String Matching

Naive Algorithm
Rabin-Karp Algorithm
Knuth-Morris-Pratt Algorithm
Boyer-Moore Algorithm

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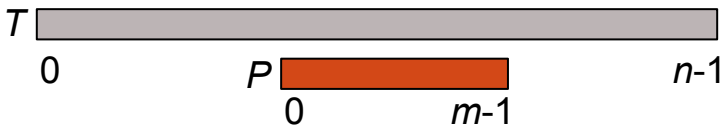
https://xkcd.com/208/

The String Matching problem



Text string containing n characters: $T[0 .. n-1]$,

Search pattern containing m characters: $P[0 .. m-1]$, $m < n$

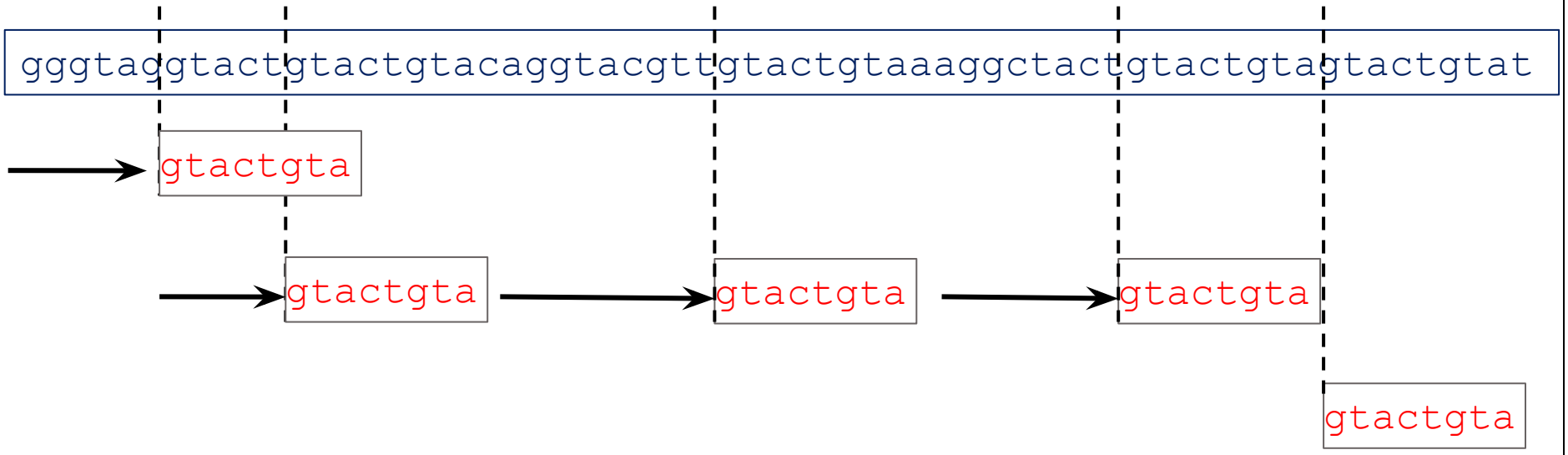
- Determine whether P occurs in T
- Report every occurrence of P in T
- Generally, n is very large compared to m.

Applications:

- Search and replace functions in text editors
- Keyword searches in databases
- Internet applications
- DNA pattern matching

Example: DNA pattern matching

Human DNA: ~ 3 billion base-pairs (chars)
One gene: typically 29,000 base-pairs



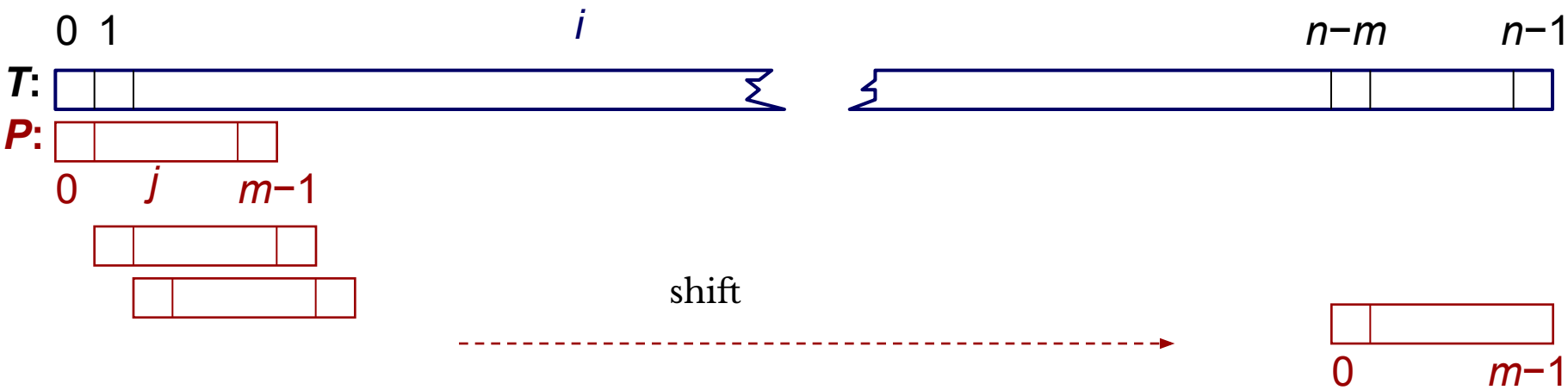
DNA Bases

DNA strings are drawn from the alphabet $\Sigma = \{a, c, g, t\}$

Naïve Algorithm

Shift the pattern from left to right, one character position at a time, and report all matching positions i such that

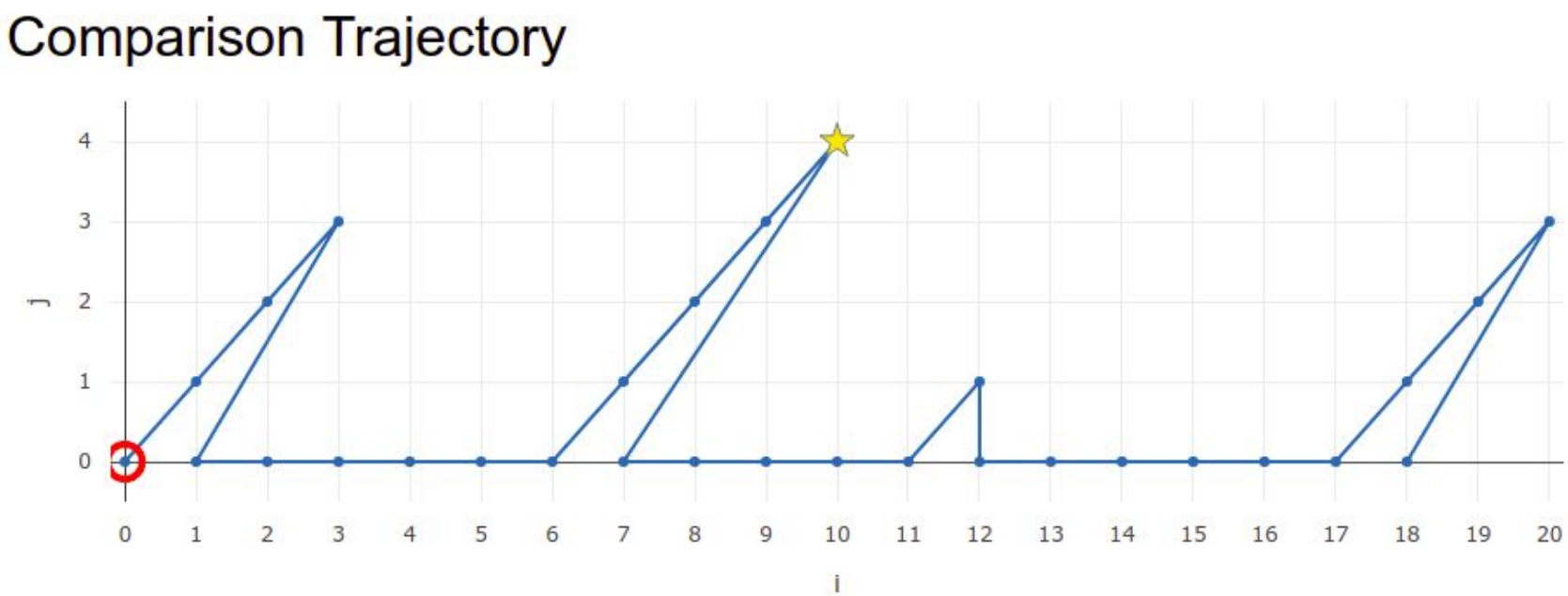
$$T[shift+j] == P[j], \quad \text{for} \quad j = 0, 1, \ldots, m-1.$$




```
for shift in range(0, n - m + 1):
    j = 0
    while j < m and T[shift+j] == P[j]:
        j = j+1
    if j == m:
        print(shift)
```

Naïve Algorithm

Watch it in action:
https://lobb.nz/stringmatchvisualiser/stringmatching.html



Naïve Algorithm - Complexity

Best case: $O(n)$

`aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa`

`bbbbbbbb`

Worst case: $O(nm)$

`aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaab`

`aaaaaab`

Expected: O(n)

With random alphabetic text, probability of mismatch in the first character is 25/26.

A good (enough) algorithm with typical written text and shortish patterns.

Python String Matching

ASIDE

Built-in pattern matching (optimised string search) functions:

str.find() (exact matching - naïve algorithm??)

```
text = 'Python string matching algorithms'
pattern = 'ing'
index = text.find(pattern)
while index > -1 :
    print (index)
    index = text.find(pattern, index+1)
```

```
10, 19
```

Sequence Matcher (partial matching - Ratcliff-Obershelp algorithm)

```
from difflib import SequenceMatcher
text = 'ctgacttggcactcg'
pattern = 'tgactacgcac'
s = SequenceMatcher(None, text, pattern)
lyst = s.get_matching_blocks()
print(lyst)
```

```
[Match(a=1, b=0, size=5), Match(a=8, b=7, size=4), Match(a=15, b=11, size=0)]
```

Improved Pattern Matching

- The naïve algorithm does not remember the structure of previously matched strings.
- The search pattern needs to be first preprocessed in order to analyze its structure.
  - **Pattern Preprocessing** Algorithm
- We consider three important algorithms for exact pattern matching:
  - **Rabin-Karp (RK)** Algorithm
  - **Knuth-Morris-Pratt (KMP)** Algorithm
  - **Boyer-Moore (BM)** Algorithm

Matching by hashing

Consider the following code to look for a pattern in a string s:

```
s = "asdfasdfsadfadsfareadgsasdasdasaesasdfadeq"
pat = "asdfa"
m, n = len(pat), len(s)
hash_pat = hash(pat)
for i in range(n - m + 1):
   if hash(s[i : i + m]) == hash_pat:
      print(f"Possible match at position {i}")
```

which prints

```
Possible match at position 4
Possible match at position 34
```

But *hash(`s[i : i + m]`)* is O(m), so this code is O(nm) even without hash collisions. Much worse than naive algorithm.

