

# The BWT and FM-Index

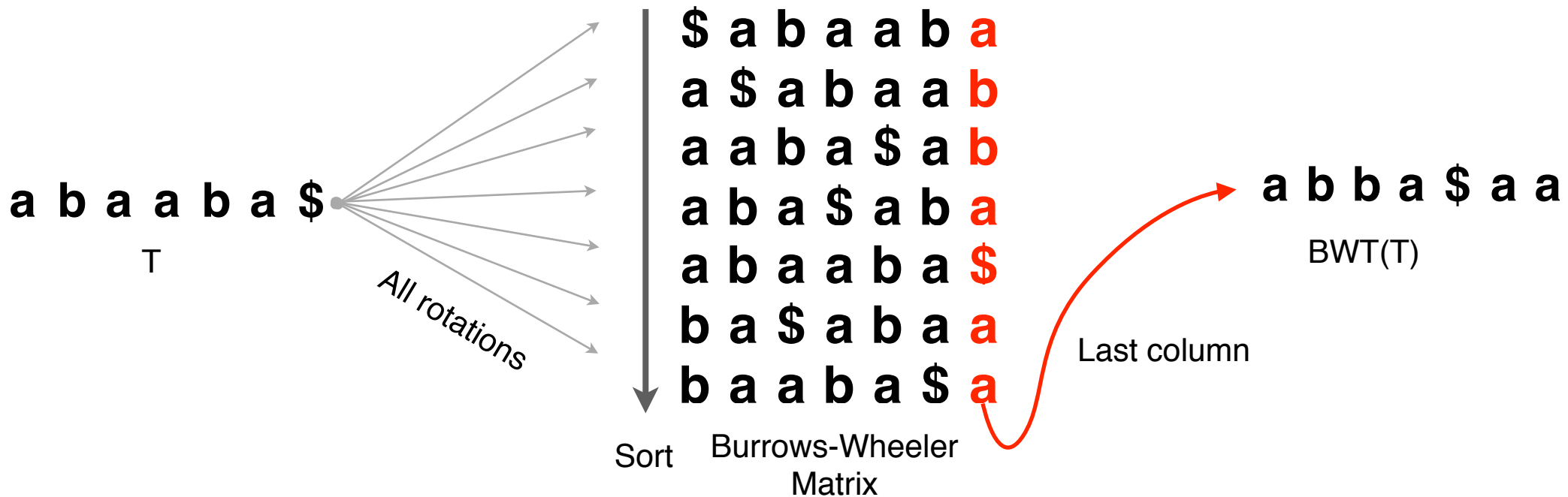
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The FM-index reduces space by building an index from the Burrows-Wheeler Transform (BWT) of the text



# Burrows-Wheeler Transform

*Reversible permutation of the characters of a string, used originally for compression*



How is it useful for compression?

How is it reversible?

How is it an index?

Burrows M, Wheeler DJ: A block sorting lossless data compression algorithm.  
Digital Equipment Corporation, Palo Alto, CA 1994, Technical Report 124;  
1994

# Burrows-Wheeler Transform

```
def rotations(t):  
    """ Return list of rotations of input string t """  
    tt = t * 2  
    return [ tt[i:i+len(t)] for i in xrange(0, len(t)) ]
```

Make list of all rotations

```
def bwm(t):  
    """ Return lexicographically sorted list of t's rotations """  
    return sorted(rotations(t))
```

Sort them

```
def bwtViaBwm(t):  
    """ Given T, returns BWT(T) by way of the BWM """  
    return ''.join(map(lambda x: x[-1], bwm(t)))
```

Take last column

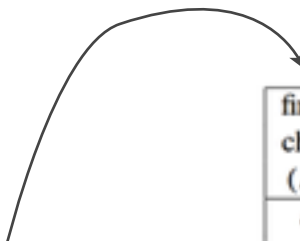
```
>>> bwtViaBwm("Tomorrow_and_tomorrow_and_tomorrow$")  
'w$wwdd__nnooaaattTmmrrrrrrrooo__ooo'  
  
>>> bwtViaBwm("It_was_the_best_of_times_it_was_the_worst_of_times$")  
's$esttssfftteww_hhmmbootttt_ii__woeeaaressIi_____  
  
>>> bwtViaBwm('in_the_jingle_jangle_morning_Ill_come_following_you$')  
'u_gleeeengj_mlh_l_nnnnt$nwj__lggIolo_iiiiarfcmylo_oo_'
```

Python example: [http://bit.ly/CG\\_BWT\\_SimpleBuild](http://bit.ly/CG_BWT_SimpleBuild)

# Burrows-Wheeler Transform

Characters of the BWT are sorted by their *right-context*

This lends additional structure to BWT(T), tending to make it more compressible



final char (L)	sorted rotations
a	n to decompress. It achieves compression
o	n to perform only comparisons to a depth
o	n transformation} This section describes
o	n transformation} We use the example and
o	n treats the right-hand side as the most
a	n tree for each 16 kbyte input block, enc
a	n tree in the output stream, then encodes
i	n turn, set \$L[i]\$ to be the
i	n turn, set \$R[i]\$ to the
o	n unusual data. Like the algorithm of Man
a	n use a single set of probabilities table
e	n using the positions of the suffixes in
i	n value at a given point in the vector \$R
e	n we present modifications that improve t
e	n when the block size is quite large. Ho
i	n which codes that have not been seen in
i	n with \$ch\$ appear in the {\em same order
i	n with \$ch\$.
o	n with Huffman or arithmetic coding. Bri
o	n with figures given by Bell\cite{bell}.

Figure 1: Example of sorted rotations. Twenty consecutive rotations from the sorted list of rotations of a version of this paper are shown, together with the final character of each rotation.

