INF-503

Table of Contents

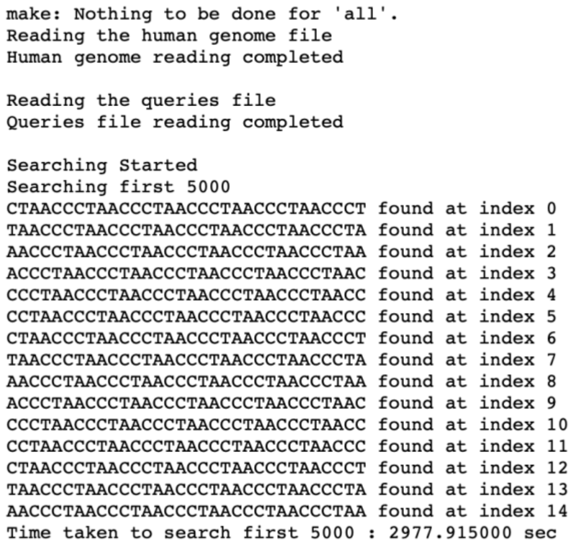
Homework – 2

Problem #1 :

(20 pts) Read in the entire query dataset and store it in an instance of the Queries_AR class. Read in the entire subject dataset into a single, concatenated character array (same way you did it in HW#1). Implement a search function which would search for 32-character fragments of the subject sequence within the Queries_AR object. The search function should return the location (index) of the match OR a negative value if a 'hit' was not found. Iterate through 32-character long fragments of the subject dataset, searching for each one in the query dataset.

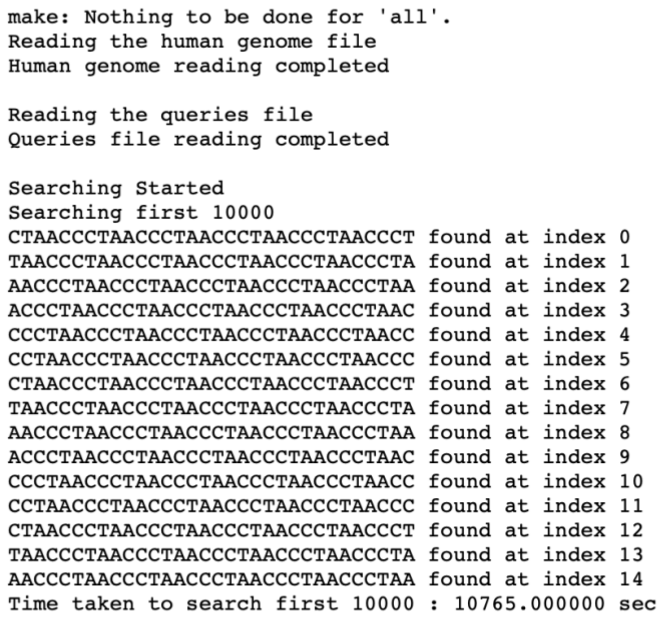
● How long did it take you to search for the first 5k, 10K, 100K, and 1M 32-character long fragments of the subject dataset within the query dataset?

1. For first 5k records



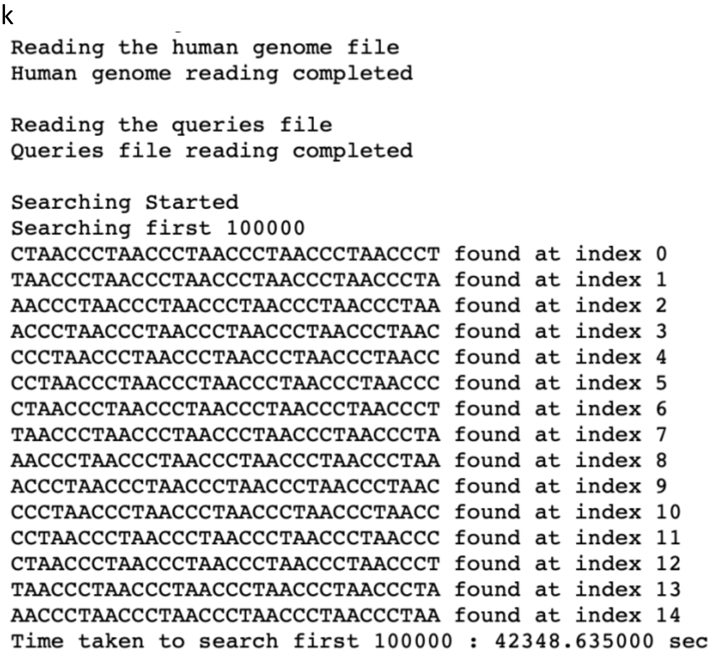
```
make: Nothing to be done for 'all'.
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Searching Started
Searching first 5000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 5000 : 2977.915000 sec
```

