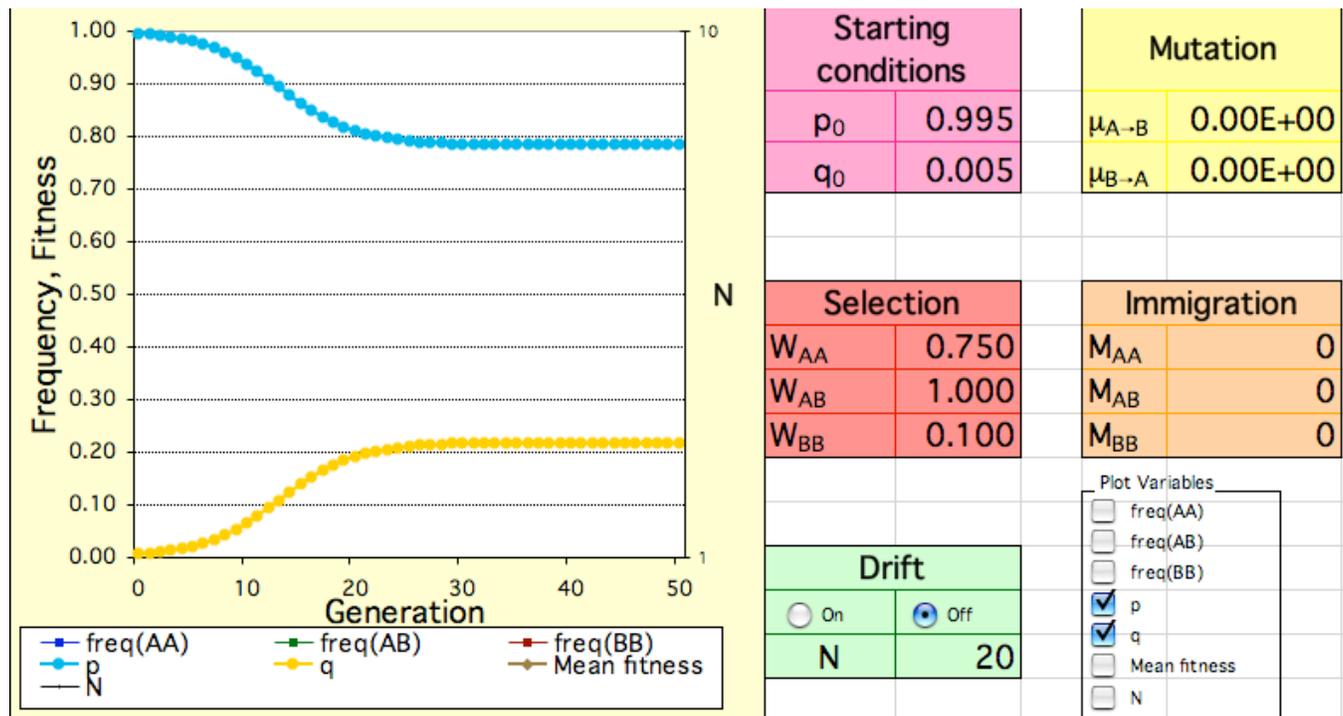
It turns out that the sickle-cell allele confers a dominant resistance to malaria:

allele	contribution to sickle-cell phenotype	contribution to malaria-resistance phenotype	frequency
A	normal (dominant)	none (recessive)	p
B	sickle-cell (recessive)	resistant (dominant)	q

therefore:

genotype	phenotype	fitness with malaria	fitness without malaria
AA	normal	low	high
AB	malaria-resistant	high	high
BB	sickle-cell (& malaria-resistant)	very low	very low

- Without malaria, the expected result is loss of the sickle-cell allele (previous page)
- With malaria, the advantage of being AB is balanced by the disadvantage of being BB.



Sexual Selection

Examples:

1) Advantages in competition with members of the same sex for mating with the opposite sex.

a) Peacock:



Males have ~170 eyespots on tail feathers

- remove 20 spots with scissors and females won't mate with them

b) Barn swallow:



Males have long tail feathers

- glue on longer tail feathers and females pick that male more often for mating

2) Sperm competition because females can mate with more than one male.
Garden spiders



Males lock their genitals onto the female's genitals, mate, and then die. The locked-on dead male prevents other males from mating.

Diversity of Life Survey

This is due by the start of the Evolution 7 lecture.

This survey is designed to see how well you understand the diversity of living organisms. There is no right or wrong answer; you will receive full credit for whatever you write. We are most interested in **your** understanding of these important biological issues.

Please do not consult any outside sources (textbook ,www, other people, etc,) when completing this survey!!

You will complete this survey on-line; once you have completed the survey, you will automatically receive 10 points for the "Diversity of Life Survey" whether your answers are correct or not.

How to complete the survey:

- 1) Go to any computer connected to the internet. Go to the Bio 111/112 home page:
<http://intro.bio.umb.edu/111-112/>
- 2) Go to the Bio 112 **Lecture Materials** and scroll down to the links for **Evolution 6** and click on the "Complete the Diversity of Life Survey" link.
- 3) Choose your name from the list and enter your UMS number as a password (leave off the "UMS"). If you do not see something like the screen shown below, your computer does not have Java installed; you should switch to another computer or download Java from the link on the **Lecture Materials** page (it is free).

Diversity of Life Survey for .Your name here

This survey is designed to see how well you understand the diversity of living organisms. There is no right or wrong answer; you will receive full credit for whatever you write. We are most interested in your understanding of these important biological issues. Please do not consult any outside sources (textbook ,www, other people, etc.) when completing this survey!!

Assume that you are working for a natural history museum like the Harvard Museum of Natural History, only smaller. Your museum has specimens of the following 20 types of organisms in its collection. Your task is to design a tree that will help orient visitors to the collection. Your tree should include all the groups of organisms listed below and communicate the ways they are evolutionarily related to one another.

Using the program in the window below, draw a tree diagram to show the relationships between these organisms. Please include additional text and graphics that you think will help visitors understand how you have organized these groups of organisms. There is no right or wrong answer to this task, but it is important that you are able to explain the logic behind your approach.

Instructions:

- Drag Organisms to where you want them
- Shift-click on the workspace to add a node
- Click on an item (organism or node) to select it. It's border will turn red
- When you have two items (organism and/or node) selected, you can link or unlink them
- Links will remain connected when you move items.
- Click "Label" to add a text label.
- Click "Delete" to delete a text label or node.
- Select two objects connected by a link and click "Split" to add a new node in the middle of the link.

 Bat
 Beetle
 Bird

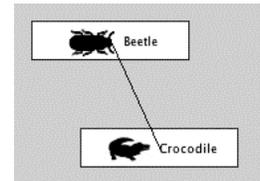
- 4) Read the instructions carefully - you are to make a tree showing the relationships between the 20 organisms shown at the lower section of the web page.

5) Draw your tree: Move the organism labels to appropriate places on the page and connect them with lines as appropriate. **PLEASE DO NOT CONSULT ANY OUTSIDE SOURCES WHEN COMPLETING THIS SURVEY!!**

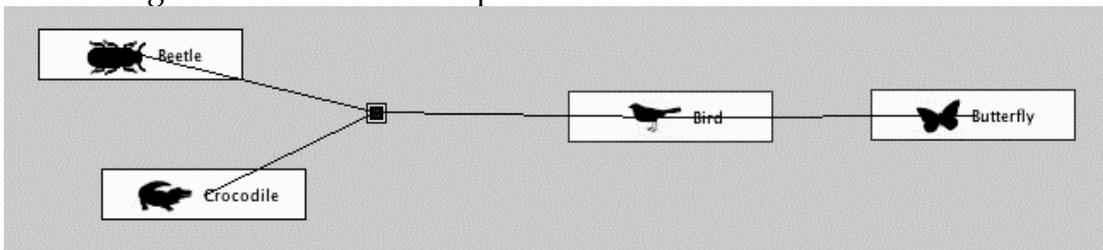
These are the things you can do to draw your tree on the web page:

- *Move the organism labels around.* Just drag them with the mouse to where you want them. Any lines you have connected them will stay connected.

- *Connect any two organism labels with a link to show that they are related.* Click on each organism label - you will see it's border turn red to indicate that it is selected - then click the **Link** button. You should see a blue line connecting them appear on the screen. See picture at right: An organism label can be linked with as many lines as you like.



