BIO3119 Practice problems - 2015

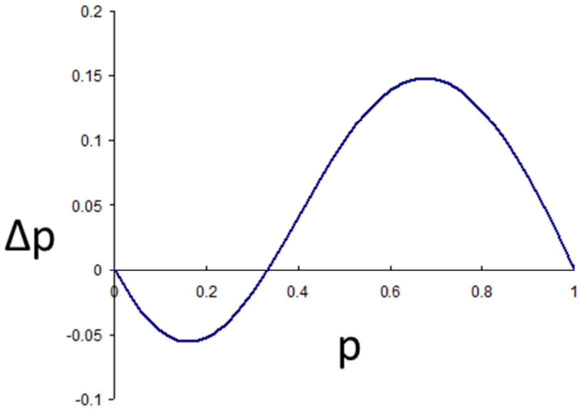
This is a set of problems to help you practice for the final exam. These will not count towards your mark in the course and are not to be submitted. Answers are provided at the end. Please do not distribute. Please note that just because a particular topic is asked here it does not mean it will be on the final. Likewise, topics not covered here may be on the exam. These are some examples of the format and type of questions on the exam.

1. The table below summarizes the number of replacement and silent substitutions for fixed differences between humans and chimpanzees, and polymorphisms within these species, for the mtDNA gene *ND3*. Determine whether these data are consistent with expectation under the neutral theory using a contingency chi-square test. P-values can be obtained using software (e.g., Excel or via web-based calculators) or using the table at the end of the problem set.

	Fixed	Polymorphic
nonsynonymous	4	8
synonymous	31	10

2. A biologist studying the major histocompatibility complex (MHC) in mice has determined that certain combinations of alleles at different loci occur much more frequently than would be predicted if they segregated independently.
    a. What is the term that describes this phenomenon?
    b. List three causes that could be responsible.

3. What form of selection does the figure below represent and what does it imply about the relative magnitudes of the relative fitnesses of the three genotypes? Label all equilibria and indicate their stability. If the initial allele frequency were 0.2, would selection increase or decrease this in the next generation?



4. For a mutation (*a*) with effects as described in the fitness set below, estimate the mutation rate to the mutant *a* allele if, at mutation-selection balance, $\hat{q} \approx 8 \text{ x } 10^{-6}$.

w_{AA}	w_{Aa}	w_{aa}
1	0.91	0.1

5. Define effective population size and give three reasons that may cause it to be less than the census population size.

6. Consider two loci with two alleles each and $p = 0.3$ at one and $p = 0.8$ at the other. What is the probability of choosing an individual at random that is a double heterozygote (i.e. heterozygous at both loci)? What two assumptions did you have to make in calculating this answer?

7. In birds and Lepidoptera (butterflies and moths), males are the homogametic sex (ZZ) while females are the heterogametic sex (ZW). This is referred to as the ZW system, which is opposite to the XY system seen in mammals where females are homogametic (XX) and males are heterogametic (XY). In parakeets, which are normally green-feathered, lutino (*l*) is a recessive Z-linked allele that causes yellow feathers.

    a. If 20% of males have yellow feathers, what percentage of females are expected to have yellow feathers, assuming Hardy-Weinberg and no sex-differences in allele frequency?

    b. Given the observed male genotypic numbers below from a set of 405 males, determine whether genotype frequencies fit Hardy-Weinberg expectation.

	Genotype	Observed Number
males	++	149
	+*l*	186
	Ll	70

8. In four sentences or less, define genetic drift, explain why it occurs, and explain why it causes no average change in allele frequency.

Solutions

1.

	fixed	polymorphic	sum
nonsynonymous	4	8	12
synonymous	31	10	41
sum	35	18	53

	fixed	polymorphic
nonsynonymous	= 12/53*35/53*53 =7.92	= 12/53*18/53*53 = 4.08
synonymous	= 41/53*35/53*53 = 27.1	= 41/53*18/53*53 = 13.9

Then calculate [(observed-expected)^2/expected] for each cell and sum them to get
$\chi^2 = 7.36$.
df = 1
$p < 0.01$
These data are not consistent with expectation under the neutral theory. This pattern is not consistent with both polymorphism and divergence at this locus being a product of the neutral mutation rate.

