A grammar compressor for collections of reads with applications to the construction of the BWT

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In Genomics, *sequencing reads* are massive and repetitive string collections of raw DNA sequences

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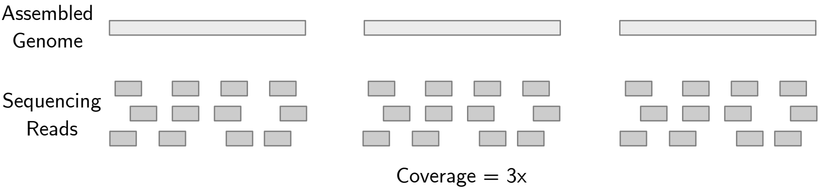

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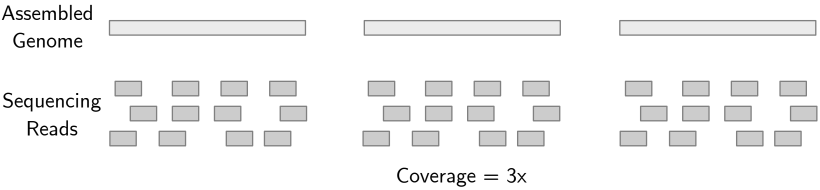

Read collections can be much more massive than assembled genomes

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Long-term goal

Producing a compact representation for reads for storage and analysis purposes

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What do we propose in this work?

A grammar compressor from which we can efficiently compute the eBWT of the reads

Related concepts

Induced suffix sorting (ISS) (**Nong *et al.* 2009**) is a technique for building the **SA** of a text $T[1..n]$ in linear time

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Definitions: (**Nong *et al.* 2009**)

- **L-type** ($\mathtt{L}$): $T[i..n] >_{lex} T[i+1..n]$
- **S-type** ($\mathtt{S}$): $T[i..n] <_{lex} T[i+1..n]$
- **LMS-type** ($\mathtt{S*}$): $T[i-1..n] >_{lex} T[i..n] <_{lex} T[i+1..n]$

A substirng $P = T[i..j]$ is a **LMS-substring** if the suffixes $T[i..n]$ and $T[j..n]$ are $\mathtt{S*}$ and no other suffix in P is $\mathtt{S*}$

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    - g is the sum of the lengths of the right hands of the rules

LMSg algorithm

$T^1 =$ `g t a t t a c c $ c t a a t a g t a c c $ g a c c a g a c c a g t $`

LMSg algorithm

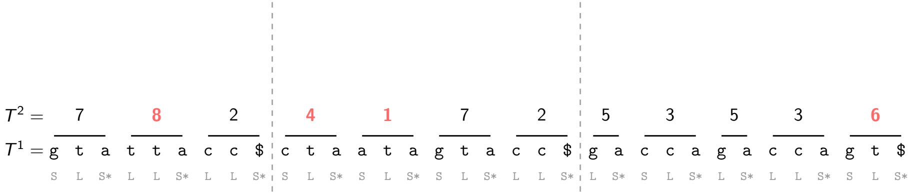
$T^1 =$	g	t	a	t	t	a	c	c	$	c	t	a	a	t	a	g	t	a	c	c	$	g	a	c	c	a	g	a	c	c	a	g	t	$
	S	L	S*	L	L	S*	L	L	S*	S	L	S*	S	L	S*	S	L	S*	L	L	S*	L	S*	S	L	S*	L	S*	L	L	S*	S	L	S*

LMSg algorithm

$$T^1 = \overline{\texttt{g t a}}\ \overline{\texttt{t t a}}\ \overline{\texttt{c c \$}}\ \vdots\ \overline{\texttt{c t a}}\ \overline{\texttt{a t a}}\ \overline{\texttt{g t a}}\ \overline{\texttt{c c \$}}\ \vdots\ \overline{\texttt{g a}}\ \overline{\texttt{c c a}}\ \overline{\texttt{g a}}\ \overline{\texttt{c c a}}\ \overline{\texttt{g t \$}}$$

