Name: ....

Question:	1	2	3	4	5	6	7	8	9	10	Total
Points:	10	10	10	10	10	10	10	10	10	10	100
Score:											

10   1. An $n \times n$ distance matrix D for a phylogenetic tree with n leaves is ultrametric if for every three leaves i, j, k, of the three distances $D[i,j]$, $D[i,k]$, $D[j,k]$,

○ the two smallest are equal   ○ the two smallest are different   ○ the two largest are equal   ○ the two largest are different   ○ the sum of the two smallest is equal to the largest

10   2. An $n \times n$ distance matrix D for a phylogenetic tree with n leaves is additive if for every four leaves i, j, k, ℓ, of the three sums of distances $D[i,j] + D[k,\ell]$, $D[i,k] + D[j,\ell]$, $D[i,\ell] + D[j,k]$,

○ the two smallest are equal   ○ the two smallest are different   ○ the two largest are equal   ○ the two largest are different   ○ the sum of the two smallest is equal to the largest

10   3. Given an $n \times n$ distance matrix D, the unique phylogenetic tree T with n leaves that fits the data, if D is ultrametric, can be reconstructed in ... time using the UPGMA algorithm.

○ $O(n)$ ○ $O(n^2)$ ○ $O(n^3)$ ○ $O(n^4)$ ○ $O(n^5)$

10   4. Given an $n \times n$ distance matrix D, the unique phylogenetic tree T with n leaves that fits the data, if D is additive, can be reconstructed in ... time using the NJ algorithm.

○ $O(n)$ ○ $O(n^2)$ ○ $O(n^3)$ ○ $O(n^4)$ ○ $O(n^5)$

10   5. Given an $n \times m$ genomic matrix M, the unique phylogenetic tree T with n leaves that fits the data, if it exists, can be reconstructed in ... time using the algorithm of Dan Gusfield (1991).

○ $O(n)$ ○ $O(m)$ ○ $O(n+m)$ ○ $O(nm)$ ○ None of the above.

10   6. What does KPCOFGS mean? Explain your answer.

10   7. What are the potential sources of bias in the taxonomic classification of sequence reads from a metagenomic sample?

10   8. Is the taxonomic assignment of sequence reads in a metagenomic sample coming from unknown sequences possible? Explain your answer.

10   9. What is the best indicator of classification error for the taxonomic annotation of sequence reads? Explain your answer.

10   10. In the taxonomic assignment of sequence reads, what does it mean for a node in the reference taxonomy to be relevant?