A New Lightweight Algorithm to compute the BWT and the LCP array of a Set of Strings

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Abstract

Indexing of very large collections of strings such as those produced by the widespread sequencing technologies, heavily relies on multi-string generalizations of the Burrows-Wheeler Transform (BWT), and for this problem various in-memory algorithms have been proposed. The rapid growing of data that are processed routinely, such as in bioinformatics, requires a large amount of main memory, and this fact has motivated the development of algorithms, to compute the BWT, that work almost entirely in external memory.

On the other hand, the related problem of computing the Longest Common Prefix (LCP) array is often instrumental in several algorithms on collection of strings, such as those that compute the suffix-prefix overlap among strings, which is an essential step for many genome assembly algorithms.

The best current lightweight approach to compute BWT and LCP array on a set of \(m\) strings, each one \(k\) characters long, has I/O complexity that is \(O(mk^2 \log |\Sigma|)\) (where \(|\Sigma|\) is the size of the alphabet), thus it is not optimal.

In this paper we propose a novel approach to build BWT and LCP array (simultaneously) with \(O(kmL(\log k + \log \sigma))\) I/O complexity, where \(L\) is the length of longest substring that appears at least twice in the input strings.

1 Introduction

In this paper we address the problem of constructing in external memory the Burrows-Wheeler Transform (BWT) and the Longest Common Prefix (LCP) array for a large collection of strings. An efficient indexing of very large collections of strings is strongly motivated by the widespread use of Next-Generation Sequencing (NGS) technologies that are producing everyday collections of data that fill several terabytes of secondary storage, that has to be processed by software applications. Common applications in metagenomics require indexing of collections of strings (reads) that are sampled from several genomes, where those genomes amount to billions of base pairs. For example, over 500 gigabases of data have been analyzed to start a catalogue of the human gut microbiome.\[20\]
The Burrows-Wheeler Transform (BWT) [6] is a reversible transformation of a text that was originally designed for text compression; it is used for example in the BZIP2 program. The BWT of a text $T$ is a permutation of its symbols and is strictly related to the Suffix Array of $T$. In fact, the $i^{th}$ symbol of the BWT is the symbol preceding the $i^{th}$ smallest suffix of $T$ according to the lexicographical sorting of the suffixes of $T$. The Burrows-Wheeler Transform has gained importance beyond its initial purpose, and has become the basis for self-indexing structures such as the FM-index [8], which allows to efficiently perform important tasks such as searching a pattern in a text [8,12,21]. The generalization of the BWT (and the FM-index) to a collection of strings has been introduced in [16,17].

An entire generation of recent bioinformatics tools heavily rely on the notion of BWT. For example, representing the reference genome with its FM-index is the basis of the most widely used aligners, such as Bowtie [10], BWA [13,14] and SOAP2 [15]. Still, to attack some other fundamental bioinformatics problems, such as genome assembly, an all-against-all comparison among the input strings is needed, especially to find all prefix-suffix matches (or overlaps) between reads in the context of the Overlap Layout Consensus (OLC) approach based on string graph [18]. This fact justifies to search for extremely time and space efficient algorithms to compute the BWT on a collection of strings [2,7,11,25]. For example, SGA (String Graph Assembler) [23] is a de novo genome assembler that builds a string graph from the FM-index of the collection of input reads. In a preliminary version of SGA [22], the authors estimated, for human sequencing data at a 20x coverage, the need of 700Gbytes of RAM in order to build the suffix array, using the construction algorithm in [19], and the FM-index.

Another technical device that is used to tackle the genome assembly in the OLC approach is the Longest Common Prefix (LCP) array of a collection of strings, which is instrumental to compute (among others) the prefix-suffix matches in the collection. The huge amount of available biological data has stimulated the development of the first efficient external-memory algorithms (called, BCR and BCRext) to construct the BWT of a collection of strings [1]. Similarly, a lightweight approach to the construction of the LCP array has been investigated [3]. Towards an external memory genome assembler, LSG [4,5] is founded upon BCRext and builds in external memory the string graph of a set of strings. In that approach, external memory algorithms to compute the BWT and the LCP array [2,3] are fundamental.

Still, the construction of the BWT (and LCP array) of a huge collection of strings is a challenging task. A simple approach is constructing the BWT from the Suffix Array, but it is prohibitive for massive datasets. A first attempt to solve this problem [24] partitions the input collection into batches, computes the BWT for each batch and then merges the results.

In this paper we present a new lightweight (external-memory) approach to compute the BWT and the LCP array of a collection of strings, which is alternative to BCRext [1]. The algorithm BCRext is proposed together with BCR and both are designed to work on huge collections of strings (the experimental analysis is on billions of 100-long strings). Those algorithms are lightweight because, on a collection of $m$ strings of length $k$, BCR uses only
$O(m \log(mk))$ RAM space and $O(km + \text{sort}(m))$ CPU time, where sort($m$) is the time taken to sort $m$ integers. The same complexity holds for the lightweight LCP algorithm given in [3]. Though the use of the RAM is negligible for DNA data, the overall I/O volume is $O(k^2m + mk \log(mk))$. Clearly, a main question is if it is possible to achieve the optimal $O(km)$ I/O complexity. Both BCR and BCReXt build the BWT with a column-wise approach, where at each step $i$ the elements preceding the suffixes of length $k - i - 1$ of each read are inserted in the correct positions of the partial BWT that considers only suffixes shorter than $k - i - 1$. Moreover, both algorithms are described as a succession of sequential scans, where the partial BWTs are read from and written to external files, thus obtaining a small main memory footprint.

Compared to BCReXt, our algorithm uses an I/O volume that is $O(Lkm \log k)$, where $L$ is the maximum length of any substring appearing at least twice in the input collection. Clearly $L \leq k$. Compared with BCR, our approach does not require an explicit sort of a generic set, but it is mainly based on the simple idea of building partial BWTs, each one for the set of suffixes of a given length $l$, then merging those partial BWTs to obtain the complete BWT by using an approach similar to the one proposed in [9], where the construction of a multi-string BWT is proposed with the main goal of merging BWTs for distinct genomic sequences.

2 Preliminaries

Let $\Sigma = \{c_0, c_1, \ldots, c_\sigma\}$ be a finite alphabet where $c_0 = \$$ (called sentinel), and $c_0 < c_1 \cdots < c_\sigma$ where $<$ specifies the lexicographic ordering over alphabet $\Sigma$. We consider a collection $S = \{s_1, s_2, \ldots, s_m\}$ of $m$ strings, where each string $s_j$ consists of $k$ symbols over the alphabet $\Sigma \setminus \{$$\}$ and is terminated by the symbol $$$. The $i^{th}$ symbol of string $s_j$ is denoted by $s_j[i]$ and the substring $s_j[i]s_j[i+1] \cdots s_j[t]$ of $s_j$ is denoted by $s_j[i : t]$. In order to simplify the presentation, we assume that all the strings in $S$ have the same length $k$. The suffix and prefix of $s_j$ of length $l$ are the substrings $s_j[k-l+1 : k]$ (denoted by $s_j[k-l+1 : ]$) and $s_j[1 : l]$ (denoted by $s_j[: l]$) respectively. Then the $l$-suffix and $l$-prefix of a string $s_j$ is the suffix and prefix with length $l$, respectively. The lexicographic ordering among strings in $S$ is defined in the usual way. Though we use the same sentinel to terminate strings, we can easily distinguish the same suffix of different strings by assuming an implicit ordering of the sentinels that is induced by the ordering of the input strings.

