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Grundlagen der Bioinformatik

SoSe 2018

Assignment 04

Submit electronically in Ilias by 14.5.2018, 10h

1 Profile alignment (2 points)

Using the sum-of-pairs score, a BLOSUM62 substitution matrix, a linear gap penalty of 5 and scoring gap-against-gap as 0, show how to produce a profile alignment of the two given profiles using dynamic programming, by filing in the matrix:

match: 2 mismatch: -2 gap penalty: 2		V V	C C	L M	W F	C C
macmatch: -2						
11431. 2 (ks: 7)	III					
gap porus 1.2	EEE					
()	C C C					
	I M I					
	EQE					
	C C C					

2 Three different multiple sequence approaches (6 points)

Summarize three different multiple sequence programs in your own words (choose three different published approaches that do not share any coauthors and whose publication dates are separated by 5 or more years.) What are the main algorithmic differences between the three approaches?

3 Application of a multiple alignment tool (2 points)

Download the fastA file data04.fasta from the Ilias webpage.

Compute a multiple alignment of these sequences, report the alignment using a color-coding of amino acids (say which coloring scheme was used) and report the score of the alignment, and details of the scoring scheme (that is, substitution model used, linear or affine gap scores, gap penalties...)

Provide details of the method used.