Beta Diversity

- Beta diversity measures the diversity *between* samples.

- The distance between each pair of samples (with respect to community composition) is calculated.

- Read depth is important here also, so rarefaction is performed

- There are many ways to calculate beta diversity; we will use one: UniFrac

Beta Diversity: UniFrac

1. Make a phylogenetic tree including all sequences
2. Label each terminal node with sample (Red, Yellow, Blue).
3. Branches that lead to sequences from more than one sample are shared (grey)
4. Distance = unique branch length / total branch length

Red vs Yellow   Red vs Blue   Yellow vs Blue
                  shared=Grey