

**PLNT3140 INTRODUCTORY CYTOGENETICS 2018**  
**FINAL EXAMINATION**  
**December 13, 2018**

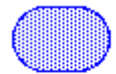
Answer any combination of questions totaling to exactly 100 points. If you answer questions totaling more than 100 points, answers will be discarded at random until the total points equal 100. There are 12 questions to choose from, totaling 120 points. This exam is worth 35% of the final grade.

Ways to write a readable and concise answer:

- i. Just answer the question. Save time by specifically addressing what is asked. Don't give irrelevant background if it doesn't contribute to the question that was asked.
- ii. Avoid stream of consciousness. Plan your answer by organizing your key points, and then write a concise, coherent answer. Make your point once, clearly, rather than repeating the same thing several times with no new information.
- iii. Point form, diagrams, tables, bar graphs, figures are welcome. Often they get the point across more clearly than a long paragraph.
- iv. Your writing must be legible. If I can't read it, I can't give you any credit.

1. (10 points) Wild type corn has blue kernels, due to the production of an anthocyanin pigment encoded by the C (colorless) locus. In one maize line, the kernels were yellow due to a mutation (cc) in the C locus. When this yellow line was crossed with another maize yellow line, the progeny often showed variegated kernels, as illustrated at right. Explain cause of the variegated kernels. In some variegated kernels, the blue patches were large, while in other kernels, the blue patches were small. What is the difference?

C: blue



cc: yellow



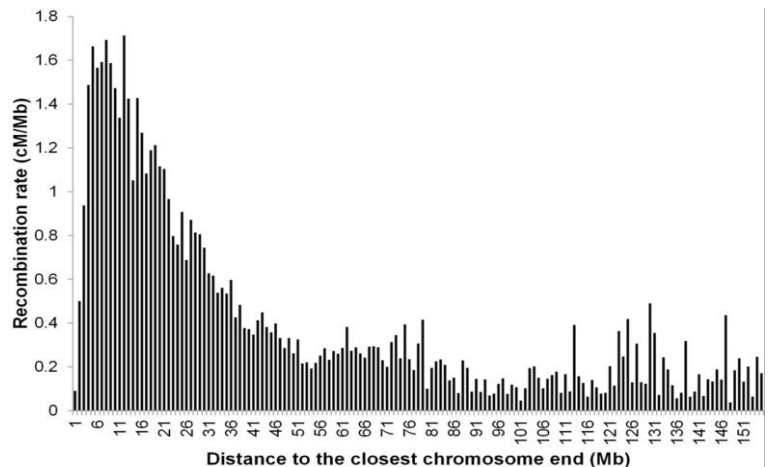
variegated



2. (10 points)

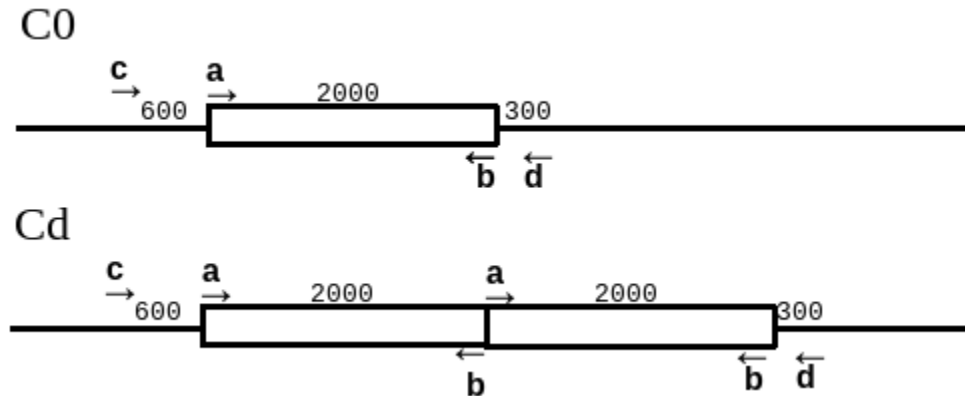
a) A high density linkage map of the pig (*Sus scrofa*) genome was made consisting of 38,599 SNP markers covering a genome whose total genetic length (averaged among several crosses) is about 2000 cM. The physical length of the genome is 2334 Mb. What is the average length, in Mb, of 1 cM in the pig genome?

b) The accompanying graph was made by measuring the recombination frequency every million bases along each of the 18 chromosomes. The graph shows pooled results for all positions on all chromosomes. What is the most important conclusion that can be drawn from these results?



