A Compressed Self-Index for Genomic Databases

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Abstract. Advances in DNA sequencing technology will soon result in databases of thousands of genomes. Within a species, individuals’ genomes are almost exact copies of each other; e.g., any two human genomes are 99.9% the same. Relative Lempel-Ziv (RLZ) compression takes advantage of this property: it stores the first genome uncompressed or as an FM-index, then compresses the other genomes with a variant of LZ77 that copies phrases only from the first genome. RLZ achieves good compression and supports fast random access; in this paper we show how to support fast search as well, thus obtaining an efficient compressed self-index.

1 Introduction

DNA sequencing technology has advanced to the point that in the foreseeable future it will be practical for many people to pay for copies their genomes \cite{1,2}. This raises the question how to store many individual genomes compactly but such that we can still search them quickly. Any two human genomes are 99.9% the same, but compressed self-indexes based on compressed suffix arrays, the Burrows-Wheeler Transform or LZ78 (see \cite{11} for a survey) do not take full advantage of this similarity. Kreft and Navarro \cite{9} recently introduced a compressed self-index based on LZ77, which compresses repetitive sequences very well; however, two drawbacks of their index is that i) it uses a lot of space for the first genome and ii) the search time depends on the depth of nesting of the LZ77 parse. A compressed self-index stores a string $S[1..n]$ in compressed form such that, given a pattern $P[1..m]$, we can quickly list the \texttt{occ} occurrences of $P$ in $S$. In this paper we show how to build a compressed self-index on top of Relative Lempel-Ziv (RLZ) compression, which allows us to i) store the first, reference genome separately and more compactly, ii) restrict the depth of nesting to 1 and iii) reduce the dependence on the pattern length from quadratic to linear in the search time.

Kuruppu, Puglisi and Zobel \cite{10} introduced RLZ specifically for compression of genomic databases. Their idea is to store the first genome either uncompressed or as an FM-index, then compresses the other genomes with a variant of LZ77 that copies phrases only from the first genome — thus restricting the depth of nesting in the parse to 1. Although they showed that RLZ compresses genomic databases well and supports fast random access, they did not show how to support search in the whole database. We show how, if $G$ is the reference genome of length $n$, $T$ is the rest of the database and the RLZ parse of $T$ with respect to $G$ has $r$ phrases, then we can store the whole database in $(1 + 1/\epsilon)nH'_k(G) + O(r \log n + \log^{1+\epsilon} r) + O(n)$ bits such that, given a pattern $P$ of length $m$, in $O((m + \text{occ}_0) \log^\epsilon n + \text{occ}_1 + \text{occ}_2)$ time we can list the \texttt{occ}_0 occurrences of $P$ in $G$ and the \texttt{occ}_1 + \text{occ}_2 occurrences of $P$ in $T$. 
2 The Data Structure

Let \( G[1..n] \) be the reference sequence and let \( T[1..N] \) be the rest of the text. We assume that the alphabet \( \Sigma \) has a polylogarithmic size in \( n \). The RLZ-parse of \( T \) with respect to \( G \) is the partitioning \( T_1 T_2 \ldots T_r \) of \( T \) into \( r \) phrases such that \( T_i \) is the longest prefix of \( T_i \ldots T_r \) that occurs in \( G \). Let \( D \) be the set of \( d \) distinct phrases in the parse.

We divide the problem of finding the occurrences of a pattern \( P[1..m] \) into three phases: (i) finding the \( \text{occ}_0 \) occurrences in \( G \), (ii) finding the \( \text{occ}_2 \) occurrences in \( T \), i.e., occurrences that are completely contained in a single phrase, and (iii) finding the \( \text{occ}_1 \) occurrences in \( T \), i.e., occurrences that cross a phrase boundary.

