homework_4.md 3/30/2021

Problem 1A

Since there are a lot of results for the total 15 readsets, I just paste some of them here:

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the score for # 6read is :97

GGACACTTCGCATGGTGGACAGCCTTTGTTACTAATGTGAATGCGTCATC
the score for # 7read is :100

GATGTAATTATCTTGGCAAACCACGCGAACAAATAGATGGTTATGTCATG
GATGTAATTATCTTGGCTAACCACGCGAACAATTGATGGTTATGTTATG
GAIGIANITAICIIGGCIAACCACGCGAACAAAIIGAIGGIIAIGIIAIG
the score for # 8read is :91

GAGGAATACCAATCCACTTGTCTCCCTATTCTTTGACATGA
the score for # 9read is :88

AGGGGTACTGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTTA GAAGGTCAAATCAATGATATGAT
AGGGGIACIGCIGITATGICITTAGAAGGICAAAICAAIGATATGAT
AGGGGTACTGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTT_AGAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTTA_GAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTTAAAAGAAGGTCAAATCAATGATATGAT
AGGGGTACTGCTGTTATGTCTTTAGAAGGTCAAATCAATGATATGAT
the score for # 10read is :85

GTAGACTTATAATTAGAGAAAACAACAGAGTTGTTATTTCTAGTGATGTT
GTAGACTTATAATTAGAGAAAACAACAGAGTTGTTATTTCTAGTGATGTT
the score for # 11read is :100 ***********************************
CAATGTTTGTTTTCTTG TTTTATTGCCACTAGTCTCTAGTCAGTGTG
CAATGTTTGTTTTCTTGCCTTTTATTGCCACTAGTCTCTAGTCAGTGTG
the score for # 12read is :90

ATTACCCCTGCATACACTAATTCTTTCACACGTGGTGTTTATTACC
ATTACCCCCTGCATACACTAGGGATTCTTTCACACGTGGTGTTTATTACC
the score for # 13read is :85 ************************************
GTTTTACATTCAACTCAGGACTTGTTCTTACCTTTCTTTTCCAATGTTAC
GTTTTACATTCAACTCAGGACTTGTTCTTACCTTTTCCAATGTTAC
he score for # 14read is :100

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Problem 1B

```
[yg336@wind ~/inf503/Homework4 ]$ tail output 1B 1000.txt
TAGGA_GAGTGTGGACACTTATG_AATGTCT_TGACACTCGTTTATAAAGT
TCGGACGCACGTCAAGACT ATGTAGGGTATGTAACACTCGCTCGTCAAGT
TAGGA GAGTGTGGACACTTATG AATGTCT TGACACTCGTTTATAAAGT
TCGGACGCACGTCAAGAC TATGTAGGGTATGTAACACTCGCTCGTCAAGT
the score for # 999read is :37
total time for 1000random sequences is 55s
[yg336@wind ~/inf503/Homework4 ]$ tail output 1B 10000.txt
TGTTCTTGCTCG CAAACATACAACGTGTTGTAGCTTGTCACACCGTTTCTAT
||| x||| ||| |x||| x||||x| ||x|x|xx|||| x| |x||||x|||
TGT ATTG TCGCCGAAC CACAAAG GTCGGACTTTGT GC CGGTTTGTAT
TGTTCTTGCTCG CAAACATACAACGTGTTGTAGCTTGTCACACCGTTTCTAT
|| |x||| || || |x||| x||||x| ||x|x|xx|||| x| |x||||x|||
TG TATTG TCGCCGAAC CACAAAG GTCGGACTTTGT GC CGGTTTGTAT
the score for # 9999read is :38
total time for 10000random sequences is 547s
[yg336@wind ~/inf503/Homework4 ]$ tail output_1B_100000.txt
CTCAGGTTTTGCTGCAT_ACAGTCGC_TACAGGATTGGCAACTATAAATTAA
CTCAT TCTTGCGGCATGACCGTTGCGGAAAGGTTGGGTCCCTA AAATTAA
CTCAGGTTTTGCTGCAT ACAGTCGC TACAGGATTGGCAACTATAAATTAA
CTCA TTCTTGCGGCATGACCGTTGCGGAAAGGTTGGGTCCCTA AAATTAA
the score for # 99999read is :48
total time for 100000random sequences is 5543s
[yg336@wind ~/inf503/Homework4 ]$ tail output 1B 1000000.txt
GCTACTGTAGTAATTGGAACAAGCAAATTCTATG GTGGTTGGCACAA
GTTGCTCTATTAATCGGA GGAGAAAATCCGGTGCCTCGTCGGCGCTA
GCTACTGTAGTAATTGGAACAAGCAAATTCTATG GTGGTTGGCACAA
GTTGCTCTATTAATCGG AGGAGAAAATCCGGTGCCTCGTCGGCGCTA
the score for # 999999read is :38
total time for 1000000random sequences is 53983s
```

