INSTRUCTIONS:

- fill out the scantron card with a #2 pencil
- PRINT your name, date and lab section in the spaces provided
- TO RECEIVE A GRADE you must print your student number, fill in corresponding bubbles in the spaces provided on the card & indicate that you have taken EXAM 1A
- read ALL questions carefully before answering any of them
- if a question has more than one correct answer, chose the one that is MOST correct
- circle answers on the exam pages BEFORE filling marking answers on the scantron
- mark only ONE answer for each question on the scantron card
- mark all answers carefully – dark and only within the bubbles for each question
- you MUST sign the sheet at the front of the room when handing in your exam to receive a grade
1. General properties of genetic material do not include

   A) change – it mutates and gives rise to variation
   **B) structure – it provides structural integrity for nearly all cellular components**
   C) replication – it copies itself and is inherited
   D) ubiquity – it is found in (or associated with) all life on earth
   E) function – it encodes polypeptides and provides the blueprint for life

2. Phenotype (P) is determined by

   A) genes (G)
   **B) genes and environment and their interaction (G + E + G*E)**
   C) environment (E)
   D) genes and environment (G + E)
   E) genes and gene interaction with the environment (G + G*E)

3. The component(s) of variation illustrated by these norms of reaction is (are)

   A) P only
   B) E only
   **C) G + E**
   D) G only
   E) G*E only

4. A trait is said to be “fixed” when it

   A) returns to a baseline state after relaxing natural selection
   B) returns to a high level after relaxing artificial selection
   C) cannot be distinguished from a trait observed in the wild
   D) can only be selected in one direction (high or low)
   **E) does not return to a baseline state after relaxing artificial selection**

5. Dominant alleles are

   A) autosomal
   **B) more common than recessive**
   C) wild type
   D) found in nature
   E) mutant
6. Phenotypes influenced by large numbers of genes are typically

A) pleiotropic
B) continuous
C) Mendelian
D) counted rather than measured
E) rare

7. Genetic variation is derived from mutation and is generally not distributed by

A) meiosis
B) recombination
C) mitosis
D) random segregation
E) independent assortment

8. Properties of a good model genetic organism include

A) large size, long generation time
B) long history of investigation, established research tools, sequenced genome
C) large genome, many chromosomes, redundant genes
D) all of the above
E) humans only – I don't think any of those other species are very useful or interesting

9. The centimorgan (cM) is a unit of measurement used for mapping genes and is equivalent to

A) 100 Morgans
B) % recombination ÷ 2
C) 1 chromomere
D) % recombination
E) ~ 5 ×10⁸ base pairs

10. Centromeres divide during

A) metaphase I
B) metaphase II
C) anaphase II
D) anaphase I
E) prophase II
11. Prior to meiosis I in fruit flies \((n = 4)\), the number of chromatids in each cell is

A) 4  
B) 8  
C) 12  
D) 16  
E) 32

12. The configuration that best illustrates a dihybrid with genes linked in **cis** is

A) \[
\begin{array}{cc}
A & b \\
a & B
\end{array}
\]

B) \[
\begin{array}{cc}
A & a \\
b & B
\end{array}
\]

C) \[
\begin{array}{c}
A \\
a
\end{array}
\cdot
\begin{array}{c}
b \\
B
\end{array}
\]

D) \[
\begin{array}{cc}
A & B \\
a & b
\end{array}
\]

E) \[
\begin{array}{c}
A \\
a
\end{array}
\cdot
\begin{array}{c}
B
\end{array}
\]

13. Assuming no new mutations, the mode of inheritance in the following pedigree could be

A) Y-linked  
B) X-linked dominant  
C) autosomal dominant  
D) X-linked recessive  
E) C) & D)

14. If the mode of inheritance in #13 is autosomal recessive, the probability that III1 will be an unaffected female is

A) 1/8  
B) 1/6  
C) 1/4  
D) 1/3  
E) 1/2
15. The number of genetically different gametes that humans can produce based on independent assortment alone is

A) \(2^{23}\)
B) \(23^2\)
C) \(2^{46}\)
D) \(46^2\)
E) \(23^4\)

16. For autosomal traits, diploid organisms receive

A) two genetically different copies of each DNA sequence from each parent
B) one genetically different copy of each chromosome from each parent
C) one genetically identical copy of each chromatid from each parent
D) two genetically different copies of each chromatid from each parent
E) two genetically identical alleles of each gene from each parent

17. When genes are unlinked, new combinations of parental alleles are generated by

A) segregation
B) independent assortment
C) mutation
D) crossing over
E) B) & D)

