

# FM-index of Alignment with Gaps

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## Abstract

Recently, a compressed index for similar strings, called the *FM-index of alignment* (FMA), has been proposed with the functionalities of pattern search and random access. The FMA is quite efficient in space requirement and pattern search time, but it is applicable only for an alignment of similar strings without gaps. In this paper we propose the *FM-index of alignment with gaps*, a realistic index for similar strings, which allows gaps in their alignment. For this, we design a new version of the suffix array of alignment by using alignment transformation and a new definition of the alignment-suffix. The new suffix array of alignment enables us to support the LF-mapping and backward search, the key functionalities of the FM-index, regardless of gap existence in the alignment. We experimentally compared our index with RLCSA due to Mäkinen et al. on 100 genome sequences from the 1000 Genomes Project. The index size of our index is less than one third of that of RLCSA.

**Keywords:** Indexes for similar strings, FM-indexes, Suffix arrays, Alignments, Backward search.

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## 1. Introduction

A lot of indexes not only storing similar strings but also supporting efficient pattern search have been developed such as RLCSA [13, 14, 20], LZ-scheme based indexes [4, 5, 11]

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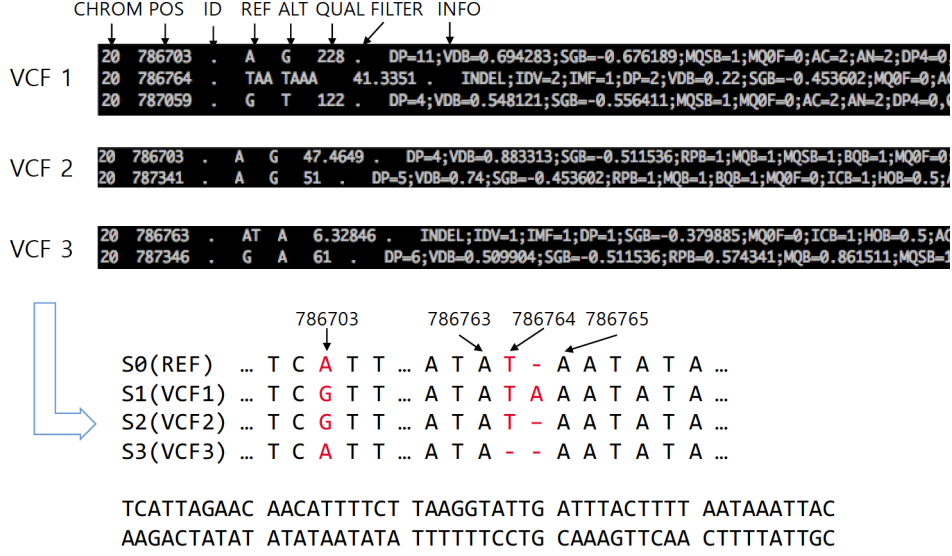


Figure 1: Example of a VCF file.

compressed suffix trees [1, 19], and so on [10, 18]. To exploit the similarity of the given strings, most of them use classical compression schemes such as run-length encoding and Lempel-Ziv compressions [12, 21]. Recently, Na et al. [15, 16, 17] took a new approach using an alignment of similar strings without classical compression schemes, and they proposed indexes of alignment called the *suffix tree of alignment* [16], the *suffix array of alignment* (SAA) [17], and the *FM-index of alignment* (FMA) [15]. The FMA, a compressed version of the SAA, is the most efficient among the three indexes but it is applicable only for an alignment of similar strings *without gaps*.

However, real-world data include gaps in alignments. Figure 1 shows Variant Call Format (VCF) files created by SAMtools (Sequence Alignment/Map tools) for sequences from the 1000 Genomes Project [3]. A VCF file contains alignment information between an individual sequence and its reference sequence. Note that not only substitutions but also indels (insertions and deletions) are contained in an alignment. For example, the first line of the ‘VCF 3’ file in Fig. 1 says that AT at position 786763 in the reference sequence is aligned with A in the individual sequence. Thus, the FMA [15] allowing only substitutions in an alignment is an unrealistic index.

In this paper we propose a new FM-index of alignment, a realistic compressed index for similar strings, allowing indels as well as substitutions in an alignment. (We call our index the FMA with gaps and the previous version the FMA without gaps.) For this, we design a new version of the SAA by using an alignment transformation and a new definition of the suffix of an alignment (called the *alignment-suffix*). In our index, an

alignment is divided into two kinds of regions, common regions and non-common regions, and gaps in a non-common region are put together into one gap in the transformed alignment. The alignment-suffix is defined for the transformed alignment but its definition is different from those defined in [15, 16, 17]. Due to the alignment transformation and the new definition of the alignment-suffix, our index supports the LF-mapping and backward search, the key functionalities of the FM-index [6, 7, 8], regardless of gap existence in the alignment.

For constructing our index, we must find common regions and non-common regions for the given strings but we do not need to find a multiple alignment for the given strings since the knowledge about positions where substitutions and indels occur are of no use in our transformed alignment. Finding common and non-common regions is much easier and simpler than finding a multiple alignment. For instance, common regions and non-common regions between an individual sequence and its reference sequence can be directly obtained from a VCF file. In the example of Fig. 1, position 786703 is a non-common region and positions 786704..786763 are a common region. Hence, based on the reference sequence, common regions and non-common regions of 100 genome sequences can be easily created.

We implemented the FMA with gaps and did experiments on 100 genome sequences from the 1000 Genomes Project. We compared our FMA with RLCSA due to Mäkinen et al. [14]. The index size of our FMA is less than one third of that of RLCSA. Our index is faster in pattern search and RLCSA is faster in random access.

This paper is organized as follows. We first describe our FMA and search algorithm for an alignment with gaps in Section 2 and give experimental results in Section 3. In Section 4, we conclude with remarks.

