

PFP Compressed Suffix Trees

Christina Boucher¹, Ondřej Cvacho², Travis Gagie³, Jan Holub², Giovanni Manzini⁴, Gonzalo Navarro⁵, and Massimiliano Rossi¹

¹ *University of Florida, Department of Computer & Information Science & Engineering.*

² *Czech Technical University in Prague, Department of Theoretical Computer Science.*

³ *Dalhousie University, Faculty of Computer Science.*

⁴ *University of Eastern Piedmont, Department of Science and Technological Innovation.*

⁵ *University of Chile, CeBiB – Center for Biotechnology and Bioengineering, Department of Computer Science.*

DSB

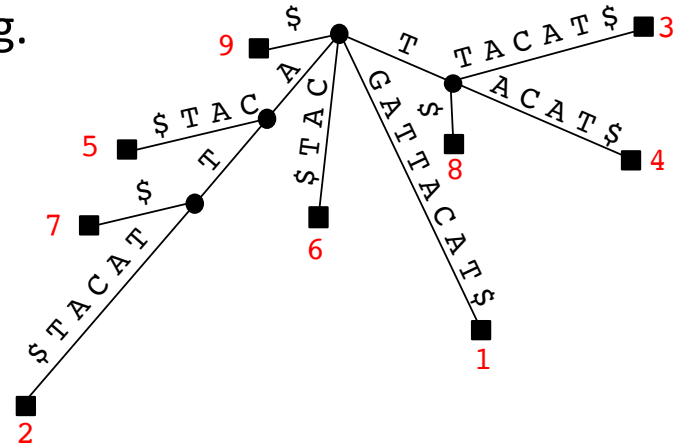
12 Feb 2021

Suffix tree

Weiner, "Linear pattern matching algorithms". [SWAT 1973]

Compact trie of the suffixes of the string.

S: G A T T A C A T \$
1 2 3 4 5 6 7 8 9



Index all the $O(n^2)$ substrings of $S[1..n]$ in $O(n)$ time and space.

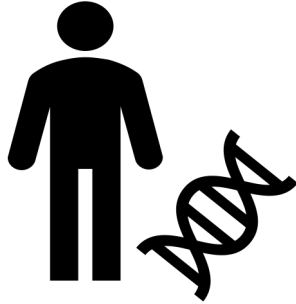
One of the most powerful data structure in stringology and bioinformatics.

E.g.,:

- Maximal Unique Matches (MUMs) (sequence alignment)
- Maximal Exact Matches (MEMs) (short read alignment)
- Tandem Repeats,
- ...

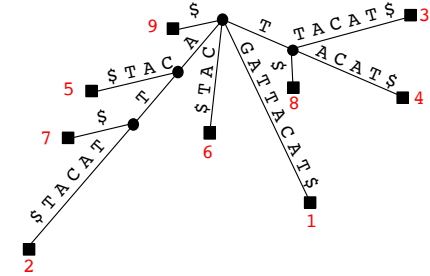
Suffix tree

Weiner, "Linear pattern matching algorithms". [SWAT 1973]



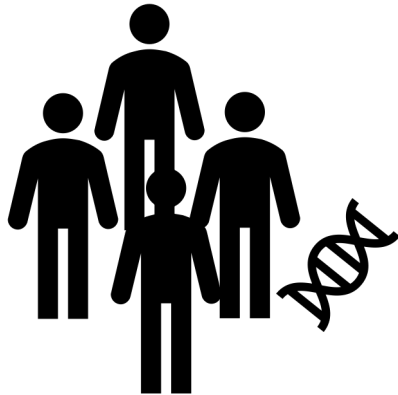
One human chromosome 19:

- 58.5 Mbp (haploid)
- Less than 16 MB (using gzip)



Classical implementation of its suffix tree:

- 1.2 GB



512 human chromosome 19:

- 29,952 Mbp (haploid)
- Less than 7.5 GB (using gzip)

Classical implementation of its suffix tree:

- 600 GB

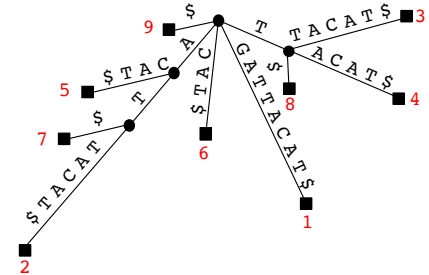
We need something smaller!

