Practice Problems: ANSWERS (Available on-line for students).

Q1) Generate a Punnett Square for a heterozygous individual (a+/a) crossed with a heterozygous individual (a+/a). In this case the mutation is recessive. Determine the genotypic ratio and phenotypic ratio. For phenotypic ratio do not refer to specific a+ or a phenotype but instead refer to them as dominant or recessive. Can this trait be sex linked in humans? **Answer: see 1) in table below. Can't be sex-linked in humans because males can't be heterozygous (except in very rare cases). Typically males are hemizygous.**

Q2) Generate a Punnett Square for a heterozygous individual crossed with a heterozygous individual. Make the mutation dominant. Notice that the phenotypic ratio for dominant/recessive is identical to Q1 (3/4 Dominant, 1/4 recessive) except you now have to realize your mutation is Dominant and wild type is recessive. **Answer: see 2) in table below. Note that the answer with respect to ratios is identical to Q1 except the notation is different in that you use upper case because the mutation is dominant.**

Q3) Generate a Punnett Square for a heterozygous individual crossed with a homozygous recessive individual. Make the mutation recessive. Determine the genotypic ratio and phenotypic ratio. Can this trait be sex linked in humans? **Answer: see 3) in table below. Can't be sex-linked in humans because males can't be heterozygous (except in very rare cases) or homozygous (except in very rare cases). Typically males are hemizygous.**

Q4) Generate a Punnett Square for a heterozygous individual crossed with a homozygous dominant individual. Make the mutation recessive. Determine the genotypic ratio and phenotypic ratio. Can this trait be sex linked in humans? How does your answer compare to 3? **Answer: see 4) in table below. Note in this case that all of the offspring must have the dominant allele and must therefore have the dominant phenotype. Again this can't be sex-linked because males are typically hemizygous.**

Q5) Generate a Punnett Square for a homozygous recessive individual crossed with a homozygous recessive individual. Determine the genotypic ratio and phenotypic ratio. Can this trait be sex linked in humans? How does your answer compare to 3? **See # 5 below. All offspring will have the same genotype and the same phenotype – homozygous recessive and they will display the recessive phenotype. Again this can't be sex-linked because males are typically hemizygous (not homozygous).**

Q6) Generate a Punnett Square for a homozygous dominant individual crossed with a homozygous dominant individual. Determine the genotypic ratio and phenotypic ratio. Can this trait be sex linked in humans? How does your answer compare to 5? **See #6 below. All offspring will have the same genotype and the same phenotype – homozygous dominant and they will display the dominant phenotype. Again this can't be sex-linked because males are typically hemizygous (not homozygous).**

Q7) Generate a Punnett Square for a homozygous dominant individual crossed with a homozygous recessive individual. Determine the genotypic ratio and phenotypic ratio. Can this trait be sex linked in humans? How does your answer compare to 5 & 6? **See #7 below. All offspring will have the same genotype and the same phenotype – heterozygous and they will display the dominant phenotype. Again this can't be sex-linked because males are typically hemizygous (not homozygous).**

Commit to memory the phenotypic and genotypic ratios for the crosses below.

The dominant phenotype is indicated by the letter D and the recessive phenotype is indicated by the letter r.

Table 1: Phenotypic and genotypic ratios for autosomal, single traits

	Phenotypic ratios (D/r)	Genotypic ratios
1) heterozygous w/heterozygous	3:1 (3/4D:1/4r)	1:2:1 (a+/a+):(a+/a): (a/a)
2) heterozygous w/heterozygous	3:1 (3/4D:1/4r)	1:2:1 (A+/A+):(A+/A): (A/A)
3*) heterozygous w/ homozygous recessive	1:1 (1/2D:1/2r)	1:1 (a+/a) : (a/a)
4*) heterozygous w/ homozygous dominant	1:0 (1D:0r)	1:1 (a+/a): (a+/a+)
5*) homozygous recessive w/homo recessive	1r:0D	1:0 (a/a)
6*) homo dominant w/homo dominant	1D:0r	1:0 (a+/a+)
7*) homozygous recessive w/homo dominant	1D:0r	1:0 (a+/a)

* For questions 3-7 the mutation was considered recessive. Changing the mutation to dominant will not change the dominant/recessive ratio nor will it change the genotypic ratio. It would change the notation (upper case).

