ALGORITHMS

Searching Algorithms

Agenda

1. Introduction
2. Demo
3. Algorithms used
    3.1. Brute Force
    3.2. Knuth–Morris–Pratt
    3.3. Boyer–Moore
4. Results
5. Conclusion

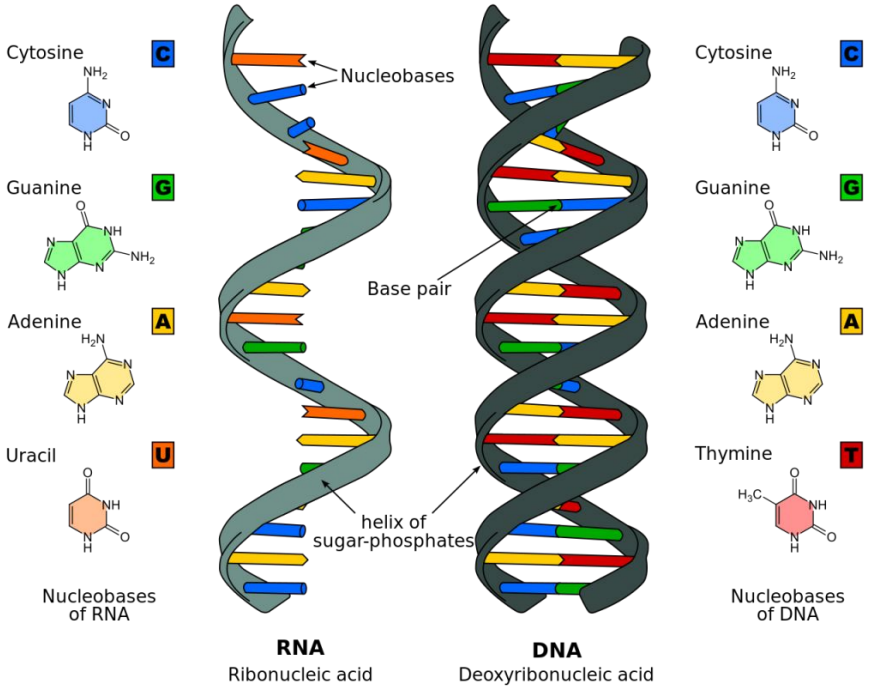
Problem Statement

Performing dna sequence searching

Consist of 4 alphabets

Genome sequence files can range from kilobytes to gigabytes

Time consuming process with bruteforce methods



Aim

Look into how we can **speed up** the searching process through **implementing smarter and better algorithms**, instead of just using brute force methods. As a result researchers would **spend less time waiting** for their search to complete, **greatly improving their efficiency**.

Data Resources Used

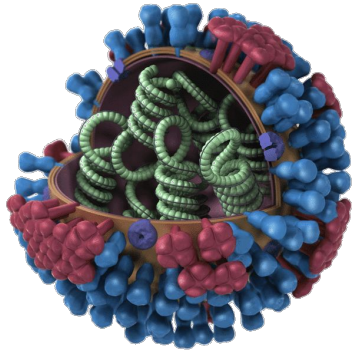
Genome sequences were downloaded from:

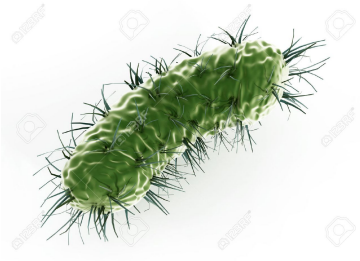
The National Center for Biotechnology Information (NCBI)

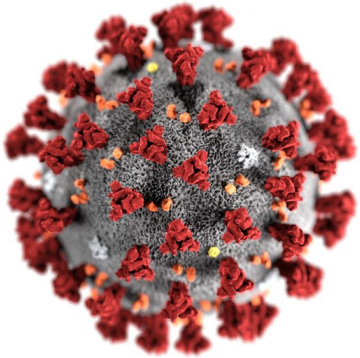
30 KB → COVID.FNA

5.0 MB → SALMONELLA.FNA

1.4 GB → INFLUENZA.FNA





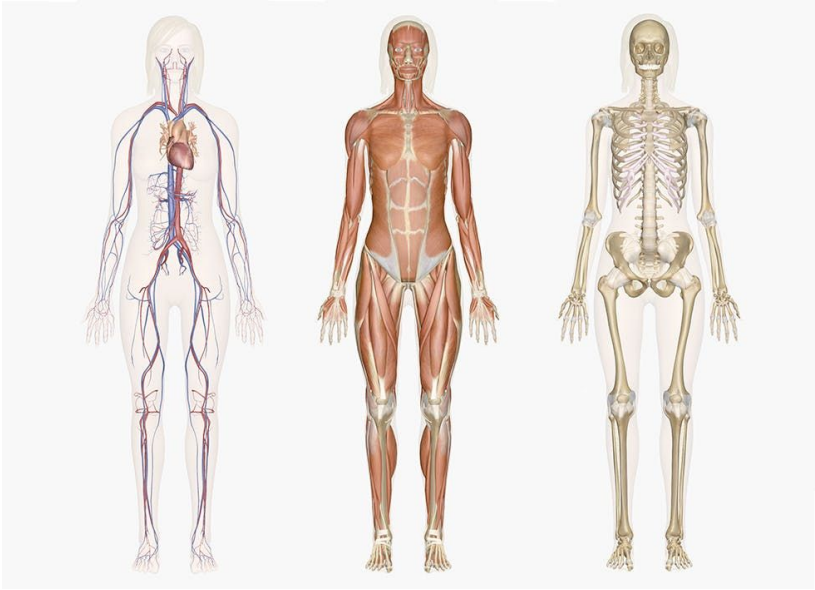


Possible Limitations

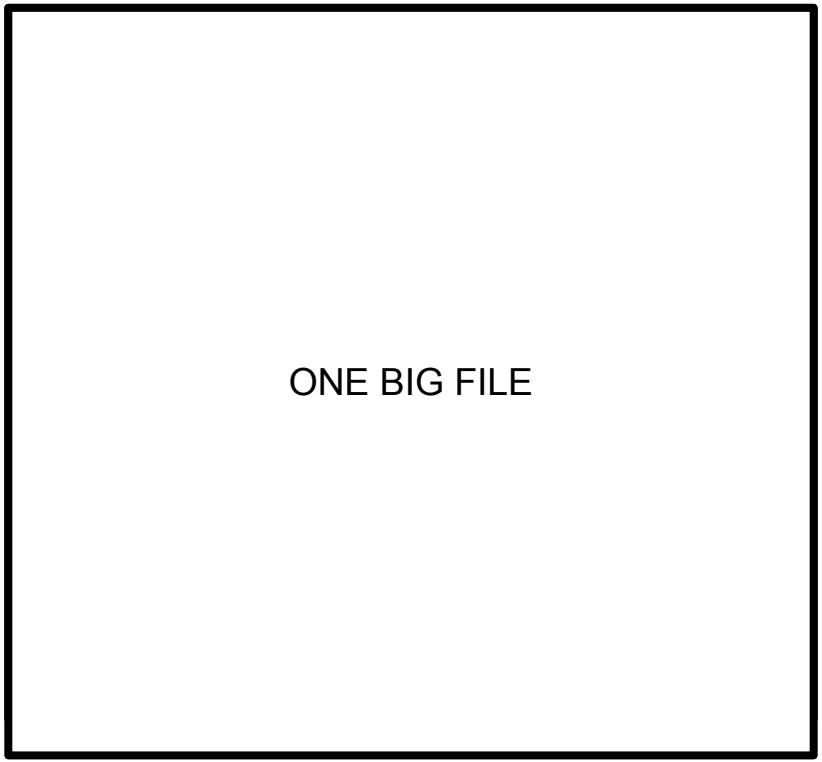
The **human genome** is over 6 billion in length equating to **6 GB**

If it were to be **directly loaded into a memory** to process

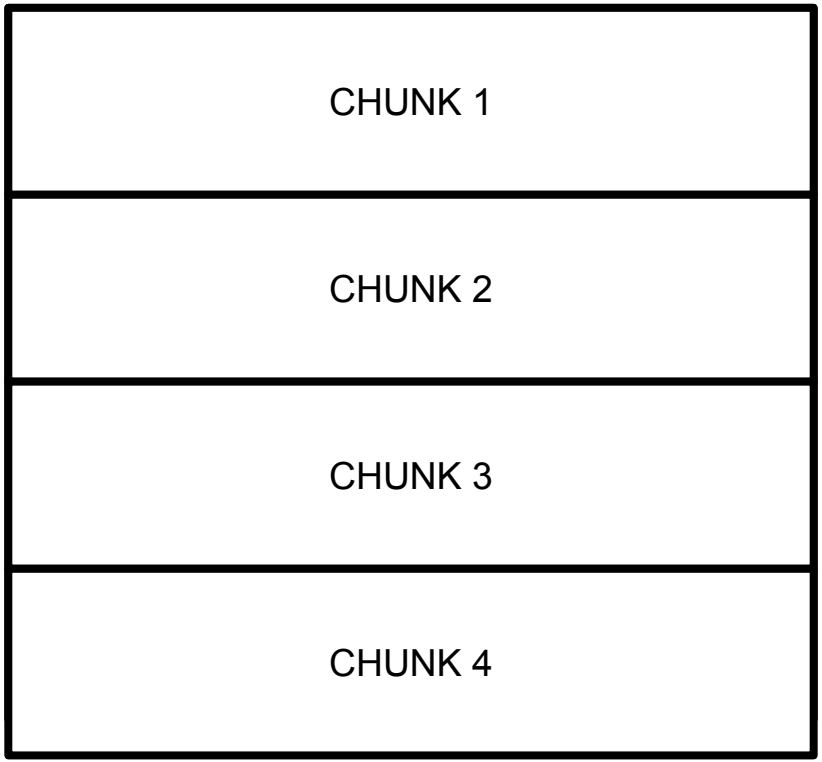
We would possibly face **memory limitations**