Compressed suffix trees (with full functionality)

Sadakane, “Compressed Suffix Trees with Full Functionality”. [Theory of Computing Systems 2007]

Simulation of the suffix tree functionality using:

1. Random access to SA, ISA, LCP.
2. Operations RMQ, NSV, PSV on LCP.



Fischer, Mäkinen, Navarro, “Faster entropy-bounded compressed suffix trees”. [TCS 2009]



One human chromosome 19:

- 58.5 Mbp (haploid)
- Less than 16 MB (using gzip)



512 human chromosome 19:

- 29,952 Mbp (haploid)
- Less than 7.5 GB (using gzip)

Compressed suffix tree (**sds1**):

- 64 MB (2.1 GB working memory)
- ~32 sec

Compressed suffix tree (**sds1**):

- 28 GB (1,106 GB working memory)
- ~16 hour and 30 minutes

The final index is small, but the working memory does not scale.

“To use [an index] one must first *build it!*”

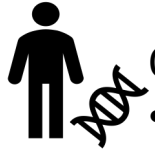
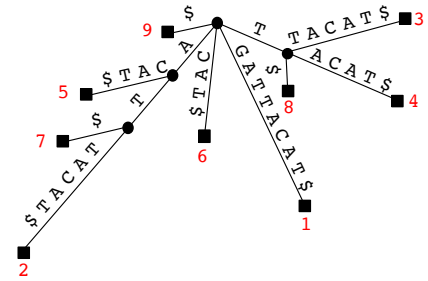
Ferragina, Gagie, Manzini, “Lightweight data indexing and compression in external memory”.
[Algorithmica 2012]

PFP Compressed suffix trees

Use prefix-free parsing as data structure.

Simulation of the suffix tree functionality using:

1. Random access to SA, ISA, and S.
2. Operation LCE + SA to simulate LCP and RMQ on LCP.
3. Operations $Prev(i, h)$ and $Next(i, h)$ to simulate PSV and NSV on LCP.



One human chromosome 19:

- 58.5 Mbp (haploid)
- Less than 16 MB (using gzip)



512 human chromosome 19:

- 29,952 Mbp (haploid)
- Less than 7.5 GB (using gzip)

PFP Compressed suffix tree (**pfp**):

- 1.6 GB (6 GB working memory)
- ~1 min

PFP Compressed suffix tree (**pfp**):

- 19 GB (27.5 GB working memory)
- ~30 minutes

Experimental results – Chr19

Setup:

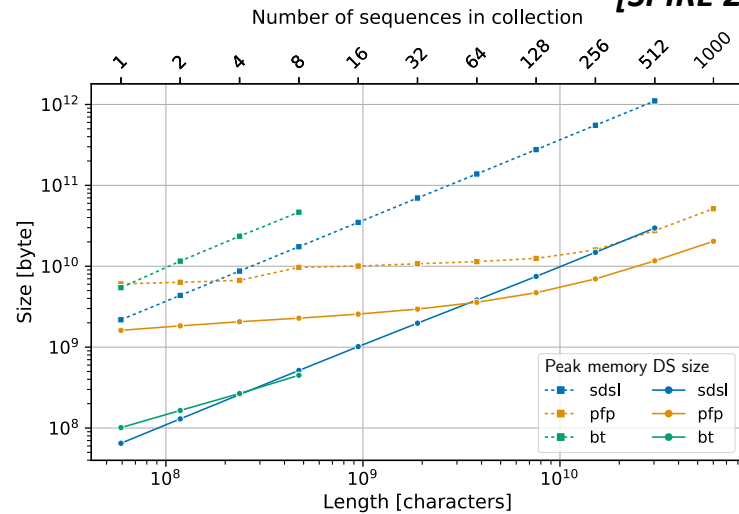
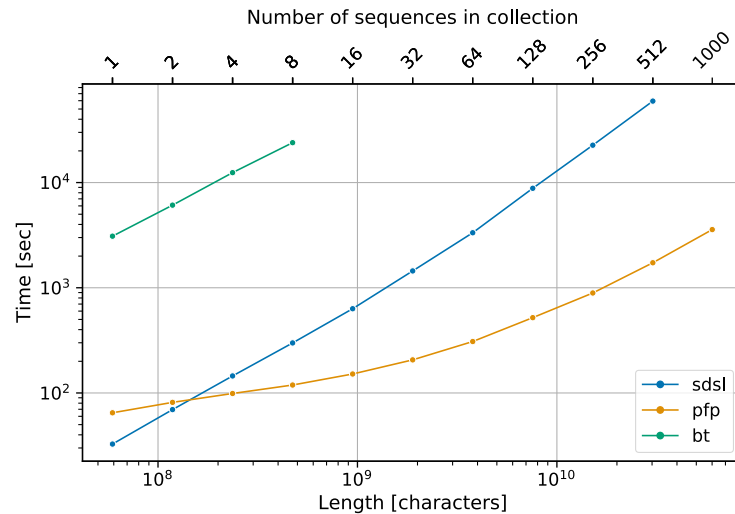
- Intel(R) Xeon(R) CPU E5-2640 v4 @ 2.40GHz
- 40 cores
- 756 GB RAM

