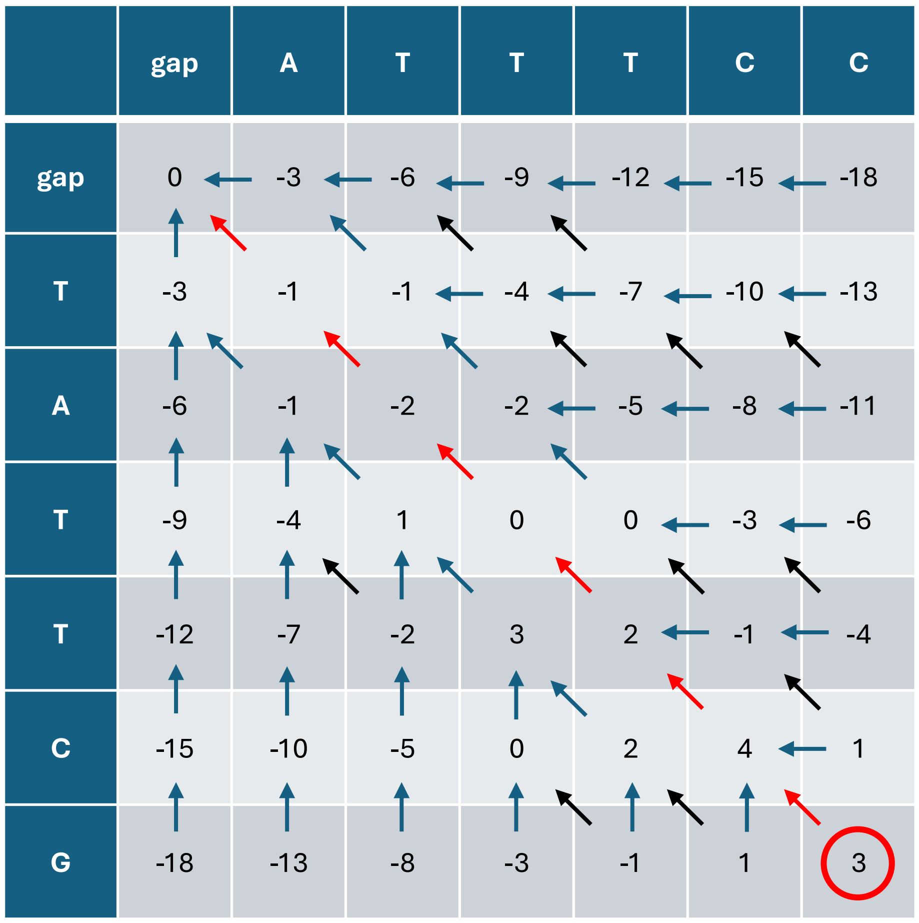
GLOBAL

Seq_2

Seq_1



	gap	A	T	T	T	C	C
gap	0	-3	-6	-9	-12	-15	-18
T	-3	-1	-1	-4	-7	-10	-13
A	-6	-1	-2	-2	-5	-8	-11
T	-9	-4	1	0	0	-3	-6
T	-12	-7	-2	3	2	-1	-4
C	-15	-10	-5	0	2	4	1
G	-18	-13	-8	-3	-1	1	3

