

BWT everywhere

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The BWT



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(Here BWT stands for: Best Water Technology)



The Burrows-Wheeler-Transform

$T = \text{fukuoka}$. The BWT is a permutation of T : $\text{bwt}(T) = \text{kaouufk}$

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kuokafu
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okafuku
kafukuo
afukuok

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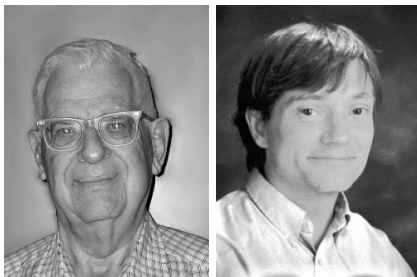
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$\text{BWT}(T) = \text{concatenation of last characters} = L$

The Burrows-Wheeler Transform

- introduced by Burrows and Wheeler in 1994
- a reversible string transform
- basis of a highly effective lossless text compression algorithm
- basis of compressed data structures (compressed text indexes)



source: Adjeroh, Bell, Mukerjee (2008)

Inventors of BW-transform and the FM-index Receive Kanellakis Award [↗](#)

Michael Burrows [↗](#), Google; **Paolo Ferragina** [↗](#), University of Pisa; and **Giovanni Manzini** [↗](#), University of Pisa, receive the **ACM Paris Kanellakis Theory and Practice Award** [↗](#) for inventing the BW-transform and the FM-index that opened and influenced the field of Compressed Data Structures with fundamental impact on Data Compression and Computational Biology. In 1994, Burrows and his late coauthor David Wheeler published their paper describing revolutionary data compression algorithm based on a reversible transformation of the input—the “Burrows-Wheeler Transform” (BWT). A few years later, Ferragina and Manzini showed that, by orchestrating the BWT with a new set of mathematical techniques and algorithmic tools, it became possible to build a “compressed index,” later called the FM-index. The introduction of the BW Transform and the development of the FM-index have had a profound impact on the theory of algorithms and data structures with fundamental advancements.

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- for BWT and FM-index (Ferragina & Manzini 2000, 2005)

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- *“... that opened and influenced the field of Compressed Data Structures with fundamental impact on Data Compression and Computational Biology”*
- some bioinformatics tools:
 - `bwa`, `bwa-sw`, `bwa-mem` (Li & Durbin, 2009, 2010, Li 2013) > 55,000 cit.
 - `bowtie`, `bowtie2` (Langmead et al., 2009, 2012) > 70,000 cit.

This talk is about other uses of the BWT.

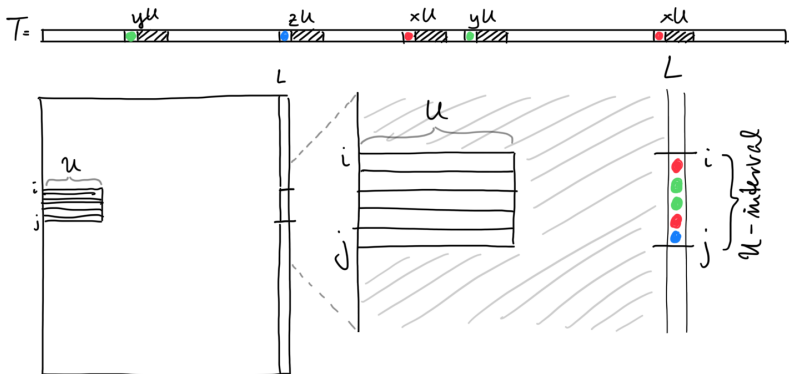
This talk is about other uses of the BWT.

1. distance measures based on the BWT
2. generating random de Bruijn sequences with the BWT
3. analyzing different BWT variants for string collections
4. why a common method for BWT of text collections is not a good idea

Our tools for this talk

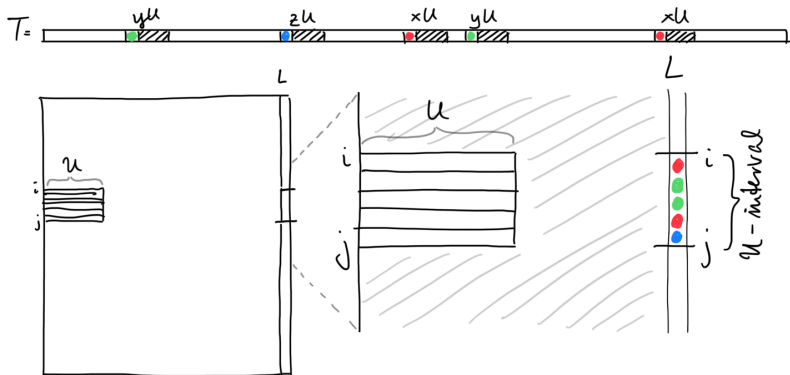
Tool 1: U -intervals

Def. Let U be a substring of T . The U -interval of $L = \text{bwt}(T)$ is $[i, j]$, where the conjugates in positions $k \in [i, j]$ are exactly those starting with U :