More precisely, we assume that given $s_i, s_j \in S$, with $i < j$, then the sentinel of $s_i$ precedes the sentinel of $s_j$.

Given the lexicographic ordering $X$ of the suffixes of $S$, the Suffix Array is the $(m(k + 1))$-long array $SA$ where the element $SA[i]$ is equal to $(p, j)$ if and only if the $i^{th}$ element of $X$ is the $p$-suffix of string $s_j$. The Burrows-Wheeler Transform (BWT) of $S$ is the $(m(k + 1))$-long array $B$ where if $SA[i] = (p, j)$, then $B[i]$ is the first symbol of the $(p + 1)$-suffix of $s_j$ if $p < k$, otherwise $B[i] = \$$. In other words $B$ consists of the symbols preceding the ordered suffixes of $X$. The Longest Common Prefix (LCP) array of $S$ is the $(m(k + 1))$-long array $LCP$ such that $LCP[i]$ is the length of the longest prefix shared by
suffixes $X[i - 1]$ and $X[i]$. Conventionally, $LCP[1] = -1$.

Now, we give the definition of *interleave* of a generic set of arrays, that will be used extensively in the following.

**Definition 1.** Given $n + 1$ arrays $V_0, V_1, \ldots, V_n$, then an array $W$ is an interleave of $V_0, V_1, \ldots, V_n$ if $W$ is the result of merging the arrays such that: (i) there is a 1-to-1 function $\psi_W$ from the set $\bigcup_{i=0}^n \{(i, j) : 1 \leq j \leq |V_i|\}$ to the set $\{q : 1 \leq q \leq |W|\}$, (ii) $V_i[j] = W[\psi_W(i, j)]$ for each $i, j$, and (iii) $\psi_W(i, j) < \psi_W(i, j_2)$ for each $j_1 < j_2$.

By denoting with $L = \sum_{i=0}^n |V_i|$ the total length of the arrays, the interleave $W$ is a $L$-long array giving a fusion of $V_0, V_1 \ldots, V_n$ which preserves the relative order of the elements in each one of the arrays. As a consequence, for each $i$ with $0 \leq i \leq n$, the $j^{th}$ element of $V_i$ corresponds to the $j^{th}$ occurrence in $W$ of an element of $V_i$. This fact allows to encode the function $\psi_W$ as a $L$-long array $I_W$ such that $I_W[q] = i$ if and only if $W[q]$ is an element of $V_i$. Given $I_W$, it is possible to reconstruct $W$ by considering that $W[q]$ is equal to $V_{I_W[q]}[j]$ where $j$ is the number of values equal to $W[q]$ in the interval $I_W[1, q]$; this number will be called *rank* at position $q$. In the following, we will refer to vector $I_W$ as *interleave-encoding* (or simply *encoding*). Algorithm 1 shows how to reconstruct an interleave from its encoding (the array *rank* is used to store the rank values), and can also be used to simulate a scan of $W$ by means of its encoding $I_W$.

**Algorithm 1:** Reconstruct the interleave $W$ from the encoding $I_W$

1. for $i \leftarrow 0$ to $n$ do
2.   rank[$i$] $\leftarrow 0$
3. for $q \leftarrow 1$ to $|I_W|$ do
4.   $i \leftarrow I_W[q]$
5.   rank[$i$] $\leftarrow$ rank[$i$] + 1
6.   $W[q] \leftarrow V_i[rank[i]]$

### 3 The lightweight algorithm for BWT and LCP array

Let $B_l$ and $X_l$ ($0 \leq l \leq k$) be $m$-long arrays such that $B_l[i]$ is the symbol preceding the $i^{th}$ smallest $l$-suffix of $S$ and $X_l[i]$ is the $i^{th}$ smallest $l$-suffix of $S$. It is easy to see that the BWT $B$ is an interleave of the $k + 1$ arrays $B_0, B_1, \ldots, B_k$, since the ordering of symbols in $B_l$ ($0 \leq l \leq k$) is preserved in $B$, i.e. $B$ is *stable* w.r.t. each array $B_0, B_1, \ldots, B_k$. This fact is a direct consequence of the definition of $B$ and $B_0$. For the same reason, the lexicographic ordering $X$ of all suffixes of $S$ is an interleave of the arrays $X_0, X_1, \ldots, X_k$. Let $I_B$ be the encoding of the interleave of arrays $B_0, B_1, \ldots, B_k$ giving the BWT $B$, and let $I_X$ be the encoding of the interleave of arrays $X_0, X_1, \ldots, X_k$ giving $X$. Then it is possible to show that $I_B = I_X$.

Our algorithm for building the BWT $B$ and the LCP array, differently from \[1\], consists of two distinct phases: in the first phase the arrays $B_0, B_1, \ldots, B_k$ are computed, while
the second phase determines $I_X$ (which is equal to $I_B$) thus allowing to reconstruct $B$ as an interleave of $B_0, B_1, \ldots, B_k$. Indeed, BCRext \cite{1} computes the BWT of the collection $S$ incrementally via $k + 1$ iterations. At each iteration $l$, with $0 \leq l \leq k$, the algorithm computes a partial BWT $bwt_l(S)$ that is the BWT for the ordered collection of suffixes of length at most $l$, that is for the lexicographic ordering of $X_0, X_1, \ldots, X_l$. This approach requires that, at each iteration $l$, the symbols preceding the $(l-1)$-suffixes of $S$ must be inserted at their correct positions into $bwt_{l-1}(S)$, that is each $l$ iteration simulates the insertion of the $l$-suffixes in the ordered collection of $\bigcup_{i=0}^{l-1}X_i$. Updating the partial BWT $bwt_l(S)$ in external memory, the process requires a sequential visit of the file containing the basic information of the partial $bwt_{l-1}(S)$. Thus the I/O volume at each iteration $l$ is at least $m(l-1)\log \sigma$ (since there are $m$ suffixes for each length $i$ between 1 to $l-1$). Consequently the total I/O volume for computing $bwt_k(S)$ is at least $O(mk^2)$. More precisely, the BCRext algorithm in \cite{1} that uses less RAM, requires at each iteration an additional I/O volume given by $m \log (km)$, due to a process of ordering special arrays used to save RAM space. Our algorithm instead consists of a first phase that has $O(mk)$ I/O volume and time complexity and produces the arrays $B_0, B_1, \ldots, B_k$ (see procedure \textbf{Partition-suffixes}), and a second phase which computes $I_X$ by implicitly merging the arrays $X_0, X_1, \ldots, X_k$ into the interleave $X$ of the overall ordered set of all suffixes (see procedure \textbf{Merge-suffixes}). As described in Section \cite{3}, the procedure does not need to compute explicitly the arrays $X_0, X_1, \ldots, X_k$ and the interleave $X$. Inspired by \cite{9}, we perform this step by a number of $L$ iterations, where $L$ the length of the longest substring that has at least two occurrences in $S$. Thus the merging operation takes fewer iterations than BCRext (the latter requires $k$).

