

**PLNT3140 INTRODUCTORY CYTOGENETICS 2016  
FINAL EXAMINATION**

Monday December 18, 2017

Time: 13:30 - 15:30

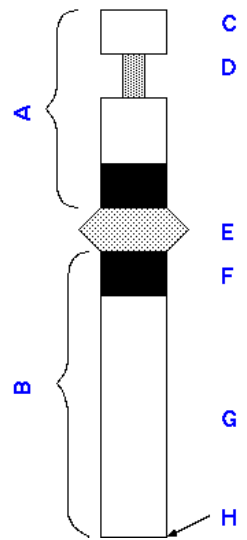
Location: Engineering E2-130, Seats 1 -27

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) What is the term for the diagram at right?  
For A - H, name each part.



2. (10 points) The 2-point distances between five loci are shown in the table (cM).

	T175	C35	T93	C66
C35	4.2			
T93	18.7	15.6		
C66	26.1	25.5	12.1	
T50B	30.4	30.5	21.1	12.2

- a) Draw a map, showing the order of markers and the distances between adjacent markers.
- b) The distances between markers do not appear to be additive. That is, if the map order was BCA, the BA distance is not equal to BC + CA. What is the most likely reason for this observation? Can you suggest a potential solution to this problem?

3. (10 points) The accompanying table lists the lengths of chromosomes in the rat (*Rattus norvegicus*).

<b>Loc</b>	<b>Type</b>	<b>Name</b>	<b>RefSeq</b>	<b>INSDC</b>	<b>Size (Mb)</b>
Nuc	Chr	1	<a href="#">NC_005100.4</a>	<a href="#">CM000072.5</a>	282.76
Nuc	Chr	2	<a href="#">NC_005101.4</a>	<a href="#">CM000073.5</a>	266.44
Nuc	Chr	3	<a href="#">NC_005102.4</a>	<a href="#">CM000074.5</a>	177.7
Nuc	Chr	4	<a href="#">NC_005103.4</a>	<a href="#">CM000075.5</a>	184.23
Nuc	Chr	5	<a href="#">NC_005104.4</a>	<a href="#">CM000076.5</a>	173.71
Nuc	Chr	6	<a href="#">NC_005105.4</a>	<a href="#">CM000077.5</a>	147.99
Nuc	Chr	7	<a href="#">NC_005106.4</a>	<a href="#">CM000078.5</a>	145.73
Nuc	Chr	8	<a href="#">NC_005107.4</a>	<a href="#">CM000079.5</a>	133.31
Nuc	Chr	9	<a href="#">NC_005108.4</a>	<a href="#">CM000080.5</a>	122.1
Nuc	Chr	10	<a href="#">NC_005109.4</a>	<a href="#">CM000081.5</a>	112.63
Nuc	Chr	11	<a href="#">NC_005110.4</a>	<a href="#">CM000082.5</a>	90.46
Nuc	Chr	12	<a href="#">NC_005111.4</a>	<a href="#">CM000083.5</a>	52.72
Nuc	Chr	13	<a href="#">NC_005112.4</a>	<a href="#">CM000084.5</a>	114.03
Nuc	Chr	14	<a href="#">NC_005113.4</a>	<a href="#">CM000085.5</a>	115.49
Nuc	Chr	15	<a href="#">NC_005114.4</a>	<a href="#">CM000086.5</a>	111.25
Nuc	Chr	16	<a href="#">NC_005115.4</a>	<a href="#">CM000087.5</a>	90.67
Nuc	Chr	17	<a href="#">NC_005116.4</a>	<a href="#">CM000088.5</a>	90.84
Nuc	Chr	18	<a href="#">NC_005117.4</a>	<a href="#">CM000089.5</a>	88.2
Nuc	Chr	19	<a href="#">NC_005118.4</a>	<a href="#">CM000090.5</a>	62.28
Nuc	Chr	20	<a href="#">NC_005119.4</a>	<a href="#">CM000091.5</a>	56.21
Nuc	Chr	X	<a href="#">NC_005120.4</a>	<a href="#">CM000092.5</a>	159.97
Nuc	Chr	Y	<a href="#">NC_024475.1</a>	<a href="#">CM002824.1</a>	3.31
MT	Chr	MT	<a href="#">NC_001665.2</a>	<a href="#">AY172581.1</a>	0.016313
	Un	-	-	-	88.16
TOTAL					2870.2063

a) Using the Clark and Carbon formula, calculate the number of BAC clones needed to ensure a 99% chance of finding at least one clone for any given gene. Assume that the BAC library has an average insert size of 100 kb.

