Directions: Listed below, by chapter, you’ll find the big ideas and key terms from the first half of our quarter. These concepts and terms will make up the majority of exam 1. In addition, you’ll find practice problems to help you prepare for the exam. The answers to these practice problems will be posted online this weekend. (Don’t ask for solutions now! We want you to work these on your own first!) Note that your quizzes and in-class worksheets also make excellent exam review materials.

Chapter 1: The Genetic Approach to Biology
Terminology: genetic polymorphism, wild type, mutant, genomics, genotype, phenotype
Big Concepts/Ideas:
- A. Forward vs Reverse Genetics
- B. Model Organisms (general characteristics; advantages and disadvantages)
- C. Developmental Noise

Chapter 2: Single-Gene Inheritance
Terminology: diploid (2n), haploid (n), homologous chromosomes, chromatin, centromere, heterochromatin, euchromatin, telomeres, introns, transposable elements, parental generation (P), first filial generation (F1), second filial generation (F2), homozygous, heterozygous, dyad, tetrad, synopsis, null alleles, leaky mutations, haplosufficient, haploinsufficient, hemizygous
Big Concepts/Ideas:
- A. Monohybrid Crosses and expected ratios
- B. Sex-Linked Inheritance, expected patterns of inheritance
- C. Pedigree Analysis: be able to both construct a pedigree from a family history, and interpret a pedigree to determine the type of inheritance (autosomal recessive, autosomal dominant, X-linked dominant and recessive, Y-linked)
- D. Calculating risk in a pedigree: product rule
- E. Be able to interpret maps of chromosomes
- F. Review the paper on gene therapy and understand the key ideas presented

Chapter 3: Independent Assortment of Genes
Terminology: independent assortment, dihybrid, hybrid vigor, recombination, quantitative trait loci (QTLs), cytohets, cytoplasmic segregation,
Big Concepts/Ideas:
- A. Mendel’s Second Law and expected ratios in F1, F2
- B. Sum and Product Rules to determine expected outcomes
- C. Chi-Square test (equation and critical values table provided)
- D. Role and Production of Pure Lines
- E. Hybrid vigor, what does it mean? How does it happen?
- F. Use of the fungus, Neurospora, as a model
- G. Role of polygenes (QTLs) in continuous variation (dose effect)
- H. Inheritance patterns in mitochondria and chloroplasts
- I. Summarize and discuss the potential impact of genetics on agriculture, especially in the developing world
Chapter 4: Mapping Eukaryote Chromosomes by Recombination

Terminology: linked genes, loci, crossover, cis and trans conformations, genetic map unit/centimorgan, recombinant frequency (RF), molecular markers, SNPs, RFLPs, haplotype, linkage disequilibrium, VNTRs, microsatellites, minisatellites, Lod score, linkage map vs physical map

Big Concepts/Ideas:
A. Using recombinant frequency to test linkage
B. Mapping genes based on RF
C. Use of Molecular Markers to map genes
D. Interpreting Lod scores
E. Effect of Double Crossover

Chapter 6: Gene Interaction

Terminology: null mutation, dominant negative, incomplete dominance, codominance, lethal allele, pleiotropy, double mutants, epistasis (epistatic and hypostatic), suppressor, penetrance, expressivity

Big Concepts/Ideas:
A. Predicting inheritance patterns with codominance, multiple alleles (e.g. human blood types)
B. Impact of lethal alleles on ratios
C. Beadle and Tatum’s use of Neurospora to decipher metabolic pathways; evolution of the one-gene-one-enzyme hypothesis
D. Designing and interpreting a complementation test
E. Interpreting/predicting ratios in dominant and recessive epistasis
F. Review the paper by Lifton (identify key ideas from chapter 4 that are present in the paper; describe the approach his group took to identifying this new allele)

Practice Problems: In addition to your quizzes and in-class work, you may find the following practice problems helpful as you prepare for the exam.

1. A disease affecting sheep grazing in Salem, Oregon was found to be due to a virus. The virus was grown on sheep kidney cells and cultured in vitro. The virus appeared to contain four chemically defined components, W, X, Y, and Z. Which of the components are part of the virus and which are part of the sheep kidney cells?

