Rank, select and access in grammar-compressed strings

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Abstract. Given a string $S$ of length $N$ on a fixed alphabet of $\sigma$ symbols, a grammar compressor produces a context-free grammar $G$ of size $n$ that generates $S$ and only $S$. In this paper we describe data structures to support the following operations on a grammar-compressed string: $\text{rank}_c(S,i)$ (return the number of occurrences of symbol $c$ before position $i$ in $S$); $\text{select}_c(S,i)$ (return the position of the $i$th occurrence of $c$ in $S$); and $\text{access}(S,i,j)$ (return substring $S[i,j]$). For $\text{rank}$ and $\text{select}$ we describe data structures of size $O(n\sigma \log N)$ bits that support the two operations in $O(\log N)$ time. We propose another structure that uses $O(n\sigma \log(\frac{N}{n})(\log N)^{1+\epsilon})$ bits and that supports the two queries in $O(\log N/\log \log N)$, where $\epsilon > 0$ is an arbitrary constant. To our knowledge, we are the first to study the asymptotic complexity of $\text{rank}$ and $\text{select}$ in the grammar-compressed setting, and we provide a hardness result showing that significantly improving the bounds we achieve would imply a major breakthrough on a hard graph-theoretical problem. Our main result for $\text{access}$ is a method that requires $O(n \log N)$ bits of space and $O(\log N + m/\log_\sigma N)$ time to extract $m = j - i + 1$ consecutive symbols from $S$. Alternatively, we can achieve $O(\log N/\log \log N + m/\log_\sigma N)$ query time using $O(n \log(\frac{N}{n})(\log N)^{1+\epsilon})$ bits of space. This matches a lower bound stated by Verbin and Yu for strings where $N$ is polynomially related to $n$.

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1 Introduction

Modern information systems and scientific experiments produce enormous amounts of highly repetitive data of various flavours. A particularly compelling example comes from the field of genomics, where recent breakthroughs in the biochemistry of DNA sequencing have drastically reduced the cost and time required to produce whole genome sequences. This has in turn given rise to databases of tens of thousands of large but highly similar individual genome sequences [10,30].

Metagenomic samples [44], increasingly used to describe the species diversity and makeup in microbial environments, are another kind of highly repetitive biological data. Each sequence in the dataset (called a read) is very short (say 200 characters), but has high overlap (perhaps 180 characters, or more) with several other sequences in the collection. A typical metagnomic sample is about a terabyte in size, but clearly also contains a great amount of redundancy.

Elsewhere, highly repetitive data takes the form of versioned document collections, like source code repositories and other large multi-author collections, such as Wikipedia. Even the web itself contains tremendous redundancy [11] in the form of copied and reused text and images [32,2] and boilerplate. An extreme example is the Web Archive (or Wayback Machine), which contains regular crawls of the web (over 400 billion web pages in all) captured over the last 20 years.

In order to store the above types of data, compression must be employed. However, effective compression alone is not enough: support for efficient queries over the original data without prior decompression is highly desirable.

Grammar compression [6] is particularly effective at compressing highly repetitive text data. Given a string $S$ of length $N$, a grammar compressor produces a context-free grammar $G$ that generates $S$ and only $S$. The size of the grammar refers to the total length of the right-hand sides of all rules. It is well known (see, e.g., [34]) that on the kind of highly repetitive data mentioned above, grammar compressors (and their close relative LZ77 [49]) can achieve compression significantly better than statistical compressors, whose performance is expressed in terms of the popular $k$th-order empirical entropy measure [31].

In this paper we consider support for three basic operations on grammar-compressed strings:

- **access**($S, i, j$) = return the symbols in $S$ between $i$ and $j$ inclusive;
- **rank**$_c(S, i)$ = number of occurrences of symbol $c \in \Sigma$ among the first $i$ symbols in $S$;
- **select**$_c(S, j)$ = position in $S$ of the $j$th occurrence of symbol $c \in \Sigma$.

The **access** operation (often called “random access”) allows one to process areas of interest in the compressed string without full decompression of all the symbols prior to $S[i, j]$. This is important, for example, in index-directed approximate pattern matching, where an index data structure first finds “seed” sites at which approximate matches to a query string may occur before more expensive alignment of the pattern by examining the text around these sites (via the **access** operation).

In their seminal paper Bille, Landau, Raman, Sadakane, Rao, and Weinmann [5] show how, given a grammar of size $n$, it is possible to build a data structure of size $O(n \log N)$ bits that supports access to any substring $S[i, j]$ in time $O(\log N + (j - i))$.

Operations **rank** and **select** are of great importance on regular (uncompressed) strings, where they serve as building blocks for fast pattern matching indexes [37], wavelet trees [20,36], and document retrieval methods [23,35,39]. On binary strings, efficient rank and select support has
been the germ for the now busy field of succinct data structures \(^{33}\). Although many space-efficient
data structures supporting rank and select operations have been presented \(^{18,20,21,42,43}\), they are not able to compress \(S\) beyond its statistical entropy.

To our knowledge we are the first to formally study algorithms for and the complexity of rank and select in grammar-compressed strings, however three related results exist in the literature. Navarro, Puglisi and Valenzuela \(^{39}\), and more recently Navarro and Ordóñez \(^{38}\), investigated practical methods for the rank operation in the context of indexed pattern matching. Their results pertain to grammars produced by a specific grammar compressor (the widely used RePair scheme \(^{29}\)), which are balanced and in Chomsky normal form (i.e. straight-line programs \(^{28}\)). They provide no formal analysis of the size of their data structure, but because their grammars are balanced their rank algorithm takes \(O(\log N)\) time. Experiments indicate the approach is practical for some applications.

Recently, Bille, Cording, and Gørtz \(^{4}\), used a weak form of select query, called select-next\(^{4}\) as part of their compressed subsequence matching algorithm. A select-next\((S,i,c)\) query returns the smallest \(j > i\) such that \(S[j] = c\).

Our Contribution. This paper provides the following results (also summarized in Table 1):

1. We show how to support access to \(m\) consecutive symbols in \(O(\log N + m/\log_\sigma N)\) time using \(O(n \log N)\) bits of space. This is an improvement over the \(O(\log N + m)\) time solution of Bille et al., within the same space. Our scheme can be seen as a grammar-compressed counterpart to the scheme of Ferragina and Venturini \(^{12}\) (see also Sadakane and Grossi \(^{36}\)), which has the same access time as ours, but only achieves \(k\)th order entropy compression (for some \(k = o(\log_\sigma N)\)).
2. We then show that by balancing the grammar and increasing space usage slightly, we obtain a data structure that supports access to \(m\) consecutive symbols in \(O(\log N/\log \log N + m/\log \sigma N)\) time and \(O(n\log N^{1+\epsilon})\) bits of space, matching a lower bound by Verbin and Yu \(^{48}\).
3. We describe a data structure supporting rank and select operations in \(O(\log N)\) time and \(O(n\sigma \log N)\) bits of space for general (unbalanced) grammars, and \(O(\log N/\log \log N)\) time and \(O(n\sigma \log N^{1+\epsilon})\) bits of space for balanced grammars.
4. The above schemes for rank and select are fairly straightforward augmentations to our access data structures, but our final result suggests that it is probably difficult to do much better. In particular, we show a reduction between rank and select operations in grammar compressed strings and the problem of counting the number of distinct paths between two nodes in a directed acyclic graph, an old and seemingly difficult problem in graph theory. No significant progress has been made so far, even on the seemingly easier problem of reachability queries \(^{9}\) (just returning whether the number of paths is non-zero).

