COT 6405 Programming Project

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Contents

Comparison of longest common subsequence (LCS) algorithms

COT 6405 Analysis of Algorithms, Spring 2020

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1 Introduction

This notebook compares **longest common subsequence** (defined below) algorithms:

- **Brute-force**: generates combinations of subseqences and check if they are common subsequences.
- **Dynamic programming**: takes advantage of common subproblems to not evaluate the same subsequence more than once.
- **Hirschberg's linear space**: a dynamic programming approach, combined with divide-and-conquer, that uses significantly less space than the dynamic programming algorithm.

The comparison measures:

- Runtime efficiency: how long it takes to find a longest common subsequence.
- Space efficiency: how much space is used to find a longest common subsequence.

The code used in the experiments is written in Pyhton 3.x. The code is available in this GitHub repository.

2 Longest common subsequence

2.1 Definiton

Given a sequence $X = < x_1, x_2, \ldots, x_m >$, another sequence Z is a **subsequence** of X if there is a strictly increasing sequence $< i_1, i_2, \ldots, i_k >$ of indices of X such that for all $j = 1, 2, \ldots, k$, we have $x_{ij} = z_j$ [CLRS01].

For example:

- Given the sequence $X = < A, B, C, B, D, A, B >$
- The sequence $Z = < B, C, D, B >$ is a subsequence of X, with indices $< 2, 3, 5, 7 >$

Given two sequences, a **common subsequence** is a sequence that is common to both sequences. A **longest common subsequence** (LCS) is a maximum-length common subsequence.

For example:

- Given the sequences $X = < A, B, C, B, D, A, B >$ and $Y = < B, D, C, A, B, A >$

- The sequence $< B, C, A >$ is a common subsequence
- The sequence $< B, C, B, A >$ is a longest common subsequence
- The sequence $< B, D, A, B >$ is another LCS, therefore LCSs do not have to be unique

2.2 Applications

Applications of LCS include determining if two organisms are similar by comparing their DNAs. In this case, "similar" can be determined by the longest common subsequence between the DNAs. The longer the subsequence, the more common the organisms are.

Building on the DNA example, LCS can be used as a form of compression. Using a pre-built suffix tree, an LCS-based solution compressed the human genome from about 3 GB to just over 8 MB [BAF16].

LCS is also used in version control systems to produce the "diff", the minimal amount of additions and deletions that transform the older version of a file into the new version, also known as the "edit distance" [NAV01]. For example, this output of Git's `diff` command between two versions of a file shows deletion and addition of two lines to transform the old version of the file into the new one:

```
@@ -33,15 +33,11 @@ class ModifiedFile(BaseCommit):
     '''Number of lines added to the file in this commit.'''
     deleted = Column(Integer)
-    '''Number of lines deleted from the file in tihs commit.'''
+    '''Number of lines deleted from the file in this commit.'''
-    commit_id = Column(String)
+    commit_id = Column(String, ForeignKey('commit_info.commit_id'))
```

3 Notebook structure

The remainder of this notebook is structured as follows:

- **Algorithms**: describes the algorithms used in the tests.
- **Planning of experiments**: describes the experiments performed, data collected for each one, the analysis performed on them.
- **Initialization and verification**: initializes the notebook (import Python modules, set important environment values) and verifies that the algorithms are working before using them.
- **Measurement and analysis**: run the tests to collect the metrics and analyzes those metrics.
- **Code**: documents relevant pieces of the code and other technical aspects found during the development and execution of the tests.

4 Algorithm descriptions

Three algorithms will be analyzed:

- Brute-force
- Dynamic programming
- Hirschberg's linear space

In all sections below, m is the lenght of the longest sequence and n is the length of the shortest sequence.

4.1 Brute-force

Brute-force is the simplest LCS algorithm: generate subsequences of the smaller sequence and check if they are also a subsequence of the larger sequence.

The pseudocode for the algorithm is:

```
LCS_BRUTE_FORCE(X, Y)
    // Pick the shortest sequence to generate subsequences
    short_seq = shortest_of(X, Y)
    long_seq = longest_of(X, Y)

    // Try all subsequences of the shortest sequence
    for i = length(short_seq) to 1
        // Try all subsequences of length i, one at a time
        while "there are subsequences of length i to try":
            subseq = next_subsequence(short_seq, i)
            if is_subsequence(subseq, long_seq)
                return subseq

    // Could not find a subsequence
    return [] // empty sequence
```

Runtime analysis: the algorithm selects the smaller sequence to generate combinations to test. Since there are 2^n combinations of subsequences that can be generated from the subsequence, and each one has to be tested against the larger sequence, the runtime is $m \times 2^n$. In most cases, the second term is much larger than m, making it a $O(2^n)$ algorithm.

Space analysis: A naive implementation would generate all combinations of the smaller sequence ahead time, using $O(2^n)$ space. An optimized implementation, as shown above, generates one combination of the smaller sequence at a time, using $O(n)$ space.

4.2 Dynamic programming

Dynamic programming makes use of the optimal substructure of the LCS, solving smaller subproblems only once, combining the solutions.

The pseudocode is shown below. It has two parts: first two matrices are constructed to determine the LCS length and how to construct it (a series of "moves"), then the LCS is extracted by going through the moves matrix.

```
LCS_LENGTH(X, Y)
    m = length(X)
    n = length(Y)

    // c is an m x n matrix with the top row and
    // left column initialized to zero
    c = matrix(m, n)
    for i = 1 to m
        c[i, 0] = 0
    for j = 1 to n
        c[0, j] = 0

    // b is an m x n empty matrix that will hold the
    // movements to build the LCS
    b = matrix(m ,n)

    for i = 1 to m
        for j = 1 to n
            if X[i] == Y[j]
                c[i,j] = c[i-1,j-1] + 1
                b[i,j] =  "diagonal"
            else if c[i-1,j] >= c[i, j-1]
                c[i,j] = c[i-1,j]
                b[i,j] =  "up"
            else
                c[i,j] = c[i,j-1]
                b[i,j] =  "down"

    // c[m,n] has the LCS length and b has the
    // sequences of moves to extract the LCS
    return c, b

EXTRACT_LCS(b, X, i, j)
    lcs = empty_list()

    while i > 0 and j > 0
        move = b[i,j]
        if move == "diagonal"
            lcs = lcs + X[i]
            i = i - 1
            j = j - 1
        else if move == "up"
            i = i - 1
        else // "down"
            j = j - 1

    // The LCS was built from the bottom up,
    // need revert it before returning
    return reverse(lcs)

LCS(X, Y)
    b, c = LCS_LENGTH(X, Y)
    lcs = EXTRACT_LCS(b, X, length(X), length(Y))
    return lcs
```

Runtime analysis: the `LCS_LENGTH` part of the algorithm is $O(m \times n)$, from its two nested loops. The `EXTRACT_LCS` is $O(m + n)$. For large values of m and n, `LCS_LENGTH` dominates the runtime, making the algorithm overall $O(m \times n)$.

