

Matthew Noack matthewnoack@csu.fullerton.edu

Project 3

1) Analyze the efficiency of the exhaustive algorithm mathematically to determine its big-O efficiency class, probably similar to the exhaustive algorithm in Project 2 .

The big O of the Exhaustive Method is $2^{(n+m)}$. This is due to number of iterations that the generate_all_subsequences() generates has a for loop of two to the power of the size of the first set of subsequences and a for loop of two to the power of second set of subsequences.

2) Analyze the efficiency of the dynamic programming algorithm mathematically to determine its big-O efficiency class .

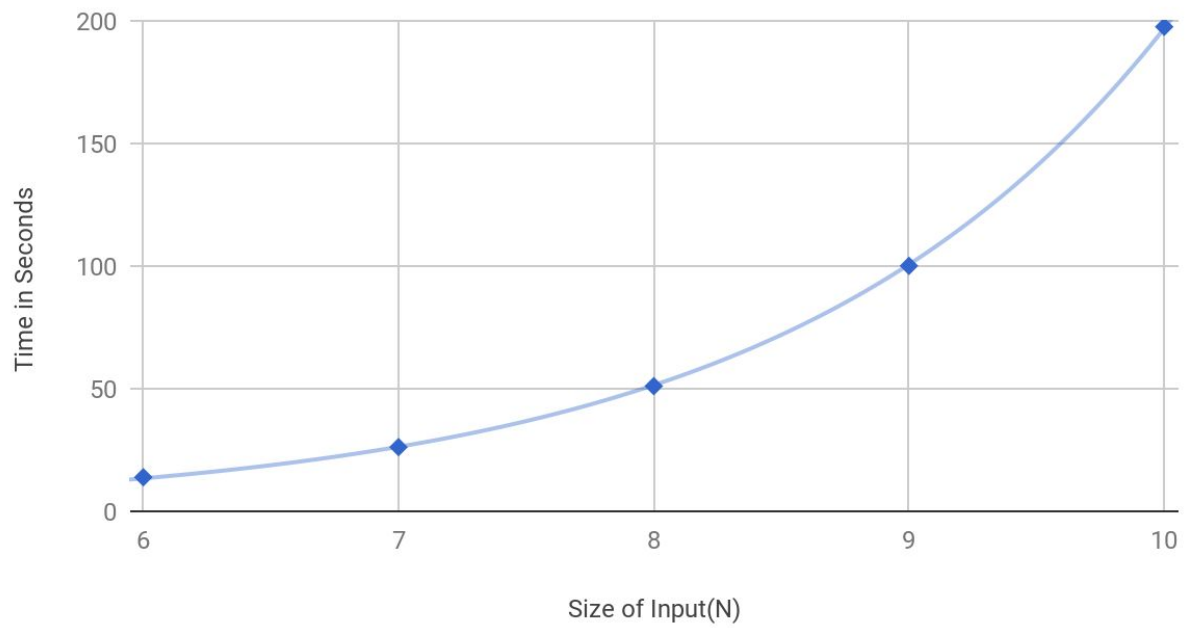
The big O of the Dynamic Programming is $O(n*m)$. This is due to a nested for loop iterating over the size of n and m.

3a) In both the exhaustive and dynamic methods, the fourth string matches to a different protein strain than sp|P32469|DPH5_YEAST Diphthine synthase. These results are still correct due to the time it took to complete the methods being within expected results predicted for each method.

4) The empirical data matches the mathematically derived big O for both the Exhaustive Method and Dynamic Programming. Since the only change that occurs with each program call is the String to Match(n), the list of proteins(m), is a constant. Therefore, the Exhaustive Method grows at a $O(2^n)$ rate, as shown in the Exhaustive Method graph, and the Dynamic programming grows at a $O(n)$ rate, as shown in the Dynamic Programming graph.

```
oscreader@OSC: ~/project-3-matthewnoack
File Edit View Search Terminal Help
oscreader@OSC:~$ cd project-3-matthewnoack
oscreader@OSC:~/project-3-matthewnoack$ ./experiment
----- Exhaustive Method -----
String to Match = QSDITV
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
13.8783
String to Match = KDITVXR
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
26.1719
String to Match = YKSDTWRN
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
51.0449
String to Match = AYKDIRNLX
sp|Q08032|CDC45_YEAST Cell division control protein 45 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC45 PE=1 SV=1
100.061
String to Match = BQSITVARGL
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
197.551
----- Dynamic Programming -----
String to Match = QSDITV
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
0.00282855
String to Match = KDITVXR
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
0.00286113
String to Match = YKSDTWRN
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
0.0034069
String to Match = AYKDIRNLX
sp|Q08032|CDC45_YEAST Cell division control protein 45 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=CDC45 PE=1 SV=1
0.00399738
String to Match = BQSITVARGL
sp|P32469|DPH5_YEAST Diphthine synthase OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c) GN=DPH5 PE=1 SV=1
0.00447403
oscreader@OSC:~/project-3-matthewnoack$
```

Exhaustive Method



Dynamic Programming

