Università Ca'Foscari Venezia

Artificial Intelligence and Data Engineering

Master Degree Thesis

A New Compressing Technique for Labeled Trees

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Abstract

Contents

Chapter 1

Introduction

1.1 Project overview

The increasing availability of large structured datasets, such as those found in XML documents, biological data, and hierarchical knowledge bases, has led to the need for efficient compression techniques for trees. Traditional compression methods, such as general-purpose text compression algorithms, often fail to exploit the hierarchical structure of trees effectively. Consequently, specialized tree compression techniques have been developed to address this issue.

Among the most prominent techniques for tree compression, the *Extended Burrows-Wheeler Transform* [7] extends the classical Burrows-Wheeler Transform to labeled trees, leveraging their structural properties to achieve significant compression. Another notable approach includes *Re-Pair-based compression* [19], which applies grammar-based compression to the tree structure.

Despite these advancements, existing techniques may not be optimal when dealing with trees characterized by a high degree of repetitiveness. Many real-world datasets, such as versioned documents or biological phylogenies, contain repeated substructures that can be exploited to achieve better compression. The aim of this thesis is to study a novel compression technique designed to efficiently handle such highly repetitive trees. We will implement and evaluate this method, comparing it with existing state-of-the-art approaches to determine its effectiveness in different scenarios.

1.2 State of the art

We begin with a brief overview of the state of the art for labeled tree compression. Subsequently, the next chapter will provide a detailed examination of the Extended Burrows-Wheeler Transform.

The Extended Burrows-Wheeler Transform [7] is a data structure designed for efficient compression and indexing of labeled trees. The XBWT works by linearizing a labeled tree into two arrays: one captures the structural properties of the tree and the other stores its labels. This transformation allows for efficient representation, navigation, and querying of the tree. The key advantage of the XBWT lies in its ability to compress labeled trees while supporting a wide range of operations, such as parent-child navigation and sophisticated path-based searches, in (near-)optimal time and space. The XBWT provides significant improvements in both compression ratio and query performance compared to traditional compression schemes, making it a valid resource for intensive applications.

Tree Re-Pair is a grammar-based compression technique specifically adapted for tree structures [19]. It extends the principles of the original Re-Pair algorithm introduced in [18], specifically designed for sequences and to handle the hierarchical nature of trees. The core idea of the tool is to identify frequently occurring patterns within the tree and represent them more compactly. The process involves the linearization of the tree (e.g., using a specific traversal order) and then the application of the Re-Pair logic. In this way, it finds the most frequent pair of adjacent elements (which could represent nodes, labels, or structural components depending on the linearization) in the sequence. The pair is then replaced by a new non-terminal symbol, and the corresponding production rule is added to a 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 (a set of production rules) 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 [20].

1.3 Challenges

In order to develop an effective tree compression scheme that can exploit repetitive structures, we need to address several key challenges:

- **Identification of repetitive structures:** The first step in compressing repetitive trees is to identify the repeated substructures efficiently. This requires the development of algorithms capable of detecting and representing these structures in a compact way.
- **Optimization of representation:** Once the repetitive structures have been identified, the challenge is to represent them in an optimized way that minimizes the overall size of the compressed tree. This involves finding the most efficient encoding for the repeated substructures.

We will address these challenges by developing a novel tree compression scheme that leverages the deterministic finite automata minimization algorithm to identify and compress repetitive structures in trees and the Minimum Weight Perfect Bipartite Matching algorithm to optimize their representation. Both algorithms are known for their efficiency and effectiveness in solving similar problems and are well-suited to the task at hand. They will be integrated into a comprehensive compression pipeline that can handle trees with repetitive structures efficiently.

1.4 The structure of the thesis

The thesis is structured as follows:

1. **Chapter 1** provides an overview of the project and its objectives.
2. **Chapter 2** contains the theoretical background on labeled trees necessary to understand the content of the subsequent chapters.
3. **Chapter 3** provides a detailed examination of the Extended Burrows-Wheeler

Transform and its implementation that we will use as a benchmark for comparison.

4. **Chapter 4** introduces the Hopcroft algorithm for minimizing deterministic finite automata and an algorithm derived from it for minimizing acyclic deterministic finite automata in linear time which we will use to identify repetitive structures in trees.

5. **Chapter 5** presents the concept of matching in bipartite graphs and the Minimum Weight Perfect Bipartite Matching problem, which we will use in our compression scheme to chain repetitive structures.

6. **Chapters 6** presents the proposed tree compression scheme, outlining the pipeline used to compress trees with repetitive structures and the algorithms used to build the compression scheme.

7. **Chapter ??** describes the implementation details of the proposed method and the experimental setup used to evaluate its performance.

8. **Chapter ??** provides a detailed analysis of the experimental results, discussing the performance of the proposed method in various scenarios.

9. **Chapter ??** discusses the implications of our findings and outlines possible directions for future research.

Chapter 2

Theoretical Background on Labeled Trees

Before delving into specific compression techniques, it is essential to establish a solid theoretical foundation regarding labeled trees. These structures are fundamental for representing hierarchical data across diverse fields, from bioinformatics to document processing. This chapter provides the necessary background, defining labeled trees, exploring their common applications, and introducing the core concepts behind their compression and indexing. Understanding these principles, including the role of succinct data structures and the information-theoretic limits of compression, is crucial for appreciating the challenges and advancements in handling large-scale tree-structured data effectively, which forms the basis for the work presented in this thesis.

2.1 Labeled Trees

A **labeled tree** is a rooted, ordered, hierarchical data structure in which every node is assigned a label from a predefined alphabet Σ. The structure consists of nodes connected by edges, forming a directed acyclic graph. Formally, a labeled tree T with t nodes can be defined as $T = (V, E, \ell)$, where:

- V is the set of nodes,
- $E \subseteq V \times V$ is the set of directed edges, and
- $\ell : V \to \Sigma$ is a labeling function that assigns a label $\ell(u) \in \Sigma$ to each node u.

In the case of ordered labeled tree, the children of a node in the tree are ordered, meaning their positions relative to each other matter. A labeled tree can have arbitrary degrees and shapes, and the alphabet Σ used for labels can be of arbitrary size.

2.1.1 Applications of Labeled Trees

Labeled trees are widely used in computer science and data representation due to their hierarchical structure and flexibility in modeling relationships. Prominent applications include:

1. **XML Data Representation:** XML documents are often modeled as labeled trees, where each element is a node labeled by its tag, and hierarchical nesting represents parent-child relationships.
2. **JSON Data Representation:** JSON objects can be viewed as labeled trees, with keys as labels and values as children.

3. **Bioinformatics:** Labeled trees are used to represent phylogenetic trees, genome annotations, and hierarchical clustering.
4. **Compiler Design:** Abstract Syntax Trees (ASTs) for programming languages are labeled trees that capture the structure of code.
5. **File Systems:** The directory structure of file systems can be viewed as labeled trees.

Efficient representation, navigation, and querying of labeled trees are essential for many applications, motivating the development of specialized data structures and algorithms.

2.2 Compressing and Indexing Labeled Trees

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 (near-)optimal time.

Let u be a node in the labeled tree T and let $c \in \Sigma$. We define the following navigation operations on T:

- **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 c.
- **Path queries:** retrieve the nodes in the subtree rooted at u (any possible order should be implemented).
- **Subpath queries:** ask for the (number of occurrences of) nodes of T that descend from a labeled subpath P. Which may be anchored anywhere in the tree (i.e., not necessarily in its root).

A naive solution to index labeled trees is to store the tree in a straightforward manner, such as a list of nodes with their labels and parent-child relationships using pointer in $O(tlogt)$. However, this representation is not space-efficient and does not support fast navigation or query operations.

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. One of the most successful approaches is the Extended Burrows-Wheeler Transform, which extends the classical Burrows-Wheeler Transform (BWT) to handle labeled trees efficiently.

Before the advent of XBWT, Kosaraju [16] proposed a method to index labeled trees by extending the concept of prefix sorting, which is commonly applied to strings, to work with labeled trees by leveraging the structure of tries (prefix trees). To achieve this, he introduced the idea of constructing a suffix tree for a reversed trie allowing subpath queries in $O(|P| \log |\Sigma| + occ)$ time, where occ is the number of occurrences of P in T but still requiring $O(t \log t)$ space and so not being compressed.

2.3 Succinct Data Structures for Trees

In order to compress the index of labeled trees, we need to avoid the use of pointers and store the tree in a space-efficient manner. Succinct data structures are a class of compressed data structures that support efficient navigation and query operations on the compressed data. These structures are designed to use close to the information-theoretic lower bound on space while providing fast access to the original data. They were first introduced by Jacobson [14] and have been applied to various problems in string processing, graph theory, and data compression.

2.3.1 Information-Theoretic Lower Bound for Trees

The information-theoretic lower bound for storing an unlabeled tree with t nodes is given by:

- The number of binary unlabeled trees with t nodes is given by the Catalan number $C_t = \frac{1}{t+1}\binom{2t}{t}$ that can can be approximated as $C_t \approx \frac{4^t}{t^{3/2}\sqrt{\pi}}$ using Stirling's approximation.
- The entropy (or the information-theoretic minimum number of bits to encode the structure of the tree) is the logarithm (base 2) of the total number of trees, which is $-\log_2 C_t \approx 2t - \frac{1}{2}\log_2 \pi t^3$.
- The correction term $\frac{1}{2}\log_2 \pi t^3$ grows slower that the linear term $2t$, we can say that $-\frac{1}{2}\log_2 \pi t^3 = -\Theta(\log t)$.
- The information-theoretic lower bound for storing an unlabeled tree with t nodes is $2t - \Theta(\log t)$ bits.

Then for labeled trees, the labels assigned to each node must be stored, which requires an additional space:

- Let Σ denote the alphabet of labels, and let $|\Sigma|$ be the size of the alphabet.
- Each node in the tree requires $\log_2 |\Sigma|$ bits to store its label.
- Therefore, for t nodes, the total space required to store the labels is $t \log_2 |\Sigma|$ bits.

Combining the structural representation and the labeling, the information-theoretic lower bound for storing a labeled tree is:

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

Chapter 3

The Extended Burros-Wheeler Transform

This chapter delves into the Extended Burrows-Wheeler Transform (XBWT) introduced Ferragina et al. [7], a prominent state-of-the-art technique for labeled tree compression. Understanding the principles and performance of XBWT is crucial as 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 method like XBWT, we can effectively demonstrate the potential advantages and contributions of our new approach, particularly for trees exhibiting high repetitiveness.

Disclaimer: The fundamental definitions, properties, and algorithms related to the Extended Burrows-Wheeler Transform presented in this chapter are based on the work introduced by Ferragina et al. 'Compressing and Indexing Labeled Trees, with Applications' [7].

3.1 Introduction to XBWT

In 2005, Ferragina et al. [7] observed that succinctness could be achieved for labeled trees by exploiting an index scheme that fit into a space proportional to the entropy-compressed edge labels plus the succinct tree's topology. This observation was the starting point for the development of the Extended Burrows-Wheeler Transform. Let's start by defining the XBWT.

XBWT works by linearizing a labeled tree into two coordinated arrays: one capturing the structural properties of the tree and the other storing its labels. This transformation allows for efficient representation, navigation, and querying of the tree. The key advantage of XBWT lies in its ability to compress labeled trees while supporting a wide range of operations, such as parent-child navigation and sophisticated path-based searches, in (near-)optimal time and space.

One of the primary applications of XBWT is in the compression and indexing of 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 chapter 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.

Let's start with a quick overview of the XBWT and its theoretical foundations.

3.1.1 How XBWT Works

The transformation process of XBWT is as follows:

1. **Path Sorting:** The labeled tree is linearized by sorting its nodes based on the *paths* from each node's parent to the root. The resulting order groups nodes with similar upward paths together, clustering related labels.
2. **Array Construction:** Two arrays, S_{last} and S_α, are generated:
   - S_{last} stores structural information, such as whether a node is the last child of its parent. This encodes the tree's structure without the need for explicit pointers.
   - S_α stores the labels of the nodes in the sorted order determined by their upward-path sorting.
3. **Compression:** Both S_{last} and S_α are highly compressible due to the clustering of similar labels and structural redundancy.