- *Make a branch-point (also called a 'node').* In order to make a branched line, you need to create a branch point - a node. To do this, you hold the shift key and click wherever you want the node to be (don't worry, you can move it with the mouse just like an organism label. You'll see a node appear. You can move the node and link to it just like an organism label. An example is shown below:



- *Add a node to the middle of a line.* Select the items at the ends of the line and click the **Split** button. A node will appear in the middle of the line. You can then move, link, etc the node.
- *Delete a link.* Select the items at the ends of the link and click the **Delete** button. The link will disappear but the items at the ends will remain.
- *Delete a node.* Select the node only (you can click twice on an item to de-select it) and click **Delete**. The node and any lines attached to it will disappear.
- *Undo a change.* Click the **Undo** button. You cannot undo an undo.

You should be sure to save your work often by clicking the Submit button.

6) Answer the questions that follow the tree.

7) Be sure to **Submit** your answers when you are done.

8) This assignment must be completed by 12:00 noon on Evolution 7; after that time, you will be able to see your survey but not save any changes or receive credit if you have not already.

Bio 112 Population Genetics Practice Problems

These are intended as practice for the exams; you should do them & write out answers before looking at the solutions. I will hand out solutions in a week or so.

1) In Shorthorn cattle, the genotype $C^R C^R$ is phenotypically red, $C^R C^W$ is roan (a mixture of red and white), and $C^W C^W$ is white.

a) Given that 108 red, 48 white and 144 roan animals were found in the central valley of California, calculate the frequencies of the C^R allele and the C^W allele in the gene pool of the population.

b) If all 5 assumptions for Hardy-Weinberg Equilibrium hold for this population, what is the expected frequency of each genotype in the next generation? Is the population represented in part (a) in Hardy-Weinberg equilibrium?

c) The rancher has observed that white Shorthorn cattle are sterile (unable to reproduce). What are the frequencies of the C^R and C^W alleles in the part of the population that is capable of reproducing? (this is harder than you'd likely find on an exam)

d) Taking into account the sterility of the white cattle, and assuming that the 5 assumptions of Hardy-Weinberg equilibrium hold for the breeding population, what are the expected frequencies of genotypes in the next generation? Would you expect this next generation to be at Hardy-Weinberg equilibrium? Why/why not?

2) Populophobia is a dreaded (but hypothetical) autosomal recessive condition in humans that causes genetics students to go into convulsions whenever they see the Hardy-Weinberg formula. That is: D is the normal allele; d is the populophobia allele (recessive phenotype), so

DD and Dd are normal

dd are populophobic - go into convulsions when they see the H-W formula

In a class of 200 genetics students, 32 had convulsions during their first population genetics lecture. Assume that students are a representative sample of a population at Hardy-Weinberg equilibrium.

a) What is the frequency of the populophobia (d) allele in this population? How many students in this class are heterozygous (Dd) for this condition?

b) During the second population genetics lecture, the professor decided to derive the Hardy-Weinberg formula for a population having 10 alleles at a given locus. The trauma induced by the derivation caused 75% of the students with populophobia to spontaneously combust...

POOF!

What is the frequency of each allele in the surviving population of genetics students? What are the frequencies of each genotype and phenotype?

c) The devious professor planned to rid the world of populophobia by forcing all young science students to derive the Hardy-Weinberg formula. Why was he a poor geneticist (besides being insane)?

3) You are studying an obnoxious weed in your backyard. These weeds are sexually-reproducing, freely-interbreeding, diploid organisms. They are either tall, medium, or short; the height is determined by one gene with two codominant alleles:

<u>Genotype</u>	<u>Phenotype</u>
HH	tall
Hh	medium
hh	short

a) Last year, you counted all the weeds in your yard and got the following results:

<u>Height</u>	<u>Number</u>
tall	16
medium	48
short	36

i) What are the frequencies of the two alleles (H and h) in this population? Show your work.

ii) Is this population at Hardy-Weinberg equilibrium? Justify your answer.

b) This year, after a particularly harsh winter, you count all the weeds in your yard again and get the following results:

<u>Height</u>	<u>Number</u>
tall	2
medium	57
short	41

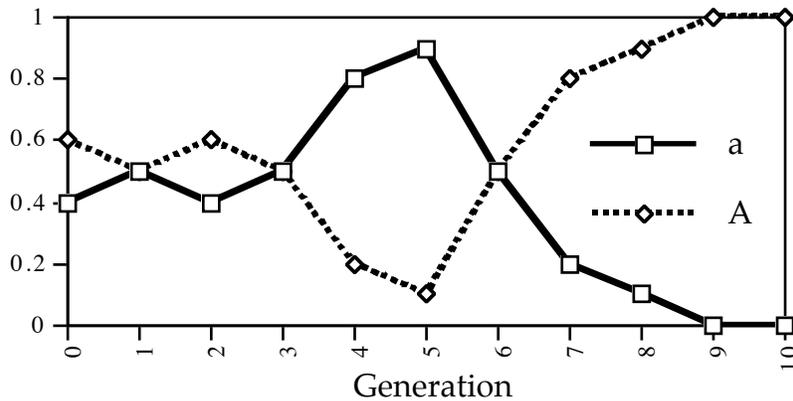
i) What are the frequencies of the two alleles (H and h) in this population? Show your work.

ii) Is this population at Hardy-Weinberg equilibrium? Justify your answer.

c) Offer a reasonable hypothesis to explain the changes in the genetic structure of the population from last year to this year assuming that the changes are **due to natural selection**.

d) Offer a reasonable hypothesis to explain the changes in the genetic structure of the population from last year to this year assuming that the changes are due to **some factor other than natural selection**.

4) Shown below is a graph similar to what you constructed in lab. It is the result of randomly killing 95% of the population in each generation.



Notice that the A allele takes over the population completely and the a allele goes extinct in generation 9. Is this the result of the A allele increasing the fitness of the organisms? Explain your reasoning briefly.

5) Microevolution

You are a time-traveling evolutionary biologist studying a particular species of snake on an island off the coast of Massachusetts. You travel 100,000 years into the past and observe that the snakes are a variety of colors (red, blue, yellow, green) and that most of the snakes are blue. This same species of snake and the same mix of colors are found on the mainland.

a) Assuming that all the snakes are descended from an ancestral blue snake, where did the other colors come from?

At the present time, the snakes are still the same variety of colors, but most of the snakes are green.

b) Explain this change in color frequency (micro-evolution) as though it were based solely on each of the following processes:

i) Bottleneck effect.

ii) Founder effect.

iii) Migration.

iv) Non-random mating.

v) Natural selection.

Bio 112 Solving Population Genetics Problems

Reminder:

Genotype frequencies are the frequencies of the three possible genotypes (AA, Aa, aa).

Allele frequencies are the frequencies of the two alleles (A with frequency p; a with frequency q)

In general:

Solving population genetics problems usually follows this pattern:

- (1) Find the allele frequencies; there are 2 methods to use depending on what you know:
 - (1a) if you know all the genotype frequencies
 - (1b) if you know at least one of the genotype frequencies **and** can assume that the population is at HWE. You can then find the other genotype

frequencies.

- (2) Predict the genotype frequencies in the next generation.

- (3) See if the population is at HWE.

The particular steps:

(1a) Find the allele frequencies given all three genotype frequencies. This is the most general way to get allele frequencies; it works under **all** conditions (at HWE and not at HWE). You do it by calculating the number of alleles contributed by each genotype to the gene pool.

