

BIM (M1) – AAGB (TD2)

Building a phylogenetic tree from a distance matrix (UPGMA¹ & NJ²)

1 UPGMA

1. What does UPGMA mean?
2. Explain it briefly.
3. Give some pros/cons of this method.
4. Give the formula that gives the distance D_{ij} between two clusters.
5. From which kind of data can one create a distance matrix?
6. Give the UPGMA algorithm. What is its complexity?
7. From this distance matrix, build the phylogenetic tree using UPGMA :

	A	B	C	D	E	F	G
A							
B	19						
C	27	31					
D	8	18	26				
E	33	36	41	31			
F	18	1	32	17	35		
G	13	13	29	14	28	12	

2 Neighbo(u)r Joigning

1. What is the improvement that NJ gives over UPGMA?
2. Explain the general principle of the algorithm.
3. Give the NJ algorithm (initialization, recursion et ending). What is the complexity?
4. From this distance matrix, build the phylogenetic tree using NJ :

	A	B	C	D	E	F
A		2	4	6	6	8
B	2		4	6	6	8
C	4	4		6	6	8
D	6	6	6		4	8
E	6	6	6	4		8
F	8	8	8	8	8	

1. Sokal R and Michener C (1958). "A statistical method for evaluating systematic relationships". University of Kansas Science Bulletin 38 : 1409–1438

2. N. Saitou and M. Nei. The neighbor-joining method : a new method for reconstructing phylogenetic trees. Molecular Biology and Evolution, 4 :406–425, 1987

3 Additive Phylogeny

1. What is a degenerate triplet ?
2. What is an additive matrix ? How can we check whether a matrix is additive ?
3. From this distance matrix, build the phylogenetic tree using Additive Phylogeny :

	A	B	C	D	E
A		11	10	9	15
B	11		3	12	18
C	10	3		11	17
D	9	12	11		8
E	15	18	17	8	