Space analysis: the $m \times n$ matrix in `LCS_LENGTH` is responsible for the space the algorithm needs, thus the space is $O(m \times n)$.

4.3 Hirschberg's linear space

Hirschberg's linear space algorithm [HIR75] is a dynamic programming approach that uses divide-and-conquer. As the name indicates, it makes efficient use of space.

The pseudocode is shown below. It has two parts: a *scoring* (also called *cost*) function to help decide where to divide the current subsequence being analyzed, and the function that divides-and-conquers, based on that score.

```
SCORE(X, Y)
    m = length(X)
    n = length(Y)

    // A list of of scores, initialized with n zeros
    scores = list(0 * n)

    for i = 1 to m
        prev_score = scores
        for j = 1 to n
            if X[i] == Y[j]
                scores[j+1] = prev_scores[j] + 1
            else
                scores[j+1] = max(scores[j], prev_scores[j + 1])

    return scores

LCS(X, Y)
    m = length(X)
    n = length(Y)
    if m == 0
        // Got to the end of the sequence
        return []
    else if m == 1
        // Last character, check if it is in subsequence
        if X[1] is in Y
            return X[1]
        else
            return []
    else
        // Find where to split the current sequences

        // X is split in the middle
        i = m / 2
        XB = X[i:i]
        XE = X[i+1:m]

        // Y is split based on the scores
        cost_top_left = SCORE(XB, Y)
        cost_bottom_right = SCORE(reverse(XE), reverse(Y)))
        cost = cost_top_left + reverse(cost_bottom_right)

        k = index of max(cost) // argmax(cost)
        YB = Y[1:k]
        YE = Y[k+1:n]

        // Solve for each part of the split sequences
        return LCS(XB, YB) + LCS(XE, YE)
```

Runtime analysis: in each step, the sequences under examination are split into two subquences at $m/2$ and a *q* based on a cost factor (this is the secret cause of the algorithm). It can be shown that the recurrence is $O(mn)$ [KT05] [FAG16].

Space analysis: a naive implementation of the algorithm creates copies of the sequences as it splits them during the recursive calls, using space $O(m+n)$. An implmentation that passes the original sequences around and uses indices to logically split them (without creating copies), uses space $O(min(m, n))$ (in the SCORE fuction).

4.4 Runtime and space summary

The following table summarizes the runtime and space characteristics of the algorithms.

Algorithm	Runtime	Space
Brute-force	$O(2^n)$	$O(n)$
Dynamic programming	$O(m \times n)$	$O(m \times n)$
Hirschberg	$O(m \times n)$	$O(min(m, n))$

5 Planning of experiments

The experiments compare the runtime and space of the brute-force, dynamic programming recursive, and Hirchberg's linear space algorithms.

To illustrate the algorithms in a typical application, the tests will use two strings that resemble DNA sequences (a combination of the letters `A`, `C`, `G`, and `T`) and will find an LCS for them. To emulate the computational biology case of searching for a common substring between two DNA strands, in each case we will search for a string that is one-tenth of the larger strings, illustrated in the table below.

5.1 Input size for tests

Strings of three sizes will be used, small, medium, large. For each size, the same strings will be used with all algorithms, to keep the comparison consistent.

Test size	The DNA strain (X)This is the *m* in RT and space analysis	The possible common sequence (Y)This is the *n* in RT and memory analysis
Small	1,000	100
Medium	10,000	1,000
Large	100,000	10,000

Table 1 - Size of strings to test and how they map to the m and n of the RT and memory analysis.

5.2 Runs

Each algorithm will be executed ten times (k=10) for each string size to remove variations in the environment. The average of these runs will be used as the final number for the algorithm.

Two values will be measured in each run, running time (RT) and memory (space) usage:

- Time: measured with Python's `time` package.
- Memory: measured with Python's `memory_profiler` package.

Details of how measurements were conducted are documented in the code section, later in this document.

5.3 Data structures

Experimental data, the strings, will be stored in the standard data structures for string representation, usually mapped to a constant-time access continuous array in programming languages. Auxiliary data structures to keep track of intermediate results will be kept either in Pythnon arrays on NumPy arrays, whichever is more performant for a specific piece of code.

5.4 Input generation

Strings for the tests will be generated using a pseudo-random number generation initialized with a seed, to ensure the repeatability of the experiments (the same sequence is generated every time). The strings will be generated only once, before each algorithm is executed, to ensure that the results can be compared with each other.

5.5 Graphs and tables

For each algorithm, two tables will be filled in:

- RT analysis: theoretical vs. empirical RT.
- Memory usage: theoretical vs. empirical memory usage.

The following table illustrates the RT analysis for the brute-force algorithm.

Test size	Theoretical complexity	Empirical RT (ms)	Ratio (empirical RT / theoretical complexity	Predicted RT	% error
Small m=1,000, n=100	$2^n = 2^{100}$				

Test size	Theoretical complexity	Empirical RT (ms)	Ratio (empirical RT / theoretical complexity	Predicted RT	% error
Medium m=10,000, n=1,000	2^n = 2^{1000}				
Large m=100,000, n=10,000	2^n = 2^{10000}				

Table 2 - RT analysis table example, using the brute-force algorithm as illustration

The table columns are computed as follows:

- *Ratio* measures the ratio between the empirical and the theoretical complexity. Its value is always > 0. It is used to calculate the constant *c*.
  - The constant *c* measures the overhead of the steps (computer instructions) that are outside the main loops (or recursive calls) of the algorithms. It is determined as the maximum of the ratio values (with outliers discarded), i.e. the maximum value of the *Ratio* column.
- *Predicted RT* is computed as the constant *c* times the *Theoretical complexity*.
- *% error* measures the discrepancy between the predicted and the empirical time: *(Empirical RT - Predicted RT) / Empirical RT * 100*.

