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A New Compression Technique for Repetitive Tries

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Abstract

This thesis introduces a novel compression technique for repetitive tries, which are fundamental data structures for representing large sets of strings in applications like bioinformatics and natural language processing. While tries are efficient for prefix-based queries, their inherent repetitiveness often leads to a large memory footprint. Traditional compression algorithms often fail to exploit this redundancy, and even specialized techniques like the Extended Burrows-Wheeler Transform (XBWT) may not be optimal in such cases.

The proposed method aims to find an effective trade-off between high compression and efficient indexing. The core idea is to identify and merge identical subtrees by reducing the trie to a minimal deterministic finite automaton (DFA). However, a fully minimized DFA is difficult to index efficiently. Therefore, this work proposes a partial minimization of the trie that ensures the resulting automaton is *p–sortable*, a property that allows for efficient indexing.

The problem is framed as a **String Partitioning Problem**, where the sequence of nodes in the trie, ordered co–lexicographically, is partitioned into p subsequences to maximize the merging of equivalent states. This optimization problem is then reduced to finding a **Minimum Weight Perfect Bipartite Matching (MW-PBM)**, which can be solved efficiently.

The result is a compressed, p–sortable automaton that supports efficient queries. Experimental results demonstrate the effectiveness of this method, particularly for highly repetitive datasets, achieving a balance of compression and indexability that prior methods could not attain. Our approach opens new possibilities for managing and querying large-scale string datasets in a memory-efficient manner.

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Chapter 1

Introduction

The problem of compressing large sets of strings, or finite languages, is a fundamental challenge in computer science with applications in areas like bioinformatics, natural language processing, and data indexing. A finite language can be naturally represented by a trie. In this representation, each string in the language corresponds to a unique path from the root to a final state. Compressing the language is therefore equivalent to compressing its corresponding trie structure.

Tries are exceptionally efficient for solving problems related to string collections and prefix-based queries. Their structure makes them ideal for a variety of applications:

1. **Autocomplete and Predictive Text:** Tries are widely used in search engines and text editors to suggest completions for a given prefix. By traversing the trie, all words sharing the prefix can be quickly retrieved.
2. **Spell Checkers:** A trie can store a dictionary of valid words. To check a word, one simply traverses the trie. If the path corresponding to the word does not end in a terminal node, the word is either misspelled or not in the dictionary.
3. **IP Routing:** In networking, routers use tries to store routing tables. This allows for efficient longest prefix matching to determine the optimal route for an IP packet.
4. **Bioinformatics:** Tries are used to store and search large collections of DNA sequences or other biological data, enabling efficient pattern matching and analysis of shared subsequences.

Traditional compression algorithms often fail to exploit the inherent structural properties of tries. To address this, specialized techniques have been developed. Among the most prominent is the *Extended Burrows-Wheeler Transform (XBWT)* [12], which extends the classical Burrows-Wheeler Transform [4] to labeled trees and can be applied to tries to achieve significant compression by capturing their structural regularities.

However, existing techniques may not be optimal when dealing with tries that exhibit a high degree of repetitiveness. Such is the case for languages containing many strings with shared substrings, leading to tries with large, identical subtrees. Many real-world datasets, such as genomic databases or dictionaries of related terms, generate such highly repetitive structures. This thesis introduces and analyzes a novel compression technique specifically designed to exploit these repetitions. The core idea is to identify and merge identical subtrees by reducing the trie to its minimal deterministic finite automaton (DFA) representation. We implement this method and evaluate its performance against state-of-the-art approaches like XBWT, assessing its effectiveness on various datasets.

1.1 Challenges and Contributions

The primary goal of this thesis is to develop a data structure that both compresses a given finite language and efficiently supports indexing queries, such as navigational and subpath queries (see Definition 17). This challenge involves navigating a fundamental trade-off between compression and indexability, which we explore in detail in Section 2.5. Two straightforward approaches highlight the extremes of this spectrum:

A **Full Compression, Difficult Indexing:** One could minimize the input trie into the smallest possible equivalent DFA using an algorithm like Revuz's [32]. While this yields optimal compression through DAG compression (see Section 2.1), indexing the resulting general DFA is a notoriously difficult problem. As shown by Equi et al. [11], polynomial-time indexing schemes for general DFAs cannot support sub-quadratic query times unless the Strong Exponential Time Hypothesis (SETH) fails, making this approach unsuitable for most indexing purposes.

B **Full Indexability, No Compression:** At the other extreme, the input trie itself can be used as an index. Tries are Wheeler graphs [14], specifically 1–sortable automata (Definition 24), a property that makes them highly amenable to efficient indexing [7]. While this provides excellent query performance through the co–lexicographic ordering of states (see Definition 26), it offers no compression, as even highly repetitive subtrees are stored explicitly.

This thesis proposes a novel algorithm that finds a sweet spot in this trade-off, which we develop throughout Chapter 3. The central idea is to partially minimize the input trie while ensuring that the resulting automaton remains efficiently indexable. We achieve this by leveraging the theory of p–sortable graphs (see Section 2.5), developing a method that strategically increases the sortability parameter p (a parameter interpolating between trade-offs A and B above described) just enough to enable significant compression. The motivation for this approach is rooted in the observation that a small increase in p can lead to substantial improved compression: as noted by Policriti et al. [27], there are cases where increasing p from 1 to 2 allows for an exponential reduction in the automaton's size, a phenomenon we explore in detail in Section 2.5.

Our compression scheme, presented in Chapter 3, works by first sorting the trie's nodes by the colexicographic order of the strings connecting them to the root. Then, the scheme partitions this sorted sequence of nodes into p disjoint subsequences called *chains*, where each chain preserves the co–lexicographic order of its nodes. Our method optimizes this organization to merge the maximum number of adjacent Myhill–Nerode–equivalent states while ensuring p–sortability. We frame this problem as a string partitioning problem. Consider the sequence of nodes in the trie, when read in co–lexicographic order (see Definition 26), as a single long string. The "character" corresponding to each node is its Myhill–Nerode equivalence class (see Theorem 1), which determines if it can be merged with other nodes. The task is to partition this string of nodes into p subsequences such that the number of equal-letter runs (Definition 1) is minimized. Minimizing the number of runs directly corresponds to maximizing the number of merged states, yielding a compact p–sortable automaton. We call this problem the *String Partitioning Problem* (Definition 4).

Definition 1 (Run)**.** *Let $S = s_1 s_2 \dots s_n$ be a string over an alphabet Σ. A substring $S[i \dots j] = s_i s_{i+1} \dots s_j$ (where $1 \le i \le j \le n$) is a run if it satisfies the following conditions:*

1. ***Homogeneity:*** *All characters in the substring are identical, i.e., $s_k = s_i$ for all k such that $i \le k \le j$.*
2. ***Maximality:*** *The substring cannot be extended to the left or right without violating homogeneity. That is:*
   - *If $i > 1$, then $s_{i-1} \neq s_i$.*
   - *If $j < n$, then $s_{j+1} \neq s_j$.*

Definition 2. *For a string $S = s_1 s_2 \dots s_n$ over an alphabet Σ, and a set $I = \{i_1, i_2, \dots, i_k\} \in [n]$ with $i_1 < i_2 < \dots < i_k$, we define $S[I] := s_{i_1} s_{i_2} \dots s_{i_k}$ as the subsequence indexed by I.*

Definition 3. *Let $\tau(S)$ be the number of runs in a string S, i.e., $\tau(S) = 1 + |\{i \in [n-1] : S[i] \neq S[i+1]\}|$.*

Definition 4 (String Partitioning Problem)**.** *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning Problem where S is a string of length n over an alphabet Σ, and p is a positive integer. The output of the problem is a partition $\mathcal{P} = I_1, \dots, I_p$ of $[n]$ such that $\gamma(\mathcal{P}) = \sum_{i=1}^{p} \tau(S[I_i])$ is minimized.*

Example 1.1: String Partitioning

Let us consider the string $S =$ `2213122152` of length 10. The number of runs in S is 8, given by the decomposition `(22)(1)(3)(1)(22)(1)(5)(2)`. We want to partition the set of indices $\{1, \dots, 10\}$ into two sets, I_1 and I_2, to minimize the total number of runs in the corresponding subsequences.

A possible partition is:

- $I_1 = \{3, 5, 8, 9\}$
- $I_2 = \{1, 2, 4, 6, 7, 10\}$

This partition yields the following subsequences:

- The subsequence corresponding to I_1 is $S[I_1] =$ `1115`. This subsequence has 2 runs: (`111`) and (`5`).
- The subsequence corresponding to I_2 is $S[I_2] =$ `223222`. This subsequence has 3 runs: (`22`), (`3`), and (`222`).

The total number of runs for this partition is $2 + 3 = 5$. This is a reduction from the original 8 runs in S. This example illustrates how partitioning a string's indices can reduce the total number of runs in the resulting subsequences.

In Section 3.3, we show that the String Partitioning Problem can be reduced to the problem of finding a minimum weight perfect matching on a bipartite graph (MWPBM), allowing us to use efficient, well-studied algorithms to find the optimal solution.

To sum up, the main contribution of the thesis is to show how to convert a trie (recognizing a finite regular language) to an equivalent small compressed automaton that is p–sortable by construction (for any parameter p specified by the user) and thus supports efficient queries using the data structure developed by Cotumaccio et al. [7]. The larger p is, the better compression we can achieve (but the slower queries will be). As our experimental results in Chapter 4 will show, in both the repetitive and non-repetitive scenarios, our method allows for a twofold reduction of the number of states by just increasing p from 1 (the original trie) to 2. By further increasing p, the number of states quickly approaches that of the smallest DFA for the language.

1.2 Structure of the Thesis

This thesis is organized into several chapters, each building upon the last to provide a comprehensive exploration of our proposed trie compression scheme.

In Chapter 2, we begin by introducing the fundamental concepts and notation that are essential for understanding the subsequent chapters. This includes theoretical background on automata theory, labeled trees and tries, the Extended Burrows-Wheeler Transform (XBWT), Wheeler and p–sortable graphs, and the min-weight perfect bipartite matching (MWPBM) problem, which form the theoretical foundations of our work.

Chapter 3 then transitions from theory to practice, presenting the core ideas behind our novel trie compression algorithm. We introduce the concept of collapsing nodes and detail the reduction to a MWPBM problem, which is the central mechanism of our approach.

Following this, Chapter 4 is dedicated to the empirical evaluation of our method. We describe the implementation of our algorithm and present a series of experiments designed to assess its performance. This includes a comparison with existing methods and an analysis of the execution time and compression ratios achieved.

Finally, in Chapter 5, we summarize our findings and discuss the implications of our results. We also outline potential avenues for future research, including possible optimizations and extensions of the proposed scheme.

Chapter 2

Preliminary Concepts

2.1 Basic Notation and Concepts

Definition 5 (String)**.** *A **string** is a sequence of characters $S = s_1 s_2 \dots s_n$ drawn from an alphabet Σ.*

We use $|S| = n$ to denote the length of S. The set of all strings is represented as Σ^*, which also contains the empty string ε.
The notation $S[i] = s_i$ denotes the i-th character of S, and $S[i \dots j]$ the substring $s_i s_{i+1} \dots s_j$, for $1 \leq i, j \leq n$. Therefore, a prefix of S is a substring of the type $S[1 \dots j]$, while a suffix is a substring $S[i \dots n]$.

Definition 6 (Subsequence)**.** *$S' = s'_1 \dots s'_m$ is a **subsequence** of some string $S = s_1 \dots s_n$ if there exist a strictly increasing sequence of indices $1 \leq i_1 < i_2 < \dots < i_m \leq n$ such that $s'_j = s_{i_j}$ for all $j = 1, \dots, m$.*

In other words, a subsequence is a sequence of characters from a string that are not necessarily contiguous, but are in the same order as they appear in the original string.

We recall the following important notation for strings from the introduction section:

Definition 2. *For a string $S = s_1 s_2 \dots s_n$ over an alphabet Σ, and a set $I = \{i_1, i_2, \dots, i_k\} \in [n]$ with $i_1 < i_2 < \dots < i_k$, we define $S[I] := s_{i_1} s_{i_2} \dots s_{i_k}$ as the subsequence indexed by I.*

A basic understanding of formal grammars is crucial for comprehending some of the state-of-the-art tree compression methods discussed in this thesis.

Definition 7 (Grammar)**.** *A **formal grammar** is a set of rules for generating strings in a formal language. A grammar is typically defined as a 4-tuple $G = (N, \Sigma, P, S)$, where:*

- *N is a finite set of non-terminal symbols.*
- *Σ is a finite set of terminal symbols, disjoint from N.*
- *P is a finite set of production rules, each of the form $(\alpha \to \beta)$, where α is a string of symbols from $(N \cup \Sigma)^*$ containing at least one non-terminal symbol, and β is a string in $(N \cup \Sigma)^*$.*
- *$S \in N$ is the start symbol.*

Example 2.1:
For example, consider the grammar $G = (\{S\}, \{a, b\}, P, S)$ with the following production rules in P:

1. $S \to aSb$
2. $S \to \epsilon$

This grammar generates the language $\{a^n b^n \mid n \geq 0\}$, which includes strings like ϵ (the empty string), ab, $aabb$, $aaabbb$, and so on.

Let us now move to the definition of a rooted tree.

Definition 8 (Tree)**.** *A **rooted tree** is a triple $T = (V, E, r)$ where:*

- *V is a finite set of vertices (or nodes),*
- *$E \subseteq V \times V$ is a set of edges such that $|E| = |V| - 1$ and the underlying graph is connected and acyclic,*
- *$r \in V$ is the root vertex.*

We denote by $t = |V|$ the number of vertices in the tree.

Definition 9 (Tree Terminology)**.** *Given a rooted tree $T = (V, E, r)$, we define the following concepts:*

- ***Parent:** For any two distinct nodes $u, v \in V$, with $v \neq r$, we say that u is the parent of v iff $(u, v) \in E$ and u lies on the unique path from r to v. It follows that each node v (except for the root) has exactly one parent, which we denote as* $\text{parent}(v)$.
- ***Children:** For a vertex $u \in V$, we define the set* $\text{children}(u) = \{v \in V | (u, v) \in E \wedge u = \text{parent}(v)\}$
- ***Leaves:** A vertex $v \in V$ is a leaf if it has no children, i.e., there is no edge $(v, w) \in E$ for any $w \in V$.*
- ***Degree:** The degree of a node u, denoted deg(u), is its number of children.*
- ***Depth:** The depth (or level) of a vertex v, denoted depth(v), is the length of the unique path from the root r to v minus 1. The root has depth 0.*
- ***Height:** The height of the tree is the maximum depth among all its leaves.*
- ***Subtree:** For any vertex $v \in V$, the subtree rooted at v is the tree $T_v = (V', E', v)$ where V' contains v and all its descendants, and E' contains all edges between vertices in V'.*
- ***Linearization:** A linearization of a tree is a total ordering of its vertices that respects some traversal order (e.g., pre-order, post-order, or in-order).*

2.2 Finite State Automata

Finite automata are fundamental computational models that recognize regular languages through a finite set of states and transitions. They provide an elegant mathematical framework for representing and manipulating collections of strings, making them particularly suitable for applications in pattern matching, lexical analysis, and data compression. In the context of this thesis, finite automata serve as the underlying representation for tries and other string data structures, enabling efficient compression through state minimization.

Let $L \subseteq \Sigma^*$ be a finite set of strings. L can be represented in many different ways, such as enumeration, context-free grammars, regular expressions, or automata.

Definition 10 (Non-deterministic Finite Automaton). *A* ***non-deterministic finite automaton*** *(NFA) is a 5-tuple $N = (Q, \Sigma, \delta, q_0, F)$ where:*

- *Q is a finite set of states,*
- *Σ is a finite alphabet,*
- *$\delta : Q \times \Sigma \to \mathcal{P}(Q)$ is the transition function, where $\mathcal{P}(Q) = \{A | A \subseteq Q\}$ is the powerset of Q,*
- *$q_0 \in Q$ is the initial state,*
- *$F \subseteq Q$ is the set of final (accepting) states.*

An NFA processes an input string $S \in \Sigma^*$ one symbol at a time, starting from q_0 and following the transitions specified by δ. Let $\hat{\delta} : Q \times \Sigma^* \to \mathcal{P}(Q)$ be the extension of δ to strings defined as follows. For all $u \in Q$, $a \in \Sigma$, and $\alpha \in \Sigma*$:

$$\hat{\delta}(u, \varepsilon) = \{u\}, \qquad \hat{\delta}(u, \alpha a) = \bigcup_{v \in \hat{\delta}(u,\alpha)} \delta(v, a).$$

Therefore, $\delta(q_0, \alpha)$ denotes the set of states that can be reached from the start state q_0 by reading α. A string S is *accepted* if $\delta(q_0, S) \cap F \neq \emptyset$, or, in other words, if the automaton ends in any state $q \in F$ after processing the entire string. The set of all strings accepted by N is called the *language* of the automaton, and is denoted as

$$\mathcal{L}(N) = \{S \in \Sigma^* \mid \delta(q_0, S) \cap F \neq \emptyset\}.$$

Deterministic Finite Automata are a special case of NFAs, where each state has exactly one outgoing transition per character, i.e., $|\delta(q, a)| = 1$.

Definition 11 (Deterministic Finite Automaton). *A* ***deterministic finite automaton*** *(DFA) is a 5-tuple $D = (Q, \Sigma, \delta, q_0, F)$ where:*

- *Q is a finite set of states,*
- *Σ is a finite input alphabet,*
- *$\delta : Q \times \Sigma \to Q$ is the transition function,*
- *$q_0 \in Q$ is the initial state,*
- *$F \subseteq Q$ is the set of final (accepting) states.*

Notice how the only difference between Definition 10 and Definition 11 is the return value of the transition function. As a consequence, the expansion of δ to strings can be simplified to

$$\hat{\delta}(u, \alpha a) = \delta(\hat{\delta}(\alpha), a)$$

Similarly to NFAs, the language of a DFA is the set of strings that end at a state $q \in F$ after being processed:

$$\mathcal{L}(D) = \{S \in \Sigma^* \mid \hat{\delta}(q_0, a) \in F\}$$

Also, we introduce the following notation for automata: For $q \in Q$, we write I_q to denote the set of strings reaching q from the initial state:

$$I_q = \{\alpha \in \Sigma^* \mid q = \delta(q_0, \alpha)\}$$

NFAs can be more compact in terms of the number of states required to represent a language: a well-known fact is that the smallest DFA for a language could be exponentially larger than the smallest equivalent NFA. In this thesis, this will not be a concern, since we will assume that the input language is presented via a DFA (more specifically, a trie).

Finally, automata are naturally represented as labeled directed graphs, where the vertices are the states and the edges represent the transitions, labeled with characters from the alphabet.

Example 2.2:
Figure 2.1 shows an example of an NFA and an equivalent DFA that both accept the language of strings over alphabet $\{a, b\}$ ending with the character 'a'.

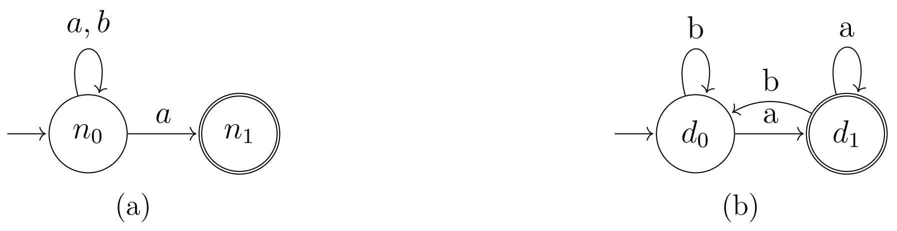


Figure 2.1: (a) An NFA and (b) an equivalent DFA for the language $(a|b)^*a$.

2.2.1 Minimization

The process of automata minimization consists of reducing the number of states in an automaton while preserving its accepted language. As extensively shown in the literature, determinism makes this problem much easier: while minimizing DFAs can be achieved in polynomial time, minimizing NFAs is a PSPACE–complete problem.

Tries are inherently deterministic, since from any node, there is at most one outgoing edge for each symbol in the alphabet. This deterministic nature will be crucial in this work to apply powerful automata minimization techniques to compress the tree structure.

The minimization of DFAs is a well-studied problem in automata theory, and there are several algorithms available for this purpose. One of the most popular algorithms for DFA minimization is Hopcroft's algorithm, which was proposed by John Hopcroft in 1971 [19]. Hopcroft's algorithm is an efficient and simple algorithm that can minimize a DFA in $O(n \log n)$ time, where n is the number of states in the DFA.

The algorithm enables computing equivalence classes of nodes, in particular, the Myhill–Nerode equivalence classes [30, 28]. The Myhill–Nerode theorem states that a language is regular if and only if it has a finite number of Myhill–Nerode equivalence classes. This theorem provides a powerful tool for determining the regularity of languages and is a cornerstone of automata theory. Let us formalize the concept of equivalence classes and the Myhill–Nerode theorem.

Definition 12 (Myhill–Nerode Equivalence Relation)**.** *For a language $L \subseteq \Sigma^*$ and any strings $x, y \in \Sigma^*$, we say x is equivalent to y with respect to L (written as $x \approx_L y$) if and only if for all strings $z \in \Sigma^*$:*

$$xz \in L \Leftrightarrow yz \in L$$

That is, strings x and y are equivalent if they have the same behavior with respect to the language L: either they both lead to acceptance or both lead to rejection when any suffix z is appended.

Theorem 1 (Myhill–Nerode theorem [30, 28])**.** *Let L be a language over an alphabet Σ. Then L is regular if and only if there exists a finite number of Myhill–Nerode equivalence classes for L. Specifically, the number of equivalence classes is equal to the number of states in the minimal DFA recognizing L.*

Throughout this section let $M = (Q, \Sigma, \delta, q_0, F)$ be a DFA. For $q \in Q$ and $a \in \Sigma$, we adopt the shorthand $q.a := \delta(q, a)$. We extend δ to words by the usual recursion:

$$\delta^*(q, \varepsilon) = q, \qquad \delta^*(q, wa) = \delta\Big(\delta^*(q, w),\, a\Big) \quad \text{for } w \in \Sigma^*,\ a \in \Sigma.$$

For a word $w = w_1 w_2 \dots w_n \in \Sigma^*$, we then write $q.w := \delta^*(q, w)$ for the (unique) state reached from q by reading w. A word w is accepted by M iff $\delta^*(q_0, w) \in F$.