Rabin-Karp algorithm

Precompute a hash of the pattern, *hash-P* $O(m)$

Think of the pattern as a sliding window over the text

for each possible window position: $O(n)$

Compute hash of text in window, *hash-W* by updating hash from previous position $O(1)$

if *hash-P == hash-W*

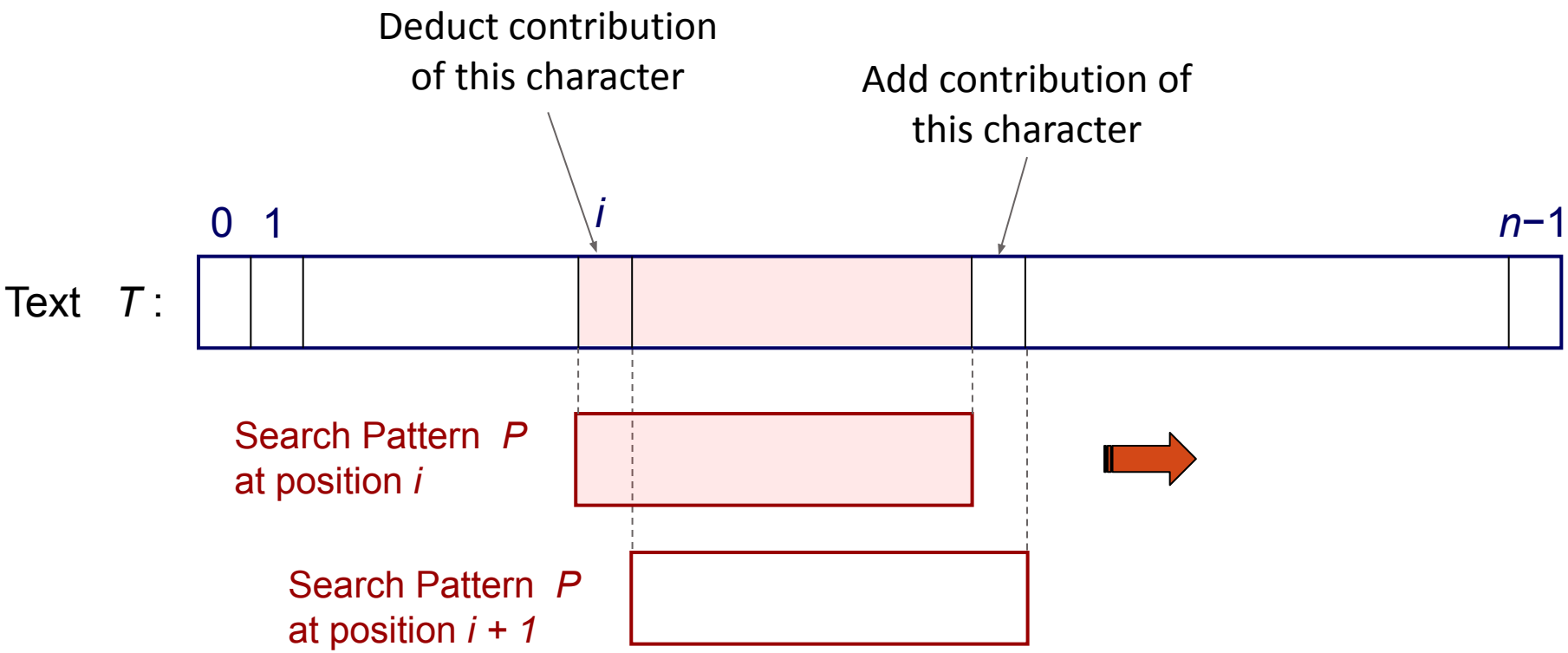
if windowed text == pattern

print matching position

Trick is to find a hash function with this property.

- Expected performance: O(n + m)
- Worst case: O(mn) - checks all chars for every hash hit
- Good if multiple patterns *P* being matched (e.g. *turnitin*??)

Rabin Karp: hash update



Rabin-Karp Hashing Function

A *"rolling hash"*

Define

$$hash(t_i \ldots t_{i+m-1}) = (t_i 2^{m-1} + t_{i+1} 2^{m-2} + \ldots + t_{i+m-1} 2^0) \bmod q$$

where t_i .. t_{i+m-1} is the text in the current window and q is a large prime number.

Then to update the hash for the window t_{i+1} .. t_{i+m} we have

$$\begin{aligned} hash(t_{i+1} .. t_{i+m}) &= (2 \times hash(t_i .. t_{m-i+1}) - t_i 2^m + t_{i+m}) \bmod q \\ &= (2 \times hash(t_i .. t_{m-i+1}) - t_i (2^m \bmod q) + t_{i+m}) \bmod q \end{aligned}$$

Written this way as 2^m could be massive.

Precompute this

Although straightforward, hash update is relatively expensive.

An improvement

Get far fewer hash collisions if use a bigger base, b > |alphabet|

e.g. b = 256

$$hash(t_i \ldots t_{i+m-1}) = (t_i b^{m-1} + t_{i+1} b^{m-2} + \ldots + t_{i+m-1} b^0) \bmod q$$

Update then becomes:

$$\begin{aligned} hash(t_{i+1} \ldots t_{i+m}) &= (b \times hash(t_i \ldots t_{m-i+1}) - t_i b^m + t_{i+m}) \bmod q \\ &= (b \times hash(t_i \ldots t_{m-i+1}) - t_i (b^m \bmod q) + t_{i+m}) \bmod q \end{aligned}$$

Written this way as b^m could be massive

Precompute this

Python code

```
BASE = 256
Q = 15487469  # Any largish prime

def rabin_karp_search(pat, text):
    m, n = len(pat), len(text)
    i = j = 0
    hash_p = 0 # hash value for pattern
    hash_t = 0  # hash value for text
    h = 1      # For calculating BASE^m % Q

    for i in range(m):
        h = (h * BASE) % Q                          # Compute BASE^m % Q
        hash_p = (BASE * hash_p + ord(pat[i])) % Q  # Computing pattern hash
        hash_t = (BASE * hash_t + ord(text[i])) % Q  # Computing window hash for i = 0

    for i in range(n - m + 1):                      # For each window position
        if hash_p == hash_t:
            if pat == text[i : i + m]:              # Char-by-char comparison only on a hash hit
                print("Pattern found at index " + str(i))

        if i < n - m:  # To prevent index error at end
            hash_t = (Q + BASE * hash_t - ord(text[i]) * h + ord(text[i + m])) % Q  # Update hash
```

Searching complete works of Shakespeare for a single string gave typically 0 or 1 hash mis-hits. But naïve algorithm 3 x faster.

A modified version of code at https://www.geeksforgeeks.org/rabin-karp-algorithm-for-pattern-searching/

When Rabin-Karp really wins ...

- … is when you're searching for any/all of a large number of patterns.
- Build a *set* of the hashes of all search patterns
- At each step, check if window hash is in the set
  - O(1)
- Is this what *turnitin* does??

Improving naive algorithm on a mismatch

Consider

Mismatch

```
T: aaaaaabaaaaaabaaaaabaaaaabaaaaabaaaaaab
P: aaaaaaa
P':        aaaaaaa
```

- Clearly, on a mismatch *in this case*, we can restart at P'

But with

Mismatch

```
T: aaaaaaabaaaaabaaaaabaaaaabaaaaabaaaaaab
P: aaaaaab
P': aaaaaab
```

- Now on a mismatch we can only move the pattern 1 step, but we **don't** need to go back to check P[0], P[1], … P[m - 2]

DFA pattern recognisers

Mismatch

```
T: aaaaaabaaaaaabaaaaabaaaaabaaaaabaaaaaab
P: aaaaaaa
P':        aaaaaaa
```

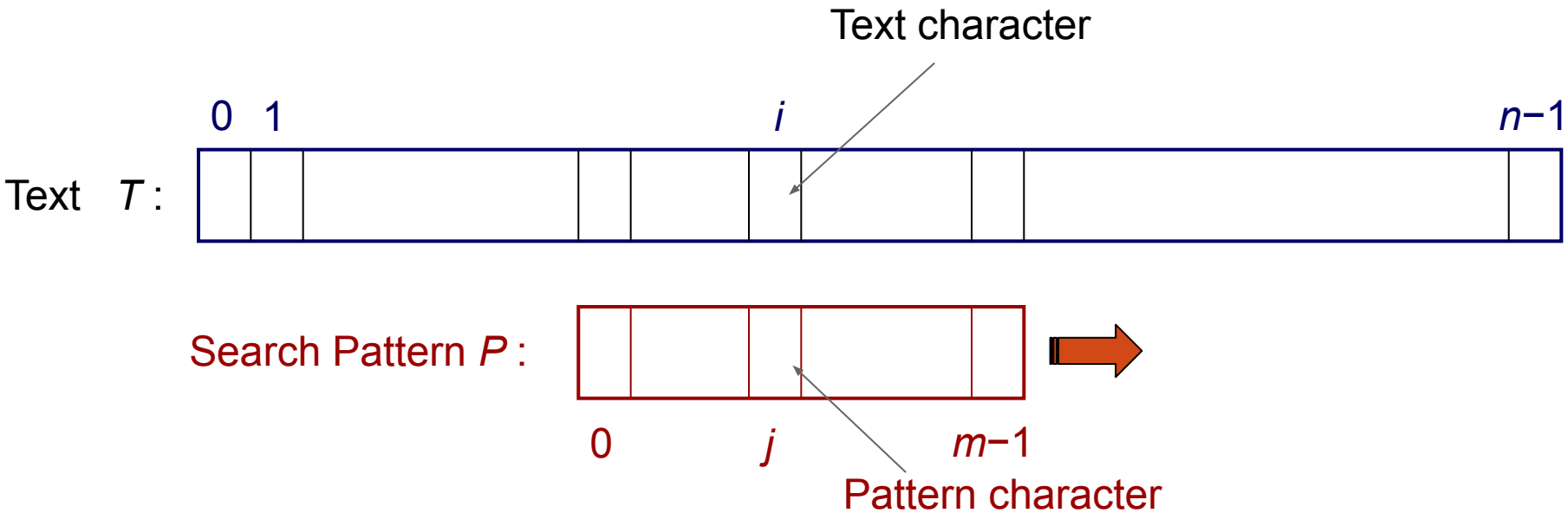
i.e. the next *shift* to try

- In general, we can precalculate the restart position for all possible mismatch positions *j* and characters *T[i]*
- Build a *Deterministic Finite State Automaton (DFA)*
  - See COSC261
- Checks T[i] exactly once - O(n)
- But the DFA is usually too expensive to build (space and time)
- So we trade off slightly slower searching for faster preprocessing.

Knuth-Morris-Pratt (KMP) Algorithm

- Uses a pre-process to skip forwards after a failed match
  - Identifies repeated sequences in the pattern
  - Like a DFA, but with a fast approximate preprocess
- We *never* back up in the text, only in the pattern.
- Pre-process O(m) in space and time
- Searching: O(n) in time
  - At most 2n - 1 character comparisons
- Overall: O(n + m)

String Matching Notation



<u>Note</u> : Here i represents the current character position in the text. $P[j]$ is compared with $T[i]$.

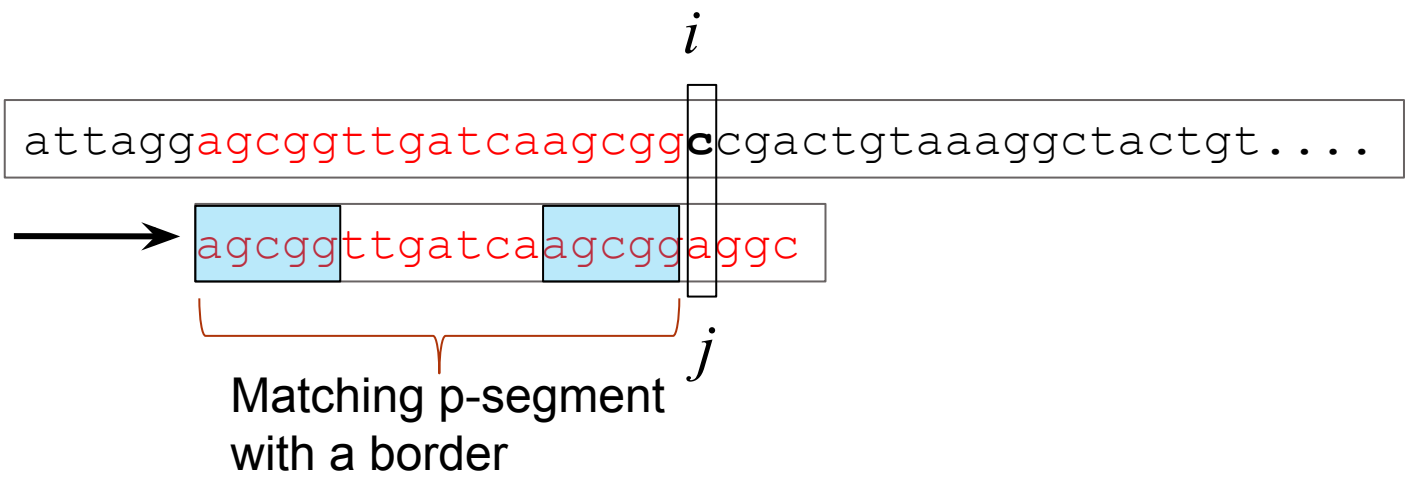
Text: $T = t_0 t_1 \ldots t_{n-1} = T[0: n]$

Pattern: $P = p_0 p_1 \ldots p_{m-1} = P[0: m]$

Matching Prefix Segment ("P-segment")

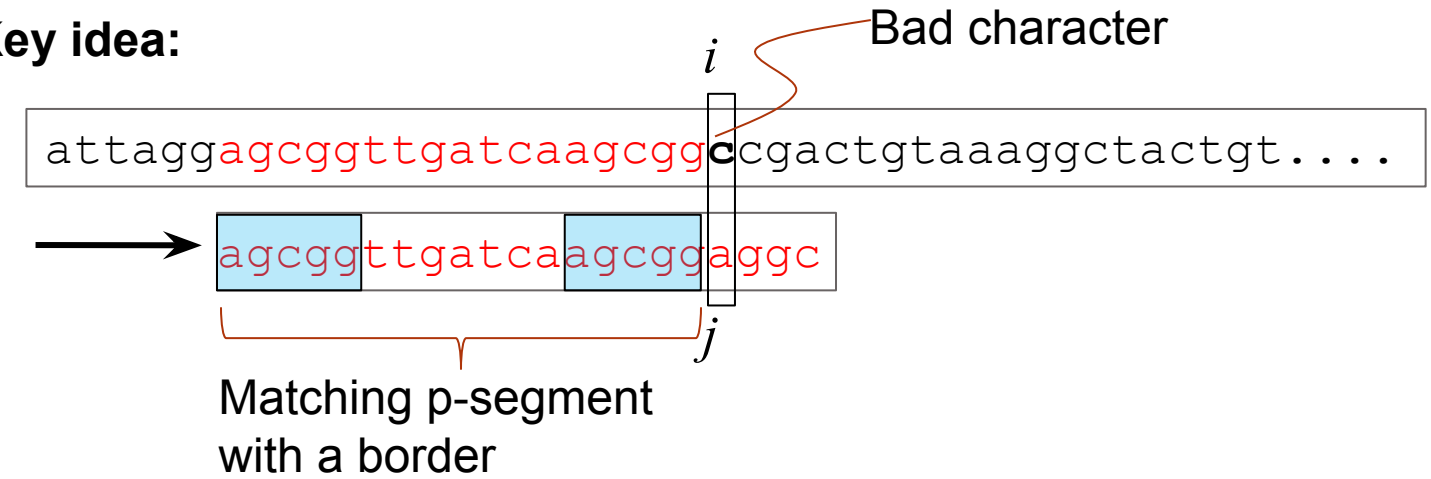
I introduce this term to reduce confusion with other prefixes in the algorithm.

