Efficient Construction of the BWT for Repetitive Text Using String Compression

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CPM 2022, Prague

June 27, 2022

Motivation

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Possible solution:

We require BWT algorithms with a cost proportional to the amount of information in the input, not the input size.

We refer to this type of methods as repetition-aware.

Our contribution

Let $\mathcal{T} = \{T_1, T_2, \ldots, T_k\}$ be a string collection of k strings and $n = \Sigma_1^k |T_i|$ symbols.

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Important aspects of our method:

- It relies on induced suffix sorting (ISS).
- We use run-length and grammar-like compression to maintain temporary data in compact form and operate faster than in a plain setting.

Induced suffix sorting (ISS)

ISS is a method developed by **Ko et al. 2005** and **Nong et al. 2009** to build the suffix array in linear time. **Okanohara et al. 2009** adapted ISS to compute the BWT without producing the suffix array.

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  (A) t c ...
  L

  (B) t t t c ...
  L L L

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  c   a   a   ...
  L $S*$ S

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- S-type suffixes (S):

- LMS-type suffixes (S_*):

- LMS-type substrings:

  t c   g   g   t   a   g $\ldots$

  L S_* S S L S_* L

Our method

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Input:
Let $\mathcal{T} = \{T_1, T_2, \ldots, T_k\}$ be a string collection of k strings and $n = \Sigma_1^k |T_i|$ symbols for which we require to build the BCR BWT.

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Observation

Let $\mathcal{S}$ be the set of distinct strings of length > 1 appearing as suffixes in the LMS substrings of $\mathcal{T}$. $\mathcal{S}$ induces a partition in the suffix array associated with the BCR BWT of $\mathcal{T}$.

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All the suffixes of $\mathcal{T}$ prefixed by some string $Y \in \mathcal{S}$ appear consecutively in the suffix array.

Our method

Consider the strings $X = \texttt{actgga}$ and $Y = \texttt{actg}$. Assume both appear as suffixes in the LMS substrings of $\mathcal{T}$.

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BWT   SA   (of $\mathcal{T}$)

	BWT								
	.	a	c	t	g_L	g	a	c	...
X	.	a	c	t	g_L	g	a	c	...
	.	a	c	t	g_L	g	a	c	...
	.	a	c	t	g_{S*}	t	...		
Y	.	a	c	t	g_{S*}	t	...		
	.	a	c	t	g_{S*}	t	...		

Our observation holds even if Y is prefix of X (or vice-versa)

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Let $Y = \texttt{actg} \in \mathcal{S}$ be a string that appears as a suffix in the strings of D.

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Let $Y = \mathtt{actg} \in \mathcal{S}$ be a string that appears as a suffix in the strings of D.

We distinguish three cases to fill the BWT range mapping the partition block for Y:

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Let $Y = \mathtt{actg} \in \mathcal{S}$ be a string that appears as a suffix in the strings of D.

We distinguish three cases to fill the BWT range mapping the partition block for Y:

Case 1: if Y is always a proper suffix that is preceded by the same character in D, then the SA block for Y maps an equal-symbol run in the BWT.

BWT	SA					
a	a	c	t	g_{s*}	t	…
a	a	c	t	g_{s*}	t	…
a	a	c	t	g_{s*}	t	…

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We distinguish three cases to fill the BWT range mapping the partition block for Y:

Case 2: if Y is not a proper suffix in the LMS substrings, then we cannot infer the BWT block for Y using D.

BWT	SA					
*	a_{s*}	c	t	g_{s*}	t	…
*	a_{s*}	c	t	g_{s*}	t	…
*	a_{s*}	c	t	g_{s*}	t	…

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Let $Y = \texttt{actg} \in \mathcal{S}$ be a string that appears as a suffix in the strings of D.

We distinguish three cases to fill the BWT range mapping the partition block for Y:

Case 3: if Y is not left-maximal, then we cannot infer the BWT block for Y either.

BWT	SA					
a	a	c	t	g_{S*}	t	…
\$	a	c	t	g_{S*}	t	…
*	a_{S*}	c	t	g_{S*}	t	…

Our method

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In each recursive step i, we proceed as follows:

Entering the recursion:

$$T^1 = \overline{\text{g t } \underline{\text{a}} \text{ t t } \underline{\text{a}} \text{ c c \$}} \; \overline{\text{g t } \underline{\text{a}} \text{ a t } \underline{\text{a}} \text{ g t } \underline{\text{a}} \text{ c c \$}}$$

$$\scriptstyle S \quad L \quad S^* \quad L \quad L \quad S^* \quad L \quad L \quad S^* \quad S \quad L \quad S^* \quad S \quad L \quad S^* \quad S \quad L \quad S^* \quad L \quad L \quad S^*$$

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

$\quad\quad S \ L \ S^* \ L \ L \ S^* \ L \ L \ S^* \ S \ L \ S^* \ S \ L \ S^* \ S \ L \ S^* \ L \ L \ S^*$

$\quad\quad\quad\quad 1 \ \ 2 \ \ 3 \ \ 4 \quad 5 \ \ 6 \ \ 7 \ \ 8 \quad 9 \ 10 \ 11 \ 12 \quad 13 \ 14 \ 15$