## 2. FM-index of alignment with gaps

### 2.1. Alignments with gaps

Consider a multiple alignment in Fig. 2 (a) of four similar strings:  $S^1 = \$cct\underline{c}aaacc\#$ ,  $S^2 = \$cct\underline{c}caaac\underline{a}\#$ ,  $S^3 = \$cct\underline{t}ataac\#$ , and  $S^4 = \$cctaacc\underline{c}\#$ . These strings are the same except the underlined characters and one string can be transformed into another strings by replacing, inserting or deleting underlined substrings. Formally, we are given an alignment  $\Upsilon$  of  $m$  similar strings  $S^j = \alpha_1\Delta_1^j \dots \alpha_r\Delta_r^j\alpha_{r+1}$  ( $1 \leq j \leq m$ ) over an alphabet  $\Sigma$ , where  $\alpha_i$  ( $1 \leq i \leq r+1$ ) is a common substring in all strings and  $\Delta_i^j$  ( $1 \leq i \leq r$ ) is a non-common substring in string  $S^j$ . In the example above,  $\alpha_1 = \$cct$ ,  $\alpha_2 = aac$ ,  $\alpha_3 = \#$ . Without loss of generality, we assume  $\alpha_1$  starts with  $\$$  and  $\alpha_{r+1}$  ends with  $\#$  where  $\$$  and  $\#$  are special symbols occurring nowhere else in  $S^j$ , and each  $\alpha_i$  is not empty.

pos.	1	2	3	4	5	6	7	8	9	0	1	2	3
$S^1 = \$$	c	c	t		<u>c</u>	-	a	-	a	a	c	<u>c</u>	#
$S^2 = \$$	c	c	t		<u>c</u>	<u>c</u>	<u>a</u>	-	a	a	c	<u>a</u>	#
$S^3 = \$$	c	c	t		<u>t</u>	-	a	<u>t</u>	a	a	c	=	#
$S^4 = \$$	c	c	t		-	-	-	-	a	a	c	<u>c</u>	#
	$\tilde{\alpha}_1^\diamond$	$\tilde{\alpha}_1^+$			$\Delta_1$				$\tilde{\alpha}_2^\diamond$	$\tilde{\alpha}_2^+$		$\Delta_2$	$\alpha_3$

(a)

Figure 2: An example of (a) an original alignment and (b) its transformed alignment.

For each common substring  $\alpha_i$ , we define  $\tilde{\alpha}_i^+$  as follows<sup>1</sup>.

**Definition 1.** The string  $\tilde{\alpha}_i^+$  ( $1 \leq i \leq r$ ) is the shortest suffix of  $\alpha_i$  occurring only once in each string  $S^j$  ( $1 \leq j \leq m$ ) and  $\tilde{\alpha}_{r+1}^+$  is an empty string.

Consider  $\alpha_1 = \text{\texttt{\$cct}}$  in Fig. 2. Since the suffix  $\text{\texttt{t}}$  of length 1 occurs more than once in  $S^3$  but the suffix  $\text{\texttt{ct}}$  of length 2 occurs only once in each string,  $\tilde{\alpha}_1^+$  is  $\text{\texttt{ct}}$ . Similarly,  $\tilde{\alpha}_2^+$  is  $\text{\texttt{ac}}$ , which is the shortest suffix of  $\alpha_2$  occurring only once in each string. Without loss of generality, for  $2 \leq i \leq r+1$ ,  $\tilde{\alpha}_i^+$  is assumed to be shorter than  $\alpha_i$ . (If  $\tilde{\alpha}_i^+$  is equal to  $\alpha_i$ , we merge  $\alpha_i$  with its adjacent non-common substrings  $\Delta_{i-1}^j$  and  $\Delta_i^j$ , and regard  $\Delta_{i-1}^j \alpha_i \Delta_i^j$  as one non-common substring).

For indexing similar strings whose alignment includes gaps, we first transform the given alignment  $\Upsilon$  into its right-justified form  $\tilde{\Upsilon}$  so that the characters in each  $\tilde{\alpha}_i^+ \Delta_j^+$  ( $1 \leq i \leq r$ ,  $1 \leq j \leq m$ ) are right-justified. See Fig. 2 for an example, where a gap is represented by a series of hyphens ‘-’ (note that ‘-’ is not a character). Hereafter, to indicate positions of characters in  $S^j$ , we use the positions in the transformed alignment  $\tilde{\Upsilon}$  and denote by  $\tilde{S}^j[i]$  the character of  $S^j$  at the  $i$ th position in  $\tilde{\Upsilon}$ . If  $\tilde{S}^j[i]$  is ‘-’, we say  $\tilde{S}^j[i]$  is empty. The positions in  $S^j$  and  $\tilde{S}^j$  can be easily converted into each other by storing gap information. Moreover, we denote the suffix of  $\tilde{S}^j$  starting at position  $q$  by suffix  $(j, q)$ , e.g., the suffix  $(3, 8)$  is **aac#** in Fig. 2.

An alignment of similar strings can be compactly represented by combining each common substring  $\alpha_i$  in all strings as in [15, 16, 17]. However, the representation is not suitable for the transformed alignment  $\tilde{\Upsilon}$  because the characters in  $\tilde{\alpha}_i^+$  are not aligned in  $\tilde{\Upsilon}$ . Thus, we introduce another representation. Let  $\tilde{\alpha}_i^\diamond$  ( $1 \leq i \leq r+1$ ) be the prefix of  $\alpha_i$  such that  $\alpha_i = \tilde{\alpha}_i^\diamond \tilde{\alpha}_i^+$ . Then, we represent the transformed alignment  $\tilde{\Upsilon}$  by combining  $\tilde{\alpha}_i^\diamond$  (rather than  $\alpha_i$ ):  $\tilde{\Upsilon} = \tilde{\alpha}_1^\diamond (\tilde{\alpha}_1^+ \Delta_1^1 / \cdots / \tilde{\alpha}_1^+ \Delta_1^m) \cdots \tilde{\alpha}_r^\diamond (\tilde{\alpha}_r^+ \Delta_r^1 / \cdots / \tilde{\alpha}_r^+ \Delta_r^m) \tilde{\alpha}_{r+1}^\diamond$ . The alignment in Fig. 2 is represented as  $\tilde{\Upsilon} = \text{\texttt{\$c(ct\underline{ca}/ct\underline{cca}/ct\underline{tat}/ct)a(ac\underline{c}/ac\underline{a}/ac/ac\underline{c})\#}}$ . We denote  $(\tilde{\alpha}_i^+ \Delta_i^1 / \cdots / \tilde{\alpha}_i^+ \Delta_i^m)$  by  $\tilde{\alpha}_i^+ \Delta_i$  and call it a *ps-region* (partially-shared region). Also, we call  $\tilde{\alpha}_i^\diamond$  a *cs-region* (completely-shared region).

<sup>1</sup>Note that the definition of  $\tilde{\alpha}_i^+$  is different from that of  $\tilde{\alpha}_i^*$  in [15, 16, 17]. The  $\tilde{\alpha}_i^+$  is longer than  $\tilde{\alpha}_i^*$  by one.

## 2.2. Suffix array and FM-index of alignment with gaps

In our index, one or more suffixes starting at an identical position  $q$  are compactly represented by one *alignment-suffix* (for short *a-suffix*) defined as follows. We have two cases according to whether the starting position  $q$  is in a cs-region or a ps-region.