3.1.2 Key Properties of XBWT

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 *information-theoretic lower bound*, which is $2t - \Theta(\log t) + t \log |\Sigma|$ bits for a tree with t nodes and an alphabet of size $|\Sigma|$.
- **Efficient Querying:** XBWT supports a range of navigational operations, such as finding the parent, child, or subtree of a node in near-optimal time.
- **Scalability:** XBWT is particularly useful for large-scale hierarchical data, such as XML documents or phylogenetic trees, where both compression and fast querying are critical.

3.1.3 XBWT implementation overview

The XBWT data structure will be 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 code is available on GitHub at `https://github.com/davide-tonetto-884585/XBWT`. The project will be structured as follows:

- **XBWT.hpp**: File containing the class definition and implementation for the generic XBWT data structure.
- **LabeledTree.hpp**: File containing the class definition and implementation for the generic labeled tree data structure used to feed and test the XBWT.

- **main.cpp**: Main file containing the test cases and examples for the XBWT implementation.
- **experiments.cpp**: File containing the experiments and performance evaluation of the XBWT construction algorithms and compression efficiency.
- **CMakeLists.txt**: CMake configuration file for building the project.

3.2 Definition of XBWT

The **Extended Burrows-Wheeler Transform** is a data structure designed to efficiently compress and index *labeled trees*. Inspired by the classical Burrows-Wheeler Transform (BWT) [2] for strings, the XBWT extends these principles to hierarchical structures, enabling efficient storage, navigation, and querying of trees. It is particularly effective for trees where each node has a label drawn from an alphabet Σ and the tree structure has an arbitrary shape and degree.

Given an ordered labeled tree T of arbitrary fan-out, depth and shape, with n internal nodes and l leaves (t nodes in total) and alphabet Σ. Let u be a node in T, we define the following information:

- $last[u]$: is a binary value that is 1 if u is the last (rightmost) child of its parent, and 0 otherwise.
- $\alpha[u]$: denotes the label of node u plus one bit that is 1 if u is a leaf and 0 otherwise.
- $\pi(u)$: is the string obtained by concatenating the labels of the nodes on the path from u's parent to the root of T (the root has an empty π component).

Then, to define the XBWT, a sorted multi-set S consisting of t triplets (one per node of T) is built, where each triplet is of the form $(last[u], \alpha[u], \pi(u))$ for some node u in T. S is built by traversing T in a pre-order fashion, for each visited node u, the triplet $(last[u], \alpha[u], \pi(u))$ is added to S, then S is stably sorted in accordance with the lexicographic order of the π component of the triplets.

Theorem 1. *The XBWT of a labeled tree T consist of the two arrays $\{S_{last}, S_\alpha\}$ after sorting, and takes $2t + t\log|\Sigma|$ bits of space.*

3.3 Properties of XBWT

The following two properties of the ordered multi-set S are crucial for the indexing scheme, they immediately follow from the composition of the transform and from the way S is built.

3.3.1 Property 1

1. S_{last} has n 1s (one for each internal node) and l 0s (one for each leaf).
2. S_α is a permutation of the labels of the nodes in T.

3. S_π contains all the upward labeled paths of T consisting internal node labels only. Also, each path is repeated a number of times equal to the number of its offsprings.

3.3.2 Property 2

1. The first triplet of S refers to the root of T.
2. The triplet of node u precedes the triplet of node v in S iff either $\pi[u] < \pi[v]$ or $\pi[u] = \pi[v]$ and u precedes v in the pre-order traversal of T.
3. Let $u_1, \ldots, u_z$ be the children of node u in T, then the triplets of $u_1, \ldots, u_z$ are consecutive in S following this order. Moreover, the subarray $S_{\text{last}}[u_1 \ldots u_z]$ provides the unary encoding of u's degree, namely $S_{\text{last}}[u_z] = 1$ and $S_{\text{last}}[u_i] = 0$ for $1 \leq i < z$.
4. Let u, v be two nodes in T having the same label $\alpha[u] = \alpha[v]$, then if the triplets of u precedes the triplets of v in S, then the contiguous block of children of u in S precedes the contiguous block of children of v in S.

3.3.3 Property 3

Let $c \in \Sigma$ be an internal node label, and let $S[j_1, j_2]$ be all triplets whose π-components are prefixed by c. If u is the i-th node labeled c in S_α, its children occur contiguously within $S[j_1, j_2]$ and delimited by the $i - 1$-th and i-th bit set to 1 in $S_{\text{last}}[j_1, j_2]$.

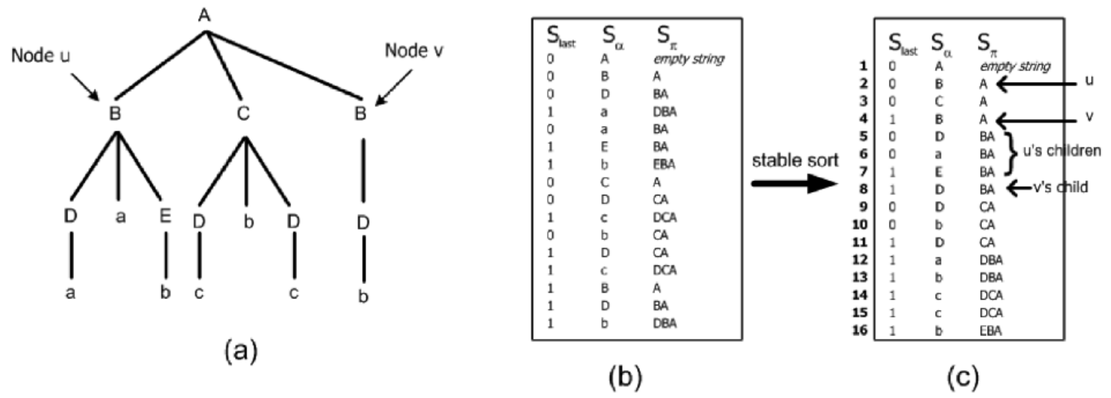
3.4 XBWT Construction

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 large deep trees. To overcome this issue, Ferragina et al. [7] proposed a more efficient algorithm that builds S in linear time and $O(t \log t)$ space.

The linear time algorithm is called **pathSort**, it is based on a generalization of the Skew algorithm for suffix array construction of strings [15]. Let's see briefly how the Skew algorithm works.

3.4.1 Skew Algorithm

The Skew algorithm is an efficient method for constructing the suffix array of a string in linear time. A suffix array is a data structure that lists the starting indices of all the suffixes of a string in lexicographical order, and it is widely used in various string processing algorithms.



S_{last}	S_{α}	S_{π}
0	A	*empty string*
0	B	A
0	D	BA
1	a	DBA
0	a	BA
1	E	BA
1	b	EBA
0	C	A
0	D	CA
1	c	DCA
0	b	CA
1	D	CA
1	c	DCA
1	B	A
1	D	BA
1	b	DBA

	S_{last}	S_{α}	S_{π}
1	0	A	*empty string*
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 3.1: (a) A labeled tree T where $\Sigma_N = \{A, B, C, D, E\}$ and $\Sigma_L = \{a, b, c\}$. Notice that $\alpha[u] = \alpha[v] = B$ and $\pi[u] = \pi[v] = A$. (b) The multi-set S obtained after the pre-order visit of T. (c) The final multi-set S after the stable sort based on the π's component of its triplets.

Algorithm Overview

1. Divide the String

The algorithm begins by partitioning the indices of the string into three groups based on their modulo 3 value:

- S_0: Indices congruent to 0 mod 3.
- S_1: Indices congruent to 1 mod 3.
- S_2: Indices congruent to 2 mod 3.

The suffixes starting at positions in S_1 and S_2 are combined into a single group called S_{12}.

2. Sort Suffixes in S_{12}

To sort the suffixes in S_{12}, the algorithm considers the triplets of characters starting at each position in S_{12}. These triplets are sorted using a linear-time sorting algorithm, such as radix sort, and then renamed by assigning each triplet an integer value representing its rank in the sorted order. If all triplets are unique, the sorting is complete; otherwise, the same procedure is applied recursively to the sequence of ranks obtained.

3. Sort Suffixes in S_0

Once the suffixes in S_{12} are sorted, the algorithm proceeds to sort the suffixes in S_0. To compare two suffixes starting at positions i and j in S_0, it compares the first characters of their respective substrings. If these are equal, it compares the suffixes starting at positions $i+1$ and $j+1$, whose ranks are already known from the sorting of S_{12}.

4. Merge the Sorted Orders

Finally, the sorted orders of the suffixes in S_0 and S_{12} are merged to obtain the complete suffix array of the original string. This merging process can be performed in linear time, ensuring the overall efficiency of the algorithm.

3.4.2 PathSort Algorithm

The pseudocode of the pathSort algorithm is shown in Algorithm 1. As we can see the algorithm is based on the Skew algorithm, but it is adapted to work on labeled trees. The main idea is to recursively sort the upward subpaths of the tree starting at nodes in levels $\not\equiv j \pmod 3$, then sort the upward subpaths starting at nodes in levels $\equiv j \pmod 3$ using the result of the previous step, and finally merge the two sets of sorted subpaths by exploiting their lexicographic names. The value of j is chosen in such a way that the number of nodes in `IntNodes` whose level is $\equiv j \pmod 3$ is at least $t/3$ so that a constant fraction of upward paths are ensured to be dropped at each recursive step. Is important to note that:

1. The height of the new (contracted) tree shrinks by a factor 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 [15], the names of the dropped subpaths can be computed in $O(t)$ time from the names of the non dropped subpaths, by radix sorting.

Algorithm 1 PATHSORT(T)

```
1: Create the array IntNodes[1, $t$], initially empty.
2: Visit the internal nodes of $T$ in pre-order. Let $u$ denote the $i$-th visited node.
3: Write in IntNodes[$i$] the symbol $\alpha[u]$, the level of $u$ in $T$, and the position in
   IntNodes of $u$'s parent.
4: 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 $\not\equiv j \pmod 3$.
5: Sort the upward subpaths starting at nodes in levels $\equiv j \pmod 3$ using the
   result of Step 3.
6: 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` (as shown in Figure 3.1-(b)), 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. These paths are then sorted using radix sort. If the sorted upward paths contain duplicates, the algorithm recursively calls the PathSort function on a new contracted tree, where nodes are renamed according to their sorted paths. Otherwise, if all upward paths are unique, the nodes in `IntNodesAtPosJ` are sorted and subsequently merged with `IntNodesNotAtPosJ` using lexicographic ordering, following the same merging strategy as in the Skew algorithm.

3.5 Inverting the XBWT

Property 3 3.3.3 ensures that the two array S_{last} and S_α of the XBWT can be used to reconstruct the original tree T. The algorithm to invert the XBWT is linear in time and requires $O(t \log t)$ bits of space.

The algorithm 2 initially builds the array F that stores the first entry in S whose π-component is prefixed by a symbol x (F approximates S_π at its first symbol). Then, it exploits the array F to efficiently build the array J that stores the position in S of the first child of each node in T. Finally, the algorithm deploys the array J to simulate a depth-first visit of T, creates its labeled nodes, and properly connects them to their parents.

Algorithm 2 RebuildTree(`xbw[`T`]`)

```
 1: $F$ = BuildF(xbw[$T$]); ▷ $F[x]$ = first entry in $S$ whose $\pi$-component is prefixed
    by symbol $x$
 2: $J$ = BuildJ(xbw[$T$], $F$);          ▷ $J[i]$ = position in $S$ of the first child of $S[i]$;
    $J[i] = -1$ if leaf
 3: Create node $r$ and set $Q = \{(1, r)\}$;                    ▷ $Q$ 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 $S_{\text{last}}[j'] = 1$;  ▷ $S[j, j']$ are the children of $u$ in $T$
11:     for $h = j'$ downto $j$ do                           ▷ Recall that $Q$ is a stack
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 3 BuildF(`xbw[T]`)

```
for $i = 1, \dots, |\Sigma_N|$ do
    $C[S_\alpha[i]] \leftarrow C[S_\alpha[i]] + 1$;            ▷ Count the occurrences of node labels
end for
$F[1] = 2$;                                                  ▷ $S_\pi[1]$ is the empty string
for $i = 1, \dots, |\Sigma_N| - 1$ do                       ▷ Consider just the internal-node labels
    $s = 0$; $j = F[i]$;
    while $s \neq C[i]$ do                                   ▷ Not all blocks of children have been passed
        if $S_{\text{last}}[j++] = 1$ then $s++$;             ▷ One further block of children has passed
        end if
    end while
    $F[i+1] = j$;
end for
return $F$.
```

Algorithm 4 BuildJ(`xbw[T]`, F)

```
for $i = 1, \dots, t$ do
    if $S_\alpha[i] \in \Sigma_L$ then
        $J[i] = -1$;                                          ▷ $S_\alpha[i]$ is a leaf label
    else
        $z = J[S_\alpha[i]]$;
        while $S_{\text{last}}[z] \neq 1$ do $z++$;           ▷ Reach the last child of $S_\alpha[i]$
        end while
        $F[S_\alpha[i]] = z + 1$;
    end if
end for
return $J$.
```

3.6 Compressing Labeled Trees

Let the k-context of a node u in a tree T be defined as the first k symbols of the π-component of the triplet associated with u. We denote this k-long prefix as $\pi_k[u]$. Thus, $\pi_k[u]$ represents the subpath of length k leading to u in T, or equivalently, the node u descends from a subpath labeled as $\pi_k[u]$, where the nodes in $\pi_k[u]$ are encountered in an upward direction.

