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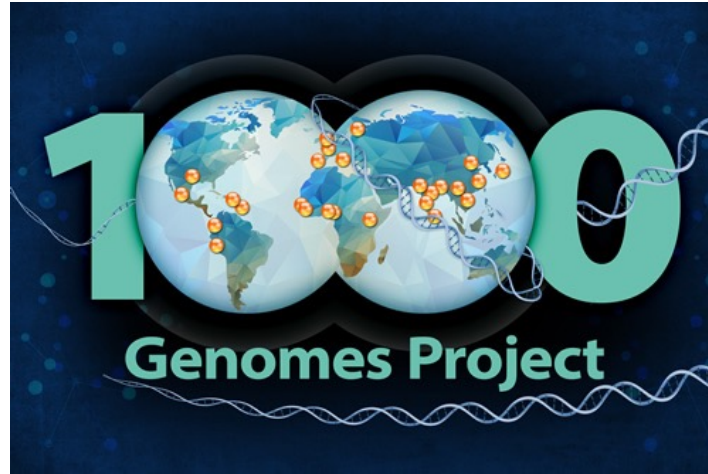
Recursive Prefix-Free Parsing for Building Big BWTs

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¹ Department of Computer and Information Science, University of Florida

² Faculty of Computer Science, Dalhousie University

Motivation



2008 - 2015

More than 3000 individual sequenced

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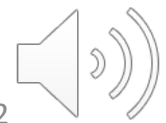
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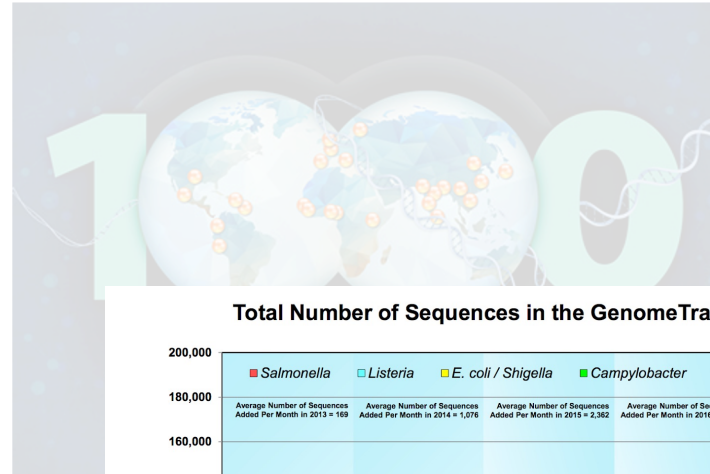
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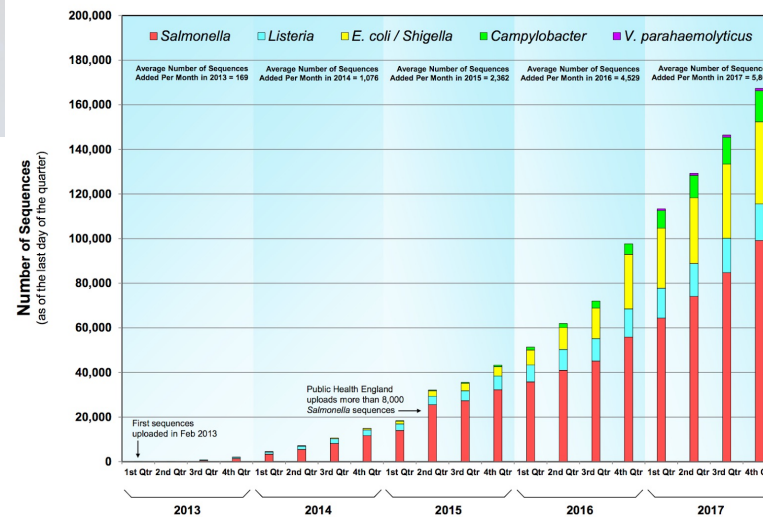
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2008- 2015

More than 3000 individual sequenced

Total Number of Sequences in the GenomeTrakr Database



2012- present

More than 580,000 isolates sequenced

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2008- 2015
 More than 3000 individual sequenced

2012- present
 More than 580,000 isolates sequenced

2012-2018
 Sequencing rare disease

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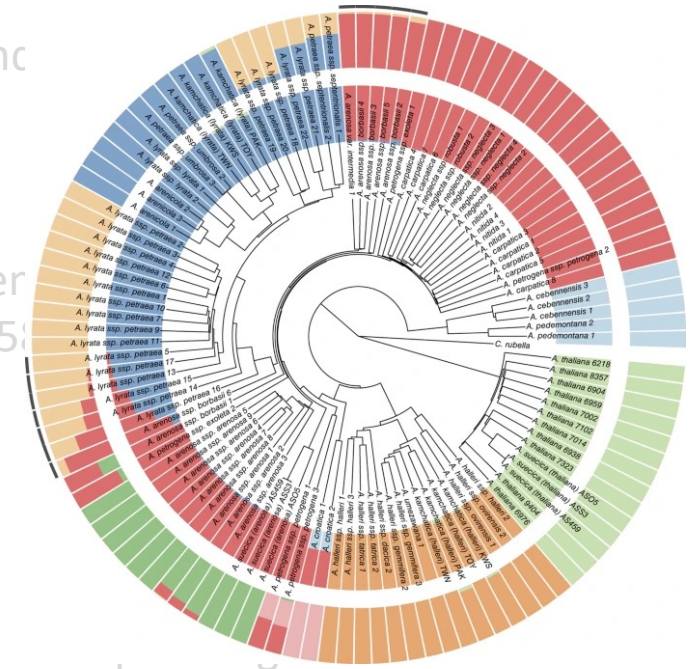
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2008- 2015
More than 3000 inc

