

# Burrows-Wheeler Transform

CMSC 423



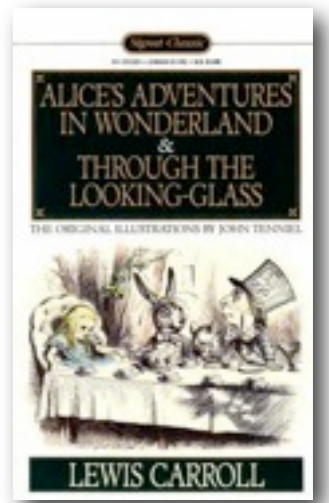
# Genome of the Cow

a sequence of 2.86 billion letters

enough letters to fill a million pages of a typical book.

```
TATGGAGCCAGGTGCCTGGGGCAACAAGACTGTGGTCACTGAATTCATCCTTCTTGGTCTAACAGAGAACATAG
AACTGCAATCCATCCTTTTTTGCCATCTTCCTCTTTGCCTATGTGATCACAGTCGGGGGCAACTTGAGTATCCTG
GCCGCCATCTTTGTGGAGCCCAAACCTCCACACCCCCATGTACTACTTCCTGGGGAACTTTCTCTGCTGGACAT
TGGGTGCATCACTGTCACCAATTCCTCCCATGCTGGCCTGTCTCCTGACCCACCAATGCCGGGTTCCTATGCAG
CCTGCATCTCACAGCTCTTCTTTTTCCACCTCCTGGCTGGAGTGGACTGTCACCTCCTGACAGCCATGGCCTAC
GACCGCTACCTGGCCATTTGCCAGCCCCTCACCTATAGCATCCGCATGAGCCGTGACGTCCAGGGAGCCCTGGT
GGCCGTCTGCTGCTCCATCTCCTTCATCAATGCTCTGACCCACACAGTGGCTGTGTCTGTGCTGGACTTCTGCG
GCCCTAACGTGGTCAACCACTTCTACTGTGACCTCCCGCCCCTTTTCCAGCTCTCCTGCTCCAGCATCCACCTC
AACGGGCAGCTACTTTTCGTGGGGGCCACCTTCATGGGGGTGGTCCCCATGGTCTTCATCTCGGTATCCTATGC
CCACGTGGCAGCCGCAGTCCTGCGGATCCGCTCGGCAGAGGGCAGGAAGAAAGCCTTCTCCACGTGTGGCTCCC
ACCTCACCGTGGTCTGCATCTTTTATGGAACCGGCTTCTTCAGCTACATGCGCCTGGGCTCCGTGTCCGCCTCA
GACAAGGACAAGGGCATTGGCATCCTCAACACTGTCATCAGCCCCATGCTGAACCCACTCATCTACAGCCTCCG
GAACCCTGATGTGCAGGGCGCCCTGAAGAGGTTGCTGACAGGGAAGCGGCCCCCGGAGTG ...
```

We can only read ~ 1000 characters at a time from a random place:



good-natured, she thought: still  
when it saw Alice. It looked  
ought to be treated  
good-natured, she thought, still  
Cat only  
a greet many  
It looked good-  
The Cat only grinned when it saw Alice.  
be treated with respect.  
still it had very long claws  
claws and a great many teeth, so she  
so she felt that it ought

The Cat only grinned when it saw Alice.  
Cat only when it saw Alice. It looked  
It looked good-  
good-natured, she thought: still  
good-natured, she thought, still  
still it had very long claws  
claws and a great many teeth, so she  
a greet many so she felt that it ought  
ought to be treated  
be treated with respect.

It's a jigsaw  
puzzle ...



...except with 35  
million pieces

# Motivation - Short Read Mapping

A Cow Genome

---

Sequencing technologies produce millions of “reads” = a random, short substring of the genome



If we already know the genome of one cow, we can get reads from a 2nd cow and map them onto the known cow genome.

Need to do millions of string searches in a long string.

# Burrows-Wheeler Transform

Text transform that is useful for compression & search.

**banana**

banana\$  
anana\$b  
nana\$ba  
ana\$ban  
na\$bana  
a\$banan  
\$banana

sort



\$banana**a**  
a\$banan**n**  
ana\$ban**n**  
anana\$b**b**  
banana\$  
nana\$b**a**  
na\$bana**a**

BWT(banana) =  
**annb\$aa**

Tends to put runs of the same character together.

Makes compression work well.

“bzip” is based on this.