S L S∗ L L S∗ L L S∗ ¦ S L S∗ S L S∗ S L S∗ L L S∗ ¦ L S∗ S L S∗ L S∗ L L S∗ S L S∗

LMSg algorithm



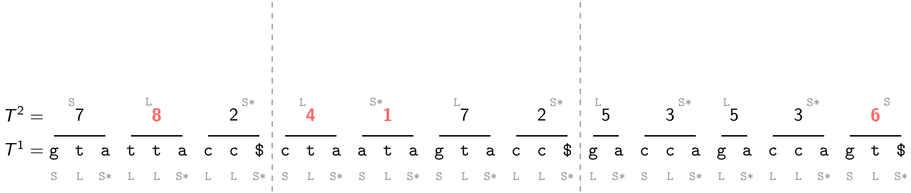
$T^2 =$ 7 8 2 | 4 1 7 2 | 5 3 5 3 6

$T^1 =$ g t a t t a c c $ | c t a a t a g t a c c $ | g a c c a g a c c a g t $

S L S∗ L L S∗ L L S∗ | S L S∗ S L S∗ S L S∗ L L S∗ | L S∗ S L S∗ L S∗ L L S∗ S L S∗

1 → ata 2 → cc$ 3 → cca 4 → cta 5 → ga 6 → gt$ 7 → gta 8 → tta

LMSg algorithm


S L S* L S* L S* L S* L S* S
$T^2 =$ 7 8 2 | 4 1 7 2 | 5 3 5 3 6
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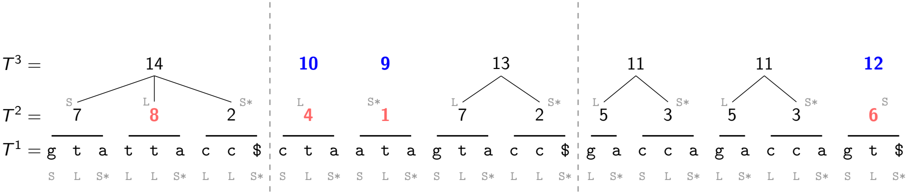

$T^3 =$ 14 | **10** **9** 13 | 11 11 **12**

S L S* | L S* L S* | L S* L S* S

$T^2 =$ 7 **8** 2 | **4** **1** 7 2 | 5 3 5 3 **6**

$T^1 =$ g t a t t a c c $ | c t a a t a g t a c c $ | g a c c a g a c c a g t $

S L S* L L S* L L S* | S L S* S L S* S L S* L L S* | L S* S L S* L S* L L S* S L S*

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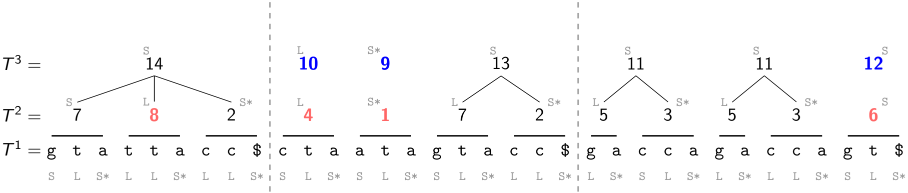
$T^3 =$
S S* L S S S S
14 10 9 13 11 11 12
$T^2 =$
S L S* L S* L S* L S* L S* S
7 8 2 4 1 7 2 5 3 5 3 6
$T^1 =$ g t a t t a c c $ c t a a t a g t a c c $ g a c c a g a c c a g t $
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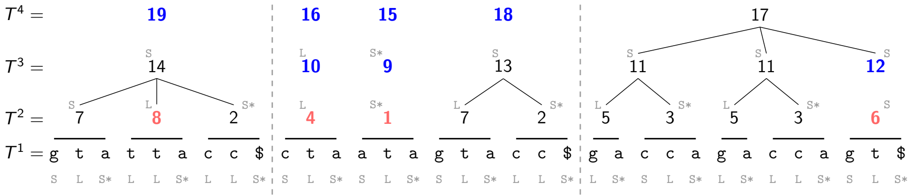
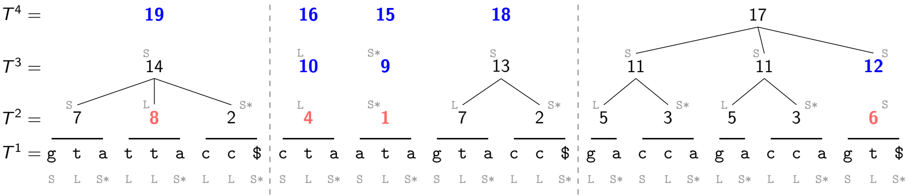

$T^4 =$ 19 16 15 18 17
$T^3 =$ 14 10 9 13 11 11 12
S L S* S S S S
$T^2 =$ 7 8 2 4 1 7 2 5 3 5 3 6
S L S* L S* L S* L S* L S* S
$T^1 =$ g t a t t a c c $ c t a a t a g t a c c $ g a c c a g a c c a g t $
S L S* L L S* L L S* S L S* S L S* S L S* L L S* L S* S L S* L S* L L S* S L S*

15 → ata   2 → cc$ 3 → cca   **16** → cta   5 → ga   **12** → gt$ 7 → gta   8 → tta