Also, Let $M = (Q, \Sigma, \delta, q_0, F)$ be a DFA recognizing L. For states (nodes) $u, v \in Q$, we say that u and v are MN–equivalent iff

$$\forall \alpha \in \Sigma^* :\ u.\alpha \in F \iff v.\alpha \in F.$$

2.2.2 Revuz' Minimization Algorithm

For our purpose, we will focus on Acyclic Deterministic Finite Automata (ADFA). An ADFA is a DFA where the transition graph contains no cycles. The acyclic property is key, as it simplifies the minimization process significantly.

In this section, we will discuss an efficient algorithm for minimizing ADFAs in linear time on the number of edges [32].

Let us begin by providing some definitions needed to understand the algorithm.

Definition 13 (Height function)**.** *For a state s in an automaton, the height $h(s)$ is defined as the length of the longest path starting at s and going to a final state.*

$$h(s) = \max\{|w| : s.w \textit{ is final}\}$$

This height function induces a partition Π_i of Q, where Π_i denotes the set of states of height i.

Now we define the canonical label of each state that will be necessary to identify MN–equivalent states. For $s \in Q$, let $l_1 < \cdots < l_k$ be the symbols of the outgoing transitions defined at s (listed in increasing order of Σ). With $b = \mathrm{F}$ if $s \in F$ and $b = \mathrm{NF}$ otherwise, we set

$$\mathrm{l}(s) := \Big(b,\, l_1,\, s.l_1,\, l_2,\, s.l_2,\, \ldots,\, l_k,\, s.l_k\Big).$$

Also, the algorithm uses a function R to map the labels of states to a new signature. This function is defined as follows:

Definition 14 (Signature map R)**.** *Let $N[\,\cdot\,]$ be the current renaming array that assigns to each state its equivalence class identifier Myhill–Nerode. For a state s labeled*

$$\mathrm{l}(s) \;=\; \Big(b,\, l_1,\, s.l_1,\, l_2,\, s.l_2,\, \ldots,\, l_k,\, s.l_k\Big),$$

where $b \in \{F, NF\}$, $l_i \in \Sigma$ (listed in increasing order), and $nl_i \in Q$, define

$$R(\mathrm{l}(s)) \;=\; \Big(b,\, l_1,\, N[s.l_1],\, l_2,\, N[s.l_2],\, \ldots,\, l_k,\, N[s.l_k]\Big).$$

It is important to notice that, since the automaton is acyclic, every transition $s \xrightarrow{a} t$ strictly decreases the height: $h(t) < h(s)$. The main loop of Algorithm 1 processes levels in increasing order $i = 0, 1, \ldots$, so by the time we handle a state $s \in \Pi_i$, all its targets t lie in $\bigcup_{j<i} \Pi_j$ and have already been assigned a Myhill–Nerode equivalence class.

Algorithm 1 RevuzMinimization(M)

```
Require: $M = (Q, \Sigma, \delta, q_0, F)$ is an ADFA.
Ensure: Minimal DFA $M' = (\{1, \ldots, n\}, \Sigma, \delta', N[q_0], F')$ with $F' = \{N[q] \mid q \in F\}$
    and $\delta'(N[q], a) = N[\delta(q, a)]$.
 1: Calculate height $h(s)$ for every state $s$
 2: Create partitions $\Pi_i = \{s \in Q \mid h(s) = i\}$
 3: $N[1, |Q|] = \{1, 2, \ldots, |Q|\}$                         ▷ Renaming array
 4: $n = 0$
 5: for $i := 0$ to $h(q_0)$ do                              ▷ $q_0$ is the initial state
 6:     Sort states in $\Pi_i$ based on $R(l(q)), q \in \Pi_i$
 7:     $n = n + 1$
 8:     $N[\Pi_i[1]] = n$;
 9:     for $j := 2$ to $|\Pi_i|$ do
10:         if $R(l(\Pi_i[j])) \neq R(l(\Pi_i[j-1]))$ then
11:             $n = n + 1$
12:         end if
13:         $N[\Pi_i[j]] = n$
14:     end for
15: end for
```

The algorithm proceeds level by level, from $i = 0$ up to the maximum height, ensuring that states at each level are correctly partitioned into Myhill–Nerode equivalence classes. For each level i, it groups the states in Π_i based on their signatures computed by the function R (see Definition 14). As explained before, when processing level i, the equivalence classes for all states in lower levels ($j < i$) have already been finalized. The signature $R(l(s))$ for a state s depends on its finality and the equivalence classes of its immediate successors. Therefore, two states $s, t \in \Pi_i$ have the same signature if and only if they are MN–equivalent. The algorithm assigns a unique class identifier to each group of states with the same signature.

The whole algorithm can be implemented to run in time $O(m)$ for an acyclic automaton with m edges. Heights may be computed in linear time by a bottom-up traversal. The lists of states of a given height are collected during this traversal. The signature of a state is easy to compute, provided the edges starting in a state have been sorted (by a bucket sort, for instance, to remain within the linear time constraint). Sorting states by their signature again is done by a lexicographic sort [2].

Example 2.3:
Now we are going to see an example of reduction for a given ADFA. The ADFA is represented in figure Figure 2.2 and, as we can notice, it is also a valid ordered rooted tree with $n = 11$ nodes, $e = 10$ edges, and the following alphabet: $\Sigma = \{0, 1\}$. The node a is the root of the tree and the initial state of the automaton, while the leaf nodes e, g, h, i, l, m are final states. It is important to note that while the algorithm applies to any ADFA, our focus is on those that are also trees, as this is the specific case relevant to our work.

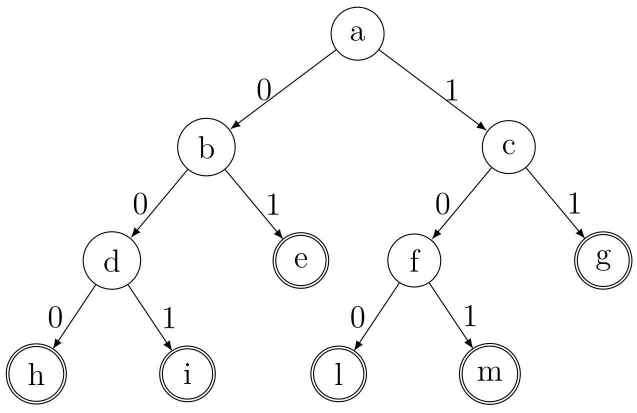


Figure 2.2: Example ADFA to be minimized

Now, let us apply the minimization algorithm step by step:

1. **Height Computation:** First, we compute the height of each state. The height is the length of the longest path to a final state. The final states (e, g, h, i, l, m) have a height of 0. For the other states, the height is calculated as follows:
   - $h(d) = 1 + \max(h(h), h(i)) = 1 + 0 = 1$
   - $h(f) = 1 + \max(h(l), h(m)) = 1 + 0 = 1$
   - $h(b) = 1 + \max(h(d), h(e)) = 1 + \max(1, 0) = 2$
   - $h(c) = 1 + \max(h(f), h(g)) = 1 + \max(1, 0) = 2$

- $h(a) = 1 + \max(h(b), h(c)) = 1 + \max(2, 2) = 3$

This gives us the following partitions based on height:

- $\Pi_0 = \{e, g, h, i, l, m\}$
- $\Pi_1 = \{d, f\}$
- $\Pi_2 = \{b, c\}$
- $\Pi_3 = \{a\}$

2. **Processing Π_0:** All states in Π_0 are final and have no outgoing transitions, so they are all equivalent. We merge them into a single class, let us call it $D = \{e, g, h, i, l, m\}$. After this step, we have a new state D which is final.

3. **Processing Π_1:** Now we examine the states in Π_1: d and f. We check their transitions:

   - State d: $\delta(d, 0) = h \in D$ and $\delta(d, 1) = i \in D$.
   - State f: $\delta(f, 0) = l \in D$ and $\delta(f, 1) = m \in D$.

   Since both states transition to the same equivalence class (D) for both symbols 0 and 1, they are equivalent. We merge them into a new class, $C = \{d, f\}$.

4. **Processing Π_2:** Next, we process the states in Π_2: b and c.

   - State b: $\delta(b, 0) = d \in C$ and $\delta(b, 1) = e \in D$.
   - State c: $\delta(c, 0) = f \in C$ and $\delta(c, 1) = g \in D$.

   Both states have transitions to class C on symbol 0 and to class D on symbol 1. Therefore, b and c are equivalent. We merge them into a new class, $B = \{b, c\}$.

5. **Processing Π_3:** Finally, we process Π_3, which contains only state a. There is nothing to compare it with, so it forms its class, $A = \{a\}$.

After applying the algorithm, we obtain the minimized ADFA represented in Figure 2.3. Each node of the original ADFA is represented by a node in the minimized ADFA (equivalence classes). The edges represent transitions between these nodes. The root node A is the initial state of the minimized ADFA, while the node D is the final state.

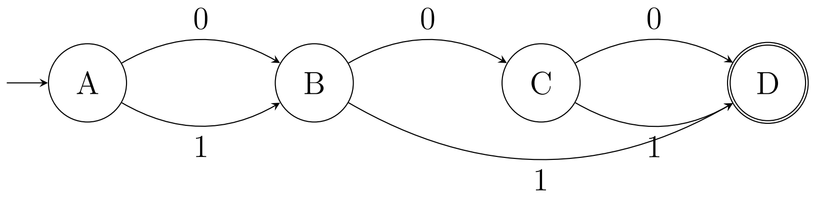

$$\begin{tikzcd} \arrow[r] & A \arrow[r, bend left, "0"] \arrow[r, bend right, "1"'] & B \arrow[r, bend left, "0"] \arrow[rr, bend right, "1"'] & C \arrow[r, bend left, "0"] \arrow[r, bend right, "1"'] & D \end{tikzcd}$$

Figure 2.3: Minimized ADFA

The equivalence classes of the nodes are listed in Table 2.1.

Class	States
A	a
B	b, c
C	d, f
D	e, g, h, i, l, m

Table 2.1: Equivalence classes of the nodes

2.3 Labeled Trees and Tries

Before delving into specific compression techniques, it is essential to establish a solid theoretical foundation regarding labeled trees and, in particular, tries. These structures are fundamental for representing hierarchical data across diverse fields, from bioinformatics to document processing. This chapter provides the necessary background, defining these two data structures, exploring their common applications, and introducing the core concepts behind their compression and indexing.

2.3.1 Definition

Definition 15 (Labeled tree). *A* ***labeled tree*** *is a 5-tuple $T = (V, E, \Sigma, \lambda, r)$, where:*

- *V, E, and r follow the same definition of the rooted tree (Definition 8),*
- *Σ is a finite set of labels, called the alphabet.*
- *$\lambda : E \to \Sigma$ is an edge-labeling function.*

In the case of *ordered* labeled trees, the children of each node are totally ordered, while the degree and shape of the tree, as well as the size of the alphabet Σ, are unconstrained.

While labeled trees encompass a broad class of hierarchical structures, this thesis focuses specifically on tries. Tries are a special case of DFAs, restricted to a tree-shaped structure, and are therefore widely used in Computer Science for representing finite sets of strings.

Definition 16 (Trie). *A* ***trie*** *is a 6-tuple $T = (V, E, \Sigma, \lambda, r, F)$ where:*

- *V is a finite set of vertices,*
- *$E \subseteq V \times V$ is a set of edges such that (V, E) forms a rooted tree,*
- *Σ is a finite set of labels, called the alphabet.*
- *$\lambda : E \to \Sigma$ is an edge-labeling function,*
- *$r \in V$ is the root vertex,*
- *$F \subseteq V$ is the set of final (accepting) vertices.*

Notice that, when expressing a trie as a DFA, each node should have a child for each character of the alphabet Σ. However, for ease of notation and representation, we will only consider nodes and edges that will eventually lead to a final state. For this reason, our definition of trie is closer to the definition of labeled trees rather than DFAs.

Key properties of a trie include:

1. **Determinism**: For every vertex $v \in V$ and every symbol $a \in \Sigma$, there is at most one edge $(v, u) \in E$ such that $\lambda((v, u)) = a$.
2. **String Representation**: For any vertex $v \in V$, let $str(v)$ be the string obtained by concatenating the labels on the unique path from the root r to v. We set $str(r) = \varepsilon$.
3. **Language Correspondence**: The language represented by the trie is exactly L, i.e., $L = \{str(v) \mid v \in F\}$.
4. **Prefix Property**: The set of all prefixes of words in L coincides with $\{str(v) \mid v \in V\}$.

These properties collectively make tries a powerful data structure. The **determinism** ensures that for any given string, there is only one path through the trie, making search operations efficient and unambiguous. The **string representation** and **language correspondence** properties formally establish the connection between the trie's structure and the set of strings it represents. Finally, the **prefix property** is fundamental to the trie's utility: it guarantees that every node corresponds to a prefix of at least one word in the language, which is the basis for autocomplete systems and is crucial for compression techniques that exploit shared prefixes.

This thesis addresses the problem of compressing repetitive collections of strings. Tries provide a natural data structure for this task, as compression can be achieved by merging their identical subtrees. Our approach, however, aims to produce not just a minimal automaton, but a p–sortable one (Definition 28) that also supports efficient indexing. The formal basis for this compression still relies on identifying equivalent states by computing the Myhill–Nerode equivalence classes (see Theorem 1), a process related to DFA minimization.

Given that a trie is a special case of DFA, we can apply automaton minimization techniques to compress its structure. This process, known as **DAG compression** (see Subsection 2.2.1) consists of transforming a tree into a directed acyclic graph (DAG) by identifying and merging its isomorphic subtrees. The result is the smallest possible automaton that recognizes the same language.

2.3.2 Indexing

The goal of compressing and indexing labeled trees is to design a compressed storage scheme for a labeled tree T with t nodes that allows for efficient navigation operations in T, as well as fast search and retrieval of subtrees or paths within T. To be effective, the compressed representation should minimize the space required to store the tree while supporting a wide range of operations in optimal (i.e., $O(1)$) or (near-)optimal time.

We focus on the following operations on labeled trees, as they will be useful in future sections:

Definition 17 (Tree Operations)**.** *Given a labeled tree $T = (V, E, \lambda, r)$, a node $u \in V$, and a symbol $s \in \Sigma$, we define the following fundamental operations:*

- ***Navigational queries:*** *ask for the parent of u, the i-th child of u, or the label of u. The last two operations might be restricted to the children of u with a specific label s.*
- ***Visualization queries:*** *retrieve the nodes in the subtree rooted at u for a given order (such as depth-first).*
- ***Subpath queries:*** *given a word $\alpha \in \Sigma^*$, answer:*
  - *Existence: determine whether $\hat{\delta}(q, \alpha) \neq \emptyset$ for some $q \in Q$, i.e., check if there exists a path in T labeled with string α.*
  - *Counting: compute the size of $\bigcup_{q \in Q} \hat{\delta}(q, \alpha)$.*
  - *Locating: return $\bigcup_{q \in Q} \hat{\delta}(q, \alpha)$.*

A naive solution to index labeled trees is to store the tree as a list of nodes with their labels and parent-child relationships using pointers in $O(t \log t)$ bits. However, this representation is not space-efficient and does not support fast subpath query operations. In order to implement fast, compressed tree indexes, we first have to understand the information-theoretic lower bounds for their lossless representation. To do so, it is essential to understand the concept of *worst-case entropy*, which is a formal measure of the minimum number of bits required to represent any object in a given set. As detailed by Navarro[29], this is a fundamental concept in data structure design.

Definition 18 (Worst-case entropy)**.** *Let U be a universe of combinatorial objects. The worst-case entropy of U is*

$$H_{wc}(|U|) = \lceil \log_2(|U|) \rceil$$

This definition establishes that the theoretical minimum number of bits needed to uniquely identify any object in a set U is the logarithm of the size of U, rounded up to the nearest integer. We now apply this principle to determine the lower bound for labeled trees.

Lemma 1. *The information-theoretic lower bound for storing an edge-labeled tree T with t nodes and m edges over an alphabet Σ is $2t + m \log_2 |\Sigma| - \Theta(\log t)$ bits.*

Proof. The total information required to store a labeled tree can be decomposed into two components: the space needed to encode the tree's structure and the space needed to encode the labels on its nodes.

1. Structural Information (Unlabeled Tree): The number of distinct unlabeled binary trees with t nodes is given by the t-th Catalan number $C_t = \frac{1}{t+1}\binom{2t}{t}$. Using Stirling's approximation for factorials, the Catalan number can be approximated as:

$$C_t \leq \frac{4^t}{t^{3/2}\sqrt{\pi}} \, .$$

Then, the worst-case entropy to encode the structure of the tree is:

$$\log_2 C_t \leq \log_2 \left(\frac{4^t}{t^{3/2}\sqrt{\pi}} \right) = \log_2(4^t) - \log_2(t^{3/2}\sqrt{\pi}) = 2t - \frac{3}{2}\log_2 t + \frac{1}{2}\log_2 \pi \ .$$

The lower-order terms can be expressed using big Theta notation as $\Theta(\log t)$. Therefore, the space required for the structure is $2t - \Theta(\log t)$ bits.

2. Labeling Information: For a tree with m edges and an alphabet Σ, each edge must be assigned a label. To distinguish between $|\Sigma|$ possible labels, a minimum of $\log_2 |\Sigma|$ bits is required for each edge. Consequently, the total space required to store the labels for all m edges is:

$$m \log_2 |\Sigma| \text{ bits.}$$

Finally, by adding the space required for the structure and the labels, the total information-theoretic lower bound for storing a labeled tree is the sum of the two components is

$$(2t - \Theta(\log t)) + (m \log_2 |\Sigma|) = 2t + m \log_2 |\Sigma| - \Theta(\log t) \text{ bits.}$$

□

2.3.3 Indexing and Compressing Labeled Trees: State of The Art

The field of tree indexing and compression has evolved through two main paradigms: succinct data structures that achieve space-optimal representations, and compression techniques that exploit structural repetitions. Neither paradigm has surpassed the other because they excel in different scenarios.

Succinct data structures provide worst-case space guarantees, aiming to store the tree in a number of bits close to the information-theoretic lower bound. This makes them highly effective for arbitrary trees with little to no repetition. On the other hand, compression techniques that exploit structural repetitions—such as representing a trie as a Directed Acyclic Graph (DAG) by merging identical subtrees—can achieve significantly better compression on datasets with high redundancy. Their effectiveness, however, is entirely dependent on the repetitiveness of the input data, and they may provide little benefit for non-repetitive structures. The choice between them depends on the expected characteristics of the data. As a consequence, many data structures have been proposed to compress and index labeled trees, each with its trade-offs in terms of space usage, query performance, and supported operations.

In the realm of succinct tree structures, early work by Kosaraju [22] proposed a method to index labeled trees by extending the concept of prefix sorting from strings to labeled trees using trie structures. He introduced the idea of constructing a suffix tree for a reversed trie, enabling subpath queries in $O(|P| \log |\Sigma| + occ)$ time, where occ is the number of occurrences of P in T. However, this approach still required $O(t \log t)$ bits of space and thus was not compressed.

A significant advancement in this direction came with the Extended Burrows-Wheeler Transform (XBWT) [12], a data structure designed for efficient compression and indexing of ordered node-labeled trees. The XBWT works by linearizing a labeled tree into two arrays, one capturing the structural properties of the tree and the other its labels. This transformation allows for a space-efficient representation, while being able to perform queries within (near-)optimal time bounds. The XBWT provides significant improvements in both compression ratio and query performance compared to traditional compression schemes, making it a valuable resource for intensive applications. We will study in detail this data structure in Section 2.4.

Complementing succinct approaches, tree compression has been extensively studied through different techniques that exploit structural repetitions in distinct ways. One of the classical approaches is *DAG compression* (equivalent to DFA minimization by interpreting the tree as a Finite State Automaton), which represents a tree as a minimal DAG by identifying and merging identical rooted subtrees. Concretely, whenever two identical subtrees occur, only one copy is stored, and all other occurrences are represented as pointers to it. The resulting structure can be exponentially smaller than the original tree and can be computed in linear time. DAG compression is widely used in programming languages, binary decision diagrams, and XML representations [3].

Another line of research extends the well-known LZ77 factorization from strings to trees. An LZ77 factorisation of a word w is a representation $w = f_1 f_2 \cdots f_\ell$, where each phrase f_i is either a single letter or it has already occurred in the text. Formally, $f_i = w[j \dots j + |f_i| - 1]$ for some $j \leq |f_1 \cdots f_{i-1}|$. If $j + |f_i| > |f_1 \cdots f_{i-1}|$, i.e. the whole phrase occurred earlier, the factorisation is called self-referencing; otherwise, it is non-self-referencing. Self-referencing factorisations can be more succinct, as with the string a^k. Each phrase f_i can be represented as either a single letter or a pair $(j, |f_i|)$, yielding a compressed representation whose size is ℓ. The smallest LZ77 factorisation of a text can be computed in linear time. This concept can be extended to trees. Here, the tree is decomposed into edge-disjoint fragments, where each fragment is either a single node or a copy of a fragment that appeared earlier in a breadth-first traversal. Each fragment is thus defined by a pointer to an earlier occurrence, much like in the string version of LZ77. This factorization uniquely determines the tree, and by minimizing the number of fragments, one obtains a compressed representation. Importantly, such factorizations can be computed in polynomial time (and in linear time for some restricted variants), yielding representations no larger than the smallest tree grammar, thus bridging block compression and grammar-based compression [15].

More recently, top tree compression has been proposed as a method that combines the advantages of subtree sharing and grammar-like approaches. The key idea is to build a hierarchical top tree decomposition, where the input tree is recursively partitioned into clusters that capture connected patterns. These clusters are then merged following a restricted set of operations, producing a binary decomposition tree whose internal repetitions are turned into subtree repeats. Finally, this decomposition is compressed using standard DAG compression, resulting in a so-called top DAG. This approach achieves close-to-optimal worst-case bounds, can be exponentially more succinct than DAG compression, and crucially, supports a wide range of navigational queries (e.g., parent, child, depth, nearest common ancestor) in logarithmic time directly on the compressed representation [3].

