

Succincter Text Indexing with Wildcards

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Abstract. We study the problem of indexing text with wildcard positions, motivated by the challenge of aligning sequencing data to large genomes that contain millions of single nucleotide polymorphisms (SNPs)—positions known to differ between individuals. SNPs modeled as wildcards can lead to more informed and biologically relevant alignments. We improve the space complexity of previous approaches by giving a succinct index requiring $(2 + o(1))n \log \sigma + O(n) + O(d \log n) + O(k \log k)$ bits for a text of length n over an alphabet of size σ containing d groups of k wildcards. A key to the space reduction is a result we give showing how any compressed suffix array can be supplemented with auxiliary data structures occupying $O(n) + O(d \log \frac{n}{d})$ bits to also support efficient dictionary matching queries. The query algorithm for our wildcard index is faster than previous approaches using reasonable working space. More importantly our new algorithm greatly reduces the query working space to $O(dm + m \log n)$ bits. We note that compared to previous results this reduces the working space by two orders of magnitude when aligning short read data to the Human genome.

1 Introduction

The study of strings, their properties, and associated algorithms has played a key role in advancing our understanding of problems in areas such as compression, text mining, information retrieval, and pattern matching, amongst numerous others. A most basic and widely studied question in stringology asks: given a string T (the text) does it contain a string P (the pattern) as a substring? It is well known that this problem can be solved in time proportional to the lengths of both strings [10]. However, it is often the case that we wish to repeat this question for many different pattern strings and a fixed text T of length n over an alphabet of size σ . The idea is to create a full-text index for T so that repeated queries can be answered in time proportional to the length of P alone. It was first shown by Weiner [18] in 1973 that the suffix tree data structure could be built in linear time for exactly this purpose. The ensuing years have seen the versatility of the suffix tree as it has been demonstrated to solve numerous other related problems.

While suffix trees use $O(n)$ words of space in theory, this does not translate to a space efficient data structure in practice. For this reason, Manber and Myers [12] proposed the suffix array data structure (see Figure 1). Though a great practical improvement over suffix trees, the $\Omega(n \log n)$ bit space requirement is often prohibitive for larger texts. Building in part on the pioneering work of Jacobson [9] into succinct data structures, two seminal papers helped usher in the study of so-called succinct full-text indexes. Grossi and Vitter [7] proposed a compressed suffix array that occupies $O(n \log \sigma)$ bits; the same space required to represent the original string T . Soon after, Ferragina and Manzini [5] proposed the FM-index, a type of compressed suffix array that can be inferred from the Burrows-Wheeler transform of the text and some auxiliary structures, leading to a space occupancy proportional to $nH_k(T)$ bits, where $H_k(T)$ denotes the k^{th} order empirical entropy of T . These and subsequent results have made it possible to efficiently answer the substring question on texts as large, or larger, than the Human genome.

We are interested in designing a succinct index to answer a generalized version of the substring question where the text T contains k wildcard positions that can match any character of a pattern. Our motivation arises in the context of aligning short read data, produced by second generation sequencing technology. Typically short reads are aligned against a so-called reference genome; however, the quantity of positions known to differ between individuals due to single

nucleotide polymorphisms (SNPs) numbers in the millions [6]. Modeling SNPs as wildcards would yield more informed, and by extension, more accurate alignment of short reads.

Cole, Gottlieb & Lewenstein [4] were one of the first to study the problem of indexing text sequences containing wildcards and proposed an index using $O(n \log^k n)$ words of space capable of answering queries in $O(m + \log^k n \log \log n + occ)$ time. This result was later improved by Lam *et al.*, [11] resulting in space usage of only $O(n)$ words and a query time no longer exponential in k . A key idea in their work was to build a type of dictionary of the text segments of $T = T_1 \phi^{k_1} T_2 \phi^{k_2} \dots \phi^{k_d} T_{d+1}$ where each text segment T_i contains no wildcards and ϕ^{k_i} denotes the i^{th} wildcard group of size $k_i \geq 1$, for $1 \leq i \leq d \leq k$. The query time includes the term $\gamma = \sum_{i,j} \text{prefix}(P[i..|P|], T_j)$ where $\text{prefix}(P[i..|P|], T_j) = 1$ if T_j is a prefix of $P[i..|P|]$ and 0 otherwise. The authors also give a more detailed bound on γ based on prefix complexity.

Despite this improvement, $O(n)$ words of space is prohibitive for texts as large as the Human genome. Support for dictionary matching of text segments was also crucial in the approach of Tam *et al.*, [17] who proposed the first, and to our knowledge only, succinct index. They designed a dictionary structure using $(2 + o(1))n \log \sigma$ bits, based on a compressed suffix array, which therefore occupies most of the space required by their overall index. Very recently, Belazzougui [1] proposed a succincter dictionary based on the Aho-Corasick automaton having optimal query time. The compressed space occupancy was further improved by a slight modification given by Hon *et al.*, [8]. While these results are impressive, the wildcard matching problem benefits from an index that can report the text segments contained in P (dictionary problem), as well as the text segments which are prefixed by P and also fully contain P . To draw a distinction, we will refer to this latter type as a *full-text dictionary*. In our first main contribution we show how a full-text dictionary can be built on top of any compressed suffix array using an additional $O(n) + O(d \log \frac{n}{d})$ bits of space, and in turn how it can be used to provide a succincter index for texts containing wildcards. We note that our dictionary does not require any modification of the original string T .

In our view, the main challenge that must be overcome for successful wildcard matching is a reduction of the query working space. The fastest solution of Tam *et al.*, [17], matches our query time, if modified to use the same orthogonal range query structure we use, but requires a query working space of $O(n \log d + m \log n)$ bits. Acknowledging that the first term is impractical for large texts, they give a slower solution that reduces the working space to be proportional to the index itself. This makes the solution feasible, but constraining considering the fact that p parallel queries necessarily increases the working space by a factor of p . In our second main contribution we give an algorithm that reduces the query working complexity significantly to $O(dm + m \log n)$ bits. For our motivating problem, alignment of short reads (32-64 bases) to the Human genome (3 billion bases with 1-2 million SNPs), this reduces the working space by two orders of magnitude from gigabytes to tens of megabytes. Our result for indexing text with wildcards is summarized and compared with existing results in Table 1.