11 → 5 3   13 → 7 2   14 → 7 8 2   17 → 11 11 12

LMSg algorithm



$T^4 =$
19
16
15
18
17
$T^3 =$
S 14
L 10
S∗ 9
S 13
S 11
S 11
S 12
$T^2 =$
S 7
L 8
S∗ 2
L 4
S∗ 1
L 7
S∗ 2
L 5
S∗ 3
L 5
S∗ 3
S 6
$T^1 =$ g t a t t a c c $ c t a a t a g t a c c $ g a c c a g a c c a g t $
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$$\mathcal{R}\begin{cases} 15 \rightarrow \texttt{ata} \quad 2 \rightarrow \texttt{cc\$} \quad 3 \rightarrow \texttt{cca} \quad 16 \rightarrow \texttt{cta} \quad 5 \rightarrow \texttt{ga} \quad 12 \rightarrow \texttt{gt\$} \quad 7 \rightarrow \texttt{gta} \quad 8 \rightarrow \texttt{tta} \\ 11 \rightarrow 5\ 3 \quad 13 \rightarrow 7\ 2 \quad 14 \rightarrow 7\ 8\ 2 \quad 17 \rightarrow 11\ 11\ 12 \end{cases}$$

$$\mathsf{S} \rightarrow 19\ 16\ 15\ 18\ 17$$

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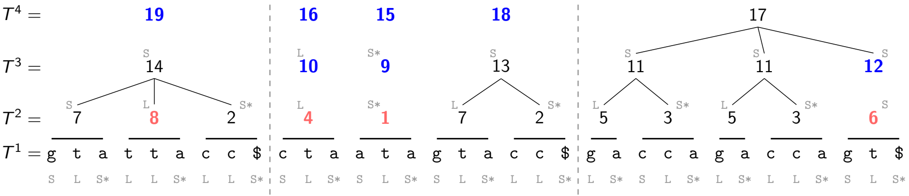

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Time complexity

The grammar construction takes $O(n \log k)$ time

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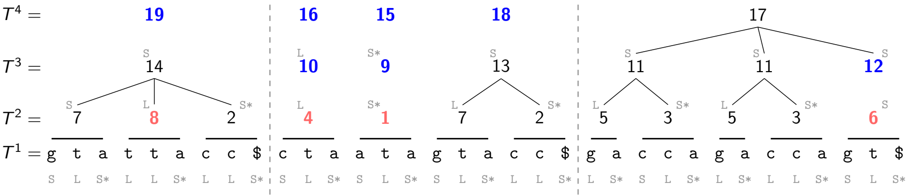

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$BWT(T^3)$	
10	9
13	10
12	11
11	11
11	12
9	13
14	14

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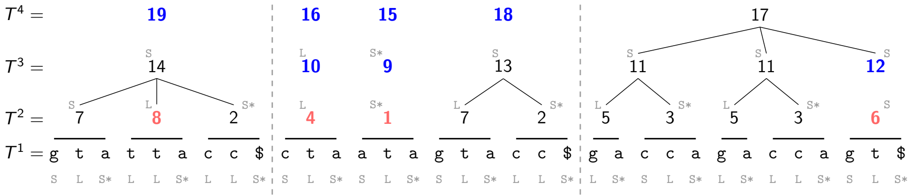

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		$BWT(T^3)$	
4	←	10	9
7 2	←	13	10
6	←	12	11
5 3	←	11	11
5 3	←	11	12
1	←	9	13
7 8 2	←	14	14

We call the replacement of a nonterminal $BWT(T^i)[j]$ its *partial decompression*

Sketch for inferring the eBWT

1	4	3	2
5	3	2	0
		8	1
2	2	3	2
3	3	12	8
	1	3	2

A range of partially decompressed phrases in some $BWT(T^i)$

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A range of partially decompressed phrases in some $BWT(T^i)$

Strings 3 2 and 3 2 0 are two distinct suffixes in partially decompressed phrases

Sketch for inferring the eBWT

1	4	3	2	5	3	2	0	L	L	S
5	3	2	0	4	3	2		L	S	
		8	1	2	3	2				
2	2	3	2	1	3	2				
3	3	12	8							
	1	3	2							

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1	4	3	2	5	3	2	0	L	L	S
5	3	2	0	4	3	2		L	S	
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2	2	3	2	1	3	2				
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In one scan of $BWT(T^i)$, we obtain the left contexts of a specific phrase's suffix

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2	2	3	2	1	3	2				
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Building $BWT(T^{i-1})$ reduces *mostly* to sort the *distinct* suffixes in the partial decompressions

