

This entire lecture is adopted (with permission) directly from a *legend* of the read-mapping world

Approximate Matching

Ben Langmead



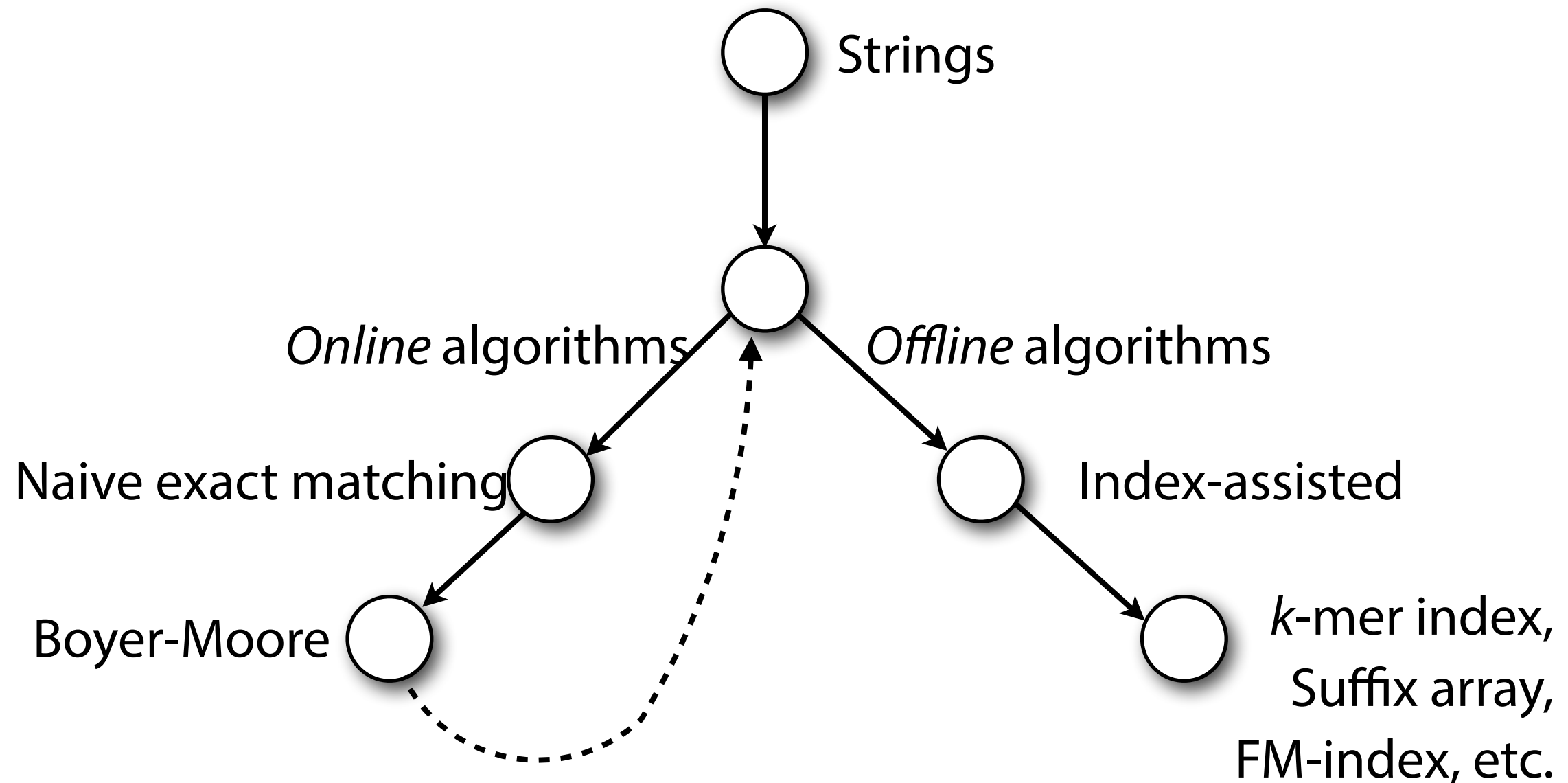
JOHNS HOPKINS

WHITING SCHOOL
of ENGINEERING

Department of Computer Science



Approximate matching



We have focused on *exact* matching...
... in reality, we have to deal with *differences*

Read

CTCAAACCTCCTGACCTTTGGTGATCCACCCGCCTNGGCCTTC

Reference

GATCACAGGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTT
CGTCTGGGGGGTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTC
GCAGTATCTGTCTTTGATTCTGCCTCATCTATTATTTATCGCACCTACGTTCAATATT
ACAGGCGAACATACTTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAATA
ACAATTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCA
AACCCCCCTCCCCGCTTCTGGCCACAGCACTTAAALACCTCTGCCAAACCCCAAAA
ACAAAGAACCCTAACACCAGCCTAACCAATTTCAAATTTTATCTTTGGCGGTATGCAC
TTTTAACAGTCACCCCCCACTAACCAATTTTCCCCTCCCCTCTCTACTACTAAT
CTCATCAATAACAACCCCCGCCATCTACCCAGCACACACACACCCCTCTAACCCCAT
CCCCGAACCAACCAAAACCCCAAAACACCCCCACAGTTTATGTAGCTCTCTCCTCAA
GCAATACACTGACCCGCTCAAACCTCTGGATTTTGGATCCACCCAGCGCTTGGCCTAAA
CTAGCCTTTCTATTAGCTCTTAGAAGATTACACATGCAAGCATCCCCCTCCAGTGAGT
TCACCCTCTAAATCACCAGCATCAAGGAACAAGCATCAAGCACGCAGCAATGCAGCTC
AAAACGCTTAGCCTAGCCACACCCCTCACGGGAAACAGCAGTGATTAACCTTAGCAATAA
ACGAAAGTTTAACTAAGCTATACTAACCCAGGGTGGTCAATTTTCGTCCAGCCACCGC
GGTCACACGATTAACCCAAGTCAATGAAGCCGGCGTAAAGAGTGTTTAGATCACCCCC
TCCCCAATAAAGCTAAAACTCACCTGATTTGTAAAAAACTCCAGTTTACAAAATAGAC
TACGAAAGTGGCTTTAACATATCTGAACAACAATAGCTAAGACCTGGGATTAGA
TACCCCACTATGCTTAGCCCTAAACCTCAACAGCTTACAAACCTGCGCCAGAA
CACTACGAGCCACAGCTTAAAACTCAAAGGACCTGGCGGTGCTTCATCTAGAGG
AGCCTGTTCTGTAATCGATAAACCCCGATCAACCTCACCACCTCTTGCTTATATA
CCGCCATCTTCAGCAAACCCTGATGAAGGCTACAAAGTAAGCGCAAGTACCTTAG
ACGTTAGGTCAAGGTGTAGCCCATGAGGTGGCAAGAAATGGGCTACATTTTCCTT
AAAACTACGATAGCCCTTATGAACTTAAAGGTGGAAGGTGGATTTAGCAGTAAT
AGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGGTACACACCCGCCGTCACCCCT
AAGTATACTTCAAAGGACATTTAACTAAACCCCTACGCATTTATATAGAGGAGACAA
CGTAACCTCAAACCTCCTGCCTTTGGTGATCCACCCGCCTTGGCCTACCTGCATAATGAAG
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GCCCCAAACCCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAA
AGTATAGGCGATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATG
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TTAACTAGAAATAACTTTGCAAGGAGAGCCAAAGCTAAGACCCCGAAACCAGACGAGCT
ACCTAAGAACAGCTAAAAGAGCACACCCGTCTATGTAGCAAAATAGTGGGAAGATTTATA
GGTAGAGGCGACAAACCTACCGAGCCTGGTGATAGCTGGTTGTCCAAGATAGAATCTTAG
TTCAACTTTAAATTTGCCACAGAACCTCTAAATCCCCTTGTAATTTAACTGTTAGTC
CAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAAGAGAGAGTAAAAAATTA
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CTACCTAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATC
ACCCTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGC
CTGCGTCAGATTAACCACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAAC
AAGTCATTATTACCCTCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTAAAA
AAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGC
ATCACCAGTATTAGAGGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCT
AACCGTGCAAAGGTAGCATAATCACTTGTTCCTTAAATAGCGACCTGTATGAATCGCTCC

Sequence differences
occur because of...

Read

CTCAAACCTCCTGACCTTTGGTGATCCACCCGCCTNGGCCTTC

Reference

GATCACAGGTCTATCACCCCTATTAACCACTCACGGGAGCTCTCCATGCATTTGGTATTTT
CGTCTGGGGGGTATGCACGCGATAGCATTGCGAGACGCTGGAGCCGGAGCACCCCTATGTC
GCAGTATCTGTCTTTGATTCTGCCTCATCCTATTATTTATCGCACCTACGTTCAATATT
ACAGGCGAACATACTTACTAAAGTGTGTTAATTAATTAATGCTTGTAGGACATAATAATA
ACAATTGAATGTCTGCACAGCCACTTTCCACACAGACATCATAACAAAAAATTTCCACCA
AACCCCCCTCCCCGCTTCTGGCCACAGCACTTAAALACCTCTGCCAAACCCCAAAA
ACAAAGAACCCTAACACCAGCCTAACCAATTTCAAATTTTATCTTTGGCGGTATGCAC
TTTTAACAGTCACCCCCCACTAACCAATTTTCCCCTCCCCTCTACTACTACTAAT
CTCATCAATAACAACCCCCGCCATCTACCCAGCACACACACACCCCTCTAACCCATA
CCCCGAACCAACCAAAACCCCAAAACACCCCCACAGTTTATGTAGCTCTCCTCAA
GCAATACACTGACCCGCTCAAACCTCTGGATTTTGGATCCACCCAGCGCTTGGCCTAAA
CTAGCCTTTCTATTAGCTCTTAGAAGATTACACATGCAAGCATCCCCCTCCAGTGAGT
TCACCCTCTAAATCACCACGATCAAGGAACAAGCATCAAGCACGCAGCAATGCAGCTC
AAAACGCTTAGCCTAGCCACACCCCTACGGGAAACAGCAGTGATTAACCTTAGCAATAA
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GGTCACACGATTAACCCAAGTCAATGAAGCCGGCGTAAAGAGTGTTTAGATCACCCCC
TCCCCAATAAAGCTAAAACTCACCTGATTGTAAAAAACTCCAGTTACAAAAATAGAC
TACGAAAGTGGCTTTAACATATCTGAACAACAATAGCTAAGACCTGGGATTAGA
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AAAACTACGATAGCCCTTATGAACTTAAGGGTGAAGGTGGATTTAGCAGTAAT
AGTAGAGTGCTTAGTTGAACAGGGCCCTGAAGCGGTACACACCCGCCGTCACCC
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CGTAACCTCAAACCTCCTGCCTTTGGTGATCCACCCGCCTTGGCCTACCTGCATAATGAAG
AAGCACCCAACTTACACTTAGGAGATTTCACTTAACTTGACCGCTCTGAGCTAAACCTA
GCCCCAAACCCACTCCACCTTACTACCAGACAACCTTAGCCAAACCATTTACCCAAATAA
AGTATAGGCGATAGAAATTGAAACCTGGCGCAATAGATATAGTACCGCAAGGGAAAGATG
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CAAAGAGGAACAGCTCTTTGGACACTAGGAAAAAACCTTGTAAGAGAGAGTAAAAAATTA
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CTACCTAAAAAATCCCAAACATATAACTGAACTCCTCACACCCAATTGGACCAATCTATC
ACCCTATAGAAGAACTAATGTTAGTATAAGTAACATGAAAACATTCTCCTCCGCATAAGC
CTGCGTCAGATTAACAACTGAACTGACAATTAACAGCCCAATATCTACAATCAACCAAC
AAGTCATTATTACCCTCACTGTCAACCCAACACAGGCATGCTCATAAGGAAAGGTTAAAA
AAAGTAAAAGGAACTCGGCAAATCTTACCCCGCCTGTTTACCAAAAACATCACCTCTAGC
ATCACCAGTATTAGAGGCACCGCCTGCCAGTGACACATGTTTAAACGGCCGCGGTACCCT
AACCGTGCAAAGCTAGCATAATCACTTGTTCCTTAAATAGCGACCTGTATGAATCGCTCC

Sequence differences
occur because of...