- The case when  $q$  is in a cs-region  $\tilde{\alpha}_i^\diamond$  ( $1 \leq i \leq r+1$ ). Let  $\alpha'_i$  be the suffix of  $\tilde{\alpha}_i^\diamond$  starting at  $q$ . All the suffixes starting at  $q$  is represented by the a-suffix  $\alpha'_i(\tilde{\alpha}_i^+ \Delta_i^1 / \dots / \tilde{\alpha}_i^+ \Delta_i^m) \dots$ . In the previous example, the suffixes starting at position 8 are represented by the a-suffix  $\mathbf{a}(\mathbf{acc}/\mathbf{aca}/\mathbf{ac}/\mathbf{acc})\#$ .
- The case when  $q$  is in a ps-region  $\tilde{\alpha}_i^+ \Delta_i$  ( $1 \leq i \leq r$ ). Let  $\delta_i^j$  ( $1 \leq j \leq m$ ) be the suffix of  $\tilde{\alpha}_i^+ \Delta_i^j$  starting at  $q$ . Then, the set of the suffixes starting at  $q$  is partitioned so that the suffixes of  $S^{j_1}$  and  $S^{j_2}$  are in the same subset if and only if  $\delta_i^{j_1} = \delta_i^{j_2}$ . For each subset  $\{\delta_i^{j_1} \dots \tilde{\alpha}_{r+1}^\diamond, \dots, \delta_i^{j_k} \dots \tilde{\alpha}_{r+1}^\diamond\}$ , all the suffixes in the subset are represented by the a-suffix  $(\delta_i^{j_1} / \dots / \delta_i^{j_k}) \dots \tilde{\alpha}_{r+1}^\diamond$ . For example, the set of the suffixes starting at position 9 is partitioned into two subsets  $\{\tilde{S}^1[9..12], \tilde{S}^4[9..12]\}$  and  $\{\tilde{S}^2[9..12]\}$ , and they are represented by the a-suffixes  $(\mathbf{acc}/\mathbf{acc})\#$  and  $\mathbf{aca}\#$ , respectively. Note that no suffix of  $\tilde{S}^3$  starts at position 9.

The suffixes represented by an a-suffix appear consecutively in the generalized suffix array of the given strings since  $\tilde{\alpha}_i^+$  occurs only once in each given string. Note that a suffix of  $\tilde{\alpha}_i^+$  may occur more than once in a string, and thus  $\tilde{\alpha}_i^+$  does not belong to a cs-region but to a ps-region.

The *suffix array of alignment* (*SAA*) is a lexicographically sorted array of all the a-suffixes of the transformed alignment  $\tilde{\Upsilon}$ . See Fig. 3 for an example, where the string number 0 indicates the string numbers  $1, \dots, m$ . We denote by  $SAA[i]$  the  $i$ th entry of the SAA. Let us consider a-suffixes in the SAA as cyclic shifts (rotated alignments) as in the Burrows-Wheeler transform [2]. Then, the array  $F[i]$  (resp.  $L[i]$ ) is the set of the first (resp. last) characters of the suffixes represented by the a-suffix in  $SAA[i]$ . By definition of the a-suffixes, the first characters of the suffixes represented by an a-suffix are of the same value and thus  $F[i]$  has one element. However,  $L[i]$  may have more than one element (at most  $|\Sigma|$  elements) as shown in Fig. 3. For example,  $F[13] = \{\tilde{S}^1[10], \tilde{S}^4[10]\} = \{\mathbf{c}\}$  and  $L[10] = \{\tilde{S}^1[10], \tilde{S}^3[10], \tilde{S}^4[10]\} = \{\mathbf{a}, \mathbf{c}\}$ . Since gaps are not considered as characters in  $\tilde{\Upsilon}$ , when letting  $q$  be the position of the characters in  $F[i]$ , the positions of the characters in  $L[i]$  may be less than  $q-1$ . (On the other hand, the position of the characters in  $L[i]$  is always  $q-1$  for an alignment without gaps when  $q > 1$ .) In Fig. 3,  $F[17] = \tilde{S}^1[4]$  and  $L[17] = \tilde{S}^1[2]$  because  $\tilde{S}^1[3]$  is empty.

We define the LF-mapping for the arrays  $L$  and  $F$ . Let  $\mathcal{L}$  be the set of pairs of a character  $\sigma$  and an entry index  $i$  such that  $\sigma \in L[i]$ . In the example of Fig. 3,  $\mathcal{L} = \{(\#, 1), (\mathbf{a}, 2), (\mathbf{c}, 2), (\mathbf{c}, 3), (\mathbf{c}, 4), (\mathbf{a}, 5), (\mathbf{t}, 5), \dots\}$ . For a pair  $(\sigma, i) \in \mathcal{L}$ , the *LF-mapping*  $LF(\sigma, i)$  is defined as the index of  $F[k]$  containing the characters corresponding

$idx$	SAA		$F$	a-suffixes (cyclic shifts)	$L$	$occ(\sigma, i) \ \& \ B_\sigma$		
	$strs$	$pos$				$a$	$c$	$t$
1	0	1	\$	\$c(ct <u>ca</u> /ct <u>cca</u> /ctt <u>at</u> /ct)a(ac <u>c</u> /ac <u>a</u> /ac/ac <u>c</u> )#	#	0	0	0
2	0	12	#	#\$c(ct <u>ca</u> /ct <u>cca</u> /ctt <u>at</u> /ct)a(ac <u>c</u> /ac <u>a</u> /ac/ac <u>c</u> )	a, c	1	1	0
3	2	11	a	a#\$cct <u>cca</u> aac	c	1	2	0
4	1,2	7	a	( <u>a</u> / <u>a</u> )a(ac <u>c</u> /ac <u>a</u> )#\$c(ct <u>c</u> /ct <u>cc</u> )	c	1	3	0
5	0	8	a	a(ac <u>c</u> /ac <u>a</u> /ac/ac <u>c</u> )#\$c(ct <u>ca</u> /ct <u>cca</u> /ctt <u>at</u> /ct)	a, t	2	3	1
6	3	10	a	ac#\$cctt <u>ata</u>	a	3	1	3
7	2	9	a	aca#\$cct <u>cca</u> a	$\langle a \rangle$	3	1	3
8	1,4	9	a	(ac <u>c</u> /ac <u>c</u> )#\$c(ct <u>ca</u> /ct)a	$\langle a \rangle$	3	1	3
9	3	6	a	ataac#\$cct <u>t</u>	t	3	3	2
10	1,3,4	11	c	( <u>c</u> / <u>c</u> / <u>c</u> )#\$c(ct <u>ca</u> /ctt <u>at</u> /ct)a(ac/a/ac)	a, c	4	4	2
11	2	10	c	ca#\$cct <u>cca</u> aa	a	5	4	2
12	1,2	6	c	( <u>ca</u> / <u>ca</u> )a(ac <u>c</u> /ac <u>a</u> )#\$c(ct/ <u>ctc</u> )	c, t	5	5	3
13	1,4	10	c	( <u>cc</u> / <u>cc</u> )#\$c(ct <u>ca</u> /ct)a(a/a)	a	6	5	3
14	2	5	c	caaaca#\$cct	t	6	5	4
15	0	2	c	c(ct <u>ca</u> /ct <u>cca</u> /ctt <u>at</u> /ct)a(ac <u>c</u> /ac <u>a</u> /ac/ac <u>c</u> )#\$	\$	6	5	4
16	4	6	c	ctaacc#\$c	c	6	6	1
17	1	4	c	ct <u>caa</u> acc#\$c	$\langle c \rangle$	6	6	1
18	2	3	c	ct <u>cca</u> aaca#\$c	$\langle c \rangle$	6	6	1
19	3	3	c	cttataac#\$c	$\langle c \rangle$	6	6	1
20	3,4	7	t	( <u>t</u> / <u>t</u> )a(ac/ac <u>c</u> )#\$c(ctt <u>a</u> /c)	a, c	7	7	4
21	3	5	t	tataac#\$cct	t	7	7	5
22	1	5	t	t <u>caa</u> acc#\$cc	c	7	8	5
23	2	4	t	t <u>cca</u> aaca#\$cc	c	7	9	5
24	3	4	t	ttataac#\$cc	c	7	10	5

