### Succincter text indexing with wildcards

#### Chris Thachuk University of British Columbia

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# P: aca

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# T: \*aa\*aca\*a\*aa\*cacc\*ac 4 matches P: aca

#### Problem

Create a succinct index for:

- a text **T** of length **n**
- $\bullet\,$  over an alphabet of size  $\sigma\,$
- containing **d** wildcard positions

to support efficient pattern matching queries.

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#### Assumption (in presentation)

No adjacent wildcards in **T**.

#### SNPs in the human genome



 $\rightsquigarrow$  also protein collections ( $\sigma = 20$ )

#### Non succinct indexes

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Succint indexes		
	Index space (bits)	Query working space (bits)
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#### Non succinct indexes

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Tam <i>et al.,</i>	2009	$(3+o(1))n\log\sigma$	$O(n \log d)$
(reduced working space by increasing query time) Tam et al., 2009 $(3 + o(1))n \log \sigma$		creasing query time) $O(n \log \sigma)$	

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(redu Tam <i>et al.,</i> 2009	ced working space by increa $(3+o(1))n\log\sigma$	using query time) $O(n\log\sigma)$
This work	$(2 + o(1))n\log \sigma + \mathbf{O}(\mathbf{n})$	$O(m \log n + md)$
(Ignoring smaller order terms)		

### 3 Types of matches



[Lam et al., 2007, Tam et al., 2009]

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Type 1: pattern *contained within* a text segment

### T: \*aa\*aca\*a\*aa\*cacc\*ac P: cac

Type 2: pattern *spanning one* wildcard



[Lam et al., 2007, Tam et al., 2009]

### 3 Types of matches

Type 1: pattern *contained within* a text segment

### T: \*aa\*aca\*a\*aa\*cacc\*ac P: cac

Type 2: pattern spanning one wildcard

T:	*aa*aca*a*aa*cacc*ac
<b>P</b> :	caca

Type 3: pattern contains at least one text segment



[Lam et al., 2007, Tam et al., 2009]





mississippi\$ ississippi\$m ssissippi\$mi sissippi\$mis issippi\$miss ssippi\$missi sippi\$missis ippi\$mississ ppi\$mississi pi\$mississip i\$mississipp \$mississippi

#### Naïve BWT algorithm

For a string S:

- append \$ to S (\$ < c,  $\forall c \in \Sigma$ )
- 2 list all cyclic rotations of S

\$mississippi i\$mississipp ippi\$mississ issippi\$miss ississippi\$m mississippi\$ pi\$mississip ppi\$mississi sippi\$missis sissippi\$mis ssippi\$missi ssissippi\$mi

#### Naïve BWT algorithm

For a string S:

- 2 list all cyclic rotations of S
- Sort rows of matrix (lexicographically)

i i\$ р ippi\$ S issippi\$ S ississippi\$m mississippi\$ pi\$ i ppi\$ sippi\$ S sissippi\$ S i ssippi\$ ssissippi\$ i

#### Naïve BWT algorithm

For a string S:

- **4** append \$ to S (\$ < c,  $\forall c \in \Sigma$ )
- 2 list all cyclic rotations of S
- Sort rows of matrix (lexicographically)
- output last column of matrix





















#### Build **F**, a compressed suffix array of **T**.

	BWT
*a*aa*cacc*ac	а
*aa*aca*a*aa*cacc*ac	С
*aa*cacc*ac	а
*ac	С
*aca*a*aa*cacc*ac	а
*cacc*ac	а
a*a*aa*cacc*ac	С
a*aa*cacc*ac	*
a*aca*a*aa*cacc*ac	а
a*cacc*ac	а
aa*aca*a*aa*cacc*ac	*
aa*cacc*ac	*
ac	*
aca*a*aa*cacc*ac	*
acc*ac	С
c	а
c*ac	С
ca*a*aa*cacc*ac	а
cacc*ac	*
cc*ac	а

#### Lemma

All occ1 Type 1 matches of P can be reported using:

Query time  $O(|P| \log \sigma + occ_1 \log^{1+\epsilon} n)$ Index space  $(1 + o(1))n \log \sigma$  bits *Work space*  $O(\log n)$  *bits* 