- Suppose that the p-segment of the pattern $P[0{:}j]$ has matched with the corresponding portion of the text.
- Match failed at $P[j]$, i.e. $T[i] \neq P[j]$

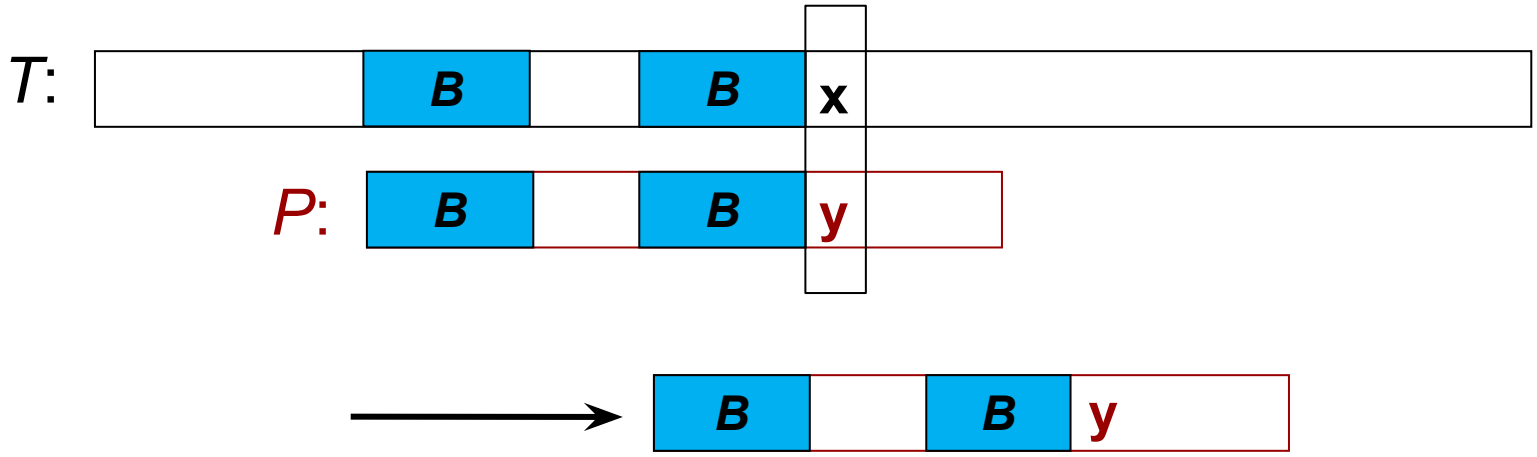


Matching P-segment and Bad Character

Key idea:



If B is the **widest** border of the matched p-segment of the pattern, the *minimum* shift worth trying is *j - len(B)* to align B again. No border => shift by j.



P-segment Borders

- We can use the information about the border of a matching prefix to shift a pattern.
- We will develop a method to pre-compute the *widest* borders of all p-segments of a given pattern, and store the border lengths in an array b[*j*]:

j :	0	1	2	3	4	5	6	7	8	9	10	11
Pattern:	M	A	T	H	E	M	A	T	I	C	S	
b[*j*]:	-1	0	0	0	0	0	1	2	3	0	0	0

The length of the widest border of matching prefix MATHEMA

- We can use b[*j*] to shift the pattern when a bad character in the text corresponding to location *j* is found.
- b[0] = -1 for use as a terminator; see later.

Teaching evaluation

I've asked for a teaching evaluation this year.

Please do respond. I want to find out how I'm doing!

Calculating borders: a brute-force approach

The brute-force way to calculate the length of the maximum borders of s is to try all border lengths from 1 up to len(s) - 1.

Need to do this for all P-segments.

```
def border_lengths(pattern):
    """A simple intuitive but inefficient implementation"""
    b = [0] * (len(pattern) + 1)          # Border lengths
    b[0] = -1       # Acts as a terminator - see later
    for i in range(1, len(pattern) + 1):  # For each p-segment
        p_seg = pattern[:i]
        for j in range(1, i):
            if p_seg[:j] == p_seg[-j:]:   # Is it a border?
                b[i] = j                  # If so, save length
    return b
```

But this is $O(m^3)$ - unacceptable. We need a better algorithm ...

Prefixes and Suffixes

Let $P = p_0 p_1 \ldots p_{m-1}$ be a string of length m.

Let $p_{-1} = p_m = \varepsilon$ (null string of length 0).

A **proper prefix of *P*** is a substring S of P such that

$S = p_0 \ldots p_{k-1}$, (or P[: k]), $0 \le k < m$.

A **proper suffix of *P*** is a substring V of P such that

$V = p_{m-k} \ldots p_{m-1}$, (or P[-k:]), $0 < k < m$.

-1	0	1	2	3	4	5	6
ε	**g**	**c**	**t**	**a**	**g**	**c**	ε

$m = 6$

Example:

Proper prefixes: ε, g, gc, gct, gcta, gctag

Proper suffixes: ε, c, gc, agc, tagc, ctagc

Border of a String

A string that is both a proper prefix and a proper suffix of P is called a **border of *P***.

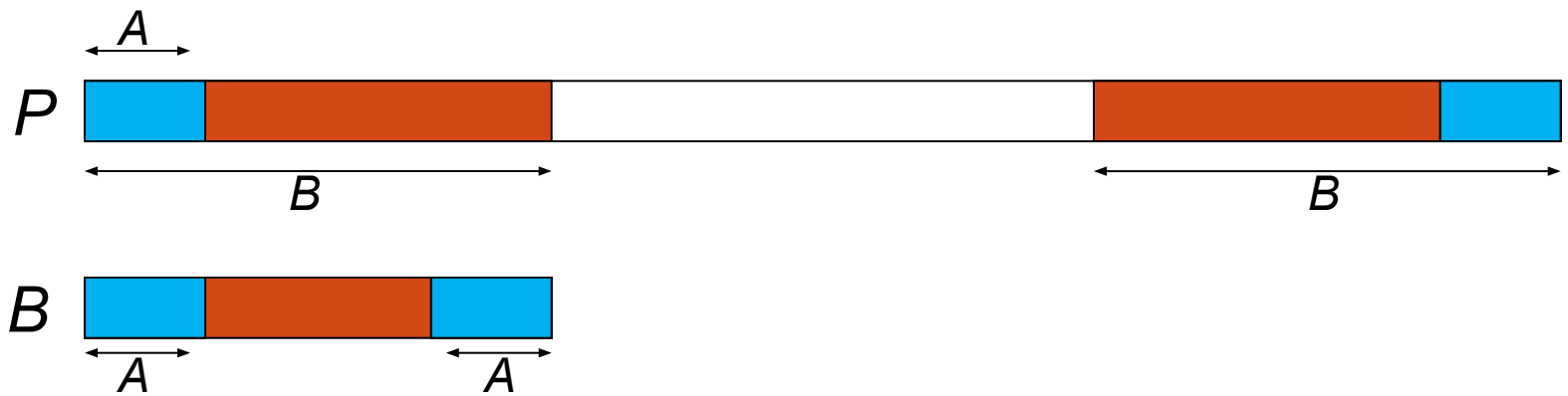
Example: P = `gctgcacggctgc`

Borders of P: ε, gc, gctgc

(ε is a border of every string).

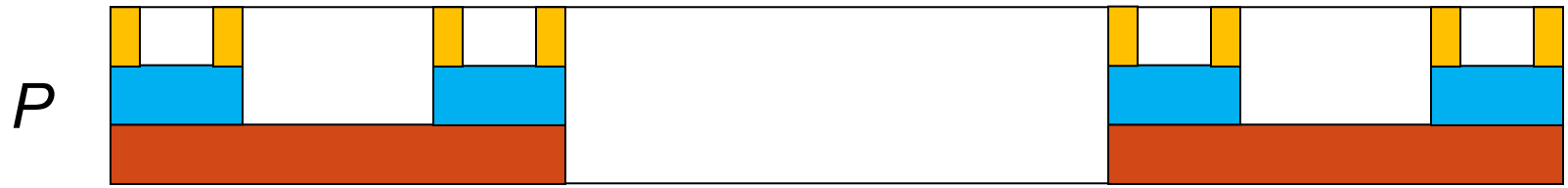
If A, B are both borders of P, and if $|A| < |B|$, then A is also a border of B.

(In the above example, 'gc' is a border of 'gctgc')



Nested Borders

In general, if a string has several borders, they will always be nested within each other in a hierarchical structure.



Example:

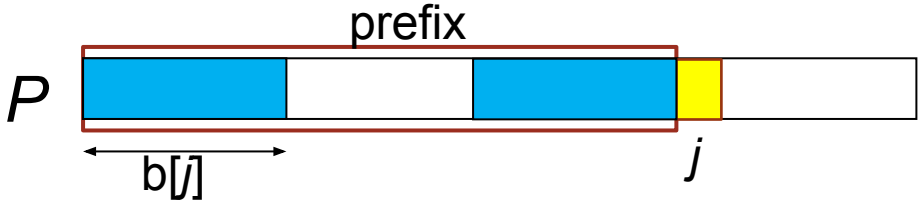
tagtacgtgtagtagcttagaggcttagtacgtgtagta

From the definition of a proper prefix/suffix, a string cannot be a border of itself.

So a single character cannot have a border other than ε.

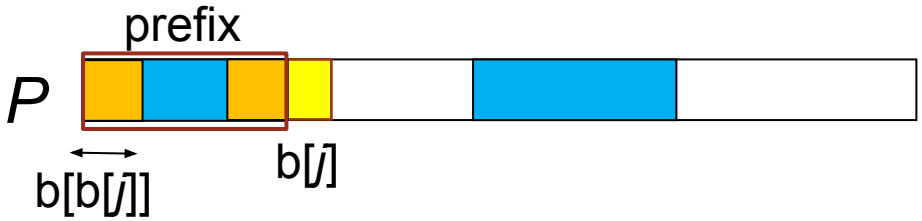
Fast Computation of P-segment Borders b[*j*]

Note: Here, by 'p-segment' at *j*, we mean the portion of the text $p_0 \ldots p_{j-1}$. (P[0:*j*])



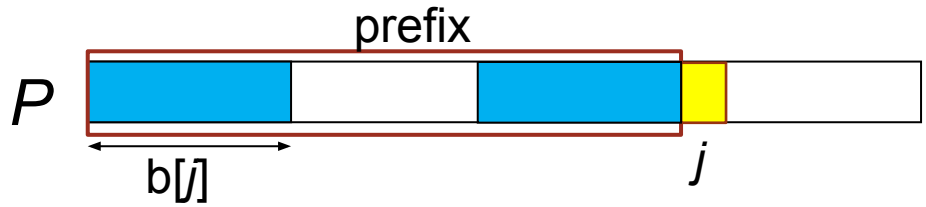
b[*j*] represents the length of the widest border of the p-segment at position *j*.

b[b[*j*]] represents the length of the widest border nested within the previous border of length b[*j*], and so on...



Computation of P-segment Borders b[*j*]

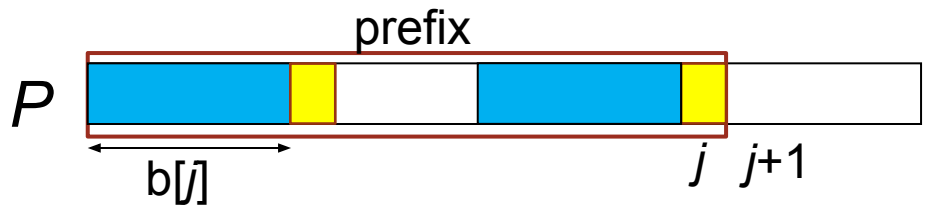
- Initialization: b[0] = −1; b[1] = 0.
- Sequential computation:



Can we compute b[*j*+1], given b[*j*]?

