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**

      • 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 empty circles with 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**