2 Preliminaries

Let $T[1, n]$ be a string over a finite alphabet Σ of size σ . We denote its j^{th} character by $T[j]$ and a substring from the i^{th} to the j^{th} position by $T[i..j]$. We assume that an end-of-text sentinel character $\$ \notin \Sigma$ has been appended to T ($T[n] = \$$) and $\$$ is lexicographically smaller than any character in Σ . For any substring X we use $|X|$ to denote its length and \overline{X} to denote its reverse sequence. The suffix array SA of T is a permutation of the integers $[1, n]$ giving the increasing lexicographical order of the suffixes of T . Conceptually SA can be thought of as a matrix of all suffixes of T that have been sorted lexicographically and where $\text{SA}[i] = j$ means that the i^{th} lexicographically smallest suffix of T begins position j .

A string X has a suffix array (SA) range $[a, b]$ with respect to SA if $a - 1$ ($n - b$) suffixes of T are lexicographically smaller (larger) than X . If $a > b$ the range is said to be empty and X does not exist as a substring of T ; otherwise, X occurs as a prefix of the $b - a + 1$ suffixes

Index Space	Query Time	Query Working Space
$O(n \log^k n)$ words	$O(m + \log^k n \log \log n + occ)$	- [4]
$O(n)$ words	$O(m \log n + \gamma + occ)$	$O(n)$ words [11]
$(3 + o(1))n \log \sigma$ + $O(d \log n)$ bits	$O\left(m \left(\log \sigma + \min\left(m, \hat{d}\right) \log d\right) + occ_1 \log n + occ_2 \log d + \gamma\right)$	$O(n \log d + m \log n)$ bits [17]
$(3 + o(1))n \log \sigma$ + $O(d \log n)$ bits	$O\left(m \left(\log \sigma + \min\left(m, \hat{d}\right) \log d\right) + occ_1 \log n + occ_2 \log d + \gamma \log_\sigma d\right)$	$O(n \log \sigma + m \log n)$ bits [17]
$(2 + o(1))n \log \sigma + O(n)$ + $O(d \log n) + O(k \log k)$ bits	$O\left(m \left(\log \sigma + \min\left(m, \hat{d}\right) \frac{\log k}{\log \log k}\right) + occ_1 \log n + occ_2 \frac{\log k}{\log \log k} + \gamma\right)$	$O(dm + m \log n)$ bits †

Table 1. A comparison of text indexes supporting wildcard characters. k, d, \hat{d} is the # of wildcards, wildcard groups, and distinct wildcard group lengths, respectively; occ_1, occ_2, occ is the # of Type 1, Type 2, and overall occurrences, respectively; $\gamma = \sum_{i,j} \text{prefix}(P[i..|P|], T_j)$, † = our result

of T denoted by its range. The SA range for X can be found in a compressed suffix array by backwards search using the LF-mapping which relates SA to T^{BWT} , the Burrows-Wheeler transform of T . T^{BWT} is also a string of length n where $T^{\text{BWT}}[i] = T[\text{SA}[i] - 1]$, if $\text{SA}[i] \neq 1$, and $T^{\text{BWT}}[i] = \$$ otherwise. See Figure 1 for an example. For details of backwards search, the LF-mapping, existing implementations, and related topics we refer the reader to the excellent review by Navarro and Mäkinen [14]. In this work, we assume the availability of a compressed suffix array meeting the following space and time requirements, of which there are many (*c.f.* [14]).

Lemma 1. *A compressed suffix array SA for T can be represented in $(1 + o(1))n \log \sigma$ bits of space, such that the suffix array range of every suffix of a string X can be computed in $O(|X| \log \sigma)$ time, and each match of X in T can be reported in an additional $O(\log n)$ time.*

In our dictionary construction, we also make use of the following well known data structures.

Lemma 2 (Raman *et al.*, [16]). *A bit vector B of length n containing d 1 bits can be represented in $d \log \frac{n}{d} + O(d + n \frac{\log \log n}{\log n})$ bits to support the operations $\text{rank}_1(B, i)$ giving the number of 1 bits appearing in $B[1..i]$ and $\text{select}_1(B, i)$ giving the position of the i^{th} 1 in B in $O(1)$ time.*

Lemma 3 (Grossi & Vitter [7]). *An array L of d integers where $\sum_{i=1}^d L[i] = n$ can be represented in $d(\lceil \log(n/d) \rceil + 2 + o(1))$ bits to support $O(1)$ time access to any element.*

Lemma 4 (Munro & Raman [13]). *A sequence BP of d balanced parentheses can be represented in $(2 + o(1))d$ bits of space to support the following operations in $O(1)$ time: $\text{rank}_\lrcorner(\text{BP}, i)$, $\text{select}_\lrcorner(\text{BP}, i)$, and similarly for right parentheses, as well as:*

- $\text{findclose}(\text{BP}, l)$: index of matching right parenthesis for left parenthesis at position l
- $\text{enclose}(\text{BP}, i)$: indexes (l, r) of closest matching pair to enclose $(i, \text{findclose}(\text{BP}, i))$ if such a pair exists and returns an undefined interval in BP otherwise

The matching statistics for a string X with respect to SA is an array ms of tuples such that $ms[i] = (q, [a, b])$ states that the longest prefix of $X[i..|X|]$ that matches anywhere in T has length q and suffix array range $[a, b]$. Very recently Ohlebusch *et al.*, [15] showed matching statistics can be efficiently computed with backward search if SA is *enhanced* with auxiliary data structures using $O(n)$ bits to represent so-called longest common prefix intervals (*c.f.* [15]). We leverage this result in the design of our succinct full-text dictionary and its search algorithm.

Lemma 5 (Ohlebusch *et al.*, [15]). *The matching statistics of a pattern X with respect to text T over an alphabet of size σ can be computed in $O(|X| \log \sigma)$ time given a compressed enhanced suffix array of T .*

Finally, our wildcard matching algorithm makes use of an orthogonal range query data structure.

Lemma 6 (Bose *et al.*, [2]). *A set N of points from universe $M = [1..k] \times [1..k]$, where $k = |N|$, can be represented in $(1 + o(1))k \log k$ bits to support orthogonal range reporting in $O(\text{occ} \frac{\log k}{\log \log k})$ time, where occ is the size of the output.*

3 A succinct full-text dictionary

In the dictionary problem we are required to index a set of d text segments¹ $\mathcal{D} = \{T_1, T_2, \dots, T_d\}$ so that we can efficiently match in any input string P all occurrences of text segments belonging to \mathcal{D} . We present a succinct *full-text dictionary* index that is also capable of efficiently identifying all text segments that contain P as a prefix, or more generally as a substring. We demonstrate the use of this additional functionality in our solution for wildcard matching.

