1. (10) Short Answer. Answer each of the following questions in the space provided. You will be counted off for explanations that are not succinct.

   a) Hemophilia is a recessive X-linked trait. Individuals with this disease lack **Blood Coagulation Factor VIII**, and are unable to stop bleeding when it occurs. Females who are carriers (heterozygous) generally take somewhat longer to stop bleeding than their noncarrier relatives. Use the **Lyon Hypothesis** to explain why they take longer to stop bleeding.

   Females who are carriers are **Hh**, only one enzyme is functioning. They may not have as much Factor VIII as females with **HH**.

   b) Describe how a Second Division Primary Nondisjunction can lead to an individual with trisomy.

   A second division primary nondisjunction can leave one gamete with an extra chromosome (trisomy). When this gamete is matched

2. (5) Briefly Describe why the following statement is false concerning heritability. It is OK to give an example demonstrating how the statement is false.

   *If a trait has a heritability of nearly zero in two separate populations, then any differences between the two populations must be due to environmental differences.*

   It is possible that the two populations are fixed for different alleles (AA vs. aa) and the difference can be explained by this. Each population could have little genetic variation within the population — but have a big genetic difference between the populations.

3. (10) We are interested in whether or not a certain gene (with two alleles) in a population has **Hardy-Weinberg Proportions**. A Chi-Square Analysis for the population gave a Chi-Square of 3.72.

   a) How many degrees of freedom for this experiment? 1

   b) State your conclusion from this experiment (the genetic conclusion). Be careful with your wording.

   The data are consistent with this population having H-h proportions for this gene.
4. (10) The following is a diagram showing Mass Selection. Match the description of the part of the diagram with the term describing it. Each letter can be used at most once. Notice that selection is to the left (smaller values) for this problem.

- **a** Selection Response
- **b** Selection Differential
- **c** Mean of The Selected Parents
- **d** Original Mean of Population
- **e** Mean of Offspring of Selected Parents

5. (9) Your instructor's wife (as strange as that may seem that he has a wife) is interested in gardening and expects him to help her. Rather than do actual work, he has developed a worm breeding program. He is interested in increasing the amount of soil a worm will go through in a day, and has discovered a variety with a mean digging length of 43.84 in (standard deviation is 1.52 in). He has estimated heritability in the narrow sense to be 0.50, and heritability in the broad sense to be 0.70. In order to increase the digging ability of the worms, he will select the best 5% in a standard mass selection scheme.

<table>
<thead>
<tr>
<th>Proportion Selected (p)</th>
<th>0.5</th>
<th>0.25</th>
<th>0.1</th>
<th>0.05</th>
<th>0.01</th>
</tr>
</thead>
<tbody>
<tr>
<td>Selection Intensity (I)</td>
<td>0.8</td>
<td>1.27</td>
<td>1.76</td>
<td>2.06</td>
<td>2.67</td>
</tr>
<tr>
<td>Standardized Selection Point (Z)</td>
<td>0</td>
<td>0.67</td>
<td>1.28</td>
<td>1.65</td>
<td>2.33</td>
</tr>
</tbody>
</table>

Include relevant units for all answers.

a) What is the selection response for this experiment?

\[
\mu + 0.05 I = (0.5)(2.04)(1.52 \text{ in}) = 1.5656 \text{ in}
\]

b) What is the expected mean length among the offspring of the selected individuals?

\[
1.5656 + 43.84 \times 0.5 = 45.9056 \text{ in}
\]

c) What is the expected mean of the group of worms that your instructor selected as the parents?

\[
\mu + 0.05 I = 43.84 + (1.52 \text{ in})(2.04) \\
= 46.9712 \text{ in}
\]
6. (8) An individual is heterozygous for an inversion as diagrammed below:

Region

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
<th>E</th>
<th>F</th>
</tr>
</thead>
</table>

Region

| A | D | C | B | E | F |

a) This inversion is **Pericentric** Paracentric

b) Give the **four** chromatids that result when there is crossing over between C and the centromere.

\[
\begin{align*}
ABC & \cdot DEF \\
AB & \cdot CD \\
AD & \cdot BC \\
FE & \cdot DC \\
\end{align*}
\]

7. (13) Consider a population with the following genotypic frequencies:

\[0.1156 TT + 0.4488 Tt + 0.4356 tt\]

a) Give the allele frequencies for alleles \( T \) and \( t \).

