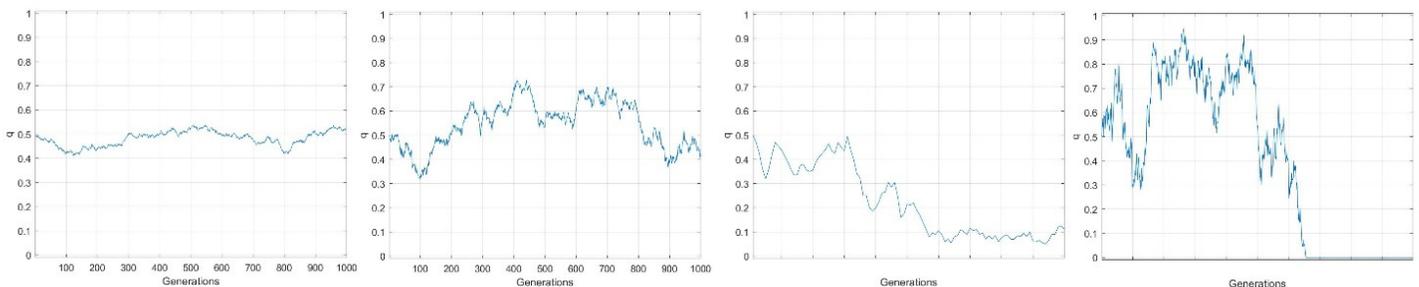


Of the **FIVE** questions on the three pages following, answer any **FOUR**. You are encouraged to use the **Excel** spreadsheet programs: you can cut and paste images into a **Word** or **PDF** program. Show your work. Submit answers in **Word** or **PDF** format.

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.



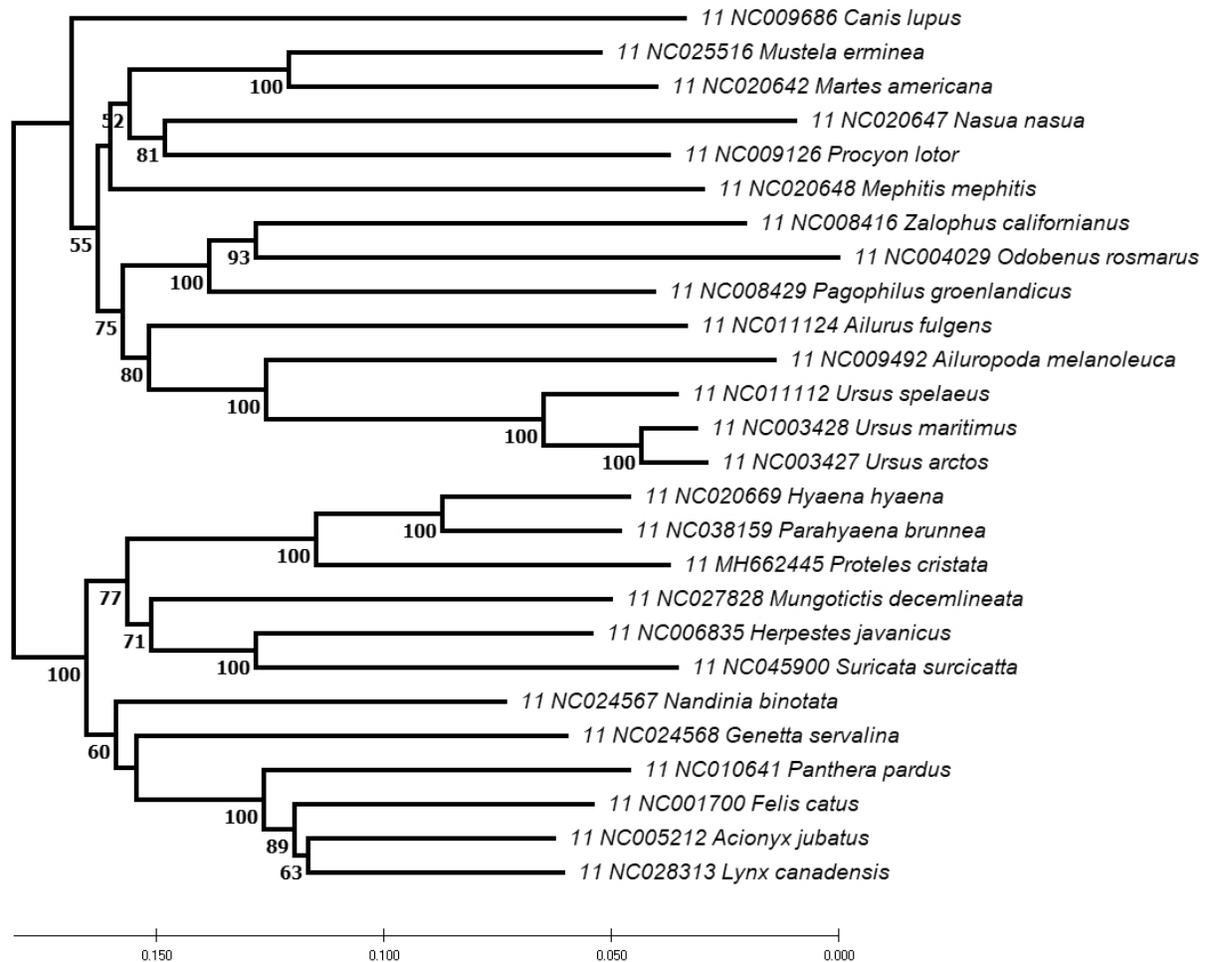
4. **BONUS:** Do this question **AFTER** any four others.

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 N_e** 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 **F_{ST}** says about the structure of the population.

Use the Excel spreadsheet. The last problem is new.

	MM	MN	NN	Local F	F-stats
Sub-Pop 1	10	180	810	0.0000	F(is) = 0.0000
Sub-Pop 2	40	320	640	0.0000	F(st) = 0.0417
Sub-Pop 3	90	420	490	0.0000	F(it) = 0.0417
Sub-Pop 1	819	162	19	0.1000	F(is) = 0.0735
Sub-Pop 2	656	288	56	0.1000	F(st) = 0.5278
Sub-Pop 3	10	180	810	0.0000	F(it) = 0.5625
Sub-Pop 1	250	500	250	0.0000	F(is) = 0.0676
Sub-Pop 2	300	400	300	0.2000	F(st) = 0.0089
Sub-Pop 3	360	480	160	0.0000	F(it) = 0.0759
Camarines Sur	20	67	13	-0.3466	F(is) = -0.0206
Palawan	39	46	15	0.0238	F(st) = 0.0635
Butuan	74	16	10	0.4580	F(it) = 0.0441



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.

- a. Felidae
- b. Mustelidae
- c. Hyaenidae
- d. 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.