Data from Tortereau F et al. (2012) A high density recombination map of the pig reveals a correlation between sex-specific recombination and GC content. *BMC Genomics* 201213:586 <https://doi.org/10.1186/1471-2164-13-586>.

3. (10 points) A 2000 bp sequence has undergone a tandem duplication. The sequences from the original chromosome (C0) and the chromosome containing the duplication (Cd) are shown below. The positions of PCR primers a, b, c and d are indicated. Note that the distance between c and a is 600 bp, while the distance between d and b is 300 bp.



Design a simple experiment in which you could use PCR to distinguish between individuals with the C0 chromosome, versus individuals with the Cd chromosome. Draw a diagram of a gel, indicating the expected sizes of PCR bands. (*It's not necessary to describe the experiment. Put all the necessary information into the diagram.*)

4. (10 points) Explain why translocations can lead to reproductive barriers between populations. What are the evolutionary consequences of these reproductive barriers?

5. (5 points) Draw a diagram showing the difference between acrocentric, metacentric, submetacentric and telocentric chromosomes. In this nomenclature, what do the terms p and q mean?

6. (10 points) Fill in the blanks.

You might think that genome size shouldn't affect mitotic cycle time. If the number of  a  per Mb stays the same, all genomes should replicate at the same rate. There must be other limiting factors eg. nuclear or cytoplasmic volume probably doesn't double when genome size doubles. For example, the concentration of dNTPs could be a major limiting factor.

In nature, annual plants tend to have  b  genomes and  c  mitotic cycles. Perennial plants tend to have  d  genomes and  e  cell cycles. Annuals have to grow very rapidly in spring, requiring rapid  f . Therefore, ecological  g  with other species forces annuals to have  b  genomes.

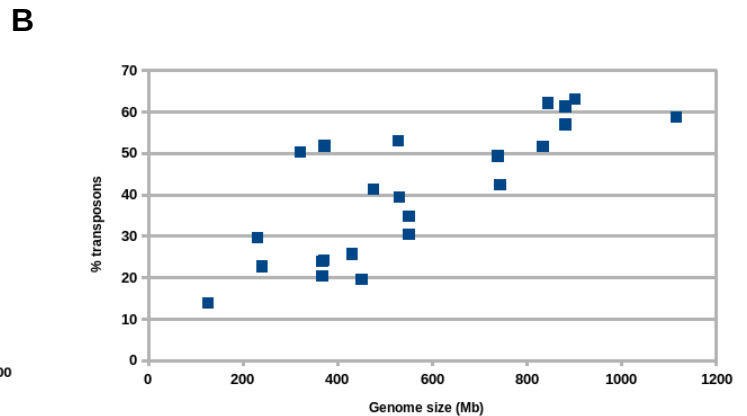
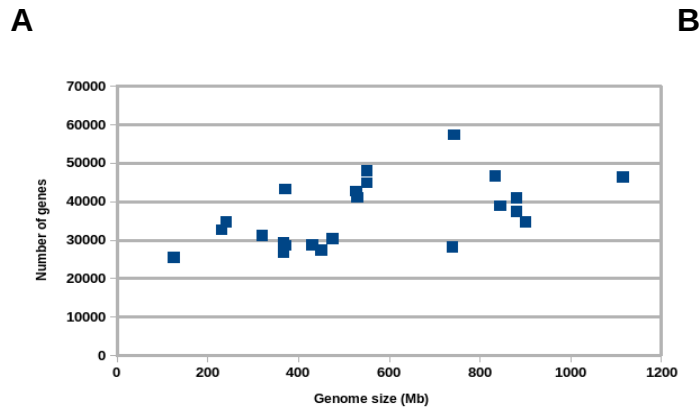
Question: Is the perennial habit more tolerant of a  e  mitotic cycle or  d  genome? Perennials pay a large metabolic price in their first year in the development of extensive root systems and above ground shoots. However, these features make them more  h  in subsequent years.

d  genomes are probably better tolerated when habitat is not limiting, in terms of food, water, light and space. The prediction would be that  b  genomes are favored when resources are  i .

