

Algorithms for the computation of phylogenetic trees

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Exercises, sheet 9 (January 17, 2006)
due by January 24, 2006

Exercise 1 (Neighbor Joining) [4 points]

Given the following distance matrix

	<i>a</i>	<i>b</i>	<i>c</i>	<i>d</i>	<i>e</i>
<i>a</i>	0	6	8	9	9
<i>b</i>		0	5	8	10
<i>c</i>			0	4	8
<i>d</i>				0	7
<i>e</i>					0

Apply the Neighbor Joining algorithm to reconstruct a phylogenetic tree. Devise the matrices of intermediate steps.

Exercise 2 (SplitsTree) [2 points]

SplitsTree uses the split decomposition method to analyze and visualize distance data. The original homepage of SplitsTree is located at <http://www.splitstree.org>. You may download SplitsTree4 for different platforms from this page. (SplitsTree is also installed at MPI. Note, that this already installed version requires input distance matrices in (peculiar) *Nexus* format, check the manual).

There is also an online version of SplitsTree available at <http://bibiserv.techfak.uni-bielefeld.de/splits/>. The online version runs into trouble for large distance matrices, but it does the job for the exercises of this sheet.

Apply SplitsTree and construct the SplitsTree graph for the distance matrix in Exercise 1. Compare the result to the Neighbor Joining tree.

Exercise 3 (SplitsTree on hominid data set) [2 points]

Analyse the alignment of 5 mitochondrial ATPases in hominids. The alignment is available from the lectures' website at

http://lectures.molgen.mpg.de/phylogeny_ws05/hominidmtdna.phy

Obtain a distance matrix by means of PHYLIP's program *dnadist* and apply SplitsTree to this distance matrix. Compare the result to the distance based reconstruction in conjunction with the bootstrap analysis of Exercise 4, sheet 8.