Related Work. Apart from the above mentioned previous results for access, rank, and select, there have been many results recently on grammar-compressed data structures for pattern matching \(^{11,18,15}\), document retrieval \(^{39,40,41}\), and dictionary matching \(^{26}\).

There has also been a significant amount of recent research effort on developing string processing algorithms that operate directly on grammar-compressed data — i.e., without prior decompression. To date this work includes algorithms for computing subword complexity \(^{3,19}\), online subsequence matching and approximate matching \(^{4,47}\), faster edit distance computation \(^{17,22}\), and computation of various kinds of biologically relevant repetitions \(^{1,27,24,25}\).

\(^{4}\) These queries are referred to as labeled successor queries in \(^{4}\).
More precisely, suppose the non-terminal that generates the whole string is \( R \). The method of Bille et al. uses heavy-weight paths in the DAG to support the access operation.

### 2. Notation and preliminaries

We consider a string \( S \) of total length \( N \) over an integer alphabet \([1..\sigma]\). The string \( S \) is generated by a grammar that contains exactly \( n \) non-terminals (variables) and \( \sigma \) terminals (corresponding to each character in the alphabet). We assume that the grammar is in Chomsky normal form (CNF). That is, each grammar rule is either of the form \( R_0 = R_1 R_2 \), where \( R_1 \) and \( R_2 \) are non-terminals, or of the form \( R_0 = c \), where \( c \) is a terminal. The grammar has thus exactly \( \sigma \) terminals. We note by \(|R|\) the length of the string generated by the non-terminal \( R \). In what follows, we only consider grammars in CNF, since every grammar of size \( n \) with \( \sigma \) terminals, can be transformed into a grammar in CNF of size \( O(n) \) with \( \sigma \) terminals.

We will often use a DAG (directed acyclic graph) representation of the grammar with one source (corresponding to the unique non-terminal that generates the whole string) and \( \sigma \) sinks (corresponding to the terminals). The height of a grammar is the maximal distance between the source and one of the sinks. The grammar is said to be balanced if its height is \( O(\log N) \). Further, it is said to be weight-balanced if there exists some absolute constants \( c_1 \) and \( c_2 \) such that for any given rule \( R_0 = R_1 R_2 \), we have that \( c_1|R_2| \leq |R_1| \leq c_2|R_2| \).

All our algorithms are in RAM model with word length at least \( \log N \) bits, and with the assumptions that all the usual arithmetic and logic operations take constant time each.

### 3. Improved access time with rank and select support

We now extend Bille et al.’s access scheme \(^5\) so that it uses the same space, \( O(n \log N) \) bits (for a grammar of length \( n \) that is not necessarily the smallest possible), but allows access to \( m \) consecutive symbols in time \( O(\log N + m/\log_\sigma N) \) instead of \( O(\log N + m) \). We also show how to support rank and select within time \( O(\log N) \) using \( O(n \sigma \log N) \) bits of space. Before that, we start by reviewing the method of Bille et al.

#### 3.1 The method of Bille et al.

The method of Bille et al. uses heavy-weight paths in the DAG to support the access operation. More precisely, suppose the non-terminal that generates the whole string is \( R_0 \). Given a position \( x \), the method of Bille et al. generates a sequence of triplets \((R_1, s_1, e_1),(R_2, s_2, e_2),...,(R_t, s_t, e_t)\), where \( t \leq \log N \), \( \sum_{1 \leq i \leq t} s_i - 1 + 1 = x \) and \( R_i \) is a non-terminal that generates a single character \( c \). Note that we have \( t \leq \log N \) because \( |R_{i+1}| \leq |R_i|/2 \) and \( R_0 \leq N \). Thus \( c \) is the character that is at position \( x \) in the substring generated by the \( R_0 \).

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**Table 1.** Summary of results for rank, select, and access in grammar-compressed strings.

|                  | Rank/select | Access |
|------------------|-------------|--------|
|                  | Unbalanced  | Balanced| Unbalanced  | Balanced  |
| **This study**   |             |        |             |          |
| Time             | \( O(\log N) \) | \( O(\log N/\log \log N) \) | \( O(\log N + m/\log_\sigma N) \) | \( O(\log N/\log \log N + m/\log_\sigma N) \) |
| Space            | \( O(n \sigma \log N) \) | \( O(n \sigma \log \log N) \) | \( O(n \log N) \) | \( O(n \log \log N) \) |
| **Bille** \(^5\) |             |        |             |          |
| Time             | –           | –      | \( O(\log N + m) \) | –        |
| Space            | –           | –      | \( O(n \log N) \) | –        |
| **Folklore**     |             |        |             |          |
| Time             | –           | –      | –           | \( O(\log N + m) \) |
| Space            | –           | –      | –           | \( O(n \log N) \) |
Each triplet \((R_i, s_i, e_i)\) indicates that a substring generated by the non-terminal \(R_i\) starts at position \(s_i\) and ends at position \(e_i\) inside the substring generated by the non-terminal \(R_{i-1}\). The non-terminal \(R_i\) is found using the heavy path that starts at the non-terminal \(R_{i-1}\). This is explained in more detail in the next subsection.

To every non-terminal \(R_i\), there is an associated position \(p_i\), which is the leaf in the heavy path that starts from the non-terminal \(R_i\). We call \(p_i\) the center of the non-terminal \(R_i\).

### 3.2 Heavy path decomposition of a DAG

Given a non-terminal \(R\), the heavy path starting from the variable \(R = P_0\) is the sequence of non-terminals \(P_1, P_2, \ldots, P_t\), such that:

1. For all \(i \in [0, t-1]\), either \(P_i = P_{i+1}Q_{i+1}\) or \(P_i = Q_i+1P_{i+1}\)
2. \(|P_i| \geq |Q_i|\).
3. The non-terminal \(P_t\) generates a single character \(c\).

Informally speaking, the heavy path starting from a non-terminal \(P_0\) is the sequence of non-terminals \(P_1, P_2, \ldots, P_t\) such that every non-terminal \(P_{i+1}\) is the heaviest among the two non-terminals in the right-hand side of the non-terminal \(P_i\) and the variable \(P_t\) generates a single character. We associate with each non-terminal \(R\) a center point \(p\), obtained as follows:

\[
p = \sum_{1 \leq i \leq k} |Q_{ij}| + 1
\]

where the \(i_j\) is the sequence of indices in \([1..t]\) such that \(P_{i_j-1} = Q_{i+1}P_{i+1}\) (that is, \(Q_{ij}\) is the left non-terminal in the right-hand side of the non-terminal of \(P_{i_j-1}\)). The character at position \(p\) in the string generated by \(R\) is precisely the character generated by the non-terminal \(P_t\).