Figure 3: The SAA and FMA for  $\tilde{\Upsilon} = \$c(ct\bar{c}a/ct\bar{c}ca/ctt\bar{a}t/ct)a(ac\bar{c}/ac\bar{a}/ac/ac\bar{c})\#$ . (Bit 0 is omitted in  $B_\sigma$ .)

to  $\sigma$  in  $L[i]$ . For example, see  $L[10] = \{\tilde{S}^1[10], \tilde{S}^3[10], \tilde{S}^4[10]\} = \{a, c\}$ . Since  $a$  in  $L[10]$  corresponds to  $\tilde{S}^3[10]$  and it is contained in  $F[6]$ ,  $LF(a, 10) = 6$ . Similarly,  $LF(c, 10) = 13$  since  $\tilde{S}^1[10]$  and  $\tilde{S}^4[10]$  (i.e.,  $c$  in  $L[10]$ ) are contained in  $F[13]$ . Note that  $LF(c, 10)$  is well defined since the characters in  $L[10]$  whose values are  $c$  are all contained in an *identical* entry  $F[13]$ . This is always true in the transformed alignment  $\tilde{\Upsilon}$  even though gaps exist in  $\tilde{\Upsilon}$ , as shown in the following lemma. (It is not true in the untransformed alignment  $\Upsilon$ .)

**Lemma 1.** *For a pair  $(\sigma, i) \in \mathcal{L}$ , the characters in  $L[i]$  whose values are  $\sigma$  are all contained in an identical entry of  $F$ .*

**Proof:** Let  $q$  be the starting position of the suffixes in  $SAA[i]$ , and  $\tilde{S}^{j_1}[q_1]$  and  $\tilde{S}^{j_2}[q_2]$  ( $j_1 \neq j_2$ ) be two characters in  $L[i]$  whose values are  $\sigma$ . Without loss of generality, we assume  $q > 1$ . Then,  $q_1$  and  $q_2$  are less than  $q$ . We have three cases according to whether  $\tilde{S}^{j_1}[q-1]$  and  $\tilde{S}^{j_2}[q-1]$  are empty.

- First, when none of  $\tilde{S}^{j_1}[q-1]$  and  $\tilde{S}^{j_2}[q-1]$  are empty (i.e.,  $q_1 = q_2 = q-1$ ),  $\tilde{S}^{j_1}[q_1]$  and  $\tilde{S}^{j_2}[q_2]$  are contained in an identical entry of  $F$  by definition of the a-suffix, which can be shown as in [15].
- Second, when both of  $\tilde{S}^{j_1}[q-1]$  and  $\tilde{S}^{j_2}[q-1]$  are empty, both  $\tilde{S}^{j_1}[q_1]$  and  $\tilde{S}^{j_2}[q_2]$  are the last character in a cs-region  $\tilde{\alpha}_i^\diamond$  since the characters in ps-region  $\tilde{\alpha}_i^+ \Delta_i$  are right-justified in  $\tilde{\Upsilon}$ . Thus,  $q_1 = q_2$  and by definition of the a-suffix, the suffixes  $(j_1, q_1)$  and  $(j_2, q_2)$  are contained in an identical entry of the SAA. Hence,  $\tilde{S}^{j_1}[q_1]$  and  $\tilde{S}^{j_2}[q_2]$  are contained in an identical entry of  $F$ .
- The third case is when only one of  $\tilde{S}^{j_1}[q-1]$  and  $\tilde{S}^{j_2}[q-1]$  is empty. We show by contradiction that this case cannot happen. Without loss of generality, assume  $\tilde{S}^{j_1}[q-1]$  is empty and  $\tilde{S}^{j_2}[q-1]$  is not empty. Since  $\tilde{S}^{j_1}[q-1]$  is empty,  $\tilde{S}^{j_1}[q_1]$  is the last character in a cs-region  $\tilde{\alpha}_k^\diamond$  and  $\tilde{S}^{j_1}[q]$  is the first character in ps-region  $\tilde{\alpha}_k^+ \Delta_k$ . It means that the suffix  $(j_1, q)$  is prefixed by  $\tilde{\alpha}_k^+$ . Since both suffixes  $(j_1, q)$  and  $(j_2, q)$  are in  $SAA[i]$ , by definition of the a-suffix, the suffix  $(j_2, q)$  is also prefixed by  $\tilde{\alpha}_k^+$ . Since  $\tilde{\alpha}_k^+$  occurs only once in each string,  $\tilde{S}^{j_2}[q_2]$  is the last character in  $\tilde{\alpha}_k^\diamond$  (i.e.,  $q_1 = q_2$ ) and  $\tilde{S}^{j_2}[q_2 + 1..q-1]$  is empty. It contradicts with the assumption that  $\tilde{S}^{j_2}[q-1]$  is not empty.

Therefore, the characters in  $L[i]$  whose values are  $\sigma$  are all contained in an identical entry of  $F$ .  $\square$

For a character  $\sigma \in \Sigma$ , a pair  $(\sigma, i) \in \mathcal{L}$  will be called an  $\mathcal{L}_\sigma$ -pair. For two  $\mathcal{L}_\sigma$ -pairs  $(\sigma, i)$  and  $(\sigma, i')$ , we say that  $(\sigma, i)$  is smaller than  $(\sigma, i')$  if and only if  $i < i'$ .

