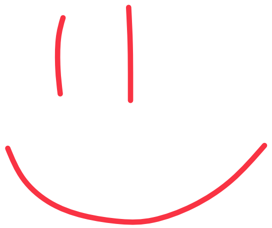
# String Algorithms and Data Structures
## Approximate Pattern Matching

CS 199-225
Brad Solomon

November 11, 2024



UNIVERSITY OF
ILLINOIS
URBANA-CHAMPAIGN

Department of Computer Science

# Learning Objectives

Review exact pattern matching and introduce approximate matching

Formally define a mismatch vs an edit

Discuss strategies for efficient approximate pattern matching…

… With mismatches ← today

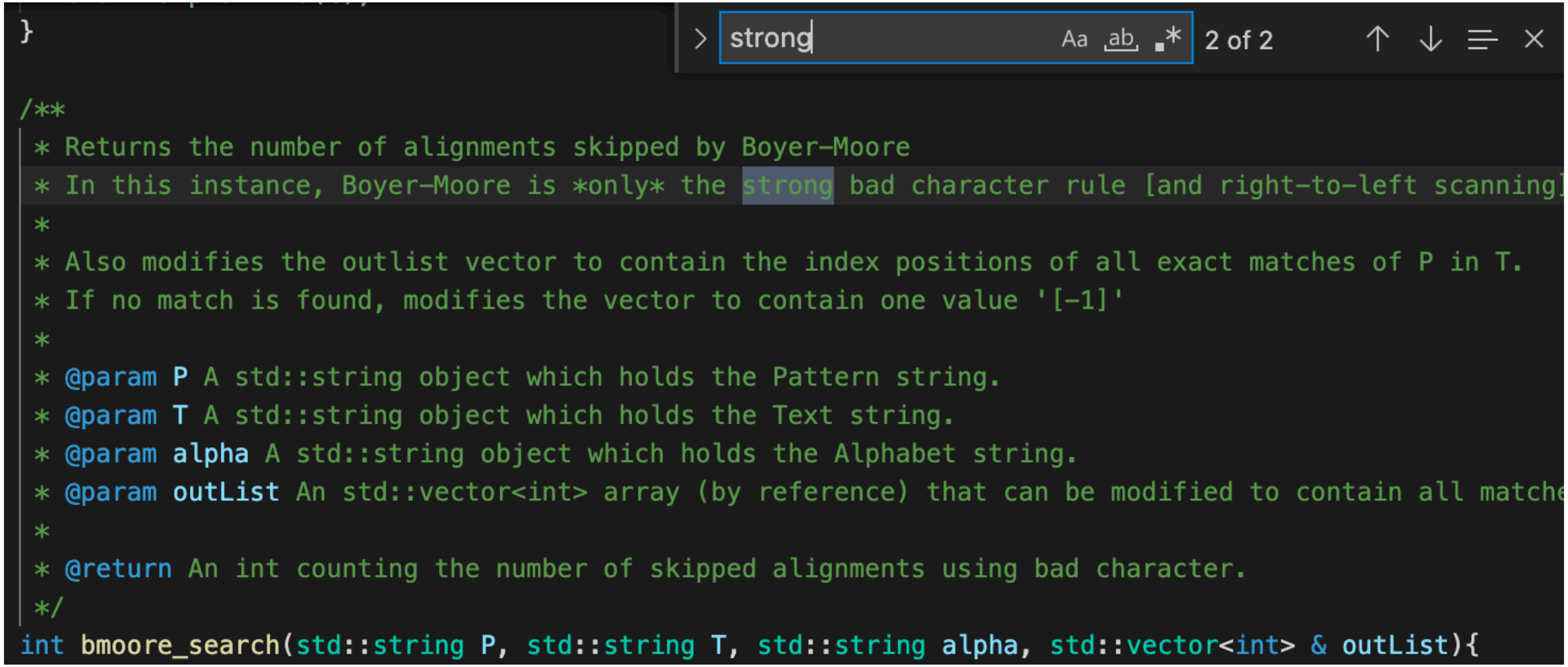
… With edits ← next week

# Suffix-Based Index Review

| | **Suffix tree** | **Suffix array** | **FM Index** |
|---|---|---|---|
| Time: Does P occur? | $O(n)$ | $O(n \log m)$ | $O(n)$ |
| Time: Count *k* occurrences of P | $O(n + k)$ | $O(n \log m)$ | $O(n)$ |
| Time: Report *k* locations of P | $O(n + k)$ | $O(n \log m + k)$ | $O(n + k)$ |
| Space | $O(m)$ | $O(m)$ | $O(m)$ |
| Needs T? | *yes* | *yes* | *no* |
| Bytes per input character | >15 | ~4 | ~0.5 |

$m = |T|$, $n = |P|$, $k$ = # occurrences of $P$ in $T$

# Limitations of exact pattern matching

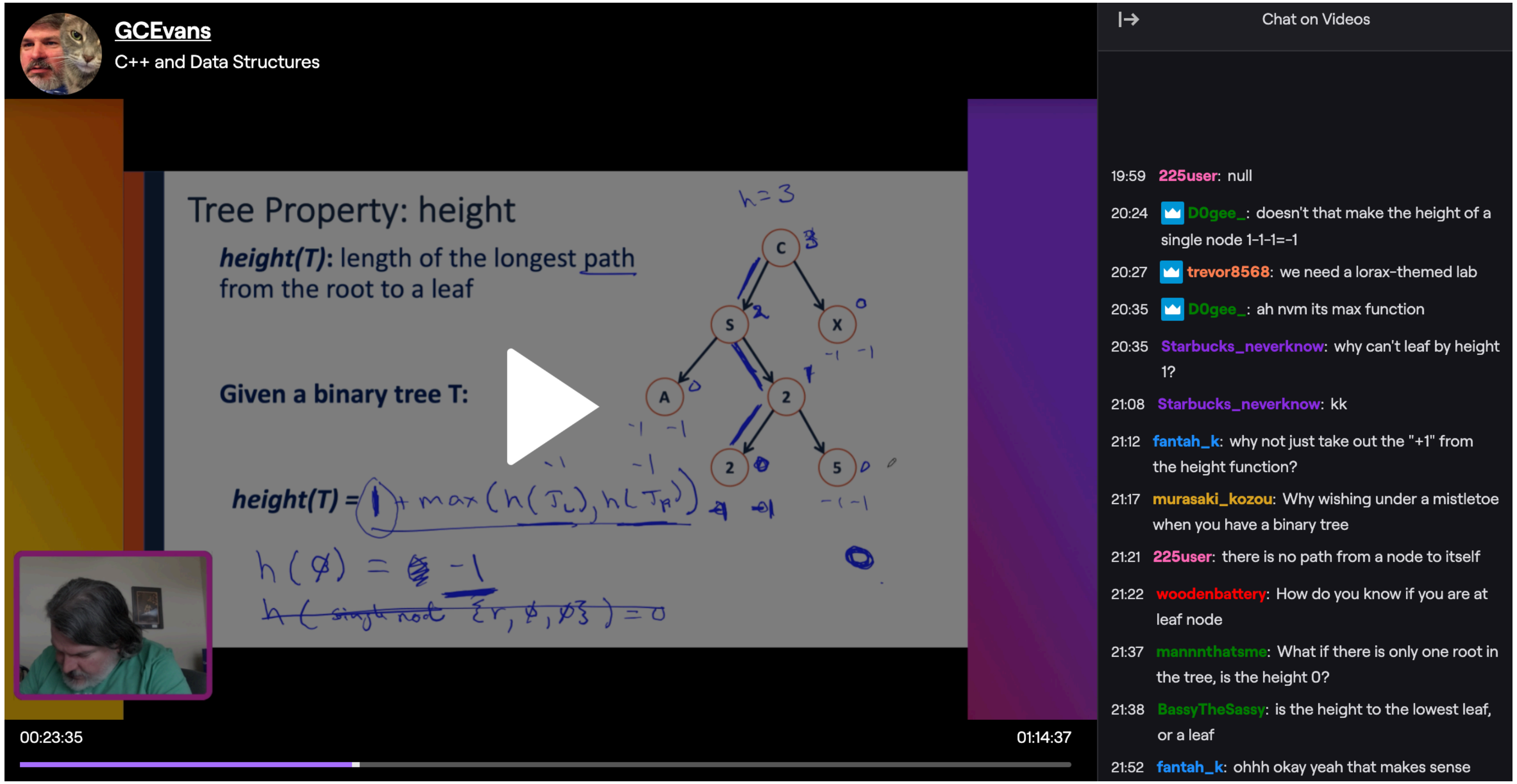


```
}

/**
 * Returns the number of alignments skipped by Boyer-Moore
 * In this instance, Boyer-Moore is *only* the strong bad character rule [and right-to-left scanning]
 *
 * Also modifies the outlist vector to contain the index positions of all exact matches of P in T.
 * If no match is found, modifies the vector to contain one value '[-1]'
 *
 * @param P A std::string object which holds the Pattern string.
 * @param T A std::string object which holds the Text string.
 * @param alpha A std::string object which holds the Alphabet string.
 * @param outList An std::vector<int> array (by reference) that can be modified to contain all matche
 *
 * @return An int counting the number of skipped alignments using bad character.
 */
int bmoore_search(std::string P, std::string T, std::string alpha, std::vector<int> & outList){
```

But what if I was actually trying to look up ‘string’?