Significance of Our Code



Significance of Our Code



Significance of Our Code

Significance of our code

Splitting up the genome that we are searching through

Influenza genome (1.4GB) → 14 Influenza chunks **(0.1GB)**

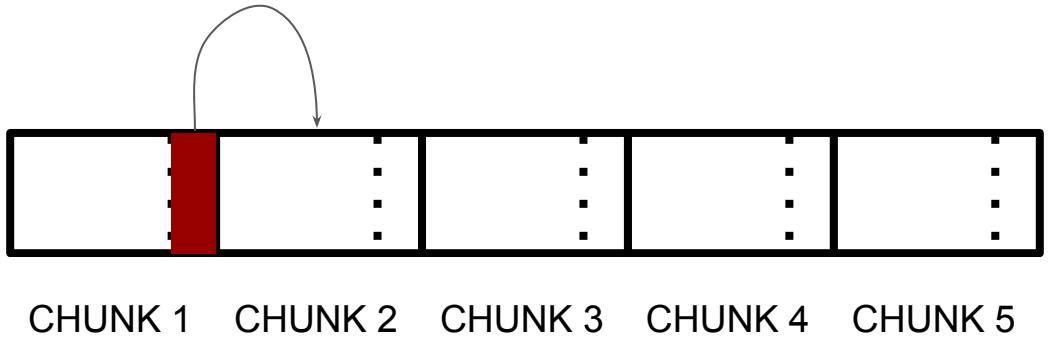
Significance of Our Code

Significance of our code

As some query sequences could be cut apart by splitting process

Ensure the there is a buffer between chunks

Makes sure that dna sequences caught in between chunks are accounted for



Plan of Action

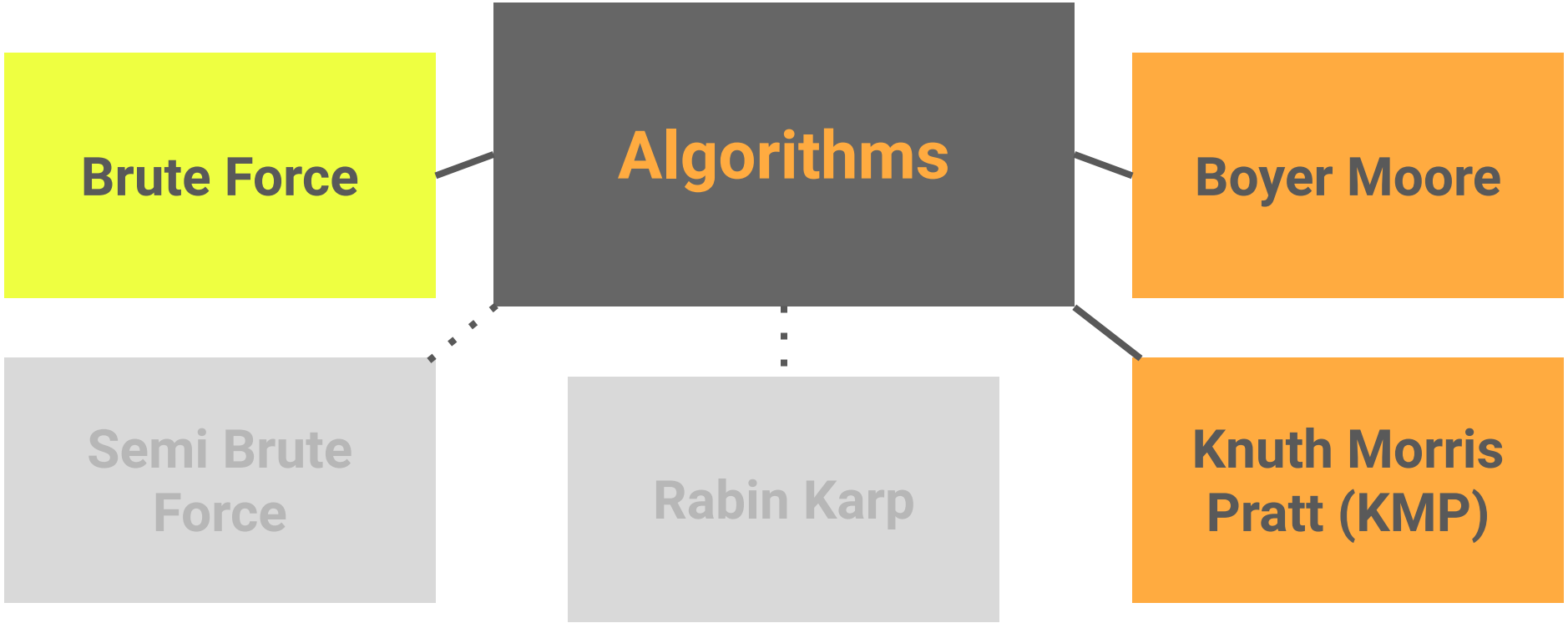
Implement Algorithms

Perform Asymptotic Analysis

Conduct Tests & Visualizing with Graphs

Leading to Conclusion

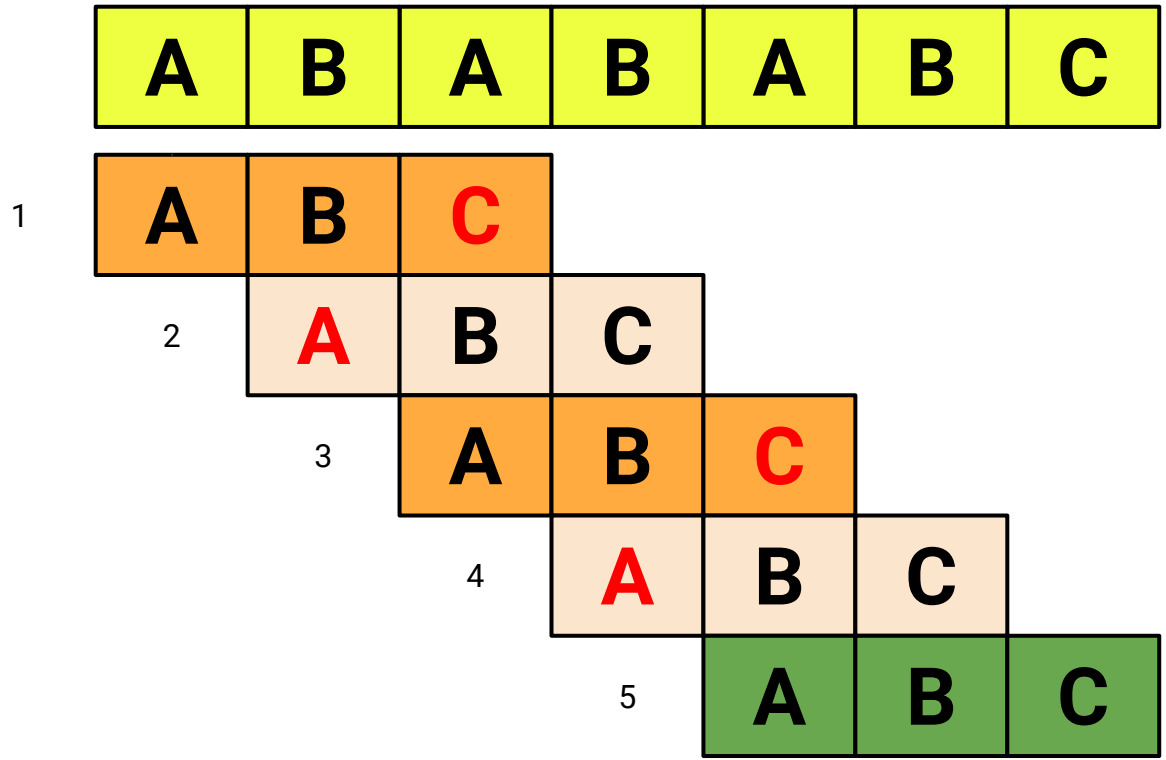
Implementing Algorithms



Implemented Algorithms - Demo with COVID.FNA

...ATCACGTAGTCGCAACAGTTCAAGAAATTCAACTCCAGGCAGCAGTAGGGGAACTTCTCCTGCTA
GAATGGCTGGCAATGGCGGTGATGCTGCTCTTGCTTTGCTGCTGCTTGACAGATTGAACCAGCTTGA
GAGCAAAATGTCTGGTAAAGGCCAACAACAACAAGGCCAAACTGTCACTAAGAAATCTGCTGCTGAG
GCTTCTAAGAAGCCTCGGCAAAAACGTACTGCCACTAAAGCATACAATGTAACACAAGCTTTCGGCA
GACGTGGTCCAGAACAAACCCAAGGAAATTTTGGGGACCAGGAACTAATCAGACAAGGAACTGATTA