<table>
<thead>
<tr>
<th></th>
<th>%A</th>
<th>%G</th>
<th>%C</th>
<th>%T</th>
<th>%U</th>
</tr>
</thead>
<tbody>
<tr>
<td>X</td>
<td>21</td>
<td>21</td>
<td>32</td>
<td>26</td>
<td>0</td>
</tr>
<tr>
<td>Y</td>
<td>26</td>
<td>32</td>
<td>21</td>
<td>21</td>
<td>0</td>
</tr>
<tr>
<td>Z</td>
<td>28</td>
<td>22</td>
<td>22</td>
<td>28</td>
<td>0</td>
</tr>
</tbody>
</table>

What can you say about the type of nucleic acid found after analyzing the infected sheep cells? Explain your answers.

You could have answered this either as X is RNA, Y is ssDNA, and Z is dsDNA. You can’t tell if the RNA is from the virus or the sheep kidney cell. The ssDNA is most likely viral and the dsDNA is from the sheep kidney cells.

Or you could say that X is RNA, Y is ssDNA, and Z is dsDNA. The virus could be a retrovirus with Y being the transcribed ssDNA and the final product being the dsDNA.
2. Draw the results of mitosis and meiosis of a cell with the following genotype A/a

You should have two cells, both with A/a from mitosis. From meiosis you should have four cells, two with A and the other two with a.

3. Duchenne Muscular dystrophy is sex-linked and usually affects only males. Victims of the disease become progressively weaker, starting early in life. Draw a pedigree for this family.

A. What is the probability that a woman whose brother has the disease will have an affected child?
Maternal grandmother had to be a carrier, X^D/X^d. Probability that the woman inherited the X^d allele from her is ½. Probability that she will pass it to her child is ½. Probability that the child is male (since this appears mostly in males) is ½. Use the product rule to determine the probability of having an affected child which is 1/2x1/2x1/2=1/8

B. If your mother’s brother (your uncle) had Duchenne’s disease, what is the probability that you have received the allele?
The maternal grandmother had to be a carrier X^D/X^d. The probability that your mother received the allele is ½. The probability that your mother passed it to you is ½. The total probability is then 1/2x1/2=1/4

C. If your father’s brother had the disease, what is the probability that you have received the allele?
Because the father does not have the disease you cannot inherit the allele from him. Consider the probability as 0.

4. A snapdragon plant that bred true for white petals was crossed with a plant that bred true for purple petals, and all the F1 had white petals. The F1 was selfed. Among the F2, three phenotypes were observed in the following numbers:

<table>
<thead>
<tr>
<th>Phenotype</th>
<th>Frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>White</td>
<td>240</td>
</tr>
<tr>
<td>Solid-purple</td>
<td>61</td>
</tr>
<tr>
<td>Spotted-purple</td>
<td>19</td>
</tr>
<tr>
<td>Total</td>
<td>320</td>
</tr>
</tbody>
</table>

a. Propose an explanation for these results, showing your genotypes of all generations (make-up and explain your symbols).

The data suggest that white is dominant to purple. The F2 are in an approximate 12:3:1 ratio which suggests epistasis must be involved. The modified 9:3:3:1 ratio is the result of a double heterozygote. I assigned the following:
The original white parents were D/D; e/e (white) X d/d; X E/E (purple) with the F1 all D/d; E/e. A self of the F1 would give a F2 generation of

9 D/-; E- white by definition
3 d/d; E- purple by definition
b. A white F2 plant was crossed with a solid-purple F2 plant, and the progeny were

- White: 50%
- Solid-purple: 25%
- Spotted-purple: 25%

What were the genotypes of the F2 plants crossed?

For this part of the question the cross is white X solid purple. The purple genotype must be d/d; e/e as defined above in part a and also to explain how you are able to get the spotted-purple (d/d; e/e). The hard part is figuring out the white genotype, which we know has to be D/d; +/-.