$D^1 = \text{a c c \$} \quad \text{a g t a} \quad \text{a a t a} \quad \text{g t a}$

$N^1 = \quad\quad 2 \quad\quad\quad\quad 1 \quad\quad\quad\quad 2 \quad\quad\quad\quad 2$

Entering the recursion:

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

$$\begin{array}{c} S \quad L \quad S^* \quad L \quad L \quad S^* \quad L \quad L \quad S^* \quad S \quad L \quad S^* \quad S \quad L \quad S^* \quad S \quad L \quad S^* \quad L \quad L \quad S^* \end{array}$$

$$\begin{array}{c} 1 \quad 2 \quad 3 \quad 4 \quad\quad 5 \quad 6 \quad 7 \quad 8 \quad\quad 9 \quad 10 \quad 11 \quad 12 \quad\quad 13 \quad 14 \quad 15 \end{array}$$

$$D^1 = \text{a c c } \$ \quad \text{a g t a} \quad \text{a a t a} \quad \text{g t a}$$

$$N^1 = \quad 2 \quad\quad\quad 1 \quad\quad\quad 2 \quad\quad\quad 2$$

$$SA_{D^1} = 4 \quad 9 \quad 1 \quad 5 \quad 10 \quad 8 \quad 12 \quad 15 \quad 3 \quad 2 \quad 6 \quad 13 \quad 7 \quad 11 \quad 14$$

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S L S* L L S* L L S* S L S* S L S* S L S* L L S*

$$D^1 = \underset{1}{\text{a}}\ \underset{2}{\text{c}}\ \underset{3}{\text{c}}\ \underset{4}{\text{\$}}\quad \underset{5}{\text{a}}\ \underset{6}{\text{g}}\ \underset{7}{\text{t}}\ \underset{8}{\text{a}}\quad \underset{9}{\text{a}}\ \underset{10}{\text{a}}\ \underset{11}{\text{t}}\ \underset{12}{\text{a}}\quad \underset{13}{\text{g}}\ \underset{14}{\text{t}}\ \underset{15}{\text{a}}$$

$$N^1 = \qquad 2 \qquad\qquad 1 \qquad\qquad 2 \qquad\qquad 2$$

$$SA_{D^1} = 4\quad 9\quad 1\quad 5\quad 10\quad 8\quad 12\quad 15\quad 3\quad 2\quad 6\quad 13\quad 7\quad 11\quad 14$$

$$pBWT^1 = \begin{matrix} \text{c} & * & * & * & \text{a} & & & \text{c} & \text{a} & * & & * \\ 2 & 2 & 2 & 1 & 2 & & & 2 & 2 & 3 & & 5 \end{matrix}$$

$$D^1 = \begin{matrix} 1 & & & 2 & & 3 & & 4 & & 5 \\ \text{a} & \text{a t a} & \text{a c c \$} & & \text{a g t a} & & \text{g t a} & & \text{t a} \\ \text{a} & 5 & & * & \$ & & \text{a} & 4 & \text{g} & 5 & & * & \text{t} \end{matrix}$$

New parse = 4 1 2 4 1 3 2

Our method

Returning from the recursion:

$$T^2 = 4 \quad 1 \quad 2 \quad 4 \quad 1 \quad 3 \quad 2$$

Our method

Returning from the recursion:

$$T^2 = \texttt{4 1 2 4 1 3 2}$$

BWT^2

4	1 2
4	1 3 2
1	2
3	2
1	3
2	4 1 2
2	4 1 3 2

Our method

Returning from the recursion:

$$T^2 = 4 \ 1 \ 2 \ 4 \ 1 \ 3 \ 2$$

BWT^2				
4	1	2		
4	1	3	2	
1	2			
3	2			
1	3			
2	4	1	2	
2	4	1	3	2

$PBWT^1$		
	c	2
1	*	2
2	*	2
3	*	1
	a	2
	c	2
	a	2
4	*	3
5	*	5

Our method

Returning from the recursion:

$$T^2 = \text{4 1 2 4 1 3 2}$$

BWT^2

4	1 2	
4	1 3 2	
1	2	
3	2	
1	3	
2	4 1 2	
2	4 1 3 2	

$PBWT^1$

	c	2
1	*	2
2	*	2
3	*	1
	a	2
	c	2
	a	2
4	*	3
5	*	5

$$D^1 = \quad \begin{array}{cccccc} & 1 & 2 & 3 & 4 & 5 \\ \text{a} & 5 & \text{* \$} & \text{a} & 4 & \text{g} & 5 & \text{* t} \end{array}$$

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$$T^2 = 4\ \ 1\ \ 2\ \ 4\ \ 1\ \ 3\ \ 2$$

BWT^2				
4	1 2			
4	1 3 2			
1	2			
3	2			
1	3			
2	4 1 2			
2	4 1 3 2			

$PBWT^1$		
c	2	
1	*	2
2	*	2
3	*	1
a	2	
c	2	
a	2	
4	*	3
5	*	5

$$D^1 = \begin{array}{ccccc} 1 & 2 & 3 & 4 & 5 \\ \text{a } 5 & * \ \$ & \text{a } 4 & \text{g } 5 & * \ \text{t} \end{array}$$