CAAACATTGGCCGCAAATTGCACAATTTGCCCCCAGCGCTTCAGCGTTCTTCGGAATGTCGCGCATTG
GCATGGAAGTCACACCTTCGGGAACGTGGTTGACCTACACAGGTGCCATCAAATTGGATGACAAAGA
TCCAAATTTCAAAGATCAAGTCATTTTGCTGAATAAGCATATTGACGCATACAAAACATTCCCACCAA
CAGAGCCTAAAAAGGACAAAAAGAAGAAGGCTGATGAAACTCAAGCCTTACCGCAGAGACAGAAGAA
ACAGCAAACTGTGACTCTTCTTCCTGCTGCAGATTTGGATGATTTCTCCAAACAATTGCAACAATCCA
TGAGCAGTGCTGACTCAACTCAGGCCTAAACTCATGCAGACCACACAAGGCAGATGGGCTATATAAA
CGTTTTCGCTTTTCCGTTTACGATATATAGTCTACTCTTGTGCAGAATGAATTCTCGTAACTACATAGC
ACAAGTAGATGTAGTTAACTTTAATCTCACATAGCAATCTTTAATCAGTGTGTAACATTAGGGAGGAC
TTGAAAGAGCCACCACATTTTCACCGAGGCCACGCGGAGTACGATCGAGTGTACAGTGAACAATGCT
AGGGAGAGCTGCCTATATGGAAGAGCCCTAATGTGTAAAATTAATTTTAGTAGTGCTATCCCCATGTG
ATTTTAATAGCTTCTTAGGAGAATGAC**AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA**

Brute Force - Linear Searching



Boyer Moore

Me: “It’s like doing grep in unix!”

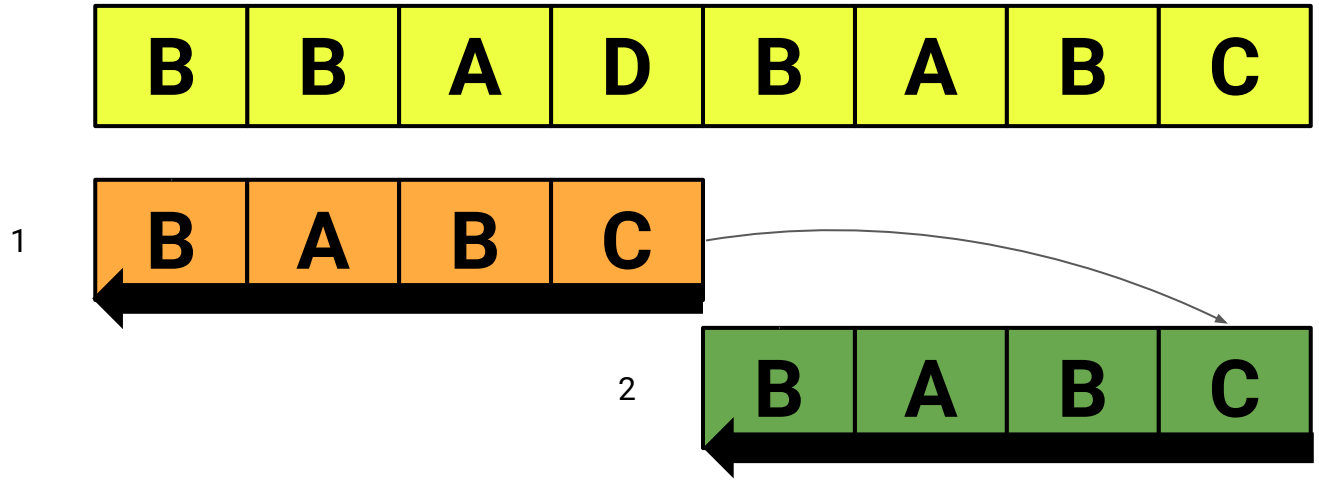
Google: “GNU grep uses the well-known Boyer-Moore algorithm.”

Boyer Moore: “Making full use of what you know to do as less as possible.”

Features

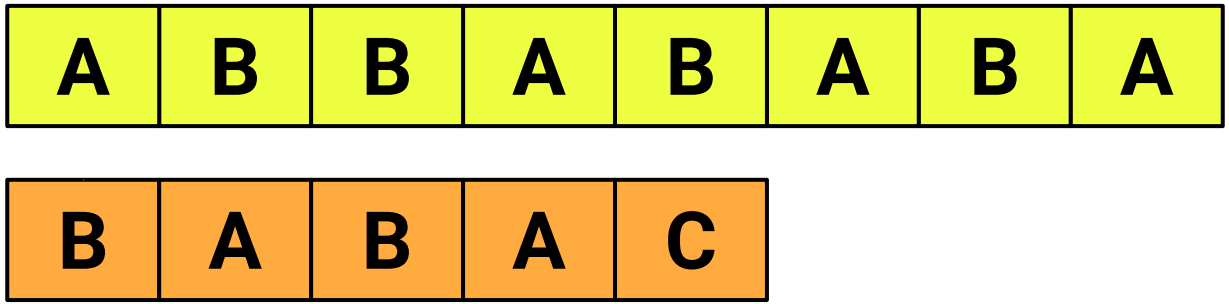
1. Right to left scan
2. Bad character rule
3. Good suffix rule + partial good suffix rule