# Burrows-Wheeler Transform

BWM bears a resemblance to the suffix array

\$ a b a a b a  
 a \$ a b a a b  
 a a b a \$ a b  
 a b a \$ a b a  
 a b a a b a \$  
 b a \$ a b a a  
 b a a b a \$ a

BWM(T)

6	\$						
5	a	\$					
2	a	a	b	a	\$		
3	a	b	a	\$			
0	a	b	a	a	b	a	\$
4	b	a	\$				
1	b	a	a	b	a	\$	

SA(T)

Sort order is the same whether rows are rotations or suffixes

# Burrows-Wheeler Transform

In fact, this gives us a new definition / way to construct BWT(T):

$$BWT[i] = \begin{cases} T[SA[i] - 1] & \text{if } SA[i] > 0 \\ \$ & \text{if } SA[i] = 0 \end{cases}$$

“BWT = characters just to the left of the suffixes in the suffix array”

\$	a	b	a	a	b	a
a	\$	a	b	a	a	b
a	a	b	a	\$	a	b
a	b	a	\$	a	b	a
a	b	a	a	b	a	\$
b	a	\$	a	b	a	a
b	a	a	b	a	\$	a

BWM(T)

6	\$
5	a \$
2	a a b a \$
3	a b a \$
0	a b a a b a \$
4	b a \$
1	b a a b a \$

SA(T)

# Burrows-Wheeler Transform

```
def suffixArray(s):  
    """ Given T return suffix array SA(T). We use Python's sorted  
        function here for simplicity, but we can do better. """  
    satups = sorted([(s[i:], i) for i in xrange(0, len(s))])  
    # Extract and return just the offsets  
    return map(lambda x: x[1], satups)
```

Make suffix array

```
def bwtViaSa(t):  
    """ Given T, returns BWT(T) by way of the suffix array. """  
    bw = []  
    for si in suffixArray(t):  
        if si == 0: bw.append('$')  
        else: bw.append(t[si-1])  
    return ''.join(bw) # return string-ized version of list bw
```

Take characters just  
to the left of the  
sorted suffixes

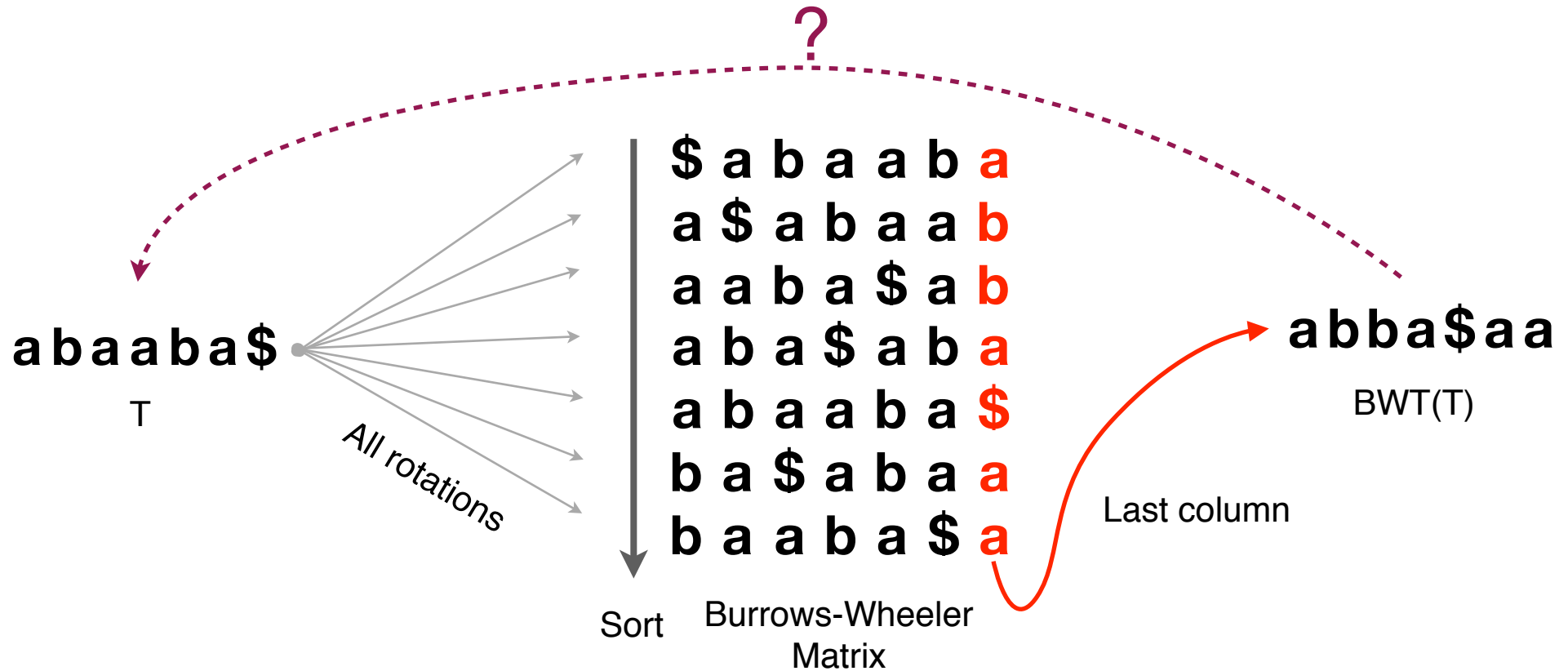
```
>>> bwtViaSa("Tomorrow_and_tomorrow_and_tomorrow$")  
'w$wwdd__nnooaaattTmmrrrrrrrooo__ooo'  
  
>>> bwtViaSa("It_was_the_best_of_times_it_was_the_worst_of_times$")  
's$esttssffteww_hhmmbootttt_ii__woeeaaressIi_____  
  
>>> bwtViaSa('in_the_jingle_jangle_morning_Ill_come_following_you$')  
'u_gleeeengj_mlh_l_nnnnt$nwj__lggIolo_iiiiarfcmlylo_oo_'
```

Python example: [http://bit.ly/CG\\_BWT\\_SimpleBuild](http://bit.ly/CG_BWT_SimpleBuild)



# Burrows-Wheeler Transform

How to reverse the BWT?



BWM has a key property called the *LF Mapping*...

# Burrows-Wheeler Transform: T-ranking

Give each character in  $T$  a rank, equal to # times the character occurred previously in  $T$ . Call this the *T-ranking*.

**a<sub>0</sub> b<sub>0</sub> a<sub>1</sub> a<sub>2</sub> b<sub>1</sub> a<sub>3</sub> \$**

Ranks aren't explicitly stored; they are just for illustration

Now let's re-write the BWM including ranks...