1. Sequencing error
2. Genetic variation

Approximate matching

T: G G 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

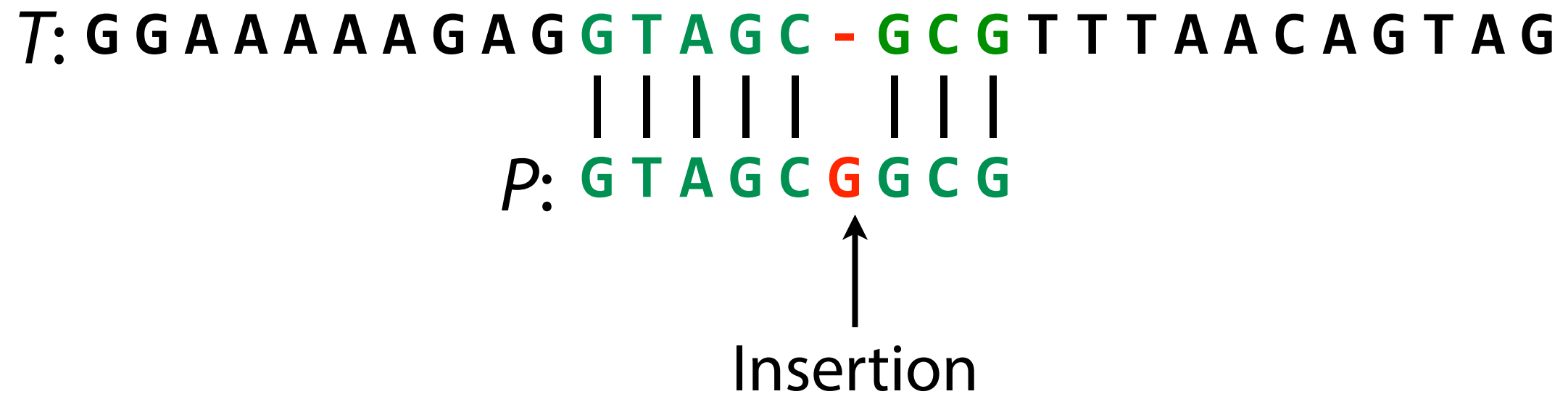
 | | | | | | |

P: G T A A C G G C G

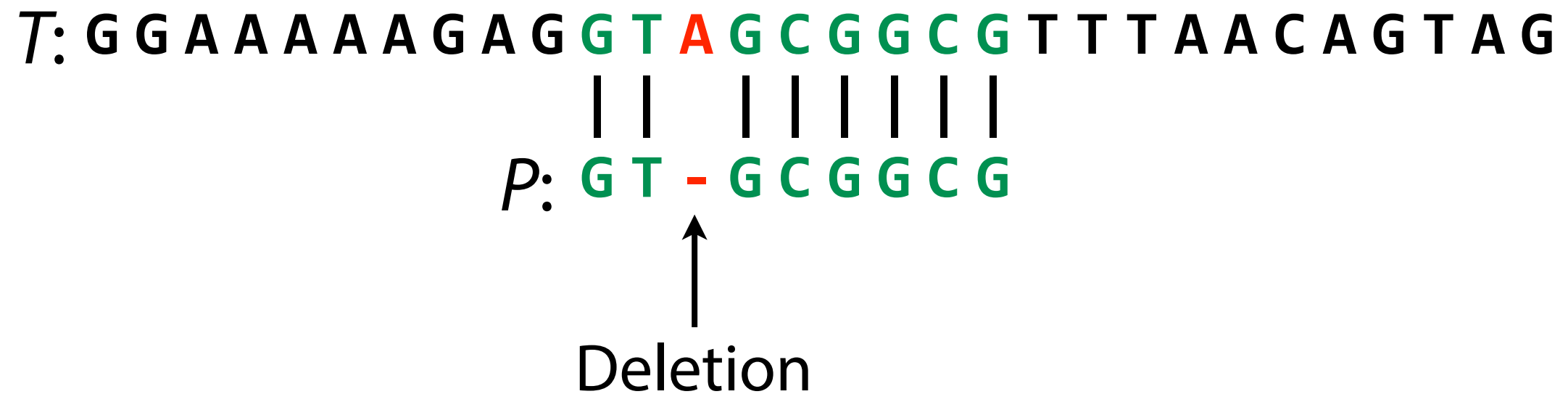
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Mismatch
(Substitution)

Approximate matching



Approximate matching



Hamming distance

For X & Y where $|X| = |Y|$, *hamming distance* =
minimum # substitutions needed to turn one into the
other

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

For X & Y where $|X| = |Y|$, *hamming distance* =
minimum # substitutions needed to turn one into the
other

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

Edit distance

(AKA Levenshtein distance)

For X & Y , *edit distance* = minimum # edits

(substitutions, insertions, deletions) needed to turn one into the other

X : T G G C C G C G C 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

Edit distance

(AKA Levenshtein distance)

For X & Y , *edit distance* = minimum # edits

(substitutions, insertions, deletions) needed to turn one into the other

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

Edit distance = 2

Edit distance

(AKA Levenshtein distance)

For X & Y , *edit distance* = minimum # edits

(substitutions, insertions, deletions) needed to turn one into the other

X : T G G C C G C G C 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

Edit distance = 2

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

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

Edit distance

(AKA Levenshtein distance)

For X & Y , *edit distance* = minimum # edits

(substitutions, insertions, deletions) needed to turn one into the other

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

Edit distance = 2

X : G C G T A T G C G G C T A - A C G C

| | | | | | | | | | | | | |

Y : G C - T A T G C G G C T A T A C G C

Edit distance = 2

Approximate matching

Like exact matching, but *pattern* P may be within a certain *distance* (usually Hamming or edit) of T . Each such place is an *approximate match*.

Allowing edits is more challenging than just allowing mismatches

We'll return to edits

Approximate matching

```
def naive(p, t):
    occurrences = []
    for i in range(len(t) - len(p) + 1):    # Loop over alignments
        match = True
        for j in range(len(p)):             # Loop over characters
            if t[i+j] != p[j]:               # compare characters
                match = False                # mismatch; reject alignment
                break
        if match:
            occurrences.append(i)             # all chars matched; record
    return occurrences
```

Approximate matching

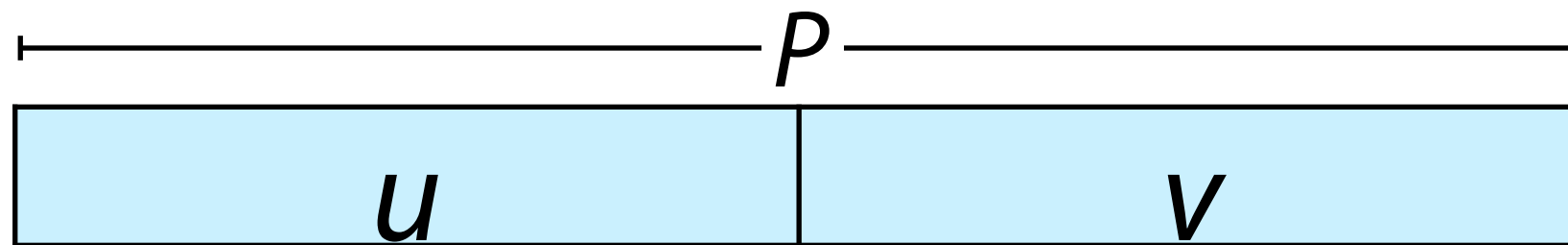
```
def naive_approx_hamming(p, t, maxDistance):
    occurrences = []
    for i in range(len(t) - len(p) + 1):  # Loop over alignments
        nmm = 0
        for j in range(len(p)):           # Loop over characters
            if t[i+j] != p[j]:            # compare characters
                nmm += 1                  # mismatch
            if nmm > maxDistance:
                break                     # exceeded max hamming dist
        if nmm <= maxDistance:
            occurrences.append(i)         # approximate match
    return occurrences
```

http://bit.ly/CG_NaiveApprox

Approximate matching

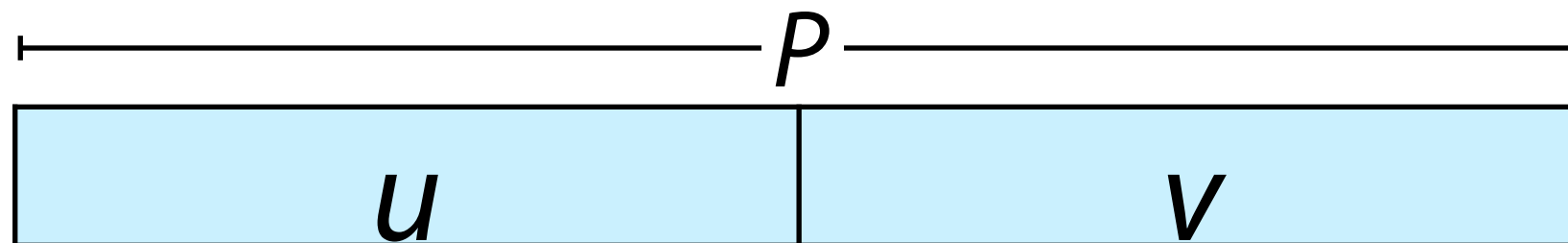
Wanted: way to apply exact matching algorithms to approximate matching problems

Approximate matching

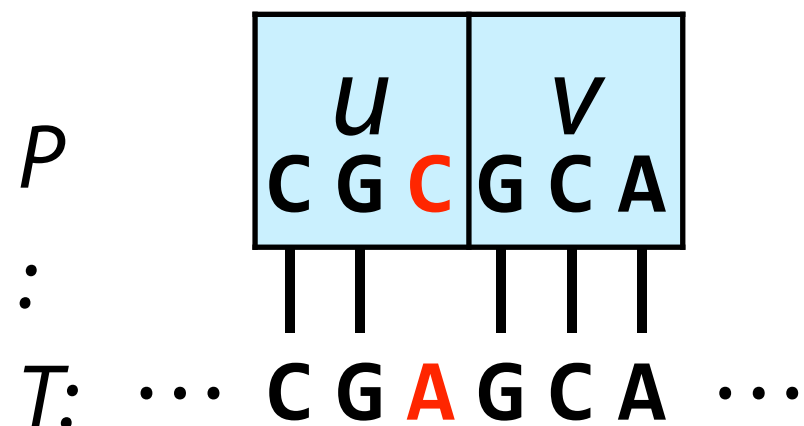


If P occurs in T with 1 edit, then u or v appears with no edits

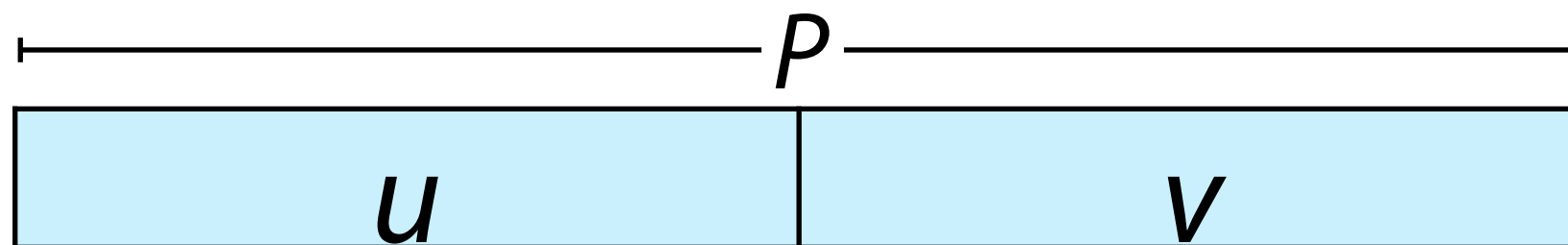
Approximate matching



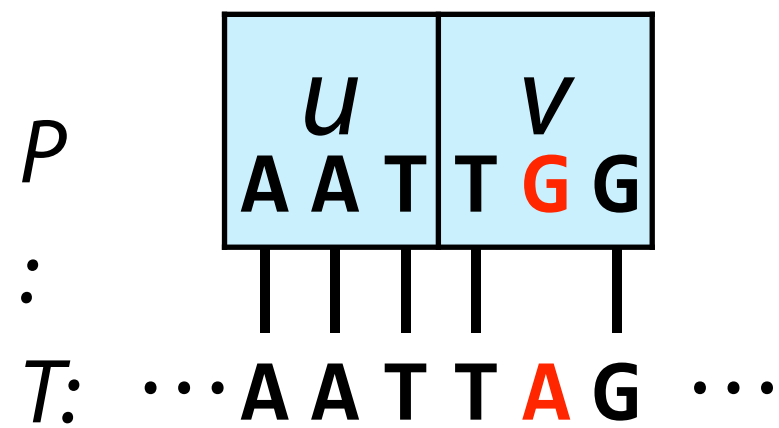
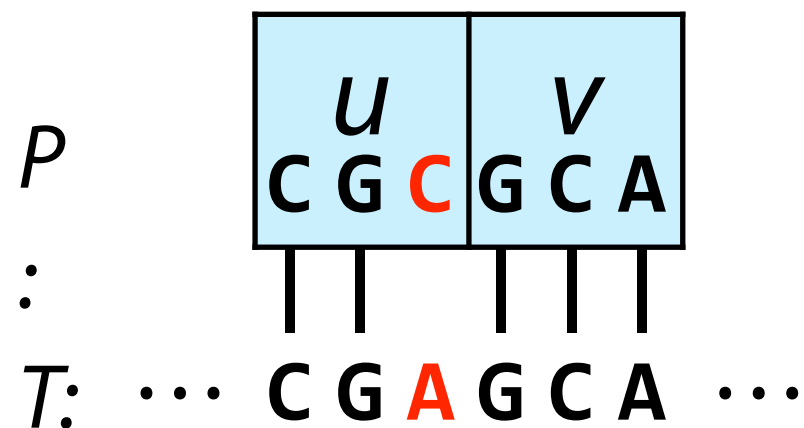
If P occurs in T with 1 edit, then u or v appears with no edits



