Burrows-Wheeler Transform and FM Index

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Lesson 04

Recapitulation

Exact string matching algorithms

on-line

Boyer-Moore

off-line

Multimap (sorted index)

Hash table

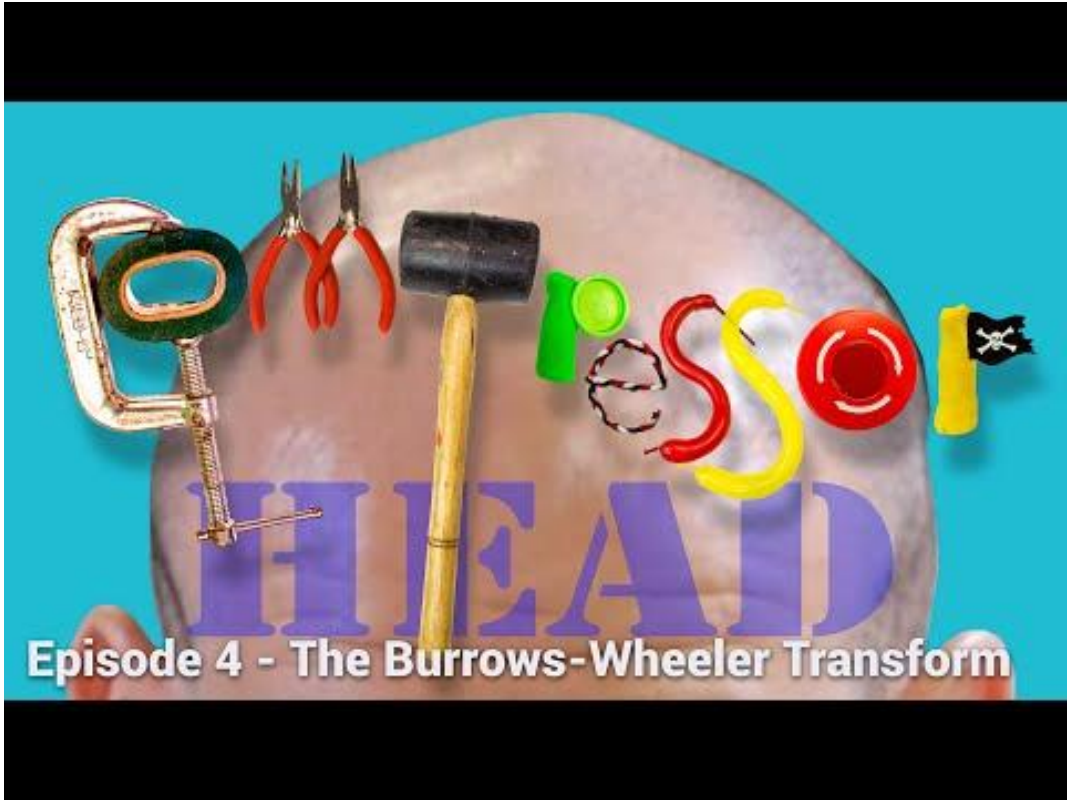
Suffix array

Suffix trie

Suffix tree

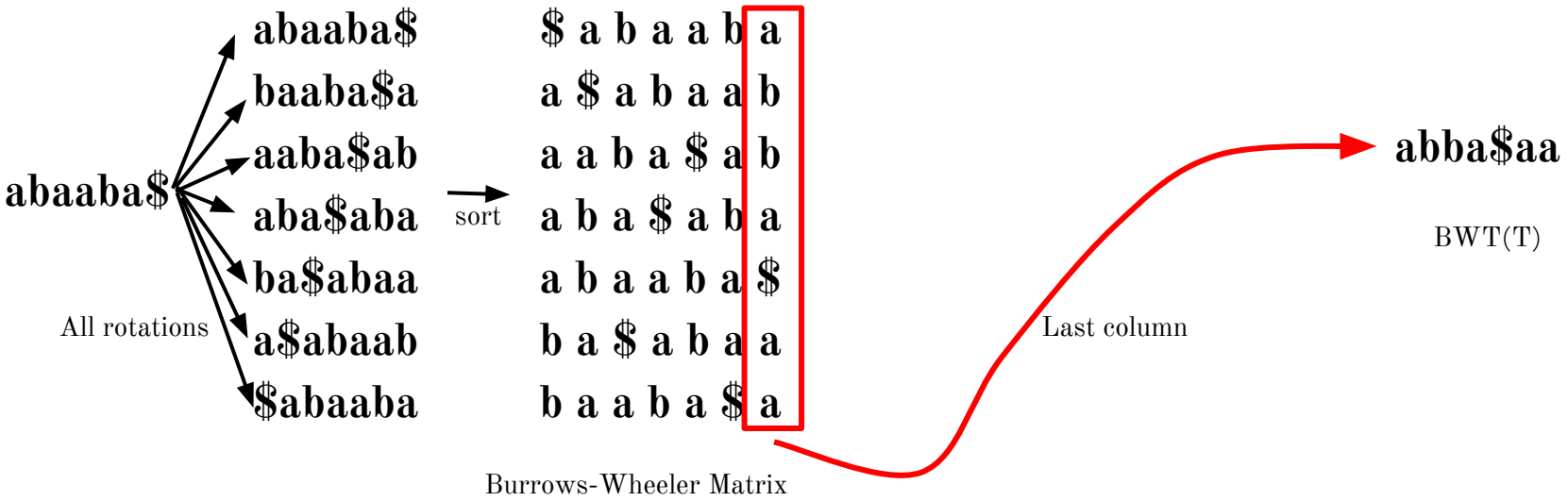
Burrows-Wheeler transform + FM index

Burrows-Wheeler Transform



Slide adapted from Ben Langmead

Burrows-Wheeler Transform



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 creating BWM """
    return ''.join(map(lambda x: x[-1], bwm(t)))
```

Take last column

```
>>>  bwtViaBwm("Tomorrow_and_tomorrow_and_tomorrow$")
'w$wwdd__nnoooaattTmmmrrrrrrooo__ooo'
>>>  bwtViaBwm("It_was_the_best_of_times_it_was_the_worst_of_times$")
's$esttssffttew_hhmmbootttt_ii__woeeaaressIi_______'
>>>  bwtViaBwm('in_the_jingle_jangle_morning_Ill_come_following_you$')
'u_gleeeengj_mlhl_nnnnt$nwj__lggIolo_iiiiarfcmylo_oo_'
```

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

Right-context from 'a'

