

Sequence alignment

(1)

Seq 1: A C C T G S

Seq 2: A C C N S

Scores:

Match: +1
 Mismatch: -2
 Gap: -1 (constant)

Gap at the beginning counts.

	A	C	C	T	G	S
A	+1	-3	-3	-3	-3	-3
C	-3	+2	+1	-2	-2	-2
C	-3	+1	+3	-1	-1	-1
N	-3	-2	-1	0	0	0
S	-3	-2	-1	0	-1	+1

A C C T G S A C C T G S
 A C C N - S A C C - N S

Dynamic programming according to Needleman and Wunsch

Smith and Waterman.

(2)

$$NW(i, j) = S(i, j) + \max$$

$$\left\{ \begin{array}{l} NW(i-1, j-1) \\ \max_k (NW(i-1, k)) + \text{Gap} \\ \max_k (NW(k, j-1)) + \text{Gap} \end{array} \right.$$

Needleman and Wunsch

$$SW(i, j) = S(i, j) + \max$$

max

$$\left\{ \begin{array}{l} SW(i-1, j-1) \\ \max_k (NW(i-1, k)) + \text{Gap} \\ \max_k (NW(k, j-1)) + \text{Gap} \end{array} \right.$$

~~SW~~

0

Smith and Waterman

	A	C	C	T	G	S
A					-3 ⁻⁴ (3)	
C					-2 ⁻³	
C				(5)	-1 ⁻²	
N	-3 -4	-2 -3	-1 -2	(1) 0	(0)	
S						+1

A C C T G S

A C C N S

Match 1

Mismatch -2

Gap -1 (constant)

Gap at the beginning counts

S W

	A	C	C	T	G	S
A	+1	0	0	0	0	0
C	0	+2	1	0	0	0
C	0	1	+3	0	0	0
N	0	0	0	1	0	0
S	0	0	0	0	0	1 0

A C C

A C C

