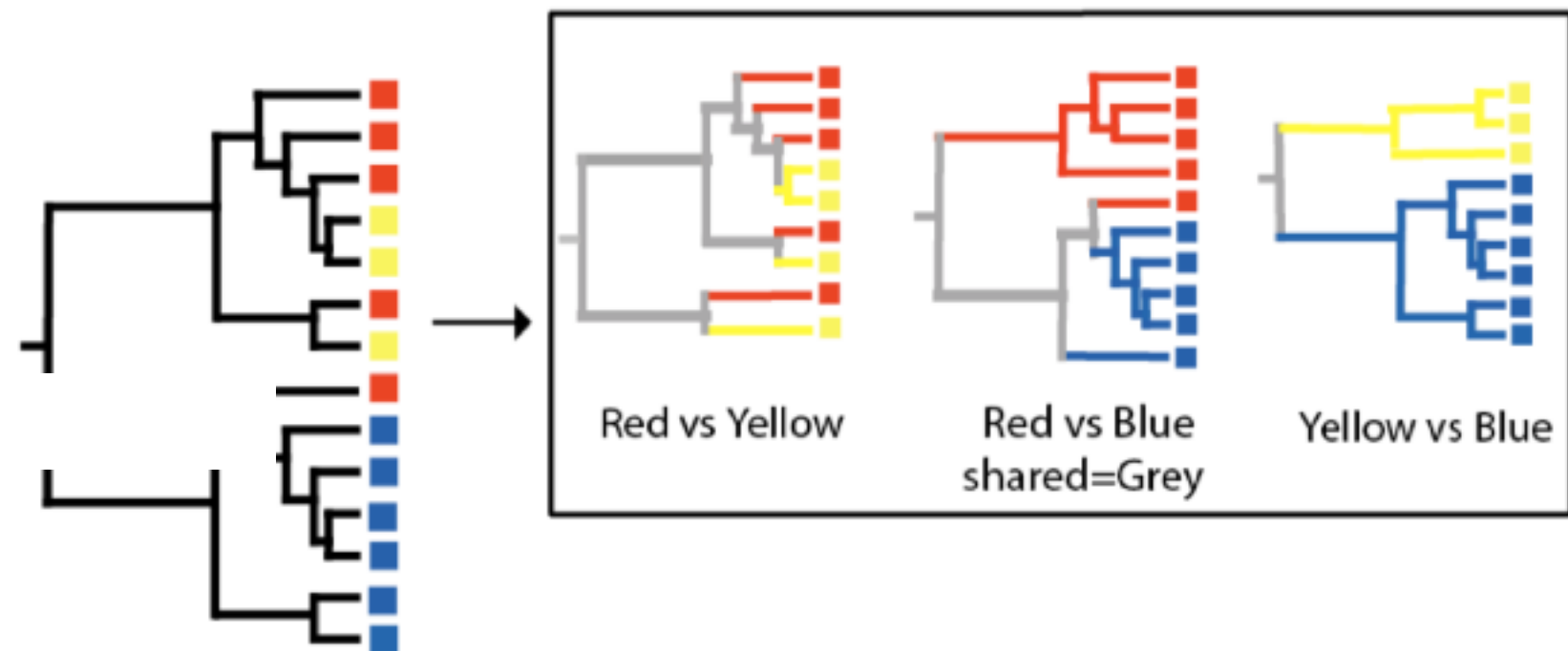


Beta Diversity: UniFrac

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



Beta Diversity: UniFrac

- Can be weighted by branch length
- Can be unweighted (sum number of branches)