# Limitations of exact pattern matching



Tree Property: height

*height(T)*: length of the longest path from the root to a leaf

Given a binary tree T:

*height(T)* = 1 + max(h(T_L), h(T_R))

h(∅) = -1

h(~~single node~~ {r, ∅, ∅}) = 0

19:59 225user: null

20:24 D0gee_: doesn't that make the height of a single node 1-1-1=-1

20:27 trevor8568: we need a lorax-themed lab

20:35 D0gee_: ah nvm its max function

20:35 Starbucks_neverknow: why can't leaf by height 1?

21:08 Starbucks_neverknow: kk

21:12 fantah_k: why not just take out the "+1" from the height function?

21:17 murasaki_kozou: Why wishing under a mistletoe when you have a binary tree

21:21 225user: there is no path from a node to itself

21:22 woodenbattery: How do you know if you are at leaf node

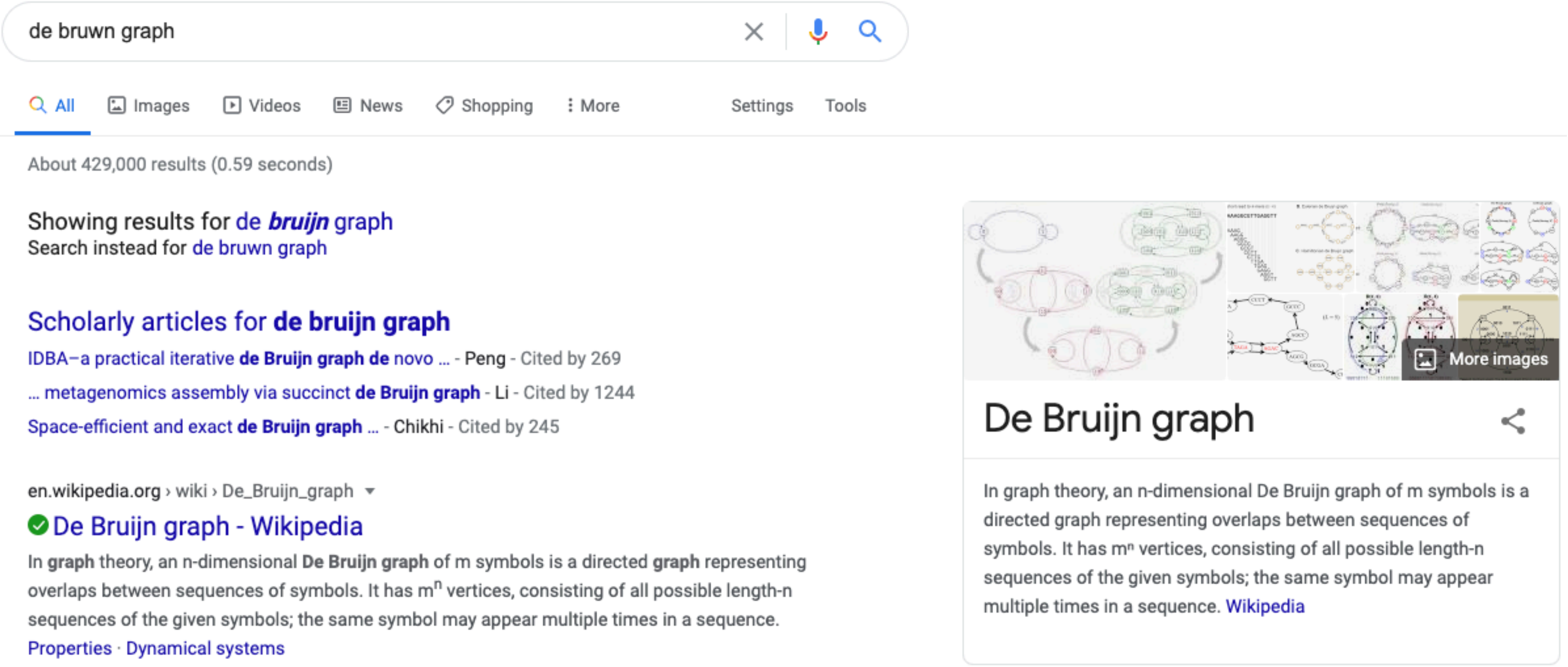
21:37 mannnthatsme: What if there is only one root in the tree, is the height 0?

21:38 BassyTheSassy: is the height to the lowest leaf, or a leaf

21:52 fantah_k: ohhh okay yeah that makes sense

If I ban “bad word”, what happens to “b@d w0rd”?

# Approximate Pattern Matching



de bruwn graph

About 429,000 results (0.59 seconds)

Showing results for de ***bruijn*** graph
Search instead for de bruwn graph

Scholarly articles for **de bruijn graph**

IDBA–a practical iterative **de Bruijn graph de** novo ... - Peng - Cited by 269
... metagenomics assembly via succinct **de Bruijn graph** - Li - Cited by 1244
Space-efficient and exact **de Bruijn graph** ... - Chikhi - Cited by 245

en.wikipedia.org › wiki › De_Bruijn_graph

De Bruijn graph - Wikipedia

In **graph** theory, an n-dimensional **De Bruijn graph** of m symbols is a directed **graph** representing overlaps between sequences of symbols. It has $m^n$ vertices, consisting of all possible length-n sequences of the given symbols; the same symbol may appear multiple times in a sequence.

Properties · Dynamical systems

De Bruijn graph

In graph theory, an n-dimensional De Bruijn graph of m symbols is a directed graph representing overlaps between sequences of symbols. It has $m^n$ vertices, consisting of all possible length-n sequences of the given symbols; the same symbol may appear multiple times in a sequence. Wikipedia

# Approximate Pattern Matching

```
Score =  248 bits (129), Expect = 1e-63
Identities = 213/263 (80%), Gaps = 34/263 (12%)
Strand = Plus / Plus

Query: 161 atatcaccacgtcaaaggtgactccaactcca---ccactccattttgttcagataatgc 217
           |||||||||||||||||||||||||||||  |     | |   || ||||||||||||||
Sbjct: 481 atatcaccacgtcaaaggtgactccaact-tattgatagtgttttatgttcagataatgc 539

Query: 218 ccgatgatcatgtcatgcagctccaccgattgtgagaacgacagcgacttccgtcccagc 277
           |||||||   ||||||||||||||||||||| || |            ||||||||||||
Sbjct: 540 ccgatgactttgtcatgcagctccaccgattttg-g------------ttccgtcccagc 586

Query: 278 c-gtgcc--aggtgctgcctcagattcaggttatgccgctcaattcgctgcgtatatcgc 334
           |  || |  | ||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 587 caatgacgta-gtgctgcctcagattcaggttatgccgctcaattcgctgggtatatcgc 645

Query: 335 ttgctgattacgtgcagctttcccttcaggcggga------------ccagccatccgtc 382
           |||||||||||||||||||||||||||||||||||            |||||||||||||
Sbjct: 646 ttgctgattacgtgcagctttcccttcaggcgggattcatacagcggccagccatccgtc 705

Query: 383 ctccatatc-accacgtcaaagg 404
            |||||||| |||||||||||||
Sbjct: 706 atccatatcaaccacgtcaaagg 728
```

edits

# Approximate Pattern Matching

**Input:** A text *T*, a pattern *P*, and a distance *d*

**Output:** All positions in *T* where *P* has at most *d* mismatches or edits

*P*: `word`

*T*: `There would have been a time for such a word`

Alignment 1: `word`

~~Not a match!~~

Distance 2 match!

Alignment 2: `word`

Match!

Distance 0 match!

# Approximate Pattern Matching

What is the distance between these two strings?

3 mismatches

X: 1 0 0 1 1

↓ ↓ ↓

Y: 0 0 1 1 0

Bag of words

= 1, 1, 1, 00

11, 0, 0, 0

2 char diff

# Approximate Pattern Matching

What is the distance between these two strings?

