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EEB 318 Midterm Exam #1

Do NOT begin before you are told to do so.

You are NOT permitted a calculator or any study aids.

Do NOT cheat. Looking in the direction of another student's paper is considered cheating. Cover your answer sheet as you work.

This midterm consists of 20 multiple choice questions AND 3 short-answer questions, and accounts for 25% of your grade for the term. Multiple choice questions are worth a total of 40 points (2 points each) and short-answer questions are worth a total of 28 points.

Pages are double-sided and numbered 1-15. A formula sheet is given on the last page. You must hand in the formula sheet with your exam.

Not all questions that have numbers and/or equations require you to do calculations!

Read each question carefully. Some may resemble questions from previous exams, but there may be important differences.

You will have approximately 1 hour 50 minutes to write this exam. You will not be allowed extra time to fill in the scantron sheet, so be sure to complete your answers before the time is up.

You must stop writing immediately when you are told to do so.

AFTER you are told to begin:

1. Check to make sure you have a complete exam.

2. Write your NAME and STUDENT NUMBER neatly on the front page (page 1) AND on EVERY PAGE THAT HAS A SHORT-ANSWER RESPONSE. Marks will be deducted if you do not follow these instructions.

3. Write your responses to the short-answer questions below the corresponding question in the space provided.

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1) Which of the following were important contributors to Darwin's conception of the theory of evolution?

R1. Lyell's notion of uniformitarianism.
R2. Dobzhansky's classic experimental observations.
R3. Lamarck's idea of acquired characteristics.
R4. Malthus' ideas on finite resources.
R5. Kimura's "Neutral Theory".

a. R1 and R2 and R3 and R4 and R5
b. R1 and R2 and R3 and R4
c. R4
d. R1 and R2
e. R1 and R4

2) Which of the following would probably have the most profound effect on an organism?

a. Insertion of 4 nucleotides within an exon.
b. Mutation of a trinucleotide repeat with motif CCA from 8 copies of the repeat to 12 copies of the repeat.
c. Insertion of a transposable element into a non-functional portion of the genome.
d. A point mutation from T to C within an intron.
e. Change of a single synonymous site in a coding sequence.

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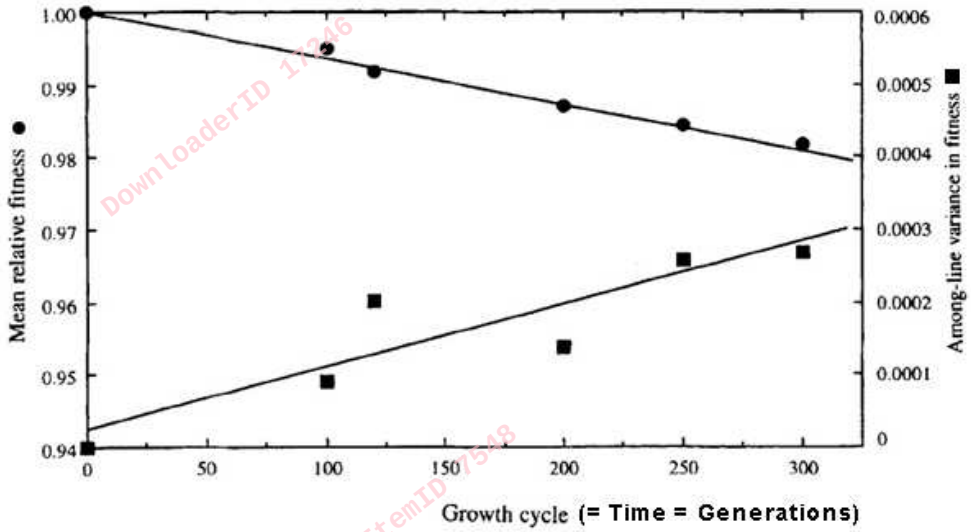
3) Which of the following statements is an ACCURATE interpretation of the following graph of data from a mutation accumulation experiment?



a. These results demonstrate how point mutations alone can affect an organism's fitness.
b. The decrease in mean relative fitness is consistent with natural selection weeding out deleterious mutations in the experimental populations.
c. The increase in among-line variance is consistent with recombination rearranging different genotype combinations.
d. Most new mutations that affect fitness have deleterious effects.
e. Genetic drift caused an allele to change in frequency from 100% to about 98% in the population, over the course of 300 generations.

