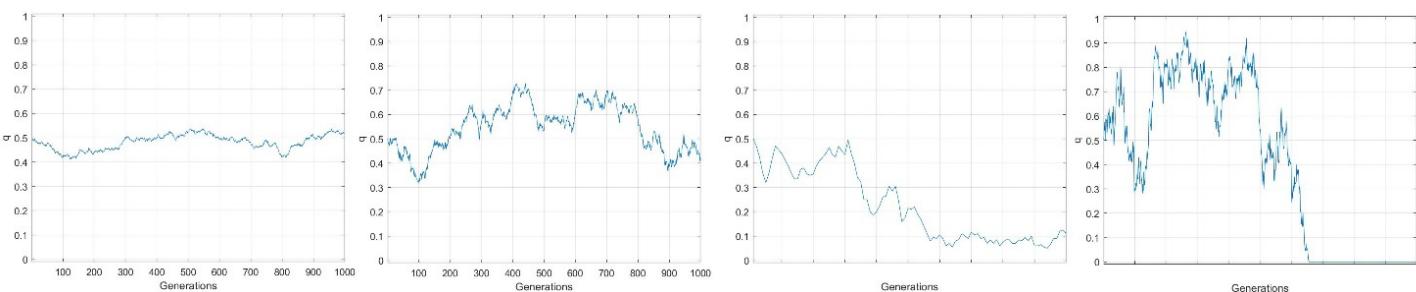


Of the **FIVE** questions on the three pages following, answer any **FOUR**. You are encouraged to use the **Excel** spreadsheet programs: you can cut and paste images into a **Word** or **PDF** program. Show your work. Submit answers in **Word** or **PDF** format.

3. The four graphs below are MATLAB simulations of **genetic drift** 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.



4. **BONUS:** Do this question AFTER any four others.

Consider a population that undergoes a severe population reduction from **10,000** individuals to **100** individuals once every **100** generations. Estimate the **effective population size Ne** over the 100 generations of this period.

5. The three grey boxes below represent three separate populations, with three sub-populations each. In each case, “**local F**” is the inbreeding coefficient calculated for each sub-population. For each problem, explain what the value of **FST** says about the structure of the population.

Use the Excel spreadsheet. The last problem is new.

	MM	MN	NN
Sub-Pop 1	10	180	810
Sub-Pop 2	40	320	640
Sub-Pop 3	90	420	490

	MM	MN	NN
Sub-Pop 1	819	162	19
Sub-Pop 2	656	288	56
Sub-Pop 3	10	180	810

	MM	MN	NN
Sub-Pop 1	250	500	250
Sub-Pop 2	300	400	300
Sub-Pop 3	360	480	160

	MM	MN	NN
Camarines Sur	20	67	13
Palawan	39	46	15
Butuan	74	16	10

	Local F	F-stats	
	0.0000	F(is) =	0.0000
	0.0000	F(st) =	0.0417
	0.0000	F(it) =	0.0417

	Local F	F-stats	
	0.1000	F(is) =	0.0735
	0.1000	F(st) =	0.5278
	0.0000	F(it) =	0.5625

	Local F	F-stats	
	0.0000	F(is) =	0.0676
	0.2000	F(st) =	0.0089
	0.0000	F(it) =	0.0759

	Local F	F-stats	
	-0.3466	F(is) =	-0.0206
	0.0238	F(st) =	0.0635
	0.4580	F(it) =	0.0441

7. Identify AND COUNT all Phylogenetically Informative Sites for species W, X, Y, & Z.

Which is most closely related to W? Explain your reasoning.

