

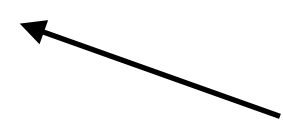

# Exact pattern matching & string search

# Why Exact Matching?

As *loose* motivation, consider the problem of mapping a read  $r$  to the genome  $G$ .

In reality, we would not use exact matching for this; why?

However, exact matching is useful here:

- Find all places where a substring of the query matches the reference exactly (seeds)  Requires efficient exact search
- Filter out regions with insufficient exact matches to warrant further investigation
- Perform a “constrained” alignment that includes these exact matching “seeds”  Here is where we use efficient algorithms for inexact matching (alignment)

# Exact String Matching Problem

Today, we'll talk about exact matching algorithms that are **quadratic** (no better than alignment!) and **linear**. Then we'll start talking about ***much*** faster approaches, but they require pre-processing the reference.

# Exact String Matching Problem

**Given:** A string **T** (called the *text*) and a string **P** (called the *pattern*).

**Find:** All occurrences of **P** in **T**.

$$|\mathbf{T}| > |\mathbf{P}|$$

An *occurrence* of **P** in **T** is a substring of **T** equal to **P**

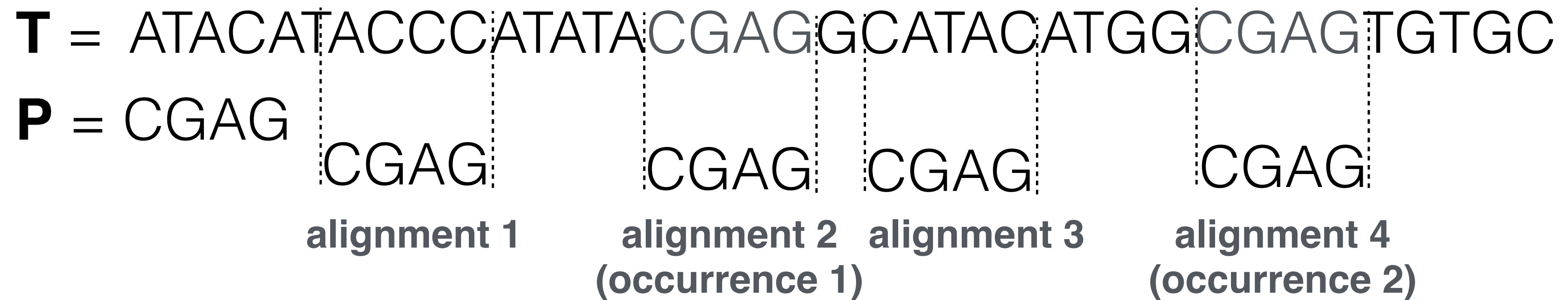
**T** = ATACATACCCATATACGAGGCATACATGGCGAGTGTGC  
**P** = CGAG

CGAG CGAG

# Occurrences vs. Alignments

An *alignment* of **P** to **T** is a correspondence (not necessarily an occurrence) between a substring of **T** and **P**

*all occurrences are alignments but not all alignments are occurrences*



# Occurrences vs. Alignments

How many possible *alignments* of **P** are there in **T**?

**T** = ATACATACCCATATACGAGGCATACATGGCGAGTGTGC

**P** = CGAG

CGAG

CGAG

CGAG

CGAG

⋮

# Occurrences vs. Alignments

How many possible *alignments* of **P** are there in **T**?

**T** = ATACATACCCATATACGAGGCATACATGGCGAGTGTGC

**P** = CGAG

CGAG

CGAG

CGAG

CGAG

⋮

$$|\mathbf{T}| - |\mathbf{P}| + 1$$

# A naive algorithm

What is the simplest algorithm you can think of to solve the exact string matching problem?

Seriously, I'm not going to change the slide until somebody suggests something really naive!



