



CSE 449 : Bioinformatics Sequence Alignment Assignment

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1. Alignment Scores results:

	Global Alignment (G)	Semi-Global Alignment (S)	Local Alignment (L)
Sequence_pair_1	77	97	106
Sequence_pair_2	-4	21	21
Sequence_pair_3	-10	21	21

2. Alignment results:

2.1 Global Alignment (G)

Alignment G1:

```
TGG-T--AGATTTC-C--CACGAGATCTACCGAG-TATGAGTAGGGGGAC-GTTCGCT-CGG-
|. | | |..| | |||||.|||||| |||||..  || | ||.| |||
-GCCTCTA-ACACACTGCACGAGATCAACCGAGATATGAGTAAT---ACAG--CGGTACGGG
```

Alignment G2:

```
CTGTCGCTGCACG
||.|| |
-TGCCG-TG----
```

Alignment G3:

```
CAGCACTTGGATTCTCGG
|||  | |  ||
CAGC----G--T----GG
```

2.2 Semi-Global Alignment (S)

Alignment S1:

```
---TGGTAGATTC-C--CACGAGATCTACCGAG-TATGAGTAGGGGGAC-GTTCGCT-CGG-
  |. || |..| | |||||.||||| ||||||.  || | ||.| ||
GCCTC-TA-ACACACTGCACGAGATCAACCGAGATATGAGTAAT---ACAG--CGGTACGGG
```

Alignment S2:

```
CTGTCGCTGCACG
 ||.|| |
-TGCCG-TG----
```

Alignment S3:

```
CAGCACTTGGATTCTCGG
 |||. | |
CAGCG-T-GG-----
```

2.3 Local Alignment (L)

Alignment L1:

```
CACGAGATCTACCGAG-TATGAGTA
 |||||.||||| |
CACGAGATCAACCGAGATATGAGTA
```

Alignment L2:

```
TGTCGCTG
 ||.|| |
TGCCG-TG
```

Alignment L3:

```
CAGCACTTGG
 |||. | |
CAGCG-T-GG
```

3. Questions

a) Was the semi-global alignment algorithm able to detected better alignments than the global alignment algorithm? Support your answer with examples of your own alignment results.

Terminal gaps may not be biologically significant

As we see at Sequence pairs 2 and 3, they have negative scores in global alignment and positive scores equals to their local alignment in global .

It happens when the second sequence is shorter than the other sequence

Sequence pari 2 : (is same inh global and semi-global) but semi-global score is greater than the golbal alignment score .

CTGTCGCTGCACG

||.|| ||

-TGCCG-TG----

b) Was the local alignment algorithm able to detect region(s) of similarity that were overlooked by

the global alignment? Support your answer with examples of your own alignment results.

Yes , As we see at Sequence pairs 2 and 3

Second sequence is detected to be simillar to a region in the first sequence

Global	Local
<p>Alignment G2:</p> <p>CTGTCGCTGCACG</p> <p> . </p> <p>-TGCCG-TG----</p>	<p>Alignment L2:</p> <p>TGTCGCTG</p> <p> . </p> <p>TGCCG-TG</p>
<p>Alignment G3:</p> <p>CAGCACTTGGATTCTCGG</p> <p> </p> <p>CAGC-----G--T-----GG</p>	<p>Alignment L3:</p> <p>CAGCACTTGG</p> <p> . </p> <p>CAGCG-T-GG</p>