Biology 202 Midterm 2011 DRAFT (PLEASE DO NOT SHARE)

1. (1 point) The following is a series of statements about a single pair of homologous autosomes:

i) They always contain the same alleles.
ii) They occur together in diploid cells.
iii) They occur together in haploid cells.
iv) They synapse during meiosis.

For statements *i* through *iv*, which are **true** statements and which are **false**?

a.) *i.* True, *ii.* False, *iii.* True, *iv.* False
b.) *i.* False, *ii.* True, *iii.* True, *iv.* False
c.) *i.* True, *ii.* False, *iii.* False, *iv.* True
d.) *i.* False, *ii.* True, *iii.* False, *iv.* True
e.) *i.* True, *ii.* True, *iii.* True, *iv.* True

Answer: d

2. (2 points) Suppose that eye color in sheep is controlled by the "E" locus. Blue eye colour (*EE* or *Ee*) is dominant to brown (*ee*). A blue-eyed sheep was crossed with a brown-eyed sheep and all four progeny were blue-eyed. Choose the most appropriate statement from below.

a.) The blue-eyed parent must have had the genotype *EE*.
b.) The blue-eyed parent must have had the genotype *Ee*, but all four of its progeny were from fertilizations with *E* gametes.
c.) There is not enough information to be certain of the genotype of the blue-eyed parent.
d.) Another locus must be involved in eye color determination.
e.) Brown-eyes are incompletely penetrant

Answer c. Note: The probability that all three progeny from an Ee x ee cross are blue-eyed, is equal to 1/16. This is sufficiently large such that it could occur easily by chance alone. Thus even though all progeny are blue-eyed, we can not with any reasonably high probability be confident that Ee or EE are genotype of the blue-eyed parent Remember that we exclude null hypotheses when the probability of acceptance is less than 1/20. In other words, the probability that an Ee blue-eyed parent produces all brown-eyed progeny when crossed with a brown-eyed parent is considered reasonably high (1 out of 16, which is well within the margin of chance alone being responsible for the outcome when the blue-eyed parent is Ee). So it is the result (i.e., the data themselves, and not the question) that is ambiguous in terms of resolving the parental genotype, leaving only answer "c" as correct response. This was intended to be a challenging question.

3. (1 point) A **rare** dominant trait, when exhibited in men, is transmitted to half their sons and to half their daughters. The gene for this trait is carried:

a. on the X chromosome or on an autosome.
b. on an autosome but not on an X chromosome.
c. on the X or on Y chromosome.
d. on the mitochondrial chromosome.
e. There is insufficient information provided to determine which chromosome it is on.

Answer: b.

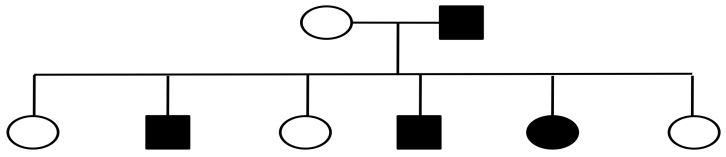
4. (2 points) You crossed true-breeding *Drosophila* females with the wild type red eye appearance and normal wing length with true-breeding males showing two autosomal recessive traits: green eyes and bent wings. If 3000 progeny of the testcross are distributed in the following phenotypic classes (see below), what is the estimated genetic distance between the loci for eye color and wing shape? (Note: the heterozygote parent in the testcross was female--recombination does not occur in Drosophila males).

Wild type	1323
Green eyes, bent wings	1452
Red eyes, vestigial wings	90
Green eyes, bent wings	135

a) 75 cM
b) 0.75 cM
c) 7.5 cM
d) 750 cM
e) Cannot be determined from the data

Answer: c. Note: A testcross, by definition, involves a cross between a heterozygous and a homozygous recessive (i.e., tester) parent.

5. (1 point) In the following pedigree, the *a* allele, responsible for the expression of the **rare** trait (filled-in symbols), is recessive to the *A* allele. Which of the assignments of genotypes to individuals is the most likely one?