# A naive algorithm

Naive algorithm 1: Consider all alignments of **P** to **T**, and report each alignment that is an occurrence.

```
def naive(T, P):  
    N = len(T)  
    M = len(P)  
    occs = []  
    for i in range(N - M + 1):  
        if P == T[i:i+M]:  
            occs.append(i)  
    return occs
```

# A naive algorithm

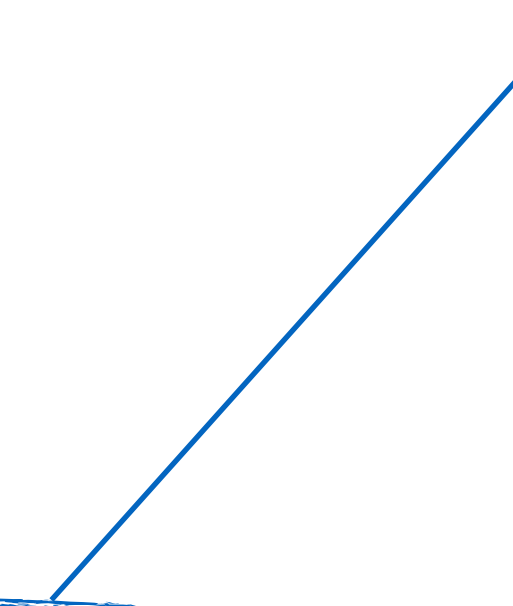
```
def naive(T, P):  
    N = len(T)  
    M = len(P)  
    occs = []  
    for i in xrange(N - M + 1):  
        if P == T[i:i+M]:  
            occs.append(i)  
    return occs
```

**Worst-case Runtime?**

# A naive algorithm

```
def naive(T, P):  
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    occs = []  
    for i in range(N - M + 1):  
        if P == T[i:i+M]:  
            occs.append(i)  
    return occs
```

$O(N)$



$O(M)$



— note,  
a “naive” implementation of  
this takes  $M$  time while a  
reasonable version quits at  
the first mismatching  
character

$$O(N) * O(M) = O(NM) \text{ time}$$

# A naive algorithm

Best scenario for naive:

**T:** GAGAGGAGTTATATATGAATAGAGATAGAGACGAG

**P:** CGAG

Because every alignment but the last disagrees  
on the very first character, the inner loop takes  $O(1)$  time,  
except for the single match which takes  $O(M)$  time  
 $O(N+M)$

# A naive algorithm

Worst scenario for naive:

**T:** CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC

**P:** C C C C G

Because every alignment is a match for **P**, the inner loop requires M char. compares each time  $O(NM)$

# A naive algorithm

There's a **big** gap between

The best case time for naive  $O(N+M)$  and

The worst case time for naive  $O(NM)$

How can we improve the worst case time?

Can we devise a method that is  $O(N+M)$  even in the worst case?