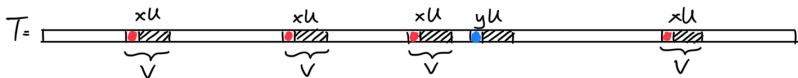
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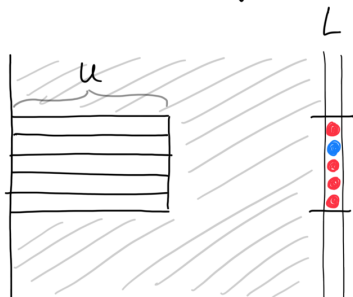


N.B.: $L[i..j]$ = left-context of U ; $[i, j] \cong$ SA-interval of U (here: CA)

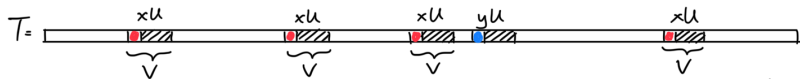
Why is the BWT so good in compression?



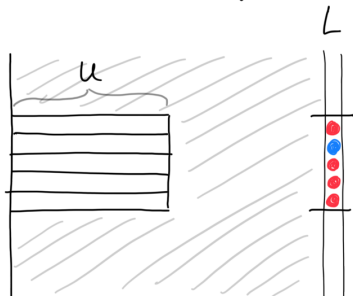
many occurrences
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many x 's in
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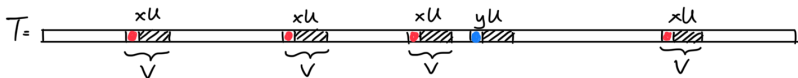


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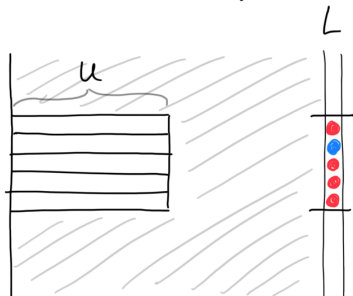


- T has many repeated substrings \Rightarrow many U -intervals mostly same character
- $L = \text{bwt}(T)$ has few runs \Rightarrow runlength encoding (RLE) is good

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- T has many repeated substrings \Rightarrow many U -intervals mostly same character
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$\text{bbbacccccccccccccccccccaaaaa} \mapsto \text{b}^3\text{a}^1\text{c}^{18}\text{a}^5$

Tool 2: The extended BWT

(Mantaci, Restivo, Rosone, Sciortino, TCS, 2007)

Ex. $\mathcal{M} = \{fu, k, uoka\}$. The eBWT is a permutation of the characters of \mathcal{M} : $eBWT(\mathcal{M}) = kuokufa$.

all rotations (conjugates)

fu
uf
k
uoka
okau
kauo
auok

→
omega order

all rotations, sorted

auok k
fu u
kauo o
k k
okau u
uf f
uoka a

N.B. $kauo <_{\omega} k$: $kauo \cdot kauo \cdots <_{lex} k \cdot k \cdot k \cdot k \cdots$

The extended BWT (cont.)

Def. (omega-order): $T <_{\omega} S$ if (a) $T^{\omega} <_{\text{lex}} S^{\omega}$, or
(b) $T^{\omega} = S^{\omega}$, $T = U^k$, $S = U^m$ and $k < m$

$\mathcal{M} = \{fu, k, uoka\}$

<i>lex-order</i>	<i>omega-order</i>
auok k	auok k
fu u	fu u
k k	kauo o
kauo o	k k
okau u	okau u
uf f	uf f
uoka a	uoka a

(**N.B.** With the lex-order, the LF-property would not hold.)

The extended BWT (cont.)

- **omega-order** instead of lex-order
- the eBWT inherits **BWT properties**: clustering effect, reversibility, useful for lossless text compression, efficient pattern matching, . . .
- However, until recently **no linear-time** algorithm was known.

The extended BWT (cont.)

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- the eBWT inherits **BWT properties**: clustering effect, reversibility, useful for lossless text compression, efficient pattern matching, ...
- However, until recently **no linear-time** algorithm was known.