2012- present
More than 50



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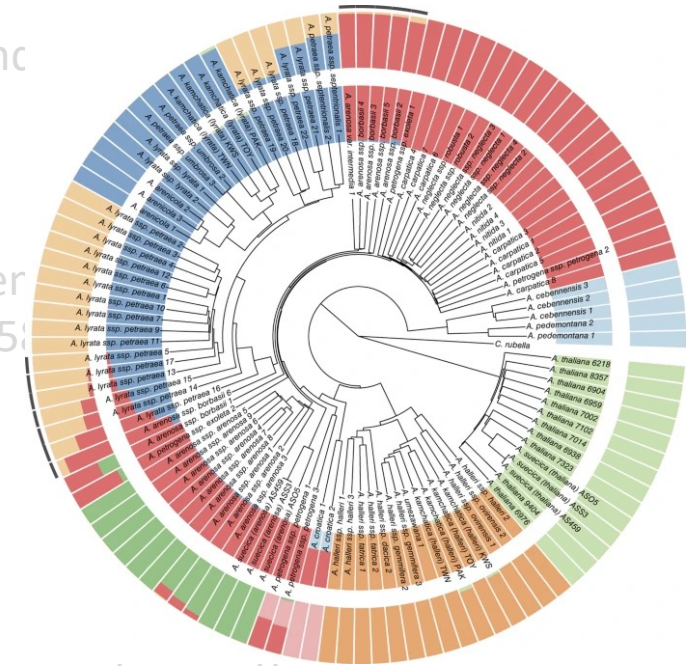
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2008- 2015

more than 3000 inc

2012- present
More than 50



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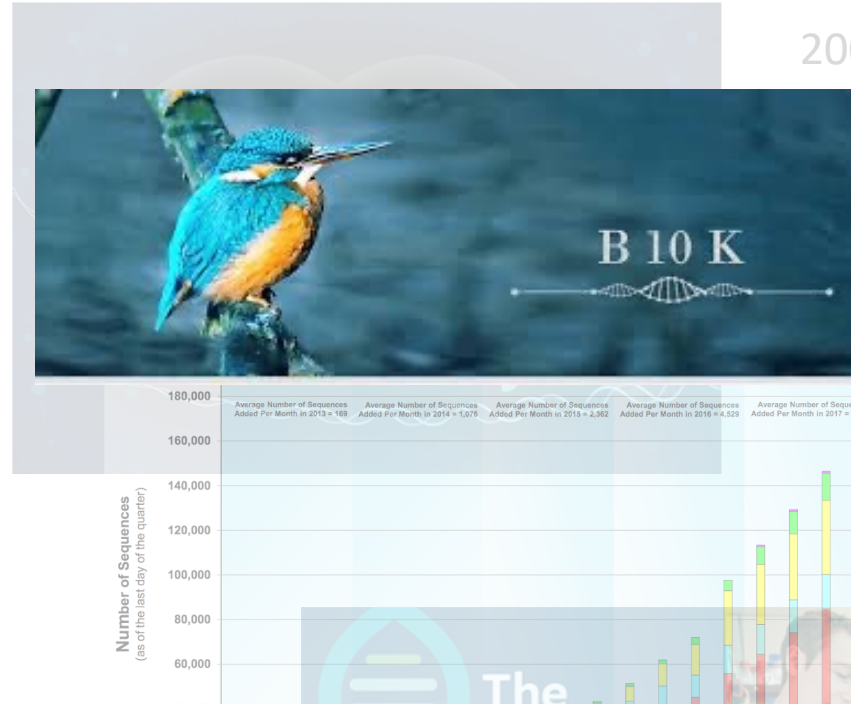
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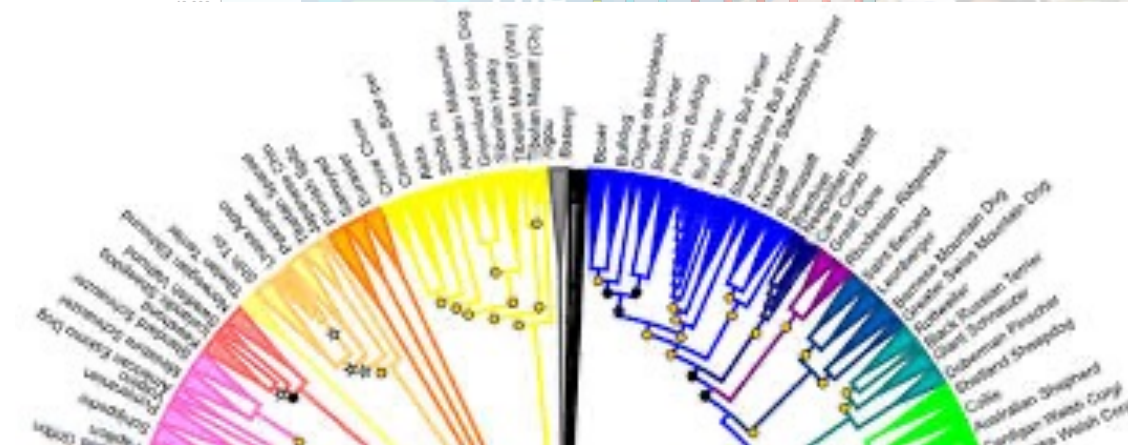
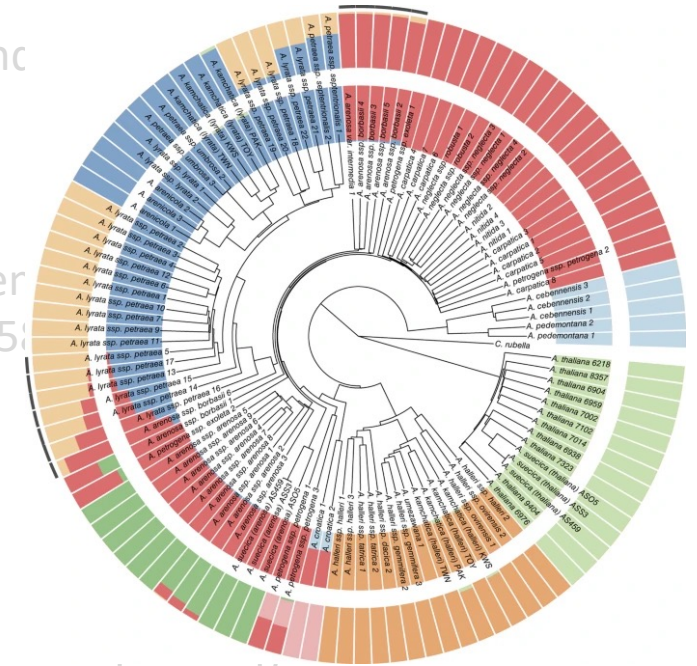
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2008- 2015