# Burrows-Wheeler Transform

BWM with T-ranking:

	<i>F</i>						<i>L</i>
	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>
	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>
	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>
	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>
	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$
	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>
	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>

Look at first and last columns, called *F* and *L*

And look at just the **a**s

**a**s occur in the same order in *F* and *L*. As we look down columns, in both cases we see: **a<sub>3</sub>**, **a<sub>1</sub>**, **a<sub>2</sub>**, **a<sub>0</sub>**

# Burrows-Wheeler Transform

BWM with T-ranking:

$F$							$L$
\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	
a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	<b>b<sub>1</sub></b>	
a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	<b>b<sub>0</sub></b>	
a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	
a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	
<b>b<sub>1</sub></b>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	
<b>b<sub>0</sub></b>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	

Same with **bs**: **b<sub>1</sub>**, **b<sub>0</sub>**

# Burrows-Wheeler Transform: LF Mapping

BWM with T-ranking:

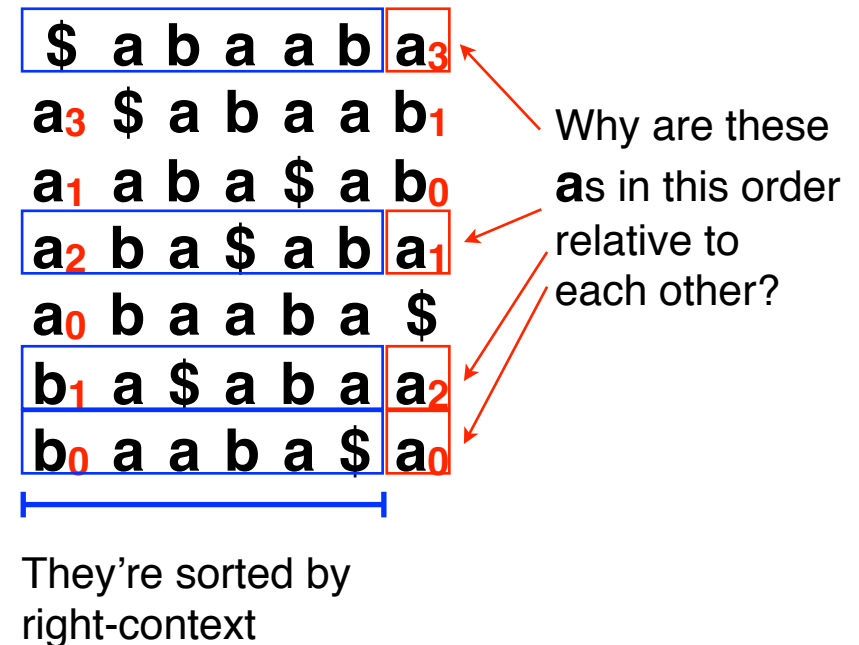
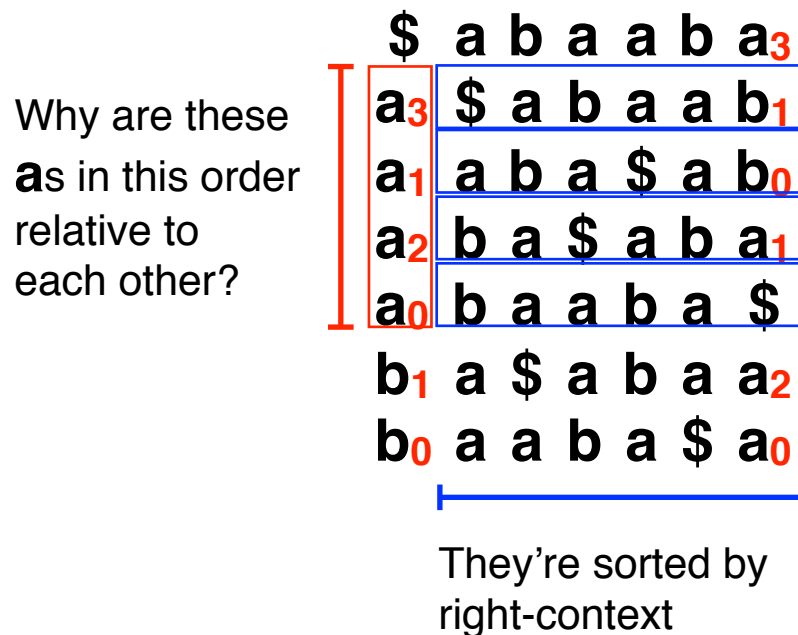
	$F$		$L$
	\$	$a_0$	$b_0$
	$a_1$	$a_2$	$b_1$
	$a_3$		

LF Mapping: The  $i^{\text{th}}$  occurrence of a character  $c$  in  $L$  and the  $i^{\text{th}}$  occurrence of  $c$  in  $F$  correspond to the *same* occurrence in  $T$  (i.e. have same rank)

However we rank occurrences of  $c$ , ranks appear in the same order in  $F$  and  $L$

# Burrows-Wheeler Transform: LF Mapping

Why does the LF Mapping hold?



Occurrences of  $c$  in  $F$  are sorted by right-context. Same for  $L$ !

Whatever ranking we give to characters in  $T$ , rank orders in  $F$  and  $L$  will match

# Burrows-Wheeler Transform: LF Mapping

BWM with T-ranking:

<i>F</i>							<i>L</i>
\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	
a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	
a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	
a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	
a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	
b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	
b <sub>0</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>1</sub>	a <sub>3</sub>	\$	a <sub>0</sub>	

We'd like a different ranking so that for a given character, ranks are in ascending order as we look down the F / L columns...

# Burrows-Wheeler Transform: LF Mapping

BWM with B-ranking:

$F$							$L$	
	\$	a <sub>3</sub>	b <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>0</sub>	a <sub>0</sub>	
	a <sub>0</sub>	\$	a <sub>3</sub>	b <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>0</sub>	
	a <sub>1</sub>	a <sub>2</sub>	b <sub>0</sub>	a <sub>3</sub>	\$	a <sub>3</sub>	b <sub>1</sub>	
	a <sub>2</sub>	b <sub>0</sub>	a <sub>0</sub>	\$	a <sub>3</sub>	b <sub>1</sub>	a <sub>1</sub>	
	a <sub>3</sub>	b <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>0</sub>	a <sub>0</sub>	\$	
	b <sub>0</sub>	a <sub>0</sub>	\$	a <sub>3</sub>	b <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	
	b <sub>1</sub>	a <sub>1</sub>	a <sub>2</sub>	b <sub>0</sub>	a <sub>0</sub>	\$	a <sub>3</sub>	