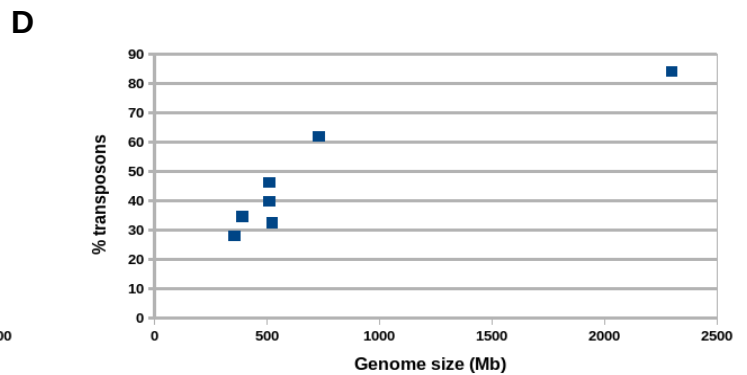
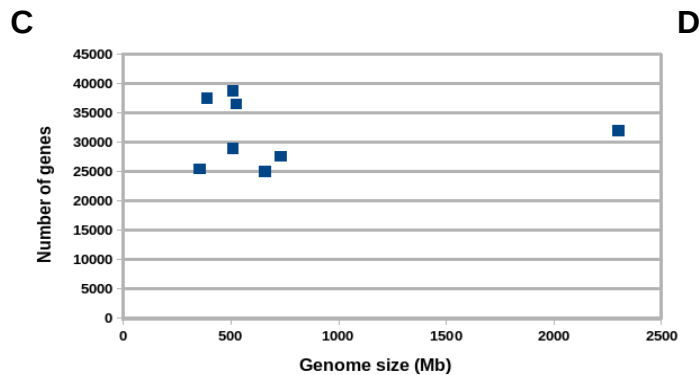
Interestingly our annual crops such as wheat and corn tend to have  d  genomes. We pamper them with fertilizers and water, and eliminate  g  through weed control. Domesticated crops are  j  competitors outside of cultivation.

7. (20 points) The graphs below plot the number or genes or the percent of the genome made up by transposons, as a function of genome size. Data are shown for various species of dicotyledonous plants (A,B) or monocotyledonous plants (C,D). What are the main conclusions you can draw from these graphs? (Hint: Points will not be given for simply stating where the data points are. What are the data telling us about plant genomes?)

### Dicots



### Monocots



Data from Raja Ragupathy, Frank M. You, Sylvie Cloutier, Arguments for standardizing transposable element annotation in plant genomes, In Trends in Plant Science, Volume 18, Issue 7, 2013, Pages 367-376, ISSN 1360-1385, <https://doi.org/10.1016/j.tplants.2013.03.005>.

8. (10 points) Suppose you want make a BAC library for a genome. Given a genome with a total haploid size of  $4 \times 10^9$  bp, how many BACs do we need to have a 99% likelihood of having a complete library ie. having at least one clone for every gene? Show your work, using the Clark and Carbon formula. Assume an average BAC insert size of 100 kb.

$$N = \frac{\ln(1 - P)}{\ln(1 - f)}$$

9. (10 points)

a) (5 points) It is commonly observed that the size of a genome can change drastically due to gain or loss of middle repetitive sequences such as transposable elements. For example an increase in transposition might double the size of the middle repetitive fraction of the genome, due to proliferation of a family of transposons. In other words, there is twice as much middle repetitive DNA, after the transposition events.

