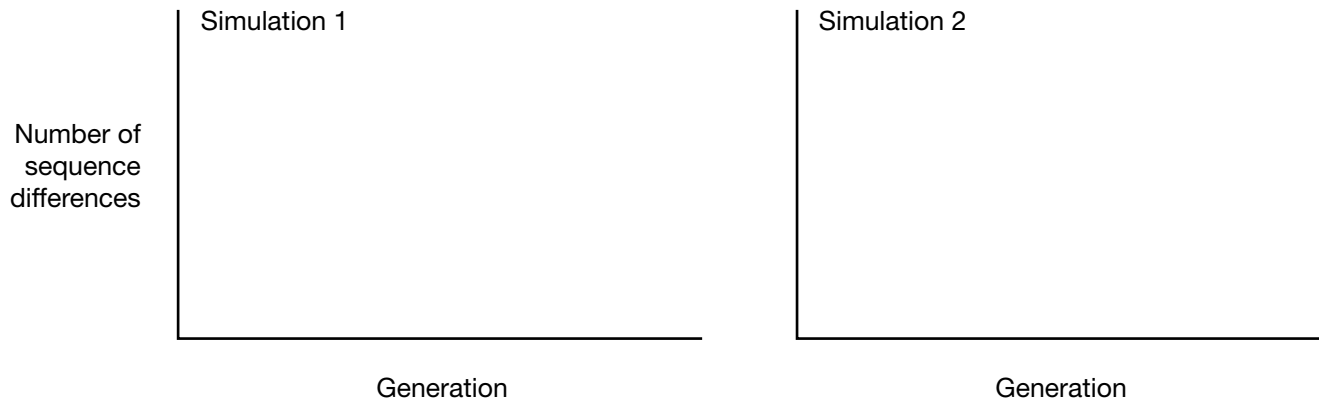# Did the surgeon give hepatitis C to his patient?

Evolution by genetic drift

1. Copy the graphs from your Drift simulations onto the axes below:

Simulation 1

Simulation 2

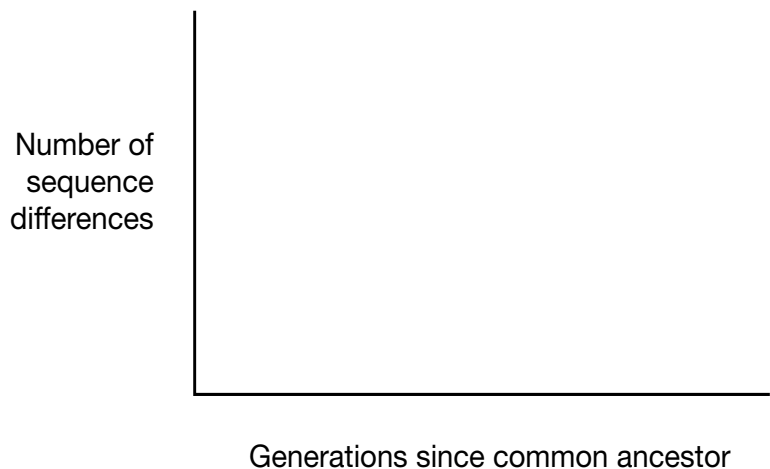Number of
sequence
differences

Generation

Generation

2. What generalizations can you make about how populations evolve under genetic drift? Why might an evolutionary biologist think of your graphs as molecular clocks?

Population divergence by genetic drift

3. Record your data on the divergence between a pair of populations in the table. Plot your data on the graph:

Generations since second pop'n was established	# of sequence diffs between randomly chosen virions
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____
_____	_____

Number of
sequence
differences

Generations since common ancestor

4. If you had nucleotide sequences from virus particles from two infected hosts, could you estimate how long it has been since the virus populations in the hosts shared a common ancestor? Explain.

Reconstructing evolutionary trees

5. Use the tables and spaces below to reconstruct the evolutionary tree you have produced with the Tree simulation. Use the tables to record pairwise differences between sequences sampled from the different virus populations, and use the spaces on the right to draw your trees.

A)

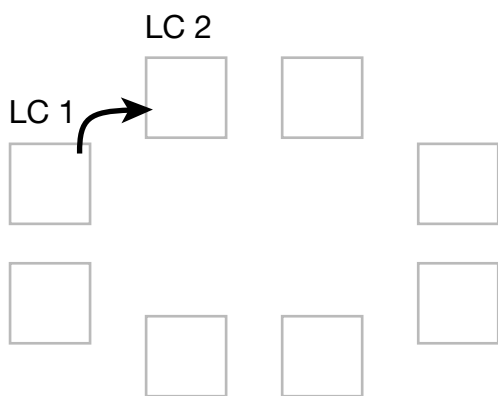B) Tree:

C)

D) Tree:

E)

F) Tree:

Blank space for calculations:

3

6. How well did UPGMA do? Draw your true tree and your reconstructed tree below. Note any differences.

7. Compare your results with those of your classmates. Are there some kinds of trees UPGMA seems to work best with? Some kinds that UPGMA seems to work poorly with? Explain.

Using UPGMA to determine whether the surgeon gave hepatitis C to his patient

8. Use the diagram at left to record the history of infections in the Archipelago simulation. Each time you establish a new population, use an arrow to record the source population, and note the generation in which you made the transfer. Use the diagram at right to record the true evolutionary tree. The first transmission of HVC has been marked for you.

LC 2

LC 1

LC 1   LC 2
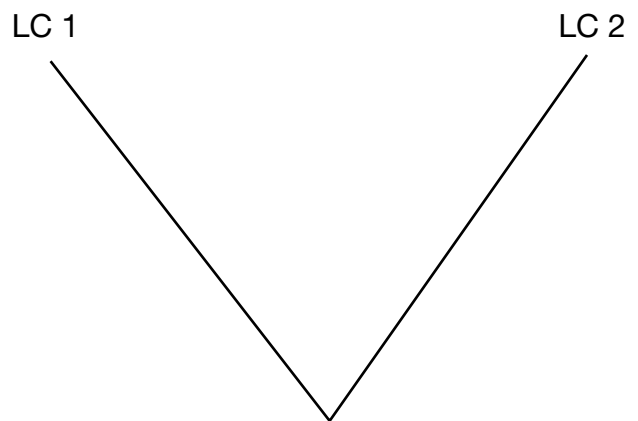
9. Use the tables and spaces below for a UPGMA reconstruction of the evolutionary history of virion populations.

A)

B) Tree:

C)

D) Tree:

E)

F) Tree:

10. How well did UPGMA do? Did the tree you reconstructed accurately reflect the origin of the patient's infection?

11. Look at the phylogeny for the real surgeon and patient in Figure 9 of the manual for this tutorial. Did the surgeon accidently infect the patient with hepatitis C? How do you know?