

CZ2001 Lab... Project 1- Searching Algorithms

Objectives

- To propose algorithms that solve **string searching problems on genome sequences**
- The algorithms should return **positions** of occurrences of a query sequence in the source sequence and the **number of occurrences**

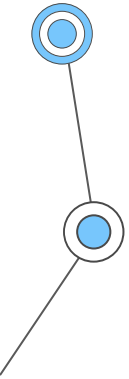
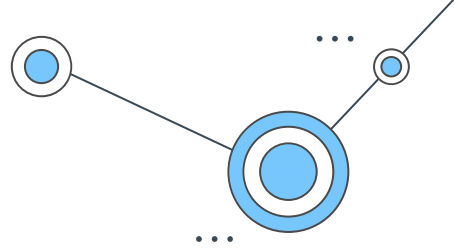
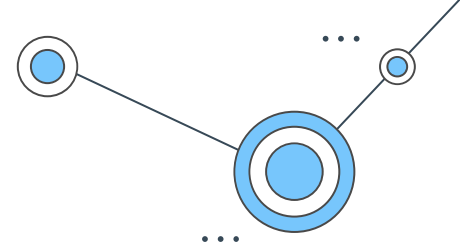


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01

Brute Force

Naive String Searching Algorithm

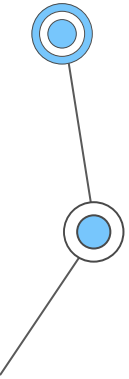
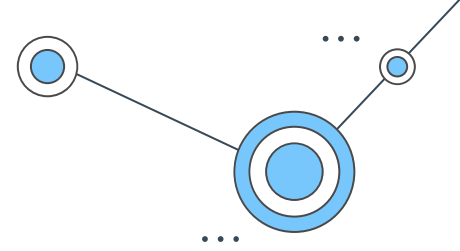


Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence

A C C G T A T Source

C G T Pattern



Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence

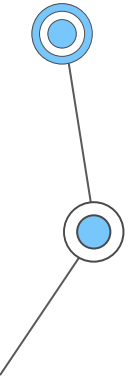
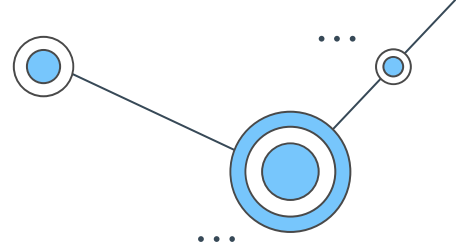


| | | | | | | |
|---|---|---|---|---|---|---|
| A | C | C | G | T | A | T |
|---|---|---|---|---|---|---|

Source

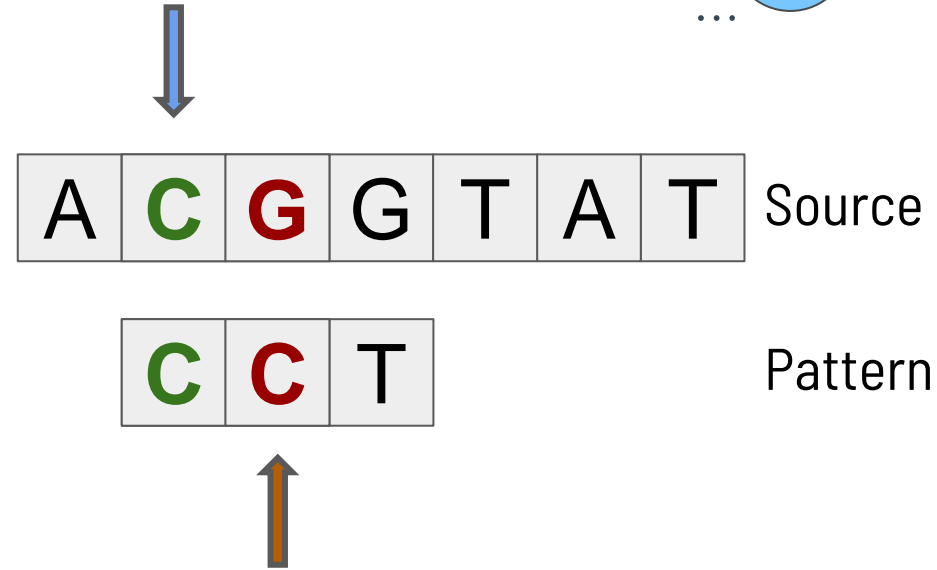
| | | |
|---|---|---|
| C | G | T |
|---|---|---|

Pattern



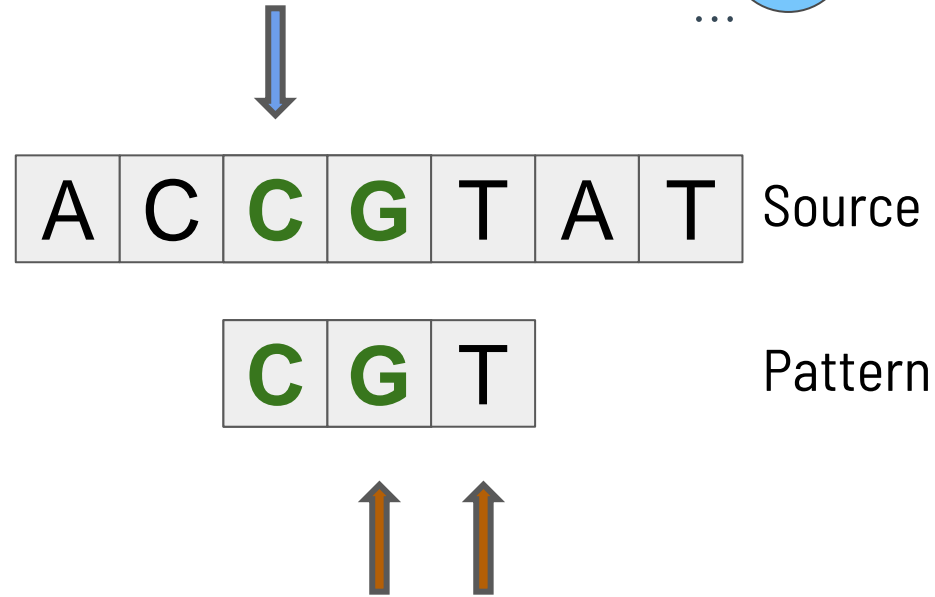
Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence



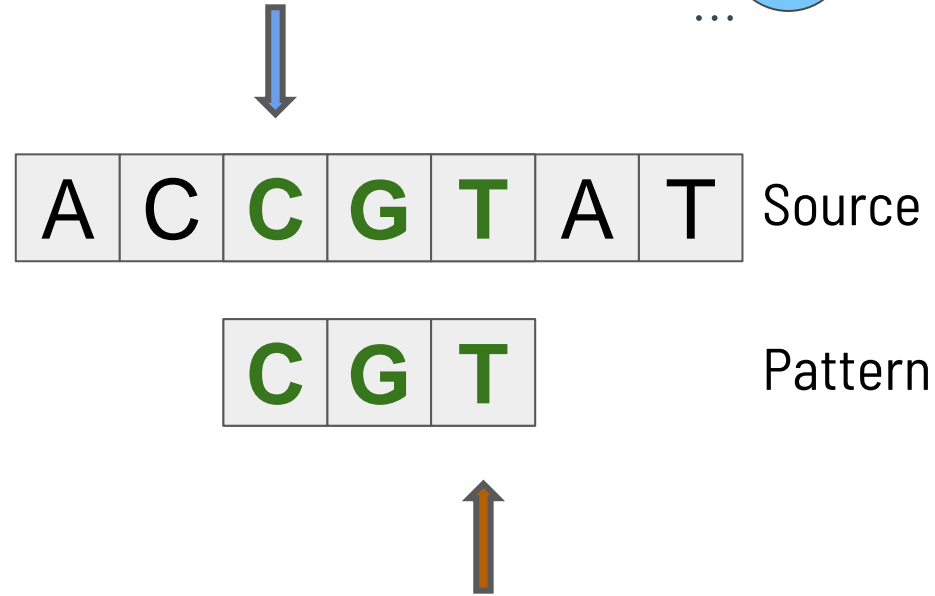
Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence



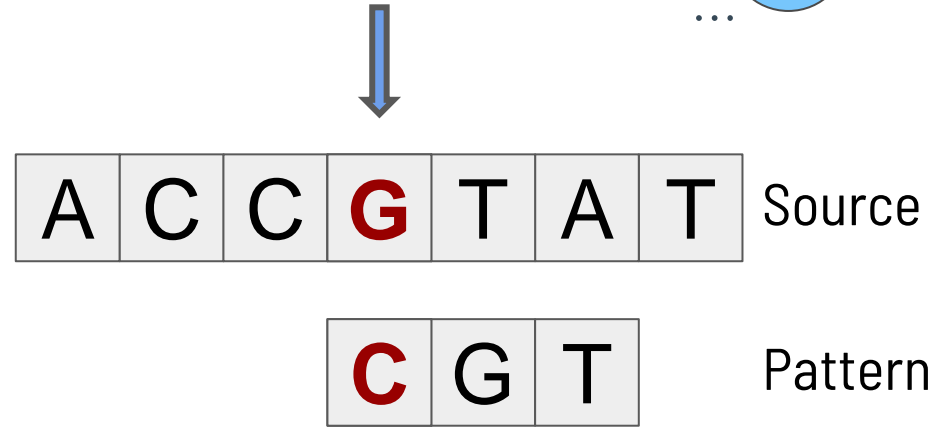
Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence



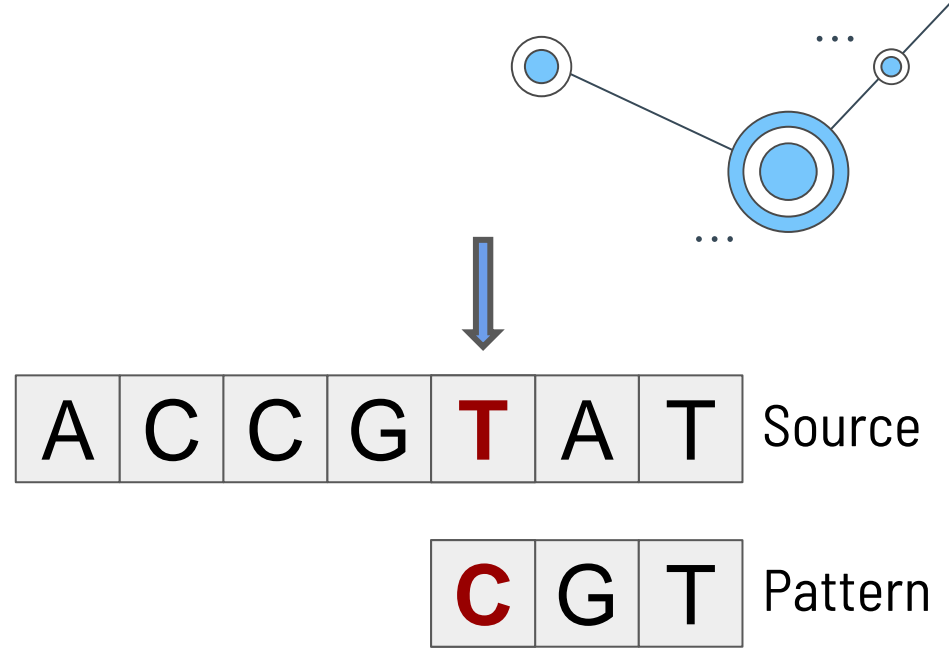
Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence



Concept

- Walk through the source sequence from the beginning till the end
- Check **at each position** if the resulting substring equals the query sequence