Practice problems:

QQ1) How many different gametic genotypes are possible from the diploid genotypes and determine the probability of each.

a) a+/a; b/b, c+/c, D/D **(2 X 1 X 2 X 1 = 4 types, each with 25% probability a+;b;c+;D a+;b;c;D a;b;c+;D and a b;c;D)**

b) AB/ab (map distance = 30%). **(4 types, P = AB = 335%, P ab = 35%, r = Ab = 15%, r aB = 15%).**

QQ2) A zygote with the genotype a+/a; b/b, cd/c+d+ will produce how many different chromosome combinations in the following cell types.

a) eye cell **– only 1, mitosis yields genetically identical cells.**

b) liver cell**– only 1, mitosis yields genetically identical cells.**

c) egg cell**– 8, nonhomologous chromosomes assort independently but the linked genes assort dependently (a+ or a, b only and then 4 possible genotypes for cd/c+d+).**

QQ3) An individual with the genotype: a/a+; B/B+; c/c+; DE/D+E was crossed with an organism with the genotype: a+/a+; B/B; c/c; DE+/D+E. What percentage of the offspring will have the following:

a) a+ phenotype (All)

b) a+/a genotype (50%)

c) B phenotype (All)

d) B/B genotype (50%)

e) a+ and B+ phenotype (100% X 0% = 0)

f) a/a+, B/B genotype (1/2 X 1/2 = 1/4, .5 X .5 = 0.25 = 25%)

g) D+ phenotype **(map distance between D & E = 30%). 25% = D+, 75% = D.**

h) make up several of your own combinations and determine the probability.

QQ4) A six-fingered man and a five-fingered woman have 20 children (10 males and 10 females) with six-fingers. Do you know if six-fingered is dominant or recessive? **Autosomal**: **Six fingered is most likely dominant. Note that if it is recessive then the five-fingered woman must be heterozygous and five fingered is dominant. If 20 out of 20 children are six fingered then the chance of mom always donating the six-fingered allele randomly is $(1/2)^{20}$ – not very likely (1 in a million since 2^{10} is about 1,000). These odds are actually much better then when you play the lottery.** Do you know if six-fingered is sex-linked? **The male must have the six-fingered allele and a Y chromosome. Thus the daughters will always get a six fingered allele from dad and the sons will get the Y chromosome from dad. Mom is either homozygous for the five-finger allele (if it is recessive) or she is heterozygous with the five-finger allele being dominant. If heterozygous with the five-fingered allele being dominant then 1/2 the boys should be five-fingered and 1/2 should be six-fingered. Likewise 1/2 the girls should be five-fingered, the other half should be six-fingered. If five finger is recessive then all the boys must be five-fingered and all the girls six-fingered. This is not the case for the boys so if the trait is sex-linked then the five-fingered allele must be dominant.** Do you know with 100% percent certainty that the male is homozygous for six-fingered? **This would imply autosomal. If autosomal and six-fingered is domiant and the male is homozygous then all of the offspring should be six-fingered. This is most likely the case.** What is the probability that if the male is heterozygous for six-fingered that all 20 children are six-fingered? As calculated earlier the chance of getting the above results is one in a million if the male is heterozygous. Possible, but not lvery ikely.

QQ5) Two traits are being examined. In the following table, the dominant phenotype is indicated by the letter D and the recessive phenotype is indicated by the letter r. D D would indicate Dominant for trait 1 and Dominant for trait 2. Likewise, r D would indicate recessive for trait 1 and Dominant for trait 2. Determine the genotype of the parents that gave rise to these offspring based upon the number of offspring. 7 problems (i to vii) are given. Note that there may be more than one cross that yields these answers, if so try to determine all of them. **IGNORE SEX LINKED FOR ALL OF THESE PROBLEMS.**

	D D	D r	r D	r r
i)	400	400	400	400
ii)	900	300	300	100
iii)	600	600	200	200
iv)	200	600	200	600
v)	200	600	600	200
vi)	1,200	0	0	0
vii)	0	0	0	1,200

General logic: The previous problems ignored the names of the traits to minimize confusion. Note how important it is to determine which traits are dominant and which are recessive. In some crosses you may not be able to determine which is dominant and which is recessive. There aren't many "rules" you can remember when it comes to genetics. There are a few however.