The LF-mapping  $LF(\sigma, i)$  is not a one-to-one correspondence. Multiple pairs can be mapped to the same entry in  $F$ . See  $L[6] = \{\tilde{S}^3[8]\} = \{\mathbf{a}\}$ ,  $L[7] = \{\tilde{S}^2[8]\} = \{\mathbf{a}\}$ , and  $L[8] = \{\tilde{S}^1[8], S^4[8]\} = \{\mathbf{a}\}$ . Since all of them are  $\mathbf{a}$  in  $F[5]$ ,  $LF(\mathbf{a}, 6) = LF(\mathbf{a}, 7) = LF(\mathbf{a}, 8) = 5$ . Thus, we classify pairs  $(\sigma, i) \in \mathcal{L}$  into two types: A pair  $(\sigma, i) \in \mathcal{L}$  is an *(m:1)-type* (many-to-one mapping-type) pair if there exists another pair  $(\sigma, i') \in \mathcal{L}$  such that  $LF(\sigma, i) = LF(\sigma, i')$ ; otherwise,  $(\sigma, i)$  is a *(1:1)-type* (one-to-one mapping-type) pair. The following lemma shows that for a (m:1)-type pair  $(\sigma, i)$ , the last characters of all the suffixes in  $SAA[i]$  are mapped to an identical entry in  $F$ . (This lemma is necessary for our search algorithm to work correctly and it is also satisfied for the FMA without gaps [15]. However, it is not satisfied when defining our index using  $\tilde{\alpha}^*$  in [15] rather than  $\tilde{\alpha}^+$ .)

**Lemma 2.** *If a pair  $(\sigma, i) \in \mathcal{L}$  is of (m:1)-type, the values of the characters in  $L[i]$  are all the same  $\sigma$ .*

**Proof:** Let  $k = LF(\sigma, i)$  and  $q_k$  be the starting position of the suffixes in  $SAA[k]$ . By definition of the a-suffix, the pair  $(\sigma, i)$  is of (m:1)-type only if  $q_k$  is the last position in a cs-region  $\tilde{\alpha}_j^\circ$  and the last character in  $\tilde{\alpha}_j^\circ$  is  $\sigma$ . Hence, all the suffixes in  $SAA[i]$  are prefixed by  $\tilde{\alpha}_j^+$ . Since  $\tilde{\alpha}_j^+$  occurs only once in each string, the preceding character of  $\tilde{\alpha}_j^+$  is the last character in  $\tilde{\alpha}_j^\circ$ , i.e.,  $\sigma$ . Therefore,  $L[i]$  has only one character  $\sigma$ .  $\square$

To handle (m:1)-type pairs in  $\mathcal{L}$  efficiently, we define bit-vectors  $B_\sigma$ 's as follows:  $B_\sigma[i] = 1$  if and only if  $(\sigma, i)$  is in  $\mathcal{L}$  and it is of (m:1)-type (see Fig. 3).

The LF-mapping can be easily computed using the array  $C$  and the function  $occ$  defined as follows [15].

- For  $\sigma \in \Sigma$ ,  $C[\sigma]$  is the total number of entries in  $F$  containing characters alphabetically smaller than  $\sigma$ .  $C[|\Sigma| + 1]$  is the size of  $F$ .
- For a character  $\sigma \in \Sigma$  and an entry index  $i$  in the SAA,  $occ(\sigma, i)$  is the number of  $\mathcal{L}_\sigma$ -pairs  $(\sigma, i')$  such that  $i' \leq i$ , i.e., the number of entries in  $L[1..i]$  containing the character  $\sigma$ . If more than one pair  $(\sigma, i') \in \mathcal{L}$  are mapped to an identical entry in  $F$ , we count only the smallest  $\mathcal{L}_\sigma$ -pair among them. For example, consider  $occ(\mathbf{a}, i)$  for  $i = 6, 7, 8$ . Since  $\mathbf{a}$ 's in  $L[6..8]$  are all contained in  $F[5]$ , we only count  $(\mathbf{a}, 6)$  and thus  $occ(\mathbf{a}, i)$ 's are the same for  $i = 6, 7, 8$ . In Fig. 3, uncounted characters in  $L$  are indicated by  $\langle \rangle$ .

Then,  $LF(\sigma, i) = C[\sigma] + occ(\sigma, i)$ . See  $L[10]$  in Fig. 3, which has two  $\mathcal{L}_\sigma$ -pairs  $(\mathbf{a}, 10)$  and  $(\mathbf{c}, 10)$ . We have  $LF(\mathbf{a}, 10) = C[\mathbf{a}] + occ(\mathbf{a}, 10) = 2 + 4 = 6$  and  $LF(\mathbf{c}, 10) = C[\mathbf{c}] + occ(\mathbf{c}, 10) = 9 + 4 = 13$ .

### 2.3. Pattern Search

Pattern search is to find all occurrences of a given pattern  $P[1..p]$  in the given strings  $S^1, \dots, S^m$ . Our pattern search algorithm proceeds backward using the LF-mapping with the array  $C$  and the function  $occ$ . It consists of at most  $p$  steps from Step  $p$  to Step 1. In Step  $\ell = p, \dots, 1$ , the algorithm finds the range  $(\text{First}_\ell, \text{Last}_\ell)$  in the SAA defined as follows:

- $\text{First}_p$  (resp.  $\text{Last}_p$ ) is the smallest (resp. largest) index  $i$  such that  $F[i] = \{P[p]\}$ .
- For  $\ell = p - 1, \dots, 1$ ,  $\text{First}_\ell$  (resp.  $\text{Last}_\ell$ ) is the LF-mapping value of the smallest (resp. largest)  $\mathcal{L}_\sigma$ -pair in the range  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ , where  $\sigma = P[\ell]$ . If there exists no  $\mathcal{L}_\sigma$ -pair in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ , then we set  $\text{First}_\ell = \text{Last}_\ell + 1$ .



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<b>Algorithm 1</b>	<b>BackwardSearch(<math>P[1..p]</math>)</b>	$\triangleright$ using the FM-index of alignment
1:	$Z \leftarrow \{1, \dots, m\};$	$\triangleright$ Set of all string numbers
2:	$\sigma \leftarrow P[p], \text{ First} \leftarrow C[\sigma] + 1, \text{ Last} \leftarrow C[\sigma + 1], \ell \leftarrow p - 1;$	
3:	<b>while</b> ( $\text{First} \leq \text{Last}$ ) <b>and</b> $Z \neq \emptyset$ <b>and</b> ( $\ell \geq 1$ ) <b>do</b>	
4:	$\sigma \leftarrow P[\ell], \text{ First}' \leftarrow \text{First}, \text{ Last}' \leftarrow \text{Last};$	$\triangleright$ Previous range
5:	$\text{First} \leftarrow C[\sigma] + \text{occ}(\sigma, \text{First} - 1) + 1, \text{ Last} \leftarrow C[\sigma] + \text{occ}(\sigma, \text{Last});$	
6:	<b>if</b> $\text{First} \geq \text{Last}$ <b>then</b>	
7:	$Z_m \leftarrow \{j \mid (j, q) \in SAA[i] \text{ such that } \text{First}' \leq i \leq \text{Last}' \text{ and } B_\sigma[i] = 1\};$	
8:	<b>if</b> $Z_m \neq \emptyset$ <b>then</b>	
9:	$\text{First} \leftarrow \text{Last}, Z \leftarrow Z \cap Z_m;$	
10:	<b>else</b>	
11:	$Z_c \leftarrow \{j \mid (j, q) \in SAA[\text{First}..\text{Last}]\},$	$\triangleright$ If $\text{First} > \text{Last}$ , $Z_c = \emptyset$
12:	$Z \leftarrow Z \cap Z_c;$	
13:	$\ell \leftarrow \ell - 1;$	
14:	<b>for all</b> $(j, q) \in SAA[\text{First}..\text{Last}]$ <b>do</b>	$\triangleright$ If $\text{First} > \text{Last}$ , no occurrence
15:	<b>if</b> $j \in Z$ <b>then</b> <b>print</b> “ $(j, q)$ ”;	$\triangleright$ Reporting an occurrence