The XBW[T] exhibits a local homogeneity property on the string S_α, which can be demonstrated through the concept of k-contexts on trees. This property mirrors the strong local homogeneity exhibited by strings under the Burrows-Wheeler Transform [Burrows and Wheeler 1994] when applied to labeled trees. Specifically, node labels in T are distributed across S_α in a manner that clusters together those labels originating from "similar" upward paths that share long prefixes.

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 squeeze the two strings that compose XBW$[T]$, by exploiting their fine specialties. Of course, many choices are possible for C_{last} and C_α, each having implications on the algorithmic time and compression bounds.

In general, 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.

3.7 Indexing a compressed labeled tree

In order to implement the efficient operations listed in 2.2 using the compressed arrays S_{last} and S_α of XBWT, we need that the chosen compressors C_α and C_{last} 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 XBWT$[T]$ 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: $A[1] = 1$, $A[j] = 1$ 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, by means of rank and select operations over A, we can succinctly implement the array F deployed in the algorithms 2 and 3.

The following methods are supported by the compressed index:

- **GetRankedChild(i, k)**: returns the position in S of the k-th child of u; the output is -1 if this child does not exist. As an example, `GetRankedChild(2, 2) = 6` in Figure 3.1.
- **GetCharRankedChild(i, c, k)**: returns the position in S of the triplet representing the k-th child of u among the ones whose label is c. The output is -1 if this child does not exist. As an example, `GetCharRankedChild(1, B, 2) = 4` in Figure 3.1.
- **GetDegree(i)**: returns the number of children of u.
- **GetCharDegree(i, c)**: returns the number of children of u labeled c.
- **GetParent(i)**: returns the position in S of the triplet representing the parent of u. The output is -1 if $i = 1$ (the root). As an example, `GetParent(8) = 4` in Figure 3.1.

- **GetSubtree(i)**: returns the node labels of the subtree rooted at u. Any possible order (i.e., pre, in, post) may be implemented.
- **SubPathSearch(P)**: determines the range $S[\text{First}, \text{Last}]$ of nodes, which are immediate descendants of each occurrence of the labeled path $P = c_1c_2\cdots c_k$ in T. Note that all strings in $S_\pi[\text{First}, \text{Last}]$ are prefixed by P^R. As an example, `SubPathSearch(BD) = [12, 13]` and `SubPathSearch(AB) = [5, 8]` in Figure 3.1.

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 5 GetChildren(i)

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

The algorithm exploits directly the properties described before, in particular the Property 3 (3.3.3). 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 $F[c]$through a select operation on A (line 6). By Property 3, the children of $S[i]$ are located at the r-th block of children following position $F[c]$. Lines $8 - 9$ identify this block.

GetParent(i)

Algorithm 6 GetParent(i)

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

Algorithm 6 is based on the Property 3 (3.3.3) and it is the inverse of the GetChildren method. At 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 3 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 properly the parent of $S[i]$.

SubPathSearch(P)

Algorithm 7 SubPathSearch(P)

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

We assume that $P = c_1c_2 \cdots c_k$ 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.

3.8 Implementation of the XBWT

The implementation of the XBWT is based on what has been described in the previous chapters. The implementation is written in C++ and is available on GitHub at the following link: `https://github.com/davide-tonetto-884585/XBWT`.

3.8.1 Implementation choices

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

- The implementation is not focused on working for 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 of the XBWT class takes as input a labeled tree, and construct directly a compressed indexing scheme for it based on the Extended Burrows-Wheeler Transform of the tree as described in the previous chapters.
- In order for the XBWT to work we assume that the labels of the leaf nodes of the given labeled tree are lexicographically greater than the labels of the internal nodes. This is necessary to ensure that the navigational and search operations work correctly.
- 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 respect the order of the labels in the alphabet and allows simplifying and reduce the space needed to store the labels in the compressed data structures. For this reason the constructor of the XBWT class takes as input a generic labeled tree.

3.8.2 Succinct Data Structure Library (SDSL)

The Succinct Data Structure Library (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 generated by 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` [10]. Let's see the implementation details of the SDSL data structures used in the XBWT implementation.

sdsl::rrr_vector

The `sdsl::rrr_vector` is a class of the Succinct Data Structure Library (SDSL), 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 [25].

The space needed by `sdsl::rrr_vector` for a 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.

sdsl::wt_int

The `sdsl::wt_int` is a class of the Succinct Data Structure Library (SDSL) that implements wavelet trees 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 [11]. The `sdsl::wt_int` uses the RRR compressed bit vectors or other succinct representations for storing the bit vectors in each node of the wavelet tree. This makes the structure space-efficient.

In the case of RRR compressed bit vectors the space needed by `sdsl::wt_int` for a sequence of length n over an alphabet of size σ is $nH_0(S)+o(n \log \sigma)+\Theta(\sigma \log n)$ bits, where $H_0(S)$ is the zero-order empirical entropy of the sequence S. Also supports query access, rank and select operations in $O(\log \sigma)$ time.

3.8.3 Details of the XBWT Class Elements

The XBWT class utilizes several data structures from the SDSL library to efficiently represent and query the compressed data. Below are the details of the main elements used in the class:

- `sdsl::rrr_vector<> SLastCompressed`: This is a compressed bit vector that stores the S_{last} array of the XBWT.
- `sdsl::wt_int<sdsl::rrr_vector<» SAlphaCompressed`: This is a wavelet tree built on top of a compressed bit vector. The wavelet tree is used to compress and index the S_α array of the XBWT.
- `sdsl::rrr_vector<> SAlphaBitCompressed`: Another compressed bit vector used to store the additional bit of S_α needed to distinguish between internal and leaf nodes.
- `sdsl::rrr_vector<> ACompressed`: A compressed bit vector representing the A array of the XBWT used to in the F array of the XBWT.
- `sdsl::rrr_vector<>::rank_1_type SLastCompressedRank`: A rank support structure for the `SLastCompressed` bit vector, allowing efficient rank queries.

- `sdsl::rrr_vector<>::select_1_type SLastCompressedSelect`: A select support structure for the `SLastCompressed` bit vector, allowing efficient select queries.
- `sdsl::rrr_vector<>::rank_1_type ACompressedRank`: A rank support structure for the `ACompressed` bit vector.
- `sdsl::rrr_vector<>::select_1_type ACompressedSelect`: A select support structure for the `ACompressed` bit vector.
- `std::unordered_map<T, unsigned int> alphabetMap`: An hash map that maps each label in the alphabet to a unique integer.
- `unsigned int cardSigma`: The cardinality of the alphabet Σ.
- `unsigned int cardSigmaN`: The cardinality of the Σ_N alphabet. Where Σ_N is the set of labels that appear in the internal nodes of the labeled tree.
- `unsigned int maxNumDigits`: The maximum number of digits that has the integer code associated to the greater label in the alphabet (needed to sort the labels in the alphabet).

The overall space complexity of the XBWT class can be derived from the space complexity of the compressed data structures used in the class.

3.8.4 Construction of the XBWT

The construction of the XBWT is done by the constructor of the XBWT class. The constructor takes as input a generic labeled tree and constructs the compressed indexing scheme using the linear pathSort (also the naive construction method can be used by passing the boolean flag `usePathSort = false`). The construction process is divided into the following steps:

1. **Alphabet Encoding**: The first step is to encode the labels of the alphabet as integers. The labels are sorted in lexicographical order and assigned a unique integer code starting from 1 to $|\Sigma|$. Two hash maps are used to map each label to a unique integer and vice versa.
2. **Construct `intNodes` array**: The next step is to construct the `intNodes` array as described in the previous chapters. `intNodes` is an array of triplets of length t in which node is represented as a triplet containing the node's label, its level, and the index of its parent node in the array (from 1 to t, root has parent 0). The nodes are inserted in preorder traversal of the labeled tree.
3. **Sort `intNodes` array:** Call the `pathSort` or `upwardStableSortConstruction` (naive method) method to get the sorted array of nodes `intNodes`.
4. **Construct S_{last} array**: Construct the S_{last} array by iterating over the sorted `intNodes` array.
5. **Construct S_α array**: Construct the S_α array by iterating over the sorted `intNodes` array, along with the additional bit array to distinguish between internal and leaf nodes.

6. **Construct A array**: Construct the A array by iterating over the sorted `intNodes` array.

7. **Construct rank and select support structures**: Construct the rank and select support structures for the compressed bit vectors.

3.8.5 Navigational Operations

The XBWT class provides several navigational operations to traverse the labeled tree and retrieve information about the nodes. The navigational operations implemented are:

- `getChildren(unsigned int i)`: This method returns a pair of integers representing the indices of the leftmost and rightmost children of the node at index `i`.
- `getRankedChild(unsigned int i, unsigned int k)`: This method returns the index of the `k`-th child of the node at index `i`.
- `getCharRankedChild(unsigned int i, T label, unsigned int k) const`: This method returns the index of the `k`-th child of the node at index `i` with the specified label.
- `getDegree(unsigned int i)`: This method returns the degree (number of children) of the node at index `i`.
- `getCharDegree(unsigned int i, T label)`: This method returns the number of children of the node at index `i` with the specified label.
- `getParent(unsigned int i)`: This method returns the index of the parent of the node at index `i`.
- `getSubtree(unsigned int i, unsigned int order = 0)`: This method returns a vector containing the labels of the nodes in the subtree rooted at index `i`. The `order` parameter specifies the traversal order (e.g., preorder, post-order).

All the methods refer to the index of the nodes in S_{last} and S_α arrays.

3.8.6 Search Operations

The XBWT class provides search operation `subPathSearch(const std::vector<T> &path)` that searches for a subpath in the XBWT structure. It uses the compressed vectors to determine the range of positions corresponding to the nodes whose upward path is prefixed by a given vector reversed.

3.9 Experiments

Davide T.: Questa sezione andrà riadattata una volta che avremo deciso quali esperimenti fare con l'altro algorimo

The experiments have been run on a machine with an AMD Ryzen 9 5600Hs CPU with 24 GB of RAM. The results are shown in Table 3.1 and Table 3.2. The source code for the experiments can be found in the `experiments.cpp` file.

3.9.1 Construction Performance of the XBWT

To evaluate the performance of the implemented algorithms, we conducted a series of experiments on randomly generated trees created using the Python library `networkx`. The trees were generated with sizes ranging from 100 to 900,000 nodes. For each tree, we executed the construction algorithms 10 times, measuring the average execution time for both the linear *PathSort* (P.S.) algorithm and the naive *UpwardStableSort* (N.S.) algorithm used for constructing the XBWT. This approach allowed us to compare their performance across different tree sizes and assess their scalability.

The results are shown in Table 3.1.