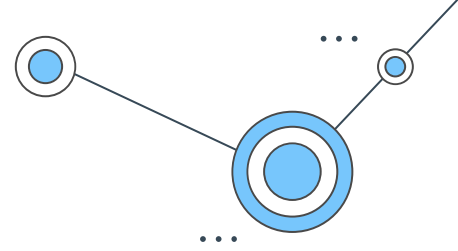


Implementation

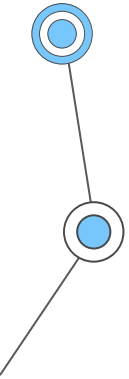
- Nested for-loop
 - Outer loop: check along all possible substrings
 - Inner loop: compare characters between the substring and the query sequence

```
occurrences = []      # create an empty list
# s1: query sequence; s2: source genome
for i in range (len(s2)-len(s1)+1):
    match = True
    for j in range (len(s1)):
        if s2[i+j] != s1[j]: # comparison failed
            match = False    # mismatch
            break
    # match found
    if match:                # append the position
        occurrences.append(i+1)
```

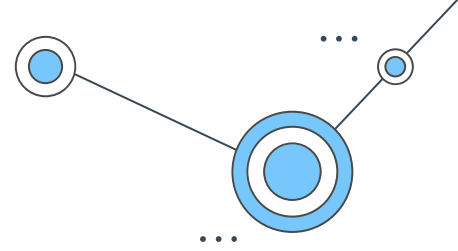
Time Complexity



- let **n** denote the length of the source genome sequence, and **m** be the length of the query sequence, where ($n \gg m$)
- To analyze the time complexity of brute force algorithm, we will be looking at the **number of character comparisons**



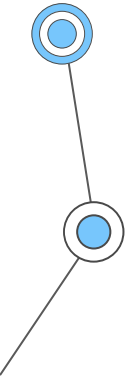
Time Complexity – Best Case Scenario

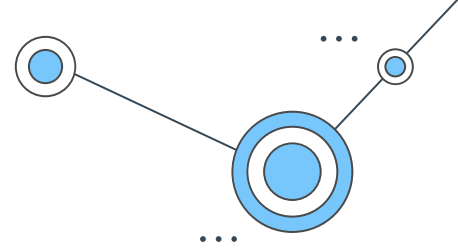


- Every first-character comparison between possible substring and query sequence results in a mismatch
- The total number of comparisons is only determined by the number of outer-loop iterations, which is **$(n-m+1)$** , or **$O(n)$**

Text: ACTGGTTCATGACCT

Pattern: BATGTC





Time Complexity – Worst Case Scenario

- The total number of comparisons is the **product** of the number of outer-loop comparisons and inner-loop comparisons, which is **$m(n-m+1)$** , or **$O(mn)$**



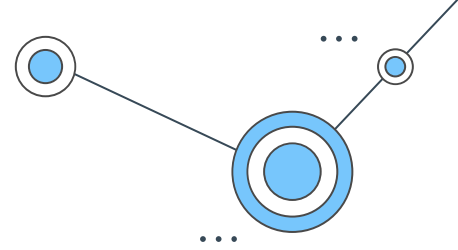
Text: TTTTTTTTTT

Pattern: TTTT

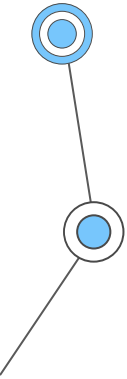
Text: TTTTTTTTTT

Pattern: TTTA

Time Complexity – Average Case Scenario



- Outer loop: it will always be executed $(n-m+1)$ times
- Inner loop: assume each number of comparisons (from 1 to m) is equally likely, expected number of comparisons = $(1+m)/2$
- The average number of comparisons = $(n-m+1)[(1+m)/2] = \mathbf{O(mn)}$

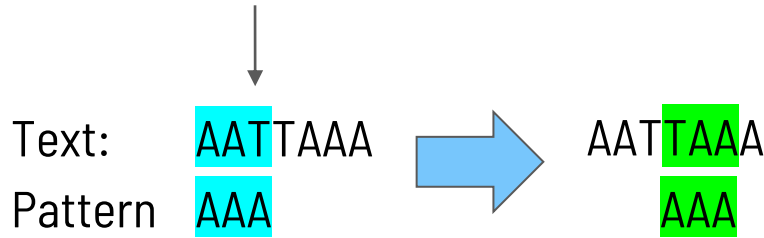


02 BMH

Boyer Moore Horspool Algorithm

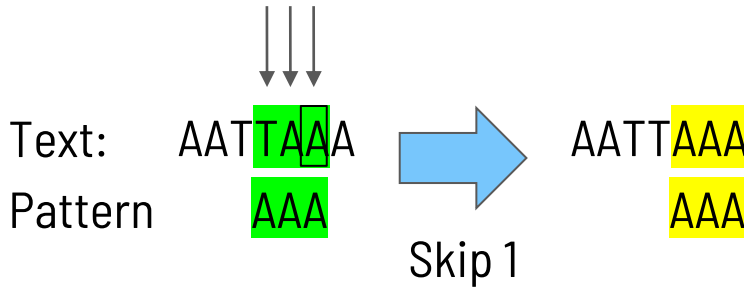
Concept

- Reduce searching time by comparing pattern with text sequences from **end to start** of pattern
- **Comparisons between first few characters** can be **skipped** when there is a **mismatch in the last few characters**



Searching in BMH

- **Bad Match Table:** Records number skips to do after mismatch with respect to the **rightmost character compared in the text**

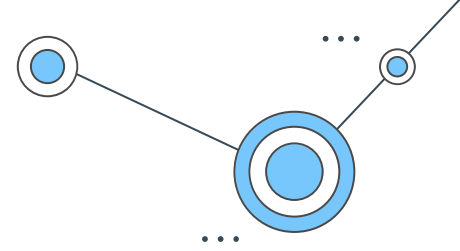


Bad Match Table

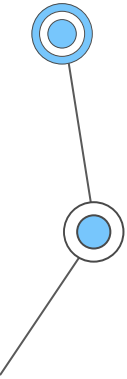
| A | C | G | T |
|---|---|---|---|
| 1 | 3 | 3 | 3 |

