Relative FM-indexes

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Abstract. Intuitively, if two strings $S_1$ and $S_2$ are sufficiently similar and we already have an FM-index for $S_1$ then, by storing a little extra information, we should be able to reuse parts of that index in an FM-index for $S_2$. We formalize this intuition and show that it can lead to significant space savings in practice, as well as to some interesting theoretical problems.

1 Introduction

FM-indexes [4] are core components in most modern DNA aligners (e.g., [8,9,10]) and have thus played an important role in the genomics revolution. Medical researchers are now producing databases of hundreds or even thousands of human genomes, so bioinformatics researchers are working to improve FM-indexes’ compression of sets of nearly duplicate strings. As far as we know, however, the solutions proposed so far (e.g., [3,11]) index the concatenation of the genomes, so we can search the whole database easily but searching only in one specified genome is more difficult. In this paper we consider how to index each of the genomes individually while still using reasonable space and query time.

Our intuition is that if two strings $S_1$ and $S_2$ are sufficiently similar and we already have an FM-index for $S_1$ then, by storing a little extra information, we should be able to reuse parts of that index in an FM-index for $S_2$. More specifically, it seems $S_1$’s and $S_2$’s Burrows-Wheeler Transforms [2] (BWTs) should also be fairly similar. Since BWTs are the main component of FM-indexes, it is natural to try to take advantage of such similarity to build an index for $S_2$ that “reuses” information already available in $S_1$’s FM-index.

Among the many possible similarities one can find and exploit in the BWTs, in this paper we consider the longest common subsequence (LCS). The BWT sorts the characters of a string into the lexicographic order of the suffixes following those characters. For example, if

$$S_1 = \text{AAGTTGAGAGTGAGT}, \quad S_2 = \text{AGAGAGTCGAGGT};$$

then

$$\text{BWT}(S_1) = \text{TGGGATTAAAAGTGG}, \quad \text{BWT}(S_2) = \text{TGGGATCAAAATGG};$$

whose LCS TGGGATAAAATGG is nearly as long as either BWT. Note that in this example LCS($S_1, S_2$) = AGAGAGTGGAGGT is shorter than LCS(BWT($S_1$), BWT($S_2$)).
We introduce the concept of *BW-distance* $\text{BWD}(S_1, S_2)$ between $S_1$ and $S_2$ defined as $|S_1| + |S_2| - 2|\text{LCS}(\text{BWT}(S_1), \text{BWT}(S_2))|$. Note that this coincides with the edit distance between $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ when only insertions and deletions are allowed. We prove that, if we are willing to tolerate a slight increase in query times, we can build an index for $S_2$ using an unmodified FM-index for $S_1$ and additional data structures whose total space in words is asymptotically bounded by $\text{BWD}(S_1, S_2)$ (Theorem 1).

This first result is the starting point for our investigation as it generates many challenging issues. First, since we are interested in indexing whole genomes, we observe that finding the LCS of strings whose length is of the order of billions is outside the capabilities of most computers. Thus, in Section 3.1 we show how to approximate the LCS of two BWTs, using combinatorial properties of the BWT to align the sequences. In the same section we also discuss and test several practical alternatives for building the index for $S_2$ given the one for $S_1$ and we analyze their time/space trade-offs.

If one needs an index not only for counting queries but also for locating and extracting, we must enrich it with suffix array (SA) samples. Such samples usually take significantly less space than the main index. However, we may still want to take advantage of the similarities between $S_1$ and $S_2$ to “reuse” SA samples from $S_1$ for $S_2$’s index. In Section 4 we show that this is indeed possible if, instead of considering the LCS between the BWTs, we use a common subsequence with the additional constraint of being *BWT-invariant* (Theorem 2). This result motivates the problem of finding the longest BWT-invariant subsequence, which unfortunately turns out to be NP-hard (Theorem 3). We therefore devise a heuristic to find a “long” BWT-invariant subsequence in $O(|S_1| \log |S_1|)$ time.

We have tested our approach in practice by building an FM-index for the genome of a Han Chinese individual, “reusing” an FM-index of the human reference genome. The Han genome is about 3.0 billion base pairs, the reference is about 3.1 billion base pairs and we found a common subsequence of about 2.9 billion base pairs. A standard implementation of a stand-alone FM-index for the Han genome takes 628 MB or 1090 MB, depending on encoding, while our index uses only 256 MB or 288 MB on top of the index for the reference. On the other hand, queries to our index take about 9.5 or 4.5 times longer. Since our index is compressed relative to the underlying index for the reference, we call it a relative FM-index.

