FH Krems	ATBI6ILV - Algorithms and Tools in Bioinformatics Pt 2: Sequence Alignment Algorithms	SS 2024

Deadline: see MS Teams

Name _____ **Effort [h]** ____

Punkte _____

1. Position Specific Scoring (25 pt)

Implement a framework for position-specific scoring in a programming language of your choice:

- Implement the import of aligned sequences (given in a text file)
- A position-specific scoring matrix is to be calculated on the basis of these read-in sequences
- Finally, it shall be possible to read in any number of sequences and output the score values of these sequences (in relation to the calculated scoring matrix)

2. Needleman-Wunsch und Smith-Waterman (35 pt)

Implement a framework for applying the Needleman-Wunsch and Smith-Waterman alignment algorithms in a programming language of your choice:

- It shall be possible to treat two sequences of any length
- Substitution matrix and gap costs must be passed to the alignment function
- The result is the alignment plus specification of its quality (score)
- Users shall be optionally enabled to treat overlaps specifically

3. BLAST (40 pt)

Implement the core routines of the BLAST algorithm:

- The algorithm is given a sequence as well as a „database“ (i.e., set of sequences)
- You do not have to implement a FSM
- Use a substitution matrix and thresholds for the similarity of words (these are also inputs to the function)
- The result is the information, which DB sequence the given sequence is similar to plus the score and the position of the alignment

Remarks: Hand in your elaborations electronically,
MS Teams or per mail to julia.vetter@fh-hagenberg.at
Hand in: Solution idea, implementation, and detailed test documentations
Accepted format: One (!) .pdf file