Approximate matching



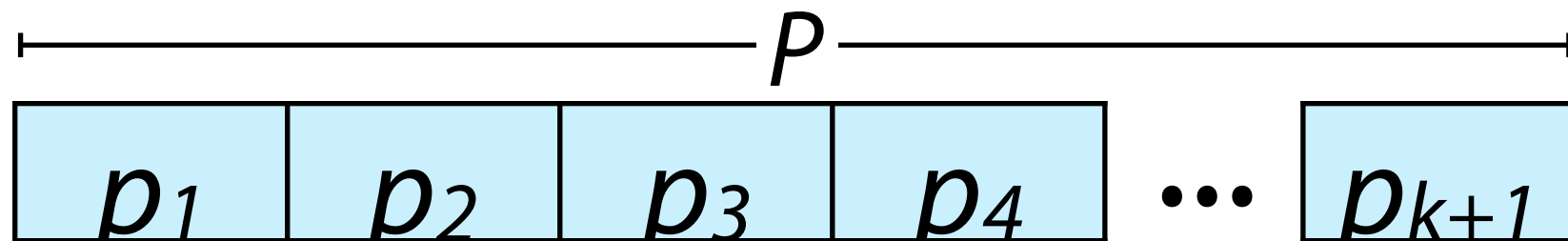
If P occurs in T with 1 edit, then u or v appears with no edits



Approximate matching

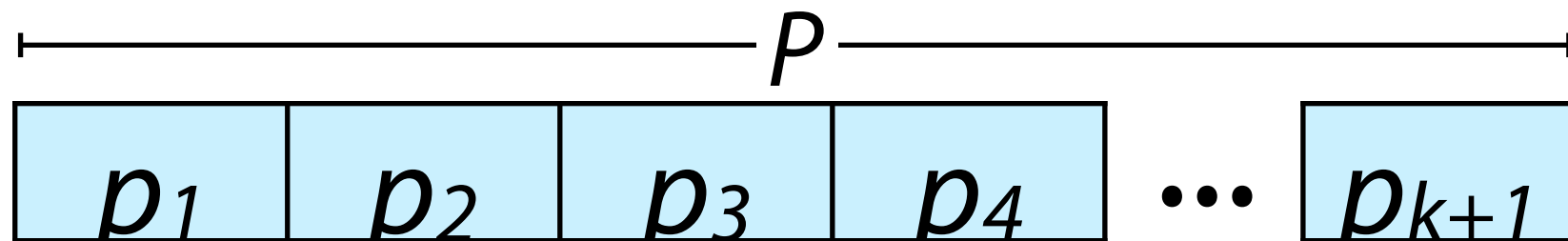
If P occurs in T with up to k edits...

Approximate matching



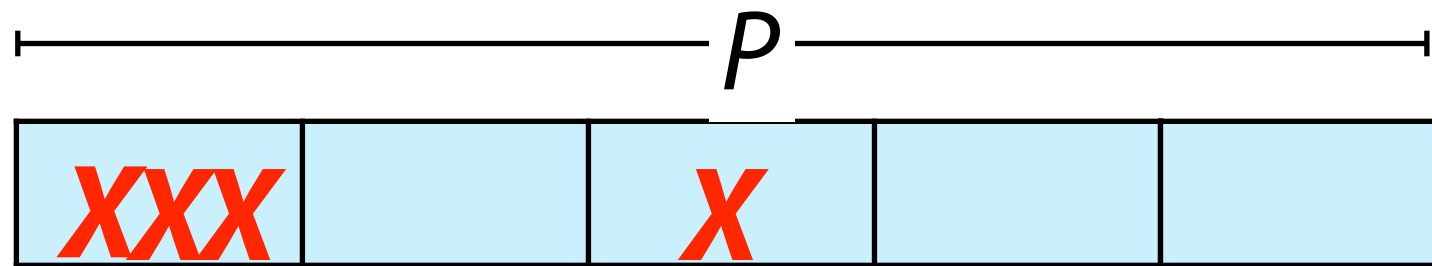
If P occurs in T with up to k edits...

Approximate matching



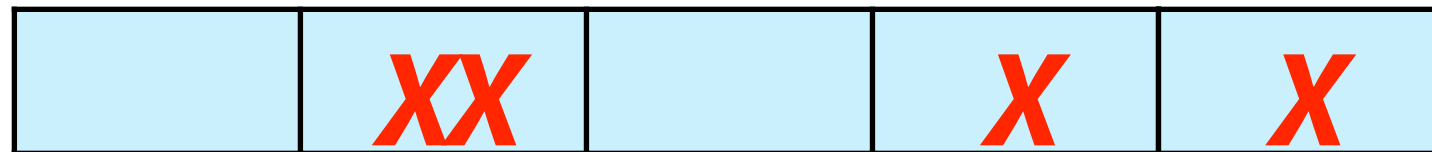
If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits

Approximate matching



5 partitions

4 edits (**x**)



Approximate matching



Pigeonhole principle: $k+1$ pigeons, k holes.

At least one has >1 pigeon!

Approximate matching



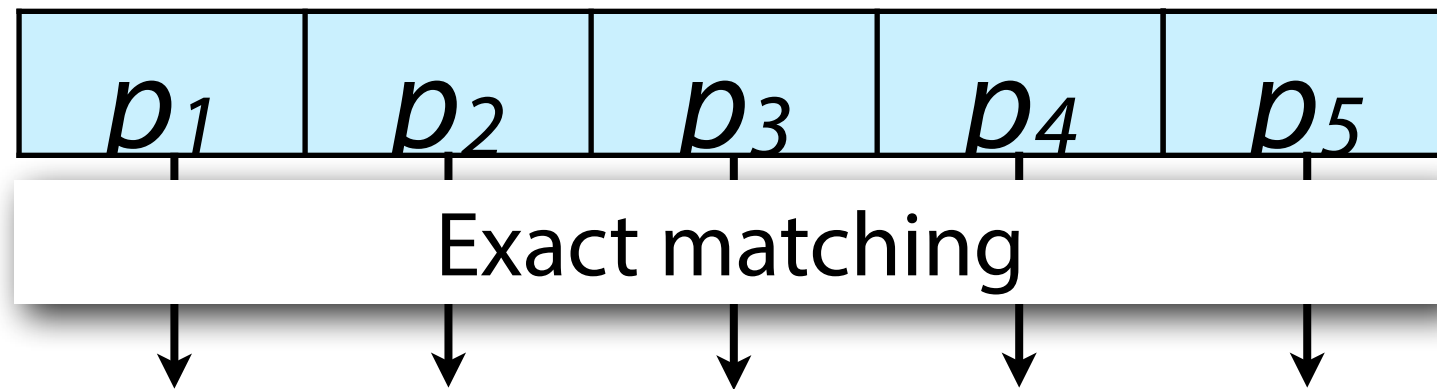
We have k pigeons, $k+1$ holes, at least one...

Approximate matching



We have k pigeons, $k+1$ holes, at least one...
...is *empty*

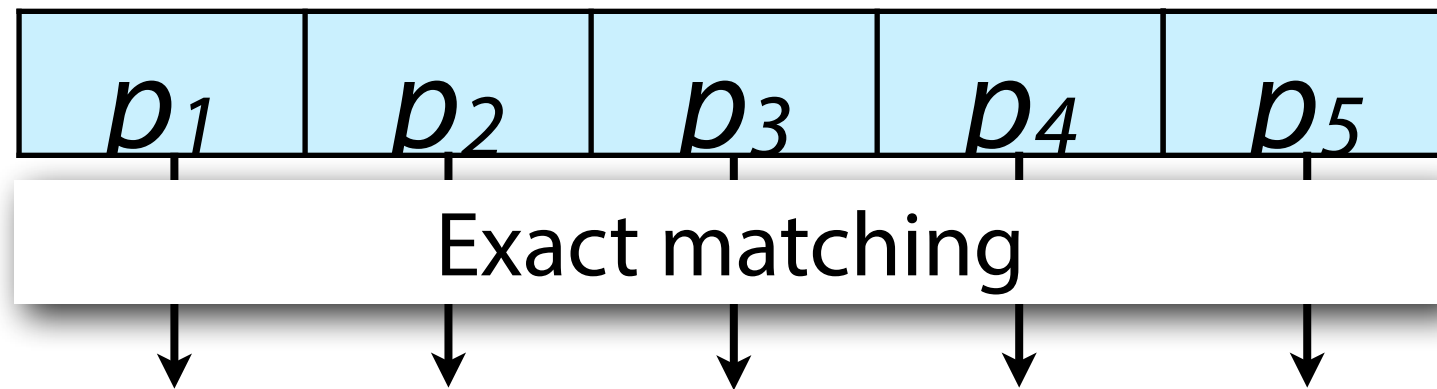
Pigeonhole principle



T

What algorithm can we use?

Pigeonhole principle

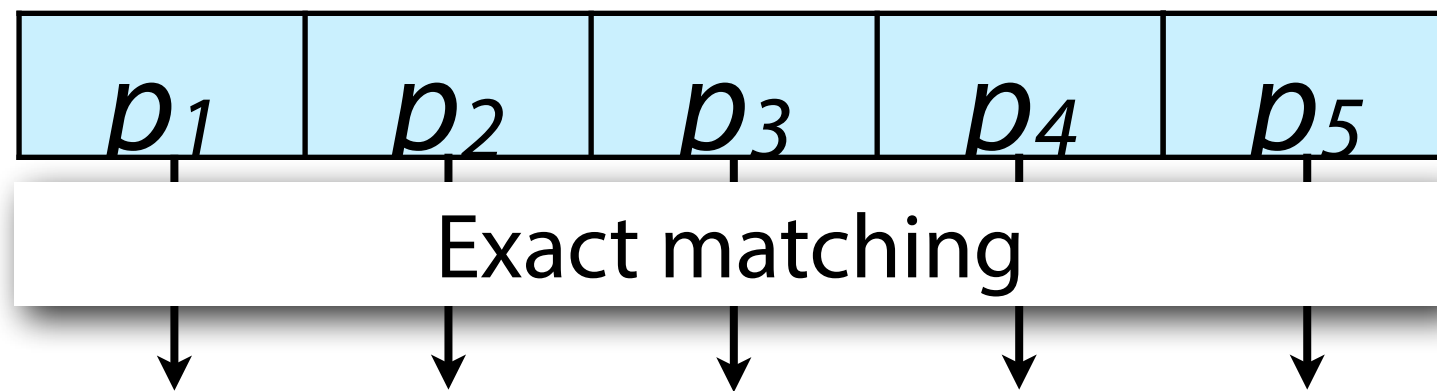


T

What algorithm can we use?

Any exact matching algorithm

Pigeonhole principle



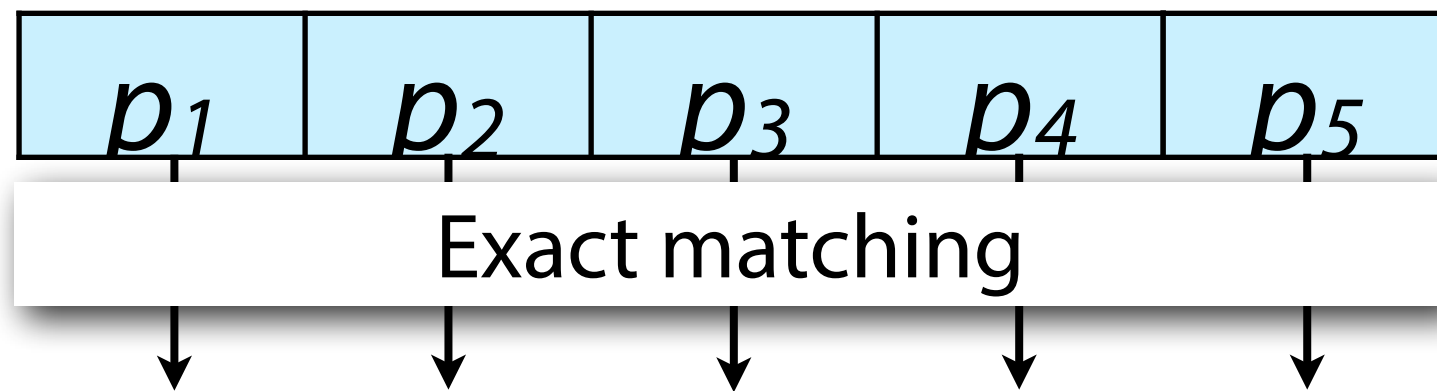
T

What algorithm can we use?