Since 2021: linear-time algorithms and implementations available

- First linear-time algorithm
(Bannai, Kärkkäinen, Köppl, Piatkowski, CPM 2021)
- We significantly simplified this algorithm
(Boucher, Cenzato, L., Rossi, Sciortino, SPIRE 2021)
- ... and gave **efficient implementations** of the eBWT (**cais, pfpebwt** 2021)
- Later we gave an **r-index** based on the eBWT (—, Inf. & Comp., 2024)

Tool 3: The standard permutation

Def. Given a string V , its **standard permutation** π_V is defined by:
 $\pi_V(i) < \pi_V(j)$ if (i) $V_i < V_j$, or (ii) $V_i = V_j$ and $i < j$.

In other words, π_V is a stable sort of the characters of V .

Example: $V = \text{kaouufk}$

0	1	2	3	4	5	6
k	a	o	u	u	f	k
a	f	k	k	o	u	u
0	1	2	3	4	5	6

$$\begin{aligned}\pi_V &= \begin{pmatrix} 0 & 1 & 2 & 3 & 4 & 5 & 6 \\ 2 & 0 & 4 & 5 & 6 & 1 & 3 \end{pmatrix} \\ &= (0, 2, 4, 6, 3, 5, 1)\end{aligned}$$

(If V is a BWT, then π_V is called **LF-mapping**.)

The standard permutation (cont.)

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- With π_V we can recover (a conjugate of) T from $\text{bwt}(T)$ back-to-front:

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- Similarly, we can recover (conjugates of) \mathcal{M} from $\text{eBWT}(\mathcal{M})$:

Ex. $V = \text{kuokufa}$, $\pi_V = (0, 2, 4, 6)(1, 5)(3)$

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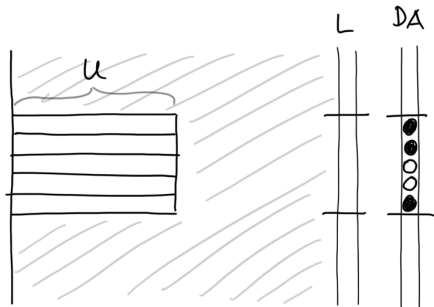
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Thm. (Folklore) A string V is the BWT of a primitive string if and only if π_V is cyclic.

Distance / similarity measures



Mantaci, Restivo, Rosone, Sciortino, **ToCS** 2007

Distance/similarity based on eBWT

Idea: Conjugates of similar strings should mix well in the eBWT.

Ex.: $S = \text{kyoto}$, $T = \text{tokyo}$.

conjugates	L	DA (document array)
kyoto	o	S
kyoto	o	T
okytot	t	S
okytot	t	T
otoky	y	S
otoky	y	T
tokyo	o	S
tokyo	o	T
yotok	k	S
yotok	k	T

runlengths of DA: i_0, i_1, \dots, i_ℓ

Def. (delta-distance)

$$\delta(S, T) = \sum_{j=0}^{\ell} (i_j - 1)$$

$$\delta(\text{tokyo}, \text{kyoto}) = 0$$

$S = \text{fukuoka},$
 $T = \text{fujioka}.$

Def. (delta-distance)

$$\delta(S, T) = \sum_{j=0}^{\ell} (i_j - 1)$$

$$DA = T^1 S^1 T^1 S^1 T^3 S^2 T^2 S^2$$

$$\delta(S, T) = 2 + 1 + 1 + 1 = 5$$

conjugates	L	DA
afujiok	k	T
afukuok	k	S
fujioka	a	T
fukuoka	a	S
iokafuj	j	T
jiokafu	u	T
kafujio	o	T
kafukuo	o	S
kuokafu	u	S
okafuji	i	T
ujiokaf	f	T
ukuokaf	f	S
uokafuk	k	S

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- δ has been used in bioinformatics, malware analysis, artwork comparison, ...
- a modification called 'BW similarity distribution' uses the expectation of the i_j and the Shannon-entropy (Yang et al. 2010, Yang et al. 2010, Louza et al. 2019)

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okafuji	i	T
ujiokaf	f	T
ukuokaf	f	S
uokafuk	k	S

Let $P_1 \cdot P_2 \cdots P_m$ a parsing \mathcal{P} of DA.