Boyer Moore - Right to Left Scan

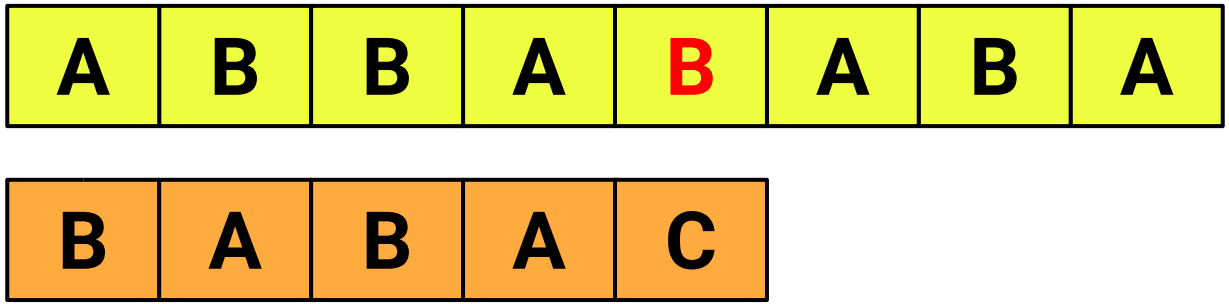


Bad Character Rule

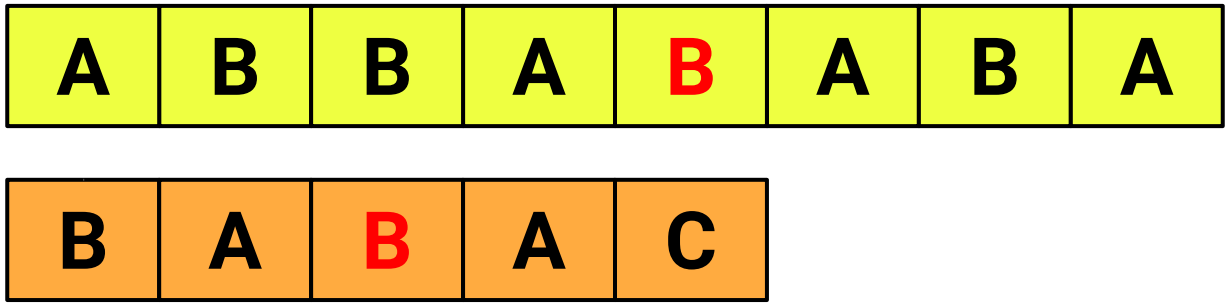
Boyer Moore - Bad Character Rule



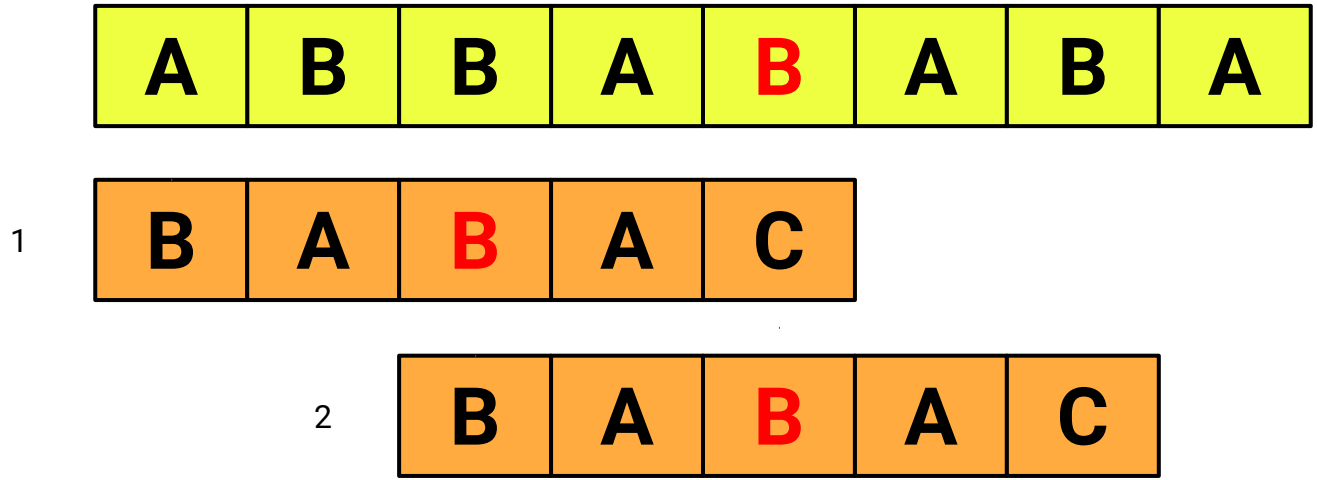
Boyer Moore - Bad Character Rule



Boyer Moore - Bad Character Rule

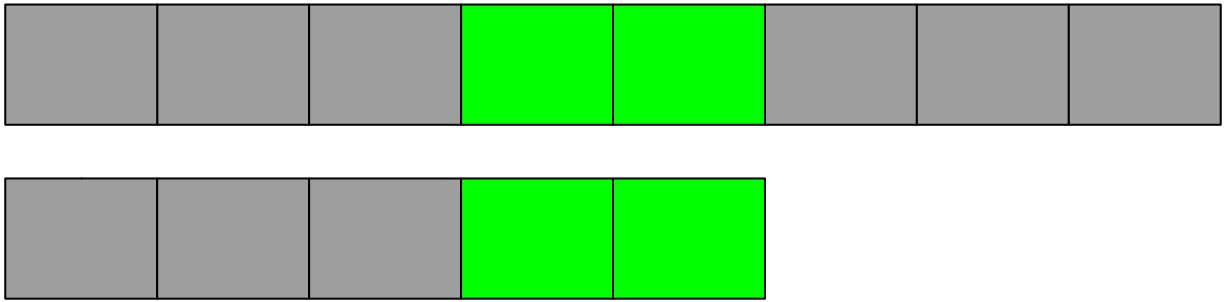


Boyer Moore - Bad Character Rule

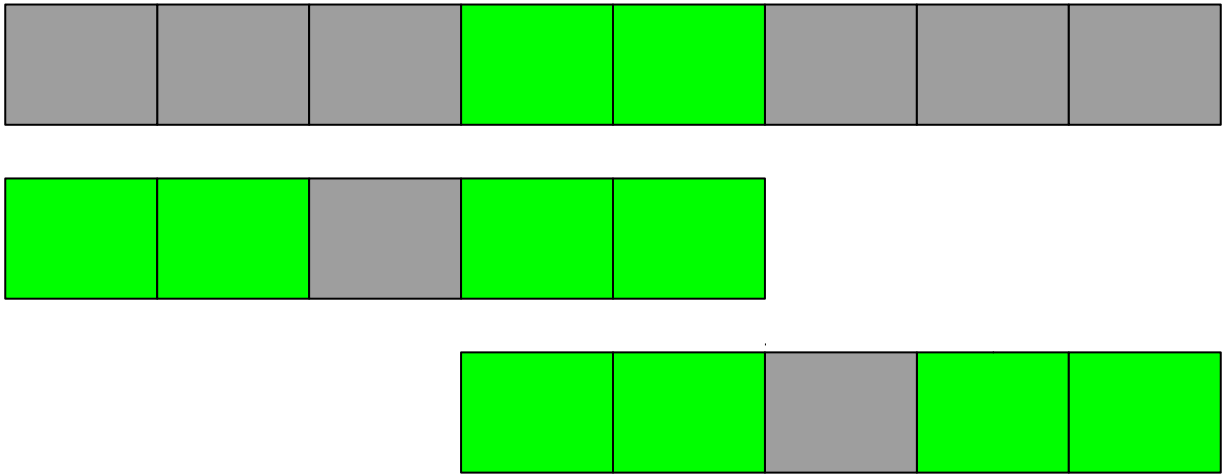


Good Suffix Rule

Boyer Moore - Good Suffix Rule

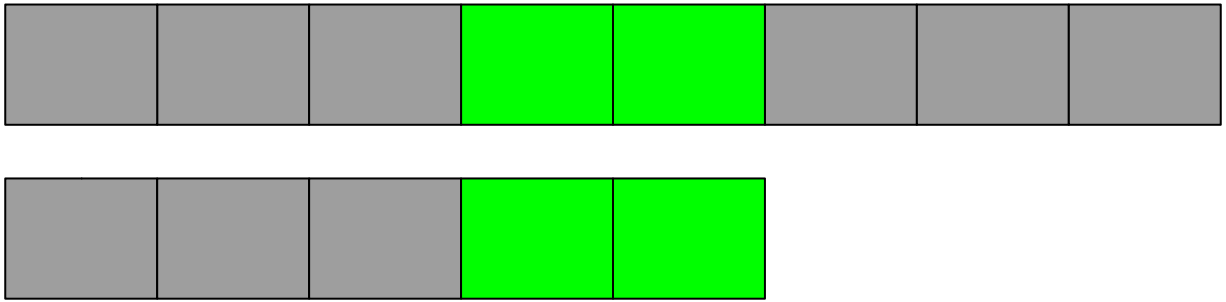


Boyer Moore - Good Suffix Rule

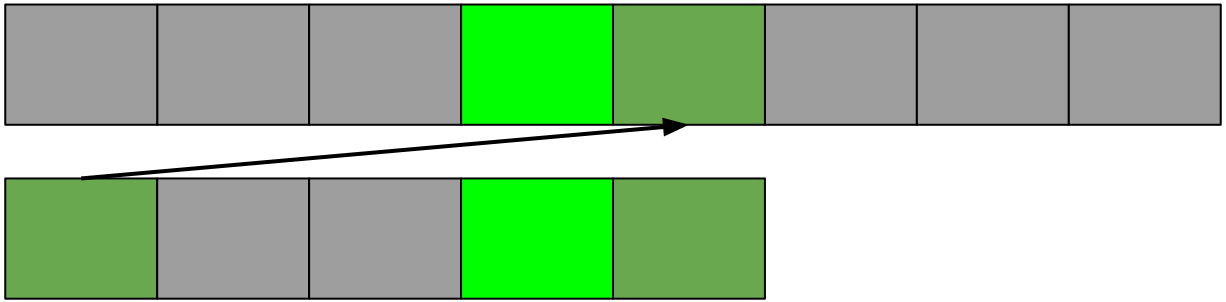


Partial Good Suffix Rule

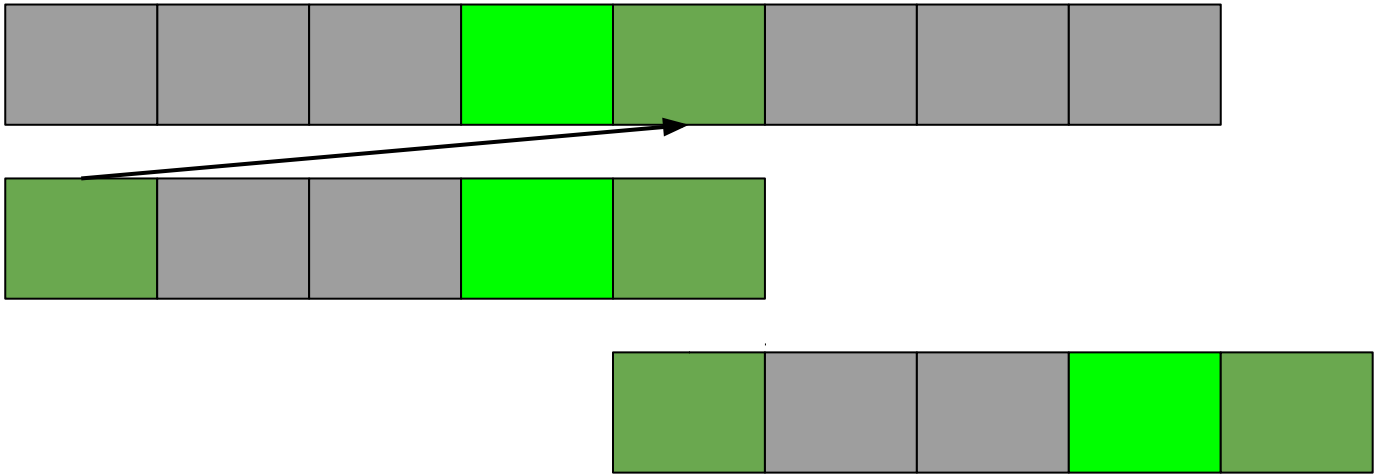
Boyer Moore - Good Suffix Rule + Partial



