1. At what stage of meiosis does a reciprocal exchange of non-sister chromatids occur?

a) haplophase I
b) telophase II
c) mitotic anaphase
d) zygotene
e) pachytene
f) cytokinesis
g) hallowene

2. A geneticist crosses two diploid plants as follows: AABbCcDDEE x aaBbCcDdee. What is the probability of obtaining progeny heterozygous at all 5 genes from this cross assuming each gene occurs on a different chromosome pair?
= 1 x 1/2 x 1/2 x 1/2 x 1 = 1/8
a) 3/4
b) 1/2
c) 1/4
d) 1/8
e) 1/16
f) 1/32
g) 1/64

3. For the cross of question # 2 above, how many progeny must the geneticist grow in order to be 99% certain of obtaining the heterozygous genotype indicated above?
prob of not getting it is 7/8 for each progeny. Therefore $0.99 = 1-(7/8)^n$
so $n\log(7/8) = \log(1-0.99)$
$n = 34.49$
a) 34.5
b) 71.4
c) 84.5
d) 99.9
e) at least 1000
f) cannot be determined

4. For the cross rrSSTtUuVVWw x RrSsttuuVVww, and assuming that dominance occurs at each gene and there is independent assortment, how many possible **genotypes** would you expect to occur from this cross?
= 2 x 2 x 2 x 2 x 1 x 2 =32
a) 4
b) 8
c) 12
d) 16
e) 32
f) 48
g) none of the above

5. For the cross in question # 4 above, how many different **phenotypes** would you expect to obtain from the cross assuming independent assortment?

= 2 x 1 x 2 x 2 x 1 x 2 =16

a) 4
b) 8
c) 12
d) 16
e) 32
f) 48
g) 64

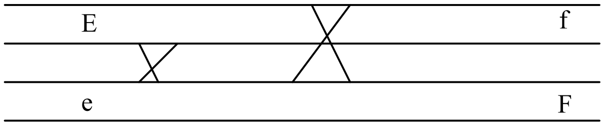
6. A geneticist begins a series of crosses with two parental lines: AABB and aabb. The parental lines are crossed to produce an F_1 and then the F_1 is test crossed. The number of various progeny from the test cross are listed below. Is there any statistical evidence that the two genes are linked?

using contingeny or test of independence there is one degree of freedom.
the expects are 44 46 44 46
chisquare = 5.69 there is just 1 df so critical value is 3.841

	AaBb	Aabb	aaBb	aabb
Observed #	52	38	36	54

a) There is **no** statistical evidence for linkage because the chisquare calculated = 0.8
b) There **is** statistical evidence for linkage because the chisquare calculated = 0.8
c) There is **no** statistical evidence for linkage because the chisquare calculated = 5.8
d) There **is** statistical evidence for linkage because the chisquare calculated = 5.8
e) There is statistical evidence for linkage because the chisquare calculated = 11.6
f) none of the above are correct

7. A three-strand double crossover occurs in a single meiosis between two genes in a double heterozygote (EeFf) where the genes are linked in repulsion (trans arrangement). Which of the following is correct with respect to the gametes resulting from this single meiosis? Here's one three strand double crossover gives: EF, Ef, ef, eF



a) gametes are 1 EF, 1 Ef , 1 eF, 1 ef
b) gametes are 2 Ef, 2 eF
c) gametes are 2 EF, 2 ef
d) gametes are 1 EF, 3 ef

e) gametes are 3 EF 1 ef
f) gametes are 1 eF, 1 Ef, 2 EF
g) cannot be determined without knowledge of the map distance

8. You cross two strains of *Neurospora* to study the inheritance of two alleles (**P**, p) of a phosphatase gene. The numbers of various kinds of asci obtained are shown below:

p	**P**	p	p	**P**	**P**
p	**P**	p	p	**P**	**P**
p	**P**	**P**	**P**	p	p
p	**P**	**P**	**P**	p	p
P	p	p	**P**	**P**	p
P	p	p	**P**	**P**	p
P	p	**P**	p	p	**P**
P	p	**P**	p	p	**P**
130	120	55	56	54	55

Which of the following is correct with respect to these data?

a) the gene must be on the mitochondrial genome
b) the gene does not show a Mendelian inheritance
c) the gene is not linked to the centromere since there are approximately as many parental asci as recombinant asci in total
d) the gene is 23.4 cM from the centromere
e) the gene is 46.8 cM from the centromere
f) none of the above

recomb freq given by 1/2 number of recombinant asci/ total number of asci
= 0.5 x (55+56+54+55)/(130+120+55+56+54+55) = 0.234