2. For first 10k records



```
make: Nothing to be done for 'all'.
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Searching Started
Searching first 10000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 10000 : 10765.000000 sec
```

3. For first 100k



```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Searching Started
Searching first 100000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 100000 : 42348.635000 sec
```

4. For 1M records

For 5000 records 2977.915 sec / 5000 records = 0.5955 sec/rec

For 10000 records 10765.00 / 10000 records = 1.07 sec / rec

For 100000 records 42388.635 sec / 100000 records = 0.42 sec / rec

Avg time per record = average of all three = 0.69 sec/rec

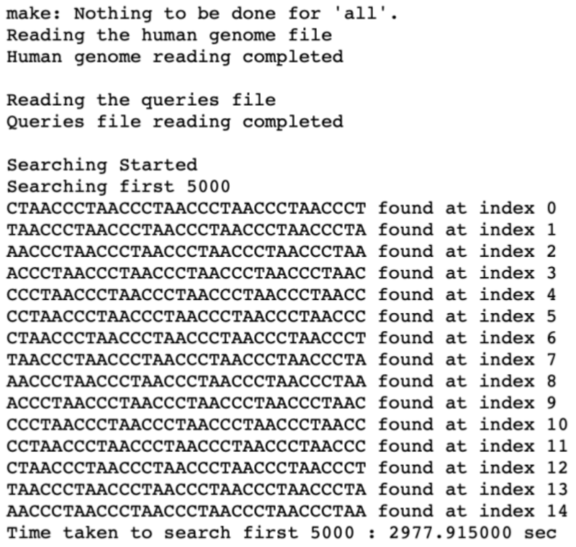
For 1000000 records = 0.69 * 1000000 = 690000seconds

● How long would it take to search for every possible 32-character long fragment of the subject dataset within the query dataset? Please note that depending on the efficiency of your algorithm, this step may take a long time. If the total time is greater than 24 CPU hours, provide an estimate rather than an exact number.

Time to run for total genome (3057186663)

3057186663 * 0.69 = 210,94,58,797.47 seconds

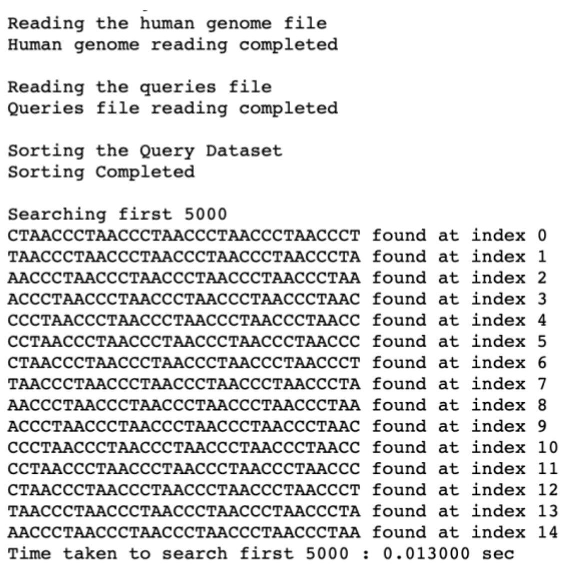
● Print the first 15 fragments of the subject dataset along with it's indices that you found within the Query AR object (if any)



```
make: Nothing to be done for 'all'.
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Searching Started
Searching first 5000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 5000 : 2977.915000 sec
```