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Then, all the suffixes prefixed by  $P[\ell..p]$  are in  $SAA[\text{First}_\ell..\text{Last}_\ell]$  and the size of the range decreases monotonically when  $\ell$  decreases.

While the size of the range  $(\text{First}_\ell, \text{Last}_\ell)$  is greater than one (i.e.,  $\text{First}_\ell < \text{Last}_\ell$ ), all the suffixes in  $SAA[\text{First}_\ell..\text{Last}_\ell]$  are prefixed by  $P[\ell..p]$ . When  $\text{First}_\ell = \text{Last}_\ell$ , however, some suffixes in  $SAA[\text{First}_\ell]$  may not be prefixed by  $P[\ell..p]$ . For example, when assuming that  $P = \text{aaacc}$ , we have  $(\text{First}_2, \text{Last}_2) = (5, 5)$ , and the suffixes  $(1, 8)$  and  $(4, 8)$  in  $SAA[5]$  are prefixed by  $\text{aacc}$  but the other suffixes  $(2, 8)$  and  $(3, 8)$  are not. Also, we have  $(\text{First}_1, \text{Last}_1) = (4, 4)$ , and the suffix  $(1, 7)$  in  $SAA[4]$  is prefixed by  $\text{aaacc}$  but the suffix  $(2, 7)$  is not. Thus, in addition to the range  $(\text{First}_\ell, \text{Last}_\ell)$ , we maintain the set  $Z_\ell$  defined as follows:

- When  $\text{First}_\ell = \text{Last}_\ell$ ,  $Z_\ell$  is the set of the string numbers of the suffixes prefixed by  $P[\ell..p]$ .

For simplicity, we define  $Z_\ell$  to be  $\{1, \dots, m\}$  when  $\text{First}_\ell < \text{Last}_\ell$ . Then, regardless of the size of the range  $(\text{First}_\ell, \text{Last}_\ell)$ , a suffix  $(j, q)$  is prefixed by  $P[\ell..p]$  if and only if  $(j, q) \in SAA[\text{First}_\ell..\text{Last}_\ell]$  and  $j \in Z_\ell$ .

Algorithm 1 shows the search algorithm using our index, which is the same as the code in [15]. (Since the definition of the a-suffix is different from that in [15], however, we need a correctness proof which will be given later.) The algorithm maintains the following loop invariant for a range  $(\text{First}, \text{Last})$  and a string number set  $Z$ :

At the end of Step  $\ell = p, \dots, 1$ , the range  $(\text{First}, \text{Last}) = (\text{First}_\ell, \text{Last}_\ell)$  and  $Z = Z_\ell$ .

Initially (in Step  $p$ ), we set  $(\text{First}, \text{Last}) = (\text{First}_p, \text{Last}_p)$  and  $Z = Z_p$  (lines 1–2). Each iteration of the while loop (lines 3–13) represents each Step  $\ell = p - 1, \dots, 1$ . In Step  $\ell = p - 1, \dots, 1$ , we first compute range  $(\text{First}, \text{Last})$  using the LF-mapping of the previous range  $(\text{First}', \text{Last}') = (\text{First}_{\ell+1}, \text{Last}_{\ell+1})$  and  $\sigma = P[\ell]$  (lines 4–5). If the size of the range  $(\text{First}, \text{Last})$  is more than one, then  $(\text{First}, \text{Last}) = (\text{First}_\ell, \text{Last}_\ell)$  and  $Z = Z_\ell = \{1, \dots, m\}$ . Thus, we continue to the next step (by skipping lines 6–12 and going to line 13). Otherwise (i.e., the size of  $(\text{First}, \text{Last})$  is one or less), we compute  $Z_\ell$  as follows (lines 6–12). Let  $Z_m$  be the set of the string numbers in  $SAA[i]$ 's such that  $\text{First}_{\ell+1} \leq i \leq \text{Last}_{\ell+1}$  and  $B_\sigma[i] = 1$ , and let  $Z_c$  be the set of the string numbers in  $SAA[\text{Last}]$ . Then,  $Z_\ell = Z_{\ell+1} \cap Z_m$  if  $Z_m \neq \emptyset$ , and  $Z_\ell = Z_{\ell+1} \cap Z_c$ , otherwise. (As in [15], lines 10–12 for  $Z_c$  can be removed by using a loose definition and a lazy update for  $Z_\ell$ .) For example, assume  $P = \text{aaacc}$ . In Step 2, given  $(\text{First}_3, \text{Last}_3) = (8, 8)$  and  $Z_3 = \{1, 2, 3, 4\}$ , we have  $Z_m = \{1, 4\}$  and thus  $Z_2 = \{1, 4\}$ . In Step 1, given  $(\text{First}_2, \text{Last}_2) = (5, 5)$  and  $Z_2 = \{1, 4\}$ , we have  $Z_m = \emptyset$  and  $Z_c = \{1, 2\}$  ( $\text{Last}_1 = 4$ ), and thus  $Z_1 = \{1, 4\} \cap \{1, 2\} = \{1\}$ . After the while loop terminates, the occurrences of  $P$  are reported using the range  $(\text{First}, \text{Last})$  and  $Z$  (lines 14–15). Since the SAA stores positions in the transformed alignment  $\tilde{Y}$ , we need to convert them to the original positions in the given strings  $S^j$ , which can be easily done by using gap information.

Now we show the invariant is satisfied at the end of each step (an iteration of the while loop) by induction. Trivially, the invariant is true at the end of Step  $p$ , which is the induction basis. At the beginning of Step  $\ell = p - 1, \dots, 1$ , by inductive hypothesis,  $(\text{First}, \text{Last}) = (\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . After executing line 5,  $\text{First} = C[\sigma] + \text{occ}(\sigma, \text{First}_{\ell+1} - 1) + 1$  and  $\text{Last} = C[\sigma] + \text{occ}(\sigma, \text{Last}_{\ell+1})$ , where  $\sigma = P[\ell]$ . Then, the following lemmas show Algorithm 1 computes correctly  $(\text{First}_\ell, \text{Last}_\ell)$  and  $Z_\ell$  at the end of Step  $\ell$ .

