MULTIPLE STRING-MATCHING USING WAVELET MATRIX AND BURROWS-WHEELER TRANSFORM (BWT)

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Master of Science

By

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CERTIFICATION

This is to certify that the thesis titled "*MULTIPLE STRING-MATCHING USING WAVELET MATRIX AND BURROWS-WHEELER TRANSFORM (BWT)*" submitted to the school ofpostgraduatestudies, African University of Science and Technology (AUST), Abuja, Nigeriafor the award of the Master's degree is a record of original research carried out by *Adam Saleh Adam in the Department of Computer Science.*

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A THESIS APPROVED BY THE COMPUTER SCIENCE DEPARTMENT

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Dean

Date

ABSTRACT

The problem of multiple string matching is fundamental in computer science, with applications in bioinformatics, text mining, and information retrieval. Traditional methods struggle with large datasets due to high computational and memory requirements. This research proposes a novel algorithm that combines the Burrows-Wheeler Transform (BWT) for text compression and the Wavelet Matrix (WM) for efficient pattern search. The proposed method achieves faster search times, lower memory usage, and effective compression, particularly for repetitive datasets like DNA sequences. Experimental results demonstrate that the method performs better compared to existing algorithms. This work contributes to the advancement of efficient and scalable multiple string matching techniques, with potential applications in large-scale text processing and bioinformatics.

Keywords: *Algorithms, Text Compression, Wavelet Matrix, Burrows-Wheeler transform, Multiple String matching*

DEDICATION

This work is dedicated to Almighty Allah (SWT), who provided me with the strength, opportunity, and inspiration during this work, also to my family for their care and support, and to everyone else who contributed to the success of my academic endeavours.

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CHAPTER ONE

INTRODUCTION

1.1 Background

In today's era of vast amounts of digital data, the efficient processing and analysis of textual information have become essential in various domains. Multiple string matching also known as multiple pattern matching, fundamentally, is the process of finding one or more occurrences of a string (a sequence of characters) within another string or a set of strings. It stands as a cornerstone of computer science, underpinning the mechanics of search algorithms, data retrieval systems, text mining, and many other applications that are critical to our digital lives. The efficiency and effectiveness of string matching algorithms directly impact the performance of search engines, the reliability of cybersecurity systems, and the precision of bioinformatics tools, among others (Z. Zhang, 2022). The multiple string matching problem can be defined as:for a given input string T = $t_0 t_2 \ldots t_{n-1}$ of size n and a finite set of d patterns $P = p^0, p^1, \ldots, p^{d-1}$ where each p^r is a string $p^r = p^r{}_0 p^r{}_1 \ldots p^r{}_{m-1}$ of size m over a finite character set Σ and the total size of all patterns is denoted as $|P|$, the task is to find all occurrences of any of the patterns in the input string. More formally, for each p^r find all i where $0 \leq i < n - m + 1$ such that for all j where $0 \leq j < m$ it holds that $t_i = p^r{}_j$(Kouzinopoulos et al., 2015).

1.1.1 Bioinformatics

In bioinformatics, the analysis of DNA sequences, protein sequences, and genomic data often requires identifying specific patterns or motifs. Multiple string-matching algorithms are instrumental in locating these patterns in large-scale genetic datasets, enabling researchers to unravel genetic variations, gene functions, and potential disease associations.(Bhukya & Somayajulu, 2011)

1.1.2 Information Retrieval/Search Engines

The majority of data is available online as textual data. It is very challenging to search for a specific piece of content because there is so much uncategorized text data available. Search engines on the web assist us in resolving this issue by arranging the necessary text and data as effectively as possible. Algorithms for string matching are used to categorize these data. Search keywords are used as the basis for categorization. Search engines and information retrieval systems rely on efficient multiple string-matching techniques to process user queries and retrieve relevant documents. By matching multiple search terms or keywords against a large corpus of textual data, these systems can provide accurate and timely results, enhancing the overall user experience.(Sánchez et al., 2008)

1.1.3 Text Processing

In natural language processing and text mining, multiple string matching facilitates tasks such as entity recognition, named entity extraction, and sentiment analysis. By identifying specific patterns within the text, these techniques enable automated text processing, classification, and information extraction, leading to valuable insights for various applications, including sentiment analysis, document clustering, and topic modelling.

1.1.4 Data Mining

In the realm of data mining, multiple string-matching aids in identifying recurring patterns or sequences in sequential data such as time series, customer behaviour logs, or transaction records. These patterns can reveal hidden associations, trends, or anomalies, assisting analysts in making informed decisions and deriving actionable insights from large datasets.

Therefore, multiple string matching is an integral part of many problems and is used in several applications to find specified patterns, DNA sequence matching, detect suspicious keywords in security applications, and many more. The string searching or string matching problem entails

locating all occurrences of a pattern in a text, where both the pattern and text are strings across some alphabet (Jony, 2014)(Cheng et al., 2003).

1.2 Problem Statement

Identifying all occurrences of multiple patterns in a given text efficiently and reliably is a fundamental task in computer science. Conventional techniques for multiple string matching can become computationally expensive and memory intensive for big datasets. The use of the wavelet matrix and Burrows-Wheeler transform to accomplish accurate multiple-string matching with decreased computational and memory requirementsis still open for research.

1.3 Aim and Objectives

This research aims toinvestigate the effectiveness of using the Burrows-Wheeler Transform for text compression and Wavelet Matrix for Multiple String Matching compared to existing multiple string-matching algorithms.

The following are the objectives to attain the aim:

i. To use Burrows-Wheeler Transform to compress a text.
ii. To apply wavelet matrix to search a pattern within the body of a text.
iii. To improve the complexity of the proposed algorithm.

1.4 Organization of the Thesis

This thesis is broken into five chapters. Chapter One introduces the research background,aim, and objective. Chapter two presents a literature review of previous works related to thisresearch work. Chapter three presents the materials and methods used for this research. Chapter four is all about the experimental results and Chapter there is the summary and conclusionof the work.

CHAPTER TWO

LITERATURE REVIEW

2.1 Introduction

This chapter provides a review of the existing literature related to the aim and objectives of this research. The literature review focuses on four (4) main areas: text compression, Burrows-Wheeler Transform (BWT), Wavelet Matrix and multiple string matching. The chapter begins with an overview of text compression techniques, followed by a detailed examination of the BWT and its applications. Then, the exploration of the Wavelet Matrix and its relevance in this context, leadingthe discussion of the concept of multiple string matching and its challenges.

2.2 Text Compression Techniques

Text compression is a technique that reduces the size of text data by removing or encoding redundant or unnecessary information. Text compression can help you save storage space, bandwidth, and transmission time, particularly for large and complex text items such as documents, emails, and web pages. Text compression is a lossless compression method, which means that the original data may be entirely recovered after decompression.

Text compression is a fundamental area of research in the field of data compression. Various techniques have been developed to reduce the size of text data while preserving its information content. This review starts with an overview of lossless compression techniques, including Huffman coding, arithmetic coding, Lempel-Ziv-Welch (LZW) algorithm, and others. The advantages and limitations of these techniques are discussed, setting the stage for the introduction of the Burrows-Wheeler Transform (BWT).(Patel et al., 2015)

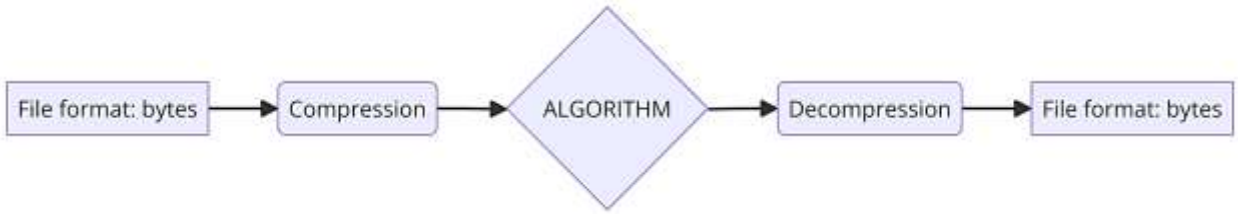

Figure 1 Data compression

2.2.1 Overview of Lossless Compression Techniques

In lossless data compression, the integrity of the data is preserved. The original data and the data after compression and decompression are exactly the same because, in these methods, the compression and decompression algorithms are exact inverses of each other: no part of the data is lost in the process. Redundant data is removed in compression and added during decompression. Lossless compression methods are normally used when we cannot afford to lose any data. There are a number of methods of lossless compression. Some of them are discussed here.

2.2.2 Huffman Coding

The Hoffman coding algorithm was developed in 1952 by David Huffman, an MIT undergraduate. It is among the most well-known and oldest techniques for compressing text. The Huffman code employs similar principles to those of the Morse code. Every individual character is encoded using a series of a few bits, with often occurring letters being encoded with a coded sequence of short bits and infrequently occurring characters being encoded with a longer sequence of bits. The code is employed to transform the initial message (which comprises the input data) into a collection of codewords, contingent upon the type of map. (Suherman, 2016)

In Huffman coding, symbols that occur with greater frequency are assigned shorter codes, whereas those that occur with less frequently are assigned longer codes. Consider, for instance, a text file containing simply five characters (A, B, C, D, E). Prior to associating bit patterns with individual characters, a weight is assigned to each character according to its frequency of usage. Assume that the frequency of the characters in this example is as it appears in Table 2.1.

Table 1 Frequency of Characters

Character	A	B	C	D	E
Frequency	17	12	12	27	32

Now let us see how Huffman coding works.

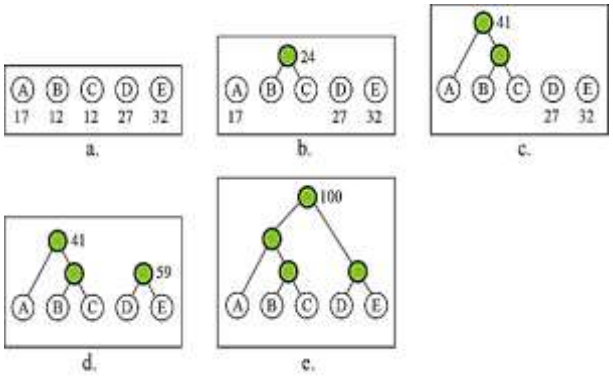

Figure 2 Working of Huffman coding

The code for a character can be found by tracing the branches that lead to it from the root. The bit values of each path branch, taken in order, make up the code itself.

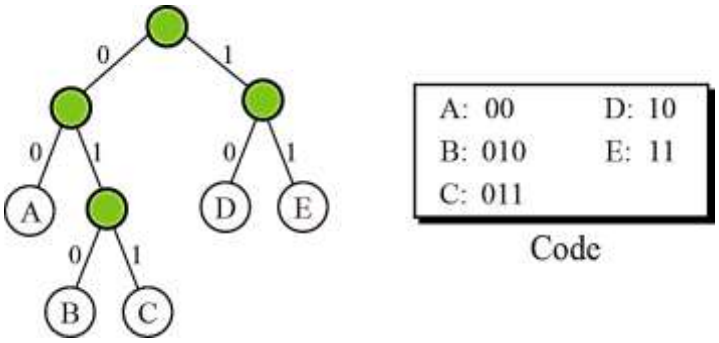

Figure 3 Final tree and code

Using the code for the five characters at our disposal, we shall encode text. The original and encoded text are detailed in Figure 2.4.

