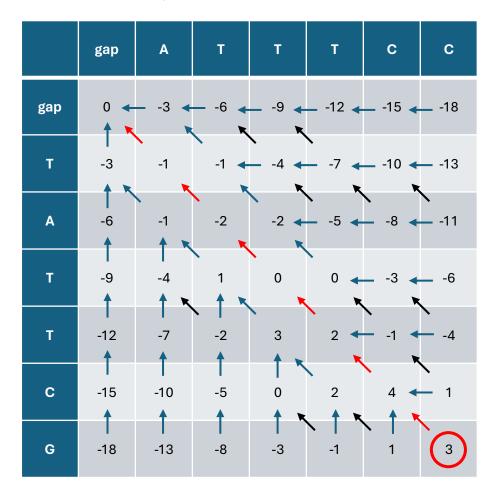
## **GLOBAL**

Seq\_2

C	$\bigcirc$	$\alpha$	1
U	$\Box$	Ч_	- 1



Seq\_1 ATTTCC

Seq\_2 TATTCG

no multiple best alignments

## LOCAL

Seq\_2

	-	
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	gap	A	т	т	т	С	С
gap	0	0	0	0	0	0	0
т	0	0	2	2	2	0	0
Α	0	2	0	1	1	1	0
т	0	0	4	2	3	0	0
т	0	0	2	6	4	2	0
С	0	0	0	3	5	6	4
G	0	0	0	0	2	4	5

Seq\_1 TATTCG TATTCG

Seq\_2 ATTTCC ATTTCC

two best alignments

```
from sequence_alignments import (
    create_submat,
    needleman_wunsch,
    smith_waterman,
    recover_align_local,
SEQ_1 = 'TATTCG'
SEQ_2 = 'ATTTCC'
MATCH = 2
MISMATCH = -1
GAP = -3
def get_alignments(
     seq_1: str = SEQ_1,
    seq_2: str = SEQ_2,
    match: int = MATCH,
    mismatch: int = MISMATCH,
    gap: int = GAP,
    Given two sequences and the match, mismatch, and gap scores,
    print all the relevant information about the global and local alignments.
     - seq_1 (str): the first sequence to be aligned
    - seq_2 (str): the second sequence to be aligned
    - gap (int): the score for a gap
    alphabet = set(seq_1 + seq_2)
    # Determine the score and traceback matrix.
    gsm, gtm = needleman_wunsch(seq_1, seq_2, sm, gap)
print('Global score matrix:', gsm)
    print('Global traceback matrix:', gtm)
    gbs = gsm[-1][-1]
print('Global alignment score:', gbs)
    oga = recover_align(gtm, seq_1, seq_2)
print('Optimal global alignment:', oga)
    # Explain if there are multiple best alignments. print('Multiple best global alignments:', 'Yes' if len(oga) > 1 else 'No')
    print()
    lsm, ltm, lbs = smith_waterman(seq_1, seq_2, sm, gap)
    print('Local score matrix:', lsm)
print('Local traceback matrix:', ltm)
    print('Local alignment score:', lbs)
    ola = recover_align_local(lsm, ltm, seq_1, seq_2)
    print('Optimal local alignment:', ola)
    # Explain if there are multiple best alignments.
print('Multiple best local alignments:', 'Yes' if len(ola) > 1 else 'No')
if __name__ == '__main__':
    get_alignments()
```