# Another Example

appellee\$

appellee\$

ppellee\$a

pellee\$ap

ellee\$app

lee\$app

lee\$appel

ee\$appell

e\$appelle

\$appellee

sort

\$appellee

appellee\$

e\$appelle

ee\$appell

ellee\$app

lee\$appel

lee\$app

pellee\$ap

ppellee\$a

BWT(appellee\$) =  
e\$elplepa

Doesn't always improve  
the compressibility...





# Inverse BWT

```
def inverseBWT(s):  
    B = [s1, s2, s3, ..., sn]  
    for i = 1..n:  
        sort B  
        prepend si to B[i]  
    return row of B that ends with $
```

# Another BWT Example

dogwood\$  
ogwood\$d  
gwood\$do  
wood\$dog  
ood\$dogw  
od\$dogwo  
d\$dogwoo  
\$dogwood

sort →

\$dogwood  
d\$dogwo  
dogwood\$  
gwood\$d  
od\$dogwo  
ogwood\$d  
ood\$dogw  
wood\$dog

last column →

BWT(dogwood\$) =  
do\$oodwg

do\$oodwg

# Another BWT Example

d \$  
o d  
\$ d  
o g  
o o  
d o  
w o  
g w

Prepend

Sort

\$d  
d\$  
do  
gw  
od  
og  
oo  
wo

d \$d  
o d\$  
\$ do  
o gw  
o od  
d og  
w oo  
g wo

Prepend

Sort

\$do  
d\$d  
dog  
gwo  
od\$  
ogw  
ood  
woo

Prepend

Sort

d\$do  
o d\$d  
\$ dog  
o gwo  
o od\$  
dogw  
wood  
gwoo

\$dog  
d\$do  
dogw  
gwoo  
od\$d  
ogwo  
ood\$  
wood

Prepend

Sort

d \$dog  
o d\$do  
\$ dogw  
o gwoo  
o od\$d  
dogwo  
wood\$  
gwood

\$dogw  
d\$dog  
dogwo  
gwood  
od\$d  
ogwo  
ood\$d  
wood\$

d \$dogw  
o d\$dog  
\$ dogwo  
o gwood  
o od\$d  
d ogwo  
w ood\$d  
g wood\$

Prepend

\$dogwo  
d\$dogw  
dogwoo  
gwood\$  
od\$dog  
ogwood  
ood\$d  
wood\$d

Sort

d \$dogwo  
o d\$dogw  
\$ dogwoo  
o gwood\$  
o od\$dog  
d ogwood  
w ood\$d  
g wood\$d

Prepend

\$dogwoo  
d\$dogwo  
dogwood  
gwood\$d  
od\$dogw  
ogwood\$  
ood\$dog  
wood\$d

Sort

d \$dogwoo  
o d\$dogwo  
\$ dogwood  
o gwood\$d  
o od\$dogw  
d ogwood\$  
w ood\$dog  
g wood\$d

Prepend

\$dogwood  
d\$dogwoo  
dogwood\$  
gwood\$d  
od\$dogwo  
ogwood\$d  
ood\$dogw  
wood\$dog

Sort

# Searching with BWT: LF Mapping

BWVT(unabashable)	LF Mapping									# of times letter appears before this position in the <b>last</b> <b>column</b> .
	\$	a	b	e	h	l	n	s	u	
\$unabashable	0	0	0	0	0	0	0	0	0	
abashable\$un	0	0	0	1	0	0	0	0	0	
able\$unabash	0	0	0	1	0	0	1	0	0	
ashable\$unab	0	0	0	1	1	0	1	0	0	
bashable\$una	0	0	1	1	1	0	1	0	0	
ble\$unabasha	0	1	1	1	1	0	1	0	0	
e\$unabashabl	0	2	1	1	1	0	1	0	0	
hable\$unabas	0	2	1	1	1	1	1	0	0	
le\$unabashab	0	2	1	1	1	1	1	1	0	
nabashable\$u	0	2	2	1	1	1	1	1	0	
shable\$unaba	0	2	2	1	1	1	1	1	1	
unabashable\$	0	3	2	1	1	1	1	1	1	
	1	3	2	1	1	1	1	1	1	

**LF Property:** The  $i^{\text{th}}$  occurrence of a letter  $X$  in the **last column** corresponds to the  $i^{\text{th}}$  occurrence of  $X$  in the **first column**.

# BWT Search

BWTSearch(aba)      Start from the **end** of the pattern

Step 1: Find the range of “a”s in the first column

Step 2: Look at the same range in the last column.

Step 3: “b” is the next pattern character. Set B = the LF mapping entry for b in the first row of the range.