- If *P*[*j*]==*P*[b[*j*]], then the border can be extended by one character:

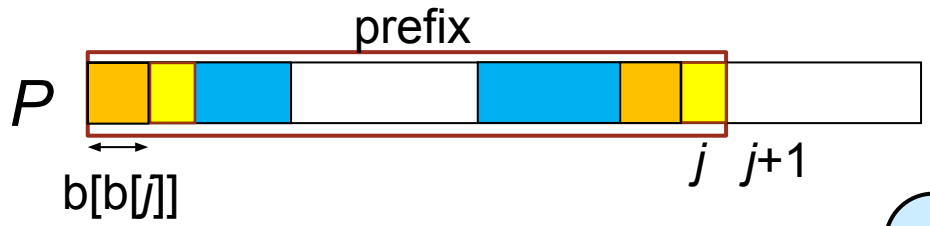
  b[*j*+1] = b[*j*]+1



- Else, if *P*[*j*]==*P*[b[b[*j*]]], the nested border can be extended by one character:

  b[*j*+1] = b[b[*j*]] + 1

- And so on



Preprocessing Patterns: Example (m = 1)

j:	0	1	2	3	4	5	**6**	7	8	9	
Pattern:	**c**	**g**	c	a	**c**	**g**	c	g	c	c	
Border length b[*j*]:	-1	0	0	1	0	1	2	3	2	3	1

b[6]=2 (The p-segment "cgcacg" has a widest border of length 2)

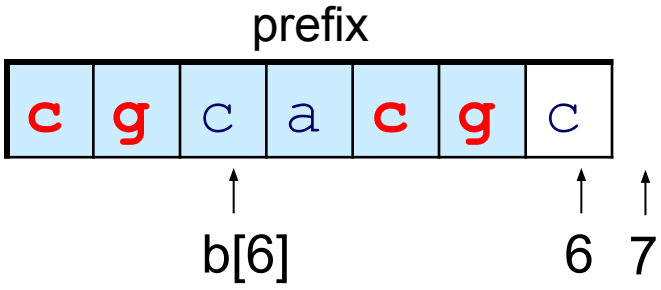
Computation of b[7] from b[6]:

j = 6

Is *P*[*j*] == *P*[b[*j*]] ?

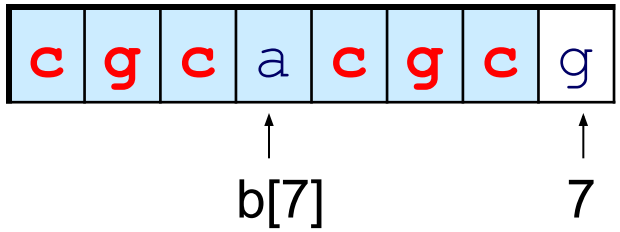
Yes: the border can be extended to 'cgc'

Therefore, b[7] = b[6] + 1 = 3.



Example (cont'd)

j:	0	1	2	3	4	5	**6**	7	8	9	
Pattern:	**c**	**g**	**c**	a	**c**	**g**	**c**	g	c	c	
Border length b[*j*]:	-1	0	0	1	0	1	2	3	2	3	1



Computation of b[8] from b[7]:

j = 7

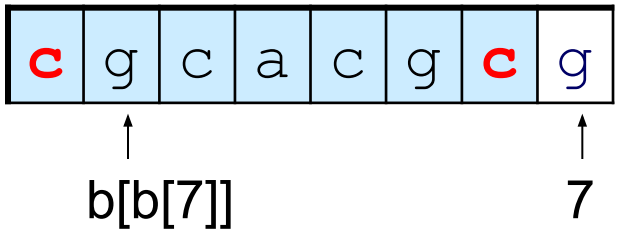
Is *P*[*j*] == P[b[*j*]] ?

No: the border 'cgc' cannot be extended.

Does the border have a sub-border? If so, can it be extended? i.e.,

Is *P*[*j*] == *P*[b[b[*j*]]] ? (b[b[7]]=b[3]=1)

Yes. We extend the sub-border.



Therefore,

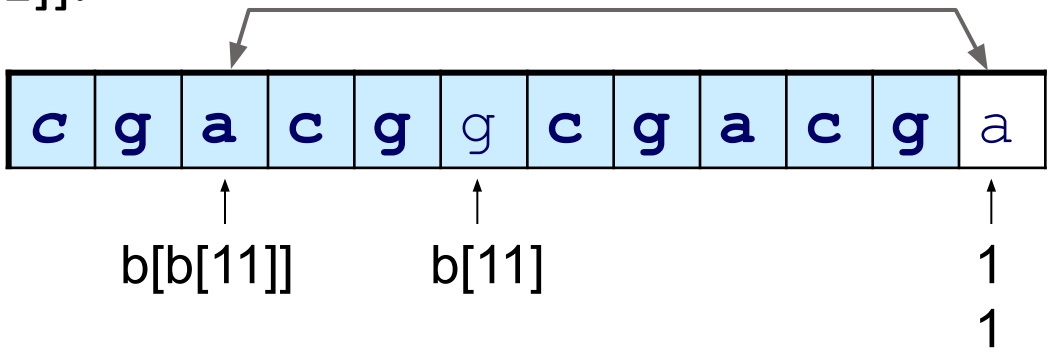
b[8] = b[b[7]] + 1 = 2.

Preprocessing Patterns

Another Example:

	0	1	2	3	4	5	6	7	8	9	10	11	12
	c	g	a	c	g	g	c	g	a	c	g	a	
b[*j*]	−1	0	0	0	1	2	0	1	2	3	4	5	?

To compute b[12], we first check if the previous border can be extended: Is *P*[11]==*P*[b[11]]? If not we compare the character at position b[b[11]].



They match. So b[12] = b[b[11]] + 1 = 3

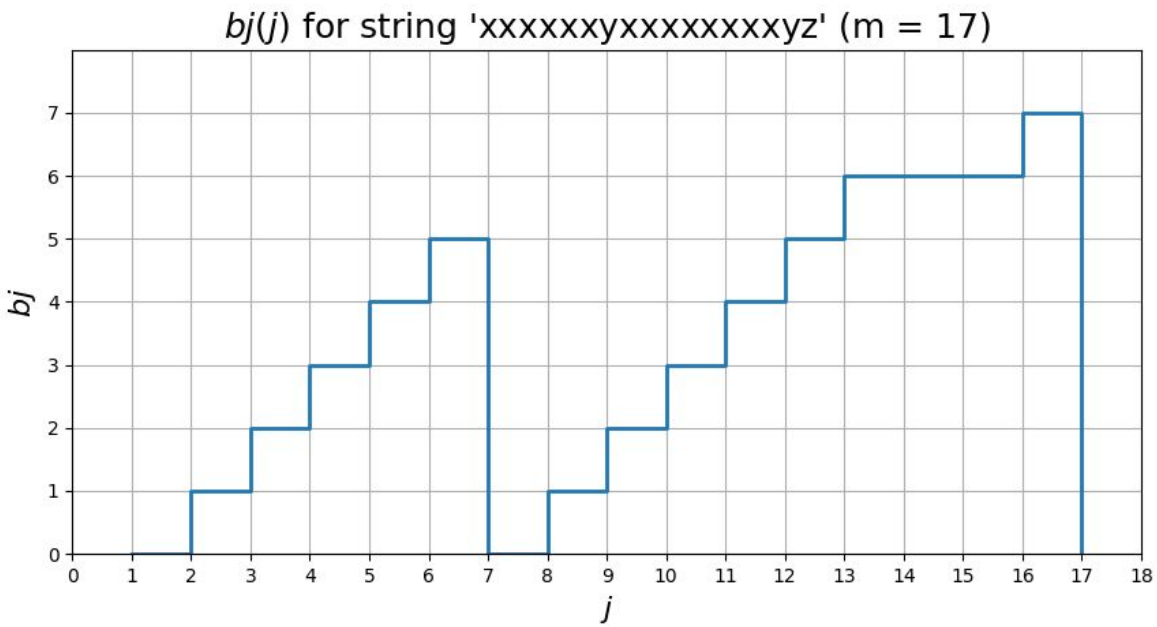
Efficient Computation of Prefix Borders

Although the explanation and proof is complicated, the code is quite simple:

```
def border_lengths(p):
    """ Computes lengths of p-segment borders """
    b = [0]*(len(p) + 1)
    b[0:2] = [-1, 0]
    j, bj = 1, 0
    while j < len(p):
        while bj >= 0 and (p[j] != p[bj]):
            bj = b[bj]
        j, bj = j+1, bj+1
        b[j] = bj
    return b
```

Preprocessing - Complexity

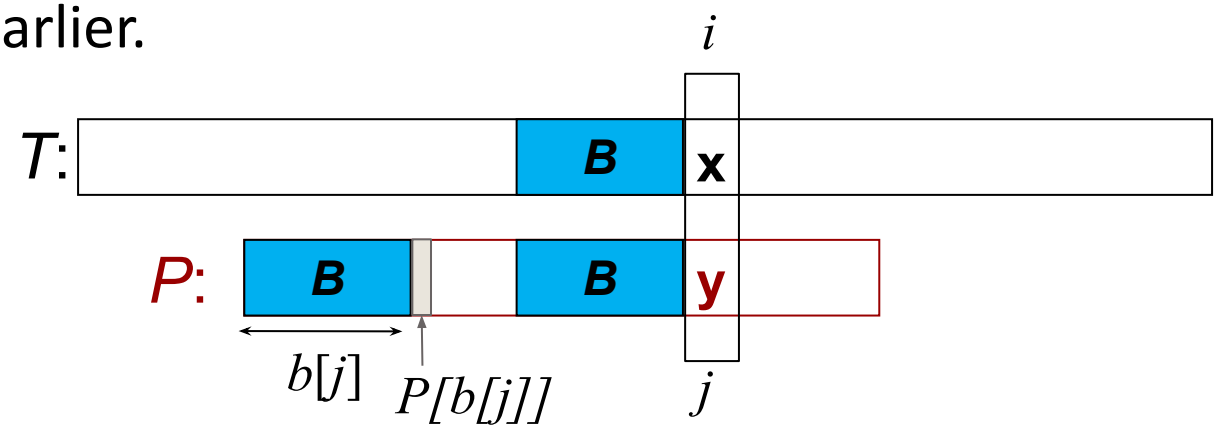
- The outer while-loop executes exactly *m*-1 times.
- The inner loop can decrease the value of *bj* at most as often as it has been increased previously by the outer loop.
- The overall number of executions of the nested loops follow a staircase pattern with an overall complexity of $O(m)$.



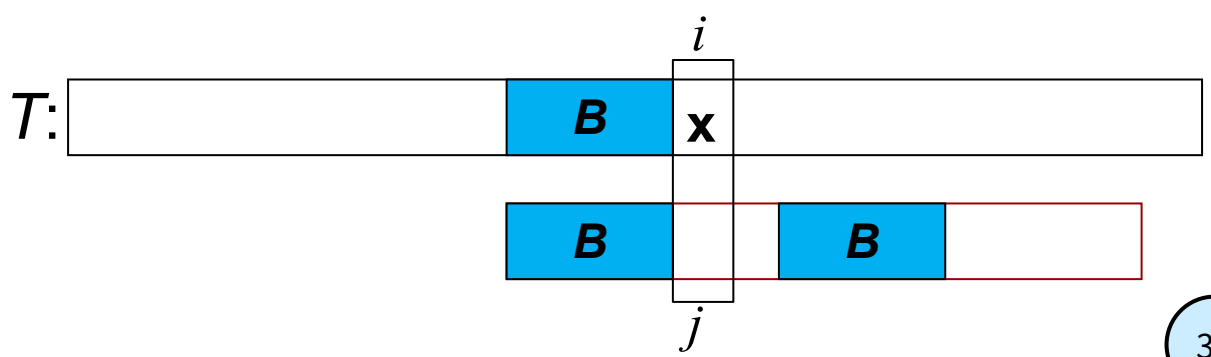
"Amortised complexity" (See COSC261)

Shifting Pattern Using P-segment Borders

- We now consider the procedure for shifting the pattern as previously shown earlier.
- $T[i] \neq P[j]$

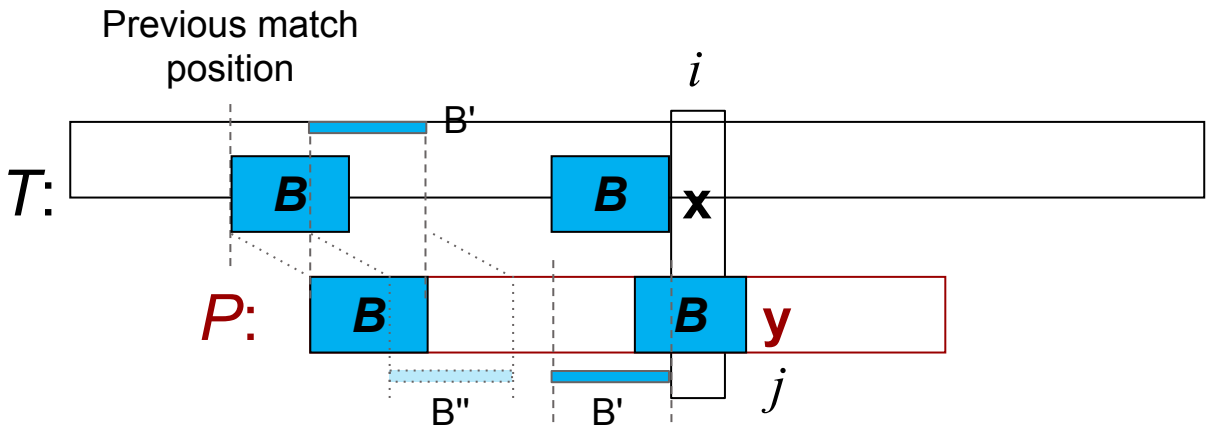


- We change the value of j to b[j] thereby **effectively** shifting the pattern as shown below. ***i* does not change.**
- $T[i]$ and $P[j]$ are now compared.