Data structures:

- PFP compressed suffix tree (**pfp**) Available at "<https://github.com/maxrossi91/pfp-cst>"
- SDSL compressed suffix tree (**sdsl1**)
- Block tree compressed suffix tree (**bt**)

Cáceres, Navarro, "Faster repetition-aware compressed suffix trees based on block trees".

[SPIRE 2019]



Also 10,000 *Salmonella* genomes in the paper with similar trends.

PFP Compressed Suffix Trees

Prefix-free parsing

Boucher, Gagie, Kuhnle, Langmead, Manzini, Mun, "Prefix-free parsing for building Big BWTs". [AMB 2019]

$S: G A T T A C A T \# G A T A C A T \# G A T T A G A T A \# \#$

We consider S to be circular and we append w copies of $\#$ $w = 2$

$E = \{AC, AG, T\#, \#\#\}$ (*trigger strings of length w*)

$S: G A T T A C A T \# G A T A C A T \# G A T T A G A T A \# \#$

$P = D[1] \quad D[2] \quad D[4] \quad D[2] \quad D[5] \quad D[3]$

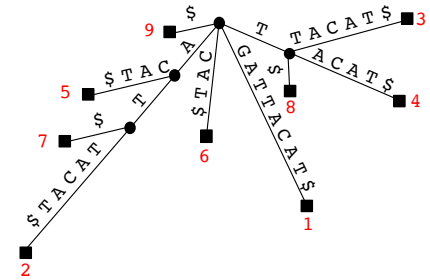
$D = \{\#\#GATTAC, ACAT\#, AGATA\#\#, T\#GATAC, T\#GATTAG\}$

PFP Compressed suffix trees

Use prefix-free parsing as data structure.

Simulation of the suffix tree functionality using:

1. Random access to SA , ISA , and S .
2. Operation $LCE(p, q)$, length of the longest common prefix of $S[p..]$ and $S[q..]$.
 1. $LCP[i] = LCE(SA[i], SA[i - 1])$
 2. $Min(i, j) = LCE(SA[i], SA[j])$, i.e., the smallest value in $LCP[i + 1..j]$
3. Operations $Prev(i, h)$ and $Next(i, h)$ the closest position preceding and following i with LCP value smaller than h



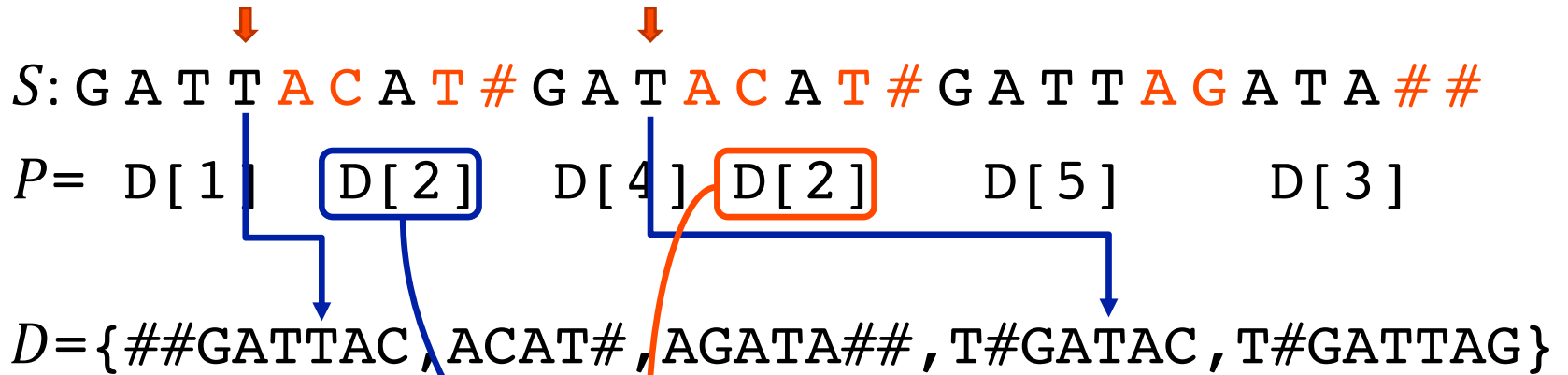
Primitives to implement:

- Random access to S .
- Random access to SA and ISA .
- Operation LCE .
- Operations $Prev(i, h)$ and $Next(i, h)$.