*X*: 1 0 0 1 1

*Y*: 0 0 1 1 0

```
X: 1 0 0 1 1
     |   |
Y: 0 0 1 1 0
```

Hamming distance is 3!

```
X: 1 0 0 1 1 -
       | | | |
Y: - 0 0 1 1 0
```

remove

insert

Edit distance is 2!

# Approximate Pattern Matching

How can I describe the relationship between two strings?

```
X: 1 0 0 1 1
     |   |
Y: 0 0 1 1 0
```

Substitution

Hamming

Dist

```
X: 1 0 0 1 1 -
     | | | |
Y: - 0 0 1 1 0
```

deletion

insertion

Substitution

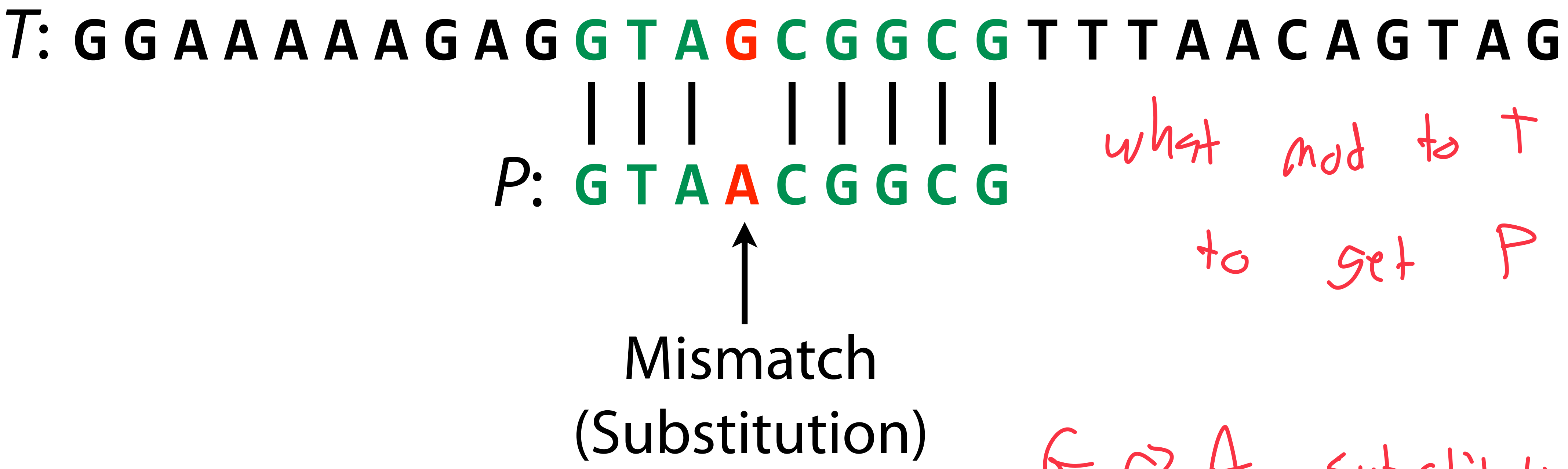
Edit

distance

# Approximate Pattern Matching

A **substitution** replaces one character with another

Described as the character swap needed to *convert T* to *P*



*T*: GGAAAAAGAGGTAGCGGCGTTTAACAGTAG

*P*: GTAACGGCG

Mismatch
(Substitution)

what mod to T
to get P

G → A substitution

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

*X*: **GAGGTAGCGGCGTT**

*Y*: **GTGGTAACGGGGTT**

3

*X*: **TGGCCGCGCAAAAACAGC**

*Y*: **TGACCGCGCAAAACAGCT**

6

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

*X*: G A G G T A G C G G C G T T<br>
|   | | | |   | | |   | | |<br>
*Y*: G T G G T A A C G G G G T T

*Hamming distance = 3*

*X*: T G G C C G C G C A A A A A C A G C

*Y*: T G A C C G C G C A A A A C A G C T

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

```
X: G A G G T A G C G G C G T T
   |   | | | |   | | |   | | |
Y: G T G G T A A C G G G G T T
```

*Hamming distance = 3*

```
X: T G G C C G C G C A A A A A C A G C
   | |   | | | | | | | | | |
Y: T G A C C G C G C A A A A C A G C T
```

*Hamming distance = 6*

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

*X*: **G G C C G G C**

*Y*: **C C G G G G G**

*X*: **T A T A T A**

*Y*: **A T A T A T**

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

```
X:  G G C C G G C
            | |
Y:  C C G G G G G
```

*Hamming distance = 5*

```
X:  T A T A T A

Y:  A T A T A T
```

# Hamming Distance

The minimum number of ***substitutions*** to turn one string into another.

```
X:  G G C C G G C
            | |
Y:  C C G G G G G
```

*Hamming distance = 5*

```
X:  T A T A T A

Y:  A T A T A T
```

*Hamming distance = 6*

# Approximate Pattern Matching

An **insertion** adds a character, shifting all other characters back

Insertion is relative! What edits *convert T* to *P*

```
T: GGAAAAAGAGGTAGC-GCGTTTAACAGTAG
             ||||| |||
P:           GTAGCGGCG
                  ↑
              Insertion
```

Added a G to T
to match pattern

# Approximate Pattern Matching

An **deletion** removes a character, shifting all other characters forward

Deletion is relative! What edits *convert T* to *P*

```
T: G G A A A A A G A G G T A G C G G C G T T T A A C A G T A G
                        | |   | | | | | |
                     P: G T - G C G G C G
                            ↑
                         Deletion
```

Delete A from T

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

*X*: **T G G C C G C G C A A A A A C A G C**

*Y*: **T G A C C G C G C A A A A C A G C T**

*X*: **G C G C T**

*Y*: **G C T**

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

```
X:  T G G C C G C G C A A A A A C A G C -
    | |   | | | | | | | | | |   | | | |
Y:  T G A C C G C G C A A A A - C A G C T
```

*Edit distance = 3*

T

X: **G C G C T**

P

Y: **G C T**

G C G C T
G C - - T

G C G C T
G - - C T

deletion ↓
G C G C T
- - G C T

2

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

```
X:  T G G C C G C G C A A A A A C A G C -
    | |   | | | | | | | | | |   | | | |
Y:  T G A C C G C G C A A A A - C A G C T
```

*Edit distance = 3*

```
X:  G C G C T      G C G C T      G G C C T
        | | |      | |     |      |     | |
Y:  - - G C T      G C - - T      G - - C T
```

*Edit distance = 2*

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

*X*: **G G C C G G C**

*Y*: **C C G G G G G**

*X*: **T A T A T A**

*Y*: **A T A T A T**

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

*X*: G G C C G G C

*Y*: C C G G G G G

G G C C G G C - -

- - C C G G G G G

*Edit distance* = *5*

A better 5?

*X*: **T A T A T A**

*Y*: **A T A T A T**

A T A T A T A

A T A T A T ?

# Edit Distance

The minimum number of substitutions, insertions, or deletions (**edits!**) needed to turn one string into another (from X to Y)!

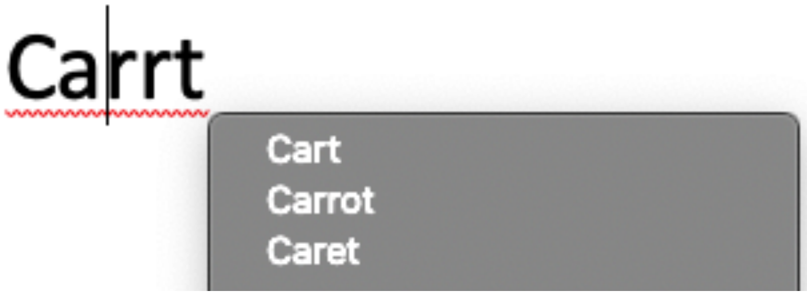
```
X:  G G C C G G C        G G C C G G C - -
            | |              | | | |
Y:  C C G G G G G        - - C C G G G G G
```

