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1. You want to know whether section A and section B students answered a particular Bio180 exam question differently. The observed counts are shown in the table to the right. Recall that

Expected value = $\frac{\text{Row total} \times \text{Column total}}{\text{Grand total}}$ (15 pts)

	Section A	Section B	Total
Correct	420	276	696
Incorrect	140	184	324
Total	560	460	1,020

a) What is the null hypothesis?

There is no ~~mean~~ difference between how students answered the question in Section A & Section B.

b) Under the null hypothesis, what is the expected value for correct answers in Section A? (Just that one cell—show your work in the space provided.)

$$\frac{\text{Row total} \times \text{Column total}}{\text{Total Sum}} = \frac{696 \times 560}{1020} = 382.18$$

382.18

c) The calculated χ^2 statistic turns out to be 26.2; the χ^2 critical value is 3.84.

The p-value is (circle one)

2

> 0.05

< 0.05

Write a sentence that explains what this p-value means.

There is less than a 5% chance of receiving these results if the null hypothesis is true.

Can you reject your null hypothesis? (circle one)

2

yes

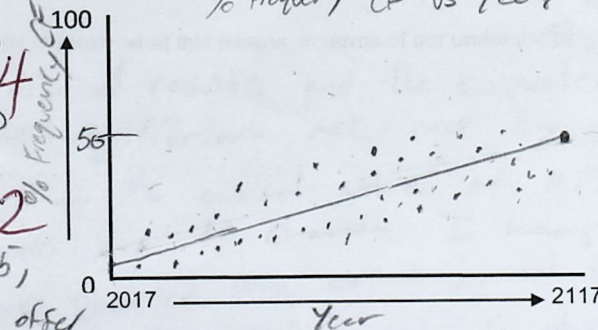
no

d) What do your results mean in terms of the question you posed originally?

The differences in correct answers in section A and B observed are not due to chance. Therefore Bio A and Bio B students did answer the exam question differently, because the p value < 0.05, so we reject the null hypothesis that there is no mean difference.

2. Cystic fibrosis (CF) is a fatal genetic disease, caused by a recessive allele CF^- . The frequency of CF^- is 5% in people of northern European ancestry, which is extremely high given how deleterious the allele is. Recent work has shown that CF^+CF^- heterozygotes are protected against cholera (an infectious disease; CF^+ is the normal, non-disease allele). Due to global warming, cholera is increasing in areas occupied by northern Europeans. (9 pts)

a. If CF^+CF^- heterozygotes are protected against cholera, and if the frequency of cholera increases over the next 100 years, make a scatterplot predicting the frequency of CF^- alleles over time. Use data points and a best-fit line that would be expected if the relationship has a p-value of 0.01 and a very low R^2 .



b. In part b, explain why you projected the 2117 frequency at the value you chose.

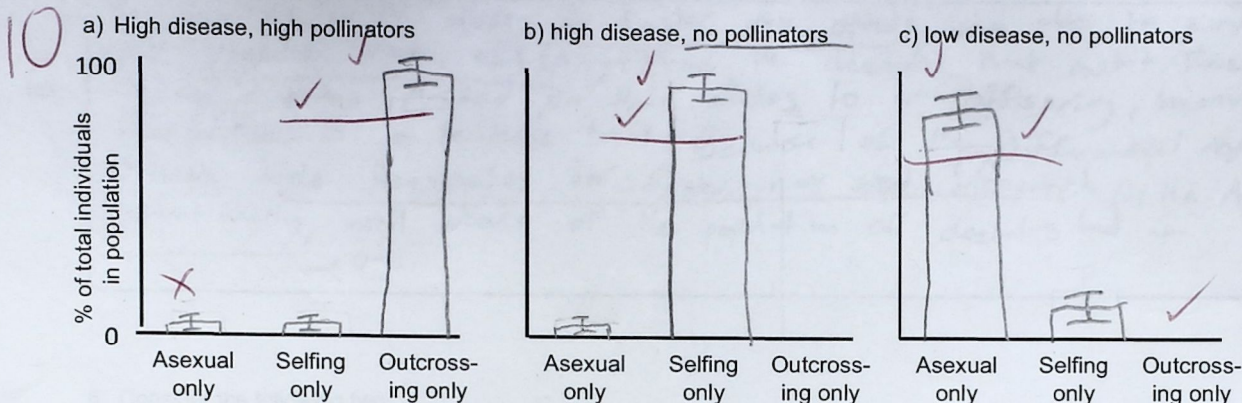
I projected the frequency at 0.5, because although the allele CF^- does offer