18. Recombination is greatest on a chromosome arm at or near the

A) centromere
B) middle
C) telomere
D) chromocenter
E) end

19. The second order (30 nm \(\varnothing\)) coiled DNA packaging structure is the

A) supercoil
B) solenoid
C) scaffold
D) nucleosome
E) chromatin
20. The following results were obtained by counting several similar ears of corn that had four distinct kernel types: 70 purple round, 90 purple wrinkled, 76 yellow round and 84 yellow wrinkled. The cross that most likely gave rise to these offspring is

A) PS/ps × ps/ps  
B) PS/ps × PS/ps  
C) P/p; s/s × p/p; S/s  
D) P/p; S/s × P/p; S/s  
E) P/P; S/s × P/p; S/S

21. When you test your hypothesis from question #20 using the contingency table method (you suspect that round kernels are physiologically challenged), the calculated $\chi^2 =$

A) 0.45, with 50% > $P$ > 75%, you do not reject the hypothesis  
B) 0.45, with 90% > $P$ > 95%, you do not reject the hypothesis  
C) 2.90, with 25% > $P$ > 10%, you do not reject the hypothesis  
D) 2.90, with 10% > $P$ > 5%, you reject the hypothesis  
E) 0.45, with 50% > $P$ > 75%, you reject the hypothesis

22. True-breeding recessive ebony mutant fruit flies (having black bodies) were bred with true-breeding recessive curved mutant flies (having curly wings). F1 siblings were bred among themselves. If the genes controlling these traits are unlinked, the proportion of F2 flies with ebony bodies and normal wings should be

A) 1/16  
B) 3/16  
C) 1/4  
D) 9/16  
E) 3/4

23. If F1 flies in #22 have 4 offspring, the chance that at least 1 will be ebony curved is

A) 0.0009  
B) 0.0206  
C) 0.2275  
D) 0.2060  
E) 0.7725
24. The most likely progeny generated from a test cross of the dihybrid $u^+/u^+; v/v^+$ would be

<table>
<thead>
<tr>
<th></th>
<th>$u^+v^+$</th>
<th>$u^+v$</th>
<th>$u^+v^+$</th>
<th>$u^v$</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>231</td>
<td>239</td>
<td>228</td>
<td>235</td>
</tr>
<tr>
<td>B</td>
<td>12</td>
<td>656</td>
<td>667</td>
<td>15</td>
</tr>
<tr>
<td>C</td>
<td>567</td>
<td>0</td>
<td>0</td>
<td>588</td>
</tr>
<tr>
<td>D</td>
<td>693</td>
<td>32</td>
<td>41</td>
<td>694</td>
</tr>
<tr>
<td>E</td>
<td>0</td>
<td>513</td>
<td>522</td>
<td>0</td>
</tr>
</tbody>
</table>

25. The distance between genes $u$ and $v$ in #24 is

A) 0 cM  
B) 2 cM  
C) 5 cM  
D) 49.9 cM  
E) not calculated because the genes are unlinked

26. Three X-linked recessive mutations were used in a Drosophila mapping experiment: *fruitless* (*fru*) flies are bisexual, *lush* flies have a heightened response to ethanol, and *ken & barbie* (*kab*) flies lack external genitalia. True-breeding $P_1$ *fru* *kab* males and *lush* females were crossed (artificially, given their reproductively challenged conditions) and $F_1$ females were bred with wild type males to give the following $F_2$ males:

<table>
<thead>
<tr>
<th>Gene order is</th>
<th>Phenotype</th>
<th># Flies</th>
</tr>
</thead>
<tbody>
<tr>
<td>A) lush fru kab</td>
<td>+ + +</td>
<td>81</td>
</tr>
<tr>
<td>B) fru kab lush</td>
<td>+ + lush</td>
<td>639</td>
</tr>
<tr>
<td>C) kab lush fru</td>
<td>+ + +</td>
<td>1044</td>
</tr>
<tr>
<td>D) kab fru lush</td>
<td>fru kab +</td>
<td>2736</td>
</tr>
<tr>
<td>E) A) and D)</td>
<td>fru kab lush</td>
<td>2844</td>
</tr>
</tbody>
</table>

27. The distance between *fru* and *kab* in #26 is

A) 25 cM  
B) 15 cM  
C) 23 cM  
D) 40 cM  
E) 36 cM
28. Interference in #26 is

A) 37.5
B) 0
C) 0.53
D) 20
E) 0.47

29. The diagram that most accurately shows the arrangement of homologous chromosomes during the first metaphase of meiosis is