9. For question # 8 above, use Haldane's mapping function to determine the map distance between the phosphatase gene and the centromere. The map distance is:
haldanes map function = -50 x ln(1 - 2 x r) = -50 x ln(1 - 2 x0.234) = 31.56

a) 0.34 cM
b) 10.1 cM
c) 20.4 cM
d) 31.6 cM
e) 137.6 cM
f) 50 cM since the gene is not linked to the centromere
g) none of the above

10. Which of the following is **INCORRECT** with respect to a trait determined by polygenic inheritance?
Heritability is the proportion of genetic variance not phenotypic variance.

a) Heritability is the proportion of phenotypic variation for the trait.
b) Dominance can occur for genes involved in the trait
c) The phenotypic variance of the trait can have an environmental component
d) The minimum number of genes involved can be estimated
e) Parent-offspring regression can provide an estimate of heritability

11) The recombination frequency between two linked genes, C & D, is r, where $0 < r < 0.5$. You cross two pure breeding lines of sunflowers, CCDD x ccdd, to obtain an F_1 individual. In terms of "r", what is the expected proportion of **CD** gametes produced by this F_1 individual?

a) r
b) r/2
c) r/4
d) (1-r)
e) (1-r)/2
f) (1-r)/4
g) none of the above

12. For question 11 above, imagine that the map distance between the genes C and D is 10 cM. You self-fertilize the F_1 individual to obtain F_2 progeny. What is the expected proportion of **ccdd** progeny in the F_2?

expect (1-r)/2 of cd, so expect (1-r)/2 x (1-r)/2 of ccdd progeny.
=0.9/2 x 0.9/2 = 0.2025

a) 0.0025
b) 0.01
c) 0.16
d) 0.2025
e) 0.45
f) 0.9
g) none of the above

13. Which one of the following is **correct** with respect to "hyrbrid vigor" in crop plants ?
a) it is a result of a single gene showing heterozygote superiority
b) it results from environmental differences between inbred and hybrid lines
c) it refers to increased yield of F_1 progeny from the cross of two inbred parental lines
d) it refers to increased yield in the F_2 and subsequent generations (F_3, F_4 etc)
e) it is determined by genes in the chloroplast genome

14. Imagine you constructed the map below using a three point test cross. Under the assumption of no crossover interference, how many double recombinant progeny would you expect to occur in a sample of 2000 progeny from this testcross?

if no interference proportion of double recs given by product of single recomb freqs
so proportion doubles = 0.02 x 0.08 = 0.0016
if there were 2000 progeny, expect 2000 x 0.0016 = 3.2

a) 0
b) 1.5
c) 3.2
d) 10
e) 16
f) 750
g) none of the above

15. For question # 14 above, how many double recombinant progeny would you have observed if the interference value, I = 1, and you grew out 10,000 progeny.
If there is interference of I=1 then there will never be any double recs.
a) 0
b) 1.5
c) 3.2
d) 10
e) 16
f) 750
g) none of the above

16. You cross two purebreeding parental lines as follows: qqRRSS x QQrrss , and then perform a three-point testcross using the triple heterozygous F_1 individual. The numbers of progeny of various genotypes are given below. There are 2000 total progeny.

Parental types are qRS and Qrs

for QR proportion recombs = 206/2000 = 0.103
for QS proportion recombs = 606/2000 = 0.303
for RS proportion recombs = 800/2000 = 0.4

map is

R 10.3 Q 30.3 S

so distance between R and S is 10.3 + 30.3 = 40.4

QRS / qrs	2
qrs / qrs	4
QRs / qrs	95
qrS / qrs	105
Qrs / qrs	594
qRS / qrs	600
QrS / qrs	295
qRs / qrs	305

Which one of the following statements is **correct**?

