

Questions for Bioinformatics 1 WiSe 2023/2024

- Practical part alignments and trees -

Please follow the instructions for the exercises and answer all questions/perform the tasks on this question sheet.

Exercise 1: Build phylogenetic trees

1 a) Which sequence accessions have you downloaded from NCBI and why?

1 b) Are the five trees you constructed any different from each other? Describe the differences (focus on three of your choice).

1 c) Explain shortly the principles of each of these five phylogenetic methods:

UPGMA:

ME:

NJ:

MP:

ML:

Exercise 2: BLAST

2 a) Which sequence in the database is most similar to the query?

2b) What is the origin of the most similar sequence? Is it a dinosaur sequence?

Exercise 3: Substitution Matrices. Delete the wrong answer.

3 a) Which substitution is more likely to appear in BLOSUM62? W ↔ F H ↔ Q

3 b) Which substitution is more likely to appear in PAM250? W ↔ F H ↔ Q

Exercise 4: Dotplot

	A	B	R	A	C	A	D	A	B	R	A	C	A	D	A	B	R	A
A																		
B																		
R																		
A																		
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Fill out the dotplot by using an “x” and answer the following questions.

4 a) How do repeated patterns look like in a dotplot?

4 b) How do palindromes look like in a dotplot? *Hint: “ANNA” is a palindrome.*

Exercise 5: Dynamic Programming

5 a) Create an alignment of the two phrases based on the presented path (see instructions sheet). Gaps are represented as a hyphen (“-”). Use the second row to write down the scores needed for exercise 5b).

G																		
G																		

5 b) Calculate the score of the alignment using the BLOSUM62 matrix and set the gap penalties as follows: gap opening = -11, gap extension = -1.

Score: _____

Exercise 6: Use BLASTx to find a hidden message

6) What is the hidden message in the dinosaur sequence?

Exercise 7: Add the human sequence ABD95911.1 to the Neighbor Joining tree