Def. $dist_{\mathcal{P}}(S, T) = \sum_{i=1}^m ||P_i|_S - |P_i|_T|$

where $|P_i|_x$ is the multiplicity of x in P_i

Ex. Let \mathcal{P} be the parsing

DA = $(TS)(TS)(T)(T)(TS)(S)(T)(T)(S)(S),$
 then $dist_{\mathcal{P}}(S, T) = 7.$

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This can be used e.g. to simulate the
[k-mer distance](#)

(aka q-gram distance, Ukkonen 1992):

Def. (*k-mer distance*)

$$dist_k(S, T) = \sum_{|U|=k} |mult(S, U) - mult(T, U)|$$

$S = \text{fukuoka},$
 $T = \text{fujioka}.$

conjugates	L	DA
afujiok	k	\bar{T}
afukuok	k	S
fujioka	a	\bar{T}
fukuoka	a	S
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Def. (k -mer distance)

$$dist_k(S, T) = \sum_{|U|=k} |mult(S, U) - mult(T, U)|$$

$$dist_2(S, T) = 7$$

$S = \text{fukuoka},$

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conjugates	L	DA
afujiok	k	T
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fujioka	a	T
fukuoka	a	S
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ujiokaf	f	T
ukuokaf	f	S
uokafuk	k	S

Let $L = eBWT(S, T)$, and $DA = P_1 \cdots P_r$ the parsing of the DA where P_i corresponds to the i th run of L .

Def. (rho: monotonic block parsing)

$$\rho(S, T) = \sum_{i=1}^r ||P_i|_S - |P_i|_T|$$

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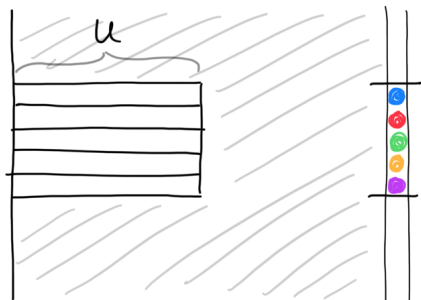
$$\rho(S, T) = \sum_{i=1}^r ||P_i|_S - |P_i|_T|$$

Ex.

$DA = (TS)(TS)(T)(T)(TS)(S)(T)(TS)(S),$

$$\rho(S, T) = 5$$

Generating random de Bruijn sequences



L. & Parmigiani, LATIN 2024

de Bruijn sequences

Def. A de Bruijn sequence (dB sequence) of order k over an alphabet Σ is a circular string in which every k -mer occurs exactly once as a substring.

k -mer = string of length k

Ex. $k = 3$: aaababbb (binary)
 01234567

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k -mer	position
aaa	0
aab	1
aba	2
abb	4
baa	7
bab	3
bba	6
bbb	5

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$k = 3$: aaacaabbabcacccabacbccbbcb
(ternary)

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$k = 3$: aaacaabbabcacccabacbccbbcb
(ternary)

Easy: length of a dB sequence is σ^k ($\sigma = |\Sigma|$)

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aaa	0
aab	1
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bbb	5

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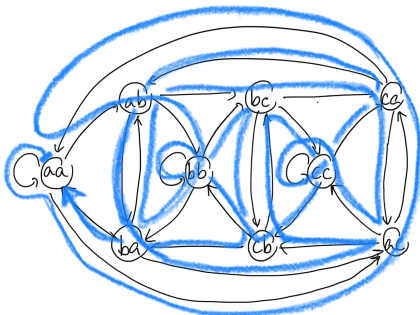
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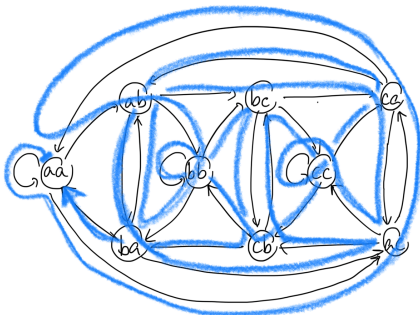
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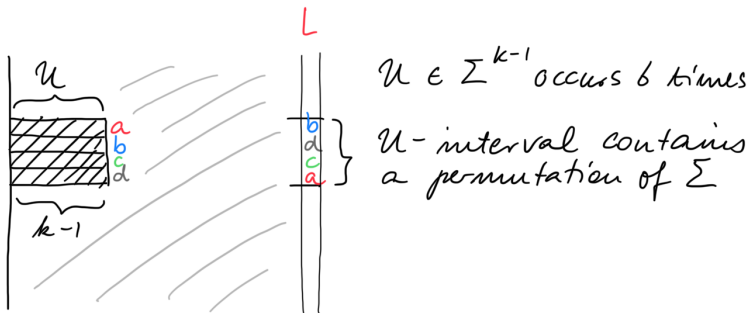
aaacaabbabcacccabacbccbbbcb

(one of the 373 248 dB seqs for $\sigma = 3, k = 3$)

Applications of de Bruijn sequences

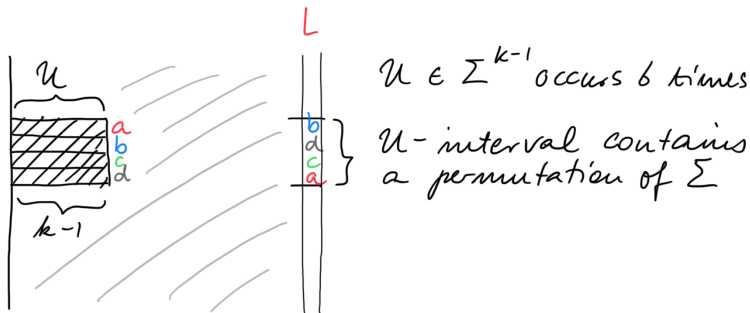
- pseudo-random bit generators
- experimental design: reaction time experiments, imaging studies (MRI)
- computational biology: DNA probe design, DNA microarray, DNA synthesis
- cryptographic protocols
- ...