Another notable approach is Tree Re-Pair [25], a grammar-based compression technique adapted for tree structures. It extends the principles of the original Re-Pair algorithm [24] to handle the hierarchical nature of trees by identifying and compactly representing frequently occurring patterns as non-terminal characters in the grammar decomposition. The process involves the linearization of the tree and then the application of the Re-Pair logic, which finds the most frequent pair of adjacent elements (which could represent nodes, labels, or structural components, depending on the linearization) in the sequence, and replaces it with a new non-terminal symbol, and the corresponding production rule is added to the resulting grammar. All this process is then repeated until no more pairs occur frequently enough or some other stopping criterion is met. The final output is a relatively small grammar and a sequence of symbols (including the newly introduced non-terminals) that can be used to reconstruct the original tree. An application of Tree Re-Pair to XML documents can be found in [26].

In summary, DAG compression is efficient but limited to subtree repeats, LZ77 factorisation captures more general repetitions while relating closely to grammar-based methods such as Tree Re-Pair, and top tree compression strikes a balance by exploiting both subtree and pattern repeats while still enabling efficient query support.

This thesis focuses on developing a novel technique specifically tailored for highly repetitive tries. Our approach leverages the structural properties unique to tries and their repetitive patterns. Therefore, we use the XBWT as our primary benchmark for comparison, as it represents a well-established and high-performance baseline specifically designed for trie compression in the field.

2.4 The Extended Burrows-Wheeler Transform

This section explores the Extended Burrows-Wheeler Transform (XBWT), a state-of-the-art technique for labeled tree compression. We are interested in the XBWT for the following reasons:

- It provides a powerful theoretical foundation for indexing labeled trees and tries. Tries are a special case of a broader class of graphs known as Wheeler graphs, and the XBWT can be understood as a compressed index specifically for this special case. This context is crucial, as the work of Cotumaccio et al. [6] later generalized the principles of the XBWT to the larger class of p–sortable graphs (Section 2.5).
- It will serve as the primary benchmark against which we will evaluate the novel compression scheme proposed in this thesis. By establishing a baseline with a well-regarded and theoretically significant method like the XBWT, we can effectively demonstrate the potential advantages and contributions of our new approach, particularly for trees exhibiting high repetitiveness.

In 2005, Ferragina et al. [12] introduced an innovative approach to labeled tree compression by transforming it into a more tractable string compression problem. Their key contribution, the XBWT, is a sophisticated data structure that achieves highly efficient compression by combining entropy-compressed edge labels with a succinct representation of the tree topology. This elegant solution not only simplifies the compression process but also maintains the structural relationships, essential for tree operations.

One of the primary applications of the XBWT is compressing and indexing hierarchical data formats, such as XML documents. It provides significant improvements in both compression ratio and query performance compared to traditional tools, making it an invaluable resource for data-intensive applications in fields like bioinformatics, information retrieval, and big data analytics.

This section aims to explore the XBWT data structure and its applications in the context of labeled trees. We will start by providing an overview of the theoretical foundations of the XBWT. Finally, we will describe and compare the algorithms for constructing the XBWT and demonstrate its use in compressing and indexing labeled trees.

2.4.1 Definition

The **Extended Burrows-Wheeler Transform** is a data structure designed to efficiently compress and index *ordered node-labeled trees.* Inspired by the classical Burrows-Wheeler Transform (BWT) [4] for strings, the XBWT extends its principles to hierarchical structures, enabling efficient storage, navigation, and querying of trees.

Definition 19 (XBWT basic notation)**.** *Let T be a totally ordered node-labeled tree of arbitrary fan-out, depth, and shape, with n internal nodes and l leaves ($n + l = t$ nodes in total) and alphabet Σ. Given a node $u \in T$, we define the following information:*

- *$last(u)$: a binary value that is 1 if u is the last (rightmost) child of its parent in the total order, and 0 otherwise.*
- *$\alpha(u)$: the label of node u concatenated with one bit that is 1 if u is a leaf and 0 otherwise.*
- *$\pi(u)$: the string obtained by concatenating the labels of the nodes on the upward path from u parent to the root of T. Formally, given the parent node u' of u, we can define $\pi(u)$ as follows:*

$$\pi(u) = \begin{cases} \varepsilon & \text{if } u \text{ is the root} \\ label(u') \circ \pi(u') & \text{otherwise} \end{cases}$$

where $\circ$ is the concatenation operator.

Let Σ_N be the alphabet of the internal nodes, and Σ_L be the alphabet of the leaves of T. If $\Sigma_L \cap \Sigma_N = \emptyset$, the additional indicator bit in $\alpha(u)$ becomes redundant and may be omitted. Without loss of generality, we will only consider this case; therefore, we identify $\alpha(u)$ with the node label, i.e., $\alpha(u) := label(u)$.

The definition of the XBWT relies on a sequence S, which contains a triplet $(last(u), \alpha(u), \pi(u))$ for each node u in the tree T.

The construction of S is a two-step process. First, an intermediate vector of triplets is created by traversing the tree T in pre-order and generating a triplet $(last(u), \alpha(u), \pi(u))$ for each node. Then, S is stably sorted according to the lexicographical order of the π component of each triplet (see Figure 2.5 for an example). From now on, we will use S_{last} (resp. S_α, S_π) to refer to the sequences made up of the *last* (resp. α, π) component of all triplets in S.

Theorem 2. *The XBWT of a labeled tree T consists of two arrays, S_{last} and S_α, after sorting. The total space required is $2t + t \log |\Sigma|$ bits.*

Therefore, S_π is not needed after the construction of the XBWT. However, in the following discussion, we will still refer to it as it possesses some important properties. See Figure 2.4 for an example of the tree T and Figure 2.5 for its corresponding sequence S.

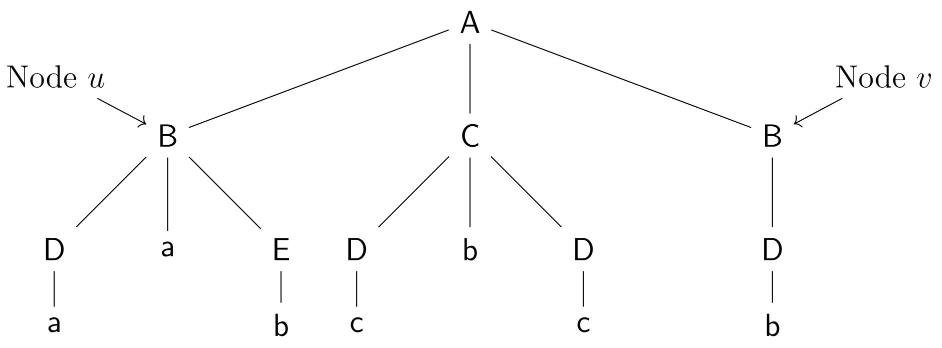


Figure 2.4: A labeled tree with $\Sigma_N = \{A, B, C, D, E\}$ and $\Sigma_L = \{a, b, c\}$. Notice that $\alpha(u) = \alpha(v) = B$ and $\pi(u) = \pi(v) = A$.

2.4.2 Properties

The XBWT's effectiveness as an indexing structure stems from a key property of the sequence S, which we call "Grouping by Parent". This property, along with its consequences, arises directly from the transform's definition and the sorting process.

Key Property: Grouping by Parent

The fundamental property of the XBWT is that the children of any node u in the tree T form a contiguous block in the sequence S. Let $u'_1, \ldots, u'_z$ be the children of node u in their original order. Their corresponding triplets will appear consecutively in S in that same order.

Example 2.4:
Consider the node u in Figure 2.4. Looking at Figure 2.5, we can see that its children form a contiguous block in positions $[5, 6, 7]$ of the sequence S.

This grouping provides several important consequent properties:

	S_{last}	S_α	S_π
1	0	A	ϵ
2	0	B	A
3	0	C	A
4	1	B	A
5	0	D	BA
6	0	a	BA
7	1	E	BA
8	1	D	BA
9	0	D	CA
10	0	b	CA
11	1	D	CA
12	1	a	DBA
13	1	b	DBA
14	1	c	DCA
15	1	c	DCA
16	1	b	EBA

Figure 2.5: Decomposition of S for the tree shown in Figure 2.4, obtained by stably sorting triplets according to S_π. In this representation, nodes u and v from the original tree T appear at indices 2 and 4, respectively. The children's block of node u occupies positions 5 through 7, while node v's single child is located at index 8.

Unary Degree Encoding: The subarray S_{last} for the block of children $[u_1, \ldots, u_z]$ encodes the degree of u in unary coding. Specifically, $S_{\text{last}}[u'_z] = 1$ and $S_{\text{last}}[u'_i] = 0$ for $1 \leq i < z$.

Example 2.5:
Consider the node u in Figure 2.4. Looking at Figure 2.5, we can observe that $S_{\text{last}}[5 \ldots 7] = [0, 0, 1]$, which is equal to 3 in unary encoding, matching the number of children of node u.

Preservation of Sibling Order: If two nodes u and v have the same label, and the triplet for u precedes the triplet for v in S, then the entire block of children of u will also precede the block of children of v.

Example 2.6:
Consider nodes u and v in Figure 2.4. In Figure 2.5, node u appears at index 2 while node v appears at index 4 in the sequence S. Following the preservation of sibling order property, all children of u (occupying positions $[5, 6, 7]$) appear before the child of v (at position 8).

Path-based Indexing: This property extends to entire paths. For any label $c \in \Sigma$, all triplets whose π-components are prefixed by c form a contiguous block in S. If u is the i-th node with label c in S_α, its children's block is located within the larger block of all nodes with paths prefixed by c. This block is delimited by the $(i-1)$-th and i-th 1s in the corresponding section of S_{last}.

Example 2.7:
Let's examine nodes u and v in Figure 2.4, both labeled 'B'. In the sequence S shown in Figure 2.5, u is the first node with label 'B' (at index 2), and v is the second (at index 4).

The children of all nodes labeled 'B' form a contiguous block in S. In this case, the children of both u and v are located in the range $[5 \dots 8]$. We can distinguish between the children of u and the children of v using the S_{last} array:

- The block of children for u (the first 'B' node) starts at the beginning of the range (index 5) and ends at the position of the first 1 (index 7) in $S_{\text{last}}[5 \dots 8]$.
- The block of children for v (the second 'B' node) starts after the first 1 (index 8) and ends at the position of the second 1 (index 8) in $S_{\text{last}}[5 \dots 8]$.

Other Properties

Additional properties of the XBWT components include:

- The first triplet in S always corresponds to the root of the tree T.
- S_{last} contains exactly n 1s (one for each internal node) and exactly l 0s (one for each leaf).
- S_α is a permutation of the node labels in T.

2.4.3 Construction

A naive approach to build the XBWT would be to explicitly construct S through the concretization of π-strings and then sort it using a stable sorting algorithm. However, this approach would require $\Theta(t^2)$ space in the worst case, which is not feasible for deep trees. To overcome this issue, Ferragina et al. [12] proposed a more efficient algorithm that builds S in linear time $O(t)$ and uses $O(t \log t)$ bits of working space. This algorithm is called PathSort, and is based on a generalization of the Skew algorithm, designed for the construction of suffix arrays on strings [20].

The Skew algorithm works by first building the suffix array recursively on a string of length two-thirds of the original one. This is done by working on the suffixes starting at positions i such that $i \bmod 3 \neq 0$. Then, the suffix array of the remaining suffixes is built using the result of the previous step, and in the end, these two are merged into the final suffix array. Thanks to linear-time radix sorting of the suffix array, a single-pass merge algorithm, and given that the recursion operates on a string of length $2n/3$, the overall time satisfies

$$T(n) = T(2n/3) + O(n) = O(n).$$

The PathSort algorithm works similarly, adapted to work on labeled trees. **Alessio:** What is an upward subpath? Is it the π component of the node or is it something with the triplets? If it is the first case, use $\pi(u)$, otherwise define upward subpath. Reading the Ferragina et al paper it seems π (or at least, some prefix), so i will edit it. The original version is in the old stuff folder. Given a value $j \in \{0, 1, 2\}$, the main idea is to recursively sort the π component of the nodes in levels $\not\equiv j$

(mod 3), then sort the π component of the nodes in levels $\equiv j \pmod 3$ using the result of the previous step, and finally merge the resulting two sets. At each step i of the recursion, the algorithm works on a labeled tree T_i, which is a *contracted* (or shrunk) version of the original tree T. We set $T_0 = T$, and note that the structure of T_{i+1} is derived from that one of T_i. The inner workings of the recursive step will be explained in detail later.

The parameter j is chosen in such a way that the number of nodes of the shrunk tree whose level is $\equiv j \pmod 3$ is at least $t/3$, so that a constant fraction of upward paths π is ensured to be dropped at each recursive step. It is important to note that:

1. the height of the new (contracted) tree shrinks by a factor of three, hence the node naming requires the radix sort over triples of names;
2. given the choice of j, the number of nodes of the new (contracted) tree will be at most $2t/3$, thus ensuring that the running time of the algorithm satisfies the recurrence $R(t) = R(2t/3) + \Theta(t) = \Theta(t)$;
3. following an argument similar to [20], the names of the dropped subpaths can be computed in $O(t)$ time from the names of the non-dropped subpaths, by radix sorting.

The pseudocode of the PathSort algorithm is shown in Algorithm 2.

Algorithm 2 PathSort(T)

```
1: Initialize the array of triplets IntNodes[$1 \dots t$].
2: Visit the internal nodes of $T$ in pre-order. For the $i$-th visited internal node $u$,
   set IntNodes[$i$] = $\big(\alpha(u), \text{level}(u), \text{parent}(u)\big)$.
3: Let $j \in \{0, 1, 2\}$ be such that the number of nodes in IntNodes whose level is
   $\equiv j \pmod 3$ is at least $t/3$. Sort recursively the upward subpaths starting at
   nodes in levels $\not\equiv j \pmod 3$.
4: Sort the upward subpaths starting at nodes in levels $\equiv j \pmod 3$ using the
   result of Step 3.
5: Merge the two sets of sorted subpaths by exploiting their lexicographic names.
```

Recursive Step of PathSort

At each recursive step, the algorithm constructs the array `IntNodes`, which stores the triplets $(\alpha(u), \text{level}(u), \text{parent}(u))$ for every internal node u in the given tree T.

Next, the algorithm selects a value j such that the number of nodes in `IntNodes` with depth $\equiv j \pmod 3$ is at least $t/3$. Based on this choice, two separate arrays are created:

- `IntNodesAtPosJ`, containing nodes at levels $\equiv j \pmod 3$,
- `IntNodesNotAtPosJ`, containing nodes at levels $\not\equiv j \pmod 3$

For each node u in `IntNodesNotAtPosJ`, the algorithm extracts the upward path consisting of the first three ancestors of u, $\pi(u)[1 \dots 3]$. These paths are then sorted using radix sort. If all upward paths are unique, the nodes in `IntNodesAtPosJ` are sorted and subsequently merged with `IntNodesNotAtPosJ` using lexicographic ordering. Otherwise, the algorithm recursively calls the PathSort function on a new contracted tree, where nodes are renamed according to their sorted paths.

2.4.4 Inversion

The ability to invert the XBWT is fundamental to its utility as a compression technique. Invertibility guarantees that the original tree can be perfectly reconstructed from its transformed representation (S_{last} and S_α). This ensures that the compression is lossless, meaning that no information is lost during the process, which is a critical requirement for most applications.

The property 'Path-based Indexing' (Subsection 2.4.2) ensures that the two arrays S_{last} and S_α of the XBWT can be used to reconstruct the original tree T. The algorithm for inverting the XBWT is linear in time and requires $O(t \log t)$ bits of space.

Algorithm 3 operates in three main steps. First, it constructs two auxiliary arrays, F and J, which are crucial for navigating the tree structure within the compressed format.

- **The F array:** This array maps each character $c \in \Sigma$ to the index of the first occurrence in S of a triplet whose π-component is prefixed by c. It essentially marks the starting points of blocks of nodes that share the same initial path label.
- **The J array:** For each entry i in S, $J[i]$ stores the index in S corresponding to the first child of the node represented by $S[i]$. If $S[i]$ represents a leaf, $J[i]$ is set to a sentinel value (e.g., -1).

Example 2.8: F and J arrays
Considering the XBWT in Figure 2.5, the F array would map 'A' to index 2 (for node r), 'B' to index 5 (for the children of nodes with label 'B'), and so on. For the J array, let's take the node u at index 2 in S. Its first child is at index 5. Therefore, $J[2]$ would be 5.

Finally, the algorithm employs the array J to simulate a depth-first visit of T, creates its labeled nodes, and properly connects them to their parents.

Algorithm 3 REBUILDTREE(S_α, S_{last})

```
 1: $F$ = BUILDF($S_\alpha$, $S_{\text{last}}$)
 2: $J$ = BUILDJ($S_\alpha$, $S_{\text{last}}$, $F$)
 3: Create node $r$ and set $Q = \{\langle 1, r\rangle\}$;                    ▷ $Q$ is a stack
 4: while $Q \neq \emptyset$ do                              ▷ We still have nodes to create in $T$
 5:     $\langle i, u\rangle$ = pop($Q$);
 6:     $j = J[i]$;                                      ▷ Take the block of $u$'s children in $S$
 7:     if $j = -1$ then                                               ▷ $u$ is a leaf of $T$
 8:         continue;
 9:     end if
10:     Find first $j' \geq j$ such that $S_{\text{last}}[j'] = 1$;  ▷ Range $[j, j']$ are the children of $u$ in $T$
11:     for $h = j'$ downto $j$ do
12:         Create the node $v$ labeled $S_\alpha[h]$;
13:         Attach $v$ as first child of $u$;
14:         push($\langle h, v\rangle$, $Q$);
15:     end for
16: end while
17: return node $r$.
```

Algorithm 4 BUILDF(S_α, S_{last})

```
 1: $C[1, |\Sigma_n|] = \{0, 0, \ldots, 0\}$;
 2: $F[1, t] = \{0, 0, \ldots, 0\}$;
 3: for $i = 1, \ldots, t$ do
 4:     $C[S_\alpha[i]] = C[S_\alpha[i]] + 1$;              ▷ Count the occurrences of node labels
 5: end for
 6: $F[1] = 2$;                                                ▷ $S_\pi[1]$ is the empty string
 7: for $i \in \{1, \ldots, |\Sigma_N| - 1\}$ do              ▷ Consider just the internal-node labels
 8:     $s = 0$; $j = F[i]$;
 9:     while $s \neq C[i]$ do                      ▷ Not all blocks of children have been passed
10:         $j = j + 1$;
11:         if $S_{\text{last}}[j] = 1$ then                 ▷ One further block of children has passed
12:             $s = s + 1$;
13:         end if
14:     end while
15:     $F[i + 1] = j$;
16: end for
17: return $F$.
```

Algorithm 5 BuildJ(S_α, S_{last}, F)

```
1: $J[1,t] = \{0, 0, \ldots, 0\}$;
2: for $i = 1, \ldots, t$ do
3:     if $S_\alpha[i] \in \Sigma_L$ then
4:         $J[i] = -1$;                                   ▷ $S_\alpha[i]$ is a leaf label
5:     else
6:         $J[i] = F[S_\alpha[i]]$;
7:         $z = J[i]$;
8:         while $S_{\text{last}}[z] \neq 1$ do           ▷ Reach the last child of $S_\alpha[i]$
9:             $z = z + 1$;
10:        end while
11:        $F[S_\alpha[i]] = z + 1$;
12:    end if
13: end for
14: return $J$.
```

2.4.5 Compressing Labeled Trees

The XBWT of a tree T exhibits a local homogeneity property on S_α: the labels (α components) of nodes whose upward paths (π components) share long common prefixes appear in S_α in contiguous (or tightly bounded) clusters. This phenomenon can be formalized via the notion of k-contexts on trees. This property mirrors the strong local homogeneity exhibited by strings under the Burrows-Wheeler Transform [4] when applied to labeled trees.

To illustrate this, let us consider two arbitrary nodes u and v in T, and examine their contexts $\pi(u)$ and $\pi(v)$. Given the sorting of S, the greater the length of the shared prefix between $\pi(u)$ and $\pi(v)$, the closer the corresponding labels $\alpha(u)$ and $\alpha(v)$ will be in the string S_α. These closely spaced labels are expected to be few in number, resulting in S_α exhibiting local homogeneity. As a consequence, we can leverage the advanced algorithmic techniques developed for BWT-based compression methods to achieve efficient compression.

At the end, the XBWT is used for turning the labeled tree compression problem into a string compression problem. To this aim, two string compressors C_α and C_{last} are used to compress the two strings S_α and S_{last}. respectively, by exploiting their fine specialties. Of course, many choices are possible for C_α and C_{last}, each having implications on the algorithmic time and compression bounds.

In general, the following theorem holds:

Theorem 3 ([12], Theorem 4)**.** *let C_α be a k-th order string compressor that compresses any string w into $|w|H_k(w) + |w| + o(|w|)$ bits, taking $O(|w|)$ time; and let C_{last} be an algorithm that stores S_{last} without compression. With this simple instantiation, the labeled tree T can be compressed within $tH_k(S_\alpha) + 2t + o(t)$ bits and takes $O(t)$ optimal time.*

Since $H_k(S_\alpha) \leq (\log|\Sigma|) + 1$ (where the additional $+1$ cost comes from the definition of α in Definition 19, since we consider the same alphabet Σ for nodes and leaves), the above bound is at most $t(\log|\Sigma| + 3) + o(t)$ bits, and can be significantly better than the information-theoretic lower bound and the plain storage of the XBWT (both taking $2t + t \log |\Sigma|$ bits), depending on the distribution of the labels among its nodes.