a heterozygote advantage, if it is homozygous recessive,

then the person dies. At allele frequency level of 0.5, it ensures that it is not too frequent to make people die, but frequent enough that under the equilibrium, heterozygote proportion will be 0.5, which are resistant to cholera.

NS acts on individual

3. In a plant species, there is heritable variation in mode of reproduction: some individuals only reproduce asexually, some only via self-fertilization, and some only via outcrossing. Make bar graphs showing the relative frequencies of individuals that mate in each mode, in the three types of environments listed. Include standard error bars. (11 pts)



- 12 4. Researchers explored *GPRA*—a gene where some alleles predispose people to asthma—by genotyping 1,738 individuals in Germany. They found alleles *T* and *C* at this gene; the observed number of genotypes is given in the table. (12 pts)

a. What are the observed allele frequencies?

T: 0.62 *C*: 0.38

b. Fill in the table, including the expected values under the null hypothesis provided by the Hardy-Weinberg Principle. Remember that the total number of individuals sampled was 1,738.

Genotype	Observed number	Observed frequency	Expected frequency
<i>TT</i>	541	0.31	0.38
<i>TC</i>	1083	0.62	0.47
<i>CC</i>	114	0.07	0.14

13 c. In this study, the χ^2 analysis returned a *p*-value of <0.0001 . Explain what this means, in terms of our understanding of *GPRA*.

The differences from the observed results and the expected results of, if they were in HW equilibrium are not by chance. The *p* value of <0.0001 is less than the critical value of 0.05, so the results received are likely not due to chance. In terms of *GPRA*, there were more heterozygotes observed than expected, and less homozygotes observed than expected. HW equilibrium is not in place for this gene. This means there is evolution or non random mating occurring with respect to this gene. There might be a heterozygote advantage.

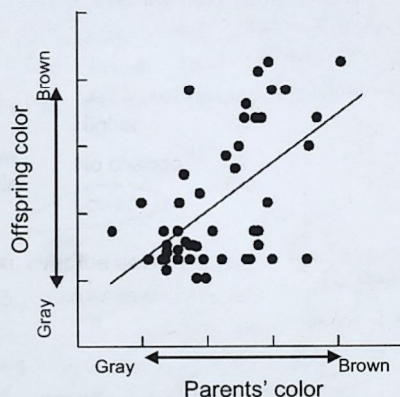
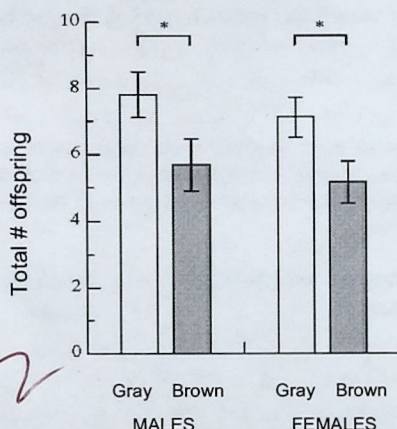
5. The following statement is incorrect: "Cheetahs evolved to run 60mph, from ancestors that only ran 20mph, because they need to be able to chase down prey." Using only the space provided, write a correct version in the space provided by completing the following statement: "In cheetahs, some alleles are associated with faster or slower running speeds. In the ancestors of today's cheetahs, ..."

(8 pts)

The cheetahs with alleles for faster max speeds were able to survive and produce more offspring than the cheetahs that couldn't. These faster cheetahs passed on their alleles to an offspring, because their fast speed is a heritable trait. Because of the differential reproductive success, allele frequencies for faster max speed increased for the population generationally, until most of the population of cheetahs had it.