![Fig. 1. An illustration of the heavy path starting from variable \(P_0\) and its center point \(p\).](image)
3.3 Biased Skip trees

The main data structure used by Bille et al. is a forest of trees built as follows. Each forest has as a root a node that corresponds to a sink in the DAG representation of the grammar. A node $x$ is a child of another node $y$ in the forest if and only if $y$ is the heavy child of $x$ in the original DAG. Thus the forest can be thought of as being built by reversing the original DAG (upside-down) and keeping only the edges that correspond to heavy paths. Then each of the resulting trees is represented using a biased skip tree. The representation allows us to find the sequence of triplets $(R_1, s_1, e_1), (R_2, s_2, e_2), \ldots, (R_t, s_t, e_t)$, given a position $x$ in the string $S$. Suppose that we are given a non-terminal $R$ with its center point $p$ and its heavy path $P_1, P_2, \ldots, P_t$. Given a point $x$ inside the substring generated by $R$ such that $x < p$, we wish to find inside the heavy path decomposition of $R$ the non-terminal $P_i$ such that either:

1. $P_i = P_{i+1}Q_{i+1}$ with $x - p_i > |P_{i+1}| - p_{i+1}$, where $p_{i+1}$ is the center of the non-terminal $P_{i+1}$ and $p_i$ is the center of the non-terminal $P_i$.
2. $P_i = Q_{i+1}P_{i+1}$ with $p_i - x > p_{i+1} - 1$, where $p_{i+1}$ is the center the non-terminal $P_{i+1}$ and $p_i$ is the center of the non-terminal $P_i$.

Informally speaking, the non-terminal $P_i$ is the last non-terminal in the heavy path that contains the point $x$ and the non-terminal $Q_{i+1}$ hangs from the heavy-path, either from the right (first case above) or from the left (second case above). The biased skip tree allows to find the non-terminal $P_i$ in time $O(\log(|R|/|Q_{i+1}|))$. Then, the algorithm produces the triplet $(R_i, s_i, e_i)$ by setting $R_i = Q_{i+1}$, $s_i = p - p_i + 1$ and $e_i = s_i + |R_i| - 1$ and starts the same procedure above by replacing $R$ by $R_1$, which results in the triplet $(R_2, s_2, e_2)$. The algorithm continues in this way until it gets the triplet $(R_t, s_t, e_t)$. The total running time of the procedure is $O(\log N)$, since $|R| = N$ and the successive running times $O(\log(|R|/|R_1|)), O(\log(|R_1|/|R_2|)), \ldots, O(\log(|R_{t-1}|/|R_t|))$ add up to $O(\log N)$ time by a telescoping argument.

3.4 Improved access time

The above scheme can be extended to allow decompression of an arbitrary substring that covers position $[x, x']$ in time $O(m + \log N)$, where $m = x' - x + 1$ is the length of the decompressed substring. The decomposition works as follows. We first find the sequence of triplets $(R_1, s_1, e_1), (R_2, s_2, e_2), \ldots, (R_t, s_t, e_t)$ corresponding to the point $x$. We then find the sequence of triplets $(R'_1, s'_1, e'_1), (R'_2, s'_2, e'_2), \ldots, (R'_t, s'_t, e'_t)$ corresponding to the point $x'$. We let $(R_i, s_i, e_i) = (R'_i, s'_i, e'_i)$ be the last common triplet between the two sequences. Then the non-terminal $R'_{i+1}$ hangs on the left of the heavy path that starts at the non-terminal $R_i$ and the non-terminal $R'_t$ hangs on the right. Without loss of generality, assume that $R'_t$ hangs at a higher point than $R_{i+1}$ and that $P_i$ is the last non-terminal on the heavy path of $R_i$ that contains point $x$ (note that $P_i = R_{i+1}P_{i+1}$). Then the non-terminal $P_{i+1}$ still contains the point $x'$ and we need to decompress all the non-terminals that hang on the right of the heavy path that starts at $P_{i+1}$ down to the non-terminal from which the non-terminal $R'_{i+1}$ hangs. Afterwards, we just need to 1) decompress all the non-terminals that hang on the right of the heavy path that starts at $R_j$ down to the non-terminal from which $R_{j+1}$ hangs for all $j \in [i + 1, t - 1]$ and then 2) symmetrically decompress all the non-terminals that hang on the left of the heavy path that starts at $D'_j$ down to the non-terminal from which $R'_{j+1}$ hangs for all $j \in [i + 1, t' - 1]$. This whole procedure takes $O(m + \log N)$ time. The main point of the procedure is to be able to decompress all the non-terminals that hang
on the right or on the left of the portion of some heavy path that starts at some non-terminal $P_i$ down to some non-terminal $P_{i+1}$ inside that heavy path.

In what follows, we show how to reduce the time to just $O(m/\log\sigma N + \log N)$. For every non-terminal $X$ that generates a right-hand side $YZ$, we will store the following additional fields, which occupy $O(\log N)$ bits:

1. The $\log N/\log\sigma$ leftmost characters in the substring generated by $X$.
2. The $\log N/\log\sigma$ rightmost characters in the substring generated by $X$.
3. Three jump pointers. Each jump pointer is a pair of the form $(R, p)$, where $R$ is non-terminal and $p$ is a position inside the substring generated by $X$.

The three jump pointers are called left, right and central (any of them may be empty). The jump pointers will allow us to accelerate the extraction of characters. The central jump pointer allows to fully decompress any given non-terminal that generates a string of length $m$ in time $O(m/\log\sigma N)$. The right and left jump pointers will allow us to jump along the heavy paths, avoiding the traversal of all the non-terminals in the heavy path. We first start by describing the central jump pointer (henceforth called central field).

**Non-terminal decompression** The central field of $X$ will contain a pointer to another variable in addition to the position, where the substring of that variable starts inside the string generated by $X$. If $X$ generates a string of length less than $2\log\sigma N$, then we do not store the central field at all. Otherwise we do the following. We use two temporary counters $C_l$ and $C_r$. If $Y$ generates a string of length less than $\log\sigma N$, then we increment $C_l$ by $|Y|$. If $Z$ generates a string of length less than $\log\sigma N$, then we increment $C_r$ by $|Z|$. If one of the two variables $Y$ or $Z$ generates a string of length at least $\log\sigma N$, we let $W$ be that variable and let its right-hand side be $UV$. We now show a recursive procedure implemented on the variable $W$. If both $U$ and $V$ are of length at least $\log\sigma N$, we stop the recursion. If either of $U$ or $V$ is of length less than $\log\sigma N$, we increment $C_l$ by $|U|$ if $C_l + |U|$ or increment $C_r$ by $|V|$ if $C_r \leq \log N/\log\sigma$. Otherwise, if we succeeded in incrementing $C_l$, we recurse on the variable $V$ by setting $W = V$. If we succeeded in incrementing $C_r$, we recurse on the variable $U$ by setting $W = U$. Whenever we stop for a variable $W$ and could no longer recurse, we set the central field to $(W, C_l + 1)$.