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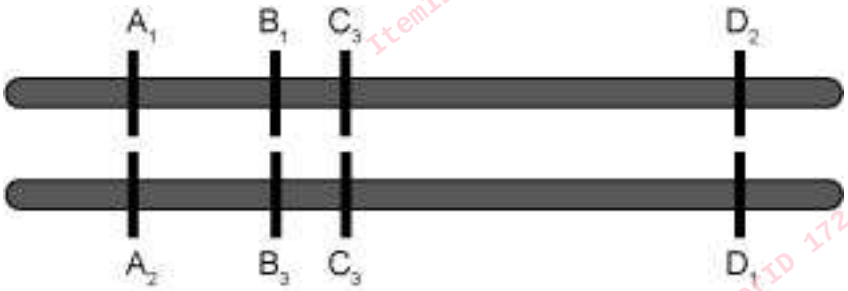
4) A population of algae is at Hardy-Weinberg Equilibrium at a locus with 2 alleles, Ccm1 and Ccm2 (recall, $p^2 : 2pq : q^2$), with Ccm1 homozygotes at frequency 0.2. Under the assumptions of the Hardy-Weinberg model, what fraction of individuals will be heterozygous in the generation experienced by the "grandchildren" of the present-day algae (2 generations in the future)?

a. $2 * 0.2 * (1 - 0.2) = 0.32$
b. $2 * \sqrt{0.2} * (1 - \sqrt{0.2}) = 0.494$
c. $[2 * \sqrt{0.2} * (1 - \sqrt{0.2})]^2 = 0.244$
d. $1 - 0.2 = 0.8$
e. Frequency can't be determined from the above information.

5) Consider the following representation of allelic states on a pair of homologous chromosomes in a diploid individual. Which of the following corresponds to a GENOTYPE?



R1. A_1-D_2
R2. B_1/B_3
R3. A_1-B_1-C_3-D_2
R4. A_1-B_1-C_3-D_2/A_2-B_3-C_3-D_1
R5. A_2-B_3-C_3-D_1

a. R1 and R3 and R5
b. R1 and R2
c. R3 and R5
d. R4
e. R2 and R4

6) Which of the following is an assumption of the standard Hardy-Weinberg model?

   a. Natural selection affects the locus under consideration.
   b. New alleles arise at the locus by mutation every generation to generate heterozygosity.
   c. Gene flow occurs only between subpopulations that are directly adjacent to one another.
   d. Genetic drift does not occur in the population.
   e. None of the above are assumptions of the standard Hardy-Weinberg model.

7) Consider two populations of annual wildflowers in which individuals reproduce only by self-fertilization. There are two selectively neutral alleles at the Eft locus (Eft1 and Eft2) in each population, but no migration between the populations. The mutation rate at Eft is very low, so we can ignore new mutations over the course of a few generations. The Eft1 allele occurs at frequency 0.2 and at frequency 0.7 in each of populations A and B, respectively. Population A has 1000 flowers, whereas population B has 5000 flowers. What fraction of the progeny coming from flowers that are heterozygous at the Eft locus in population B will be homozygous for Eft2?

   a. 0
   b. 0.25
   c. $(1 - 0.7) = 0.3$
   d. $(1 - 0.7)^2 = 0.09$
   e. $(1000 / 5000) * [(1 - 0.2) / (1 - 0.7)] = 0.533$

8) Imagine a population of garden snails in which the inbreeding coefficient is 0.6, but all other Hardy-Weinberg assumptions are met. A related species – the sidewalk snail – has an inbreeding coefficient of 0.1, also subject to the other assumptions of the Hardy-Weinberg principle. What differences would you expect to see between these two species?

   a. There is more gene flow in the sidewalk snails.
   b. The fraction of individuals that are heterozygous at any given locus will probably be greater in the sidewalk snail population.
   c. Individuals of the garden snail population would be harder to find because they would be less common.
   d. Genetic drift will have a more pronounced effect in the garden snail population.
   e. The mutation rate will be higher in the garden snail population.