The following table illustrates memory usage for the brute-force algorithm.

Test size	Theoretical memory usage (KiB)	Empirical memory usage (KiB)	% error
Smallm=1,000, n=100	n / 1024 = 0.98		
Mediumm=10,000, n=1,000	9.8		
Largem=100,000, n=10,000	97.7		

Table 3 - Memory usage analysis table example, using the brute-force algorithm as illustration

The table columns are computed as follows:

- *Theoretical memory usage* is the number of characters needed, times 1 byte per character, divided by 1,024 to transform to KiB.

  - "1 byte per character" comes from the variable-length encoding of strings in Python using the CPython environment. Because we are representing DNA strands, we are using only ASCII characters, which are represented as 1 byte [CPY20] [GOL20].

- *% error* measures the discrepancy between the theoretical and empirical memory usage: *Empirical memory usage / Predicted memory usage) / Empirical memory usage * 100*.

For the other algorithms, the theoretical values will be adjusted as follows:

- Dynamic programming:
  - Theoretical RT = $m \times n$
  - Theoretical memory usage = $m \times n$
- Hirschberg's linear space algorithm
  - Theoretical RT = $m \times n$
  - Theoretical memory usage = $m + n$

Once the tables are filled in, two sets of graphs will be created:

- **Algorithm comparison**: this set of graphs compares the empirical runtime and memory usage of the algorithms. There will be one runtime and one memory usage plot for all algorithms (two graphs).
- **Theoretical vs. empirical results**: this set of graphs compares the empirical runtime and memory usage of each algorithm. There will be one set of plots for each algorithm and each size, for a total of 9 graphs (3 algorithms, 3 sizes).

The following graphs will be generated for algorithm comparison:

- RT comparison: a horizontal bar graph with the runtime in ms (horizontal axis) for each algorithm, grouped by the input size. A horizontal bar graph will be used because of the expected large values for large input sizes. This representation makes better use of space.
- Memory comparison: similar to the graph above, using memory usage as the horizontal axis.

The following graphs will be generated for each algorithm for the theoretical vs. empirical results:

- Theoretical vs. empirical runtime in ms for each input size
- Theoretical vs. empirical memory usage in KiB for each input size

5.6 Programming language

The experiments use Python 3.x in a Jupyter Notebook environment.

6 Initialization and verification

Load commonly-used modules.

```
import pandas as pd
import matplotlib.pyplot as plt
import seaborn as sns
pd.set_option('precision', 3)
```

Check that the algorithms work by testing them against controlled input.

There are three part to the tests:

1. Automated tests that check against well-defined inputs. They are meant to be easy to debug, in case an algorithm fails.
2. Tests with longer inputs that simular DNA strands. They test more realistic scenarios, but still short enough to run fast.
3. A visual check, by printing the aligned subsequence. They guard against the test code itself having a failure that generates false positives.

```
import utils.lcs_test

lcs_test.test(visualize=True)
```

```
All basic tests passed
All DNA tests passed
Visual inspection:
                         lcs_brute_force:  CACATTGCCTGGATAGGGGCTAGGATCGAG
                         lcs_brute_force:  ....TT......AT.GG....AGGA.CGA. size=13
    lcs_dynamic_programming_matrix_numpy:  ....TT......AT.GG....AGGA.CGA. size=13
                    lcs_hirschberg_numpy:  ....TT......AT.GG....AGGA.CGA. size=13
```

7 Runtime tests and analysis

To illustrate a real-life scenario, the code checks if a DNA strand is part of a larger DNA sequence [WIK20a].

```
# Force reload because this piece of code frequently changes
import importlib
import metrics as m
importlib.reload(m);
```

7.1 Constant *c* calculation

This section calculates the constant *c* for each algorithm. This is the constant that accounts for instructions that are not in the loops. For example, given a runtime $O(n^2)$, the constant *c* allows us to write the runtime more precisely as $c \times n^2$.

The constant is also affected by the language and compiler or intepreter used. In this notebook it is calculated with dynamic analysis: run the code and calculate the overhead.

Each algorithm was executed once with different input sizes, with the pairs representing the length of X and Y, respectively: (1,000, 100), (2,000, 200), (3,000, 300), (4,000, 300), (4,000, 500), (4,000, 1,000).

Once the algorithms are run, we calculate *c* as $max(rt1, rt2, ..., rt_n)$, excluding outliers where applicable.

```
rt_results_raw, rt_results_summary = m.runtime(m.seq_phase1, verbose=1,
    file='runtime-phase1')
```

```
Loading from file
```

We now have two Pandas DataFramse:

- `rt_results_raw`: results from all 10 executions of each algorithms and each input size.
- `rt_results_summary`: average of the executions for each each algorithm and input size.

Using these DataFrames, the following sections calculate three constants, one for each algorithm. They are stored in the following variables:

- `c_bf`: the constant for the brute-force algorithm.
- `c_dp`: the constant for the dynamic programming algorithm.
- `c_h`: the constant for the Hirschberg linear space algorithm.

The dataframes contain metrics for all algorithms. The sections below filter the dataframe for the algorithm analyzed as needed.

7.1.1 Constant *c* for brute-force

```
rt_bf, c_bf = m.add_runtime_analysis(rt_results_summary, m.ALG_BRUTE_FORCE)
print('c_bf={}'.format(c_bf))
display(rt_bf)
```

```
c_bf=5.206481974415714e-32
```

```
     Algorithm  Sequence size  Subsequence size  Empirical RT (ms)  \
0  Brute-force           1000               100              0.066
1  Brute-force           2000               200              0.173
2  Brute-force           3000               300              0.206
3  Brute-force           4000               300              0.256
4  Brute-force           4000               500              0.495
5  Brute-force           4000              1000            156.909
6  Brute-force           5000               900              0.601
7  Brute-force           5000              1000              0.658
8  Brute-force           5000              1200              0.760

   Theoretical complexity       Ratio  Predicted RT    % error
0               1.268e+30   5.206e-32     6.600e-02  0.000e+00
1               1.607e+60   1.077e-61     8.366e+28 -4.836e+31
2               2.037e+90   1.011e-91     1.061e+59 -5.148e+61
3               2.037e+90   1.257e-91     1.061e+59 -4.143e+61
4              3.273e+150  1.512e-151    1.704e+119 -3.443e+121
5              1.072e+301  1.464e-299    5.579e+269 -3.555e+269
6              8.453e+270  7.110e-272    4.401e+239 -7.323e+241
7              1.072e+301  6.141e-302    5.579e+269 -8.478e+271
8                     inf   0.000e+00           inf       -inf
```

We can see in the table a very large error for most tests of the brute-force algorithm. This is caused by the "luck factor" of this algorithm: if we are lucky and generate a combination early on that happens to be a common subsequence, the algorithm terminates quickly. The probability of generating a common subsequence is high in this case because of the reduced amount of possible combinations we have when using only the four letter of a DNA sequence.