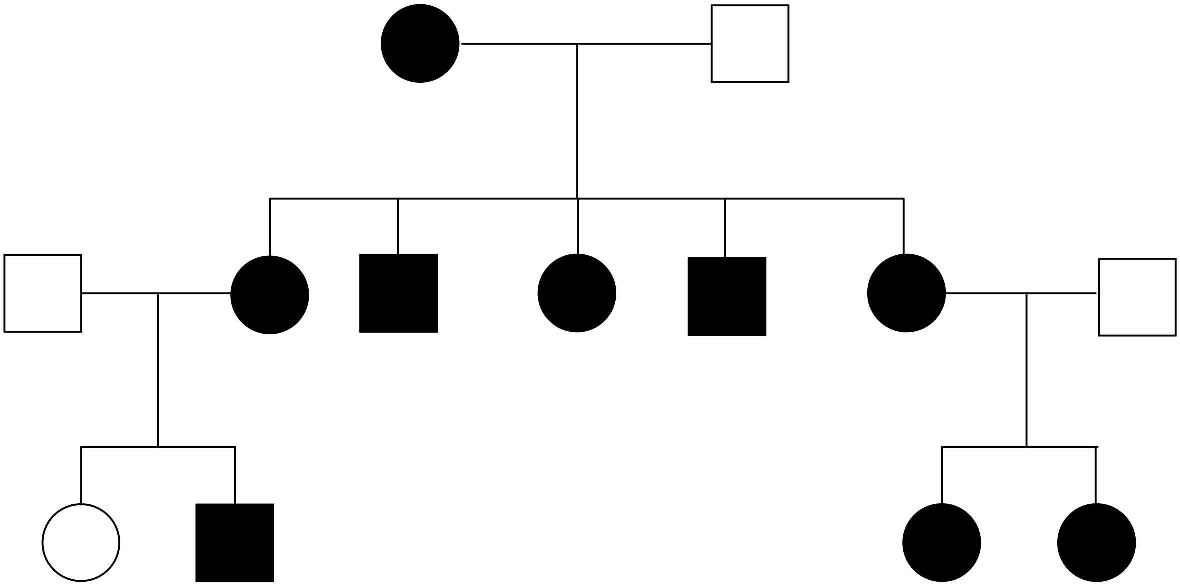
a) map order is QRS and the distance between Q and R is equal to 40 cM
b) map order is QRS with the distance between Q and R equal to 40.6 cM
c) R and Q are 10.3 cM apart but not linked to S
d) R and S are 10.3 cM apart
e) there are no double recombinants
f) none of the above

17. Tay Sachs disease is caused by a recessive autosomal allele "*t*". A husband and wife who are both normal (and who had normal parents), each have a sister with the disorder. The husband and wife wish to have 2 offspring. What is the probability that both offspring will be normal ?

Husband and wife are both Tt with probability 2/3 each.
Prob of an affected child is 1/4 from Tt by Tt mating
so prob of an affected child is 2/3 x 2/3 x 1/4 = 1/9.
so prob of a normal child is 8/9
prob of two normal children is 8/9 x 8/9 = 64/81
note that the other approach to the solution involves working out the probabilities of having a normal child for all four possible genotypes of the parents and then adding the probs (ie TT x TT, Tt x TT, TT x Tt, Tt x Tt)

a) 0
b) 1/2
c) 8/27
d) 27/64
e) 64/81
f) 1/64
g) none of the above

18. Below is a pedigree for a commonly occurring single gene trait in cheetahs.



Which of the following is correct with the respect to the possible mechanism(s) of inheritance of this trait?

it can't be mitochondrial
it cant' be xlinked recessive
it could be autosomal dominant , autosomal recess, xlinked dom

a) It must be due to a gene in the mitochondrial genome
b) It must be due to an autosomal dominant
c) It must be due to an X-linked dominant
d) It could be due to any of X-linked recessive, X-linked dominant or mitochondrial gene
e) It could be due to any of autosomal dominant or autosomal recessive or X-linked recessive
f) It could be due to any of autosomal dominant or autosomal recessive or X-linked dominant
g) It could be due to any of autosomal dominant or autosomal recessive or X-linked recessive or X-linked dominant or mitochondrial gene

19. *Silene dioica* is a plant that has separate sexes that are determined just as in humans. Red flowers are determined by an X-linked dominant allele, R, while white flowers are determined by an X-linked recessive. Purple stripes are determined by an autosomal dominant allele while absence of stripes is the result of a recessive allele.
You cross a pure breeding red female with stripes, to a white male with no stripes. You then cross 1 male and 1 female from these F_1 progeny to obtain F_2 progeny. Which of the following is correct?

a) more males than females will have red flowers
b) 3/16 of the progeny will be males with red flowers without stripes
c) 1/16 of the progeny will be females with red flowers and no stripes
d) 3/8 of the progeny will be males with white flowers with stripes
e) 3/8 of the prgeny will be females with white flowers and stripes
f) none of the above

Parents female is X^RX^RPP male is X^rYpp

F_1 females X^RX^rPp males X^RYPp

F_2 obtained by crossing an F_1 male with an F_1 female
(perhaps easiest to do this using branch diagrams, although punnett square would work).