$	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

Burrows-Wheeler Matrix

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

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

BWT(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)

Which structure is very similar to BWM?

Sort order is the same whether rows are rotations or suffixes

Burrows-Wheeler Transform

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

$ 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

BWT(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)

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

Burrows-Wheeler Transform

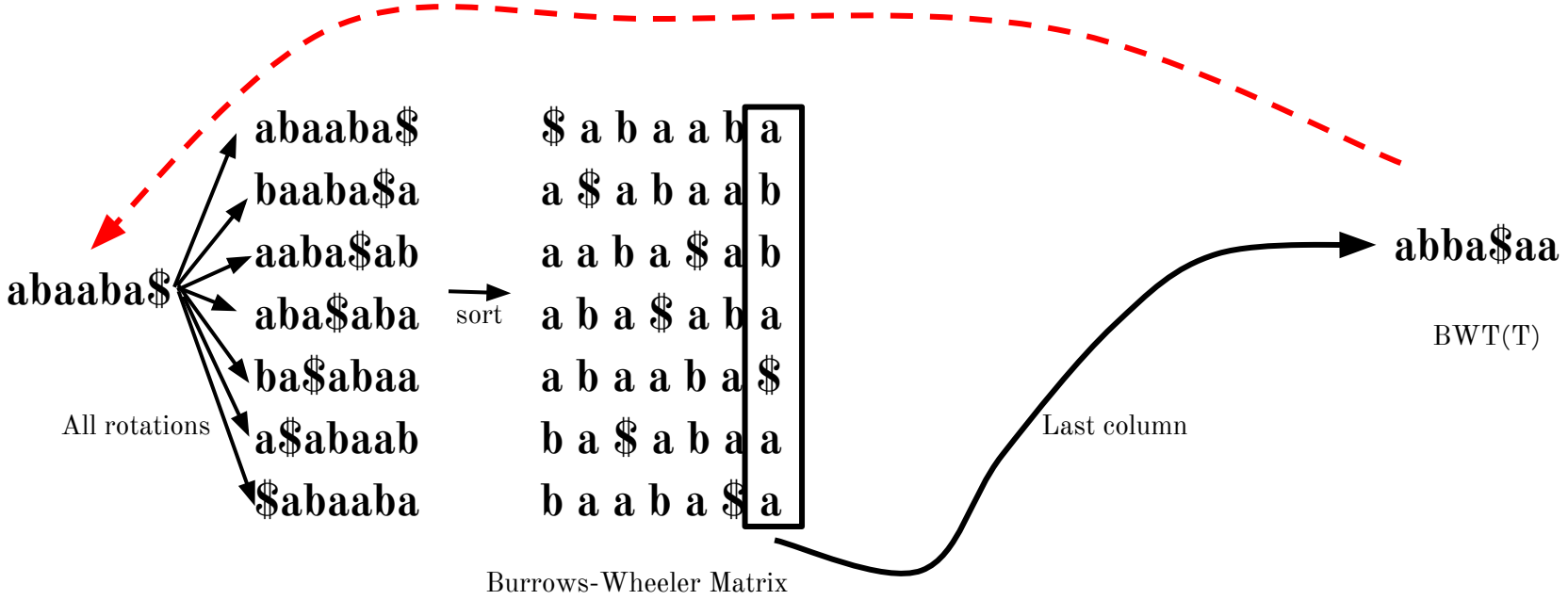
```
def suffixArray(s):
    """ Given T return suffix array SA(T).  We use Python's sorted
        function here for simplicity, but we can do better. """
    satups = sorted([(s[i:], i) for i in range(len(s))])
    # Extract and return just the offsets
    return map(lambda x: x[1], satups)
def bwtViaSa(t):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