Given the "luck factor" of this case, analyzing the predicted vs. empirical runtime will not be insightful.

7.1.2 Constant *c* for dynamic programming

```
rt_dp, c_dp = m.add_runtime_analysis(rt_results_summary, m.ALG_DYNAMIC_PROGRAMMING
    )
print('c_dp={}'.format(c_dp))
display(rt_dp)
```

```
c_dp=0.0001627695555555558
```

```
              Algorithm  Sequence size  Subsequence size  Empirical RT (ms)  \
9   Dynamic programming           1000               100             15.257
10  Dynamic programming           2000               200             62.163
11  Dynamic programming           3000               300            142.757
12  Dynamic programming           4000               300            182.718
13  Dynamic programming           4000               500            308.720
14  Dynamic programming           4000              1000            612.753
15  Dynamic programming           5000               900            732.463
16  Dynamic programming           5000              1000            777.084
17  Dynamic programming           5000              1200            938.708

    Theoretical complexity      Ratio  Predicted RT  % error
9                   100000  1.526e-04        16.277   -6.685
10                  400000  1.554e-04        65.108   -4.737
11                  900000  1.586e-04       146.493   -2.617
12                 1200000  1.523e-04       195.323   -6.899
13                 2000000  1.544e-04       325.539   -5.448
14                 4000000  1.532e-04       651.078   -6.255
15                 4500000  1.628e-04       732.463    0.000
16                 5000000  1.554e-04       813.848   -4.731
17                 6000000  1.565e-04       976.617   -4.038
```

Since all results are within a small margin of error, none of them will be discarded for the calculation.

7.1.3 Constant *c* for Hirschberg's linear space

```
rt_h, c_h = m.add_runtime_analysis(rt_results_summary, m.ALG_HIRSCHBERG)
print('c_h={}'.format(c_h))
display(rt_h)
```

```
c_h=0.00034574999999999363
```

```
     Algorithm  Sequence size  Subsequence size  Empirical RT (ms)  \
18  Hirschberg           1000               100             34.575
19  Hirschberg           2000               200            135.058
20  Hirschberg           3000               300            290.896
21  Hirschberg           4000               300            387.301
22  Hirschberg           4000               500            621.257
23  Hirschberg           4000              1000           1226.753
```

```
24  Hirschberg          5000            900          1399.517
25  Hirschberg          5000           1000          1542.752
26  Hirschberg          5000           1200          1846.447

    Theoretical complexity      Ratio  Predicted RT  % error
18                  100000  3.457e-04        34.575    0.000
19                  400000  3.376e-04       138.300   -2.400
20                  900000  3.232e-04       311.175   -6.971
21                 1200000  3.228e-04       414.900   -7.126
22                 2000000  3.106e-04       691.500  -11.307
23                 4000000  3.067e-04      1383.000  -12.737
24                 4500000  3.110e-04      1555.875  -11.172
25                 5000000  3.086e-04      1728.750  -12.056
26                 6000000  3.077e-04      2074.500  -12.351
```

Some of the results are of by more than 10%, but not by much, so we will keep all of them for the calculation.