The decompression is done in a straightforward way. Whenever we want to decompress a variable that generates a string of length at most $2\log N/\log\sigma$, we just write the left and right substrings of lengths $\log N/\log\sigma$, which are already stored with the variable. Whenever we want to decompress a variable $X$ that has a central field $(R, p)$, we decompress everything inside the substring generated by $X$ that lies on the left and right of $R$ (that is, substrings that span characters $[1, p - 1]$ and $[p + |R|, |X|]$) which are both stored inside the left and right substrings of $X$. We then recurse on the variable $R$. Otherwise, if $X$ does not have a central field simply recurse on the two variables of its right-hand side. We will now prove that the total time to decompress any variable that generates a string of length $m$ is $O(1 + m/\log\sigma N)$.

To prove this, we will analyze the virtual decompression tree traversed during the decompression and prove that the total number of nodes in such a tree is $O(1 + m/\log\sigma N)$. To that purpose we will first prove that the number of leaves is at most $O(1 + m/\log\sigma N)$. In order to reach a leaf $X$ during the decompression, there could be two cases.

1. We reach $X$ from a node $Y$ that has two children of weight at least $\log\sigma N$ and one of them is $X$ and we followed the pointer to $X$.  


2. We reach $X$ from a node $Y$ that contains in its central field a pointer to $X$.

In the first case, $X$ generates a string of length at least $\log N/\log \sigma$. Thus, there can be at most $m/(\log \sigma N)$ such leaves since they all generate disjoint substrings.

If we reach $X$ from a node $Y$ that has a central field, then necessarily $Y$ generates a substring of length more than $2\log \sigma N$. We can therefore uniquely associate $Y$ with $X$ and thus conclude that there can be at most $m/(2\log \sigma N)$ such leaves. We have proved that the number of leaves is at most $O(m/\log \sigma N)$. This implies that the number of nodes of degree two in the decompression tree is at most $O(m/\log \sigma N)$. It remains to show that the number of unary nodes in the decompression tree is at most $O(m/\log \sigma N)$. For that, it suffices to show that we decompress a substring of length $\Theta(\log \sigma N)$ everytime we traverse two consecutive unary nodes $N_0$ and then $N_1$ in the decompression tree. This is obvious, since if we do not do so, then we can merge both the right substring and the left substring of $N_1$ into the ones of $N_0$ and delete $N_1$. We thus have proved the following lemma.

Lemma 1. Suppose that we are given a grammar of size $n$ that generates a string $S$ of length $N$ over an alphabet of size $\sigma$ is of size $n$. Then we can build a data structure that uses $O(n \log N)$ bits so that decompressing the string generated by any non-terminal takes $O(\log N + m/\log \sigma N)$ time, where $m$ is the length of the string generated by the non-terminal.

Decompression of arbitrary substrings We now show how to decompress an arbitrary substring that is not necessarily aligned on a non-terminal.

Recall that the core procedure for decompression is as follows. We are given a non-terminal $R$ and another non-terminal $Q$ that hangs from the heavy path down from $R$ and we want to decompress what hangs from the left (respectively right) of the heavy path down to the point where $Q$ hangs from the heavy path. To accelerate the decompression we will use the right and left jump pointers. Since the right and left decompression are symmetric, we only describe the case of left decompression.

Before describing the decompression itself, we first describe how the left jump pointer for non-terminal $R$ is set. We will keep a counter $C$, assume $P_0 = R$ and inspect the sequence $P_1, P_2, \ldots, P_t$. For every $i$ starting from 1 such that $P_{i-1} = Q_i P_i$, we increment $C$ by $|Q_i|$ and stop when $C + |Q_i| > \log N/\log \sigma$. Then the left jump pointer will point to the non-terminal $P_{i-1} = L$ along with its starting point $p_L$ inside $R$. If $P_0 = Q_1 P_1$ and $|Q_1| > \log N/\log \sigma$ or $C + |Q_i|$ never exceeds $\log N/\log \sigma$, then we do not store a left jump pointer at all.

The decompression of the left of a heavy path is done as follows. We are given the non-terminal $Q$ and its starting position $p_Q$ inside $P$. At first, we first check whether $p_Q \leq \log N/\log \sigma$, in which case everything to the left of $Q$ inside $P$ is already in the left substring of $P$ and it can be decompressed in time $O(1 + p_Q/\log \sigma N)$ and we are done.

If $p_Q > \log N/\log \sigma$, then we have two cases:

1. If $P$ has a left jump pointer $(L, p_L)$ then $p_Q \geq p_L$ and we decompress the first $p_L \leq \log N/\log \sigma$ characters of the string generated by $P$ (from the left substring of $P$), then replace $P$ by $L$ and recurse on $L$ and $Q$.

2. If $Q$ does not have a left jump pointer, then we necessarily have that $P = Q_1 P_1$ with $|Q_1| > \log N/\log \sigma$ and $p_Q > |Q_1|$, we just decompress $Q_1$ (using the procedure shown above for fully decompressing non-terminals using central jump pointers). replace $P$ by $P_1$ and recurse on $P_1$ and $Q$. 

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It remains to show that the bound for the procedure is $O(1 + y / \log_\sigma N)$, where $y$ is the total length of the decompressed string. Analyzing the recursion, it can easily be seen that when we follow two successive left jump pointers, we are decompressing at least $\log_\sigma N$ characters from left substrings.

Otherwise, if we do not follow a jump pointer, then we are either decompressing a non-terminal of length at least $\log_\sigma N$ characters in optimal time or we terminate by decompressing at most $\log_\sigma N$ characters.

We thus have shown the following theorem.

**Theorem 1.** Suppose that we are given a grammar of size $n$ that generates a string $S$ of length $N$ over an alphabet of size $\sigma$ is of size $n$. Then we can build a data structure that uses $O(n \log N)$ bits that supports the access to $m$ consecutive characters in time $O(\log N + m / \log_\sigma N)$ time.

### 3.5 Rank and select

In order to support rank we will reuse the same forest of biased skip trees used by Bille et al. (see above). For every node $\alpha$ representing a non-terminal $R$ with center point $p_R$, we associate $\sigma$ values $v_{R,1}, \ldots, v_{R,\sigma}$, where $v_{R,c}$ represents the number of occurrences of character $c$ in the interval $R[1, p_R]$. The rank operation can be supported by using the values $v_i$ stored at each node. That is counting the number of occurrences of character $c$ before position $p$ in the string generated by $R = R_0$ can be done by first finding the sequence of triplets (see above) $(R_1, s_1, e_1), (R_2, s_2, e_2), \ldots, (R_t, s_t, e_t)$, where $R_i$ is in the right hand-side of some non-terminal $P_i$ that is the heavy path of $R_{i-1}$. Then the result of the rank operation will clearly be

$$\sum_{i=0}^{t-1} (v_{R_i,\sigma} - v_{P_{i+1},\sigma})$$

The total space will be $O(n\sigma \log N)$ bits, while the query time still remains $O(\log N)$.