4 The Procedure Partition-suffixes

The input set $S = \{s_1, s_2, \ldots, s_m\}$ is preprocessed in order to have a fast access to its symbols, and $k$ $m$-long arrays $S_0, S_1, \ldots, S_{k-1}$ are obtained. More in detail, the element $S_l[i]$ ($0 \leq l \leq k-1$) is the $(k-l)^{th}$ symbol of the string $s_i$, that is $s_i[k-l]$. In other words $S_l[i]$ is the symbol preceding the $l$-suffix of $s_i$. The procedure Partition-suffixes (see Algorithm \cite{2}) takes in input the arrays $S_0, S_1, \ldots, S_{k-1}$ and computes the arrays $B_0, B_1, \ldots, B_k$ by using $k + 1$ $m$-long arrays $N_l$ ($0 \leq l \leq k$), where $N_l[i] = q$ if and only if the $l$-suffix of the input string $s_q$ is the $i^{th}$ element of $X_l$. Notice that the symbol $B_l[i]$ precedes the $l$-suffix $s_q[k-l+1:]$, that is $B_l[i] = s_q[k-l]$. In particular, $N_0$ contains the sequence of indexes $(1, 2, 3, \ldots, |S|)$ and $B_0$ contains the sequence $(s_1[k], s_2[k], \ldots, s_m[k])$ of the last symbols of the input strings (i.e. the symbols before the sentinels). In order to specify the structure of the Procedure Partition-suffixes, given a symbol $c_h$ of the alphabet $\Sigma$, we define the $c_h$-projection operation $\Pi_{c_h}$ over the array $N_l$ that consists in taking from $N_l$ only the entries $i$ such that $s_i[k-l] = c_h$. In other words $\Pi_{c_h}(N_l)$ is the vector that projects the entries of $N_l$ corresponding to strings whose $l$-suffix is preceded by the symbol $c_h$. Then the following Lemma directly follows from definition of $N_{l-1}$.

\textbf{Lemma 1.} Given the array $N_{l-1}$, the sequence of indexes of strings, whose $l$-suffix starts
with symbol \( c_h \) and ordered w.r.t. the \( l \)-suffix, is equal to vector \( \Pi_{c_h}(N_{l-1}) \).

As a main consequence of the above Lemma the array \( N_l \) can be simply obtained from \( N_{l-1} \) as the concatenation \( \Pi_{c_0}(N_{l-1}) \cdot \Pi_{c_1}(N_{l-1}) \cdots \Pi_{c_\sigma}(N_{l-1}) \) where \( c_0 \cdot c_1 \cdots c_\sigma \) is the lexicographic order of symbols of alphabet \( \Sigma \). Notice that the \( c_h \)-projection of \( N_{l-1} \), is computed by listing the positions \( i \) of \( N_{l-1} \) such that \( B_{l-1}[i] = c_h \). Indeed, \( B_{l-1} \) lists the symbols precedings the ordered \((l-1)\)-suffixes.

The procedure Partition-suffixes computes arrays \( B_0, \ldots, B_k \) in \( k \) iterations. At each iteration \( l \), arrays \( B_l \) and \( N_l \) are computed from arrays \( B_{l-1} \) and \( N_{l-1} \). The array \( N_{l-1} \) is stored in \(|\Sigma|\) lists \( N_{l-1}(c_h) \), where \( N_{l-1}(c_h) \) is the \( c_h \)-projection of \( N_{l-1} \). In the following, the arrays are treated as lists which can be stored in external files.

The basic procedure to compute \( N_l \) from \( B_{l-1} \) and \( N_{l-1} \) is the following. First, \( B_{l-1} \) is sequentially read and, for each position \( i \), \( N_{l-1}[i] \) is appended to the list \( N_{l-1}(c_h) \), where \( c_h = B_{l-1}[i] \). At this point, \( N_l \) is given by the concatenation of lists \( N_{l-1}(c_0)N_{l-1}(c_1) \cdots N_{l-1}(c_\sigma) \). After computing \( N_l \), the vector \( B_l \) can be obtained. Indeed, assuming that the \( j^{th} \) element in the ordered list of \( l \)-suffixes is the suffix of string \( i \) (that is, \( N_l[j] = i \)) the symbol preceding such suffix is \( s_i[|s_i| - l] \) and is directly obtained by accessing position \( i \) of vector \( S_l \) (recall that \( S_l \) has been computed in the preprocessing phase). More precisely, \( N_l \) is sequentially read and, for each position \( j \), if \( N_l[j] = i \) then \( B_l[j] = S_l[i] \). Due to a random access, array \( S_l \) it is assumed to be kept in RAM with a space cost of \( O(m \log \sigma) \).

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**Algorithm 2: Partition-suffixes**

- **Input**: The arrays \( S_0, \ldots, S_k \).
- **Output**: The arrays \( B_0, \ldots, B_k \).

1. for \( i \leftarrow 1 \) to \( m \) do
2.   \( B_0[i] \leftarrow S_0[i] \);
3.   \( N_0[i] \leftarrow i \);
4. for \( l \leftarrow 1 \) to \( k \) do
5.   foreach \( c \in \Sigma \) do
6.     \( N_{l-1}(c) \leftarrow \) empty list;
7.   \( B_l \leftarrow \) empty list;
8.   \( N_l \leftarrow \) empty list;
9. for \( i \leftarrow 1 \) to \( m \) do
10.   \( c \leftarrow B_{l-1}[i] \);
11.   Append \( N_{l-1}[i] \) to \( N_{l-1}(c) \);
12. for \( i \leftarrow 0 \) to \(|\Sigma|\) do
13.   Append \( N_{l-1}(c_i) \) to \( N_l \);
14. for \( i \leftarrow 1 \) to \( m \) do
15.   Append \( S_l[N_l[i]] \) to \( B_l \);
The procedure Merge-suffixes

The second step of our algorithm computes the encoding $I_X$ of the interleave $X$ of the arrays $X_0, X_1, \cdots, X_k$, giving the lexicographic ordering of all suffixes of $S$ and (at the same time) computes the LCP array. Recall that $I_X$ is equal to the encoding $I_B$ of the interleave of the arrays $B_0, B_1, \cdots, B_k$ giving the BWT $B$. This section is devoted to describe how to compute $I_X$ from which it is easy to obtain the BWT $B$ as explained in Algorithm [1], while the description of the approach to obtain the LCP array is postponed until Section 5.1.