Data structures on PFP:

- Parse P and Dictionary D .
- Bitvector B_P
- Bitvector B_{BWT}
- Grid W
- Table and grid M
- Suffix ranks on D
- Suffix tree data structure on P

Operation LCE



Lexicographically sorted phrase suffixes of D LCP

ACAT#	0
AGATA#	1
##GATTAC	2
T#GATAC	3
T#GATTAG	2
##GATTAC	1
T#GATTAG	3

SLCP Lexicographically sorted suffixes of P

0	D[1]D[2]D[4]D[2]D[5]D[3]
0	D[2]D[4]D[2]D[5]D[3]
8	D[2]D[5]D[3]
1	D[3]
0	D[4]D[2]D[5]D[3]
5	D[5]D[3]

$$LCE(4,12) = 3 + 8 - 2 = 9$$

SLCP: LCP of P in characters

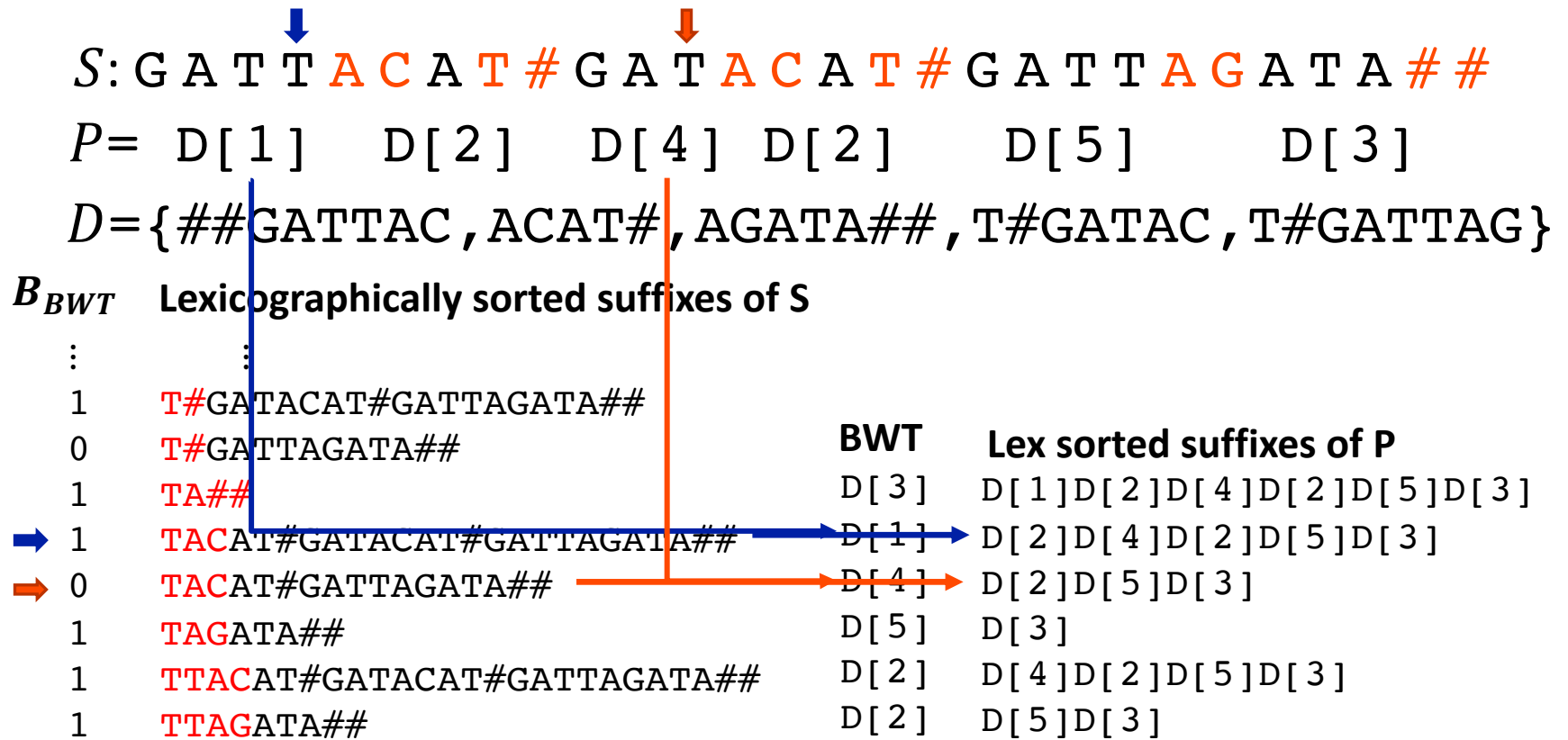
Operation SA

$S: G A T T A C A T \# G A T A C A T \# G A T T A G A T A \# \#$
 $P = D[1] \quad D[2] \quad D[4] \quad D[2] \quad D[5] \quad D[3]$
 $D = \{ \# \# G A T T A C, A C A T \#, A G A T A \# \#, T \# G A T A C, T \# G A T T A G \}$

	B_{BWT}	Lexicographically sorted suffixes of S