More than 3000 inc

2012- present
More than 50



FM-index, BWT

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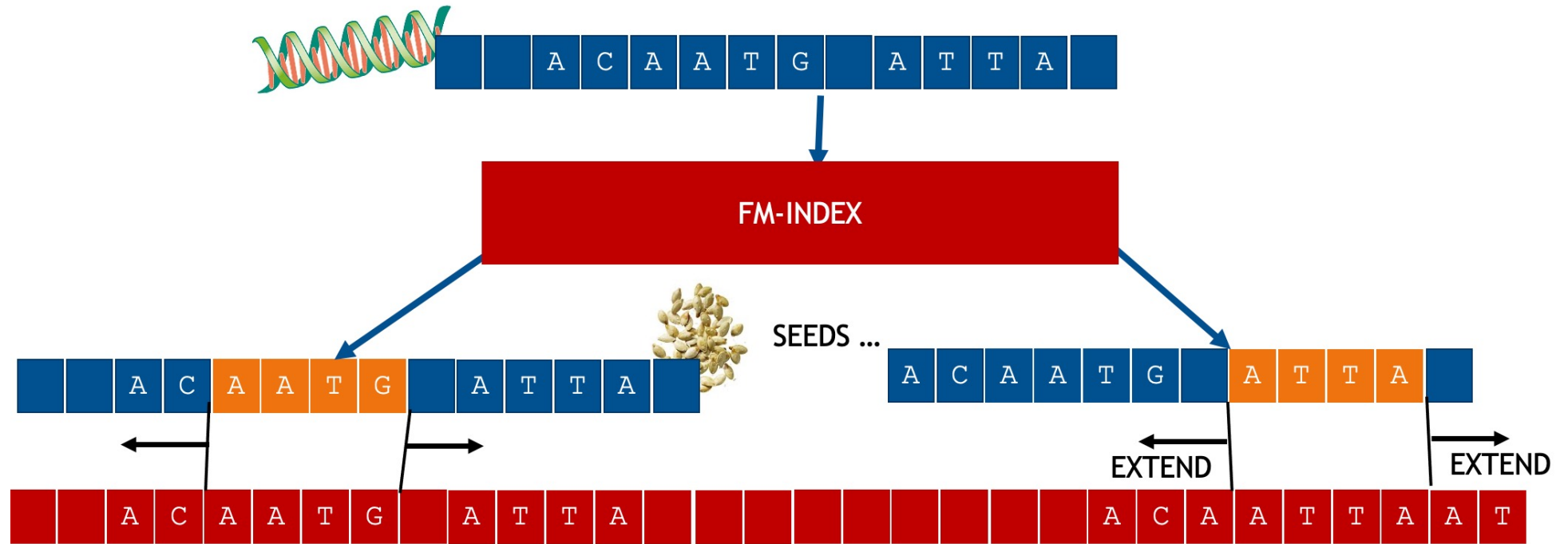
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S: AAGGTNTATACCTTCCCAGGTAA**C**AAACCAACCAA\$
 AAGGTNTATACCTTCCCAGGTAA**A**AAACCAACCAA\$
 AAGGTNTATACCTTCCCAGGTAA**T**AAACCAACCAA\$



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```
S:   ##AAGGTNTATACCTTCCCAGGTAACAAACCAACCAA$  
     AAGGTNTATACCTTCCCAGGTAAAAAACCAACCAA$  
     AAGGTNTATACCTTCCCAGGTAATAAACCAACCAA$##
```



Prefix Free Parsing

```
S:   ##AAGGTNTATACCTTCCCAGGTAACAAACCAACCAA$  
      AAGGTNTATACCTTCCCAGGTAAAAAACCAACCAA$  
      AAGGTNTATACCTTCCCAGGTAATAAACCAACCAA$##
```