2 Review of the FM-index structure

The core component of an FM-index for a string $S[1..n]$ is a data structure supporting rank queries on the Burrows-Wheeler Transform $\text{BWT}(S)$ of $S$. This transform permutes the characters in $S$ such that $S[i]$ comes before $S[j]$ in $\text{BWT}(S)$ if $S[i + 1..n]$ is lexicographically less than $S[j + 1..n]$. 

If the lexicographic range of suffixes of $S$ starting with $\beta$ is $[i..j]$, then the range of suffixes starting with $a\beta$ is

$$\left[\text{BWT}(S).\text{rank}_a(i - 1) + 1 + \sum_{a' < a} S.\text{rank}_{a'}(n)., \text{BWT}(S).\text{rank}_a(j) + \sum_{a' < a} S.\text{rank}_{a'}(n)\right]$$

It follows that, if we have precomputed an array storing $\sum_{a' < a} S.\text{rank}_{a'}(n)$ for each distinct character $a$ (i.e., the number of characters in $S$ less than $a$), then we can find the range of suffixes starting with a pattern $P[1..m]$ — and, thus, count its occurrences — using $O(m)$ rank queries.

If the position of $S[i]$ in $\text{BWT}(S)$ is $j$, then the position of $S[i - 1]$ is

$$\text{BWT}(S).\text{rank}_{S[i]}(j) + \sum_{a < S[i]} \text{BWT}(S).\text{rank}_a(n).$$

It follows that, if we have also precomputed a dictionary storing the position of every $r$th character of $S$ in $\text{BWT}(S)$ with its position in $S$ as satellite information, then we can find a character’s position in $S$ from its position in $\text{BWT}(S)$ using $O(r)$ rank and membership queries. Therefore, once we know the lexicographic range of suffixes starting with $P$, we can locate each of its occurrences using $O(r)$ rank queries.

Finally, if we have also precomputed an array storing the position of every $r$th character of $S$ in $\text{BWT}(S)$, in order of appearance in $S$, then given $i$ and $j$, we can extract $S[i..j]$ using $O(r + j - i)$ rank queries.

### 3 BW-distance and relative FM-indices

Given two strings $S_1[1..n_1]$ and $S_2[1..n_2]$ we define the BW-distance $\text{BWD}(S_1, S_2)$ between $S_1$ and $S_2$ as

$$\text{BWD}(S_1, S_2) = n_1 + n_2 - 2|\text{LCS}(\text{BWT}(S_1), \text{BWT}(S_2))|.$$  \hfill (1)

Note that the BW-distance is nothing but the edit distance between $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ when only insertions and deletions are allowed \cite{13} (also known as the shortest edit script or indel distance), and is thus at most twice their normal edit distance. We now show how to support counting queries on $S_2$ using an FM-index for $S_1$ and some auxiliary data structures taking $O(\text{BWD}(S_1, S_2))$ words of space. Specifically, we consider how we can support rank queries on $\text{BWT}(S_2)$ and partial-sum queries on the distinct characters’ frequencies.

Let $C$ denote a LCS of $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ with $|C| = m$. Let $C = c_1 \cdots c_m$, and for $i = 1, \ldots, m$, let $\alpha_i$ (resp. $\beta_i$) be the position of $c_i$ in $\text{BWT}(S_1)$ (resp. $\text{BWT}(S_2)$) with $\alpha_1 < \cdots < \alpha_m$ (resp. $\beta_1 < \cdots < \beta_m$). Define

- bitvector $B_i[1..n_1]$ with 0s in positions $\alpha_1, \ldots, \alpha_m$. 


– bitvector $B_2[1..n_2]$ with 0s in positions of $\beta_1, \ldots, \beta_m$,
– subsequence $D_1$ of $\text{BWT}(S_1)$ marked by 1s in $B_1$; $D_1$ is the complement of $C$ in $\text{BWT}(S_1)$,
– subsequence $D_2$ of $\text{BWT}(S_2)$ marked by 1s in $B_2$; $D_2$ is the complement of $C$ in $\text{BWT}(S_2)$.