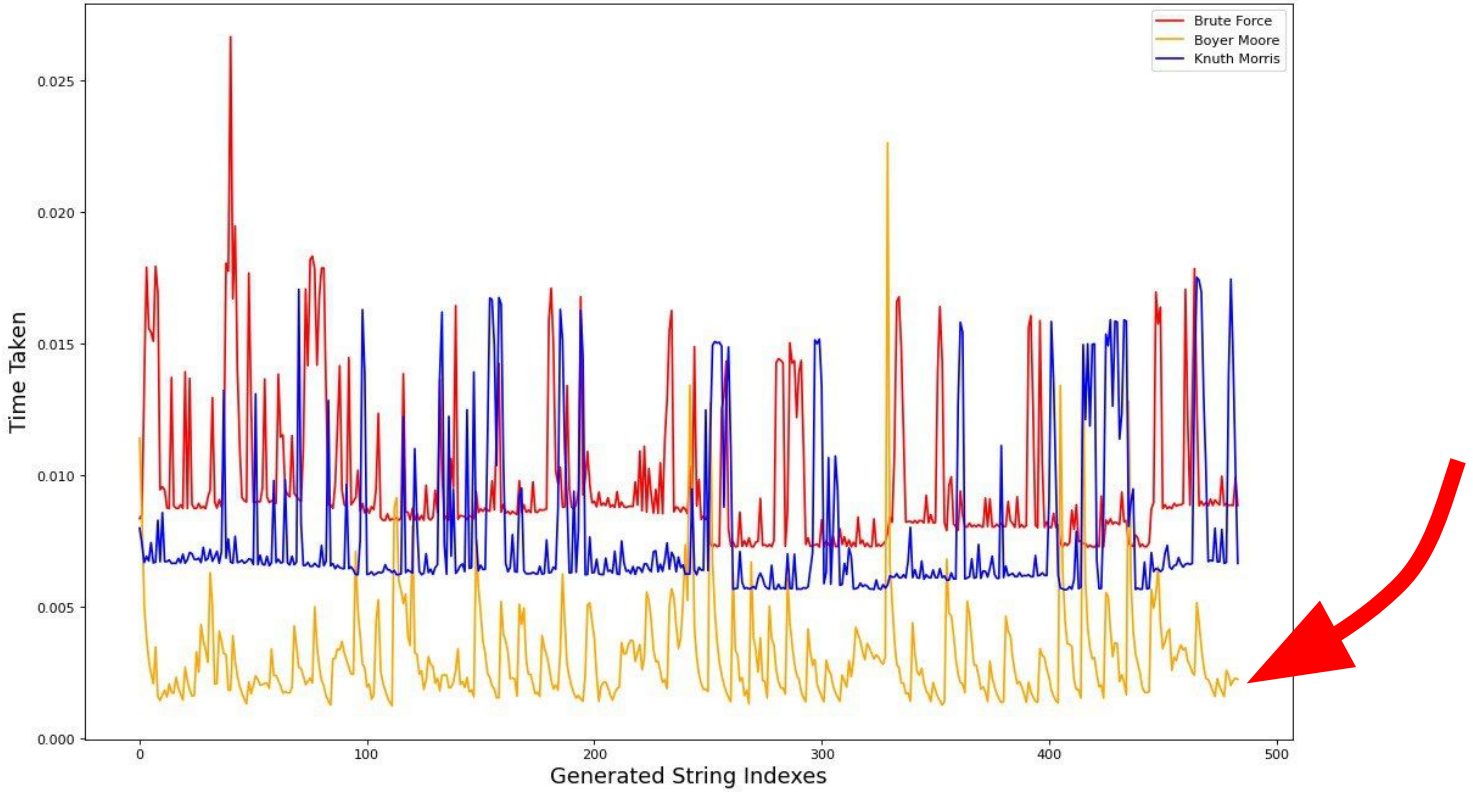
Boyer Moore - Good Suffix Rule + Partial



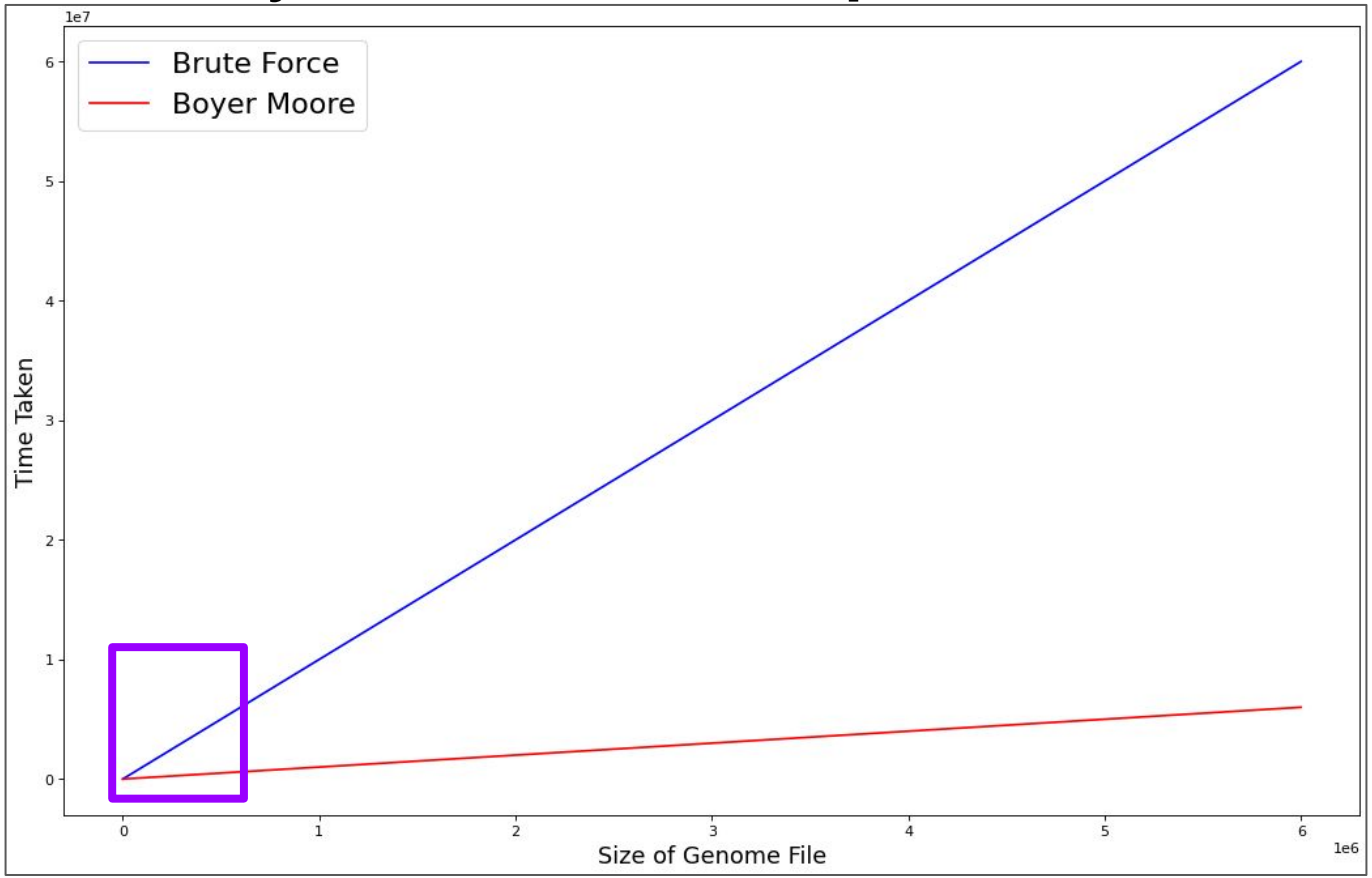
Boyer Moore - Good Suffix Rule + Partial