9) A student majoring in Ecology & Evolutionary Biology isolated DNA from 12 members of her boyfriend's extended family, after getting permission from each of them, and then sequenced 600 nucleotides from the mitochondrial NADH locus as part of a research project. When she got the results back, she identified a total of 3 single nucleotide polymorphisms, all at synonymous sites. She also determined that 10 of the sequences were unique and that the other 2 were identical to each other. How many haplotypes did the student identify at the NADH locus in this sample of people?

a. Can't be determined without more information about the DNA sequence.
b. 1
c. 10
d. 11
e. 12

10) Reproduction in red-winged blackbirds follows a polygynous mating system, in which a small number of males successfully defend a food-rich territory and then mate with many female partners who rear their young in the corresponding territory. Consequently, the sex ratio among breeding individuals can be as high as 10 females to 1 male in a given territory. How would you expect this mating system to influence the effective population size relative to the adult census population size of red-winged blackbirds?

a. Because both are measures of population size, they would give equivalent values.
b. The effective population size would be larger, because males have many mating partners.
c. The census population size would be larger, because some males don't have a territory.
d. It is not possible to determine how effective and census population sizes relate without knowing the sex ratio of the juvenile birds in the nests.
e. Only population bottlenecks will cause a difference between effective and census population size, so as long as the red-winged blackbirds are demographically stable, then the two measures of population size would be the same.

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11) Which of the following are ways that phenotypic variation can be distributed?

R1. Into two or more partially sympatric populations.
R2. In a gradual cline of trait values across a geographic range.
R3. Into effects due purely to environmental differences across space.
R4. With effects due to differences in many genes.
R5. With effects due to differences in exactly one gene.

a. R1 and R4.
b. R2 and R3.
c. R1 and R2 and R5.
d. R1 and R2 and R3 and R4.
e. R1 and R2 and R3 and R4 and R5.

12) A postdoctoral fellow working on their research project measured the surface area of the foreheads of 360 randomly selected students as well as each of the students' parents. A mid-parent value was calculated as the average of the forehead surface areas for the two parents, which was equal to 245 cm^2 with a variance of 62.4. After calculating the heritability from a regression of offspring and mid-parent values, she determined that the genetic variance was exactly equal to the environmental variance for the trait. From this information alone, what is the heritability of forehead surface area that she calculated?

a. Not enough information is given to calculate the heritability.
b. 0
c. 0.5
d. 1
e. 62.4 / 245 = 0.255

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13) Consider populations of diploid trout that managed to colonize 40 small lakes from fishermen transporting them from Lake Huron, but then experience no further migration between any of the water bodies. The source population contained 2 selectively neutral alleles at the TFT locus, with allele TFT_1 at frequency 0.3. Each of the small lakes initially contained the TFT_1 and TFT_2 alleles at the frequency at which they were present in Lake Huron, and reach a demographic equilibrium effective population size of 1000 in each small lake. What is the probability that the TFT_2 allele will eventually be lost in the Lake Huron population?

a. 0
b. 0.30
c. 0.70
d. 1 – 2 * 0.3 * 0.7 = 0.58
e. 40 / 1000 = 0.04

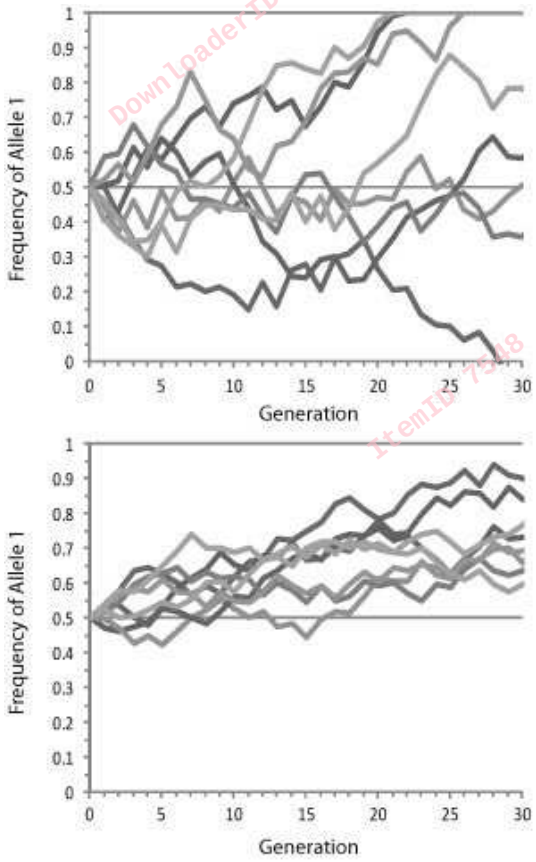
14) Based on the information about the trout populations given in the previous question, answer the following question. After the trout populations in this system reach equilibrium, after many (>4000) generations, what value of F_{st} would you expect to observe between any pair of lakes?

a. 0
b. 1 / 4001 = 0.00025
c. 0.3
d. 0.7
e. 1

15) Consider the measurement of genetic variation by allozymes and by sequencing DNA of coding regions. Which of the following is/are accurate?

a. Only allozymes will detect differences at replacement sites.
b. Only DNA sequences will detect insertion and deletion mutations.
c. Both approaches will detect differences at synonymous sites.
d. All of the above.
e. None of the above.