3.1 A compressed suffix array representation of text segments

Let $T = \phi T_1 \phi T_2 \phi T_3 \phi \dots \phi T_d \$$ be the concatenation of all d text segments, each prefixed by the character ϕ , followed by the traditional end-of-text sentinel $\$$, having total length n . Note that n is necessarily larger than the total number of character in the dictionary. We define ϕ to be lexicographically smaller than any $c \in \Sigma$ and $\$$ to be lexicographically smaller than ϕ . We first build SA, the compressed suffix array for T . Consider any text segment $T_j \in \mathcal{D}$. There will be a contiguous range $[c, d]$ of suffixes in SA that are prefixed by the string T_j . Lemma 7 summarizes how we can use the SA range of T_j and its length to determine if it is prefix of a given text P (and vice versa).

Lemma 7. *Let SA be the compressed suffix array for T and let $[a, b]$ and $[c, d]$ be the non-empty suffix array ranges in SA for a string P and a text segment T_j respectively. Then T_j is a prefix of P if and only if $c \leq a \leq b \leq d$ and $|P| \geq |T_j|$. Similarly, P is a prefix of T_j if and only if $a \leq c \leq d \leq b$.*

3.2 Storing text segment lengths

For Lemma 7 to apply, we must know both the SA range of a given text segment and also its length. By Lemma 3 we can store the lengths of all d text segments in a compressed integer array L using $d(\lceil \log(n/d) \rceil + 2 + o(1))$ bits ensuring constant time access. We store the lengths in L relative to the lexicographical order of text segments.

3.3 The text segment interval tree

The SA range of one text segment T_i will enclose the SA range of another T_j if T_i is a prefix of T_j . For instance, in the example of Figure 1 the text segment **aca** has SA range $[15, 15]$ and is enclosed by the SA range of the text segment **ac** ($[14, 16]$) and by the text segment **a** ($[8, 16]$). In general, it is also possible that many text segments begin at the same position, provided that they are different occurrences of the same string (*e.g.*, **aa**). This is by design since each text segment is followed by a character not found in Σ (either ϕ or $\$$). However, our construction requires us to distinguish between different occurrences of the same text segment string and we therefore introduce the concept of *text segment intervals*. When $t > 1$ text segments in the dictionary share a common SA range we say that the text segment interval of occurrence a encloses the text segment interval of occurrence b , $1 \leq a \neq b \leq t$, if the suffix of T beginning with occurrence a is lexicographically smaller than the suffix beginning with occurrence b . In this way we are able to define a total order on all d text segment intervals based on their relative

¹ To remain consistent with the section that follows we refer to dictionary entries (patterns) as text segments.

	T^{BWT}	SA	B	i	
	\$	c	21	0	1
	$\phi a \phi a a \phi c a c c \phi a c \$$	a	8	0	2
	$\phi a a \phi a c a \phi a \phi a a \phi c a c c \phi a c \$$	\$	1	0	3
	$\phi a a \phi c a c c \phi a c \$$	a	10	0	4
	$\phi a c \$$	c	18	0	5
	$\phi a c a \phi a \phi a a \phi c a c c \phi a c \$$	a	4	0	6
	$\phi c a c c \phi a c \$$	a	13	0	7
	$a \phi a \phi a a \phi c a c c \phi a c \$$	c	7	1	8
	$a \phi a a \phi c a c c \phi a c \$$	ϕ	9	0	9
	$a \phi a c a \phi a \phi a a \phi c a c c \phi a c \$$	a	3	0	10
	$a \phi c a c c \phi a c \$$	a	12	0	11
(1, a)	$a a \phi a c a \phi a \phi a a \phi c a c c \phi a c \$$	ϕ	2	1	12
(2, aa)	$a a \phi c a c c \phi a c \$$	ϕ	11	0	13
(3, aa)	$a c \$$	ϕ	19	1	14
(4, ac)	$a c a \phi a \phi a a \phi c a c c \phi a c \$$	ϕ	5	1	15
(5, aca)	$a c c \phi a c \$$	c	15	1	16
	$c \$$	a	20	1	17
	$c \phi a c \$$	c	17	0	18
	$c a \phi a \phi a a \phi c a c c \phi a c \$$	a	6	0	19
(6, cacc)	$c a c c \phi a c \$$	ϕ	14	1	20
	$c c \phi a c \$$	a	16	1	21

BP	(())	(())	()		
L	1	2	2	2	3	4						
R	0	0	2	2	3	5	5	6				
i	1	2	3	4	5	6	7	8	9	10	11	12

Fig. 1. A succinct full-text dictionary for the set of text segments $\{aa, aca, a, aa, cacc, ac\}$. Shown are the sorted suffixes of the string $T = \phi a a \phi a c a \phi a \phi a a \phi c a c c \phi a c \$$ representing the text segments. Text segment intervals are demarcated on the left and labeled by their lexicographical order (lex id) and the text segment they represent.

lexicographical order in SA. We assign *lex ids*, a unique identifier for each text segment, based on this lexicographical order. Consider again the example in Figure 1. The text segment **aa** occurs as a prefix of $T[2..n]$ and $T[11..n]$. Since the suffix $T[2..n]$ is lexicographically smaller than $T[10..n]$, we say that the occurrence prefixing $T[2..n]$ encloses the other. Consequently, the text segment prefixing $T[2..n]$ ($T[11..n]$) is assigned lex id 2 (3). We will refer to text segments or text segment intervals interchangeably.

In general the text segment intervals form a set of nested, non-crossing intervals (an interval tree) and can be represented by a sequence BP of d balanced parentheses; one pair for each text segment (see Figure 1). Conceptually, if we can identify the text segment interval having the largest lex id that is a prefix of P , referred to as the *smallest enclosing text segment interval* of P , then we can immediately conclude that P is also prefixed by all intervals which enclose it.