# Z boxes and the Z algorithm

**T:** ATACGGGCACATACCATACGAATATACAAA

**Def:** Let  $Z_i$  be the length of the *longest* substring *starting at*  $i$  that matches a prefix of  $T$ .

# Z boxes and the Z algorithm

**T:** ATACGGGCACATACCATACGAATATACAAA  
**Z<sub>T</sub>:** -10100001040100501001304010111

**Def:** Let  $Z_i$  be the length of the longest substring *starting at*  $i$  that matches a prefix of  $T$ .



# Z boxes and the Z algorithm

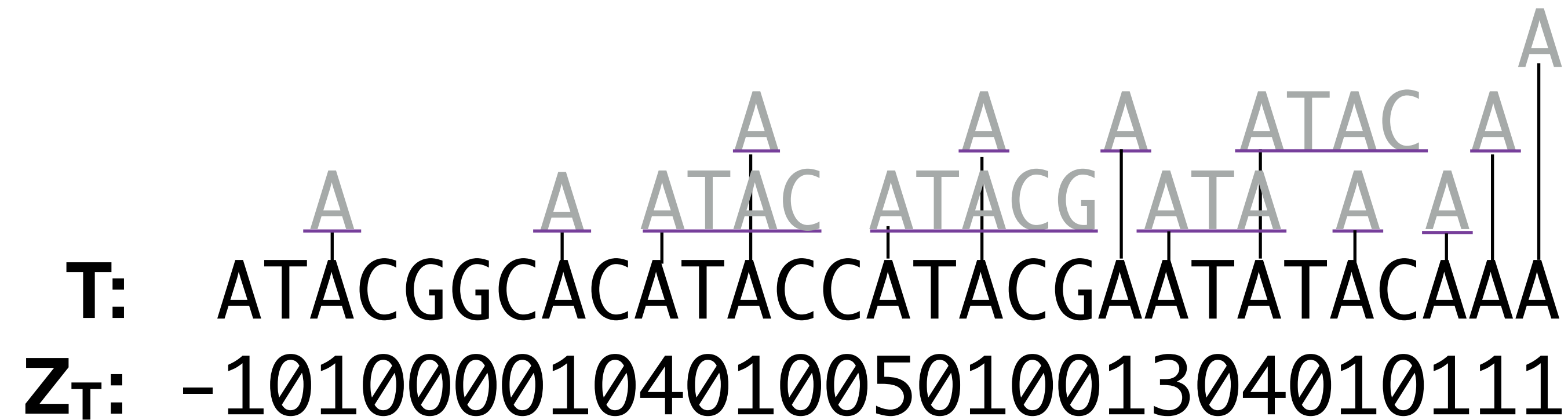
**T:** ATACGGGCACATACCATACGAATATACAAA

**Z<sub>T</sub>:** -1 0 1 0 0 0 0 1 0 4 0 1 0 0 5 0 1 0 0 1 3 0 4 0 1 0 1 1 1

**Def:** Let  $Z_i$  be the length of the longest substring *starting at*  $i$  that matches a prefix of  $T$ .

Naïvely, there is an  $O(?)$  algorithm to compute the  $z$  values

# Z boxes and the Z algorithm



**T:** ATACGGCACATACCATACGAATATACAAA  
**Z<sub>T</sub>:** -1 0 1 0 0 0 1 0 4 0 1 0 0 5 0 1 0 0 1 3 0 4 0 1 0 1 1 1

**Def:** Let  $Z_i$  be the length of the longest substring *starting at i* that matches a prefix of T.

Naïvely, there is an  $O(T^2)$  algorithm to compute the z values

Ignore this complexity for a second; **how could we use z values to solve exact pattern matching?**

# Z boxes and the Z algorithm

**P:** ACA

**T:** ATACGGCACATACCATACGAATATACAAA

**Def:** Let  $Z_i$  be the length of the longest substring *starting at*  $i$  in  $T$  that matches a prefix of  $P$ .

Ignore this complexity for a second; **how could we use z values to solve exact pattern matching?**

# Z boxes and the Z algorithm

**P\$T:** ACA\$ ATACGGCACATACCATACGAATATACAAA

**Def:** Let  $Z_i$  be the length of the longest substring *starting at*  $i$  in  $T$  that matches a **prefix of  $P$** .

Now, any  $Z_i$  value =  $|P|$  designates that an occurrence of  $P$  exists at position  $i$  in  $T$ .

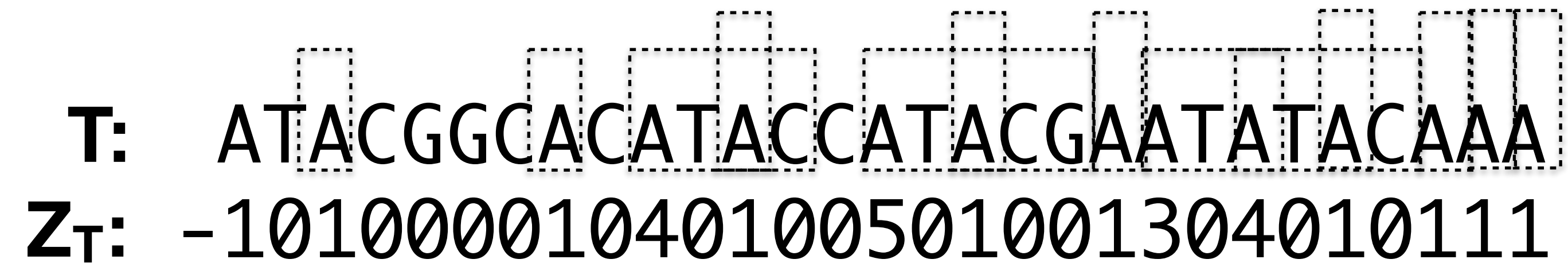
Note:  $\$ \notin \Sigma$  ensures that  $Z_i$  is always  $\leq |P|$