```
W:   2  
TS:  {NT, AG, A$, ##}
```



Prefix Free Parsing

S: **##AAGGTNT**ATACCTTCCC**AGGTAA**C**AAACCAACCA**A\$
 AAGGTNTATACCTTCCC**AGGTAA**A**AAACCAACCA**A\$
 AAGGTNTATACCTTCCC**AGGTAA**T**AAACCAACCA**A\$##

W: 2
TS: {NT, AG, A\$, ##}

Prefix Free Parsing

S: **##**AGGTNTATACCTTCCCAGGTAA**C**AAACCAACCA**A**\$
AAGGTNTATACCTTCCCAGGTAA**A**AAACCAACCA**A**\$
AAGGTNTATACCTTCCCAGGTAA**T**AAACCAACCA**A**\$##

W: 2
TS: {NT, AG, A\$, ##}

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S: **##A**AGGTNTATACCTTCCC**AG**GTAACAAACCAACCA**A**\$
A**AG**GTNTATACCTTCCC**AG**GTA**A**AAAACCAACCA**A**\$
A**AG**GTNTATACCTTCCC**AG**GTA**A**TAAACCAACCA**A**\$##

W: 2
TS: {NT, AG, A\$, ##}



Prefix Free Parsing

S: **##**A**AGGTNT**ATACCTTCCC**AGGTAA**C**AAACCAACCA****A\$**
 AAGGTNTATACCTTCCC**AGGTAA**A**AAACCAACCA****A\$**
 AAGGTNTATACCTTCCC**AGGTAA**T**AAACCAACCA****A\$##**

W: 2
TS: {NT, AG, A\$, ##}

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S: **##A****AG**GTNTATACCTTCCC**AG**GTAA**C**AAACCAACCA**A**\$
 AAGGTNTATACCTTCCC**AG**GTAA**A**AAACCAACCA**A**\$
 AAGGTNTATACCTTCCC**AG**GTAA**T**AAACCAACCA**A**\$##

W: 2
TS: {NT, AG, A\$, ##}

Prefix Free Parsing

S: **##AAGGTNT**ATACCTTCCC**AGGTAA**C**AAACCAACCA**A\$
 AAGGTNTATACCTTCCC**AGGTAA**A**AAACCAACCA**A\$
 AAGGTNTATACCTTCCC**AGGTAA**T**AAACCAACCA**A\$##

W: 2
TS: {NT, AG, A\$, ##}

D: {##AAG}
P: [h(##AAG)]

Prefix Free Parsing

S: **##AAGTNT**ATACCTTCCC**AGGTAA**C**AAACCAACCA**A\$
 AAGTNTATACCTTCCC**AGGTAA**A**AAACCAACCA**A\$
 AAGTNTATACCTTCCC**AGGTAA**T**AAACCAACCA**A\$##

W: 2
TS: {NT, AG, A\$, ##}

D: {##AAG, AGGTNT}
P: [h(##AAG), h(AGGTNT)]

Prefix Free Parsing

S: **##AAGGTNT**ATACCTTCCC**AGGTAA**C**AAACCAACCAA****A\$**
 AAGGTNTATACCTTCCC**AGGTAA****AAAACCAACCAA****A\$**
 AAGGTNTATACCTTCCC**AGGTAA****TAAACCAACCAA****A\$##**

W: 2
TS: {NT, AG, A\$, ##}

D: {##AAG, A\$##, A\$AAG, AGGTAAAAACCAACCAA\$,
 AGGTAACAAACCAACCAA\$, AGGTAATAACCAACCAA\$,
 AGGTNT, NTATACCTTCCCAG}

P: [1, 7, 8, 5, 3, 7, 8, 4, 3, 7, 8, 6, 2]

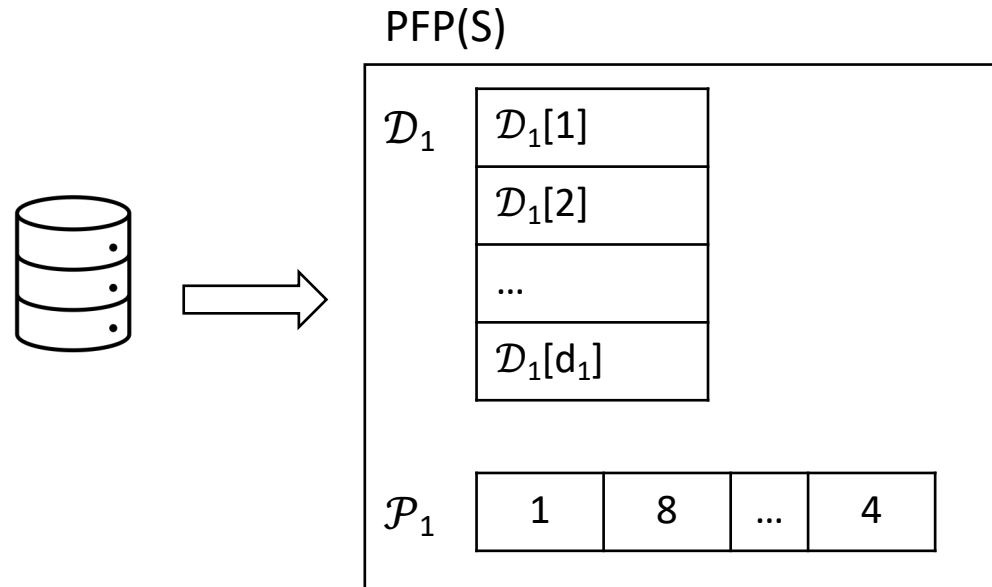
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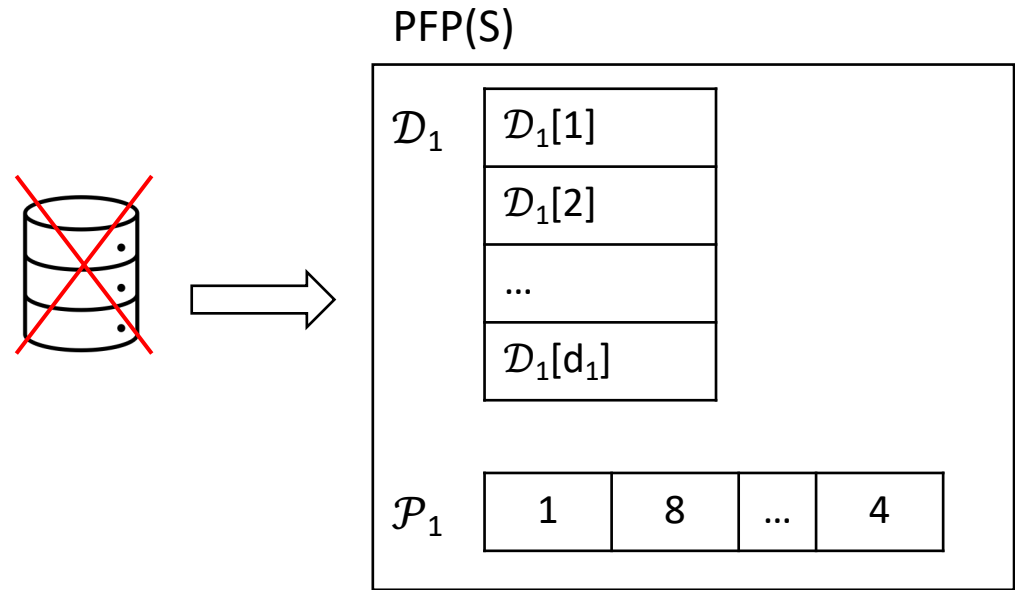
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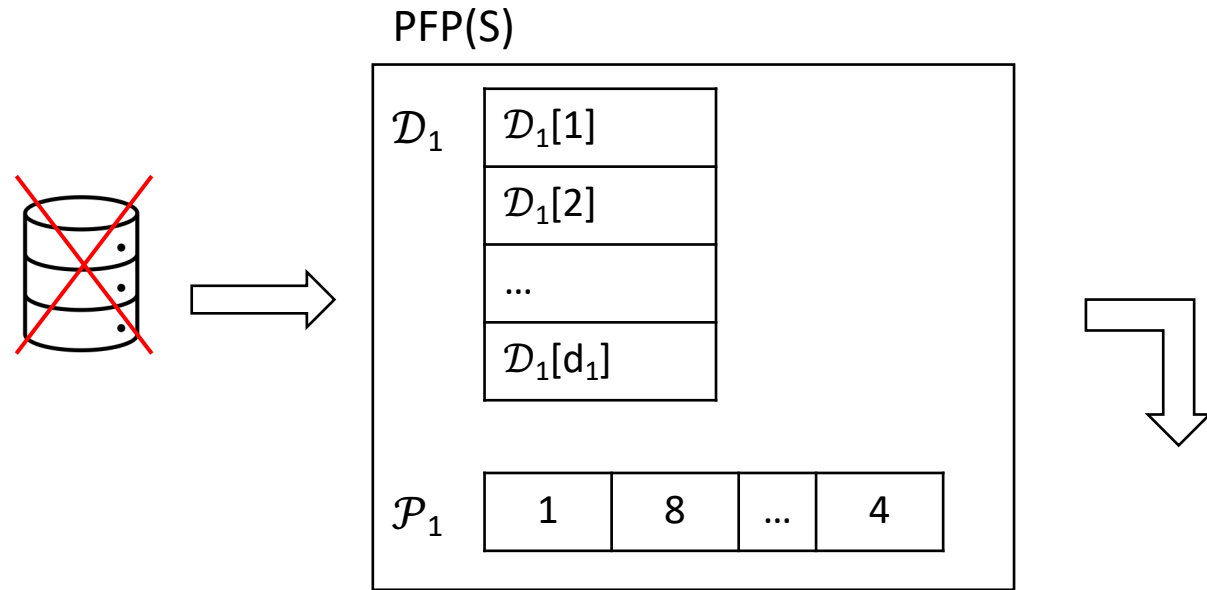
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```

CCCCC$CCCTTTTC$$$GGTATAATTACCC$$
$$$GGGAGCAAAGGTTTTTGGGTTTAAAAAA
AAAGGTGTTTTTTTTTTTAAAATTTTTCCCCC
CTTTAAAAAAACCCAAAACAAGGGGGTGGGGG
CCCCCGGGGGGGGCCCCCCCCAAGCCAAAAC
GAAAAACCCCCGTCCTTTTCACCCACGGGT
GGTGTGTTTTTTTTTGGGGGTGGGGCCCGCGGG
  