To keep the math simple, consider an imaginary species with a diploid DNA content of 10 pg per nucleus. The following describes the components of that genome:

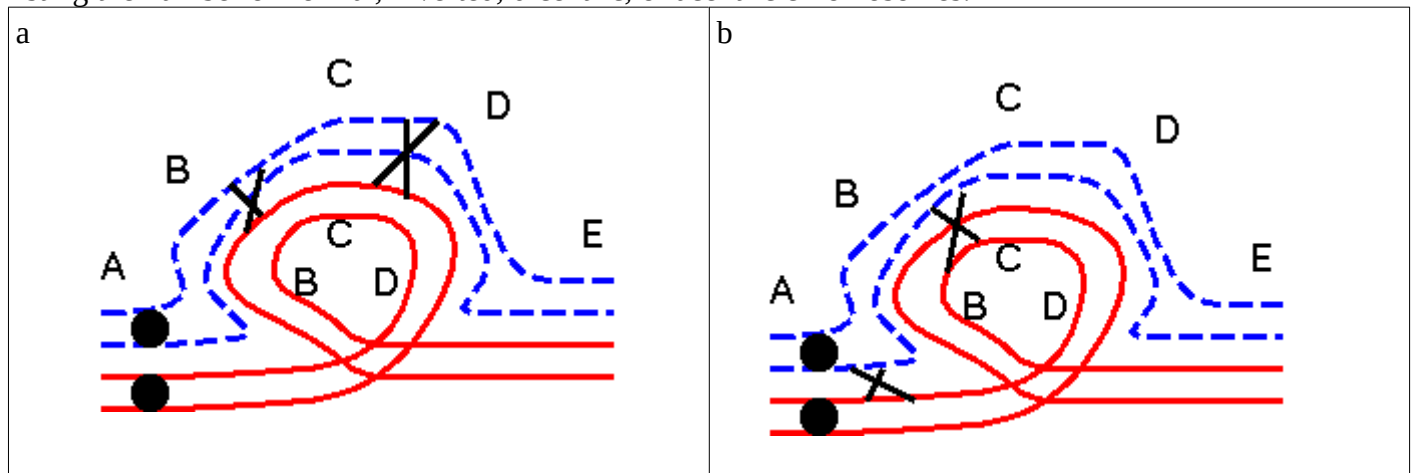
Population A - Original population

	percent of genome	pg DNA per nucleus
highly repetitive	15%	1.5
middle repetitive	75%	7.5
single copy	10%	1
total	100%	10.0

Suppose that in one population of this species (Population B), a drastic amplification of transposons took place, such that the middle repetitive fraction doubled in size. Create a new table, similar to the one above, for the genome of Population B.

b) (5 points) With Population A as a starting point, what would happen if a third population of this species (Population C) had undergone a tetraploidization event. Create a table to represent Population C.

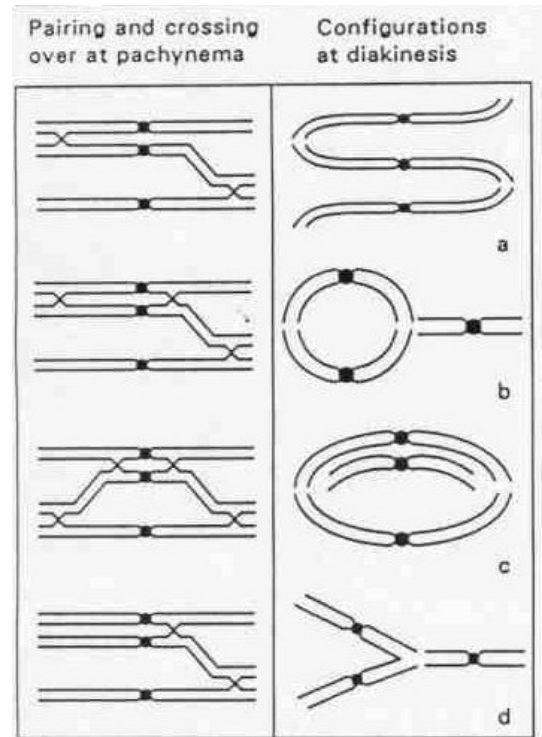
10. (10 points) For each of the following diagrams, indicate the outcome of double crossovers in meiosis by listing the number of normal, inverted, dicentric, or acentric chromosomes.



11. (10 points)

a) What is being illustrated in the figure at right?

b) Why do the chromosomes in diakinesis form chains?



12. (5 points) Define the term "homeologous chromosomes".