# Z boxes and the Z algorithm

**P\$T:** ACA\$ ATACGGCACATACCATACGAATATACAAA

Now that the longest possible  $Z_i$  is  $\leq |P|$  then we are back to an  $O(|T| |P|)$  algorithm ... back to the problem at hand; how do we make this better?

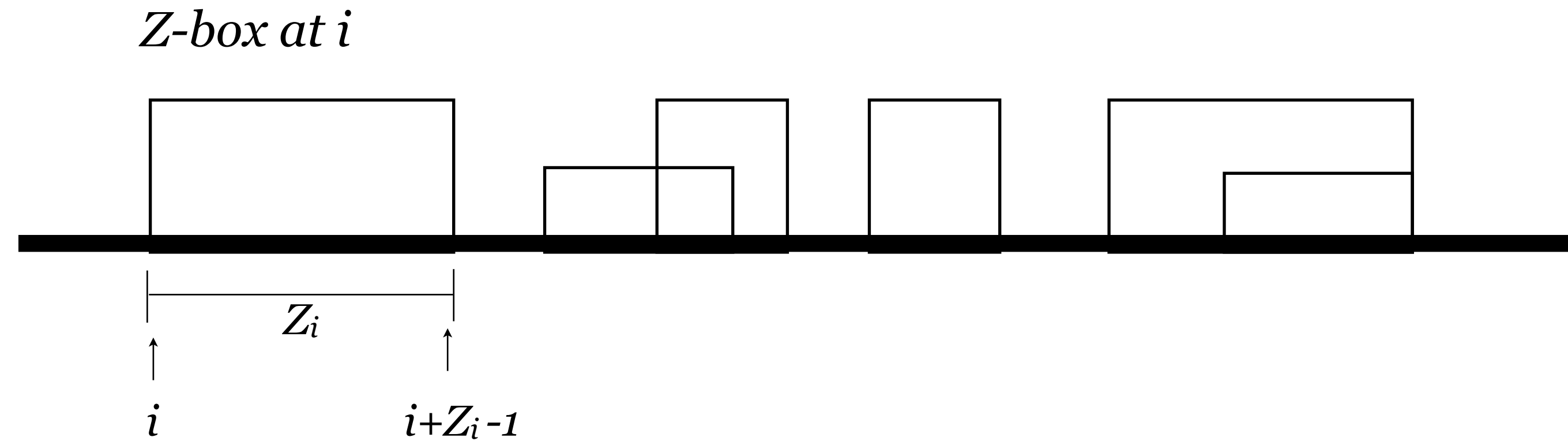
# Z boxes (boxen?)



**T:** ATACGGCACATACCATACGAATATACAAA  
**Z<sub>T</sub>:** -10100001040100501001304010111

Imagine a “box” (possibly of length 0) starting at every position. The left-most end of the box is where the match with the prefix begins, and each box extends  $Z_i$  characters to the right (to position  $i + Z_i - 1$ ).