Time Complexity: Preprocessing

- Counting the number of character comparisons.
- For all cases: $O(m+\sigma)$
 - Assign position to alphabet in Bad Match Table (σ)
 - Calculate number of skips (m)

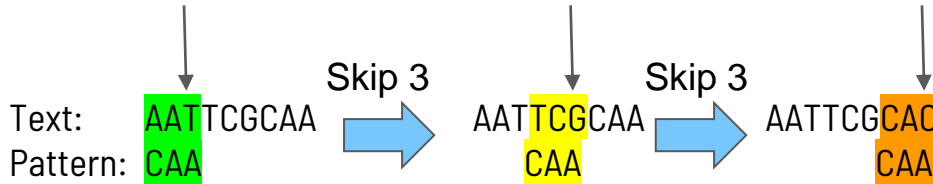


n: Length of text
m: Length of pattern
 σ : Number of alphabets



Time Complexity: Searching

- Best Case Scenario: $O(n/m)$
 - When the first compared character is always not found in the pattern
 - 1 Comparison and m skips per outer loop

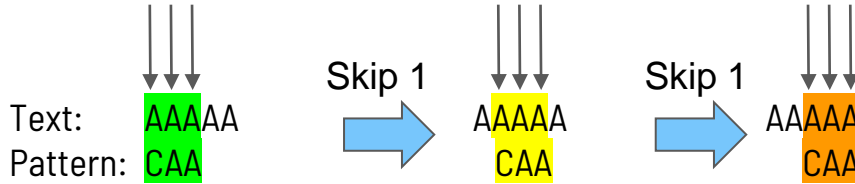


| A | C | G | T |
|---|---|---|---|
| 1 | 2 | 3 | 3 |

n: Length of text
m: Length of pattern
 σ : Number of alphabets
↓
: Comparison

Time Complexity: Searching

- Worst Case Scenario: $O(nm)$
 - When all characters in the pattern matches or when all but the last match
 - m comparisons and 1 skips per outer loop



n : Length of text
 m : Length of pattern
 σ : Number of alphabets
↓ : Comparison

| A | C | G | T |
|---|---|---|---|
| 1 | 2 | 3 | 3 |

Time Complexity: Searching

- Average Case Scenario: $O(n)$

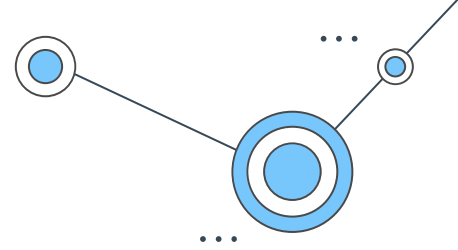
E (Number of comparisons)

= E(Times outer loop executed) * E(Comparisons per outer loop)

= $n / E(\text{Skips per outer loop}) * E(\text{Comparisons per outer loop})$

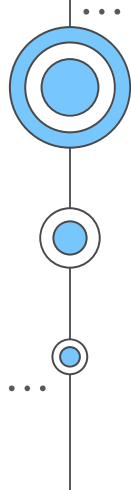
= $n = O(n)$

- Assume each skip (from 1 to m) is equally likely
 - $E(\text{Skips per outer loop}) = (1+m)/2$
- Assume each number of comparisons (from 1 to m) is equally likely
 - $E(\text{Comparisons per outer loop}) = (1+m)/2$



n: Length of text
m: Length of pattern
 σ : Number of alphabets

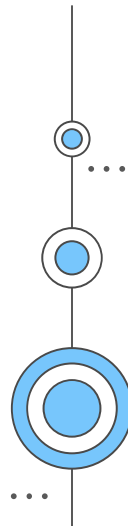




03

Modi-KMP

Modified Knuth-Morris-Pratt algorithm



Concept

- Uses two preprocessing techniques to reduce comparisons:
Bad match table(BMT) & **Longest Prefix-Suffix array(LPS)**
- Implements bad character heuristic within KMP algorithm, which initially use only lps array.

Bad Match Table

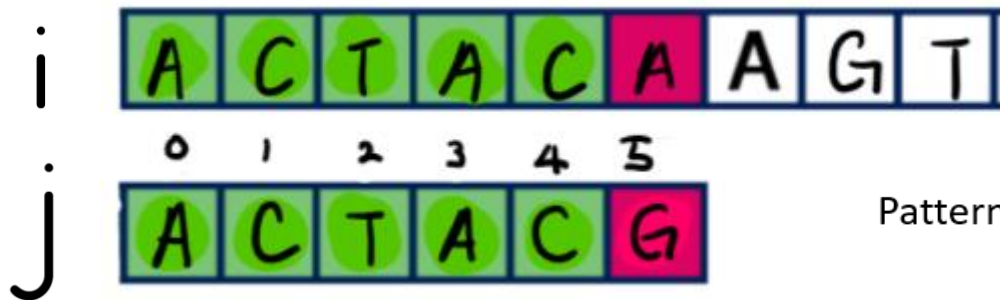
| A | C | G | T |
|---|---|---|---|
| 1 | 3 | 3 | 3 |

Pattern: ACTACG

lps array

| A | C | T | A | C | G |
|---|---|---|---|---|---|
| 0 | 0 | 0 | 1 | 2 | 0 |

Lps array



Pattern: ACTACG

lps array

| | | | | | |
|---|---|---|---|---|---|
| A | C | T | A | C | G |
| 0 | 0 | 0 | 1 | 2 | 0 |

$$i = 5$$

Lps array

i

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| A | C | T | A | C | A | A | G | T |
|---|---|---|---|---|---|---|---|---|

0 1 2 3 4 5

j

| | | | | | |
|---|---|---|---|---|---|
| A | C | T | A | C | G |
|---|---|---|---|---|---|

i

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| A | C | T | A | C | A | A | G | T |
|---|---|---|---|---|---|---|---|---|

