Exercises – Phylogenetics

Universität Bielefeld, SS 2019
Dr. Roland Wittler, M. Sc. Tizian Schulz
https://gi.cebitec.uni-bielefeld.de/Teaching/2019summer/Phylogenetik

Exercise Sheet 10 — 27.06.2019

Due: 04.07.2019

Task 1 Modeling Amino Acid Replacements. **(4 points)**
Assume the alphabet of amino acids $\mathcal{A} = \{A, D, R\}$. Consider the following alignment of sequences A and B:

$$A = \texttt{R D A A A D R A R R D D R A R D R D R D}$$
$$B = \texttt{R D A R A A A D D D A A D R A A A D D A}$$

(a) Write down the values for all $m_{i,j}$, all f_i and N. Use them to calculate the transition matrix P.

(b) Obviously (without computing it), P is not calibrated to 1 PAM. Why?

(c) Calculate the score matrix S using P and $\pi_i = f_i$. If you do not have any results from (a) use

$$P = \begin{pmatrix} \frac{4}{15} & \frac{2}{5} & \frac{1}{3} \\ \frac{3}{7} & \frac{2}{7} & \frac{2}{7} \\ \frac{5}{11} & \frac{4}{11} & \frac{2}{11} \end{pmatrix} \text{ and } \pi = \left(\frac{3}{8}, \frac{7}{20}, \frac{11}{40}\right).$$

Task 2 Maximum Likelihood Estimation of Evolutionary Distances. **(4 points)**
Assume the evolution of the sequences A and B from Task 1 follows an EMP with the following transition matrix:

$$P = \begin{pmatrix} 1 - \frac{4}{6}t & \frac{1}{6}t & \frac{1}{6}t \\ \frac{1}{6}t & 1 - \frac{4}{6}t & \frac{1}{6}t \\ \frac{1}{6}t & \frac{1}{6}t & 1 - \frac{4}{6}t \end{pmatrix}$$

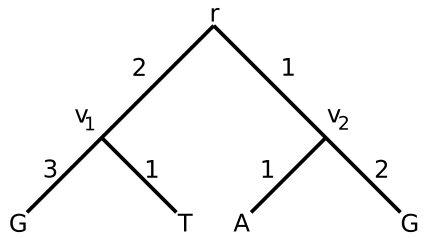
Determine the time t such as to maximize the likelihood $Pr(A, B \mid t)$.

Task 3 Computing the Likelihood of a Given Tree. **(4 points)**
Consider the given transition probability matrix $P(t)$ and the given tree T. Compute the *likelihood* of T.

$$P(t) = \begin{pmatrix} 1 - 3a_t & a_t & a_t & a_t \\ a_t & 1 - 3a_t & a_t & a_t \\ a_t & a_t & 1 - 3a_t & a_t \\ a_t & a_t & a_t & 1 - 3a_t \end{pmatrix}$$

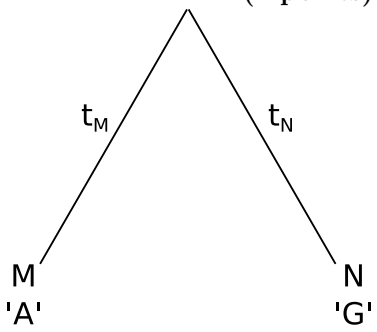
where

$$a_t = \frac{1 - exp(-4t/30)}{4}$$



Task 4 Pulley Principle. **(4 points)**

The *Pulley Principle* from Joseph Felsenstein says that the likelihood for a phylogenetic tree is independent of the location of the root node.
Consider the simplified scenario of an alphabet $\{A, G\}$ and the given tree.
Show that the likelihood for that tree is independent of the exact location of the root node, i.e., it is only dependent on the **sum** of the lengths: $t_M + t_N$. Proceed as follows:



(a) Write down the likelihood in dependence of t_M and t_N. (Example: formular on top of page 82 in the lecture notes.)

(b) Use the assumption that the process of evolution is *reversible* to write the likelihood in a way such that it only contains one π_i (e.g. π_G).

(c) Since P is a stochastic matrix, we can use the *Chapman-Kolmogorov Equation*: $P(t_M + t_N) = P(t_M)P(t_N)$. You can simplify the likelihood with one of the four entries of $P(t_M + t_N)$ such that it is only dependent on the sum $t_M + t_N$.