The BWT of de Bruijn sequences



(in particular, BWT+RLE does not compress well: many runs!)

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N.B. From now on: binary dB sequences (for simplicity).

Construction algorithms

Many algorithms for constructing dB sequences:

- H. Fredricksen: *A survey of full length nonlinear shift register cycle algorithms*, 1982 (classic survey)
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- a small subset of dB sequences (e.g. linear feedback shift registers)

k	4	5	6	7	10	15	20
#LFSRs	2	6	6	18	60	1 800	24 000
#dBseqs	16	2048	67 108 864	$1.44 \cdot 10^{17}$	$1.3 \cdot 10^{151}$	$3.63 \cdot 10^{4927}$	$2.47 \cdot 10^{157820}$

- number of binary dB sequences = $2^{2^{k-1}-k}$

Construction of random dB sequences

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 $\alpha =$ inverse Ackermann function
- ... and it is beautifully simple at that!

The BWT of a dB sequence

$T = \text{aaababbb}, k = 3$

a	a	a	b	a	b	b	b
a	a	b	a	b	b	b	a
a	b	a	b	b	b	a	a
a	b	b	b	a	a	a	b
b	a	a	a	b	a	b	b
b	a	b	b	b	a	a	a
b	b	a	a	a	b	a	b
b	b	b	a	a	a	b	a

$\text{bwt}(\text{aaababbb}) = \text{baabbaba}$

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b	b	a	a	a	b	a	b	b
b	b	b	a	a	a	b	a	a

$\text{bwt}(\text{aaababbb}) = \text{baab**a**ba}$

$\text{bwt}(T) \in \{\text{ab}, \text{ba}\}^{2^k-1}$

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A. No! e.g. $V = abbababa$, its standard permutation is

$$\pi_V = \begin{pmatrix} 0 & 1 & 2 & 3 & 4 & 5 & 6 & 7 \\ 0 & 4 & 5 & 1 & 6 & 2 & 7 & 3 \end{pmatrix} = (0)(1, 4, 6, 7, 3)(2, 5)$$

Indeed, $V = \text{eBWT}(\{a, aabbb, ab\})$.

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Indeed, $V = \text{eBWT}(\{\mathbf{a}, \mathbf{aabbb}, \mathbf{ab}\})$.

Def. (Higgins, 2012) A binary **de Bruijn set of order k** is a multiset of total length 2^k such that every k -mer is the prefix of some rotation of some power of some string in \mathcal{M} .

Ex. $\mathcal{M} = \{\mathbf{a}, \mathbf{ab}, \mathbf{aabbb}\}$ k -mers: $\mathbf{aaa}, \mathbf{aab}, \mathbf{bab}, \dots$

The basic theorem

Thm (Higgins, 2012) The set $\{ab, ba\}^{2^{k-1}}$ is the set of eBWTs of binary de Bruijn sets of order k .

Corollary A string $V \in \{ab, ba\}^{2^{k-1}}$ is the BWT of a dB sequence if and only if π_V is cyclic.

Our idea: Take a random $V \in \{ab, ba\}^{2^{k-1}}$ and turn it into the BWT of a dB sequence.

Lemma (Swap Lemma) Let V be a binary string, $V_i \neq V_{i+1}$, and V' the result of swapping V_i and V_{i+1} .

- If i and $i + 1$ belong to **distinct cycles** in of π_V then the number of cycles **decreases by one**,
- otherwise it **increases by one**.

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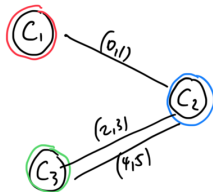
- swap V_0 and V_1 : babababa, st. perm. $(0, 4, 6, 7, 3, 1)(2, 5)$
- swap V_2 and V_3 : baabbaba, st. perm. $(0, 4, 6, 7, 3, 5, 2, 1)$

Invert baabbaba and output the dB seq $T =$ aaababbb.