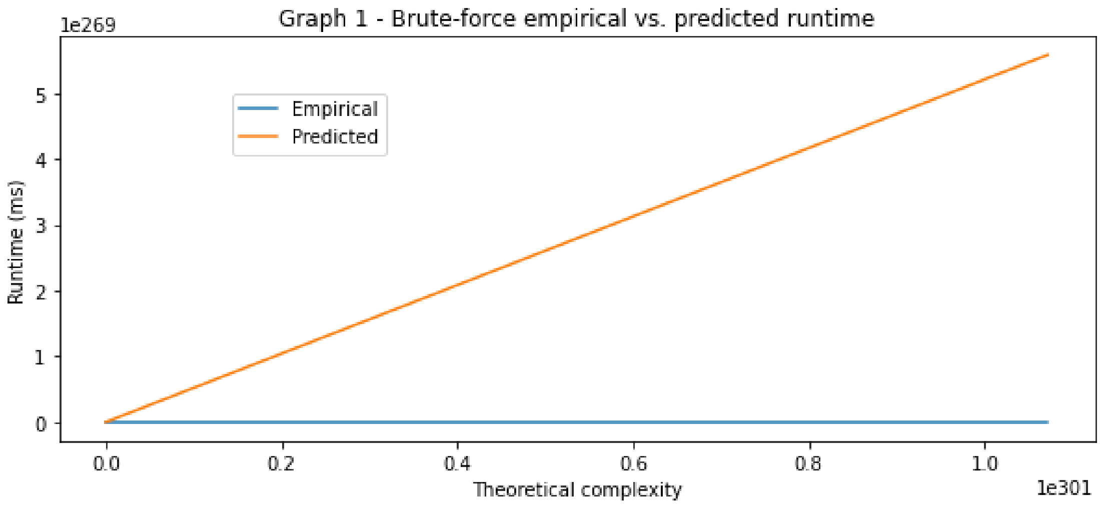
7.2 Empirical vs. predicted RT graphs

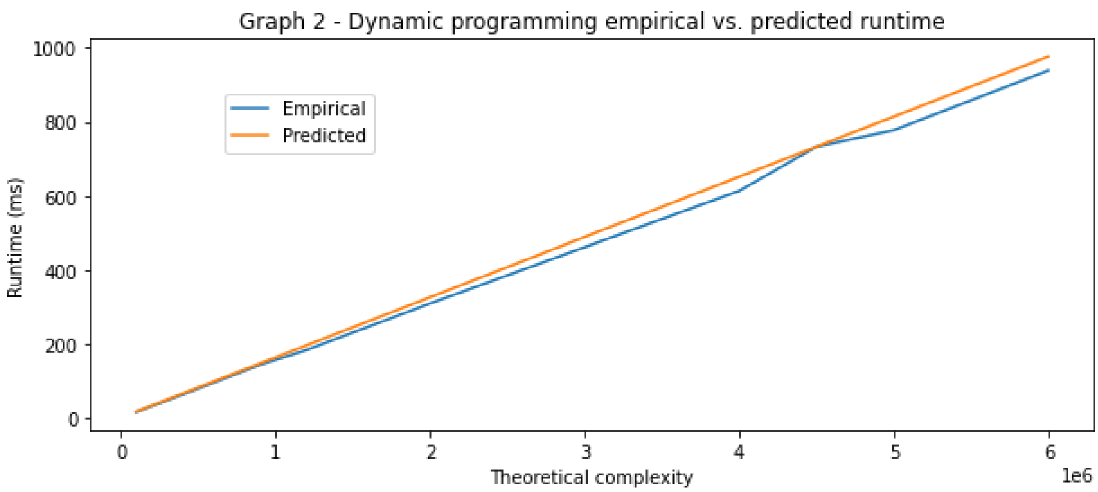
The graphs below compare the empirica runtime with the predicted runtime using the smaller input sizes. The predicted runtime is calcutated as $c \times$ *theoretical complexity*.

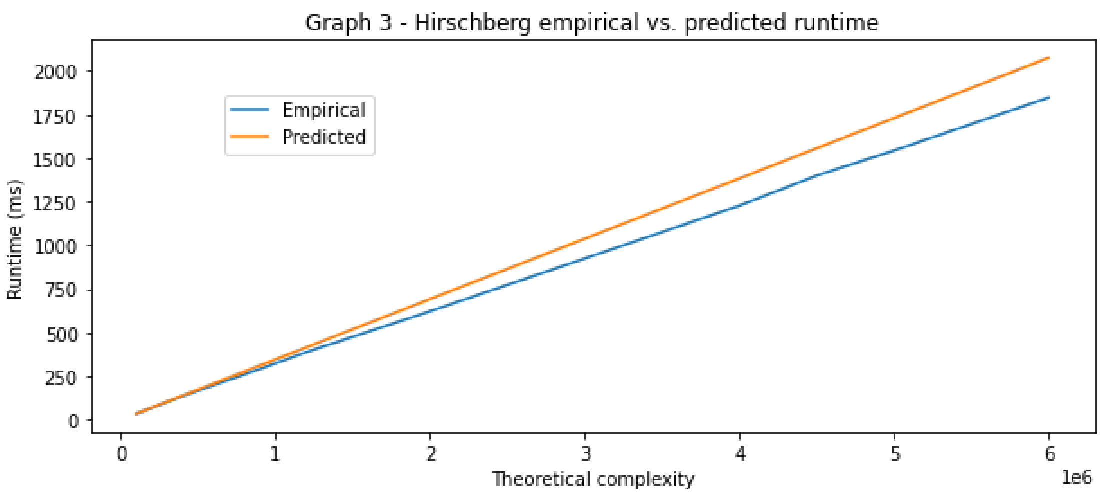
Each of the graphs below shows the empirical vs. predicted runtime for an algorithm. The empirical runtime is the actual running time of the algorithms, while the empirical runtime is calculated as $c \times$ the theoretical complexity.

```
graph_number = 0
def plot_empirical_predicted_rt(data, title):
    '''Auxiliary function to plot the graphs consistently for all algorithms.'''
    global graph_number
    graph_number +=1
    fig = plt.figure(figsize=(10,4))
    sns.lineplot(x=m.DF_THEORETICAL_COMPLEXITY, y=m.DF_EMPIRICAL_RT, data=data)
    sns.lineplot(x=m.DF_THEORETICAL_COMPLEXITY, y=m.DF_PREDICTED_RT, data=data)
    plt.title('Graph {} - {} empirical vs. predicted runtime'.format(
        graph_number, title))
    plt.ylabel("Runtime (ms)")
    fig.legend(['Empirical', 'Predicted'], bbox_to_anchor=(0.3, 0.8))
    plt.show()
```

```
for alg in (rt_bf, rt_dp, rt_h):
    plot_empirical_predicted_rt(alg, alg.iloc[0][m.DF_ALGORITHM])
```







From these graphs we can see that:

1. The brute-force graph shows again the "luck" effect, where the runtime is low because a subsequence just happens to be found early on. It could have gone the other way, as it in fact did in one of the experiments, where after running for eight hours, it still did not find a common subsequence for m = 5,000 and n = 2,000.

2. Both the dynamic programming and the Hirschberg algorithms track closely to their predicted runtime.
3. The Hirschberg algorithm's error is larger for larger input sizes, likely because the nature of the implementation and the programming language. It is a recursive algorithm and Python does not support tail recursion optimization [WIK20b] [ROS09]. Thus the loops have the extra cost of function calls that the dynamic programming algorithm does not have. The cost of the function calls is relatively more expensive for small input size, resulting in overstimating c. An improvement for this case could be to do a more rigorous outlier elimination when calculating c.

7.3 Graphs for larger input sizes

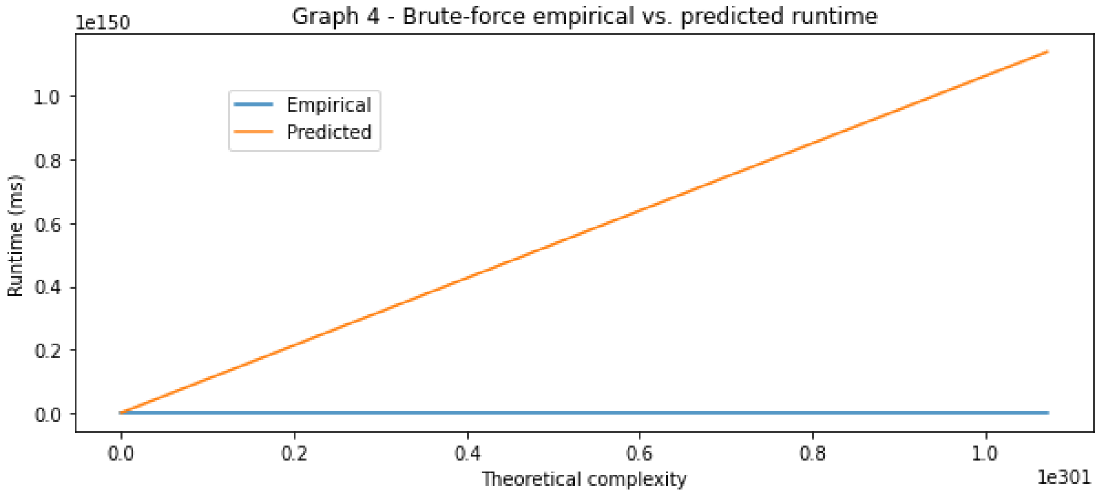
The graphs below compare the empirical runtime with the predicted runtime using the larger input sizes. As before, the predicted runtime is calcutated as $c \times$ *theoretical complexity*.

