

# Needleman-Wunsch Sequence Alignment

## Linear Gap Penalty Mode

**Sequences:** GATTACA vs GCATGCU

**Scoring:** Match = +1, Mismatch = -1, Gap = -1

**Score:** 0

**Number of optimal paths:** 2

### Alignment 1

G-ATTACA

	-	G	C	A	T	G	C	U
-	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	0	-1	-2	-3	-4	-5
A	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
T	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	-1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

GCAT-GCU

### Alignment 2

G-ATTACA

	-	G	C	A	T	G	C	U
-	0	-1	-2	-3	-4	-5	-6	-7
G	-1	1	0	-1	-2	-3	-4	-5
A	-2	0	0	1	0	-1	-2	-3
T	-3	-1	-1	0	2	1	0	-1
T	-4	-2	-2	-1	1	1	0	-1
A	-5	-3	-3	-1	0	0	0	-1
C	-6	-4	-2	-2	-1	-1	1	0
A	-7	-5	-3	-1	-2	-2	0	0

GCATG-CU

## Test alignment (EDNAFULL)

Score: 1

Number of optimal paths: 1

AG--ATTACA-

-GCCCWT-GCWG

	-	G	C	C	C	W	T	G	C	W	G
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20
A	-2	-4	-6	-8	-10	-7	-9	-11	-13	-15	-17
G	-4	3	1	-1	-3	-5	-7	-4	-6	-8	-10
A	-6	1	-1	-3	-5	-2	-4	-6	-8	-5	-7
T	-8	-1	-3	-5	-7	-4	3	1	-1	-3	-5
T	-10	-3	-5	-7	-9	-6	1	-1	-3	0	-2
A	-12	-5	-7	-9	-11	-8	-1	-3	-5	-2	-4
C	-14	-7	0	-2	-4	-6	-3	-5	2	0	-2
A	-16	-9	-2	-4	-6	-3	-5	-7	0	3	1