Needleman-Wunsch

Christopher B.   Sebastian C.

Jennifer M.   Whitney T.

Ned S.   Drew M.

Objectives

- Understand why Needleman-Wunsch was developed.
- Comprehend how Needleman-Wunsch works.
- Show how our GUI works.
- Display analysis of our implementations.

History

- Developed in 1970
- Saul B. Needleman and Christian D. Wunsch
- Dynamic Programming for Global Alignment

Motivation

- Global Alignment
- Find Common Ancestry
- Find Genetic Mutations
- A high percentage of what we know about DNA has been discovered in the past 50 years

GUI Prototypes & Final Product

Needlemen Wursh

Selection

[ ]

Selection

[ ]

Score:

[ ]

String1:

[ ]

String 2:

[ ]

Alignment:

[ ]

NeedlemenWursh

Selection

[ ]

[select]

[ ]

[select]

Score:

[ ]

String1:

[   ] Score?

String2:

[   ]

alignment:

Neeldeman- Wunsh Algorithms

File Select

```
[                    ]
```

[Button]

File select

[~~Butt~~]

[BUTTON]

Algorithm

```
[              |v]
```

Score [|▪]   **mismatch** [   ]   **Match** [   ]

String 1

```
[                                                    ]
```

String 2

```
[                                                    ]
```

Alignment

```
[                                                    ]
```

Alignment Algorithms

File Selection

C:/Users

[Select]

C:/Users

[Select]

Algorithm

[Random ⌐]

Scoring

Match:

`1`

Mismatch:

`-1`

Gap:

`-2`

[Run]

File 1:

```
AAGGCTATTCTAGTCTCAAAACATAGTCAAGGGAGAGACG
GGACGTGGAGCGGTGAATTCAAAACCAGGAGTAGCCCATC
GTTACGGAGTGCGCGCCCCCCCCGTAAGAAAAGTAATCCG
CCTAACGTTCTAGCACATAGAGCACAGGCTCCGCGTTAGT
```

File 2:

```
AAGGCTATTCTAGTCTCAAAACATAGTCAAGGGAGAGACG
GGACGTGGAGCGGTGAATTCAAAACCAGGAGTAGCCCATC
GTTACGGAGTGCGCGCCCCCCCCGTAAGAAAAGTAATCCG
CCTAACGTTCTAGCACATAGAGCACAGGCTCCGCGTTAGT
```

Output Difference:

```
AAGGCTATTCTAGTCTCAAAACATAGTCAAGGGAGAGACG
GGACGTGGAGCGGTGAATTCAAAACCAGGAGTAGCCCATC
-GTTACGGAGTGCGCGCCCCCCCCGTAAGAAAAGTAATCC
GCCTAACGTTCTAGCACATAGAGCACAGGCTCCGCGTTAG
T-GCTGTTGCCAATGGATGGCTTTTACCAAAATTAACCTA
```

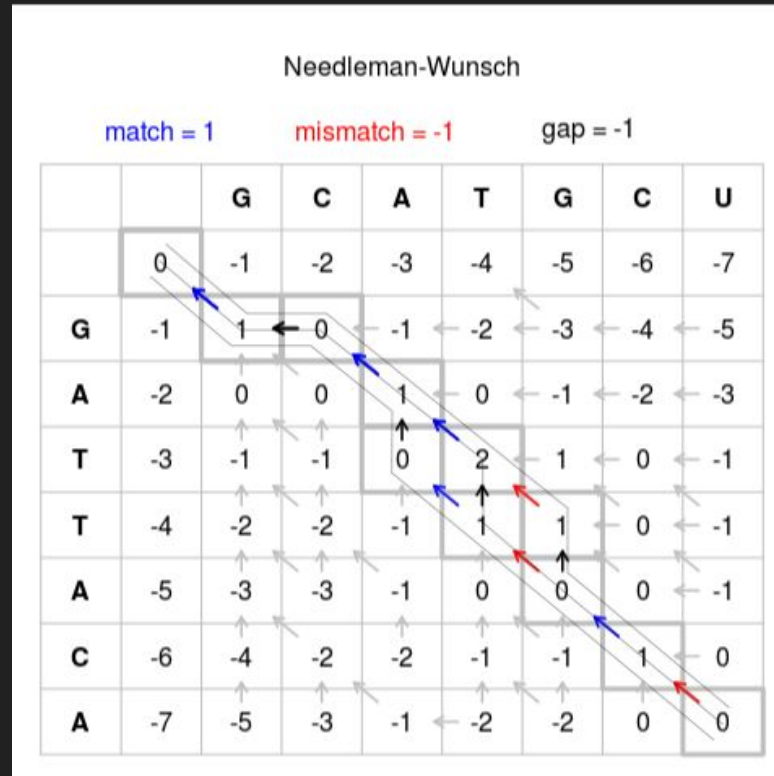### Score:

`47504`

Time (Seconds):

`13.71727`

Algorithms Implemented

- Needleman-Wunsch
  - Implementation from researcher's information
- Brute Force
  - Longest runtime
- Random
  - Not great, scoring not consistent
- Greedy
  - $$$$$

