**Case Study 1 Questions**

Name:

1. What mitochondrial markers could be helpful to determine whose who? Why?

2. Which mitochondrial genome did you select (A, B or C)?

3. a. What type of files did this job produce (annotate.sh)?

b. What directory are they stored in?

4. What type of file did this job produce (blast\_nt.sh)?

5. a. Based on the BLAST report, what is the closest organism that your sequence matched in the nt database?

b. What is the Max Score of the top hit?

c. What is Query Coverage of the top hit?

d. What is the Percent Identity of the top hit?

e. What is the E-value? Is this considered a good E-value?

6. Try another mitochondrial gene. Do the results converge on the same top hit? If not, why do you think this could happen?

7. Which marker are you more confident for your taxonomic assignment? Why?

8. Does it appear that the mitochondrial genome of this specimen is present in the nt database?

9. List 3 pros and 3 cons of using mitochondrial markers in the space below. For each, put a literature reference to support your point.

Pro 1:

Pro 2:

Pro 3:

Con 1:

Con 2:

Con 3:

10. How does the sampled assembled mitogenome you produced compare to the assembly from all reads?

11. How does it compare to the reference mitogenome? What are the number of variants (mutations)?

12. What species is the reference mitogenome? What is the lowest taxonomic group (Phylum, Class, Order, Family, Genus, Species) that your specimen and the reference specimen share?