Proof that this is the minimum shift

- Suppose we try some smaller shift in P and get a match



- Sections B' in T and P must match B as well.
- Hence the B/B' union is a border of the p-segment P[j]
- But it's wider than just B
- So B *wasn't* the widest border of the p-segment P[j]
- CONTRADICTION => aligning borders *is* the minimum shift

KMP Algorithm (Code)

```
b = border_lengths(pattern)

i, j = 0, 0
while i < len(text):
    while j >= 0 and text[i] != pattern[j]:
        j = b[j]
    i, j = i+1, j+1
    if j == len(pattern):
        # Match found. Print position.
        print (i-j)
        j = b[j]
```

KMP Example with Visualiser

https://lobb.nz/stringmatchvisualiser/stringmatching.html

Use the string match visualiser on the following:

Text: `cgacggcgacggcggcgaccgacggcgacgac`

Pattern: `cgacggcgacga`

Border table (slide 33):

j	0	1	2	3	4	5	6	7	8	9	10	11	12
pattern	c	g	a	c	g	g	c	g	a	c	g	a	
b[*j*]	−1	0	0	0	1	2	0	1	2	3	4	5	3

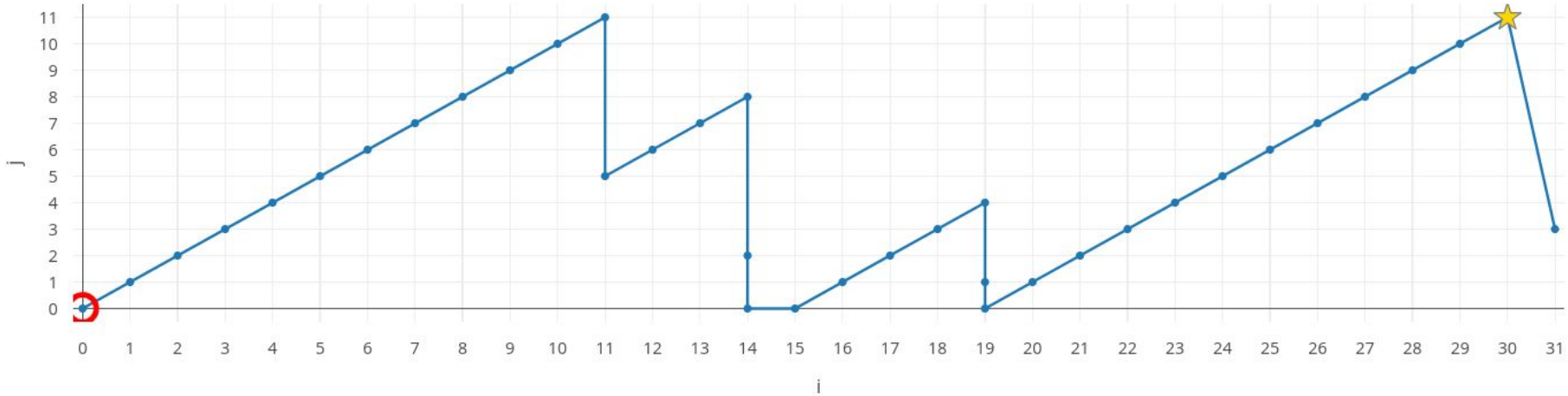
KMP Algorithm visualised

i:	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31
Text:	c	g	a	c	g	g	c	g	a	c	g	g	c	g	g	c	g	a	c	c	g	a	c	g	g	c	g	a	c	g	a	c
Pattern:	c	g	a	c	g	g	c	g	a	c	g	a																				

Previous Next

Show state table

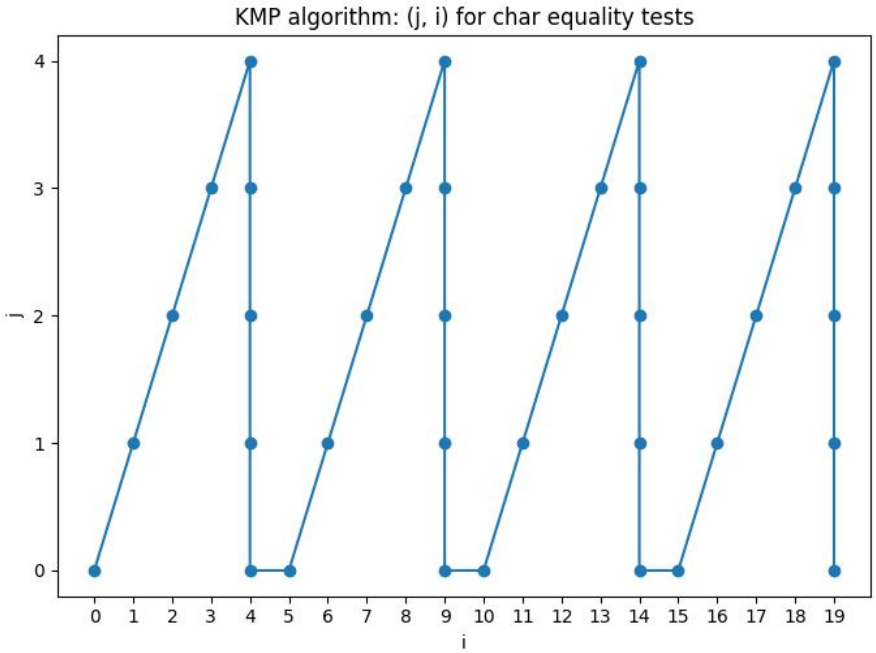
Comparison Trajectory

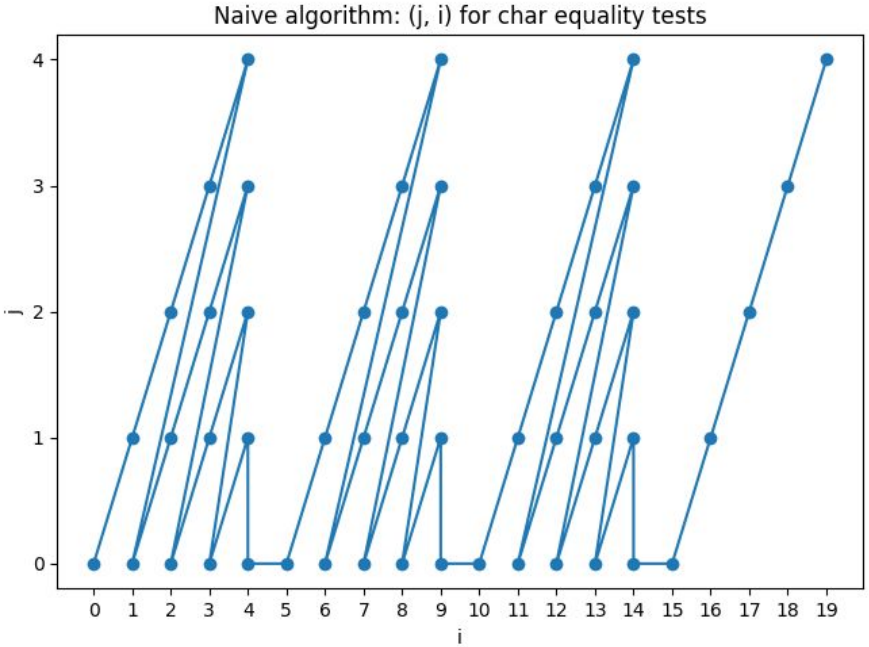


KMP: Another example (worst case)

XXXXOXXXXOXXXXOXXXXO

XXXXX





KMP Algorithm Complexity

- The previous examples show that comparisons form a "sawtooth" pattern. There are two cases:

  T[*i*] = P[*j*]. Here *i* and *j* are both incremented in the outer while loop.

  T[i] ≠ P[j]. Here the value of j is repeatedly reduced to b[j] in the inner loop, effectively moving the pattern towards the right. *i* does not change (until j = -1 when the inner loop terminates).

- Each "tooth" has at most as many points in the vertical bit as in the sloped bit, so at most 2*n* comparisons in total.
- Preprocessing requires $O(m)$ comparisons.
- The overall complexity of KMP algorithm is $O(m+n)$

Boyer-Moore Algorithm

- A very efficient string matching algorithm
- Often implemented in search and replace functions in text editors.
- Preprocesses the search string to derive information about its structure
- Compares the search pattern from **right to left** of the search string
- Uses two types of heuristics:
  - “Bad character” heuristics
  - “Good suffix” heuristics

Bad Character Heuristics

If a mismatch occurs for the **rightmost character** $P[m-1]$ of the search pattern, and if the corresponding character in the text does not appear in the pattern at all, then the whole pattern can be shifted by m positions.

```
agtacgtgctcaaccgagtatagccgagatacg
gccgaga
        gccgaga
```

Shift

Boyer-Moore Complexity (Best Case)

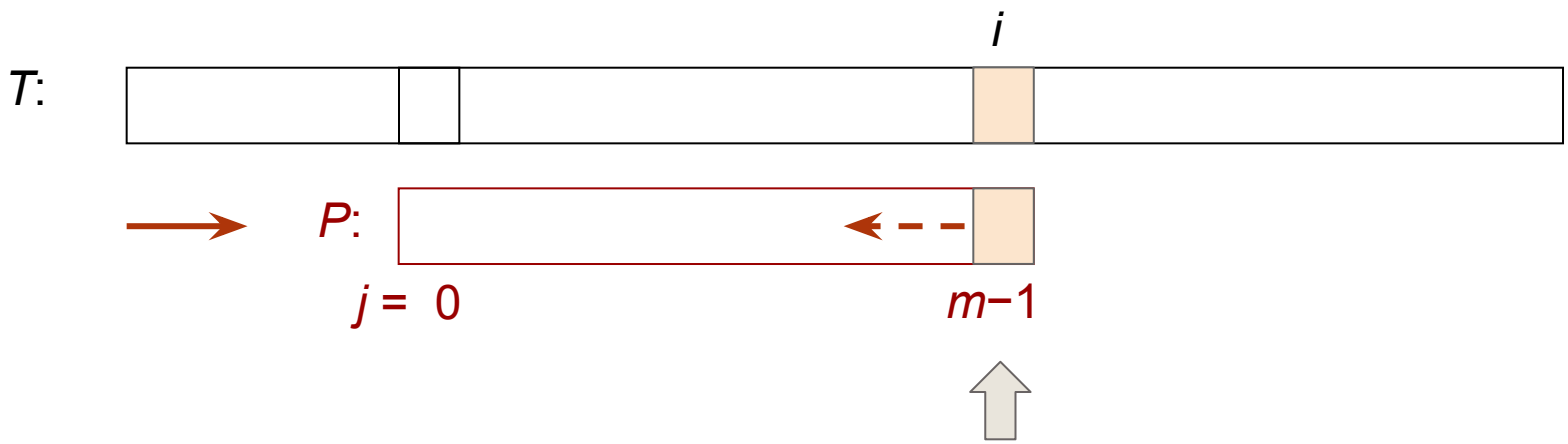
If the first compared text symbol does not occur in the pattern for each attempt, the number of comparisons would be of the order of $O(n/m)$ (Sub-linear complexity!)

