

### Q1. the global max similarity matrix

	-	A	A	G	T	G	C	C	T	C	A	A	G	A	T	A
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30
A	-2	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19	-21	-23	-25	-27
C	-4	-1	0	-2	-4	-6	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24
C	-6	-3	-2	-1	-3	-5	-5	-5	-7	-9	-11	-13	-15	-17	-19	-21
G	-8	-5	-4	-1	-2	-2	-4	-6	-6	-8	-10	-12	-12	-14	-16	-18
T	-10	-7	-6	-3	0	-2	-3	-5	-5	-7	-9	-11	-13	-13	-13	-15
C	-12	-9	-8	-5	-2	-1	-1	-2	-4	-4	-6	-8	-10	-12	-14	-14
T	-14	-11	-10	-7	-4	-3	-2	-2	-1	-3	-5	-7	-9	-11	-11	-13
C	-16	-13	-12	-9	-6	-5	-2	-1	-3	0	-2	-4	-6	-8	-10	-12
A	-18	-15	-12	-11	-8	-7	-4	-3	-2	-2	1	-1	-3	-5	-7	-9
G	-20	-17	-14	-11	-10	-7	-6	-5	-4	-3	-1	0	0	-2	-4	-6
C	-22	-19	-16	-13	-12	-9	-6	-5	-6	-3	-3	-2	-1	-1	-3	-5
A	-24	-21	-18	-15	-14	-11	-8	-7	-6	-5	-2	-2	-3	0	-2	-2
A	-26	-23	-20	-17	-16	-13	-10	-9	-8	-7	-4	-1	-3	-2	-1	-1
T	-28	-25	-22	-19	-16	-15	-12	-11	-8	-9	-6	-3	-2	-4	-1	-2
A	-30	-27	-24	-21	-18	-17	-14	-13	-10	-9	-8	-5	-4	-1	-3	0

### Q2. the best global upmost alignment

	-	A	A	G	T	G	C	C	T	C	A	A	G	A	T	A
-	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30
A	-2	1	-1	-3	-5	-7	-9	-11	-13	-15	-17	-19	-21	-23	-25	-27
C	-4	-1	0	-2	-4	-6	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24
C	-6	-3	-2	-1	-3	-5	-5	-5	-7	-9	-11	-13	-15	-17	-19	-21
G	-8	-5	-4	-1	-2	-2	-4	-6	-6	-8	-10	-12	-12	-14	-16	-18
T	-10	-7	-6	-3	0	-2	-3	-5	-5	-7	-9	-11	-13	-13	-13	-15
C	-12	-9	-8	-5	-2	-1	-1	-2	-4	-4	-6	-8	-10	-12	-14	-14
T	-14	-11	-10	-7	-4	-3	-2	-2	-1	-3	-5	-7	-9	-11	-11	-13
C	-16	-13	-12	-9	-6	-5	-2	-1	-3	0	-2	-4	-6	-8	-10	-12
A	-18	-15	-12	-11	-8	-7	-4	-3	-2	-2	1	-1	-3	-5	-7	-9
G	-20	-17	-14	-11	-10	-7	-6	-5	-4	-3	-1	0	0	-2	-4	-6
C	-22	-19	-16	-13	-12	-9	-6	-5	-6	-3	-3	-2	-1	-1	-3	-5
A	-24	-21	-18	-15	-14	-11	-8	-7	-6	-5	-2	-2	-3	0	-2	-2
A	-26	-23	-20	-17	-16	-13	-10	-9	-8	-7	-4	-1	-3	-2	-1	-1
T	-28	-25	-22	-19	-16	-15	-12	-11	-8	-9	-6	-3	-2	-4	-1	-2
A	-30	-27	-24	-21	-18	-17	-14	-13	-10	-9	-8	-5	-4	-1	-3	0

**Upmost alignment:**

AAGTGCCTCAAGA-TA  
- ACCGTCTCAGCAATA  
= \* \_ \_ \* \_ \* \* \* \* \_ \_ \* = \* \*

**The score of the alignments:**

**9 matches(+1X9), 5 mismatches(-1X5), 2 gaps(-2X2) = 0**