In order to support select, we will construct $\sigma$ DAGs, where DAG number $c$ is built as follows. We remove every non-terminal whose corresponding substring does not contain the character $c$. We also remove every non-terminal for which one of the two non-terminals in the right-hand side generates a string that does not contain $c$. We then construct a biased skip tree rooted at the terminal $c$, but replacing the size of the strings generated by the non-terminals with the number of occurrences of character $c$ in the string generated by the non-terminal (the heavy paths are constructed by taking into account the number of occurrences of character $c$ instead of the total size of the strings generated by the non-terminals). Given a non-terminal $P$, the centerpoint $p_c$ determined by the heavy path will indicate the occurrence number $p_c$ of character $c$. We now associate the value $u_{P,c}$ which stores the position of the occurrence number $p_c$ inside the substring generated by $c$. Given a non-terminal $R = R_0$ and an occurrence number $x$ of $c$, we can determine the position $p$ of terminal $c$ in the substring generated by $R$ as follows: we first use the biased skip tree to determine the sequence $(R_1, s_1, e_1), (R_2, s_2, e_2), \ldots, (R_t, s_t, e_t)$, where $R_i$ is in the right hand-side of some non-terminal $P_i$ that is the heavy path of $R_{i-1}$. Then the result of the select query will be $\sum_{0 \leq i \leq t-1} (u_{R_i,\sigma} - u_{P_{i+1},\sigma}) + 1$. Overall the time taken to answer a select query will be $O(\log N_c) \leq O(\log N)$, where $N_c$ is the number of occurrences of character $c$ in the whole string. The total space will clearly be $O(n\sigma \log N)$ bits of space. We have proved the following.

**Theorem 2.** Suppose that we are given a grammar of size $n$ that generates a string $S$ of length $N$ over an alphabet of size $\sigma$. Then we can build a data structure that uses $O(n\sigma \log N)$ bits that supports rank and select queries in time $O(\log N)$. 

8
4 Optimal access time for not-so-compressible strings

Theorem 3. Given a weight-balanced grammar of size \( n \) generating a string \( S \) of length \( N \) over an alphabet of size \( \sigma \), we can build a data structure that uses \( O(n \log^{1+\epsilon} N) \) bits (for any constant \( \epsilon \)), that supports random access to any character of \( S \) in \( O(\log N / \log \log N) \) time, and access to \( m \) consecutive characters in \( O(\log N / \log \log N + m / \log \sigma N) \) time. Furthermore, we can build a data structure that uses \( O(n \sigma \log^{1+\epsilon} N) \) bits of space and that supports rank and select in \( O(\log N / \log \log N) \) time.

Because the grammar is balanced it will have the property that any root-to-leaf path in the corresponding tree will have depth \( O(\log N) \). For every variable \( X \) we generate a new right-hand side that contains at most \( \log^\epsilon N \) variables by iteratively expanding the right-hand side of \( X \) down \( \epsilon \log \log N \) levels (or less if we reach a terminal). We then store in a fusion tree the prefix-sum of the lengths of the strings generated by each variable in the right-hand side. Every fusion tree uses \( O(\log^{1+\epsilon} N) \) bits of space and allows constant time predecessor search on the prefix-sums. More precisely, assuming that the expanded right-hand side of \( R \) is \( R_1 R_2 \ldots R_t \) with \( t \leq 2^{\epsilon \log \log N} \), the prefix sums are \( v_1, v_2, \ldots v_t \), where \( v_i = |R_1| \ldots |R_{i-1}| \).

The fusion tree is a data structure which uses linear space and allows predecessor searches on a set of \( t \) integers of \( w \) bits in \( O(\log t / \log w) \). Since in our case, we have \( t = \log^\epsilon N \) and \( w \geq \log N \), the query time is constant. It is clear that a top-down traversal of the tree can now be done in time \( O(\log N / \log \log N) \). This is because we are moving \( \epsilon \log \log N \) levels at a time at each step and a leaf is reached after descending at most \( O(\log N) \) levels.

We note that our upper bound for access matches the lower bound of Verbin and Yu who have shown that for “not-so-compressible” strings — those that have a grammar of length \( n \) such that \( N \leq n^{1+\epsilon} \) for some constant \( \epsilon \) — the query time cannot be better than \( O(\log N / \log \log n) = O(\log N / \log \log N) \) if the used space is not more than \( O(n \log^c n) \) for some constant \( c \). Extending the scheme to select and rank queries is not so hard and multiplies the space by a factor \( \sigma \). For supporting rank queries it suffices to augment every node that corresponds to a variable \( R \) with the prefix-sums of the number of occurrences of character \( c \) in the strings generated by the variables in the expanded right-hand side for every character \( c \). That is supposing that a variable \( R \) has an expanded right-hand-side \( R_1 \ldots R_t \) with \( t \leq 2^{\epsilon \log \log N} \), we store \( t \) values \( v_{1,c}, \ldots, v_{t,c} \) such that \( v_{i,c} \) is the sum of the number of occurrences of character \( c \) in the strings generated by rules \( R_1, \ldots R_i \). Then a rank query can be answered during a top-down traversal of the DAG. We initially set a counter to zero. Then whenever we traverse a node corresponding to the variable \( R \) with right-hand side \( R_1, \ldots R_t \), and the fusion tree indicates to continue through the node \( R_i \), we add the value \( v_{i-1} \) to the counter (or zero if \( i = 1 \)) and at the end return the value of the counter.

For select queries, we can build \( \sigma \) DAGs, where in the DAG for character \( c \) we replace the length of the strings by the count of character \( c \). Answering select queries for character \( c \) is then easily done by a top-down traversal of the DAG with expanded right-hand side. Suppose that for a node corresponding to a variable \( R \), we store the sequence \( v_{1,c}, v_{2,c}, \ldots, v_{t,c} \) in a fusion tree associated to variable \( R \) and character \( c \), where \( v_{i,c} \) is the total number of occurrences of character \( c \) in \( R_1, \ldots, R_i \). We start by setting a counter \( C = 0 \) and then traverse the DAG top-down. For each traversed node, we query a fusion tree associated with character \( c \) and a rule \( R \) to determine which variable in the expanded right-hand side of \( R \) to continue the traversal to. If the variable indicated is \( R_i \), then we increment \( C \) by \( v_i = |R_1| + \ldots + |R_{i-1}| \) (the value \( v_i \) is stored in the original DAG used to support access queries).
It remains to show how access queries are supported. We can show that in time $O(\log N/\log \log N + m/\log_\sigma N)$ we can decompress a substring of length $m$ at an arbitrary position, while using the same $O(n \log^{1+\epsilon} N)$ bits of space.

Consider any variable $X$ that generates two variables $Y$ and $Z$. If $Y$ generates a string of length at most $\log_\sigma N$, then we keep the whole string generated by $Y$ in the node corresponding to $X$ instead of writing the identifier of $Y$. Similarly if $Z$ generates a string of length at most $\log_\sigma N$, we keep in the node $X$ the whole string generated by $Z$ instead of keeping the identifier of $Z$.