# Z Boxes



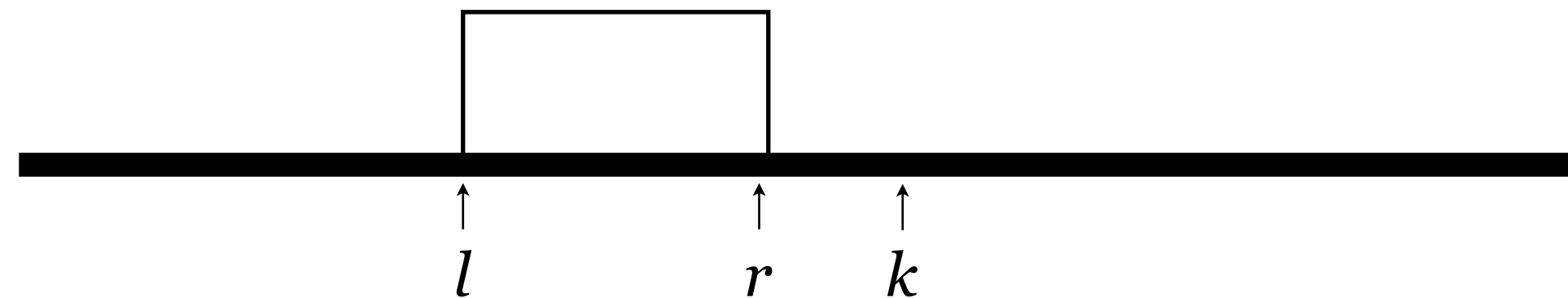
**Def.** *Z-box at  $i$*  is the substring starting at  $i$  and continuing to  $i+Z_i-1$ . This is the substring that matches the prefix. There is no Z-box at  $i$  if  $Z_i = 0$ .

- Algorithm for computing  $Z_i$  will iteratively compute  $Z_k$  given:
  - $Z_2 \dots Z_{k-1}$ , and
  - the boundaries  $l, r$  of the rightmost Z-box found starting someplace in  $2 \dots k-1$ .
  - you don't need  $l$  to understand how the algorithm works, but it is required to efficiently compute the necessary quantities

# Z Algorithm

- Input:  $Z_2 \dots Z_{k-1}$ , and the boundaries  $l, r$  of the rightmost Z-box found starting someplace in  $2 \dots k-1$ .
- Output:  $Z_k$ , and updated  $l, r$

1. If  $k > r$ , explicitly compute  $Z_k$  by comparing with prefix.  
If  $Z_k > 0$ :  $l = k$  and  $r = k + Z_k - 1$  (since this is a new farther right Z-box).



The current index is *beyond* the bound of the rightmost z-box.

The structure of the rightmost z-box can not tell us what to expect for  $Z_k$

Compute  $Z_k$  by explicit comparison and update  $l, r$  if  $Z_k > 0$



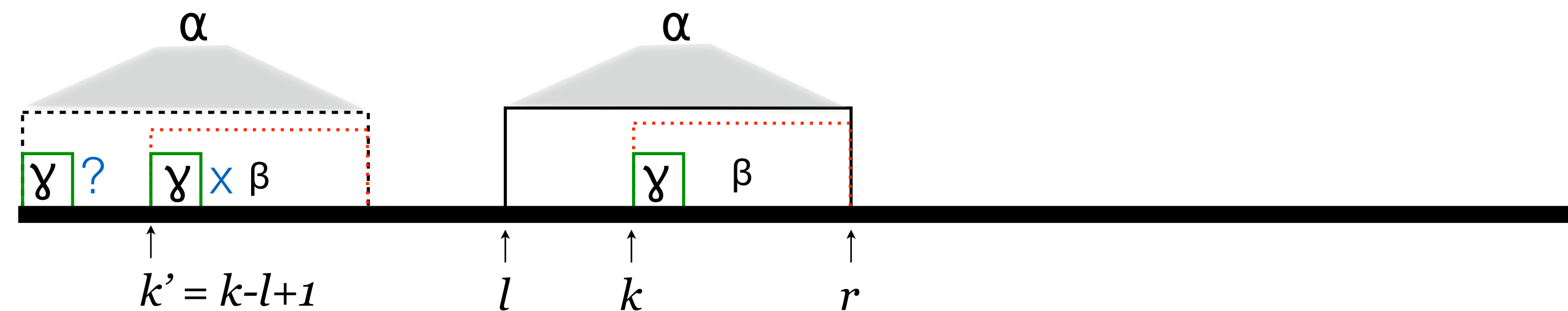
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If  $k \leq r$ , this is the situation:

Case 2a :  $Z_{k'} < |\beta|$ :

$Z_{k'} < |\beta|$  : Then the  $\gamma$  that is a prefix of  $\beta$  is also a prefix of  $\alpha$ , **but** the character occurring after the  $\gamma$  starting at  $k'$  is *not* the same as the character after the  $\gamma$  starting at the beginning of the string ... why?



