

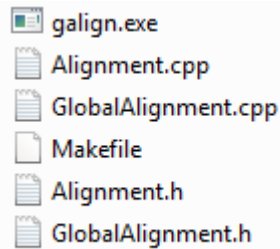
MATH 578A Programming Assignment #1

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- **Summary**

As the memory-length and time-length curves show, when the lengths of the both sequences are 15,935, the running time is 8.284 seconds, and the memory is 1.18 GB. Thus, as the two sequences become longer, the biggest problem of this global alignment algorithm is computer memory.

- **Code and executable file**



- **Compiler**

MinGW GCC 4.7.2

```
>g++ -o galign.exe Alignment.cpp GlobalAlignment.cpp
```

- **Running Environment**

Windows 7 Professional

Processor: Inter(R) Core(TM) 2 Duo CPU T6570 @2.10GHz 2.10GHz

Installed memory (RAM): 2.00 GB

1) Result of the first example:

```
C:\Windows\system32\cmd.exe

E:\coding\workspace\Alignment>galign.exe testData\test1-A.txt testData\test1-B.t

The two sequences are:
TCGCTTGTAGATGAG
TCGCTAAGAGATCAG

The alignment of the two sequences is:
TCGCTTGTAGATGAG
|||||      ||||| ||
TCGCTAAGAGATCAG

Alignment score:      18
% of Identity: 73.33%
Running time: 0.00s
Memory used: 1.31 kilobytes

E:\coding\workspace\Alignment>_
```

2) Result of the second example:

```

C:\Windows\system32\cmd.exe
E:\coding\workspace\Alignment>galign.exe -m2 -s1 -i2 testData\test2-A.txt testData\test2-B.txt
The two sequences are:
TATAGTTAGAGATAACTATTCCCCGTTTGGGGTCTGTATACAGGTGCTGCATG
TCCNGCTAGAAAATAGTGGAGTGTCTAGCTTGCTAGACCTTGAAAACAGGTGCTGCACG
The alignment of the two sequences is:
TATAGTTAGAGATA-ACTA-TTCCCCGTTTG--GGGTC-TGTATACAGGTGCTGCATG
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TCCNGCTAGAAATAGTGGAGTGTCTAGCTTGCTAGACCTTGAAAACAGGTGCTGCACG
Alignment score: 39
% of Identity: 58.62%
Running time: 0.00s
Memory used: 15.78 kilobytes
E:\coding\workspace\Alignment>

```

3) Part result of the third example:

```
C:\Windows\system32\cmd.exe
acgcccataacgatggatgctagttgttggagggcttagtctctccagtaatgcagctaacgcattaagcatcccgcctg
acgctgtataacgatgcacacttggtgtt-aatcg-aaag-gt-t--agtaccgaagctaacgtgttaagtgtgccgcctg
gggagtaagggtcgcaagattaaaactcaaaggaatagacggggacccgcacaagcgggtggagcangtgggtttaattcgan
gggagtatgttcgcaagaatgaaaactcaaaggaattgacgggggcccgcacaagcgggtggagcatgtgggtttaattcgat
nnnacacgaagaaccttacccttaggcttgacattgagagaaat-cgctagaaatagtggagtgcttagcttgctagacctt
gatacgcgaggaaccttaccagggttgacatatacaggatagtagtagagata-acta-ttccccgttg--gggtc-t
gaaaacagggtgctgcacggctgtcgtcagctcgtgtcgtgagatgttgggttaagtcccgcacaacgagcgcaaccccnttt
gtatacagggtgctgcattggtgtcgtcagctcgtgccgtgaggtgtcgggttaagtcccgcacaacgagcgcaaccccttggtt
cttagttgctaacagggttatgtctgagaactctaaggatactgcctccg-taaggaggaggaaggtggggcgcagctcaag
gtctgttaccagcatgtaaagatggggactcagacgagactgccgggtgataagccggaggaaggtgaggatgacgtcaaa
tcacatcatggcccttacg-cctagggttacacacgtgctacaatgggggtgcacaaagagaagcaatactgtgaagtggagc
tcacatcatggcccttatgtcct-ggggtacacacgtgctacaatggcctgtacaaagcagatgcgaacagtgatgtgaagc
caatcttca-aaa-cacctctcagttcggattgtaggctgcaactcgcctgcatgaagctggaatcgctagtaatcgcaa
aaaac-gcagaaagcagggtctcagtcagattgaagtctgaaactcggcttcacatgaagttggaatcgctagtaatcgat
atcagccatgttgccgtgaatacgttcccggtcttggtactcaccgcccgtcacaccatgggagttgtgtttgccttaag
atcag-aatgatacgggtgaatacgtt--c--tc--g-----g--g-----cc-----ttg--t-a-
tcaggatgctaaattgggtactgcccacggcacacacagcgactgggg
-c---a--c---a---c--c-g--cc-c-g-----tc-ac-----
Alignment score: 1438
% of Identity: 69.22%
Running time: 0.08s
Memory used: 9704.97 kilobytes
E:\coding\workspace\Alignment>
```

