1. Examine the tree below. Is population A an ancestor of population C? (1 point)

Population A is not the ancestor of population C. All of the populations at the tips of the branches are contemporary, existing at the same time. They share a common ancestor but none of these extant populations is an ancestor of another. None of these populations is a descendant of another.

2. Using the tree pictured in question 1, can we tell the order of peak colonization from the phylogenetic tree? Can we tell the order of colonization events (assuming populations split at colonization)? (2 points)

We can not tell which the order that the peaks were colonized. We only know the order that the splits happened. So we can tell the order that the colonizations occurred, but we cant tell which population was the source population and which population is new.

3. Draw circles around all of the monophyletic groups or clades. (2 points)
4. How is maximum parsimony used to choose between two phylogenetic trees? (1pt)

The principle of maximum parsimony states that the simplest tree is the best tree. We consider the tree with the fewest character changes to be the simplest tree. Using maximum parsimony, we pick the tree with the fewest character changes as the best representation of the evolutionary history of the group of taxa that we are looking at.

5. Consider 4 populations of flowers with the following traits (4 points):

   (a) red flowers, 5 petals, tall stems
   (b) red flowers, 5 petals, short stems
   (c) red flowers, 4 petals, short stems
   (d) blue flowers, 4 petals, short stems

Draw a rooted phylogenic tree for these populations and label the character changes on the branches.

Above is an example of one way that you could have drawn the tree for these taxa. You did not need to have drawn the most parsimonious tree. You needed to draw a tree that had a root, shown at the top of the tree. You also needed to have all of the taxa at the tips of the branches. You also needed to label the character changes. You could have done this in a few ways, but you should not have labeled the same trait change on two sister branches of the tree. You also should have picked one of the traits to be ancestral and you should not have labeled both versions of the trait changing on sister branches.