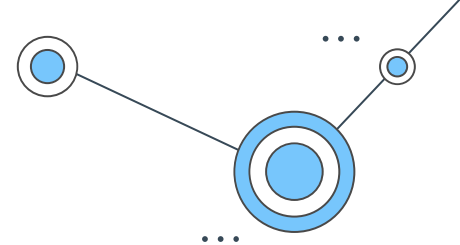
0 1 2 3 4 5

j

| | | | | | |
|---|---|---|---|---|---|
| A | C | T | A | C | G |
|---|---|---|---|---|---|

Pattern: ACTACG

i = 5

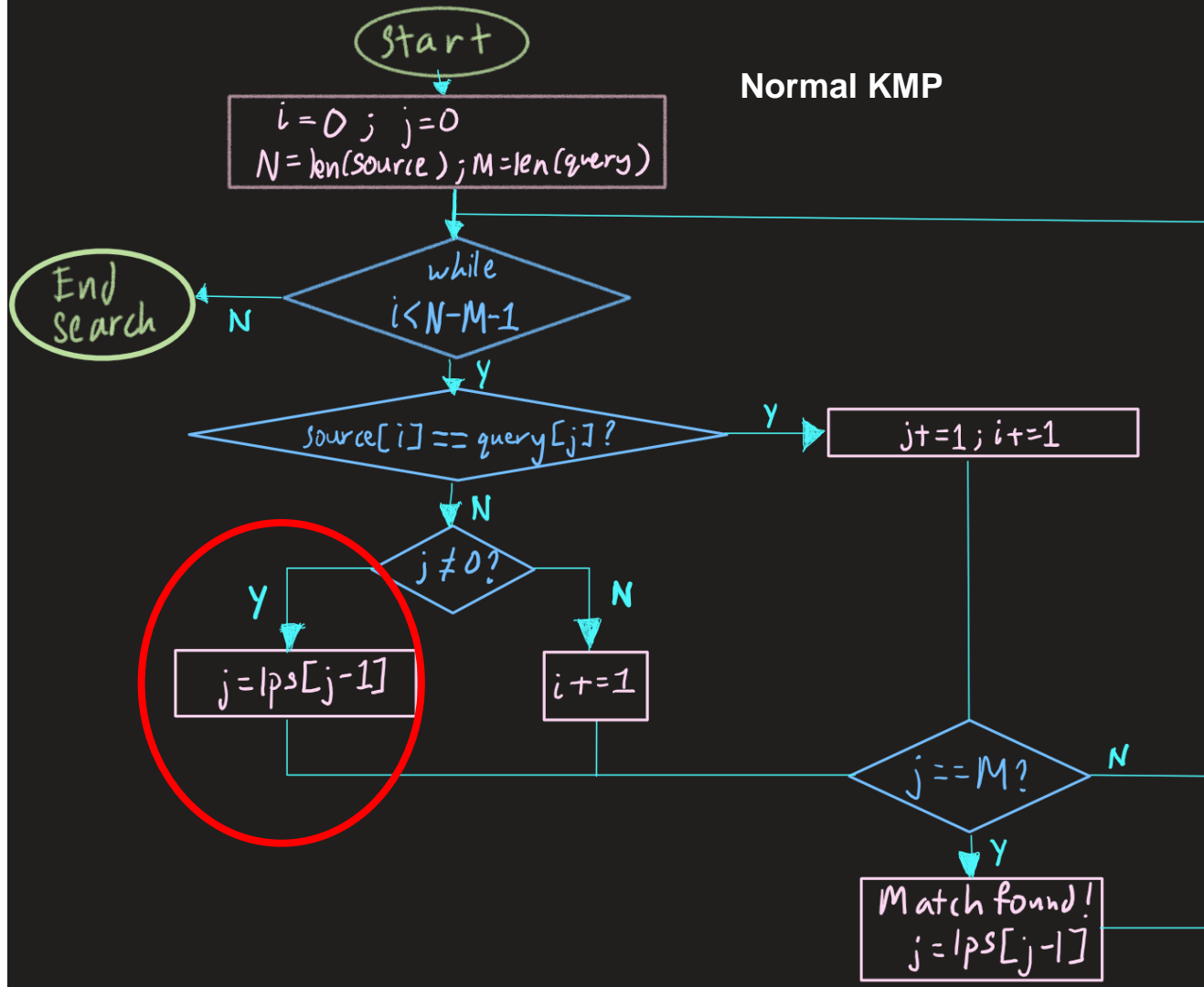


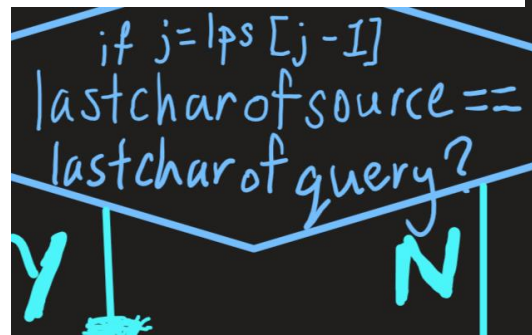