2.4.6 Indexing a Compressed Labeled Tree

In order to implement the efficient operations listed in Subsection 2.3.2 using the compressed arrays S_{last} and S_α of XBWT, we need the chosen compressors C_α and C_{last} to support the following operations:

Given a string $S[1,t]$ over alphabet Σ

- $rank_c(S,q)$: gives the number of times the symbol $c \in \Sigma$ appears in $S[1,q]$.
- $select_c(S,i)$: gives the position of the i-th occurrence of the symbol $c \in \Sigma$ in S.

The compressed indexing of the XBWT will be based on three compressed data structures that support rank and select queries over the two strings S_α and S_{last}, and over an auxiliary binary array $A[1,t]$ defined as: $A[1] = 0$, $A[j] = 1$ if and only if the first symbol of $S_\pi[j]$ differs from the first symbol of $S_\pi[j-1]$. Hence, A contains at most $|\Sigma| + 1$ bits set to 1 out of t positions. It is also easy to see that, through rank and select operations over A, we can succinctly implement the array F employed in Algorithms 3 and 4.

In this section, let $S \coloneqq (S_{\text{last}}, S_\alpha)$ such that $S[i] = (S_{\text{last}}[i], S_\alpha[i])$ for $i = 1, \ldots, t$, denote the XBWT obtained after the construction phase. The compressed index supports the following methods:

GetRankedChild(i, k): Returns the position in S of the k-th child of the node at index i. If the child does not exist, it returns -1.

Example 2.9:
In Figure 2.6, `GetRankedChild(2, 2)` returns 6.

GetCharRankedChild(i, c, k): Returns the position in S of the k-th child labeled c of the node at index i. If the child does not exist, it returns -1.

Example 2.10:
In Figure 2.6, `GetCharRankedChild(1, B, 2)` returns 4.

GetDegree(i): Returns the total number of children of the node at index i in S.

GetCharDegree(i, c): Returns the number of children of the node at index i in S that have the label c.

GetParent(i): Returns the position in S of the parent of the node at index i. If the node is the root (at index 1), it returns -1.

Example 2.11:
In Figure 2.6, `GetParent(8)` returns 4.

	A	S_{last}	S_α	S_π
1	0	0	A	ϵ
2	1	0	B	A
3	0	0	C	A
4	0	1	B	A
5	1	0	D	BA
6	0	0	a	BA
7	0	1	E	BA
8	0	1	D	BA
9	1	0	D	CA
10	0	0	b	CA
11	0	1	D	CA
12	1	1	a	DBA
13	0	1	b	DBA
14	0	1	c	DCA
15	0	1	c	DCA
16	1	1	b	EBA

Figure 2.6: The sequence S for the tree shown in Figure 2.4, obtained by stably sorting triplets according to their 'π' components. In contrast to Figure 2.5, the auxiliary binary array A is shown in the second column.

GetSubtree(i): Retrieves the labels of all nodes in the subtree rooted at the node at index i in S. The labels can be returned in any standard traversal order (e.g., pre-order, in-order, or post-order).

SubPathSearch(P): For a given labeled path $P = c_1c_2 \cdots c_k$, this function finds the range [First . . . Last] such that all strings in S_π[First . . . Last] are prefixed by the reversed path $P^R = c_k \cdots c_2c_1$.

Example 2.12:
In Figure 2.6, `SubPathSearch(BD)` results in the range [12, 13], and `SubPathSearch(AB)` gives the range [5, 8].

It is important to note that their time complexity is dependent on the specific implementation for rank and select over the compressed strings S_α and S_{last}.

Let's now see how to implement some of the above methods (from which the others can be derived) using the rank and select operations over the compressed strings S_α and S_{last}.

GetChildren(i)

Algorithm 6 exploits directly the properties described before, in particular Property 'Path-based Indexing' (Subsection 2.4.2). The rank operation at line 5 is used to get the number r of nodes labeled c up to position i in S_α. Then, the position $F[c]$ is obtained through a select operation on A (line 6). By Property 'Path-based Indexing', the children of $S[i]$ are located at the r-th block of children following position $F[c]$. Lines $8 - 9$ identify this block.

Example 2.13:
Let's walk through an example using Figure 2.6. Consider the node u at index 2 labeled with B. To find its children:

1. First, we compute $r = 1$ since this is the first occurrence of B in S_α up to position 2.
2. Next, we find $y = F[B] = 5$, which marks the start of the block containing children of all nodes labeled B.
3. Then, we count $z = 1$ ones in S_{last} up to position $y - 1$.
4. Finally, the children block is delimited by the $z+r-1 = $ 1st and $z+r = $ 2nd ones in S_{last}, giving us the range $[5, 7]$.

This range $[5, 7]$ indeed contains the three children of the node at index 2, as we can verify from the tree structure in Figure 2.4.

Algorithm 6 GetChildren(S_α, S_{last}, i)

```
1: if $S_\alpha[i] \in \Sigma_L$ then
2:     return $-1$                                  ▷ $S[i]$ is a leaf
3: end if
4: $c = S_\alpha[i]$                                ▷ $S[i]$ is labeled $c$
5: $r = \text{rank}_c(S_\alpha, i)$
6: $y = \text{select}_1(A, c)$                      ▷ $y = F[c]$
7: $z = \text{rank}_1(S_{\text{last}}, y - 1)$
8: First $= \text{select}_1(S_{\text{last}}, z + r - 1) + 1$
9: Last $= \text{select}_1(S_{\text{last}}, z + r)$
10: return (First, Last)
```

GetParent(i)

Algorithm 7 is based on Property 'Path-based Indexing' (Subsection 2.4.2) and it is the inverse of the GetChildren method. In line 4, the algorithm computes the label c of the parent of $S[i]$ that prefixes the upward path leading to $S[i]$. Then, the parent of $S[i]$ is searched among the nodes labeled c in S_α by exploiting Property 'Path-based Indexing' in a reverse manner. Namely, the number k of children-blocks in the range $S[y, i]$ is computed; these are children of nodes labeled c and preceding i in the stable sort of S. Then, the k-th occurrence of c in S_α is selected, which is indeed the parent of $S[i]$.

Example 2.14:
Let's illustrate how to find a node's parent using Figure 2.6. Consider node v located at index 4 with label B. The process to find its parent involves:

1. Computing $c = \text{rank}_1(A, 4) = 1$, which tells us the parent has label 'A' (as A contains exactly one 1 up to position 4).
2. Locating $y = F[A] = 2$, which indicates where the block of children for nodes labeled 'A' begins.

3. Calculating $k = \text{rank}_1(S_{\text{last}}, 4-1) - \text{rank}_1(S_{\text{last}}, 2-1) = 0$, meaning no complete child blocks appear before position 4.
4. Therefore, v's parent is the first ($(k+1)$-th) occurrence of 'A' in S_α, corresponding to index 1 (the root of $\mathcal{T}$).

This example demonstrates how the XBWT structure efficiently encodes parent-child relationships using just the S_{last} and S_α arrays.

Algorithm 7 GetParent(S_α, S_{last}, i)

```
1: if $i = 1$ then
2:     return $-1$                                  ▷ $S[i]$ is the root of $\mathcal{T}$
3: end if
4: $c = \text{rank}_1(A, i)$
5: $y = \text{select}_1(A, c)$
6: $k = \text{rank}_1(S_{\text{last}}, i-1) - \text{rank}_1(S_{\text{last}}, y-1)$
7: $p = \text{select}_c(S_\alpha, k+1)$
8: return $p$
```

SubPathSearch(P)

We assume that $P = c_1 c_2 \cdots c_k$ algorithm SubPathSearch computes the range $[First, Last]$ in $|P| = l$ phases, each one preserving the following invariant:

- Invariant of Phase i. At the end of the phase, $S_\pi[First]$ is the first entry prefixed by $P[1,i]^R$, and $S_\pi[Last]$ is the last entry prefixed by $P[1,i]^R$, where s^R is the reversal of string s.

At the beginning (i.e., $i = 1$), First and Last are easily determined via the entries $F[c_1]$ and $F[c_1+1]-1$, which point to the first and last entry of S_π prefixed by c_1 (by definition of array F). Since we do not have the F array, we implement these operations via rank and select queries over array A. Let us assume that the invariant holds for Phase $i-1$, and prove that the i-th iteration of the for-loop in algorithm SubPathSearch preserves the invariant. More precisely, let $S_\pi[First, Last]$ be all entries prefixed by $P[1, i-1]^R$. So $S[First, Last]$ contains all nodes descending from $P[1, i-1]$. SubPathSearch determines $S[z_1]$ (respectively $S[z_2]$) as the first (respectively last) node in $S[First, Last]$ that descends from $P[1, i-1]$ and is labeled c_i, if any. Then it jumps to the first child of $S[z_1]$ and the last child of $S[z_2]$. From Property 2 (item 2) and the correctness of algorithms GetChildren and GetDegree, we infer that the positions of these two children are exactly the first (respectively last) entry in S whose π-component is prefixed by $P[1,i]^R$.

The time complexity of the SubPathSearch algorithm is $O(l)$, where l is the length of the input path P.

Example 2.15:
Consider the tree in Figure 2.4, and let $P = BD$. The algorithm SubPathSearch(P) returns the range $[12, 13]$ through the following steps:

1. Initially, $First = F[B] = 5$ and $Last = F[C] - 1 = 8$. The range $S[5, 8]$ contains all nodes descending from paths prefixed by B.

2. For $c_2 = D$:
    - Compute $k_1 = 0$ and $k_2 = 2$
    - This yields $z_1 = 5$ and $z_2 = 8$
    - The first child of $S[5]$ is at position 12
    - The last (and only) child of $S[8]$ is at position 13
3. Therefore, the algorithm returns the range $[12, 13]$

Note that the number of occurrences of subpath P is 2, as evidenced by the two occurrences of 1 in range $S_{\text{last}}[12, 13]$.

Algorithm 8 SubPathSearch(S_α, S_{last}, P)

```
1:  $First = F(c_1)$; $Last = F(c_1 + 1) - 1$
2:  if $First > Last$ then
3:      return "$P$ is not a subpath of $T$"
4:  end if
5:  for $i = 2, \ldots, k$ do
6:      $k_1 = \text{rank}_{c_i}(S_\alpha, First - 1)$;
7:      $z_1 = \text{select}_{c_i}(S_\alpha, k_1 + 1)$          ▷ first entry in $S_\alpha[First, t]$ labeled $c_i$
8:      $k_2 = \text{rank}_{c_i}(S_\alpha, Last)$;
9:      $z_2 = \text{select}_{c_i}(S_\alpha, k_2)$          ▷ last entry in $S_\alpha[1, Last]$ labeled $c_i$
10:     if $z_1 > z_2$ then
11:         return "$P$ is not a subpath of $T$"
12:     end if
13:     $First = \text{GetRankedChild}(z_1, 1)$          ▷ get the first child of $S[z_1]$
14:     $Last = \text{GetRankedChild}(z_2, \text{GetDegree}(z_2))$          ▷ get the last child of $S[z_2]$
15: end for
16: return $(First, Last)$
```

2.4.7 Summary

To sum up, the XBWT has several key properties that make it an effective tool for labeled tree compression and indexing:

- **Succinctness:** The XBWT representation of a labeled tree uses space close to the worst-case entropy (Lemma 1), which is $H_{wc} = 2t + t \log|\Sigma| - \Theta(\log t)$ bits for a tree with t nodes and an alphabet of size $|\Sigma|$. Notice that the second component of H_{wc} is $t \log|\Sigma|$ and not $m \log|\Sigma|$ since the XBWT works on *node* labeled trees.
- **Efficient Querying:** The XBWT supports navigational queries (Definition 17) in optimal time $O(1)$ if $|\Sigma| = O(polylog(t))$, otherwise in $O(\log\log^{1+\epsilon}|\Sigma|)$ time. Whereas, given $s \in \Sigma^*$, subpath queries (Definition 17) are supported in $O(|s|)$ if $|\Sigma| = O(polylog(t))$, otherwise in $O(|s| \log\log^{1+\epsilon}|\Sigma|)$ time.
- **Scalability:** The XBWT is particularly useful for large-scale hierarchical data, such as XML documents or phylogenetic trees, where both compression and fast querying are critical.

2.5 Wheeler and p–sortable Graphs

2.5.1 Introduction and Motivation

As established in the introduction, the primary goal of this thesis is to find an effective balance between compressing a finite language and preserving its indexability. The two extremes — full DFA minimization and the raw input trie — are inadequate, as one sacrifices indexing for compression and the other sacrifices compression for indexing. The solution to this problem lies in a specific class of graphs that are structured enough to be indexed efficiently yet flexible enough to allow for significant compression. This chapter introduces the theoretical framework that underpins our approach: Wheeler graphs and their generalization, p–sortable graphs (Wheeler graphs corresponding to the case $p = 1$).

A crucial observation is that the input trie representing our language is already a highly structured object. It is a Wheeler graph, a type of graph that admits a special ordering on its nodes and edges, making it exceptionally well-suited for indexing. In formal terms, a trie is a 1–sortable graph. This property explains both its powerful indexing capabilities and its inherent lack of compression.

The concept of p–sortability offers a way to navigate the trade-off. By controllably increasing the sortability parameter p, we can begin to merge MN–equivalent states (see Theorem 1), thereby compressing the graph. The resulting automaton is no longer a simple trie but a more general p–sortable graph that retains strong indexing properties. This chapter will formally define these concepts, which are the foundation of our algorithm for achieving a practical compromise between compression and indexability.

2.5.2 Orders

The core property that makes Wheeler and p–sortable graphs efficiently indexable is the existence of a specific ordering on their states. This ordering provides the necessary structure to navigate the automaton and answer queries quickly, a task that is computationally hard on general graphs. The fundamental ordering used in this context is the *co–lexicographic* (co–lex) *order*, which compares states based on the labels of the paths that reach them. This section formally defines this order and the related concepts that are essential for understanding the structure of indexable automata.

Definition 20 (co–lexicographic order on Σ^*). *The co–lex order $\preceq$ is defined as follows. Given two strings $\alpha, \beta \in \Sigma^*$, we say that $\alpha \preceq \beta$ if and only if either:*

- *α is a suffix of β, or*
- *there exist strings $\alpha', \beta', \gamma \in \Sigma^*$ and symbols $a, b \in \Sigma$, such that $\alpha = \alpha' a \gamma$, $\beta = \beta' b \gamma$, and $a \prec b$.*

Now, let us define the formal concept of partial order and the width of a partial order.

Definition 21 (Partial Order). *A partial order is a binary relation $\leq$ over a set S that is reflexive, antisymmetric, and transitive. That is, for all $a, b, c \in S$:*

- *$a \leq a$ (reflexivity)*
- *if $a \leq b$ and $b \leq a$, then $a = b$ (antisymmetry)*
- *if $a \leq b$ and $b \leq c$, then $a \leq c$ (transitivity)*

A partial order $(S, \leq)$ can be visualized using a *Hasse diagram.* In a Hasse diagram, each element of S is represented by a node, and given $a, b \in S$, there is a line segment or curve going upward from a to b if $a \leq b$ and there is no element $c \in S$ such that $a \leq c \leq b$. The direction of the relation is implicitly upwards, so arrows are not needed. An example is given in Example 2.16.

Example 2.16:
In the example shown in Figure 2.7, the set is composed of the divisors of 12, and the relation is divisibility. An edge is drawn from a to b if a divides b and there is no other element c in the set such that a/c and c/b. For instance, there is an edge from 2 to 4 because 2 divides 4, and no other element in the set is a multiple of 2 and a divisor of 4. There is no direct edge from 2 to 12 because the relationship is captured transitively through other elements, such as 2/4/12 or 2/6/12.

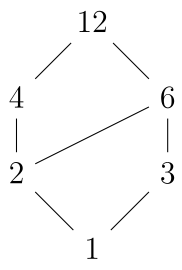


Figure 2.7: Hasse diagram for the set $\{1, 2, 3, 4, 6, 12\}$ on the "divides" relation.

Now we can define the concept of the width of a partial order.

Definition 22 (Antichain)**.** *An antichain of a partial order $(S, \leq)$ is a subset of S where any two distinct elements are incomparable. That is, for any two distinct elements a, b in the antichain, neither $a \leq b$ nor $b \leq a$ holds.*

Definition 23 (Width of a partial order, [8])**.** *The width of a partial order $\leq$, denoted by width$(\leq)$, is the size of the largest possible antichain.*

By Dilworth's Theorem [8], the width of a partial order $(S, \leq)$ is equal to the cardinality of its largest antichain; this can be equivalently defined as the minimum number of chains needed to partition S, where each chain is a totally ordered subset of S under the relation $\leq$.

2.5.3 Wheeler Graphs

With the concept of co–lex order established, we can now define the class of graphs that form the starting point of our work. A Wheeler automaton is an automaton where the states can be arranged in a strict, total order.

Definition 24 (Wheeler automaton, [14])**.** *A finite state automaton $\mathcal{A} = (Q, \Sigma, \delta, q_0, F)$ is a Wheeler automaton if there exists a total order $\leq$ on its set of states Q that satisfies the following axioms:*

1. *The initial state precedes all other states in the order.*

For any two transitions $u \in \delta(u', a)$ and $v \in \delta(v', b)$:

2. $a < b \implies u \leq v$,
3. $a = b \wedge u' < v' \implies u \leq v$.

The order $\leq$ is called a Wheeler order.

Consequently, we define the concept of Wheeler language.

Definition 25 (Wheeler language)**.** *A Wheeler language L is a language accepted by a deterministic Wheeler automaton.*

The most important example of a Wheeler automaton for this thesis is the trie. Any trie representing a finite language is a Wheeler automaton. The co–lexicographic order of the strings spelling the paths from the root to each node provides the required total ordering of the states. This is why tries are inherently indexable. However, this rigid structure also means they are uncompressed, as every unique path must be stored explicitly, even if it corresponds to a substring that appears many times in the language. Our work begins with this observation: we start with a Wheeler automaton (the trie) and seek to compress it while preserving efficient indexability.

2.5.4 The co–lex Width of an Automaton

Now that we have the concepts of co–lex order and width, we can combine them to formally define the class of indexable automata that are central to this thesis. The width of the co–lex partial order on an automaton's states is the critical measure of its structural complexity from an indexing perspective.

The co–lex order can be extended to the set of states of an automaton. This idea was first introduced with the notion of Wheeler graphs by Gagie et al. [14] and was later generalized to arbitrary finite automata by Cotumaccio and Prezza [6], where a partial order replaces the total order. Let $\lambda(q) = \{a \in \Sigma \mid q \in \delta(u, a), \forall u \in Q\}$ denote the set of transition labels entering in state q, and $\min \lambda(q)$ and $\max \lambda(q)$ represent the minimum and maximum elements of the set, respectively. The definition of co–lex order on an automaton is as follows:

Definition 26 (co–lexicographic order on an NFA, [7])**.** *Let $N = (Q, \Sigma, \delta, q_0, F)$ be an NFA. A co–lex order on N is a partial order $\leq$ on Q that satisfies the following two axioms:*

1. *For every $u, v \in Q$, if $u < v$, then $\max \lambda(u) \leq \min \lambda(v)$.*
2. *For every $a \in \Sigma$ and $u, v, u', v' \in Q$, if $u \in \delta(u', a)$, $v \in \delta(v', a)$ and $u < v$, then $u' \leq v'$.*

The two axioms in Definition 26 allow for states of a finite automaton to be compared. When $\leq$ is total, we say that the co–lex order is a Wheeler order (introduced in [14] and Definition 24).

Consequently, we can introduce the concept of co–lex width of an automaton.

Definition 27 (Width of an NFA, [7]). *The co–lex width of an NFA N is the minimum width of a co–lex order on N, i.e.,*

$$width(N) = \min\{width(\leq) \mid \leq \text{ is a co–lex order on } N\}$$

The requirement of a Wheeler order is powerful but restrictive. Many automata, especially those resulting from DAG compression, may not satisfy it (see Example 2.17). This introduces a fundamental trade-off: while DAG compression minimizes an automaton's size, it can destroy the very structure that enables efficient indexing. In fact, it has been shown that indexing general graphs — and thus, highly compressed automata — to support fast string matching is computationally expensive [11]. The second axiom of Definition 26 does not always enforce an ordering between any two states, leading to a partial order instead of a total one. This gives rise to the more general notion of a *p–sortable automaton*:

Definition 28 (p–sortable automaton). *Let $\mathcal{A} = (Q, \Sigma, \delta, q_0, F)$ be a finite-state automaton. We call $\mathcal{A}$ p–sortable if there exists a co–lexicographic order $\leq$ on Q such that Q can be partitioned into p chains $\{Q_i\}_{i=1}^{p}$, where each $(Q_i, \leq)$ is totally ordered.*

Under these definitions, a Wheeler automaton is a 1–**sortable automaton**, since a total order has a width of 1 (all its antichains are singletons).

Example 2.17:
State incomparability can arise in several situations. For example, consider two states u and u'.

- As illustrated in Figure 2.8a, if there are two same-labeled transitions to the target states u and v from two incomparable states u' and v', then u and v are also incomparable.
- Conflicting constraints from different labels can force incomparability, as shown in Figure 2.8b. An existing order on the sources of a-transitions (e.g., $u' < v'$) may require $u < v$ to satisfy the Wheeler axioms, while an order on the sources of b-transitions (e.g., $v'' < u''$) may require the opposite, $v < u$. Since neither can be true, the targets u and v must be incomparable.

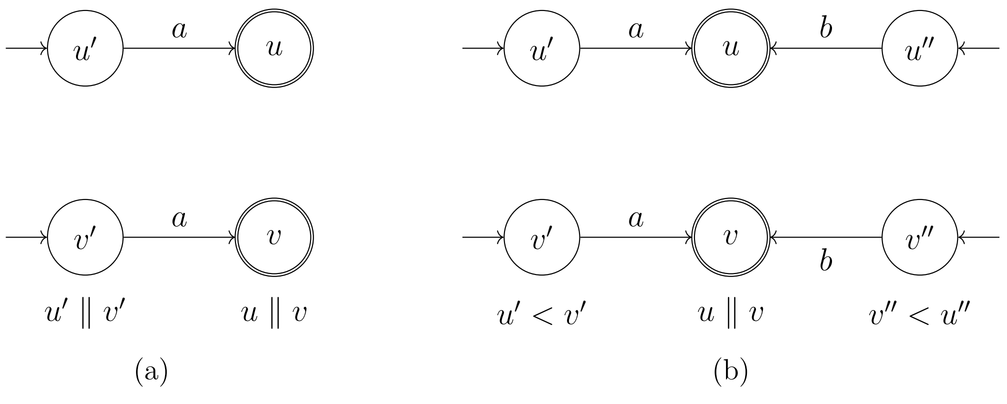


Figure 2.8: Examples of state incomparability in automata.