A)

B)

C)

D)

E)

30. If the genes yellow \( (y) \) and white \( (w) \) in Drosophila are separated by 1 cM and you score \( 2.5 \times 10^4 \) flies in a mapping experiment, the expected number of recombinants is

A) 100
B) 250
C) 400
D) 1000
E) impossible to determine without knowing the parental genotypes
31. Accuracy in recombination mapping experiments is compromised by

A) inability to detect multiple recombination events
B) interference
C) differential viability of recombinant phenotypes
D) small sample sizes (“sample error”)
E) all of the above

46. Genes in fungi are probably linked when

A) # tetratypes (TT) << # non-parental ditypes (NPD)
B) # parental ditypes (PD) >> # non-parental ditypes (NPD)
C) # parental ditypes (PD) ≅ # tetratypes (TT)
D) # non-parental ditypes (NPD) ≅ # parental ditypes (PD)
E) # tetratypes (TT) ≅ # non-parental ditypes (NPD)

32. When mapping linked genes in fungi, parental ditypes (PD) can arise from

A) one (of two) types of double cross-over events involving three chromatids
B) double cross-over events involving one chromatid
C) double cross-over events involving two chromatids
D) both types of double cross-over events involving three chromatids
E) double cross-over events involving four chromatids

33. A strain of *Neurospora*, auxotrophic for serine (s), glycine (g) and isoleucine (i) was crossed to a wild type strain and the following asci were counted:

<table>
<thead>
<tr>
<th>1</th>
<th>2</th>
<th>3</th>
<th>4</th>
<th>5</th>
<th>6</th>
<th>7</th>
<th>8</th>
<th>9</th>
<th>10</th>
<th>11</th>
<th>12</th>
<th>13</th>
</tr>
</thead>
<tbody>
<tr>
<td>igs</td>
<td>+gs</td>
<td>ig+</td>
<td>igs</td>
<td>+gs</td>
<td>igs</td>
<td>+g+</td>
<td>igs</td>
<td>+gs</td>
<td>+gs</td>
<td>+gs</td>
<td>+gs</td>
<td>igs</td>
</tr>
<tr>
<td>i+s</td>
<td>+++</td>
<td>ig+</td>
<td>i++</td>
<td>+++</td>
<td>+gs</td>
<td>igs</td>
<td>+s+</td>
<td>ig+</td>
<td>+g+</td>
<td>+gs</td>
<td>+s+</td>
<td>i++</td>
</tr>
<tr>
<td>+g+</td>
<td>igs</td>
<td>++s</td>
<td>+g+</td>
<td>ig+</td>
<td>i++</td>
<td>+++</td>
<td>ig+</td>
<td>+s+</td>
<td>i+s</td>
<td>i++</td>
<td>ig+</td>
<td>+gs</td>
</tr>
<tr>
<td>+++</td>
<td>i++</td>
<td>++s</td>
<td>++s</td>
<td>i+s</td>
<td>+++</td>
<td>+++</td>
<td>i+s</td>
<td>+++</td>
<td>i+s</td>
<td>i++</td>
<td>i++</td>
<td>+++</td>
</tr>
<tr>
<td>17</td>
<td>9</td>
<td>5</td>
<td>4</td>
<td>3</td>
<td>3</td>
<td>83</td>
<td>3</td>
<td>29</td>
<td>24</td>
<td>77</td>
<td>22</td>
<td>7</td>
</tr>
</tbody>
</table>

The linked genes are

A) i and s
B) g and s
C) i and g
D) all three
E) none – they are all on different chromosomes
34. A ser⁻ mutant

A) is resistant to serine
B) can utilize serine as a carbon source
C) requires serine in growth media
D) can make its own serine
E) can grow without serine

35. Processes that facilitate recombination in bacteria do not include

A) generalized transduction
B) conjugation
C) transformation
D) specialized transduction
E) translocation

36. When mapping bacterial genes by conjugation

A) the recipient is F⁺ and str⁺
B) the donor is Hfr and str⁺
C) the recipient is F⁻ and str⁻
D) the donor is F⁺ and str⁻
E) the recipient is Hfr and str⁻

37. Three Hfr strains were derived from one E. coli F⁺ strain, each shown below with the first three markers transferred during an Hfr × F⁻ cross:

Hfr 1 … E C D ►
Hfr 2 … D A F ►
Hfr 3 … E B F ►

A is shown (below) at both ends to represent circularity – assume that the Hfr picks up all intermediates between any two represented genes. Gene order on the bacterial chromosome must be