Before entering into the details, we need some definitions.

**Definition 2.** Let $\alpha = s_{i_{\alpha}}[k - l_{\alpha} + 1 :]$ and $\beta = s_{i_{\beta}}[k - l_{\beta} + 1 :]$ be two generic suffixes of $S$, with length respectively $l_{\alpha}$ and $l_{\beta}$. Then, given an integer $p$, $\alpha \prec_p \beta$ (and we say that $\alpha$ $p$-precedes $\beta$) iff one of the following conditions hold: (1) $\alpha[:, p]$ is lexicographically strictly smaller than $\beta[:, p]$, (2) $\alpha[:, p] = \beta[:, p]$ and $l_{\alpha} < l_{\beta}$, (3) $\alpha[:, p] = \beta[:, p]$, $l_{\alpha} = l_{\beta}$ and $i_{\alpha} < i_{\beta}$.

**Definition 3.** Given the arrays $X_0, X_1, \cdots, X_k$, the $p$-interleave $X^p$ ($0 \leq p \leq k$) is the interleave such that $X^p[i]$ is the $i^{th}$ smallest suffix in the $\prec_p$-ordering of all the suffixes of $S$.

It is immediate to verify that $X^k$ (that is, the suffixes sorted according to the $\prec_k$ relation) is equal to $X$, hence $I_X = I_{X^k}$. Therefore, our approach is to determine $I_{X^k}$ by iteratively computing $I_{X^p}$ by increasing values of $p$, starting from $I_{X^0}$. Observe that $X^0$ lists the suffixes in the same order given by the concatenation of arrays $X_0, X_1, \cdots, X_k$ and the encoding $I_{X^0}$ is trivially given by $|X_0| 0$s, followed by $|X_1| 1$s, $\ldots$, followed by $|X_k|$ values equal to $k$.

**Definition 4.** Let $X^p$ be the $p$-interleave of $X_0, X_1, \cdots, X_k$, and let $i$ be a position. Then, the $p$-segment of $i$ in $X^p$ is the maximal interval $[b, e]$ such that $b \leq i \leq e$ and all suffixes in $X^p[b, e]$ have the same $p$-prefix. Positions $b$ and $e$ are called respectively begin and end position of the segment, and the common $p$-prefix is denoted by $w_p(b, e)$.

It is immediate to observe that the set of all the $p$-segments of a $p$-interleave form a partition of its positions $(1, \cdots, (k + 1)m)$. Observe that, by definition, a suffix smaller than $p$ belongs to a $p$-segment $[b, e]$ having $b = e$. In other words, such suffix is the unique element of the $p$-segment.

Before describing the approach, the computation of $X^p$ from $X^{p-1}$ is explained. Let $Q^p$ ($0 \leq p \leq k$ and $0 \leq l \leq k$) be the $m$-long array such that $Q^p[i]$ is the $p^{th}$ symbol of the suffix $X[i]$. In particular, $Q^p[i]$ is the sentinel $\$ if the suffix is smaller than $p$. Moreover, let $Q^p$ be the interleave of the arrays $Q^0_0, Q^0_1, \cdots, Q^0_k$ such that $I_{Q^0} = I_{X^{p-1}}$. In other words, $Q^p[i]$ is the $p^{th}$ symbol of the suffix $X^{p-1}[i]$.

**Lemma 2.** Let $[b, e]$ be a $(p - 1)$-segment of $X^{p-1}$. Then, $X^p[b, e]$ is a permutation of $X^{p-1}[b, e]$ defined by the permutation $\Pi_{b, e}^{p-1}$ of the indexes $(b, b + 1, \cdots, e)$ producing the stable ordering of the symbols in $Q^p[b, e]$, such that the $r^{th}$ suffix of $X^p[b, e]$ is the suffix of $X^{p-1}$ in position $\Pi_{b, e}^{p-1}[r]$.
Proof. First we prove that $X^p[b,e]$ is a permutation of $X^{p-1}[b,e]$. Let us denote with $w$ the $(p-1)$-prefix common to suffixes in $X^{p-1}[b,e]$, and let $i$ be a position in $[b,e]$. Given a position $q < b$, by definition, the $(p-1)$-prefix $w_q$ of $X^{p-1}[q]$ is strictly smaller than $w$. Then, the $p$-prefix of $X^{p-1}[q]$ is strictly smaller than the $p$-prefix of $X^{p-1}[i]$. In the same way, given a position $q' > e$ by definition, the $(p-1)$-prefix $w'_q$ of $X^{p-1}[q']$ is strictly greater than $w$. Then, the $p$-prefix of $X^{p-1}[q']$ is strictly greater than the $p$-prefix of $X^{p-1}[i]$. Hence, the set of the suffixes of $X^{p-1}$ before $b$ and the set of the suffixes after $e$ are equal (respectively) to the set of the suffixes of $X^p$ before $b$ and to the set of the suffixes after $e$, thus deriving that for $b < i < e$ the suffix $X^{p-1}[i]$ is equal to $X^p[j]$ for some $j$ in $[b,e]$, completing the proof of the first part.

Furthermore, all suffixes in $X^{p-1}[b,e]$ share the common $(p-1)$-prefix $w$, and therefore their $<_p$-order can be determined by ordering their $p$th symbols. More specifically, the suffix $X^{p-1}[i]$ ($b < i < e$) is the $r^{th}$ suffix in $X^p[b,e]$, where $r$ is the rank of its $p$th character in the stable order of $Q^p[b,e]$. □

Given the suffix in position $i$ of $X^{p-1}$, such that $i$ is in the $(p-1)$-segment $[b,e]$, the Lemma 2 allows to compute its position $i' \in [b,e]$ on $X^p$. Let $\#< be the number of symbols of $Q^p[b,e]$ that are strictly smaller than $Q_q[i]$ and let $\#>_ be the number of symbols of $Q^p[b,q]$ which are equal to $Q^p[i]$. Then, the rank of suffix $X^{p-1}[i]$ in $X^p[b,e]$ is $r = \#<_ + \#>_$, thus deriving that its position in $X^p$ is $i' = b + r - 1$. It is possible to notice that the positions $(b, b+1, \ldots, e)$ on $X^p$ are partitioned into $n$ $p$-segments $[b, c_1], \ldots, [b_n, e]$ (referred as induced by the $(p-1)$-segment $[b, e]$ of $X^{p-1}$), where $n$ is the number of distinct non-$\$ symbols in $Q^p[b,e]$ plus the number $\#_<$ of symbols $<$ in $Q^p[b,e]$. Observe that the first $\#_<$ $p$-segments $[b_1, e_1], \ldots, [b_{\#_<}, e_{\#_<}]$ have width 1, while the width of the last $n - \#_<$ $p$-segments $[b_{\#_<+1}, e_{\#_<+1}], \ldots, [b_n, e_n]$ can be computed as follows. Let $\{c_1, \ldots, c_{n-\#_<}\}$ be the ordered set of the distinct non-$\$ symbols in $Q^p[b,e]$. Then, the width of $[b_{\#_<+1}, e_{\#_<+1}]$ (1 $\leq i \leq n - \#_<$) is equal to the number of occurrences of the symbol $c_i$ in $Q^p[b,e]$. From what described above, it derives that the $p$-segments on $X^p$ form a partition of its positions $(1, \ldots, (k+1)m)$ that is a refinement of the partition formed by the $(p-1)$-segments on $X^{p-1}$.