How to choose the blocks to swap

0	1	2	3	4	5	6	7
a	b	b	a	b	a	b	a
a	a	a	a	b	b	b	b
0	1	2	3	4	5	6	7

(0) $(1, 4, 6, 7, 3)$ $(2, 5)$
 C_1 C_2 C_3



- **unhappy block**: elements $2i, 2i + 1$ are in different cycles
- **cycle graph** Γ_V : vertices = cycles, edges = unhappy blocks
- Spanning Trees of $\Gamma_V =$ (BWTs of) dB sequences closest to V
- here 2 STs: BWTs of **aaabbbbab**, **aaababbbb**

BWT-based algorithm for generating random dB sequences

- first practical algorithm for constructing a random dB sequence which produces **any** dB sequence with positive probability
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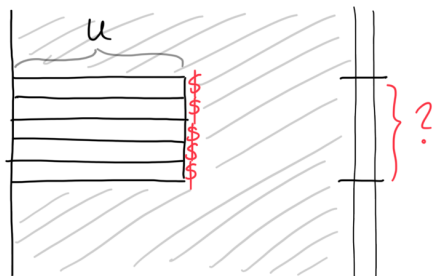
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- can be straightforwardly extended to any constant-size alphabet (present on github)

On text indexes for string collections



Cenzato & L., CPM 2022, Bioinformatics 2024

Cenzato, Guerrini, L., Rosone, DCC 2023

BWT of string collections

All that glisters is not gold. (W. Shakespeare, The Merchant of Venice)

All that is referred to as **extended BWT** is **not extended BWT**.

BWT of string collections

- Often, **any** BWT of a string collection is called **extended BWT**.
- Many tools exist for BWT of string collections, but until 2021 none computed the original eBWT.

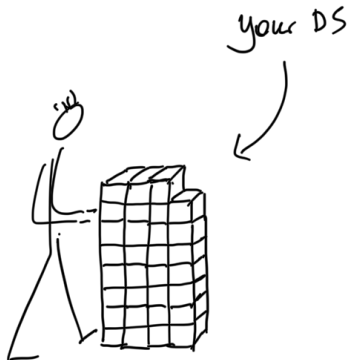
Q. So what **do** these tools compute?

The different BWT variants

(Cenzato & L., CPM 2022, Bioinformatics 2024)

- We surveyed 18 different tools and the resulting BWT variants
- We identified **5 distinct BWT variants** for string collections, ...
- ... and later added a 6th variant, the **optimalBWT**, which **minimizes r** (see later)
- All but the original eBWT use end-of-string symbols ($\$$).
- The BWT variants differ also in the number of runs r .

size of data structures is $O(r)$



BWT of text collections with dollars

- Most commonly, the strings are concatenated and then treated like one string.
- Two methods: multidollarBWT (and variations) and concatBWT

multidollarBWT (different dollars: $\$i < \$_{i+1}$)

— $\$1$ — $\$2$ — $\$3$ — $\$4$ — $\$5$

Concat BWT (same dollar plus $\# < \$$)

— $\$$ — $\$$ — $\$$ — $\$$ — $\$ \#$

- We showed that all variants can be reduced to multidollarBWT.

Interesting intervals

Q. Where exactly do these BWT variants differ? **A.** in interesting intervals

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Ex. $\mathcal{M} = \{ATATG, TGA, ACG, ATCA, GGA\}$

BWT variant	example
<i>non-sep. based</i> eBWT(\mathcal{M})	CGGGATGTACGTTAAAAA
<i>separator-based</i> dollarEBWT(\mathcal{M})	GGAAACGG\$\$\$TTACTGT\$AAA\$
multidolBWT(\mathcal{M})	GAGAAGCG\$\$\$TTATCTG\$AAA\$
colexBWT(\mathcal{M})	AAAGGCGG\$\$\$TTACTGT\$AAA\$
concatBWT(\mathcal{M})	AAGAGGCG\$\$\$TTACTGT\$AAA\$
optimalBWT	AAAGGGCG\$\$\$TTACTTG\$AAA\$

in color: **interesting intervals**

colex a.k.a. 'rlo'

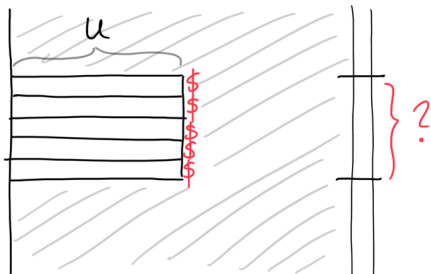
Def. An interval $[i, j]$ is **interesting** if it is the U -interval of a left-maximal shared suffix U .