▪ Running Time and Memory used

I randomly generated 13 pairs dataset to test the running time and memory used in different length of sequences. The two sequences have the same length in all the 13 datasets. The results are shown in Table 1. Figure 1 and 2 are the plots of the memory and running time used in different length of sequences, respectively. The running time is calculated by the deviation of the end and the start of alignment algorithm. The memory is the sum of memory used in array s and l, sequence U, V, and the alignment results rU and rV.

Table 1. Running Time and Memory Used in different Sequence Length

Sequence Length	5	15	45	135	405	1,215	3,645	10,935	11,935	12,935	13,935	14,935	15,935
Running Time (s)	0	0	0	0	0.015	0.063	0.483	4.306	4.898	5.60	6.443	7.395	8.284
Memory Used	0.20 KB	1.3 KB	10.51 KB	90.86 KB	806.50 KB	7.06 MB	63.40 MB	570.32 MB	679.39 MB	797.99 MB	926.13 MB	1.04 GB	1.18 GB

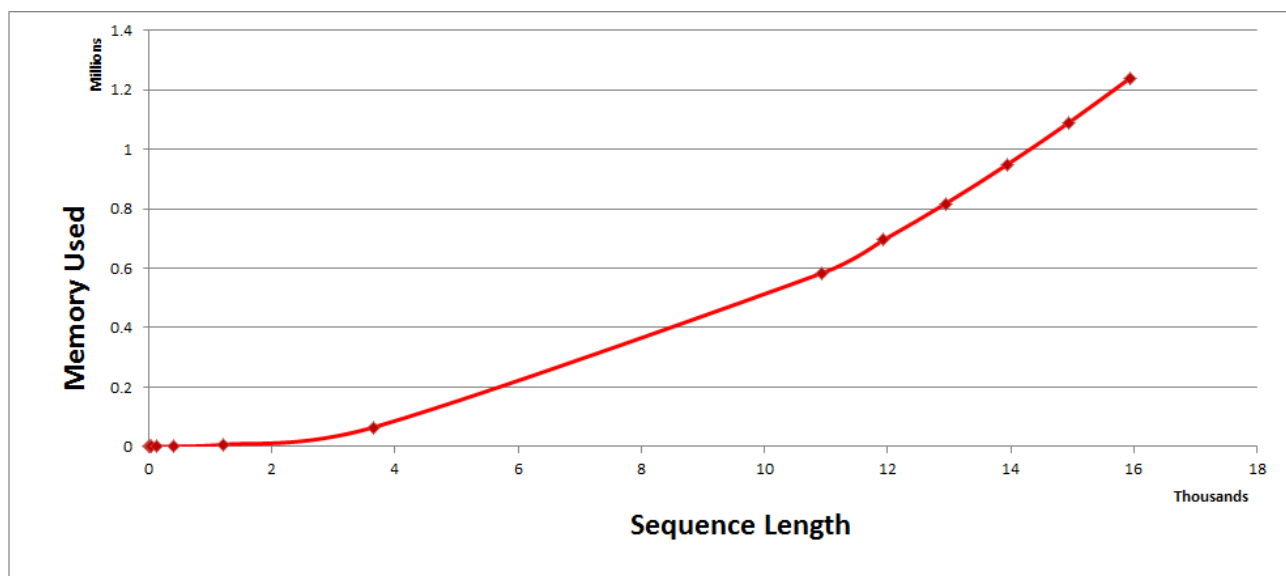


Figure 1 Memory Used in different Sequence Length

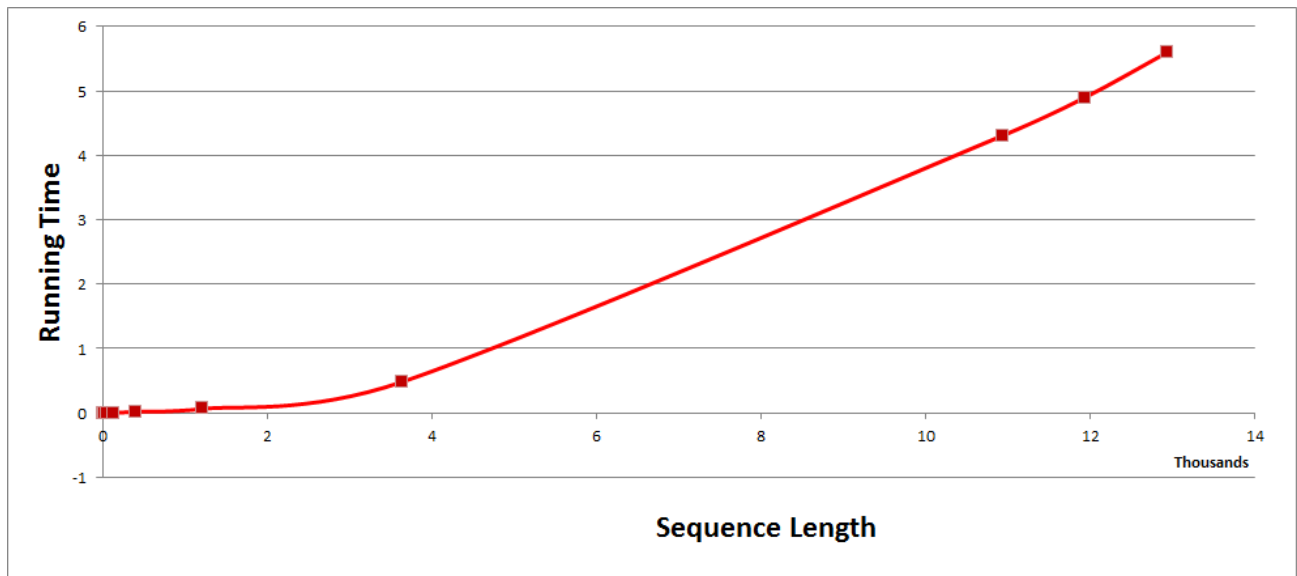


Figure 2 Running Time in different Sequence Length

■ Running log

Running log file records all run of galign.exe and the corresponding results.

```

globalAlignment.log - Notepad
File Edit Format View Help
-----
Sun Feb 24 23:10:43 2013

testData\test1-A.txt
testData\test1-B.txt
The two sequences are:
TCGCTTGATGATGAG
TCGCTAAGAGATCAG

The alignment of the two sequences is:
TCGCTTGATGATGAG
||||| |||||
TCGCTAAGAGATCAG

Alignment score: 18
% of Identity: 73.3333
Running time: 0
Memory used: 1.30859 kilobytes
Memory used: 1.30859 kilobytes
The length of the sequence is 15

-----
Sun Feb 24 23:10:28 2013

testData\test1-A.txt
testData\test1-B.txt
The two sequences are:
TCGCTTGATGATGAG
TCGCTAAGAGATCAG

The alignment of the two sequences is:

```