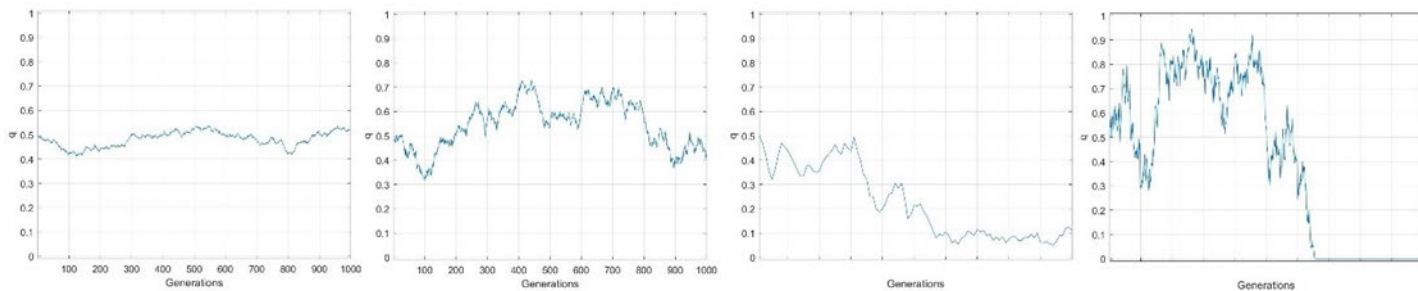


The final exam will include FIVE of the following, of which you must answer FOUR. [I may require an answer to one, and any THREE others]. The exam format will be identical to that of the midterm. The numbers & examples will change. You may bring half of an 8.5"x11" sheet as notes for the exam.

3. The graphs below are MATLAB simulations of **genetic drift** on $q = f(B)$ under different conditions.
- Which graph (**1st** or **2nd**) is likelier to have the **larger starting population**? Explain.
 - Which graph (**3rd** or **4th**) is likelier to have gone for the **longer number of generations**? Explain.
 - Which (if any) of the simulations is likely to lead to **loss** ($q=0$) or **fixation** ($q=1$) of $f(B)$? Explain.



1. The grey boxes below give genotype frequencies of **AA AB** and **BB** for four separate populations, with three sub-populations each. In all sub-populations, $N = 1,000$. For each, explain what the **value of F_{ST}** says about the **structure of the population**.

	AA	Aa	aa	Local F	F-stats
Sub-Pop 1	250	500	250	0.0000	F(is) = 0.0000
Sub-Pop 2	250	500	250	0.0000	F(st) = 0.0000
Sub-Pop 3	250	500	250	0.0000	F(it) = 0.0000
Sub-Pop 1	275	450	275	0.1000	F(is) = 0.1000
Sub-Pop 2	275	450	275	0.1000	F(st) = 0.0000
Sub-Pop 3	275	450	275	0.1000	F(it) = 0.1000
Sub-Pop 1	810	180	10	0.0000	F(is) = 0.5814
Sub-Pop 2	500	0	500	1.0000	F(st) = 0.4267
Sub-Pop 3	10	180	810	0.0000	F(it) = 0.7600
Sub-Pop 1	810	180	10	0.0000	F(is) = 0.0000
Sub-Pop 2	250	500	250	0.0000	F(st) = 0.4267
Sub-Pop 3	10	180	810	0.0000	F(it) = 0.4267
Luzon	118	132	50	0.0723	F(is) = 0.0916
Mindanao	110	157	33	-0.1205	F(st) = 0.0412
Palawan	222	48	30	0.4580	F(it) = 0.1290

2. From the following matrix of sequence differences among the mtDNA genomes of five species of Carnivora, calculate **by hand** a **UPGMA phenogram**. **Label** the pairwise differences at all nodes.

	<i>Felis</i>	<i>Spilogale</i>	<i>Ailuropoda</i>	<i>Helarctos</i>	<i>Ursus</i>
<i>Felis</i>	0				
<i>Spilogale</i>	412	0			
<i>Ailuropoda</i>	404	306	0		
<i>Helarctos</i>	402	304	242	0	
<i>Ursus</i>	406	308	244	130	0