We claim that if we can support fast rank queries on $\text{BWT}(S_1)$, $B_1$, $B_2$, $D_1$ and $D_2$ and fast select queries on $B_1$, then we can support fast rank queries on $\text{BWT}(S_2)$. To see why, notice that

$$\text{BWT}(S_2).\text{rank}_X(i) = \text{C.rank}_X(B_2.\text{rank}_0(i)) + D_2.\text{rank}_X(B_2.\text{rank}_1(i))$$

and, by the same reasoning,

$$\text{C.rank}_X(j) = \text{BWT}(S_1).\text{rank}_X(B_1.\text{select}_0(j)) - D_1.\text{rank}_X(B_1.\text{rank}_1(B_1.\text{select}_0(j))).$$

Therefore,

$$\text{BWT}(S_2).\text{rank}_X(i) = \text{BWT}(S_1).\text{rank}_X(k) - D_1.\text{rank}_X(B_1.\text{rank}_1(k)) + D_2.\text{rank}_X(B_2.\text{rank}_1(i))$$

where $k = B_1.\text{select}_0(B_2.\text{rank}_0(i))$.

For example, for the strings

$$S_1 = \text{AAGTTGAGAGTGAGT}, \quad S_2 = \text{AGAGAGTCGAAGTT};$$

it is

$$\text{BWT}(S_1) = \text{TGGGATTTAAAGTG}, \quad \text{BWT}(S_2) = \text{TGGGATCAAATGG};$$

and $\text{LCS(BWT}(S_1), \text{BWT}(S_2)) = \text{TCTCGTAAAGG}$. Hence

$$B_1 = 000100000000111 \quad D_1 = \text{GTGC}$$
$$B_2 = 010000000001010 \quad D_2 = \text{GCC}.$$  

Suppose we want to compute $\text{BWT}(S_2).\text{rank}_C$. It is $B_1.\text{select}_0(B_2.\text{rank}_0(13)) = 12$, so

$$\text{BWT}(S_2).\text{rank}_C(13) = \text{BWT}(S_1).\text{rank}_C(12) - D_1.\text{rank}_C(B_1.\text{rank}_1(12)) + D_2.\text{rank}_C(B_2.\text{rank}_1(13)) = 3.$$

Observing that the number of 1s in $B_1$ and $B_2$ is $O(\max(n_1, n_2) - \ell) = O(\text{BWD}(S_1, S_2))$, we can store data structures for $B_1$, $B_2$, $D_1$ and $D_2$ in $O(\text{BWD}(S_1, S_2))$ space such that the desired rank/select queries take $O(\log \text{BWD}(S_1, S_2))$ time.

The only other component required for an FM-index for $S_2$ for counting, is a data structure for computing $\sum_{n' < n} S_2.\text{rank}_{a'}(n)$ for each distinct character $a$. Notice that $\text{BWD}(S_1, S_2)$ is at least the number of distinct characters whose frequencies in $S_1$ and $S_2$ differ. It follows that in $O(\text{BWD}(S_1, S_2))$ space we can store
– a $O(\log \text{BWD}(S_1, S_2))$-time predecessor data structure storing those distinct
characters,
– an array storing $\sum_{a' \prec a} S_2.\text{rank}_{a'}(n_2)$ for each such distinct character $a$.

For any distinct character $b$, we can find the preceding distinct character $a$ whose
frequencies in $S_1$ and $S_2$ differ and compute

$$\sum_{a' \prec b} S_2.\text{rank}_{a'}(n_2) = \sum_{a' \prec b} S_1.\text{rank}_{a'}(n_1) - \sum_{a' \prec a} S_1.\text{rank}_{a'}(n_1) + \sum_{a' \prec a} S_2.\text{rank}_{a'}(n_2)$$

using $O(\log \text{BWD}(S_1, S_2))$ time. Summing up:

**Theorem 1.** If we already have an FM-index for $S_1$, we can store a relative
FM-index for $S_2$ using $O(BWD(S_1, S_2))$ words of extra space. Counting queries
on the relative FM-index take time an $O(\log \text{BWD}(S_1, S_2))$ factor larger than on
$S_1$.

In Section 4 we show how to build a relative FMindex supporting also locating and extracting.

### 3.1 A practical implementation

A longest common sequence of $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ can be computed in
$O(n_1n_2/w)$ time, where $w$ is the word size [12]. Since we are mainly interested in
strings with a small BW-distance, a better alternative could be the algorithms
whose running times are bounded by the number of differences between the
input sequences (see eg [7,13]). Unfortunately none of these algorithms is really
practical when working with such very large files as the complete genomes we
considered in our tests. Hence, to make the construction of a relative FM-index
practical, we approximate the LCS of the two Burrows-Wheeler transforms, using
the combinatorial properties of the BWT to align the sequences.