Any exact matching algorithm

If we have a k-mer index, we can use that

Pigeonhole principle



T

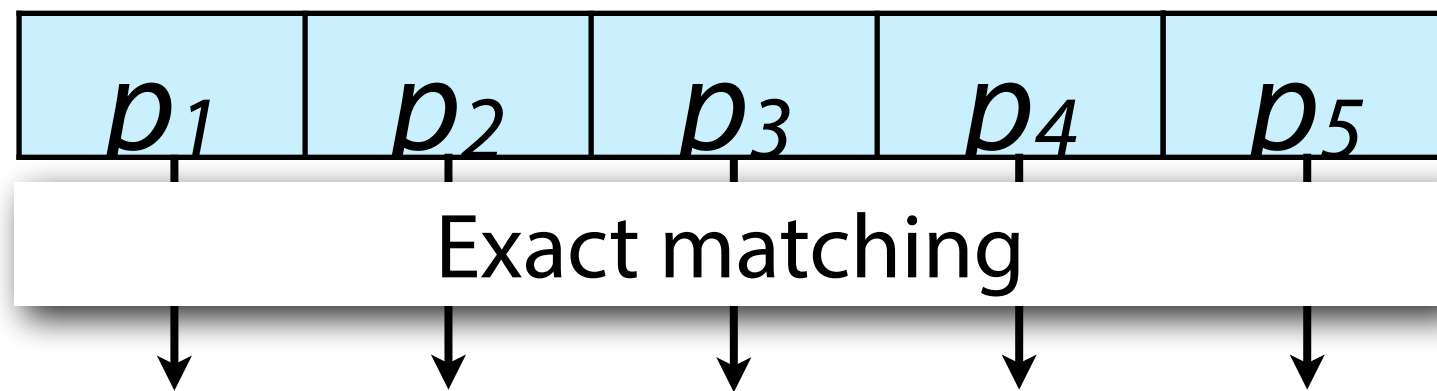
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Any exact matching algorithm

If we have a k-mer index, we can use that

Naive exact matching

Pigeonhole principle



T

What algorithm can we use?

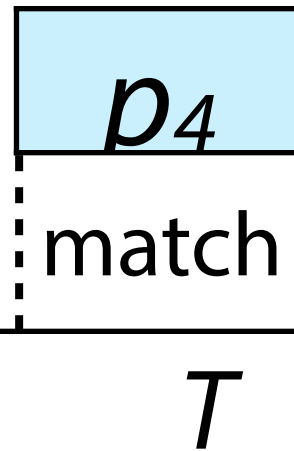
Any exact matching algorithm

If we have a k-mer index, we can use that

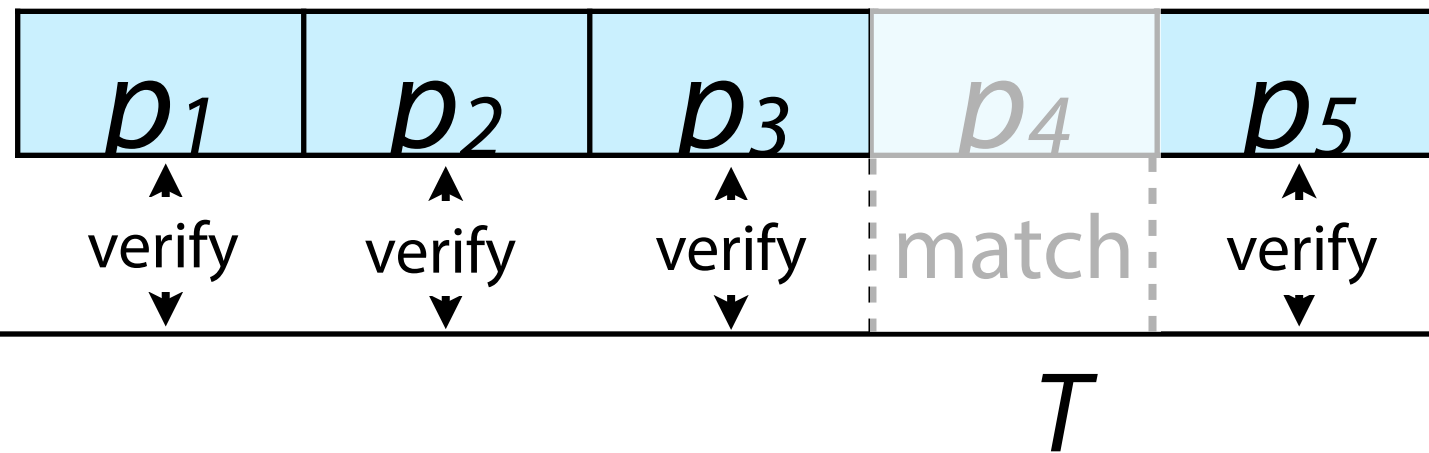
Naive exact matching

Boyer-Moore

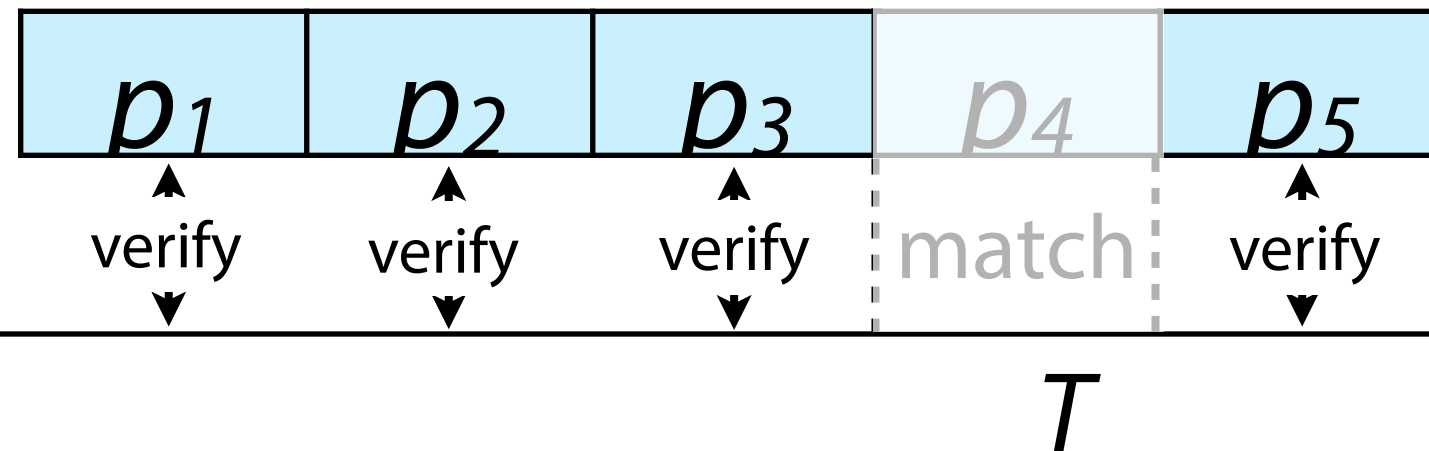
Pigeonhole principle



Pigeonhole principle

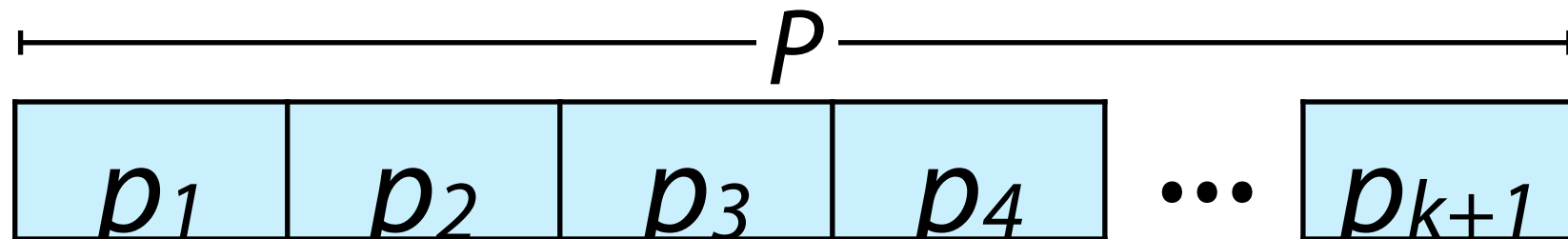


Pigeonhole principle



For Hamming distance, verification is essentially just the inner loop of **naive_approx_hamming** from before

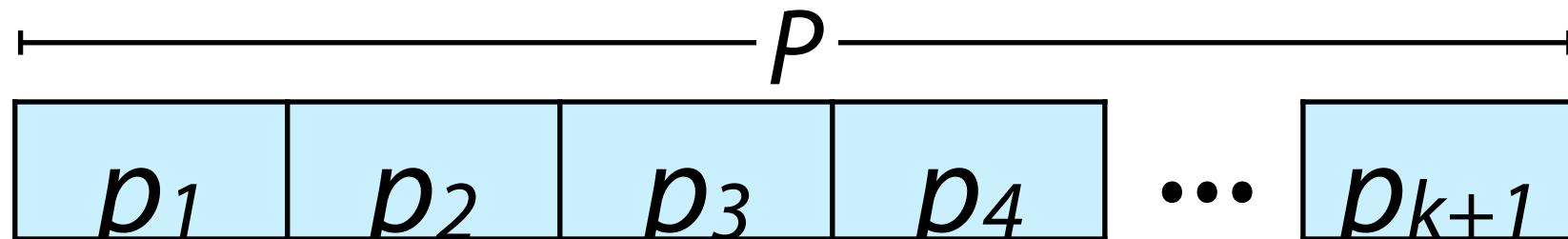
Pigeonhole principle



Advantages

Disadvantages

Pigeonhole principle

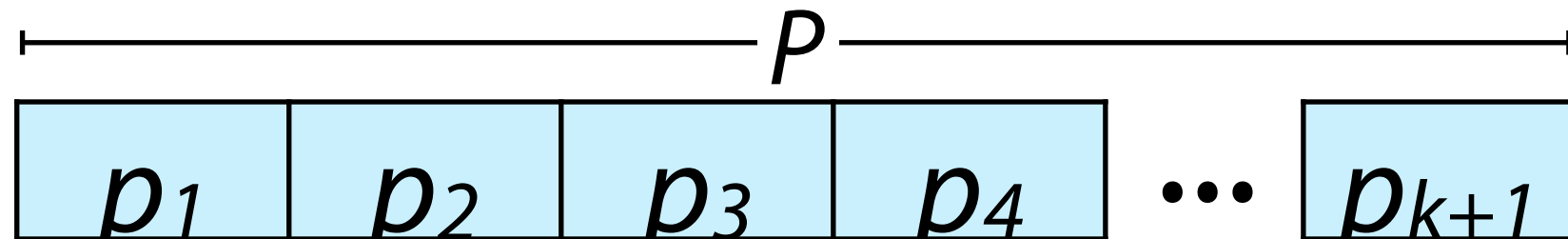


Advantages

Reuse favorite exact
matching algos; fast and
easy

Disadvantages

Pigeonhole principle



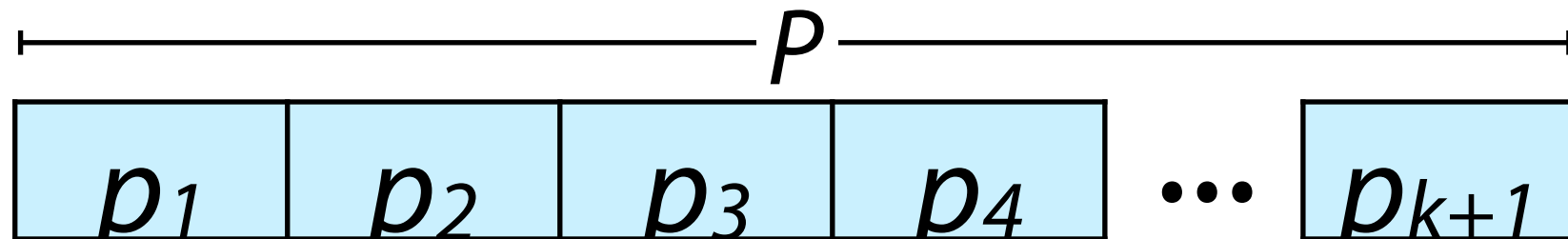
Advantages

Reuse favorite exact
matching algos; fast and
easy.
Flexible; works for
Hamming and edit
distance*

Disadvantages

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

Pigeonhole principle



Advantages

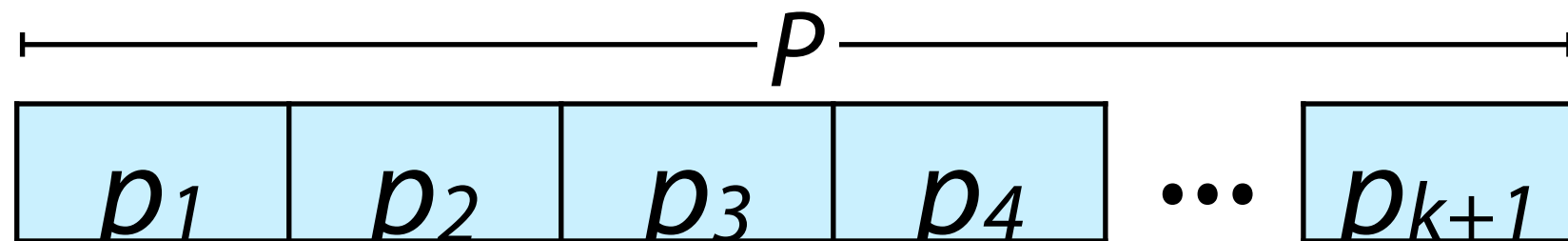
Reuse favorite exact matching algos; fast and easy.
Flexible; works for Hamming and edit distance*