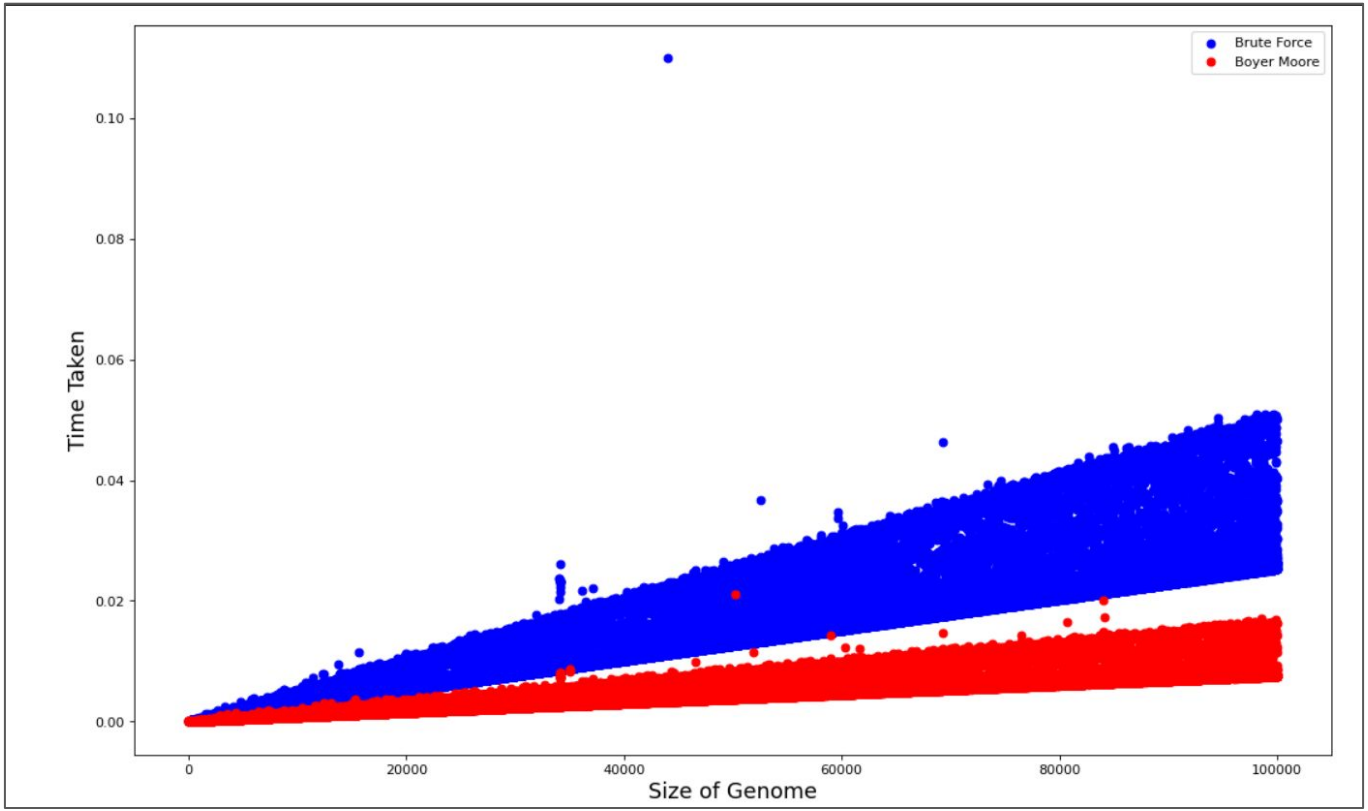
Results of Analysis - As A Whole



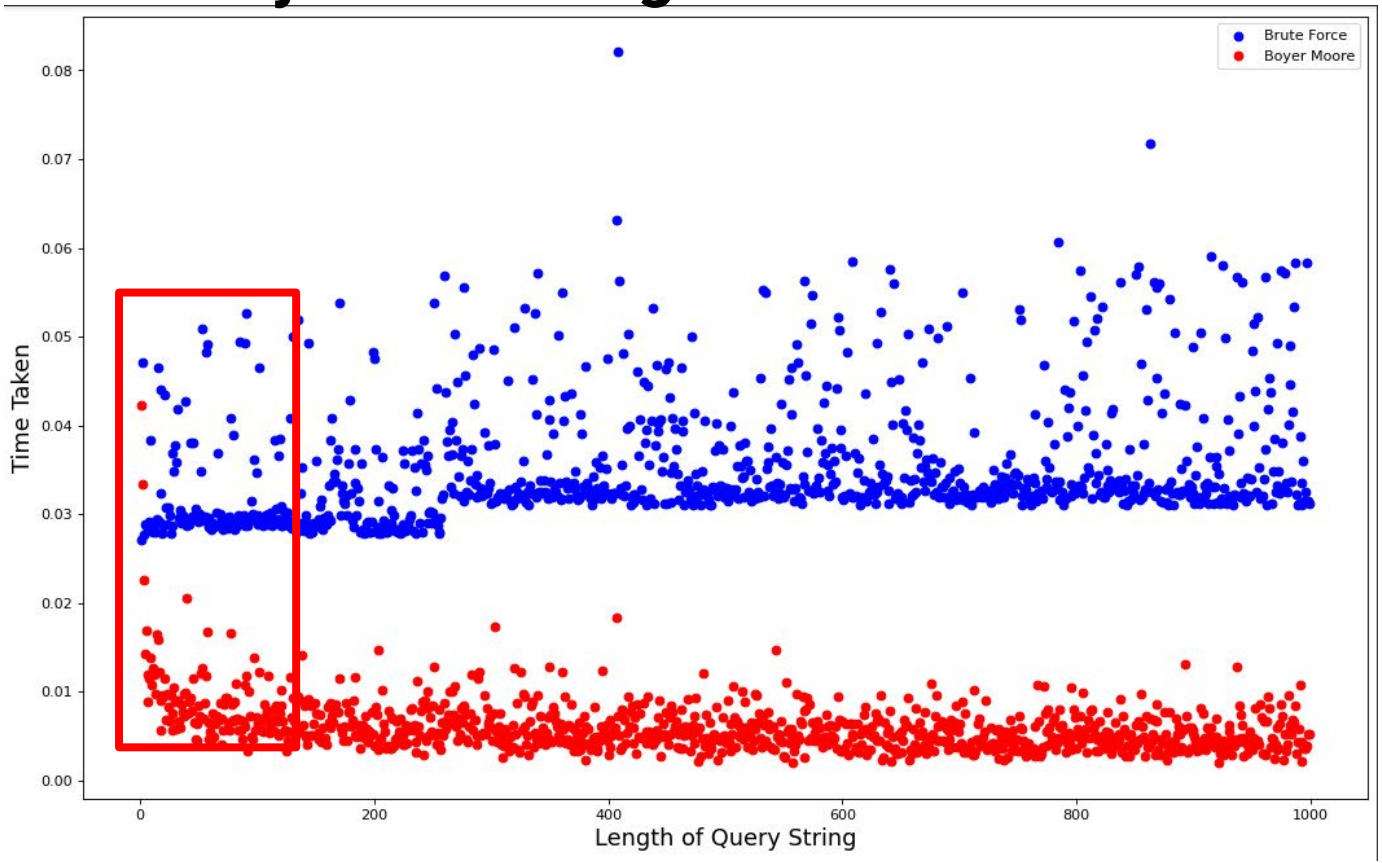
Results of Analysis - Theoretical Speed



Results of Analysis - How Time Taken Affected as Size



Results of Analysis - Testing



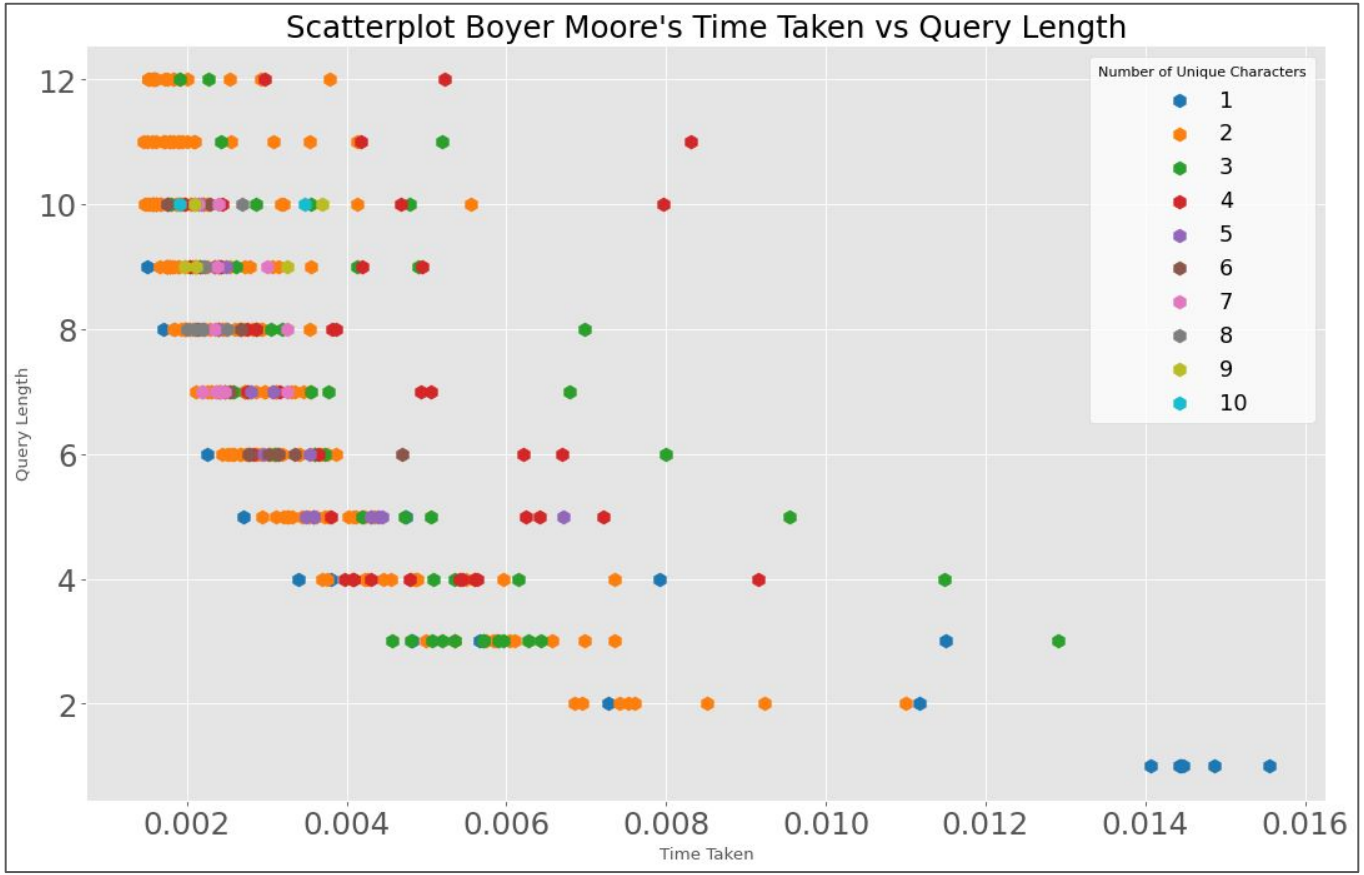
Results of Analysis - Testing

Query Size	BF Time	BM Time
