Evolution
Fall 2011
Midterm Exam #2

Name: KEY
Student number:

There are 15 questions totaling 42 points on this exam. Point allocation is given next to each question. Your final mark for the exam will be the percentage of points out of 42. The exam is worth 20% of your final course grade.

No notes or textbook can be used during the exam. There is a formula sheet at the back of the exam.

No assistance between students is allowed.

If a question is unclear to you raise your hand and an instructor will try to help.

- This key gives baseline points for correct answers. Partial marks were given for partially correct answers.
- Given that the exam took longer than expected and students may have been rushed to finish the exam, I was lenient in terms of clarity of explanations, giving the benefit of the doubt to students.
- In principle, this exam should facilitate learning and help prepare you for the final exam, so do not hesitate to ask questions about the exam.

[1] [a] Identify four processes that cause allele frequencies to change in a subpopulation. (2 points)

Mutation
migration
drift

selection

(½) point for each correct answer

[b] Identify two processes that by themselves do not change allele frequencies, but change the genetic composition of a subpopulation. (1 point)

inbreeding
recombination
assortative mating

(½) point for each correct answer up to 1

[2] A diploid population consists of 350 A_1A_1, 1102 A_1A_2 and 1548 A_2A_2 genotypes. Assess whether there is evidence for inbreeding in this population. Provide support for your analysis. (3 points)

$N = 350 + 1102 + 1548 = 3000$

$p_{A_1} = \frac{2 \cdot 350 + 1102}{2 \cdot 3000} = 0.30 \qquad p_{A_2} = 1 - p_{A_1} = 0.7$

$H = \frac{1102}{3000} = 0.37 \qquad H_0 = 2 \cdot p_{A_1} \cdot p_{A_2} = 2 \cdot 0.3 \cdot 0.7 = 0.42$

$F = \frac{H_0 - H}{H_0} = \frac{0.42 - 0.37}{0.42} = 0.12$ $F > 0$ ∴ evidence for inbreeding

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① → H ① → F

① → H_0

[3] At two loci the following haplotype counts are observed: 140 A_1B_1, 340 A_2B_2, 60 A_1B_2, 460 A_2B_1. What is the expected <u>number</u> of A_1B_2 haplotypes if the haplotypes were in linkage equilibrium? (2 points)

$P_{A_1} = \frac{140+60}{1000} = 0.2$ $\qquad$ $P_{B_2} = \frac{340+60}{1000} = 0.4$

$N_{A_1 B_2} = P_{A_1} \cdot P_{B_2} \cdot 2N = 0.2 \cdot 0.4 \cdot 1000 = 80$

(1/2) P_{A_1} $\qquad$ ① $P_{A_1B_2} = P_{A_1} = P_{B_2}$

(1/2) P_{B_2}

[4] An asexual population consists of 0.2 *A* genotypes and 0.8 *B* genotypes. The per capita growth rate of the *A* genotype is 1.7 and the per capita growth rate of the *B* genotype is 2.3. What will the frequency of the *B* genotype be in the next generation? (3 points)

$P_B' = P_B \frac{w_B}{\bar{w}}$

$w_A = \frac{1.7}{2.3} = 0.74 \quad w_B = 1$ $\qquad$ (note: could standardize by A genotype also)

$\bar{w} = 0.2 \cdot 0.74 + 0.8 \cdot 1 = 0.948$

$P_B' = 0.8 \cdot \frac{1}{0.948} = 0.844$

① → $\bar{w}$

$P_B' = 0.8 \cdot \frac{1}{0.948}$ ↙①

①

[5] In a diploid and sexually reproducing population there is a genetic locus with two alleles. The frequency of the A_1 allele is 0.45 and the frequency of the A_2 allele is 0.55. The relative fitnesses of genotypes are given in the table below.

	A_1A_1	A_1A_2	A_2A_2
Relative fitness	0.97	1	0.96

[a] What type of fitness model occurs at this locus? (1 point)

Heterozygote advantage ①

[b] What is the frequency of the A_1 allele in the next generation? (Answer to an accuracy of 3 decimal places). (3 points)

$$\bar{\omega} = 0.45^2 \cdot 0.97 + 2 \cdot 0.45 \cdot 0.55 \cdot 1 + 0.55^2 \cdot 0.96 = 0.981$$ ①

①

$$p'_{A_1} = 0.45 \cdot \frac{\boxed{0.45 \cdot 0.97 + 0.55 \cdot 1}}{0.981} = 0.452$$

①

[c] What is the expected equilibrium frequency of A_1? (1 point)

$$\hat{p}_{A_1} = \frac{t}{s+t} = \frac{0.04}{0.03+0.04} = 0.571$$ ①

[6] [a] In words, explain what determines the marginal fitness of an allele. (2 points)

(1) Genotypes the allele occurs in

(2) Probability the allele is in a genotype

(1.5) for (1) or (2) → ② for both (1) & (2)

① for discussion of survivorship/fecundity of allele

[b] If the marginal fitness of an allele is greater than the mean fitness of a population will the frequency of the allele increase or decrease? (1 point)

increase ①

[7] What processes cause a geographic cline in allele frequency? (2 points)

migration - selection balance

↗ ↗

① ①

Partial marks for migration & drift, isolation-by-distance ...