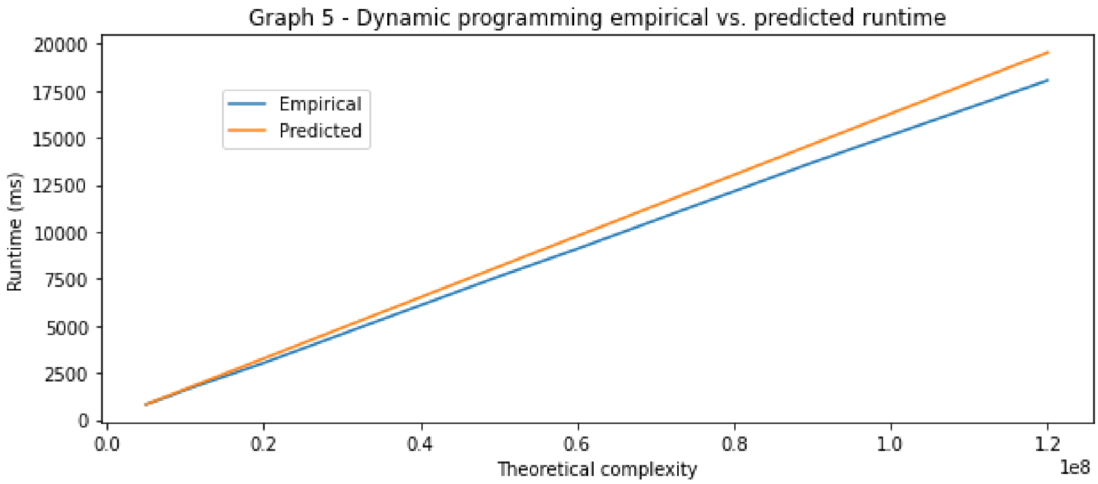
The graphs show the same trend lines as the graphs for the smaller input sizes.

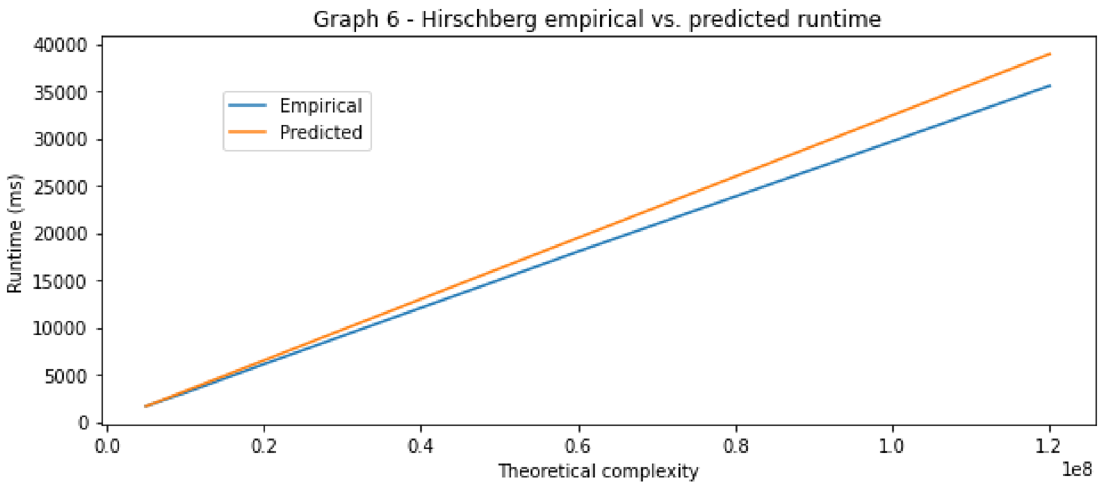
```
rt_results_raw, rt_results_summary = m.runtime(m.seq_phase2, verbose=1,
    file='runtime-phase2')
```

```
Loading from file
```

```
for alg in (m.ALG_BRUTE_FORCE, m.ALG_DYNAMIC_PROGRAMMING, m.ALG_HIRSCHBERG):
    rt, _ = m.add_runtime_analysis(rt_results_summary, alg)
    plot_empirical_predicted_rt(rt, rt.iloc[0][m.DF_ALGORITHM])
```





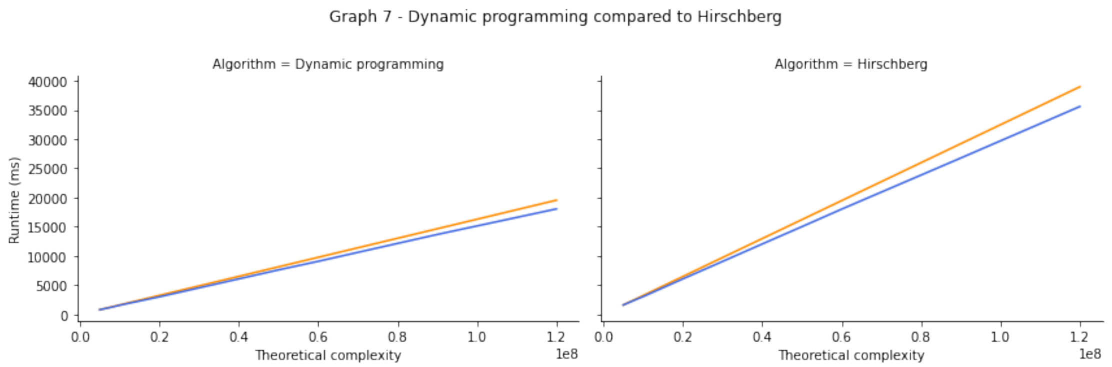


Graphing the algorithms separately does not clearly show how their runtime compare with each other. The graph below shows the dynamic programming and the Hirschberg algorithm with the same scale for the vertical axis (the brute-force algorithm is not shown because its complexity is in another scale entirely, therefore not comparable with the other two algorithms).