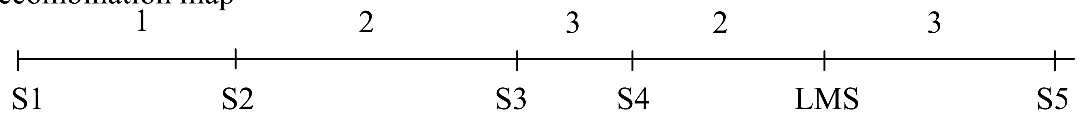
1/4 PP } 3/8 Female Redflower Purplestripes
1/2 Female X^RX^r 1/2 Pp }
1/4 pp 1/8 Female Redflower no stripes

1/4 PP } 3/16 male Redflower Purplestripes
1/4 male X^RY 1/2 Pp }
1/4 pp 1/16 male Redflower no stripes

1/4 PP } 3/16 male whiteflower Purplestripes
1/4 male X^rY 1/2 Pp }
1/4 pp 1/16 male whiteflower no stripes

20. To find the gene or genes that cause the genetic disorder known as Laurence-Moon syndrome (indicated as LMS on the recombination map below), you obtain a recombination map comprised of single nucleotide polymorphism markers (SNPs) that you have mapped in addition to LMS. You use the human genome sequence to produce a corresponding physical map of the same region of the genome. The maps are shown below. SNP markers are numbered S1, S2, S3 etc and the distances between them are indicated in centimorgans. The location of the SNPs are shown on both the physical and recombination maps. The physical map also includes the positions of all the genes in the region indicated as G1, G2, G3 etc and represented as black boxes.

Recombination map



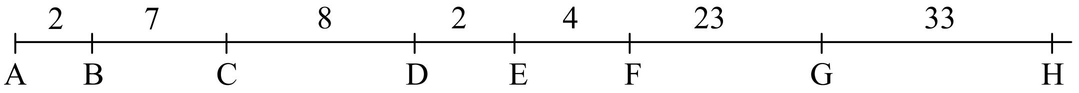
Physical map

Based upon these maps, which of the following is correct?

a) LMS is caused by gene G6
b) LMS is caused by one or both of genes G6 and G7.
c) LMS is caused by any one of the genes shown on the physical map
d) LMS is caused by gene G5
e) none of the above

21. A man and woman decide to have four children. Both the man and woman are normal but carriers of a recessive allele for the autosomal disorder alkaptonuria in which urine is black in colour. What is the probability that 2 of their four children will be normal.
mating is Aa x Aa
use binomial distn prob (2normal) = 4!/(2!2!) x $(3/4)^2$ x $(1/4)^2$
= 54/256 = 27/128
or realize there are 6 possible ways to have 2 normal and 2 affected offspring
and probability of having 2 normal and 2 affected is 3/4 x 3/4 x 1/4 x 1/4
a) 1/16
b) 3/4
c) 9/16
d) 27/64
e) 8/9
f) none of the above

22. The recombination map below provides distances between genes A, B, C etc, in cM. What is the best estimate of the distance between genes C and G?



= 8+2+4+23 = 37

a) 2 cM
b) 14 cM
c) 37 cM
d) 47 cM
e) none of the above

23. For question # 22 above, imagine you explored only the genes B and H in the cross BH/bh x bh/bh. What is the expected proportion of recombinant progeny based solely upon this cross?

Given that B and H are well over 50cM apart, the recomb freq would be 0.5

a) 0.02
b) 0.15
c) 0.35
d) 0.5
e) 0.77
f) none of the above

24. A geneticist maps over 1200 markers including genes, RFLPs, SNPs, and CAPS in a blackfly species. She is able to assemble the markers and genes into 4 separate genetic maps (or linkage groups). How many chromatids would you expect to occur at first metaphase of meiosis in this blackfly species?

with so many markers, you would have likely assembled one map for each chromosome, so haploid number is 4 so expect 16 chromatids at first metaphase.

a) 4
b) 8
c) 12
d) 16
e) 1200
f) none of the above