	:	:
	1	T #GATACAT#GATTAGATA##
#1s: lexicographic rank of the proper phrase suffix.	0	T #GATTAGATA##
	1	TA ##
	1	TAC AT#GATACAT#GATTAGATA##
	0	TAC AT#GATTAGATA##
	1	TAG ATA##
	1	TTAC AT#GATACAT#GATTAGATA##
	1	TTAG ATA##

Each suffix of S **starts with a proper phrase suffix** of length at least w

Operation SA

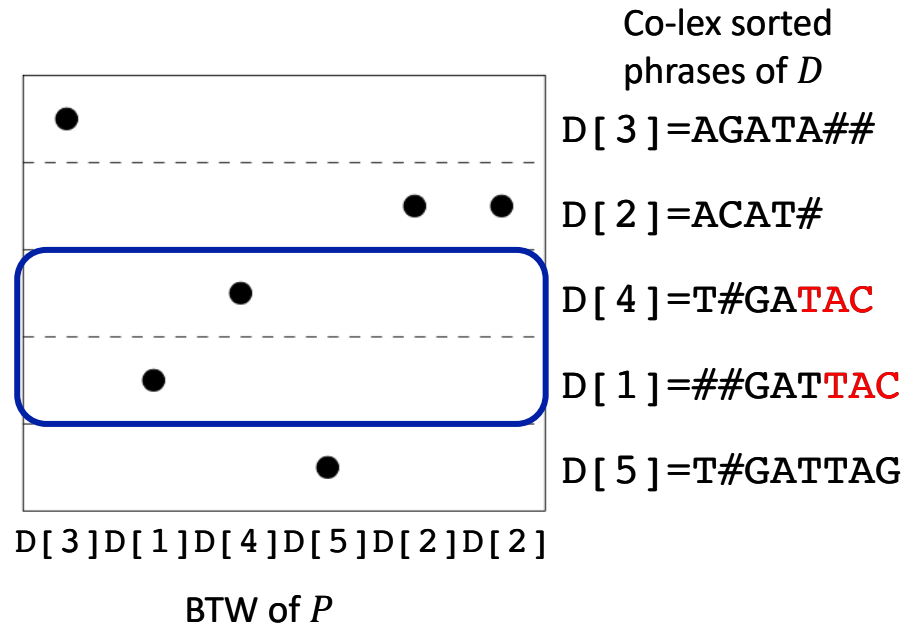


The relative order of suffixes of S starting with the same proper phrase suffix is given by the relative order of the corresponding suffixes of P

Operation SA

$S: G A T T A C A T \# G A T A C A T \# G A T T A G A T A \# \#$
 $P = D[1] \quad D[2] \quad D[4] \quad D[2] \quad D[5] \quad D[3]$
 $D = \{ \# \# G A T T A C, A C A T \#, A G A T A \# \#, T \# G A T A C, T \# G A T T A G \}$

Find the **relative order** of occurrences in BWT of P of **phrases with the same proper phrase suffix**