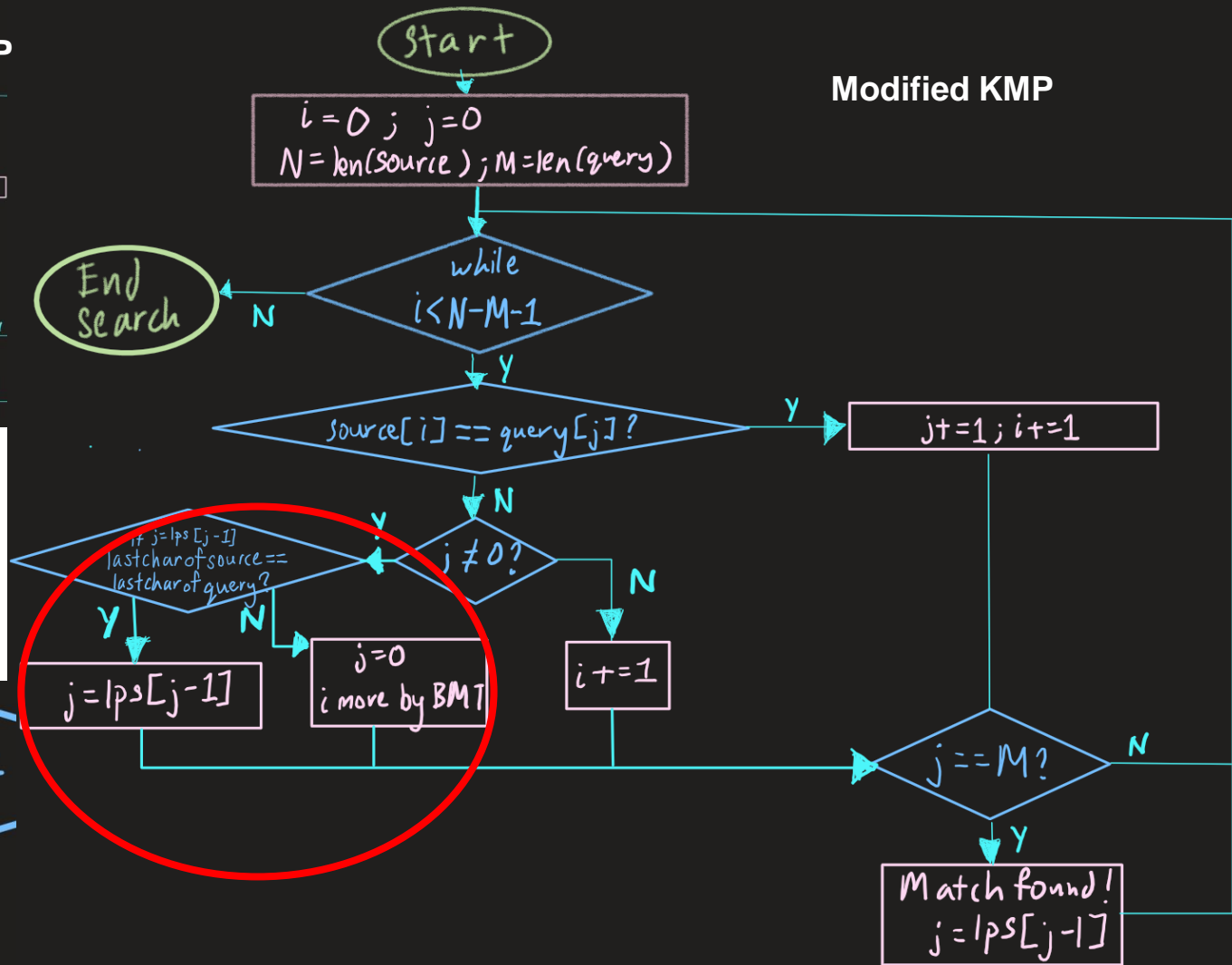
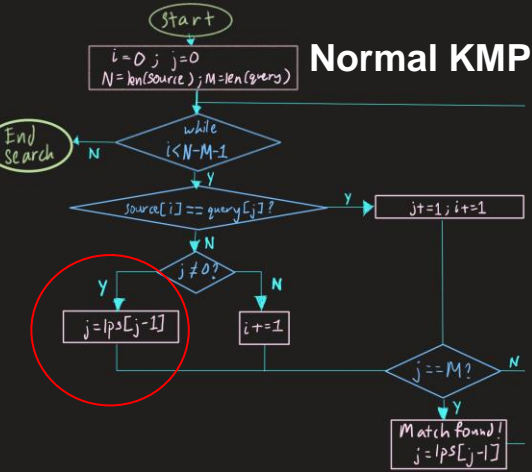
0 1 2 3 4 5

lps array

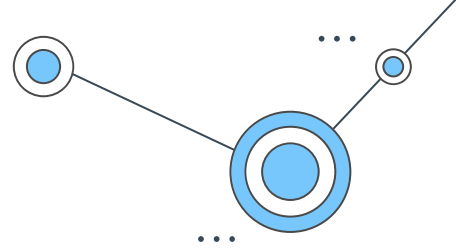
| | | | | | |
|---|---|---|---|---|---|
| A | C | T | A | C | G |
| 0 | 0 | 0 | 1 | 2 | 0 |