Make suffix array

Take characters just to the left of the sorted suffixes

```
>>>  bwtViaBwm("Tomorrow_and_tomorrow_and_tomorrow$")
'w$wwdd__nnoooaattTmmmrrrrrrooo__ooo'
>>>  bwtViaBwm("It_was_the_best_of_times_it_was_the_worst_of_times$")
's$esttssffttew_hhmmbootttt_ii__woeeaaressIi_______'
>>>  bwtViaBwm('in_the_jingle_jangle_morning_Ill_come_following_you$')
'u_gleeeengj_mlhl_nnnnt$nwj__lggIolo_iiiiarfcmylo_oo_'
```

Burrows-Wheeler Transform



How to reverse the BWT?

BWM has a key property called the LF Mapping

Burrows-Wheeler Transform: T-ranking

T-ranking: Give each character in T a rank, equal to # times the character occurred previously in T.

$$\mathbf{a}_{0}\ \mathbf{b}_{0}\ \mathbf{a}_{1}\ \mathbf{a}_{2}\ \mathbf{b}_{1}\ \mathbf{a}_{3}\ \$$$

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

Burrows-Wheeler Transform: T-ranking

BWT with T-raking:

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

Look at first and last columns, called F and L

"a" occur in the same order in F and L

As we look down columns, in both cases we see: a_3, a_1, a_2, a_0

Burrows-Wheeler Transform: T-ranking

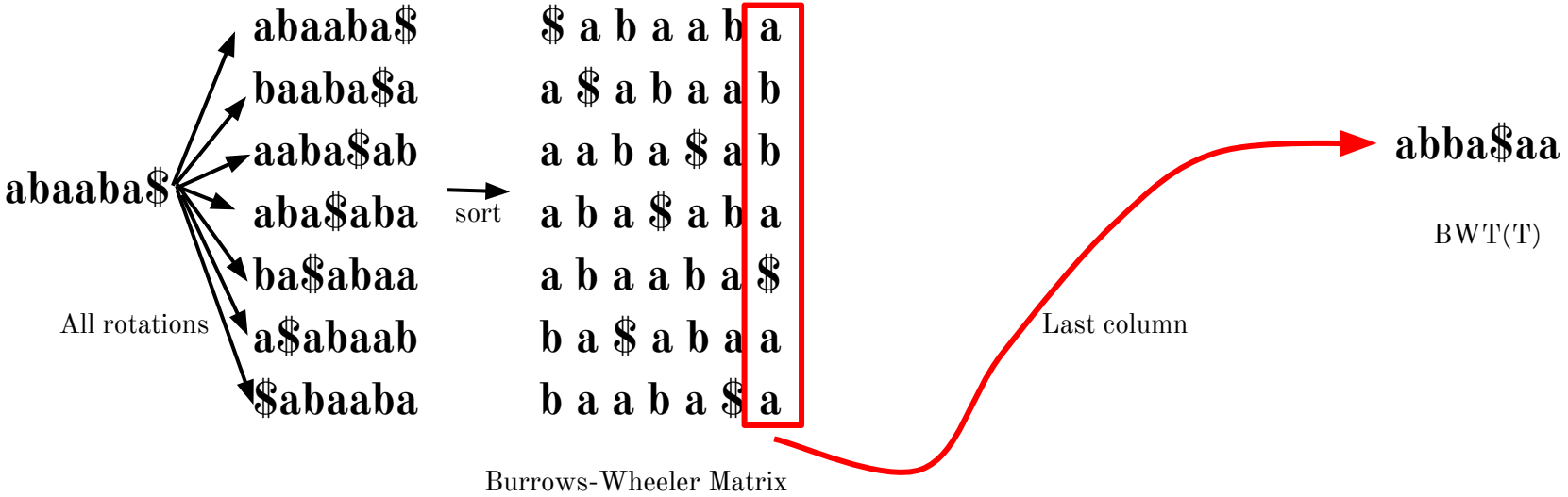
BWT with T-raking:

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

Same is with “b”

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?

Slide adapted from Ben Langmead

Burrows-Wheeler Transform: LF Mapping

BWT with T-raking:

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

Order of ranks in L is preserved in F!

LF Mapping: The i-th occurrence of a character c in L and the i th occurrence of c in F correspond to the same occurrence in T

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?
Why are these "a" in this order relative to each other?

They're sorted by right-context!!!

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

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

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 B-ranking:

$	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

Ascending rank

F now has very simple structure: a $, a block of “a” with ascending ranks, a block of “b” with ascending ranks (we do not have to store its ranks)

Burrows-Wheeler Transform

	F	L
	$	a_0
	a_0	b_0
	a_1	b_1
	a_2	a_1
	a_3	$
	b_0	a_2
row 6 →	b_1	a_3

Which BWM row begins with b_1?
Skip row starting with $ (1 row)
Skip rows starting with "a" (4 rows)
Skip row starting with b_0 (1 row)

Answer: row 6

Burrows-Wheeler Transform

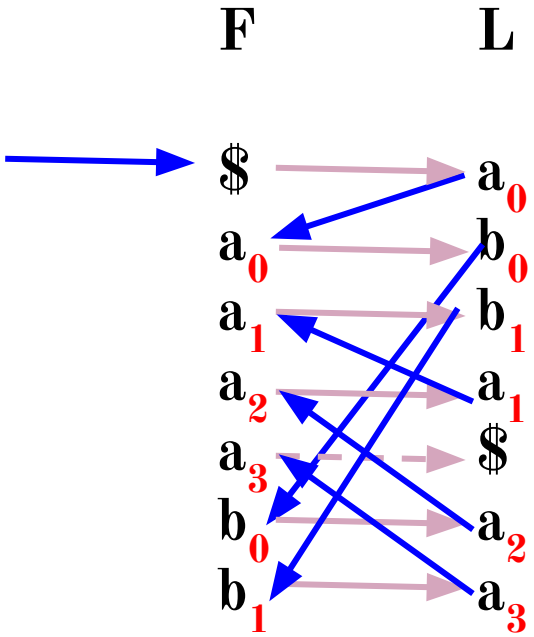
Say T has 300 As, 400 Cs, 250 Gs and 700 Ts and $\$ < A < C < G < T$
Which BWM row (0-based) begins with G_{100}? (Ranks are B-ranks.)

