Needleman-Wunsch & Hirschberg Unit Tests

```
Hints:  Many test values are taken from project Algorithms
        for Bioninformatics of Alexander Mattheis or the lectures.
        For Hirschberg the input values were negated.
```

Test 1
Input

```
Sequence A:          AGTC
Sequence B:          ATC

Deletion:            -2
Insertion:           -2
Match:                1
Mismatch:            -1
```

Output

		A	T	C
	0	-2	-4	-6
A	-2	1	-1	-3
G	-4	-1	0	-2
T	-6	-3	0	-1
C	-8	-5	-2	1

```
Seq1    AGTC
        * **
Seq2    A_TC
```

Test 2
Input

```
Sequence A:          GGGTGAGACCCCAGTTCAACCC
Sequence B:          CCCCGCGACTCGGGTTCAAGGG

Deletion:            -2
Insertion:           -2
Match:                4
Mismatch:            -1
```

Output

		C	C	C	C	G	C	G	A	C	T	C	G	G	G	T	T	C	A	A	G	G	G
	0	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30	-32	-34	-36	-38	-40	-42	-44
G	-2	-1	-3	-5	-7	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30	-32	-34	-36	-38
G	-4	-3	-2	-4	-6	-6	-5	-2	-4	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26	-28	-30	-32
G	-6	-5	-4	-3	-5	-2	-4	-1	-3	-5	-7	-9	-6	-8	-10	-12	-14	-16	-18	-20	-22	-24	-26
T	-8	-7	-6	-5	-4	-4	-3	-3	-2	-4	-1	-3	-5	-7	-9	-6	-8	-10	-12	-14	-16	-18	-20
G	-10	-9	-8	-7	-6	0	-2	1	-1	-3	-3	-2	1	-1	-3	-5	-7	-9	-11	-13	-10	-12	-14
A	-12	-11	-10	-9	-8	-2	-1	-1	5	3	1	-1	-1	0	-2	-4	-6	-8	-5	-7	-9	-11	-13
G	-14	-13	-12	-11	-10	-4	-3	3	3	4	2	0	3	3	4	2	0	-2	-4	-6	-3	-5	-7
A	-16	-15	-14	-13	-12	-6	-5	1	7	5	3	1	1	2	2	3	1	-1	2	0	-2	-4	-6
C	-18	-12	-11	-10	-9	-8	-2	-1	5	11	9	7	5	3	1	1	2	5	3	1	-1	-3	-5
C	-20	-14	-8	-7	-6	-8	-4	-3	3	9	10	13	11	9	7	5	3	6	4	2	0	-2	-4
C	-22	-16	-10	-4	-3	-5	-4	-5	1	7	8	14	12	10	8	6	4	7	5	3	1	-1	-3
C	-24	-18	-12	-6	0	-2	-1	-3	-1	5	6	12	13	11	9	7	5	8	6	4	2	0	-2
A	-26	-20	-14	-8	-2	-1	-3	-2	1	3	4	10	11	12	10	8	6	6	12	10	8	6	4
G	-28	-22	-16	-10	-4	2	0	1	-1	1	2	8	14	15	16	14	12	10	10	11	14	12	10
T	-30	-24	-18	-12	-6	0	1	-1	0	-1	5	6	12	13	14	20	18	16	14	12	12	13	11
T	-32	-26	-20	-14	-8	-2	-1	0	-2	-1	3	4	10	11	12	18	24	22	20	18	16	14	12
C	-34	-28	-22	-16	-10	-4	2	0	-1	2	1	7	8	9	10	16	22	28	26	24	22	20	18
A	-36	-30	-24	-18	-12	-6	0	1	4	2	1	5	6	7	8	14	20	26	32	30	28	26	24
A	-38	-32	-26	-20	-14	-8	-2	-1	5	3	1	3	4	5	6	12	18	24	30	36	34	32	30
C	-40	-34	-28	-22	-16	-10	-4	-3	3	9	7	5	3	3	4	10	16	22	28	34	35	33	31
C	-42	-36	-30	-24	-18	-12	-6	-5	1	7	8	11	9	7	5	8	14	20	26	32	33	34	32
C	-44	-38	-32	-26	-20	-14	-8	-7	-1	5	6	12	10	8	6	6	12	18	24	30	31	32	33

```
Seq1    GGGTGAGACCCCAGTTCAACCC
        ||||*|***|*||******|||
Seq2    CCCCGCGACTCGGGTTCAAGGG
```

Test 3
Input

```
Sequence A:        TCCGA
Sequence B:        TACGCGC

Deletion:          -1
Insertion:         -1
Match:              1
Mismatch:           0
```

Output

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

```
Seq1    T_C_CGA
        * * **|
Seq2    TACGCGC
```

Test 4
Input

```
Sequence A:        AATCG
Sequence B:        AACG

Deletion:          -2
Insertion:         -2
Match:              1
Mismatch:          -1
```

Output

		A	A	C	G
	0	-2	-4	-6	-8
A	-2	1	-1	-3	-5
A	-4	-1	2	0	-2
T	-6	-3	0	1	-1
C	-8	-5	-2	1	0
G	-10	-7	-4	-1	2

```
Seq1    AATCG
        ** **
Seq2    AA_CG
```

Test 5: **Multiple existing Tracebacks** (only for Hirschberg – computed with NW implementation)

Input

```
Sequence A:        AATCG
Sequence B:        ACG

Deletion:          -2
Insertion:         -2
Match:              1
Mismatch:          -1
```

Output (first alignment is found, because most left tracecell is selected)

		A	C	G
	0	-2	-4	-6
A	-2	1	-1	-3
A	-4	-1	0	-2
T	-6	-3	-2	-1
C	-8	-5	-2	-3
G	-10	-7	-4	-1

```
Seq1    AATCG
          * **
Seq2    _A_CG
```

		A	C	G
	0	-2	-4	-6
A	-2	1	-1	-3
A	-4	-1	0	-2
T	-6	-3	-2	-1
C	-8	-5	-2	-3
G	-10	-7	-4	-1

```
Seq1    AATCG
         *  **
Seq2    A__CG
```