Now, we describe a simple procedure (see Algorithm 3) to compute $X^p[b,e]$ from the $(p-1)$-segment $[b,e]$ of $X^{p-1}$. The procedure uses $\sigma+1$ (initially empty) lists $L_{c_0}, \ldots, L_{c_\sigma}$. Each position $i \in [b,e]$ is considered from $b$ to $e$ and each suffix $X^{p-1}[i]$ is appended to the list $L_c$ such that $c$ is the $p^{th}$ symbol of $X^{p-1}[i]$. Afterwards, each list of the sequence $\langle L_{c_0}, \ldots, L_{c_\sigma} \rangle$ is read sequentially, and each suffix $x$ in position $r_h$ of the list $L_{c_h}$ is put in the position $b + r - 1$ of $X^p$, where $r$ is given by the total size of the lists $L_{c_0}, \ldots, L_{c_{h-1}}$ (which have been previously read) plus the position $r_h$ of $x$. Observe that $r$ contains the rank of $x$ in the $<_p$-ordering of the suffixes of the $(p-1)$-segment.

Algorithm 3 can be easily modified in order to produce also the $p$-segments $[b, c_1], [b_2, e_2], \ldots, [b_n, e]$ induced by the $(p-1)$-segment $[b, e]$. Observe that the first $|L_{c_0}|$ $p$-segments have width 1, while for the last $n - |L_{c_0}|$ $p$-segments it is easy to prove that $c_i = b + T_i - 1$ where $T_i$ is the total size of the first $i - |L_{c_0}| + 1$ nonempty lists $L_{c_0}, L_{c_1}, \ldots, L_{c_{\sigma}}$. The entire interleave $X^p$ is obtained by computing $X^p[b,e]$ for each distinct $(p-1)$-segment $[b,e]$ of $X^{p-1}$. 8
Algorithm 3: Compute $p$-segment on $X$ from a $(p-1)$-segment

1. $L_{c_0}, L_{c_1}, \ldots, L_{c_a} \leftarrow$ empty lists;
2. for $i \leftarrow b$ to $e$ do
   3. $c \leftarrow Q^p[i];$
   4. Append $X^{p-1}[i]$ to $L_c$;
   5. $r \leftarrow 1$;
6. for $h \leftarrow 0$ to $\sigma$ do
   7. for $r_h \leftarrow 1$ to $|L_{c_h}|$ do
    8. $x \leftarrow L_{c_h}[r_h];$
    9. $X^p[b+r-1] \leftarrow x;$
   10. $r \leftarrow r + 1$;

At this point, it is immediate to extend the definition of $p$-segment $[b, e]$ from $X^p$ to its encoding $I_{X^p}$, and to see that the Algorithm 3 can be slightly modified to compute $I_{X^p}[b, e]$ from the $(p-1)$-segment $[b, e]$ of $I_{X^{p-1}}$ (see Algorithm 4).

Algorithm 4: Compute $p$-segment on $I$ from a $(p-1)$-segment

1. $L_{c_0}, L_{c_1}, \ldots, L_{c_a} \leftarrow$ empty lists;
2. for $i \leftarrow b$ to $e$ do
   3. $c \leftarrow Q^p[i];$
   4. Append $I_{X^{p-1}}[i]$ to $L_c$;
   5. $r \leftarrow 1$;
6. for $h \leftarrow 0$ to $\sigma$ do
   7. for $r_h \leftarrow 1$ to $|L_{c_h}|$ do
    8. $j \leftarrow L_{c_h}[r_h];$
    9. $I_{X^p}[b+r-1] \leftarrow j;$
   10. $r \leftarrow r + 1$;

Based on Algorithm 4 we designed the iterative procedure Merge-suffixes (see Algorithm 6) to compute the encoding $I_{X^k}$ starting from the encoding $I_{X^0}$ that can be easily obtained as explained before. Recall that $I_{X^k}$ is the encoding of the interleave of the arrays $B_0, \ldots, B_k$ giving the BWT $B$ of the input set $S$. The iteration $p$ of the procedure computes $I_{X^p}$ from $I_{X^{p-1}}$, by scanning the array $I_{X^{p-1}}$, and is detailed in Algorithm 5. Precisely, the procedure, for each $(p-1)$-segment $[b, e]$, computes the portion $I_{X^p}[b, e]$ of $I_{X^p}$. We point out that it is not actually necessary to reconstruct the interleave $Q^p$ from the arrays $Q^p_0, Q^p_1, \ldots, Q^p_k$, since its encoding is $I_{X^{p-1}}$, and therefore a scan of $I_{X^{p-1}}$ allows also to simulate a scan of $Q^p$ (see Algorithm 1).

The conditions at line 13 of Algorithm 5 and at line 6 of Algorithm 6 are checked by using an auxiliary binary array $E^{p-1}$ storing the $(p-1)$-segments. More specifically, $E^{p-1}[i]$ is true iff $i$ is the end position of some $(p-1)$-segment. The array $E^{p-1}$ is sufficient to reconstruct the set of all $(p-1)$-segments since they form a partition of positions.
Algorithm 5: Compute $I_{X^p}$ from $I_{X^{p-1}}$

1 $L_{c_0}, L_{c_1}, \ldots, L_{c_\sigma} \leftarrow$ empty lists;
2 for $j \leftarrow 0$ to $k$ do
3     rank[$j$] $\leftarrow$ 0;
4 pick_up_start $\leftarrow$ true;
5 for $i \leftarrow 1$ to $(k+1)m$ do
6     if pick_up_start = true then
7         $b \leftarrow i$;
8         pick_up_start = false;
9         $j \leftarrow I_{X^{p-1}}[\bar{i}]$;
10        rank[$j$] $\leftarrow$ rank[$j$] + 1;
11        $c \leftarrow Q^p_{\text{index}}[\text{rank}[j]]$;
12        Append $j$ to $L_c$;
13     if $i$ is the end position of a $(p-1)$-segment then
14         pick_up_start = true;
15         $r \leftarrow 1$;
16     for $h \leftarrow 0$ to $\sigma$ do
17         for $r_h \leftarrow 1$ to $|L_{c_h}|$ do
18             $j \leftarrow L_{c_h}[r_h]$;
19             $I_{X^p}[b + r - 1] \leftarrow j$;
20         if $r_h > 1$ and $h > 0$ then
21             $L_{c_p}[b + r - 1] = p$;
22         else
23             $L_{c_p}[b + r - 1] = L_{c_{p-1}}[b + r - 1]$;
24             $r \leftarrow r + 1$;
25 $L_{c_0}, L_{c_1}, \ldots, L_{c_\sigma} \leftarrow$ empty lists;

$(1, \ldots, (k+1)m)$, and it is read sequentially with the other arrays. For the sake of brevity the computation of $E^{p-1}$ (of each iteration $p$) is omitted.