```



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From Prefix Free Parsing to the BWT

Lemma

No phrase suffix of length greater than w is a proper prefix of any phrase suffix.

Proof sketch

Every phrase starts with a trigger strings and ends with a trigger string and contains no other trigger string. If a phrase suffix α with $|\alpha| > w$ were a proper prefix of a phrase suffix β then β would contain a trigger string $|\alpha| - w$ characters from its start and $|\beta| - |\alpha|$ characters from its end.

From Prefix Free Parsing to the BWT

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Corollary

If two characters $S[i]$ and $S[j]$ are followed by different phrase suffixes α and β with $|\alpha|, |\beta| \geq w$, then $S[i]$ precedes $S[j]$ in BWT if and only if $\alpha < \beta$.

Proof sketch

Suppose $|\alpha| \leq |\beta|$. Since $\alpha \neq \beta[0..|\alpha| - 1]$, either $\alpha < \beta$ or $\beta < \alpha$. In the first case $S[i]$ precedes $S[j]$ in BWT and in the second case $S[j]$ precedes $S[i]$.



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From Prefix Free Parsing to the BWT

Lemma

If two characters $S[i]$ and $S[j]$ are followed by the same phrase suffix α with $|\alpha| \geq w$, then $S[i]$ precedes $S[j]$ in BWT if and only if $S[i + |\alpha| - w + 1] < S[j + |\alpha| - w + 1]$.

Corollary

If two characters $S[i]$ and $S[j]$ in phrases $P[i']$ and $P[j']$ are followed by the same phrase suffix α with $|\alpha| \geq w$, then $S[i]$ precedes $S[j]$ in $BWT(S)$ if and only if $P[i']$ precedes $P[j']$ in $BWT(P)$.

Scaling PFP

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Haplotypes	Input Size	$ P_1 $	$ D_1 $	$ D_1 + P_1 $	$ P_2 $	$ D_2 $	$ D_2 + P_2 $
200	22.08	0.96	0.16	1.11	0.08	0.05	0.13
400	44.11	1.91	0.23	2.14	0.16	0.09	0.25
600	66.13	2.86	0.27	3.13	0.24	0.12	0.36
800	88.16	3.82	0.32	4.14	0.32	0.15	0.48
1000	110.18	4.77	0.36	5.13	0.73	0.16	0.89
1200	132.21	5.72	0.40	6.13	0.49	0.22	0.71
1400	154.24	6.68	0.43	7.11	0.57	0.25	0.82
1600	176.26	7.63	0.46	8.09	0.65	0.27	0.92
1800	198.29	8.59	0.48	9.07	0.73	0.29	1.02
2000	220.31	9.54	0.51	10.05	0.81	0.31	1.12
2200	242.34	10.49	0.54	11.03	0.89	0.34	1.22
2400	264.36	11.45	0.56	12.00	0.97	0.35	1.32

Table 1: In order to illustrate the advantage of our recursive algorithm, we illustrate the size of the input, the size of the dictionary and parse from prefix-free parsing of the input sequences, and the size of the dictionary and parse from prefix-free parsing PFP(T). All sizes are shown in gigabytes.

