**Homework 6**

1. When we use the molecular data to build the phylogeny tree, we often assume that nucleotide changes should accumulate in some constant proportion to time, where the constant of proportionality may differ in different lineages. In reality, what factors could make this hypothesis not true?
2. We have talked about methods for phylogeny estimation. Discuss how we could measure the accuracy of the estimated phylogeny. What approaches would you take to assess the utility of different methods or algorithms?
3. In class, we discussed two different greedy sequential tree construction method, one with O(n^3) and another with O(n^2) complexity where n is the number of leaves. Suggest another possible greedy tree construction method with polynomial time complexity. Give the time complexity for your approach. Analyze pros and cons with respect to the two O(n^3) and O(n^2) algorithms discussed in class.