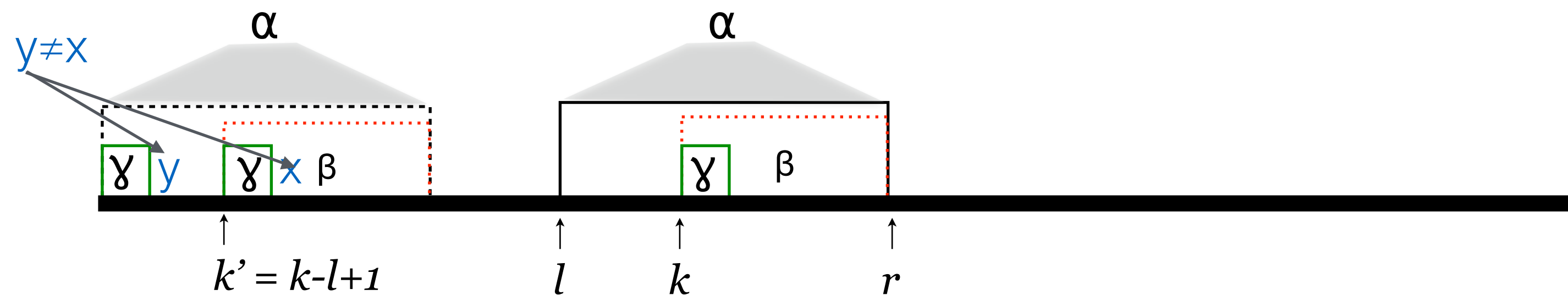
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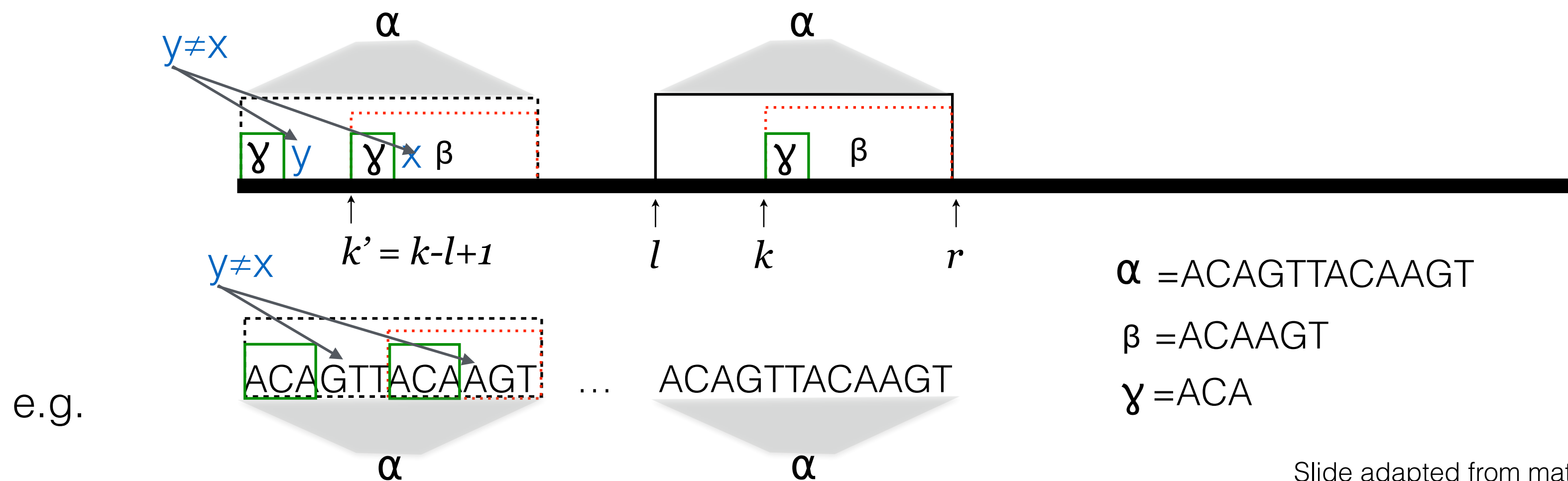
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# Z Algorithm