Disadvantages

Large k yields small partitions matching many times by chance; lots of verification work

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

Pigeonhole principle



Advantages

Reuse favorite exact matching algos; fast and easy.
Flexible; works for Hamming and edit distance*

Disadvantages

Large k yields small partitions matching many times by chance; lots of verification work
 $k+1$ exact matching problems, one per partition

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

Implementation of pigeonhole principle with Boyer-Moore as exact matching algorithm: http://j.mp/CG_ApproxBM

	Boyer-Moore, exact			Boyer-Moore, ≤ 1 mismatch with pigeonhole			Boyer-Moore, ≤ 2 mismatches with pigeonhole		
	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches
P: "tomorrow" T: Shakespeare's complete works	786 K	1.91s	17						
P: 50 nt string from Alu repeat* T: Human reference (hg19) chromosome 1	32.5 M	67.21 s	336						

* GCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG

Implementation of pigeonhole principle with Boyer-Moore as exact matching algorithm: http://j.mp/CG_ApproxBM

	Boyer-Moore, exact			Boyer-Moore, ≤ 1 mismatch with pigeonhole			Boyer-Moore, ≤ 2 mismatches with pigeonhole		
	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches
P: "tomorrow" T: Shakespeare's complete works	786 K	1.91s	17	3.05 M	7.73 s	24			
P: 50 nt string from Alu repeat* T: Human reference (hg19) chromosome 1	32.5 M	67.21 s	336	107 M	209 s	1,045			

* GCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG

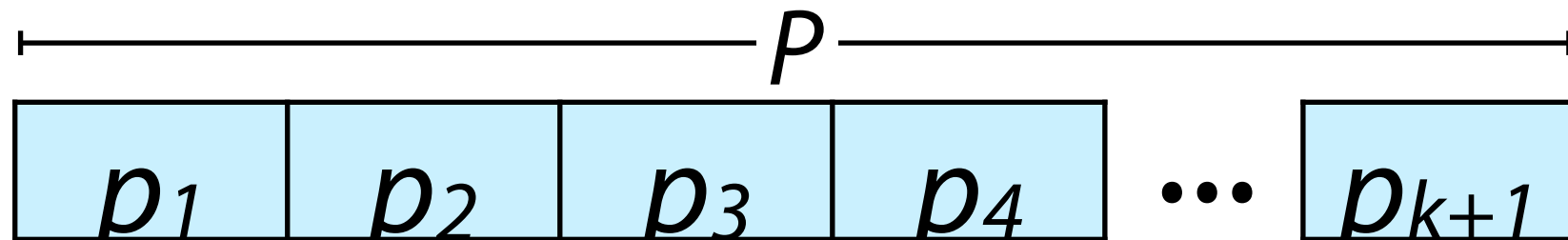
Implementation of pigeonhole principle with Boyer-Moore as exact matching algorithm: http://j.mp/CG_ApproxBM

	Boyer-Moore, exact			Boyer-Moore, ≤ 1 mismatch with pigeonhole			Boyer-Moore, ≤ 2 mismatches with pigeonhole		
	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches	# character comparisons	wall clock time	# matches
P: "tomorrow" T: Shakespeare's complete works	786 K	1.91s	17	3.05 M	7.73 s	24	6.98 M	16.83 s	382
P: 50 nt string from Alu repeat* T: Human reference (hg19) chromosome 1	32.5 M	67.21 s	336	107 M	209 s	1,045	171 M	328 s	2,798

* GCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG

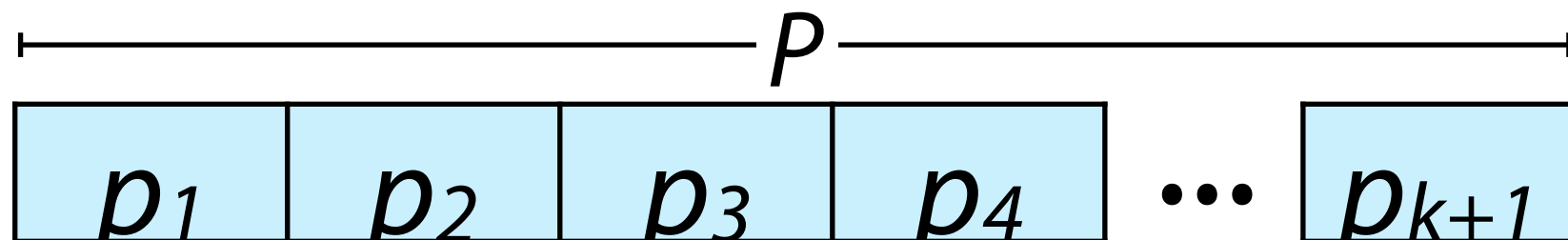
Generalizing pigeonhole, part 1

If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits



Generalizing pigeonhole, part 1

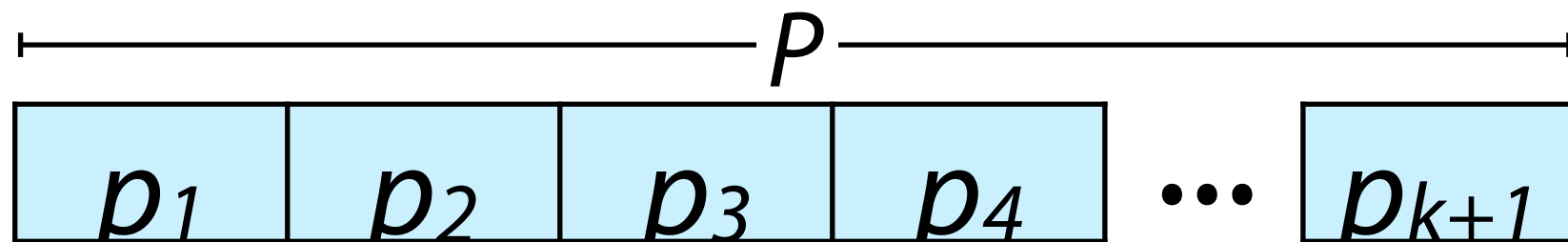
If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits



But doesn't *have to* be “at least one of” ...

Generalizing pigeonhole, part 1

If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits

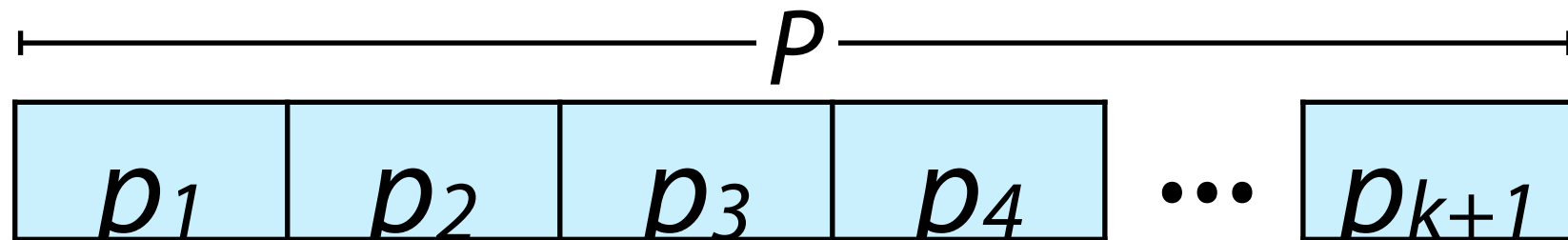


But doesn't *have to* be “at least one of” ...

what would we have to change for “at least two of”?

Generalizing pigeonhole, part 1

If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits



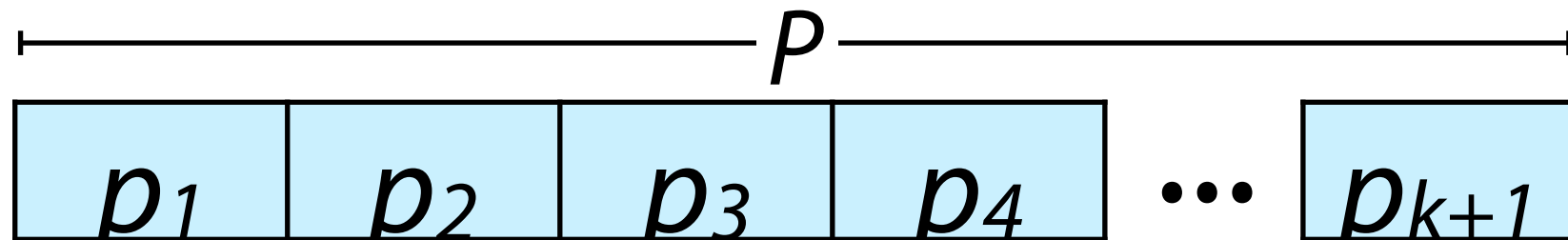
But doesn't *have to* be “at least one of” ...

what would we have to change for “at least two of”?

If P occurs in T with up to k edits, then at least **two** of _____ must appear with 0 edits

Generalizing pigeonhole, part 1

If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits



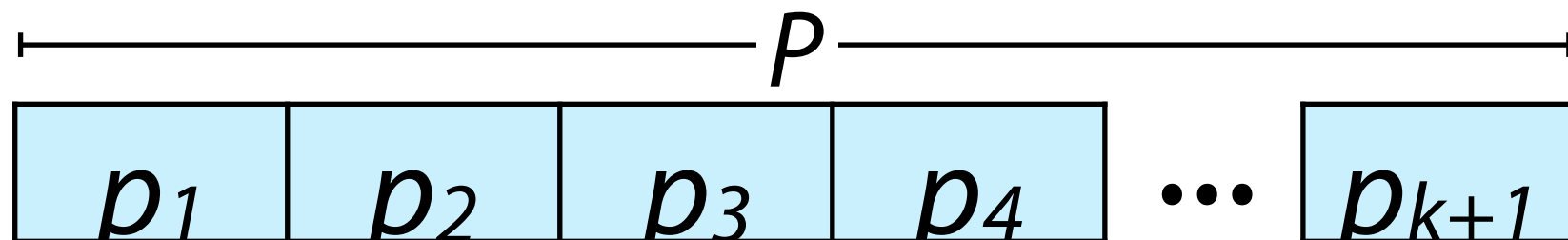
But doesn't *have to* be “at least one of” ...

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If P occurs in T with up to k edits, then at least **two** of p_1, p_2, \dots, p_{k+2} must appear with 0 edits

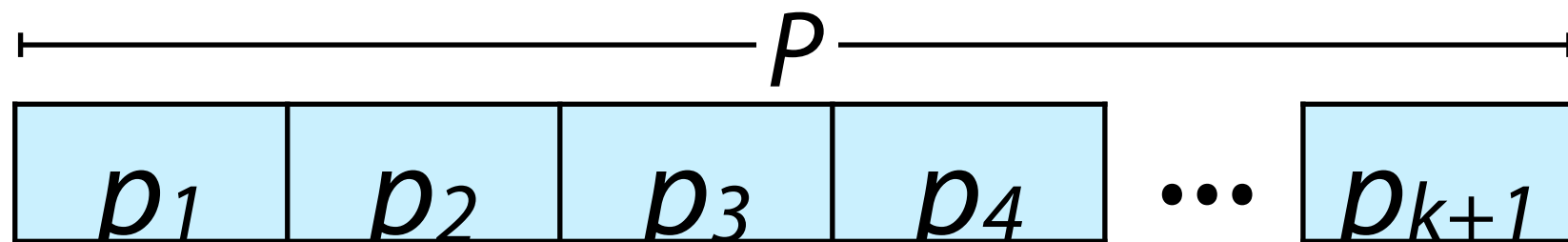
Generalizing pigeonhole, part 2

If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits

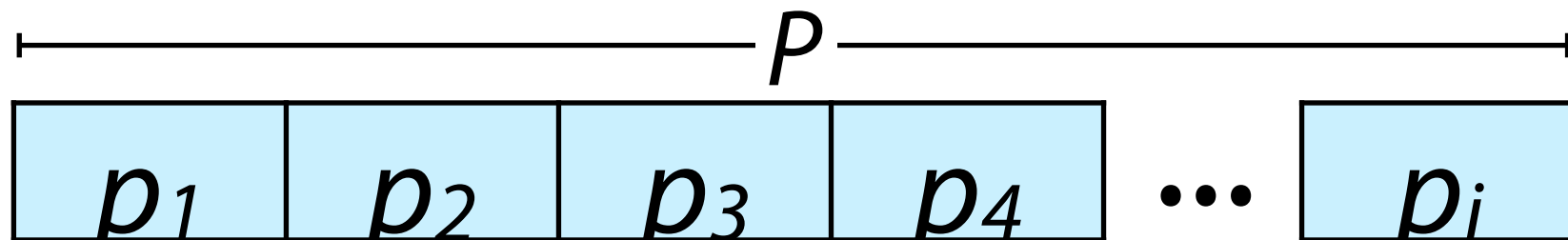


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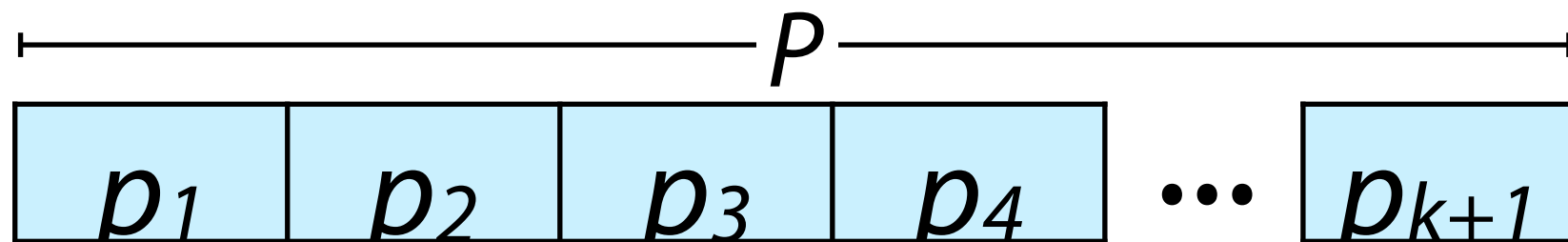


Let p_1, p_2, \dots, p_i be a partitioning of P . If P occurs with up to k edits, then at least one of p_1, p_2, \dots, p_i must occur with \leq ??? edits.