- since each individual has two alleles to contribute, the size of the gene pool is the number of individuals times 2.
- each AA individual contributes 2 A's to the pool
- each Aa individual contributes one A and one a to the pool
- each aa individual contributes 2 a's to the pool

For example: given this population

<u>genotype</u>	<u>number</u>
AA	30
Aa	20
aa	50

you calculate the total # of individuals = $30 + 20 + 50 = 100$; this lets you calculate the genotype frequencies:

<u>genotype</u>	<u>number</u>	<u>genotype frequency (number divided by total)</u>
AA	30	$30/100 = 0.3$
Aa	20	$20/100 = 0.2$
aa	50	$50/100 = 0.5$

Now, you can get the allele frequencies in two ways:

⇒ either calculate the contributions using the numbers of each genotype (easy):

<u>genotype</u>	<u>number</u>	<u>contributions to gene pool</u>		
		<u>total alleles</u>	<u>A alleles</u>	<u>a alleles</u>
AA	30	60	60	0
Aa	20	40	20	20
aa	50	100	0	100
total # of alleles = $100 \times 2 = 200$		(or $60 + 40 + 100 = 200$)		
total # of A's = $60 + 20 = 80$		frequency of A = $p = 80/200 = 0.4$		
total # of a's = $20 + 100 = 120$		frequency of a = $q = 120/200 = 0.6$		

⇒ or calculate using the frequencies of each genotype (more advanced):

$$\text{frequency of } A = p = (\text{frequency of } AA) + (\text{frequency of } Aa) / 2 \\ = 0.3 + (0.2) / 2 = 0.3 + 0.1 = 0.4$$

$$\text{frequency of } a = q = (\text{frequency of } aa) + (\text{frequency of } Aa) / 2 \\ = 0.5 + (0.2) / 2 = 0.5 + 0.1 = 0.6$$

(1b) Find the allele frequencies given at least one genotype frequency and assuming the population is at HWE. This **only** works if you can assume that the population is at HWE; this will be given in the problem. To do this, you need to find one of the genotype frequencies and then use the following relationships which only hold at HWE:

$$\text{frequency of } AA = p^2$$

$$\text{frequency of } Aa = 2pq$$

$$\text{frequency of } aa = q^2$$

Once you've found either p or q , you know that $p + q = 1$ always, so you can get the other.

For example: "Sickle-cell anemia is an autosomal recessive genetic disease:

allele contribution to phenotype

A normal (dominant)

a sickle-cell anemia (recessive)

In a particular population, 99% (frequency = 0.99) are normal (AA and Aa) and 1% (frequency = 0.01) are sickle-cell (aa). Assuming that this population is at HWE, find the frequencies of each allele."

If we call the frequency of the normal allele (A) p , and the disease allele (a) q :

From above, we know that $0.99 = p^2 + 2pq$ (a difficult equation to solve)

but, we also know that $0.01 = q^2$ (this is much easier to solve)

take the square root of both sides:

since we know that $p + q = 1$, $p = 1 - q$ so $p = 1 - 0.01$ so $p = 0.9$

Now we have both allele frequencies. We can then go on to find the frequencies of the other genotypes using the relationships above:

$$\text{frequency of homozygous normal (AA)} = p^2 = (0.9)^2 = 0.81 \quad 81\% \text{ AA}$$

$$\text{frequency of carriers (Aa)} = 2pq = 2(0.1)(0.9) = 0.18 \quad 18\% \text{ Aa}$$

(note that $81\% + 18\% = 99\%$, the number of phenotypically normal individuals).

Note that the sum of the allele frequencies ($p + q$) is **always** = 1 whether at HWE or not.

(2) Predict the genotype frequencies in the next generation. To do this, you must assume that the 5 conditions for HWE hold for the population. In the case where they do not hold (like in lab where there was selection), you can assume that they hold for the breeding population (the part of the population that can reproduce). As long as you are using the allele frequencies (p & q) for the breeding population, you can use the relationships below:

$$\text{frequency of } AA = p^2$$

$$\text{frequency of } Aa = 2pq$$

$$\text{frequency of } aa = q^2$$

(3) See if the population is at HWE. If the conditions of HWE hold, the next generation calculated using (2) will be at HWE. You can use this as a test to see if a population is at HWE.

- calculate the allele frequencies using (1a). You cannot use (1b) because (1b) **assumes** that you are at HWE already!
- predict what the genotype frequencies will be at HWE using (2)
- compare the predicted genotype frequencies with the actual ones. If they're equal, then the population is at HWE.

For example: the population in 1a has $p = 0.4$ and $q = 0.6$. If it were at HWE, the frequency of AA would be $p^2 = 0.16$; the frequency of Aa would be $2pq = 0.48$; and the frequency of aa would be $q^2 = 0.36$ – since the actual frequencies are 0.3, 0.2 and 0.5, respectively, the population is **not** at HWE.

Note that $p^2 + 2pq + q^2$ **always** = 1, whether at HWE or not; so testing to see if $p^2 + 2pq + q^2 = 1$ does **not** test to see if the population is at HWE.

Hints for solving the practice problems: (numbers in [brackets] are appropriate steps as above)

#1a = [1a] #1b = [2] #1c = [not above] #1d = [2]
#2a = [1b] #2b = [1a] #2c = [not above]
#3ai = [1a] #3aii = [3] #3bi = [1a] #3bii = [3]

You should try the problems before using these hints.

Solutions to: Population Genetics Practice Problems

1) a)

	C^R	C^W	
108 red cows $C^R C^R$	216		frequency of C^R allele = p
144 roan cows $C^R C^W$	144	144	p = 360/600 = 0.6
48 white cows $C^W C^W$		96	frequency of C^W allele = q
	<u>360</u>	<u>240</u>	q = 240/600 = 0.4
	600	600	

b) Assuming that the population satisfies the 5 requirements for HWE, we can predict that:
 frequency of $C^R C^R = p^2 = (0.6)^2 = 0.36 = 36\%$ red cows
 frequency of $C^R C^W = 2pq = 2(0.6)(0.4) = 0.48 = 48\%$ roan cows
 frequency of $C^W C^W = q^2 = (0.4)^2 = 0.16 = 16\%$ white cows

If the assumptions required for Hardy-Weinberg equilibrium are met, then any population will reach equilibrium in one generation. Therefore, we know that the frequencies above are equilibrium frequencies. To find if the population in part (a) is in equilibrium, take these frequencies, multiply by the population size, and compare the numbers to those given in part a.

number of red cows = $0.36(300) = 108$
 number of roan cows = $0.48(300) = 144$
 number of white cows = $0.16(300) = 48$

Since these are the same as those in part (a), then the population in part (a) was already in equilibrium.

c) To answer this, one recalculates p and q in the same way as in part a, but does not include the 48 sterile (unable to reproduce, infertile) white cows. It is important to realize that the breeding population is reduced to 252 cows, or a total of 504 alleles.

	C^R	C^W	
108 red cows $C^R C^R$	216		frequency of C^R allele = p
144 roan cows $C^R C^W$	144	144	p = 360/504 = 0.71
			frequency of C^W allele = q
	<u>360</u>	<u>144</u>	q = 144/504 = 0.29
	504	504	

d) Assuming that the conditions for HWE hold for the breeding population, we can calculate:
 frequency of $C^R C^R = p^2 = (0.71)^2 = 0.504 = 50.4\%$ red cows
 frequency of $C^R C^W = 2pq = 2(0.71)(0.29) = 412 = 41.2\%$ roan cows
 frequency of $C^W C^W = q^2 = (0.29)^2 = 0.084 = 8.4\%$ white cows

This population is not in equilibrium due to the reproductive selection against the C^W allele resulting from the sterility of white ($C^W C^W$) cows. Realize that $p^2 + 2pq + q^2 = 1$ **at all times**, even when not in equilibrium. That is, the frequencies will always add to 100% of the population. ($50.4\% + 41.2\% + 8.4\% = 1$ but is not in equilibrium.)

2) a) You need to use the Hardy-Weinberg equilibrium formula for 2 alleles to solve this problem. If we define q as the frequency of the populophobia allele (d) and p as the frequency of the normal allele (D):

$$1 = p^2 + 2pq + q^2$$

where, q^2 represents the fraction of individuals who are homozygous recessive (dd - populophobic). Thus,

$$q = \sqrt{\frac{32}{200}} = \sqrt{0.16} = 0.4$$

since $p + q = 1$, $p = 1 - q$ or: $p = 1 - 0.4 = 0.6$

The frequency of heterozygotes (Dd) is:

$$2pq = 2(0.6)(0.4) = 0.48$$

$(0.48)(200) = 96$ individuals are heterozygous.