Nodes	**Depth**	**P.S. Time (s)**	**N.S. Time (s)**
100	22	0.002	0.001
500	45	0.004	0.002
1000	74	0.006	0.003
5000	175	0.028	0.015
10000	288	0.056	0.053
50000	486	0.31	0.35
100000	754	0.69	1.25
500000	2246	4.7	16.46
900000	2658	8.51	34.2

Table 3.1: Performance comparison between PathSort and Naive Sort algorithms.

3.9.2 Space Analysis of the XBWT

To evaluate the space savings achieved through XBWT compression, we conducted experiments on the same set of randomly generated trees used for the construction performance tests. For each tree, we compared the memory usage (in bytes) of three representations: the plain tree, the uncompressed XBWT, and the compressed XBWT.

The plain tree representation consists of the simple balanced parenthesis encoding of the tree structure combined with the edge labels. For example for tree in Figure 3.1, the plain tree representation would be:

`(A(B(D(a))(a)(E(b)))(C(D(c))(b)(D(c)))(B(D(b)))).`

By *uncompressed XBWT*, we refer to the XBWT arrays S_{last} and S_α (including the additional bit) stored without any compression. Specifically, S_{last} is represented as a plain bitvector (`sdsl::bit_vector`), and S_α is stored as a wavelet tree (`sdsl::wt_int`) with plain bitvectors (`sdsl::bit_vector`). In contrast, the *compressed XBWT* representation stores S_{last} and S_A as compressed RRR bitvectors (`sdsl::rrr_vector`), and S_α as a wavelet tree with RRR bitvectors, as described in the previous chapter.

Table 3.2 reports the sizes (in bytes) for each representation of the trees across different sizes. The last column highlights the space savings achieved by the compressed XBWT compared to the plain tree representation, expressed as a percentage. These results illustrate the substantial space reductions achieved through compression, especially as the tree size increases.

Nodes	Plain tree (B)	U. XBWT (B)	C. XBWT (B)	Saving (%)
100	390	424	496	-27.18
500	2390	1112	1136	52.47
1000	4890	2242	2056	57.96
5000	28890	12911	10400	64
10000	58890	45625	21848	62.90
50000	338890	175146	123216	63.64
100000	688890	349478	259376	62.35
500000	3888890	1850850	1451570	62.67
900000	7088890	3480190	2718570	61.65

Table 3.2: Space analysis of the XBWT. Plain tree is the size in bytes of the tree in the simple balanced parenthesis representation plus the edge labels, U. XBWT is the size in bytes of the tree in the uncompressed XBWT, and C. XBWT is the size in bytes of the tree in the compressed XBWT. The last column shows the space-saving percentage between plain tree and compressed XBWT.

3.9.3 Conclusions

From the results shown in Table 3.1, we can draw several conclusions about the performance of the PathSort (P.S.) algorithm compared to the Naive Sort (N.S.) algorithm and the space savings achieved by compressing the XBWT.

Firstly, 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.

Secondly, the depth of the tree appears to increase with the number of nodes, which is expected in randomly generated trees. This increase in depth does not seem to adversely affect the performance of the PathSort algorithm as much as it does the Naive Sort algorithm.

For small trees, the compressed XBWT does not always provide immediate savings due to the overhead of succinct data structures. For instance, for 100 nodes, the compressed representation is larger than the plain tree, showing a -27.18% increase in space. However, as the number of nodes increases, the compression becomes more effective, achieving savings of over 60% for large trees.

The space reduction becomes particularly evident for trees with more than 500 nodes. These results confirm that the compressed XBWT provides a scalable and space-efficient alternative for storing and indexing labeled trees. The efficiency gains are particularly beneficial for applications requiring large-scale tree processing, such as bioinformatics and text indexing.

In conclusion, the PathSort algorithm is a more efficient choice for constructing the XBWT, especially for larger trees, and the compression method provides significant space savings, making the overall process more efficient in terms of both time and space.

Chapter 4

Hopcroft's algorithm for Minimization of DFA

Tree compression schemes that effectively exploit repetitive structures require efficient techniques for identifying and representing such repetitions in a compact manner. In our approach, we leverage deterministic finite automata (DFA) minimization as a foundational tool for recognizing and compressing recurring patterns within trees. Among the various DFA minimization algorithms, Hopcroft's algorithm stands out due to its optimal time complexity and efficiency in reducing state redundancies. This chapter provides the necessary theoretical background on Hopcroft's algorithm and DFA minimization, explaining their relevance to our proposed compression scheme. Also, we introduce a linear-time algorithm for minimizing acyclic deterministic finite automata, which is particularly suitable for identifying repetitive structures in trees. Let's start by introducing what are deterministic finite automata and why minimizing them is important for tree compression.

4.1 Deterministic Finite Automata (DFA)

Definition 1 (Deterministic Finite Automaton). *A deterministic finite automaton (DFA) is a 5-tuple $M = (Q, \Sigma, \delta, q_0, F)$ where:*

- *Q is a finite set of states*
- *Σ is a finite set of input symbols (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*

The DFA processes an input string s one symbol at a time by starting from the initial state q_0 and following transitions based on the input symbols. The string s is accepted if the DFA ends in an accepting state after processing all input symbols, otherwise, it is rejected. The language recognized by a DFA is the set of all strings that lead to an accepting state. DFA are widely used in various applications, including lexical analysis, pattern matching, and formal language theory.

4.1.1 DFA Minimization

The process of automata minimization consists in reducing the number of states in a DFA while preserving the language accepted by the DFA. The minimization of DFA is crucial for a variety of applications, such model checking, hardware design, and compilers, as it produces a more effective and compact representation of the automaton allowing for faster processing and reduced memory usage.

The minimization of DFA 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 the Hopcroft's algorithm, which was proposed by John Hopcroft in 1971 [13]. The 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.

4.2 The Need for DFA Minimization in the novel scheme

A key challenge in tree compression is the identification of structurally similar or identical subtrees. By modeling repetitive substructures as states in a DFA, we can transform the problem into one of minimizing redundant states, thereby reducing the size of the representation. DFA minimization ensures that equivalent substructures are merged efficiently, leading to a more compact encoding.

The minimized DFA provides a canonical representation of the repetitive structures, which can then be leveraged in our compression pipeline. This theoretical foundation enables us to systematically identify and encode tree patterns, ultimately improving the compression efficiency.

In the subsequent sections, we delve into the formal definition of the Hopcroft's algorithm. Then, we introduce an algorithm for minimizing acyclic DFAs in linear time, which is particularly relevant for identifying repetitive structures in trees.

4.3 Hopcroft's Minimization Algorithm

Minimization of DFA is a classical and widely studied problem in automata theory and Formal Languages. It consists of finding the unique (up to isomorphism) finite automaton with the minimal number of states, recognizing the same regular language of a given DFA.

Algorithm 8 works by iteratively refining a partition of the states until no further refinement is possible, meaning all states within each set of the partition are indistinguishable. The final partition represents the equivalence classes, which correspond to the states of the minimal DFA. Here's a step-by-step explanation based on the provided pseudocode:

1. **Initialization:** The algorithm starts with an initial partition P containing two sets: the set of final states F and the set of non-final states $Q \setminus F$. These are the coarsest sets of potentially distinguishable states. A working set W is initialized, typically containing the set of final states F (or the smaller of the two initial sets as an optimization). W holds the sets that are used as "splitters" to refine the partition P.

2. **Refinement Loop:** The algorithm iterates as long as the working set W is not empty. In each iteration, a set A (a "splitter") is removed from W. Then,

Algorithm 8 Hopcroft's Algorithm for DFA Minimization

```
Require: A DFA $M = (Q, \Sigma, \delta, q_0, F)$
 1: $P \leftarrow \{F, Q \setminus F\}$                              ▷ Initial partition
 2: $W \leftarrow \{F\}$                  ▷ Working set initialized with final states
 3: while $W \neq \emptyset$ do
 4:     Remove a set $A$ from $W$
 5:     for all $c \in \Sigma$ do
 6:         $X \leftarrow \{q \in Q \mid \delta(q, c) \in A\}$            ▷ Predecessors of $A$ via $c$
 7:         for all $Y \in P$ such that $X \cap Y \neq \emptyset$ and $Y \setminus X \neq \emptyset$ do
 8:             Replace $Y$ in $P$ with $Y_1 = X \cap Y$ and $Y_2 = Y \setminus X$
 9:             if $Y \in W$ then
10:                 Replace $Y$ in $W$ with $Y_1$ and $Y_2$
11:             else
12:                 Add the smaller of $Y_1$ and $Y_2$ to $W$
13:             end if
14:         end for
15:     end for
16: end while
17: return the minimized DFA built from partition $P$
```

for each input symbol $c \in \Sigma$:

- Calculate the set $X = \{q \in Q \mid \delta(q, c) \in A\}$. This is the set of all states that transition *into* the set A upon reading symbol c.
- For each set Y currently in the partition P, check if Y needs to be split by X. A split is necessary if some states in Y are in X and some are not (i.e., $X \cap Y \neq \emptyset$ and $Y \setminus X \neq \emptyset$). This indicates that states in Y are distinguishable based on whether their c-transition leads into A.
- If Y needs to be split, replace Y in the partition P with two new sets: $Y_1 = X \cap Y$ (states in Y that transition into A) and $Y_2 = Y \setminus X$ (states in Y that do not transition into A).
- Update the working set W: If the original set Y was in W, remove Y and add both new sets Y_1 and Y_2 to W. If Y was not in W, add only the smaller of the two new sets (Y_1 or Y_2) to W. This optimization helps maintain the algorithm's efficiency.

3. **Termination:** The loop continues until the working set W is empty. At this point, no set in the partition P can be further refined. The partition P now contains the final equivalence classes of states.

4. **Result:** The final partition P defines the states of the minimized DFA. Each set in P corresponds to a single state in the minimal DFA, and transitions are defined based on the original DFA's transitions between these sets.

The algorithm enables to compute equivalence classes of nodes in $O(n \log n)$, in particular, the Myhill-Nerode equivalence classes [24, 22]. 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's formalize the concept of equivalence classes and the Myhill-Nerode theorem.

Definition 2 (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.

Definition 3 (Regular Language)**.** *A language L over an alphabet Σ is called a* ***regular language*** *if it can be recognized by a deterministic finite automaton (DFA). Equivalently, a language is regular if it can be described by a regular expression or generated by a regular grammar. Regular languages form the simplest class in the Chomsky hierarchy of formal languages.*

Theorem 2 (Myhill-Nerode theorem [24, 22])**.** *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.*

4.4 Minimization of acyclic DFA in linear time

For our purpose, we will focus on a specific type of finite automaton: an acyclic deterministic finite automaton (or DAWG). An acyclic DFA is one where there are no cycles within the transitions. This property simplifies the minimization process since it ensures that every state can be reached from the start state through a unique path.

Let's start by giving the notion of directed acyclic word graph (DAWG):

Definition 4 (DAWG)**.** *A* ***DAWG*** *(directed acyclic word graph) or automaton $\mathcal{A}$ is defined by the following 5-uple:*

$$\mathcal{A} = (Q, \Sigma, F, T, q_0),$$

where

- *Q is a set of states;*
- *Σ is an alphabet of finite cardinal denoted by $|\Sigma|$;*
- *q_0 is the initial state;*
- *T is the subset of terminal states of Q;*
- *F is a function of $Q \times \Sigma$ into Q defining the transitions (arcs) of the automaton.*

The state reached by a transition labeled a from state q is denoted by $q.a = F(q, a)$. This notation extends transitively to words: if w is a word, then $q.w$ denotes the state reached by following the transitions labeled by each letter $w_1, w_2, \ldots, w_n$ of w. A word w is accepted by the automaton if $q_0.w \in T$.

In this section, we will discuss an efficient algorithm for minimizing acyclic deterministic finite automata in linear time on the number of states [26]. Let's start by giving some definitions and theorems introduced in the paper [26].

Definition 5 (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.*

$$h(s) = \{|w|| s.w \text{ is final}\}$$

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

Definition 6 (Distinguished set)**.** *We say that a set Π_i is distinguished if no pair of states in Π_i are equivalent.*

4.4.1 The algorithm

The minimization algorithm introduced in [26] operates by labeling each state with a unique identifier that represents the structure of the automaton from that state onward. It proceeds in the following steps:

1. **Height Computation:** The height of each state is determined, where the height of a state is the length of the longest path from that state to a final state.
2. **State Labeling:** Each state is labeled based on the structure of its transitions. The label consists of:
   - Whether the state is final or not.
   - The transitions, recorded as ordered pairs of symbols and target state identifiers.
3. **Lexicographic Sorting:** States at each height level are sorted lexicographically based on their labels using a bucket sort technique.
4. **Merging Equivalent States:** After sorting, states with identical labels are merged, ensuring that equivalent states are unified.