**Lemma 3.** *If  $\text{First} < \text{Last}$ , then  $(\text{First}_\ell, \text{Last}_\ell) = (\text{First}, \text{Last})$  and  $Z_\ell = Z_{\ell+1}$ .*

**Proof:** By definition of the LF-mapping, the suffixes in  $SAA[\text{First}..\text{Last}]$  are prefixed by  $P[\ell..p]$ . We show that no suffix outside  $SAA[\text{First}..\text{Last}]$  are prefixed by  $P[\ell..p]$ . Suppose that a suffix prefixed by  $P[\ell..p]$  is contained in an  $SAA[i]$  outside  $SAA[\text{First}..\text{Last}]$ . Then, all suffixes in  $SAA[i]$  are prefixed by  $P[\ell..p]$ . (If two suffixes in two distinct entries of the SAA are prefixed by  $P[\ell..p]$ , then all the suffixes in the two entries are prefixed by  $P[\ell..p]$ , which can be easily shown using the definition of the a-suffix.) Let  $(\sigma, k)$  be the smallest  $\mathcal{L}_\sigma$ -pair such that  $LF(\sigma, k) = i$ . Since the suffixes in  $SAA[k]$  are prefixed by  $P[\ell + 1..p]$ ,  $k$  is included in the previous range  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$  by definition and thus its LF-mapping value  $i$  is also included in  $(\text{First}, \text{Last})$  (note that the pair  $(\sigma, k)$  is always counted in the function  $\text{occ}$ ). It contradicts with the assumption that  $i$  is outside the range  $(\text{First}, \text{Last})$ . Therefore, we get  $(\text{First}_\ell, \text{Last}_\ell) = (\text{First}, \text{Last})$ . Furthermore, since  $\text{First}_\ell \neq \text{Last}_\ell$ ,  $Z_\ell = Z_{\ell+1} = \{1, \dots, m\}$  by definition.  $\square$

**Lemma 4.** *If  $\text{First} \geq \text{Last}$  and  $Z_m \neq \emptyset$ , then  $(\text{First}_\ell, \text{Last}_\ell) = (\text{Last}, \text{Last})$  and  $Z_\ell = Z_{\ell+1} \cap Z_m$ .*

**Proof:** Since  $Z_m \neq \emptyset$ , there exist  $\mathcal{L}_\sigma$ -pairs of (m:1)-type in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . Furthermore, all of the  $\mathcal{L}_\sigma$ -pairs are mapped to one entry  $F[\text{Last}]$  of  $F$  since  $\text{First} \geq \text{Last}$ . Therefore,  $(\text{First}_\ell, \text{Last}_\ell) = (\text{Last}, \text{Last})$ .

Next, let us consider  $Z_\ell$ . In this case,  $\mathcal{L}_\sigma$ -pairs in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$  are all of (m:1)-type. Moreover, for every  $\mathcal{L}_\sigma$ -pair  $(\sigma, i)$  in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ , the last characters of the suffixes in  $SAA[i]$  are all  $\sigma$  by Lemma 2. Thus,  $Z_m$  is the set of the string numbers of the suffixes whose last characters are  $\sigma$  in  $SAA[\text{First}_{\ell+1}..\text{Last}_{\ell+1}]$ . By definition,  $Z_{\ell+1}$  is the set of the string numbers of the suffixes prefixed by  $P[\ell+1..p]$ . Thus, a suffix  $(j, q)$  in  $SAA[\text{Last}]$  is prefixed by  $\sigma P[\ell+1..p]$  ( $= P[\ell..P]$ ) if and only if  $j \in Z_m$  and  $j \in Z_{\ell+1}$ . Therefore, we get  $Z_\ell = Z_m \cap Z_{\ell+1}$ .  $\square$

**Lemma 5.** *If  $\text{First} \geq \text{Last}$  and  $Z_m = \emptyset$ , then  $(\text{First}_\ell, \text{Last}_\ell) = (\text{First}, \text{Last})$  and  $Z_\ell = Z_{\ell+1} \cap Z_c$ .*

**Proof:** Since  $Z_m = \emptyset$ , there is no  $\mathcal{L}_\sigma$ -pair of (m:1)-type in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . If  $\text{First} = \text{Last}$ , there is one  $\mathcal{L}_\sigma$ -pair of (1:1)-type in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . If  $\text{First} > \text{Last}$ , there is no  $\mathcal{L}_\sigma$ -pair of (1:1)-type in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . In both cases,  $(\text{First}_\ell, \text{Last}_\ell) = (\text{First}, \text{Last})$ .

Next, let us consider  $Z_\ell$  when  $\text{First} = \text{Last}$ . Let  $(\sigma, i)$  be the only one  $\mathcal{L}_\sigma$ -pair in  $(\text{First}_{\ell+1}, \text{Last}_{\ell+1})$ . Since  $(\sigma, i)$  is of (1:1)-type, the set of the string numbers in  $SAA[\text{Last}]$  (i.e.,  $Z_c$ ) is the same as the set of the string numbers of the suffixes whose last characters are  $\sigma$  in  $SAA[\text{First}_{\ell+1}..\text{Last}_{\ell+1}]$ . Thus, a suffix  $(j, q)$  in  $SAA[\text{Last}]$  is prefixed by  $\sigma P[\ell+1..p]$  ( $= P[\ell..P]$ ) if and only if  $j \in Z_c$  and  $j \in Z_{\ell+1}$ . Therefore, we get  $Z_\ell = Z_c \cap Z_{\ell+1}$ .  $\square$

Therefore, we can get the following theorem.

**Theorem 1.** *Algorithm 1 finds correctly all the occurrences of a pattern  $P$ .*

#### 2.4. Data structures

Our index consists of the function  $occ$ , the array  $C$ , the bit-vectors  $B_\sigma$ , and a sampled SAA. Furthermore, we store gap information for mutual conversion between positions in an original string  $S^j$  and positions in its transformed string  $\tilde{S}^j$ .

We store the SAA using two kinds of sampling as in [15], the *regular-position sampling* and the *irregular-position sampling*. For the regular-position sampling, we sample  $SAA[i]$  storing every  $d$ -th position in the transformed alignment  $\tilde{Y}$  where  $d$  is a given parameter. Then, we get an  $SAA[i]$  in a sampled SAA by repeating the LF-mapping from  $SAA[i]$  until a sampled entry  $SAA[k]$  is encountered. In order to guarantee that the string

Table 1: The index sizes (in MBytes) where “sampling” means the space for sampling, “gap” means the space for storing gap information, and “core” means the space except for sampling and gap.

