Reading guide for Maximum Likelihood Estimation (MLE) and Model Section
Nov 12, 2015

Page and Holmes:

- Read Section 6.5 on maximum likelihood estimation (pp. 193 – 201), but skip the section on rate variation (pp. 198, 199) which is out of date.
- Read Section 5.2 on genetic distance (pp. 144-162), keeping the following in mind:
    - In class, we introduced sequence evolution models in the context of the maximum likelihood method. In Page and Homes, sequence evolution models are introduced in the context of estimating pairwise distances between taxa, which we will discuss in the upcoming lectures. The underlying models are the same although they are applied differently in the distance-based and MLE methods.
    - The section on "Models of sequence evolution" covers the DNA substitution models we discussed in class, using a matrix representation. You should understand the characteristics of each of the models. You are not responsible for the formal matrix representation used in Page and Holmes. Pay particular attention to figures 5.14 and 5.15.
    - Skip Box 5.2 on LogDet distances.
- Kosiol, C., Bofkin, L., & Whelan, S. (2006). Phylogenetics by likelihood: evolutionary modeling as a tool for understanding the genome. *Journal of biomedical informatics*, *39*(1), 51-61.
    - Read Sections 1-3 for an overview of phylogeny reconstruction by MLE.
    - Section 4 explains the Akaike and Bayesian Information Criteria. The last paragraph deals with other types of statistical testing that will be covered later in the course when we discuss quality control.
    - Sections 5.3 and 5.4 deal with rate heterogeneity and adaptive evolution. Read these sections to understand the problems that arise when working with heterogeneous evolutionary processes. You are not required to understand the details of specific models not covered in class.