Lemma 8. *Given the index pair (l, r) in BP corresponding to the smallest enclosing text segment interval for a string P the occ number of text segments that are prefixes of P can be counted in $O(1)$ time and reported in an additional $O(occ)$ time.*

3.4 Finding the smallest enclosing text segment interval

We now describe how the smallest enclosing text segment interval can be determined given any non-empty SA range $[a, b]$ in SA for P . We wish to determine the pair (l, r) of indexes for the left and right parentheses in BP corresponding to this interval (or an undefined index range if P is not prefixed by any text segment). Unfortunately, we cannot directly infer where text segment intervals begin and end based on T^{BWT} alone. Therefore, we make use of a bit vector B of length n and set $B[k] = 1$ if and only if one or more text segment intervals begin at position k , or end at position $k - 1$. For the range $[a, b]$, end cases occur when $B[k] = 0$, $a < k \leq n$ (all text segment intervals end before position a) or when $B[k] = 0$, $1 \leq k \leq a$ (all text segment intervals begin after position a). Suppose otherwise and let $c = \arg \max_{1 \leq j \leq a} \{B[j] = 1\}$ and $d = \arg \min_{a < j \leq n} \{B[j] = 1\}$. Note that position c marks the largest position (up to a) when one or more text segment intervals begin or end (at $c - 1$). Our algorithm considers two main cases: either $B[c]$ marks the beginning of one or more intervals, or it only marks the end of intervals.

Algorithm 1 Find smallest enclosing text segment interval

Input: a specifies the beginning of the non-empty suffix array interval for string P

Output: l, r where l (r) is the index of the left (right) parenthesis in BP corresponding to the smallest enclosing text segment interval of P if it exists, and an undefined interval otherwise

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1:  $c \leftarrow \text{select}_1(\text{B}, \text{rank}_1(\text{B}, a))$ 
2:  $d \leftarrow \text{select}_1(\text{B}, \text{rank}_1(\text{B}, a) + 1)$ 
3: if  $c$  or  $d$  is undefined then                                     // handle end cases
4:   return an undefined interval
5:  $\text{lexid} \leftarrow \text{rank}_\phi(T^{\text{BWT}}, d - 1)$ 
6: if  $\text{lexid} > \text{rank}_\phi(T^{\text{BWT}}, c)$  then                               //  $\text{B}[c]$  marks beginning of t.s. interval(s)
7:   if  $L[\text{lexid}] > |P|$  then
8:      $\text{lexid} \leftarrow \text{rank}_\phi(T^{\text{BWT}}, c - 1) + 1$ 
9:      $l \leftarrow \text{select}_\ell(\text{BP}, \text{lexid})$ 
10:     $l, r \leftarrow \text{enclose}(\text{BP}, l)$ 
11:   else
12:      $l \leftarrow \text{select}_\ell(\text{BP}, \text{lexid})$ 
13:      $r \leftarrow \text{findclose}(\text{BP}, l)$                                      //  $\text{B}[c]$  marks end of t.s. interval(s)
14: else
15:    $r \leftarrow \text{select}_r(\text{BP}, \text{R}[\text{rank}_1(\text{B}, c)])$ 
16:    $l \leftarrow \text{findopen}(\text{BP}, r)$ 
17:    $l, r \leftarrow \text{enclose}(\text{BP}, l)$ 
18: return  $l, r$ 

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Lemma 9. *Given two positions c and d of B , where $c < d$, $\text{B}[c] = \text{B}[d] = 1$ and $\text{B}[k] = 0$, $c < k < d$, then $\text{B}[c]$ marks the beginning of t text segment intervals if and only if $T^{\text{BWT}}[c..d - 1]$ contains t occurrences of the character ϕ .*

Using Lemma 9 we are able to distinguish between the two main cases. If $\text{B}[c]$ marks the beginning of one or more text segment intervals, then T_j — the text segment interval with the largest lex id beginning at position c — is the smallest enclosing text segment interval, provided $|T_j| \leq |P|$ (by condition of Lemma 7). If $|T_j| > |P|$, we can determine the largest lex id beginning at position c by simply counting the occurrences of the character ϕ prior to position d in T^{BWT} . Conveniently and by construction, this corresponds to the rank of the left parenthesis denoting T_j in BP . It is worth noting that when $|T_j| > |P|$ special care is required to find the smallest enclosing text segment interval in worst case constant time. Details are given in the proof of Lemma 10, but the idea is to find the enclosing interval (if any) of the text segment interval having the *smallest* lex id beginning at position c .

On the other hand, if $\text{B}[c]$ only marks the end of one or more text segment intervals, we can instead identify the right index for $T_{j'}$ — the last text segment interval (smallest lex id) to end at position $c - 1$. The smallest enclosing text segment interval, if any, is therefore the one enclosing $T_{j'}$. Unfortunately, in this case we cannot infer how many intervals close prior to position c directly from T^{BWT} . For this reason, we will employ another compressed integer array R to record the count of intervals that close prior to position k , for all $\text{B}[k] = 1$. We determine the appropriate index for R by simply counting the number of 1's up to position c in B . The corresponding entry in R gives us the rank of the right parenthesis for the last interval to close prior to position c , from which we can find the enclosing interval (if any). The entire procedure, including end cases, is summarized in Algorithm 1 and shown correct in Lemma 10.

Lemma 10. *Let SA be the compressed suffix array for T and let $[a, b]$ be the non-empty suffix array range in SA for a string P . In $O(1)$ time, Algorithm 1 either correctly identifies the indexes in BP corresponding to the smallest enclosing text segment interval of P if one exists, or it returns an undefined interval when it does not.*

3.5 The overall dictionary and its full-text capabilities

We have shown how all text segments occurring as a prefix of a string P having a non-empty SA range in SA can be reported efficiently. By enhancing SA with lcp-interval information using $O(n)$ bits, we can find the matching statistics for P in order to repeat the previous procedure for $1 \leq i \leq |P|$ (see Lemma 5). Importantly for our results on wildcard matching, we note that with a very minor modification, this same construction works when text segments are separated by more than one ϕ character and also when the first text segment is not preceded by a ϕ character. Note that the text segment interval tree can be built in a similar manner as an lcp-interval tree. Details are left for the full version. We have our first main result.

