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Bioinformatics II

Assignment No. 3

Forms:

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name: | Main |  |  |  |
| Inputs | Outputs | Calls | Called by | Files |
| String Sequence 1 | ‘Similarity score’ | similarity(String sequence1, String sequence 2) | none | none |
| String Sequence 2 | ‘aligned sequence 1’ | getAlignment(long[][] alignMatrix, String sequence 1, String sequence 2) |  |  |
|  | ‘aligned sequence 2’ |  |  |  |
| Processing: | Drives the program |  |  |  |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name: | p |  |  |  |
| Inputs | Outputs | Calls | Called by | Files |
| String aminoA1 | ‘substitution score’ | none | similarity | none |
| String aminoA2 |  |  | getAlignment |  |
| Processing: | Compares amino acids and returns substitution score | | | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name: | max |  |  |  |
| Inputs | Outputs | Calls | Called by | Files |
| int xLeft | 'max score' | none | similarity | none |
| int xAbove |  |  |  |  |
| int xDiagonal |  |  |  |  |
| Processing: | Compares the three paths and returns the max score | | | |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name: | similarity |  |  |  |
| Inputs | Outputs | Calls | Called by | Files |
| String sequence1 | Long[][] alignmentMatrix | p | main | none |
| String sequence2 |  | max |  |  |
| Processing: | Computes the values of each cell | | |  |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Name: | getAlignment |  |  |  |
| Inputs | Outputs | Calls | Called by | Files |
| Long[][] alignMatrix | String[] sequences | p | main | none |
| String sequence1 |  |  |  |  |
| String sequence2 |  |  |  |  |
| Processing: | Does the traceback on the matrix and returns the global alignment | | | |

Variables:

Global variable:

String[][] blosum62: BLOSUM62 substitution matrix

Function p:

Int x: value that holds the position of the currently looped amino acid in sequence 1

Int y: that holds the position of the currently looped amino acid in sequence 2

String aminoA1: substring that is used to compare for substitution score

String aminoA2: substring that is used to compare for substitution score

Function max:

Int xLeft: holds the score from the cell from the left plus the gap score for comparing which path yields the highest score

Int xAbove: holds the score from the cell from above plus the gap score for comparing which path yields the highest score

Int xDiagonal: holds the score from the diagonal plus the match/mismatch score

Function similarity:

String sequence1: holds sequence to be aligned

String sequence2: holds other sequence

Int matchScore: holds a substitution score for filling out matrix

Long[][] alignmentMatrix: holds scores for the alignmentMatrix

Function getAlignement:

Long[][] alignMatrix: same as alignmentMatrix

String sequence1: same as before

String sequence2: same as before

Int maxCellX: holds the x-value of the max score cell

Int maxCellY: holds the y-value of the max score cell

Int currentX: holds an x-value for keeping track of what cell the loop is on

Int currentY: holds an y-value for keeping track of what cell the loop is on

String[] sequences: holds the aligned sequences to be returned

Main method:

String seq1: sequence from input

String seq2: sequence from input

Long[][] alignMatrix: alignment matrix

String[] sequences: holds the aligned sequence