With this graph we can see that although they have the same growth rate (both have $O(mn)$ complexity), the Hirschberg algorithm has a higher slope, resulting from its higher *c* constant.

```
dp_summary, _ = m.add_runtime_analysis(rt_results_summary, m.
    ALG_DYNAMIC_PROGRAMMING)
h_summary, _ = m.add_runtime_analysis(rt_results_summary, m.ALG_HIRSCHBERG)
summary = pd.concat([dp_summary, h_summary])
```

```
graph_number += 1
g = sns.FacetGrid(summary, col=m.DF_ALGORITHM, height=4, aspect=1.5)
g.map(plt.plot, m.DF_THEORETICAL_COMPLEXITY, m.DF_PREDICTED_RT,
    color='darkorange')
g.map(plt.plot, m.DF_THEORETICAL_COMPLEXITY, m.DF_EMPIRICAL_RT,
    color='royalblue')
g.set_ylabels('Runtime (ms)').fig.subplots_adjust(top=0.8)
g.fig.suptitle('Graph {} - Dynamic programming compared to Hirschberg'.format(
    graph_number))
plt.show()
```



8 Space tests and analysis

```
mem_results_raw, mem_results_summary = m.memory(m.seq_phase2, verbose=1,
    file='memory-phase2')
mem_results_summary = m.add_memory_analysis(mem_results_summary)
```

```
Loading from file
```

We now have two Pandas DataFramse:

- `mem_results_raw`: results from all 10 executions of each algorithms and each input size.
- `mem_results_summary`: average of the executions for each each algorithm and input size.

The DataFrames contain metrics for all algorithms. Sections below filters the row for the algorithm analyzed in that section.

The tables below show the empirical and predicted space in MiB. Using these values, an eror column is also shown.

Observations from these tables:

1. Measuring small amounts of memory used in short period of times, as used by the brute-force algorithm in all cases and by the other algorithms with smaller input sizes, is unreliable. There is a discussion about the method used later in the notebook, in the code section. Based on these observations, the results from the brute-force algorithm will not be used in further analysis.
2. As the runtime increases and the amount of memory used grows larger, the measurements become more reliable.

```
for alg in [m.ALG_BRUTE_FORCE, m.ALG_DYNAMIC_PROGRAMMING, m.ALG_HIRSCHBERG]:
    df = mem_results_summary[mem_results_summary[m.DF_ALGORITHM] == alg]
    print('\n{} memory analysis'.format(alg))
    display(pd.pivot_table(df, values=[m.DF_EMPIRICAL_SPACE, m.DF_PREDICTED_SPACE,
         m.DF_ERROR],
     index=[m.DF_SEQ_SIZE, m.DF_SUBSEQ_SIZE]))
```

```
Brute-force memory analysis
```

```
                                 % error  Empirical space (MiB)   \
Sequence size Subsequence size
```

```
10000         500              -inf                 0.000
              800              -inf                 0.000
              1000             -inf                 0.000
20000         1000             -inf                 0.000
              2000             -inf                 0.000
              2500           38.965                 0.004
30000         2000             -inf                 0.000
              3000           75.586                 0.012
              4000           87.793                 0.031

                              Predicted space (MiB)
Sequence size Subsequence size
10000         500                        4.768e-04
              800                        7.629e-04
              1000                       9.537e-04
20000         1000                       9.537e-04
              2000                       1.907e-03
              2500                       2.384e-03
30000         2000                       1.907e-03
              3000                       2.861e-03
              4000                       3.815e-03
```

```
Dynamic programming memory analysis
```

```
                                 % error  Empirical space (MiB)  \
Sequence size Subsequence size
10000         500            -162660.417                  0.012
              800                  0.134                 30.559
              1000                 0.167                 38.211
20000         1000                 0.101                 76.371
              2000                 0.058                152.676
              2500                 0.047                190.824
30000         2000                 0.057                229.012
              3000                 0.037                343.449
              4000                 0.029                457.895

                              Predicted space (MiB)
Sequence size Subsequence size
10000         500                           19.073
              800                           30.518
              1000                          38.147
20000         1000                          76.294
              2000                         152.588
              2500                         190.735
30000         2000                         228.882
              3000                         343.323
              4000                         457.764
```

```
Hirschberg memory analysis
```

```
                              % error  Empirical space (MiB)  \
Sequence size Subsequence size
10000         500              -inf                 0.000
              800            92.188                 0.039
              1000           91.862                 0.047
20000         1000           91.862                 0.047
              2000           91.862                 0.094
              2500           91.862                 0.117
30000         2000           86.979                 0.059
              3000           97.287                 0.422
              4000           97.543                 0.621

                              Predicted space (MiB)
Sequence size Subsequence size
10000         500                            0.002
              800                            0.003
              1000                           0.004
20000         1000                           0.004
              2000                           0.008
```

```
              2500                          0.010
 30000        2000                          0.008
              3000                          0.011
              4000                          0.015
```

Memory analysis for the dynamic programming and Hirschberg's linear space is more interesting.

Before going into the analysis, a review of some implementation details that affect the space characteristics of the algorithms:

1. The classic dynamic programming algorithm uses two $m \times n$ matrices, one for the length and another for the direction of the moves. Space-optimized implementations combine these matrices into one, reserving bits in each cell for the length and direction. Such an implementation was used here. It is discussed in the code section of the notebook.
2. Hirschberg's traditional implementation is recursive. In languages that do not support tail recursion, such as Python, each recursion creates a new stack frame. Thus, some of the memory used by the algorithm is in the form of the stack frames, in addition to the arrays it needs for the algorithm itself.
3. Also for Hirschberg's, a simplistic implementation of the algorithm creates copies of the sequences as it finds where to split them. A space-optimized algorithm uses indices into the original sequence to avoid creating copies. Such an implementation was used here. It is discussed in the code section of the notebook.

With that in mind, from the tables we observe that:

1. The dynamic programming algorithm tracks closely to the predicted space. This is due to two factors. First, it uses a large amount of memory, which seems to favor this particular method of measuring memory utilization (discusion in the code section). And second, it uses loops, as opposed to recursion, which does not create the overhead of stack frames (in languages without tail recursion).
2. The Hirschberg's linear space algorithm has a large error. This error is likely caused by it being a recursive algorithm. Some of the memory measured during the execution comes from the stack frames created in each recursion.