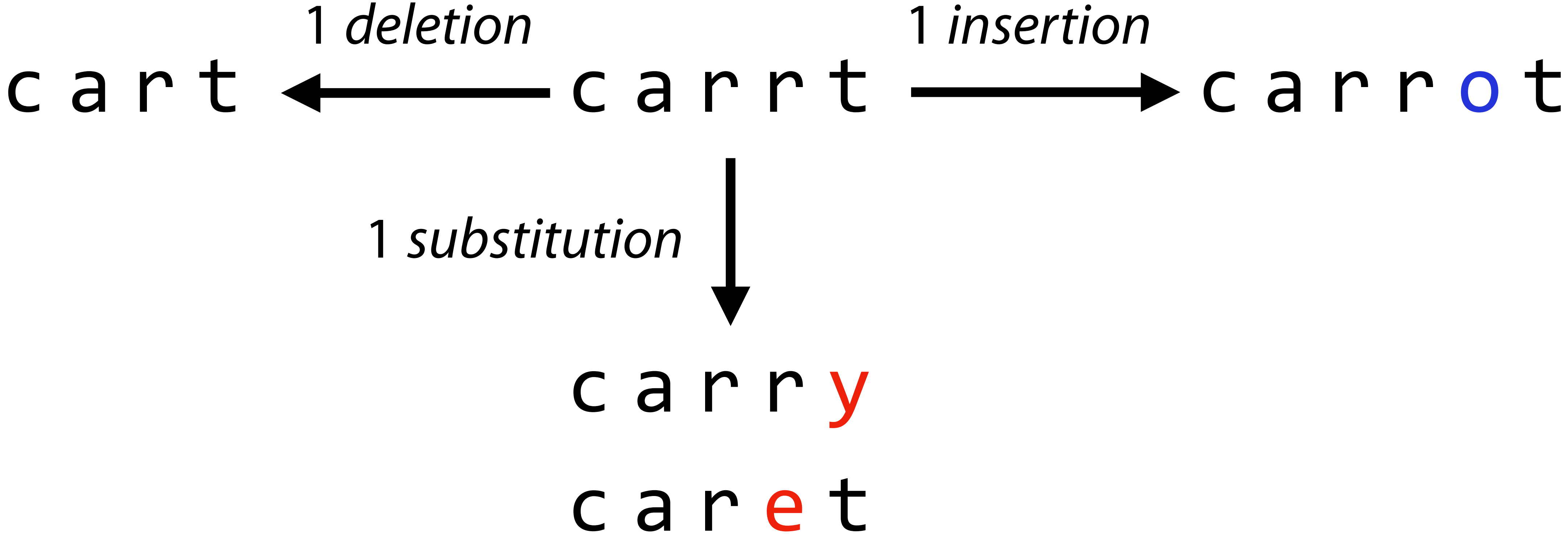
*Edit distance = 5*

```
X:  T A T A T A -
      | | | | |
Y:  - A T A T A T
```

*Edit distance = 2*

# Edit Distance


Carrt


cart ← 1 *deletion* carrt 1 *insertion* → carrot

1 *substitution* ↓

carry

caret

# Edit Distance

```
Score =  248 bits (129), Expect = 1e-63
Identities = 213/263 (80%), Gaps = 34/263 (12%)
Strand = Plus / Plus
```

Substitution

```
Query: 161 atatcaccacgtcaaaggtgactccaactcca---ccactccattttgttcagataatgc 217
           |||||||||||||||||||||||||||||  |     | |   || ||||||||||||||
Sbjct: 481 atatcaccacgtcaaaggtgactccaact-tattgatagtgttttatgttcagataatgc 539

Query: 218 ccgatgatcatgtcatgcagctccaccgattgtgagaacgacagcgacttccgtcccagc 277
           |||||||   ||||||||||||||||||||| || |            ||||||||||||
Sbjct: 540 ccgatgactttgtcatgcagctccaccgattttg-g------------ttccgtcccagc 586
```

Deletion

```
Query: 278 c-gtgcc--aggtgctgcctcagattcaggttatgccgctcaattcgctgcgtatatcgc 334
           |  || |  | ||||||||||||||||||||||||||||||||||||||| |||||||||
Sbjct: 587 caatgacgta-gtgctgcctcagattcaggttatgccgctcaattcgctgggtatatcgc 645

Query: 335 ttgctgattacgtgcagctttcccttcaggcggga------------ccagccatccgtc 382
           |||||||||||||||||||||||||||||||||||            |||||||||||||
Sbjct: 646 ttgctgattacgtgcagctttcccttcaggcgggattcatacagcggccagccatccgtc 705
```

Insertion

```
Query: 383 ctccatatc-accacgtcaaagg 404
            |||||||| |||||||||||||
Sbjct: 706 atccatatcaaccacgtcaaagg 728
```

# Approximate Pattern Matching

How can I describe the relationship between two strings?

```
X: 1 0 0 1 1
     |   |
Y: 0 0 1 1 0
   S M S M S
```

```
X: 1 0 0 1 1 -
     | | | |
Y: - 0 0 1 1 0
   D M M M M I
```

**Edit string:** Describe the changes you would make to X to become Y

# Approximate Pattern Matching

**Input:** A text *T*, a pattern *P*, and a distance *d*

**Output:** All positions in *T* where *P* has at most *d* mismatches or edits

**Hamming Distance:** Min number substitutions (mismatches)

**Edit Distance:** Min number edits (substitution, insertions, deletions)

# Approximate Pattern Matching

$\Sigma = 0, 1$ $P = 000$

**Hamming Distance 1 strings:** 100 010 001

**Edit Distance 1 strings:**

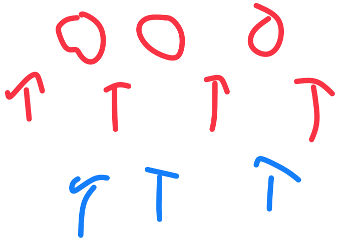
100

010

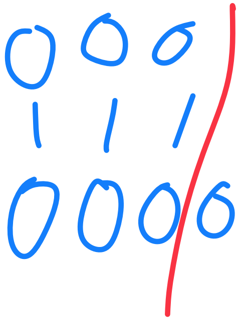
001

# Approximate Pattern Matching

$\Sigma = 0, 1$      $P = 000$



Must compare same length



**Hamming Distance 1 strings:** 100 010 001

**Edit Distance 1 strings:**

| Substitutions | Inserts | Delete |
|---|---|---|
| 100 | 1000 | 00 |
| 010 | 0100 | |
| 001 | 0010 | |
| | 0001 | |
| | 0000 | |

N Sub

$\left[(N+1)\cdot|\Sigma|\right]$ In

N Del

# Approximate Pattern Matching

$P = \text{abb}$ $d = 1$

Using ***Hamming*** distance, what are valid approximate matches for P?

Using ***edit*** distance, what are valid approximate matches for P?

**A)** aba

**B)** aabb

insert

**C)** bbb

**D)** ab

del

# Approximate Pattern Matching

How do we find all approximate matches for a pattern in a text?

```
P:  word
T:  There would have been a time for such a word
    word word word word word word word word word
     word word word word word word word word
      word word word word word word word word
       word word word word word word word word
        word word word word word word word word
```

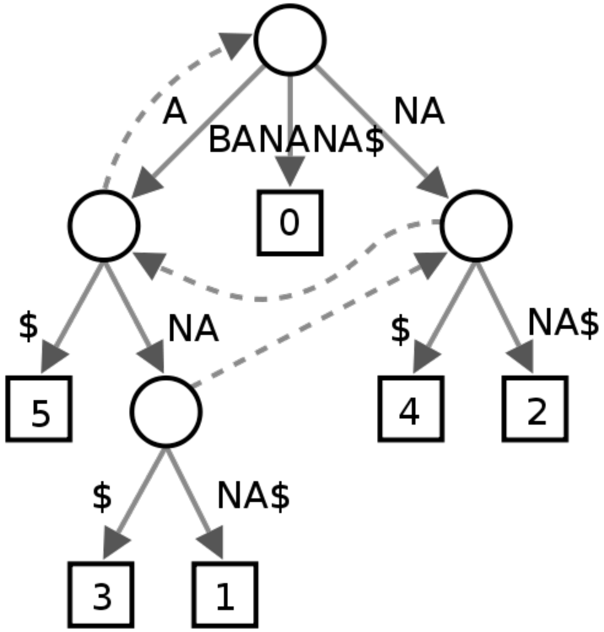
# Approximate Pattern Matching

How do we find all approximate matches for a pattern in a text?

**Can we use our efficient exact pattern matching algorithms?**

|  | **A** | **C** | **G** | **T** |
|---|---|---|---|---|
| **A** | 0 | 0 | 1 | 2 |
| **C** | 0 | 1 | 0 | 1 |
| **G** | 0 | 1 | 2 | 0 |
| **T** | 0 | 1 | 2 | 3 |

Boyer-Moore



Suffix Tree

|  |  |
|---|---|
| 6 | **$** |
| 5 | **A$** |
| 3 | **ANA$** |
| 1 | **ANANA$** |
| 0 | **BANANA$** |
| 4 | **NA$** |
| 2 | **NANA$** |

Suffix Array

**$** BANAN **A**
**A** $BANA **N**
**A** NA$BA **N**
**A** NANA$ **B**
**B** ANANA **$**
**N** A$BAN **A**
**N** ANA$B **A**

FM Index

# Approximate Pattern Matching

$D = 1$

**Can we use our efficient exact pattern matching algorithms?**

For Hamming distance (mismatches), we can!