Set E = the LF mapping entry for b in the last + 1 row of the range.

Step 4: Find the range for “b” in the first row, and use B and E to find the right subrange within the “b” range.

	LF Mapping									
		$\Sigma$								
BWT(unabashable)	\$	a	b	e	h	l	n	s	u	
\$unabashable	0	0	0	0	0	0	0	0	0	
→ abashable\$un ←	0	0	0	1	0	0	0	0	0	
able\$unabash	0	0	0	1	0	0	1	0	0	
ashable\$unab ←	0	0	0	1	1	0	1	0	0	
→ bashable\$una ←	0	0	1	1	1	0	1	0	0	
→ ble\$unabasha	0	1	1	1	1	0	1	0	0	
e\$unabashabl	0	2	1	1	1	0	1	0	0	
hable\$unabas	0	2	1	1	1	1	1	0	0	
le\$unabashab	0	2	1	1	1	1	1	1	0	
nabashable\$u	0	2	2	1	1	1	1	1	0	
shable\$unaba	0	2	2	1	1	1	1	1	1	
unabashable\$	0	3	2	1	1	1	1	1	1	
	1	3	2	1	1	1	1	1	1	

# BWT Searching Example 2

pattern = "bana"

	a	\$	a	b	n
→	\$bananna	0	0	0	0
→	a\$banann	0	1	0	0
	ananna\$b	0	1	0	1
→	anna\$ban	0	1	1	1
→	bananna\$	0	1	1	2
	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
	nna\$bana	1	2	1	3
		1	3	1	3

	n	\$	a	b	n
	\$bananna	0	0	0	0
←	a\$banann	0	1	0	0
	ananna\$b	0	1	0	1
	anna\$ban	0	1	1	1
←	bananna\$	0	1	1	2
	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
	nna\$bana	1	2	1	3
		1	3	1	3

	n	\$	a	b	n
	\$bananna	0	0	0	0
	a\$banann	0	1	0	0
	ananna\$b	0	1	0	1
	anna\$ban	0	1	1	1
→	bananna\$	0	1	1	2
→	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
→	nna\$bana	1	2	1	3
→		1	3	1	3

(B,E) = 0, 2

	a	\$	a	b	n
	\$bananna	0	0	0	0
	a\$banann	0	1	0	0
	ananna\$b	0	1	0	1
	anna\$ban	0	1	1	1
	bananna\$	0	1	1	2
←	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
←	nna\$bana	1	2	1	3
		1	3	1	3

(B,E) = 1, 2

	a	\$	a	b	n
	\$bananna	0	0	0	0
→	a\$banann	0	1	0	0
→	ananna\$b	0	1	0	1
→	anna\$ban	0	1	1	1
→	bananna\$	0	1	1	2
	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
	nna\$bana	1	2	1	3
		1	3	1	3

(B,E) = 0, 1

	b	\$	a	b	n
	\$bananna	0	0	0	0
	a\$banann	0	1	0	0
	ananna\$b	0	1	0	1
	anna\$ban	0	1	1	1
→	bananna\$	0	1	1	2
→	na\$banan	1	1	1	2
	nanna\$ba	1	1	1	3
	nna\$bana	1	2	1	3
		1	3	1	3

# BWT Searching Notes

- Don't have to store the LF mapping. A more complex algorithm lets you compute it in  $O(l)$  time on the fly with only a little bit of storage.
- To find the range in the first column corresponding to a character:
  - Pre-compute array  $C[c] = \#$  of occurrences in the string of characters lexicographically  $< c$ .
  - Then start of the "a" range, for example, is:  $C["a"] + 1$ .
- Running time:  $O(|\text{pattern}|)$ 
  - Finding the range in the first column takes  $O(l)$  time using the  $C$  array.
  - Updating the range takes  $O(l)$  time using the LF mapping.