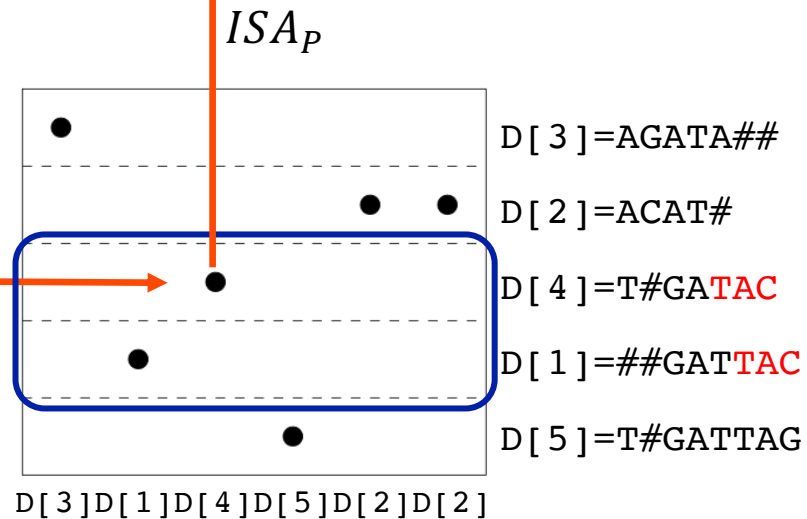


Operation SA

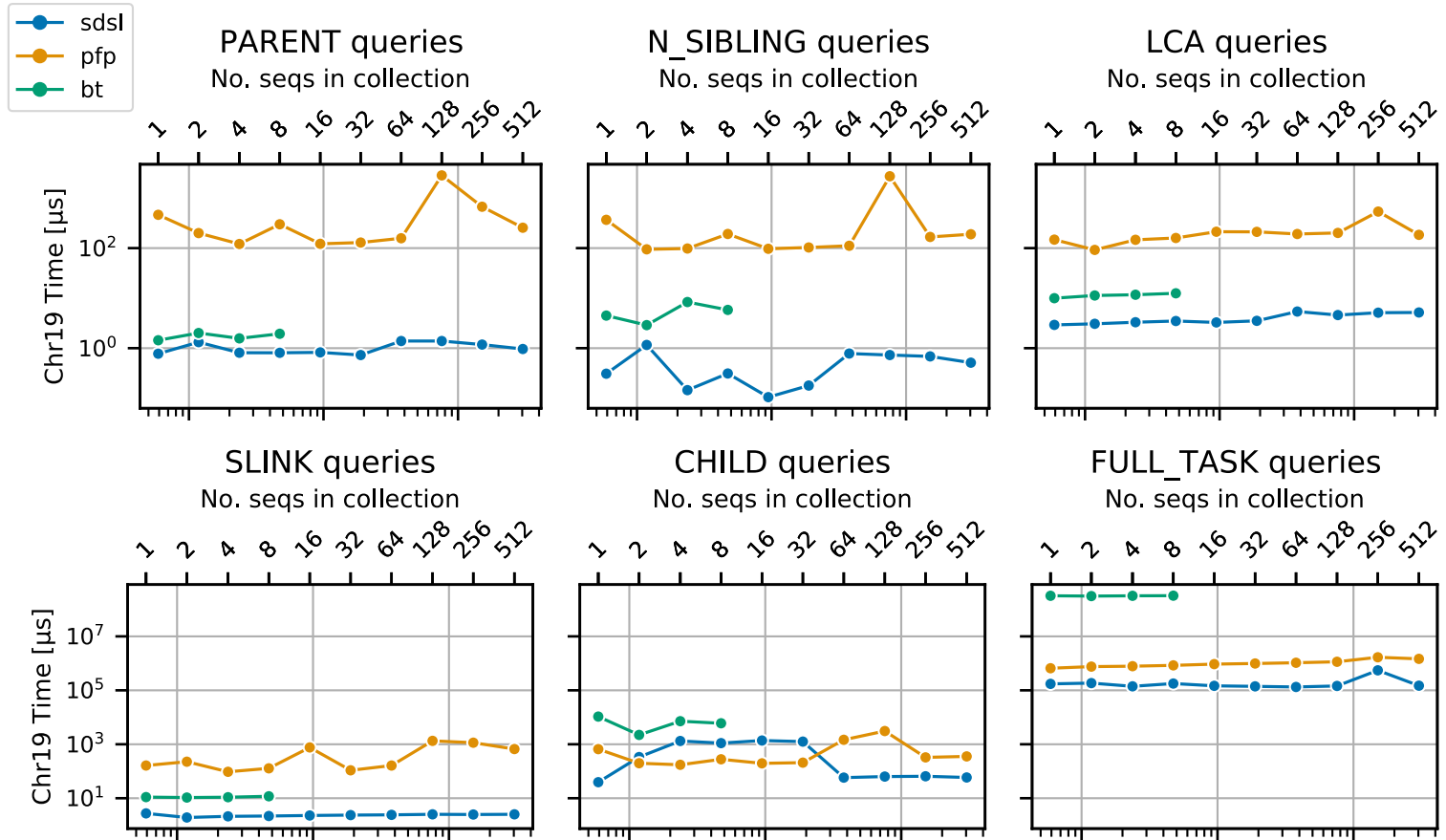
$S: G A T T A C A T \# G A T A C A T \# G A T T A G A T A \# \#$
 $P = D[1] \quad D[2] \quad D[4] \quad D[2] \quad D[5] \quad D[3]$
 $D = \{ \# \# G A T T A C, A C A T \#, A G A T A \# \#, T \# G A T A C, T \# G A T T A G \}$