- 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

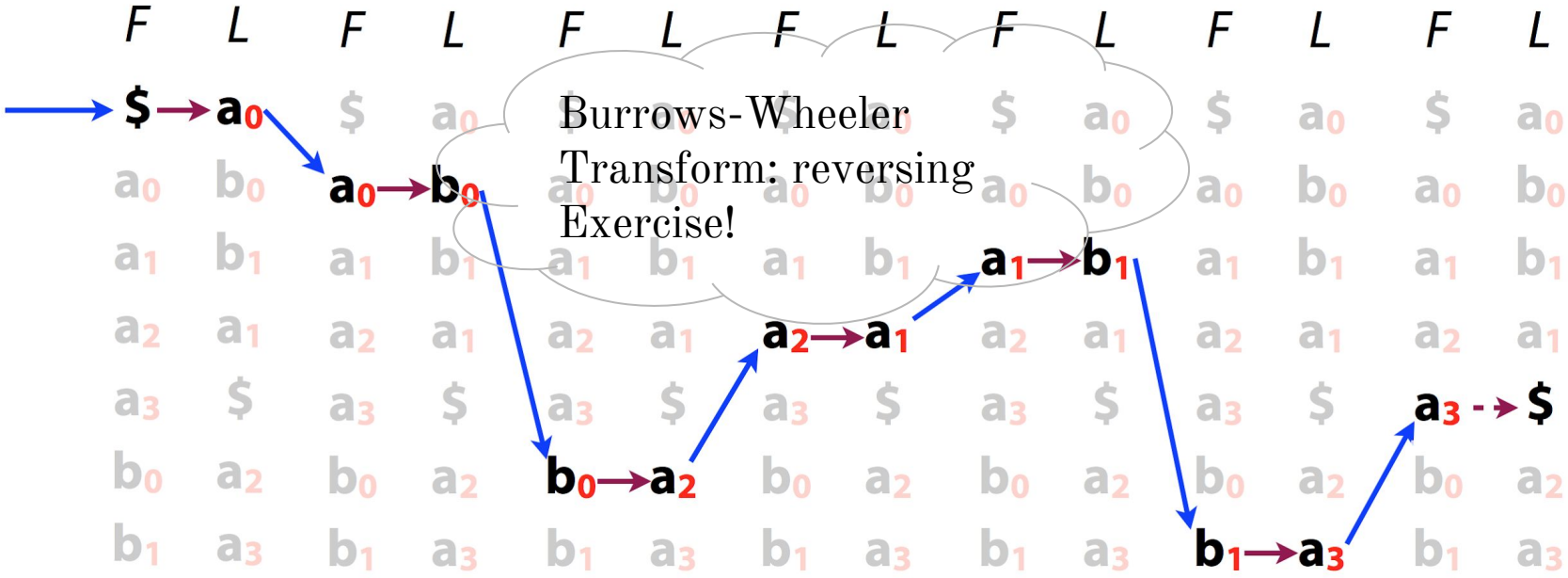
Start in first row. F must have \$.
L contains character just prior to \$: a_0
...



Reverse of chars we visited = $\mathbf{a_3\ b_1\ a_1\ a_2\ b_0\ a_0\ \$}$ = T

Burrows-Wheeler Transform: reversing

Another way of visualizing Reverse BWT(T)



Burrows-Wheeler Transform: reversing

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

- An index combining the BWT with a few small auxilliary data structures

“FM” supposedly stands for “Full-text Minute-space.” (But inventors are named Ferragina and Manzini)

- 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!

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

Easy to find all the rows beginning with a, thanks to F's simple structure

$	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

$\mathbf{P = aba}$

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 = aba

$	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

P = aba

$	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

FM Index: querying

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

P = aba

$	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

Occurs just to the left

P = 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

Use LF mapping

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

FM Index: querying

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

$\mathbf{P = bba}$

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	$
b_0	a	a	b	a	$	a_2
b_1	a	$	a	b	a	a_3

Use LF mapping

No b!

FM Index: querying

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

P = 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

[3, 5)

Where are these?

SA(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 $

[3, 5)

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

FM Index: querying

$\mathbf{P} = \mathbf{aba}$

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

Scan looking for **b!**

FM Index: Current issues

(1) Scanning for preceding character is slow

$	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

(2) Storing ranks takes too much space

```
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
```

m integers

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

$	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?

FM Index: fast rank calculations

Is there an O(1) way to determine which **b** precede the **a** in our range?