Seq_1 ATTTCC

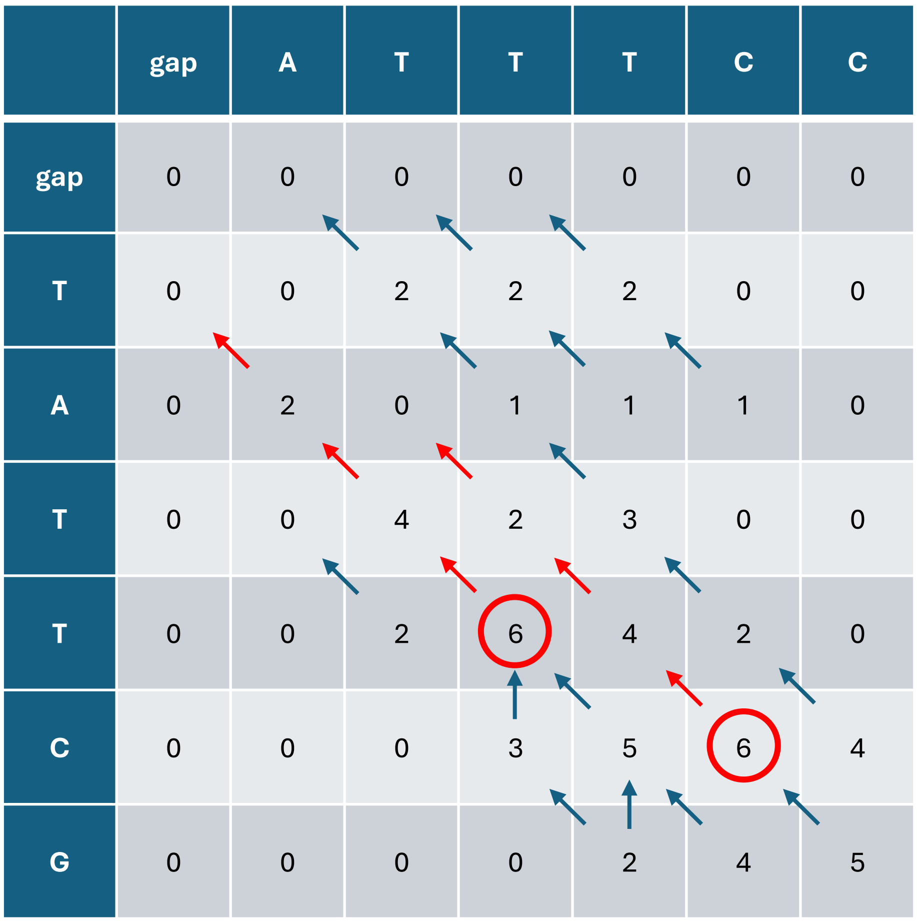
Seq_2 TATTCG

no multiple best alignments

LOCAL

Seq_2

Seq_1



	gap	A	T	T	T	C	C
gap	0	0	0	0	0	0	0
T	0	0	2	2	2	0	0
A	0	2	0	1	1	1	0
T	0	0	4	2	3	0	0
T	0	0	2	6	4	2	0
C	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

```python
from sequence_alignments import (
    create_submat,
    needleman_wunsch,
    smith_waterman,
    recover_align,
    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.

    Args:
    - seq_1 (str): the first sequence to be aligned
    - seq_2 (str): the second sequence to be aligned
    - match (int): the score for a match
    - mismatch (int): the score for a mismatch
    - gap (int): the score for a gap
    '''
    alphabet = set(seq_1 + seq_2)

    # GLOBAL ALIGNMENT
    # Determine the score and traceback matrix.
    sm = create_submat(match, mismatch, alphabet)
    gsm, gtm = needleman_wunsch(seq_1, seq_2, sm, gap)
    print('Global score matrix:', gsm)
    print('Global traceback matrix:', gtm)

    # Determine the best score.
    gbs = gsm[-1][-1]
    print('Global alignment score:', gbs)

    # Retrieve the optimal sequence alignment.
    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()

    # LOCAL ALIGNMENT
    # Determine the score and traceback matrix.
    lsm, ltm, lbs = smith_waterman(seq_1, seq_2, sm, gap)
    print('Local score matrix:', lsm)
    print('Local traceback matrix:', ltm)

    # Determine the best score.
    print('Local alignment score:', lbs)

    # Retrieve the optimal sequence alignment.
    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()
```

Note: *To solve part 3.d), I slightly altered the functions from the lab, so that the possibility of multiple optimal alignments is considered. That resulted in a changed signature of the 'recover_align' functions, where instead of one optimal alignment they now return a list of optimal alignments. I also made some naming changes regarding some of the functions. I hope this is not an issue for the grading of the assignment, otherwise I would be happy to provide my altered code.*