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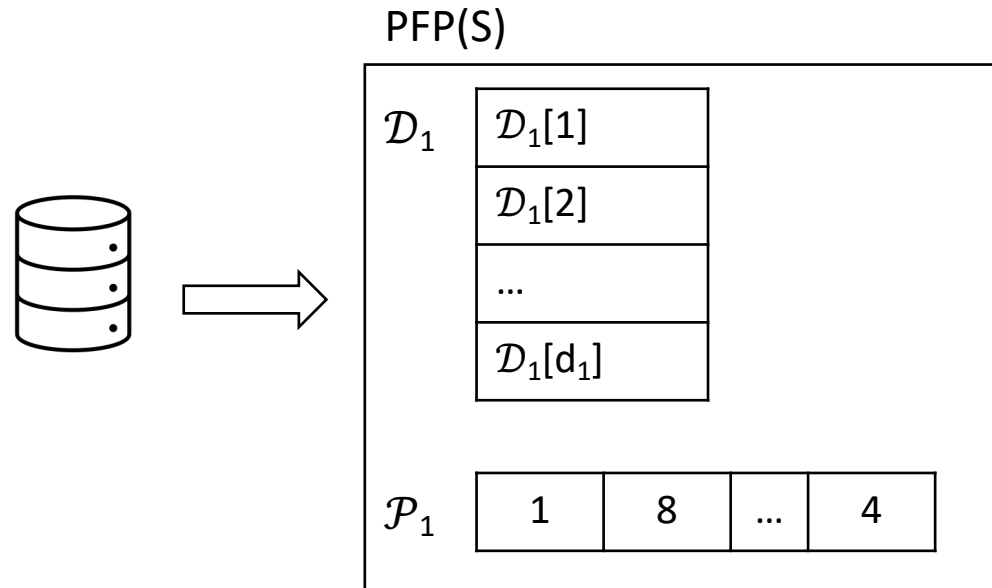
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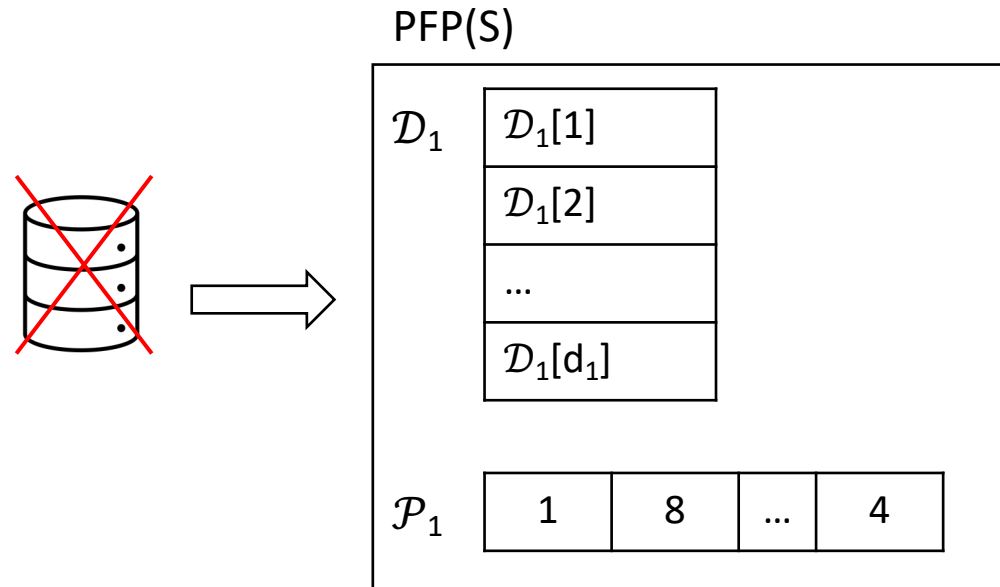
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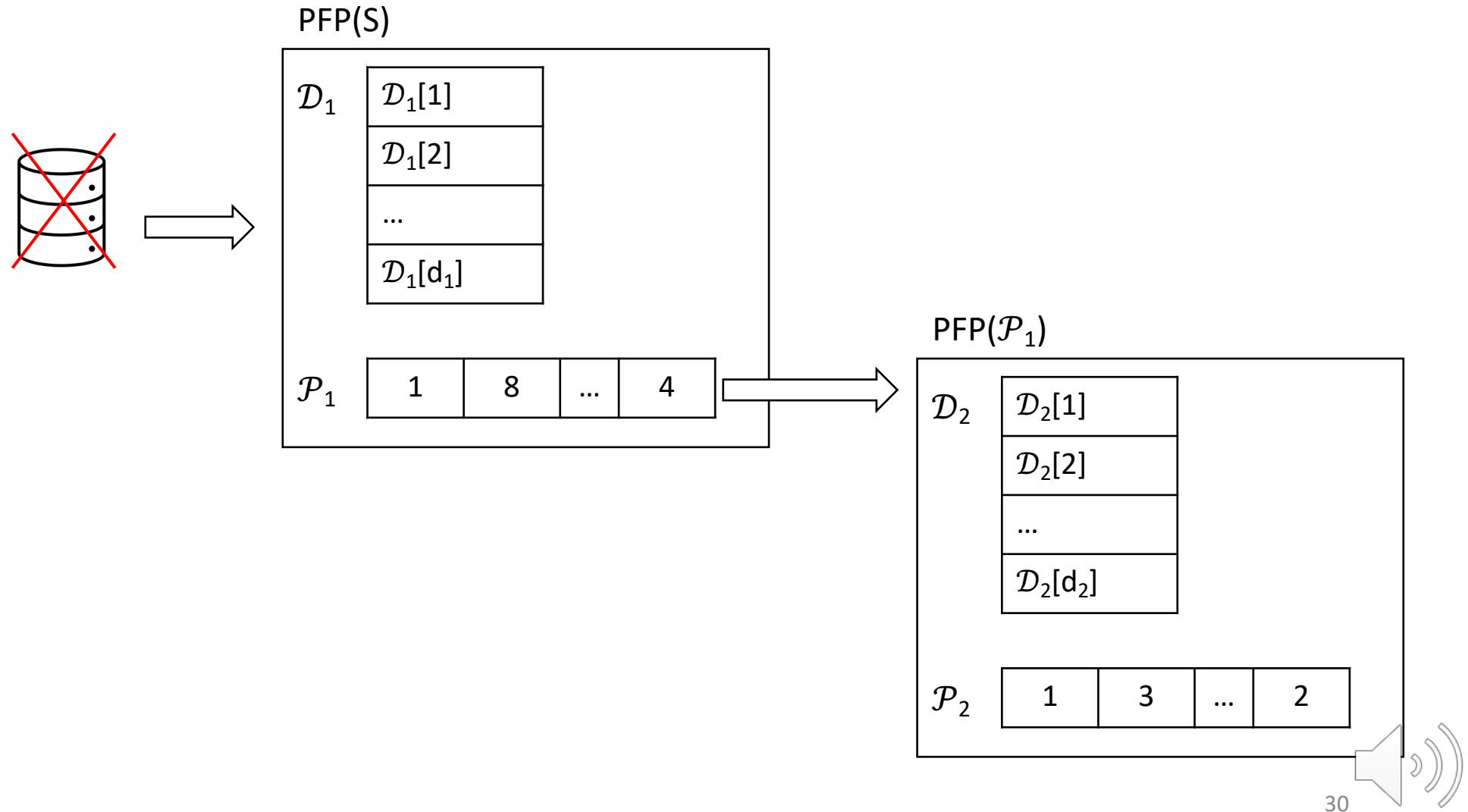
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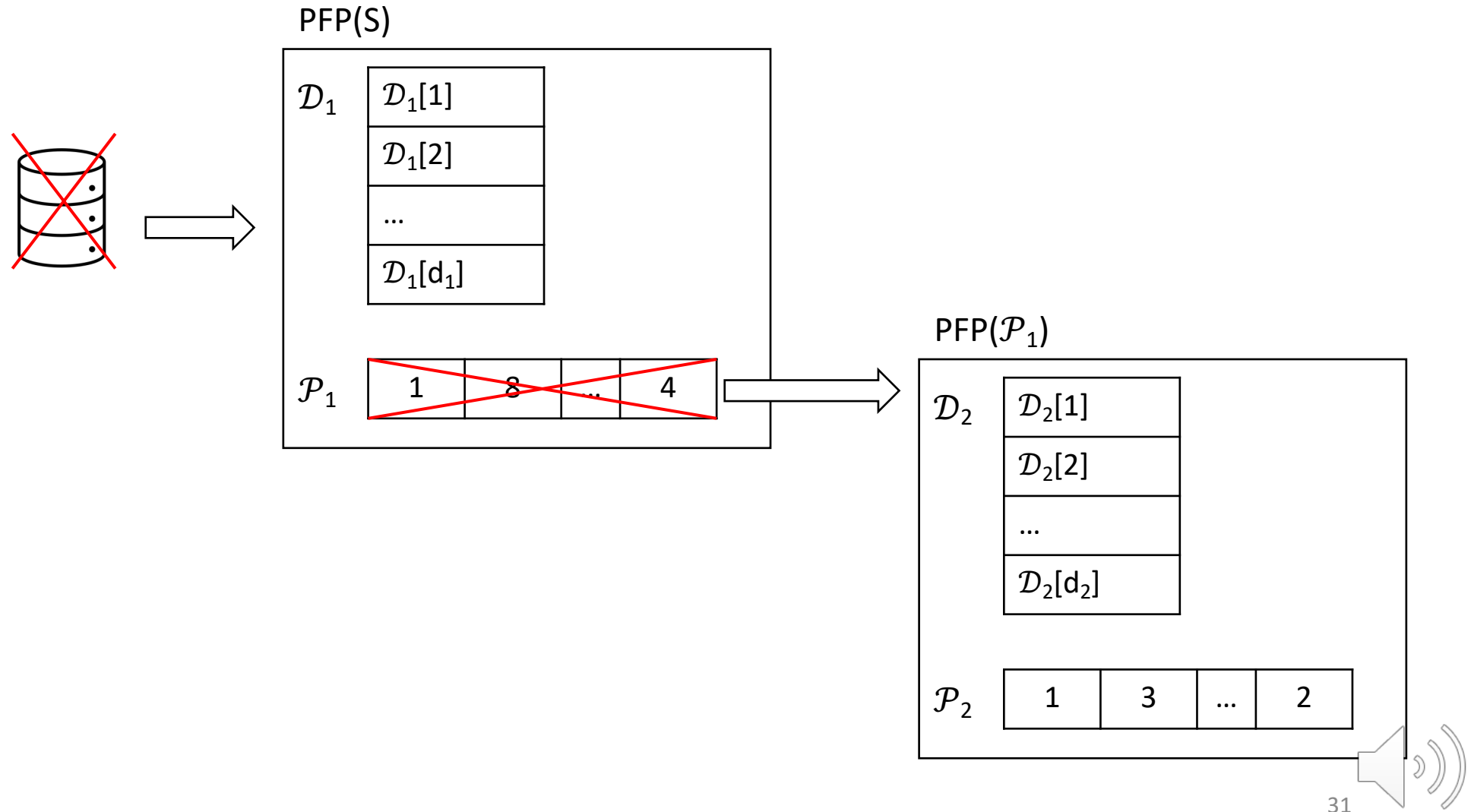
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Extending Previous Results

