

# 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

## 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	-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	