i↓ / j→	O	⊘	1 T	2 C	3 G ←j
0 L	O	⊘	-2	-4	-6
1 T	-2		-1	-3	-5
2 T	-4		-1	-2	-4
3 C	-6		-3	0	-2
4 G	-8		-5	-2	1

$V = a[i-1][j]$

$a[i][i] = a[0][i] + gap$

i S1: —
j S2: —

UP i-1 j

L : i, j-1   S2: —

D: i-1, j-1 S1, S2 fill.

TTACTGC
TGATGA

A C G T

	A	C	G	T
#	-2	1	-2	
-2	4	-2	1	
	-2	4	-2	
1	-2		4	
-2	1	-2	4	

Semi-Global:

Traceback Path:
starting Point : max score found in last row/column

Traceback ends: when u reach beginning of either sequence. (cuz ends r not penalized).

Local : find best matching subsequences within 2 large sequences.

high similarity regions are considered.

if score -ve fill zero. so

Traceback starts from cell with highest score. in matrix.

Stops: when similarity drops below certain threshold (zero)

Semi-Global: seq1: ACTG   Seq2: CT
Match = +1, mismatch = -1, Gap = -1.

high score: last row / last column.
    end when 1 seq is aligned
       gaps ignored.

A C T G
_ C T _

		0	1	2	3	4 ← j
		—	A	C	T	G
0	—	0	0	0	0	0
1	C	0	0	1	0	-1
2	T	0	-1	0	2	1

i ↓

Local: Seq1: ACCGT   Seq2: CCG
-ve value set to zero.   match = +1, mismatch = -1, Gap = -1

Start from highest score.
ends when score reaches
zero.

A C C G A
_ C C G _

		0	1	2	3	4 ← j	
		—	A	C	C	G	T
0	—	0	0	0	0	0	0
1	C	0	0	1	1	0	0
2	C	0	0	1	2	1	0
3	G	0	0	0	1	3	2

i ↓