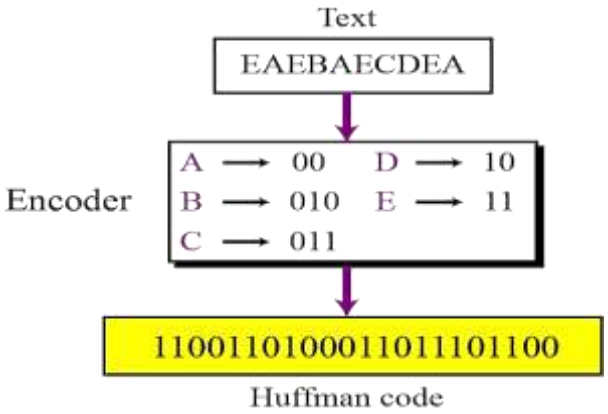

Figure 4 Huffman Encoding

The recipient's task of decoding the received data is exceedingly straightforward. As illustrated in Figure 2.5, decoding is performed.

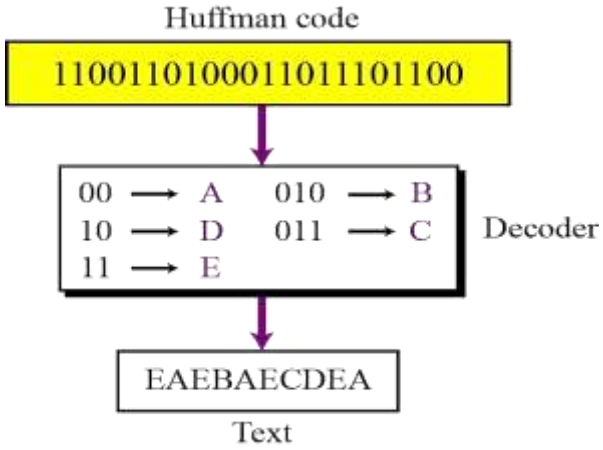

Figure 5 Huffman Decoding

Huffman coding, which is computationally straightforward and generates prefix codes with the condition that each symbol is represented by a code consisting of an integral number of bits, consistently attains the shortest predicted code word length.

2.2.3 Shannon-Fano Coding

Another lossless compression technique is Shannon-Fano coding, which gives the symbols in the data variable-length codes determined by their probabilities. The algorithm splits the symbols into two equal-probability groups, giving each group a bit value of either 0 or 1. After that, it iteratively goes through each group's steps until every symbol has a distinct code. Similar to Huffman coding,

Shannon-Fano coding is less effective and could not yield the best codes. (Elakkiya & Thivya, 2022)

2.2.4 Arithmetic Coding

Arithmetic coding, is a popular entropy coder, but its main drawback is its speed; nonetheless, compression is typically better than what Huffman can accomplish. Arithmetic coding works on the basis of a probability line ranging from 0 to 1. Each symbol is assigned a range in this line according to its probability; the greater the probability, the larger the range assigned to that symbol. Start encoding the symbols when the ranges and probability line have been established. Each symbol indicates the location of the output floating point number. Since arithmetic coding can encode in fractional amounts of bits, which more closely resemble the actual information content of the symbol, it can typically generate more overall compression than either Huffman or Shannon–Fano. Arithmetic coding is more computationally expensive and has more patent protection than Huffman, thus it hasn't replaced it in the same way that Huffman has supplanted Shannon–Fano. Let's imagine that we have

Table 2 Symbol , their frequency and range

Symbol	Occurrence	Range
a	2	[0,0.5)
b	1	[0.5,0.75)
c	1	[0.75,1]

We begin by encoding the symbols and calculating the resultant number. The algorithm to compute the output number is:

- Low = 0
- High = 1

Loop. For all the symbols.

- Range = high – low
- High = low + range * high range of the symbol being coded
- Low = low + range * low range of the symbol being coded

Where: Range, which maintains track of the location of the subsequent range, and Give an output number and set it to high and low.

Table 3 Symbol, Range and Values

Symbol	Range	Low Value	High Value
		0	1
b	1	0.5	0.75
a	0.25	0.5	0.625
c	0.125	0.59375	0.625
a	0.03125	0.59375	0.609375

The output number will be 0.59375.

2.2.5 Lempel-Ziv-Welch (LZW) Algorithm

The Lempel Ziv Algorithm is a lossless data compression algorithm. As depicted in Figure 2.6, it is not a single algorithm, but rather derives from algorithms proposed by Jacob Ziv and Abraham Lempel in their seminal articles of 1977 and 1978.

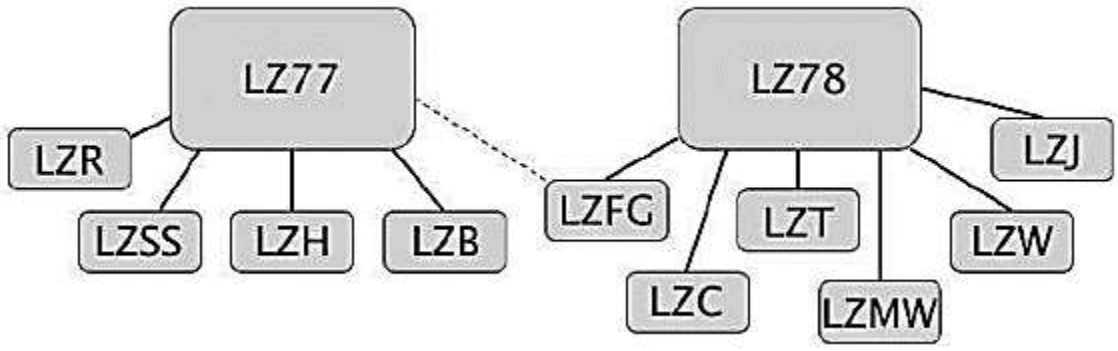

Figure 6 Classification of lempel ziv family

Based on LZ78, Terry Welch has proposed his LZW (Lempel–Ziv–Welch) algorithm. It essentially implements the LZSS principle by which the subsequent non-matching symbol is not transmitted explicitly to the LZ78 algorithm. Initiating the dictionary requires including every conceivable symbol from the input alphabet. It ensures that a match is consistently discovered. (Fitriya et al., 2017)

LZW would just provide the dictionary with the index. The encoder accumulates the input into a pattern denoted by 'w', provided that 'w' is present in the dictionary. The index of 'w' is broadcast to the receiver, the pattern 'w*K' is appended to the dictionary, and another pattern commencing with the letter 'K' is generated if the addition of an additional letter 'K' yields a pattern 'w*K' that is not present in the dictionary.

2.2.6 Run-Length Encoding

This is a lossless compression algorithm that compresses the data by replacing consecutive identical symbols with a pair of the symbol and its count. For example, the string "AAAAABBBBCCCC" can be compressed as "A5B4C4".

Run-length encoding is probably the simplest method of compression. It can be used to compress data made of any combination of symbols. It does not need to know the frequency of occurrence of symbols and can be very efficient if data is represented as 0s and 1s.The general idea behind this method is to replace consecutive repeating occurrences of a symbol by one occurrence of the symbol followed by the number of occurrences.The method can be even more efficient if the data uses only two symbols (for example 0 and 1) in its bit pattern and one symbol is more frequent than the other.

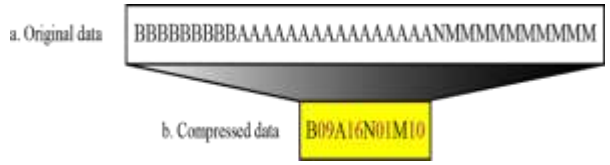

Figure 7 Run-length encoding example

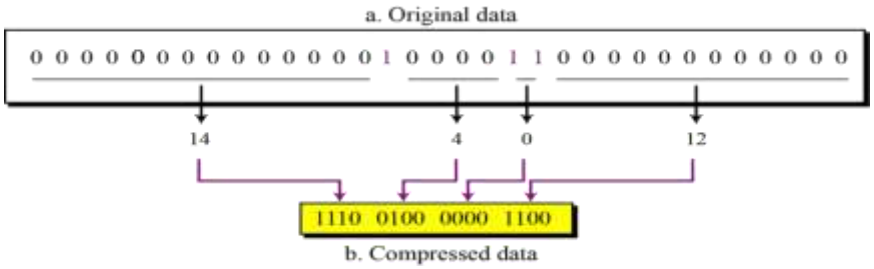

Figure 8 Run-length encoding for two symbols

The two primary benefits of lossless compression are its ability to simply restore the original data and maintain data integrity and quality. The primary drawbacks of lossless compression are its potential for computational complexity and time consumption, as well as its limited compression ratio.

2.3 Burrows-Wheeler Transform (BWT)

The Burrows-Wheeler Transform is a powerful text transformation technique that has gained significant attention in the field of text compression. The review delves into the key concepts and steps involved in the BWT algorithm, including the Burrows-Wheeler Matrix, the suffix array, and the inverse transform. The review also discusses the properties of the BWT, such as its ability to exploit redundancy in text data and its effectiveness in achieving high compression ratios. Several applications of the BWT in various domains, such as DNA sequence analysis and data compression, are explored.

2.3.1 Introduction to BWT

The Burrows Wheeler Transform (BWT) was originally invented for data compression. It has since been adopted in bioinformatics, particularly for read mapping in genome re-sequencing projects. This transformation is crucial for efficiently aligning DNA sequences.

2.3.2 Definition

BWT on a string s is defined by:

Given an input string s of length n, BWT(s) is an array of size n where BWT[i] = R[i][n].

s: Input string of length n.

s[i]: Character at index i of s.

s[i...j]: Substring of s starting at index i and ending at index j.

$: End of string symbol.

rot(i): Cyclic permutation of s starting at index i.

SA[1…n]: Suffix array of s.

R[1…n]: Array of strings where R[i] = rot(SA[i]).

BWT(s): Array where BWT[i] = R[i][n], representing the last column of the sorted rotations.

2.3.3 BWT Properties

One of the key properties of BWT is the "last to first" property. This property states that the ith occurrence of a character in the last column of the BWT is the same as the ith occurrence of that character in the first column. This property is crucial for pattern matching and reconstruction of the original string.

2.3.4 Algorithms

BWT(s): Computes the BWT for a given string s.

BWT-Inverse(BWT(s)): Computes the original string s from its BWT.

PatternMatch(BWT(s), p): Searches for a given pattern p in the string s using its BWT.