A) A D C E B F A
B) A B C D F E A
C) A F B D E C A
D) A E F B C D A
E) A C D F E B A
38. Interrupted-mating crosses in *E. coli* between Hfr *gal*<sup>+</sup> *arg*<sup>+</sup> *gly*<sup>+</sup> and F− *gal*<sup>−</sup> *arg*<sup>−</sup> *gly*<sup>−</sup> show that *arg*<sup>+</sup> enters the F− last. In a fine mapping study using the same two strains *arg*<sup>+</sup> recombinants are selected and tested by replica plating for the presence of the *gal*<sup>+</sup> *gly*<sup>+</sup> alleles with the following results:

Gene order and map distances are

<table>
<thead>
<tr>
<th>Gene Order</th>
<th>Map Distances</th>
</tr>
</thead>
<tbody>
<tr>
<td>A) arg</td>
<td>10 cM</td>
</tr>
<tr>
<td>B) gly</td>
<td>4 cM</td>
</tr>
<tr>
<td>C) gal</td>
<td>10 cM</td>
</tr>
<tr>
<td>D) arg</td>
<td>10 cM</td>
</tr>
<tr>
<td>E) arg</td>
<td>4 cM</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Genotypes</th>
<th># Colonies</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>gal</em>&lt;sup&gt;+&lt;/sup&gt; <em>arg</em>&lt;sup&gt;+&lt;/sup&gt; <em>gly</em>&lt;sup&gt;+&lt;/sup&gt;</td>
<td>1036</td>
</tr>
<tr>
<td><em>gal</em>&lt;sup&gt;−&lt;/sup&gt; <em>arg</em>&lt;sup&gt;+&lt;/sup&gt; <em>gly</em>&lt;sup&gt;−&lt;/sup&gt;</td>
<td>116</td>
</tr>
<tr>
<td><em>gal</em>&lt;sup&gt;−&lt;/sup&gt; <em>arg</em>&lt;sup&gt;−&lt;/sup&gt; <em>gly</em>&lt;sup&gt;+&lt;/sup&gt;</td>
<td>44</td>
</tr>
<tr>
<td><em>gal</em>&lt;sup&gt;+&lt;/sup&gt; <em>arg</em>&lt;sup&gt;−&lt;/sup&gt; <em>gly</em>&lt;sup&gt;−&lt;/sup&gt;</td>
<td>4</td>
</tr>
</tbody>
</table>

39. Closely linked markers *A* and *B* is demonstrated by transformation when

A) co-transformation is more than the sum of individual transformation frequencies
B) co-transformation is less than the product of individual transformation frequencies
C) co-transformation is more than the product of individual transformation frequencies
D) transformation by *A* is equal to transformation by *B*
E) co-transformation is less than the sum of individual transformation frequencies

40. Mapping genes in humans is difficult because

A) controlled breeding programs cannot be employed
B) the human genome is relatively large
C) sample sizes in human populations tend to be relatively small
D) distances between genes associated with known phenotypes are large
E) all of the above

**BONUS QUESTIONS**

41. If you calculate a map distance between two genes as being 20 cM, the corrected distance (taking into account multiple cross over events) estimated using a mapping function would be

A) 21.1 cM
B) 23.3 cM
C) 25.5 cM
D) 27.7 cM
E) 29.9 cM
42. The distance between \textit{i} and the centromere in #33 is
\begin{itemize}
  \item[A)] 0.21 cM
  \item[B)] 0.41 cM
  \item[C)] \textbf{0.52 cM}
  \item[D)] 0.63 cM
  \item[E)] 0.72 cM
\end{itemize}

43. The distance between \textit{s} and the centromere in #33 is
\begin{itemize}
  \item[A)] 10.52 cM
  \item[B)] 11.36 cM
  \item[C)] 12.03 cM
  \item[D)] \textbf{13.81 cM}
  \item[E)] 14.34 cM
\end{itemize}

44. The distance between the linked genes in #33 is
\begin{itemize}
  \item[A)] 17.88 cM
  \item[B)] 19.33 cM
  \item[C)] 21.17 cM
  \item[D)] 24.22 cM
  \item[E)] \textbf{25.70 cM}
\end{itemize}

45. The Department seminar on Friday, October 6 (and the review article posted on the GENETICS web page) by Dr. David Arnosti discussed temporal and spatial control of gene expression by
\begin{itemize}
  \item[A)] \textit{exons}
  \item[B)] \textbf{enhancers}
  \item[C)] \textit{introns}
  \item[D)] \textit{operons}
  \item[E)] \textit{enzymes}
\end{itemize}