Ascending rank

$F$  now has very simple structure: a \$, a block of **a**s with ascending ranks, a block of **b**s with ascending ranks



# Burrows-Wheeler Transform

<i>F</i>	<i>L</i>	
\$	a <sub>0</sub>	
a <sub>0</sub>	b <sub>0</sub>	
a <sub>1</sub>	b <sub>1</sub>	← Which BWM row <i>begins</i> with <b>b<sub>1</sub></b> ?
a <sub>2</sub>	a <sub>1</sub>	Skip row starting with \$ (1 row)
a <sub>3</sub>	\$	Skip rows starting with <b>a</b> (4 rows)
b <sub>0</sub>	a <sub>2</sub>	Skip row starting with <b>b<sub>0</sub></b> (1 row)
row 6 → b <sub>1</sub>	a <sub>3</sub>	Answer: row 6

# Burrows-Wheeler Transform

Say  $T$  has 300 **A**s, 400 **C**s, 250 **G**s and 700 **T**s and  $\$ < \mathbf{A} < \mathbf{C} < \mathbf{G} < \mathbf{T}$

Which BWM row (0-based) begins with **G**<sub>100</sub>? (Ranks are B-ranks.)

Skip row starting with **\$** (1 row)

Skip rows starting with **A** (300 rows)

Skip rows starting with **C** (400 rows)

Skip first 100 rows starting with **G** (100 rows)

Answer: row  $1 + 300 + 400 + 100 =$  **row 801**

# Burrows-Wheeler Transform: reversing

Reverse BWT( $T$ ) starting at right-hand-side of  $T$  and moving left

**Start** in first row.  $F$  must have  $\$$ .  $L$  contains character just **prior** to  $\$$ :  **$a_0$**

**$a_0$** : LF Mapping says this is same occurrence of  **$a$**  as first  **$a$**  in  $F$ . **Jump** to row *beginning* with  **$a_0$** .  
 $L$  contains character just **prior** to  **$a_0$** :  **$b_0$** .

Repeat for  **$b_0$** , get  **$a_2$**

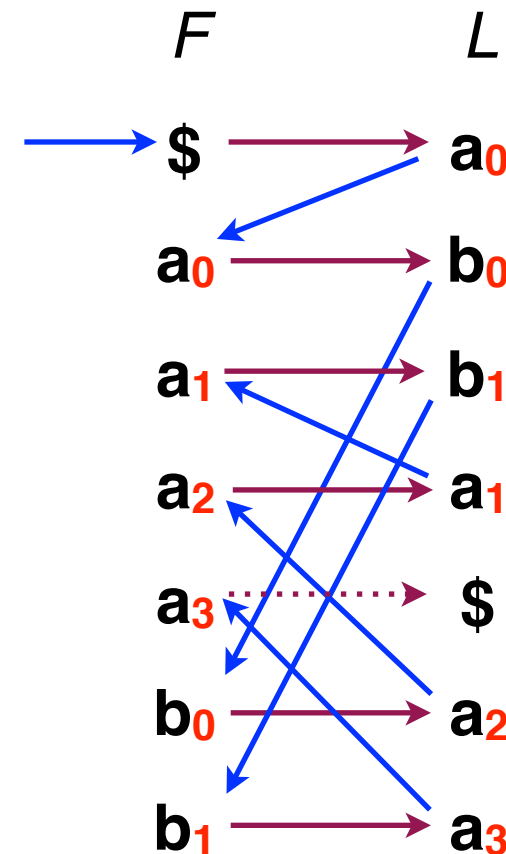
Repeat for  **$a_2$** , get  **$a_1$**

Repeat for  **$a_1$** , get  **$b_1$**

Repeat for  **$b_1$** , get  **$a_3$**

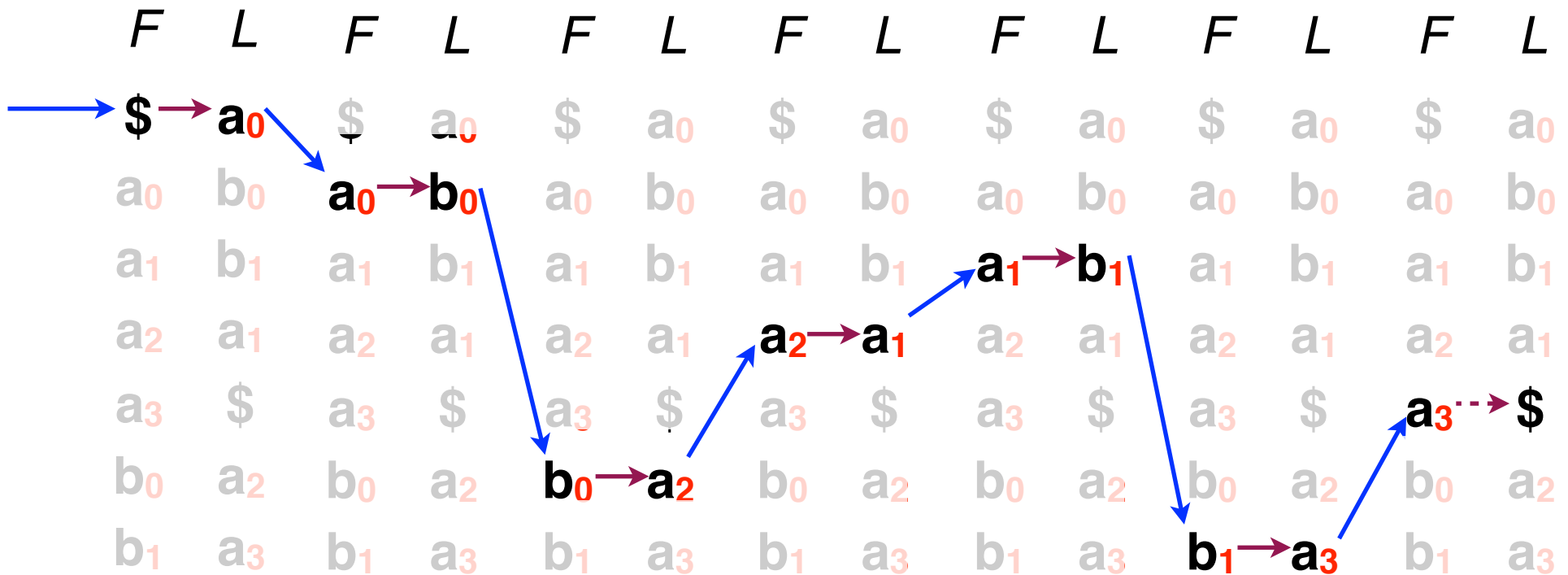
Repeat for  **$a_3$** , get  $\$$ , done