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

b) Suppose that you didn't care about getting a complete genomic library, but rather were only interested in getting genes from chromosome 18. (Assume flow cytometry is not an option.) Does that make any difference to your cloning strategy? Explain why or why not.

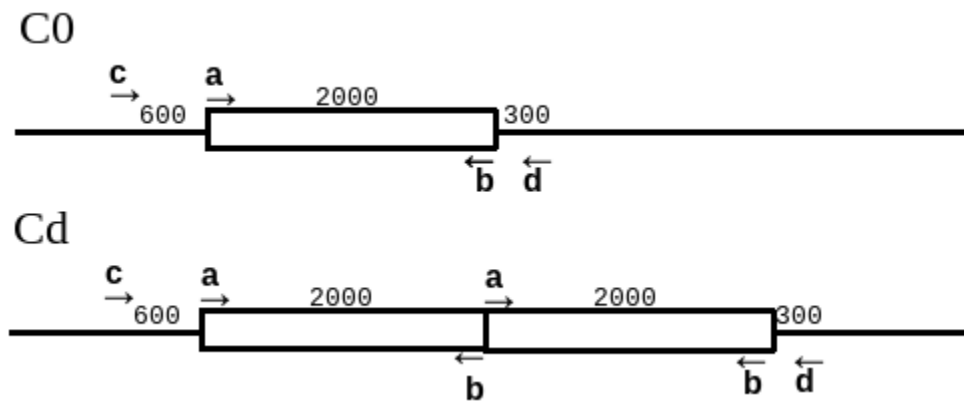
4. (10 points) Explain one reason why eukaryotic genomes sequenced by Whole Genome Sequencing usually give incomplete sequences for most chromosomes. Illustrate your answer using one or more diagrams.

5. (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?



6. (5 points) Explain the concept of microsynteny, in the context of comparing genomes between two related species.

7. (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.)

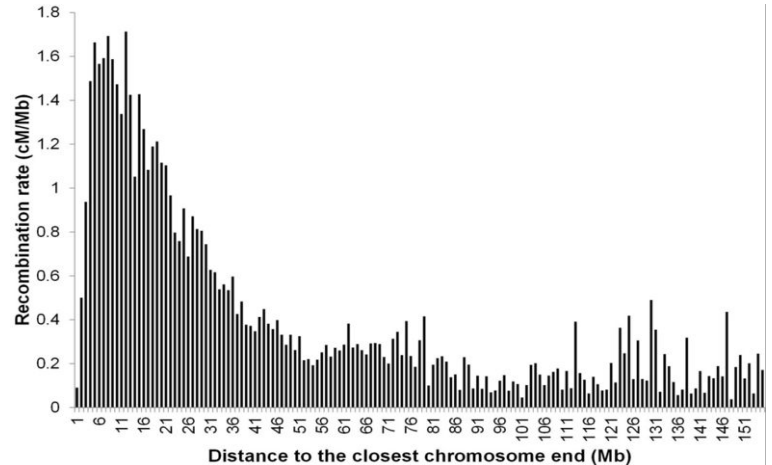
8. (10 points) Explain why translocations can lead to reproductive barriers between populations. What are the evolutionary consequences of these reproductive barriers?

9. (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?

10. (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>.

11. (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.