Observe that, under the assumption that the input set $S$ does not contain duplicates, all the $k$-segments of the encoding $I_{X^k}$ have width equal to 1. Moreover, after $L$ iterations, where $L$ is the length of the longest common substring of two strings in $S$, (1) the encoding $I_{X^L}$ is equal to $I_{X^k}$ and (2) each $I_{X^j}$ with $j > L$ is identical to $I_{X^L}$. Those two facts are a consequence of the following two observations: (i) the length $p$ of the longest common prefix between two strings is equal to the length of the longest common substring in $S$, if all the $(p+1)$-prefixes of the suffixes are distinct, (ii) the $\prec_{p+1}$ order relation does not effect the ordering given by $I_{X^p}$, that is $I_{X^{p+1}} = I_{X^p}$.

Algorithm 4 computes also the LCP array whose description is in the following Section 5.1. Section 5.2 is devoted to describe how to compute the arrays $Q^p_i$ used by iteration $p$. 

10
Algorithm 6: Merge-suffixes

Input: The arrays $B_0, B_1, \ldots, B_k$
Output: The encoding $I_{X^k}$.

1. for $l \leftarrow 0$ to $k$ do
2.  \hspace{1em} for $i \leftarrow 1$ to $m$ do
3.  \hspace{2em} $I_{X^0}[lm + i] \leftarrow l$; $Lcp[lm + i] \leftarrow 0$;
4. Compute lists $Q_i^l$ for $0 \leq l \leq k$;
5. $p \leftarrow 1$;
6. while there exists some $(p - 1)$-segment on $I_{X^{p-1}}$ which is wider than 1 do
7.  Compute $I_{X^p}$ from $I_{X^{p-1}}$;
8.  Compute lists $Q_{p+1}^l$ for $0 \leq l \leq k$;
9. Output $I_{X^p}$;

5.1 Computing the LCP array

The LCP array is obtained by exploiting Proposition 3 which easily follows from the definition of $p$-segment.

Proposition 3. Let $i$ be a position on the LCP array $LCP$. Then $LCP[i]$ is the largest $p$ such that $i$ is the start of a $(p + 1)$-segment (of $I_{X^{p+1}}$) and is not the start of a $p$-segment (of $I_{X^p}$).

Proof. Notice that, since the $(p + 1)$-segments are a refinement of the $p$-segments, then there can be only one such $p$. Let $\alpha_{i-1}$ and $\alpha_i$ be respectively the $(i - 1)^{th}$ and the $i^{th}$ lexicographically smallest suffix of $S$. Assume initially that $i$ is the start of a $(p + 1)$-segment, but not of a $p$-segment. Since $i$ is not a start of a $p$-segment, then $i - 1$ and $i$ belong to the same $p$-segment hence, by definition of segment, they share the same $p$-prefix. Since $i$ is the start of a $(p + 1)$-segment, then $i - 1$ and $i$ cannot belong to the same $(p + 1)$-segment, hence they do not share the same $(p + 1)$-prefix. Thus, $LCP[i] = p$. Assume now that $LCP[i] = p$, that is $\alpha_{i-1}$ and $\alpha_i$ share a common $p$-prefix, but not a $(p + 1)$-prefix. Again, by definition of segment, $i - 1$ and $i$ belong to the same $p$-segment but not to the same $(p + 1)$-segment.

At this point, let $Lcp_p$ be the $(k + 1)m$-long array such that $Lcp_p[i]$ is the length of the longest common prefix between the $p$-prefix of suffix $X^p[i]$ and the $p$-prefix of suffix $X^p[i - 1]$. The array $Lcp_k$ is clearly equal to the LCP array of the input set $S$.

Each iteration $p$ (see Algorithm 4) of our procedure computes $Lcp_p$ from $Lcp_{p-1}$ and the array $Lcp_0$ is set to all 0s before starting the iterations. The following invariant, which directly implies its correctness, is maintained.

Lemma 4. At the end of iteration $p$, $Lcp_p[i] = p$ iff $i$ is not the start position of any $p$-segment.
Proof. We will prove the lemma by induction on \( p \). Before the first iteration, the array \( Lcp_0 \) is set to all 0s, therefore we only have to consider the general case. Observe that (at the beginning of iteration \( p \)), given a \((p - 1)\)-segment \([b, e]\), we have \( Lcp_{p-1}[i] = p - 1 \) for \( b + 1 \leq i \leq e \). Then, the procedure (see Algorithm 4) sets to \( p \) the array \( Lcp_p \) in all positions of the induced \( p \)-segments different from their start positions (line 21), completing the proof.

5.2 Computing the \( Q^p_l \) arrays

In this section we describe how to compute the arrays \( Q^p_0, Q^p_1, \ldots, Q^p_k \) used by iteration \( p \). Recall that \( Q^p_i \) is the \( m \)-long array such that \( Q^p_i[i] \) is the \( p \)th symbol of the \( i \)th smallest \( l \)-suffix of \( X_l \) (\( Q^p_i[i] \) is a sentinel \$ if the suffix is smaller than \( p \)). The following proposition establishes a recursive definition of \( Q^p_i \).

Lemma 5. Let \( X_l \) and \( X_{l-1} \) be respectively the sorted \( l \)-suffixes and \((l - 1)\)-suffixes of the set \( S \). Let \( \alpha_l \) and \( \alpha_{l-1} \) be respectively the \( l \)-suffix and the \((l - 1)\)-suffix of a generic input string \( s_l \). Then the \( p \)th symbol of \( \alpha_l \) is the \((p - 1) \)th symbol of \( \alpha_{l-1} \).

Since the suffixes \( \alpha_l \) and \( \alpha_{l-1} \) can have different positions in \( X_l \) and \( X_{l-1} \), the list \( Q^p_l \) is a permutation of \( Q^{p-1}_{l-1} \). Still, Algorithm 7 exploits the construction of \( Q^{p-1}_{l-1} \) to quickly compute \( Q^p_l \). Notice that, for \( l \geq 1 \), \( Q^1_l \) is the result of sorting \( B_{l-1} \) whereas for \( l = 0 \), \( Q^1_0 \) is a sequence of sentinels Therefore the arrays \( Q^0_0, Q^1_2, \ldots, Q^1_k \) can be trivially computed.