Reverse of chars we visited =  **$a_3$**   **$b_1$**   **$a_1$**   **$a_2$**   **$b_0$**   **$a_0$**   $\$$  =  $T$



# Burrows-Wheeler Transform: reversing

Another way to visualize reversing BWT(T):



$T$ : a<sub>3</sub> b<sub>1</sub> a<sub>1</sub> a<sub>2</sub> b<sub>0</sub> a<sub>0</sub> \$



# Burrows-Wheeler Transform: reversing

```
def rankBwt(bw):  
    ''' Given BWT string bw, return parallel list of B-ranks. Also  
        returns tots: map from character to # times it appears. '''  
    tots = dict()  
    ranks = []  
    for c in bw:  
        if c not in tots: tots[c] = 0  
        ranks.append(tots[c])  
        tots[c] += 1  
    return ranks, tots
```

Calculate B-ranks and count occurrences of each char

```
def firstCol(tots):  
    ''' Return map from character to the range of rows prefixed by  
        the character. '''  
    first = {}  
    totc = 0  
    for c, count in sorted(tots.iteritems()):  
        first[c] = (totc, totc + count)  
        totc += count  
    return first
```

Make concise representation of first BWM column

```
def reverseBwt(bw):  
    ''' Make T from BWT(T) '''  
    ranks, tots = rankBwt(bw)  
    first = firstCol(tots)  
    rowi = 0 # start in first row  
    t = '$' # start with rightmost character  
    while bw[rowi] != '$':  
        c = bw[rowi]  
        t = c + t # prepend to answer  
        # jump to row that starts with c of same rank  
        rowi = first[c][0] + ranks[rowi]  
    return t
```

Do reversal

Python example: [http://bit.ly/CG\\_BWT\\_Reverse](http://bit.ly/CG_BWT_Reverse)



# Burrows-Wheeler Transform: reversing

```
>>> reverseBwt("w$wwdd__nnoooaattTmmrrrrrrrooo__ooo")
'Tomorrow_and_tomorrow_and_tomorrow$'

>>> reverseBwt("s$esttssfftteww_hhmmbootttt_ii__woeeaaressIi_____")
'It_was_the_best_of_times_it_was_the_worst_of_times$'

>>> reverseBwt("u_gleeeengj_mlh1_nnnnt$nwj__lggIolo_iiiiiarfcmlylo_oo_")
'in_the_jingle_jangle_morning_Ill_come_following_you$'
```

ranks list is  $m$  integers  
long! We'll fix later.

```
def reverseBwt(bw):
    ''' Make T from BWT(T) '''
    ranks, tots = rankBwt(bw)
    first = firstCol(tots)
    rowi = 0 # start in first row
    t = '$' # start with rightmost character
    while bw[rowi] != '$':
        c = bw[rowi]
        t = c + t # prepend to answer
        # jump to row that starts with c of same rank
        rowi = first[c][0] + ranks[rowi]
    return t
```

# Burrows-Wheeler Transform

We've seen how BWT is useful for compression:

Sorts characters by right-context, making a more compressible string

And how it's reversible:

Repeated applications of LF Mapping, recreating  $T$  from right to left

How is it used as an index?

# FM Index

FM Index: an index combining the BWT *with a few small auxiliary data structures*

Core of index consists of  $F$  and  $L$  from BWM:

$F$  can be represented very simply  
(1 integer per alphabet character)

And  $L$  is compressible

Potentially very space-economical!

$F$		$L$
\$	a b a a b	a
a	\$ a b a a	b
a	a b a \$ a	b
a	b a \$ a b	a
a	b a a b a	\$
b	a \$ a b a	a
b	a a b a \$	a

└────────────────┘  
Not stored in index

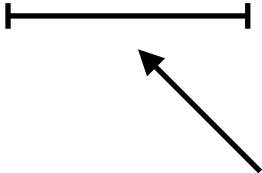
Paolo Ferragina, and Giovanni Manzini. "Opportunistic data structures with applications." *Foundations of Computer Science, 2000. Proceedings. 41st Annual Symposium on*. IEEE, 2000.



# FM Index: querying

Though BWM is related to suffix array, we can't query it the same way

\$	a	b	a	a	b	a
a	\$	a	b	a	a	b
a	a	b	a	\$	a	b
a	b	a	\$	a	b	a
a	b	a	a	b	a	\$
b	a	\$	a	b	a	a
b	a	a	b	a	\$	a



6	\$
5	a \$
2	a a b a \$
3	a b a \$
0	a b a a b a \$
4	b a \$
1	b a a b a \$

We don't have these columns; binary search isn't possible

# FM Index: querying

Look for range of rows of BWM(T) with  $P$  as prefix

Do this for  $P$ 's shortest suffix, then extend to successively longer suffixes until range becomes empty or we've exhausted  $P$

$P = \mathbf{ab}\mathbf{a}$

Easy to find all the  
rows beginning with  
 $\mathbf{a}$ , thanks to  $F$ 's  
simple structure

$F$		$L$
\$	a b a a b	$\mathbf{a_0}$
$\mathbf{a_0}$	\$ a b a a	$\mathbf{b_0}$
$\mathbf{a_1}$	a b a \$ a	$\mathbf{b_1}$
$\mathbf{a_2}$	b a \$ a b	$\mathbf{a_1}$
$\mathbf{a_3}$	b a a b a	\$
$\mathbf{b_0}$	a \$ a b a	$\mathbf{a_2}$
$\mathbf{b_1}$	a a b a \$	$\mathbf{a_3}$

# FM Index: querying

We have rows beginning with **a**, now we seek rows beginning with **ba**

$P = \mathbf{aba}$

$F$						$L$
\$	a	b	a	a	b	$a_0$
$a_0$	\$	a	b	a	a	$b_0$
$a_1$	a	b	a	\$	a	$b_1$
$a_2$	b	a	\$	a	b	$a_1$
$a_3$	b	a	a	b	a	\$
$b_0$	a	\$	a	b	a	$a_2$
$b_1$	a	a	b	a	\$	$a_3$

← Look at those rows in  $L$ .  
 $b_0, b_1$  are **b**s occurring just to left.