That leaves: $200 - (96 + 32) = 72$ who are homozygous normal

b) If 75% of the individuals with populophobia spontaneously combust, then:

$$(0.75)(32) = 24 \text{ } dd \text{ individuals lost from the population}$$

$32 - 24 = 8$ individuals remaining who are homozygous recessive (dd)

Thus, the surviving population is:

72 DD

96 Dd

8 dd

total: 176

To calculate the new allele frequencies, you must determine the total number of p and q alleles remaining in the population. This is equal to the number of heterozygotes plus *twice* the number of homozygotes.

$$\text{total } D \text{ alleles} = 2(72) + 96 = 240$$

$$\text{total } d \text{ alleles} = 96 + 2(8) = 112$$

$$\text{total alleles in population} = 240 + 112 = 352$$

The frequency of each allele in the new population is:

$$\text{frequency of } D = p = 240/352 = 0.68$$

$$\text{frequency of } d = q = 112/352 = 0.32$$

The frequencies of each *genotype* are:

$$\text{frequency of homozygous normal} = 72/176 = 0.41$$

$$\text{frequency of heterozygotes} = 96/176 = 0.545$$

$$\text{frequency of homozygous populophobia} = 8/176 = 0.045$$

The frequencies of each *phenotype* are:

$$\text{frequency of normal} = 0.41 + 0.545 = 0.955$$

$$\text{frequency with populophobia} = 0.045$$

c) Most recessive alleles are masked in heterozygotes and are unaffected by selection pressures. Even if there was complete selection against populophobia (100% spontaneously combust), it would take almost 100 generations to reduce the populophobia allele from 40% to 1%.

3) a) i)

<u>height</u>	<u>Number</u>	<u>Genotype</u>	<u>#H's contributed</u>	<u>#h's contributed</u>
tall	16	HH	32	0
medium	48	Hh	48	48
short	36	hh	0	72
total H's = 80		total h's = 120		total alleles = 200

frequency of H = $p = 80/200 = 0.4$
frequency of h = $q = 120/200 = 0.6$

ii) If it were at HWE, then:

frequency of HH = $p^2 = (0.4)^2 = 0.16$	so in 100 plants $0.16 \times 100 = 16$ plants
frequency of Hh = $2pq = 2(0.4)(0.6) = 0.48$	so in 100 plants $0.48 \times 100 = 48$ plants
frequency of hh = $q^2 = (0.6)^2 = 0.36$	so in 100 plants $0.36 \times 100 = 36$ plants

These are the same numbers as observed, so the population is at HWE.

b) i)

<u>height</u>	<u>Number</u>	<u>Genotype</u>	<u>#H's contributed</u>	<u>#h's contributed</u>
tall	2	HH	4	0
medium	57	Hh	57	57
short	41	hh	0	82
total H's = 61		total h's = 139		total alleles = 200

frequency of H = $p = 61/200 = 0.305$
frequency of h = $q = 139/200 = 0.695$

ii) If it were at HWE, then:

frequency of HH = $p^2 = (0.305)^2 = 0.093$	so in 100 plants $0.093 \times 100 = 9$ plants
frequency of Hh = $2pq = 2(0.305)(0.695) = 0.424$	so in 100 plants $0.424 \times 100 = 42$ plants
frequency of hh = $q^2 = (0.695)^2 = 0.483$	so in 100 plants $0.483 \times 100 = 48$ plants

These are not the same numbers as observed, so the population is not at HWE. One of the 5 assumptions must be violated. Note that there are much fewer tall plants than expected.

c) The number of tall plants must have dropped because the tall plants were at a disadvantage because of their height. Perhaps they poked out of the snow more than the other plants and were frozen by the cold winds and died. The shorter plants were protected by the snow.

d) There are several possibilities, here are some:

- genetic drift: all the tall plants happened to be near a tree that fell down and crushed most of them.
- migration: your neighbor has mostly short and medium plants and seeds from them blew onto your yard.

4) No. Survivors are randomly selected (not on the basis of genotype) so frequencies are not related to fitness. Because of this, the results would likely have been different if the experiment were run again.

5) a) Mutation. Mutations in the pigment-producing genes of the snake could have resulted in progeny of different colors.

b) i) It happened that most of the snakes on the island were killed by a flood that did not discriminate on the basis of color. Although there was no selective advantage to green, it just so happened (chance events) that most of the surviving snakes happened to be green (the survivors were not a representative sample of the original population); resulting in a mostly green population.

ii) Although there was no selective advantage to green, it just so happened that a catastrophe killed all the snakes on the island. It then happened that the island was colonized by a group of snakes from the mainland of different colors, most of which were green, resulting in a large population of green snakes on the island.

iii) A large number of green snakes migrated to the island from the mainland; the mainland population happens to be mostly green. This increased the frequency of the green allele in the island population, resulting in mostly green snakes.

iv) For some reason (a genetic influence on behavior), green snakes become the "mate of choice" among the snakes on the island, leading to an increase in the frequency of the green allele in the population.

v) Some selective force acts against the non-green snakes, reducing their number or reproductive output, resulting in a relative increase in green snakes. For example, a predator could come to the island which is unable to see the green snakes against the green foliage and therefore eats only the other snakes.

Bio 112 Handout for Evolution 7

This handout contains:

- Today's iClicker Questions
- Figures for this lecture

iClicker Question #4A - before lecture

You will need to look these up on the web (hint: try Googling "broccoli species" for example). Which of the following sets of organisms are all members of the same species?

- A. broccoli, cauliflower, brussels sprouts.
- B. tomato, potato, deadly nightshade (belladonna)
- C. cow, pig, sheep
- D. human, chimpanzee
- E. more than one of the above

iClicker Question #4B - after lecture

Which of the following scenarios could not lead to the formation of a new species.

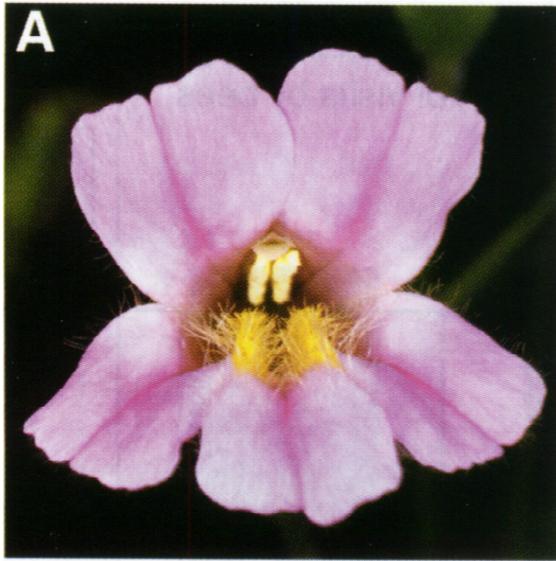
- A. A mutation occurs that allows seeds with that mutation to survive chewing and passage through the digestive tract of birds that eat the plant. Note that the birds that eat the plant travel many miles between eating the plant and depositing the seeds in their feces.
- B. A mutation occurs that changes the color of a flower such that it is no longer visible to its usual pollinator.
- C. A mutation occurs that causes animals with that mutation to be fertile in the fall instead of the spring.
- D. A mutation that leads to a behavioral alteration such that birds with the mutation prefer to nest on high cliffs instead of in the branches of trees.
- E. None of the above.

Beaming in your answers

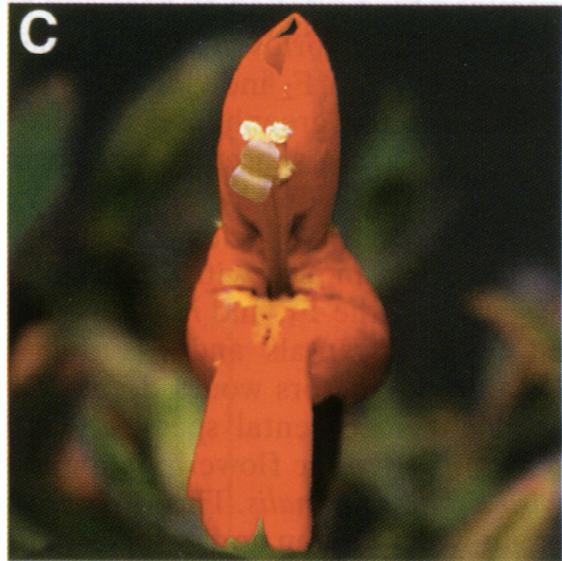
1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
3. Transmit your answer as follows:
 - a. Press the button corresponding to the answer you've selected (A thru E).
 - b. The "STATUS" light will flash green to indicate that your answer has been received. If the "STATUS" light flashed red, your answer was not received; you should re-send it until you get a green "STATUS" light.