[8] Describe a type of frequency dependent selection. Discuss whether this type of frequency dependent selection can or cannot maintain genetic or phenotypic diversity in a species. (3 points)

Examples from class:

(1) positive frequency-dependent selection

(2) inverse frequency-dependent selection

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② Correct description

① Correct discussion of maintenance of diversity

[9] The effective population size of humans is about 10,000 to 20,000, yet our current census size is about 7,000,000,000. Indicate and explain a likely reason for why the effective size is so much lower than our current census size. (2 points)

Likely reason is humans had a small population size historically.

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② for discussion of historically small population size or unequal sex ratio. Partial marks for other answers depending on degree of correctness.

[10] In lions, about 25% of adults are reproductive males and 75% are reproductive females. If a subpopulation of lions consisted of 32 adults, what is its effective population size? (2 points)

$$N_m = 0.25 \cdot 32 = 8 \qquad N_f = 0.75 \cdot 32 = 24$$

$$N_e = \frac{4 \cdot N_m \cdot N_f}{N_m + N_f} = \frac{4 \cdot 8 \cdot 24}{8+24} = 24$$

(1/2) for N_m & N_f (1.5) for N_e given your N_m & N_f values

[11] Is the change in allele frequency of a codominant and deleterious allele with selection coefficient s=-0.001 affected more by random genetic drift or selection, on average, in a population with an effective population size equal to 10,000? Explain why. (3 points)

Ideal answer:

$$\frac{\text{rate of } \Delta \text{ by drift}}{\text{rate of } \Delta \text{ by selection}} = \frac{\dfrac{p(1-p)}{2N_e}}{\dfrac{|s|\, p(1-p)}{2}} = \frac{\dfrac{\cancel{p(1-p)}}{\cancel{2} \cdot 10^4}}{\dfrac{|-0.001|\, \cancel{p(1-p)}}{\cancel{2}}}$$

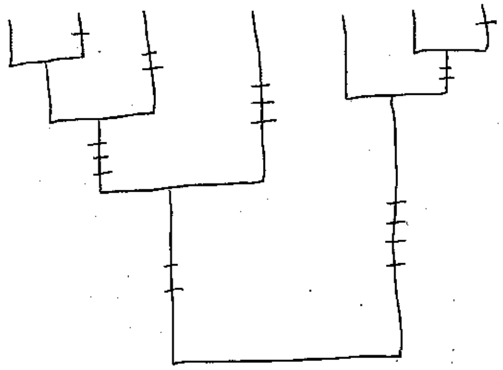
$$= 0.1$$

Since ratio of Δ due drift relative to Δ by selection is < 1, selection has a greater effect

① Identifying selection correctly

② Correct explanation

[12] Below is the gene tree for a sample of 7 alleles at a genetic locus. Hash marks in the tree indicate mutations.



What type of selection may be occurring at this locus? Support your answer with an analysis. (4 points)

$k_e = 7$ ①

$k_i = 11$ ①

$a = 1 + \frac{1}{2} + \cdots + \frac{1}{7-1} = 2.45$ (1/2)

$k_e - k_i/(a-1) = 7 - 11/(2.45-1) = -0.59$ (1/2)

Since $k_e - k_i/(a-1) < 0$, suggests ①
balancing selection is occurring

[13] What type of data can be used to detect a recent selective sweep of an allele in a sexually reproducing population undergoing recombination? Given this type of data, what would be indicative of a recent selective sweep? (2 points)

Levels of linkage disequilibrium ①

Large L.D. is indicative of a ①
selective sweep

Also, could use gene trees & the G-statistic

[14] [a] Identify four sources of variation that contribute to phenotypic variation in a population. (2 points)

Additive effects
dominance
epistasis
environmental
genotype × environment

(1/2) for each correct answer up to 2

Partial marks for mutation, migration, etc.

[b] What source of phenotypic variation contributes to narrow-sense heritability? (1 point)

additive

[15] Describe two approaches that can be used to estimate narrow-sense heritability. (2 points)

(1) Regress phenotypes of offspring on parent. Slope = h_N^2 ①

(2) Apply a selection differential to a population (S). Measure its response (R). Estimate

$$h_N^2 = \frac{R}{S}$$ ①

Also accepted $h_N^2 = \frac{V_A}{V_P}$ for ① point