

Assignment 1: Sequence alignment

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1 Global Alignment

```
1 (1) for sequences "ATCGAT" and "ATACGT":
2
3         AT-CGAT
4         || || |
5         ATACG-T
6
7 (2) for sequences "PAWHEAE" and "GAWGHEQ":
8
9         PAW-HEAE
10        || ||
11        GAWGHE-Q
12
13 (3) for sequences "ATTA" and "ATTTTA":
14
15        A--TTA
16        |  |||
17        ATTTTA
```

Listing 1: Global Alignment Results

2 Percent Identity& Hamming Distance

2.1 Sequence "ATCGAT", "ATACGT"

Results are shown in the Figure1.

```
• (particle_hana) (base) user@dell-XPS:~/Project_thesis/Bio-Info$
3.py
AT-CGAT
|| || |
ATACG-T
Percent Identity:
- Divided by the length of the alignment (7): 71.43%
- Divided by the number of non-gap positions (5): 100.00%
Hamming Distance: 2
```

Figure 1: Global Alignment 1

2.2 Sequence "ACGATAGCGAAACCAAAA", "CACGTAGCCGATGTC"

Due to the different lengths of two sequences, the Hamming distance calculation is not feasible. Results are shown in the Figure2.

```

-ACGATAG-CGAAACCAAAA
||| ||| ||| |
CACG-TAGCCGATGTC----
Percent Identity:

- Divided by the length of the alignment (20): 50.00%
- Divided by the number of non-gap positions (13): 76.92%
Hamming Distance: None

```

Figure 2: Global Alignment 2

3 Optimal Local Alignment

3.1 Sequence "PAWHEAE", "HDAGAWGHEQ"

Results are shown in the Figure3.

```

● (particle_hana) (base) user@
ions/ms-python.debugpy-2024.
.py
Max alignment score: 6
Optimal Local Alignment:
AW-HE
|| ||
AWGHE

```

Figure 3: Local Alignment 1

3.2 Sequence "KQTGKGS", "KSAGKGAI"

Results are shown in the Figure4.

```

ons/ms-python.debugpy-2024.12.0
y
Global Alignment:
KQTGKG-S
|  |||
KSAGKGAI

Max alignment score: 6
Optimal Local Alignment:
GKG
|||
GKG

```

Figure 4: Local Alignment 2

4 Levenshtein Distance

Results are shown in the Figure5.

```

KQTGKGS
KSAGKGAI
Levenshtein Distance: 4

TAAACGTCGT
AAACGTCGTA
Levenshtein Distance: 2

○ (particle_hana) (base) user@dell-XPS:~/P

```

Figure 5: Levenshtein distance

5 Optimal Alignments

5.1 Sequence "ATTA", "ATTTTA"

Results are shown in the Figure6.

```
OUTPUT  DEBUG CONSOLE  TERMINAL  PORTS

ATTA
ATTTTA

1. Number of optimal alignments: 6

2. All optimal alignments:

Alignment 1:
A--TTA
ATTTTA

Alignment 2:
A-T-TA
ATTTTA

Alignment 3:
AT--TA
ATTTTA

Alignment 4:
A-TT-A
ATTTTA

Alignment 5:
AT-T-A
ATTTTA

Alignment 6:
ATT--A
ATTTTA
```

Figure 6: Optimal Alignments 1

5.2 Sequence "AAAAA", "AAAABAAAA"

Results are shown in the Figure7.

```
AAAAA  
AAAABAAAA
```

```
1. Number of optimal alignments: 56  
o (particle_hana) (base) user@dell-XPS:~
```

Figure 7: Optimal Alignments 2