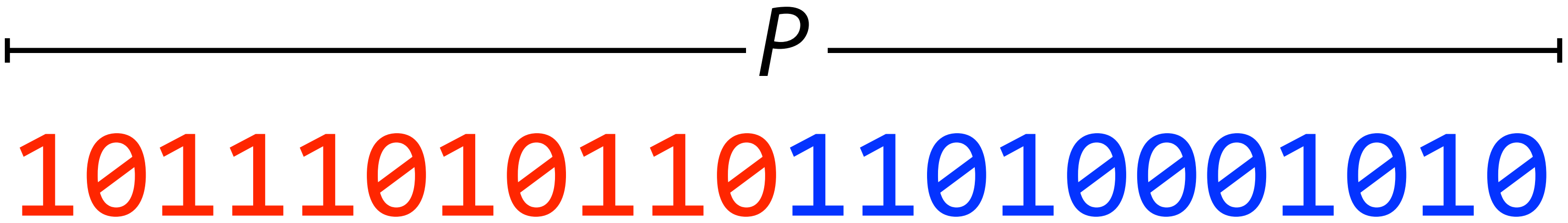
$P$

1011101011011010001010

# Approximate Pattern Matching

**Can we use our efficient exact pattern matching algorithms?**

For Hamming distance (mismatches), we can!



10111010110 11010001010

# Approximate Pattern Matching

D=1

**Can we use our efficient exact pattern matching algorithms?**

For Hamming distance (mismatches), we can!

u ✓

10111101011011010001010

10111111011011010001010

10111101011011010000010

10111101011111010001010

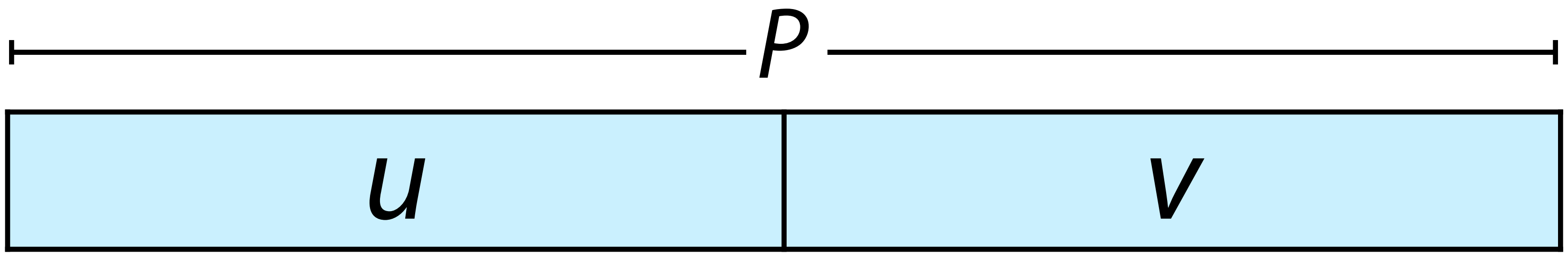
10111101011011110001010

Errors in black

# Approximate Pattern Matching

**Can we use our efficient exact pattern matching algorithms?**

For Hamming distance (mismatches), we can!



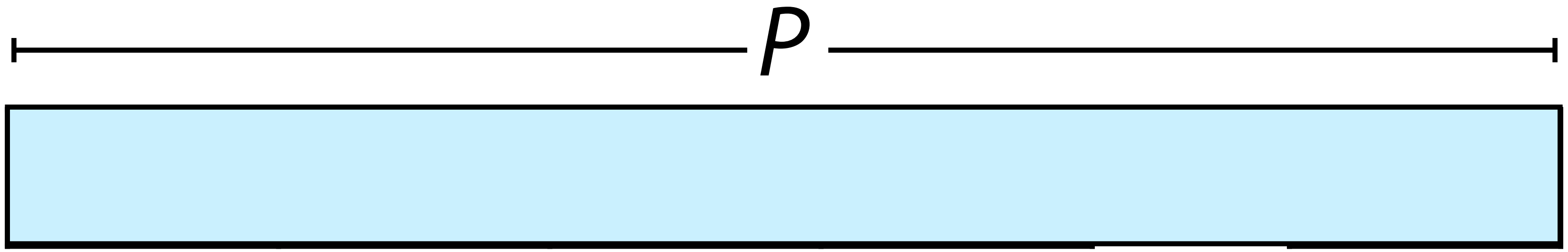
If *P* occurs in *T* with 1 mismatch, then *u* or *v* has no mismatch

**We can search for *u* and *v* in T as a proxy for *P*!**

# Approximate Pattern Matching

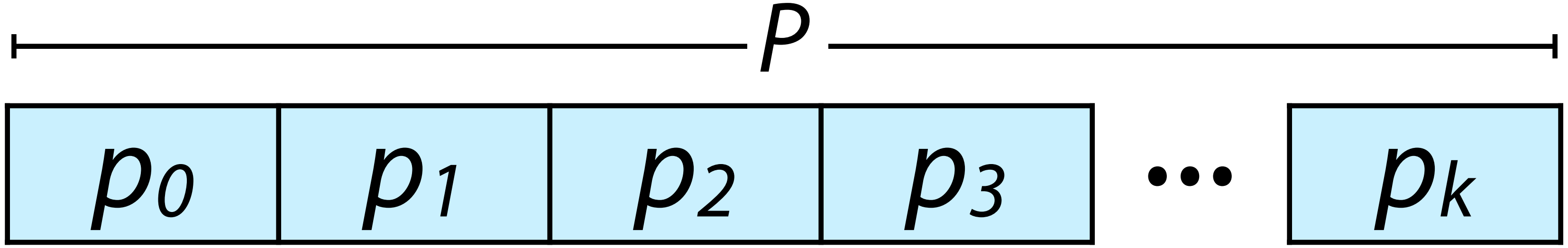
If *P* occurs in *T* with up to *k* mismatches…

$K+1$



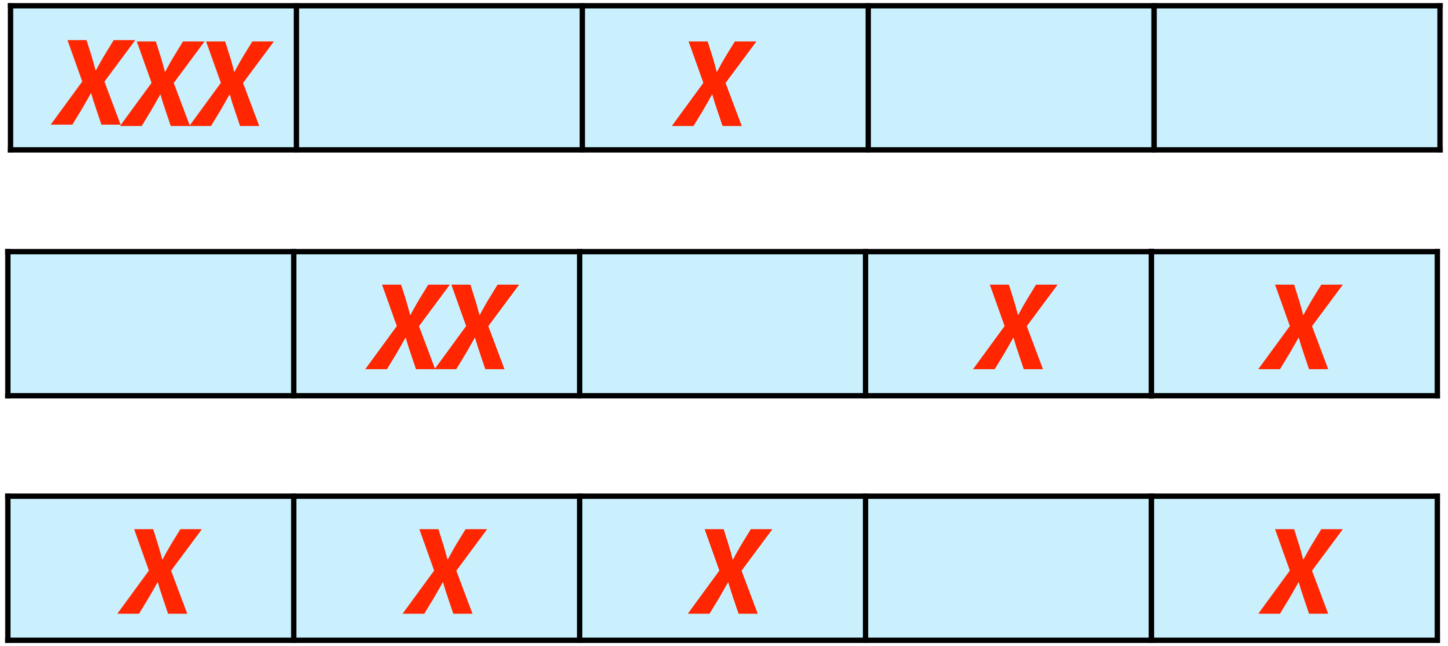
# Approximate Pattern Matching

If *P* occurs in *T* with up to *k* mismatches, then if we split P into *k+1* partitions, at least one of $p_0$, $p_1$, ..., $p_k$ must appear with 0 mismatches.