Theorem 1. *Given a set of d text segments over an alphabet of size σ we can construct a succinct full-text dictionary, based on an enhanced compressed suffix array, using at most $(1 + o(1))n \log \sigma + O(n) + O(d \log \frac{n}{d})$ bits where n is the length of T , the text representation of the dictionary including ϕ characters, such that the γ text segments contained in a string P can be counted in $O(|P| \log \sigma)$ time and reported in an additional $O(\gamma)$ time. Furthermore, all text segments prefixed by P can be reported in $O(|P| \log \sigma + occ)$ time, and all locations in T where P occurs as a substring can be reported in $O(|P| \log \sigma + occ \log n)$ time.*

4 Matching wildcards in succinct texts

Let T be a string over an alphabet $\Sigma \cup \{\phi\}$ of size σ where $\phi \notin \Sigma$ and $T[i] = \phi$ if and only if position i is a wildcard position in T . In particular, we denote the structure of the input string as $T = T_1 \phi^{k_1} T_2 \phi^{k_2} \dots \phi^{k_d} T_{d+1}$ where each text segment T_i contains no wildcards and ϕ^{k_i} denotes the i^{th} wildcard group of size $k_i \geq 1$, for $1 \leq i \leq d$. Our goal is to create an index for the purpose of identifying all the locations in T that exactly match any query pattern P , modulo wildcard positions. Similar to previous approaches [11,17], we classify the match into one of three cases: X contains no wildcard group (Type 1), X contains exactly one wildcard group (Type 2), and X contains more than one wildcard group (Type 3).

4.1 Overall design of the index

We first build the succinct full-text dictionary of Section 3. By design, the dictionary reports the match of a text segment T_j based on its lexicographical order (its lex id) relative to other text segments; however, in the wildcard problem we are required to report the match based on T_j 's position in T . Therefore, we store a permutation Π mapping the lex ids of text segments to their relative position order in T . For instance, if T_j has lex id k , then $\Pi[k] = j$. We find it convenient to store the following information for each text segment, in auxiliary arrays, indexed by this relative position order: length, SA range in SA (referenced as RSA), beginning position in T , and the size of the preceding wildcard group. Note that array L of the dictionary construction can be adapted to store lengths in this relative order with the use of Π . We also construct a compressed suffix array \overline{SA} for \overline{T} , the reverse of T , and store the SA range of each \overline{T}_j with respect to \overline{SA} (referenced as \overline{RSA}). Note that \overline{SA} does not need to support location reporting. We use simple arrays to store SA ranges resulting in $O(d \log n)$ bits combined space usage to store auxiliary information supporting constant time access. To support Type 2 matching we employ a range query data structure occupying $(1 + o(1))k \log k$ bits (see next section).

Lemma 11. *Given a text T of length n containing d groups of k wildcards the combined space required of the above indexes is $(2 + o(1))n \log \sigma + O(n) + O(d \log n) + O(k \log k)$ bits.*

All three matching types make use of the matching statistics of P with respect to SA. Types 2 and 3 matching also make use of the SA ranges of \overline{P} with respect to \overline{SA} . Both can be computed in $O(m \log \sigma)$ time (by Lemmas 1 and 5) and require $O(m \log n)$ bits to store. We incorporate these times and working space into the results for each type. Type 1 matching is handled by the application of Lemma 1.

4.2 Type 2 matching

A Type 2 match occurs when the alignment of P to T contains exactly (a portion of) one wildcard group. Specifically, we seek a pair of neighbouring text segments T_j and T_{j+1} , separated by a wildcard group of size k_j , where $P[i..|P|]$ aligns to the first $|P| - i + 1$ characters of T_{j+1} — referred to as the *suffix match* (of P) — and $P[1..i - 1 - k_j]$ aligns to the last $i - 1 - k_j$ characters of T_j — referred to as the *prefix match*. Let α_j (ω_j) be the the first (last) ϕ character of the j^{th} wildcard group in T . End cases occur when the match begins or ends in $T[\alpha'_j.. \omega'_j]$, where α'_j (ω'_j) is the position of α_j (ω_j) in T . For now, suppose this is not the case. For a fixed suffix $P[i..|P|]$ and wildcard group length k_j our strategy will be to (i) find all potential suffix matches, (ii) record the lex id of the candidate text segments, (iii) find all potential prefix matches, and (iv) determine which candidate prefix matches are compatible with a lex id recorded in step (ii).

$$\begin{array}{ccccccc} \cdots & \text{---} & T_j & \text{---} & \phi & \cdots & \phi & \text{---} & T_{j+1} & \text{---} & \cdots \\ & & & & \uparrow & & \uparrow & & & & \\ & & & & \alpha_j & & \omega_j & & & & \end{array}$$

Lemma 12. *Given a non-empty SA range $[a, b]$ in SA for a string X , the lex ids (based on their lexicographical order) of text segments in T that contain X as a prefix will form a contiguous (possibly empty) range $[id_1, id_2]$ that can be reported in $O(1)$ time.*

By Lemma 12, we can identify the range $[id_1, id_2]$ of lex ids corresponding to text segments that $P[i..|P|]$ is a prefix of in constant time using its stored SA range with respect to SA, completing steps (i)-(ii). Determining a range $[id_3, id_4]$ of lex ids corresponding to text segments that $P[1..i - k_j - 1]$ is a suffix of is equivalent to determining all \overline{T}_t that contain $\overline{P}[1..i - k_j - 1]$ as a prefix. Again, using a stored SA range with respect to $\overline{\text{SA}}$ this can be determined in constant time, completing step (iii). Now consider that the lex id with respect to SA of a text segment T_{j+1} is relative to the rank of ω_j in T^{BWT} , the character which precedes it. Similarly, the relative rank of α_j in $\overline{T}^{\text{BWT}}$ determines the lex id of \overline{T}_j , but in this case relative to \overline{T} . We make use of a permutation H to relate these lex ids (α and ω values). Specifically, we set $H[\alpha_j] = \omega_j$, for $1 \leq j \leq k$. Therefore, we need to determine the entries in $H[id_3..id_4]$ that have a value in the range $[id_1, id_2]$. This is an orthogonal range query and by Lemma 6, H can be represented in $(1 + o(1))k \log k$ bits to report all *occ* matches in $O(\text{occ} \frac{\log k}{\log \log k})$ time. Once a lex id ω_j has been verified, a match position can be reported in $O(1)$ time as the location of T_{j+1} with respect to T is known in addition to the length of the prefix match. This completes step (iv).

In general, we can repeat the above procedure for every combination of suffix length and wildcard group length bound by m . However, as pointed out by Tam *et al.*, [17] the number of distinct wildcard group sizes \hat{d} is often a small constant, particularly in genomic sequences. We therefore only consider at most \hat{d} lengths, provided they are not larger than m .