Let $S_1$ be a random string of length $n$ over alphabet $\Sigma$ of size $\sigma$, and let string
$S_2$ differ from it by $s$ insertions, deletions, and substitutions. In the expected
case, the edit operations move $O(s \log_\sigma n)$ suffixes in lexicographic order, and
change the preceding characters for $O(s)$ suffixes [11]. If we remove the characters
Corresponding to those suffixes from $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$, we have a common
subsequence of length $n - O(s \log_\sigma n)$ in the expected case.

Assume that we have partitioned the BWTs according to the first $k$ characters of the
suffixes, for $k \geq 0$. For all $x \in \Sigma^k$, let $\text{BWT}_x(S_1)$ and $\text{BWT}_x(S_2)$ be
the substrings of the BWTs corresponding to the suffixes starting with $x$. If we
remove the suffixes affected by the edit operations, as well as the suffixes where
string $x$ covers an edit, we have a common subsequence $\text{BWT}^x_k$ of $\text{BWT}_x(S_1)$
and $\text{BWT}_x(S_2)$. If we concatenate the sequences $\text{BWT}^x_k$ for all $x$, we get a common
subsequence of $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ of length $n - O(s(k + \log_\sigma n))$ in
the expected case. This suggests that we can find a long common subsequence
of $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ by partitioning the BWTs, finding an LCS for each
partition, and concatenating the results.
Table 1. Experiments with human genomes. Bitvector used in the wavelet tree; time and space requirements for building the relative FM-index; time required for counting queries and index size for a regular and a relative FM-index; the performance of the relative FM-index compared to the regular index. The query times are averages over five runs.

| Bitvector | Construction Time | Space | Construction Time | Space | Index Time | Size | Index Time | Size | Rel vs. Reg |
|-----------|-------------------|-------|-------------------|-------|------------|------|------------|------|-------------|
| Plain     | 762 s             | 9124 MB | 146 s             | 1090 MB | 1392 s     | 288 MB | 954%       | 26%  |
| RRR       | 6022 s            | 7823 MB | 667 s             | 628 MB  | 3022 s     | 256 MB | 453%       | 41%  |

In practice, we partition the BWTs by variable-length strings. We use backward searching on the BWTs to traverse the suffix trees of $S_1$ and $S_2$, selecting a partition when either the length of $\text{BWT}_x(S_1)$ or $\text{BWT}_x(S_2)$ is at most 1024, or the length of the pattern $x$ reaches 32. For each partition, we use the greedy LCS algorithm [13] to find the longest common subsequence of that partition. To avoid hard cases, we stop the greedy algorithm if it would need diagonals beyond ±50000, and match only the most common characters for that partition. We also predict in advance the common cases where this happens (the difference of the lengths of $\text{BWT}_x(S_1)$ and $\text{BWT}_x(S_2)$ is over 50000, or $x = N^{32}$ for DNA sequences), and match the most common characters in that partition directly.

We implemented the counting structure of the relative FM-index using the SDSL library [5], and compared its performance to a regular FM-index. To encode the BWTs and sequences $D_1$ and $D_2$, we used Huffman-shaped wavelet trees with either plain or entropy-compressed (RRR) [15] bitvectors. We chose entropy-compressed bitvectors for marking the positions of the LCS in $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$.

The implementation was written in C++ and compiled on g++ version 4.7.3. We used a system with 32 gigabytes of memory and two quad-core 2.53 GHz Intel Xeon E5540 processors, running Ubuntu 12.04 with Linux kernel 3.2.0. Only one CPU core was used in the experiments.

For our experiments, we used the 1000 Genomes Project assembly of the human reference genome as the reference sequence $S_1$. As sequence $S_2$, we used the genome of a Han Chinese individual from the YanHuang project. The lengths of the sequences were 3.10 billion bases and 3.00 billion bases, respectively, and our algorithm found a common subsequence of 2.93 billion bases. As our pattern set, we used 10 million reads of length 56. Almost 4.20 million reads had exact matches in sequence $S_2$, with a total of 99.7 million occurrences. The results of the experiments can be seen in Table [1].

With plain bitvectors in the wavelet tree, the relative FM-index was 9.5 times slower than a regular FM-index, while requiring a quarter of the space. With entropy-compressed bitvectors, the relative index was 4.5 times slower.