Lemma

If two characters $T[i]$ and $T[j]$ in phrases $P_1[i']$ and $P_1[j']$ are followed by the same phrase suffix $\alpha \in S_1$, then $T[i]$ precedes $T[j]$ in the *BWT* of T if one of the following two conditions is true: (a) $P_1[i']$ and $P_1[j']$ precede two different phrase suffixes $\alpha', \beta' \in S_2$ with $\alpha' < \beta'$; or (b) the phrase $P_2[k']$ containing $P_1[i']$ precedes the phrase $P_2[l']$ containing $P_1[j']$ in the *BWT* of P_2 .



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Definition

We define a table T_1 containing $O(|S_1|)$ rows and $O(1)$ columns, such that for each, $\alpha \in S_1$ we store in T_1 its range in $\text{BWT}(T)$ along with the co-lexicographic sub-range of the elements of D_1 which store the occurrence of α .

phrase suffix	BWT range	co-lex sub-ranges				
		\$	A	C	G	T
\$\$	0-0			0-0		
\$AAC	1-3			3-3		
\$AC	4-8	1-1		2-2		
AAC	9-16	3-3		4-4		5-7
AATAGT	17-18				21-21	
AC	19-43	1-2	3-7	8-9	10-11	12-13
AGGT	44-45				25-25	
...						