Use LF Mapping. Let new range delimit those **b**s

\$	a	b	a	a	b	$a_0$
$a_0$	\$	a	b	a	a	$b_0$
$a_1$	a	b	a	\$	a	$b_1$
$a_2$	b	a	\$	a	b	$a_1$
$a_3$	b	a	a	b	a	\$
$b_0$	a	\$	a	b	a	$a_2$
$b_1$	a	a	b	a	\$	$a_3$

Now we have the rows with prefix **ba**

# FM Index: querying

We have rows beginning with **ba**, now we seek rows beginning with **aba**

$P = \mathbf{aba}$

$F$							$L$
\$	a	b	a	a	b		$a_0$
$a_0$	\$	a	b	a	a		$b_0$
$a_1$	a	b	a	\$	a		$b_1$
$a_2$	b	a	\$	a	b		$a_1$
$a_3$	b	a	a	b	a		\$
$b_0$	a	\$	a	b	a		$a_2$
$b_1$	a	a	b	a	\$		$a_3$

←  $a_2, a_3$  occur just to left.

$P = \mathbf{aba}$

Use LF Mapping →

$F$							$L$
\$	a	b	a	a	b		$a_0$
$a_0$	\$	a	b	a	a		$b_0$
$a_1$	a	b	a	\$	a		$b_1$
$a_2$	b	a	\$	a	b		$a_1$
$a_3$	b	a	a	b	a		\$
$b_0$	a	\$	a	b	a		$a_2$
$b_1$	a	a	b	a	\$		$a_3$

Now we have the rows with prefix **aba**

# FM Index: querying

$P = \text{aba}$  Now we have the same range,  $[3, 5)$ , we would have got from querying suffix array

$F$		$L$
\$	a b a a b	$a_0$
$a_0$	\$ a b a a	$b_0$
$a_1$	a b a \$ a	$b_1$
$a_2$	b a \$ a b	$a_1$
$a_3$	b a a b a	\$
$b_0$	a \$ a b a	$a_2$
$b_1$	a a b a \$	$a_3$

$[3, 5)$

Where are these?

6	\$
5	a \$
2	a a b a \$
3	a b a \$
0	a b a a b a \$
4	b a \$
1	b a a b a \$

$[3, 5)$

Unlike suffix array, we don't immediately know *where* the matches are in T...

# FM Index: querying

When  $P$  does not occur in  $T$ , we eventually fail to find next character in  $L$ :

$P = \mathbf{bba}$

	$F$		$L$
	\$	a b a a b	$a_0$
	$a_0$	\$ a b a a	$b_0$
	$a_1$	a b a \$ a	$b_1$
	$a_2$	b a \$ a b	$a_1$
	$a_3$	b a a b a	\$
Rows with <b>ba</b> prefix	$b_0$	a \$ a b a	$a_2$
	$b_1$	a a b a \$	$a_3$

← No **bs**!

# FM Index: querying

If we *scan* characters in the last column, that can be very slow,  $O(m)$

$P = \mathbf{ab}\mathbf{a}$

$F$						$L$
\$	a	b	a	a	b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$	a	b	a	a	<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a	b	a	\$	a	<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b	a	\$	a	b	<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b	a	a	b	a	\$
<b>b<sub>0</sub></b>	a	\$	a	b	a	<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a	a	b	a	\$	<b>a<sub>3</sub></b>

Scan, looking for **bs**

# FM Index: lingering issues

(1) Scanning for preceding character is slow

	\$	a	b	a	a	b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$	a	b	a	a		<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a	b	a	\$	a		<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b	a	\$	a	b		<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b	a	a	b	a		<b>\$</b>
<b>b<sub>0</sub></b>	a	\$	a	b	a		<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a	a	b	a	\$		<b>a<sub>3</sub></b>

$O(m)$   
scan

(2) Storing ranks takes too much space

$m$  integers

```
def reverseBwt(bw):
    """ Make T from BWT(T) """
    ranks, tots = rankBwt(bw)
    first = firstCol(tots)
    rowi = 0
    t = "$"
    while bw[rowi] != '$':
        c = bw[rowi]
        t = c + t
        rowi = first[c][0] + ranks[rowi]
    return t
```

(3) Need way to find where matches occur in  $T$ :

Where?

	\$	a	b	a	a	b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$	a	b	a	a		<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a	b	a	\$	a		<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b	a	\$	a	b		<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b	a	a	b	a		<b>\$</b>
<b>b<sub>0</sub></b>	a	\$	a	b	a		<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a	a	b	a	\$		<b>a<sub>3</sub></b>



# FM Index: fast rank calculations

Is there an  $O(1)$  way to determine which **bs** precede the **as** in our range?

<i>F</i>		<i>L</i>
\$	a b a a b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$ a b a a	<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a b a \$ a	<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b a \$ a b	<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b a a b a	\$
<b>b<sub>0</sub></b>	a \$ a b a	<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a a b a \$	<b>a<sub>3</sub></b>

Idea: pre-calculate #  
**as**, **bs** in *L* up to every  
row:

<i>F</i>	<i>L</i>	<i>Tally</i>	
		<b>a</b>	<b>b</b>
\$	a	1	0
<b>a</b>	<b>b</b>	1	1
<b>a</b>	<b>b</b>	1	2
<b>a</b>	a	2	2
<b>a</b>	\$	2	2
<b>b</b>	a	3	2
<b>b</b>	a	4	2

