

# Exercises – Phylogenetics

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<http://wiki.techfak.uni-bielefeld.de/gi/Teaching/2015winter/Phylogenetik>

## Exercise List 10 — 12.01.2016

Due to: 19.01.2016

### Exercise 1 Programming exercise: Splitstree.

(4 Points)

Implement a function that calculates the “isolation index” for the *split decomposition*: For two given sets  $J$  and  $K$  calculate  $\alpha_{J,K}(d)$  w.r.t a matrix  $d$ :

$$\alpha_{J,K}(d) = \frac{1}{2} \min_{\substack{i,j \in J \\ k,l \in K}} (\max\{d_{ij} + d_{kl}, d_{ik} + d_{jl}, d_{il} + d_{jk}\} - d_{ij} - d_{kl})$$

Send a version of your program to your TA<sup>1</sup> and describe how to use the program. Make it as easy as possible to calculate all the  $\alpha$  in task 3. You’ll find another matrix and some solutions on the back of this sheet if you want to test your implementation.

### Exercise 2 Calculation of $d$ -Splits.

(4 Points)

Look at the algorithm that calculates  $d$ -Splits (lecture notes, page 62).

- Explain: If a split  $J, K$  is extended by one taxon ( $J', K$ , where  $J' := J \cup \{i\}$ ),  $\alpha_{J',K}$  does not have to be recalculated completely to decide whether  $J', K$  is a valid split ( $\alpha_{J',K} \neq 0$ ). A complete recalculation would take  $\mathcal{O}(n^4)$ . Without the recalculation it is possible to do in  $\mathcal{O}(n^3)$ . How?
- Explain the running time of  $\mathcal{O}(n^6)$ .  
 Hint: There are  $\binom{n}{2}$  splits for  $n$  taxa maximally (you don’t need to show this.)

### Exercise 3 Splitstree.

(3 Points)

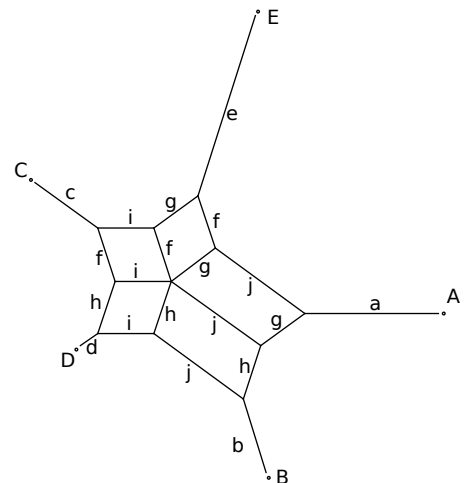
Consider the following distance matrix and the corresponding splitstree:

	A	B	C	D	E
A :	0	9	13	12	13
B :		0	12	7	15
C :			0	6	10
D :				0	12
E :					0

Calculate the length of the edges  $a$  bis  $j$  in the given network.

(Hint:  $a = \alpha_{\{A\},\{B,C,D,E\}}$ ,  $g = \alpha_{\{A,E\},\{B,C,D\}}$ , etc.)

Solve this exercise with your implementation. You can also use the software *Splitstree* ([www.splitstree.org](http://www.splitstree.org)) — describe the format of your input and your proceeding.



Turn around!

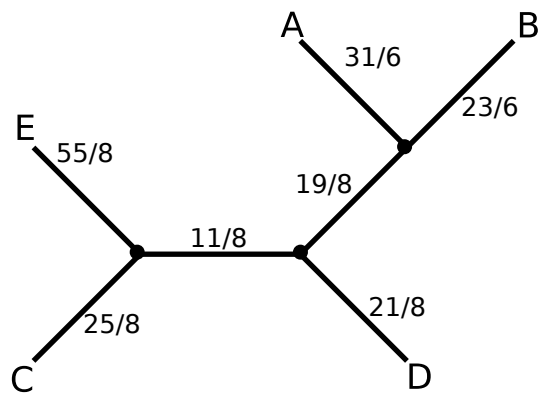
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**Exercise 4 Comparison of methods.**

**(2 Points)**

If one uses the *Neighbor Joining* algorithm on the distance matrix from task 3, the result is the following tree. Compare the tree with the result from task 3.

*Neighbor Joining*-Tree:



Matrix and some solution to test your implementation in task 1 (optional!):

	<i>A</i>	<i>B</i>	<i>C</i>	<i>D</i>	<i>E</i>
<i>A</i> :	0	6	8	5	10
<i>B</i> :		0	5	8	10
<i>C</i> :			0	4	8
<i>D</i> :				0	7
<i>E</i> :					0

<i>J</i>	<i>K</i>	$\alpha_{J,K}$
{ <i>A, B, C, E</i> }	{ <i>D</i> }	0.5
{ <i>A, B, D, E</i> }	{ <i>C</i> }	0.5
{ <i>A, B, E</i> }	{ <i>C, D</i> }	0.5
{ <i>A, C, D, E</i> }	{ <i>B</i> }	1.5
{ <i>A, C, E</i> }	{ <i>B, D</i> }	0.0
{ <i>A, D, E</i> }	{ <i>B, C</i> }	1.5
{ <i>A, E</i> }	{ <i>B, C, D</i> }	0.0
{ <i>B, C, D, E</i> }	{ <i>A</i> }	1.5
{ <i>B, C, E</i> }	{ <i>A, D</i> }	1.0
{ <i>B, D, E</i> }	{ <i>A, C</i> }	0.0
{ <i>B, E</i> }	{ <i>A, C, D</i> }	0.0
{ <i>C, D, E</i> }	{ <i>A, B</i> }	2.0
{ <i>C, E</i> }	{ <i>A, B, D</i> }	0.0
{ <i>D, E</i> }	{ <i>A, B, C</i> }	0.0
{ <i>E</i> }	{ <i>A, B, C, D</i> }	4.5