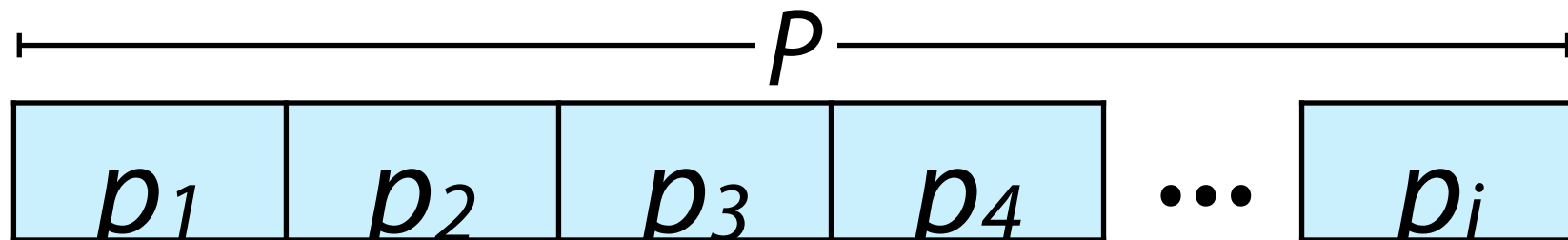


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If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits



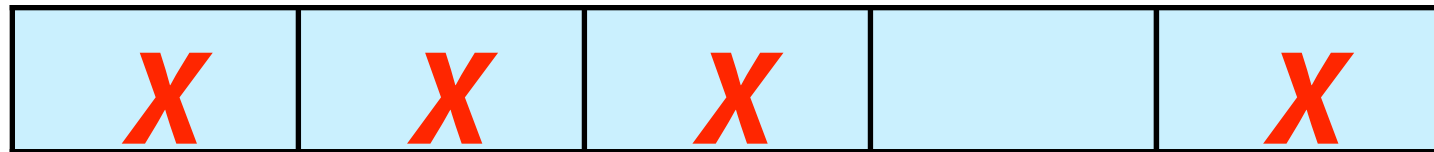
Let p_1, p_2, \dots, p_j be a partitioning of P . If P occurs with up to k edits, then at least one of p_1, p_2, \dots, p_j must occur with $\leq \text{floor}(k / j)$ edits.



Generalizing pigeonhole, part 2

At least one
of p_1, p_2, \dots, p_5
occurs with...

— p —



$k = 4$ edits

Generalizing pigeonhole, part 2

At least one
of p_1, p_2, \dots, p_5
occurs with...

┌─────────── p ───────────┐



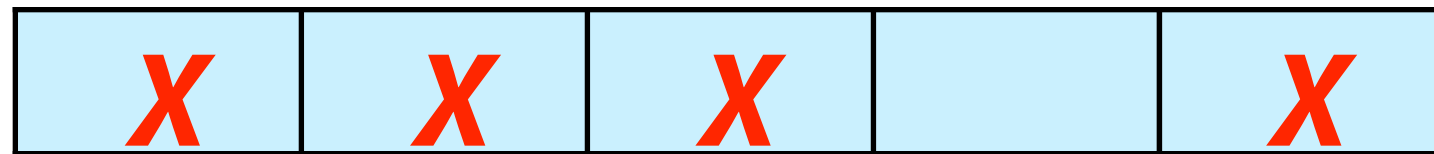
$k = 4$ edits

≤ 0 edits

Generalizing pigeonhole, part 2

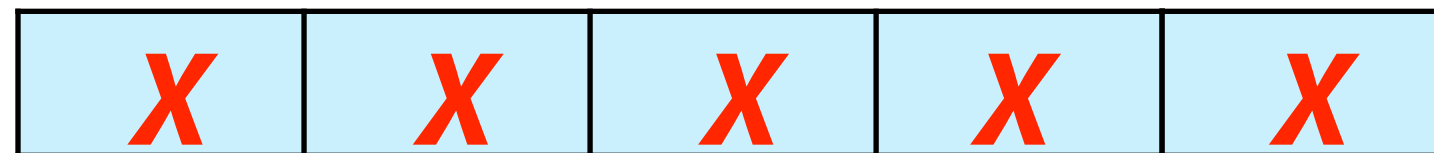
At least one
of p_1, p_2, \dots, p_5
occurs with...

┌────────── p ─────────┐



$k = 4$ edits

≤ 0 edits



$k = 5$ edits

Generalizing pigeonhole, part 2

At least one
of p_1, p_2, \dots, p_5
occurs with...

┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



$k = 5$ edits ≤ 1 edits

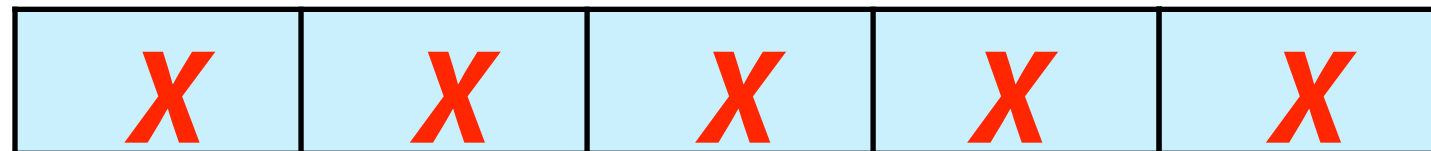
Generalizing pigeonhole, part 2

At least one
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┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



$k = 5$ edits ≤ 1 edits



$k = 9$ edits

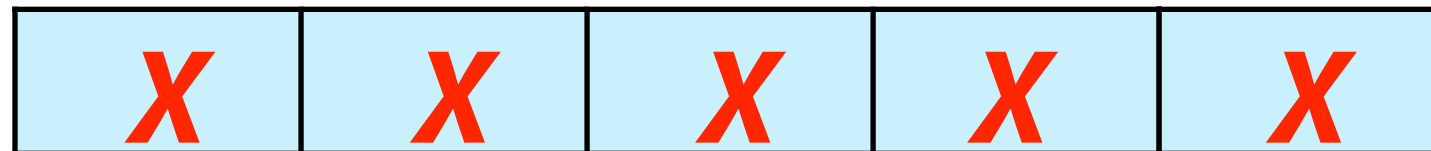
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┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



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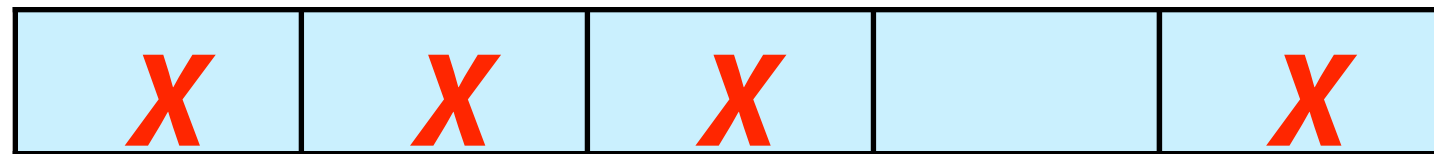


$k = 9$ edits ≤ 1 edits

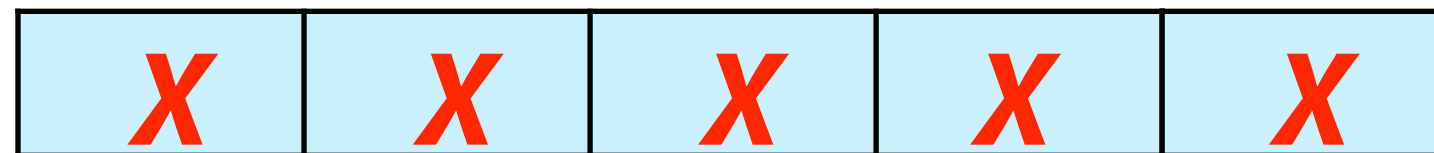
Generalizing pigeonhole, part 2

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┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



$k = 5$ edits ≤ 1 edits



$k = 9$ edits ≤ 1 edits



$k = 10$ edits

Generalizing pigeonhole, part 2

At least one
of p_1, p_2, \dots, p_5
occurs with...

┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



$k = 5$ edits ≤ 1 edits



$k = 9$ edits ≤ 1 edits



$k = 10$ edits ≤ 2 edits

Generalizing pigeonhole, part 2

At least one
of p_1, p_2, \dots, p_5
occurs with...

┌────────── p ─────────┐



$k = 4$ edits ≤ 0 edits



$k = 5$ edits ≤ 1 edits



$k = 9$ edits ≤ 1 edits



$k = 10$ edits ≤ 2 edits

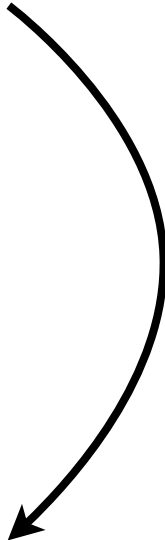
etc

Generalizing pigeonhole, part 2

General	<p><i>Pigeonhole principle</i></p> <p>If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_j must appear with $\text{floor}(k / j)$ edits</p>
Specific	<p><i>Pigeonhole principle with $j = k + 1$</i></p> <p>If P occurs in T with up to k edits, then at least one of p_1, p_2, \dots, p_{k+1} must appear with 0 edits</p>

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Generalizing pigeonhole, part 2

Let $j = k + 1$

Why?

General

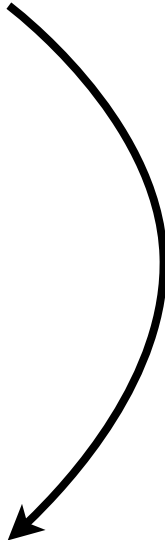
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Specific

Pigeonhole principle with $j = k + 1$

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then at least one of p_1, p_2, \dots, p_{k+1}
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Generalizing pigeonhole, part 2

Let $j = k + 1$

Why?
Smallest value s.t. $\text{floor}(k / j)$
 $= 0$

General

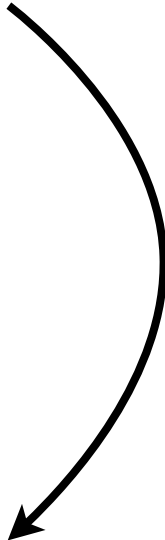
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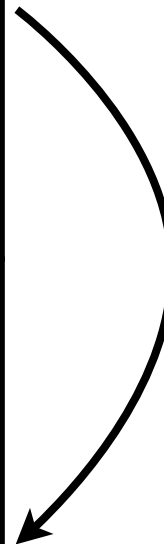
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Let $j = k + 1$

Why?
Smallest value s.t. $\text{floor}(k / j) = 0$

Why make $\text{floor}(k / j) = 0$?



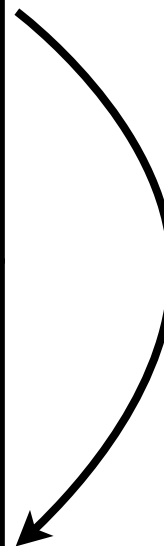
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Why make $\text{floor}(k / j) = 0$?
So we can use exact matching



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Why is smaller j good?

Generalizing pigeonhole, part 2

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Why is smaller j good?
Yields fewer, longer partitions

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Why are long partitions good?