9. For the **mutation model** at

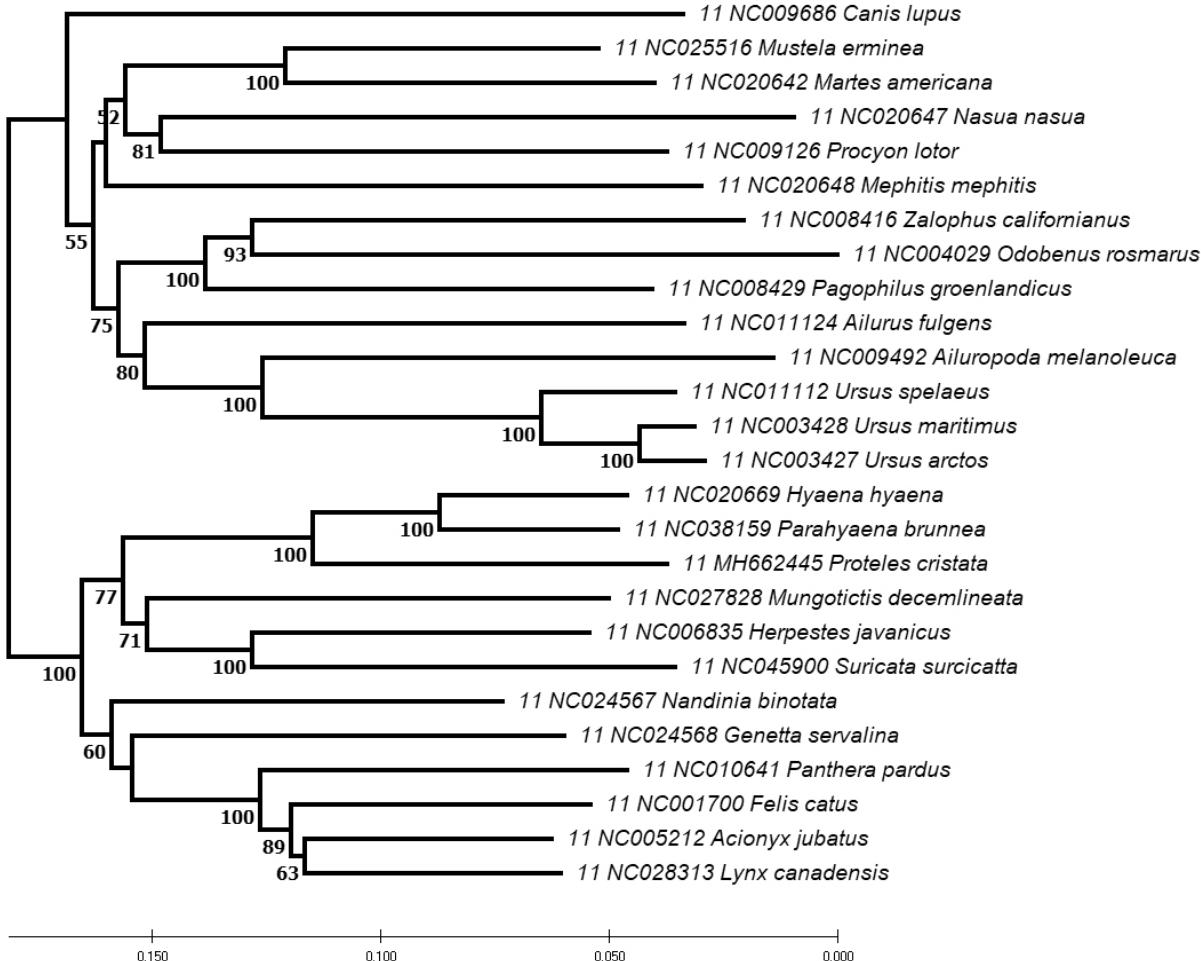
[https://www.mun.ca/biology/scarr/4250_Mutation-Selection_equilibrium.html]

If the **mutation rate** for the recessive condition Trumphair is 2×10^{-5} / gamete, and persons with Trump Hair have a fitness **W = 0.6**, what is the **equilibrium frequency** of the allele for Trump hair?

For the **migration model** described at

[https://www.mun.ca/biology/scarr/4250_Migration-Selection_equilibrium_2020.html]

If $q = 1.0$ on the mainland, the migration rate from the mainland to the island is $m = 0.1$, and the fitness of BB homozygotes on the island is $W = 0.8$, calculate the **equilibrium frequency of q** on the island.



12. The phylogenetic tree above is based on a **Neighbor-Joining Analysis** in MEGA of 3,000 bp of two mitochondrial DNA genes. Numbers in **BOLD** below each node indicate the **percent bootstrap support** from 3,000 bootstrap replications. Bootstrap values < 50% are not shown.

The network has been rooted to separate the dog-like **Caniformia** species (above) from the cat-like **Feliformia** species (below). Species arrangements within each suborder are unmodified from the MEGA output.

QUESTIONS: The tree allows molecular inferences about relationships among Carnivore families. **Use the information in the tree**, rather than any external sources.

a. According to the tree, which of the following **families** as recognized by conventional morphology-based taxonomy are **monophyletic** OR **paraphyletic**? Explain your reasoning as supported by the tree.

- Felidae*
- Mustelidae*
- Hyaenidae*
- Viverridae*

b. Is the **Giant Panda** more closely related to **Ursidae** or to the **Lesser Panda**?

Explain your reasoning as supported by the tree.

c. Are the marine mammals (**Pinnipedia**) **monophyletic** or **polyphyletic**?

Explain your reasoning as supported by the tree.