\[
\begin{align*}
T & = 0.34 \\
t & = 0.66
\end{align*}
\]

b) Assume that this population (in part a) is undergoing mutation. The mutation rates are \(3 \times 10^{-4}\) and \(2 \times 10^{-5}\) for \( T \rightarrow t \) and \( t \rightarrow T \), respectively. Give the allele frequency for \( T \) after a single generation. **For this problem, do not round. Give all digits.**

\[
T = 0.3399112 \cdot 0.34 \left(1 - 3 \times 10^{-4}\right) + 0.4488 \cdot 2 \times 10^{-5} = 0.3399112
\]

c) Consider the original population in a). Assume that \( TT \) has a fitness of 1.0, \( Tt \) has a fitness of 0.6, and \( tt \) has a fitness of 0.1. Compute the allele frequency of \( T \) for the next generation.

\[
\begin{align*}
T & = 0.584072 \\
\begin{array}{cccc}
0.1156 & 0.4928 & 0.4356 \\
0.1156 & 0.6285 & 0.8935 \\
\end{array}
\end{align*}
\]

\[
\begin{align*}
A_{T} & = 0.26916 + 0.28913 = 0.55829 \\
p(T) &= 0.26916 + \frac{0.28913}{2} = 0.584072
\end{align*}
\]

You may need to use some of these equations:

\[
\begin{align*}
p^2W_{AA} + 2pqW_{As} + q^2W_{ss} & \quad (1-m)p + mP \\
p^2 + Fpq & \quad (1-\mu)p + q
\end{align*}
\]
8. (7) A certain population has a molecular marker locus with three alleles. We have surveyed the population and found the following data:

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Number</th>
<th>Expected</th>
<th>Chi-Square</th>
</tr>
</thead>
<tbody>
<tr>
<td>FF</td>
<td>345</td>
<td>0.35976</td>
<td>(6.32&lt;4.7)</td>
</tr>
<tr>
<td>MM</td>
<td>32</td>
<td>XXX</td>
<td></td>
</tr>
<tr>
<td>SS</td>
<td>78</td>
<td>XXX</td>
<td></td>
</tr>
<tr>
<td>FM</td>
<td>150</td>
<td>XXX</td>
<td></td>
</tr>
<tr>
<td>FS</td>
<td>30</td>
<td>G0.9639</td>
<td></td>
</tr>
<tr>
<td>MS</td>
<td>53</td>
<td>XXX</td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>688</td>
<td>XXX</td>
<td>XXX</td>
</tr>
</tbody>
</table>

a) Compute the frequencies of each of the alleles.

\[
\begin{align*}
F & \quad 0.632 \pm 0.67 \\
M & \quad 0.1940 \pm 0.41 \\
S & \quad 0.173 \pm 0.92 \\
\end{align*}
\]

\[
\frac{295}{688} + \frac{152}{688} + \frac{30}{688} = 4.35 / 688
\]

b) Complete the Chi-Square Table for this problem. Do not compute any of the cells with XXX.

c) \[f_{-3=3}\] Give the degrees of freedom for a Chi-Square test to determine if this population has Hardy-Weinberg proportions. Do not calculate the Chi-Square.

9. (4) The following is a list of the three processes that make up the Central Dogma of Genetics. Fill in the number of the process BEST described by each phrase. Each number is used at most once.

1. Transcription
2. Translation
3. Replication

\[\_\_\_\_\_\_\_\] This process is the only one of the three that is not reversible.

\[\_\_\_\_\_\_\_\] Process that creates an intermediate product.

10. (4) The following is a list of the three molecules that make up the Central Dogma of Genetics. Fill in the number of the process BEST described by each phrase. Each number is used at most once.

1. DNA
2. Protein
3. RNA

\[\_\_\_\_\_\_\_\] Used in the storage of genetic information.

\[\_\_\_\_\_\_\_\] Beadle & Tatum’s hypothesis concerned genes and this molecule.
11. (6) Below are the structures found in Meiosis Prophase I for various chromosomal mutations. For each arrangement during synapsis, indicate the type of mutation that can give rise to the arrangement.

a) Interstitial Deletion
b) Terminal Deletion
c) Paracentric Inversion
d) Pericentric Inversion

Possible Choices:
1. Interstitial Deletion
2. Paracentric Inversion
3. Terminal Deletion
4. Pericentric Inversion
5. Fission
6. Translocation
7. Fusion
8. Trisomy

12. (10) These are several statements about chromosomal mutations.

1. A result of nondisjunction.
2. Can lead to problems with genes in the wrong regulatory context.
3. May be important for evolution by reinforcing reproductive isolation.
4. Possible mechanisms why chimpanzees have more chromosomes than humans.

For each type of chromosomal mutation, circle the number for ALL statements that are true for that type. Each attribute can be used more than one time.

a) Trisomy
b) Translocation
c) Fusion
d) Inversion
e) Duplication

13. (4) Genetic Load, as described by your instructor, is (Circle ALL that are true)

a) The reduction in fitness in the population due to deleterious alleles (hint: this is the right one)

b) Taking more than one genetics course in a semester.

d) What is done just before a researcher does shotgun DNA sequencing.

e) Other