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Definition

We define a table T_2 containing $O(|S_2|)$ rows and $O(1)$ columns, such that for each $\alpha' \in S_2$, we store in T_2 the co-lexicographic range of the phrases of D_2 that contain α' along with the meta-characters that precede α' in P_1 .

phrase suffix	co-lex range	preceding meta- character
\$ \$	0--0	\$
1 7 17	4--4	\$
...		
5 20 15 18 3 10	2--2	19
5 20 16 23 \$ \$ \$	0--0	12
6 12 5 20 16 23 \$ \$ \$	0--0	4
7 17	4--8	1, 14, 4, 4
8 4 6 12 5 20 16 23 \$ \$ \$	0--0	14
...		

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Definition

We define the grid G_2 containing $O(|P_2|)$ rows and $O(|D_2|)$ columns, such that for each element l of D_2 , G_2 stores the positions in the BWT of P_2 where l appears.

0	7	17	25	17	21	9	24	14	8	4	6	12	5	20	16	23	2	\$	\$	•																							
1							7	17	25	17	19	9	24	16	23	3	10			•																							
2								3	10	17	19	5	20	15	18	3	10			•																							
3									7	17	25	13	24	15	22	3	10			•																							
4																		\$	1	7	17	•																					
5									7	17	25	11	9	20	16	23	4	7	17		•																						
6																				7	17	26	4	7	17	•																	
7																										3	10	13	20	14	8	4	7	17	•								
8																																			3	10	12	5	20	14	7	17	•

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Algorithm

Given a string T , the dictionary D_1 and the parse P_1 obtained by running PFP on T , and the dictionary D_2 and the parse P_2 obtained by running PFP on P_1 , we can compute the BWT of T from D_1 , D_2 and P_2 using $O(|D_1| + |D_2| + |P_2|)$ workspace.

```
for each  $\alpha$  in table  $T_1$  :  
    if  $\alpha$  is preceded by only one character:  
        output corresponding BWT range  
    else:  
        for each  $\alpha'$  in  $T_2$  preceded by  $D_1(\alpha)$ :  
            if  $\alpha'$  is preceded by only one element of  $D_1(\alpha)$ :  
                output corresponding BWT range  
            else:  
                for each occurrence of  $d \in D_1(\alpha)$  in  $G_2$ :  
                    output corresponding BWT character
```

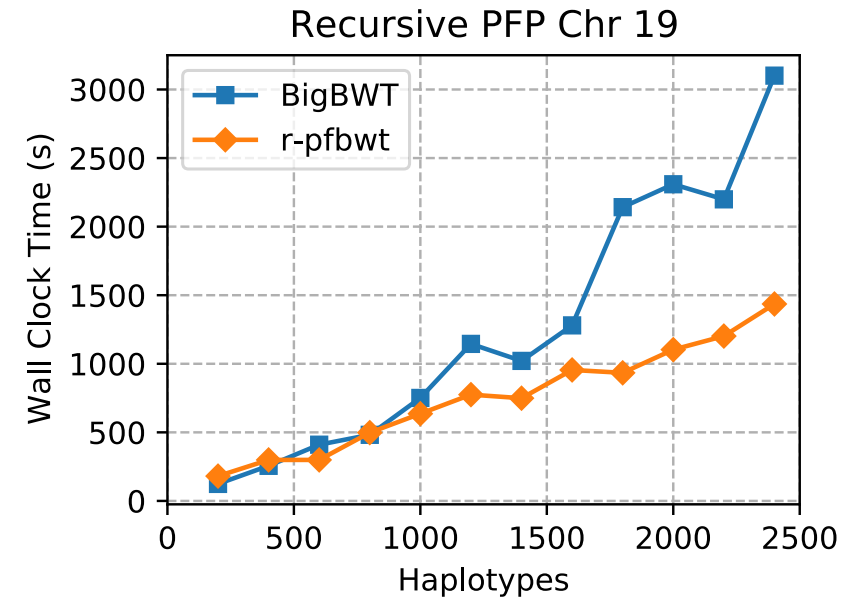
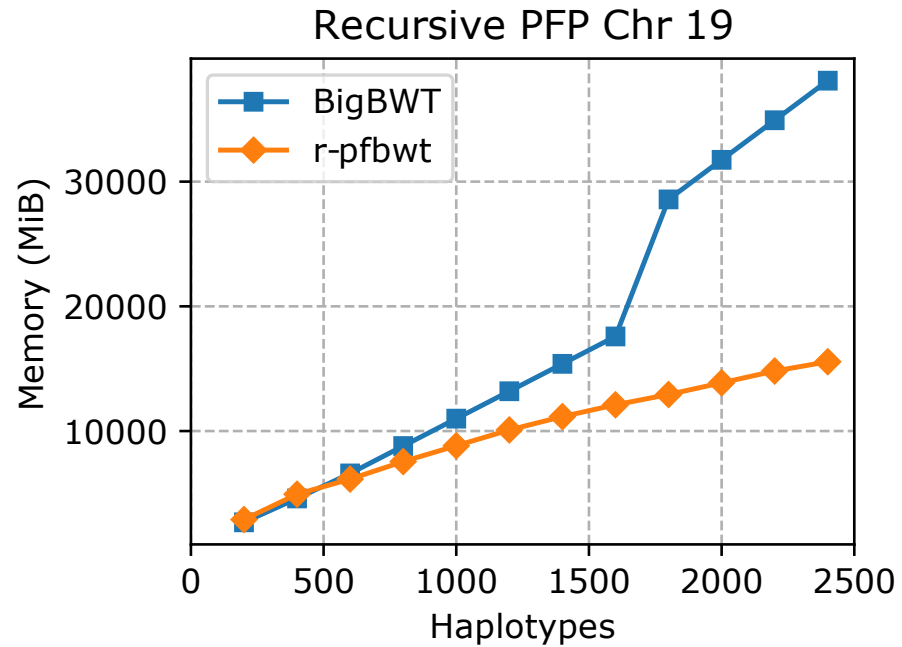
Results on Chromosome 19

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Thank you!

Source Code: <https://github.com/marco-oliva/r-pfbwt>

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