

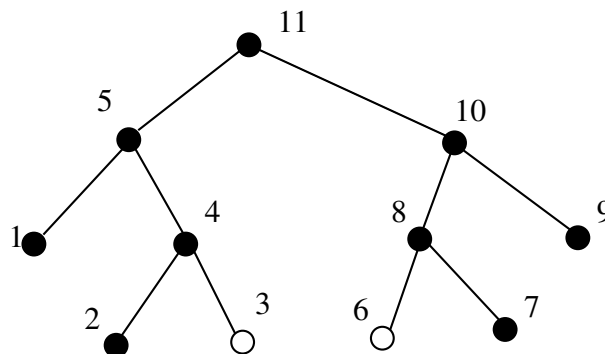
23. January 2013

Exercise 1: Simulate sequence datasets for various trees and various substitution models. Explore which models are preferred for these datasets by jmodeltest and by the Bayes-factor analysis in MrBayes. How does the accuracy of phylogeny reconstruction depend on which of the proposed models is used?

Exercise 2: Compute the transition probabilities between the states \bar{B} , \bar{B} and $\frac{B}{B}$ for the simplified TKF92 model (with $\lambda = \mu$ and fragments of geometrically distributed length).

Exercise 3: Simulate data with the program indelible to analyze the accuracy of phylogenies and alignments estimated by BAli-Phy compared to the standard approach with separate steps for the alignment and the phylogeny estimation.

Exercise 4: The black filled circles in the following tree are the active nodes, and the numbers show the priority order.



Let a branch length t_i for each branch i be given. Assume the simplified TKF91 model (with $\lambda = \mu$, only single positions are inserted or deleted at a time).

- Compute the probability that the next “tihl” places a B to node 10.
- If this happens, how probable is it then that this tihl has an N at nodes 6 and 8, an E at node 7, and a H at node 9?
- Which nodes are then active in the next step?