Homework #2

1. Fill out the three worksheets that follow:
   ‣ using a step-matrix in which each transition (A↔G, C↔T) costs 1 step and each transversion (A↔C, A↔T, G↔C, G↔T) costs 2 steps
   ‣ using the following data from one DNA site:
     taxon 1 = A; taxon 2 = A; taxon 3 = C; taxon 4 = T

2. On each of the three worksheets:
   ‣ fill in all circles with either observed or ancestral states (there are 16 possible combinations of ancestral states, hence the 16 trees)
   ‣ use 0, 1 or 2 tick marks on each edge to show number of steps
   ‣ indicate the number of steps below each of the 16 trees
   ‣ indicate all most-parsimonious ancestral state reconstructions by circling the trees requiring the minimum number of steps

3. Indicate which of the three possible tree topologies is most parsimonious