3. A strategy to lower illegal poaching of Rhinoceros horns is to craft '*horns*' from horse hair glued together and shaped into a horn. The plan is to flood the market with fake '*horns*', so that the value of real horns falls. **The DNA data on the next page** are from horns of two rhinos and one horse. If *Tapirus* is the outgroup to the other three, (1) identify the number of **Phylogenetically Informative Sites** ' [http://www.mun.ca/biology/scarr/Bio4250 - Cladistic_dataset.html] favoring XY, XZ, or YZ as rhinos. (2) **Which of X, Y, or Z is the horse? Explain your decision.**
4. A population of Hangashores on Merasheen Island typically has a census count of **10,000**. Approximately **1,000** years ago, a fire reduced the population to **10** trees. Calculate the long-term **effective population size N_e** . (a) Show the **exact** calculation, leaving it in the numerical format. (b) Calculate an **approximate** numerical estimation.
5. For the **mutation model** [http://www.mun.ca/biology/scarr/4250_Mutation-Selection_equilibrium.html]
If the **mutation rate** for the recessive condition *Mulligan* is **2×10^{-5} / gamete**, and persons with *Mulligan* have a fitness **$W = 0.6$** , what is the **equilibrium frequency** of the allele for Mulliganism?
6. For the **migration model** described at [http://www.mun.ca/biology/scarr/4250_Migration-Selection_equilibrium.html]
If **$q = 1.0$** on the mainland, the **migration rate** from the mainland to the island **$m = 0.01$** , and the fitness of **BB** homozygotes on the island **$W = 0.8$** , calculate the **equilibrium frequency of q** on the island.
7. Based on the **Genetic Drift** lab at [http://www.mun.ca/biology/scarr/4250_Genetic_Drift.html] and the **MatLab** program, identify a set of conditions of **N** and **s_2** in which one or more populations go to **fixation ($q = 1$)** of an allele that is at a **selective disadvantage**. Draw the result. Explain how this happens.
8. At [http://www.mun.ca/biology/scarr/4250_F-statistics.html], two ways of calculating **F_{ST}** are shown, in terms of **F_{IT} & F_{IS}** or **H_T & H_S** . **Show** that the two calculations are equivalent.

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1 1111111112 2222222223 3333333334 4444444445 5555555556 ]
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#Tapirus ATGACTAACA TCCGAAAATC CCACCCACTA ATCAAAATCA TCAATCATTC ATTTATCGAC
#X .....A..... ..G..... T..... ..T..... .....C.. T.....T...
#Y ..... ..T..... .....T..... .....C.. ...C.....
#Z ..... ..T..... .....T..... .....C..C.. ...C.....T

[
[
1 1111111111 1111111111 ]
6666666667 7777777778 8888888889 9999999990 0000000001 1111111112 ]
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 ]
#Tapirus CTACCAGCCC CATCAAACAT CTCATCCTGA TGAAACTTTG GCTCACTCTT AGGAATCTGC
#X ..... .C..... T....A... .....C. ....C...C. ....
#Y .....CA... ..T...G.... ....T.... ....C..AC. ....
#Z ..G..CA... ..... ..G....G .....T.... ....C..GC. ....

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2222222223 3333333334 4444444445 5555555556 6666666667 7777777778 ]
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 ]
#Tapirus CTGATCCTAC AAATTATTAC AGGCCTATTT CTAGCTATAC ACTATACATC AGACACAAC
#X ..A.....C. ....CT.A.. .....C .....C.... ....C..... .....G..A
#Y ..A..... ..CC.A.. C..A..... ..T..C.... ..T..C...C. ...T....A
#Z T.A...T... .....C.A.. C..A.....C ..T..C.... ....C...C. ....TA

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1111111111 1111111112 2222222222 2222222222 2222222222 2222222222 ]
8888888889 9999999990 0000000001 1111111112 2222222223 3333333334 ]
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#Tapirus ACCGCTTTCT CATCTGTAAC CCACATTTGT CGAGATGTAA ATTACGGATG AATCATCCGC
#X ..T..C.... ....C..C.. T.....C..C .....C..T. .C..... ...T..T...
#Y ..T..C.... .....TG. ....C... ....C.... .C.....C.. ...T.....
#Z ..T..C.... .....CG. ...T..C... ....C..G. ....C... ..T.....

[
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2222222222 2222222222 2222222222 2222222222 2222222222 2222222223 ]
4444444445 5555555556 6666666667 7777777778 8888888889 9999999990 ]
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 ]
#Tapirus TACCTTCACG CCAACGGAGC ATCCATATTT TTTATCTGCC TGTTTATTCA CGTAGGACGA
#X .....C..T. .... ..A..... .....C..C..... .....C
#Y .....A.... .T..... .....C .....A..C..C.. TA.....C
#Z ..T..C..T. .... .....C .....A..C..C.. .....C

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3333333333 3333333333 3333333333 3333333333 3333333333 3333333333 ]
0000000001 1111111112 2222222223 3333333334 4444444445 5555555556 ]
1234567890 1234567890 1234567890 1234567890 1234567890 1234567890 ]
#Tapirus GGCCTATATT ATGGATCCTA CACATTCCTA GAAACATGAA ATATTGGAAT CATCCTACTA
#X .....C..C. .C..C..T.. ..... ..G..... .C..... .....T
#Y .....C.... .C..... ...C..... ....C.... .C..C...G. T.....
#Z ..TA.C.... .C....A.. T..C..... ....C.... .C..C...G. T...T....

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