# Approximate Pattern Matching

If $P$ occurs in $T$ with up to $k$ mismatches, then if we split P into $k+1$ partitions, at least one of $p_0$, $p_1$, ..., $p_k$ must appear with 0 mismatches.



5 partitions
4 mismatches (X)

# Approximate Pattern Matching

**Pigeonhole principle:** A direct relationship between containers and objects from either perspective below.

*k+1* pigeons, *k* holes?

*At least one hole has two pigeons!*

*k* pigeons, *k+1* holes?

*At least one hole is empty!*

# Approximate Pattern Matching

Pigeonhole principle lets us use exact matching algorithms:

*P*: `word`

*T*: `There would have been a time for such a word`

# Approximate Pattern Matching

Pigeonhole principle lets us use exact matching algorithms:

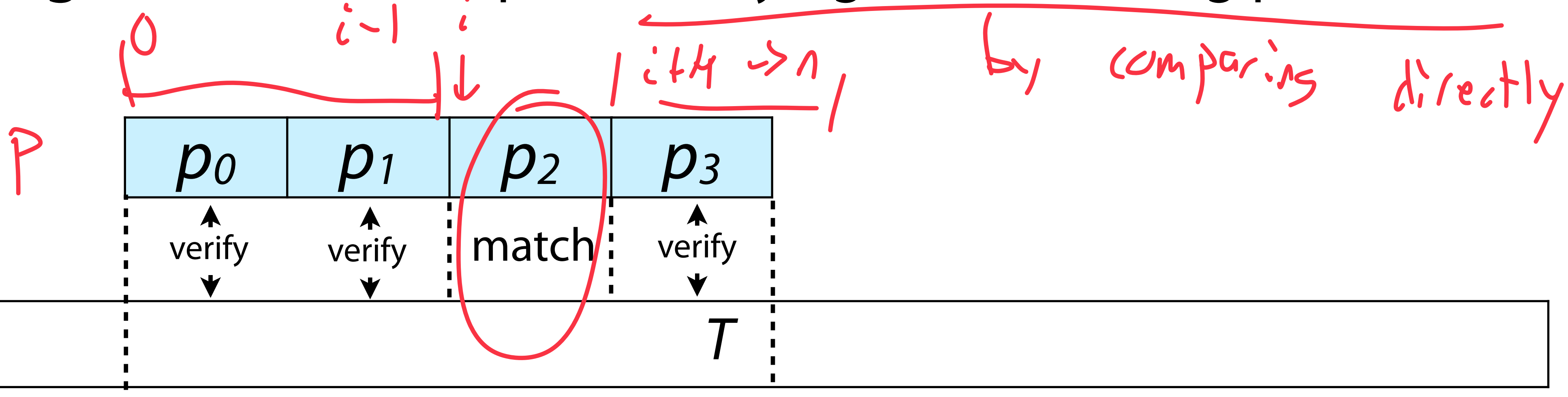
```
P: word
T: There would have been a time for such a word
u: wo    wo                                wo
v: rd                                        rd
```

1) Given *k* allowed mismatches, break the pattern up into *k+1* partitions

What do we do with these partial matches?

# Approximate Pattern Matching

**Counting mismatches** requires verifying non-matching partitions



→

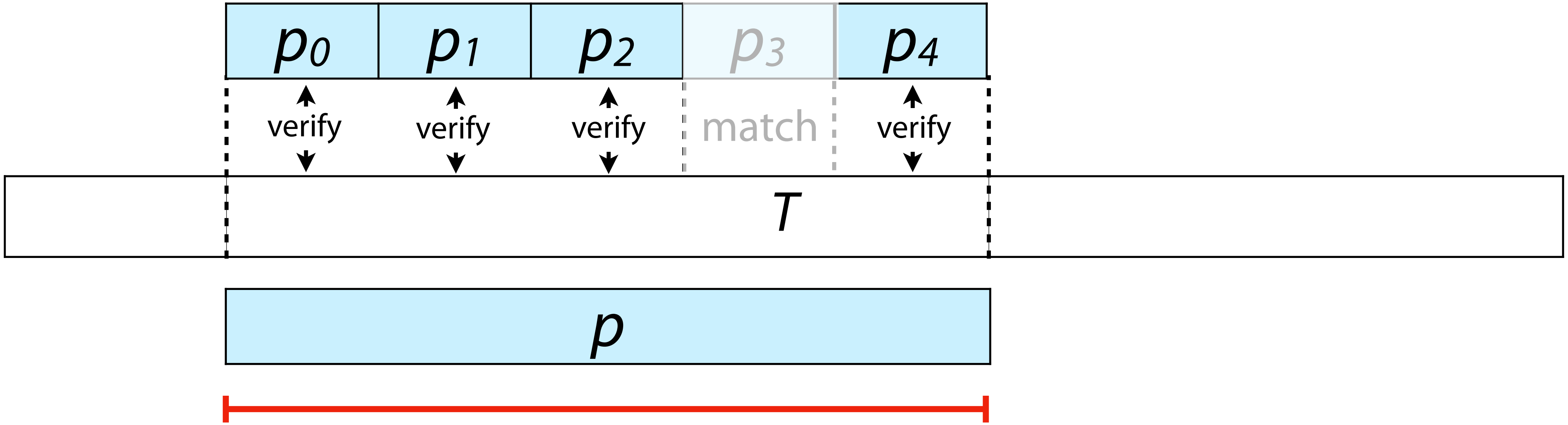
**WORD**

**THERE WOULD HAVE BEEN A TIME**

# Approximate Pattern Matching

This is known as the ***seed and extend*** heuristic

```
T:  There would have been a time for such a word
          word                                   word
                                                 word
```



Only consider mismatches while verifying a seed hit

# **Seed and Extend** Approximate Pattern Matching

*P*: `word`

*T*: `There would have been a time for such a word`

*u*: `wo`      `word`      `word` 0

2

*v*: `rd`      `word` 0

1) Given *k* allowed mismatches, break the pattern up into *k+1* partitions

2) For every partial exact match, **inspect** the full alignment

(Count mismatches in the remaining characters in the alignment)

3) Return all matches (but don't duplicate!)

# Approximate Pattern Matching

Find all edit distance 2 approximate matches

*P*: **`CATS`**

*T*: **`THE CART WAS CARRIED BY THE CATS`**

# Approximate Pattern Matching

Find all edit distance 2 approximate matches

*P*: **CATS**

*T*: **THE CART WAS CARRIED BY THE CATS**

C THE CART WAS CARRIED BY THE CATS

A THE CART WAS CARRIED BY THE CATS

T THE CART_WAS CARRIED BY_THE CATS

S THE CART_WAS CARRIED BY THE CATS

# Approximate Pattern Matching

As a ***heuristic***, seed and extend reduces the overall search space

```
T:  There would have been a time for such a word
          word                              word
                                            word
```

Consider the likelihood of seeing ‘wo’ or ‘rd’ **by chance**:

256 characters : $$\frac{1}{256}^{2} = 0.000015$$

# Approximate Pattern Matching in Genomics

**Partition Seed:** Length ~40

`CTCAAACTCCTGACCTTTGGTGATCCACCCGCCTAGGCCTTC`

**T:** Length 3 billion

Likelihood of random seed string:

$$\frac{1}{4}^{40} = 8.27e - 25$$

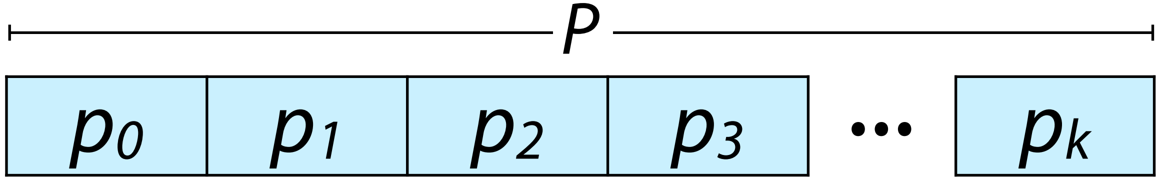
# of times seed will occur by chance in T:

Likelihood * (~ length)

$$2.48e - 15$$

# Approximate Pattern Matching

**"Seed and extend"** approach to pattern matching



$P$

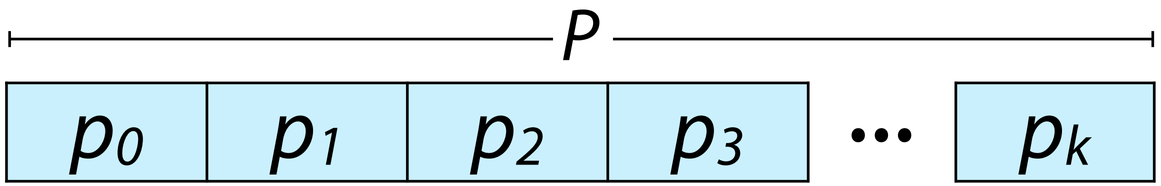
$p_0$ $p_1$ $p_2$ $p_3$ … $p_k$

**Pros:**

**Cons:**

# Approximate Pattern Matching

**"Seed and extend"** approach to pattern matching



$P$

$p_0$ $p_1$ $p_2$ $p_3$ … $p_k$

**Pros:**

Reuse exact matching algs

Works for Hamming and edit distance*

As a heuristic, reduces search space

**Cons:**

Slow for large $k$

- small partitions matching many times by chance
- $k$+1 exact matching problems, one per partition

---

* we don't know how to do edit distance verification yet

# Assignment 10: a_pigeon

Learning Objective:

Preprocess text into kmers and a hash table

Use pigeonhole principle to perform approximate matching

**Consider:** Do the partitions need to be contiguous runs of characters? Do they need to all be the same length?

# `kmerMap text_to_kmer_map(string & T, int k)`

Input:

- **`string & T`:** The input text — can be very large this week!
- **`int k`:** The fixed size for each kmer (substring)

Output:

- **`kmerMap`:** `unordered_map<string, vector<int>>`

*T*: **`aaaaabbbbbb`** $k = 4$

# `kmerMap text_to_kmer_map(string & T, int k)`

Input:

- **`string & T`:** The input text — can be very large this week!
- **`int k`:** The fixed size for each kmer (substring)

Output:

- **`kmerMap`:** `unordered_map<string, vector<int>>`

*T*: **aaaaabbbbbb** *k = 4*

```
aaaa bbbb
 aaaa bbbb
  aaab bbbb
   aabb
    abbb
```

**Output**

```
aaaa : {0, 1}
aaab : {2}
aabb : {3}
abbb : {4}
bbbb : {5, 6, 7}
```

## `vector<Seed> partitionPattern(string P, int np)`

Input:

- **`string P`**: The input pattern — can be large this week!
- **`int np`**: The number of non-overlapping partitions to split P

Output:

- **`vector<Seed>`**: Vector of partitioned strings and their index
- **`typedef std::pair<std::string, int> Seed;`**

$P$: **ABCDEFGH** $np = 2$

# `vector<Seed> partitionPattern(string P, int np)`

Input:

- **`string P`**: The input pattern — can be large this week!
- **`int np`**: The number of non-overlapping partitions to split P

Output:

- **`vector<Seed>`**: Vector of partitioned strings and their index
- **`typedef std::pair<std::string, int> Seed;`**

*P*: **`ABCDEFGH`** $np = 2$ `{ {ABCD, 0}, {EFGH, 4} }`

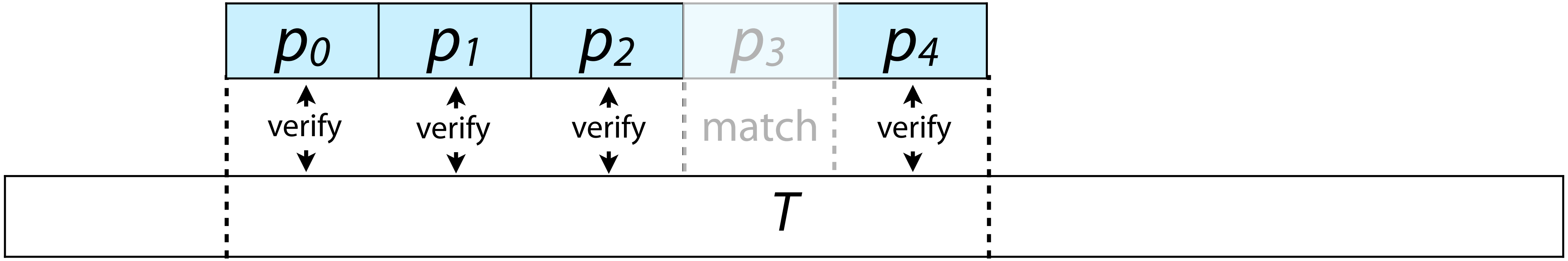
# `vector<int> approximate_search(fname, P, mm)`

Input:

- **`string fname`:** The file storing the text T
- **`string P`:** The pattern text
- **`int mm`:** The number of allowed mismatches

Output:

- **`vector<int>`:** The index positions in T of all approximate matches



$p_0$ $p_1$ $p_2$ $p_3$ $p_4$

verify verify verify match verify

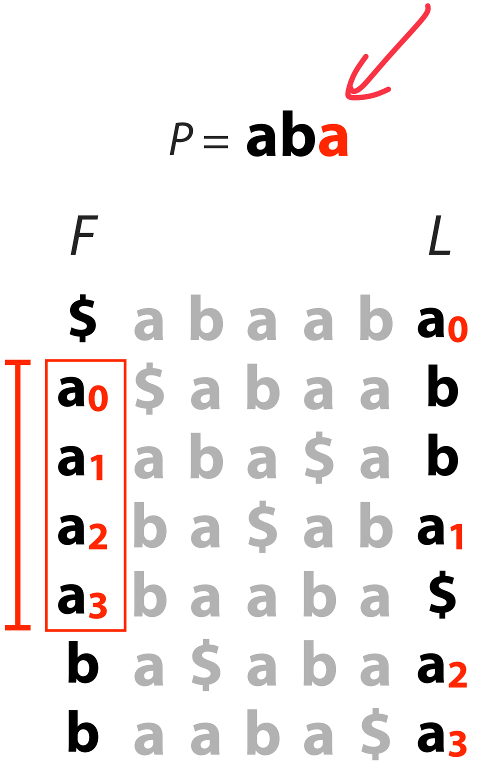
$T$

# Bonus Slides

# FM Index w/ mismatches

Start with shortest suffix, then match successively longer suffixes

Keep track of mismatches for each suffix



*P* = **aba**

| F | | | | | | L |
|---|---|---|---|---|---|---|
| $ | a | b | a | a | b | $a_0$ |
| $a_0$ | $ | a | b | a | a | b |
| $a_1$ | a | b | a | $ | a | b |
| $a_2$ | b | a | $ | a | b | $a_1$ |
| $a_3$ | b | a | a | b | a | $ |
| b | a | $ | a | b | a | $a_2$ |
| b | a | a | b | a | $ | $a_3$ |