We store the reference sequence \( G \) in an compressed suffix array (CSA) of \( (1/\epsilon)nH_k + O(n) \) bits [8], where \( \epsilon \) is an arbitrary constant with \( 0 < \epsilon \leq 1 \). Then we can find all the \( \text{occ}_0 \) occurrences of a pattern \( P[1..m] \) in \( O(m \log \sigma + \text{occ}_0 \log^\epsilon n) \) time.

To support search for secondary occurrences, we build a data structure for 2-dimensional, 2-sided range-reporting on an \( n \times n \) grid, on which we place \( r \) points, with each point \((i,j)\) indicating that a phrase is copied from \( G[i..j] \). Since the queries will be 2-sided — in particular, given a query point \((x,y)\) we want to find all the points \((i,j)\) on the grid such that \( i \leq x \) and \( j \geq y \), and the associated phrase, whose source \( G[i..j] \) includes \( G[x..y] \) — this data structure can be implemented with a predecessor data structure for the points’ horizontal coordinates, a range-maximum for their vertical coordinates (sorted by their horizontal coordinates) and a map from points to text positions. These data structures take \( O(r \log(n + r)) + o(n) \) bits and answer queries in \( O(p) \) time, where \( p \) is the number of points returned. For each occurrence \( G[x..y] \) of \( P \) in \( G \), we query the 2-sided range-reporting data structure to find all \( p \) phrases whose sources include \( G[x..y] \), in \( O(p) \) time.

Lemma 1. There is a data structure of \( O(r \log(n + r)) + o(n) \) bits such that, given the \( \text{occ}_0 \) occurrences of \( P \) in \( G \), in \( O(\text{occ}_0 + \text{occ}_2) \) time we can list the \( \text{occ}_2 \) secondary occurrences of \( P \) in \( T \).

To find primary occurrences, we represent each phrase boundary with a pair \((i,j)\), where \( i \) is the rank of the suffix of \( T \) starting at the phrase boundary in the lexicographical ordering of all suffixes of \( T \) starting at phrase boundaries, and \( j \) is the rank of the phrase ending at the phrase boundary in the lexicographical ordering of \( D^R \), the set of reversed distinct phrases. We store the pairs in a data structure for 2-dimensional range reporting by Alstrup et al. [3], which requires \( O(r \log^{1+\epsilon} n) \) bits of space and answers queries in \( O(\log \log r + p) \) time, where \( p \) is the number of points returned. Given the lexicographical interval of suffixes of \( T \) starting at phrase boundaries and having \( P[i..m] \) as a prefix and the lexicographical interval of \( D^R \) of reversed phrases having \( (P[1..i-1])^R \) as a prefix, we can find all primary occurrences of \( P \) such that first phrase boundary inside the occurrence is at position \( i \). The rest of the section describes how these intervals can be computed efficiently.

We augment the CSA of \( G \) with \( O(n) \)-bit data structures storing the longest common prefix (LCP) array [6] and its next/previous-smaller-value (NSV/PSV) array [7]. Then, for any string \( X \) and symbol \( c \), given the lexicographical interval of suffixes of \( G \) beginning with \( X \) we can compute the interval for \( cX \) in \( O(\log \sigma) \) time, and given the interval for \( Xc \) we can compute the interval for \( X \) in \( O(\log^\epsilon n) \) time. Given a pattern \( P[1..m] \), for all \( i \in [1..m] \), let \( \ell(i) \) be an integer such that \( P[i..\ell(i) - 1] \) is the longest prefix of \( P[i..m] \) that occurs in \( G \). We can compute \( \ell(i) \) for all \( i \) in...
\[ O(m \log \epsilon n) \] time using the CSA and the LCP and NSV/PSV data structures. Then, for some \( k \), \( P[i..\ell(i) - 1]P[\ell(i)..\ell^2(i) - 1] \ldots P[\ell^k(i)\ldots m] \) is the RLZ-parse of \( P[i..m] \) with respect to \( G \). If \( P[i..m] \) occurs in \( T \) starting at a phrase boundary, then the first \( k \) phrases following that phrase boundary must match \( P[i..\ell(i) - 1], P[\ell(i)..\ell^2(i) - 1], \ldots, P[\ell^{k-1}(i)\ldots \ell^k[i] - 1] \) exactly, and the \((k + 1)\)st phrase must begin with \( P[\ell^k[i]..m] \).