Example 2.18:
Consider the following DFA D of Figure 2.9a and its partial co–lex order Figure 2.9b. The DFA is not Wheeler because states u_3 and u_5 and states u_4 and u_7 are incomparable (as shown in the Hasse diagram). D admits a partition into two chains of totally ordered states, for example, one possible chain partition is given by:

- Chain 1: $u_1 \leq u_2 \leq u_3 \leq u_4$
- Chain 2: $u_5 \leq u_6 \leq u_7$

meaning that the DFA in Figure 2.9a is a 2–sortable automaton. This is also evident from Figure 2.9b, since the largest antichains are $\{u_3, u_5\}$ and $\{u_4, u_7\}$.

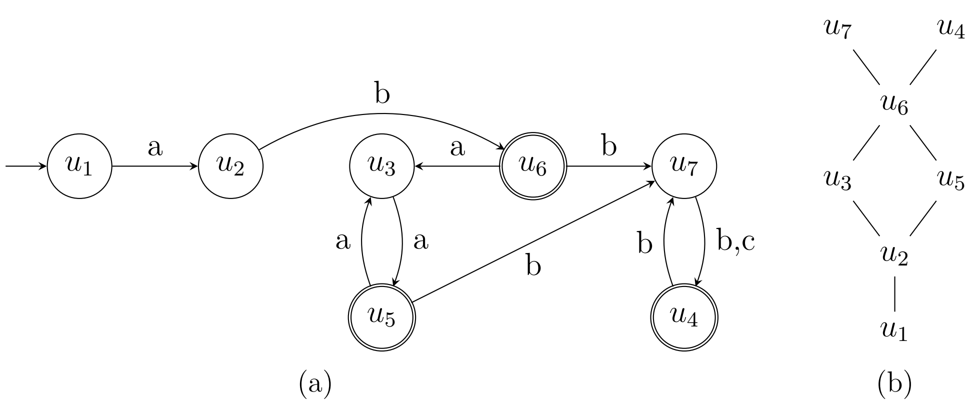


Figure 2.9: An example of (a) a 2–sortable DFA and (b) the corresponding Hasse diagram of its partial order.

We now introduce another important result by [27]. Let $D = (Q, \Sigma, \delta, s, F)$ denote the minimal DFA accepting a Wheeler language L, and let $D^w = (Q^w, \Sigma, \delta^w, s^w, F^w)$ denote the minimal Wheeler DFA (WDFA) accepting L, i.e. the DFA with the minimum number of states among all Wheeler DFAs accepting L. Since D^w is Wheeler, for any two distinct states $q, q' \in Q^w$ the associated sets $I_q, I_{q'}$ are disjoint. This property does not generally hold for D, where states may correspond to overlapping sets of prefixes. As a consequence, when transforming D into D^w, certain states of D may need to be *split* into several states in D^w, potentially leading to an exponential blow-up in the number of states (see Example 2.19).

Example 2.19: [27]
We now provide a simple example of an automaton D with width n that accepts a Wheeler language, yet its minimum equivalent Wheeler DFA, D^w, is exponentially larger. Let D be the automaton depicted in Figure 2.10.

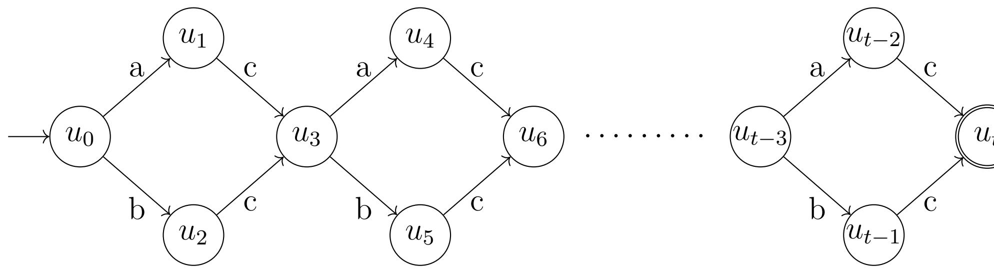


Figure 2.10: A DFA accepting a finite (and thus Wheeler) language, for which the minimal equivalent Wheeler DFA is exponentially larger.

The language $L = \mathcal{L}(D)$, being finite, is a Wheeler language [1]. However, any Wheeler automaton accepting L must have a number of states that is exponential in n. Since there are exponentially many such pairwise distinct strings leading to t, a Wheeler automaton must partition the set I_{u_t} into an exponential number of sub-intervals. This forces the state u_t to be "split" into exponentially many copies, leading to an exponential blow-up in the size of the minimal Wheeler DFA.

The previous example highlights a crucial trade-off: enforcing the strict ordering of a Wheeler DFA can lead to an exponential increase in the number of states compared to a minimal DFA. This work is motivated by this significant result, which demonstrates that even a modest increase in sortability (for instance, from $p = 1$ to $p = 2$) can yield exponential compression. Consequently, the objective is to convert a trie (a 1–sortable automaton) into a more general p–sortable graph (with $p > 1$), in a manner that enables DAG compression while preserving efficient indexability. This highlights the potential of exploring the trade-off between sortability and size, which is the central theme of this thesis.

2.5.5 Indexing Finite State Automata

Now we introduce the current state of the art in indexing finite state automata. In 2023, Cotumaccio et al. [6] introduced a compressed data structure for automata whose performance and space complexity are directly tied to the automaton's co–lex width p. This structure generalizes the famous Burrows-Wheeler transform [4].

Theorem 4 ([6]). *Let $\mathcal{A}$ be a p–sortable automaton. There exists a compressed data structure for A that supports subpath queries (Definition 17) on a query word α of length m in $O(mp^2 \log\log(p|\Sigma|))$ time. The space required is:*

- $\log(|\Sigma|) + \log p + 2$ *bits per edge if A is a DFA.*
- $\log(|\Sigma|) + 2\log p + 2$ *bits per edge if A is an NFA.*

This highlights a direct trade-off: both query time and space per edge depend on the width parameter p, which governs the automaton's compressibility.

To highlight the importance of this data structure, we recall that the final output of our compression pipeline is a p–sortable DAG-compressed automaton with a controlled co–lex width p. This allows us to leverage these advanced indexing capabilities on the compressed automata produced by our method.

2.6 Min-Weight Perfect Bipartite Matching

2.6.1 Introduction and Motivation

The fundamental goal of our compression scheme is to transform an input trie into a compressed, p–sortable automaton by partitioning its nodes into p chains in an optimal way.

To make this optimization problem more concrete, we can frame it as a string partitioning problem. Imagine the sequence of nodes in the trie, when read in co–lexicographic order, as a single long string. The "character" corresponding to each node is its Myhill–Nerode equivalence class, which determines if it can be merged with other nodes. The task is to partition this string of nodes into p substrings such that the number of runs is minimized (consecutive nodes of the same MN–equivalence class are merged into a single run). For instance, a subsequence $AAABBA$ contains three runs (see Example 1.1). Minimizing the number of runs directly corresponds to maximizing the number of merged states, yielding a compact p–sortable automaton.

In this section, we will provide the necessary background on the Minimum Weight Perfect Bipartite Matching (MWPBM) problem, a fundamental challenge in combinatorial optimization. We will then demonstrate in Section 3.3 a formal reduction from our partitioning problem to the MWPBM problem. This reduction is the key to our method, as it allows us to model our problem as a bipartite graph and leverage well-known efficient algorithms to find the optimal solution for our compression task.

2.6.2 Bipartite Graphs

Definition 29 (Bipartite graph). *A graph $G = (V, E)$ is called **bipartite** if its vertex set V can be partitioned into two disjoint subsets $V = V_1 \cup V_2$ such that every edge in E has the form (u_1, u_2) where $u_1 \in V_1$ and $u_2 \in V_2$.*

In other words, the vertices of the graph can be divided into two separate groups such that all edges connect a vertex from the first group to a vertex from the second group. An example of a bipartite graph is shown in Figure 2.11.

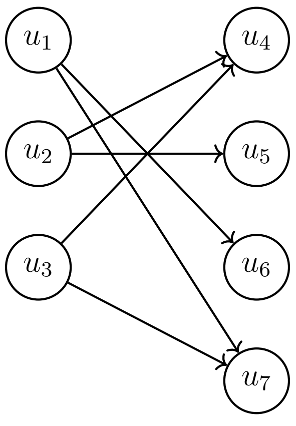


Figure 2.11: Example of a bipartite graph $G = (V, E)$ where $V_1 = \{u_1, u_2, u_3\}$, $V_2 = \{u_4, u_5, u_6, u_7\}$ and $E = \{(u_1, u_6), (u_1, u_7), (u_2, u_4), (u_2, u_5), (u_3, u_4), (u_3, u_7)\}$.

Definition 30 (Weighted bipartite graph)**.** *A* ***weighted bipartite graph*** *is a bipartite graph $G = (V, E, w)$, where w is a weight function $w : E \to \mathbb{R}$ that assigns a real-valued weight to each edge.*

In other words, in a weighted bipartite graph, each edge has a numerical value, called *weight*, associated with it.

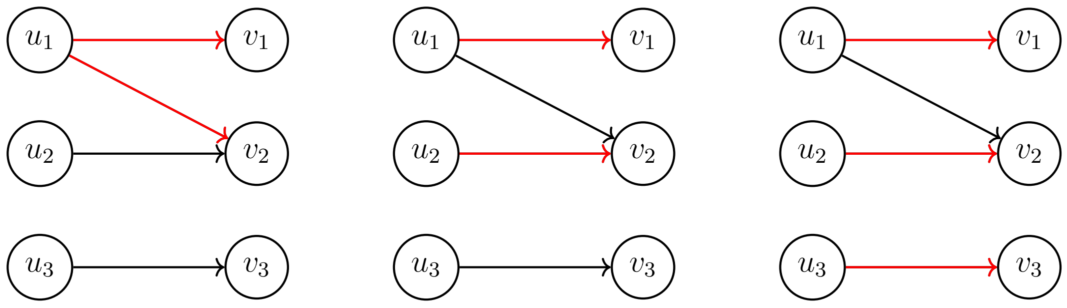
2.6.3 Problem Definition

Given a bipartite graph $G = (V, E)$, we define the concept of a matching as follows.

Definition 31 (Matching)**.** *Given a bipartite graph $G = (V, E)$, a* ***matching*** *$M \subseteq E$ is a collection of edges such that every vertex of V is incident to at most one edge of M.*

In other words, a matching is a set of edges such that no two edges share a common vertex. If a vertex v has no edge of M incident to it, then v is said to be **exposed** (or unmatched). A matching is **perfect** if no vertex is exposed; in other words, a matching is perfect if its cardinality is equal to $|V_1| = |V_2|$. We cite [16] as the source for the definitions and terminology used in this section.

Example 2.20:
In Figure 2.12, we illustrate three distinct scenarios. Subfigure (a) depicts a set of edges that does not constitute a valid matching, as vertex u_1 is incident to more than one edge, namely (u_1, v_1) and (u_1, v_2), violating the definition of a matching. Subfigure (b) presents a valid, yet non-perfect matching; here, vertices u_3 and v_3 are exposed, meaning they are not incident to any edge in the matching. Finally, subfigure (c) shows a perfect matching, where every vertex in the graph is incident to exactly one edge in the matching, satisfying the condition $|M| = |V_1| = |V_2| = 3$.



(a) Non-matching (b) Matching (c) Perfect matching

Figure 2.12: Examples of (a) a non-matching, (b) a non-perfect matching, and (c) a perfect matching in a bipartite graph. The edges in the set M are highlighted in red.

The problem of finding a minimum weight perfect matching in a weighted bipartite graph (Definition 30) is a well-known problem in combinatorial optimization. The problem can be formulated as follows:

Definition 32 (Minimum weight perfect matching in weighted bipartite graphs)**.** *Given a weighted bipartite graph $G = (V, E, w)$, find a perfect matching M such that the sum of the weights of the edges in M is minimized.*

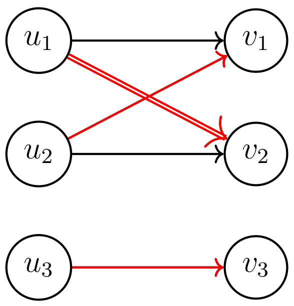
The weight of a matching is the sum of the weights of the edges in the matching. We define the weight of a matching M as follows:

$$w(M) = \sum_{e \in M} w(e) \tag{2.1}$$

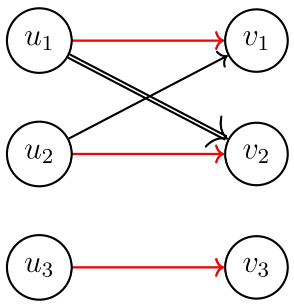
Example 2.21:
Consider the weighted bipartite graph in Figure 2.13, where single edges have weight 1 and double edges have weight 2. The goal is to find a perfect matching with the minimum possible total weight. Both subfigures show a valid perfect matching; however, only one of them has the minimum weight.

- Subfigure (a) shows the perfect matching $M_a = \{(u_1, v_2), (u_2, v_1), (u_3, v_3)\}$. Its total weight is $w(M_a) = w(u_1, v_2) + w(u_2, v_1) + w(u_3, v_3) = 2 + 1 + 1 = 4$. This is a valid perfect matching, but it is not optimal.
- Subfigure (b) shows the perfect matching $M_b = \{(u_1, v_1), (u_2, v_2), (u_3, v_3)\}$. Its total weight is $w(M_b) = w(u_1, v_1) + w(u_2, v_2) + w(u_3, v_3) = 1 + 1 + 1 = 3$.

Since $w(M_b) < w(M_a)$, the matching in (b) is a minimum weight perfect matching for this graph, while the matching in (a) is a non-minimum perfect matching.



(a) Non-min. weight perfect matching.



(b) Min. weight perfect matching.

Figure 2.13: Example of (a) a non-minimum weight perfect matching and (b) a minimum weight perfect matching in a bipartite graph. Double edges have weight 2, while single edges have weight 1. The edges in a matching are highlighted in red.

2.6.4 State of the Art

There are several algorithms to solve the problem of finding a minimum-weight perfect matching in a bipartite graph. The first algorithm to solve this problem was proposed by Kuhn in 1955 [23]. The algorithm is based on the Hungarian method, which is a combinatorial optimization algorithm that solves the MWPBM problem in polynomial time. In the original paper, the complexity of the algorithm was $O(n^4)$ where n is the number of nodes in the bipartite graph. Later Dinic and Kronrod [9] showed that the algorithm can be implemented in $O(n^3)$ time.

The Hungarian method is a powerful algorithm; however, it is not very intuitive and can be difficult to implement. In recent years, several other algorithms have been proposed to solve this problem. In 1970, Edmonds and Karp [10] proposed an algorithm that solves the problem in $O(nm + n^2 \log n)$ time, where m is the number of edges. In 1989, Gabow and Tarjan [13] proposed an algorithm that solves the problem in $O(\sqrt{n}m \log(nW))$ time, where W denotes the highest edge weight in the graph; costs are assumed to be integral. The algorithms work by scaling. Lastly, in 2009, Sankowski and Piotr [33] introduced a randomized algorithm that solves the problem in $O(Wn^{\omega})$ time, where ω is the exponent of matrix multiplication, and W is the highest edge weight in the graph.

In 2022, Chen, Li, et al. [5] proposed a nearly linear time algorithm for the Minimum Cost Flow (MCF) problem, running in $O(m'^{1+o(1)})$ on a network with m' edges. This is highly relevant as the MWPBM problem can be reduced to MCF. Specifically, an MWPBM instance on a bipartite graph with n vertices and m edges can be transformed into an MCF problem on a network with $m' = 2n + m$ edges.

Chapter 3

Trie Compression Scheme

As introduced in the first chapter, the primary goal of this thesis is to develop a novel trie compression scheme that effectively leverages repetitive structures within the input trie. The proposed algorithm is designed to identify and compactly represent these recurring patterns, thereby improving compression performance, particularly for highly repetitive tries. This chapter provides an overview of the proposed compression scheme.

3.1 Compression Scheme Pipeline

The overall pipeline of our proposed method is outlined in Algorithm 9. It takes an input trie T and a width parameter p and produces a compressed, p–sortable automaton.

Algorithm 9 COMPRESSTRIE(T, p)

```
Require: Input trie $T$, width integer parameter $p$
Ensure: A compressed, $p$–sortable automaton $\mathcal{A}$
1: $V_{sorted} = \textsc{PathSort}(T)$
2: $N[1, \ldots, |Q|] = \text{RevuzMinimization}(T)$
3: $G_{bipartite} = \text{ConstructMWPBMInstance}(V_{sorted}, N, p)$
4: $M = \text{SolveMWPBM}(G_{bipartite})$
5: $C[1, \ldots, p] = \text{ExtractChainsFromMatching}(M, V_{sorted})$
6: $\mathcal{A} = \text{CollapseChains}(C, N)$
7: return $\mathcal{A}$
```

The first step of the pipeline (line 2) establishes a total order on the nodes of the trie. This is achieved by sorting the nodes co–lexicographically using the **Path Sort** algorithm, which we described in Algorithm 2. This sorting is fundamental, as it arranges the nodes in the order required for a Wheeler automaton.

Next, the algorithm identifies which nodes are candidates for merging (line 3). This is done by partitioning the nodes into equivalence classes based on the structure of the subtrees rooted at each node. Two nodes are in the same class if and only if their subtrees are isomorphic. This is equivalent to computing the Myhill–Nerode equivalence classes for the finite language accepted by the trie, a process we adapt from Revuz's algorithm for minimizing acyclic DFAs (Algorithm 1).

The core of the algorithm lies in lines 4 and 5, where we solve the **String Partitioning Problem**. The input to this problem is the string formed by concatenating the Myhill–Nerode classes of the sorted nodes. As detailed in Section 3.3, we reduce this problem to finding a Minimum Weight Perfect Bipartite Matching (MWPBM). A bipartite graph is constructed where the weight of each edge corresponds to the cost of placing two characters adjacent in a subsequence. By finding a perfect matching with minimum weight using standard algorithms (Subsection 2.6.4), we can reconstruct a partition of the string into p subsequences that minimizes the total number of runs, thereby maximizing compression.

Finally, the DAG compressed automaton is constructed (line 6). The algorithm iterates through each of the p subsequences and "collapses" any consecutive sequence of nodes belonging to the same Myhill–Nerode equivalence class into a single state. This compression, which we describe in Section 3.2, produces the final p–sortable automaton, which can then be indexed for efficient querying (Subsection 2.5.5).

Example 3.1: Compression pipeline

In our running example, we begin with the trie shown in Figure 3.1. Each node in this trie is labeled with its corresponding Myhill–Nerode equivalence class, as determined in Example 2.3. By traversing the nodes in co–lexicographic order, we construct a string S where each character represents the Myhill–Nerode equivalence class of a node:

$$S = \text{ABCDDCBDDDD}$$

This string S then becomes the input to the String Partitioning Problem (see Definition 4), where the objective is to partition S into p subsequences while minimizing the total number of runs.

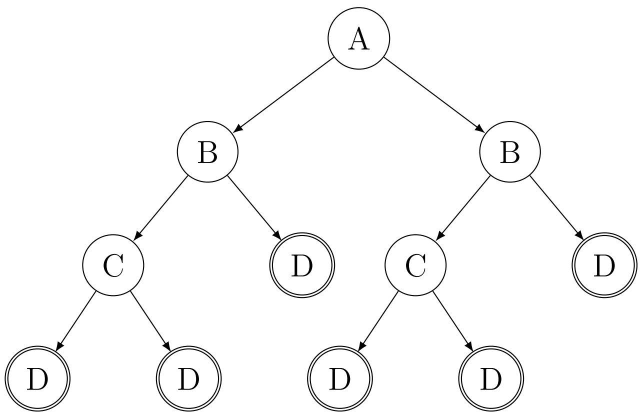


Figure 3.1: ADFA of Figure 2.2, with each node labeled with its equivalence class.

Given $p = 2$, one way to partition the string is $C = [\text{ABCDCBD}, \text{DDDD}]$, which is clearly suboptimal as the total number of runs is $runs(C) = 7 + 1 = 8$. An optimal solution would be $C' = [\text{ABCCB}, \text{DDDDDD}]$, since $runs(C') = 4 + 1 = 5$ is the minimum number of runs for the partition of S into two chains.

3.2 Collapsing Nodes in Chains

This chapter introduces our **node collapsing** technique, designed to reduce the size of the trie by collapsing runs of Myhill–Nerode-Equivalent states adjacent in the same chain. The String Partitioning Problem provides us with a set of subsequences whose characters correspond to the nodes of the original trie; we call them chains. Within these chains, we often find consecutive nodes that are redundant from a language-theoretic perspective, specifically because they belong to the same Myhill–Nerode equivalence class.

The core idea is to merge any such sequence of consecutive, equivalent nodes into a single representative node. This operation reduces the graph structure while preserving its language. The new representative node inherits all unique incoming and outgoing transitions from the nodes it replaces, ensuring that the overall language accepted by the graph remains unchanged.

In this section, we will formally define the collapsing procedure and then rigorously prove that this transformation is language-preserving (Lemma 2), guaranteeing the correctness of our compression scheme.