Number of sequences		30			100		
Sampling rate		32	128	512	32	128	512
FMA	total	57.5	49.2	47.1	85.5	75.6	73.1
	core	38.2	38.2	38.2	49.7	49.7	49.7
	gap	1.4	1.4	1.4	5.1	5.1	5.1
	sampling	17.9	9.6	7.5	30.7	20.8	18.3
RLCSA	total	390	193	141	1113	417	233
	core	122	122	122	168	168	168
	sampling	268	71	19	945	249	65

numbers in  $SAA[i]$  are the same as the ones in  $SAA[k]$ , we also need the following irregular sampling: an  $SAA[i]$  is sampled when  $L[i]$  has multiple characters or, for any  $\sigma \in \Sigma$ , the pair  $(\sigma, i)$  is of (m:1)-type. Note that such an  $SAA[i]$  has different string numbers from the string number in  $SAA[i']$  where  $i' = LF(\sigma, i)$  for a character  $\sigma \in L[i]$ .

For supporting retrieval operations, we also need a sampled inverse SAA. In the FMA without gaps [15], the regular-position sampling is enough for the inverse SAA. Due to gaps, however, we need also an irregular sampling for the inverse SAA. Suppose that a gap in a transformed string  $\tilde{S}^j$  includes a regular sampling position  $q$ . Then, we cannot sample the position  $q$  in  $\tilde{S}^j$ . Let  $q'$  be the leftmost position such that  $q' > q$  and no gap in  $\tilde{S}^j$  includes  $q'$ . Then, the position  $q'$ , instead of  $q$ , is sampled in  $\tilde{S}^j$ . For example, assuming position 4 is a regular sampling position in Fig. 2, instead of position 4, position 6 is sampled in  $\tilde{S}^4$  since  $\tilde{S}^4[3..5]$  is a gap.

### 3. Experiments

To compare our FM-index of alignment (FMA) with the RLCSA [14], we measured their sizes, pattern search time and retrieval time. Our index was implemented using SDSL (Succinct Data Structure Library [9]) and all experiments were conducted on a computer with Intel Xeon X5672 CPU and 32GB RAM, running the Linux debian 3.2.0-4-amd64 operating system.

The experimental data set is a reference sequence and 99 individual sequences, which are downloaded from the 1000 Genomes Project website. The reference genome is hs37d5 and each individual sequence consists of a pair of BAM and BAI files, where a BAM file contains reads (short segments of length 90-125) of each individual and a BAI file contains the alignment of the reads. Each pair of BAM and BAI files is fed to SAMtools (Sequence Alignment/Map tools) to obtain a VCF file which stores genetic mutations such as substitutions, insertions and deletions relative to the reference genome.

Table 2: Pattern search (location) time (in secs) for 500 queries of length 10.

Number of sequences	30			100		
Sampling rate	32	128	512	32	128	512
FMA	6.40	19.86	48.63	15.13	25.53	37.84
RLCSA	6.94	31.08	177.89	20.04	102.36	622.42

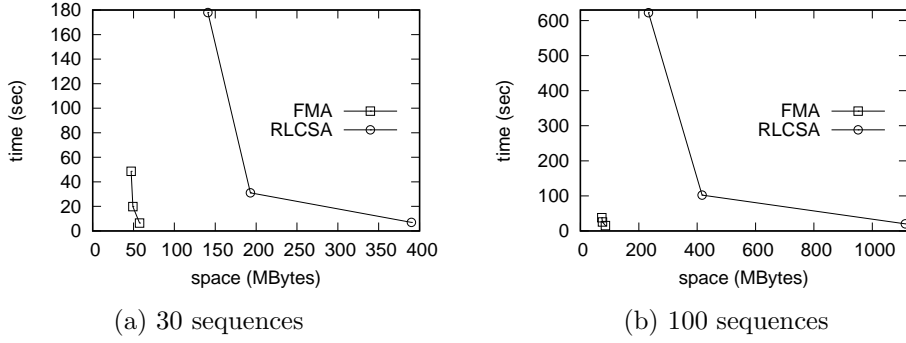


Figure 4: Total index sizes and pattern search (location) times for 500 queries of length 10. Each index was tested with sampling rates  $d = 32, 128$ , and  $512$ .

First, we compared the sizes of our FMA with those of RLCSA. We created these indexes with sampling rates  $d = 32, 128$ , and  $512$  from 30 and 100 sequences (Table 1). The table shows that the FMA requires less than one third of the space of RLCSA in every case. Furthermore, the size of the FMA varies little regardless of the sampling rates because irregular sampling occupies most space for sampling.

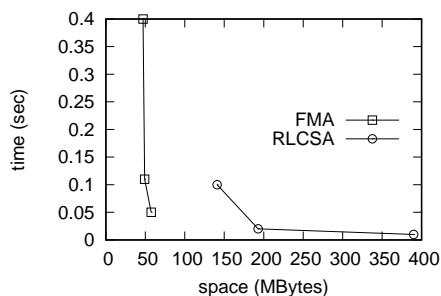
Second, we compared the running time of pattern search (location) reporting all occurrences. We performed the pattern search with patterns of length 10 on the indexes with sampling rates  $d = 32, 128$ , and  $512$  from 30 and 100 sequences (Table 2 and Fig. 4), and FMA is the fastest in all cases. We also compared the retrieval time (Table 3 and Fig. 5). In all cases, RLCSA shows the best performance in retrieval time.

#### 4. Concluding Remarks

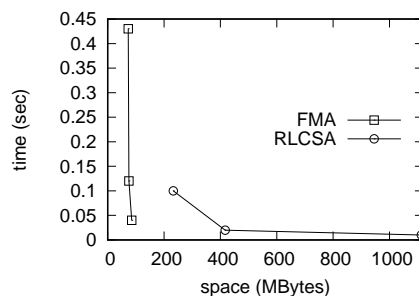
We have proposed the FM-index of alignment with gaps, a realistic index for similar strings, which allows gaps in their alignment. For this, we have designed a new version of suffix array of alignment by using alignment transformation and a new definition of the alignment-suffix. The new SAA enabled us to support the LF-mapping and backward search regardless of gap existence in alignments. Experimental results showed that our index is more space-efficient than RLCSA and it is faster than RLCSA in pattern search even though its retrieval time is slower than that of RLCSA. It remains as future work to do extensive experiments and analysis on various real-world data.

Table 3: Retrieval time (in secs) for 500 queries of length 10.

Number of sequences	30			100		
Sampling rate	32	128	512	32	128	512
FMA	0.05	0.11	0.40	0.04	0.12	0.43
RLCSA	0.01	0.02	0.10	0.01	0.02	0.10



(a) 30 sequences



(b) 100 sequences

Figure 5: Total index sizes and retrieval times for 500 queries of length 10. Each index was tested with sampling rates  $d = 32, 128$ , and  $512$ .

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