Algorithm 7: Compute all lists \( Q^p_l \) for any given \( p \geq 2 \).

| Input | The lists \( B_0, \ldots, B_k \) on alphabet \( c_0, \ldots, c_\sigma \), an integer \( p \) with \( 2 \leq p \leq k \), and all \( Q^{p-1}_{l-1} \). |
|-------|---------------------------------------------------------------|
| Output | The lists \( Q^p_l \) for each \( k \geq l \geq p \) |
| 1     | for \( l \leftarrow p \) to \( k \) do |
| 2     | \( Q^p_l \) \leftarrow \text{empty list}; |
| 3     | for \( h \leftarrow 0 \) to \( \sigma \) do |
| 4     | \( Q^p_l(c_h) \) \leftarrow \text{empty list}; |
| 5     | for \( j \leftarrow 1 \) to \( m \) do |
| 6     | \( \text{Append } Q^{p-1}_{l-1}[j] \) to \( Q^p_l(B_{l-1}[j]) \); |
| 7     | for \( h \leftarrow 0 \) to \( \sigma \) do |
| 8     | \( \text{Append } Q^p_l(c_h) \) to \( Q^p_l \); |

In order to prove the correctness of Algorithm 7 we need to show that the permutation \( St^{l-1} \) over indexes \( 1, \ldots, m \) of \( B_{l-1} \) induced by the lexicographic ordering of \( B_{l-1} \), is the correct permutation of \( Q^{p-1}_{l-1} \) to obtain \( Q^p_l \). Indeed, observe that \( St^{l-1} \) is the permutation that relates positions of indexes of strings in \( X_{l-1} \) to their positions in \( X_l \). More precisely, given a string \( s_q \) of \( S \), such that its \((l - 1)\)-suffix is in position \( j \) of list \( X_{l-1} \), then if \( St^{l-1}[j] = t \), it means that the \( l \)-suffix is of the string \( s_q \) is in position \( t \) of list \( X_l \).
The above observation is a consequence of the fact that in order to get the lexicographic ordering of $X_l$ from the list $X_{l-1}$ we simply sort the $(l-1)$-suffixes by the first symbol that precedes them, i.e., they are sorted by the list $B_{l-1}$.

6 Complexity

First of all, notice that all the arrays are accessed sequentially, therefore they can be stored in external files and it is immediate to view our procedure as an external memory approach, where only the arrays $S_l$ ($0 \leq l \leq k-1$) of the symbols of the input strings are kept in main memory (together with some additional data structures).

First we will consider the procedure Partition-suffixes which mainly consists of $k$ iterations. At iteration $l$, the coordinated scans of $N_{l-1}$ and $B_{l-1}$ suffice to construct $N_l$ and successively $B_l$. Notice that we keep array $S_l$ in main memory, since it is the only array that we access randomly. This procedure has $O(km)$ I/O complexity and a matching running time. Moreover, keeping the array $S_l$ in main memory requires $O(m \log \sigma)$ space.

Mainly the procedure Merge-suffixes is a loop where each iteration $p$ consists of a coordinated scan of the arrays $I_{X_{p-1}}$, $E_{p-1}$ and $Lcp_{p-1}$, and of the arrays $Q_{p}^l$ for $0 \leq l \leq k$, as well as writing the arrays $I_{X_{p}}$, $E_{p}$ and $Lcp_{p}$, and computing all the $Q_{p+1}^l$ arrays. Both $Lcp_{p-1}$ and $I_{X_{p-1}}$ have $O(km)$ elements, each requiring $O(\log k)$ space, therefore their scan implies $O(km \log k)$ I/O complexity. The $E_{p}$ array has $O(km)$ elements, each requiring $O(\log \sigma)$ space, which implies an $O(km \log \sigma)$ I/O complexity. There are at most $k$ $Q_{p}^l$ arrays, each consisting of $m$ elements where each element requires $O(\log \sigma)$ space, which implies an $O(km \log \sigma)$ I/O complexity. There are some additional data structures, whose I/O complexity is smaller than the $O(km(\log k + \log \sigma))$ of the other parts.

The only relevant data structure of Merge-suffixes that must reside in main memory is the rank array, which has $k$ elements, each requiring $O(\log k)$ space.

The last component of our complexity analysis is the number of iterations of Merge-suffixes. Notice that the condition of the while loop at line 6 is equivalent to testing whether all $p$-segments contain only one suffix. Notice that, if $L$ is the length of the longest substring appearing at least twice, then each $(L+1)$-long substring appears once in the input strings $S$, that is all $(L+1)$-prefixes of some suffixes are unique. Consequently, the procedure iterates exactly $L$ times over the loop at line 6. Therefore, the overall I/O complexity of the algorithm is $O(kmL(\log k + \log \sigma))$.

7 Conclusions

We have presented a new lightweight algorithm to compute the BWT and the LCP array of a set of strings, whose I/O complexity is competitive with BCRext. More precisely, our overall I/O complexity is $O(kmL(\log k + \log \sigma))$, while BCRext has $O(mk(k \log \sigma + \log(mk)))$.

While our focus has been on the theoretical aspects, it would be interesting to implement
the proposed algorithm and perform an experimental analysis to determine the practical behavior. Since the number of iterations of the Merge-suffixes procedure is not fixed a priori, we expect a finely tuned implementation to provide great improvements.
|                  | BCR (with LCP) | BCRext (BWT only) | This paper (with LCP) |
|------------------|----------------|-------------------|-----------------------|
| CPU Time         | \(O(k(m + \text{sort}(m)))\) | \(O(km)\)       | \(O(km\lambda)\)     |
| RAM usage (bits) | \(O((m + \sigma^2) \log(mk))\) | \(O(\sigma^2 \log(mk))\) | \(O(m \log(\sigma))\) |
| I/O (bits)       | \(O(mk^2 \log(\sigma))\) (partial BWT) | \(O(mk^2 \log(\sigma))\) (partial BWT) | \(O(mk \log(\sigma))\) (vectors \(B_*\)) |
|                  | \(O(mk^2 \log(k))\) (partial LCP) | \(O(mk^2 \log(\sigma))\) (sequences) | \(O(mk \log(m))\) (vectors \(N_*\)) |
|                  | \(O(mk \log(\sigma))\) (current symbols) | \(O(mk\log(mk))\) (P array) | \(O(mkL \log(k))\) (interleave) |
|                  |                  | \(O(mk\log(m))\) (N array) | \(O(mkL \log(\sigma))\) (vectors \(Q_*\)) |
|                  |                  | \(O(mkL)\) (vectors \(\text{End}_p\)) | \(O(mkL)\) (vectors \(\text{End}_p\)) |

Table 1: Time and space complexity comparison with BCR and BCRext.