Algorithm 10 COLLAPSE(N, u, v)

```
Require: $N = (Q, \Sigma, \delta, q_0, F)$ is an NFA; $u, v \in Q$ and are MN–equivalent.
Ensure: A collapsed automaton $N' = (Q', \Sigma, \delta', q_0', F')$
1: Create a new state $w$
2: $Q' = (Q \setminus \{u, v\}) \cup \{w\}$
3: $\phi(z) = w$ if $z \in \{u, v\}$ else $z$
4: $\delta' = \{(\phi(q), a, \phi(r)) \mid (q, a, r) \in \delta\}$
5: $q_0' = \phi(q_0)$
6: $F' = \{\phi(f) \mid f \in F\}$
```

The COLLAPSE procedure forms the core of our compression strategy. By recursively applying this operation to all consecutive MN–equivalent nodes in each chain, we merge redundant states. The restriction to merge only consecutive states is critical: merging non-consecutive states, even if they share the same MN–class, would violate the total order of the chains, a property that must be preserved for the construction of the p–sortable automaton (Definition 28) to be valid. This process transforms the initial trie into a compact p–sortable automaton. Such an automaton can result in an NFA, as the COLLAPSE operation may introduce non-determinism. For example, if two states u and v are merged into a new state w, and there exist transitions (u, a, s) and (v, a, t) and $s \neq t$ after the collapsing procedure, the resulting state w will have two distinct transitions for the same label a, which is a feature of NFAs.

Example 3.2:
Assume that we extract the chains C_1 = ACCB and C_2 = BDDDDDD from the trie in Figure 2.2 by applying the reduction from String Partitioning to MWPBM. The nodes inside each chain are the following:

- $C_1 = \{a, d, f, c\}$
- $C_2 = \{b, h, l, e, i, m, g\}$

Applying Algorithm 10 we obtain:

- For $C_1 = (a, d, f, c)$ with classes (A, C, C, B):
  - Block $B_1 = \{a\}$ (class A) $\rightarrow$ collapsed node v_1. The node a is the initial state. It has two outgoing edges: $a \xrightarrow{0} b$ and $a \xrightarrow{1} c$. Since b and c collapse to w_1 and v_3 respectively, we obtain $v_1 \xrightarrow{0} w_1$ and $v_1 \xrightarrow{1} v_3$.
  - Block $B_2 = \{d, f\}$ (class C) $\rightarrow$ collapsed node v_2. The outgoing edges of d and f are:

    $$d \xrightarrow{0} h,\ d \xrightarrow{1} i, \qquad f \xrightarrow{0} l,\ f \xrightarrow{1} m.$$

    After collapsing, we obtain:

    $$v_2 \xrightarrow{0} w_2, v_2 \xrightarrow{1} w_2, \qquad v_2 \xrightarrow{0} w_2, v_2 \xrightarrow{1} w_2.$$

    Since we have two identical edges we can keep only one of each.
  - Block $B_3 = \{c\}$ (class B) $\rightarrow$ collapsed node v_3. It has two outgoing edges: $c \xrightarrow{0} f$ and $c \xrightarrow{1} g$. Since f and g collapse to v_2 and w_2 respectively, we obtain $v_3 \xrightarrow{0} v_2$ and $v_3 \xrightarrow{1} w_2$.

  Result: $C_1' = (v_1, v_2, v_3)$ with classes (A, C, B). Here, v_1 is the initial state.
- For $C_2 = (b, h, l, e, i, m, g)$ with classes (B, D, D, D, D, D, D):
  - Block $B_1 = \{b\}$ (class B) $\rightarrow$ collapsed node w_1. It has two outgoing edges: $b \xrightarrow{0} d$ and $b \xrightarrow{1} e$. As d, e collapse to v_2 and w_2 respectively, we obtain $w_1 \xrightarrow{0} v_2$ and $w_1 \xrightarrow{1} w_2$.
  - Block $B_2 = \{h, l, e, i, m, g\}$ (all class D) $\rightarrow$ collapsed node w_2. The node w_2 collects all incoming edges formerly targeting any of b, h, l, e, i, m, g, and it is accepting.

  Result: $C_2' = (w_1, w_2)$ with classes (B, D), and w_2 is the unique accepting state for this example.

The collapsed chains preserve all distinct outgoing and incoming edges through the collapse map Φ, significantly reducing the space complexity from 11 nodes to 5 nodes total. The resulting 2–sortable automaton is shown in Figure 3.2.

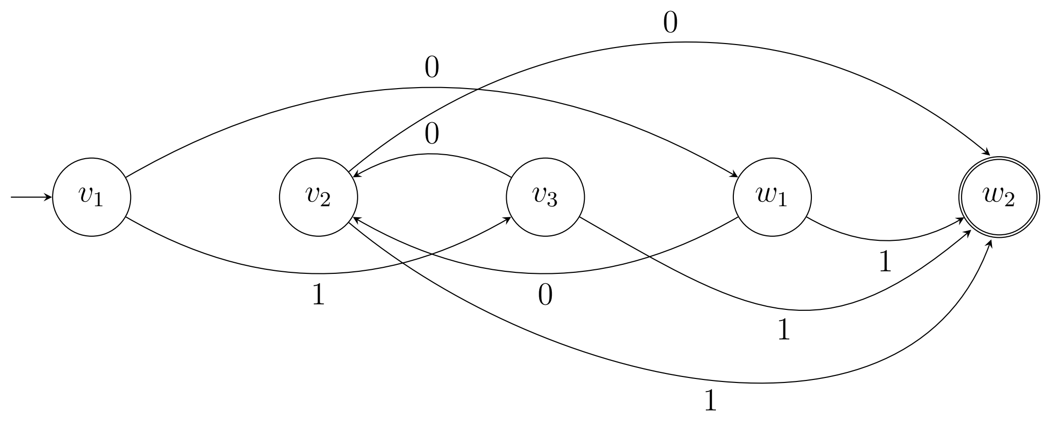


Figure 3.2: 2–sortable automaton obtained after collapsing consecutive MN–equivalent nodes in chains C_1 and C_2 from Example 3.7.

We now need to prove that the language recognized by an automaton obtained after collapsing two MN–equivalent nodes following Algorithm 10 is equivalent to the language of the original automaton.

Lemma 2. *Let $N = (Q, \Sigma, \delta, q_0, F)$ be an automaton recognizing $L \subseteq \Sigma^*$. If two states $l, q \in Q$ correspond to the same Myhill–Nerode class for L (Theorem 1), then merging l and q into a single state yields an automaton (possibly nondeterministic) that still recognizes exactly L.*

Proof. By the Myhill–Nerode theorem (Theorem 1), every state of M corresponds to a unique Myhill–Nerode equivalence class, and L is exactly the union of those classes that intersect L. If l and q belong to the same equivalence class, then for every continuation $z \in \Sigma^*$ we have

$$\delta(l, z) \in F \iff \delta(q, z) \in F.$$

Thus, replacing l with q (or vice versa) in any path does not affect whether the run ends in an accepting state. Therefore, merging l and q does not alter the set of accepted strings, i.e. the recognized language remains L. □

Collapsing two MN–equivalent nodes as in Algorithm 10 preserves the language of the original automaton, and the resulting chains inherit a total order. This directly implies that the obtained NFA is p–sortable and enables the application of the NFA indexing scheme of Cotumaccio et al. [7].

3.3 Reducing the String Partitioning Problem to the MWPBM Problem

In the previous chapters, we modeled the task of partitioning trie nodes into p chains as the String Partitioning Problem (see Definition 4). We now demonstrate that this problem can be solved in polynomial time by reducing it to the MWPBM problem. This section will first detail the construction of a bipartite graph from an instance of the String Partitioning Problem. Then, we will prove that a minimum-weight perfect matching in this graph directly corresponds to an optimal solution for the partitioning problem. Let's start with an example.

Example 3.3: String Partitioning Problem
Let S = AABACABB be the input string and let $p = 2$ be the desired number of subsequences. Our goal is to partition the characters of S into two subsequences, S_1 and S_2, such that the total number of runs (Definition 1) is minimized.

Consider the following partition:

- S_1 is formed by taking the 1st, 2nd, 4th, and 6th characters of S: AAAA.
- S_2 is formed by the remaining characters (3rd, 5th, 7th, and 8th): BCBB.

The number of runs for each subsequence is:

- Runs(S_1) = 1 (the run is "AAAA").
- Runs(S_2) = 3 (the runs are "B", "C", "BB").

The total number of runs for this partition is $1 + 3 = 4$. An optimal solution to the String Partitioning Problem would be a partition that achieves the minimum possible total number of runs. In this case, 4 is indeed the optimal value.

3.3.1 Bipartite Graph Construction

Now, we will show how to construct a bipartite graph that allows us to solve the String Partitioning problem.

Definition 33 (Bipartite graph construction)**.** *Let S be a string of size n from an alphabet Σ and let p be the number of subsequences we want to partition S into. We can construct a weighted bipartite graph $G = (V, E, w)$ such that vertices are divided in two disjoint sets $V = V_1 \cup V_2$ in the following way:*

- *V_1 contains $n + p$ nodes composed of p source nodes $s_1, s_2, \ldots, s_p$ (referred to collectively as $\mathcal{S}$) followed by n character nodes $a_1, a_2, \ldots, a_n$ (referred to collectively as $\mathcal{T}_1$).*
- *V_2 contains $n + p$ nodes composed of n character nodes $b_1, b_2, \ldots, b_n$ (referred to collectively as $\mathcal{T}_2$) followed by p destination nodes $d_1, d_2, \ldots, d_p$ (referred to collectively as $\mathcal{D}$).*

Then the edges of the graph G are constructed in the following way:

- ***Source Edges:*** *For each source node $s \in \mathcal{S}$ and each node $v_j \in \mathcal{T}_2$, an edge (s, v_j) is created with weight $w(s, v_j) = 1$.*
- ***Internal Edges:*** *For each pair of indices i, j such that $1 \le i < j \le n$, an edge is created between $u_i \in \mathcal{T}_1$ and $v_j \in \mathcal{T}_2$. The weight of this edge, $w(u_i, v_j)$, is 0 if the characters $S[i]$ and $S[j]$ are the same, and 1 otherwise. Formally:*

$$w(u_i, v_j) = \begin{cases} 0 & \textit{if } S[i] = S[j] \\ 1 & \textit{if } S[i] \neq S[j] \end{cases}$$

- ***Destination Edges:*** *For each node $u_i \in \mathcal{T}_1$ and each destination node $d \in \mathcal{D}$, an edge (u_i, d) is created with weight $w(u_i, d) = 1$.*

Example 3.4: Vertices

Let's apply the reduction to the string $S = \text{ABCDDCBDDDD}$ from our running example (Example 3.1), with a target of $p = 2$ subsequences. Following the construction rules, we build a bipartite graph. The vertices of this graph are structured as shown in Figure 3.3.

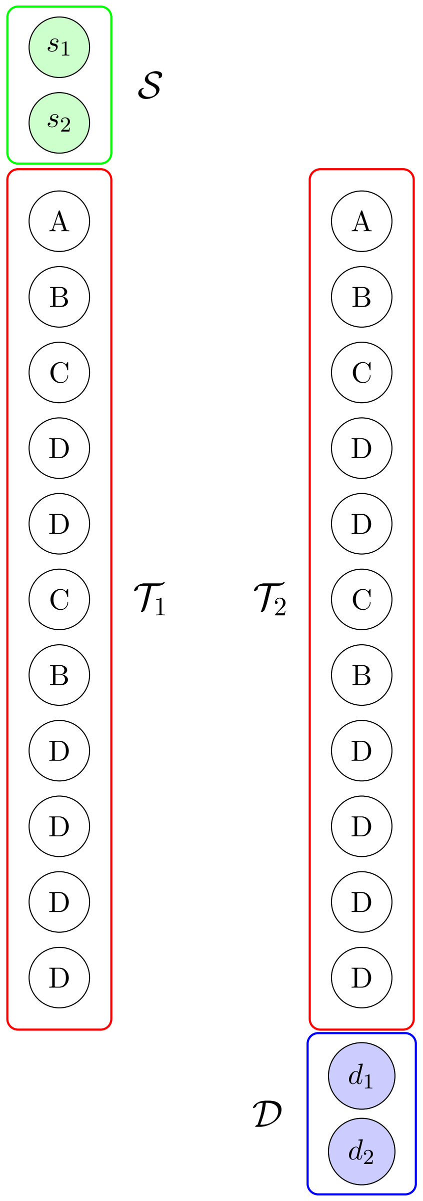


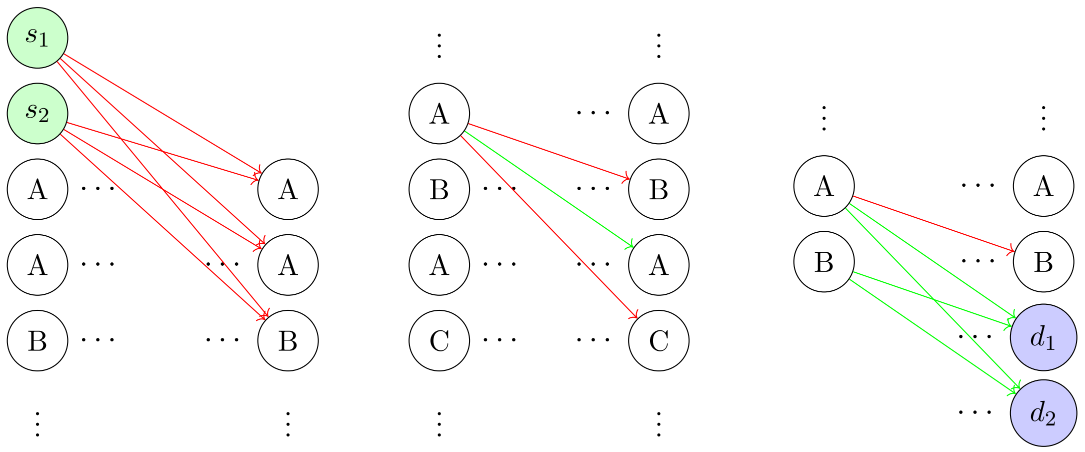
Figure 3.3: Bipartite graph vertices structure for string $S = \text{ABCDDCBDDDD}$ with $p = 2$. The nodes are ordered from top to bottom.

Example 3.5: Edges

Let us see a small example for each case of Definition 33. Consider $p = 2$. In Figure 3.4-(a), there is an example for the sources' edges. As stated before, each source is connected with weight 1 to all nodes in $\mathcal{T}_2$.

In Figure 3.4-(b), we illustrate the edges from $\mathcal{T}_1$ to $\mathcal{T}_2$. These edges model the cost of appending a character to a subsequence. An edge from u_i to v_j (for $j > i$) has weight 1 if $S[i] \neq S[j]$ (starting a new run) and weight 0 if $S[i] = S[j]$ (extending an existing run). For instance, the node for the first 'A' connects to the nodes for 'B' and 'C' with weight 1, and to the node for 'A' with weight 0.

Lastly, Figure 3.4-(c) shows the destination edges. These edges terminate a subsequence. An edge from any node $u_i \in \mathcal{T}_1$ to any destination node $d_k \in \mathcal{D}$ has weights 0, ensuring that ending a chain does not increase the run count. For example, if the node for 'B' is the last element of a subsequence, it is matched with a destination node, and this edge (u_B, d_k) contributes 0 to the total weight.



(a) (b) (c)

Figure 3.4: Examples of the connection construction in the bipartite graph for $p = 2$, showing the cases for source nodes $\mathcal{S}$ (a), internal nodes $\mathcal{T}_1$ and $\mathcal{T}_2$ (b), and destination nodes $\mathcal{D}$ (c). Red arrows indicate edges with weight 1, while green arrows indicate edges with weight 0.

We now state the following theorem regarding the number of edges in the bipartite graph resulting from Definition 33. This theorem is essential for understanding the complexity of the final algorithm employed to solve the MWPBM problem and, thus, the String Partitioning problem.

Lemma 3 (Bipartite graph properties). *The bipartite graph G constructed as stated in Definition 33 has $2n + 2p$ nodes and $2np + \frac{n(n-1)}{2}$ edges.*

Proof. The total number of edges in the graph G is the sum of the edges from the three categories defined in the construction:

- **Source Edges:** There are p source nodes in $\mathcal{S}$ and n nodes in $\mathcal{T}_2$. Each source node connects to every node in $\mathcal{T}_2$, resulting in $p \times n = np$ edges.
- **Destination Edges:** There are n nodes in $\mathcal{T}_1$ and p destination nodes in $\mathcal{D}$. Each node in $\mathcal{T}_1$ connects to every node in $\mathcal{D}$, resulting in $n \times p = np$ edges.
- **Internal Edges:** For each node $u_i \in \mathcal{T}_1$, edges are created to all nodes $v_j \in \mathcal{T}_2$ where $j > i$. The number of such edges is $\sum_{i=1}^{n-1} i = \frac{n(n-1)}{2}$.

Summing these up, the total number of edges is $2np + \frac{n(n-1)}{2}$. □

3.3.2 Proof

In this section, we will prove that a minimum-weight perfect matching in a bipartite graph constructed as stated in Definition 33 directly corresponds to an optimal solution for the String Partitioning problem defined as follows. We recall the following definitions from the intro.

Definition 1 (Run)**.** *Let $S = s_1 s_2 \dots s_n$ be a string over an alphabet Σ. A substring $S[i \dots j] = s_i s_{i+1} \dots s_j$ (where $1 \le i \le j \le n$) is a run if it satisfies the following conditions:*

1. ***Homogeneity:*** *All characters in the substring are identical, i.e., $s_k = s_i$ for all k such that $i \le k \le j$.*
2. ***Maximality:*** *The substring cannot be extended to the left or right without violating homogeneity. That is:*
   - *If $i > 1$, then $s_{i-1} \neq s_i$.*
   - *If $j < n$, then $s_{j+1} \neq s_j$.*

Definition 3. *Let $\tau(S)$ be the number of runs in a string S, i.e., $\tau(S) = 1 + |\{i \in [n-1] : S[i] \neq S[i+1]\}|$.*

Definition 4 (String Partitioning Problem)**.** *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning Problem where S is a string of length n over an alphabet Σ, and p is a positive integer. The output of the problem is a partition $\mathcal{P} = I_1, \dots, I_p$ of $[n]$ such that $\gamma(\mathcal{P}) = \sum_{i=1}^{p} \tau(S[I_i])$ is minimized.*

We introduce the following notation:

Definition 34. *Let $r : \mathcal{I}_{StringPartitioning} \to \mathcal{M}_{MWPBM}$ be the reduction function that maps an instance $(S, p) \in \mathcal{I}_{StringPartitioning}$ to an instance $G \in \mathcal{M}_{MWPBM}$, i.e., G is the bipartite graph constructed as stated in Definition 33.*

Lemma 4. *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning Problem. Any partition $\mathcal{P} = I_1, \dots, I_p$ of $[n]$ induces a perfect matching $M(\mathcal{P})$ in the bipartite graph $G = r(\mathcal{I})$.*

Proof. Let $\mathcal{P} = I_1, \dots, I_p$ be a partition. Write I_q as $I_q = \{i_1, i_2, \dots, i_k\}$ such that $i_1 < i_2 < \dots < i_k$, then define

$$M(I_q) := \{(s_q, b_{i_1}), (a_{i_k}, d_q)\} \cup \{a_{i_j}, b_{i_{j+1}} : j \in [k-1]\}$$

and

$$M(\mathcal{P}) := \bigcup_{i=1}^{p} M(I_i).$$

To see that $M(\mathcal{P})$ is a perfect matching, observe that every node in G is covered exactly once. For each $q \in [p]$, the source s_q and destination d_q are used once in $M(I_q)$ and are not part of any other $M(I_z)$ for $z \neq q$. Furthermore, as $\mathcal{P}$ is a partition of $[n]$, every index $j \in [n]$ belongs to exactly one set I_q. The definition of $M(I_q)$ creates a chain of edges for the indices in I_q, covering each corresponding node a_j and b_j exactly once within that chain. Thus, every node in G is included in precisely one edge of $M(\mathcal{P})$. □

Lemma 5. *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning Problem. Every perfect matching M on $G = r(\mathcal{I})$ induces a partition $\mathcal{P}(M)$ of $[n]$.*

Proof. Let M be a perfect matching on G. For a node u in the bipartite graph, we let $M(u)$ be the node matched to u in M. The matching M naturally defines p sets $I_q = \{i_1, \ldots, i_k\}$ for $q \in [p]$, such that $i_1 < i_2 < \cdots < i_k$, that can be inductively defined as follows: i_1 is such that $b_{i_1} = M(s_i)$, i_2 is such that $b_{i_2} = M(a_{i_1})$, …, i_k is such that $t_i = M(a_{i_k})$. It remains to show that $I_1, \ldots, I_p$ form a partition of S.

Assume that an index $j \in [n]$ does not appear in any set I_q. By the construction of our bipartite graph, the node b_j corresponds to position j in the string. If j is not included in any partition, then b_j cannot be matched to any node in V_1, contradicting the requirement that M is a perfect matching.

Moreover, assume that an index $j \in [n]$ appears in two distinct sets I_i and I_z where $i \neq z$, and assume also that j is the smallest index with that property. Let $I_i = \{i_1, \ldots, i_k\}$ with $i_1 < \cdots < i_k$ and $I_z = \{i'_1, \ldots, i'_{k'}\}$ with $i'_1 < \cdots < i'_{k'}$ and assume that $j = i_l = i'_s$. There are three cases:

1. if $l = s = 1$, it follows that b_j is matched to s_i and s_z, a contradiction to M being a perfect matching.
2. if one of the two is 1 and the other one not, assume without loss of generality $l = 1$ and $s \neq 1$ then b_j is matched to s_z and $a_{i'_{s-1}}$, a contradiction to M being a perfect matching.
3. Both $l \neq 1$ and $s \neq 1$, then by the minimality of j we have $a_{i_{l-1}} \neq a_{i'_{s-1}}$ and thus b_j is matched to two distinct nodes, again a contradiction to M being a perfect matching.

Hence, as M is a perfect matching, each index $j \in [n]$ must appear in exactly one set I_i, ensuring that the sets $\{I_1, I_2, \ldots, I_p\}$ form a partition of $[n]$. □

Lemma 6. *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning Problem. Let moreover M be a perfect matching on $G = r(\mathcal{I})$. Then $W(M) = \gamma(\mathcal{P}(M))$. Conversely, let $\mathcal{P}$ be a partition of S, then $\gamma(\mathcal{P}) = W(M(\mathcal{P}))$.*

Proof. The weight $W(M)$ is the sum of the weights of all edges in the matching. By construction of the bipartite graph:

- Each source node s_i contributes weight 1 to connect to the first element of I_i,
- Each edge (a_j, b_k) with $j < k$ contributes weight 0 if $S[j] = S[k]$, or weight 1 if $S[j] \neq S[k]$,
- Each edge to destination node d_i contributes weight 0.