+2

6. Consider the following two graphs, from a study of gray and brown "color morphs" in the same population of tawny owls in Finland. A * and bracket indicate a statistically significant comparison. The bar chart shows standard error bars; the scatterplot shows the best-fit line, $p < 0.01$. (13 pts)



a) Which graph supports the hypothesis that color is a trait with heritable variation? (Circle one)

BarChart

Scatterplot

Explain your reasoning.

Color is a continuous variable in this case, and the scatterplot shows the relationship between two continuous variables that we have: parent's color and offspring color. Scatterplot shows heritable variation relationship between offspring's color is related to parent's color.

b) Which graph supports the hypothesis that color is a trait associated with differential reproductive success? (Circle one)

BarChart

Scatterplot

Explain your reasoning:

The bar chart shows how many offspring males and females of different colors produced. This clearly shows differential reproductive success as the bar chart allows us to compare how many offspring a male of gray produced vs how many a male of brown produced, and same thing with females.

c) Would you expect that genotypes involved in coloration are in Hardy-Weinberg proportions in this population, at this time? Explain why or why not.

No. HW model assumes that there is no non random mating in the population, so the alleles would be in correct HW frequencies. However, the gray males and females in this population are experiencing greater reproductive success, which means there is non random mating, which violates the model.

32 7. Woodland caribou are a highly endangered species found in southern British Columbia and northern Idaho, where less than 1400 individuals remain from a population that numbered in the tens of thousands only 100 years ago. Woodland caribou live in old-growth forests; in winter their most important food consists of lichens that grow on old trees. They have adaptations to these environments, including extraordinarily large hooves that make it efficient for them to walk in deep snow. Use your understanding of evolutionary processes to analyze their situation. (32 pts)

a. How did the recent reduction in population size affect overall genetic diversity—meaning, the total number of different alleles at each gene? Circle one:

Higher

No change

Lower 2

b. What evolutionary process was responsible for this change or lack of change? 2 Genetic drift.

3 c. Explain your answer to part b.

Because there was a reduction of sample size, due to sample error and genetic drift, there is now a loss of genetic diversity. There are less individuals and genetic drift means that some individuals and their genotypes have been lost from the population. This is a loss of alleles and therefore diversity.

d. Predict how this change or lack of change in genetic diversity will impact the population, over the next 100 years.

This will hurt the population. The population, with low diversity, will not be as adapted, if there are environmental changes in the 100 years. They have low diversity so they will not be able to survive and reproduce because the environment changes.

e. Logging and road construction have broken what were formerly large areas of habitat into small, isolated patches. Compared to the population 100 years ago, how has gene flow among individuals throughout the occupied area changed? Circle one:

Higher

No change

Lower 2

f. Predict how this change or lack of change in gene flow will impact the population, over the next 100 years.

6 Because the population has been split into small subsets, inbreeding will happen because the population is small and isolated. Inbreeding depression will probably occur over the next 100 years as well, because homozygosity will increase as inbreeding occurs. This could cause deleterious alleles showing up more, because of more homozygotes.

g. Climate change is reducing snowfall and forcing tree species to shift their ranges north and to higher elevations. Predict how this change in the environment will impact woodland caribou over the next 100 years.

3 Because the caribou's environment is changing, evolution, a change of frequencies in alleles, could take place. If there is a mutation that occurs that allows a caribou to survive in a different environment, then it would have greater fitness and pass this on to its offspring, while other caribou would not survive, and the population would gradually change.

h. How did the recent drastic reduction in population size impact the mutation rate per gene, in each generation? Circle one:

Higher

No change 2

Lower

Explain your reasoning:

Mutations occur randomly, so decreasing the population size would not change the mutation rate per gene.

i. How did the recent drastic reduction in population size impact the total number of mutations that occur in each generation at any given gene (e.g. a gene that affects hoof size) in the population as a whole? Circle one:

Higher

No change

Lower 2

Explain your reasoning:

4 Mutation happens in every population in every generation. However, the rate is very low. Decreasing the sample size means that although the rate does not decrease, because there are less individuals in the population, there are less mutations that occur for a given gene.