

PS5 DNA Sequence Alignment

Overview:

This program calculates the optimal sequence alignment of two DNA strings. A major part of this assignment was analyzing the time and space usage with Valgrind.

Implementation:

This program is implemented with a dynamic programming approach that creates a N by M matrix, N and M being the sizes of the DNA strings. This matrix is used to find the edit distance and the optimal alignment.

What I Learned:

- How to use dynamic programming.
- How to display my program execution time.
- How to analyze the results of running valgrind to find memory usage of the program.
- How to calculate the largest input my program could theoretically handle with 8GB of RAM, or if it had to 24 hours to execute.

Output:

```
osboxes@osboxes:~/Documents/ps5$ ./ED < example10.txt
Edit distance = 7
A T 1
A A 0
C - 2
A A 0
G G 0
T G 1
T T 0
A - 2
C C 0
C A 1
Execution time is 4.4e-05 seconds.
```