1	0.02707	0.04225

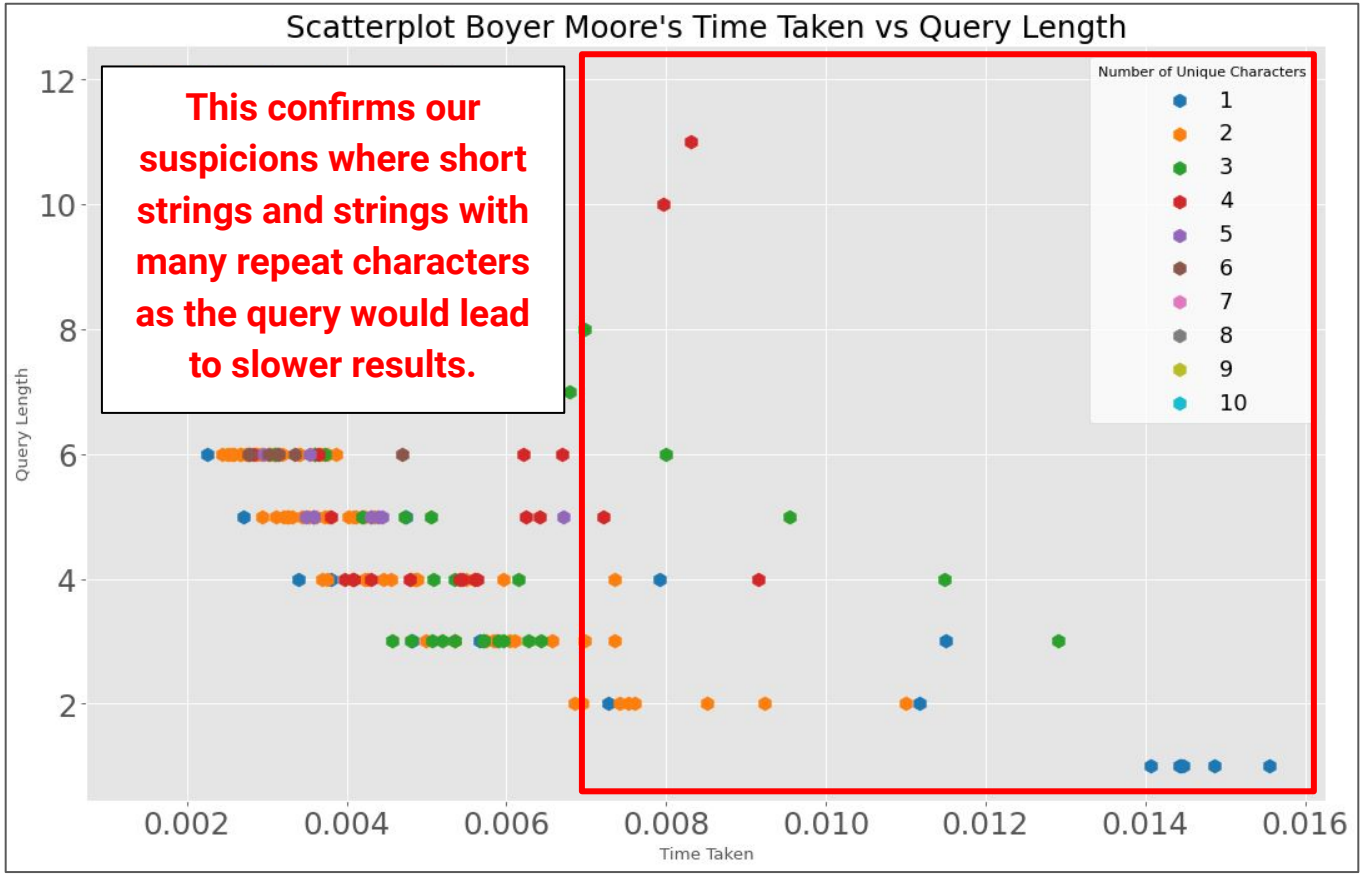
Which is intuitive as longer query length means bigger skips!

As lookup tables are only generated for the query string.

Results of Analysis - Deeper Dive into Boyer Moore



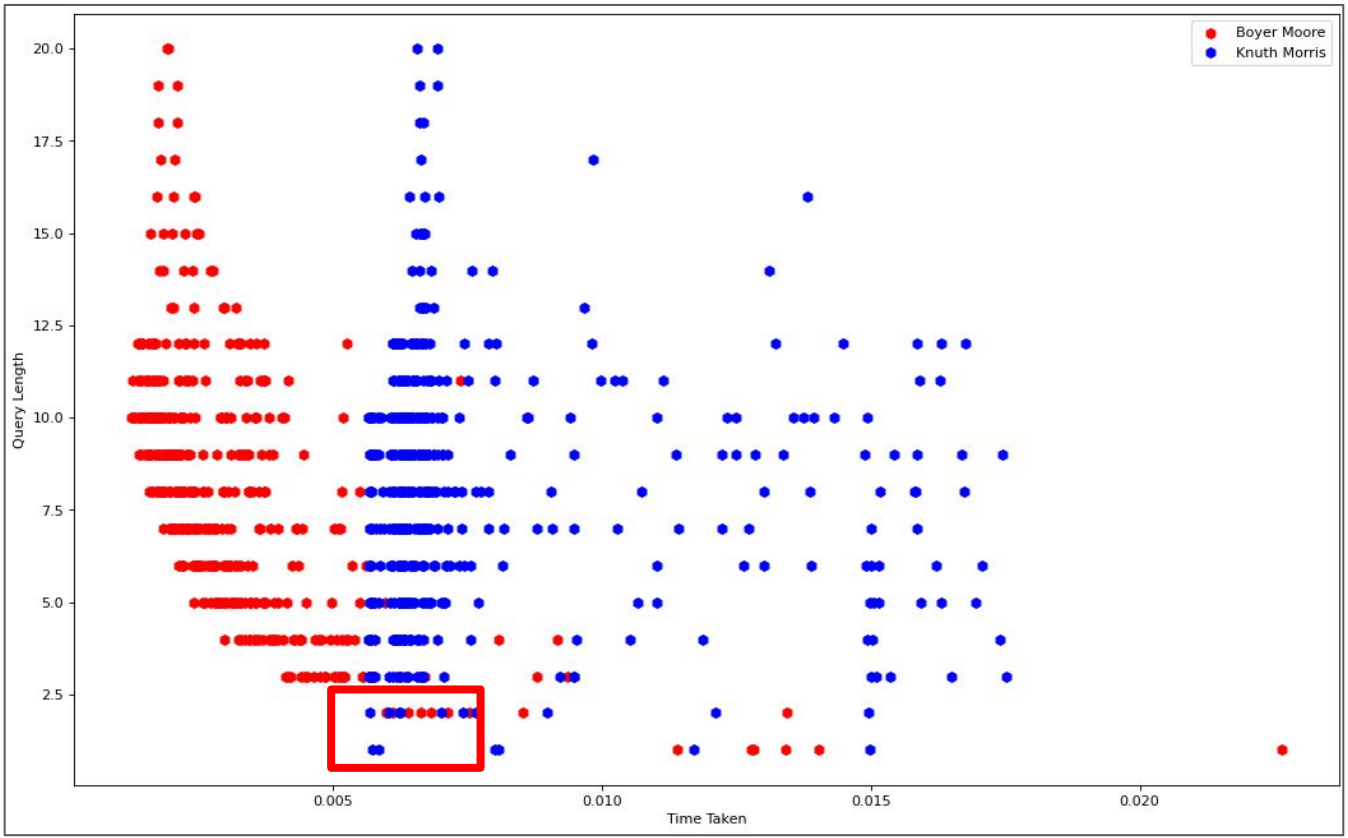
Results of Analysis - Deeper Dive into Boyer Moore