Examples of Speciation/Reproductive-isolation

Flowers:

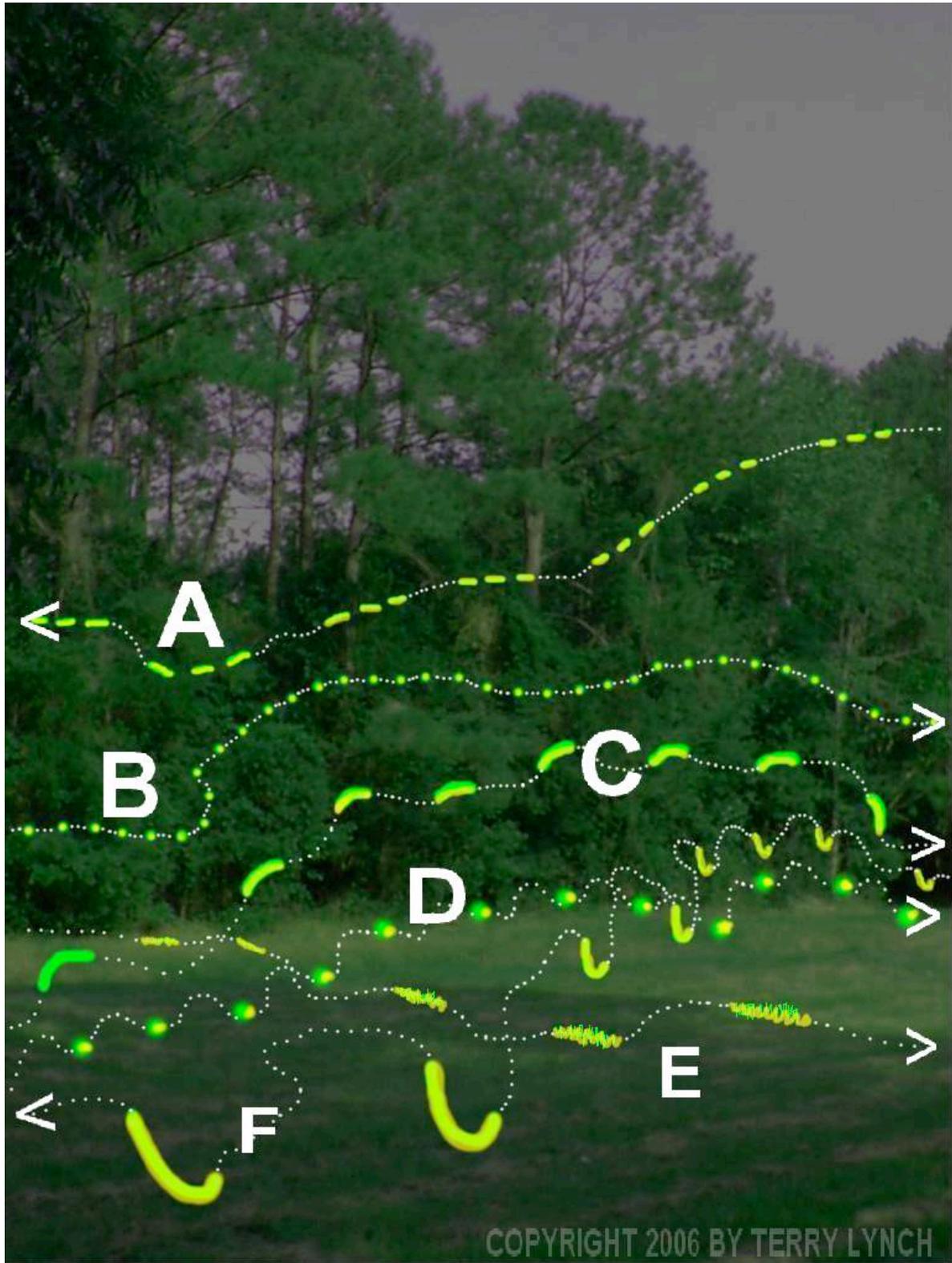


Mimulus lewisii



Mimulus cardinalis

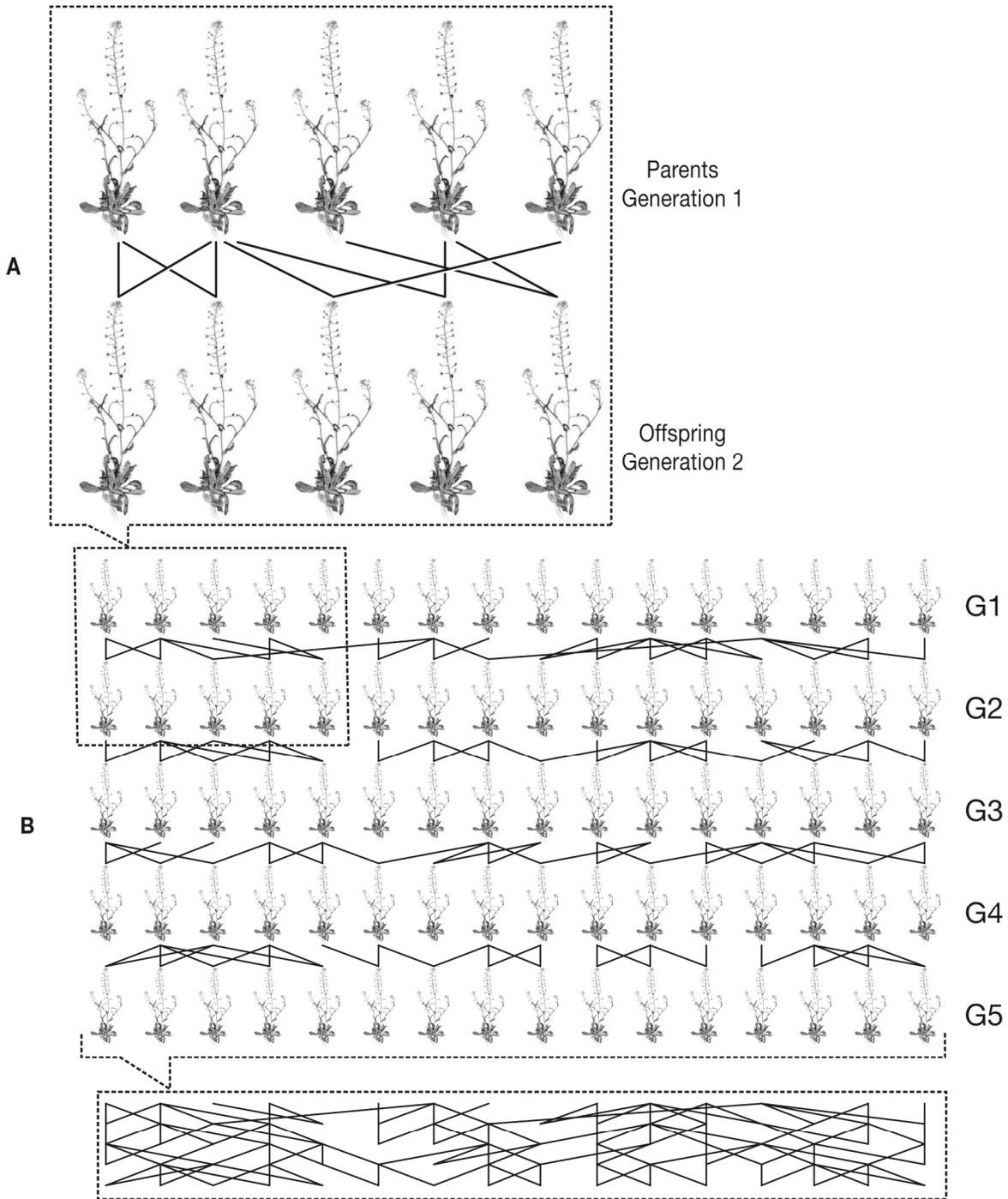
Fireflies



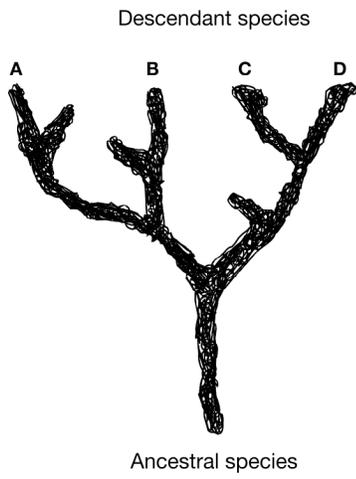
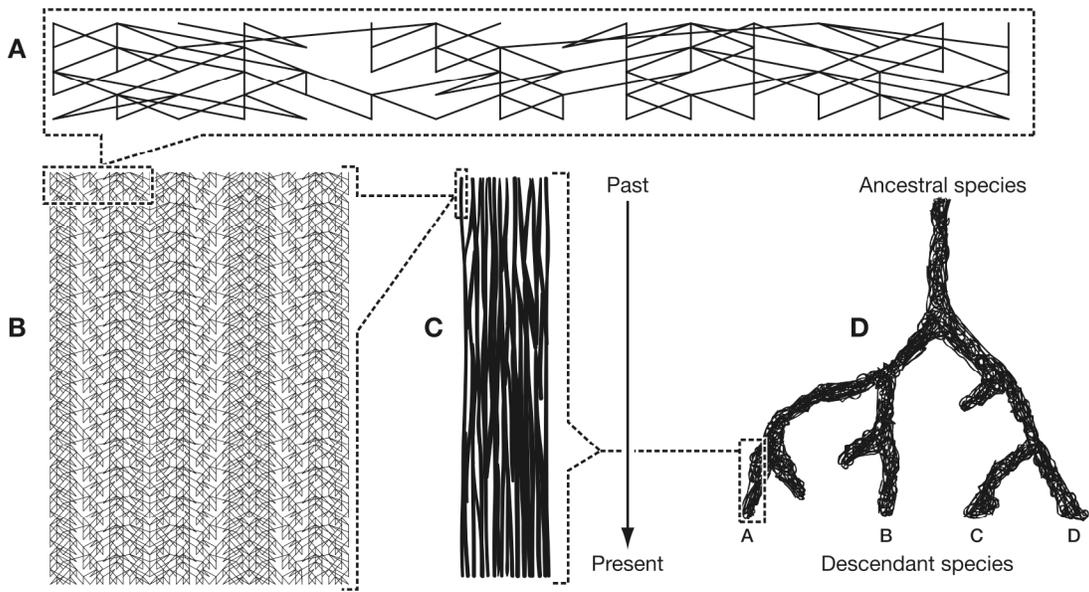
http://byteland.org/naturalist/firefly_faq.html

Evolution 7 - 3

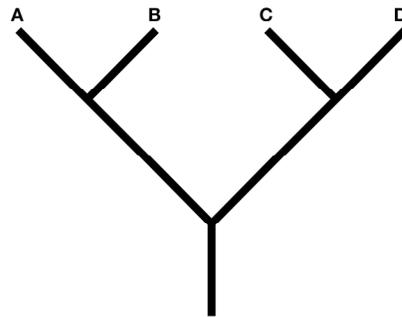
Speciation: the process



From ("Phylogenies & Tree Thinking" by David A. Baum and Susan Offner *American Biology Teacher* 70:4 222 [2008])

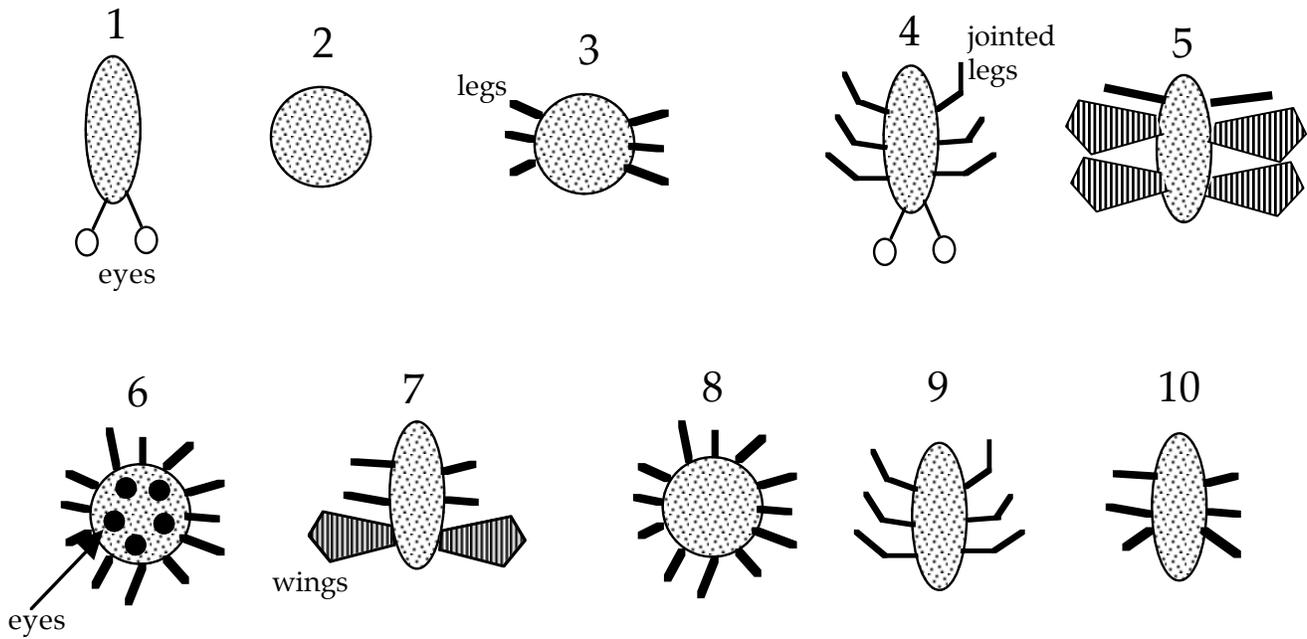


A



B

Bio 112 Phylogeny Demonstration Problem



Other info:

- in a layer of rock that is 600 million years old, you only find type 2.
- in a layer of rock 200 million years old, you find 4, 5, and 6 but not 1.

Suppose you found these fossil creatures on Mars. What might you conjecture about their evolutionary history?

Bio 112 Handout for Evolution 8

This handout contains:

- Today's iClicker Questions
- Handouts for today's lecture

iClicker Question #5A - before lecture

Consider the hypothetical creatures on the last page of this handout. Which of the following is the most likely order of evolution for the creatures listed?

- A. (first) 6 8 3 2 (last)
- B. (first) 2 8 3 6 (last)
- C. (first) 2 3 6 8 (last)
- D. (first) 2 3 8 6 (last)
- E. none of the above

iClicker Question #5B - after lecture

Put the following events in order from the first (happened longest ago) to the last (happened most recently).

- (A) First plants on land.
- (B) First plants.
- (C) First animals on land.

- A. A then B then C.
- B. A then C then B.
- C. B then C then A.
- D. B then A then C.
- E. C then A then B.

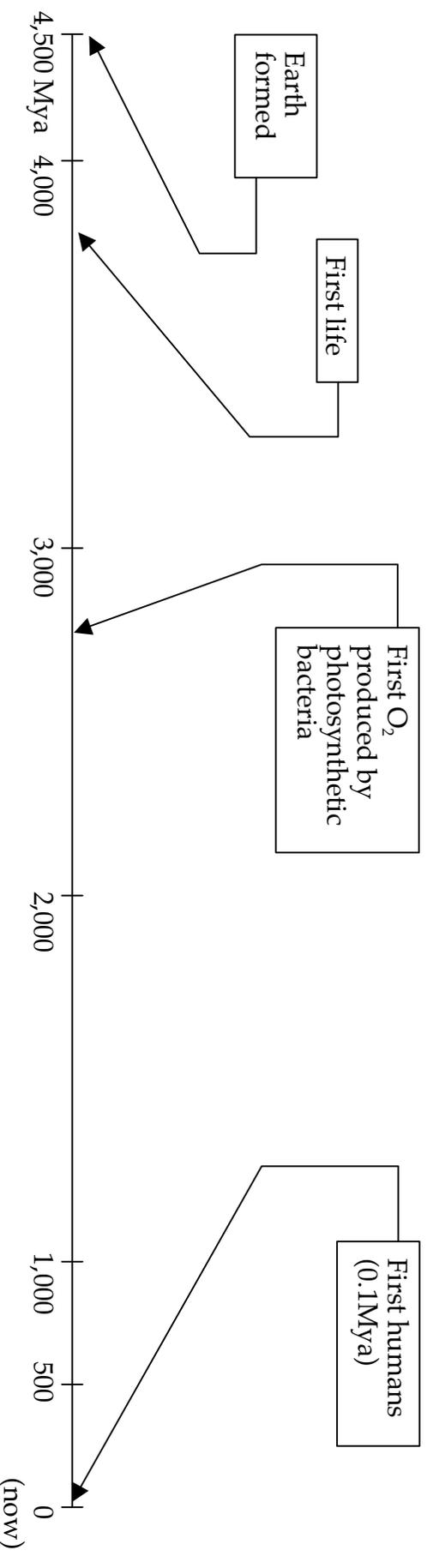
Beaming in your answers

1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
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Bio 112 Earth History I (the *very* big picture)