In details, the algorithm minimizes an acyclic deterministic finite automaton by leveraging the concept of state height. The algorithm partitions the states based on their height. It then processes these partitions in increasing order of height, starting from height 0.

The core idea relies on the 'height property': If every Π_j with $j < i$ is distinguished, then two states p and q in Π_i (the set of states with height i) are equivalent if and only if for every letter a in the alphabet Σ, the transitions $p.a$ and $q.a$ lead to the same state (or both are undefined).

The algorithm iteratively ensures that each Π_i is distinguished. It starts with Π_0, where all states are trivially equivalent (as they are final states with no outgoing paths to other final states contributing to height) and merges them. Then, for each subsequent height i, it sorts the states in Π_i based on their transitions. Specifically, states are grouped based on the target states of their transitions for each symbol in the alphabet. Since all lower levels ($j < i$) are already distinguished by the inductive step, states in Π_i that have identical transitions for all symbols (leading to equivalent states in lower levels) are themselves equivalent according to the height property. These equivalent states are then merged.

This process uses a specialized lexicographic sorting technique (related to bucket sort) optimized for this task, which helps achieve linear time complexity relative to the size of the automaton (number of states and transitions). The algorithm leverages a technique similar to the one presented in [1] for testing tree isomorphism. Specifically, Revuz adopt a renumbering scheme during the lexicographic sorting phase to optimize both time and space complexity.

4.4.2 Renumbering Scheme Explained

The core minimization algorithm relies on sorting states at the same height level based on their transitions. A state s can be represented by a label or tuple: $(F/NF, l_1, nl_1, l_2, nl_2, \dots, l_k, nl_k)$, where F/NF denotes final/non-final status, l_i is the i-th transition symbol (alphabet character), and nl_i is the target state of that transition.

The challenge arises when performing the lexicographic sort (using repeated bucket sorts) on these labels, specifically concerning the nl_i components. If the actual state numbers (ranging from 1 to $|Q|$, the total number of states) are used directly as the values for nl_i:

- The range of values for these components becomes large (1 to $|Q|$). This forces the bucket sort step that handles these components to use a bucket array of size $|Q|$, potentially making the sort non-linear in the size of the automaton if $|Q|$ is large compared to the number of transitions e.
- Alternatively, representing state numbers as strings of digits would increase the length of the labels by a factor proportional to $\log |Q|$, again potentially breaking the overall linear time complexity.

The renumbering scheme overcomes this issue by assigning temporary, small integer names to the target states (nl_i) during the sorting process for each height level Π_i. The key idea is that when sorting states at height i, we only need to distinguish between the equivalence classes of the target states nl_i from lower levels ($j < i$), as those levels have already been processed and minimized. The renumbering scheme ensures that the bucket array size is bounded by the maximum of $|C|$ (the alphabet size) and E_i (the total number of edges from states at height i). The renumbering function adopted is the following:

4.4.3 Pseudocode

The paper presents the core minimization logic and a more detailed sorting (or distinguishing) algorithm separately. Here's a combined representation based on the 'Final algorithm' section of the paper.

Algorithm 11 distinguishes states within a given height level Π_i. It iteratively refines

Algorithm 9 Renumbering Function

```
1: function Renumber(s, h, n)
2:     if $s$.ch $\neq h$ then
3:         $s$.ch $= h$
4:         $s$.num $= n$
5:         $n = n + 1$
6:     end if
7:     return $s$.num
8: end function
```

Algorithm 10 Minimization Algorithm for Acyclic DFAs

```
1: Calculate height $h(s)$ for every state $s$.
2: Create partitions $\Pi_i = \{s \in Q \mid h(s) = i\}$.
3: Merge all states in $\Pi_0$.
4: for $i := 1$ to $h(q_0)$ do                              ▷ $q_0$ is the initial state
5:     ▷ Distinguish states in $\Pi_i$ using the sorting/distinguishing algorithm below
6:     Put states in $\Pi_i$ into a list $L$.               ▷ May pre-split by Final/NonFinal
7:     Call Distinguish($L$)
8:     Merge resulting groups of equivalent states identified by Distinguish.
9: end for
```

partitions based on transitions. Each state s is labeled with the following:

$$label(s) = (F/NF, l_1, nl_1, l_2, nl_2, \ldots, l_k, nl_k)$$

where F/NF indicates final/non-final, l_k is the k-th transition symbol, and nl_k is the (renumbered) target state name. The sorting happens component by component.

Note: The pseudocode in the paper is slightly intertwined with the bucket sort details. This representation attempts to capture the logic described. The renumbering function is called implicitly when accessing nl_j. The handling of merging might occur after the Distinguish procedure completes for level i, or potentially within it as groups become fully distinguished. The pseudocode merges states within bucket Q[$], which relates to the end-of-string marker in the generic sort; for state labels, equivalence is confirmed when a group remains together after checking all label components.

Algorithm 11 Distinguish Algorithm

```
1: function DISTINGUISH(List_of_States)
2:     Place List_of_States into QUEUE2        ▷ Queue of lists of potentially equivalent states
3:     $k := 0$        ▷ Represents the component index of the label being compared
4:     repeat
5:         Move QUEUE2 to QUEUE1; Clear QUEUE2
6:         $k := k + 1$
7:         while QUEUE1 not empty do
8:             Let $L$ be the first list in QUEUE1
9:             Clear Buckets $Q[1 \dots m]$        ▷ $m$ depends on alphabet size and renumbered state names
10:            Clear NONEMPTY list of bucket indices
11:            while $L$ not empty do
12:                Let $S$ be the first state in $L$
13:                Determine the $k$-th component value $v$ for state $S$
14:                if $Q[v]$ is empty then
15:                    Add $v$ to NONEMPTY
16:                end if
17:                Move $S$ from $L$ to bucket $Q[v]$
18:            end while
19:            for each index $v$ in NONEMPTY do
20:                if Bucket $Q[v]$ contains more than one state then
21:                    Add $Q[v]$ as a list to QUEUE2        ▷ These still need further distinguishing
22:                else if $k$ corresponds to the end-of-label marker '$S$' then
23:                    Merge all states in $Q[v]$ (they are equivalent)
24:                end if
25:            end for
26:        end while
27:    until QUEUE2 is empty        ▷ No more lists need refinement
28: end function
```

Chapter 5

Min-Weight Perfect Bipartite Matching

5.1 Problem definition

Given a weighted bipartite graph $G = (V, E)$ (remember that a bipartite graph is a graph whose vertices can be divided into two disjoint sets V_1 and V_2 such that every edge connects a vertex in V_1 to a vertex in V_2), let's define the concept of a matching.

Definition 7 (Matching)**.** *A matching $M \in E$ 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 $|V_1| = |V_2|$ [9].

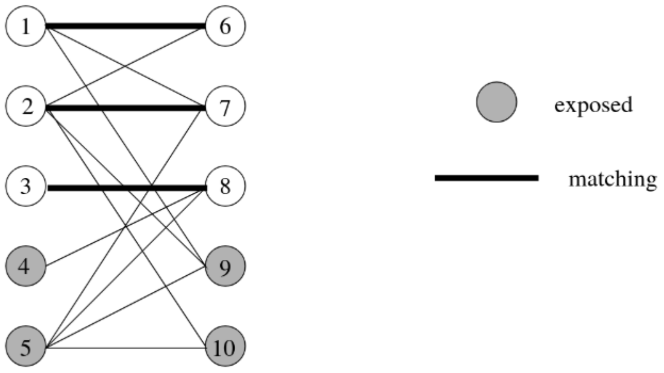


Figure 5.1: Example of a perfect matching in a bipartite graph.

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

Definition 8 (Minimum weight perfect matching in bipartite graphs (MWPBM))**.** *Given a weighted bipartite graph $G = (V, E)$, where $V = V_1 \cup V_2$ and $V_1 \cap V_2 = \emptyset$, 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. The weight of an edge $e = (u, v)$ is denoted by $w(e)$. This problem is also called **the assignment problem**.*

5.2 The existence of perfect matchings in bipartite graphs

In this section two theorems that states a condition for the existence of perfect matchings in bipartite graphs are introduced. These theorems will be useful in the following chapter to proof our reduction [23].

5.2.1 The Tutte matrix and its determinant

Let's start with the definition of the **Tutte matrix** of a bipartite graph.

Definition 9 (Tutte matrix)**.** *The Tutte matrix of bipartite graph $G = (U, V, E)$ is an $n \times n$ matrix M with the entry at row i and column j*

$$M_{i,j} = \begin{cases} 0, & \text{if } (u_i, u_j) \notin E \\ x_{i,j}, & \text{if } (u_i, u_j) \in E \end{cases} \tag{5.1}$$

The determinant of the Tutte matrix is useful in testing whether a graph has a perfect matching or not, as the following theorem introduced in [21] shows.

Theorem 3 (Existence of perfect matchings in bipartite graphs [21])**.** *Given a bipartite graph G and the Tutte matrix M for G then the following equivalence holds:*

$$Det(M) \neq 0 \iff \textit{There exists a perfect matching in } G$$

Proof. We have the following expression for the determinant:

$$\text{Det}(M) = \sum_{\pi \in S_n} (-1)^{sgn(\pi)} \prod_{i=1}^{n} M_{i,\pi(i)}$$

where S_n is the set of all permutations on $[n]$, and $sgn(\pi)$ is the sign of the permutation π. There is a one-to-one correspondence between a permutation $\pi \in S_n$ and a (possible) perfect matching

$$\{(u_1, v_{\pi(1)}), (u_2, v_{\pi(2)}), \cdots, (u_n, v_{\pi(n)})\} \text{ in } G.$$

Note that if this perfect matching does not exist in G (i.e., some edge $(u_i, v_{\pi(i)}) \notin E$), then the term corresponding to π in the summation is 0. So we have

$$\text{Det}(M) = \sum_{\pi \in P} (-1)^{sgn(\pi)} \prod_{i=1}^{n} x_{i,\pi(i)}$$

where P is the set of perfect matchings in G. This is clearly zero if $P = \emptyset$, i.e., if G has no perfect matching. If G has a perfect matching, there is a $\pi \in P$ and the term corresponding to π is

$$\prod_{i=1}^{n} x_{i,\pi(i)} \neq 0.$$

Additionally, there is no other term in the summation that contains the same set of variables. Therefore, this term is not cancelled by any other term. So in this case, $\mathrm{Det}(M) \neq 0$. □

5.2.2 The Hall's Marriage Theorem

Hall's Marriage Theorem [12] provides a necessary and sufficient condition for the existence of a matching in a bipartite graph that saturates one side of the partition. It's often stated in the context of finding pairings (like marriages) between two sets of entities.

Definition 10 (Neighborhood). *For a subset of vertices $W \subseteq V_1$, the* ***neighborhood*** *of W, denoted by $N(W)$, is the set of all vertices in V_2 that are adjacent to at least one vertex in W.*

$$N(W) = \{v \in V_2 \mid \exists u \in W \text{ such that } \{u, v\} \in E\}$$

Theorem 4 (Hall's Marriage Theorem [12]). *Let $G = (V_1 \cup V_2, E)$ be a bipartite graph. There exists a perfect matching M in G if and only if for every subset $W \subseteq V_1$, the following condition holds:*

$$|N(W)| \geq |W|$$

This condition is known as ***Hall's condition****.*

In simpler terms, a matching that covers all vertices in V_1 exists if and only if every group of vertices chosen from V_1 collectively has at least as many neighbors in V_2 as there are vertices in the chosen group.