(a) I-1: *A/a*, I-2: *a/a* and II-1: *A/a*, II-2: *a/a*, II-3: *A/a*, II-4: *a/a*, II-5: *a/a*, II-6: *A/a*

(b) I-1: *a/a*, I-2: *A/a* and II-1: *A/a*, II-2: *a/a*, II-3: *A/a*, II-4: *a/a*, II-5: *a/a,* II-6: *A/a*

(c) I-1: *A/A*, I-2: *A/a* and II-1: *A/a*, II-2: *A/A* II-3: *A/a*, II-4: *A/A*, II-5: *A/a,* II-6: *A/a*

(d) I-1: X_A/X_a, I-2: X_a/Y and II-1: X_A/X_a, II-2: X_a/Y, II-3: X_A/X_a, II-4: X_a/Y, II-5: X_a/X_a, II-6: X_A/X_a

(e) All of the above assignments are equally possible.

Answer d. *While the assignment of I-1: A/a, I-2: a/a would give the progeny phenotypes as shown, this would require an unexpected event (the coming together of parents with three rare alleles). On the other hand, the assignment I-1: X_A/X_a, I-2: X_a/Y, while unusual, requires that parents with only two of the rare alleles need come together to produce the family, and thus it is the more likely assignment. (Note: the probability of transmission of the disease from parents to offspring is identical in the assignments listed in answers (a) and (d)--it is one-half; the overall probability of the two competing assignments is governed by the chances of particular parents coming together).*

6. (1 point) Females homozygous for the recessive mutant characters *a*, *b,* and *c* were crossed with wild-type males from a pure-breeding stock. A testcross was then done by taking the F_1 females (all wild-type in appearance) and crossing them with triple mutant males (*a, b, c*) taken from a pure-breeding stock. The following offspring were counted (Note: lower case letter indicates a mutant phenotype, while "+" indictes wild type):

Phenotype	Number
a, b, c	840
a + +	231
b + +	69
c + +	375
a, b +	381
a, c +	75
b, c +	225
wild-type	804

Here are some possible recombination maps.

Map 1: ***a*** ___ ___ ***b*** _____ ***c***
20 cM 30 cM

Map 2: ***c*** ___ ___ ***b*** _____ ***a***
20 cM 30 cM

Map 3: ***c*** ___ _____ ***b*** _____ ***a***
30 cM 20 cM

Map 4: ***a*** ***b*** ***c***

30 cM 20 cM

Which answer below is correct?

a.) Map 1 is consistent with the data presented, and there is no evidence of interference.
b.) Maps 1 and 3 are consistent with the data presented, and there is evidence of interference.
c.) Maps 2 and 4 are consistent with the data presented, and there is evidence of interference.
d.) Map 1 is consistent with the data presented, and there is evidence of interference.
e.) Map 2 is consistent with the data presented, and there is no evidence of interference.

Answer: b

7. (1 point) Genes *X*, *Y*, and *Z* assort independently and control the production of green pigment. Suppose that *X*, *Y*, and *Z* act in the following pathway:

Colourless precursor $\xrightarrow{X}$ *intermediate 1* $\xrightarrow{Y}$ *intermediate 2* $\xrightarrow{Z}$ *green pigment*

The alternative (and recessive) alleles of these three genes (*a*, *b*, and *c*) all code for abnormal products that interrupt the pathway. The intermediates 1 and 2 are colourless.
A single green *X/X Y/Y Z/Z* individual is crossed with a single colourless individual *x/x y/y z/z* to give a green F_1. The F_1 is self-fertilized. What proportion of the F_2 individuals would be expected to be colourless?

(a) 1/64
(b) 27/64
(c) 37/64
(d) 9/64
(e) 3/64

Answer c.

8. (1 point) Recessive mutant allele "$" is NOT capable of complementing another recessive mutant allele "#". Read the following statements below and choose the correct answer.