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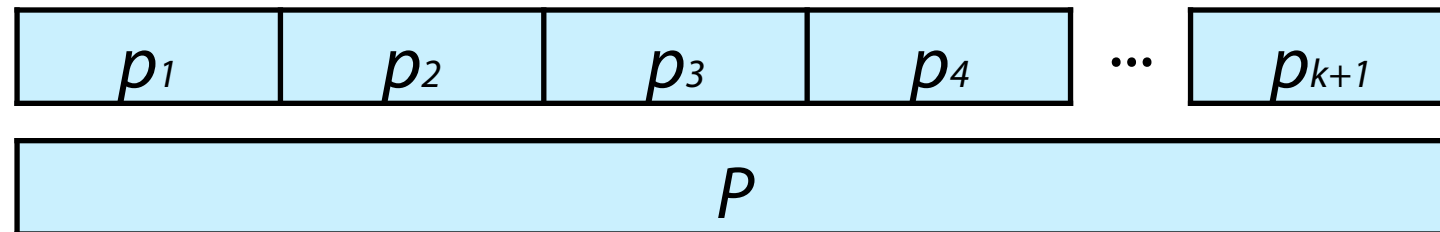
Why make $\text{floor}(k / j) = 0$?
So we can use exact matching

Why is smaller j good?
Yields fewer, longer partitions

Why are long partitions good?
Makes exact-matching filter more specific, minimizing # candidates

A different principle

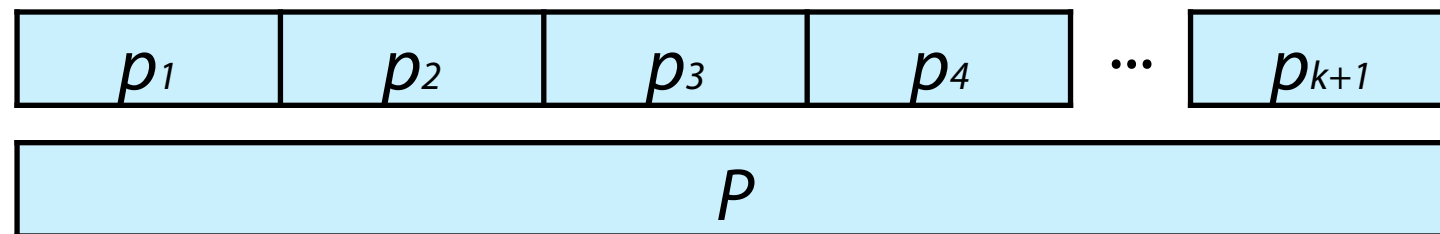
We partitioned P into non-overlapping substrings



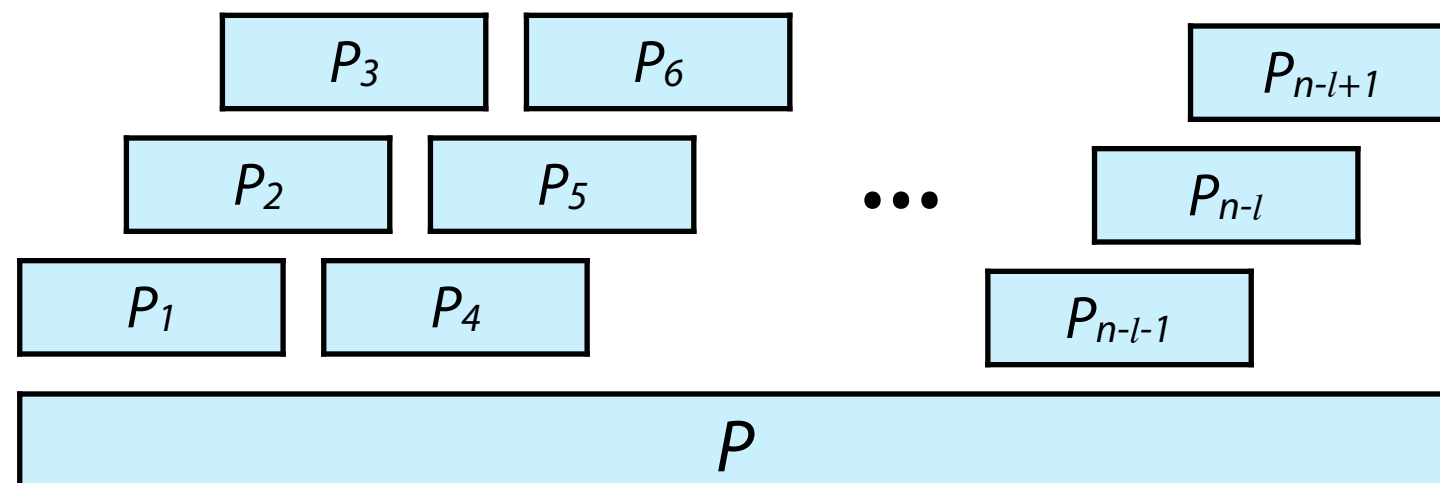
Now consider *overlapping* substrings

A different principle

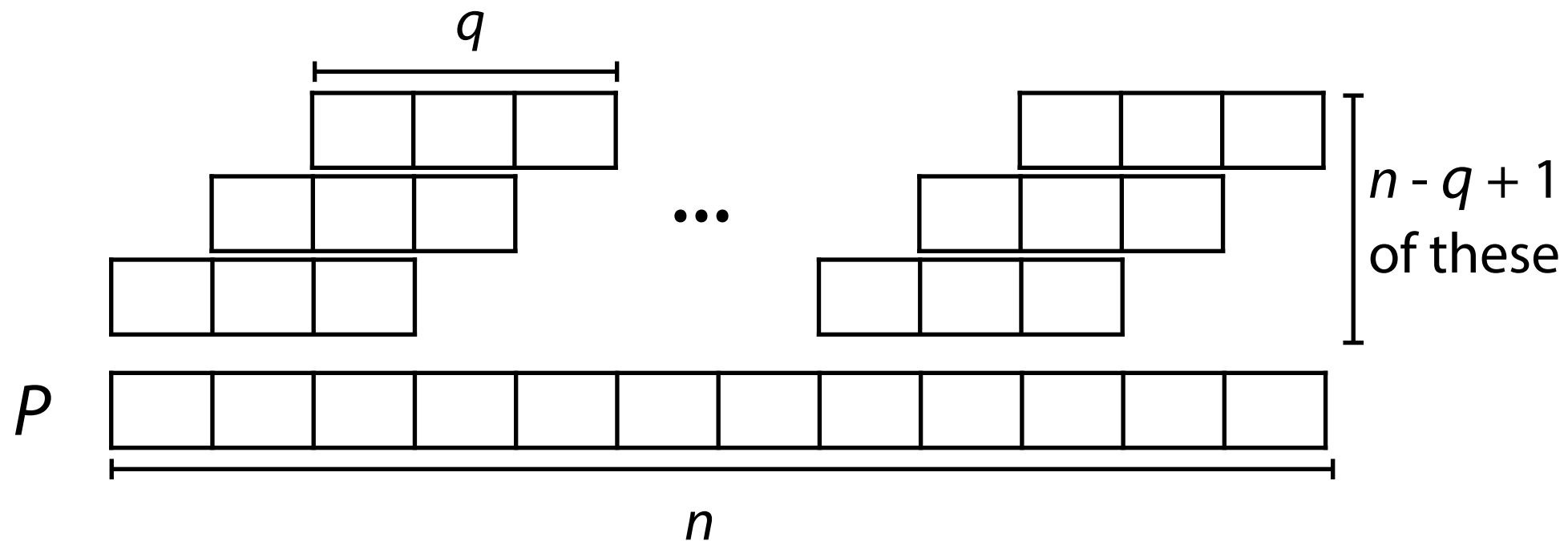
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Now consider *overlapping* substrings

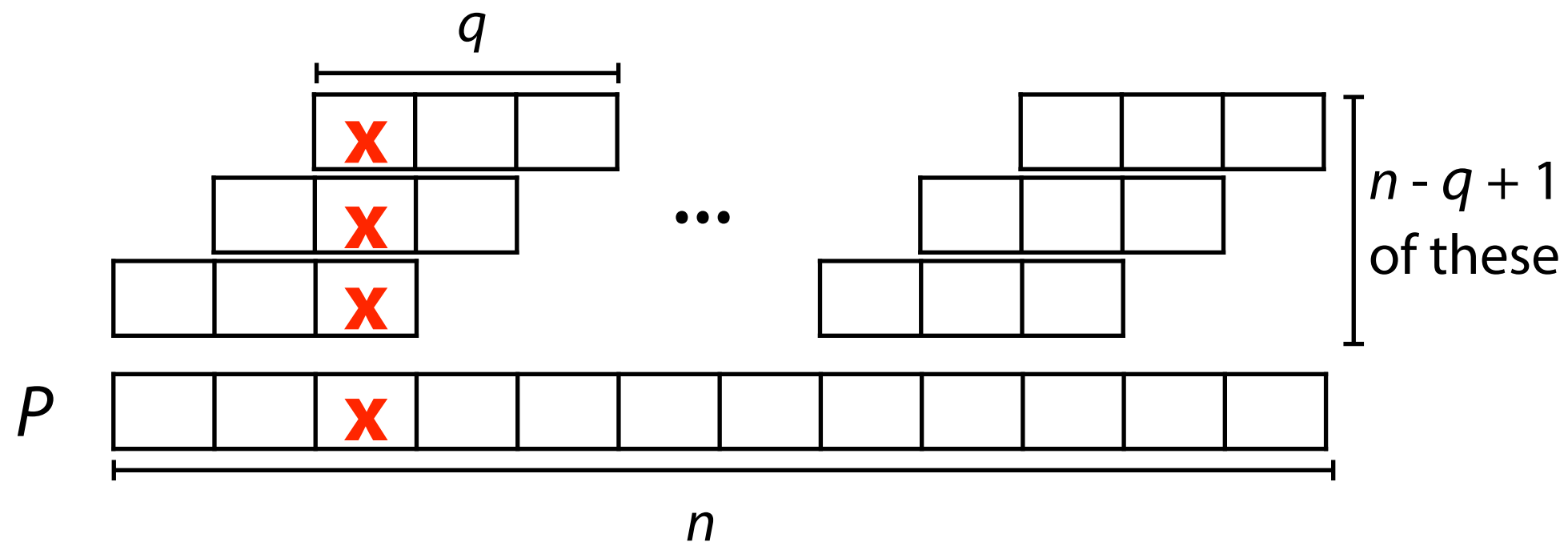


Approximate string matching: more



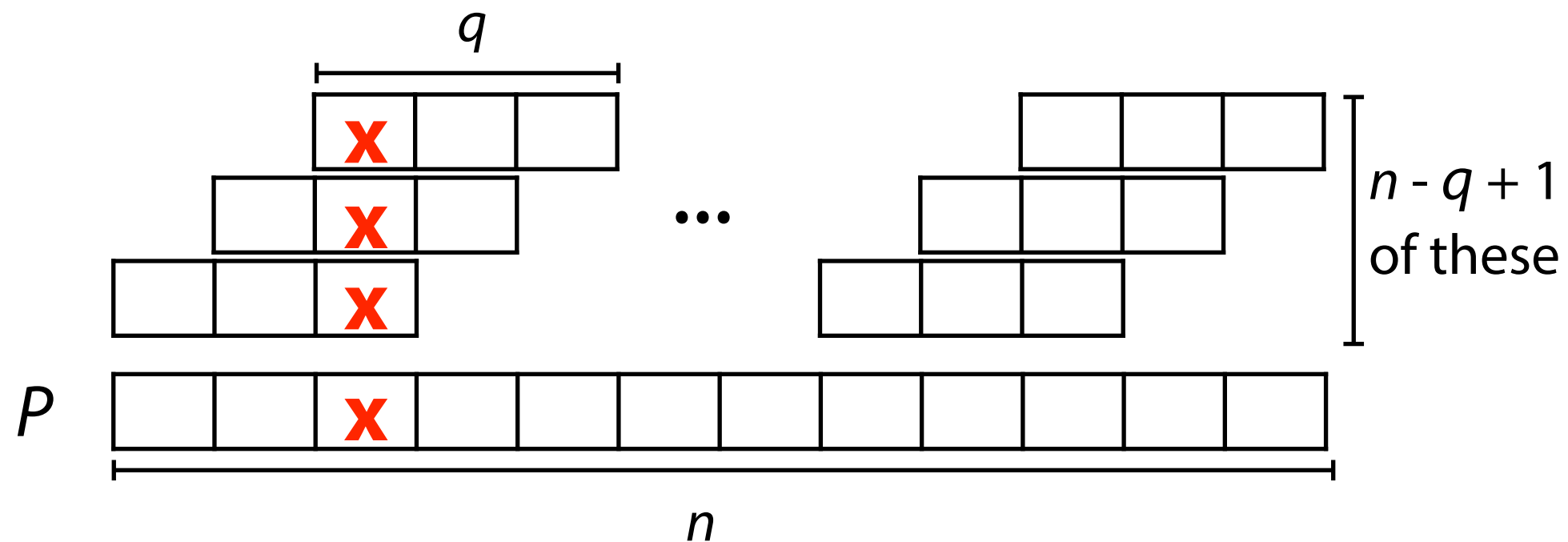
Say substrings are length q . There are $n - q + 1$ such substrings.