Sketch for inferring the eBWT

1	4	3	2	S	L	L	S
5	3	2	0	L	L	L	S
		8	1			L	S
2	2	3	2	S	S	L	S
3	3	12	8	S	S	L	S
	1	3	2		S	L	S

We do not have enough information for sorting suffixes of length 1

We use $BWT(T^i)$ to obtain the right context of suffix 1 in row 3

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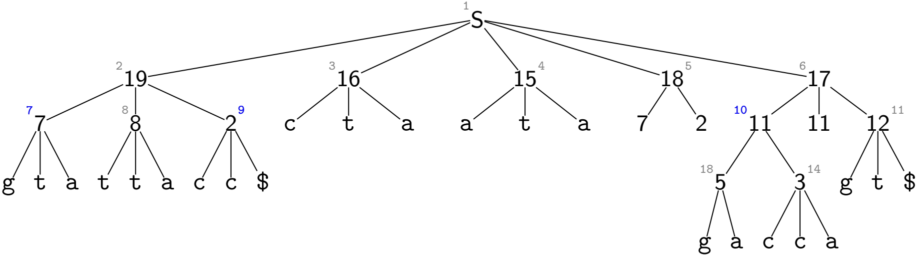
- The first occurrence of a nonterminal is stored as an internal node
    - The next occurrences are stored as leaves
    - The leaf's label is the first occurrence of the nonterminal
- We encode the topology in **LOUDS**
- The leaf labels are stored in a succinct array

Representing the grammar



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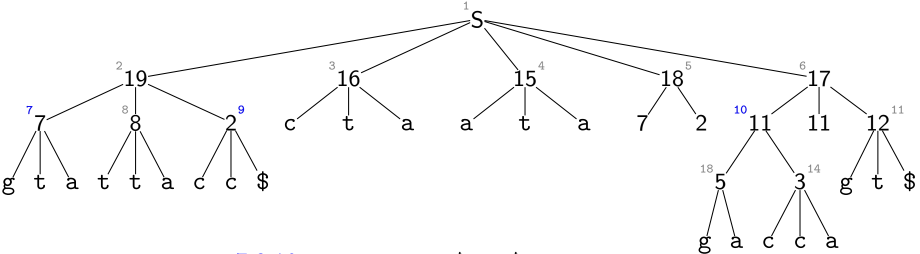

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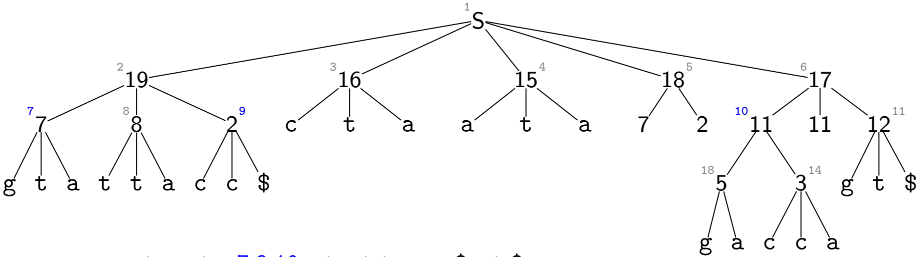

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Space usage

The grammar tree uses $2g + (g - r)\log(r)$ bits of space

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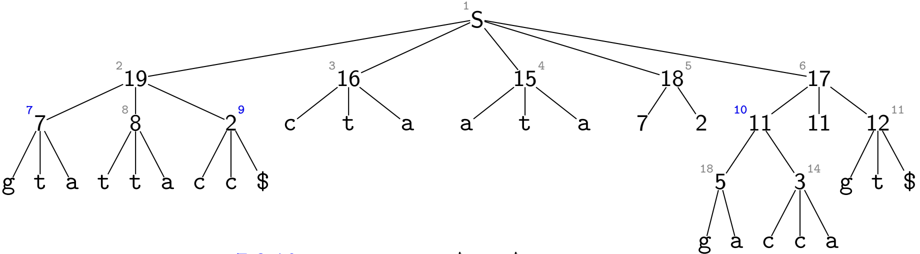

c t a a t a 7 9 10 g t a t t a c c $ g t $ g a c c a

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We have to reconstruct the original nonterminal symbols to get eBWT

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Number of genomes	Uncompressed size (GB)
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3	34.30
4	45.89
5	57.37

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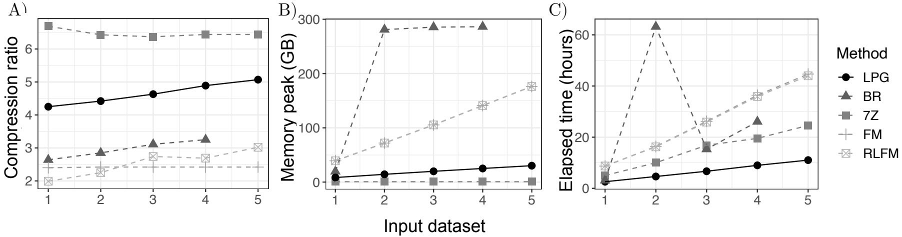
We use 10 threads with all the methods (when possible)

Results



The compression ratio was measured as the size of the plain representation divided by the compressed representation

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- Build other data structures: LCP, de Bruijn graphs ...

Questions?