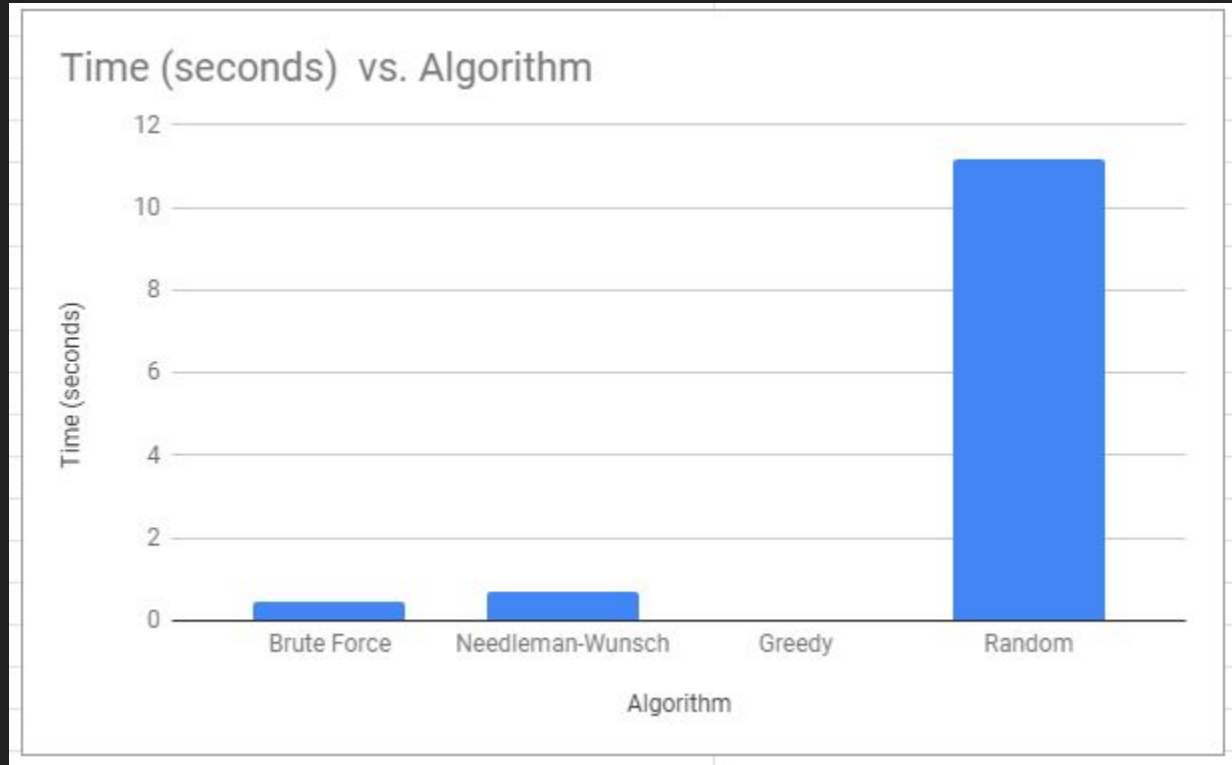# Needleman-Wunsch

Analysis

- Edge Cases
  - Completely different sequences
  - Exact same sequences
  - Sequences of different lengths
  - Invalid characters
  - Small sequences
  - Large Genomes

Analysis Chart

Runtime Chart (n= length of first sequence, m= length of second sequence)

Algorithm	Time(seconds)	Runtime	Best Input
Brute Force	0.440652	Best Case: O(n^2) or O(nm), Worst Case: O(n^3)	AGTCTA, AGTTA Alignment: AGT-TA, Score: 3
Needleman-Wunsch	0.678185	O(nm)	ATGTAGTGTATAAAG TACATGCA ATGTAGTACATGCA Score: -4
Greedy	0.00001	Best Case: O(n^2) or O(nm), Worst Case: O(n^3)	ACGTCAGGG ACGTCAGGC Score: 8
Random	11.16014	O(n^2)	ATGTAGTGTATAAAG TACAATGCA, ATGTAGTACATAAAG TCCGCTGCA Score: 14

Analysis Graph

Github Page

- https://jsebcort.github.io/NeedlemanWunsch/

Managing

- Communication
- Time management
- Scheduling
- Configuration management
- Tasking

Bibliography

- bindipatel2008. "Needleman-Wunsch Algorithm." YouTube, YouTube, 19 Apr. 2016, www.youtube.com/watch?v=aD4Cc4L3qW0.
- Lab 12 - Needleman Wunsch Algorithm, www.iiserpune.ac.in/~farhat/courses/idc205/lab12.html.
- KonstantinKonstantin. "Details of Needleman–Wunsch Algorithm." Biology Stack Exchange, biology.stackexchange.com/questions/68440/details-of-needleman-wunsch-algorithm.
- "2.1 Pairwise Sequence Alignment [Edit]¶." *An Introduction to Applied Bioinformatics*, readiab.org/book/0.1.3/2/1.