5.3 Problem formulation

The problem of finding a minimum weight perfect matching in a bipartite graph can be formulated as an integer linear program (ILP), i.e.an optimization problem in which the variables are restricted to integer values and the constraints and the objective function are linear as a function of these variables. Given a matching M, let x be its incidence vector where $x_{ij} = 1$ if edge (i, j) is in the matching, and $x_{ij} = 0$ otherwise. Then, the problem can be formulated as follows:

$$\begin{aligned} \text{minimize} \quad & \sum_{(i,j)\in E} w_{ij} x_{ij} \\ \text{subject to} \quad & \sum_{j \in V_2} x_{ij} = 1, \quad \forall i \in V_1 \\ & \sum_{i \in V_1} x_{ij} = 1, \quad \forall j \in V_2 \\ & x_{ij} \in \{0, 1\}, \quad \forall (i, j) \in E \end{aligned} \tag{5.2}$$

Notice that any solution to this integer program corresponds to a matching and therefore this is a valid formulation of the minimum weight perfect matching problem in bipartite graphs.

The linear program relaxation of the above integer program is as follows:

$$\begin{aligned} \text{minimize} \quad & \sum_{(i,j)\in E} w_{ij}x_{ij} \\ \text{subject to} \quad & \sum_{j\in V_2} x_{ij} = 1, \quad \forall i \in V_1 \\ & \sum_{i\in V_1} x_{ij} = 1, \quad \forall j \in V_2 \\ & 0 \le x_{ij} \le 1, \quad \forall (i,j) \in E \end{aligned} \tag{5.3}$$

The set of feasible solutions to the constraints in (P) forms a polytope. When optimizing a linear constraint over a polytope, the optimum will be achieved at one of the "corners" or extreme points of the polytope. An extreme point x of a set Q is an element $x \in Q$ that cannot be expressed as $\lambda y + (1-\lambda)z$ with $0 < \lambda < 1$, $y, z \in Q$, and $y \neq z$. (This concept will be formalized and discussed in more detail when we cover polyhedral theory.)

In general, even if all the coefficients of the constraint matrix in a linear program are either 0 or 1, the extreme points of a linear program are not guaranteed to have all coordinates integral. This is not surprising since the general integer programming problem is NP-hard, while linear programming is solvable in polynomial time. Consequently, there is no guarantee that the value Z_{IP} of an integer program is equal to the value Z_{LP} of its LP relaxation. However, since the integer program is more constrained than the relaxation, we always have $Z_{IP} \geq Z_{LP}$, implying that Z_{LP} is a lower bound on Z_{IP} for a minimization problem. Moreover, if an optimal solution to a linear programming relaxation is integral, then it must also be an optimal solution to the integer program.

In our problem, the constraint matrix has a special form that lead to the following result:

Theorem 5. *Any extreme point of (P) is a $0-1$ vector and, hence, is the incidence vector of a perfect matching.*

Consequently, the polytope

$$\begin{aligned} P = \{x : & \sum_{j\in V_2} x_{ij} = 1, \quad \forall i \in V_1, \\ & \sum_{i\in V_1} x_{ij} = 1, \quad \forall j \in V_2, \\ & 0 \le x_{ij} \le 1, \quad \forall (i,j) \in E\} \end{aligned} \tag{5.4}$$

is called the bipartite perfect matching polytope.

5.4 Solutions to the problem

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 [17]. The algorithm is based on the Hungarian method, which is a combinatorial optimization algorithm that solves the assignment problem in polynomial time. In the original paper the complexity of the algorithm was $O(n^4)$, but later Dinic and Kronrod [5] showed that the algorithm can be implemented in $O(n^3)$ time.

The Hungarian method is a powerful algorithm, however, the algorithm is not very intuitive and can be difficult to implement. In recent years, several other algorithms have been proposed to solve the problem of finding a minimum weight perfect matching in a bipartite graph. In 1970, Edmonds and Karp [6] proposed an algorithm that solves the problem in $O(nm + n^2 \log n)$ time. In 1989 Gabow and Tarjan [8] proposed an algorithm that solves the problem in $O(\sqrt{n}m \log(nW))$ time, where n, m and W denote the number of vertices, number of edges, and largest magnitude of a cost; costs are assumed to be integral. The algorithms work by scaling. Lastly, in 2009, Sankowski and Piotr [27] introduced a randomized algorithm that solves the problem in $O(Wn^w)$ time, where w is the exponent of matrix multiplication, and W is the highest edge weight in the graph.

In 2022, Chen, Li, et al. [3] proposed a new solution to the Minimum-Cost Flow problem that woks in almost-linear time, precisely in $O(m^{1+o(1)})$ time. The minimum-cost flow problem is a classic combinatorial graph problem that find numerous applications in engineering and scientific computing. This result is important also for our problem, since the maximum weight perfect matching problem can be reduced to the minimum-cost flow problem, allowing to solve the problem in almost-linear time.

5.5 Implementation used in this work

Davide T.: Da completare una volta deciso come procedere

In this section, we will present an implementation of the Gabow and Tarjan algorithm to solve the problem of finding a minimum weight perfect matching in a bipartite graph. The algorithm is based on scaling and is a generalization of the Hungarian method. The algorithm works by scaling the edge weights and then finding a perfect matching in the scaled graph.

Chapter 6

Tree compression scheme focused on repetitive structures

As introduced in the first chapter of this thesis, the main goal of this work is to develop a new tree compression scheme that is able to exploit the presence of repetitive structures in the input tree. The idea is to design a compression algorithm that is able to identify and compress the repetitive parts of the input tree, while still being able to represent the non-repetitive parts of the tree in a compact way. The main motivation behind this work is to improve the compression performance of tree compression algorithms when dealing with trees that contain repetitive structures. In this chapter, we provide an overview of the proposed tree compression scheme.

6.1 The novel compression scheme pipeline

Let T be an ordered tree of arbitrary fan-out, depth, and shape. T consists of n internal nodes and ℓ leaves, for a total of $t = n + \ell$ nodes. Every node of T is labeled with a symbol drawn from an alphabet Σ. We assume that Σ is the set of labels effectively used in the nodes of T and that these labels are encoded with the integers in the range $[1, |\Sigma|]$. Then we need to define the array π where, for each node u, $\pi(u)$ is the string obtained by concatenating the labels on the **upward path** from the parent of u to the root of the tree (root has an empty π component).

The following pipeline is used to compress the tree T:

1. Initially the array π is computed for the tree T by traversing the tree in a pre-order fashion. Then the nodes are stably sorted by the lexicographic order of their π strings. In order to sort the nodes, the **Path Sort** algorithm introduced in [7] is used, allowing to sort nodes in linear time and $O(t \log t)$ space. An implementation of this algorithm in C++ is available in the author's GitHub in the following repository: `https://github.com/davide-tonetto-884585/XBWT`.

2. Then, using a variant of the Hopcroft algorithm for minimization of DFA [13] that works over directed acyclic graphs [26] and so over trees, the nodes are partitioned into equivalence classes where two nodes are equivalent (has the same class) if they have the same subtree rooted at them.

3. Given a width p, the nodes previously sorted are then divided into p chains with the aim of minimizing the run-length encoding of each chain (by considering the equivalence classes). In order to do so we reduced this problem (CHAINS-DIVISION problem) to the Minimum Perfect Bipartite Matching problem, which can be solved in polynomial time as introduced in [3] and [27].

4. Lastly, the resulting deterministic finite automaton (DFA) or non-deterministic finite automaton (NFA) can be indexed using the indexing scheme introduced by Cotumaccio et al. [4]. Also, the chains may be compressed using some techniques such as run-length encoding, Huffman encoding, and Elias-Fano encoding.

6.2 Reducing Chains-Division Problem to the Assignment Problem

In this section, we will show how we can reduce the problem of finding the optimal partition of the nodes of a tree T given their equivalence classes into p with $p \leq |E| \leq t$ chains to the Minimum Weight Perfect Bipartite Matching problem, where E is the set of equivalence classes of the nodes of T and t is the number of nodes of the tree. This reduction will allow us to solve the problem in polynomial time as shown in the previous chapter.

Then we will show how to optimize the reduction by introducing some constraints that will allow us to reduce the number of edges in the bipartite graph, and we will also show how to move from the Minimum Weight Perfect Bipartite Matching problem to the more studied Maximum Weight Perfect Bipartite Matching problem without losing generality.

6.2.1 Chains-Division problem definition

It is important to start by defining the problem we want to solve.

Definition 11 (CHAINS-DIVISION problem). *Given a tree T with t nodes, and given the equivalence classes E coming from the Hopcroft algorithm applied to the tree T, the sorted order of the nodes in T according to the upward path π, and the number of chain $2 \leq p \leq t$, we want to find the optimal partition of the nodes of T into p chains such that the run length encoding of each chain is minimized.*

Let's give a formal definition of run length encoding.

Definition 12 (Run length encoding). *Given a sequence $S = \{s_1, s_2, \dots, s_n\}$, the run length encoding of S is the sequence $R = \{r_1, r_2, \dots, r_m\}$ where r_i is the number of times the element s_i is repeated in S. It allows us to represent the sequence S in a more compact way.*

So, we aim to divide the nodes of the tree into p chains such that the run length encoding of the chains is minimized meaning that we want to minimize the number of distinct equivalence classes in each chain. Follows the definition of chain.

Definition 13 (Chains). *Given a tree T with t nodes and p chains, a chain C is a sequence of nodes $C = \{c_1, c_2, \dots, c_m\}$ such that c_i is a node of T for $i = 1, 2, \dots, m$ and $m \leq t$. Also, Each node of T is in exactly one chain and the nodes of the chain are ordered according to the upward path π of the tree.*

6.2.2 Bipartite graph construction

Now we will show how to construct a bipartite graph that will allow us to solve the problem of finding the optimal partition of the nodes of a tree T given their equivalence classes into p with $p \leq |E| \leq t$ chains.

Let T be a tree with t nodes and p, which is the number of chains we want to partition the nodes into. Let E be the set of equivalence classes of the nodes of T. We can construct a bipartite graph $G = (V, E)$ such that vertices are divided in two disjoint sets $V = V_1 \cup V_2$ in the following way:

Definition 14. *The two sets V_1 and V_2 of the bipartite graph G are constructed in the following way:*

- *V_1 contains $t + p$ nodes composed by p source nodes $s_1, s_2, \ldots, s_p$ and the t elements of E ordered.*
- *V_2 contains $t + p$ nodes composed by the t elements of E ordered and p destination nodes $d_1, d_2, \ldots, d_p$.*

Then the edges of the graph G will be constructed in the following way:

1. *The sources nodes $s_i \in V_1$ for $i = 1, 2, \ldots, p$ are connected to the first p nodes with distinct equivalence class in V_2 with weight 1.*
2. *Each of the t nodes of the tree in V_1 is connected to the first p (at most) nodes with distinct class in V_2 (and without the same class of the considered node) coming after it in the ordering of the nodes with weight 1.*
3. *Each of the t nodes of the tree in V_1 is also connected to the first node with its same class in V_2 coming after it in the ordering of the nodes of t with weight 0 iff there is one, otherwise p edges with weight 0 are added to each of the destination nodes $d_i \in V_2$ for $i = 1, 2, \ldots, p$.*

Notice that it is important to consider the order of the nodes of the two sets V_1 and V_2 as stated above, because we will need to connect the source nodes to the destination nodes in a way that will allow us to find the optimal partition of the nodes of the tree. In Figure 6.3 the nodes are ordered from top to bottom. An example of the node structure is shown in Figure 6.1.

Notice also that when we talk about the same V_1 node placed in V_2 we are referring to the corresponding node in V_2 that derives from the same node in the original tree T since the nodes of the tree are placed ordered in both sets V_1 and V_2. In Figure 6.1, 6.3 and 6.2 the node's correspondence is achieved by putting the two nodes at the same level.

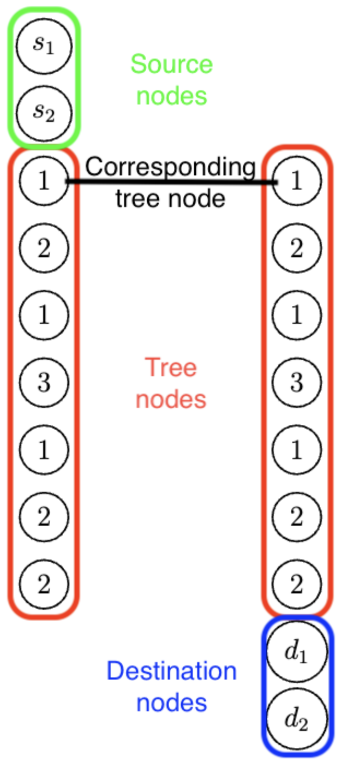


Figure 6.1: Example of a bipartite graph nodes constructed from a tree with the following equivalence classes $E = \{1, 2, 1, 3, 1, 2, 2\}$. The nodes are ordered from top to bottom.