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Ex. $U = A$

$\mathcal{M} = \{ATATG, TGA, ACG, ATCA, GGA\}$

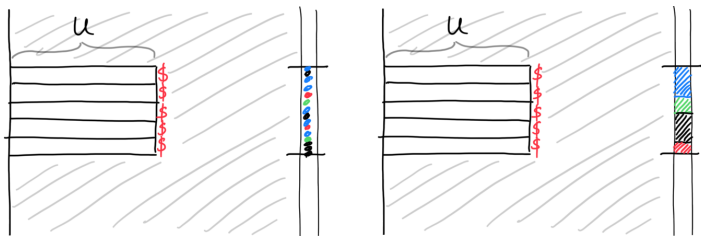
$A\$_2 \dots$	G	$A\$_1 \dots$	C
$A\$_4 \dots$	C	$A\$_2 \dots$	G
$A\$_5 \dots$	G	$A\$_3 \dots$	G
(input)		(colex)	



$U \in \Sigma^*$ is called a **left-maximal shared suffix** if there exist two strings $S_1, S_2 \in \mathcal{M}$ such that U is a suffix of S_1 and S_2 and is preceded by different characters in S_1 and S_2 .

The colexBWT

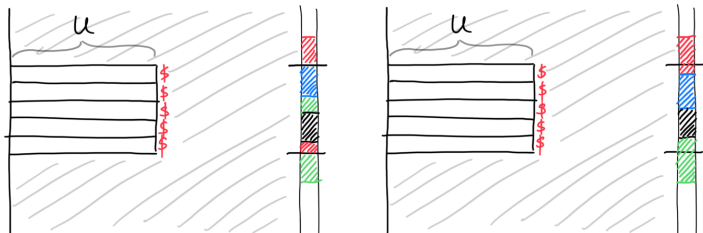
colexBWT: sort input strings colexicographically, then multidollarBWT



In the colexBWT, each interesting interval has at most σ runs.

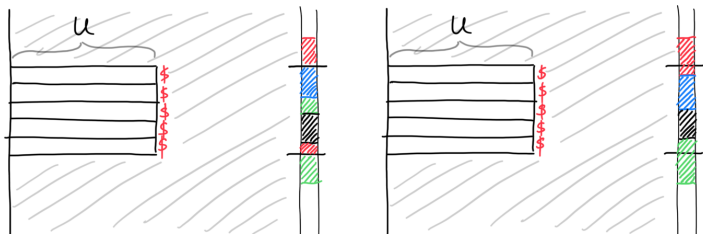
The optimal BWT

(Cenzato, Guerrini, L., Rosone, DCC 2023)

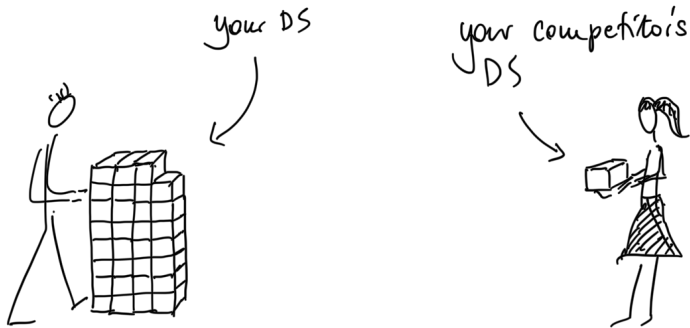


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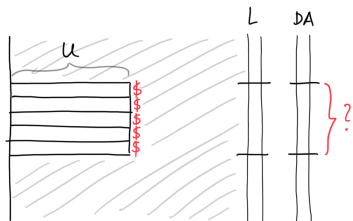
- complication due to successive interesting intervals
- based on algorithm by Bentley, Gibney, Thankachan (ESA, 2020)
- we implemented it, combining it with SAIS and BCR
- negligible computational overhead



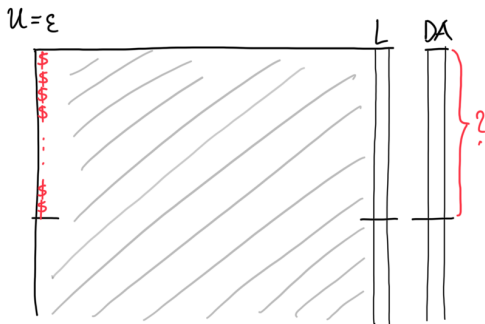
Improvement by [optimalBWT](#) on real biological data:

- in Cenzato & L. (2022, 2024): multipl. factor of up to **4.2**
- in Guerrini, Cenzato, L., Rosone (2023): – " – of up to **31.5**

What is the output order of the concatBWT?



Cenzato, L., Masillo, Rossi, forthcoming



Observation

- Let $U = \epsilon$. Then the U -interval is $[1, k]$, where $k = |\mathcal{M}|$.
- k -prefix of the $DA =$ **output order**.
- The order in all other interesting intervals is induced by this.