We will now prove that decompressing the substring generated by any variable $X$ can be done in time $O(1 + |X|/\log_\sigma N)$. The decompression is done as follows. If both $|Y| \leq \log_\sigma N$ and $|Z| \leq \log_\sigma N$, then we directly output the substrings of $X$ and $Y$, since the two strings are stored in $X$. If we have $|Y| \leq \log_\sigma N$ and $|Z| > \log_\sigma N$, then we output $Y$ and recurse on $Z$. If we have $|Z| \leq \log_\sigma N$ and $|Y| > \log_\sigma N$, then we output $Z$ and recurse on $Y$. If we have both, i.e., $|Y| > \log_\sigma N$ and $|Z| > \log_\sigma N$, then we recurse on both $Y$ and $Z$.

We will now analyze the decompression by proving that the (virtual) decompression tree contains always at most $O(1 + |X|/\log_\sigma N)$ nodes. We assume that $|X| = m \geq \log_\sigma N$. Otherwise the decompression of $X$ is immediate since both $|Y| \leq \log_\sigma N$ and $|Z| \leq \log_\sigma N$. We first prove that the number of leaves is $O(m/\log_\sigma N)$. Since each leaf must contain a string of length at least $\log_\sigma N$ (recall that the string corresponding to variable of length less than $\log_\sigma N$ is stored in the corresponding parent of the leaf), we must output at least $\log_\sigma N$ characters per leaf and thus we cannot have more than $m/\log_\sigma N$ leaves. The number of nodes of degree at least $2$ in any tree is less than the number of leaves, and those nodes correspond to the case where both $|Y| > \log_\sigma N$ and $|Z| > \log_\sigma N$. It remains to bound the number of unary internal nodes which correspond to the case where either $|Y| \leq \log_\sigma N$ and $|Z| > \log_\sigma N$ or $|Z| \leq \log_\sigma N$ and $|Y| > \log_\sigma N$. We note that in this case, we output the substring associated with either $Y$ or $Z$. Since the grammar is weight-balanced, and $|X| \geq \log_\sigma N$, it is easy to see that $Y \geq c_0 \log_\sigma N$ and $Z \geq c_0 \log_\sigma N$. We thus output a string of length $c_0 \log_\sigma N$ every time we traverse a unary node.

We now show how to decompress an arbitrary substring of length $m$ in time $O(\log N/\log \log N + m/\log_\sigma N)$. For that, we build the access structure above for each variable. In addition, for each variable $X$, we store the first and the last $\log_\sigma N \log^e N$ characters of the substring generated by $X$. This adds $O(\log^{1+\epsilon} N)$ bits of space per variable. The decompression of a substring that spans positions $[x, y]$ inside the $R$ will first start by traversing the DAG top-down for position $x$ and $y$. We collect the two paths that consist of the $O(\log N/\log \log N)$ traversed nodes for positions $x$ and $y$. We note by $R$, the variable that corresponds to the lowest common node between the two paths. The variable $R$ will have an expanded right-hand-side $R_1 R_2 \ldots R_t$, such that the next nodes on the paths of positions $x$ and $y$ have respectively associated variables $R_i$ and $R_j$ with $j > i$. We thus need to decompress all variables $R_k$ for $i < k < j$ and then decompress the prefix of the string generated by $R_j$ up to the position that corresponds to $y$ and the suffix of the string generated by $R_i$ up to the position that corresponds to $x$. It remains to show how to decompress a prefix of the string generated by a variable $R$ up to an arbitrary position $x$ in optimal time. Suppose that $R = R_0 R_1 \ldots R_t$ and that $x$ is in variable $R_i$. We will have to decompress the substring generated by $R_0 R_1 \ldots R_{i-1}$. In order to do that we first check whether $\ell = |R_0| + |R_1| + \ldots + |R_{i-1}| \geq \log^e N \log_\sigma N$. If that is the case, we decompress all the variables $R_0, R_1, \ldots, R_t$ in time $O(\ell/\log_\sigma N + i - 1)$. Since $i - 1 \leq \ell \leq \log^e N$ and $\ell/\log_\sigma N \geq \log^e N$, we deduce that the time is $O(\ell/\log_\sigma N)$, which is optimal. If $\ell < \log^e N \log_\sigma N$, we can directly decompress the first $\ell$ characters of the substring generated by $R$ in optimal $O(1 + \ell/\log_\sigma N)$ time, since we have stored the first $\log^e N \log_\sigma N$ characters of
In the subsequent steps, we can continue from $R_i$ and the relative position of $x$ in the substring generated by $R_i$. Since we traverse at most $\log N / \log \log N$ levels and we spend optimal time for decompression at each level, the total time is $O(\log N / \log \log N + m / \log_\sigma N)$, which is optimal.

Decompressing the suffix generated by a variable $R$ up to an arbitrary $x$ is symmetric.

We keep the consecutive nodes that we have traversed in a stack. Once we reach a leaf (which is a node generating a substring of length between $\log_\sigma N$ and $2 \log_\sigma N - 2$), we can get the leaf’s content in $O(1)$ time. We then traceback in the tree, collecting the substrings contained in the nodes or the leaves until we will have decompressed $O(m)$ characters. It is easy to see that we will not traverse more than $O(\log N / \log \log N + \log \sigma N)$ nodes.

**Corollary 1.** Given an arbitrary context-free grammar of size $n$ generating a string $S$ of length $N$ over an alphabet of size $\sigma$, we can build a data structure that uses $O(n \log(N/n) \log^{1+\epsilon} N)$ bits (for any constant $\epsilon$) such that access to $m$ consecutive characters supported in time $O(\log N / \log \log N + m / \log_\sigma N)$ time. Furthermore we can build a data structure that uses $O(n \sigma \log(N/n) \log^{1+\epsilon} N)$ bits of space and that supports rank and select in $O(\log N / \log \log N)$ time.

To achieve the corollary we can use the scheme of Charikar et al. [6], which can generate a weight-balanced grammar from an unbalanced one such that the balanced grammar generates the same string as the unbalanced one, but is of size larger by a factor at most $O(\log(N/n))$.

## 5 The hardness of rank and select in grammar-compressed strings

We will now show a reduction from the problem of rank and select in grammar compressed strings to path counting in DAGs.

Suppose that we are given a DAG with $m$ nodes and $n$ edges that has $\beta$ nodes with indegree 0 (sources) and $\sigma$ nodes with outdegree 0 (sinks) and we want to answer the following type of query: given any node $u$ and any sink $v$, compute the number of distinct paths that connect $u$ to $v$. We allow multi-edges. That is, we allow more than one edge $uv$ with the same nodes $u$ and $v$. Let $N$ be the total number of distinct paths that connect the $\beta$ sources to the $\sigma$ sinks. We can show that we can construct a grammar-compressed string of (uncompressed) length $N$ that contains $O(n)$ non-terminals and $\sigma$ terminals and such that answering the described query on the graph reduces to answering rank queries on the grammar compressed string.