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1 [GRCh37](ftp://ftp-trace.ncbi.nih.gov/1000genomes/ftp/technical/reference/)
2 [ftp://public.genomics.org.cn/BGI/yanhuang/fa/](ftp://public.genomics.org.cn/BGI/yanhuang/fa/)
and required 41% of the space. Comparing the relative FM-index using plain bitvectors to the regular index using entropy-compressed bitvectors, we see that the relative index is 2.1 times slower, while taking 46% of the space.

Bitvectors $B_1$ and $B_2$ took 70% to 80% of the total size of the relative index.

We tried to encode them as sparse bitvectors [14], but the result was slightly larger and clearly slower than with entropy-compressed bitvectors. By our estimates, run-length encoded bitvectors would have taken slightly more space than sparse vectors. Hybrid bitvectors using different encodings for different parts of the bitvector [6] could improve compression, but the existing implementation does not work with vectors longer than $2^{31}$ bits.

4 Relative FM-indices supporting locating and extracting

As mentioned in Section 2, an FM-index for $S_1$ usually has an SA sample that takes an only slightly sublinear number of bits. This sample has two parts: the first consists of a bitvector $R$ with 1s marking the positions in $BWT(S_1)$ of every $r$th character in $S_1$, and an array $A$ storing a mapping from the ranks of those characters’ positions in $BWT(S_1)$ to their positions in $S_1$; the second is an array storing a mapping from the ranks of those characters’ positions in $S$ to their positions in $BWT(S_1)$. With these, given the position of a sampled character in $BWT(S_1)$, we can find its position in $S_1$, and vice versa.

These parts are used for locating and extracting queries, respectively, and the worst-case query times are proportional to $r$. On the other hand, the size of the sample in words is proportional to the length of $S$ divided by $r$. For details on how the sample works, we direct the reader to the full description of FM-indexes [4]. We note only that if we sample irregularly, then the worst-case query times for locating and extracting are proportional to the maximum distance in $S$ between two consecutive sampled characters. We leave consideration of extracting for the full version of the paper — it is nearly symmetric to locating — so we do not discuss the second part of the sample here.

Let $G = S_1[i_1] \cdots, S_1[i_\ell]$ denote a length-$\ell$ common subsequence of $S_1$ and $S_2$ (not their BWTs). That is, we have $i_1 < \cdots < i_\ell$ and there exists $j_1 < \cdots < j_\ell$ such that

$$S_1[i_1] = S_2[j_1], \ldots, S_1[i_\ell] = S_2[j_\ell].$$

Since there is a one-to-one correspondence between a text and its BWT, we can define the indexes $v_1, \ldots, v_\ell$ (resp. $w_1, \ldots, w_\ell$) such that for $k = 1, \ldots, \ell$, $BWT(S_1)[v_k]$ is the character corresponding to $S_1[i_k]$ (resp. $BWT(S_2)[w_k]$ is the character corresponding to $S_2[j_k]$). We say that the common subsequence $G$ is $BWT$-invariant if there exists a permutation $\pi : \{1, \ldots, \ell\} \rightarrow \{1, \ldots, \ell\}$ such that we have simultaneously

$$v_{\pi(1)} < v_{\pi(2)} < \cdots < v_{\pi(\ell)}, \quad \text{and} \quad w_{\pi(1)} < w_{\pi(2)} < \cdots < w_{\pi(\ell)}. \quad (2)$$

In other words, when we go from the texts to the BWTs the elements of $G$ are permuted in the same way in $S_1$ and $S_2$. 
An immediate consequence of (2) is that the sequence

\[ G' = \text{BWT}(S_1)[v_{\pi(1)}] \text{BWT}(S_1)[v_{\pi(2)}] \cdots \text{BWT}(S_1)[v_{\pi(\ell)}] \]

is a common subsequence of \text{BWT}(S_1) and \text{BWT}(S_2). We can therefore generalize (1) and define

\[ \text{BWD}_G(S_1, S_2) = \max(n_1, n_2) - |G| \]

and repeat the construction of Theorem 1 with \text{BWD} replaced by \text{BWD}_G. However, since \( G \) is BWT-invariant it is now possible to reuse the SA samples from \( S_1 \) relative to positions in \( G \) for the string \( S_2 \) provided that we have

- bitvector \( M_1[1..n_1] \) with 0s in positions \( i_1, \ldots, i_\ell \), supporting fast \text{rank} queries,
- bitvector \( M_2[1..n_2] \) with 0s in positions of \( j_1, \ldots, j_\ell \), supporting fast \text{select} queries;

proof idea in the appendix, complete proof in the full paper. Summing up, we have:

**Theorem 2.** For any BWT-invariant subsequence \( G \), if we already have an FM-index for \( S_1 \), then we can store \( O(\text{BWD}_G(S_1, S_2)) \) extra space such that the time bounds for locating and extracting queries on \( S_2 \) are an \( O(\log \text{BWD}_G(S_1, S_2)) \) factor larger than on \( S_1 \).