Easy to find all the rows beginning with **a**

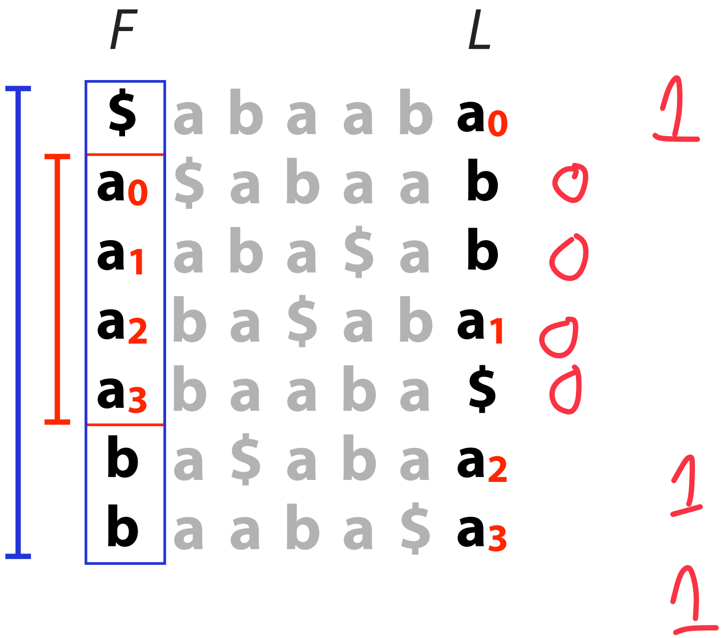
# FM Index w/ mismatches

Start with shortest suffix, then match successively longer suffixes

Keep track of mismatches for each suffix

But we count everything else as a potentially valid mismatch

$P$ = **ab**a

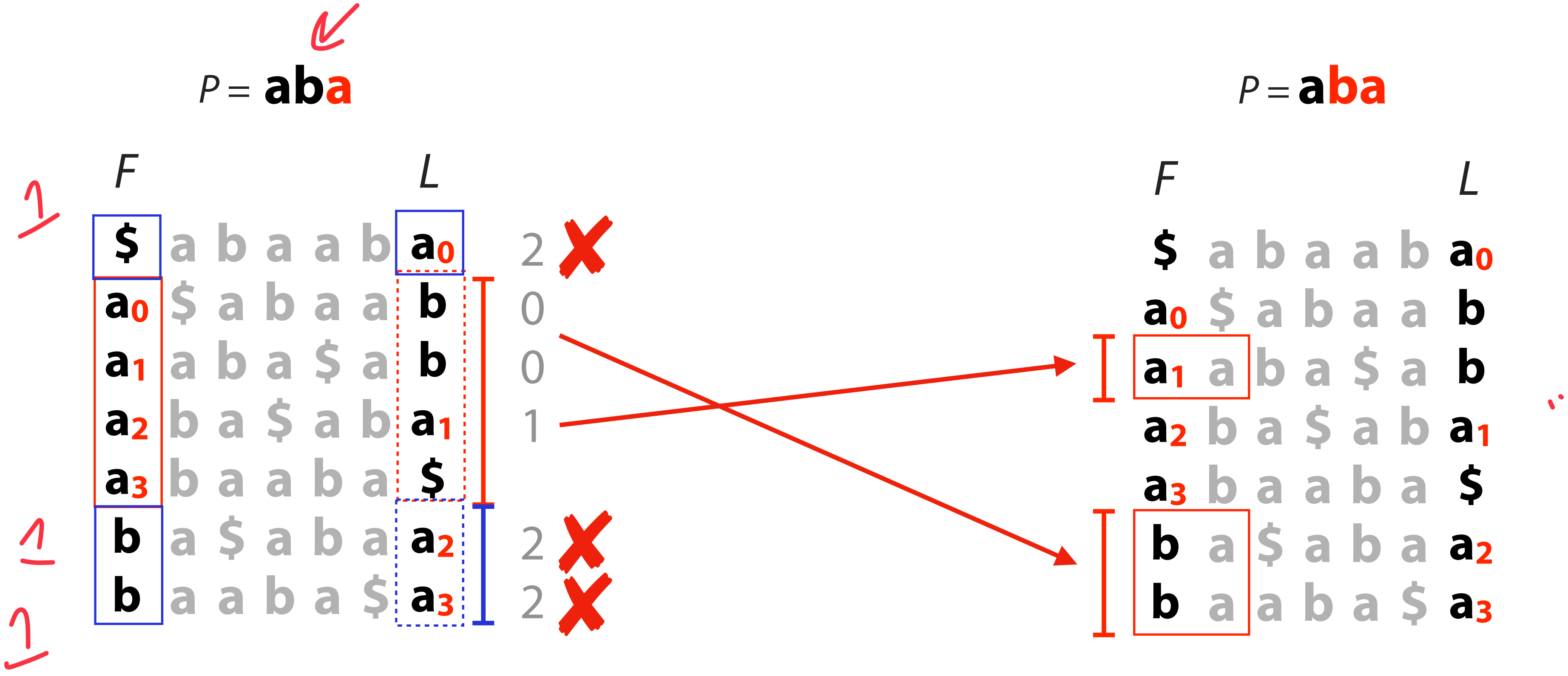


| F | | | | | | L | |
|---|---|---|---|---|---|---|---|
| \$ | a | b | a | a | b | $a_0$ | 1 |
| $a_0$ | \$ | a | b | a | a | b | 0 |
| $a_1$ | a | b | a | \$ | a | b | 0 |
| $a_2$ | b | a | \$ | a | b | $a_1$ | 0 |
| $a_3$ | b | a | a | b | a | \$ | 0 |
| b | a | \$ | a | b | a | $a_2$ | 1 |
| b | a | a | b | a | \$ | $a_3$ | 1 |

1

# FM Index w/ mismatches

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



P = **aba**

F L

1 $ a b a a b $a_0$ 2 ✗

$a_0$ $ a b a a b 0

$a_1$ a b a $ a b 0

$a_2$ b a $ a b $a_1$ 1

$a_3$ b a a b a $

1 b a $ a b a $a_2$ 2 ✗

1 b a a b a $ $a_3$ 2 ✗

P = **aba**

F L

$ a b a a b $a_0$

$a_0$ $ a b a a b

$a_1$ a b a $ a b

$a_2$ b a $ a b $a_1$

$a_3$ b a a b a $

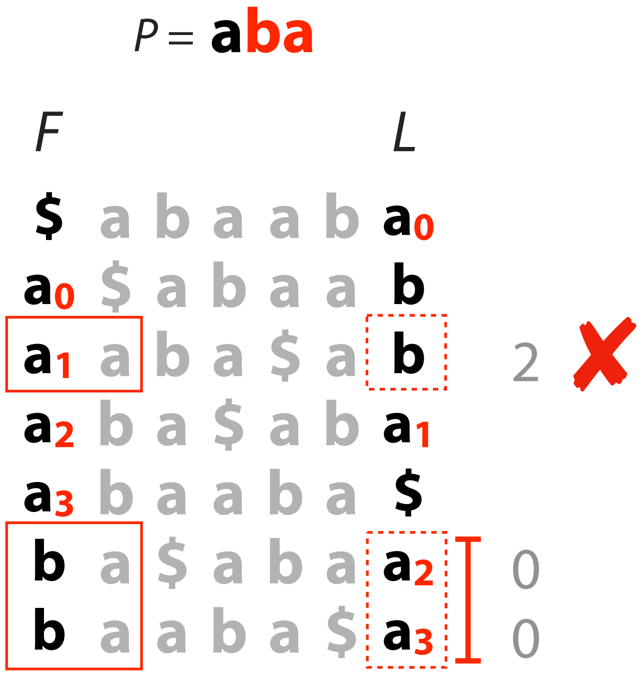
b a $ a b a $a_2$

b a a b a $ $a_3$

No longer have just one search range!

# FM Index w/ mismatches

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



$P =$ **aba**

$F \qquad L$

$\$ \; a \; b \; a \; a \; b \; a_0$

$a_0 \; \$ \; a \; b \; a \; a \; b$

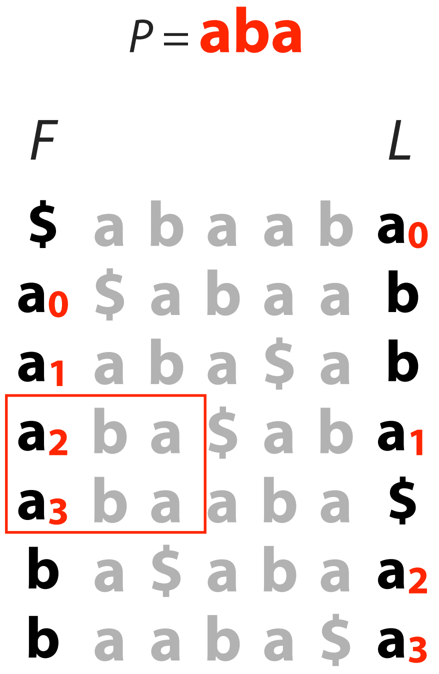
$a_1 \; a \; b \; a \; \$ \; a \; b$ 2 ✗

$a_2 \; b \; a \; \$ \; a \; b \; a_1$

$a_3 \; b \; a \; a \; b \; a \; \$$

$b \; a \; \$ \; a \; b \; a \; a_2$ 0

$b \; a \; a \; b \; a \; \$ \; a_3$ 0



$P =$ **aba**

$F \qquad L$

$\$ \; a \; b \; a \; a \; b \; a_0$

$a_0 \; \$ \; a \; b \; a \; a \; b$

$a_1 \; a \; b \; a \; \$ \; a \; b$

$a_2 \; b \; a \; \$ \; a \; b \; a_1$

$a_3 \; b \; a \; a \; b \; a \; \$$

$b \; a \; \$ \; a \; b \; a \; a_2$

$b \; a \; a \; b \; a \; \$ \; a_3$

Only works for Hamming Distance (mismatches)!