Example:

```
aaaaaabaaaaaabaaaaaabaaaaaabbbbbbbbbb
aaaaaaa
        aaaaaaa
                aaaaaaa
```

Comparison of characters

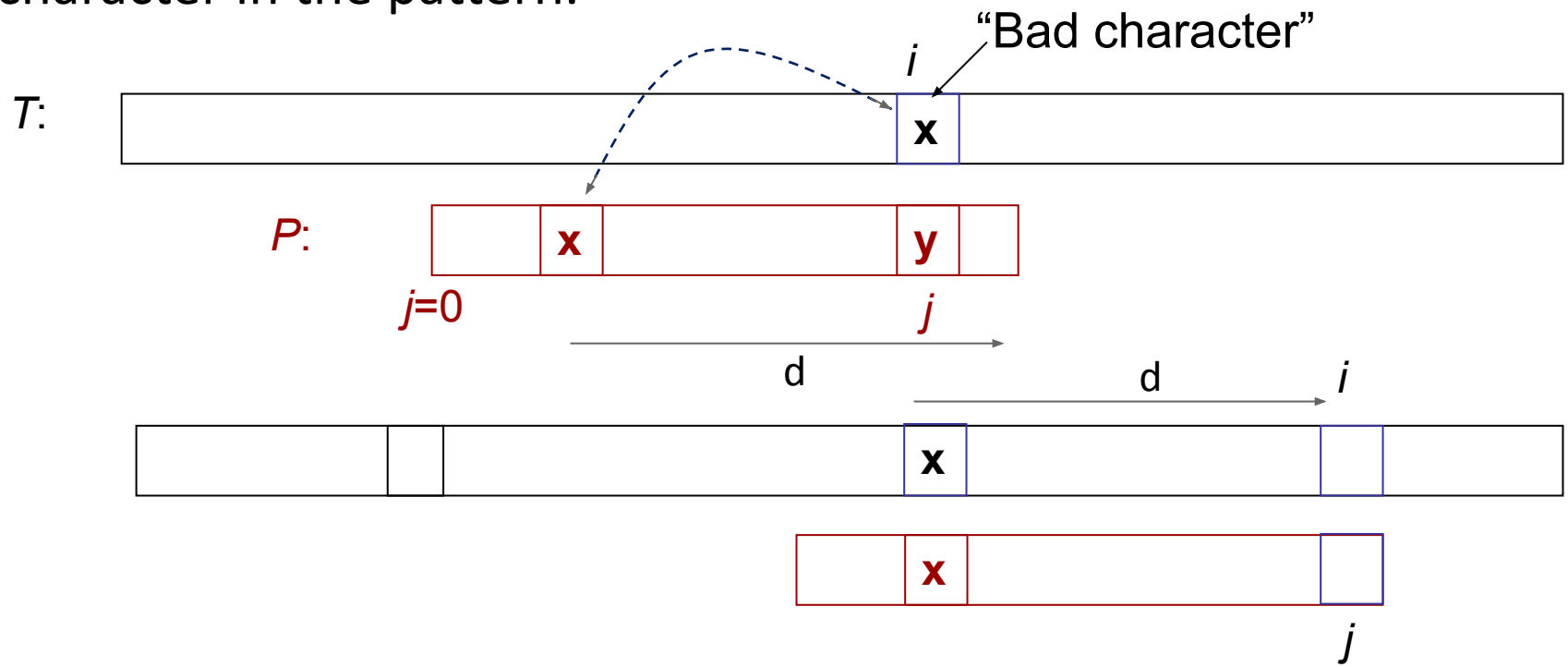
- In Boyer-Moore algorithm, we always start comparisons from the rightmost end of the pattern and work backwards.
- The pattern is always moved from left to right.



Start comparing here and move left

Bad Character Heuristics

If a text symbol that causes a mismatch at $P[j]$ is found somewhere in the pattern, then the pattern can be shifted so that the text symbol aligns with the rightmost occurrence of that character in the pattern.



Restart comparisons at $i = i + d$, $j = m - 1$ where d is the distance of 'x' from the end of the pattern.

Shift array *delta1* ('d' in previous slide)

We create an array "delta1[]" that contains the distance **from the end of the pattern** of the last (rightmost) occurrence of each character (*m*, if the character does not appear in the pattern).

Example: Pattern: gccgaga

m = 7

Symbol *s*	'a'	'c'	'g'	't'
delta1[*s*]	0	4	1	7

```
agtacgtgctcaaccgagtatagccgagatacg
        gccgaga
            gccgaga
             gccgaga
                 gccgaga
```

Shift distance = 4

Shift distance = 1

Shift distance = 7

Computation of "delta1" array

Code for computing the values of "delta1" array:

pat = "agccgcaga"

Symbol *s*	'a'	'c'	'g'	't'
delta1[*s*]	0	3	1	9

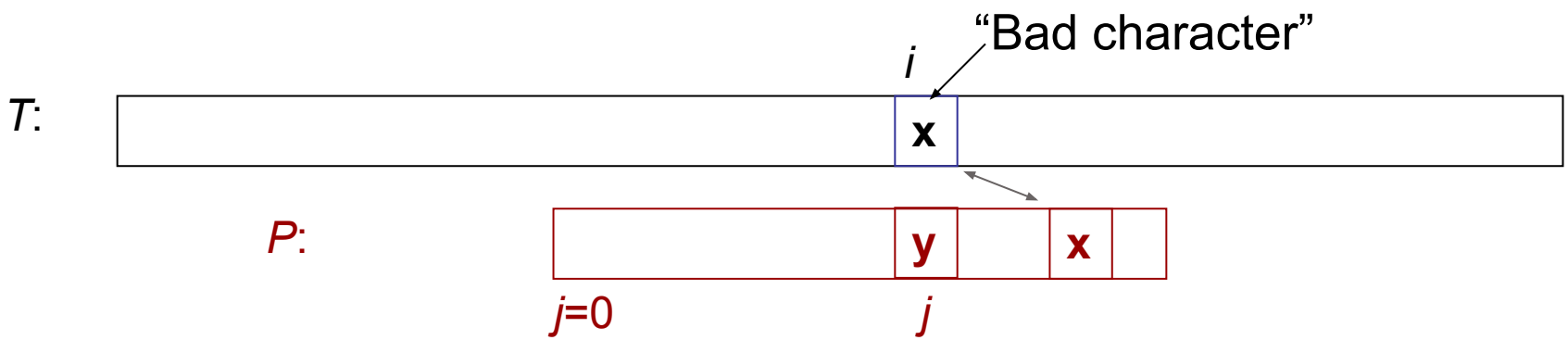
```
LEN_ALPHABET = 256  # Assume ASCII
def bad_char_shifts(pattern):
    m = len(pattern)
    delta1 = LEN_ALPHABET * [m]
    for i, c in enumerate(pattern):
        delta1[ord(c)] = m - i - 1
    return delta1
```

Complexity = $O(m + |\Sigma|)$

Size of alphabet (4 for a DNA sequence if encode *a, c, g, t* as 0, 1, 2, 3)

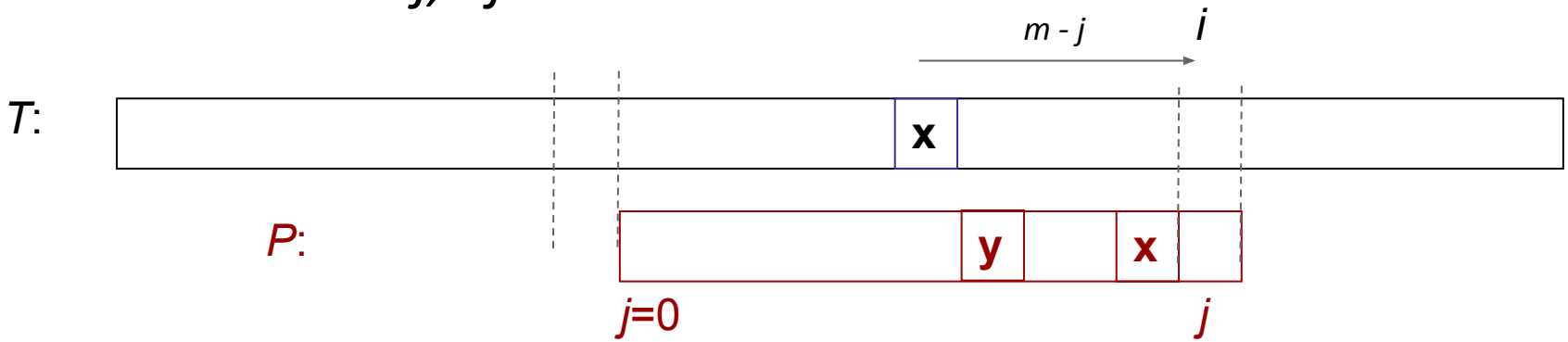
A complication

What if the character we want to match appears *after* P[j]?

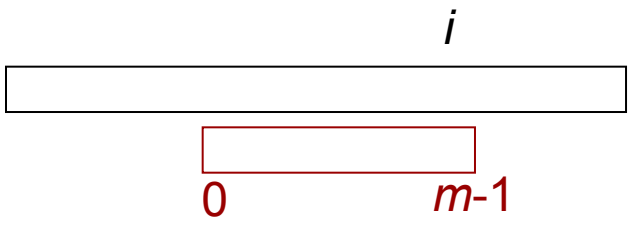


Mustn't slide pattern *back*. Instead just advance it by 1.

Restart at $i \mathrel{+}= m - j, \quad j = m - 1$



Simplified Boyer-Moore (Boyer-Moore-Horspool)



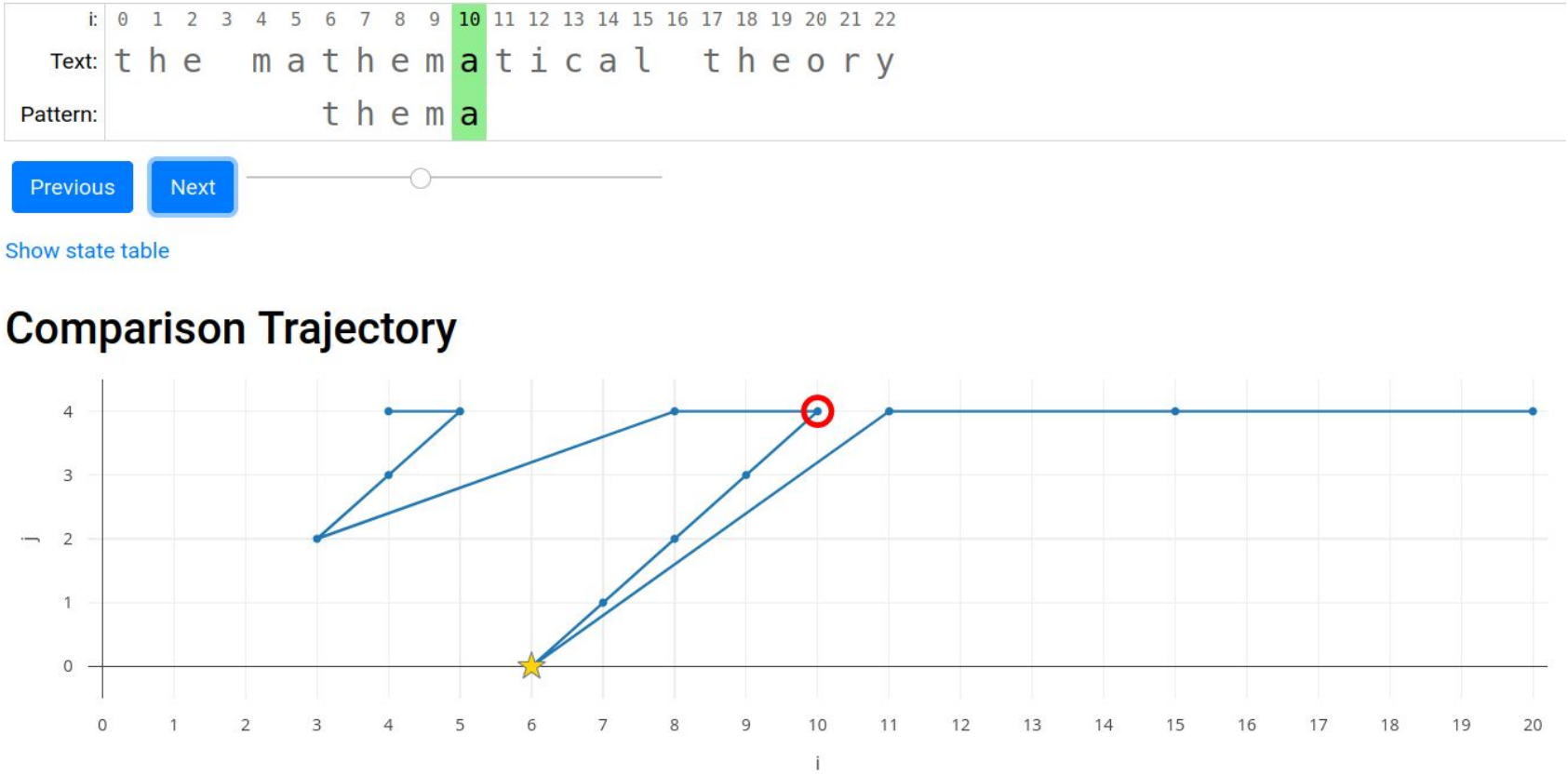

```
def main():
    delta1 = bad_char_shifts(pattern)
    m = len(pattern)
    i = m - 1
    while i < len(text):
        j = m - 1
                while  j  >=  0  and  pattern[j]  ==  text[i]:
            i -= 1
            j -= 1
        if j < 0:
            print (i)
            i += m + 1
        else:
            i += Math.max(m - j, delta1[ord(text[i])])
```

Deals with complication in last slide

delta1 is the increment in *i* **not** the shift

Simplified Boyer-Moore (Boyer-Moore-Horspool)

Watch it in action:
https://lobb.nz/stringmatchvisualiser/stringmatching.html



Simplified Boyer-Moore

- For most practical applications, the simplified version of the Boyer-Moore algorithm gives very good results.