2.

  a. The phenomenon is linkage disequilibrium.
  b. Any of these are plausible explanations: 1) selection favouring certain combinations of alleles; 2) Insufficient time has passed to reach linkage equilibrium; 3) genetic drift; 4) Non-random mating

3. heterozygote inferiority: $w_{Aa} < w_{aa}, w_{AA}$.
   Equilibrium exist wherever the function intersects the x-axis (i.e. where $\Delta p = 0$): $p = 0$ (stable), $p \approx 0.325$ (unstable), $p = 1$ (stable). If $p = 0.2$, selection will decrease p in the next generation ($\Delta p < 0$).

4. $w_{aa} = 1 - s = 0.1$, so s = 0.9. $w_{Aa} = 1 - hs = 1 - h(0.9) = 0.91$, so h = 0.09/0.9 = 0.1

   partially recessive ($h = 0.1$)

$$\hat{q} \approx \frac{\mu}{hs}$$

$$\mu \approx qhs = 8\times10^{-6}(.1)(.9) \approx 7.2\times10^{-7}$$

5. Effective population size is the census size of an ideal population (i.e. one that meetings all HW assumptions) in which the effects of drift are the same as the observed population. Factors: fluctuating population size, unequal sex ratio, variation in family size.

6. 1st locus: $2pq = 2(0.3)(0.7) = 0.42$
2nd locus: $2pq = 2(0.8)(0.2) = 0.32$
$Pr = 0.42 \times 0.32 = 0.1344$
Must assume (1) random mating with respect to both loci and (2) that there is no linkage disequilibrium between them.

7.

a. $p^2 = 0.20$ so $p = \sqrt{0.20} = 0.4472$
   Approximately 45% of females are expected to have yellow feathers.
b. $p = (149/405) + 1/2\ (186/405) = 0.598$
   $q = 1 - 0.598 = 0.402$

Genotype	Obs	Exp	O-E	(O-E)^2/E
++	149	144.6	4.4	0.134
+l	186	194.8	-8.8	0.397
ll	70	65.6	4.4	0.295
Total	405	405		0.826

df = 3-2 = 1, $\chi^2_{crit} = 3.84$
$\chi^2 < \chi_{crit}$, so $P > 0.05$. Therefore we fail to reject the null hypothesis that genotype frequencies at this locus in this population meet HWE.

8. Genetic drift is the random change in allele frequencies across generations caused by the finite sampling of alleles in parents to form offspring. It occurs because populations are not infinite and are therefore subject to variation inherent to random sampling, the amount of which is inversely related to the effective population size. It causes no average change in allele frequency because, in any given population, allele frequency is equally likely to increase or decrease, so the average effect across many populations (i.e. the expected value) is no change.

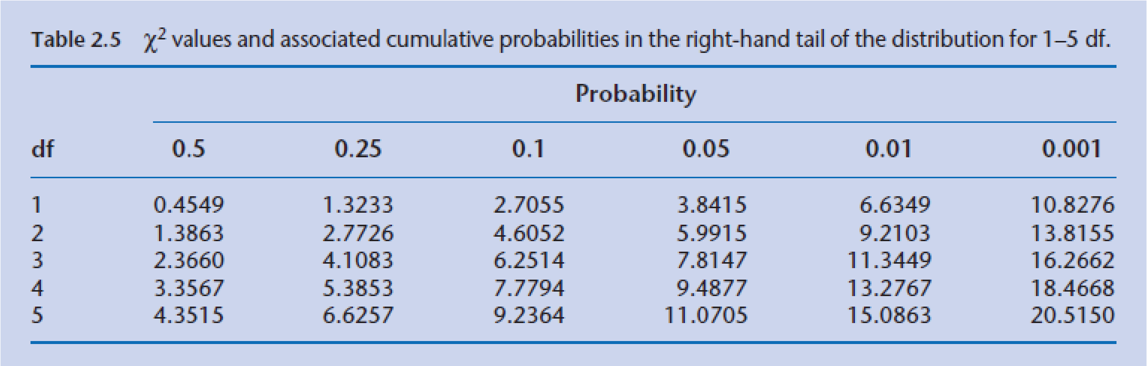


Table 2.5 χ^2 values and associated cumulative probabilities in the right-hand tail of the distribution for 1–5 df.

	Probability					
df	**0.5**	**0.25**	**0.1**	**0.05**	**0.01**	**0.001**
1	0.4549	1.3233	2.7055	3.8415	6.6349	10.8276
2	1.3863	2.7726	4.6052	5.9915	9.2103	13.8155
3	2.3660	4.1083	6.2514	7.8147	11.3449	16.2662
4	3.3567	5.3853	7.7794	9.4877	13.2767	18.4668
5	4.3515	6.6257	9.2364	11.0705	15.0863	20.5150