When computing \( \ell(i) \), we also obtain the lexicographical interval of the suffixes of \( G \) that begin with \( P[i..\ell(i) - 1] \), and the next step is to turn these into lexicographical ranks and intervals in \( D \), the set of distinct phrases. We represent each phrase in \( D \) with the integer \( qn + k \), where \( q \) is the lexicographical rank of the smallest of \( G \) that begins with the phrase, and \( k \) is the length of the phrase. Note that the integer is a complete description of the phrase, given \( G \), and it is consistent with the lexicographical ordering of the phrases. We store the integers in a data structure of \( O(d \log n) \) bits supporting \( O(\log \log d) \) time predecessor queries. If \([p..q]\) is the lexicographical interval of suffixes of \( G \) that begin with \( P[i..\ell(i) - 1] \), then \([pn + \ell(i) - i..qn + n]\) is the interval of phrases beginning with \( P[i..\ell(i) - 1] \). If the first phrase in that interval is \( pn + \ell(i) - i \), then it matches \( P[i..\ell(i) - 1] \) exactly.

Let \( R \) be the representation of the text \( T \) as a sequence of phrases, with each phrase represented by its rank in the lexicographical ordering of \( D \). The suffixes of \( R \) correspond to suffixes of \( T \) starting at phrase boundaries. We store a predecessor data structure of \( O(r + d + o(r)) \) bits, which maps a phrase in \( D \) into the lexicographical interval of suffixes of \( R \) that begin with that phrase. We also store the FM-index \([4, 5]\) of \( R \) in \( O(r \log d) \) bits supporting a backward search step in \( O(\log \log d) \) time. Let \( h \) be the smallest integer such that \( P[h..m] \) occurs in \( G \). For all \( i \in [h..m] \), we map the interval of phrases beginning with \( P[i..m] \) into the interval of suffixes of \( R \) beginning with those phrases. Then, for \( i = h - 1, \ldots, 1 \), having the interval of \( R \)'s suffixes for \( P[\ell(i)\ldots m] \) and the rank of the phrase matching \( P[i..\ell(i) - 1] \), we can compute the interval for \( P[i..m] \) with one backward search step. Thus the intervals for \( P[i..m] \) for all \( i \) can be computed in \( m \log \log d \) time.

Finally, to find reversed phrases beginning with \( (P[1..i - 1])^R \), we store an FM-index for the reverse \( G^R \) of \( G \) in \( nH_k(G) + o(n) \) bits. We use the FM-index to compute the lexicographical interval of suffixes of \( G^R \) that begin with \( (P[1..i - 1])^R \) for all \( i \in [1..m] \) in \( O(m) \) time. Using the technique of representing phrases with integers as above, we can store \( D^R \) in \( O(d \log n) \) bits so that the interval of reversed phrases beginning with \( (P[1..i - 1])^R \) can be computed in \( O(\log \log d) \) time.

**Theorem 1.** We can store a reference sequence \( G \) of length \( n \) and a text \( T \), whose RLZ-parse with respect to \( G \) has \( r \) phrases, in

\[
(1 + 1/\epsilon)nH_k(G) + O\left( r(\log n + \log^{1+\epsilon}r) \right) + O(n)
\]

bits such that, given a pattern \( P \) of length \( m \), in

\[
O((m + \text{occ}_0) \log^\epsilon n + \text{occ}_1 + \text{occ}_2)
\]

time we can list the \text{occ}_0 occurrences of \( P \) in \( G \) and the \text{occ}_1 + \text{occ}_2 occurrences of \( P \) in \( T \).

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