Problem 2A

Since there are a lot of results for the total 15 readsets, I just paste some of them here:

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```
ATGCGTTAGCTTACTACAACAACAACAAGGGAGGTAGGT
|x|| |x|||x|| ||||||||||xx|x|x|x|x
AGGC_TAAGCTAAC__CAACAACAACAGAATCTCGCT
CTAACTTTAGAGTC_CAACCAACAGAATCT
CTAAGCTAACCAACACAAC AACAGAATCT
CTAACTTTAG AGTCCAACCAACAGAATCT
CTAACTTTA_GAGTCCAACCAACAGAATCT
||||xx|x| x|xxx|||| |||||||||
CTAAGCTAACCAACAAC_AACAGAATCT
CTAA_CTTTAGAGTCCAACCAACAGAATCT
|||| |||xxxx|xxx|||| ||||||||||
CTAAGCTAACCAACAAC_AACAGAATCT
CTAACTTTAGAGTC CAACCAACAGAATCT
||||xx|x|xxxx| ||| |||||||||
CTAAGCTAACCAACACAA CAACAGAATCT
CTAACTTTAG AGTCCAACCAACAGAATCT
CTAACTTTA_GAGTCCAACCAACAGAATCT
||||xx|x| x|xxx||| |||||||||
CTAAGCTAACCAACACAA_CAACAGAATCT
CTAA_CTTTAGAGTCCAACCAACAGAATCT
|||| ||xxxx|xxx||| |||||||||
CTAAGCTAACCAACAA CAACAGAATCT
AACATGGCAAGGAAGACCTTAAAT
AACATGGCAAGGAAGACCTTAAAT
AACATGGCAAGGAA ATC AAAAT
```

All the results can be found in the txt file "output_2A.txt".

Problem 2B

The BLAST method is faster than Smith-Waterman algorithm.

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```
[yg336@wind ~/inf503/Homework4 ]$ tail output 2B_1000.txt
FTTCTTGGCACTGATAACACTCGCTACT
|x|x|x||xxx|| |||||||||||xx|
TATGTAGGGTATG_TAACACTCGCTCGT
TTTCTTGGCACTGATAACACTCGCTACTT
TATGTAGGGTATG TAACACTCGCT CGT
total time for 1000random sequences is 0s
[yg336@wind ~/inf503/Homework4 ]$ tail output_2B_10000.txt
CGAG_TGCACCAGTGACCAAGCAAGAAAGAGACAATTTCTAGAGGGT
CCAGATCCATCA_AAACCAAGCAAG__AG_GTC_ATTTATTGAAGAT
total time for 10000random sequences is 0s
[yg336@wind ~/inf503/Homework4 ]$ tail output_2B_100000.txt
CTACAGTTTCTGTTTC_TTCACCTGATG_CTGTTAC_AGCGTATAAT_GG
||| ||| xxx|xxx| |||||||||| || x|| |x| x|x|| ||
CTA_AGT_CAAGACCCTTTCACCTGATGCCTG_GACGAAC_CACAATCGG
CTACAGTTTCTGTTTC_TTCACCTGATG_CTGTTAC_AGCGTATAAT_GG
||| || |xxx|xxx| |||||||||| ||| x|| ||x| x|x||| ||
CTA AG TCAAGACCCTTTCACCTGATGCCTG GACGAAC CACAATCGG
otal time for 100000random sequences is 8s
yg336@wind ~/inf503/Homework4 | $ tail output 28 1000000.txt
 CAAAGAATACTGT TAAGAGTGTCG
CAAGGGAT C GTATAAGAGTGTCG
total time for 1000000random sequences is 79s
```

Problem 2C

```
yg336@wind:~/inf503/Homework4

The number of arguments passed: 5

The first argument is: main

The second argument is: problem2C

The third argument is: /common/contrib/classroom/inf503/SARS_COV2.txt

The fourth argument is: /home/yg336/inf503/Homework4/readsets.txt

The fifth argument is: 1000

random select 100,000 fragments from SARS-COV2 genome:
fragment found in SARS-COV2: 99998

random select 100,000 fragments from SARS-COV2 genome with 5% mutation:
fragment found in SARS-COV2: 8907
```

Note: All the fragments should be found in the SARS-COV2 genome if they are randomly selected with no mutation. The mismatch here is because of the boundary condition.