Statements:
1. Alleles "$" and "#" are alleles of the same gene.
2. Alleles "$" and "#" are alleles of two different genes.
3. Alleles "$" and "#" are always linked.
4. Alleles "$" and "#" are never linked.
5. Alleles "$" and "#" may or may not be linked.

(a) Statements 1 and 3 are correct.
(b) Statements 2 and 3 are correct.
(c) Statements 2 and 4 are correct.
(d) Statements 1 and 5 are correct.
(e) Statements 1 is correct.

Answer e. *Lack of complementation occurs when combining two mutant alleles of same genes. Since we are talking about a single gene, linkage is not relevant.*

9. (1 points) Four spontaneous auxotrophic mutants are isolated from natural populatons of a haploid, wild type fungus. These strains respond to the addition of certain nutritional supplements to minimal medium either by growth (symbolized below by "+"), or no growth ("0"). The table below shows the growth observed for each of these single mutant strains when provided with different supplements:

Mutant	A	B	C	D	E
1	+	0	+	0	0
2	+	+	+	+	0
3	+	0	+	+	0
4	0	0	+	0	0

Which of the following biochemical pathways is consistent with these data?

(a) A→B→C→D→E

(b) B→D→A→C→E

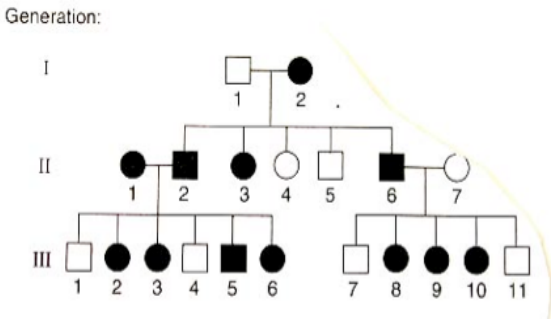
(c) C→E→B→D→A

(d) E→B→D→A→C

(e) E→B→D→C→A

Answer d *Adding compound "E" does not rescue any of the mutants, and so it must be upstream of all the other compounds in the pathway--this eliminates all answers but (d) and (e). Adding compound "B" rescues one mutant, whereas adding compound "D" rescues two different mutants. Thus, compound "B" must be upstream of "D", as listed in answer (d).*

10. (1 point) The pedigree below shows the inheritance over three generations of a common condition. Which of the following is the most likely mode of inheritance of this condition?



(a) X-linked recessive

(b) Two linked autosomal recessives

(c) Y-linked dominant

(d) Autosomal dominant

(e) None of the above

Answer d. *Autosomal dominance is the only mode that is compatible with the pedigree.*

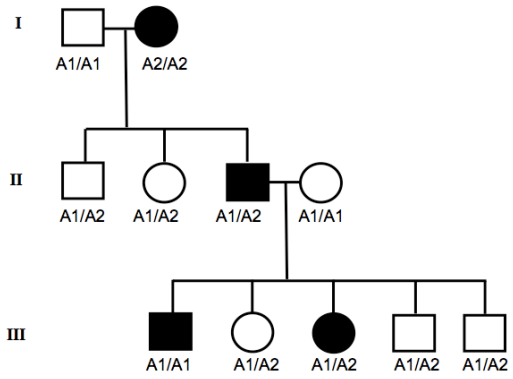
11. (1 point) The critical value ($P < 0.05$) of the Chi-square distribution with one degree of freedom is 3.84. The critical value ($P < 0.05$) of the Chi-square distribution with two degrees of freedom is 5.991. The critical value ($P < 0.05$) of the Chi-square distribution with three degrees of freedom is 7.815. From a testcross *D/d* x *d/d* in which the dominant *D* allele codes for "dark eyes" and the recessive *d* allele codes for "light eyes", which of the following results *is statistically compatible with* the hypothesis of single gene control of eye colour?