We infer **b<sub>0</sub>** and **b<sub>1</sub>**  
appear in *L* in this  
range

$O(1)$  time, but requires  
 $m \times |\Sigma|$  integers

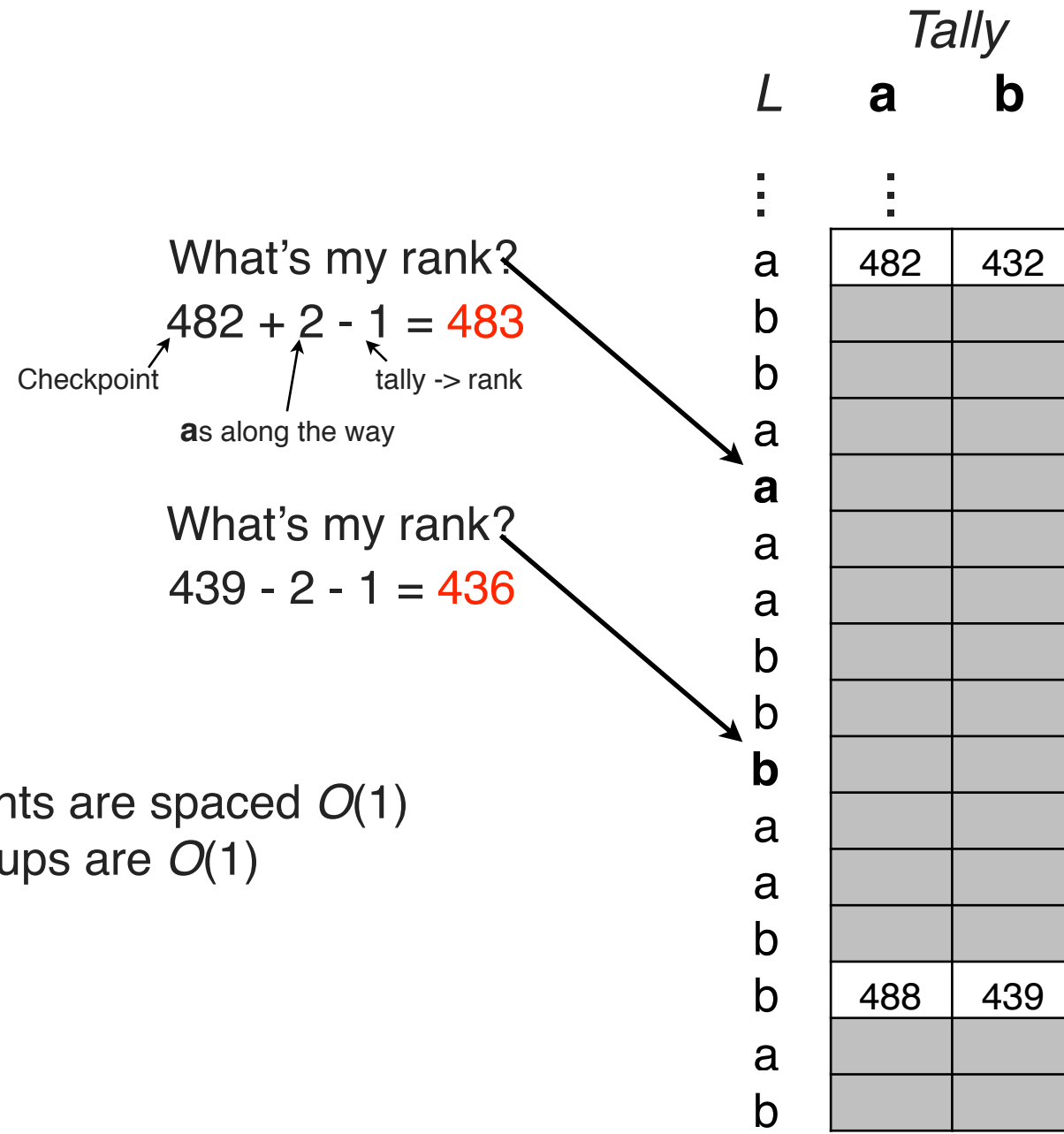
# FM Index: fast rank calculations

Another idea: pre-calculate # **a**s, **b**s in  $L$  up to *some* rows, e.g. every 5<sup>th</sup> row. Call pre-calculated rows *checkpoints*.

		<i>Tally</i>		
$F$	$L$	<b>a</b>	<b>b</b>	
\$	a	1	0	← Lookup here succeeds as usual
<b>a</b>	<b>b</b>			
<b>a</b>	<b>b</b>			
<b>a</b>	<b>a</b>			
<b>a</b>	\$			← Oops: not a checkpoint
<b>b</b>	<b>a</b>	3	2	← But there's one nearby
<b>b</b>	<b>a</b>			

To resolve a lookup for character  $c$  in non-checkpoint row, scan along  $L$  until we get to nearest checkpoint. Use tally at the checkpoint, *adjusted for # of cs we saw along the way*.

# FM Index: fast rank calculations



Assuming checkpoints are spaced  $O(1)$   
distance apart, lookups are  $O(1)$

# FM Index: a few problems

Solved! At the expense of adding checkpoints ( $O(m)$  integers) to index.

(1)

	<i>F</i>		<i>L</i>
	\$	a b a a b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$	a b a a	<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a	b a \$ a	<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b	a \$ a b	<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b	a a b a	\$
<b>b<sub>0</sub></b>	a	\$ a b a	<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a	a b a \$	<b>a<sub>3</sub></b>

← This scan is  $O(m)$  work

With checkpoints it's  $O(1)$

(2) Ranking takes too much space

$m$  integers

```
def reverseBwt(bw):
    """ Make T from BWT(T) """
    ranks, tots = rankBwt(bw)
    first = firstCol(tots)
    rowi = 0
    t = "$"
    while bw[rowi] != '$':
        c = bw[rowi]
        t = c + t
        rowi = first[c][0] + ranks[rowi]
    return t
```

