

# Computing the Longest Common Prefix Array Based on the Burrows-Wheeler Transform

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# Suffix-Array

$i$		$S_{SA[i]}$
1	1	annasanannas\$
2	2	nnaSANANNAS\$
3	3	naSANANNAS\$
4	4	saNANNAS\$
5	5	naNANNAS\$
6	6	naNNAS\$
7	7	naNNAS\$
8	8	naNAS\$
9	9	naNAS\$
10	10	naS\$
11	11	aS\$
12	12	s\$
13	13	\$
14		

# Suffix-Array

$i$	$SA[i]$	$S_{SA[i]}$
1	13	\$
2	6	anannas\$
3	8	annas\$
4	1	annasanannas\$
5	11	as\$
6	4	asanannas\$
7	7	nannas\$
8	10	nas\$
9	3	nasananannas\$
10	9	nna\$
11	2	nnasanannas\$
12	12	s\$
13	5	sanannas\$
14		

# Suffix-Array construction algorithms

Many algorithms, see survey paper of Puglisi et al. 2007:

- Time:  $\mathcal{O}(n)$  to  $\mathcal{O}(n^2 \log n)$
- Space:  $5n$  to  $18n$  bytes

DivSufSort of Yuta Mori 2008:

- Time:  $\mathcal{O}(n \log n)$
- Space:  $5n$  bytes

InducedSort of Nong et al. 2009:

- Time:  $\mathcal{O}(n)$
- Space:  $5n$  bytes

# BWT (Burrows–Wheeler transform)

$i$	$SA[i]$	$S_{SA[i]}$
1	13	\$
2	6	anannas\$
3	8	annas\$
4	1	annasanannas\$
5	11	as\$
6	4	asanannas\$
7	7	nannas\$
8	10	nas\$
9	3	nasananannas\$
10	9	nna\$
11	2	nnasanannas\$
12	12	s\$
13	5	sanannas\$
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# BWT (Burrows–Wheeler transform)

$i$	$SA[i]$	$BWT[i]$	$S_{SA[i]}$
1	13	s	\$
2	6	s	anannas\$
3	8	n	annas\$
4	1	\$	annasanannas\$
5	11	n	as\$
6	4	n	asanannas\$
7	7	a	nannas\$
8	10	n	nas\$
9	3	n	nasananannas\$
10	9	a	nna\$
11	2	a	nnasanannas\$
12	12	a	s\$
13	5	a	sanannas\$
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# BWT construction algorithms

Compute BWT from suffix array:

- Time:  $\mathcal{O}(n)$
- Space:  $n$  bytes

Direct computation, e.g.:

- Lippert et al. 2005:
  - Time:  $\mathcal{O}(n \log n)$
  - Space:  $\frac{1}{2}(1 + \sigma)(1 + \epsilon)$  bits
- Okanohara and Sadakane 2009:
  - Time:  $\mathcal{O}(n)$
  - Space:  $\mathcal{O}(n \log_\sigma \log(\log_\sigma n)) \approx 2.5n$  bytes

# LCP array (Longest Common Prefix array)

$i$	$SA[i]$	$BWT[i]$	$S_{SA[i]}$
1	13	s	\$
2	6	s	anannas\$
3	8	n	annas\$
4	1	\$	annasanannas\$
5	11	n	as\$
6	4	n	asanannas\$
7	7	a	nannas\$
8	10	n	nas\$
9	3	n	nasananannas\$
10	9	a	nna\$
11	2	a	nnasanannas\$
12	12	a	s\$
13	5	a	sanannas\$
14			

# LCP array (Longest Common Prefix array)

$i$	$SA[i]$	$BWT[i]$	$LCP[i]$	$S_{SA[i]}$
1	13	s	-1	\$
2	6	s	0	anannas\$
3	8	n	2	annas\$
4	1	\$	5	annasanannas\$
5	11	n	1	as\$
6	4	n	2	asanannas\$
7	7	a	0	nannas\$
8	10	n	2	nas\$
9	3	n	3	nasananannas\$
10	9	a	1	nna\$
11	2	a	4	nnasanannas\$
12	12	a	0	s\$
13	5	a	1	sanannas\$
14			-1	

# LCP construction algorithms from suffix array

KLAAP-algorithm of Kasai et al. 2001:

- Time:  $\mathcal{O}(n)$
- Space:  $13n$  bytes
- Space improvement by Manzini 2004:  $9n$  bytes