- 1 Mya = 1 Million years ago

The Environment:



too hot
for life

atmosphere

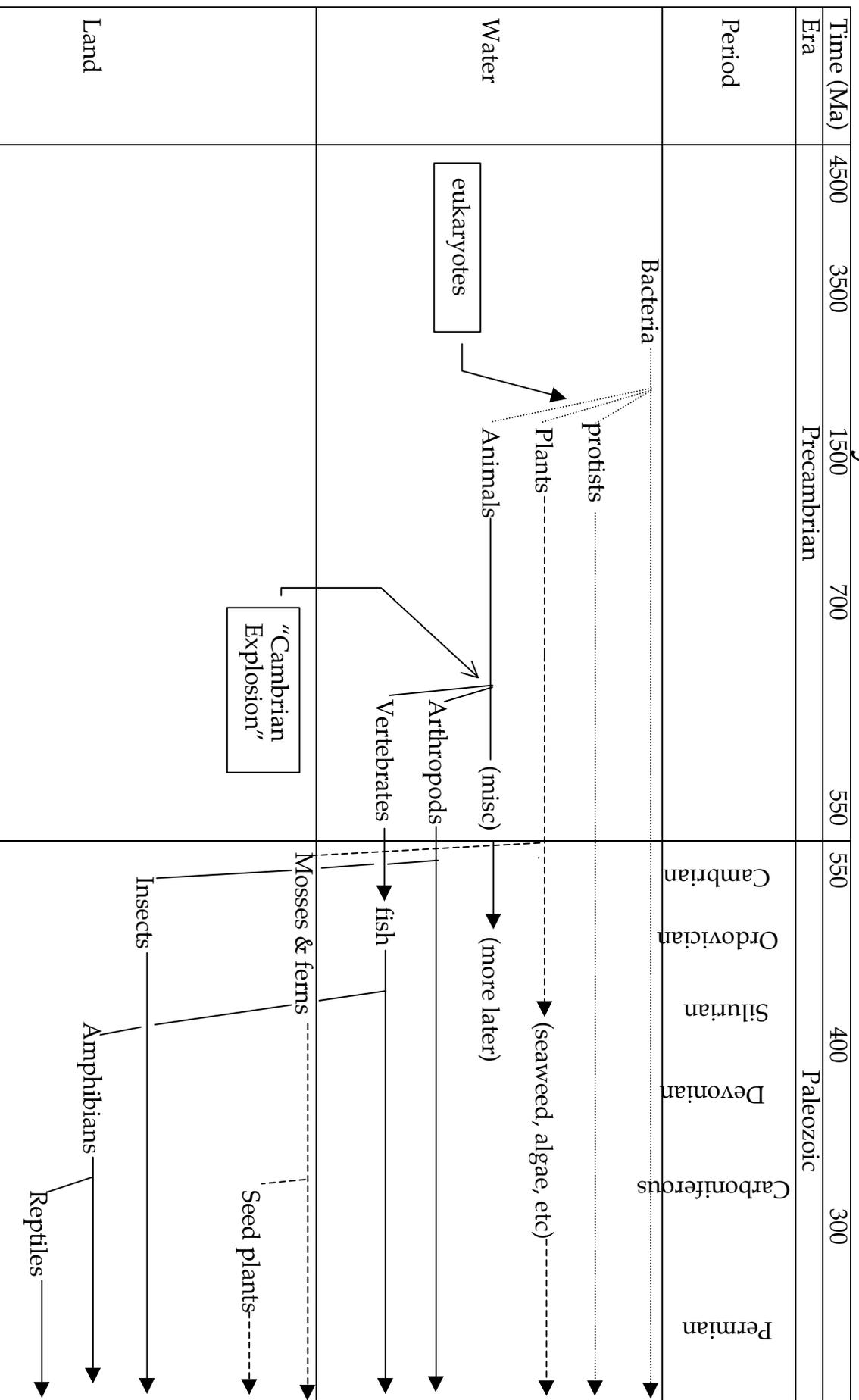
- N₂
- H₂
- H₂O
- CO₂
- NH₃ (toxic!)
- no O₂!

