Name: Parth Patel
Nau Id: 6293553

Usage: ./main --genome <genome_file_path> --fragments <fragment_count>

Arguments:
–genome - Genome Filepath
–fragments - the number of randomly generated fragments we want to search through the suffix tree

Ans 1 and 2:
The size of the tree and the number of matches for different numbers of fragments

    5K:

        Nodes: 84489
        Matches:5000

    50K:

        Nodes: 84304
        Matches:50000

    100K:

        Nodes: 82497
        Matches:100000

Explanation:
The matches and the number of searches are equal and it's not surprising, as we pushed the subject genome of 50k length into the suffix tree, which means it has every possible subsequence of the subject ranging in length from 50k down to 1,
Where 1 would constitute each nucleotide individually on its own.

Now when we are searching for fragments we are just looking to see if they exist in the tree, which they will be because we are picking these fragments from the subject that was pushed into the suffix tree. As I said earlier it has every possible subsequence of the subject inside it, and the fragments are subsequences of the subject, hence the number of matches is equal to the number of searches.

Ans 3:
Time Complexity:
O(N)*O(n)
Where,
N = number of searches/queries.
n = size of each query(here 36).

Raw Output:

```
[pp594@wind ~/hw6 ]$ make runa
./main --genome /scratch/pp594/data/human.txt  --fragments 5000
----------------------------------------------------------------
Genome Length: 3057186663
Chosen index: 957914073
subject length: 50000
Number of nodes: 84489
Searching for 5000 fragments of length 36
Matches: 5000

----------------------------------------------------------------
./main --genome /scratch/pp594/data/human.txt  --fragments 50000
----------------------------------------------------------------
Genome Length: 3057186663
Chosen index: 1010981242
subject length: 50000
Number of nodes: 84304
Searching for 50000 fragments of length 36
Matches: 50000

----------------------------------------------------------------
./main --genome /scratch/pp594/data/human.txt  --fragments 100000
----------------------------------------------------------------
Genome Length: 3057186663
Chosen index: 1357108254
subject length: 50000
Number of nodes: 82497
Searching for 100000 fragments of length 36
Matches: 100000

----------------------------------------------------------------
```