(a) 210 dark, 305 light
(b) 21 dark, 31 light
(c) 1020 dark, 1300 light
(d) 5 dark, 15 light
(e) 5 dark, 26 light

Answer b *We seek a Chi-square value less than 3.841 (there are two progeny classes expected in 1:1 ratio, and thus 1 degree of freedom). The only set of numbers yielding this low a Chi- square value are 21 dark:31 light. Chi Square = 1.92.*

12. (2 points) Assume that a disease trait is inherited as an autosomal dominant.

You genotype individuals in your pedigrees with many markers and localize the trait to a region on chromosome 4. *A1* and *A2* are two codominant alleles of the A marker gene on chromosome 4. The pedigree and genotypes at the A marker are shown below.



Calculate a LOD score for linkage between the disease locus and the marker locus A at a distance of 20 cM.

a. 0.00004
b. 0.00097
c. -1.3876
d. 0.04096
e. -2.5406

Answer c. *We must inspect the 5 testcross progeny present in generation III and consider the gamete types produced by II-3. Note that parental gametes of II-3 are either A1d or A2D (where D denotes the dominant disease allele), and recombinant gametes are A1D or A2d. Among the 5 testcross progeny, there is one that is the product of a parental gamete of II-3 (individual III-3), whereas the remaining 4 progeny are each the product of recombinant gametes of II-3. Thus, the appropriate calculation of the LOD for 10 cM is:*

LOD = Log $[(0.10^4)*(0.40^1)/.25^5] = -1.3876$ *(where Log denotes the Base 10 log of the quantity in square brackets).*

13. (1 point) In beagles, black color (*B*) is dominant over brown (*b*), and solid color (*S*) is dominant over mottled (*s*). The genes for these two characters are located on different chromosomes. Suppose that a dog with genotype *B/b s/s* is mated to a dog with genotype *b/b S/s*. What fraction of their offspring are expected to be black and mottled?

a. 1/16
b. ¼
c. 9/16
d. 3/4
e. None of the above.

Answer b.

14. (1 point) A man with blood type "A" marries a woman with blood type "A". Which of the following blood types might you expect to see in their children?

a. Type A and B would be possible.
b. Only type O would be possible.
c. Only type B would be possible.
d. Types A and O would be possible.
e. Only Type AB would be possible

Answer d.

15. (1 point) An individual who is heterozygous has a disease in which the mutant heterozygote has an abnormal protein monomer that combines with another monomer and distorts the way in which a protein signaling molecule folds, making it inactive. This type of mutation is:

a. leaky mutation

b. dominant mutation

c. recessive mutation

d. haplo-insufficient mutation

e. non-penetrant mutation

Answer b. *Note: "Haplo-insufficient mutation" is an incorrect answer. While this is a dominant mutation, the phenotypic basis does NOT arise because two functional doses of an enzyme are required* ***for completion of a biosynthetic pathway****. Rather, the mechanism is that of "poisoning" of one protein unit by another (a* ***dominant negative****), as discussed in the text and class (and contrasted with haplo-insufficient mutations) under the topic of dominant mutations.*

16. (1 point) A population is scored for variation at a single locus that contains three alleles. It is found to contain no homozygotes. But there are 100 heterozygotes for A1A2, 300 heterozygotes for A1A3, and 200 heterozygotes for A2A3.

a.) The inbreeding coefficient is -2.
b.) The inbreeding coefficient (*F*) equals 0.
c.) The population has experienced recent migration.
d.) The allele frequency of *A1* is 1/3
e.) The population has experienced recent genetic drift.