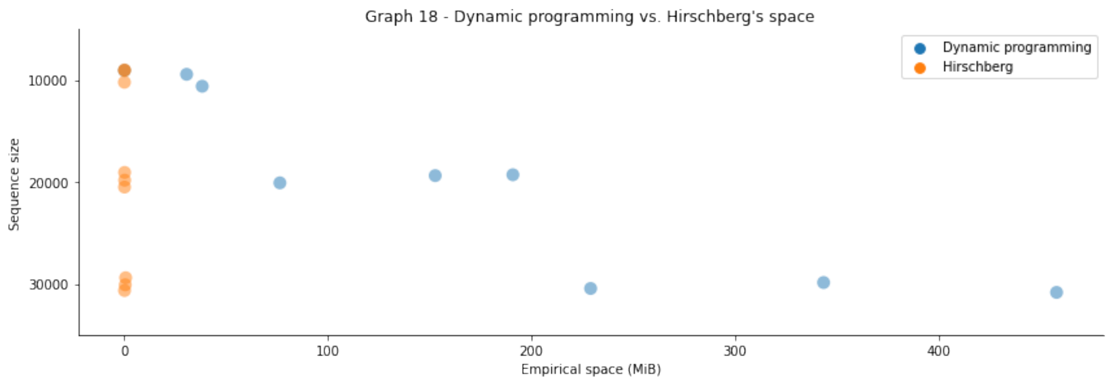
Finally, the most important observation is the difference between the dynamic programming and Hirschberg's linear space algorithm. As expected, dynamic programming uses significantly more memory.

On the other hand, in this implementation, dynamic programming is twice as fast as Hirschberg's. In another programming language, with better support for tail recursion, their performance may be comparable.

In most real-life applications, with large input sizes, a fine-tuned implementation of Hirschberg's linear space is the preferable option. In some cases, for very large input sizes, it may be the only feasible option.

To illustrate the dramatic difference in space, the graph below shows the emprical space used by the two algorithms side-by-side, for each input size. The horizontal axis is the empirical space. Each dot represent a subsequence for a sequence size (vertical axis). We can see that Hirschberg's linear space algorithm (orange) never goes past one MiB, while the dynamic programming algorithm (blue) escalates quickly, going past hundreds of MiBs, reaching almost half a gigabyte for the largest combination of sequences.

```
graph_number += 1
df = mem_results_summary[(mem_results_summary[m.DF_ALGORITHM] == m.
     ALG_DYNAMIC_PROGRAMMING) | (mem_results_summary[m.DF_ALGORITHM] == m.
     ALG_HIRSCHBERG)]
sns.catplot(y=m.DF_SEQ_SIZE, x=m.DF_EMPIRICAL_SPACE, hue=m.DF_ALGORITHM, data=df,
     orient='h', height=4, aspect=3, legend=False, s=10, alpha=0.5)
plt.title('Graph {} - Dynamic programming vs. Hirschberg\'s space'.format(
     graph_number))
plt.legend(loc='upper right')
plt.show()
```



9 Conclusions

9.1 Runtime

From the runtime experiments we can conclude that:

1. The brute-force algorithm is basically a coin flip, where the odds for "it will run quickly" are much slower than the odds for "it will run very, very slowly". It may find an LCS in extremely fast times (under 100 ms), or it may take hours and still not find an LCS (as it happened once during the research for this project). However, in some applications, where the probability of finding a common subsequence is high (a combination of small input sizes and small set of characters to pick from), running the brute-force algorithm in parallel with a dynamic programming algorithm may be worthwhile. When it pays off, it pays off big.
2. The dynamic programming and Hirschberg's algorithm have stable runtime characteristics, that is given an input size, it is easy to calculate how long it will take to find an LCS. Predictability is a desirable characteristic in real-life applications.

9.2 Space

1. The pseudocode for the algorithms are, as a general rule, not a good example of memory efficiency. For example, the pseudocode for the dynamic programming algorithm usually shows two tables, one for the length and another for the moves. While this approach makes the pseudocode easy to understand, it is not an efficient utilization of space. To make the most space-intensive algorithms work, careful use of memory management techniques is needed.
2. The difference in space utilization between the dynamic programming adn the Hirschberg's linear space algorithms is astounding when they are put side by side. It shows one of them barealy needing one MiB, while the other reaching half of a gigabyte to perform the same work. Hats off to Dr. Hirschberg.

9.3 Methodology and tools

1. Getting the algorithms to run fast and use a reasonable amount of memory requires knowledge of the particular environment (e.g a Python environment, compared to a C++ environment). The naive implementation, one that follows the pseudocode from textbooks closely, is usually slow, uses too much memory, or both.
2. Python is a good choice for experimenation, but not for performance. For example, for the brute-force algorithm Python's `itertools` is a fast and efficient way to generate combinations. On the other hand, the lack of tail recursion handicaps algorithms that make use of recursion, such as Hirschberg's. This introduces potentially artificial differences between the algorithms, i.e. differences that are caused by the environment, not necessarily by fundamental differences in the algorithms.
3. Jupyter speeds up the "experiment, evaluate" cycle greatly. It also makes the process repeatable and transparent by exposing the code used for analysis, facilitating peer review of the methods and assumptions used in the work.
4. Measuring memory usage was surprisingly hard, especially when the usage was on the low side (less than one MiB). Part of the reason is the environment (Python, which is a mixture of referene counting and garbage collection) and tools (`memory_profile`). If I had to do this again, I would write these pieces of the code in C or C++, as written in another point, and spawn individual processed for each test case, measuring memory usage with operating system tools, instead of language modules/libraries.

To summarize, if I had to do it again, I would have written the algorithms in C or C++ to take advantage of their performance and write the results into a file, then use Python to read the file and perform the analysis in a Jupyter notebook. This approach would combine the best of both worlds.

10 Code structure and description

This section highlights pieces of the code that are significant for the experiments.

10.1 Code structure

10.2 How reproducibility is ensured

10.3 How time was measured

10.4 How memory was measured

10.5 Code optimizations

11 References

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[WIK20b] Wikipedia. *Tail call*. https://en.wikipedia.org/wiki/Tail_call, accessed 2020-04-28.

References used in the code are annotated directly in the code.

12 Appendix

> Show full data from the experiments here