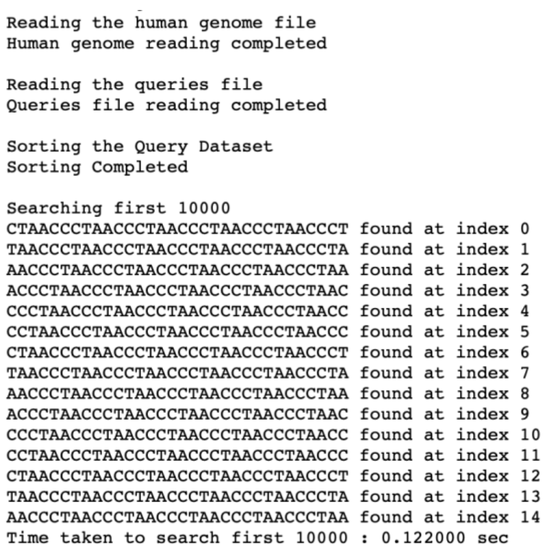
B. 20 pts) Read in the entire query dataset and store it in an instance of the Queries_AR class. Sort all character fragments in alphabetic (lexicographic) order. Any sorting algorithm will do. Read in the entire subject dataset into a single, concatenated character array (same way you did it in HW#1). Implement a search function which would search for 32 character fragments of the subject sequence within the Queries_AR object. The search function you implement should be optimal in time compared to the search function implemented in Part A and should return the location (index) of the match OR a negative value if a 'hit' was not found. Iterate through 32-character long fragments of the subject dataset, searching for each one in the query dataset.
● How long did it take you to search for the first 5k, 10K, 100K, and 1M 32-character long fragments of the subject dataset within the query dataset?

1. For first 5k records



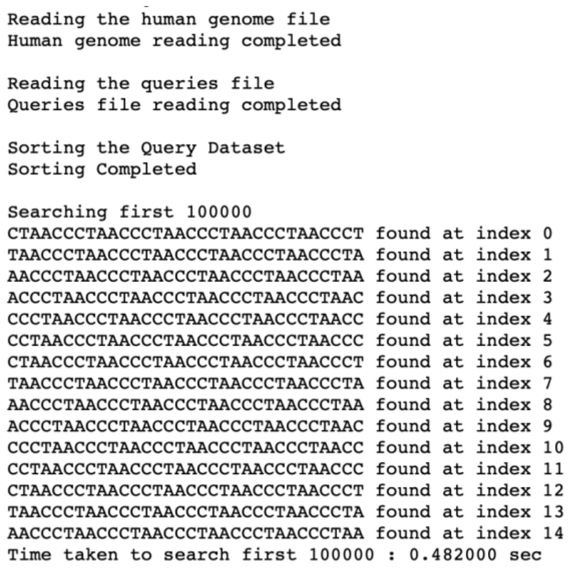
```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching first 5000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 5000 : 0.013000 sec
```

2. For first 10k records



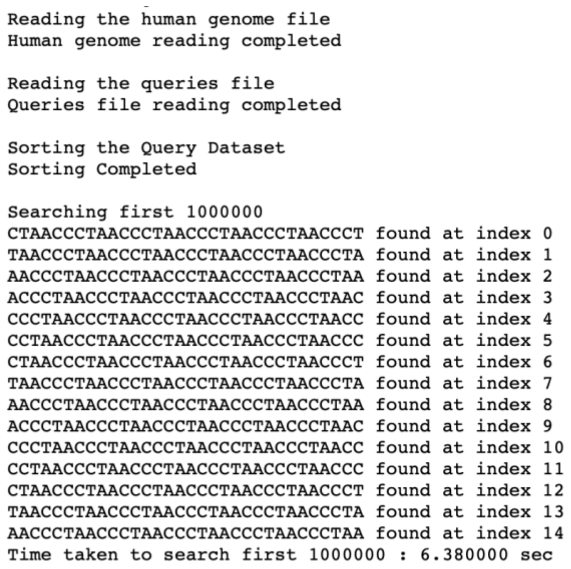
```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching first 10000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 10000 : 0.122000 sec
```

