

Needleman-Wunsch algorithm for Global Alignment

DNA sequences:

a - GATGCGCAG

b - GGCAGTA

Scoring scheme:

Match = +2

Mismatch = -3

Gap = -1

Here we have the Score matrix. We have the sequence a in columns and sequence b in rows. It is the bidimensional array used to store the optimal scores.

The pointer matrix stores the information useful to traceback the optimal path.

Score Matrix

0	-1	-2	-3	-4	-5	-6	-7
-1	2	1	0	-1	-2	-3	-4
-2	1	0	-1	2	1	0	-1
-3	0	-1	-2	1	0	3	2
-4	-1	2	1	0	3	2	1
-5	-2	1	4	3	2	1	0
-6	-3	0	3	2	5	4	3
-7	-4	-1	2	1	4	3	2
-8	-5	-2	1	4	3	2	5
-9	-6	-3	0	3	6	5	4

Pointer Matrix

9	9	9	9	9	9	9	9
8	7	16	9	9	16	9	9
8	8	17	17	7	9	9	16
8	8	17	17	8	17	7	9
8	15	7	9	17	7	17	17
8	8	8	7	9	17	17	17
8	15	15	8	17	7	9	9
8	8	8	15	17	8	17	17
8	8	8	8	7	17	17	7
8	15	15	8	8	7	9	17

We initialize the pointer matrix's first row and first column with 8 and 9, respectively; all other entries are 0. In the Pointer matrix:

- 8 means that the cell is reached from the cell above it
- 9 means that the cell is reached from the cell to the left of it
- 7 means that the cell is reached from the cell diagonally above and to the left of it
- 15 means that the cell can be reached from the cell above it or the cell diagonally above and to the left of it
- 16 means that the cell can be reached from the cell to the left of it or the cell diagonally above and to the left of it
- 17 means that the cell can be reached from the cell above it or the cell to the left of it

These are the different optimal alignments for the given sequences.

Optimal Alignments

GATGC-G-CAG
G--GCAGT-A-
Score: 4

GATGC-GC-AG
G--GCAG-TA-
Score: 4

GATGCGCAG--
G--GC--AGTA
Score: 4

GATGCGCAG--
G--G--CAGTA
Score: 4

GATGCGCAG--
G----GCAGTA
Score: 4

GATGCGCAG--
---G-GCAGTA
Score: 4

Smith Waterman algorithm for Local Alignment

DNA sequences:

a - GATGCGCAG

b - GGCAGTA

Scoring Scheme:

Match = +2

Mismatch = -1

Gap = -3

Here we have the Score matrix. We have the sequence a in columns and sequence b in rows.

Score Matrix

0	0	0	0	0	0	0	0
0	2	2	0	0	2	0	0
0	0	1	1	2	0	1	2
0	0	0	0	0	1	2	0
0	2	2	0	0	2	0	1
0	0	1	4	1	0	1	0
0	2	2	1	3	3	0	0
0	0	1	4	1	2	2	0
0	0	0	1	6	3	1	4
0	2	2	0	3	8	5	2

Pointer Matrix

9	9	9	9	9	9	9	9
8	7	7	0	0	7	0	0
8	0	7	7	7	0	7	7
8	0	0	7	7	7	7	7
8	7	7	0	0	7	7	7
8	0	7	7	9	0	7	0
8	7	7	8	7	7	9	7
8	0	7	7	9	7	7	0
8	0	0	8	7	9	7	7
8	7	7	0	8	7	9	9

to store the optimal scores.

information useful to traceback the optimal path.

Optimal Alignments
GCAG
GCAG
Score: 8