1) First determine which traits are you looking at and determine the alleles of each.
2) Determine which alleles are dominant or recessive.
3) Examine the ratio for each trait SEPARATELY.
4) Match the ratio to the genotype for each trait. For example a 3:1 ratio would imply that a heterozygous individual was crossed with a heterozygous recessive individual! The dominant allele is the one that is more prevalent (3/4). What would a 1:1 ratio imply for the individuals genotype for the second trait? If you don't know the answer instantly then go back and look at the table on the first page. The table lists the ratios you should commit to memory.
5) Now figure out the probability of the two events occurring if they are independent. If the numbers match your predictions then the traits are genetically unlinked. If the numbers don't match then the traits are genetically linked (or maybe you made a mistake, or they may be sex-linked). If the traits are linked then the offspring that are most numerous are due to the fact that they received a parental type of chromosome. (See iv and v on the previous page). Double check this. Look at #8 on the GMB III worksheet.

	D D	D r	r D	r r	
i)	400	400	400	400	D1 = 800, r1 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r), D2 = 800, R2 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r). If assort independently expect 1/2 X 1/2 for all 4 possible. Matches the data so they assort independently.
ii)	900	300	300	100	D1 = 1,200, r1 = 400 implies 3:1 ratio, 3/4 D so hetero with hetero for trait 1. Trait 2: D2 = 1,200, r2 = 400 implies 3:1 ratio, 3/4 D so hetero with hetero for trait 2. Expect 9:3:3:1 ratio if the two traits assort independently. Matches the data.
iii)	600	600	200	200	D1 = 1,200, r1 = 400 implies 3:1 ratio, 3/4 D so hetero with hetero for trait 1. D2 = 800, r2 = 800 implies hetero with hetero for with homorecessive (1/2 D, 1/2 r). If the traits assort independently you expect 3/4 x 1/2 = D D, 3/4 X 1/2 = D r, 1/4 X 1/2 = r D, 1/4 X 1/2 r r. You find those ratios so they must assort independently.
iv)	600	200	200	600	D1 = 800, r1 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r), D2 = 800 r2 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r). Unlike the first case i) you don't find 1:1:1:1 so the two traits do not assort independently. Clearly the two categories with the most offspring must be due to having received a parental type of chromosome. I would assume D D/r r represent the two parental chromosomes.

v)	200	600	600	200	D1 = 800, r1 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r), D2 = 800 r2 = 800 implies hetero w/homo recessive (1/2 D, 1/2 r). Unlike the first case i) you don't find 1:1:1:1 so the two traits do not assort independently. Clearly the two categories with the most offspring must be due to having received a parental type of chromosome. I would assume D r/ r D represent the two parental chromosomes.
vi)	1,200	0	0	0	Implies homozygous D for traits 1 & 2 crossed with anything autosomal, for each of the two traits. Could be X linked homozygous D crossed with male any genotype for each of the two traits.
vii)	0	0	0	1,200	Implies homozygous r crossed with homozygous recessive for each of the two traits. Could be X linked homozygous recessive for each of the two traits with male hemizygous recessive for each of the two traits.

Application:

QQQ1) A wild-type male fly (normal wings and normal body color) was crossed to a mutant female fly from a true breeding with vestigial wings and ebony body. Based upon the following results can you determine the genotype?

a) 1/4 = wild type for both traits, 1/4 = normal wings and ebony body, 1/4 = vestigial wings and normal body, 1/4 = vestigial wings and ebony body.

Again look at each trait separately. Each trait shows a 1:1 ratio so that we must have a heterozygous crossed with a homozygous recessive. If the two traits assort independently then you expect 1:1:1:1 and you see that. Since the female came from a true breeding population you know that the mutant alleles must be recessive.

QQQ2) Given the following genotypes make a punnett square for the cross. Be sure to include the genotype and phenotype of each box within your Punnett square. Determine the probability of each box. Now go back and actually list the 4 types of phenotypes (D D; D r; r D; r r and give the percentage of each of the four types.

Ab+/A+b crossed with Ab/Ab. **Map distance = 20.**
Ab+/A+b crossed with ab/ab. **Map distance = 20.**

	Ab 1.0
Ab+ .4	Ab+/ Ab .4
A+b .4	A+b /Ab .4
Ab .1	Ab / Ab .1
A+b+ .1	A+b+ / Ab .1

	ab 1.0
Ab+ .4	Ab+/ ab .4
A+b .4	A+b /ab .4
Ab .1	Ab / ab .1
A+b+ .1	A+b+ / ab .1

QQQ3) In humans, normal tooth enamel is white. A mutant allele that is dominant and linked to the X chromosome results in the production of defective tooth enamel that is brown in color. A man with brown tooth enamel marries a woman with normal teeth (no history of brown tooth enamel in her family history). Their daughter marries a man with normal tooth enamel. Answer the following questions.

a) What is the probability that a son from this couple will have brown teeth?

