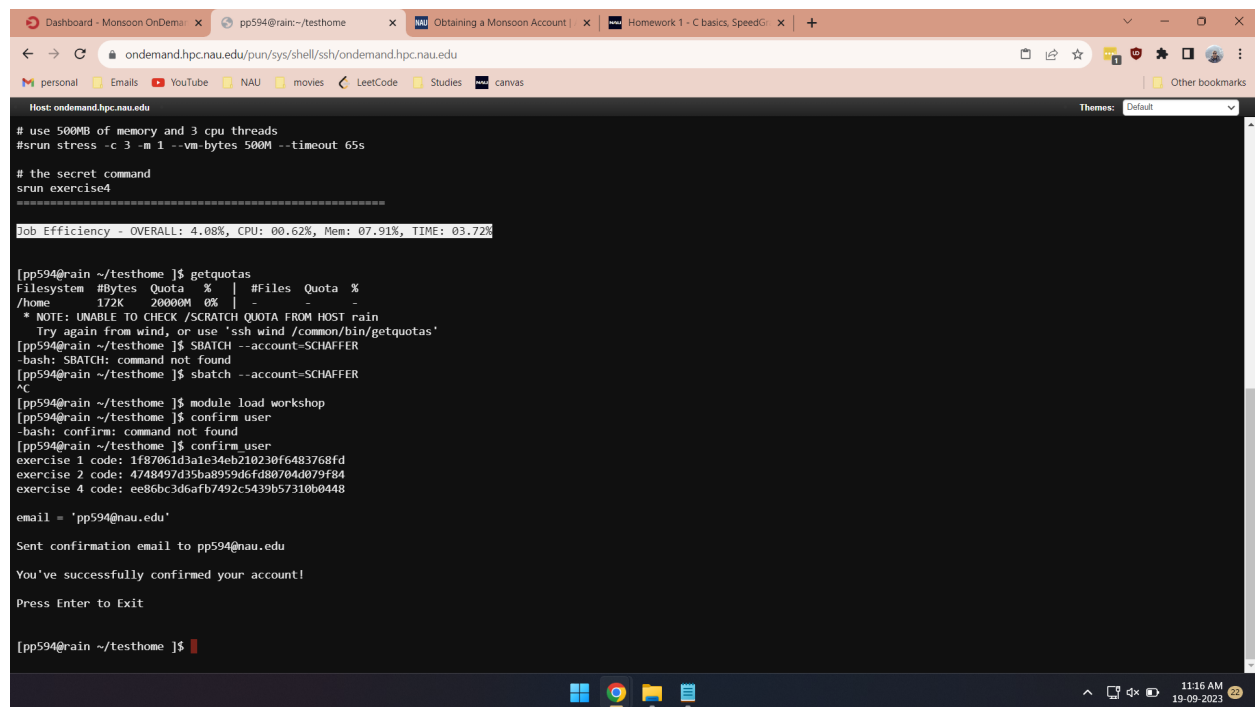


Problem 1-



```
Dashboard - Monsoon OnDemand | x pp594@rain:~/testhome | x Obtaining a Monsoon Account | x Homework 1 - C basics, SpeedG | x +
ondemand.hpc.nau.edu/pun/sys/shell/ssh/ondemand.hpc.nau.edu
personal | Emails | YouTube | NAU | movies | LeetCode | Studies | canvas
Host: ondemand.hpc.nau.edu
Themes: Default

# use 500MB of memory and 3 cpu threads
#srun stress -c 3 -m 1 --vm-bytes 500M --timeout 65s

# the secret command
srun exercise4

Job Efficiency - OVERALL: 4.08%, CPU: 00.62%, Mem: 07.91%, TIME: 03.72%

[pp594@rain ~/testhome]$ getquotas
Filesystem      #bytes  Quota  % | #Files  Quota  %
/home           172K   20000M  0% | -        -        -
* NOTE: UNABLE TO CHECK /SCRATCH QUOTA FROM HOST rain
  Try again from wind, or use 'ssh wind /common/bin/getquotas'
[pp594@rain ~/testhome]$ SBATCH --account=SCHAFFER
-bash: SBATCH: command not found
[pp594@rain ~/testhome]$ sbatch --account=SCHAFFER
^C
[pp594@rain ~/testhome]$ module load workshop
[pp594@rain ~/testhome]$ confirm user
-bash: confirm: command not found
[pp594@rain ~/testhome]$ confirm user
exercise 1 code: 1f87061d3a1e34ab210230f6483768fd
exercise 2 code: 4748497d35ba8959d6fd80704d079f84
exercise 4 code: ee86bc3d6afb7492c5439b57310b0448

email = 'pp594@nau.edu'

Sent confirmation email to pp594@nau.edu

You've successfully confirmed your account!

Press Enter to Exit

[pp594@rain ~/testhome]$
```

Problem 2:

I've created the functions computeCharacters, calculateGenomeSize, and readHumanGenome.

Compute Characters-

This function iterates over the file and reads each character that is not a scaffold header, It updates the ACGT counters, after all the characters have been read, it will compute the results i.e. GC content of the human genome, by calculating the sum of G count and C count and then the percentage of them in the whole genome.

Also, the Time Complexity to search the genome was $O(N)$ as we just assessed each character once.

Time Complexity- $O(N*M)$

calculateGenomeSize-

The calculate genome size function does exactly as the name suggests, opens the given file, And iterates through each line and if the line is not a scaffold name, it will count all the member characters and return it.

Time complexity- $O(N)$

readHumanGenome -

This function reads the file line by line and if the line is not a scaffold header, then it will keep on reading the characters to calculate the scaffold length, minimum scaffold length, maximum scaffold length, and the total number of scaffolds in the file.

Also after the file is exhausted we find the average scaffold length and the total genome length.

Time Complexity- $O(N)$