LSDS Assignment 4

Command for running Problem A: srun homework_4 1 human.txt human_reads_trimmed.fa

Command for running Problem B: srun homework_4 2 human.txt human_reads_trimmed.fa

- A) Needleman Wunch(Random and Completely Random):
 - a. For each of your searches (10K, 100K, and 1M), how many 'hits' with up to 2 mismatches did you find?

For Random:

- a) For 10k: Number of hits are 9864
- b) For 100k: Number of hits are 99003
- c) For 1M: Number of hits are 990003

For Completely Random:

- a) For 10k: Number of hits are 8657
- b) For 100k: Number of hits are 87005
- c) For 1M: Number of hits are 870005
- b. For each of your searches (10K, 100K, and 1M), how long did the search take?

For Random:

- a) For 10k: Total time taken is 83765.3 seconds
- b) For 100k: Total time taken is 85938.48 seconds
- c) For 1M: Total time taken is 8617538.48 seconds

For Completely Random:

- d) For 10k: Total time taken is 276091 seconds
- e) For 100k: Total time taken is 2768202.26 seconds
- f) For 1M: Total time taken is 27689202.26 seconds

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 ondemand.hpc.nau.edu/pun/sys/dashboard/files/fs//scratch/au282/HW_4/part1_trimmed_output.txt
File size of genome data is 3057186663
File size of query dataset is 27772294
Generating random indices using random function
The best score is 32
Found for string TAACCCTAACCCTAAC in query buffer
Found for string TAACCCTAACCCTAAC in genome buffer
Total number of hits observed in 500 n-mers are 496
Total time taken for searching all hits for 500 n-mers are 1849.82 seconds
The best score is 29
Found for string GGAAGAAAGCTTTCTG in query buffer
Found for string GGAAGAAAGCCTTCTG in genome buffer
Total number of hits observed in 1000 n-mers are 965
Total time taken for searching all hits for 1000 n-mers are 10882.8 seconds
The best score is 26
Found for string TGCCCGGACCTGGCGG in query buffer Found for string CGCCCAGACCTGGCGG in genome buffer
Total number of hits observed in 10000 n-mers are 9864
Total time taken for searching all hits for 10000 n-mers are 83765.3 seconds
                                         Generating completely random indices using custom function
The best score is 28
Found for string ACCGTCCTTGCTGGCG in query buffer
Found for string ACCGTCCTGCTGCGCG which was generated completely random Total number of hits observed in 500 n-mers are 437
Total time taken for searching all hits for 500 n-mers are 13046.7 seconds
The best score is 26
Found for string TATGTTCTATATCTAG in query buffer
Found for string TATGTTCTCTATCGAG which was generated completely random
Total number of hits observed in 1000 n-mers are 853
Total time taken for searching all hits for 1000 n-mers are 28222.9 seconds
The best score is 26
Found for string TAGCCTCCATCCATTA in query buffer
Found for string TAGCCTCCGTCCGTTA which was generated completely random
Total number of hits observed in 10000 n-mers are 8657
Total time taken for searching all hits for 10000 n-mers are 276091 seconds
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c. How long would the search take for the entire subject dataset?

For Random -> human genome(approx. 3 billion):

Number of hits are 2659752401

Total time taken is 835.646 years(approx. 8 centuries)

For Completely Random -> human genome(approx. 3 billion):

Number of hits are 2659752401

Total time taken is 2684.34 years(approx. 20 centuries)

B) BLAST(Random and Completely Random):

a. For each of your searches (10K, 100K, and 1M), how many 'hits' with up to 2 mismatches did you find?

For Random:

a) For 10k: Number of hits are 21325

b) For 100k: Number of hits are 209867

c) For 1M: Number of hits are 1437699

For Completely Random:

g) For 10k: Number of hits are 19692

h) For 100k: Number of hits are 258651

i) For 1M: Number of hits are 2871541

b. For each of your searches (10K, 100K, and 1M), how long did the search take?

For Random:

a) For 10k: Total time taken is 113.82 seconds

b) For 100k: Total time taken is 246.79 seconds

c) For 1M: Total time taken is 316.57 seconds

For Completely Random:

j) For 10k: Total time taken is 120.24 seconds

k) For 100k: Total time taken is 176.4 seconds

I) For 1M: Total time taken is 373.45 seconds

🕙 https://ondemand.hpc.nau.edu/pun/sys/dashboard/files/fs//scratch/au282/HW_4/output_2.txt - Google Chrome ondemand.hpc.nau.edu/pun/sys/dashboard/files/fs//scratch/au282/HW_4/output_2.txt File size of genome data is 3057186663 File size of query dataset is 27772294 Using BLAST WAY Generating random indices using random function The best score is 32 Found for string TAACCCTAACCCTAAC in query buffer Found for string TAACCCTAACCCTAAC in genome buffer Total number of hits observed in 10000 n-mers are 21325 Total time taken for searching all hits for 10000 n-mers are 113.82 seconds The best score is 28 Found for string GAAGATGAAGAATAAC in query buffer Found for string GAGATGTAAGAATAAC in genome buffer Total number of hits observed in 100000 n-mers are 209867 Total time taken for searching all hits for 100000 n-mers are 246.79 seconds The best score is 28 Found for string TTGATTGAGGGCTCAA in query buffer Found for string TTGTTGAGGGCTGCAA in genome buffer Total number of hits observed in 1000000 n-mers are 1437699 Total time taken for searching all hits for 1000000 n-mers are 316.57 seconds Generating completely random indices using custom function The best score is 28 Found for string TGAGCAAGTTCTAGGC in query buffer Found for string TGAGCAAGTCTCTAGC which was generated completely random Total number of hits observed in 10000 n-mers are 19692 Total time taken for searching all hits for 10000 n-mers are 120.24 seconds The best score is 26 Found for string CGAGACCTCTACCACT in query buffer Found for string CAAGACGTCTACCACT which was generated completely random Total number of hits observed in 100000 n-mers are 258651 Total time taken for searching all hits for 100000 n-mers are 176.4 seconds ______ The best score is 26 Found for string CCCAGCCAACGTTTGG in query buffer Found for string CCCAGCCAACGTTTCT which was generated completely random Total number of hits observed in 1000000 n-mers are 2871541

Total number of hits observed in 1000000 n-mers are 2871541

Total time taken for searching all hits for 1000000 n-mers are 373.45 seconds

c. How long would the search take for the entire subject dataset?

For Random -> human genome(approx. 3 billion):

Number of hits are 4371783947
Total time taken is 7.24 days

For Completely Random -> human genome(approx. 3 billion):

Number of hits are 8804688475
Total time taken is 9.05 days

d. How does that compare with the benchmarks from problem 1, part B?

For completely random using NW it took us approximately 20 centuries but when we used BLAST for the same it took approximately 9.05 days which is a drastic change. This is because BLAST is a heuristic approach and we ignore the k-mers which never resulted to a hit sequence but we wasted our time in NW still evaluating for it.

Time complexity for NW : O(N) * O(G) * O(n * n)
Time complexity for BLAST : O(N) * O(n) * O(n)