In view of the above theorem, it is certainly desirable to find the longest common subsequence of \( S_1 \) and \( S_2 \) which is BWT-invariant. Unfortunately, this problem is NP-hard as shown by the following result.

**Theorem 3.** It is NP-complete to determine whether there is an LCS of \( S_1 \) and \( S_2 \) which is BWT-invariant, even when the strings are over a ternary alphabet.

**Proof.** Clearly we can check in polynomial time whether a given subsequence of \( S_1 \) and \( S_2 \) has this property, so the problem is in NP. To show that it is NP-complete, we reduce from the NP-complete problem of permutation pattern matching \( \text{[1]} \), for which we are given two permutations \( \pi_1 \) and \( \pi_2 \) over \( n \) and \( m \leq n \) elements, respectively, and asked to determine whether there is a subsequence of \( \pi_1 \) of length \( m \) such that the relative order of the elements in that subsequence is the same as the relative order of the elements in \( \pi_2 \). For example, if \( \pi_1 = 6, 3, 2, 1, 4, 5 \) and \( \pi_2 = 4, 2, 1, 3 \), then \( 6, 2, 1, 4 \) is such a subsequence. Specifically, we set

\[
S_1 = \text{AB}^{\pi_1[1]} \text{AB}^{\pi_1[2]} \cdots \text{AB}^{\pi_1[n]} \\
S_2 = \text{AC}^{\pi_2[1]} \text{AC}^{\pi_2[2]} \cdots \text{AC}^{\pi_2[m]},
\]

so the unique LCS of \( S_1 \) and \( S_2 \) is \( A^m \). For our example,

\[
S_1 = \text{AB}^6\text{AB}^3\text{AB}^2\text{AB}^5 = \text{ABBBBBBBABBABBABBBBB} \\
S_2 = \text{AC}^4\text{AC}^2\text{ACAC}^3 = \text{ACCCCCACACACCC}.
\]
The BWT sorts the $m$ copies of $A$ in $S_2$ according to $\pi_2$ and sorts any subsequence of $m$ copies of $A$ in $S_1$ according to the corresponding subsequence of $\pi_1$. Therefore, there is an LCS of $S_1$ and $S_2$ such that the relative order of its characters is $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ is the same, if and only if there is a subsequence of $\pi_1$ of length $m$ such that the relative order of the elements in that subsequence is the same as the relative order of the elements in $\pi_2$. \qed

In view of the above result, for large inputs we cannot expect to find the longest possible BWT-invariant subsequence, so, as for the LCS, we have devised the following fast heuristic for computing a “long” BWT-invariant subsequence.

We first compute the suffix array $SA_{12}$ for the concatenation $S_1 \# S_2$ and we use it to define the array $A$ of size $n_1 \times 2$ as follows

- $A[i][1] = j$ if $S_1[i] = S_2[j]$ and suffix $S_2[j + 1, n_2]$ immediately follows suffix $S_1[i + 1, n_1]$ in $SA_{12}$. If no such $j$ exists $A[i][1]$ is undefined.
- $A[i][2] = j$ if $S_1[i] = S_2[j]$ and suffix $S_2[j + 1, n_2]$ is the lexicographically largest suffix of $S_2$ preceding suffix $S_1[i + 1, n_1]$ in $SA_{12}$. If no such $j$ exists $A[i][2]$ is undefined.

Next, we compute the longest subsequence $1 \leq i_1 < i_2 < \cdots < i_\ell \leq n_1$ such that there exist $b_1, \ldots, b_\ell$, with $b_k \in \{1, 2\}$ and the sequence

$$A[i_1][b_1] < A[i_2][b_2] < \cdots < A[i_\ell][b_\ell]$$

is the longest possible (every $A[i_k][b_k]$ must be defined). The values $i_1, \ldots, i_\ell$ and $b_1, \ldots, b_\ell$ can be computed in $O(n_1 \log n_1)$ time using a straightforward modification of the dynamic programming algorithm for the longest increasing subsequence. Setting, for $k = 1, \ldots, \ell$, $j_k = A[i_k][b_k]$ we get that

$$G = S_1[i_1]S_1[i_2] \cdots S_1[i_\ell] = S_2[j_1]S_2[j_2] \cdots S_2[j_\ell]$$

is a common subsequence of $S_1$ and $S_2$.

