

FYS 102: Bioinformatics
Homework 8
Due Friday, December 7
(Start now!)

Use the UPGMA algorithm to construct a phylogenetic tree based on the following distance matrix D .¹

	dog	bear	raccoon	weasel	seal	sea lion	cat	monkey
dog	0	32	48	51	50	48	98	148
bear	32	0	26	34	29	33	84	136
raccoon	48	26	0	42	44	44	92	152
weasel	51	34	42	0	44	38	86	142
seal	50	29	44	44	0	24	89	142
sea lion	48	33	44	38	24	0	90	142
cat	98	84	92	86	89	90	0	148
monkey	148	136	152	142	142	142	148	0

Start early and have fun!

¹This matrix is based on a research comparison of the albumins (blood proteins) in various species. This work was conducted by Vincent Sarich and published in 1969. The table was taken from the book *Inferring Phylogenies* by Joseph Felsenstein.