B_{BWT} Lexicographically sorted suffixes of S

:	:
1	T#GATACAT#GATTAGATA##
0	T#GATTAGATA##
1	TA##
→ 1	TACAT#GATACAT#GATTAGATA##
→ 0	TACAT#GATTAGATA##
1	TAGATA##
1	TTACAT#GATACAT#GATTAGATA##
1	TTAGATA##



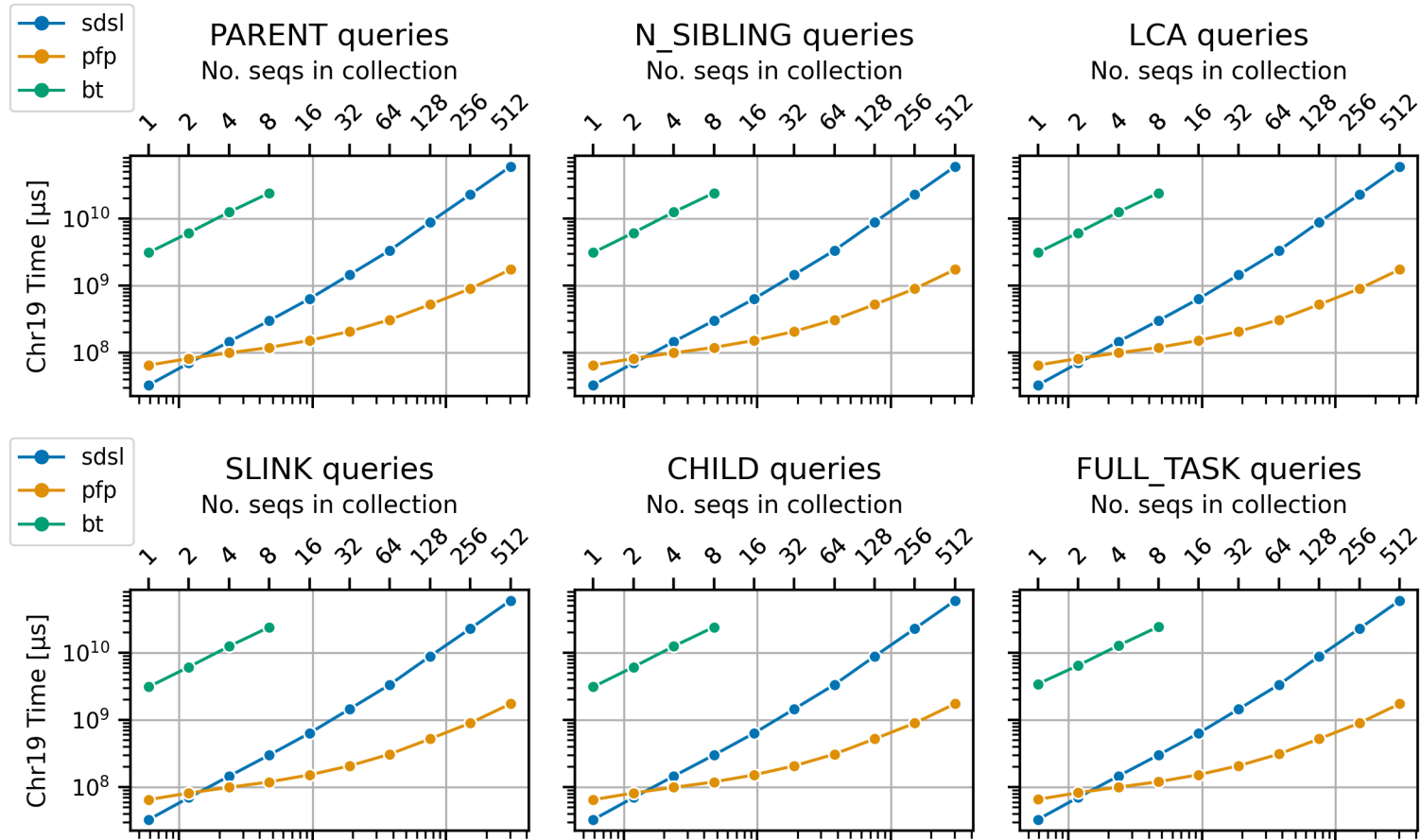
Experimental results – Queries



“To use [an index] one must first *build it!*”

Ferragina, Gagie, Manzini, “Lightweight data indexing and compression in external memory”.
 [Algorithmica 2012]

Experimental results – Queries + Build



“To use [an index] one must first *build it!*”

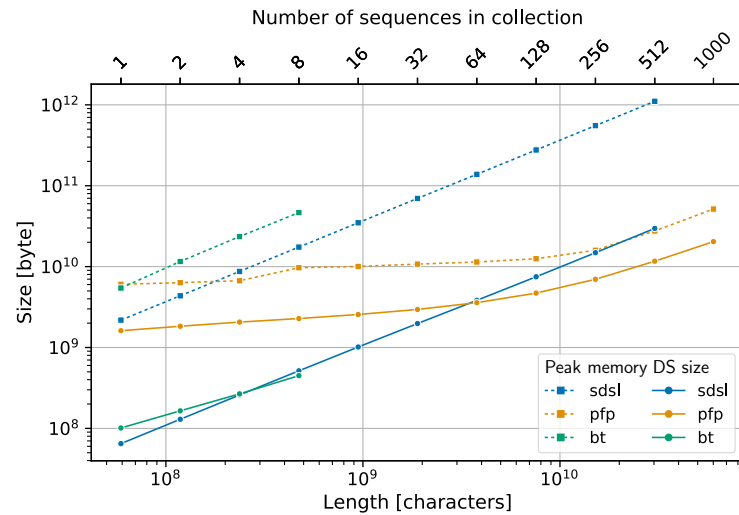
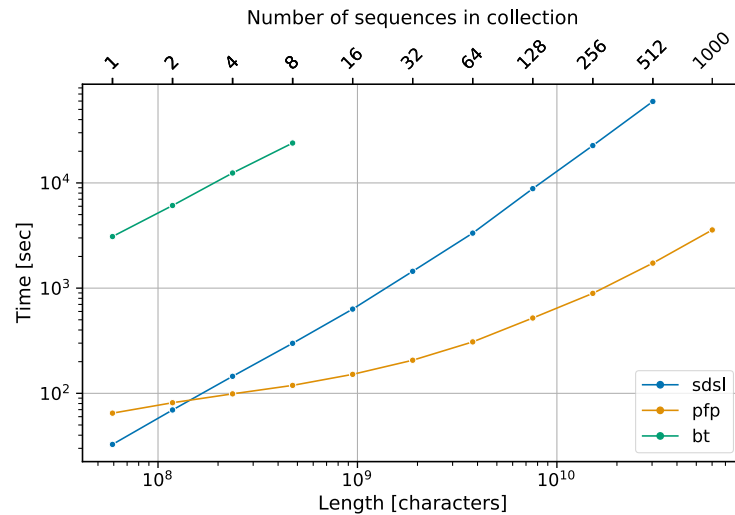
Ferragina, Gagie, Manzini, “Lightweight data indexing and compression in external memory”.
 [Algorithmica 2012]

Construction time

“To use [an index] one must first *build it!*”

Ferragina, Gagie, Manzini, “*Lightweight data indexing and compression in external memory*”.
[Algorithmica 2012]

We build it!



Thank you for your attention!

Paper at ALENEX21 <https://doi.org/10.1137/1.9781611976472.5>

Github <https://github.com/maxrossi91/pfp-cst>

Funded by:

- National Science Foundation (NSF) IIS (Grant No. 1618814),
- National Science Foundation (NSF) IIBR (Grant No. 2029552),
- National Institutes of Health (NIH) R01 (Grant No. HG011392),
- OP VVV project Research Center for Informatics (no. CZ.02.1.01/0.0/0.0/16 019/0000765),
- PRIN grant 2017WR7SHH,
- ANID Basal Funds FB0001 and Fondecyt Grant 1-200038, Chile.