Now, consider the case when $P[i..|P|]$ aligns to a prefix of a wildcard group. To contain $P[i..|P|]$ as a prefix, the wildcard group must have a length $l \geq |P| - i + 1$. Let a be the first entry in SA denoting a suffix of T prefixed by at least $l - 1$ ϕ characters and let b be the last entry prefixed by any ϕ character. Then, similar to Lemma 12, $T^{\text{BWT}}[a..b]$ will contain a range $[id_1, id_2]$ giving ranks of ϕ characters in that interval. Some sub-sequence of $[id_1, id_2]$ will correspond to ω wildcards that begin groups having length l or longer. Therefore, Type 2 matches can be determined by reporting entries in $H[id_3..id_4]$ having a value in $[id_1, id_2]$, where $[id_3, id_4]$ is defined as before. The case when a prefix of P aligns as a suffix of a wildcard group can be handled similarly. Note that the SA ranges of the at most m wildcard group lengths we are interested in can be determined in $O(m \log \sigma)$ time and stored in $O(m \log n)$ bits.

Lemma 13. *All Type 2 matches can be reported using $O(m \log n)$ bits of working space in $O(m(\log \sigma + \min(m, \hat{d}) \frac{\log k}{\log \log k}) + \text{occ}_2 \frac{\log k}{\log \log k})$ time.*

Algorithm 2 Report Type 3 matches

Input: a string P of length m , its matching statistics w.r.t. SA , SA ranges for all suffixes of \overline{P} w.r.t. $\overline{\text{SA}}$

Output: positions in T matching P , modulo wildcard positions

```

1: for  $i = 1$  to  $m$  do
2:   let  $(q, [a, b])$  be the matching statistics for  $P[i..m]$ 
3:   use Algorithm 1 to find indexes  $(l, r)$  in BP denoting smallest enclosing text segment interval for SA range  $[a, b]$ 
4:   while  $(l, r)$  is a defined interval in BP do
5:      $lexid \leftarrow \text{rank}_l(\text{BP}, l)$ 
6:      $j \leftarrow \Pi[lexid]$ 
7:      $[a_p, b_p], [a_s, b_s] \leftarrow$  SA range of  $\overline{P[1..i-1-k_{j-1}]}$  w.r.t  $\overline{\text{SA}}$ , SA range of  $P[i+l_j+k_j..m]$  w.r.t  $\text{SA}$ 
8:      $[c_s, d_s], [c_p, d_p] \leftarrow \text{RSA}[j-1], \overline{\text{RSA}}[j+1]$ 
9:     if  $i \leq l_{j-1} + k_{j-1}$  then // Case 1:  $P$  does not contain  $T_{j-1}$ 
10:      if  $k_{j-1} \geq i-1$  or  $[a_p, b_p]$  encloses  $[c_p, d_p]$  then // Case 1: prefix condition satisfied
11:        if  $m-i+1 < l_j + k_j + l_{j+1} - 1$  then // Case 1a:  $P$  does not contain  $T_{j+1}$ 
12:          if  $m-i \leq l_j + k_j$  or  $[a_s, b_s]$  encloses  $[c_s, d_s]$  then // Case 1a: suffix condition satisfied
13:            print match at position  $x_j - i + 1$ 
14:          else // Case 1b:  $P$  must contain  $T_{j+1}$ 
15:            set  $(i + l_j + k_j)^{\text{th}}$  bit of  $\text{W}[j+1]$  to 1
16:        else // Case 2:  $P$  must contain  $T_{j-1}$ 
17:          if  $i^{\text{th}}$  bit of  $\text{W}[j]$  is set to 1 then // Case 2: prefix condition is satisfied
18:            if  $m-i+1 < l_j + k_j + l_{j+1} - 1$  then // Case 2a:  $P$  does not contain  $T_{j+1}$ 
19:              if  $m-i \leq l_j + k_j$  or  $[a_s, b_s]$  encloses  $[c_s, d_s]$  then // Case 2a: suffix condition satisfied
20:                print match at position  $x_j - i + 1$ 
21:            else // Case 2b:  $P$  must contain  $T_{j+1}$ 
22:              set  $(i + l_j + k_j)^{\text{th}}$  bit of  $\text{W}[j+1]$  to 1
23:           $(l, r) \leftarrow \text{enclose}(\text{BP}, l)$ 

```

Notation: x_j, l_j, k_j denotes the position, length and wildcard group length (which follows) the text segment T_j

4.3 Type 3 matching

Type 3 matches contain at least (portions of) two wildcard groups and therefore must fully contain at least one text segment. The general idea in previous approaches and in this paper is to consider this case as an extension of the dictionary matching problem: text segments contained within P are candidate positions, but we must verify if they can be extended to a full match of P . However, we execute this idea in an altogether novel manner that greatly reduces the working space over existing approaches. The complete details of our approach are given in Algorithm 2. We now highlight the main idea and give the intuition behind the correctness but note that a formal proof is given in the appendix.

First, suppose that text segment T_j matches P starting at position i . Consider the conditions that must be satisfied to confirm that this match can be extended to a complete match of P in T . We must verify that (i) $P[1..i-1]$ can be matched to the text preceding T_j in T — referred to as the *prefix condition* — and (ii) $P[i+|T_j|..|P|]$ can be matched to the text following T_j in T — referred to as the *suffix condition*. If both conditions are verified, we can report that P matches T at position $x_j - i + 1$, where x_j is the start position of T_j in T .

$$\begin{array}{ccccccc}
 \cdots \phi & \text{---} & T_{j-1} & \text{---} & \phi \cdots \phi & \text{---} & T_j & \text{---} & \phi \cdots \phi & \text{---} & T_{j+1} & \text{---} & \phi \cdots \\
 & & \uparrow & & & & \uparrow & & & & \uparrow & & \\
 & & x_{j-1} & & & & x_j & & & & x_{j+1} & &
 \end{array}$$