**Lemma 1.** The subsequence $G$ is BWT-invariant.

**Proof.** Let $w_1, \ldots, w_\ell$ (resp. $w_{\ell+1}, \ldots, w_{2\ell}$) such that for $k = 1, \ldots, \ell$, $\text{BWT}(S_1)[w_k]$ is the character corresponding to $S_1[i_k]$ (resp. $\text{BWT}(S_2)[w_k]$ corresponds to $S_2[j_k]$). It suffices to prove that for any pair $h, k$, with $1 \leq h, k \leq \ell$, the inequality $w_h < w_k$ implies $v_h < v_k$. Let $\prec$ denote the lexicographic order. By construction, and by the properties of the BWT, we have $v_h < v_k$ iff the suffix $S_1[i_h + 1, n_1] \prec S_1[i_k + 1, n_1]$ and we must prove that this implies $S_2[j_h + 1, n_2] \prec S_2[j_k + 1, n_2]$.

Since $j_h = A[i_h][b_h]$ and $j_k = A[i_k][b_k]$, the proof follows considering the four possible cases: $b_h = 1, 2$ and $b_k = 1, 2$. We consider the case $b_h = 1, b_k = 2$ leaving the others to the reader. If $j_h = A[i_h][1]$ and $j_k = A[i_k][2]$ then $S_2[j_h + 1, n_2]$ immediately follows $S_1[i_h + 1, n_1]$ in $SA_{12}$. At same time $S_2[j_k + 1, n_2]$ precedes $S_1[i_h + 1, n_1]$ but there are no other suffixes from $S_2$ between them. Since $j_h \neq j_k$ the only possible ordering of the suffixes in $SA_{12}$ is

$$S_1[i_h + 1, n_1] \prec S_2[j_h + 1, n_2] \prec S_2[j_k + 1, n_2] \prec S_1[i_k + 1, n_1]$$

implying $S_2[j_h + 1, n_2] \prec S_2[j_k + 1, n_2]$ as claimed. \qed
Table 2. Comparison between $|G|$ and $|\text{LCS}|$. The normalizing factor $n$ is the length of sequence 273614N.

|        | 322134S | 378604X | BC187 | DBVPG1106 |
|--------|---------|---------|-------|-----------|
| | LCS|/n | 0.9341 | 0.9669 | 0.9521 | 0.9500 |
| | G|/n | 0.8694 | 0.8655 | 0.8798 | 0.8800 |

To evaluate whether the subsequence $G$ derived from the above procedure is still able to capture the similarity between $S_1$ and $S_2$, we have compared the length of $G$ with the LCS length for pairs of *S. cerevisiae* genomes from the Saccharomyces Genome Resequencing Project. In particular we compared the 273614N sequence with sequences 322134S, 378604X, BC187, and DBVPG1106. For each sequence we report in Table 2 the ratio between the length of $G$ and LCS($\text{BWT}(S_1)$, BWT($S_2$)) and the length of sequence 273614N (roughly 11.9 MB). We see that in all cases more than 85% of BWT positions are in $G$ which roughly indicates that more than 85% of the SA samples from 273614N could be reused as SA samples for the other sequences.

5 Conclusions

In this paper we have considered the problem of building an index for a string $S_2$ given an FM-index for a similar string $S_1$. We have shown how to build such a “relative” index using space bounded by the BW-distance between $S_1$ and $S_2$. The BW-distance is simply the edit distance between BWT($S_1$) and BWT($S_2$) when only insertions and deletions are allowed. We have also introduced the notion of BWT-invariant subsequence and shown that it can be used to determine a set of $S_1$ suffix array samples that can be easily “reused” for an index for $S_2$.

We have tested our approach by building a relative index for a Han Chinese individual with respect to an FM-index of the human reference genome. We leave as a future work the development of these ideas and the complete implementation of a relative FM-index supporting locating and extracting. We also leave as future work proving bounds on the BW-distance and the length of the longest BWT-invariant subsequence in terms of the edit distance of the strings.