The genotype that works to give the correct ratio is d/d; E/e X D/d; e/e.

5. A well-known geneticist, Cuenot, studied the genetic basis of the yellow coat color in mice. He carried out a number of crosses between two yellow mice and obtained what he thought was a 3:1 ratio of yellow to gray mice in the progeny. The following table gives Buenot’s actual results, along with the results of a much larger series of crosses carried out by Castle and Little (Science, 32: 868-870, 1910).

<table>
<thead>
<tr>
<th>Investigators</th>
<th>Yellow Progeny</th>
<th>Non-Yellow Progeny</th>
<th>Total Progeny</th>
</tr>
</thead>
<tbody>
<tr>
<td>Cuenot</td>
<td>263</td>
<td>100</td>
<td>363</td>
</tr>
<tr>
<td>Castle and Little</td>
<td>800</td>
<td>435</td>
<td>1235</td>
</tr>
<tr>
<td>Both Combined</td>
<td>1063</td>
<td>535</td>
<td>1598</td>
</tr>
</tbody>
</table>

a. Using a chi-square test, determine whether Cuenot’s results are significantly different from the 3:1 ratio that he thought he observed. Are they different from a 2:1 ratio?

A chi-squared analysis of 3:1 ratio is 1.18, with one degree of freedom. When referencing the chart this falls between 0.5-0.1 which is a p value that would be accepted (since it is greater than 0.05).

A chi-squared analysis of the 2:1 ratio is 5.46, with one degree of freedom. When referencing the chart this falls between 0.025 and 0.01 which is not in the acceptable range. In other words, there is very little chance your data was this far from your expected values due strictly to chance. (So you must reject your null hypothesis.)

b. Combine the results of Castle & Little and Cuenot and determine whether they are significantly different from a 3:1 ratio and a 2:1 ratio.

After analyzing the combined results, a chi-squared of the 3:1 ratio is 60.7. Again with one degree of freedom this number is way too large and not even on the charts. This would not be accepted. Again, you need to reject your null hypothesis and look for an alternate explanation.
A 2:1 ratio of the combined results gives a chi-squared of 0.177 which with one degree of freedom is between 0.995 and 0.975. This falls within the acceptable range.

c. Suggest an explanation for the different ratios that Cuenot and Castle obtained.

Cuenot’s initial results suggested that the results he obtained were consistent with the expected 3:1 ratio for this cross. However, when geneticists combined his results with other studies, the new analysis suggested that the results were most consistent with a 2:1 ratio. A 2:1 ratio is a distorted ratio, often suggestive of a lethal condition. In this case, if the yellow allele is dominant, and lethal in the homozygous condition, the cross would yield the observed 2:1 ratio.

d. Why are the results of your chi-square analysis different when you consider just Cuenot’s results compared to the combined results?

Castle’s sample size was much larger. This larger sample size reduces the sampling error inherent in the experiment, allowing for greater confidence in the results.

6. A researcher trying to identify the location of a new disease allele (a) has identified a potentially useful SNP, known as rs1582. This SNP has two known variants, abbreviated “1” and “2” below.

a. Working in mice, the research conducts the following cross. Predict the genotypic ratios that would result:

\[
A/a * 1/2 \quad \text{X} \quad a/a * 1/1
\]

Genotypes would be:

- A/a*1/1
- A/a*1/2
- a/a*1/1
- a/a*1/2

These would be expected to occur in a 1:1:1:1 ratio.

b. When the research finishes genotyping the mouse pups, she finds the following:

\[
\begin{align*}
A/a * 1/1 & = 24 \text{ pups} \\
A/a * 1/2 & = 4 \text{ pups} \\
a/a * 2/1 & = 22 \text{ pups} \\
a/a * 1/1 & = 3 \text{ pups}
\end{align*}
\]

c. Draw the chromosomes of the original parents and indicate the relative positions of the A/a locus and rs1582 SNP.

\[
\begin{align*}
\_A & \quad \text{______________1}\_ \\
\_a & \quad \text{______________2}\_
\end{align*}
\]