**Time complexity**

BCR requires \(O(k^2 \text{sort}(m))\) time, \(O(m \log(\sigma) + m \log(mk) + m \log(m))\) main memory, and \(O(mk^2 \log(\sigma))\) I/O. At each iteration \(i\), it maintains in main memory 3 lists of length \(m\) that contain the characters that have to be inserted at the current step (\(m \log(\sigma)\) bits), the position where the characters have to be inserted (\(m \log(mk)\) bits), and the indexes of the reads sorted by their \(k - i\) suffix (\(m \log(m)\) bits) respectively. Note that the computation of the position where the current characters have to be inserted (i.e., the rank of such character) is performed by a sequential scan of the partial BWT and that at each position an occurrence counter is modified. This means that at each iteration BCR performs \(O(km)\) computations.

BCRext requires \(O(k^2 m)\) time, \(O(\sigma^2 \log(mk))\) main memory, and \(O(mk^2 \log(\sigma) + mk \log(mk) + mk \log(m))\) I/O. It aims to lower the main memory requirement of BCR by storing the 3 lists of the previous approach in external memory and accesses them sequentially. Moreover, this method requires to read and write the input sequences at each iteration and has an additional \(O(mk^2 \log(\sigma))\) I/O. At each iteration \(i\), BCRext sequentially reads the external files and implicitly sorts the reads by their \(k - i\) suffix, thus obtaining the correct sorting of the elements to be added at iteration \(i + 1\).
References

[1] Markus Bauer, Anthony Cox, and Giovanna Rosone. Lightweight BWT construction for very large string collections. In *Combinatorial Pattern Matching*, volume 6661 of *LNCS*, pages 219–231. Springer, 2011.

[2] Markus Bauer, Anthony Cox, and Giovanna Rosone. Lightweight algorithms for constructing and inverting the BWT of string collections. *Theoretical Computer Science*, 483:134–148, 2013.

[3] Markus Bauer, Anthony Cox, Giovanna Rosone, and Marinella Sciortino. Lightweight LCP construction for next-generation sequencing datasets. In *Algorithms in Bioinformatics*, volume 7534 of *LNCS*, pages 326–337, Berlin, Germany, 2012. Springer.

[4] Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi. Constructing string graphs in external memory. In Daniel G. Brown and Burkhard Morgenstern, editors, *Algorithms in Bioinformatics - 14th International Workshop, WABI 2014, Wroclaw, Poland, September 8-10, 2014. Proceedings*, volume 8701 of *Lecture Notes in Computer Science*, pages 311–325. Springer, 2014.

[5] Paola Bonizzoni, Gianluca Della Vedova, Yuri Pirola, Marco Previtali, and Raffaella Rizzi. LSG: An external-memory tool to compute string graphs for NGS data assembly. *J. of Computational Biology*, in press.

[6] M. Burrows and D. J. Wheeler. A block-sorting lossless data compression algorithm. Technical report, Digital Systems Research Center, 1994.

[7] Paolo Ferragina, Travis Gagie, and Giovanni Manzini. Lightweight data indexing and compression in external memory. *Algorithmica*, 63(3):707–730, 2012.

[8] Paolo Ferragina and Giovanni Manzini. Indexing compressed text. *J. of the ACM*, 52(4):552–581, 2005.

[9] James Holt and Leonard McMillan. Merging of multi-string BWTs with applications. *Bioinformatics*, 30(24):3524–3531, 2014.

[10] Ben Langmead, Cole Trapnell, Mihai Pop, and Steven Salzberg. Ultrafast and memory-efficient alignment of short dna sequences to the human genome. *Genome Biology*, 10:R25, 2009.

[11] Heng Li. Exploring single-sample SNP and INDEL calling with whole-genome de novo assembly. *Bioinformatics*, 28(14):1838–1844, July 2012.

[12] Heng Li. Fast construction of FM-index for long sequence reads. *Bioinformatics*, 30(22):3274–3275, 2014.
[13] Heng Li and Richard Durbin. Fast and accurate short read alignment with burrows–wheeler transform. *Bioinformatics*, 15:1754–1760, 2009.

[14] Heng Li and Richard Durbin. Fast and accurate long-read alignment with burrows–wheeler transform. *Bioinformatics*, 26:589–595, 2010.

[15] Ruiqiang Li, Chang Yu, Yingrui Li, Tak-Wah Lam, Siu-Ming Yiu, Karsten Kristiansen, and Jun Wang. Soap2: an improved ultrafast tool for short read alignment. *Bioinformatics*, 25:1966–1967, 2009.

[16] Sabrina Mantaci, Antonio Restivo, Giovanna Rosone, and Marinella Sciortino. An extension of the burrows wheeler transform and applications to sequence comparison and data compression. In Alberto Apostolico, Maxime Crochemore, and Kunsoo Park, editors, *Combinatorial Pattern Matching*, volume 3537 of *Lecture Notes in Computer Science*, pages 178–189. Springer Berlin Heidelberg, 2005.

[17] Sabrina Mantaci, Antonio Restivo, Giovanna Rosone, and Marinella Sciortino. An extension of the burrows-wheeler transform. *Theoretical Computer Science*, 387:298–312, 2007.

[18] Eugene Myers. The fragment assembly string graph. *Bioinformatics*, 21(suppl. 2):ii79–ii85, 2005.

[19] Ge Nong, Sen Zhang, and Wai Hong Chan. Linear suffix array construction by almost pure induced-sorting. In *Data Compression Conference, 2009. DCC’09.*, pages 193–202. IEEE, 2009.

[20] Junjie Qin, Ruiqiang Li, Jeroen Raes, Manimozhiyan Arumugam, Kristoffer Solvsten Burgdorf, Chaysavanh Manichanh, Trine Nielsen, Nicolas Pons, Florence Levenez, Takuji Yamada, et al. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, 464(7285):59–65, 2010.

[21] Giovanna Rosone and Marinella Sciortino. The Burrows-Wheeler transform between data compression and combinatorics on words. In *The Nature of Computation. Logic, Algorithms, Applications*, volume 7921 of *LNCS*, pages 353–364. Springer Berlin Heidelberg, 2013.

[22] Jared Simpson and Richard Durbin. Efficient construction of an assembly string graph using the FM-index. *Bioinformatics*, 26(12):i367–i373, 2010.

[23] Jared Simpson and Richard Durbin. Efficient de novo assembly of large genomes using compressed data structures. *Genome Research*, 22:549–556, 2012.

[24] Jouni Sirén. Compressed suffix arrays for massive data. In *Proceedings of the 16th International Symposium on String Processing and Information Retrieval*, SPIRE ’09, pages 63–74, Berlin, Heidelberg, 2009. Springer-Verlag.
[25] Niko Välimäki, Susana Ladra, and Veli Mäkinen. Approximate all-pairs suffix/prefix overlaps. In Amihood Amir and Laxmi Parida, editors, *Combinatorial Pattern Matching*, volume 6129 of *Lecture Notes in Computer Science*, pages 76–87. Springer Berlin Heidelberg, 2010.