Definition 15 (Bipartite graph properties)**.** *The resulting bipartite graph G will have $2t + 2p$ nodes and $O(t(p + 1) + p^2 + tp)$ edges, where the $O(t(p + 1))$ edges come from the tree nodes, the $O(p^2)$ edges come from the sources since each source node is connected to p nodes, and the $O(tp)$ edges come from the destination nodes since in the worst case we have t distinct equivalence class and so all the nodes are connected to the destination nodes. The weight of the edges will be* 0 *or* 1*.*

Let's see a small example for each case, consider $p = 2$. In Figure 6.2-(a) there is an example for the sources' edges, as stated before, for each source p nodes with weight 1 are created and connected to the first p nodes with distinct equivalence class in V_2.

In Figure 6.2-(b) there is an example for the tree nodes' edges, for each node in the tree T edges with weight 1 are created and connected to the first p nodes with distinct equivalence class in V_2 after the corresponding node in V_2 (coming after the node itself in the ordering), and edges with weight 0 are created and connected to the first node with the same class in V_2 after the corresponding node in V_2. As we can see from the image, we consider the first node in V_1 labelled 1 that is connected to the node 2 with weight 1 and to the node 3 with weight 1, and to the second node labelled 1 in V_2 with weight 0.

Lastly, in Figure 6.2-(c) there is an example for the destination nodes' edges, we start by considering the first node in V_1 that is labelled 1, it is connected to the node 2 with weight 1, then since there is no node with the same class in V_2 we connect it to the destination nodes d_1 and d_2 with weight 0. The same is done for the second node in V_1 that is labelled 2 since no nodes are coming after it in the order it is connected to the destination nodes d_1 and d_2 with weight 0.

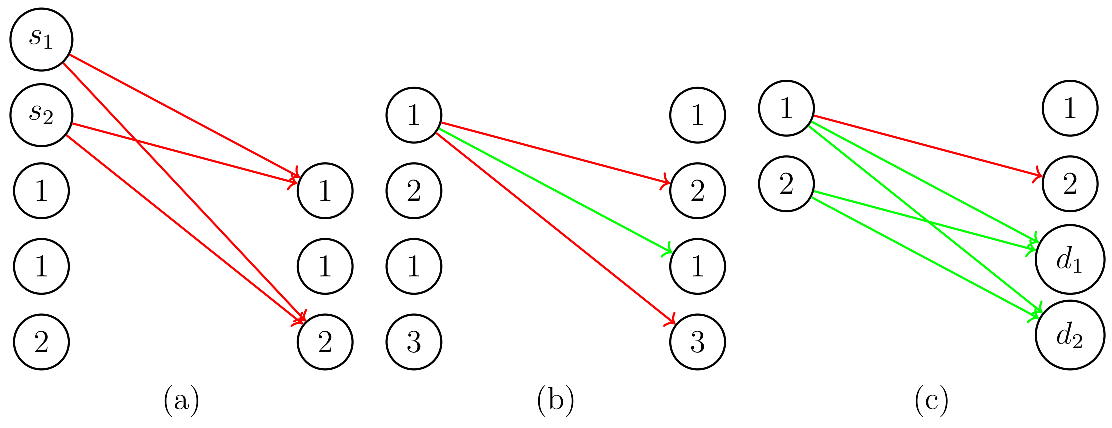


Figure 6.2: Considering $p = 2$ these three examples show how to connect nodes in the bipartite graph in the case of sources (a), tree nodes (b), and destinations (c).

6.2.3 Proof of correctness

Let's start by stating the following lemmas.

Lemma 1. *Exactly $|E|$ nodes of the tree T of the set V_1 are connected each to all the destination nodes $d_i \in V_2 \quad \forall i = 1, 2, \ldots, p$ with weight 0. Where E is the set of equivalence classes of the nodes of T coming from the Hopcroft algorithm applied to the tree T.*

Proof. Since the destination nodes $d_i \in V_2$ are connected to the nodes of the tree T with weight 0 only if there is no other node with the same class in V_2 coming after the node in the ordering, then for sure there are $|E|$ nodes of the tree T in V_1 that have no other node with the same class in V_2 coming after the node in the ordering. □

Lemma 2. *The optimal solution of the CHAINS-DIVISION problem for an instance $\mathcal{I}$ for a tree T is always greater or equal to the number of equivalence classes coming from the Hopcroft algorithm applied to the tree T.*

Proof. Since we aim to minimize the run length encoding of the chains, and the minimum cost of a chain is 1, then the optimal cost of the *CHAINS-DIVISION* problem for the tree T is always greater or equal to the number of equivalence classes since if we dispose them in $|E|$ chains we will have a cost of $|E|$ since each chain contains only nodes with the same class, and if we dispose them in $p < |E|$ chains we will have a cost greater or equal to $|E|$ since we will have to put at least two nodes with the same class into one chain or more. □

Claim 1. *The solutions for the CHAINS-DIVISION problem for the instances where the number p of chains is greater than $|E|$ are not better than the solutions for the instances where $p \leq |E|$.*

Proof. The proof comes directly from lemma 2. □

Lemma 3. *Given a bipartite graph G constructed as stated in Definition 14 from a tree T, for each node $u \in V_1$ coming from the nodes of T it is impossible for u to be* *connected to node $v \in V_2$ coming from the nodes of T such as $v < u$ in the order of the nodes of the tree T.*

Proof. The proof comes from the construction of G where the nodes of V_1 are always connected to the nodes of V_2 coming after them in the ordering of the nodes of the tree T. □

Lemma 4. *For every possible instance of the CHAINS-DIVISION problem, a perfect matching exists in the bipartite graph G constructed as specified in Definition 14.*

Proof. The proof comes from the construction of the bipartite graph G and from theorem 4. We are going to proof that the bipartite graph G constructed as stated in Definition 14 satisfies the Hall's condition and so, since by construction $|V_1| = |V_2|$, a perfect matching for G exists.

To verify Hall's condition we need to prove that for any subset $W \subseteq V_1$ we have that $|W| \leq |N(W)|$, where $N(W)$ is the neighborhood of W (Definition 10). We have the following cases (we refer to the set of source nodes $s_i \in V_1$ as S, the set of destination nodes $d_i \in V_2$ as D, and the set of tree nodes $u_i \in V_1$ as U):

1. W **contains only source nodes** ($W \subseteq S$): Let $W = \{s_{i_1}, \ldots, s_{i_k}\}$ where $k = |W| \leq p$. By construction rule 1, each source s_i is connected to the first p distinct-class nodes v_j in V_2. Let these target nodes be $T = \{v_{j_1}, \ldots, v_{j_p}\}$. The neighborhood $N(W)$ is a subset of T. Since all sources in W connect to nodes within T, $|N(W)| \leq |T| = p$. However, the construction connects each source s_i to p distinct nodes in V_2. A precise analysis of $N(W)$ is needed. In the definition, where all sources connect to the same first p distinct class nodes, $N(W)$ would be exactly those p nodes if W is non-empty. So, $|N(W)| = p$. Since $|W| = k \leq p$, we have $|N(W)| \geq |W|$.

2. W **contains only tree nodes** ($W \subseteq U$): Let $W = \{u_{j_1}, \ldots, u_{j_k}\} \subseteq V_1$ where $k = |W|$. This is the most complex case. We need to consider the neighborhood $N(W) \subseteq V_2 = V \cup D$. By construction:

   - Each $u_j \in W$ connects only to nodes v_l in V_2 where $l > j$ (lemma 3)
   - Each node connects to the next node of the same class with weight 0 (same-class connections)
   - Each node connects to the next p distinct-class nodes with weight 1 (distinct-class connections)
   - Nodes that are last of their class connect to all destination nodes $d_1, \ldots, d_p$ (destination connections)

   We distinguish the following cases:

   - In W there are only nodes which are not last of their class, by lemma 3, u_m connects to nodes v_l or d_l where $l > m$. For sure at least one neighbor is distinct from those of earlier nodes in W meaning that $|N(W)| \geq |W|$.
   - In W there are only nodes which are last of their class, also in this case for sure we have $|N(W)| \geq |W|$ since the last node of W in the ordering connects only to all destination nodes $d_1, \ldots, d_p$ (with $p \geq 2$) but the previous

ones in the ordering connect to destinations but also to the next node of distinct class with weight 1 allowing to connect not only the destination nodes but also to other distinct tree nodes in V_2.

- In W there are both nodes which are last of their class and nodes which are not last of their class, in this last case we have $|N(W)| \geq |W|$ as a derivation from the previous cases.

3. W **contains both source and tree nodes** ($W = W_S \cup W_U, where W_S \subseteq S, W_U \subseteq U$): We have $|N(W)| \geq |W|$ as a derivation from the previous cases and lemma 3.

□

Now we can prove the correctness of the reduction.

Theorem 6. *An optimal solution of an instance $\mathcal{I}$ with $p \leq |E|$ of the problem defined in Definition 11 is equivalent to an optimal solution of the Minimum Weight Perfect Bipartite Matching for the instance $r(\mathcal{I})$ where $r : \mathcal{I}_{CHAINS-DIVISION} \to \mathcal{I}_{MWPBM}$ is the reduction function that maps an instance of the problem defined in Definition 11 to an instance of the Minimum Weight Perfect Bipartite Matching problem defined in Definition 8 constructed as stated in Definition 14.*

Proof. Let $\mathcal{I}$ be an instance of the CHAINS-DIVISION problem with a tree T (having t nodes), its equivalence classes E, and a target number of chains p. From claim 1, we only consider $p \leq |E|$. Let $G = (V_1 \cup V_2, E')$ be the bipartite graph constructed according to Definition 14, which is the instance $r(\mathcal{I})$ for the MWPBM problem. We need to show that an optimal solution to CHAINS-DIVISION for $\mathcal{I}$ corresponds directly to an optimal solution (a minimum weight perfect matching) for MWPBM on G, and vice versa.

By construction, $|V_1| = |V_2| = t + p$. Lemma 4 guarantees that a perfect matching always exists in G.

Consider a perfect matching M in G. Since $|V_1| = |V_2|$ and M is perfect, every node in V_1 is matched to exactly one node in V_2, and vice versa. The matching M consists of $t+p$ edges. Due to the construction and Lemma 3 (nodes $u \in V_1 \cap T$ only connect to $v \in V_2 \cap T$ with $v > u$ or to destination nodes d_j), the matching M naturally decomposes into p paths starting from the source nodes $s_1, \ldots, s_p$ and ending at the destination nodes $d_1, \ldots, d_p$. Each path traverses a sequence of nodes corresponding to the nodes of the tree T. Specifically, a path starting at s_i will match s_i to some tree node $u_{j_1} \in V_2$. Then, the corresponding node $u_{j_1} \in V_1$ must be matched to some $u_{j_2} \in V_2$ (where $j_2 > j_1$) or a destination node d_k. This continues until a tree node $u_{j_m} \in V_1$ is matched to a destination node d_k. This forms a sequence $s_i \to u_{j_1} \to u_{j_2} \to \cdots \to u_{j_m} \to d_k$.

Let this set of p paths define a partition of the tree nodes into p chains $C_1, \ldots, C_p$, where each chain C_k contains the sequence of tree nodes visited by the k-th path. The ordering within each chain respects the original tree ordering π due to Lemma 3.

Now, let's analyze the weight of the matching M. The total weight $W(M)$ is the sum of the weights of its edges. According to Definition 14:

- Edges from source nodes s_i have weight 1. There are p such edges in M. These correspond to the start of each chain, contributing a base cost of 1 per chain.
- Edges (u_j, u_k) between tree nodes in V_1 and V_2 have weight 0 if u_j and u_k belong to the same equivalence class ($class(u_j) = class(u_k)$). These edges continue a run of the same class within a chain.
- Edges (u_j, u_k) between tree nodes have weight 1 if $class(u_j) \neq class(u_k)$. These edges signify a change in the equivalence class within a chain, thus starting a new run in the RLE sense.
- Edges (u_j, d_k) from a tree node to a destination node have weight 0. These edges terminate a chain and do not contribute to the RLE cost.