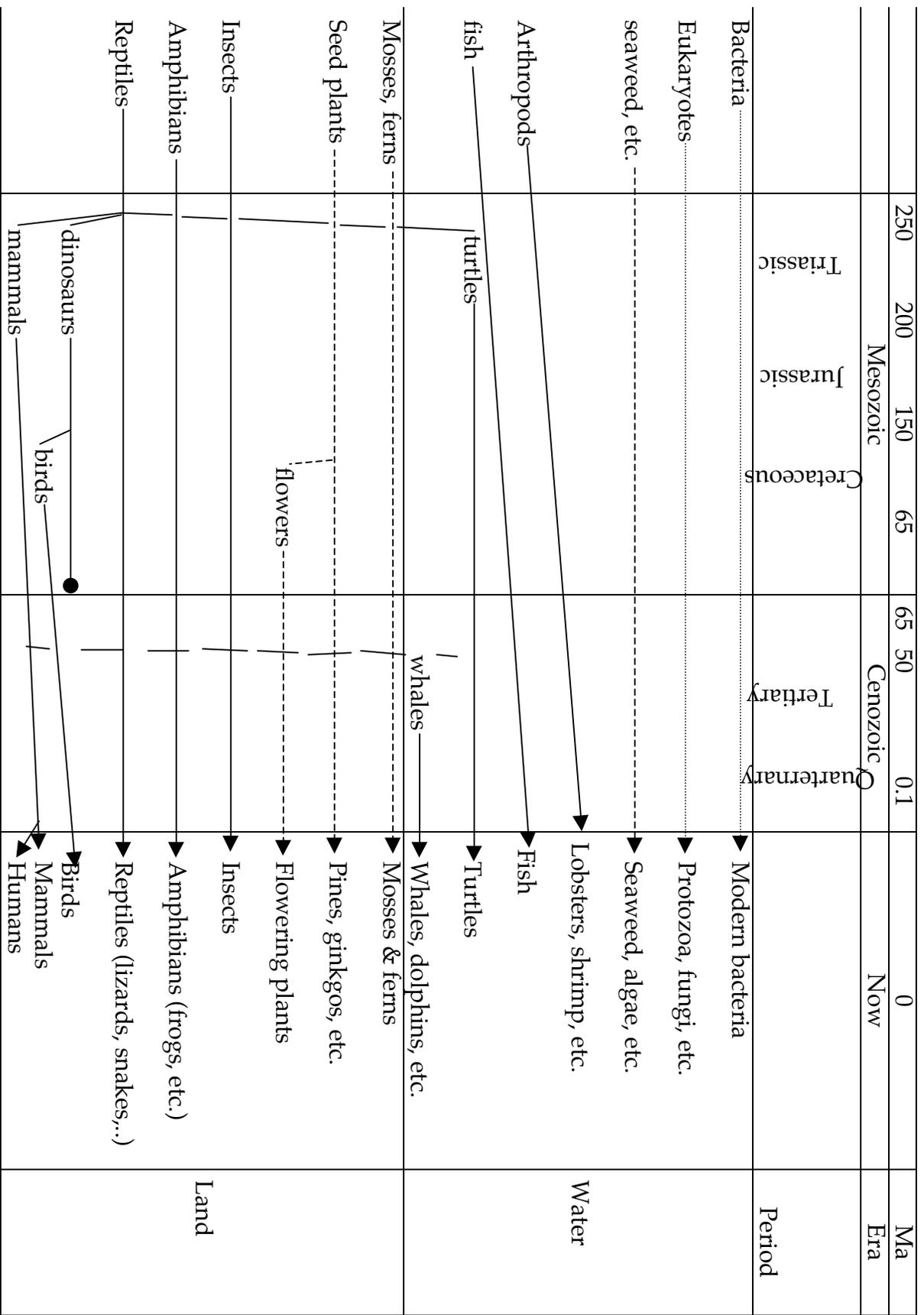
O₂ in air increases

atmosphere

- low CO₂
- 20% O₂
- 80% N₂
- no NH₃

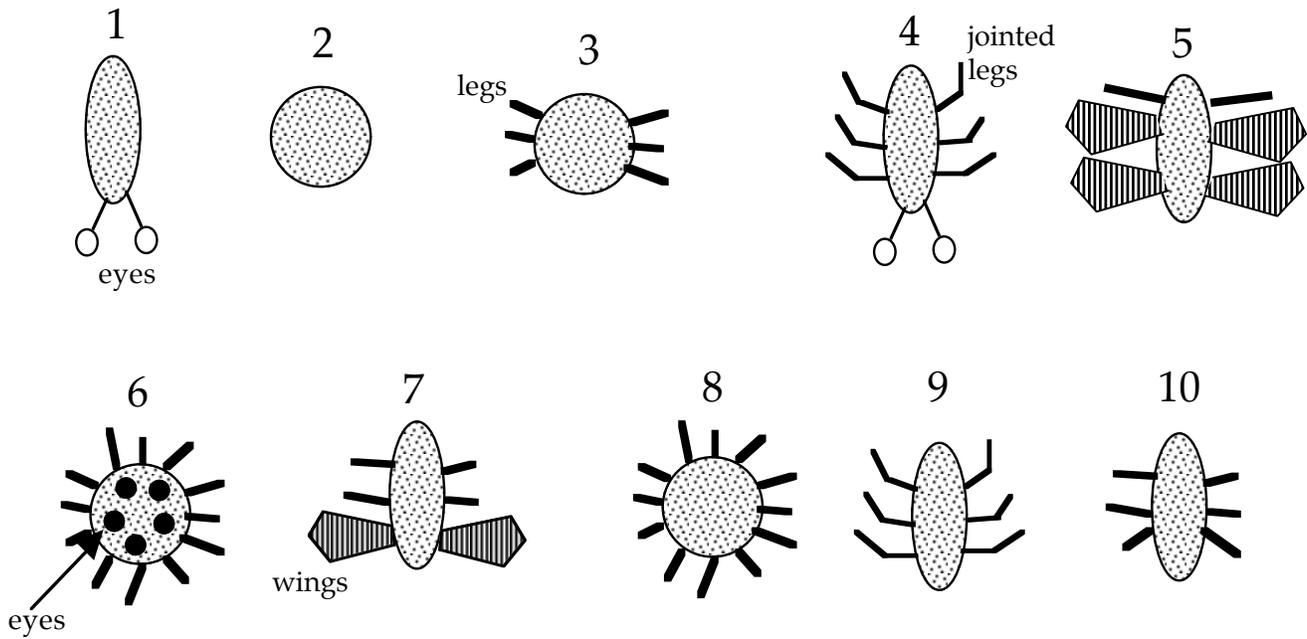
Bio 112 Earth History II





Evolution 8 - 4

Bio 112 Phylogeny Demonstration Problem



Other info:

- in a layer of rock that is 600 million years old, you only find type 2.
- in a layer of rock 200 million years old, you find 4, 5, and 6 but not 1.

Suppose you found these fossil creatures on Mars. What might you conjecture about their evolutionary history?

Bio 112 Handout for Evolution 9

This handout contains:

- Today's iClicker Questions
- Handout for today's lecture

iClicker Question #6A - before lecture

Which of the following statements are true?

- A. The amino acid sequence of any given enzyme is the same in all organisms.
- B. Any change in the amino acid sequence of a protein will cause it to be non-functional.
- C. If there is a difference in the amino acid sequence of a given enzyme in two organisms, it reflects the fact that one is fitter than the other.
- D. More than one is true.
- E. None of the above are true.

iClicker Question #6B - after lecture

There are several assumptions that go into using molecular data to generate phylogenies. Which of the following assumptions is(are) **not** essential if you want to use molecular data to generate a phylogeny?

- A. Mutation rates are constant over time and constant in all species.
- B. Proteins with similar amino acid sequences reflect common ancestry rather than coincidence.
- C. Mutations do not change the amino acid sequence of proteins.
- D. The changes in amino acid sequence used to calculate molecular phylogenies do not cause changes in function.
- E. More than one of the above.

Beaming in your answers

1. Figure out your answer and select the appropriate letter (A-E).
2. Turn on your iClicker by pressing the "ON/OFF" button; the blue "POWER" light should come on. If the red "LOW BATTERY" light comes on, you should replace your batteries soon.
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Bio 112 Molecular Phylogeny Example

- Here is an example of molecular phylogeny; it uses the single-letter code for amino acids:
 P = proline F = phenylalanine L = leucine I = isoleucine
- Consider the hydrophobic core of a protein where the exact sequence is not important for the function of the protein:

Long ago

PPPPP
Species A₁

PFPPP
Species B

Now
IFPPP
Species D

Original Protein:

PPPPP
Species A

PPPPP
Species A₂

PPLPP
Species C

PPLFP
Species E

PPLPF
Species F

- Reconstructing the history from the modern species (D, E, F):
 • Species E vs. Species F

E: PPLFP

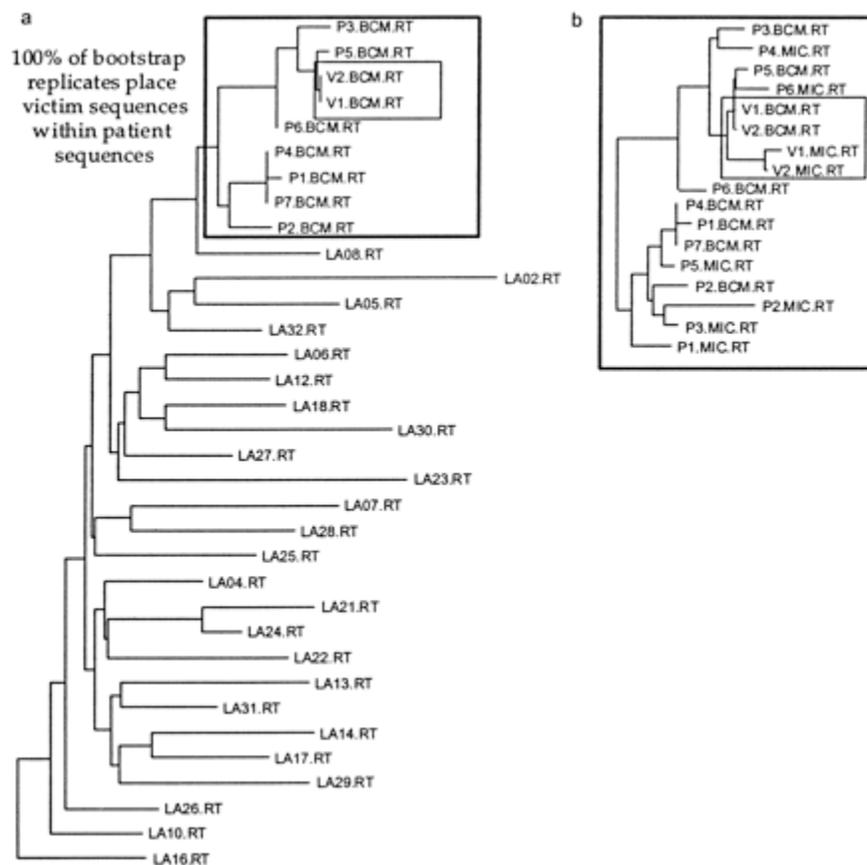
D: IFPPP

F: PPLPF

E: PPLFP

Molecular phylogeny & criminal justice

- 1994: Dr. Richard Schmidt accused of injecting his ex-girlfriend (the Victim) with HIV (AIDS virus) from one of his patients.
- HIV evolves very rapidly, even leading to multiple different sequences *in the same patient!*
- Police collected HIV samples from victim (V), Dr. Schmidt's patient (P), and many local HIV⁺ individuals from the community who were unrelated to the case (LA)
- They then used computer tools to construct the following phylogeny.



From: "Molecular evidence of HIV-1 transmission in a criminal case" by Michael L. Metzker, David P. Mindell, Xiao-Mei Liu, Roger G. Ptak, Richard A. Gibbs, and David M. Hillis. *Proceedings of the National Academy of Sciences* 99:22 14292-14297 (2002).