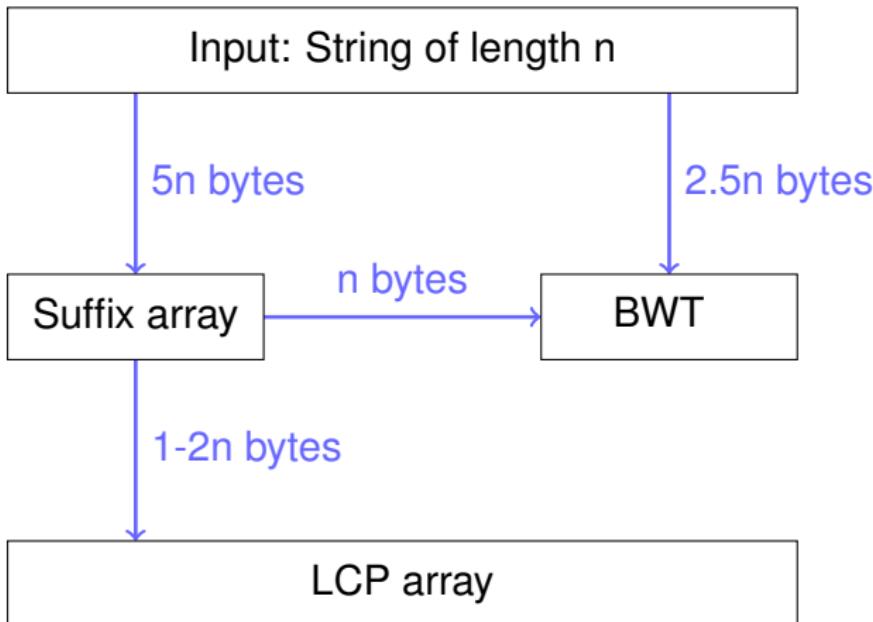
$\Phi$ -algorithm of Kärkkäinen et al. 2009:

- Time:  $\mathcal{O}(n)$
- Space:  $5n + \frac{4n}{k}$  bytes or  $n + \frac{4n}{k}$  bytes (semi-external)

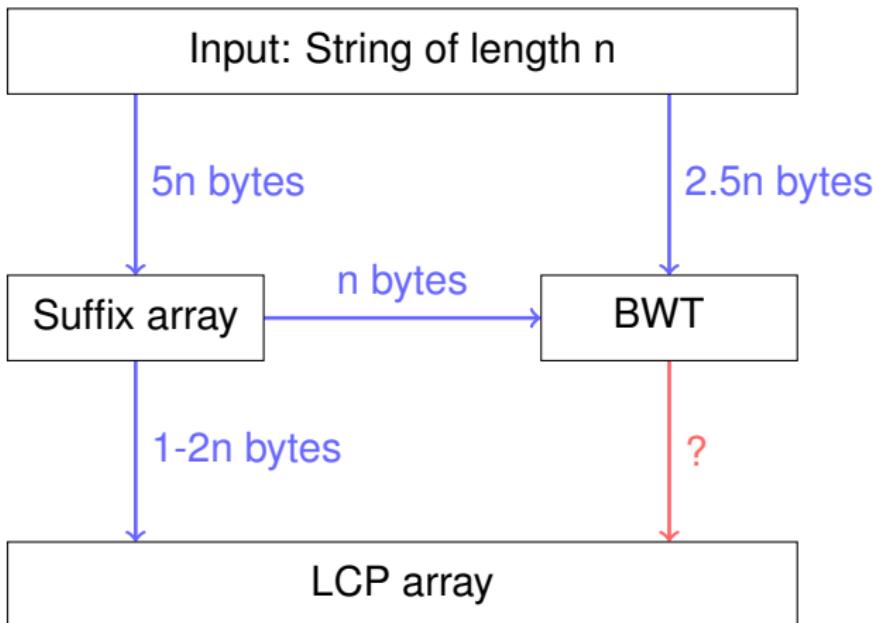
go- $\Phi$ -algorithm of Gog and Ohlebusch 2010:

- Time:  $\mathcal{O}(n)$
- Space:  $2n$  bytes

# Overview



# Task



# Observation

Assume the string  $\omega$  occurs  $t$  times in a string  $S$ :

- There are  $t$  suffixes of  $S$  that start with  $\omega$ .
- These suffixes occur consecutively in the suffix array.
- Let  $j$  be the largest index, so that the corresponding suffix starts with  $\omega$ .
- $LCP[j + 1] < |\omega|$

# Example: annasanannas\$

$i$	$BWT[i]$	$LCP[i]$	$S_{SA[i]}$
1	s	-1	\$
2	s	0	anannas\$
3	n	2	annas\$
4	\$	5	annasanannas\$
5	n	1	as\$
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# Idea

- Calculate all substrings of  $S$ , in the order of their length.
- Determine for each substring  $\omega$  the corresponding interval  $[lb \dots rb]$ .
- If  $LCP[rb + 1]$  wasn't set before, set  $LCP[rb + 1] = |\omega| - 1$ .