Our method

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$$T^2 = 4\ \ 1\ \ 2\ \ 4\ \ 1\ \ 3\ \ 2$$

BWT^2				$PBWT^1$		
4	1	2			c	2
4	1	3	2	1	*	2
1	2			2	*	2
3	2			3	*	1
1	3				a	2
2	4	1	2		c	2
2	4	1	3	2	a	2
				4	*	3
4				5	*	5
g	t	a				

$D^1 =$	1		2		3		4		5	
	a	5	*	$	a	4	g	5	*	t

Our method

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BWT^2

4	1 2
4	1 3 2
1	2
3	2
1	3
2	4 1 2
2	4 1 3 2

$PBWT^1$

c		2
1	*	2
2	*	2
3	*	1
a		2
c		2
a		2
4	*	3
5	*	5

4
g   t   a

$D^1 =$ a 5   * $ a 4   g 5   * t
          1   2   3   4   5

Experiments: datasets

Dataset	σ	n (GB)	n/r
ILL1	5	12.77	3.18
ILL2	5	24.36	4.07
ILL3	5	35.84	4.67
ILL4	5	46.50	5.03
ILL5	5	57.37	5.33
HGA05	16	14.27	4.82
HGA10	16	29.63	8.76
HGA15	16	45.04	12.02
HGA20	16	60.01	15.67
HGA25	16	75.05	19.42

Table: ILLX= Illumina reads. HGAXX= assembled human genomes.

Experiments: competitors

- `ropebwt2`: a variation of the original BCR algorithm of **Bauer et al. 2013** that uses rope data structures.
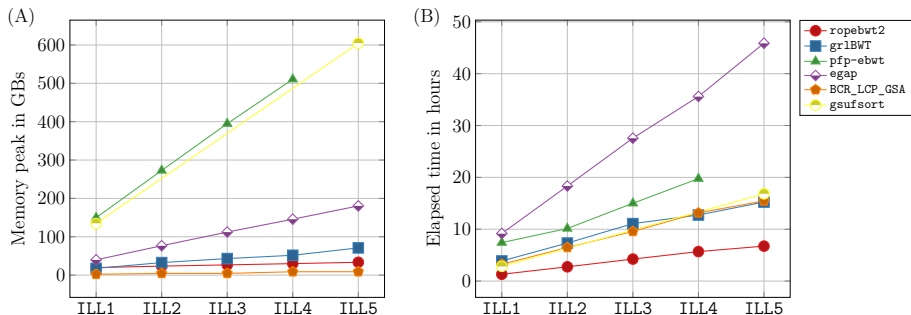
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- `BCR_LCP_GSA`: the current implementation of the semi-external BCR algorithm.

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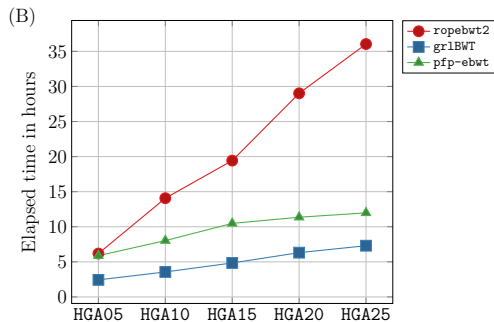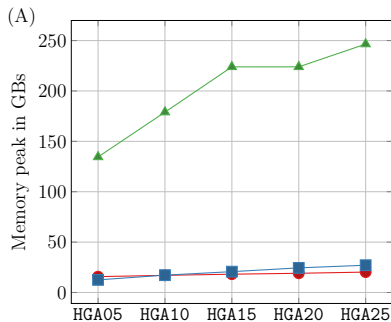- `egap`: a semi-external algorithm of **Edigi et al. 2019** that builds the BCR BWT.

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- `pfp-eBWT`: the eBWT algorithm of **Boucher et al. 2021** that builds on prefix-free parsing + ISS.
- `BCR_LCP_GSA`: the current implementation of the semi-external BCR algorithm.
- `egap`: a semi-external algorithm of **Edigi et al. 2019** that builds the BCR BWT.
- `gsufsort`: an in-memory method proposed by **Louza et al. 2020** that computes the BCR BWT and (optionally) other data structures.

Experiments: results

Non-repetitive data (Illumina reads)

Experiments: results

Repetitive data (assembled genomes)

(A) Memory peak in GBs plotted against HGA05, HGA10, HGA15, HGA20, HGA25.

(B) Elapsed time in hours plotted against HGA05, HGA10, HGA15, HGA20, HGA25.

Legend:
- ropebwt2
- gr1BWT
- pfp-ebwt

Future work

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- Modify the algorithm to build different BWT variations (e.g., the eBWT).
- Improve our hash table implementation.
- Use our repetition-aware strategy to perform other calculations: MEMs, MUMs, or suffix-prefix overlaps.

Questions?