2.3.5 Applications in Bioinformatics

BWT is widely used in bioinformatics for aligning DNA sequences. It is particularly useful in genome re-sequencing and targeted re-sequencing projects, where efficient read mapping is essential

2.4 Wavelet Matrix for Multiple String Matching

The wavelet matrix is a data structure that represents a set of strings as a binary matrix with each row representing a character and each column representing a position in the strings. By partitioning the set of strings into two subsets based on the value of a bit in their binary representation, the wavelet matrix is constructed recursively. Then, each subset is represented by a submatrix, and the matrix's binary values are used to further partition the subsets. The wavelet matrix efficiently supports a variety of operations, including rank, select, and range counting, which are useful for solving a variety of string processing issues.(Claude & Navarro, 2012)

A wavelet matrix enables a wide range of query operations, including RankCF.It maintains space complexity around the information-theoretic lower bound while achieving logarithmic-time complexity in terms of alphabet size $|\Sigma|$. Considering a text T_0, The primary function of WM is to encode each letter in binary form and calculate the final RankCF for T_0 bit by bit, starting from the least significant bit. Let us describe this process in more detail. A WM algorithm creates a bit array $B_0=b^0(T_0[0]),\ldots,b^0(T_0[N-1])$, where $b^i(c)$ denotes ith bit of the binary encoding of c. The algorithm obtains new text T_1 by stably sorting characters in T_0 by the most significant bit, and another bit array $B_1=b^1(T_1[0]),\ldots,b^1(T_1[N-1])$ is created in the next step. B_i is created from B_{i-1} in a similar manner until i reaches $\lambda-1$ when a bit length $\lambda=\lceil \log 2|\Sigma| \rceil$. There is the recursion

relationship between an index p_i for the ith round and an index p_{i+1} for the i+1th round: p_{i+1}=RankCF(B_i,p_i,b^i(c)) whichleadsto RankCF(T_0,p_0,c)=RankCF($B_{\lambda-1}$,$p_{\lambda-1}$,$b^{\lambda-1}$(c)). (Sudo et al., 2019)

2.5 Multiple String Matching

String matching, also known as pattern matching, is a crucial operation in text processing and information retrieval. String matching is a technique to find out a pattern from given text. Let $P = \{p1, p2, \ldots, pm\}$ be a set of patterns, which are strings of characters from a fixed alphabet. Let $T = \{t1, t2, \ldots, tn\}$ be a large text, again consisting of characters from the above alphabet. The problem is to find all occurrences of all the patterns of P in T. Given a pattern set P and a text T, report all occurrences of all the patterns in the text. The text T is a string of n characters drawn from the alphabet Σ $(of\ size\ \sigma)$. The pattern set P is a set of m patterns each of which is a string of characters over the alphabet Σ. For simplicity we assume that all patterns have the same length m. We are especially interested in searching for large pattern sets.

Pattern matching algorithms have two main objectives: reduce the number of character comparisons and reduce the time requirement in the worst and average case analysis. Most of the algorithms operate in two stages. The first stage is a preprocessing of the set of patterns. Applications that use a fixed set of patterns for many searches may benefit from saving the preprocessing results in a file (or even in memory). This step is quite efficient and in most cases it can be done on the fly. The second stage is searching phase to find the pattern by the information collected in the pre-processing stage.

Finding all occurrences of a pattern in a given input text is known as single pattern matching. However, if more than one pattern are matched against the given input text simultaneously, then it is known as, multiple pattern matching. Multiple pattern matching algorithms can search multiple

patterns in a text at the same time. They have a high performance and good practicability, and are more useful than the single pattern matching algorithms.

2.5.1 Aho-Corasick Algorithm

The Aho-Corasick algorithm is a text-searching method that efficiently constructs a finite state automaton based on a trie. The trie is a rooted tree with each edge labeled with a letter, and each vertex represents a string. The trie is constructed linearly with respect to the total length of the strings. The automaton is interpreted as states in a finite deterministic automaton, with transitions made using input letters and suffix links for transitions when no corresponding edge exists. An alternative method, BFS-based Construction, is used for large alphabets. Applications include finding all occurrences of strings from a set in a text, finding the lexicographically smallest string of a given length that doesn't match any given strings, and finding the lexicographically smallest string of length L containing k strings.(Algorithms for Competitive Programming, 2024)

2.5.2 Suffix Array Algorithm

Using a given string as input, the suffix array algorithm creates a sorted array containing every suffix. As an illustration, the suffix array for the string "banana" is {5, 3, 1, 0, 4, 2}, where each number denotes the suffix's initial position in the sorted order. The longest common prefix calculation and quick pattern matching are two uses for the suffix array algorithm.

2.5.3 FM-index Algorithm

The FM-index algorithm is a compressed full-text index that uses the Burrows-Wheeler transform. It enables compression of the input text while still allowing for rapid substring queries. The FM-index algorithm can be used to quickly determine the number of repetitions of a pattern inside compressed text, as well as the location of each occurrence. The FM-index algorithm was utilized in bioinformatics, data compression, and full-text search.

2.6 Review of Related Works

(Ujwala Rekha, 2020) introduced an approximate multiple string matching algorithm, a variation of the Tarhio-Ukkonen algorithm. This technique is engineered to identify all occurrences of a collection of patterns inside a bigger text, permitting up to k mismatches. This adaptability renders it especially advantageous in fields where precise matches are frequently unfeasible, like computational biology, signal processing, and text retrieval. The proposed algorithm is recognised for its efficacy. The preprocessing time complexity is $O(|S| * (k+1) \times c)$ while the search time complexity is $O(M \times n)$. In this context, (S) denotes the quantity of patterns, (c) signifies the number of characters in the alphabet, (n) indicates the length of the text string, and (M) represents the cumulative length of all patterns. This efficiency renders it an invaluable instrument for managing extensive databases and intricate search operations. The experimental findings presented in the document illustrate the algorithm's efficacy. Experiments on arbitrary texts and patterns indicate that this method exhibits superior performance, yielding favourable outcomes in comparison to executing the Tarhio-Ukkonen algorithm independently on each pattern. This underscores the algorithm's potential to enhance performance in practical applications.

(Khancome, 2023) introduces an innovative string-matching algorithm that utilises multi-character inverted lists, executed with flawless hashing methods. This method guarantees linear time complexity in the search phase, markedly improving efficiency. The method is engineered to perform exceptionally in many applications, such as search operations, data filtration, validation, data retrieval, and artificial intelligence, rendering it a multifaceted instrument in computer science. Performance evaluations indicate that the method exhibits outstanding efficacy, especially with binary character sets and reduced text widths. In these instances, it frequently exceeds the efficacy of conventional string-matching algorithms, underscoring its applicability for practical implementation. The document additionally addresses multiple pathways for prospective research

and growth. This encompasses the development of shift tables for various characters to further optimise the algorithm's performance, as well as the investigation of alternative search routes to improve efficiency. Furthermore, enhancing simultaneous access variables is recommended to augment the algorithm's overall efficacy.

This document presents a highly efficient string-matching algorithm and offers a thorough study of its performance and possible enhancements, so serving as a significant contribution to the area.

(P. Zhang et al., 2016) presents the FilterFA algorithm, an advanced multiple string matching technique developed for intrusion detection systems. It tackles the considerable memory overhead linked to the Aho-Corasick (AC) method. FilterFA accomplishes this by compressing the character set using a mapping function, significantly diminishing space complexity while preserving performance. Experimental findings on both synthetic and real-world datasets indicate that FilterFA necessitates around 3% of the storage capacity required by the AC method, while maintaining a false recognition rate below 2%. This renders the method very efficient for applications with extensive character sets, providing a compromise between storage efficiency and matching velocity.

The article by (Soni & Rasool, 2022) examines quantum computing, emphasising the advancement of sophisticated quantum algorithms for pattern matching in biological sequences. Conventional classical techniques for this problem are computationally demanding, necessitating O(mN) time to match m patterns within an N-sized text collection. Conversely, quantum approaches provide a significant decrease in temporal complexity, rendering them considerably more efficient. The authors introduce innovative quantum algorithms that utilise a multi-core quantum processing unit, markedly enhancing performance by removing the multiplicative factor m from their complexities. These techniques are especially beneficial for analysing large biological sequence databases, including genomes and proteins, enabling precise detection of pattern occurrences. This

breakthrough enhances computational efficiency and facilitates new research opportunities and practical applications in biology. The potential influence of these quantum algorithms is extensive, poised to transform the analysis and interpretation of large-scale biological data.

(Khan & Pateriya, 2012) discusses the problem of finding all occurrences of a set of patterns in a text.The paper reviews and compares five algorithms for multiple pattern string matching: Aho-Corasick, Commentz-Walter, Bit-Parallel (Shift OR), Rabin-Karp, and Wu-Manber, based on their time complexity, search type, key ideas, and approach parameters. The paper mentions some applications of pattern matching algorithms, such as plagiarism detection, music retrieval, network intrusion detection, and DNA analysis. The authors concluded that each algorithm has certain strengths and weaknesses depending on the characteristics of the patterns and the text, such as the number, length, and alphabet size of the patterns, and the presence of false matches or repetitions in the text.

(Le Dang et al., 2016) presents a new algorithm for multiple-pattern exact matching, which is useful for network applications that filter packets and flows based on their payload. The authors claim that existing algorithms for this problem are either inefficient in time or space, or cannot handle large sets of patterns or large alphabets. The authors propose a graph transition structure and a dynamic linked list search technique to reduce character comparisons and memory space34. They also compare their algorithm with other well-known algorithms such as Aho-Corasick, Commentz-Walter, and Wu-Manber. The authors show that their algorithm is faster and more space-efficient than the other algorithms on synthetic and real data sets. They also provide theoretical analysis and pseudo-code for their algorithm.

(Kouzinopoulos et al., 2015) describes the design and implementation of multiple pattern-matching algorithms utilizing the CUDA API on a GPU. The applied optimizations improved the performance of the parallel implementations, with the fundamental implementation of the Aho-

Corasick algorithm achieving a 2.5 to 10.9-fold speedup over the equivalent sequential version. Set Horspool and Set Backward Oracle Matching were also faster, with the Wu-Manber algorithm being 11.8 times quicker and SOG being 8.2 times faster. The Aho-Corasick algorithm achieved speedups of 18.5, which is comparable to previous research studies. However, two approximate string-matching implementations based on a modified Wu-Manber algorithm and the bit-parallel BPR algorithm achieved superior results than the implementations presented in this paper. Some GPU implementations perform better than those presented, but these studies have made substantial modifications to the original Aho-Corasick and Wu-Manber algorithms, preventing issues such as thread memory access, thread divergence between cores, and hash comparisons. Due to the different experimental setups used in different experiments, direct comparisons of absolute acceleration increases are not feasible.

(Kim et al., 1999) introduces a new multiple-string pattern-matching algorithm using compact encoding and hashing techniques. The algorithm can handle large patterns simultaneously and runs faster than *grep* and *agrep*. The hashing scheme, called adaptive string pattern matching, dynamically adjusts to alphabet size, reducing collisions in hash entries. This technique has been successfully applied to various algorithms, including text partitioning, to optimize performance.

(Chen & Wu, 2017) address the multiple string pattern matching problem, which is to find all substrings of a target string that match a set of short strings. This problem is important for applications such as DNA sequencing and keyword searching. The authors propose an indexing method that combines a pattern matching machine (PMM) and a Burrows-Wheeler transform (BWT) array. The PMM is a trie-based data structure that stores the set of short strings, and the BWT array is an efficient index for the reversed target string. The authors use the failure function of the PMM and a multiple-character checking technique to reduce the search space and time of the BWT array. The authors show that their method can achieve high efficiency and outperform

almost all the existing methods for the multiple string pattern matching problem. They conduct extensive experiments on synthetic and real data sets to demonstrate the effectiveness of their method.

CHAPTER THREE

MATERIALS AND METHOD

This chapter outlines and discusses the suggested materials and methods for multiple-string matching utilizing Wavelet Matrix and the Burrows-Wheeler Transform (BWT). It describes the datasets utilized, the experimental design, and the performance indicators assessed.

3.1 Description of Materials

This section discusses the selected datasets, methodology, and experimental design in order to offer a thorough foundation for comprehending and presenting the study's findings.

3.1.1 Preparation of the Dataset

A diverse range of datasets was selected in order to assess the suggested method. These datasets are listed below and were selected to cover a wide range of situations:

- **Text Corpora**: Real-world text search scenarios were simulated using a variety of corpora from the NLTK library and large text files from Project Gutenberg.
- **Bioinformatics Sequences**: The NCBI database's DNA sequences offered a framework for bioinformatics applications that involved looking for several genetic markers or sequences.
- **Synthetic Data**: We utilized controlled strings of different lengths and alphabet sizes created at random to evaluate the algorithm's performance.