- The worst-case running time of the simplified Boyer-Moore algorithm is still $O(nm)$

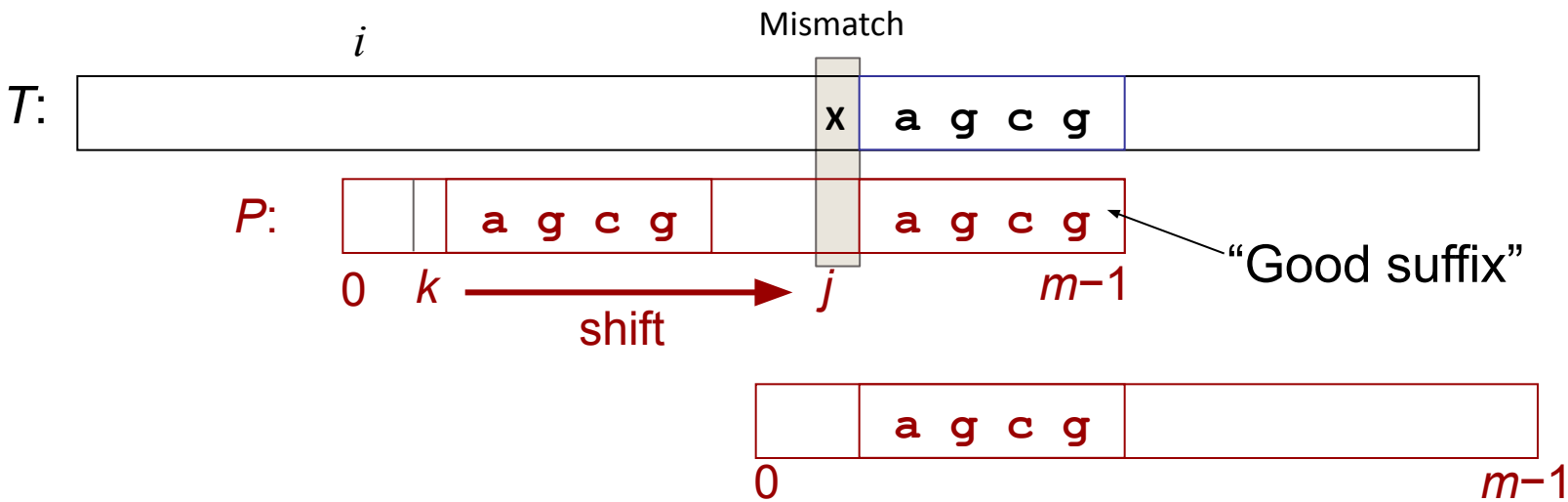
Example:

```
aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
baaaaaa
 baaaaaa
  baaaaaa
```

Good Suffix Heuristic

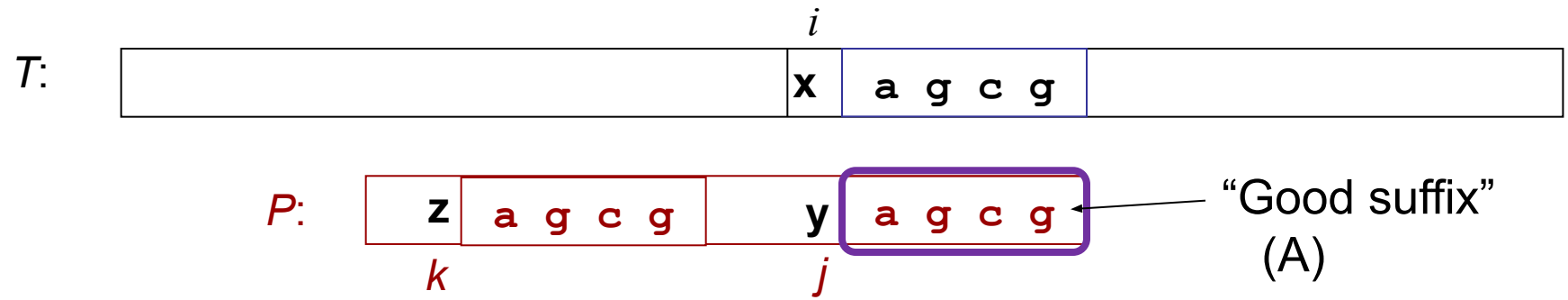
Assume that at the current position, a suffix of *P* ("good suffix") matches with the corresponding characters in *T*.

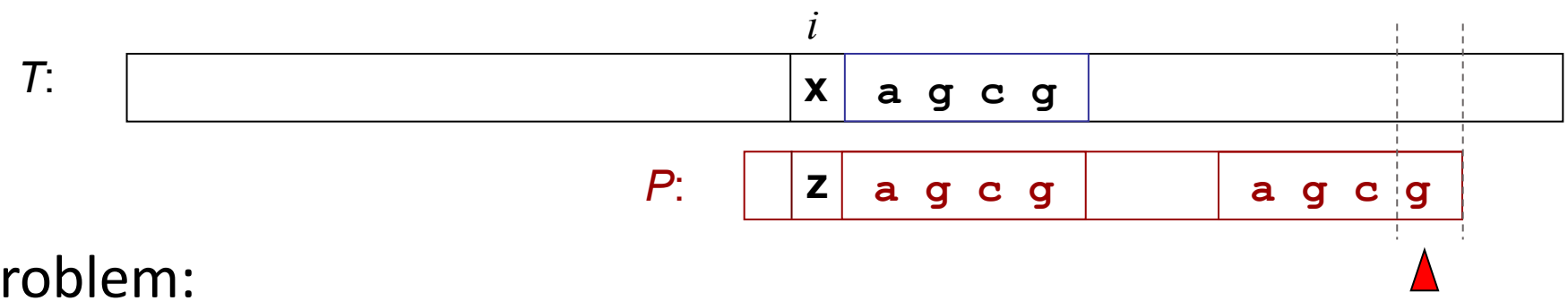
- If x is in this suffix (e.g. x == 'c'), we cannot use delta1[x] to shift the pattern. Simplified Boyer-Moore uses a shift distance = 1.
- BUT if the matching suffix appears elsewhere within the pattern, then we may be able to shift the pattern by a distance > 1.



<u>Note:</u> P[k] must be different from P[*j*], or shifting the pattern will cause another mismatch.

Good Suffix Heuristic



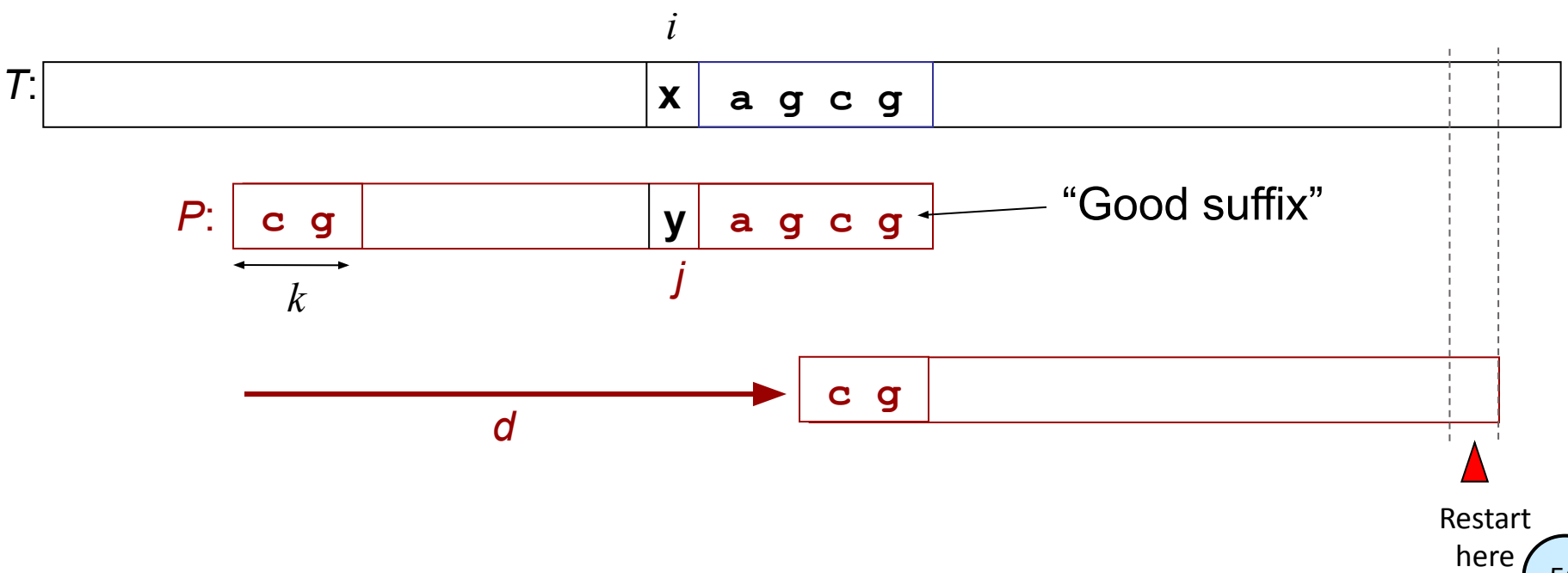


Problem:

- Does the suffix A exist earlier in the pattern (before *j*)?
- If so, and if P[*k*] ≠ P[*j*], then shift distance = *j* − *k*
  - If there are multiple such occurrences, choose the last one

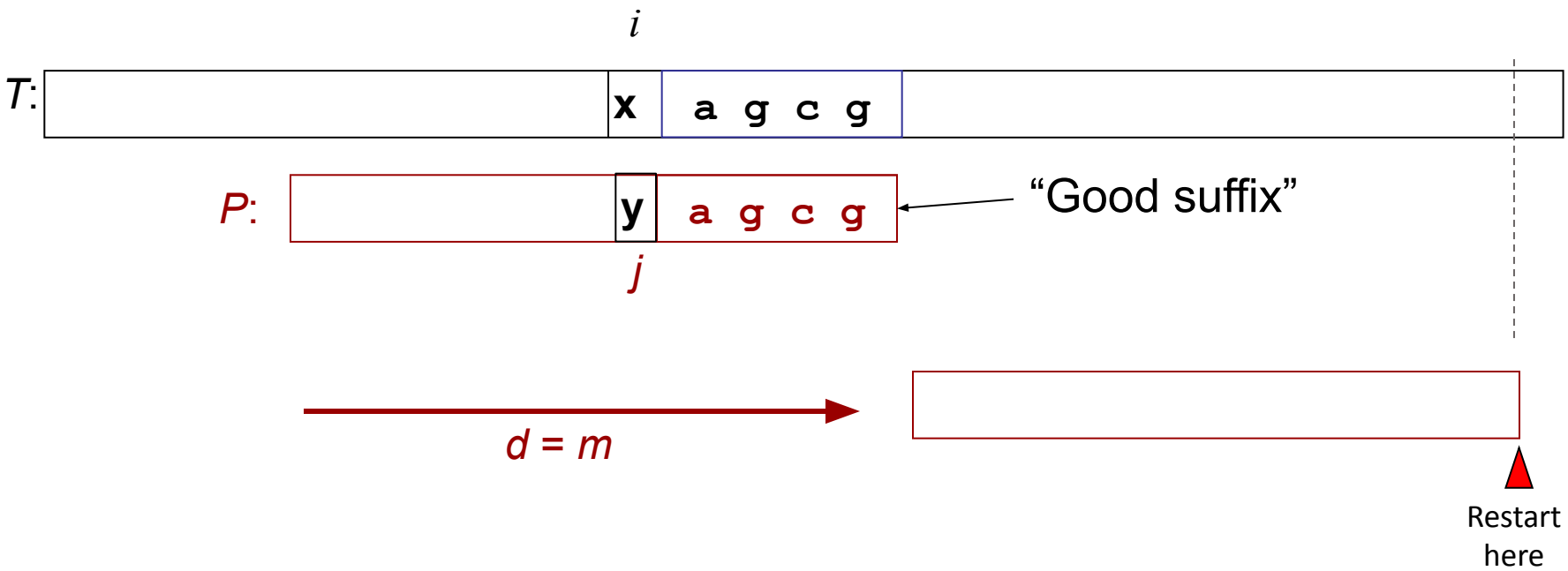
Good Suffix Heuristic

If only a part of the good suffix appears at the beginning of the pattern (the pattern has a border of length k), we can shift the pattern by a distance $d = m - k$