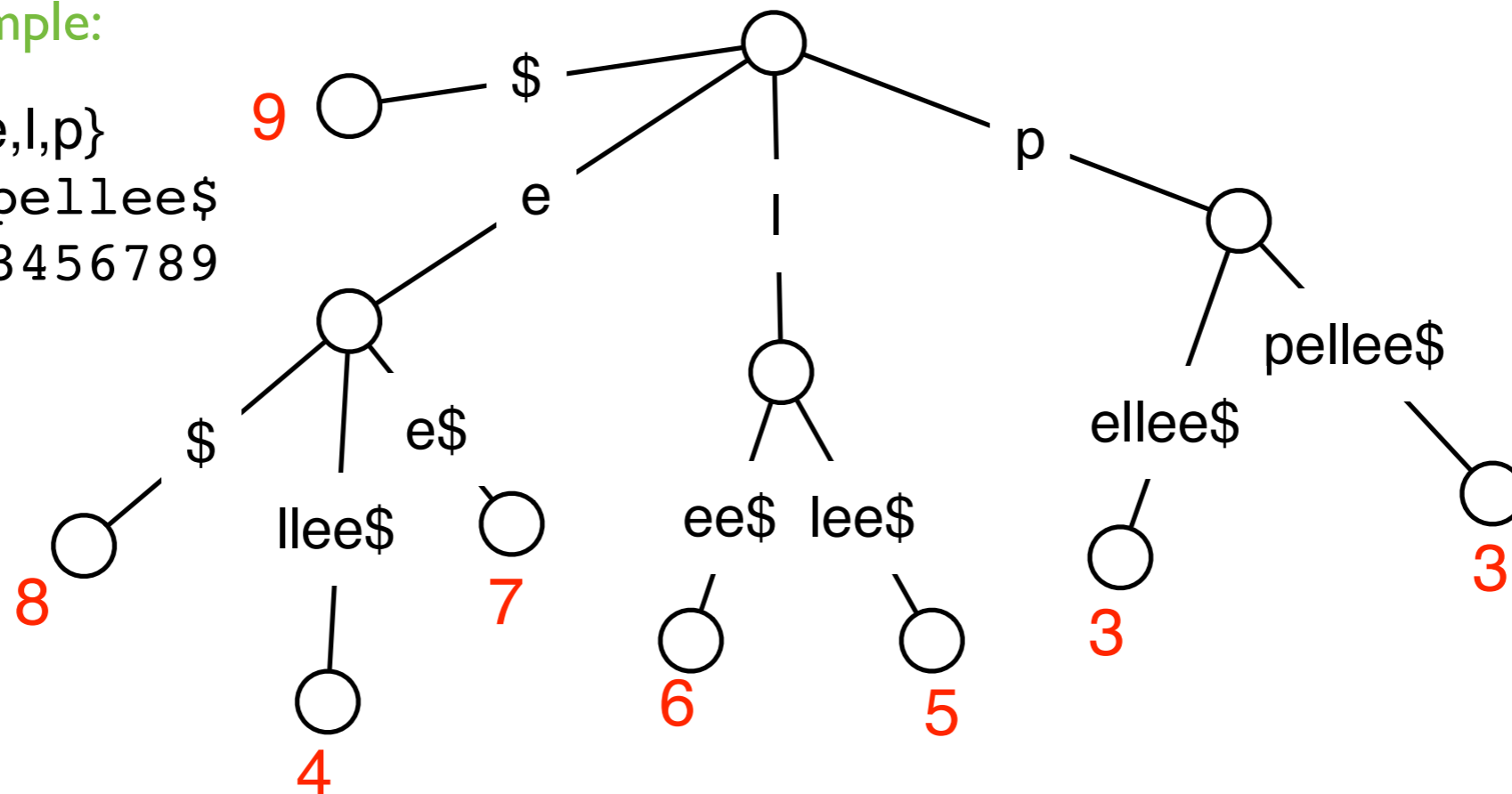
# Relationship Between BWT and Suffix Trees

- Remember: Suffix Array = suffix numbers obtained by traversing the leaf nodes of the (ordered) Suffix Tree from left to right.
- Suffix Tree  $\Rightarrow$  Suffix Array  $\Rightarrow$  BWT.

Ordered suffix tree  
for previous example:

$\Sigma = \{\$,e,l,p\}$

$s = \text{appellee}\$$   
123456789



# Computing BWT in $O(n)$ time

- Easy  $O(n^2 \log n)$ -time algorithm to compute the BWT (create and sort the BWT matrix explicitly).
- Several direct  $O(n)$ -time algorithms for BWT. These are space efficient.
- Also can use suffix arrays or trees:
  - Compute the suffix array, use correspondence between suffix array and BWT to output the BWT.
  - $O(n)$ -time and  $O(n)$ -space, but the constants are large.

# Recap

BWT useful for searching and compression.

BWT is *invertible*: given the BWT of a string, the string can be reconstructed!

BWT is computable in  $O(n)$  time.

Close relationships between Suffix Trees, Suffix Arrays, and BWT:

- Suffix array = order of the suffix numbers of the suffix tree, traversed left to right
- BWT = letters at positions given by the suffix array entries - 1