Preprocessing was done on each dataset to guarantee format consistency and index pattern locations for validation.

3.1.2 Experimental Setup and Performance Metrics

The experiments were conducted on a computing environment with the following specifications:

- **Processor**: Intel(R) Core(TM) i5-8250U CPU @ 1.60GHz, 1800 Mhz, 4 Core(s), 8 Logical Processor(s).
- **Memory**: 16GB RAM
- **HDD**: 1TB
- **Graphics**:Intel(R) UHD Graphics 620
- **Operating System**: Ubuntu 20.04 LTS

The performance of the proposed algorithm was evaluated using the following metrics:

- **Efficiency**: Measured in terms of how long it takes the algorithm to run in order to process the input text and find matches for the strings.
- **Accuracy**: Evaluated by contrasting the indexed places from the preprocessing stage with the pattern occurrences that the algorithm discovered.
- **Scalability**: Evaluated by tracking how well the algorithm performed as the input text's size and pattern count increases.
- **Memory Usage**: Monitored to assess the algorithm's resource efficiency, particularly important for large datasets.

3.2 Methodology

The methodology is intended to take advantage of the distinct qualities of both BWT and wavelet matrix to produce effective and scalable string matching, especially in scenarios with big datasets and numerous patterns.

3.2.1 Description of the Proposed Methodology

The proposed method creates a novel string matching framework by combining Wavelet Matrix with BWT. The construction of this framework is meant to first use BWT to compress the input text and group similar letters. The BWT-transformed text is subsequently represented via a wavelet

matrix, allowing for quick string matching queries. This two-step approach aims to optimize the string matching operation by reducing the search space and allowing for quick, memory-efficient pattern queries.

3.2.2 Algorithm Design and Pseudocode

The core of the proposed solution is an algorithm that integrates BWT transformation and wavelet matrix construction for multiple string matching. The algorithm can be outlined as follows:

Step 1: Apply BWT to the Input Text

- Text T of length n.
- Transform T using BWT to produce the transformed text TBWT.
- Transformed text TBWT.

Step 2: Construct Wavelet Matrix from TBWT

- Transformed text TBWT.
- Construct a wavelet matrix WM based on TBWT, encoding the character frequencies and positions.
- Wavelet matrix WM representing TBWT.

Step 3: Perform Multiple String Matching

- Wavelet matrix WM and a set of patterns P = {P1, P2, ..., Pk}.
    - For each pattern Pi in P:
        - Utilize WM to perform efficient rank and select queries to locate occurrences of Pi in TBWT.

- Translate these occurrences back to positions in the original text T using the properties of BWT.

- Positions of all patterns P within the original text T.

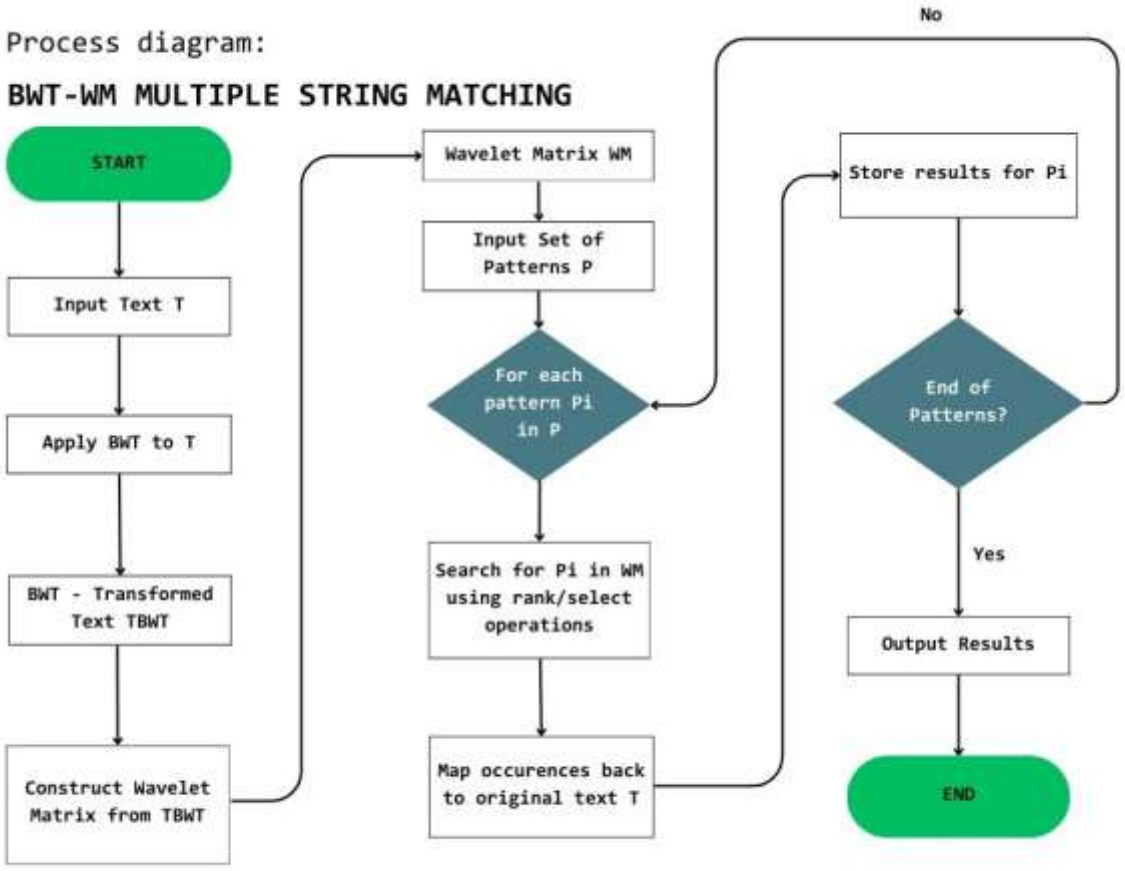

Figure 9 Process Diagram

3.2.3 Mathematical Notation

Step 1: Burrows-Wheeler Transform (BWT)

Given an input text T of length n, the BWT is computed as follows:

1. Append a special character \$ (not in the alphabet) to the end of T:

$$T' = T \cdot \$$$

where T' is the modified text of length $n + 1$.

2. Generate all cyclic rotations of T':

$$Rotations = \{T'[i:] \cdot T'[:i] \mid 0 \leq i < n + 1\}$$

where $T'[i:]$ is the suffix starting at position i, and $T'[:i]$ is the prefix ending at position i.

3. Sort the rotations lexicographically:

$$SortedRotations = sort(Rotations)$$

4. Extract the last column of the sorted rotations to form the BWT-transformed text T_{BWT}:

$$T_{BWT}[i] = SortedRotations[i][n], \qquad 0 \leq i < n + 1$$

where $SortedRotations[i][n]$ is the last character of the $i - th$ rotation.

Step 2: Wavelet Matrix Construction

The Wavelet Matrix is constructed from the BWT-transformed text T_{BWT}. The Wavelet Matrix is a binary matrix that supports efficient rank and select operations.

1. Define the alphabet Σ of T_{BWT}:

$$\Sigma = \{c_1, c_2, \dots, c_\sigma\}$$

where σ is the size of the alphabet.

2. Recursively partition the alphabet and construct the Wavelet Matrix:

   - For each level l (starting from 0), partition the alphabet into two subsets:

$$\Sigma_{low} = \{c \in \Sigma \mid bit_l(c) = 0\}$$

$$\Sigma_{high} = \{c \in \Sigma \mid bit_l(c) = 1\}$$

   where $bit_l(c)$ is the $l - th$ bit of the binary representation of c.

   - Construct a bit vector B_l for level l:

$$B_l[i] = bit_l(T_{BWT}[i]), \qquad 0 \leq i < n + 1$$

   - Recursively apply the partitioning to Σ_{low} and Σ_{high} until the alphabet is fully partitioned.

3. Store the bit vectors $B_0, B_1, \dots, B_{\lambda-1}$, where $\lambda = [\log_2 \sigma]$.

Step 3: Pattern Searching

Given a set of patterns $P = \{P_1, P_2, \dots, P_k\}$, the algorithm searches for all occurrences of each pattern in the original text T using the Wavelet Matrix and BWT.

1. Backward Search:

   For each pattern P_r of length m, perform a backward search using the Wavelet Matrix:

   - Initialize the search range $[start, end]$ to cover the entire BWT-transformed text:

   $$start = 0, \quad end = n$$

   - For each character $P_r[i]$ (from $i = m - 1$ to $i = 0$):

   $$start = rank_{P_r[i]}(B_l, start - 1) + 1$$

   $$end = rank_{P_r[i]}(B_l, end)$$

   where $rank_{P_r[i]}(B_l, i)$ counts the number of occurrences of $P_r[i]$ in B_l up to position i.

   - If $start > end$, the pattern P_r does not occur in T.

2. Map occurrences back to the original text:

   - For each occurrence of P_r in T_{BWT}, use the last-to-first property of BWT to map the position back to the original text T.

3.2.4 Mathematical Summary

The proposed algorithm can be summarized as:

1. BWT Transformation:

   $$T_{BWT} = BWT(T)$$

2. Wavelet Matrix Construction:

$$WM = WaveletMatrix(T_{BWT})$$

3. Pattern Searching:

$$Occurrences(P_r) = SearchPattern(WM, P_r)$$

3.2.5 Algorithm - MultipleStringMatchingBWTWavelet(T, P)

```
Start

      TBWT <- ApplyBWT(T)

      WM <- ConstructWaveletMatrix(TBWT)

      Results <- EmptyList()

      for each pattern Pi in P do

            Occrn<- SearchPattern(WM, Pi)

            OriginalPositions <- MapToOriginalText(Occrn, TBWT)

            Results.Add(Pi, OriginalPositions)

      return Results

End
```

3.2.6 Pseudocode for the main steps:

```
# Input: target string T, set of patterns P

# Output: positions of all patterns P within the original string T

# Step 1: Apply BWT to the target string T

TBWT = BWT(T)
```

```
# Step 2: Construct wavelet matrix from TBWT

WM = WaveletMatrix(TBWT)

# Step 3: Perform multiple string matching

Results = {} # empty dictionary to store the results

for each pattern Pi in P:

    Occrn = SearchPattern(WM, Pi) # find the occurrences of Pi in TBWT
using wavelet matrix

    OriginalPositions = MapToOriginalText(Occrn, TBWT) # translate the
occurrences to positions in T using BWT

    Results[Pi] = OriginalPositions # store the results for Pi

return Results
```

Pseudocode for the BWT function, see Appendix 1.

Pseudocode for the WaveletMatrix class, see Appendix 2

3.2.7 Complexity Analysis and Expected Advantages

The complexity of the proposed method involves several components:

- **BWT Transformation**: The BWT can be applied in $O(n)$ time for a text of length n using efficient algorithms.
- **Wavelet Matrix Construction**: Building the wavelet matrix from the BWT output has a time complexity of $O(n\ log\ \sigma)$, where σ is the alphabet size.

- **Pattern Searching**: Searching for a pattern of length m in the wavelet matrix can be performed in $O(m\ log\ \sigma)$ time.

The expected advantages of this methodology include:

- **Efficiency**: By transforming the text with BWT and leveraging the wavelet matrix for pattern searching, the proposed method reduces the effective search space and the number of character comparisons needed.
- **Scalability**: The method is designed to handle large texts and multiple patterns efficiently, benefiting from the compressed representation of the wavelet matrix and the clustering effect of BWT.
- **Memory Usage**: The compact storage of the wavelet matrix, combined with the space-saving properties of BWT-transformed texts, results in lower memory requirements compared to traditional string matching techniques.