$	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

Idea: pre-calculate # **a**-s, **b**-s in L up to every row:

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

Tally

a	b
1	0
1	1
1	2
2	2
2	2
3	2
4	2

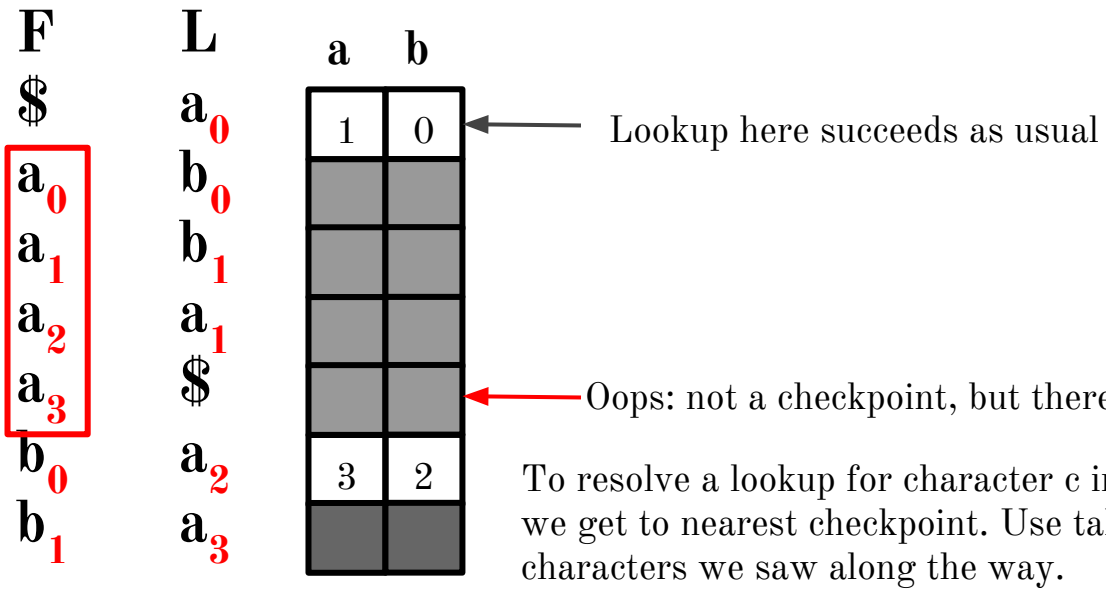
We infer b_0 and b_1 appear in L in this range:

Tally(b, i) - Tally(b,j) = 2

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

FM Index: fast rank calculations

Another idea: pre-calculate # as, bs in L up to some rows, e.g. every 5th row.
Call pre-calculated rows checkpoints.



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 characters we saw along the way.

FM Index: fast rank calculations

What's my rank?

$482 + 2 - 1 = 483$

checkpoint + as along the way - tally->rank

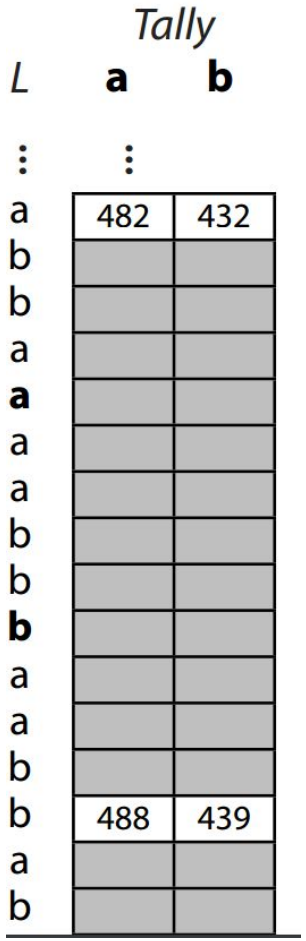
What's my rank?

$439 - 2 - 1 = 436$

checkpoint + as along the way - tally->rank

What's my rank?

439 - 2 - 1 = 436



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

FM Index: Current issues

(1) Scanning for preceding character is slow

$ 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

With checkpoints it's O(1)

(2) Storing ranks takes too much space

```
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
```

m integers

With checkpoints, we greatly reduce # integers needed for ranks - but it's still O(m) space - there's literature on how to improve this space bound

FM Index: Not yet solved!