3. For first 100k records



```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching first 100000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 100000 : 0.482000 sec
```

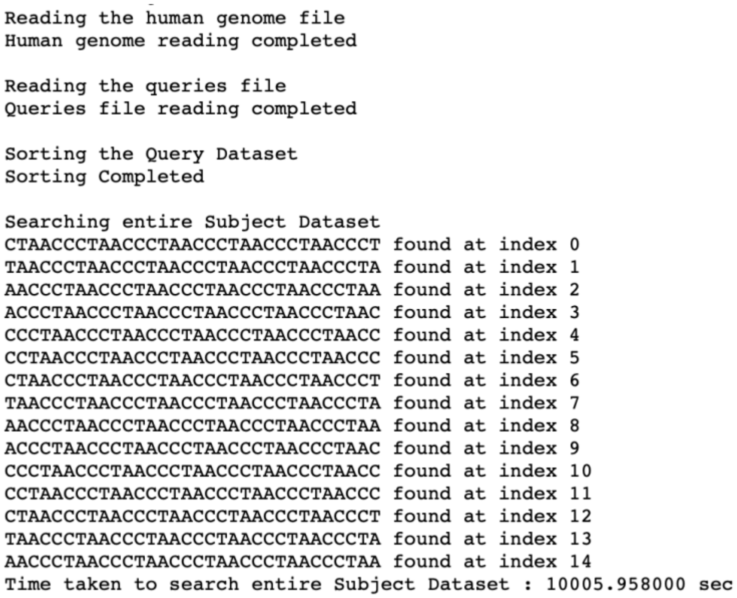
4. For first 1M records



```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching first 1000000
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search first 1000000 : 6.380000 sec
```

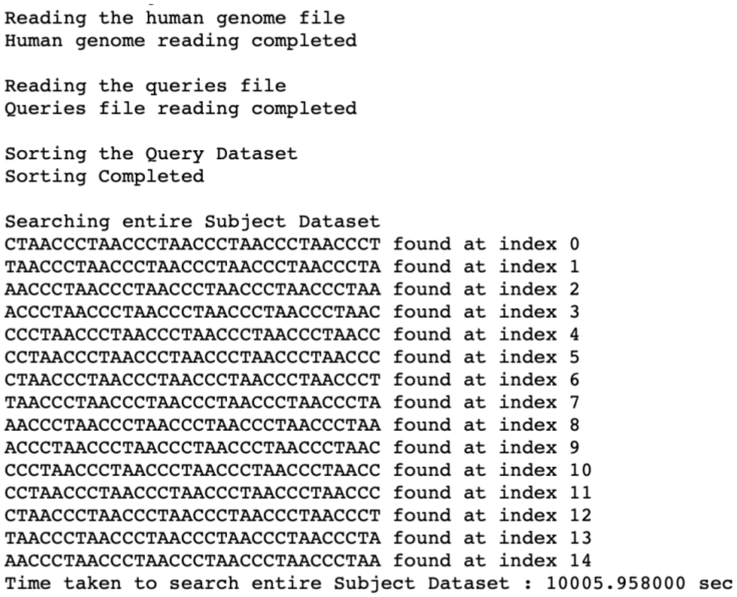
● How long would it take to search for every possible 32-character long fragment of the subject dataset within the query dataset? Please note that depending on the efficiency of your algorithm, this step may take a long time. If the total time estimate is greater than 24 CPU hours, provide an estimate rather than an exact number.