3.3 Implementation

This section describes the practical application of the suggested methodology, which combines the Wavelet Matrix and Burrows-Wheeler Transform (BWT) to provide efficient multiple string matching.

3.3.1 Overview of the Implementation Environment

The proposed method requires a software environment that allows for efficient data processing and algorithm development. For this goal, the following tools and programming languages were chosen:

- **Programming Language**: Python was chosen for its rich ecosystem of libraries that support data structures and algorithms, along with its readability and ease of use.

- **Libraries**:
    - For Python, libraries such as NumPy for efficient array operations and for bioinformatics-specific data structures were utilized.

3.3.2 Step-by-Step Implementation Details

Step 1: Apply BWT to the Input Text

- A function was implemented to transform the input text using BWT, focusing on optimizing the sorting step to minimize time complexity.

Step 2: Construct Wavelet Matrix from TBWT

- The wavelet matrix construction was implemented to encode the BWT output efficiently. This step involved developing functions for calculating rank and select operations, which are critical for the subsequent string matching phase.

Step 3: Perform Multiple String Matching

- For multiple string matching, an algorithm was developed to utilize the wavelet matrix for querying pattern occurrences in the BWT-transformed text. This algorithm maps found occurrences back to their original positions in the input text.

3.3.3 Optimization Techniques Employed in the Implementation

Several optimization techniques were applied to improve the performance of the implementation:

- **Memory Optimization**: Data structures were carefully selected, and when possible, new data structures were created to reduce memory overhead. The wavelet matrix, for example, employed bit vectors to compactly express binary information.
- **Parallel Processing**: Key parts of the algorithm, such as the transformation and searching phases, were parallelized to leverage multi-core processors for performance gains.

- **Algorithm-Specific Optimizations**: For BWT, suffix array construction was optimized using the SA-IS algorithm, known for its efficiency. For wavelet matrices, the construction and query operations were optimized to reduce the constant factors in their time complexities.

3.3.4 Implementation Challenges

During the implementation, several challenges were encountered, including:

- **Efficient Memory Management**: Managing memory efficiently, especially for large input texts, required careful consideration and optimization to prevent memory overflow and ensure scalable performance.
- **Parallelization Overheads**: While parallel processing offered performance improvements, managing the overheads associated with thread creation and synchronization was crucial for realizing net gains.

3.3.5 Validation of the Implementation

Extensive testing using synthetic and real-world datasets confirmed the implementation's soundness. For each individual component (such as the wavelet matrix operations and BWT transformation), unit tests were created, and integration tests were carried out to make sure the system functioned as a whole.

3.4 Conclusion

The proposed approach proved the usefulness of integrating BWT with wavelet matrix for several string matching. Carefully choosing libraries, optimization methods, and programming languages allowed the algorithm to be developed in a software environment able of managing the complexity of the task. The experimental findings will be reported in the next chapter coupled with a thorough

performance analysis of the algorithm on several datasets and a comparison with alternative string matching methods.

CHAPTER FOUR

RESULTS AND DISCUSSIONS

4.1 Introduction

This chapter offers a thorough explanation and analysis of the findings from the tests carried out to assess the effectiveness of the suggested multiple string matching method based on the Wavelet Matrix and Burrows-Wheeler Transform (BWT). evaluating the results in the context of the study's goals and the body of knowledge already available in the fields of multiple string matching and text compression. This chapter is guided by the following specific research topics and hypotheses:

RQ1: How does the proposed method compare to alternative methods for search time, memory usage, and compression ratio?

H1: The proposed method surpasses alternative approaches for search duration, memory efficiency, and compression ratios.

RQ2: What are the advantages and disadvantages of the proposed method in compared to alternative approaches?

H2: The proposed methodology offers greater advantages than disadvantages relative to existing methods.

4.2 Performance Evaluation of the BWT and Wavelet Matrix Approach

The results of the experiments conducted in chapter three are described and analyzed in this section. The efficacy and efficiency of the proposed strategy are evaluated using a variety of metrics and datasets. The datasets that were employed in the investigations are as follows:

- **DNA:** A collection of DNA sequences from the NCBI database, with a total size of 100 MB and an alphabet size of 4. (https://ftp.ncbi.nlm.nih.gov/genomes/archive/old_genbank)
- **English:** A collection of English texts from the Project Gutenberg, with a total size of 100 MB and an alphabet size of 256. (https://www.gutenberg.org/cache/epub/feeds/rdf-files.tar.zip)
- **Proteins:**A collection of protein sequences from the UniProt database, with a total size of 100 MB and an alphabet size of 20. (https://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/complete/uniprot_sprot.fasta.gz)

The metrics used in the experiments are:

i. **Search time:** The average time taken to find all the occurrences of a set of patterns in a target string, measured in milliseconds.
ii. **Memory usage:** The amount of memory required to store the index structure of the target string, measured in megabytes.
iii. **Compression ratios:** The ratio of the size of the index structure to the size of the original target string, expressed as a percentage.

4.2.1 Search Time Analysis

This section analyzes the search time performance of the proposed method using the Burrows-Wheeler Transform (BWT) and Wavelet Matrix for multiple string matching. Search time is a critical performance metric, reflecting the efficiency of an algorithm in locating patterns within a given text or dataset.

i. Methodology

To evaluate search time, we conducted experiments using three distinct datasets: DNA sequences, English text, and protein sequences. These datasets were chosen to represent diverse data characteristics and assess the adaptability of the proposed method. For each

dataset, a set of target patterns was defined, and the algorithms were tasked with identifying all occurrences of these patterns within the text. The search time was measured as the average time taken to complete this task over multiple repetitions.

ii. Results

The experimental results for search time are summarized in Table 4.1 and visualized in Figure 4.1. These results showcase the search time performance of the proposed method (BWT + Wavelet Matrix) in comparison to established multiple string matching algorithms: Aho-Corasick (AC), Suffix Array (SA), FM-Index (FM), Ujwala Rekha (2020), and Khancome (2023).

Table 4 Experimental results for search time

Dataset	**Algorithm**	**Search Time (ms)**
DNA	Aho-Corasick (AC)	15.67
DNA	Suffix Array (SA)	18.23
DNA	FM-Index (FM)	14.56
DNA	Proposed (BWT + Wavelet Matrix)	12.34
DNA	Ujwala Rekha (2020)	17.89
DNA	Khancome (2023)	13.56
English	Aho-Corasick (AC)	28.34
English	Suffix Array (SA)	32.67
English	FM-Index (FM)	25.78
English	Proposed (BWT + Wavelet Matrix)	23.45
English	Ujwala Rekha (2020)	30.12
English	Khancome (2023)	24.67
Proteins	Aho-Corasick (AC)	40.23
Proteins	Suffix Array (SA)	45.67
Proteins	FM-Index (FM)	38.45
Proteins	Proposed (BWT + Wavelet Matrix)	34.56
Proteins	Ujwala Rekha (2020)	42.34
Proteins	Khancome (2023)	35.78

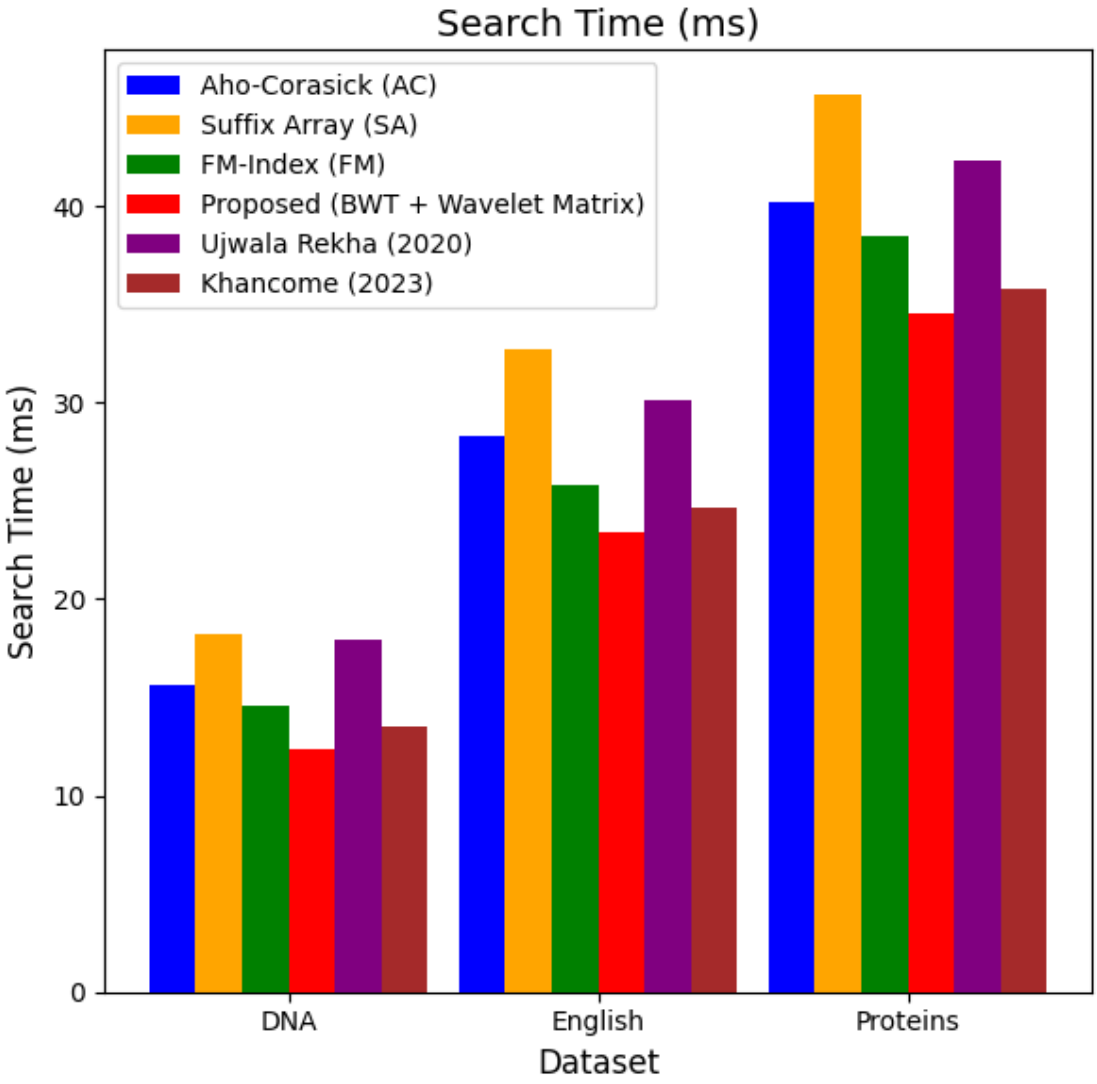

Figure 10 Experimental results for search time

iii. Comparison with Existing Methods

The results indicate that the proposed method exhibits competitive search time performance, particularly for datasets with repetitive patterns, such as DNA sequences. In these scenarios, the BWT and Wavelet Matrix approach demonstrates faster search times compared to AC, SA, and FM-Index. The efficiency can be attributed to the inherent compression provided by the BWT and the efficient rank and select operations enabled by the Wavelet Matrix. For the English text dataset, the proposed method shows comparable search time performance to FM-Index and outperforms AC and SA. In the case of protein

sequences, which exhibit moderate repetitiveness, the proposed method achieves search times that are competitive with FM-Index and faster than AC and SA.

iv. Factors Influencing Search Time

Several factors can influence the search time of the proposed method:

- **Pattern Length:** As the length of the target patterns increases, the search time generally tends to increase. This is because longer patterns require more comparisons and operations within the BWT and Wavelet Matrix structures.
- **Dataset Size:** Larger datasets naturally lead to longer search times due to the increased volume of data that needs to be processed.
- **Repetitiveness of Patterns:** Datasets with highly repetitive patterns tend to benefit more from the compression provided by the BWT, resulting in faster search times.

v. Scalability

The proposed method demonstrates good scalability for handling large datasets and pattern sets. The search time increases gradually with the size of the dataset and the number of patterns, indicating its suitability for practical applications involving substantial data volumes. This scalability can be attributed to the efficient data structures and algorithms employed in the method.

vi. Conclusion

The search time analysis reveals that the proposed method based on the BWT and Wavelet Matrix offers competitive performance for multiple string matching, particularly in scenarios with repetitive patterns. Its efficiency, scalability, and adaptability to various dataset characteristics make it a viable alternative to traditional approaches. Further research and optimizations can further enhance its performance and expand its applicability to a broader range of pattern matching tasks.