# Pseudocode

```
LCP[1] ← -1
LCP[i] ← ⊥  ∀i : 2 ≤ i ≤ n
LCP[n + 1] ← -1
initialize an empty queue
enqueue(ε)
while not all lcp values are calculated do
     $\omega \leftarrow \text{dequeue}()$ 
    for each  $a \in \Sigma$  do
        enqueue( $a\omega$ )
         $[lb \dots rb] \leftarrow \text{getIntervalBounds}(a\omega)$ 
        if  $rb \neq \perp$  and  $\text{LCP}[rb + 1] = \perp$  then
             $\text{LCP}[rb + 1] \leftarrow |a\omega| - 1$ 
```

# Pseudocode

$LCP[1] \leftarrow -1$

$LCP[i] \leftarrow \perp \quad \forall i : 2 \leq i \leq n$

$LCP[n + 1] \leftarrow -1$

initialize an empty queue

*enqueue( $\epsilon$ )*

**while** queue is not empty **do**

$\omega \leftarrow dequeue()$

**for each**  $a \in \Sigma$  **do**

*enqueue( $a\omega$ )*

$[lb \dots rb] \leftarrow getIntervalBounds(a\omega)$

**if**  $rb \neq \perp$  **and**  $LCP[rb + 1] = \perp$  **then**

$LCP[rb + 1] \leftarrow |a\omega| - 1$

*enqueue( $a\omega$ )*

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1	s	-1	\$
2	s	0	anannas\$
3	n	⊥	annas\$
4	\$	⊥	annasanannas\$
5	n	⊥	as\$
6	n	⊥	asanannas\$
7	a	0	nannas\$
8	n	⊥	nas\$
9	n	⊥	nasanannas\$
10	a	⊥	nnas\$
11	a	⊥	nnasanannas\$
12	a	0	s\$
13	a	1	sanannas\$
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# Saving space

Store interval boundaries  $[lb \dots rb]$  of  $\omega$  not  $\omega$  itself:

- Store two integers:  $2 \log n$  bit for each substring.
- Mark  $lb$  and  $rb$  in two bit vectors  $B_{lb}$  and  $B_{rb}$  of length  $n$ :  
 $2n$  bit for all substrings of same length.

Reserve only  $n$  byte for the LCP array:

- Use the fact, that algorithm calculates the LCP values in ascending order.
- If new LCP value cannot be stored into the LCP array, write LCP array to disk.

# Calculation of the subintervals

Problem: Given the interval  $[lb \dots rb]$  of  $\omega$ , if  $a\omega$ ,  $a \in \Sigma$  is a substring of  $S$ , then find the interval of  $a\omega$ .

Modified backward search with wavelet tree of the BWT:

- Find all subintervals by traversing the wavelet tree in a depth-first manner.
- Use Huffman-shaped wavelet trees to save time and space.
- Time:  $\mathcal{O}(\sigma)$
- Space:  $n$  bytes

# Runtime and space

Time complexity:  $\mathcal{O}(\sigma n)$

Practical and space efficient implementation:

- Time:  $\mathcal{O}(n \log n)$
- Space:  $\approx 2.2n$  bytes

# Experimental Results

## Test cases

- Pizza&Chili Corpus
- Some DNA-files from [www.ensembl.org](http://www.ensembl.org) (Release 62)

## Implementation

- uses the *sdsL*-library of Simon Gog  
([www.uni-ulm.de/in/theo/research/sdsL.html](http://www.uni-ulm.de/in/theo/research/sdsL.html))
- uses bit compressed arrays (i.e.  $\log n$  bits, not 4 bytes or 8 bytes per integer)