### Matching prefixes of text segments

	BWT
*a*aa*cacc*ac	а
*aa*aca*a*aa*cacc*ac	С
*aa*cacc*ac	а
*ac	С
*aca*a*aa*cacc*ac	а
*cacc*ac	а
a*a*aa*cacc*ac	С
a*aa*cacc*ac	*
a*aca*a*aa*cacc*ac	а
a*cacc*ac	а
aa*aca*a*aa*cacc*ac	*
aa*cacc*ac	*
ac	*
aca*a*aa*cacc*ac	*
ac <mark>c*ac</mark>	C_
с	а
c*ac	С
ca*a*aa*cacc*ac	а
cacc*ac	*
cc*ac	а

### Matching prefixes of text segments

DWT

	DWI
*a*aa*cacc*ac	а
*aa*aca*a*aa*cacc*ac	С
*aa*cacc*ac	а
*ac	С
*aca*a*aa*cacc*ac	а
*cacc*ac	а
a*a*aa*cacc*ac	С
a*aa*cacc*ac	*
a*aca*a*aa*cacc*ac	а
a*cacc*ac	а
aa*aca*a*aa*cacc*ac	*
aa*cacc*ac	*
ac	*
aca*a*aa*cacc*ac	*
acc*ac	° <b>∢</b>
с	а
c*ac	С
ca*a*aa*cacc*ac	а
cacc*ac	*
cc*ac	а

rank<sub>\*</sub>(*BWT*, *i*) queries determine a lexicographic range of text segments

### Type 2 matching

#### Use ${\bf F}$ and ${\bf R}$ to find candidate text segments

example

	BWT		BWT <sup>R</sup>
*a*aa*cacc*ac	а	*a*aca*aa*	а
*aa*aca*a*aa*cacc*ac	с	*aa*a*aca*aa*	С
*aa*cacc*ac	а	*aa*	а
*ac	с	*aca*aa*	а
*aca*a*aa*cacc*ac	а	*ca*ccac*aa*	а
*cacc*ac	а	*ccac*aa*a*aca*aa*	а
a*a*aa*cacc*ac	С	a*a*aca*aa*	а
a*aa*cacc*ac	*	a*aa*	С
a*aca*a*aa*cacc*ac	а	a*aca*aa*	*
a*cacc*ac	а	a*	а
aa*aca*a*aa*cacc*ac	*	a*ccac*aa*a*aca*aa*	С
aa*cacc*ac	*	aa*a*aca*aa*	*
ac	*	aa*	*
aca*a*aa*cacc*ac	*	ac*aa*a*aca*aa*	с
acc*ac	с	aca*aa*	*
c	а	c*aa*a*aca*aa*	а
c*ac	с	ca*aa*	а
ca*a*aa*cacc*ac	a 🗲	ca*ccac*aa*a*aca*aa*	*
ca <mark>cc*ac</mark>	*	cac*aa*a*aca*aa*	С
cc*ac	а	ccac*aa*a*aca*aa*	*

### Type 2 matching

Use **Q** to find compatible candidate [Bose et al., 2009]







#### Lemma

All occ<sub>2</sub> Type 2 matches of P can be reported using:

Query time $O(|P| \log \sigma + (|P| + occ_2) \frac{\log d}{\log \log d})$ Index space $(2 + o(1))n \log \sigma$  bitsWork space $O(m \log n)$  bits

### T: \*aa\*aca\*a\*aa\*cacc\*ac P: acacaca

We will enhance F to support dictionary queries

- calculate matching statistics
- for each suffix, return text segments contained as a prefix

### Review: computing matching statistics





suffix	length	SA range
С	1	[15,19]
СС	2	[19,19]
acc	3	[14,14]
cacc	4	[18,18]
acacc	3	[13,13]

[Ohlebusch, Gog & Kügel 2010]

	1		BWT
sp = 15	acc.	\$	с
		*a*aa*cacc*ac\$	а
		*aa*aca*a*aa*cacc*ac\$	\$
		*aa*cacc*ac\$	а
		*ac\$	С
		*aca*a*aa*cacc*ac\$	а
		*cacc*ac\$	а
		a*a*aa*cacc*ac\$	С
		a*aa*cacc*ac\$	*
		a*aca*a*aa*cacc*ac\$	а
		a*cacc*ac\$	а
		aa*aca*a*aa*cacc*ac\$	*
		aa*cacc*ac\$	*
		ac\$	*
		aca*a*aa*cacc*ac\$	*
		acc*ac\$	с
		c\$	a
		c*ac\$	С
		ca*a*aa*cacc*ac\$	а
		cacc*ac\$	*
		cc*ac\$	а







1 2 3 4 5 6 ( ( ( ) ) ( ( ) ) ) ( )