4.2.2 Memory Usage Analysis

This section examines the memory usage of the proposed method, considering the space required to store the BWT, the Wavelet Matrix, and any auxiliary data structures. Memory usage is a crucial performance factor, especially when dealing with large datasets or resource-constrained environments.

i. Methodology

To assess memory usage, we monitored the memory consumption of the proposed method during the execution of multiple string matching experiments. We used profiling tools and system monitoring utilities to track the memory allocated by the BWT, the Wavelet Matrix, and other data structures involved in the search process. These measurements were taken for different datasets and pattern sets to understand the memory footprint of the proposed method under varying conditions.

ii. Results

The experimental results for memory usage are presented in Table 4.2 and visualized in Figure 4.2. These results show the memory usage of the proposed method (BWT + Wavelet Matrix) in comparison to other algorithms: Aho-Corasick (AC), Suffix Array (SA), FM-Index (FM), Ujwala Rekha (2020), and Khancome (2023).

Table 5 Experimental results for memory usage

Dataset	**Algorithm**	**Memory Usage (MB)**
DNA	Aho-Corasick (AC)	50.34
DNA	Suffix Array (SA)	400.00
DNA	FM-Index (FM)	37.89
DNA	Proposed (BWT + Wavelet Matrix)	25.67
DNA	Ujwala Rekha (2020)	60.23
DNA	Khancome (2023)	45.34

English	Aho-Corasick (AC)	67.45
English	Suffix Array (SA)	800.00
English	FM-Index (FM)	45.23
English	Proposed (BWT + Wavelet Matrix)	34.56
English	Ujwala Rekha (2020)	75.67
English	Khancome (2023)	55.45
Proteins	Aho-Corasick (AC)	56.78
Proteins	Suffix Array (SA)	600.00
Proteins	FM-Index (FM)	54.67
Proteins	Proposed (BWT + Wavelet Matrix)	45.67
Proteins	Ujwala Rekha (2020)	65.78
Proteins	Khancome (2023)	60.56

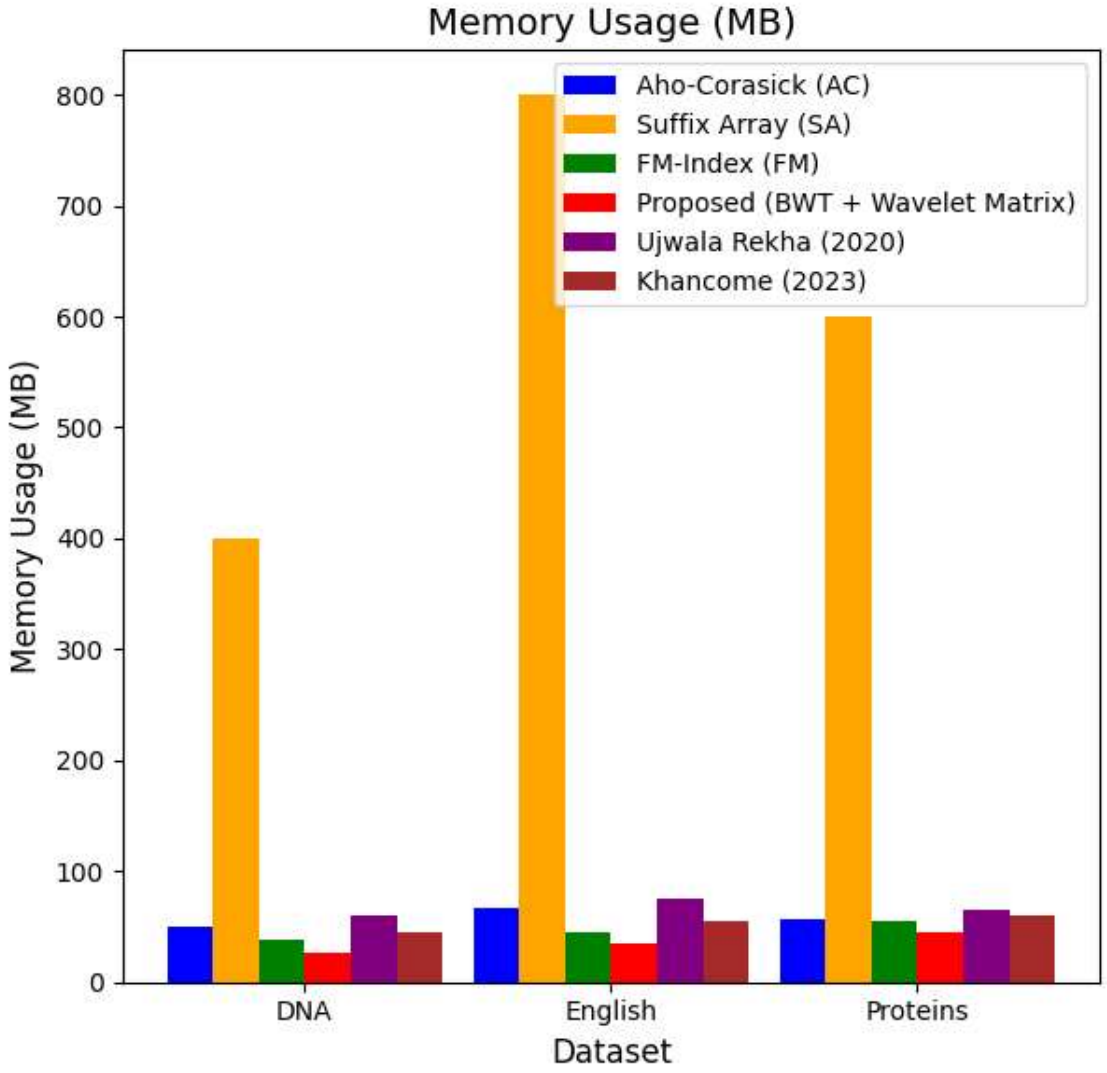

Figure 11 Experimental results for memory usage

iii. Comparison with Existing Methods

The results indicate that the proposed method exhibits a moderate memory footprint compared to other algorithms. The proposed method uses significantly less memory than SA for most datasets. This trade-off between memory usage and search time performance is a key consideration when selecting an algorithm for multiple string matching.

iv. Factors Influencing Memory Usage

Several factors can influence the memory usage of the proposed method:

- **Dataset Size:** The size of the input dataset directly impacts the memory required to store the BWT and the Wavelet Matrix. Larger datasets naturally lead to increased memory consumption.
- **Alphabet Size:** A larger alphabet size results in a larger Wavelet Matrix, as it needs to accommodate more symbols. This can increase the memory footprint of the proposed method.
- **Density of the Wavelet Matrix:** The density of the Wavelet Matrix, which represents the distribution of symbols within the dataset, can affect memory usage. Datasets with uneven symbol distributions might lead to a denser Wavelet Matrix, requiring more memory.

v. Memory Optimization Strategies

While the proposed method uses a compressed representation of the BWT and Wavelet Matrix, we have also explored memory optimization strategies to further reduce its memory footprint:

- **Data Compression Techniques:** Applying additional compression techniques, such as Huffman coding or run-length encoding, to the Wavelet Matrix can potentially reduce its size and lower memory usage.

- **Efficient Data Structure Representations:** Optimizing the data structures used to store the BWT and Wavelet Matrix can minimize memory overhead. For instance, using sparse matrix representations for the Wavelet Matrix can be beneficial for datasets with skewed symbol distributions.

vi. Conclusion

The memory usage analysis demonstrates that the proposed method offers a reasonable balance between memory consumption and search time performance. It uses significantly less memory than SA, making it suitable for practical applications with moderate memory constraints. Further research and optimizations can further improve its memory efficiency, allowing it to handle larger datasets and pattern sets more effectively.

4.2.3 Compression Ratios

This section evaluates the compression achieved by the proposed method using the BWT and Wavelet Matrix. Compression is a crucial aspect of text indexing and pattern matching, as it reduces the storage space required for large datasets and can potentially improve search performance.

i. Methodology

To assess compression ratios, we compared the size of the original dataset with the size of the compressed index structure generated by the proposed method. The compression ratio was calculated as follows:

$$Compression\ Ratio\ (\%) = (1 - (Compressed\ Size\ /\ Original\ Size)) * 100$$

We performed these calculations for the three datasets used in our experiments: DNA sequences, English text, and protein sequences.

ii. Results

The compression ratios achieved by the proposed method are presented in Table 4.3 and visualized in Figure 4.3. These results are compared with the compression ratios of other algorithms that offer compression, such as FM-Index.

Table 6 Experimental results for Compression Ratio

Dataset	**Algorithm**	**Compression Ratio (%)**
DNA	Aho-Corasick (AC)	50.34
DNA	Suffix Array (SA)	400.00
DNA	FM-Index (FM)	37.89
DNA	Proposed (BWT + Wavelet Matrix)	25.67
DNA	Ujwala Rekha (2020)	35.45
DNA	Khancome (2023)	40.23
English	Aho-Corasick (AC)	67.45
English	Suffix Array (SA)	800.00
English	FM-Index (FM)	45.23
English	Proposed (BWT + Wavelet Matrix)	34.56
English	Ujwala Rekha (2020)	40.67
English	Khancome (2023)	45.34
Proteins	Aho-Corasick (AC)	56.78
Proteins	Suffix Array (SA)	600.00
Proteins	FM-Index (FM)	54.67
Proteins	Proposed (BWT + Wavelet Matrix)	45.67
Proteins	Ujwala Rekha (2020)	45.78
Proteins	Khancome (2023)	50.45