16) Consider the two figures below, which show the changes in allele frequency for the XYZ locus with 2 alleles within isolated experimental populations. The lines in each figure represent replicate populations, each of which was initiated with 50% of each allele (XYZ-1 and XYZ-2). Which of the following statements are accurate interpretations of these figures?



R1. Genetic drift is evident only in the top figure.
R2. The two alleles at the XYZ locus are probably selectively neutral.
R3. The experimental populations for the top figure probably have a larger effective population size than the populations represented in the bottom figure, because the differences among the replicates are larger.
R4. The fact that more of the replicates fixed for an allele at the XYZ locus in the top figure than in the bottom figure indicates that natural selection must have been stronger in the top figure.
R5. Both genetic drift and selection appear to influence evolution at the XYZ locus.

a. R5
b. R1 and R2
c. R3 and R4
d. R1 and R2 and R5
e. R1 and R2 and R3 and R4 and R5

17) An undergraduate student conducting a 4th year research project surveyed genetic variation for biting-flies that inhabit 22 islands in Hudson Bay. Based on her analysis of 14 microsatellite loci, she calculated $F_{st} = 0.02$. What is an appropriate conclusion from these findings?

a. Recombination between the microsatellite loci is highly restricted.
b. Inbreeding is very strong within the biting-fly populations.
c. There is very little gene flow among the biting-fly populations.
d. Genetic variation is very low in the biting-fly species.
e. The biting-flies on Hudson Bay islands act much like a panmictic population, in an evolutionary sense.

18) Anthony Allison described how the sickling phenotype evolved independently 5 times in different human subpopulations and that in each case the causal change was due to valine being replaced by glutamic acid at one amino acid residue in the hemoglobin gene. What does this observation imply?

S1. There are two distinguishable sickling haplotypes at the hemoglobin locus in humans.
S2. There are five distinguishable sickling haplotypes at the hemoglobin locus in humans.
S3. Genetic drift can lead to one allele increasing in frequency in some populations, but another allele increasing in other populations.
S4. There has been convergent evolution in the hemoglobin gene.
S5. Point mutations can happen only once at a given nucleotide site.

a. S2 and S4.
b. S2 and S5.
c. S1 and S3.
d. S1 and S4.
e. S2 and S3 and S4 and S5.

19) Which of the following statements about the Neutral Theory of molecular evolution is ACCURATE?

S1. The rate of substitution of neutral mutations depends on the effective population size, which can be different from the census size.
S2. The Neutral Theory predicts that most molecular differences within species have absolutely no effect on the fitness of organisms.
S3. The Neutral Theory applies to the evolution of DNA sequences, but not necessarily to the evolution of phenotypes.
S4. Natural selection does not influence the probability of fixation of neutral mutations.
S5. Genetic drift is the major force controlling the change in allele frequency of deleterious mutations.

a. S1 and S5
b. S1 and S2 and S4
c. S2 and S3 and S4
d. S1 and S2 and S3 and S4 and S5
e. All are false statements about the Neutral Theory.

20) Which of the following are ACCURATE assumptions or predictions by the Neutral Theory regarding beneficial alleles?

S1. Beneficial alleles contribute, at most, only in a minor way to DNA differences between species.
S2. Beneficial mutations only arise from point mutations in replacement sites.
S3. Beneficial alleles arise rarely, but get fixed rapidly by selection.
S4. Beneficial alleles arise by mutation just as frequently as deleterious alleles.
S5. Beneficial mutations have an initial frequency of 1/N in a haploid population.

a. S2 and S3.
b. S2 and S5.
c. S4 and S5.
d. S1 and S3 and S5.
e. S1 and S3 and S4.

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Short Answer Questions

1. Design an experiment to test the key ideas and predictions of genetic drift. Be sure to: (1) describe the important components of the experimental setup, (2) describe what you would measure, (3) describe what observations would be consistent with the predictions of genetic drift. (15 points)

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2a. What are the stochastic evolutionary processes? List them and provide 1-2 sentences explanation for each. (5 points)

2b. What is meant by “stochastic” with respect to evolution? (2 points)

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3. Consider the following histogram that summarizes how particular chromosome copies from wild populations influence the viability of individuals that have those chromosome copies. What interpretations can you make from this figure (list and explain at least 2)? (6 points)