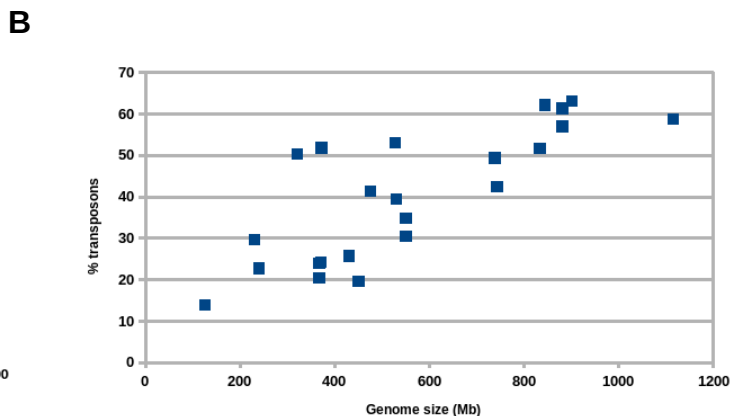
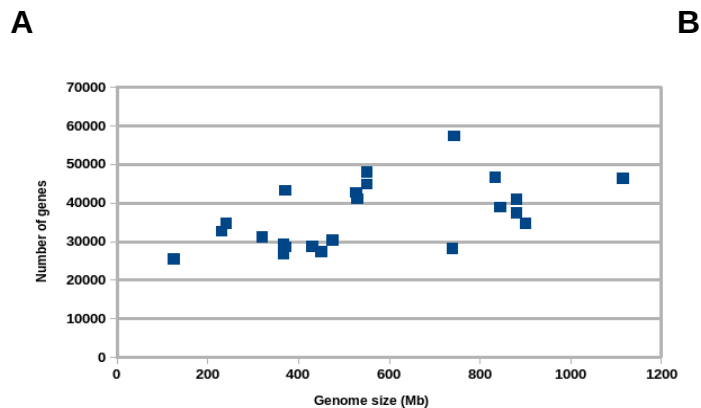
Question: Is the perennial habit more tolerant of a     e     mitotic cycle or     d     genome? Perennials pay a large metabolic price in their first year in the development of extensive root systems and above ground shoots. However, these features make them more     h     in subsequent years.

    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    .

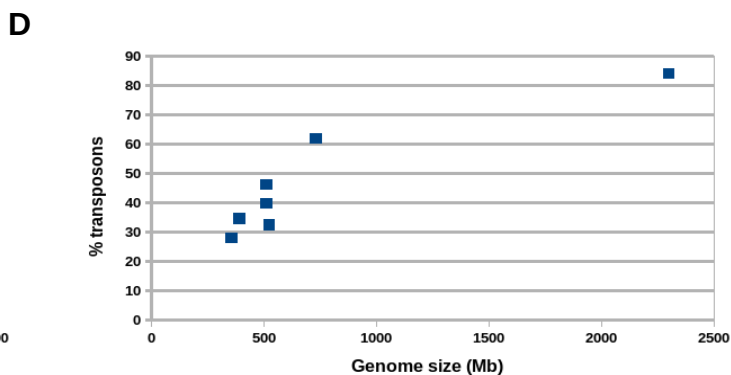
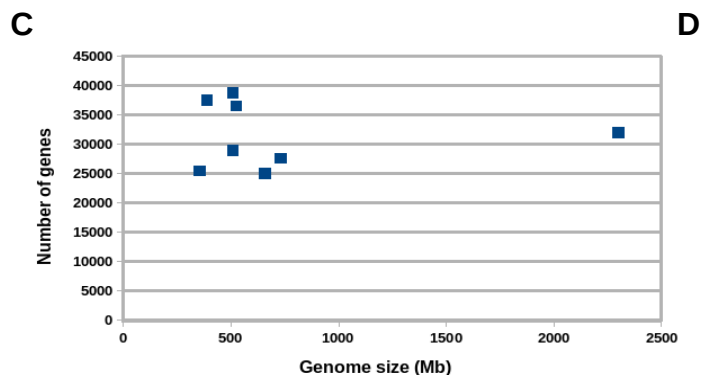
Interestingly our annual crops such as wheat and corn tend to have     d     genomes. We pamper them with fertilizers and water, and eliminate     g     through weed control. Domesticated crops are     j     competitors outside of cultivation.

12. (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>.