



## Grundlagen der Bioinformatik

SoSe 2018

### Assignment 06

Submit electronically in Ilias by 4.6.2018, 10h

In this assignment, the goal is to compare the result of the Fitch and Margoliash 1967 method for building a tree with UPGMA and Neighbor joining and to report on the topological differences of the resulting trees. The paper is available as a PDF on Ilias.

#### 1 Distances (3 points)

In their 1967 paper, Fitch and Margoliash present a distance matrix for 20 different species, based on the cytochrome C gene. Extract the distance matrix from the paper (use copy and paste, and some hand editing). (PDF is downloadable from Ilias).

Determine a suitable file format for a phylogenetic distance matrix and format the distances accordingly. Give a brief description of the file format used (name and associated program or programs).

#### 2 UPGMA tree (3 points)

Compute a UPGMA tree from your distances matrix. Compare the topology of the tree shown in Figure (2) of the paper with your topology. List all clades in which the two trees differ.

Report which program or website you used for computing the tree.

#### 3 Rooted Neighbor Joining tree (4 points)

Compute a Neighbor Joining tree from your distances matrix.

Root the tree using the tree fungal species as "outgroup".

Compare the topology of the tree shown in Figure (2) of the paper with your topology. List all clades in which the two trees differ.

Report which program or website you used for computing the tree and how you performing the rooting.