1. To run entire Genome



```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching entire Subject Dataset
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search entire Subject Dataset : 10005.958000 sec
```

- Print the first 15 fragments of the subject dataset along with it’s indices that you found within the Query AR object (if any)



```
Reading the human genome file
Human genome reading completed

Reading the queries file
Queries file reading completed

Sorting the Query Dataset
Sorting Completed

Searching entire Subject Dataset
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 0
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 1
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 2
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 3
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 4
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 5
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 6
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 7
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 8
ACCCTAACCCTAACCCTAACCCTAACCCTAAC found at index 9
CCCTAACCCTAACCCTAACCCTAACCCTAACC found at index 10
CCTAACCCTAACCCTAACCCTAACCCTAACCC found at index 11
CTAACCCTAACCCTAACCCTAACCCTAACCCT found at index 12
TAACCCTAACCCTAACCCTAACCCTAACCCTA found at index 13
AACCCTAACCCTAACCCTAACCCTAACCCTAA found at index 14
Time taken to search entire Subject Dataset : 10005.958000 sec
```

c. (20 pts) Explain the following in a video recording of duration for at most 8 minutes.

- Using your write-up (.pdf format) that you have submitted, please provide a detailed explanation of your approach to solving the problem. You should cover the following points within a maximum time limit of 3 minutes:

i. Provide a detailed explanation of the answers submitted in the write-up document for both Part A and Part B. Elaborate on why the results obtained are logical, and present your conclusions based on those results.

- During your code explanation, which should last no more than 5 minutes, please cover all aspects of your code, including:

i. Explain the logic used in implementing the search algorithm in Part A for

searching the first 5k, 10K, 100K, and 1M 32-character long fragments of the subject dataset within the query dataset. Clearly state the motive of this function and detail the steps taken in its implementation.
ii. Describe the specific bugs and issues you encountered while solving this assignment. These bugs could be from any part of your code for this homework. Provide detailed explanations of these challenges, avoiding trivial errors such as "missing a semicolon in the code."
iii. Highlight at least one specific optimization you made to improve the code's efficiency or readability.

Code Execution:

Firstly, run the make command to ready the executable file

```
srun make
```

To run code for all the lengths given in the assignment **without sort**, use the below command(s)

5000 - unsorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 5000 unsorted
```

10000 - unsorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 10000 unsorted
```

100000 - unsorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 100000 unsorted
```

1000000 - unsorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 1000000 unsorted
```

Entire Genome - unsorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 0 unsorted
```

To run code for all the lengths given in the assignment **with sort**, use the below command(s)

5000 - sorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 5000 sorted
```

10000 - sorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 10000 sorted
```

100000 - sorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 100000 sorted
```

1000000 - sorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 1000000 sorted
```

Entire Genome - sorted

```
srun ./homework2 /common/contrib/classroom/inf503/genomes/human.txt /common/contrib/classroom/inf503/human_reads_125_32.fa 0 sorted
```

Part A: Searching Fragments Using Linear Search

1. Loaded genome data into Queries_AR from files using functions (ReadFile() and ReadQueriesFile()).
2. Implemented a basic linear search to find 32-character fragments within the genomic data (HumanGenome).

3. Iterated through each fragment in the dataset and compared it with all fragments in QueriesArray until a match was found or all possibilities completed and returing -1.
4. Calculated the time taken for different fragment counts (5k, 10k, 100k, 1M) using a timer (chrono library) to assess efficiency.
5. Displayed the first 15 matching fragments and indices

Part B: Sorting and Searching with Binary Search

1. Used Quick Sort to alphabetically sort all fragments in QueriesArray.
2. Utilized binary search, a more efficient method post-sorting, to find 32-character fragments within QueriesArray.
3. Started searching from the middle of the sorted list, dividing possibilities with each comparison until finding a match or not.
4. Measured search time for various fragment counts (5k, 10k, 100k, 1M) using binary search.
5. Validated results by printing the first 15 matching fragments and their positions in the sorted dataset.

Video Presentation Link

https://nau.zoom.us/rec/play/kKG-5MQ9lV-8DYW2yqWbv__fcm1sOe4Yh4K09iiTMujN22U6tnYCdIIq53tYN9Z7RNMP1DM1qe6g-S93.KFlYx3_O5PKCiuO3?autoplay=true&startTime=1720070672000