Note: 1st couple = X^B/Y male crossed with X^{B+}/X^{B+}

Their daughter is X^B/X^{B+}. Her husband is X^{B+}/Y

Punnett square for their mating.

	X^{B+}	Y
X^B	X^B / X^{B+}	X^B / Y
X^{B+}	X^{B+} / X^{B+}	X^{B+}/ Y

1/2 the sons will have brown teeth, genotype = X^B / Y

b) What is the probability that a son from this couple will have normal teeth?

1/2 the sons will have normal teeth, genotype = X^{B+}/ Y

c) What is the probability that a daughter from this couple will have brown teeth?

1/2 the daughters will have brown teeth, genotype = X^B / X^{B+}

d) What is the probability that a daughter from this couple will have normal teeth?

1/2 the daughters will have normal teeth, genotype = X^{B+} / X^{B+}

QQQ4) An individual is heterozygous for four genes, named a, b, c and d. The mutations are recessive. This individual is test-crossed with another individual who is homozygous recessive for all 4 traits. 1,000 progeny are found as follows:

phenotype	# of progeny
$ab^+c^+d^+$	42
a^+bcd	43
$a^+b^+c^+d$	140
$abcd^+$	145
ab^+cd^+	6
a^+bc^+d	9
a^+b^+cd	305
abc^+d^+	310

Which genes, if any, are linked? Look at each trait independently – note that it should always be about 1:1 for each trait. Thus looking at the a and b loci you should find 1:1:1:1 if they assort independently (1/2 X 1/2 for each of the 4 phenotypes). Do you see that? If not then they must not assort independently. Repeat for b and c, c and d.
For phenotype
a = 42 + 145 + 6 + 310 = 503
a+ = 43 + 140 + 9 + 305 = 497
b = 43 + 145 + 9 + 310 = 507
b+ = 42 + 140 + 6 + 305 = 493
c = 43 + 145 + 6 + 305 = 499
c+ = 42 + 140 + 9 + 310 = 501
d = 43 + 140 + 9 + 305 = 497
d+ = 42 + 145 + 6 + 310 = 503

In all cases we see a 1:1 which implies a heterozygous individual crossed with homozygous recessive. Actually you were already told that. If they assort independently we would expect to find a 1:1:1:1 for ab, ab+, a+b, a+b+. Do we see that? ab = 145 + 310 = 455, ab+ = 42 + 6 = 48, a+b = 43 + 9 = 52, a+b+ = 140 + 305 = 445. We don't see a 1:1:1:1 and instead see ab as one parental chromosome and a+b+ as the other. Map distance = 100/1,000. **10 map units between a & b.** I would then look at bc. b+c+ = 42 + 140 = 182, bc = 43 + 145 = 188, b+c = 6 + 305 = 311, bc+ = 9 + 310 = 319. Map distance = 370/1,000 = **37 map units between b and c.** Check c and d. c+d+ = 42 + 310 = 352, cd = 43 + 305 = 348, c+d = 140 + 9 = 149, cd+ = 145 + 6 = 151. **Map distance = 300/1,000 = 30 map units between c and d.** Check a and c. a c+ = 42 + 310 = 352, a+ c = 43 + 305 = 348, a+ c+ = 140 + 9 = 149, a c = 145 + 6 = 151. 300/1,000 = **30 map units between a and c.**

a 10 map units b look for location of c relative to b. So far a ---- 10 map units ---- b. The distance between b and c is about 37 map units. Is c located to the left of b or to the right of b. If to the left then the distance between a and c should be about 30 and it is. We now have c ---- 27 map units ---- a ---- 10 map units --- b. Where is d? We know that between c and d it should be about 30 map units, d can be to the left of c or to the right. Notice that if we move d to the right of C it makes a and d very close. Ad+ = 42 + 145, 6 + 310 = 503, a+d = 43 + 140 + 9 + 305 = 497. No recombinants found thus it must be close. Gene order is c a d b. The a and d alleles are actually very close to one another. The parental chromosomes are c+a d+ b/c a+ d b+.

In each case they do not show independent assortment – thus all 4 are genetically linked. **Determine the parental types**!