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

$P = aba$

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

Offsets (0, 3)

SA(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 $

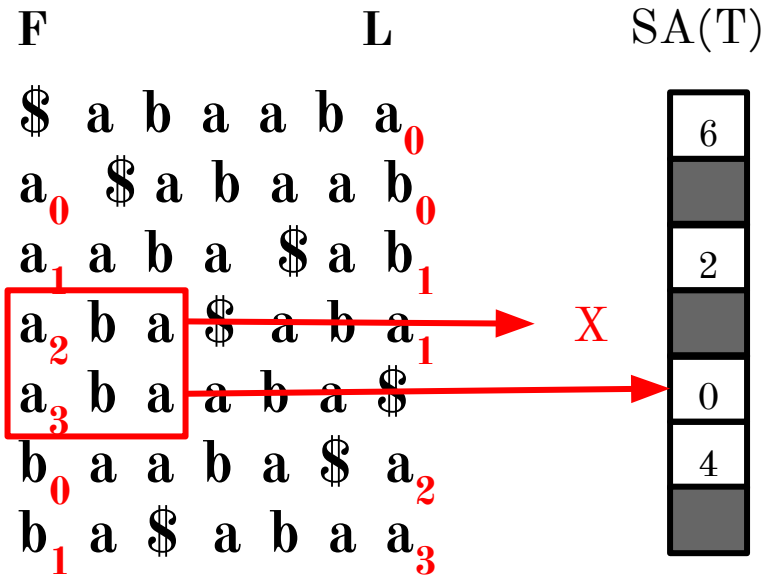
$	a	b	a	a	b	a_0
a_0	$	a	b	a	a	b_0
a_1	a	b	a	$	a	b_1
a_2	b	a	$	a	b	a_1
a_3	b	a	a	b	a	$
b_0	a	a	b	a	$	a_2
b_1	a	$	a	b	a	a_3

Where are these?

If suffix array were part of index, we could simply look up the offsets...
But, SA requires m integers...

FM Index: resolving offsets

P = aba



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

P = 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	$\boxed{a_1}$
a_3	b	a	a	b	a	$
b_0	a	a	b	a	$	a_2
b_1	a	$	a	b	a	a_3

X

SA(T)

6
2
0
4

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

...the **a** at the beginning of row 2

And row 2 has a suffix array value = 2

So row 3 has suffix array value:

2 (row 2's SA val) + 1 (# steps to row 2) = **3**

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

FM Index: resolving offsets

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

SA sample(T)

$ 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

Where are these?
In SA sample!

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):	$\sim \lvert \Sigma \rvert$ integers
Last column (L):	m characters
SA sample:	$m \cdot a$ integers, where a is fraction of rows kept
Checkpoints:	$m \times \lvert \Sigma \rvert \cdot b$ 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 = ~ 400 MB
Checkpoints:	*3 billion* * 4 bytes/char / *128* = ~ 100 MB

Total < 1.5 GB

Secondary DNA analysis

—

Lesson 04

FASTQ

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>>CCCCCCC65

...
```

A FASTQ (FQ) file normally uses four lines per sequence.

- Line 1 begins with a '@' character and is followed by a sequence identifier and an optional description.
- Line 2 is the raw sequence letters.
- Line 3 begins with a '+' character and is optionally followed by the same sequence identifier (and any description) again.
- Line 4 encodes the quality values for the sequence in Line 2, and must contain the same number of symbols as letters in the sequence.

FASTA

```
> CONTIG_NAME
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
GATTTGGGGTTCAAAGCAGTAATTTGGGGTTCAAAGCAGTATCGACAAATAGTAAATCCA
TTTGTTCATTCAAAGCAGTAATTTGGGGTTATTTGGGGTTCAAAGCAGTATCGATCAAAT
AGTAAATCCATTTGTTCAACTCACAGTTT
GATT
```

FASTA is used for storing the sequence of nucleotides or amino acids

What is CIGAR string?

- Describes similarity between sequences

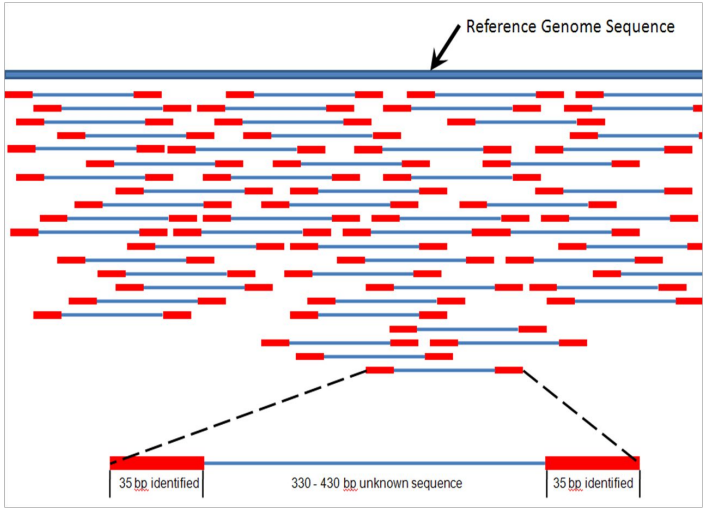
```
RefPos:     1  2  3  4  5  6  7     8  9 10 11 12 13 14 15 16 17 18 19
Reference:  C  C  A  T  A  C  T     G  A  A  C  T  G  A  C  T  A  A  C
Read:                   A  C  T  A  G  A  A     T  G  G  C  T