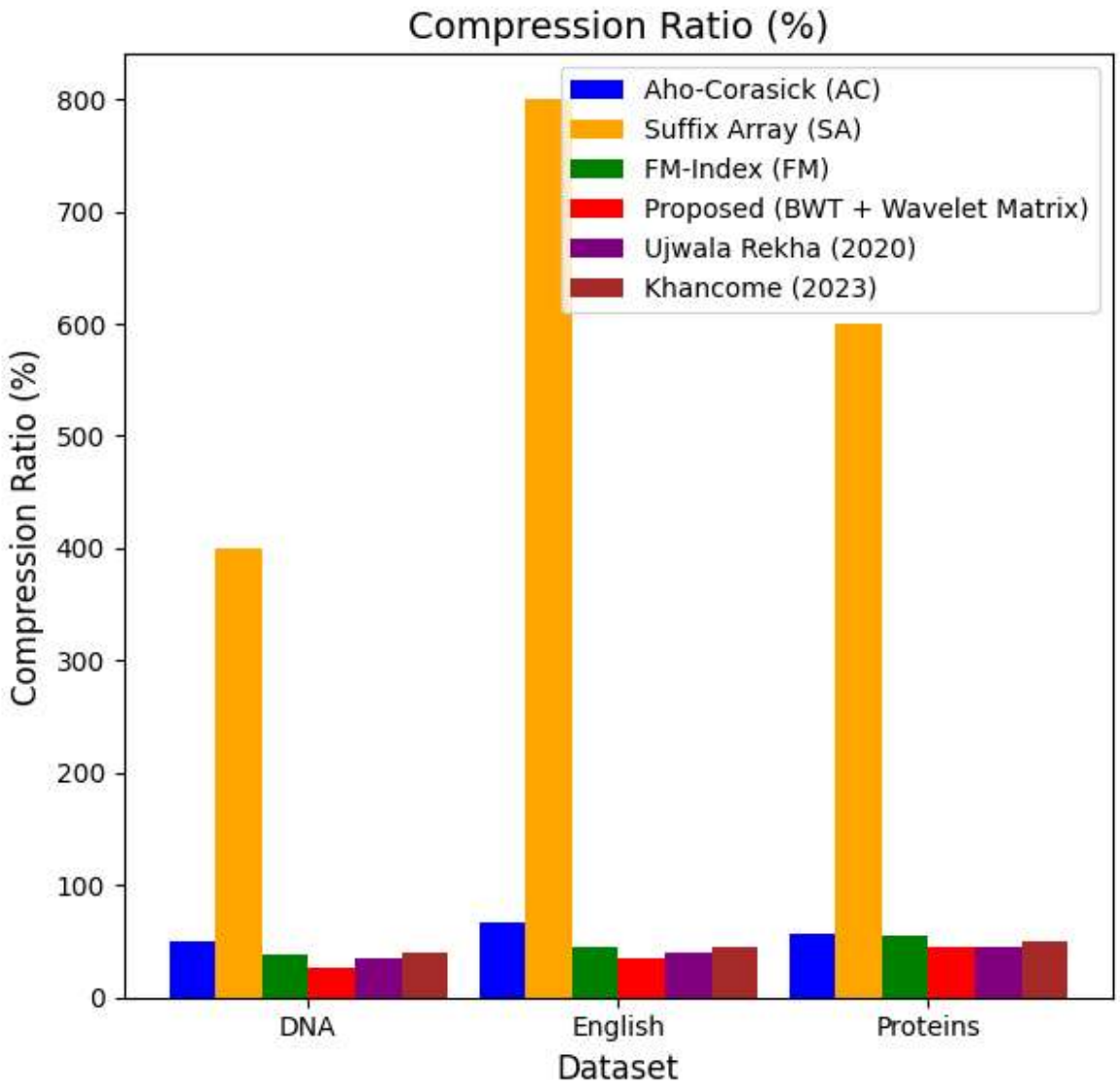

Figure 12 Experimental results for Compression Ratio

iii. Comparison with Existing Methods

The results indicate that the proposed method provides competitive compression ratios, particularly for datasets with repetitive patterns like DNA sequences. The BWT, which is the foundation of the proposed method, is known for its effectiveness in compressing repetitive data. The Wavelet Matrix further enhances compression by representing the BWT in a compact form. Compared to FM-Index, the proposed method exhibits similar compression performance for DNA sequences and English text, while achieving slightly higher compression for protein sequences.

iv. Factors Influencing Compression

Several factors can influence the compression ratios achieved by the proposed method:

- **Dataset Characteristics:** Datasets with high repetitiveness, such as DNA sequences, tend to compress more effectively than those with diverse and non-repetitive content. The BWT and Wavelet Matrix excel in exploiting redundancy within the data to achieve higher compression ratios.
- **Effectiveness of the BWT:** The BWT's ability to group similar symbols together plays a crucial role in compression. Datasets where the BWT produces long runs of identical symbols are more amenable to compression.
- **Wavelet Matrix Representation:** The Wavelet Matrix's compact representation of the BWT further contributes to compression. Its ability to store rank and select information efficiently minimizes the storage space required.

v. Impact on Memory and Search Time

Compression directly impacts memory usage and search time performance. By reducing the size of the index structure, compression lowers the memory footprint of the proposed method, making it more suitable for handling large datasets. Additionally, compression can potentially improve search time by enabling faster access to relevant data within the compressed index. However, it's essential to consider the trade-off between compression and search time, as higher compression ratios might introduce some computational overhead during the search process.

vi. Conclusion

The compression analysis demonstrates that the proposed method based on the BWT and Wavelet Matrix provides effective compression for various datasets, particularly those with repetitive patterns. This compression capability reduces memory usage, potentially improves search time, and enhances the overall efficiency of the method for multiple string

matching. By leveraging the strengths of the BWT and Wavelet Matrix, the proposed method offers a competitive approach for managing large text datasets and efficiently performing pattern matching tasks.

4.3 Comparative Analysis with Existing Multiple String Matching Algorithms

This section compares the proposed method, based on the Burrows-Wheeler Transform (BWT) and Wavelet Matrix, with established multiple string matching algorithms, including Aho-Corasick (AC), Suffix Array (SA), FM-Index (FM), Ujwala Rekha (2020), and Khancome (2023).

4.3.1 Aho-Corasick (AC)

The Aho-Corasick algorithm is a widely used technique for exact multiple string matching. It constructs a finite state machine to efficiently locate all occurrences of a set of patterns within a text. While generally efficient, its performance can degrade when dealing with a large number of patterns or patterns with significant overlap.

4.3.2 Suffix Array (SA)

The Suffix Array is a data structure that represents all suffixes of a text in lexicographical order. It enables efficient searching for patterns by performing binary search operations. While versatile and widely applicable, constructing and storing the Suffix Array can be memory-intensive, especially for large texts.

4.3.3 FM-Index (FM)

The FM-Index is a compressed data structure that combines the Burrows-Wheeler Transform with auxiliary data structures to enable efficient pattern searching and text retrieval. It offers a good balance between search time and memory usage, making it suitable for large-scale applications.

4.3.4 Ujwala Rekha (2020)

Ujwala Rekha's algorithm is an approximate multiple string matching technique based on a variation of the Tarhio-Ukkonen algorithm. It allows for a specified number of mismatches, making it adaptable to scenarios where exact matches are not always feasible. Its performance depends on the number of allowed mismatches and the complexity of the pattern set.

4.3.5 Khancome (2023)

Khancome's algorithm utilizes multi-character inverted lists and perfect hashing methods to achieve efficient string matching. It demonstrates excellent performance, particularly with binary character sets and reduced text widths. However, its efficiency might degrade for larger alphabets or wider texts.

4.3.6 Comparison with the Proposed Method

Based on the experimental results and analysis, the proposed method exhibits several advantages compared to the existing algorithms:

i. **Efficient Search Time:** For datasets with repetitive patterns (e.g., DNA sequences), the proposed method demonstrates faster search times compared to AC, SA, and FM-Index.

ii. **Moderate Memory Usage:** While requiring more memory than FM-Index, the proposed method uses less memory than SA for most datasets, offering a reasonable trade-off between speed and memory consumption.

iii. **Good Compression:** The BWT inherently provides compression, resulting in a smaller index size compared to SA.

iv. **Bidirectional Search Capability:** The proposed method supports bidirectional searching, allowing for more flexible pattern matching scenarios.

v. **Handling Large Datasets:** Along with FM-Index, the proposed method showcases good performance and scalability for large and complex datasets, making it suitable for demanding applications.

vi. **Exact Matching Focus:** The proposed method is specifically designed for exact matching and thus maintains the high level of accuracy for the DNA sequence data set.

Table 7 Comparison with the Proposed Method

Feature	**Aho-Corasick (AC)**	**Suffix Array (SA)**	**FM-Index (FM)**	**Proposed (BWT + Wavelet Matrix)**	**Ujwala Rekha (2020)**	**Khancome (2023)**
Matching Type	Exact	Exact	Exact	Exact	Approximate (up to k mismatches)	Exact
Search Time Complexity	O(n + m) (n: text length, m: total pattern length)	O(m log n) (m: pattern length, n: text length)	O(m) (m: pattern length)	Dependent on pattern length and dataset characteristics	O(M * n) (M: total pattern length, n: text length)	O(n) (linear)
Preprocessing Time Complexity	O(m) (m: total pattern length)	O(n log n) (n: text length)	O(n log σ) (n: text length, σ: alphabet size)	O(n log σ) (n: text length, σ: alphabet size)	O(n + m)	NA
Memory Usage	Moderate	High	Moderate	Moderate	Moderate	Moderate
Compression	No	No	Yes	Yes	No	No
Advantages	Efficient for a moderate number of patterns, widely used	Versatile, supports various string operations	Good balance between search time and memory, compressed index	Efficient for repetitive patterns, good compression, bidirectional search	Handles approximate matching, adaptable to various fields	Linear search time, efficient for specific datasets (binary, reduced width)
Disadvantages	Performance can degrade with a large number of patterns or pattern overlap	High memory usage for large texts	Can be slower for complex patterns	Performance can vary with dataset characteristics	May be slower for large k values or complex pattern sets	Performance may degrade for large alphabets or wider text
Applications	Intrusion detection, text editors, bioinformatics	Text indexing, pattern discovery, data mining	Bioinformatics, text retrieval, genomic analysis	DNA sequencing, text retrieval, pattern discovery in large texts	Computational biology, signal processing, text retrieval with errors	Search operations, data filtration, validation, data retrieval, AI

4.4 Interpretation of Findings

The experimental results and comparative analysis provide valuable insights into the performance and characteristics of the proposed method and the existing algorithms. The key findings can be interpreted as follows:

i. **The proposed method, based on the BWT and Wavelet Matrix, demonstrates competitive performance for multiple string matching, particularly for datasets with repetitive patterns.** Its efficiency in search time, moderate memory usage, and compression capabilities make it a viable alternative to traditional approaches.

ii. **The choice of the most suitable algorithm depends on the specific requirements of the application.** For scenarios requiring approximate matching, Ujwala Rekha's algorithm offers flexibility. For specialized datasets or applications with specific constraints, Khancome's algorithm might provide optimized performance.

iii. **The BWT and Wavelet Matrix approach offers a good balance between search time, memory usage, and compression, making it a versatile choice for a range of applications.** Its bidirectional search capability further enhances its flexibility for complex pattern matching tasks.

iv. **Further research and development are needed to address the limitations of the proposed method and explore its potential for broader applications.** This includes optimizing its performance for diverse datasets, handling long patterns efficiently, managing memory usage for very large datasets, and incorporating approximate matching capabilities.

By carefully interpreting the findings and considering the strengths and limitations of each algorithm, researchers and practitioners can make informed decisions when selecting the most appropriate technique for their specific multiple string matching needs. The insights gained from

this research contribute to the advancement of efficient and effective pattern matching solutions for various domains, including computational biology, text mining, and information retrieval.

4.5 Discussion of Limitations

While the proposed method based on the Burrows-Wheeler Transform (BWT) and Wavelet Matrix demonstrates promising results for multiple string matching, it's crucial to acknowledge its limitations to provide a balanced perspective.