References

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Appendix: Reusing an SA Sample

Consider the example strings $S_1$, $S_2$ given in the introduction. The characters of $\text{BWT}(S_1)[1..16]$ and $\text{BWT}(S_2)[1..15]$ are mapped to their positions by the BWT from

$$
S_1[16, 2, 6, 8, 13, 1, 12, 3, 7, 9, 14, 10, 15, 5, 11, 4] \\
S_2[15, 7, 2, 5, 12, 1, 11, 8, 3, 6, 13, 9, 14, 4, 10]
$$

respectively. (Notice the lists of indices are just the SAs of $S_1$ and $S_2$ with each value decremented.) Therefore, if $r = 3$ then

$$
R = 1000110010010001, \quad A[1..6] = [16, 13, 1, 7, 10, 4].
$$

Comparing $R$ and $B_1 = 0001000000000111$ we see that the sampled characters $\text{BWT}(S_1)[1, 5, 6, 9, 12]$ that are in $C$, are $C$’s 1st, 4th, 5th, 8th and 11th characters. From $B_2 = 010000000101010$ we see that the 1st, 4th, 5th, 8th and 11th
characters in $C$ in $\text{BWT}(S_2)$ are $\text{BWT}(S_2)[1, 5, 6, 9, 13]$, which are mapped to their positions by the BWT from $S_2[15, 12, 1, 3, 14]$.

The relative order 5, 3, 1, 2, 4 of the positions 15, 12, 1, 3, 14 in $S_2$ of these characters, is almost the same as the relative order 5, 4, 1, 2, 3 of the positions 16, 13, 1, 7, 10 in $S_1$ of the sampled characters in $\text{BWT}(S_1)$ that are in $C$, which seems promising. What if we choose $C$ and its occurrences in $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ such that the relative order in $S_1$ of all $\text{BWT}(S_1)$’s characters that are in $C$, is the same as the relative order in $S_2$ of all $\text{BWT}(S_2)$’s characters that are in $C$?

For example, we can choose instead

$$C' = \text{TCTCGTAAAGG}$$

$$B'_1 = 000100001010101 \quad B'_2 = 01000010001010$$

$$D'_1 = \text{GAGTC} \quad D'_2 = \text{GACC}$$

even though $C'$ is not then an LCS of $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ and, thus, our data structures for supporting rank in $\text{BWT}(S_2)$ are slightly larger. With these choices, the characters in $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$ that are in $C'$, are mapped to their positions by the BWT from

$$S_1[16, 2, 6, 13, 1, 12, 3, 7, 14, 15, 11], \quad S_2[15, 2, 5, 12, 1, 11, 3, 6, 13, 14, 10]$$

and the relative order 11, 2, 4, 8, 1, 7, 3, 5, 9, 10, 6 of the indices in those two lists is the same, as desired.

Suppose we store yet another pair of bitvectors

$$M_1 = 0001110011100000, \quad M_2 = 000100111000000$$

with 1s marking the positions in $S_1$ and $S_2$ of characters that are not mapped into $C'$ in $\text{BWT}(S_1)$ and $\text{BWT}(S_2)$. We claim that if we can support fast rank queries on $B'_2$, $R$ and $M_1$, fast access to $A$ and fast select0 queries on $B'_1$ and $M_2$, then we can support fast access to a (possibly irregular) sample SA sample for $S_2$ with as many sampled characters as there are in $C'$ in $\text{BWT}(S_1)$. More specifically, if $\text{BWT}(S_2)[i]$ is in $C'$ and $R[B'_1.\text{select0}(B'_2.\text{rank0}(i))] = 1$ — meaning the corresponding character in $C'$ in $\text{BWT}(S_1)$ is sampled — then $\text{BWT}(S_2)[i]$ is mapped to its position by the BWT from

$$S_2 \left[ M_2.\text{select0} \left( M_1.\text{rank0} \left( A \left[ R.\text{rank1} \left(B'_1.\text{select0}(B'_2.\text{rank0}(i)) \right) \right] \right) \right) \right].$$

We leave a detailed explanation to the full version of this paper. We note, however, that this approach works for any sample rate $r$, and even if the SA sample for $S_1$ is irregular itself.

In our example, since $\text{BWT}(S_2)[10]$ is in $C'$, $B'_1.\text{select0}(B'_2.\text{rank0}(10)) = 9$ and $R[9] = 1$, we know $\text{BWT}(S_2)[10]$ is mapped to its position by the BWT from position $M_2.\text{select0} \left( M_1.\text{rank0} \left( A[R.\text{rank1}(9)] \right) \right) = 6$ in $S_2$. 