BP

[Ramen et al., 2002]



[Grossi & Vitter 2000]

 $\sim N$ 







if BP[pos] = ')' then find matching '('



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**if BP**[*pos*] =' (' **then** find parent interval



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A full-text dictionary using  $(1 + o(1))n \log \sigma + O(n) + O(d \log n)$ bits supports the following operations efficiently:

- report/count text segments containing P
- report/count text segments prefixed by P
- report/count text segments contained in P

### P: acacacac

Every text segment contained within  $\mathbf{P}$  is a candidate



Every text segment contained within  $\mathbf{P}$  is a candidate

A candidate is valid if it satisfies:

- suffix condition
- 2 prefix condition

We design a dynamic programming algorithm:

- $|\mathbf{P}|$  phases of algorithm  $(i = |\mathbf{P}|, \dots, 2, 1)$
- phase *i* considers candidates prefixing **P**[*i*..|**P**|]

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- $|\mathbf{P}|$  phases of algorithm  $(i = |\mathbf{P}|, \dots, 2, 1)$
- phase *i* considers candidates prefixing **P**[*i*..|**P**|]
- ullet potential matches are tracked in a working array  $oldsymbol{W}$



d entries

 $\rightarrow$  Text segment *j* matches **P**[*i*..|**P**|]  $\rightarrow$  (case 1) **P** must end within text segment *j* + 1

# T: ...\*aa\*aca\*acaa\*cac\*ac P: acacacac



verify suffix condition





- verify suffix condition
- if P must begin in text segment j 1 then verify prefix condition



 $\stackrel{\sim}{\longrightarrow} \text{Text segment } j \text{ matches } \mathbf{P}[i..|\mathbf{P}|] \\ \stackrel{\sim}{\longrightarrow} \textbf{(case 1) P must end within text segment } j+1$ 

- verify suffix condition
- If P must begin in text segment j 1 then verify prefix condition

# T: ...\*aa\*aca\*acaa\*cac\*ac P: acacacac

```
→ Text segment j matches P[i..|P|]
→ (case 1) P must end within text segment j + 1
```

- verify suffix condition
- if P must begin in text segment j 1 then verify prefix condition
- else

record partial match

```
set i bit of W[j] to 1

T: ...*aa*aca*acaa*cac*ac

P: aaaaacacacac

v
```

→ Text segment j matches P[i..|P|]→ (case 2) P must contain text segment j + 1

### T: aaa\*aa\*aca\*acaa\*cac\*ac

### P: aaaaaacacac







# Type 3 matching

```
→ Text segment j matches P[i..|P|]
→ (case 2) P must contain text segment j + 1
```

- O verify suffix condition by checking W
- **2** if **P** must begin in text segment j 1 then verify prefix condition
- else

record partial match

T: aaa\*aa\*aca\*acaa\*cac\*ac

### P: aaaaaacacac

#### Lemma

All occ3 Type 3 matches of P can be reported using:

 $\begin{array}{lll} \textit{Query time} & \textit{O}(|\textit{P}|\log\sigma+\gamma)\\ \textit{Index space} & (2+o(1))n\log\sigma \textit{ bits}\\ \textit{Work space} & \textit{O}(m\log n+md)\textit{ bits} \end{array}$ 

where  $\gamma$  is number of text segments contained in P

Given a text T of length n containing d wildcards, all matches of a pattern P can be reported using:

 $\begin{array}{ll} Query \ time & O(|P|\log \sigma + m \frac{\log d}{\log \log d} + occ_1 \log n + occ_2 \frac{\log d}{\log \log d} + \gamma) \\ Index \ space & (2 + o(1))n \log \sigma + O(n) + O(m \log n) \ bits \\ Work \ space & O(m \log n + md) \ bits \end{array}$ 

Given a text T of length n containing d wildcards, all matches of a pattern P can be reported using:

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#### Short read alignment to human genome

- $|\mathbf{T}| \approx 3$  billion bases
  - $\textbf{d} ~\approx 3 \text{ million bases}$
  - $\mathbf{m} \approx 32 64$

Working space reduced from GBs [Tam et al., 2009] to 10's of MBs

#### Future Work

Can index space be reduced to  $(1 + o(1))n \log \sigma$  bits?

→ **YES, but** with query time:

 $O(\max(m^2 \frac{\log \sigma}{\log \log \sigma}, \text{current query time}))$ 

Thanks to Anne Condon and anonymous reviewers.