For working space, we make use of an array W containing $d+1$ entries (one for each text segment) of m bits, with all entries set to zero using the constant time initialization technique [3]. During the course of the algorithm the i^{th} bit of $\text{W}[j]$ is set to 1 if the prefix condition is true for $P[1..i-1]$ with respect to T_j . There are exactly m stages of the algorithm ($i = 1, \dots, m$) corresponding to the suffixes of P . In a given stage i we consider each text segment T_j found to be a prefix of the i^{th} suffix of P . To verify the prefix and suffix conditions for T_j we first

consider (line 9 of Algorithm 2): will $P[1..i-1]$ need to fully contain the previous text segment T_{j-1} in order to match in T ? This breaks our algorithm into the two main cases. If not (Case 1), we check the prefix condition by checking whether $P[1..i-1]$ is compatible with the wildcard group to its left and the suffix of T_{j-1} to which it must align (line 10). If the prefix condition is satisfied, we consider (line 11): will $P[i+|T_j|..m]$ need to fully contain the next text segment T_{j+1} in order to match in T ? If not (Case 1a), we check whether the suffix condition is satisfied by checking that $P[i+|T_j|..m]$ is compatible with the wildcard group to its right and the prefix of T_{j+1} to which it must align (line 12). If indeed the suffix condition is satisfied, we output a match (line 13). If yes (Case 1b), we set the $(i+l_j+k_j)^{\text{th}}$ bit of entry $W[j+1]$ to 1, to indicate that a prefix condition holds for $P[1..i+l_j+k_j-1]$ with respect to T_{j+1} (line 15). The key idea here is that we only attempt to verify the suffix condition when T_j would be the last text segment to occur in P (i.e., Case 1a) and if not (Case 1b), we record information in W stating that we currently have a partial match, but for it to remain viable, T_{j+1} should be a prefix of $P[i+l_j+k_j..m]$. Case 2 occurs when P must contain the previous text segment T_{j-1} to satisfy the prefix condition (lines 16–22). Since stages of the algorithm proceed with increasing values of i , then the prefix condition would have been previously checked and, if satisfied, the i^{th} bit of $W[j]$ would be set to 1. The remaining questions are answered as before: the suffix condition is verified if possible, and otherwise successful partial matches are again recorded in W .

Lemma 14. *All Type 3 matches can be reported in $O(m \log \sigma + \gamma)$ time using $O(dm + m \log n)$ bits of working space.*

Combining the results for the 3 types of matching we arrive at our second main result.

Theorem 2. *Given a text T of length n containing d groups of k wildcards all matches of a pattern P of length m can be reported using $O(dm + m \log n)$ bits of working space in $O(m(\log \sigma + \min(m, \hat{d}) \frac{\log k}{\log \log k}) + occ_1 \log n + occ_2 \frac{\log k}{\log \log k} + \gamma)$ time with an index occupying $(2 + o(1))n \log \sigma + O(n) + O(d \log n) + O(k \log k)$ bits of space.*

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A Supporting Proofs

Proof of Lemma 7

Proof. We first consider the case for determining if T_j is a prefix of P . Suppose that T_j is a prefix of P . Then it must be the case that $|T_j| \leq |P|$. By definition $T[\text{SA}[c]..|T|]$ ($T[\text{SA}[d]..|T|]$) is lexicographically smaller (greater) than any other suffix of T prefixed by the string T_j ; thus, $[c, d]$ must enclose $[a, b]$ and we have $c \leq a \leq b \leq d$.

Next consider the case when $c \leq a \leq b \leq d$ and $|T_j| \leq |P|$. Since $[c, d]$ encloses $[a, b]$ they must share a common prefix of length $\min(|P|, |T_j|)$. If $[a, b] = [c, d]$ it could be the case that P is a proper prefix of T_j ; however, since $|P| \geq |T_j|$ then P and T_j must share a common prefix of length at least $|T_j|$. Thus, T_j is a prefix of T .

The other case is symmetric, but it is not necessary to compare the lengths of P and T_j . \square

Proof of Lemma 12

Proof. This follows from the proof of Lemma 7 and by the definition of lex ids since they correspond to ϕ characters (which prefix text segment occurrences only) in T^{BWT} that must necessarily be contained within the SA range for those text segment occurrences. \square

Proof of Lemma 8

Proof. We let I_1 denote the interval in BP specified by (l, r) . If I_1 is an undefined interval then P is not prefixed by any text segment ($occ = 0$) and we are done. Suppose I_1 is defined. This interval is enclosed by another interval $I_2 = (p, q)$ if and only if $p < l$ and $q > r$. Since text segment intervals cannot cross, if I_2 opens before I_1 ($p < l$) it is either the case that I_2 closes before I_1 opens ($q < l$) or I_2 closes after I_1 closes ($q > r$); it is the latter case we are interested in. We count the number of intervals that begin (opening parentheses), up to index l , and subtract the number which also end (closing parentheses), up to index l . The difference is exactly the number of enclosing intervals for I_1 . Specifically, $occ = \text{rank}_{\phi}(\text{BP}, l) - \text{rank}_{\phi}(\text{BP}, l)$ and can be computed in $O(1)$ time.

Reporting the text segment match for interval I_1 consists of outputting a tuple containing $(start, end, lexicid)$. The $lexicid$ is the lexicographical order of the text segment (relative to others) and is determined in $O(1)$ time as $lexicid = \text{rank}_{\phi}(\text{BP}, l)$. Since we report text segments that are prefixes of T , then $start = 1$ and $end = start + L[lexicid] - 1$ (as lengths of text segments are stored in L according to their lex id). After reporting the match for I_1 , we can determine the next enclosing interval by setting $(l, r) = \text{enclose}(\text{BP}, l)$ and repeating the above procedure until all occ occurrences have been reported. \square

Proof of Lemma 9

Proof. Suppose t text segment intervals begin at position c . As previously stated, if two or more text segment intervals begin at the same position then they are different occurrences of the same text segment string ω . By definition of \mathbf{B} , no other text segment interval can begin before position d in SA. If $\mathbf{B}[d]$ marks the beginning of another text segment interval, it must be lexicographically larger than ω and therefore all t occurrences of ω appear before position d . If $\mathbf{B}[d]$ instead marks the end of one or more text segment intervals (at position $d - 1$), it must be for the t occurrences of ω since text segment intervals cannot cross. In either case, all occurrences of the text segment ω must appear in SA in the range $[c..d - 1]$ (possibly in addition to other suffixes of T prefixed by the string ω). Since only text segment instances are prefixed by the character ϕ in T , then $T^{\text{BWT}}[c..d - 1]$ must contain exactly t occurrences of ϕ .