What is the output order of the concatBWT?

Concat BWT (name dollar plus #<\$)

— \$ — \$ — \$ — \$ — \$ #

$\mathcal{M} = \{\text{ATATG}, \text{TGA}, \text{ACG}, \text{ATCA}, \text{GGA}\}$

$\text{concatBWT}(\mathcal{M}) = \text{BWT}(\text{ATATG}\$ \text{TGA}\$ \text{ACG}\$ \text{ATCA}\$ \text{GGA}\$ \#)$

rotation	concatBWT	DA
$\$ \# \text{ATATG}\$ \text{TGA}\$ \text{ACG}\$ \text{ATCA}\$ \text{GGA}$	A	5
$\$ \text{ACG}\$ \text{ATCA}\$ \text{GGA}\$ \# \text{ATATG}\$ \text{TGA}$	A	2
$\$ \text{ATCA}\$ \text{GGA}\$ \# \text{ATATG}\$ \text{TGA}\$ \text{ACG}$	G	3
$\$ \text{GGA}\$ \# \text{ATATG}\$ \text{TGA}\$ \text{ACG}\$ \text{ATCA}$	A	4
$\$ \text{TGA}\$ \text{ACG}\$ \text{ATCA}\$ \text{GGA}\$ \# \text{ATATG}$	G	1
...

Map the strings to their lexicographic rank:

ACG	↦	a
ATATG	↦	b
ATCA	↦	c
GGA	↦	d
TGA	↦	e

$\underbrace{\text{ATATG}}_b \$ \underbrace{\text{TGA}}_e \$ \underbrace{\text{ACG}}_a \$ \underbrace{\text{ATCA}}_c \$ \underbrace{\text{GGA}}_d \$ \# \mapsto \text{beacd}\#.$

input: b e a c d # **output:** d e a c b ($DA : 5, 2, 3, 4, 1$)

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b e a c d

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b e a c d #	→	# b e a c d
e a c d # b	lexicographic	a c d # b e
a c d # b e	order	b e a c d #
c d # b e a		c d # b e a
d # b e a c		d # b e a c
# b e a c d		e a c d # b

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# b e a c d		e a c d # b

output order: $\text{bwt}(\text{beacd}\#) = \text{de}\# \text{acb} \rightsquigarrow \text{deacb}$

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- the concatBWT **cannot produce all BWT variants**:

k	3	4	5	6	7	8	9	10	11
	83.33%	75.0%	68.33%	63.89%	60.12%	57.29%	54.8%	52.81%	51.0%

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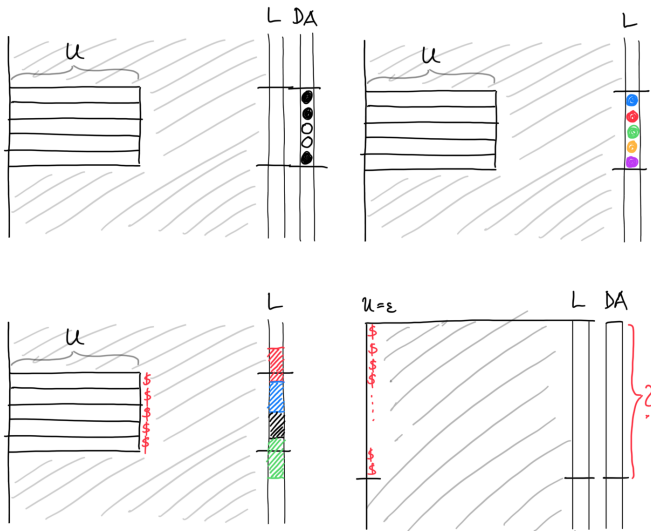
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- examples already on 3 strings where it **cannot produce the optimalBWT**

- the output order of the concatBWT is the **BWT of the meta-string of the input** (almost)
- on most datasets, the concatBWT and the multidolBWT will **differ**
- the concatBWT **cannot produce all BWT variants**:

k	3	4	5	6	7	8	9	10	11
	83.33%	75.0%	68.33%	63.89%	60.12%	57.29%	54.8%	52.81%	51.0%

- only those which, inserting $\#$ somewhere, can become the BWT of some meta-string
- examples already on 3 strings where it **cannot produce the optimalBWT**
- a first study of strings which are the **bwt*** of some string in (Giuliani, L., Masillo, Rizzi: *When a dollar makes a BWT*, TCS 2021)

Summary (BWT everywhere)



Conclusions

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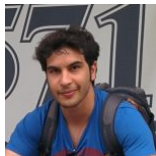
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3. Definition of the number of runs r for string collections **should be standardized** (optBWT or colexBWT).

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