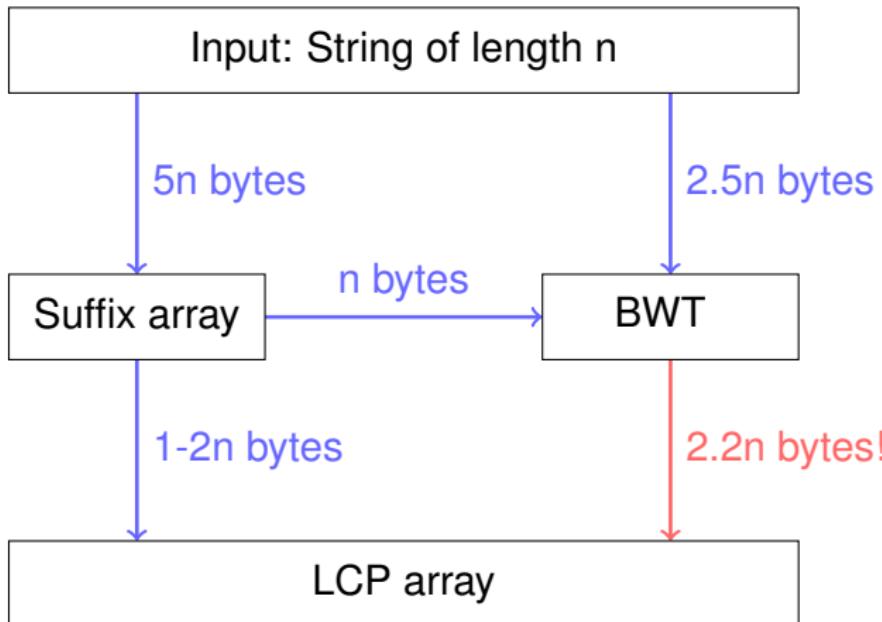
# Experimental Results

	dna 200MB		english 200MB		proteins 200MB		sources 200MB		xml 200MB	
SA constr.	71	5	64	5	72	5	45	5	49	5
BWT constr.	93	1.9	109	2.2	150	2.6	87	2.2	83	2.2
KLAAP	58	9	48	9	48	9	33	9	32	9
Φ1	37	9	30	9	30	9	22	9	22	9
Φ4	83	6	74	6	78	6	60	6	63	6
Φ64	80	5.1	76	5.1	78	5.1	64	5.1	75	5.1
Φ4-Semi	78	2	72	2	72	2	59	2	63	2
Φ64-Semi	76	1.1	70	1.1	70	1.1	56	1.1	73	1.1
go-Φ	53	2	74	2	70	2	51	2	49	2
new algorithm	66	1.8	124	2	137	2	131	2.2	99	2.1
KLAAP	129	9	112	9	120	9	78	9	81	9
Φ1	108	9	94	9	102	9	67	9	71	9
Φ4	154	6	138	6	150	6	105	6	112	6
Φ64	151	5.1	140	5.1	150	5.1	109	5.1	124	5.1
Φ4-Semi	149	5	136	5	144	5	104	5	112	5
Φ64-Semi	147	5	134	5	142	5	101	5	122	5
go-Φ	124	5	138	5	142	5	96	5	98	5
new algorithm	159	1.9	233	2.2	287	2.6	218	2.2	182	2.2

# Experimental Results

	Stickleback 446 MB		Chicken 1.050 MB		Sloth 2.060 MB		Orangutan 3.093 MB	
SA constr.	171	5	471	5	1.100	5	2.013	9
BWT constr.	204	2	549	1,9	1.062	1,9	1.686	1,9
KLAAP	150	9	454	9	951	9	1.527	9
Φ1	98	9	318	9	756	9	1.183	9
Φ4	187	6	534	6	1.236	6	-	-
Φ64	193	5,1	522	5,1	1.163	5,1	-	-
Φ4-Semi	182	2	523	2	1.183	2	1.786	2
Φ64-Semi	180	1,1	454	1,1	1.064	1,1	1.648	1,1
go-Φ	117	2	316	2	685	2	1.041	2
new algorithm	141	1,8	338	1,8	800	1,8	1.270	1,8
KLAAP	321	9	925	9	2.051	9	3.540	9
Φ1	269	9	789	9	1.856	9	3.196	9
Φ4	358	6	1.005	6	2.336	6	-	-
Φ64	364	5,1	993	5,1	2.263	5,1	-	-
Φ4-Semi	353	5	994	5	2.283	5	3.799	9
Φ64-Semi	351	5	925	5	2.164	5	3.661	9
go-Φ	288	5	787	5	1.785	5	3.054	9
new algorithm	345	2	887	1,9	1.862	1,9	2.956	1,9

# Solution



Thank you!  
Any Questions?