

Key

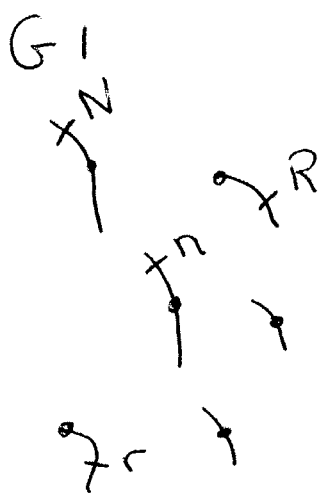
Answer all questions. You must show your work clearly to get full credit. Also, you may be eligible for partial credit even if your answer is wrong. It is probably better NOT to erase as sometimes there is work worth some credit in that scribbling.

1. (6 points, a freebie!). a) In what year did you take Intro Biology (first semester Biol 111 or equivalent)?  
 b) Where (what school) did you take Introductory Biology?  
 c) Who was your instructor for that intro course if you can remember?

2. (24 point Donut Question). The number of chromosomes in the wing cell of a mosquito is six. i) Using chromosomes with different morphologies (**different positions of the centromere and/or different lengths**), draw the chromosomes (i.e. assume that you can see them clearly) in an adult mosquito in a) G1 stage of the cell cycle; b) anaphase of mitosis; c) metaphase I of meiosis; d) the telophase II cells resulting from the metaphase I meiosis drawn in part c.

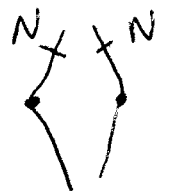
ii) Your mosquito is heterozygous for two **independent** genes, the *notch* wing locus  $Nn$  and the *ridge* back locus  $Rr$ . Label **ALL** copies of your genes in your four (a,b,c,d) figures. There is **no crossing over** in this species.

iii) Assuming that there are 3 picograms (pg) of DNA in a sperm cell of mosquito, how many pg are in your figures a, b, c, and d above?



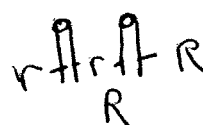
6 pg

Anaphase  
Mitosis



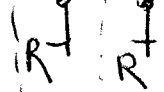
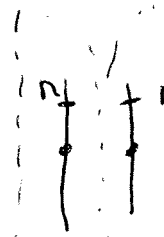
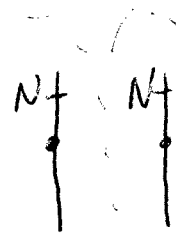
12 pg

Met I  
meiosis



12 pg

Telo phase II



3 pg

3 pg

**3. (12 points).** How similar are the genes, position of the centromere and the DNA sequence of sister chromatids? How similar are the genes, position of the centromeres and the DNA sequence for homologous chromosomes? Be clear and precise in your answers.

Sister chromatids are identical barring a mutation during the S stage of the cell cycle. The genes are the same and in the same positions, the centromeres are in the same place, and the DNA is identical.

Homologous chromosomes are very similar. Genes are the same and in the same positions. Centromeres are in the same position. The DNA differs a little since the alleles at a locus contributed by the different parents may differ often by as little as a few base pairs in 1000s.

**4. (16 points).** Wing color in butterflies is very diverse. A series of crosses were performed to examine inheritance patterns. Given the available data, determine the number of genes and alleles involved and indicate the genotypes for the following crosses. **Be sure to define clearly, your gene notations and dominance relationships.**

blue B1 B2	x	blue B1 B2	87 blue, 28 green B1__ B2 B2	Segregates 3:1 so must be Het x Het, Blue is Dom to Green
brown B2 B3	x	brown B2 B3	55 brown, 26 green, 31 dusty B2 B3 B2 B2 B3 B3	Segregates 1:2:1 must be Het x Het but co dominance, brown = Het
blue B1 B2	x	brown B2 B3	42 blue, 19 green, 22 brown B1__ B2 B2 B2 B3	Segregates 1:2:1 must be Het x Het
dusty B3 B3	x	blue B1 B2	23 brown, 28 blue B2 B3 B1 B3	Segregates 1:1 must be test cross

Genotypes:

B1 \_\_ = Blue      B1 (Blue) is dominant to B2 (green) and B3 (dusty)

B2 B2 = Green

B3 B3 = Dusty

B2 B3 = Brown      B2 and B3 are codominant

There is also a two gene system that works. In that model, at one locus A\_\_ \_\_ = Blue. If the first locus is a a, then at the second locus (say B) there are two alleles which are codominant. aa B1 B1 = Green; aa B1 B2 = Brown; aa B2B2 = dusty ... or something similar.

5. (12 points). You are a squirrel breeder (you must be nuts), and you have the following genotypes of two independent genes determine coat color.

$A\_B\_ =$  gray;  $A\_bb =$  red;  $aaB\_ =$  black;  $aabb =$  golden.

A third gene (D) deposits color in the coat and the recessive mutant (d) creates albinos. Show the **genotypes of the offspring** below and show a possible **genotype and phenotype** of the parents who produced them.

3/8 Red  $A\_bb Dd$       1/8 golden  $aa bb Dd$       1/2 Albino  $\_\_ bb dd$

Parents Genotype  $Aa bb Dd$  x  $Aa bb dd$

Parents Phenotype **Red** x **albino**

6. (20 points). A cross was made between a true breeding black haired rat and a true breeding white haired rat. All of the F1 were black. The F1 animals were intercrossed and produced **46 black, 21 white, 13 brown** offspring. Propose a model for the inheritance of coat color and define genes, alleles and genotypes of your crosses. Test your model with  $\chi^2$ . Give an explanation of the biochemical interactions or pathways involved.