Normal KMP





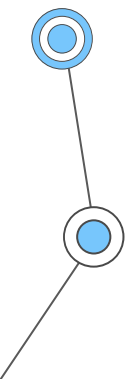
Time Complexity: Preprocessing



n is length of Source DNA, m is length of query pattern

- Bad Match Table: For all cases: approx. $O(m)$
- LPS: For all cases $O(m)$

Bad Match Table



| A | C | G | T |
|---|---|---|---|
| 1 | 3 | 3 | 3 |

Pattern: ACTACG

lps array

| A | C | T | A | C | G |
|---|---|---|---|---|---|
| 0 | 0 | 0 | 1 | 2 | 0 |

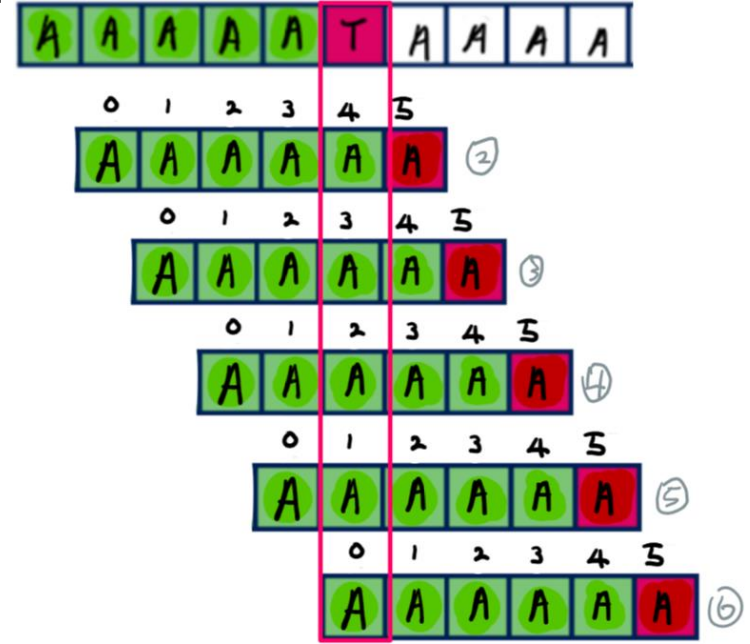
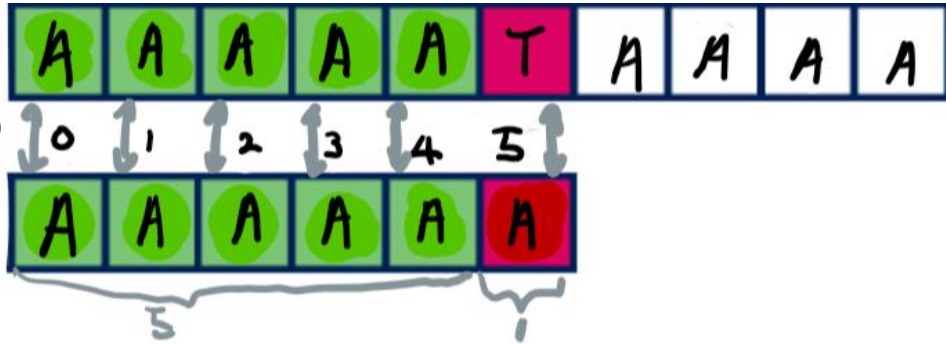
Time Complexity:

- Best Case Scenario: $O(n/m)$
 - Occurs when if-else allows BMT \Rightarrow causing algorithm to run like Boyer-Moore
 - Pointer i signifying pattern moving along source code increments by m each time, causing only n/m comparisons



Time Complexity:

- Worst Case Scenario: $O(n)$
 - Text=AAAAA**T**AAAAA**T**AAAAA**T**AAAA...
 - Pattern=AAAAA**A**, length of pattern = 6
 - Compares approx. $2n$ times: has complexity of $O(n)$



Time Complexity:

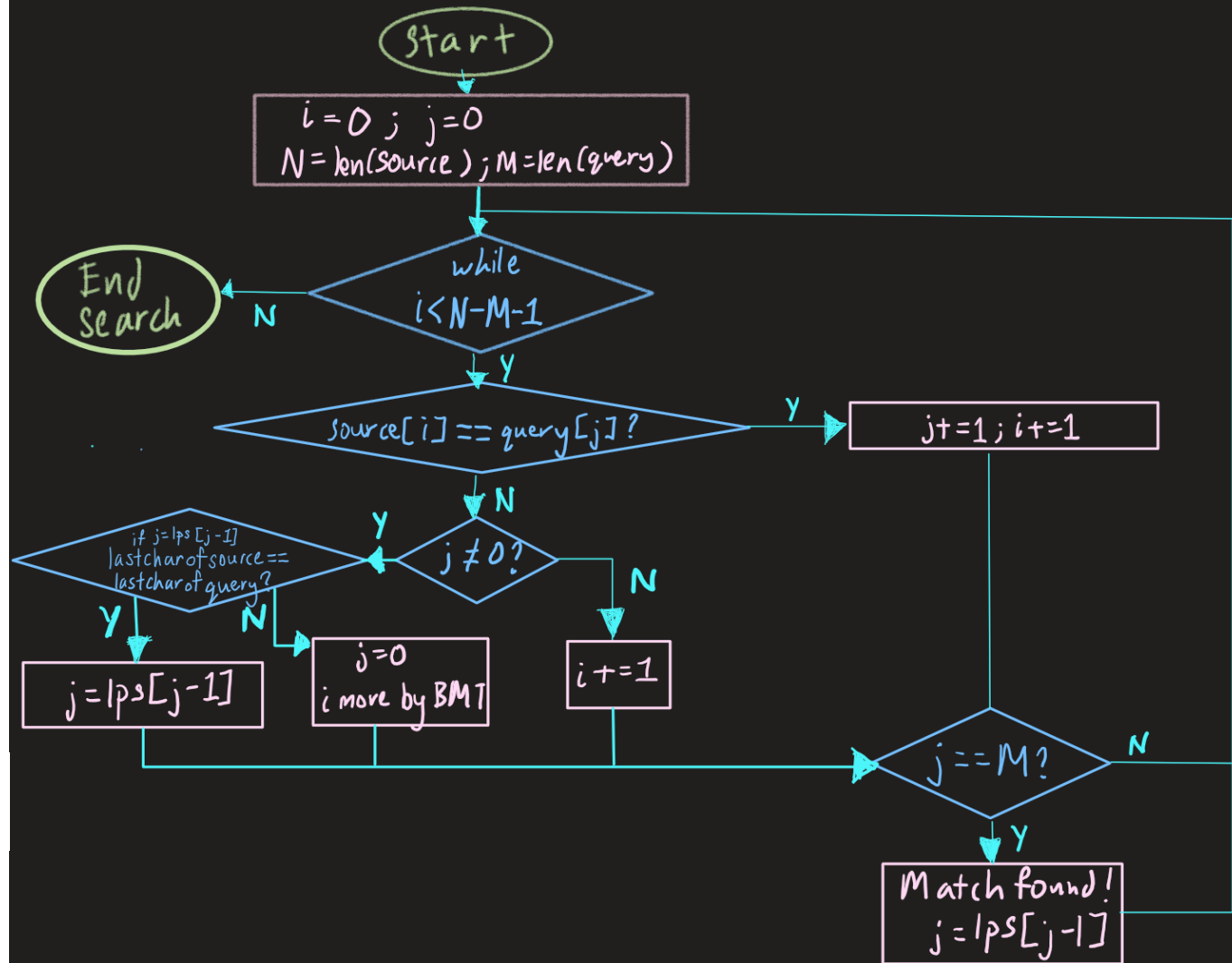
- Average Case Scenario: $O(n)$

Expected i shifts per iteration:

$$\frac{1}{4} + \frac{15+9m^2}{32m}$$

Expected number of comparisons:

$$n / \left(\frac{15+8m+9m^2}{32m} \right) = O(n)$$



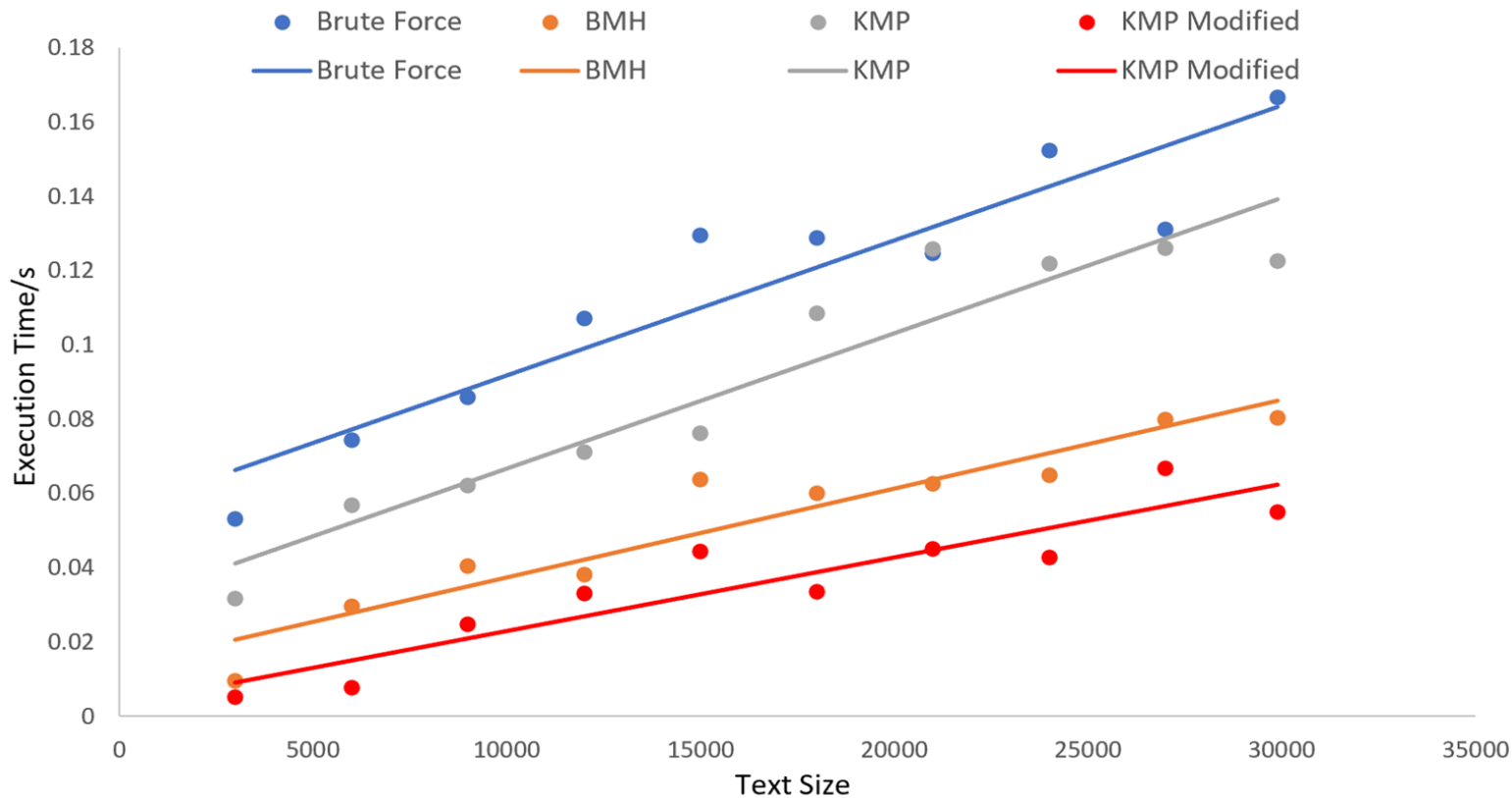
04

Conclusion

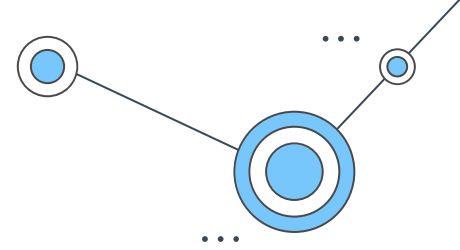
Comparison between algorithms

Comparison for empirical runs

Run Time for Empirical Runs



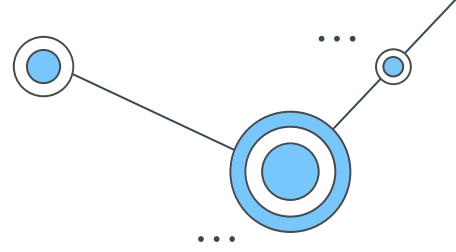
Theoretical Complexity



* n : Length of text, m : Length of pattern, σ : Number of alphabets

| Algorithms | Preprocessing Time complexity | | Best Case Time Complexity | Worst Case Time Complexity | Average Case Time Complexity | Preprocessing Space Complexity | Overall Space Complexity |
|--------------|---------------------------------------|----------------------|---------------------------|----------------------------|------------------------------|--|--------------------------|
| Brute Force | | | $O(n)$ | $O(mn)$ | $O(mn)$ | - | $O(1)$ |
| BMH | $O(m+\sigma)$ for bad character table | | $O(\frac{n}{m})$ | $O(mn)$ | $O(n)$ | $O(1)$ for building bad character table | $O(1)$ |
| KMP | $O(m)$ for lps array | | $O(n)$ | $O(n)$ | $O(n)$ | $O(m)$ for lps Table | $O(m)$ |
| Modified KMP | $O(m+\sigma)$ for bad character table | $O(m)$ for lps array | $O(\frac{n}{m})$ | $O(n)$ | $O(n)$ | $O(m)$ for lps Table & $O(1)$ for building bad character table | $O(m)$ |





Thank You :)