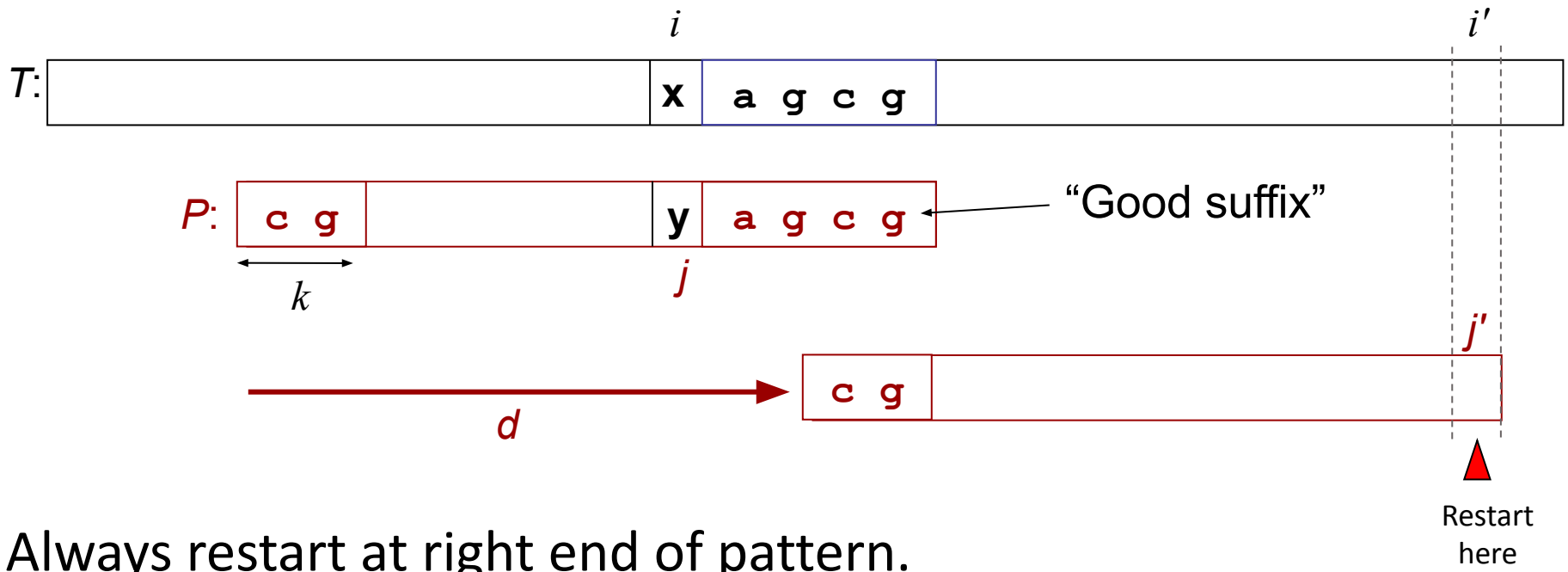


Good Suffix Heuristic

If the good suffix does not appear anywhere else in the pattern and if the pattern does not have a border, then the pattern can be shifted through its entire length ($d = m$)



Updating i and j on a pattern shift



Always restart at right end of pattern.

$j' = m - 1$

Old pattern shift = $i - j$

New pattern shift = $i' - j'$ = old pattern shift + d = $i - j + d$

Hence $\Delta i = i' - i = \boxed{m - 1 - j + d}$ ⇦ Call this *delta2[j]*

Good Suffix Heuristic: Example

delta2[*j*] gives the update to *i* when a bad character is found at position *j*: $\Delta i = i' - i = m - 1 - j + d$, where *d* is the pattern shift.

Good suffix = P[*j*+1:]

Example: *m* =12

j	0	1	2	3	4	5	6	7	8	9	10	11
pat[j]	g	a	t	c	a	c	a	c	a	t	c	a
d	12	12	12	12	12	12	12	7	12	3	10	1
delta2[*j*]	23	22	21	20	19	18	17	11	15	5	11	1

Good suffix: 'ca' , *d* = 3

We won't bother with the code to compute these shifts.

Earlier occurrence of tca is preceded by 'a' so not useful. See note slide 54.

Full Boyer-Moore Algorithm

```
delta1  = bad_char_shifts(pattern)
delta2 = good_suffix_shifts(pattern) # Not in course

m = len(pattern)
i = m - 1
while i < len(text):
    j = m - 1
    while j >= 0 and pattern[j] == text[i]:
        i -= 1
        j -= 1
    if j < 0:
        print(i)
        i += m + 1
    else:
        i += max(delta2[j], delta1[ord(text[i])])
```

Compare with simplified B-M code

Full Boyer-Moore

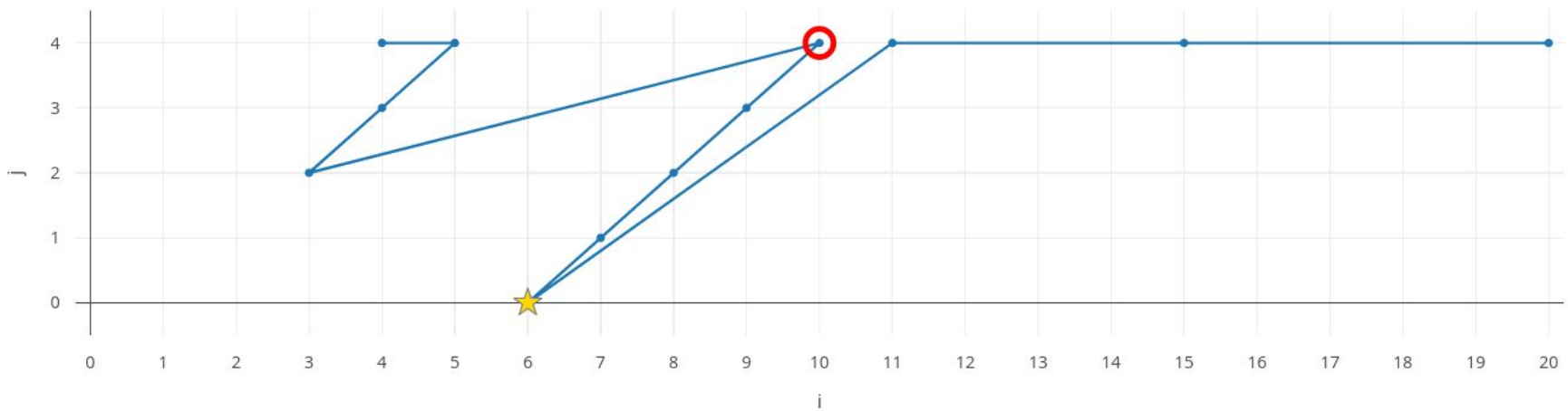
Watch it in action:
https://lobb.nz/stringmatchvisualiser/stringmatching.html

i:	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22
Text:	t	h	e		m	a	t	h	e	m	a	t	i	c	a	l		t	h	e	o	r	y
Pattern:							t	h	e	m	a												

Previous Next

Show state table

Comparison Trajectory



Compare with Simplified Boyer-Moore trajectory. Explain the difference!

Full Boyer-Moore Complexity

- Worst-case time complexity of the full Boyer-Moore algorithm is $O(n+m)$ unless there are lots of hits.
  - Can then be O(nm), e.g. find pattern *aaaaaa* in a string of one thousand *a*'s
- Boyer-Moore is an efficient algorithm for searching natural language text, particularly with large patterns.

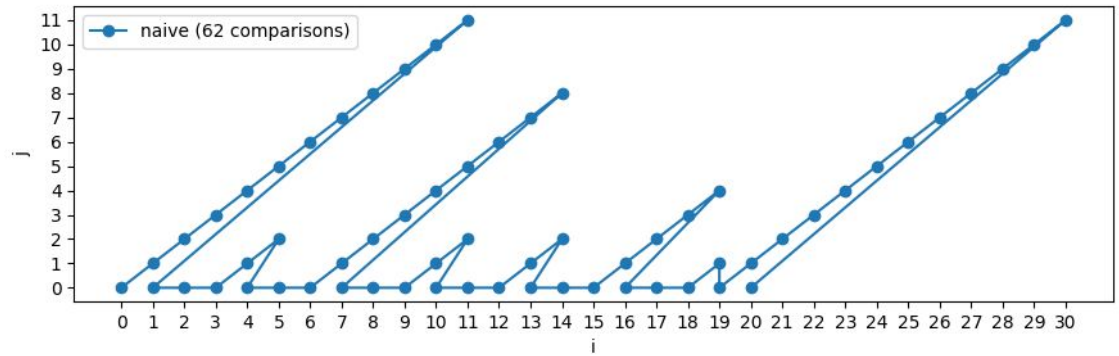
	Best Case	Worst Case
Naïve	$O(n)$	$O(nm)$
KMP	$O(n+m)$	$O(n+m)$
BM	$O(n/m)$	$O(nm)$

Further refinements are possible to B-M to achieve O(n + m) in worst case, namely when there are lots of hits. See Wikipedia (Galil rule).

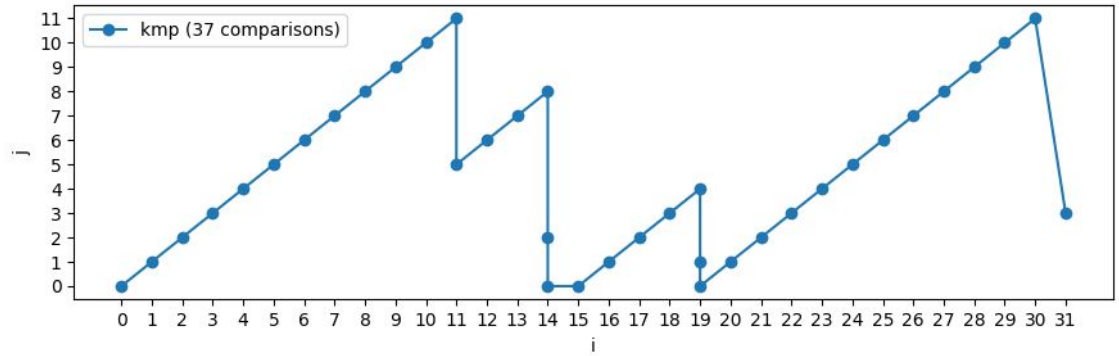
Comparison on DNA example

search("cgacggcgacga", "cgacggcgacggcggcgaccgacggcgacgac")

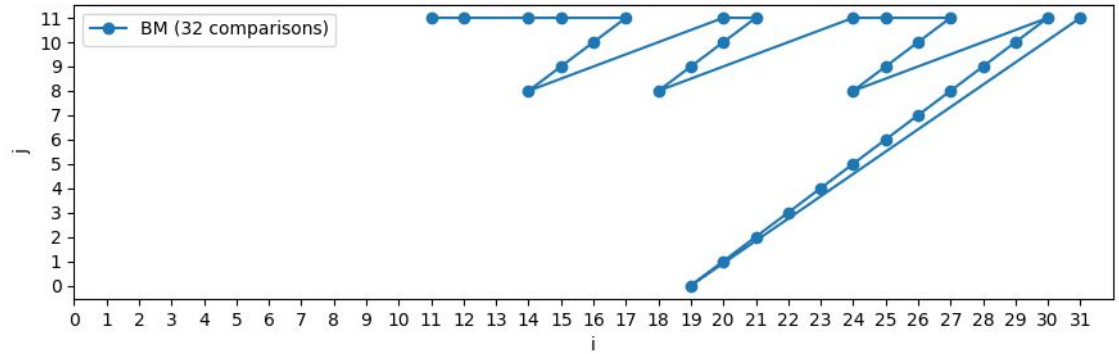
Naive: 62 comparisons



KMP: 37 comparisons



Boyer-Moore: 32 comparisons



Summary

- Naive algorithm is fine for short patterns
- Rabin-Karp is best for searching a large text for a large number of different patterns.
- Boyer-Moore is the best algorithm with large patterns and large texts
  - Boyer-Moore-Horspool is relatively easy to program and gives most of the benefits
  - The full algorithm is difficult and tables are large, especially with a large alphabet
- KMP has best worst case performance; no restriction on alphabet size.
  - And easier to understand and program.