Now, let M be a perfect matching on G. By Lemma 5, M induces a partition $\mathcal{P}(M) = \{I_1, \ldots, I_p\}$ of $[n]$ as the matching M naturally defines p sets $I_q = \{i_1, \ldots, i_k\}$ such that $i_1 < i_2 < \cdots < i_k$, that were inductively defined as: i_1 was such that $b_{i_1} = M(s_i)$, i_2 was such that $b_{i_2} = M(a_{i_1})$, $\ldots$, i_k was such that $t_i = M(a_{i_k})$. Thus, the following equation holds:

$$\begin{aligned} W(M) &= p + |\{(a_j, b_k) \in M : S[j] \neq S[k]\}| \\ &= p + \sum_{i=1}^{p} |\{j \in [|I_i| - 1] : (S[I_i])[j] \neq (S[I_i])[j+1]\}| \end{aligned}$$

Where the first equality holds because the total weight $W(M)$ is the sum of weights from the p source edges (each with weight 1) and the internal edges with weight 1. The second equality rewrites this count by summing the run boundaries for each partition set I_i. By distributing the constant p into the summation, we get:

$$\begin{aligned} W(M) &= \sum_{i=1}^{p} \Big(1 + |\{j \in [|I_i| - 1] : (S[I_i])[j] \neq (S[I_i])[j+1]\}|\Big) \\ &= \sum_{i=1}^{p} \tau(S[I_i]) \\ &= \gamma(\mathcal{P}(M)) \end{aligned}$$

We used the definition of $\tau(S[I_i])$ as the number of runs (1 plus the number of character changes). The final equality is by the definition of $\gamma(\mathcal{P}(M))$.

Conversely, let $\mathcal{P} = \{I_1, \ldots, I_p\}$ be a partition of S. By Lemma 4, $\mathcal{P}$ induces a perfect matching $M(\mathcal{P}) = \bigcup_{q=1}^{p} M(I_q)$. Since the edge sets $M(I_q)$ are disjoint, the total weight of the matching is the sum of the weights of each part, i.e., $W(M(\mathcal{P})) = \sum_{q=1}^{p} W(M(I_q))$.

Let's analyze the weight of a single component $M(I_q)$ for a set $I_q = \{i_1, \ldots, i_k\}$ with $i_1 < \cdots < i_k$. The edges in $M(I_q)$ are (s_q, b_{i_1}), (a_{i_k}, d_q), and $(a_{i_j}, b_{i_{j+1}})$ for $j \in [k-1]$. According to the weight definitions, $w(s_q, b_{i_1}) = 1$, $w(a_{i_k}, d_q) = 0$, and $w(a_{i_j}, b_{i_{j+1}})$ is 1 if $S[i_j] \neq S[i_{j+1}]$ and 0 otherwise. The weight of $M(I_q)$ is therefore:

$$\begin{aligned} W(M(I_q)) &= w(s_q, b_{i_1}) + \sum_{j=1}^{k-1} w(a_{i_j}, b_{i_{j+1}}) + w(a_{i_k}, d_q) \\ &= 1 + |\{j \in [k-1] : S[i_j] \neq S[i_{j+1}]\}| \\ &= \tau(S[I_q]) \end{aligned}$$

Summing over all sets in the partition, we directly equate the matching weight to the partition cost:

$$W(M(\mathcal{P})) = \sum_{q=1}^{p} W(M(I_q)) = \sum_{q=1}^{p} \tau(S[I_q]) = \gamma(\mathcal{P})$$

This confirms that the weight of the induced matching is equal to the cost of the partition. □

Theorem 5. *Let $\mathcal{I} = (S, p)$ be an instance of the String Partitioning problem. An optimal solution of $r(\mathcal{I})$ can be used to compute an optimal solution of $\mathcal{I}$.*

Proof. By the previous lemmas, we have established a bijective correspondence between partitions of S and perfect matchings in the bipartite graph G constructed by $r(\mathcal{I})$:

- Any partition $\mathcal{P}$ of S induces a perfect matching $M(\mathcal{P})$ in G (Lemma 4).
- Any perfect matching M in G induces a partition $\mathcal{P}(M)$ of S (Lemma 5).
- The weight equivalence holds: $W(M) = \gamma(\mathcal{P}(M))$ and $\gamma(\mathcal{P}) = W(M(\mathcal{P}))$ (Lemma 6).

Therefore, finding a minimum weight perfect matching M in G is equivalent to finding an optimal partition $\mathcal{P}$ for the String Partitioning Problem. □

In the following example, we show how a perfect matching can be used to retrieve a partition.

Example 3.6:
Consider the example in Figure 3.5, which shows a perfect matching for the instance $r(\mathcal{I})$ with $\mathcal{I} = (S = \text{AAB}, p = 2)$. The solid arrows represent the edges of the matching M. The dashed arrows are a visual aid showing the correspondence between a character's representation in $\mathcal{T}_2$ (on the right) and its representation in $\mathcal{T}_1$ (on the left), which is essential for tracing the paths.

We extract two substrings:

- **Substring 1 (red):**
  1. Start at source s_1. The matching edge is (s_1, v_1), where v_1 corresponds to the first character, $S[1] = \text{A}$. The subsequence is now "A".
  2. Following the conceptual link to u_1, we find the matching edge (u_1, v_2), where v_2 corresponds to the second character, $S[2] = \text{A}$. The subsequence is now "AA".
  3. Following the link to u_2, we find the matching edge (u_2, d_1). Since d_1 is a destination node, the path terminates.
  4. The final subsequence is $S_1 = \text{AA}$.
- **Substring 2 (blue):**
  1. Start at source s_2. The matching edge is (s_2, v_3), where v_3 corresponds to the third character, $S[3] = \text{B}$. The subsequence is "B".
  2. Following the link to u_3, we find the matching edge (u_3, d_2). Since d_2 is a destination, the path terminates.
  3. The final subsequence is $S_2 = \text{B}$.

This example illustrates how the procedure correctly reconstructs the two substrings from the perfect matching, yielding the partition $\Pi = \{S_1, S_2\}$.

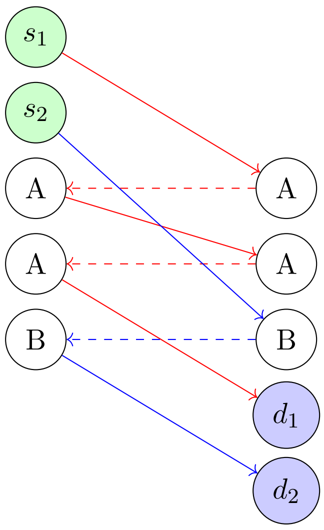


Figure 3.5: An example of a perfect matching (solid lines) in the constructed bipartite graph. The matching defines a partition into two paths (red and blue), which are traced by following the solid and dashed arrows.

Example 3.7:
Let's apply the reduction to the string $S = \text{ABCDDCBDDDD}$ from our running example (Example 3.1), with a target of $p = 2$ subsequences. In Figure 3.6 we have one of the possible minimum perfect matchings for the instance having weight 5.

We can trace the two paths from the source nodes to the destination nodes to obtain the following optimal partition:

- **Subsequence 1:** The path starting from s_1 traces the characters corresponding to indices in the set $I_1 = \{1, 3, 6, 7\}$, yielding the subsequence $S[I_1] = \text{ACCB}$. The number of runs is $\text{runs}(S[I_1]) = 3$.
- **Subsequence 2:** The path starting from s_2 traces the characters for indices in the set $I_2 = \{2, 4, 5, 8, 9, 10, 11\}$, yielding the subsequence $S[I_2] = \text{BDDDDDD}$. The number of runs is $\text{runs}(S[I_2]) = 2$.

The total cost of this partition is the sum of the runs, $3 + 2 = 5$, which matches the weight of the perfect matching. This demonstrates how the reduction finds an optimal solution for the String Partitioning Problem.

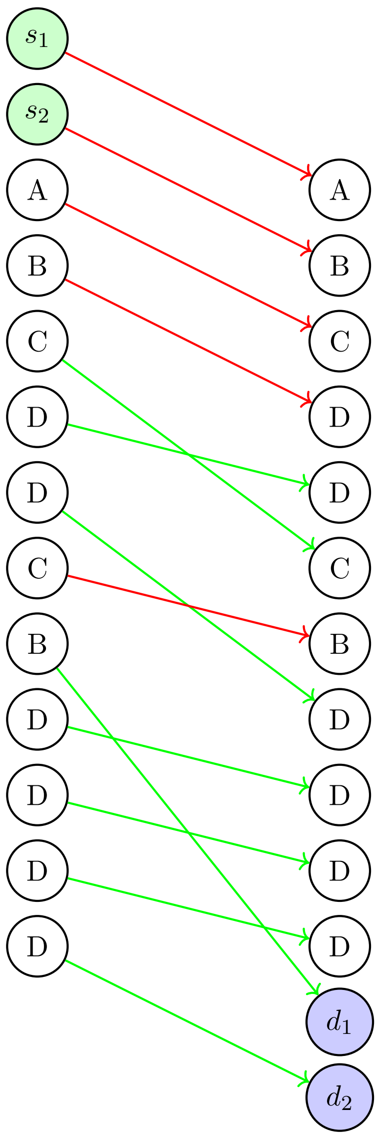


Figure 3.6: Example of an optimal perfect matching for the graph G of the MWPBM instance $r((S = ABCDDCBDDDD, p = 2))$. Green edges weigh 0, while red edges weigh 1.

3.3.3 Future Improvements

The reduction proposed in this thesis allows us to find an optimal solution for the String Partitioning Problem. However, it requires the construction of a graph with $O(n^2)$ edges, where n is the length of the input string. This is a significant drawback, as it makes the pipeline unfeasible for real-world datasets.

A more efficient bipartite graph construction is currently under study. The goal is to reduce the number of edges in the graph to $O(np)$, while maintaining the same optimal solution cost as the reduction with $O(n^2)$ edges.

To improve the efficiency of the reduction, we are studying a more sparse construction for the bipartite graph, replacing the dense connection of each node $u_i \in \mathcal{T}_1$ to every node $v_j \in \mathcal{T}_2$ (where $j > i$). Consider an instance $\mathcal{I} = (S, p)$ of the String Partitioning problem. In the refined weighted bipartite graph $G = (V_1 \cup V_2, E, w)$ of $r(\mathcal{I})$, for each node $u_i \in V_1$, we define the edge set as follows:

1. **Zero-weight edge:** If there exists $j \in \{i+1, i+2, \dots, n\}$ such that $S[i] = S[j]$, then we add edge $(u_i, v_{j'})$ with weight 0, where

$$j' = \min\{j \in \{i+1, i+2, \dots, n\} : S[i] = S[j]\}$$

2. **Unit-weight edges:** Let $\mathcal{C}_i = \{c \in \Sigma : c \neq S[i]\}$ be the set of characters distinct from $S[i]$. For each character $c \in \mathcal{C}_i$, define

$$j_c = \min\{j \in \{i+1, i+2, \dots, n\} : S[j] = c\}$$

   if such j exists. Then we add edges (u_i, v_{j_c}) with weight 1 for the first p distinct characters in $\mathcal{C}_i$.

This leads to a graph with $O(np)$ edges, where n is the size of S. It can be shown that such a graph preserves the optimal solutions of the original reduction.

Example 3.8:
Consider the example in Figure 3.7, where $p = 2$. The first node labeled A in V_1 is connected to the first node labeled A in V_2 with weight 0. Also, it is connected only to the first p distinct nodes in V_2 with weight 1.

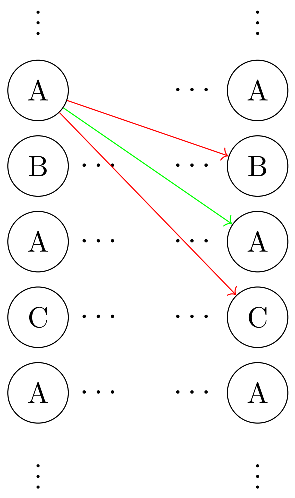


Figure 3.7

Chapter 4

Implementation and Experiments

4.1 Experimental Setup

All experiments were conducted on a consistent hardware and software platform to ensure fair and reproducible comparisons. This section details the environment and datasets used in our evaluation.

4.1.1 Hardware

The experimental platform is a MacBook Pro equipped with an Apple M4 Pro processor and 24 GB of RAM, running macOS.

4.1.2 Datasets

To systematically evaluate performance under controlled conditions, particularly with respect to repetitiveness, we generated a suite of synthetic labeled tries. Real-world datasets often lack ground-truth information about their repetitive structures, making it difficult to isolate the effects of this property. Our synthetic generation approach allows us to create tries with tunable characteristics.

The tries were generated using a custom Python script that constructs a trie and introduces repetitiveness by randomly copying subtries to different locations. At each step of the trie's growth, with a certain probability, a random existing subtrie is selected and duplicated as a new branch. This "copy-paste" mechanism allows us to create complex, highly repetitive structures that mimic patterns found in real-world data.

The generation process was controlled by the following key parameters:

Max Branching Factor The maximum number of children for any node.

Repetition Probability The probability of copying an existing subtrie instead of creating a new random branch.

Subtrie Depth Range The minimum and maximum depth of subtries eligible for copying.

Max Nodes The target maximum number of nodes in the generated trie.

Alphabet Size The number of unique characters in the alphabet.

Seed The seed used for random number generation to ensure reproducibility.

By varying these parameters, we can produce a diverse range of tries to thoroughly test the limits and behaviors of each compression algorithm.

4.2 XBWT Implementation and Experiments

Before presenting the implementation and the experiments related to our proposed trie compression scheme, it is necessary to detail our implementation of the XBWT introduced in Section 2.4. This implementation serves a dual purpose. Firstly, it provides the PathSort algorithm, a fundamental component required by our compression method. Secondly, it will serve as a benchmark for comparison against our scheme in future work. For now, our focus is on the experiments conducted to evaluate the performance of the PathSort algorithm, particularly its execution time.

4.2.1 Implementation

The XBWT data structure has been implemented in C++ using the Succinct Data Structure Library 2.0 (SDSL) for efficient representation and manipulation of compressed data structures. We will develop two algorithms for constructing the XBWT: one efficient linear-time recursive algorithm and one more straightforward iterative algorithm. Also, we will implement the necessary data structures and algorithms for navigating and querying the XBWT, such as parent-child navigation and path-based searches.

The implementation of the XBWT is based on the descriptions provided in Section 2.4. Also, it is available on GitHub at the following link: `https://github.com/davide-tonetto-884585/XBWT`.

Implementation Choices

Follows a list of the main choices made during the implementation of the XBWT:

- The implementation is not focused on a specific kind of data, such as XML documents or JSON files, but it is designed to work with any kind of labeled tree.
- The construction method takes as input a labeled tree. It constructs directly a compressed indexing scheme based on the Extended Burrows-Wheeler Transform of the tree as described in the previous sections.
- The implementation is based on the Succinct Data Structure Library (SDSL) to handle the compressed data structures generated by the XBWT. The SDSL library provides efficient implementations of various compressed data structures and algorithms, which are essential for representing and querying the XBWT efficiently.
- The labels of the alphabet are encoded as integers, starting from 0 to $|\Sigma| - 1$, where $|\Sigma|$ is the cardinality of the alphabet. This encoding respects the order of the labels in the alphabet and allows simplifying and reducing the space needed to store the labels in the compressed data structure. For this reason, the constructor of the XBWT class takes as input a generic labeled tree.

Succinct Data Structures

The implementation of the XBWT relies heavily on succinct data structures to achieve space efficiency while maintaining fast query operations. In particular, we use succinct data structures to compress the two main arrays of the XBWT: S_α and S_{last}. These arrays, which can be quite large for substantial trees, benefit significantly from compression.

The compression is achieved through the Succinct Data Structure Library (SDSL), which provides efficient implementations of various compressed data structures. For S_{last}, which is a binary sequence, we utilize a compressed bit vector that supports fast rank and select operations. For S_α, which contains labels from a potentially large alphabet, we employ a wavelet tree structure that provides both compression and efficient query capabilities.

The SDSL is a C++ library that provides efficient implementations of various compressed data structures and algorithms. It is used in this project to handle the compressed data structures composing the XBWT. The SDSL library provides a wide range of succinct data structures, such as bit vectors, wavelet trees, and compressed suffix arrays, which are essential for representing and querying the XBWT efficiently. The library is available at `https://github.com/simongog/sdsl-lite` [17]. Let's see the implementation details of the SDSL data structures used in the XBWT implementation.

RRR Bit Vector

The RRR bit vector is designed to provide space-efficient representations of bit vectors while supporting efficient rank and select operations. This data structure implements the RRR (Raman, Raman, and Rao) encoding method, which compresses bit vectors by partitioning them into fixed-size blocks and encoding each block based on its population count (the number of 1s) and specific configuration [31].

The space needed for an RRR bit vector of length n with m set bits is $nH_0 + o(n)$ ($\approx \lceil \log \binom{n}{m} \rceil$). The rank support is provided by `sdsl::rank_support_rrr`, adding 80 bits and requiring $O(\log k)$ time for rank queries, where k is the number of set bits. The select support is provided by `sdsl::select_support_rrr`, adding 64 bits and requiring $O(\log n)$ time for select queries.

This data structure is used to represent S_{last}, a dedicated binary array B_α that stores the additional information associated with each entry of S_α (i.e., $B_\alpha[i] = 1$ if the i-th symbol in S_α corresponds to a leaf and 0 otherwise), and the A array of the XBWT.

Wavelet Tree

The Wavelet tree is designed to efficiently handle sequences over large alphabets, such as integer sequences. It provides a space-efficient representation while supporting fast access, rank, and select operations. The wavelet tree is a balanced binary tree that recursively partitions the alphabet into two equal-sized subsets and encodes the sequence based on the partitioning [18]. The `sdsl::wt_int` uses the RRR bit vectors or other succinct representations for storing the bit vectors in each node of the wavelet tree. This makes the structure space-efficient.

If RRR-compressed bitvectors are used for the internal bitmaps, a wavelet tree over a sequence $S \in \Sigma^n$ (with $|\Sigma| = \sigma$) occupies $nH_0(S) + o(n \log \sigma) + \Theta(\sigma \log n)$ bits of space, where $H_0(S)$ is the zero-order empirical entropy of S, and it supports access, rank, and select queries in $O(\log \sigma)$ time.

This data structure is used to represent the S_α array of the XBWT.

4.2.2 Construction Time Experiments

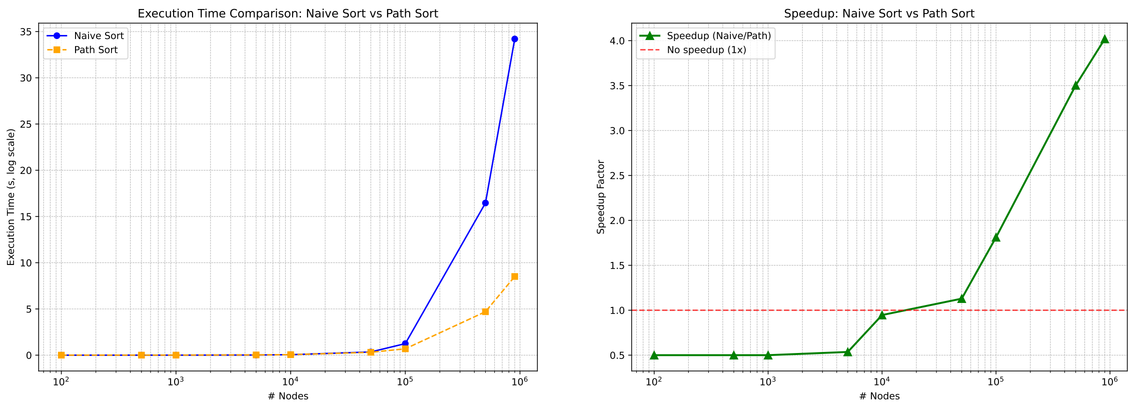
To evaluate the performance of the implemented algorithms, we conducted a series of experiments on randomly generated trees, with sizes ranging from 100 to 900,000 nodes. For each tree, we executed the construction algorithms 10 times, recording the average execution time for both the linear PathSort algorithm and the Naive Sort algorithm used for constructing the XBWT. By "Naive Sort", we refer to a straightforward approach that first precomputes all the upward paths in the tree and then sorts them using a standard sorting algorithm. This method contrasts with PathSort, which is specifically designed to achieve linear time complexity in path sorting. This approach enabled us to compare their performance across various tree sizes and evaluate their scalability.

From the results shown in Table Table 4.1, we can draw several conclusions about the performance of the PathSort algorithm compared to the Naive Sort algorithm.

The PathSort algorithm consistently outperforms the Naive Sort algorithm in terms of execution time, especially as the number of nodes increases. For smaller trees, the difference in execution time between the two algorithms is minimal. However, as the number of nodes grows, the PathSort algorithm demonstrates significantly better scalability. For instance, with 900,000 nodes, the PathSort algorithm takes 8.51 seconds, whereas the Naive Sort algorithm takes 34.2 seconds, giving a speedup of more than 4×. A visual representation of the results can be seen in Figure 4.1 where both the time comparison and the speedup are shown.

# Nodes	Depth	Naive Sort (s)	PathSort (s)
100	22	0.001	0.002
500	45	0.002	0.004
1,000	74	0.003	0.006
5,000	175	0.015	0.028
10,000	288	0.053	0.056
50,000	486	0.350	0.310
100,000	754	1.250	0.690
500,000	2,246	16.460	4.700
900,000	2,658	34.200	8.510

Table 4.1: Performance comparison of the execution times for the Naive Sort and PathSort algorithms on randomly generated trees of varying sizes.