We modify the DAG such that it contains a single source and all nodes it contains are either of outdegree 0 or 2:

1. For every node $v$ of outdegree 1 do the following. If the successor of the node is $w$, then for every edge $uv$ create a new edge $uw$ and remove the edge $uv$. After making these changes, node $v$ will become of indegree 0. We remove the node $v$ and keep a data structure that maps the node $v$ to node $w$. Since any path starting at $v$ must pass through $w$, we will know that counting the number of paths starting at $v$ and ending at a node $x$ will be exactly the same as the number of paths starting at $w$ and ending in $x$. Note that all the paths that went through node $v$ will be preserved. Thus the count of the number of paths will not change.

2. If the number of nodes having indegree 0 is $t \geq 2$, then create a new root and connect the root to all the nodes of indegree 0 by creating $t - 2$ intermediate nodes. The root and the newly created nodes will have outdegree 2.

3. For every node $v$ of outdegree $d \geq 3$, we will add exactly $d - 2$ intermediate nodes of outdegree 2 that connect the original nodes with the destination and modify $v$ so that it has outdegree 2.
Clearly, the constructed DAG will have $O(m)$ nodes and will generate a string of length exactly $N$, where $N$ is the total number of distinct paths between one of the original $\beta$ sources and one of the original $\sigma$ sinks. Figure 2 in the appendix illustrates this transformation.

For every non-terminal, we will store two pointers that delimit the leftmost occurrence of the rule in the text (the beginning and ending positions). This array occupies $O(n)$ words of space. Then, in time $T(n, \sigma, N)$, we build a data structure of size $S(n, \sigma, N)$ that answers rank queries on the string generated by the grammar in time $t(n, \sigma, N)$. To answer a query that counts the number of paths between a node $u$ and a designated sink $v$, we will find the non-terminal $R$ that corresponds to $u$ and the terminal $c$ that corresponds to $v$. We then find (using the array of pointers) the two positions $i$ and $j$ that correspond to the leftmost occurrences of $R$ in the text. Finally, the count is returned by doing two rank queries for symbol $c$ at positions $i$ and $j$ respectively.

**Theorem 4.** Suppose there exists a scheme that can preprocess a grammar of size $n$ with $\sigma$ non-terminals that generates a string of length $N$ in $T(n, \sigma, N)$ time and produces a data structure of size $S(n, \sigma, N)$ that answers to rank queries on the string generated by the grammar in time $t(n, \sigma, N)$. Then given a DAG with $m$ nodes, $n$ edges (possibly with multiedges), $\beta$ sources and $\alpha$ sinks, we can, after preprocessing time $O(n + T(n, \sigma, N))$, produce a data structure of size $O(n + S(n, \sigma, N))$ that can count the number of distinct paths from any node of the DAG to one of the $\sigma$ sinks in time $O(t(n, \sigma, N))$, where $N$ is the number of distinct paths that connect the $\beta$ sources to the $\alpha$ sinks.

6 Concluding Remarks

Perhaps the most important open question we raise is whether our results for rank and select are optimal. As we have shown, proving this one way or the other would lead to progress on the path counting problem in DAGs, an old and interesting problem in graph theory. Relatedly, similar approaches may prove fruitful in judging the hardness of other problems on grammar-compressed strings, many solutions to which currently seem to be loose upperbounds [4,1,27,24,25].

Our result for access closes the gap between Bille et al.’s random access result [5] and the lowerbound of Verbin and Yu [48] for the (large) set of strings whose grammar-compressed size $n$ is polynomially related to $N$. We leave closing the gap for the remaining strings as an open problem.

Another interesting problem for future work is to support these queries in compressed text whose size is bounded in terms of the size of the LZ77 parsing, $z$, which is a lowerbound on $n$. The block graph data structure of Gagie, Gawrychowski and Puglisi [16] supports access queries for $m$ symbols of text in $O(\log N + m)$ time and $O(z \log N)$ words of space. Perhaps it is possible to augment their data structure to also support rank and select. Also, is it possible to improve their access time to $O(\log N + m/\log_\sigma N)$ as we have done here for grammar compressed strings?
References

1. Bannai, H., Gagie, T., I, T., Inenaga, S., Landau, G.M., Lewenstein, M.: An efficient algorithm to test square-
    freeness of strings compressed by straight-line programs. Information Processing Letters 112(19), 711–714 (2012)
2. Bendersky, M., Croft, W.B.: Finding text reuse on the web. In: Proc. 2nd International Conference on Web
    Search and Web Data Mining (WSDM). pp. 262–271 (2009)
3. Bille, P., Cording, P.H., Görtz, I.L.: Compact q-gram profiling of compressed strings. In: Proc. 24th Symposium
    on Combinatorial Pattern Matching (CPM). pp. 62–73. LNCS 7922 (2013)
4. Bille, P., Cording, P.H., Görtz, I.L.: Compressed subsequence matching and packed tree coloring. In: Proc. 25th
    Symposium on Combinatorial Pattern Matching (CPM). pp. 40–49. LNCS 8486 (2014)
5. Bille, P., Landau, G.M., Raman, R., Sadakane, K., Satti, S.R., Weimann, O.: Random access to grammar-
    compressed strings. In: Proc. 22nd Symposium on Discrete Algorithms (SODA). pp. 373–389. SIAM (2011)
6. Charikar, M., Lehman, E., Liu, D., Panigrahy, R., Prabhakaran, M., Sahai, A., Shelat, A.: The smallest grammar
    problem. IEEE Transactions on Information Theory 51(7), 2554–2576 (2005)
7. Claude, F., Navarro, G.: Self-indexed grammar-based compression. Fundamenta Informaticae 111(3), 313–337
    (2010)
8. Claude, F., Navarro, G.: Improved grammar-based compressed indexes. In: Proc. 19th International Symposium on
    String Processing and Information Retrieval (SPIRE). pp. 180–192. LNCS 7608 (2012)
9. Cohen, E., Halperin, E., Kaplan, H., Zwick, U.: Reachability and distance queries via 2-hop labels. SIAM Journal on
    Computing 32(5), 1338–1355 (2003)
10. Consortium, .G.P.: A map of human genome variation from population-scale sequencing. Nature 467, 1061–1073
    (2010)
11. Ferragina, P., Manzini, G.: On compressing the textual web. In: Proc. 3rd Conference on Web Search and Data
    Mining (WSDM). pp. 391–400 (2010)
12. Ferragina, P., Venturini, R.: A simple storage scheme for strings achieving entropy bounds. Theoretical Computer
    Science 372(1), 115–121 (2007)
13. Fredman, M.L., Willard, D.E.: Blasting through the information theoretic barrier with fusion trees. In: Proceedings of
    the twenty-second annual ACM symposium on Theory of computing. pp. 1–7. ACM (1990)
14. Fredman, M.L., Willard, D.E.: Surpassing the information theoretic bound with fusion trees. Journal of computer
    and system sciences 47(3), 424–436 (1993)
15. Gagie, T., Gawrychowski, P., Kärkkäinen, J., Nekrich, Y., Puglisi, S.J.: A faster grammar-based self-index. In:
    Proc. International Conference on Language and Automata Theory and Applications (LATA). pp. 240–251.
    LNCS 7183 (2012)
16. Gagie, T., Gawrychowski, P., Puglisi, S.J.: Faster approximate pattern matching in compressed repetitive texts. In:
    Proc. International Symposium on Algorithms and Computation (ISAAC). pp. 653–662. LNCS 7074 (2011)
17. Gawrychowski, P.: Faster algorithm for computing edit distance between SLP-compressed strings. In: Proc.
    Symposium on String Processing and Information Retrieval (SPIRE). pp. 229–236. LNCS 7608 (2012)
18. Golyński, A., Munro, J.I., Rao, S.S.: Rank/select operations on large alphabets: a tool for text indexing. In: Proc.
    17th Symposium on Discrete Algorithms (SODA). pp. 368–373. SIAM (2006)
19. Goto, K., Bannai, H., Inenaga, S., Takeda, M.: Fast q-gram mining on SLP compressed strings. Journal of Discrete
    Algorithms 18, 89–99 (2013)
20. Grossi, R., Gupta, A., Vitter, J.S.: High-order entropy-compressed text indexes. In: Proc. 14th Symposium on
    Discrete Algorithms (SODA). pp. 841–850. SIAM (2003)
21. Grossi, R., Gupta, A., Vitter, J.S.: When indexing equals compression: experiments with compressing suffix
    arrays and applications. In: Proc. 15th Symposium on Discrete Algorithms (SODA). pp. 636–645. SIAM (2004)
22. Hermelin, D., Landau, G.M., Landau, S., Weimann, O.: Unified compression-based acceleration of edit-distance
    computation. Algorithmica 65(2), 339–353 (2013)
23. Hon, W.K., Patil, M., Shah, R., Thankachan, S.V., Vitter, J.S.: Indexes for document retrieval with relevance. In:
    Space-Efficient Data Structures, Streams, and Algorithms. pp. 351–362. LNCS 8066 (2013)
24. I, T., Matsubara, W., Shimohira, K., Inenaga, S., Bannai, H., Takeda, M., Narisawa, K., Shinohara, A.: Detecting
    regularities on grammar-compressed strings. In: Proc. 38th International Symposium on Mathematical Foundations of
    Computer Science (MFCS). pp. 571–582. LNCS 8087 (2013)
25. I, T., Nakashima, Y., Inenaga, S., Bannai, H., Takeda, M.: Faster Lyndon factorization algorithms for SLP and
    LZ78 compressed text. In: Proc. 20th International Symposium on String Processing and Information Retrieval
    (SPIRE). pp. 174–185. LNCS 8214 (2013)
26. I, T., Nishimoto, T., Inenaga, S., Bannai, H., Takeda, M.: Compressed automata for dictionary matching. In: Proc. 18th International Conference on Implementation and Application of Automata (CIAA). pp. 319–330. LNCS 7982 (2013)