P **Black** x **White**

F1 **Black**

F2 **46 Black 21 White 13 Brown**

Total offspring = 80

Can not be 1 locus because F2 would have to segregate 3:1. Try two loci. Since there are only 3 phenotypes in F2, it must be a modified Mendelian ratio (epistasis).

With two genes the F2 should segregate as:

Expected Numbers

$A\_B\_ \quad 9/16 \quad x \ 80 \quad = \quad 45 \quad \text{Black}$

$A\_bb \quad 3/16 \quad x \ 80 \quad = \quad 15 \quad \text{Brown}$

$aa B\_ \quad 3/16 \quad x \ 80 \quad = \quad 15 \quad \text{White}$

$aa bb \quad 1/16 \quad x \ 80 \quad = \quad 5 \quad \text{White}$

Since one category is missing and none of the phenotypes seems to have just 5 individuals, it appears that the least frequent category is combined with one of the others

This creates a 9:4:3 modified ratio

Test the model

$$\chi^2 = \frac{(46-45)^2}{45} + \frac{(21-20)^2}{20} + \frac{(13-15)^2}{15}$$

$\approx 0.34 \quad df=2$

$0.5 < P < 0.9$  that we would get a deviation this big if the model is correct. We can accept the model (or fail to reject). Why might we get this modified ratio?

white precursor  $\xrightarrow{\text{Gene A}}$  Brown Intermediate  $\xrightarrow{\text{Gene B}}$  Black

	Probability (p)					
	0.90	0.50	0.20	0.05	0.01	0.001
1	0.02	0.46	1.64	3.84	6.64	10.83
2	0.21	1.39	3.22	5.99	9.21	13.82
3	0.58	2.37	4.64	7.82	11.35	16.27
4	1.06	3.36	5.99	9.49	13.28	18.47
5	1.61	4.35	7.29	11.07	15.09	20.52
6	2.20	5.35	8.56	12.59	16.81	22.46
7	2.83	6.35	9.80	14.07	18.48	24.32
8	3.49	7.34	11.03	15.51	20.09	26.13
9	4.17	8.34	12.24	16.92	21.67	27.88
10	4.87	9.34	13.44	18.31	23.21	29.59
15	8.55	14.34	19.31	25.00	30.58	37.30
25	16.47	24.34	30.68	37.65	44.31	52.62
50	37.69	49.34	58.16	67.51	76.15	86.60

$\chi^2$  values

7. (12 points). Sickle cell anemia (SC) and muscular dystrophy (MD) are independent, recessive mutations in humans. Two normal parents have a girl with SC and MD. A) What is the probability that their next child will have a mutant phenotype? B) What is the probability that their next child will be a normal girl? C) What is the probability that their next two children will be the same sex and SC but **not** MD?

S \_ = not SC (normal)    M \_ = Not MD (normal)  
 ss = SC                    mm = MD

Ss Mm                    x                    Ss Mm                    both parents must be heterozygotes at both loci

Girl ssmm

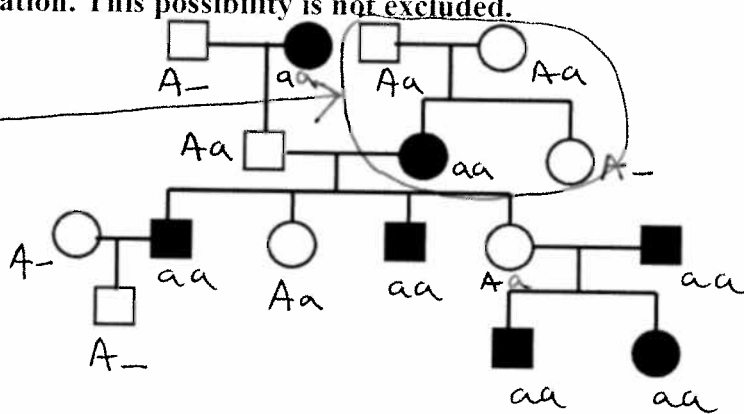
A) Next child has 3/4 chance of being normal at SC and 3/4 being normal at MD, so the probability of being normal at both is  $3/4 \times 3/4 = 9/16$ . All the rest will have one or two mutants  $1 - 9/16 = 7/16$

B) Probability of not SC = 3/4; Prob of not MD = 3/4; Prob of Girl = 1/2. All three events must happen simultaneously within this next child so the probability =  $3/4 \times 3/4 \times 1/2 = 9/32$

C) Probability of two SC kids =  $1/4 \times 1/4 = 1/16$ ; Prob of two kids not MD =  $3/4 \times 3/4 = 9/16$ ; Prob of two boys =  $1/2 \times 1/2 = 1/4$ . All of these need to happen to get two boys with SC and not MD =  $1/16 \times 9/16 \times 1/4 = 9/1024$ . There is the same probability of having this with two girls so either alternative will answer this question and the joint probability is 18/1024 or 9/512

8. (12 points). For the human pedigree below, identify mode(s) of inheritance (single gene dominant, single gene recessive) **that can be excluded** (if any), explain why and give an explanation for the most likely mode. Clearly identify individuals in the pedigree that support your arguments.

This portion of the pedigree excludes a dominant allele as the cause of this mutation. One of the parents would have to show the trait since the first girl shows the trait. The trait could be caused by a single gene recessive mutation. This possibility is not excluded.



Showing that single gene with a recessive mutation could account for the pattern in this pedigree.

We have not proven this to be a single gene recessive however. Additional information could exclude that possibility as well!