(a) Time Comparison (b) Speedup

Figure 4.1: Time comparison and speedup plots for the experiments in Table 4.1. Image (a) shows PathSort time in seconds (yellow dashed line) vs. Naive Sort time (blue line). Image (b) shows the speedup of PathSort over Naive Sort. The area below the red dashed line indicates points where the speedup is less than or equal to 1, representing no improvement of PathSort over Naive Sort.

4.3 Trie Compression Scheme Implementation and Experiments

4.3.1 Implementation

Our proposed trie compression scheme was implemented in C++ to run some preliminary experiments, and it is available at `https://github.com/davide-tonetto-884585/trie-compression`. We compiled it using Apple Clang 17.

In particular, we utilized the PathSort algorithm implementation of the XBWT introduced in Subsection 4.2.1. Moreover, we used a C++ implementation by Vladimir Kolmogorov of the minimum cost perfect matching algorithm described in [21]. The implementation is available at `https://pub.ista.ac.at/~vnk/software.html`.

4.3.2 Compression as a Function of p

Our first experiment investigates the relationship between the co–lexicographical width, p, of the automaton produced by our compression pipeline and the final compression size. Our central hypothesis is that a larger value of p can lead to a better compression ratio. This is motivated by the fact that enforcing the strict total ordering of a Wheeler DFA (which corresponds to $p = 1$) can lead to an exponential increase in the number of states compared to a minimal DFA representing the same language [27] (see Section 2.5). A p–sortable automaton relaxes this strict requirement by partitioning the states into p totally ordered chains. By increasing p, we provide more flexibility, allowing the automaton to be represented with fewer states—potentially moving closer to the size of a minimal DFA. We therefore expect that a larger p will result in a smaller automaton, leading to better compression.

To generate automata with varying co–lex widths, we controlled the structural repetitiveness of the input tries using the `repetition_probability` parameter in our data generator. We conducted two main experiments:

1. **Low-Repetitiveness Scenario:** We generated a set of 100 tries with a target size of 100,000 nodes, an alphabet size of 26 characters, and a low repetition probability of 0.2.
2. **High-Repetitiveness Scenario:** We generated a second set of 100 tries with a target size of 100,000 nodes, an alphabet size of 26 characters, but with a high repetition probability of 0.8.

We run our full compression pipeline on each trie with different values of p in the range $[1, 15]$. We then report the maximum, mean, and minimum number of nodes and edges obtained after compression. By correlating the measured p with the final compression ratio in both scenarios, we aim to empirically demonstrate that the compression of our method is fundamentally governed by the co–lex width of the resulting automaton.

For each value of p, the experimental results are presented as boxplots, which provide a comprehensive statistical summary of the compression performance across all 100 trials. Each boxplot displays:

- The **median** (middle line): the central value that separates the upper and lower halves of the results.
- The **first quartile (Q1)** and **third quartile (Q3)** (box boundaries): representing the 25th and 75th percentiles, respectively, with the box containing the middle 50% of the data.
- The **interquartile range (IQR)**: the spread of the middle 50% of observations, calculated as Q3 - Q1.
- The **whiskers**: extending to the most extreme data points within $1.5 \times$ IQR from the box boundaries.
- **Outliers**: individual points beyond the whiskers, representing unusually high or low compression ratios.

This visualization allows us to assess not only the central tendency of compression performance for each p value, but also the variability and distribution shape of the results across different trie structures. Additionally, the mean compression value for each p is highlighted with a red line plot that is overlaid on the boxplots to show the overall trend. To provide a theoretical baseline, a green horizontal line indicates the mean number of distinct Myhill–Nerode classes across all tries in the experiment. Since the number of states in a minimal DFA for the language is equal to the number of MN–classes, this line represents the minimum possible number of states. Observing the red line trend approaching the green line shows that as p increases, the average number of nodes in the compressed automaton approaches this theoretical minimum.

The results from our experiments, presented in Figure 4.2 and Figure 4.3, strongly confirm our initial hypothesis. The findings are particularly interesting: simply increasing the co–lexicographical width from $p = 1$ to $p = 2$ is sufficient to halve the number of states in the resulting automaton. Furthermore, the benefits of increasing p are most pronounced for small values. As shown in the plots, the number of states rapidly approaches the theoretical minimum (indicated by the green line), with the compression performance essentially reaching its optimum at around $p = 8$ for Figure 4.2 and around $p = 11$ for Figure 4.3. This demonstrates that even with a very small co–lexicographical width, our method can achieve near-optimal compression by effectively identifying and merging MN–equivalent nodes.

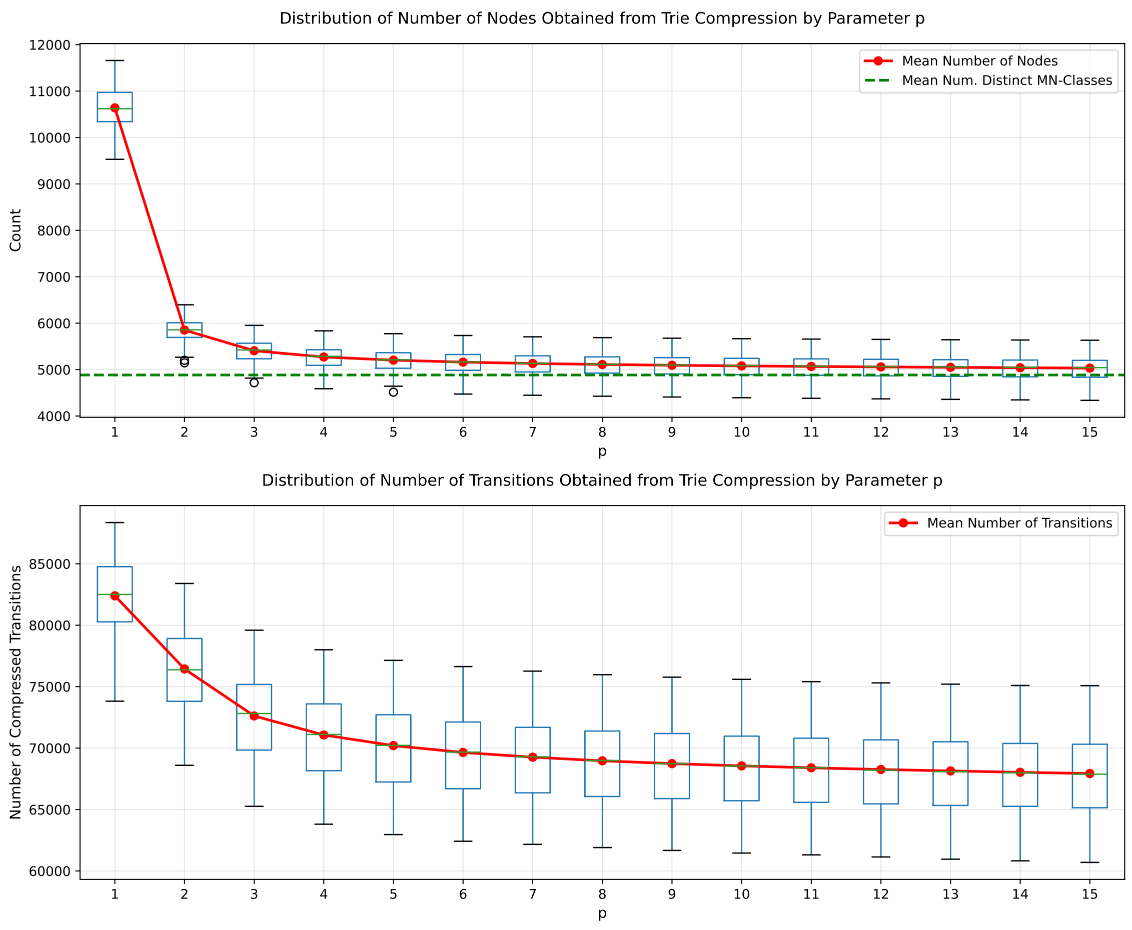


Figure 4.2: Experimental results for the **low-repetition** scenario. The plots show the number of nodes (top) and transitions (bottom) in the compressed automaton as a function of the co–lexicographical width, p. Each boxplot illustrates the distribution of results for a given p. The red line tracks the mean, showing a rapid decrease that approaches the theoretical minimum number of states (the mean number of MN–classes, shown by the green line).

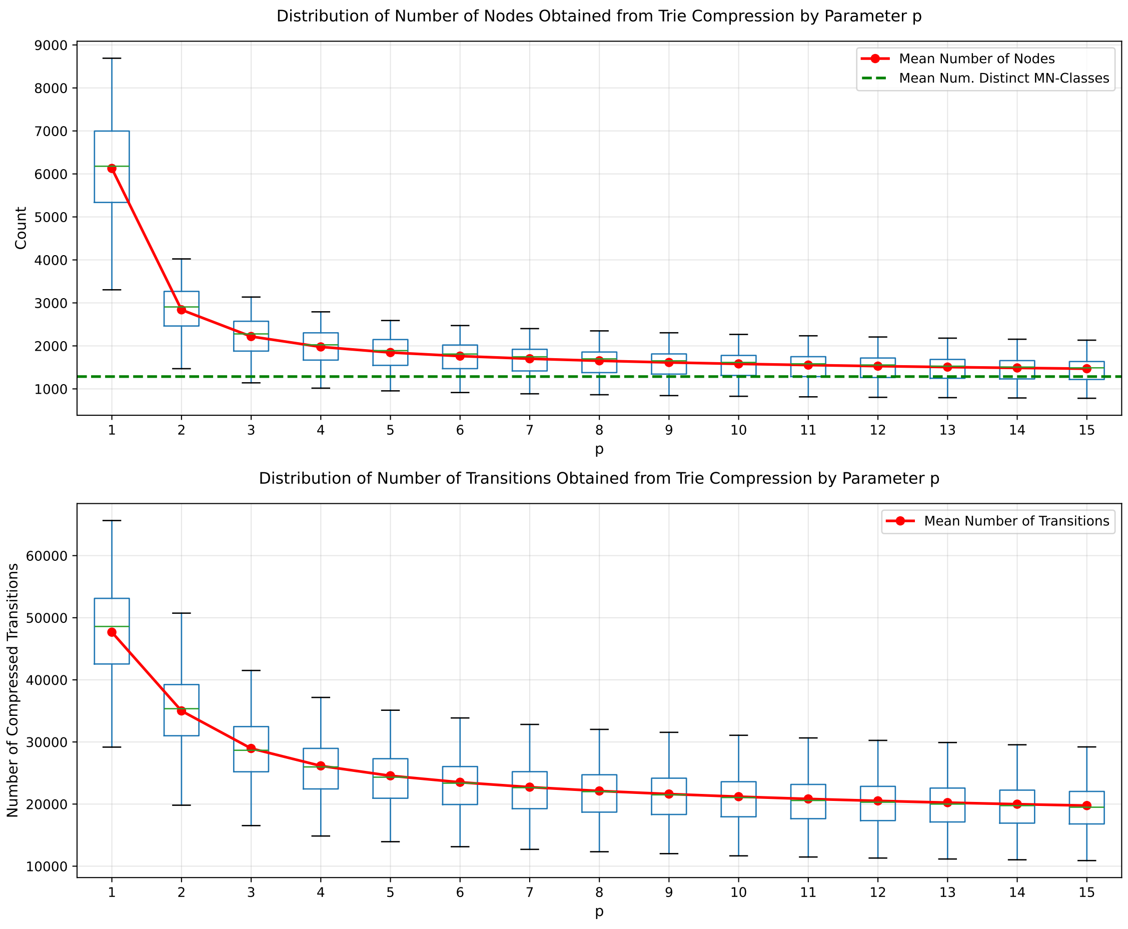


Figure 4.3: Experimental results for the highly-repetitive scenario. The plots show the number of nodes (top) and transitions (bottom) in the compressed automaton as a function of the co–lexicographical width, p. Each boxplot illustrates the distribution of results for a given p. The red line tracks the mean, showing a rapid decrease that approaches the theoretical minimum number of states (the mean number of MN–classes, shown by the green line).

To provide a clear comparison between the two scenarios, Figure 4.4 shows the mean and standard deviation for both the low- and high-repetitive datasets. The results confirm our hypothesis: tries with higher trie repetitiveness achieve significantly better compression, as evidenced by the lower number of nodes and transitions for all values of p. This is expected, as a more repetitive trie allows for a more compact representation in the compressed automaton.

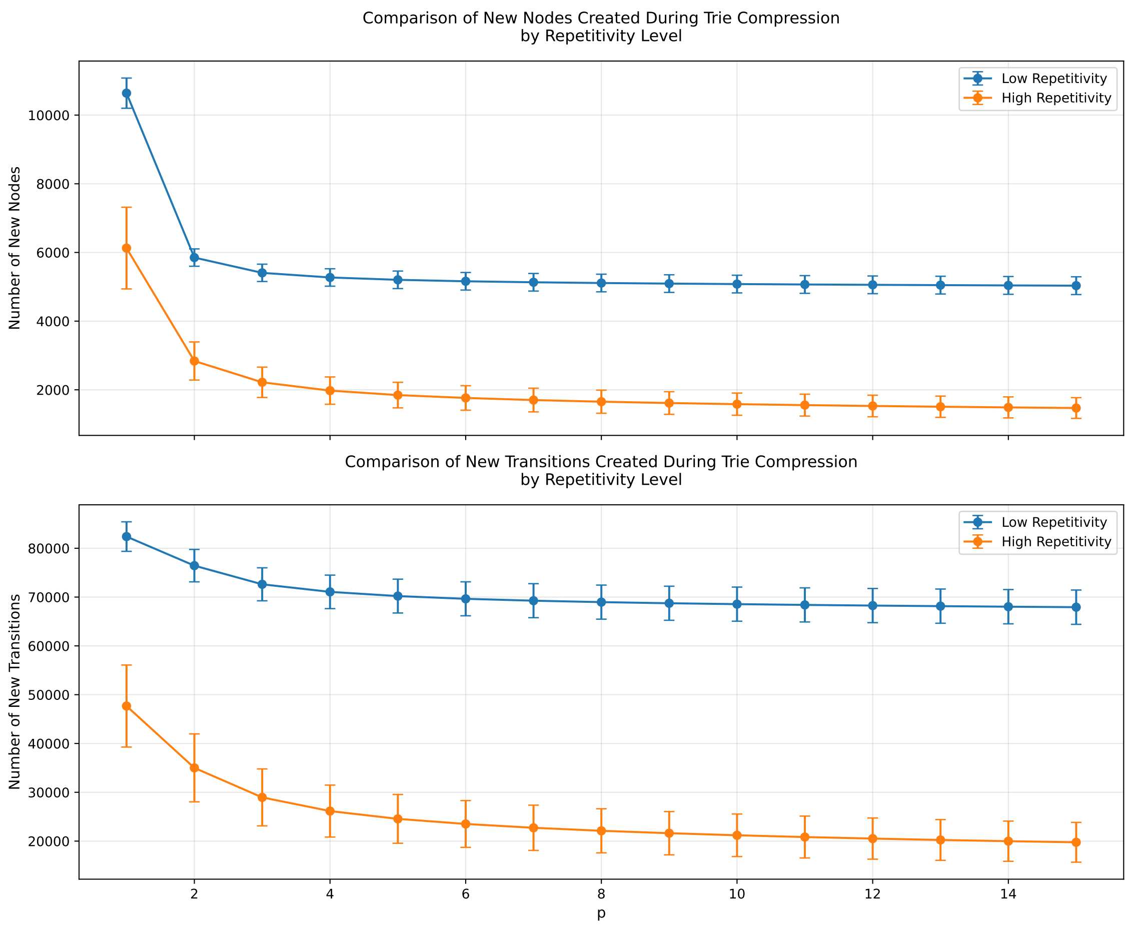


Figure 4.4: Direct comparison of compression performance for low-repetitive versus high-repetitive datasets. The plots track the mean number of nodes (top) and transitions (bottom) as a function of p. The results clearly show that high-repetitive datasets (orange) yield significantly better compression across all values of p, resulting in a much smaller final automaton. This highlights the effectiveness of our method in exploiting the redundancy present in highly repetitive data.

4.3.3 Preliminary Execution Time Experiments

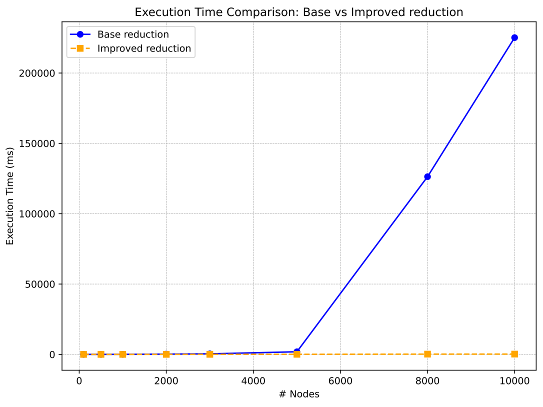
In this section, we present a comparative analysis of the execution times for two different approaches to the trie compression problem. The first approach is the standard reduction to a minimum weight perfect matching problem, as detailed in Section 3.3. The second is an optimized version of this reduction that reduces the number of edges in the bipartite graph to $O(np)$, which is proposed as a future research direction in Subsection 3.3.3.

Our experimental setup involved generating tries of various sizes using the method described earlier. For each trie, we ran both the standard and the optimized algorithms with a fixed parameter $p = 8$. A critical part of our evaluation was to confirm that the optimized algorithm is correct. We did this by verifying that for every instance, the optimal cost of the matching produced by the optimized version was identical to the one produced by the standard reduction. The formal proof of correctness for this optimization is intended to be a component of the author's future PhD research.

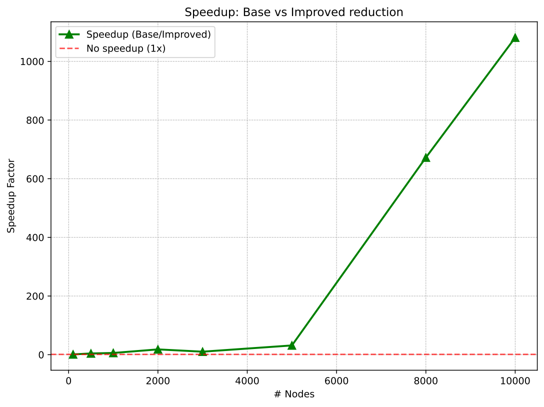
The results presented in Table 4.2 clearly demonstrate the effectiveness of the optimized approach. While the number of nodes resulting after the collapse procedure remains the same for both methods, the execution time is significantly reduced with the optimization. For smaller tries, the difference is minimal, but as the trie size increases, the performance gap widens dramatically. This substantial improvement highlights the practical benefits of the optimization, especially for large-scale applications.

# Nodes	# New Nodes	$O(n^2)$ Time (ms)	$O(np)$ Time (ms)
100	9	0.33	0.33
500	38	8.61	2.04
1000	71	32.69	5.57
2000	111	190.38	10.54
3000	147	393.58	38.35
5000	226	1870.17	59.34
8000	323	126308.08	187.95
10000	359	225162.19	208.29

Table 4.2: Performance comparison of standard $O(n^2)$ vs. optimized $O(np)$ reduction algorithms, for $p = 8$.



(a) Time Comparison



(b) Speedup

Figure 4.5: Time comparison and speedup plots for the experiments in Table 4.2. Figure (a) shows the standard $O(n^2)$ reduction method execution time in milliseconds (yellow dashed line) vs. the improved $O(np)$ reduction time (blue line). Figure (b) shows the speedup of the improved reduction over the standard one. The area below the red dashed line indicates points where the speedup is less than or equal to 1.

Chapter 5

Conclusions and Future Works

This thesis has presented a preliminary study of a novel pipeline designed for trie compression. The initial results are promising and suggest a strong potential for this approach. Specifically, our findings demonstrate that a minor increase in the co–lexicographical width of the input trie can achieve significant compression, particularly when applied to tries with a high degree of internal repetitiveness.

A central contribution of this research is the development of a methodology to balance trie compression with indexability. We framed this challenge as a String Partitioning problem, aiming to identify the optimal p–sortable compressed automaton for a given input trie. The core of our approach lies in a strategic partitioning of the trie's nodes. This partitioning is designed to maximize compression while ensuring the resulting automaton is p–sortable, thus controlling the balance between a compact representation and efficient indexing. Furthermore, we demonstrated that this optimization problem can be reduced to finding a minimum-weight perfect matching in a bipartite graph, which allows for the identification of optimal node pairings to achieve the highest degree of compression.

The reason we specifically aim for a p–sortable automaton is that it allows us to find a balance between storage efficiency and usability. While maximum compression could be achieved by converting the trie into a minimal directed acyclic graph (DAG), such a structure is generally difficult to index, rendering it inefficient for search operations. A p–sortable automaton, however, allows for the creation of an effective index. This index enables fast querying and data retrieval directly on the compressed form, thereby avoiding the performance bottleneck of decompressing the data before use. This method produces a p–sortable automaton that can be indexed effectively, allowing for efficient subsequent querying and data retrieval operations without a notable sacrifice in performance. This approach offers a valuable compromise in the trade-off between the extremes of full, un-indexable compression and uncompressed, fully-indexable structures.

5.1 Future Works

The research presented in this thesis is preliminary, and several avenues for future work have been identified. The reduction we have proposed for the String Partitioning problem, while effective, exhibits a quadratic time complexity with respect to the number of nodes in the trie. This computational cost renders it inefficient for very large-scale applications. A critical next step is to investigate improvements to this reduction to develop more scalable and efficient solutions (see Subsection 3.3.3 for further details). Subsequently, these optimized algorithms should be rigorously evaluated on real-world datasets to validate their performance and practical applicability.

Another significant direction for future research is the exploration of methods to produce a p–sortable deterministic finite automaton directly from our pipeline, rather than the current p–sortable non-deterministic finite automaton. A deterministic representation would offer further advantages in terms of space efficiency. One potential approach to achieve this is to develop a pruning strategy for the output NFA. Such a method would need to carefully remove states and transitions in a way that transforms the NFA into an equivalent DFA, ensuring that the recognized language remains unchanged. It would also be interesting to minimize the size of the returned automaton (for instance, providing explicit guarantees of minimality of the returned p–sortable DFA), and to accept as input an arbitrary Wheeler DFA.

The research and development of these future works will be continued during the author's PhD program.

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