27. Inenaga, S., Bannai, H.: Finding characteristic substrings from compressed texts. International Journal of Foundations of Computer Science 23(2), 261–280 (2012)

28. Karpinski, M., Rytter, W., Shinozaha, A.: An efficient pattern-matching algorithm for strings with short descriptions. Nordic Journal of Computing 4, 172–186 (1997)

29. Larsson, N.J., Moffat, A.: Offline dictionary-based compression. Proc. of the IEEE 88(11), 1722–1732 (2000)

30. Mäkinen, V., Navarro, G., Sirén, J., Välimäki, N.: Storage and retrieval of highly repetitive sequence collections. Journal of Computational Biology 17(3), 281–308 (2010)

31. Manzini, G.: An analysis of the Burrows-Wheeler transform. Journal of the ACM 48(3), 407–430 (2001)

32. Metzler, D., Bernstein, Y., Croft, W.B., Moffat, A., Zobel, J.: Similarity measures for tracking information flow. In: Proc. 14th ACM Int. Conf. Information and Knowledge Management (CIKM). pp. 517–524. ACM Press (2005)

33. Munro, J.I.: Tables. In: Proc. 16th Conference on Foundations of Software Technology and Theoretical Computer Science (FSTTCS). pp. 37–42. LNCS 1180 (1996)

34. Navarro, G.: Indexing highly repetitive collections. In: Proc. 23rd International Workshop on Combinatorial Algorithms (IWOCA). pp. 274–279. LNCS 7643 (2012)

35. Navarro, G.: Spaces, trees and colors: The algorithmic landscape of document retrieval on sequences. ACM Computing Surveys 46(4), article 52 (2014), 47 pages

36. Navarro, G.: Wavelet trees for all. Journal of Discrete Algorithms 25, 2–20 (2014)

37. Navarro, G., Mäkinen, V.: Compressed full-text indexes. ACM Computing Surveys 39(1), article 2 (2007)

38. Navarro, G., Ordóñez, A.: Grammar compressed sequences with rank/select support. In: Proceedings of the 21st International Symposium on String Processing and Information Retrieval (SPIRE) (2014), to appear

39. Navarro, G., Puglisi, S.J., Valenzuela, D.: Practical compressed document retrieval. In: Proc. 10th International Symposium on Experimental Algorithms (SEA). pp. 193–205. LNCS 6630 (2011)

40. Navarro, G., Puglisi, S.J., Valenzuela, D.: General document retrieval in compact space. ACM Journal of Experimental Algorithmics (2014), to appear

41. Navarro, G., Valenzuela, D.: Space-efficient top-k document retrieval. In: Proc. 11th International Symposium on Experimental Algorithms (SEA). pp. 307–319. LNCS 7276 (2012)

42. Okanohara, D., Sadakane, K.: Practical entropy-compressed rank/select dictionary. In: Proc. 9th workshop on Algorithm Engineering and Experiments. pp. 60–70. SIAM (2007)

43. Raman, R., Raman, V., Rao, S.S.: Succinct indexable dictionaries with applications to encoding k-ary trees, prefix sums and multisets. ACM Transactions on Algorithms 3(4) (2007)

44. Riesenfeld, C., Schloss, P.D., Handelsman, J.: Metagenomics: genomic analysis of microbial communities. Annual Review of Genetics 38, 525–552 (2004)

45. Rytter, W.: Application of Lempel-Ziv factorization to the approximation of grammar-based compression. Theoretical Computer Science 302(1–3), 211–222 (2003)

46. Sadakane, K., Grossi, R.: Squeezing succinct data structures into entropy bounds. In: Proc. 17th Symposium on Discrete Algorithms (SODA). pp. 1230–1239. SIAM (2006)

47. Tiskin, A.: Towards approximate matching in compressed strings: Local subsequence recognition. In: Proc. 6th International Computer Science Symposium in Russia (CSR). pp. 401–414. LNCS 6651 (2011)

48. Verbin, E., Yu, W.: Data structure lower bounds on random access to grammar-compressed strings. In: Proc. 24th Symposium on Combinatorial Pattern Matching (CPM). pp. 247–258. LNCS 7922 (2013)

49. Ziv, J., Lempel, A.: A universal algorithm for sequential data compression. IEEE Transactions on Information Theory 23(3), 337–343 (1977)
Fig. 2. An illustration of the transformation required in our reduction of rank queries on a grammar compressed string to a path counting queries in DAGs.