Approximate string matching: more



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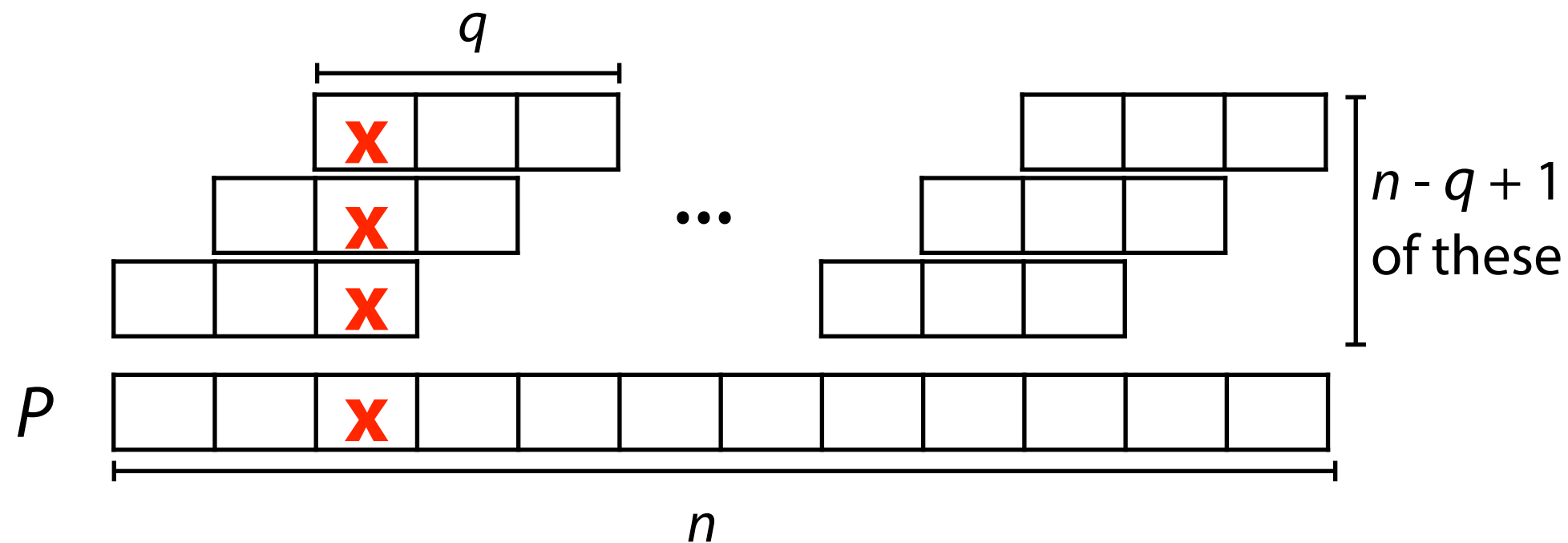
Approximate string matching: more



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1 edit to P changes *at most* q substrings

Approximate string matching: more

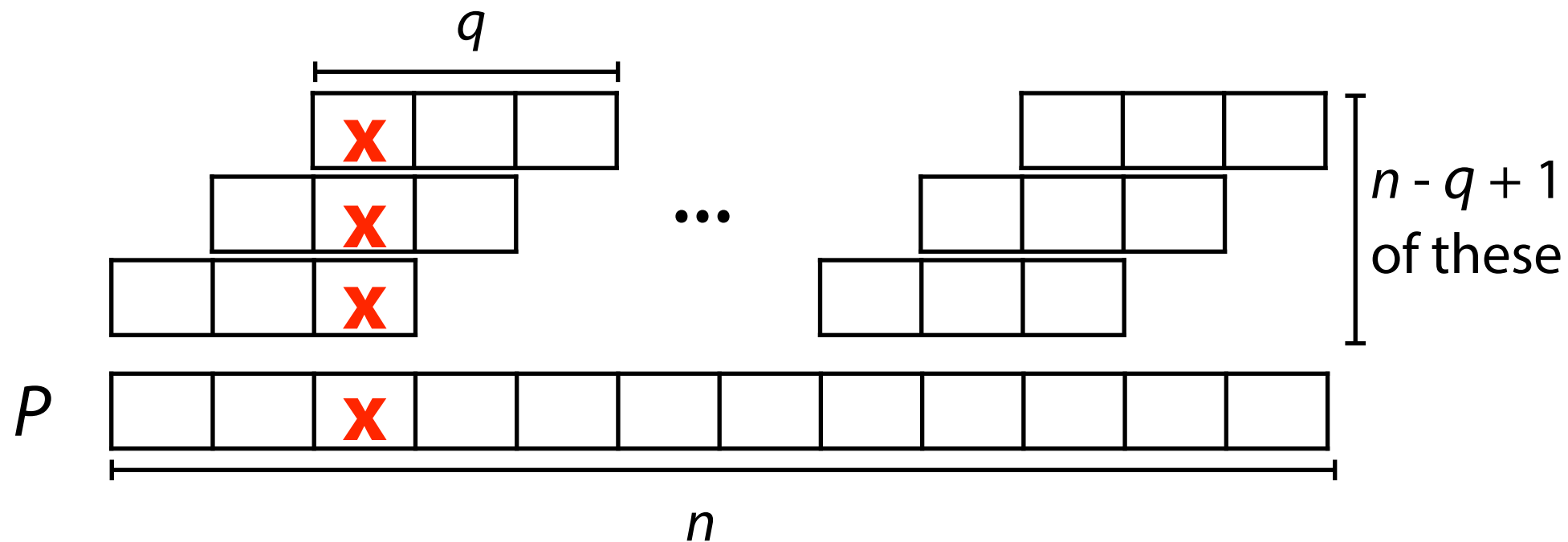


Say substrings are length q . There are $n - q + 1$ such substrings.

1 edit to P changes *at most* q substrings

Minimum # of length- q substrings unedited after k edits?

Approximate string matching: more



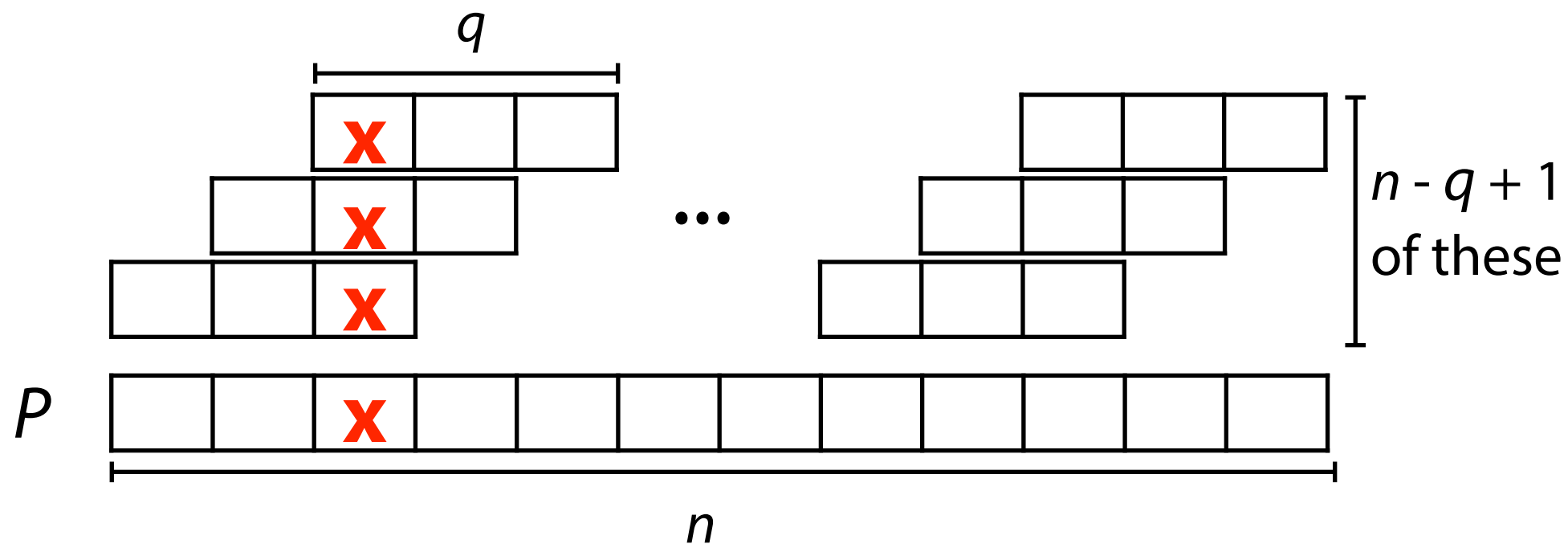
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*kq is worst case;
could be $< kq$*

Minimum # of length- q substrings unedited after k edits? $n - q + 1 - kq$

Approximate string matching: more



Say substrings are length q . There are $n - q + 1$ such substrings.

1 edit to P changes *at most* q substrings

*kq is worst case;
could be $< kq$*

Minimum # of length- q substrings unedited after k edits? $n - q + 1 - kq$

q -gram lemma: if P occurs in T with up to k edits, alignment must contain t exact matches of length q , where $t \geq n - q + 1 - kq$

Approximate string matching: more

If P occurs in T with up to k edits, alignment contains an exact match of length q , where $q \geq \text{floor}(n / (k + 1))$

Obtained by solving for q : $n - q + 1 - kq \geq 1$

Approximate string matching: more

If P occurs in T with up to k edits, alignment contains an exact match of length q , where $q \geq \text{floor}(n / (k + 1))$

Obtained by solving for q : $n - q + 1 - kq \geq 1$

Exact matching filter: find matches of length $\text{floor}(n / (k + 1))$ between T and *any* substring of P . Check vicinity for full match.

Approximate matching principles

Non-overlapping substrings

Overlapping substrings

General

Pigeonhole principle

p_1, p_2, \dots, p_j is a partitioning of P . If P occurs with $\leq k$ edits, at least one partition matches with $\leq \text{floor}(k / j)$ edits.

q-gram lemma

If P occurs with $\leq k$ edits, alignment contains t exact matches of length q , where $t \geq n - q + 1 - kq$

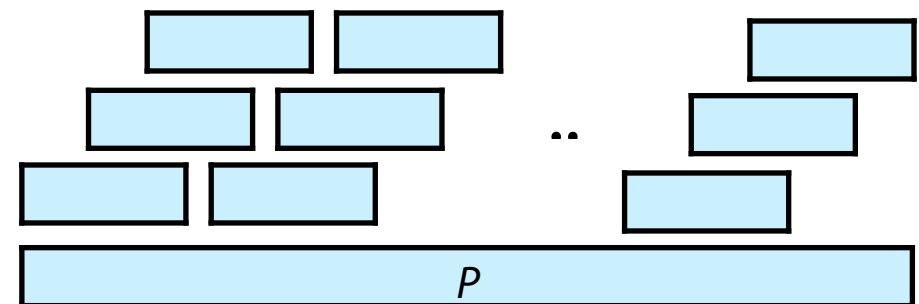
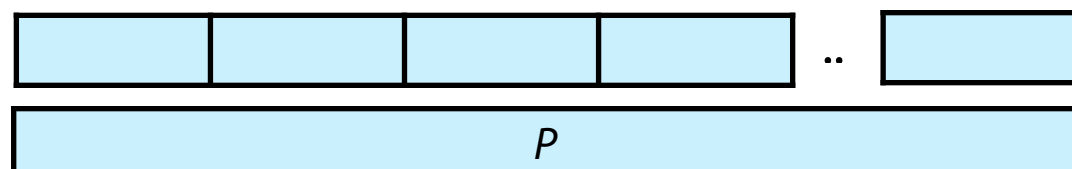
Specific

Pigeonhole principle with $j = k + 1$

p_1, p_2, \dots, p_{k+1} is a partitioning of P . If P occurs in T with $\leq k$ edits, at least one partition matches exactly.

q-gram lemma with $t = 1$

If P occurs with $\leq k$ edits, alignment contains an exact match of length q where $q \geq \text{floor}(n / (k + 1))$

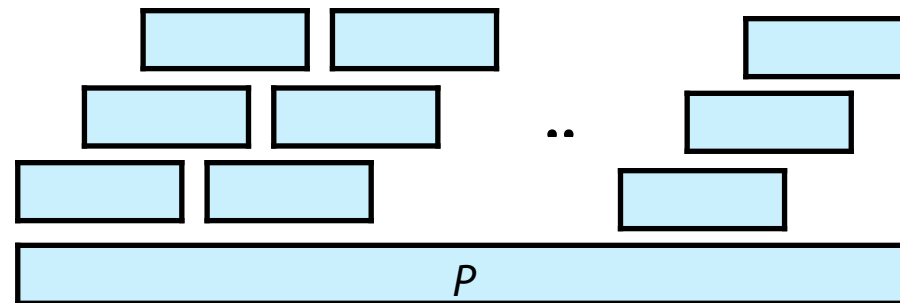


Sensitivity

Sensitivity = fraction of “true” approximate matches discovered by the algorithm

Lossless algorithm finds all of them, *lossy* algorithm doesn't necessarily

We've seen *lossless* algorithms. Most everyday tools are *lossy*. Lossy algorithms are usually much speedier & still acceptably sensitive.



Example lossy algorithm: pick $q > \text{floor}(n / (k + 1))$