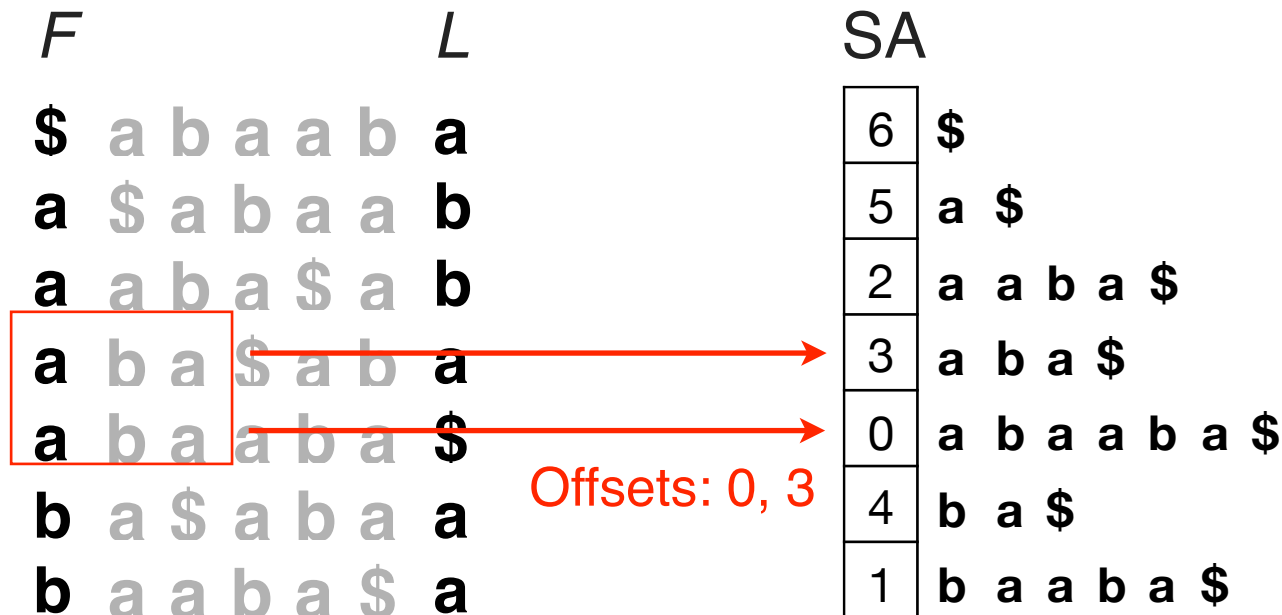
With checkpoints, we greatly reduce  
# integers needed for ranks

# FM Index: a few problems

Not yet solved: **(3)** Need a way to find where these occurrences are in  $T$ :

\$	a	b	a	a	b	<b>a<sub>0</sub></b>
<b>a<sub>0</sub></b>	\$	a	b	a	a	<b>b<sub>0</sub></b>
<b>a<sub>1</sub></b>	a	b	a	\$	a	<b>b<sub>1</sub></b>
<b>a<sub>2</sub></b>	b	a	\$	a	b	<b>a<sub>1</sub></b>
<b>a<sub>3</sub></b>	b	a	a	b	a	\$
<b>b<sub>0</sub></b>	a	\$	a	b	a	<b>a<sub>2</sub></b>
<b>b<sub>1</sub></b>	a	a	b	a	\$	<b>a<sub>3</sub></b>

If suffix array were part of index, we could simply look up the offsets



But SA requires  
 $m$  integers

# FM Index: resolving offsets

Idea: store some, but not all, entries of the suffix array

<i>F</i>	<i>L</i>	SA
\$ a b a a b a		6
a \$ a b a a b		
a a b a \$ a b		2
a b a \$ a b a		
a b a a b a \$		0
b a \$ a b a a		4
b a a b a \$ a		

a b a	\$ a b a	X
a b a	a b a \$	

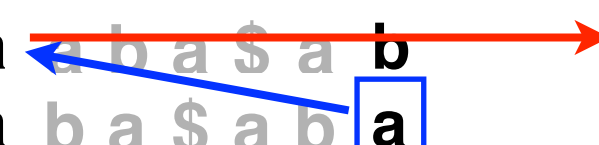
Lookup for row 4 succeeds - we kept that entry of SA

Lookup for row 3 fails - we discarded that entry of SA

# FM Index: resolving offsets

But LF Mapping tells us that the **a** at the end of row 3 corresponds to...  
...the **a** at the beginning of row 2

<i>F</i>		<i>L</i>		<i>SA</i>			
\$	a	b	a	a	b	a	6
a	\$	a	b	a	a	b	
a	a	b	a	\$	a	b	2
a	b	a	\$	a	b	<b>a</b>	
a	b	a	a	b	a	\$	0
b	a	\$	a	b	a	a	4
b	a	a	b	a	\$	a	



And row 2 has a suffix array value = 2

So row 3 has suffix array value = 3 = 2 (row 2's SA val) + 1 (# steps to row 2)

If saved SA values are  $O(1)$  positions apart in  $T$ , resolving offset is  $O(1)$  time

# FM Index: problems solved

Solved! At the expense of adding some SA values ( $O(m)$  integers) to index  
Call this the “SA sample”

**(3)** Need a way to find where these occurrences are in  $T$ :

\$	a	b	a	a	b	a <sub>0</sub>
a <sub>0</sub>	\$	a	b	a	a	b <sub>0</sub>
a <sub>1</sub>	a	b	a	\$	a	b <sub>1</sub>
a <sub>2</sub>	b	a	\$	a	b	a <sub>1</sub>
a <sub>3</sub>	b	a	a	b	a	\$
b <sub>0</sub>	a	\$	a	b	a	a <sub>2</sub>
b <sub>1</sub>	a	a	b	a	\$	a <sub>3</sub>

With SA sample we can do this  
in  $O(1)$  time per occurrence



# FM Index: small memory footprint

Components of the FM Index:

First column ( $F$ ):  $\sim |\Sigma|$  integers

Last column ( $L$ ):  $m$  characters

SA sample:  $m \cdot a$  integers, where  $a$  is fraction of rows kept

Checkpoints:  $m \cdot |\Sigma| \cdot b$  integers, where  $b$  is fraction of rows checkpointed

Example: DNA alphabet (2 bits per nucleotide),  $T$  = human genome,  $a = 1/32$ ,  $b = 1/128$

First column ( $F$ ): 16 bytes

Last column ( $L$ ): 2 bits \* 3 billion chars = 750 MB

SA sample: 3 billion chars \* 4 bytes/char / 32 =  $\sim$  400 MB

Checkpoints: 3 billion \* 4 bytes/char / 128 =  $\sim$  100 MB

Total < 1.5 GB

# FM Index: small memory footprint

Paolo Ferragina, and Giovanni Manzini. "Opportunistic data structures with applications."  
*Foundations of Computer Science, 2000. Proceedings. 41st Annual Symposium on.* IEEE, 2000.

FM Index described here is simplified version of what's described in paper

Also discussed in paper: how to compress  $BWT(T)$  for further savings

# Indexing summary

Memory cost to index a human genome:

- Suffix tree: ~47 GB

- Suffix array: 12 GB

- FM-index: 1.5 GB

Suffix-based data structures allow *count* and *locate* queries for arbitrary patterns

Substring indices we saw earlier are restricted to a small set of patterns with a fixed length

# Paper discussion

Short break then we'll discuss "Fast and accurate short read alignment with the Burrows-Wheeler transform"