The total weight of the matching M is therefore

$$W(M) = p + \text{(number of weight-1 edges between tree nodes)}$$

The cost of the chain partition, defined as the sum of the lengths of the run-length encodings of the chains, is precisely $p +$ (number of class changes within chains). A class change occurs exactly when a path in the matching uses a weight-1 edge between tree nodes. Therefore, $W(M)$ is exactly equal to the RLE cost of the partition defined by the matching M.

Conversely, any valid partition of T into p ordered chains $C_1, \dots, C_p$ can be mapped to a perfect matching M in G. For each chain $C_k = [u_{k,1}, \dots, u_{k,m_k}]$, we construct a path in G: match s_k to $u_{k,1} \in V_2$. Then match $u_{k,i} \in V_1$ to $u_{k,i+1} \in V_2$ for $i = 1, \dots, m_k - 1$. Finally, match $u_{k,m_k} \in V_1$ to one of the available destination nodes d_j. Since we have p chains and p source/destination nodes, and every tree node is in exactly one chain, this process uses all $t + p$ nodes in V_1 and V_2, forming a perfect matching. The weight of this matching will correspond to the RLE cost of the partition, as argued above.

Since there is a one-to-one correspondence between valid chain partitions and perfect matchings in G, and the cost of a partition (total RLE length) is equal to the weight of the corresponding matching, minimizing the matching weight is equivalent to minimizing the RLE cost. Thus, an optimal solution to MWPBM on G yields an optimal solution to CHAINS-DIVISION on T. □

6.2.4 Full example

Consider The example in Figure 6.3 where we have a tree T with $t = 7$ nodes, $p = 2$ chains and the equivalence classes $E = \{1, 2, 1, 3, 1, 2, 2\}$ sorted accordingly to the upward path π of each node of the tree. We can construct the two distinct sets V_1 and V_2 of the bipartite graph G as follows: $V_1 = \{s_1, s_2, 1, 2, 1, 3, 1, 2, 2\}$ and $V_2 = \{1, 2, 1, 3, 1, 2, 2, d_1, d_2\}$. The edges of the graph G will be constructed as stated in Definition 14. In Figure 6.3-(a) we have the resulting bipartite graph, and in Figure 6.3-(b) we have one of the possible minimum perfect matchings for the graph in (a) having weight 4. A the end we can see that the optimal partition of the nodes of the tree T is $C_1 = \{1, 1, 1, 2, 2\}$ and $C_2 = \{2, 3\}$ with a total cost of

4, this can be obtained starting from the sources and by following the edges of the nodes, jumping to the corresponding node in V_1 and following the edges again until we reach the destination nodes.

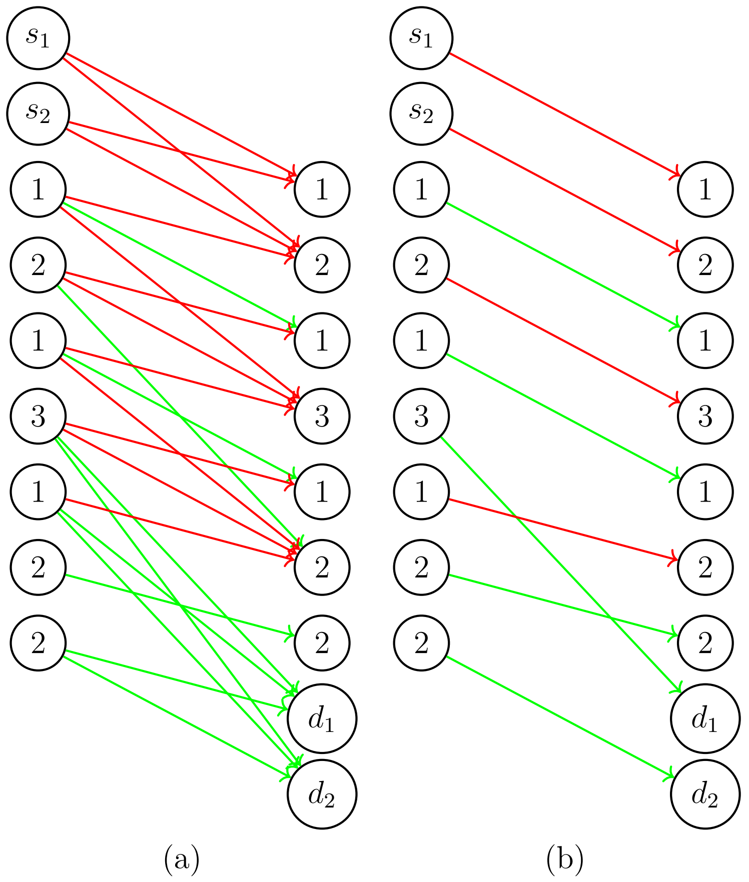


Figure 6.3: Example of a reduction for the sorted nodes' equivalency classes $E = \{1, 2, 1, 3, 1, 2, 2\}$. In (a), we have the resulting bipartite graph constructed from E. In (b), we have the resulting perfect matching for the graph in (a) having weight 4. Green edges weigh 0, while red edges weigh 1.

6.2.5 Heuristics and Improvements

Some changes can be made to the reduction in order to optimize it and to reduce the number of edges in the bipartite graph. Here are some of the improvements that can be made.

- **Sources' edges optimization**:

  Lemma 5. *The sources' edges can be optimized by connecting each source only to the smaller node (considering the order of the nodes) in V_2 coming from the tree T that is not connected to any other source.*

  Proof. Since the source nodes are needed to distinguish the chains as starting points, we need that each source is connected to at least one node in V_2 coming from the tree T. Having the sources connected to the first p nodes with distinct equivalence class in V_2 is not necessary since allows us just to invert the chains starting from each source and so it is redundant. We can connect each source to the smaller node in V_2 coming from the tree T that is not connected to any other source since we need to connect each source to at least one node in V_2 coming from the tree T and this will allow us to distinguish the chains. □

This will reduce the number of edges coming from the sources from $O(p^2)$ to $O(p)$. In Figure 6.4-(a) the removed edges are shown in green.

- **Tree nodes' edges optimization 1**:

  Lemma 6. *The tree nodes' edges can be optimized by removing the edges of tree nodes that are connected to nodes in V_2 already linked to a source node in V_1.*

  Proof. From definition 7 we know that a matching $M \in E$ 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. Given that, in all the solutions to the problem all sources will be connected to exactly one node in V_2 coming from the tree T and so we can remove the edges of the tree nodes that are connected to nodes in V_2 already linked to a source node in V_1 since they will not be part of the final matching. □

  This will reduce the number of edges by a factor of $O(p-1)$. In Figure 6.4-(a) the removed edges are shown in blue.

- **Tree nodes' edges optimization 2**:

  Lemma 7. *The tree nodes' edges can be optimized by removing the edges with weight 1 starting from a node $u \in V_1$ to a node $v \in V_2$ if the node u has another edge with weight 0 connected to a node $z \in V_2$ such that $z < v$ in the ordering of the nodes.*

  Proof. Since every time we have an edge with weight 0 between two nodes of V_1 and V_2 it means that those two nodes have the same equivalence class and so there is no need to add additional cost trying to connect that node to nodes with different classes coming after in the ordering, as that would only increase the cost without providing any benefit to the solution. Also, we know that connecting nodes with the same class is always the best choice for optimizing the run length encoding of each chain. □

  In Figure 6.4-(a) the removed edges are shown in red.

In figure 6.4-(b) we can see the resulting bipartite graph for the example shown in previous section after the optimizations.

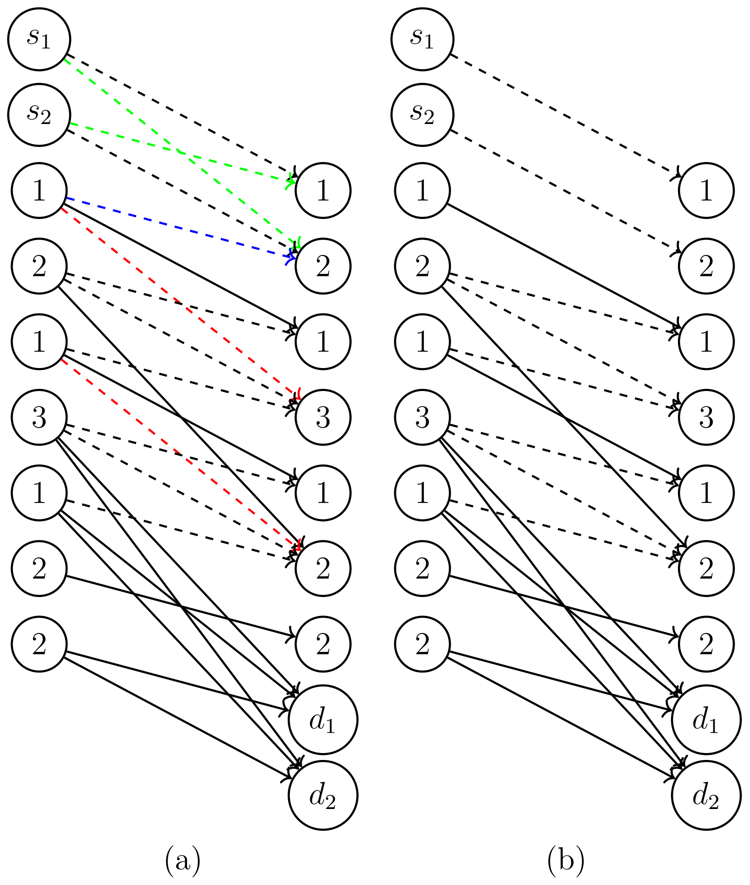


Figure 6.4: Example of a reduction for the sorted nodes' equivalency classes $E = \{1, 2, 1, 3, 1, 2, 2\}$ applying also the heuristics showed. In (a), the edges removed are shown in green for lemma 5, blue for lemma 6, and red for lemma 7. In (b), we have the resulting bipartite graph after the heuristics applied. Dashed edges weigh 1, while solid edges weigh 0.

6.2.6 Moving to Maximum weight perfect bipartite matching

In this section, we will discuss how to slightly modify the reduction process to move from a minimum weight perfect bipartite matching problem to a maximum weight perfect bipartite matching problem. This will be helpful in solving the problem more efficiently by using some known algorithms to solve the maximum weight perfect bipartite matching problem.

Theorem 7. *An optimal solution of an instance $\mathcal{I}$ with $p \leq |E|$ of the CHAINS-DIVISION problem is equivalent to an optimal solution of the Maximum Weight Perfect Bipartite Matching for the instance $r(\mathcal{I})$ where $r : \mathcal{I}_{CHAINS-DIVISION} \rightarrow \mathcal{I}_{MWPBM}$ is the reduction function that maps an instance of the CHAINS-DIVISION problem to an instance of the Maximum Weight Perfect Bipartite Matching problem constructed as stated in Definition 14 but with inverted weights (weight 0 becomes 1 and weight 1 becomes 0).*

Proof. Let M be a perfect matching in the bipartite graph G constructed as stated in Definition 14. Let $w(M)$ be the sum of the weights of the edges in the matching M. From the previous theorem, we know that the optimal solution of the CHAINS-DIVISION problem is equivalent to finding a perfect matching M in G that minimizes $w(M)$.

Let G' be a bipartite graph constructed as G but with inverted weights (weight 0 becomes 1 and weight 1 becomes 0). Let M' be a perfect matching in G' and let $w'(M')$ be the sum of the weights of the edges in the matching M'. Let k be the number of edges in the matching.

We can see that for any matching M in G:

$$w'(M) = k - w(M)$$

This means that maximizing $w'(M)$ is equivalent to minimizing $w(M)$. Therefore, finding the maximum weight perfect matching in G' is equivalent to finding the minimum weight perfect matching in G, which in turn is equivalent to finding the optimal solution of the CHAINS-DIVISION problem. □

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