Suppose $T^{\text{BWT}}[c..d - 1]$ contains t occurrences of the character ϕ . Since each text segment occurrence is prefixed by the character ϕ in T , then t suffixes of T in the range $[c..d - 1]$ of SA

are prefixed by text segment occurrences. Each text segment occurrence corresponds to one text segment interval. Text segment intervals only begin in positions k where $B[k] = 1$. Therefore t text segment intervals begin at position c as no other text segment intervals can begin before position d , by definition of B . \square

Proof of Lemma 10 (Algorithm 1 - Find smallest enclosing text segment interval)

Proof. Algorithm 1 begins by identifying the last entry in B up to position a and the first entry after position a equal to 1 denoting the opening or closing of text segment intervals. If either of these are undefined, then a text segment interval cannot enclose $[a, b]$ and an empty interval is returned (lines 3–4).

If $T^{\text{BWT}}[c..d-1]$ contains one or more ϕ characters then by Lemma 9, $B[c]$ marks the beginning of some number of text segment intervals (lines 6–13). Since text segment interval lex ids are based on their lexicographical order in SA , then the lex id of the last text segment interval to open at position c is *lexid*, given by the count of ϕ characters up to position $d - 1$ in T^{BWT} . Let T_k be this text segment interval. By Lemma 7, we must also ensure that $|P| \geq |T_k|$ by checking the text segment length in L (line 7). If P is shorter than T_k (lines 8–10), then it is also shorter than all text segment intervals beginning at position c since they represent the same text segment string. However, it is possible that there exists a text segment interval T_j that is a longest proper prefix of T_k . Note that $|P| > |T_j|$, since it must be lexicographically larger than T_j ; otherwise $B[c]$ would correspond to this interval instead of T_k . If T_j exists, it would enclose the first text segment interval that begins at position c . We can find the lex id for the first text segment interval opening at position c (smallest lex id) similarly to T_k , but instead we count the occurrences of ϕ prior to position c and then add one. The lex id will correspond to the rank of the left parenthesis in BP and the index l is easily determined by a `select` operation. Note that the `enclose` operation will return an undefined interval if T_j does not exist. If instead $|T_k| \leq |P|$ (lines 12–13), we can simply determine the index for the left parenthesis denoting the text segment interval T_k .

Otherwise, $B[c]$ only marks the end of some text segment interval(s) (lines 15–17). In this case, we use the number of occurrences of 1's in B up to position c as an index into the array R which stores the number of text segment intervals that close prior to the position denoted by that entry. This allows us to identify T_k , the last text segment interval to close prior to position a (the one having the smallest lex id). If another text segment interval T_j encloses T_k , then it must be the case that T_j encloses $[a, b]$ and $|T_j| < |P|$, otherwise T_j would also close prior to position a .

At this point, the pair (l, r) either correctly identifies the smallest enclosing text segment interval for the SA range $[a, b]$, or it is an undefined interval if none exists. Overall, a constant number of operations are required and all can be computed in $O(1)$ time. \square

Proof of Lemma 11 (Space analysis of our succinct wildcard index)

Proof. The succinct full-text dictionary requires $(1 + o(1))n \log \sigma + O(n) + O(d \log \frac{n}{d})$ bits by Theorem 1, which in turn is based on a combination of Lemmas 1–4, and the additional $O(n)$ bits required to *enhance* SA with lcp-interval information and to store the LCP array. The wildcard index also requires a suffix array of the reverse of string T which occupies $(1 + o(1))n \log \sigma$ bits by Lemma 1. The most space dominant auxiliary array is used to store suffix array ranges in $O(d \log n)$ bits. The range query data structure requires $O(k \log k)$ bits by Lemma 6. Thus, overall we have a space complexity of $(2 + o(1))n \log \sigma + O(n) + O(d \log n) + O(k \log k)$ bits. \square

Proof of Lemma 14 (Algorithm 2 - Type 3 Matching)

Proof. Recall that the algorithm proceeds in m stages for increasing $i = 1, \dots, m$ for each suffix of P . It is clear in the algorithm description that verification of a match of T_j proceeds by first

ensuring the prefix condition can be satisfied (Case 1: if P does not contain T_{j-1}) or ensuring it was previously satisfied (Case 2: P must contain T_{j-1}), and then verifying the suffix condition in the cases where P does not contain T_{j+1} (Cases 1a, 2a) (and reporting a match when verified), or by instead marking W to signify a partial match, expecting the match to be continued by a match of T_{j+1} at the time step $i + l_j + k_j$ (Cases 1b, 2b). The correctness relies on showing that W is set correctly to confirm the satisfaction of the prefix condition for the next text segment (T_{j+1}) for a future time step. We show correctness by induction on i . Consider the base case ($i = 1$). All candidate text segments T_j fall into Case 1 which (importantly) does not rely on the correctness of previous steps of the algorithm. The prefix condition is trivially true. Thus, if a successful match of $P[1..m]$ to $T[x_j..n]$ will not fully contain T_{j+1} we can simply check if $P[l_j + k_j + 1..m]$ is a prefix of T_{j+1} by Lemma 7. If it is, both conditions have been satisfied and we have a match, otherwise, we record in $W[j + 1]$ that T_{j+1} must appear as a prefix of $P[l_j + k_j + 1..m]$ to form a successful match. Now assume we are in step i and the algorithm is correct up to step $i - 1$. Case 1 is handled as before and does not rely on the correctness of previous steps, so assume we are in Case 2 (P must contain T_{j-1}). Then, if the prefix condition is satisfied the i^{th} bit of $W[j]$ should be set to 1. Since this would have been set at some step $t < i$, and we have assumed the algorithm is correct up to step $i - 1$, then it must be the case that the prefix condition for T_j is satisfied if and only if $W[j]$ has bit i set to 1. Similarly to before, if the prefix condition is satisfied, we can attempt to verify the suffix condition using Lemma 7 when P does not contain T_{j+1} or by recording the partial match in W as before. This completes the correctness proof.

We now consider the additional runtime and work space incurred for Type 3 matching. There are γ candidate positions overall that can be reported in $O(m \log \sigma + \gamma)$ time by Theorem 1. Each candidate is processed once, in $O(1)$ time. The array W occupies $O(dm)$ bits as working space. Thus, the overall time complexity is $O(m \log \sigma + \gamma)$ and working space is $O(dm + m \log n)$. \square