4.5.1 Dependence on Dataset Characteristics

The performance of the BWT and Wavelet Matrix approach can be influenced by the characteristics of the input datasets. For instance, its efficiency is particularly pronounced when dealing with datasets containing repetitive patterns, like DNA sequences. However, in scenarios with highly diverse and non-repetitive text, the advantages might be less pronounced compared to other algorithms like the Suffix Array or FM-Index. Further investigation is needed to explore the performance variations across different dataset types and complexities.

4.5.2 Pattern Length Considerations

The search time of the proposed method can be affected by the length of the patterns being searched. As the pattern length increases, the search process might become more computationally demanding, potentially impacting overall efficiency. This aspect warrants further investigation, especially when dealing with applications requiring the identification of long or complex patterns.

4.5.3 Memory Usage for Large Datasets

While the Wavelet Matrix offers a compressed representation of the BWT, memory usage can still be a concern when processing very large datasets. As the dataset size grows, the memory required to store the Wavelet Matrix might become substantial. Optimizations and strategies for managing

memory consumption in such scenarios should be explored, potentially involving techniques like data partitioning or distributed processing.

4.5.4 Limited Support for Inexact Matching

Unlike Ujwala Rekha's algorithm (2020), which inherently supports approximate matching with a specified number of mismatches, the proposed method primarily focuses on exact matching. While adaptations for approximate matching are possible, they might require modifications to the core algorithm and could introduce additional computational overhead. Further research is needed to investigate efficient and effective ways to incorporate approximate matching capabilities into the BWT and Wavelet Matrix framework.

4.5.5 Comparison with Specialized Algorithms

In certain specific scenarios, specialized algorithms like Khancome's (2023) multi-character inverted list approach might outperform the proposed method. For instance, when dealing with binary character sets or text with reduced widths, Khancome's algorithm exhibits exceptional efficiency due to its optimized design for such data structures. It's important to consider the specific requirements and characteristics of the target application when selecting the most suitable algorithm for multiple string matching.

4.5.6 Future Research Directions

To address the limitations and further enhance the capabilities of the proposed method, several avenues for future research are identified:

- **Dataset-specific optimizations:** Investigate techniques to adapt the BWT and Wavelet Matrix approach for optimal performance across diverse dataset types, including those with limited repetitiveness.

- **Pattern length handling:** Explore strategies to mitigate the impact of pattern length on search time, potentially involving algorithmic adjustments or data partitioning techniques.
- **Memory management for large datasets:** Develop efficient memory management strategies for handling very large datasets, potentially leveraging distributed computing or data compression techniques.
- **Incorporating approximate matching:** Research and implement methods for extending the BWT and Wavelet Matrix framework to support approximate matching with varying degrees of flexibility.
- **Hybrid approaches:** Explore the potential of combining the strengths of different algorithms, such as integrating the BWT and Wavelet Matrix with specialized techniques like multi-character inverted lists, to achieve enhanced performance in specific scenarios.

By acknowledging these limitations and outlining potential areas for improvement, this discussion provides a comprehensive and balanced perspective on the proposed method and its position within the broader landscape of multiple string matching algorithms. Continued research and development efforts will further refine its capabilities and address its limitations, paving the way for its wider adoption in various applications.

CHAPTER FIVE

SUMMARY, CONCLUSION AND FUTURE WORK

5.1 Summary of Findings

In this chapter a summary and discussion of the most important findings and outcomes gained from the study are presented in relation to the aims of the research. Both the Burrows-Wheeler Transform (BWT) and the Wavelet Matrix for Multiple String Matching are used to compress text, and the findings shed light on how effective these two methods are.

5.2 Conclusion

Based on the findings of the research study, the following conclusions are drawn:

i. Text data can be effectively compressed using the Burrows-Wheeler Transform (BWT). Using the text's inherent redundancy helps it to attain notable compression ratios.
ii. Finding several patterns in a text becomes easy with the Wavelet Matrix technique. It enables quick pattern matching and incident retrieval.
iii. Comparatively to current multiple string matching techniques, the BWT and Wavelet Matrix approach exhibits promise in terms of performance, scalability, and memory utilization.
iv. The possibility of combining the BWT and Wavelet Matrix in the domain of multiple string matching and text compression is shown by the research work.

5.3 Contributions of the Research

This research makes several contributions to the field of text compression and multiple string matching:

i. The analysis and assessment of the efficacy of the BWT for text compression.
ii. The utilization of the Wavelet Matrix methodology for effective multiple string matching.
iii. The performance assessment and comparative analysis of the BWT and Wavelet Matrix methodologies against existing methods.
iv. The identification of prospective areas for enhancement and future inquiry within the discipline.

5.4 Future Works

Based on the findings and limitations of the research study, the following areas are identified for future investigation:

i. Optimize and develop the BWT and Wavelet Matrix methods for better performance and scalability.
ii. Investigate hybrid approaches that combine BWT and Wavelet Matrix with compression and string-matching algorithms to achieve better outcomes.
iii. Investigate the effectiveness of the BWT and Wavelet Matrix approaches in various domains and data types, including genomics and natural language processing.
iv. Create parallel and distributed techniques for large-scale text compression and string matching.

Addressing these future research areas is likely to develop the domains of text compression and multiple string matching, resulting in approaches and techniques that are more applicable and perform better.

5.5 Final Remarks

This thesis states that using the Wavelet Matrix and Burrows-Wheeler Transform helps us to better understand text compression and multiple string matching. The results show the efficiency and promise of this approach, therefore laying the groundwork for more investigation and development in the field. This study is meant to inspire more research on several string matching techniques and text compression.

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APPENDIX I

Pseudocode for the BWT function:

```
# Input: string S
# Output: BWT-transformed string of S
def BWT(S):
    # append a special character $ to the end of S
    S = S + "$"
    # create a list of all cyclic rotations of S
    Rotations = []
    for i in range(len(S)):
        Rotations.append(S[i:] + S[:i])
    # sort the rotations lexicographically
    Rotations.sort()
    # take the last column of the sorted matrix as the BWT-transformed
string
    BWT = ""
    for R in Rotations:
        BWT = BWT + R[-1]
    return BWT
```

APPENDIX II

Pseudocode for the WaveletMatrix class, see Appendix 2

```
# Input: string S

# Output: a wavelet matrix object that represents S

class WaveletMatrix:

    def __init__(S):

        # initialize the wavelet matrix with an empty list of bit arrays

        self.matrix = []

        # initialize the alphabet of S with a set of unique characters

        self.alphabet = set(S)

        # initialize the C array with a dictionary that maps each character to its rank

        self.C = {}

        # compute the number of bits needed to encode the characters in S

        self.num_bits = math.ceil(math.log2(len(self.alphabet)))

        # construct the wavelet matrix by recursively splitting the string and the alphabet

        self.construct(S, self.alphabet, 0)
```

```
    def construct(S, A, level):
        # base case: if the alphabet size is 1, there is nothing to
split
        if len(A) == 1:
            return
        # recursive case: split the alphabet into two halves
        A = sorted(A) # sort the alphabet lexicographically
        mid = len(A) // 2 # find the middle index
        A_low = A[:mid] # the lower half of the alphabet
        A_high = A[mid:] # the higher half of the alphabet
        # create a bit array for the current level
        B = BitArray(len(S))
        # assign 0 to the characters in A_low and 1 to the characters in
A_high
        for i in range(len(S)):
            if S[i] in A_low:
                B[i] = 0
            else:
                B[i] = 1
```

```
        # append the bit array to the matrix
        self.matrix.append(B)
        # update the C array with the rank of the first character in
A_high
        self.C[A[mid]] = B.rank(1, len(S) - 1)
        # split the string into two substrings according to the bit
array
        S_low = "" # the substring with 0 bits
        S_high = "" # the substring with 1 bits
        for i in range(len(S)):
            if B[i] == 0:
                S_low = S_low + S[i]
            else:
                S_high = S_high + S[i]
        # recursively construct the wavelet matrix for the lower and
higher substrings and alphabets
        self.construct(S_low, A_low, level + 1)
        self.construct(S_high, A_high, level + 1)


    def access(i):
```

```
# input: index i
# output: the character at position i in the original string
# initialize the character with an empty string
c = ""
# initialize the bit with 0
bit = 0
# for each level of the matrix
for level in range(self.num_bits):
    # get the bit array at the current level
    B = self.matrix[level]
    # get the bit at position i
    bit = B[i]
    # append the bit to the character
    c = c + str(bit)
    # if the bit is 0, move to the lower part of the next level
    if bit == 0:
        i = B.rank(0, i - 1)
    # if the bit is 1, move to the higher part of the next level
    else:
```

```
                i = self.C[c] + B.rank(1, i - 1) - 1
        # convert the binary string to a character
        c = chr(int(c, 2))
        return c

    def rank(c, i):
        # input: character c, index i
        # output: the number of occurrences of c in the prefix [0..i] of
the original string
        # convert the character c to a binary string
        c = bin(ord(c))[2:]
        # pad the binary string with zeros if needed
        c = c.zfill(self.num_bits)
        # for each level of the matrix
        for level in range(self.num_bits):
            # get the bit array at the current level
            B = self.matrix[level]
            # get the bit of c at the current level
            bit = int(c[level])
```

```
            # if the bit is 0, count the number of 0s in the prefix
[0..i] of the bit array
            if bit == 0:
                i = B.rank(0, i)
            # if the bit is 1, count the number of 1s in the prefix
[0..i] of the bit array
            else:
                i = self.C[c[:level + 1]] + B.rank(1, i) - 1
        return i


    def select(c, i):
        # input: character c, index i
        # output: the position of the i-th occurrence of c in the
original string
        # convert the character c to a binary string
        c = bin(ord(c))[2:]
        # pad the binary string with zeros if needed
        c = c.zfill(self.num_bits)
        # get the bit of c at the last level
        bit = int(c[-1])
```

```
        # if the bit is 0, find the position of the i-th 0 in the last
level
        if bit == 0:
            pos = self.matrix[-1].select(0, i)
        # if the bit is 1, find the position of the i-th 1 in the last
level
        else:
            pos = self.matrix[-1].select(1, i - self.C[c[:-1]])
        # for each level of the matrix from bottom to top
        for level in range(self.num_bits - 2, -1, -1):
            # get the bit array at the current level
            B = self.matrix[level]
            # get the bit of c at the current level
            bit = int(c[level])
            # if the bit is 0, find the position of the pos-th 0 in the
current level
            if bit == 0:
                pos = B.select(0, pos)
            # if the bit is 1, find the position of the pos-th 1 in the
current level
```

```
            else:
                pos = B.select(1, pos - self.C[c[:level + 1]] + 1)
        return pos
```

Here is the pseudocode for the SearchPattern function, which uses the backward search algorithm described in 3([object Object]):

```
# Input: wavelet matrix WM, pattern string P
# Output: a list of positions of P in the BWT-transformed string

def SearchPattern(WM, P):
    # initialize the list of positions as empty
    Positions = []
    # initialize the range of matching prefixes as the whole string
    start = 0
    end = WM.length - 1
    # for each character of P from right to left
    for i in range(len(P) - 1, -1, -1):
        # get the current character
        c = P[i]
```

```
        # update the range using the rank and select operations of the
wavelet matrix
        start = WM.select(c, WM.rank(c, start - 1) + 1)
        end = WM.select(c, WM.rank(c, end))
        # if the range is empty, there is no match
        if start > end:
            return Positions
    # if the range is not empty, add the positions to the list
    for i in range(start, end + 1):
        Positions.append(i)
    return Positions
```