POS: 5
CIGAR: 3M1I3M1D5M
```

D - delete, I - insert, M - match/mismatch, H - hard clip,
S - soft clip, N - skipped from the sequence, P - padding silent

BWA-MEM

```
bwa mem ref.fa read1.fq read2.fq > aln.sam
```

- http://bio-bwa.sourceforge.net/
- Reference genome index must exist
- Paired-end reads
- Primary and secondary alignment (random)



BWA-MEM output

Line from SAM file:

```
SRR035022.2621862 163 16 59999 37 22S54M = 60102 179 CCAACCCAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCGACCCTCACCCTCACCC
>AAA=>?AA>@@B@B?AABAB?AABAB?AAC@B?@AB@A?A>A@A?AAAAB??ABAB?79A?AAB;B?@?@<=8:8 XT:A:M XN:i:2 SM:i:37 AM:i:37 XM:i:0 XO:i:0 XG:i:0 RG:Z:SRR035022 NM:i:2
MD:Z:0N0N52 OQ:Z:CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCBCCCCCCBBCC@CCCCCCCCCCACCCCC;CCCBBC?CCCACCACA@
```

QNAME	SRR035022.2621862
FLAG	163
RNAME	16
POS	59999
MAQ	37
CIGAR	22S54M
MRNM	=
MPOS	60102
ISIZE	179
SEQ	CCAACCCAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCCTAACCGACCCTCACCCTCACCC
QUAL	>AAA=>?AA>@@B@B?AABAB?AABAB?AAC@B?@AB@A?A>A@A?AAAAB??ABAB?79A?AAB;B?@?@<=8:8
TAG	XT:A:M
TAG	XN:i:2
TAG	SM:i:37
TAG	AM:i:37
TAG	XM:i:0
TAG	XO:i:0
TAG	XG:i:0
TAG	RG:Z:SRR035022
TAG	NM:i:2
TAG	MD:Z:0N0N52
TAG	OQ:Z:CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCBCCCCCCBBCC@CCCCCCCCCCACCCCC;CCCBBC?CCCACCACA

1	the read is paired in sequencing, no matter whether it is mapped in a pair
1	the read is mapped in a proper pair
0	not unmapped
0	mate is not unmapped
0	forward strand
1	mate strand is negative
0	the read is not the first read in a pair
1	the read is the second read in a pair

BWA-MEM aligned reads

```
coor    12345678901234  5678901234567890123456789012345
ref     AGCATGTTAGATAA**GATAGCTGTGCTAGTAGGCAGTCAGCGCCAT

r001+         TTAGATAAAGGATA*CTG
r002+       aaaAGATAA*GGATA
r003+     gcctaAGCTAA
r004+                   ATAGCT..............TCAGC
r003-                          ttagctTAGGC
r001-                                      CAGCGCCAT
```

Paired-end

Multipart

```
@SQ SN:ref LN:45
r001 163 ref  7 30 8M2I4M1D3M = 37  39 TTAGATAAAGGATACTA *
r002   0 ref  9 30 3S6M1P1I4M *  0   0 AAAAGATAAGGATA    *
r003   0 ref  9 30 5H6M       *  0   0 AGCTAA    *   NM:i:1
r004   0 ref 16 30 6M14N5M    *  0   0 ATAGCTTCAGC       *
r003  16 ref 29 30 6H5M       *  0   0 TAGGC     *   NM:i:0
r001  83 ref 37 30 9M         =  7 -39 CAGCGCCAT         *
```

Ins & padding

Soft clipping

Splicing

Hard clipping

References

JOHNS HOPKINS
WHITING SCHOOL
of ENGINEERING

Seven
Bridges