Answer d: *There are 400 A1 alleles (100 from the A1A2 and 300 from the A1A3 heterozygotes) in a population with 1200 alleles. This gives an allele frequency of 1/3 for A1.*

17. (1 point) You are studying a population of beetles on an island (beetles that hatch, mate, produce offspring, and die each year, with the dormant beetle embryos surviving the winter). Suppose that an island population receives migrants of this insect from a large, mainland source population each summer, in time for the mating season. The fraction of the total number of mating parents on the island that arrive on the island each summer is 0.1, the remaining fraction (0.9) of mating parents are from resident island individuals of this insect population. Locus **A** has two alleles (alleles *A* and *a*). The frequency of *A* on the mainland is 0.4, whereas on the island it is 0.05. Migration is unidirectional (from mainland to the island). (*Assume for this question that the **A** locus is not influenced by either selection, drift, or mutation).*

a.) It will take 6 generations for the frequency *A* on the island to exceed 0.3.
b.) It will take 4 generations for the frequency *A* on the island to exceed 0.3.
c.) The allele frequency of *A* on the island and mainland will eventually be equal.
d.) The population will attain Hardy-Weinberg proportions in a single generation.
e.) The island will eventually lose the *a* allele.

Answer c.

18. (2 points) Locus **S** affects the probability of survival in a mouse population. Out of 1000 individuals with the genotype *S1/S1*, 750 survive. Out of 1000 individuals with the genotype *S1/S2*, 500 survive. Out of 1000 individuals with the genotype *S2/S2*, 250 survive. The genotype frequencies of *S1/S1, S1/S2,* and *S2/S2* in this population, prior to selection are 0.6, 0.3, and 0.1

a.) The relative fitness of the *S1/S2* and *S2/S2* genotypes are 0.5 and 0.25, respectively.
b.) The relative fitness of the *S1/S1* and *S2/S2* genotypes are 1.0 and 0.25 respectively.
c.) The average population relative fitness before selection is 0.833.
d.) The average population relative fitness after two generations of selection will be 0.986
e.) Statements “c” and “d” are correct.

Answer c. *The concept of relative fitness was discussed in the last of my series of lectures on population genetics. The relative fitnesses of the genotypes S1/S1: 1.0; S1/S2 0.667; and S2/S2 0.333. The genotype frequencies are given. For S1S1, S1S2, and S2S2, they are 0.6, 0.3, and 0.1, respectively (Note: One can not assume the population is in Hardy-Weinberg proportions, as we have been given these genotype frequencies). With*

this information, the average relative fitnesses (relative fitnesses averaged across the genotype frequencies) can be calculated as 0.833.

19. (2 points) A genetic disease is caused by a rare recessive allele and symptoms develop early in life such that affected individuals do not survive to reproduce. Assume that the genotype frequencies in human populations are in Hardy-Weinberg proportions for the locus in which this mutation occurs. The disease affects 4 out of every 10,000 individuals. A man who is a known carrier of the disease mutation marries an unrelated woman who does not have the disease. What is the probability that their first-born child will inherit the disease?

a.) 0.0004

b.) 0.0392

c.) 0.0098

d.) 0.02

e.) 0.0001

Answer c. This question asks you to use population information to determine the probability that the "unrelated woman" is a carrier, that is, is heterozygous for the normal and mutant alleles. From the incidence of the disease and the fact that the genotype frequencies are in HW proportions, we can deduce that the frequency of the mutation is the square root of 0.0004, or in other words, 0.02. Knowing this, we can say that the expected frequency of carriers is 2 x 0.98 x 0.02 = 0.0392. From a mating of two heterozygotes, we expect ¼ to be affected; ¼ x 0.0392 = 0.0098.

20. (1 point) You conduct a cross with *Neurospora crassa* involving a wild type indicated by "+") and histidine-deficient mutant (indicated by "*h*"). Out of 1000 octads that you collect and plate out the spores from to characterize the octad, you see the following results:

Octad type	Number
h h h h + + + +	495
+ + + + *h h h h*	505

Choose the most appropriate statement from below:

a.) There is evidence of unequal segregation of this mutation.
b.) There is evidence that this mutation is closely linked to the centromere.
c.) There is evidence for complementation of *h* by a second mutation.

d.) There is for an epistatic interaction of *h* with a second mutation.
e.) There is evidence for second-division segregation of *h* and +.

Answer b