Results of Analysis - Deep Dive into Boyer Moore

Query	Query Length	Time Taken	Search Successful	Position Placed	Unique
E	1	0.02260	True	272	1
C	1	0.01996	True	1053	1
B	1	0.01849	True	4913	1
A	1	0.01844	True	642	1
BBBAAAA	7	0.01770	True	2997	2
J	1	0.01497	True	426	1
D	1	0.01430	True	3845	1
CB	2	0.01368	True	1720	2
TTT	3	0.01147	True	4628	1

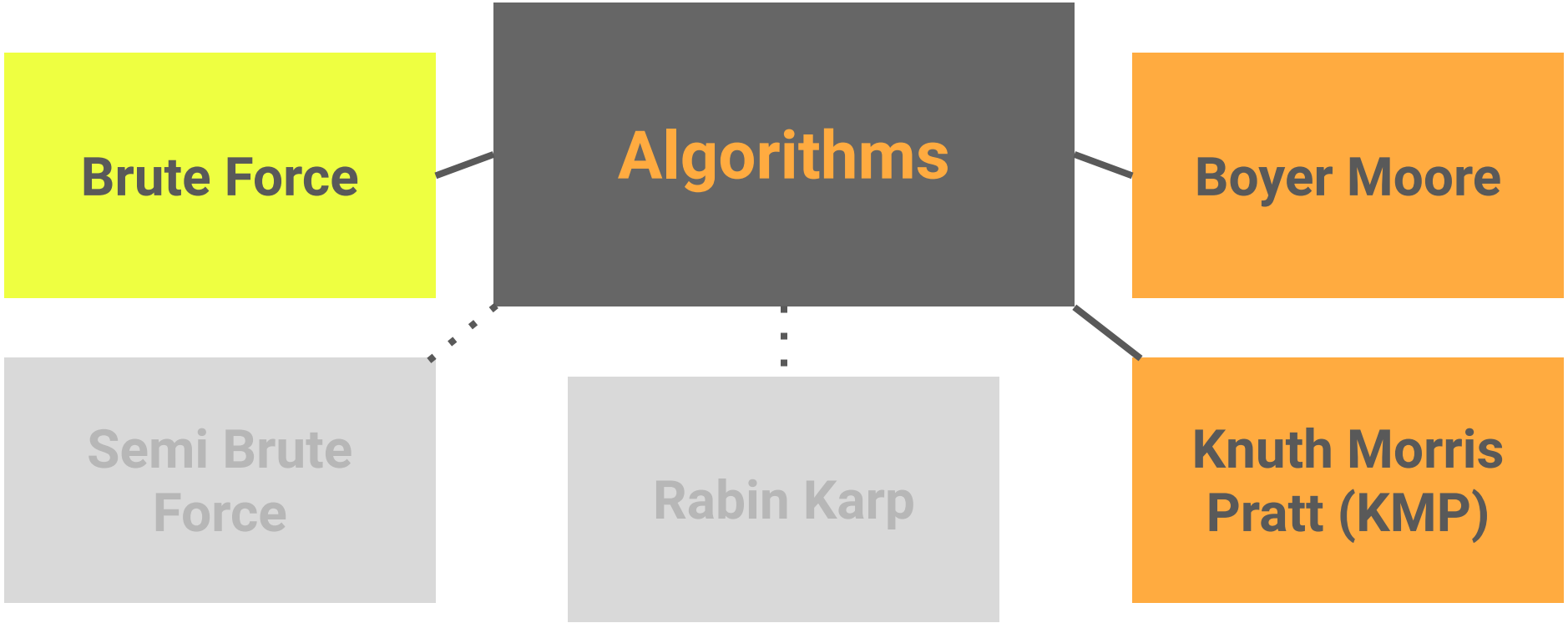
Conclusion - KMP Complementing BM



Conclusion - KMP Complementing BM

- Generally, BM performs the best out of all 3
- When string lengths get long, BM performs better, while KMP’s performance is similar to brute force.
- When string lengths gets shorter, especially when searching for one char, KMP performs better than brute force and BM, since the inner loop is not activated.

Implementing Algorithms



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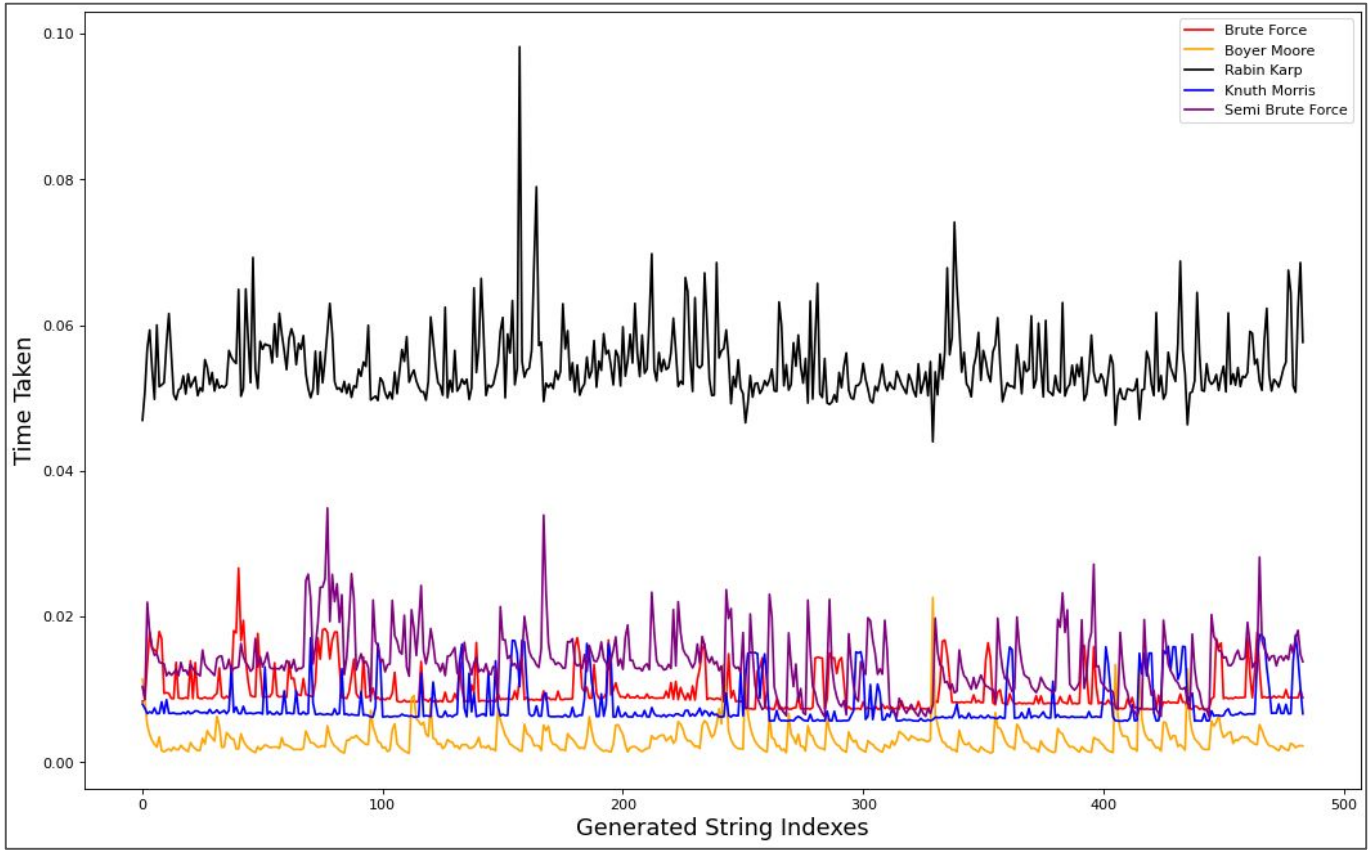

Modern Solutions to Solving Problems

Just like the search for our query string in a genome sequence,

Looking for a needle in a haystack, can be a nearby impossible task…

Why not just burn it all down?