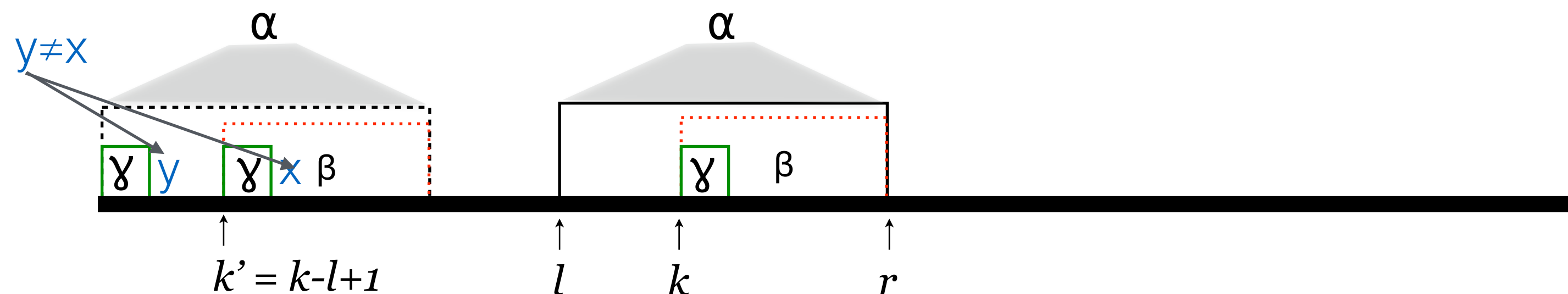
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If  $k \leq r$ , this is the situation:

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$Z_{k'} < |\beta|$ : Then the  $y$  that is a prefix of  $\beta$  is also a prefix of  $\alpha$ , **but** the character occurring after the  $y$  starting at  $k'$  is *not* the same as the character after the  $y$  starting at the beginning of the string ... **why?**

If  $x = y$ , then  $Z_{k'} > |y|$ , because the shared prefix starting at  $k'$  and 0 would had to have been longer.



# Z Algorithm

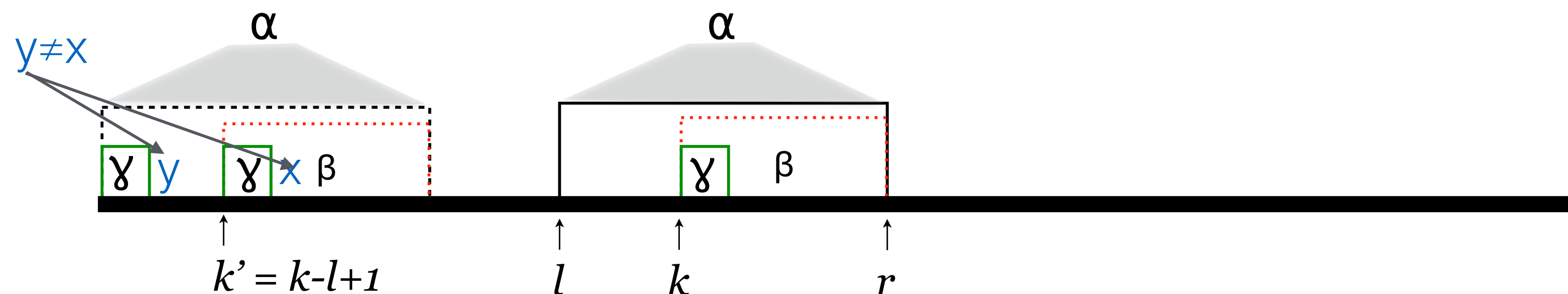
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If  $x = y$ , then  $Z_{k'} > |y|$ , because the shared prefix starting at  $k'$  and 0 would had to have been longer. But  $\beta = \beta$ , so  $Z_k = Z_{k'}$



In this case, set  $Z_k = Z_{k'}$  and leave  $l, r$  unchanged.

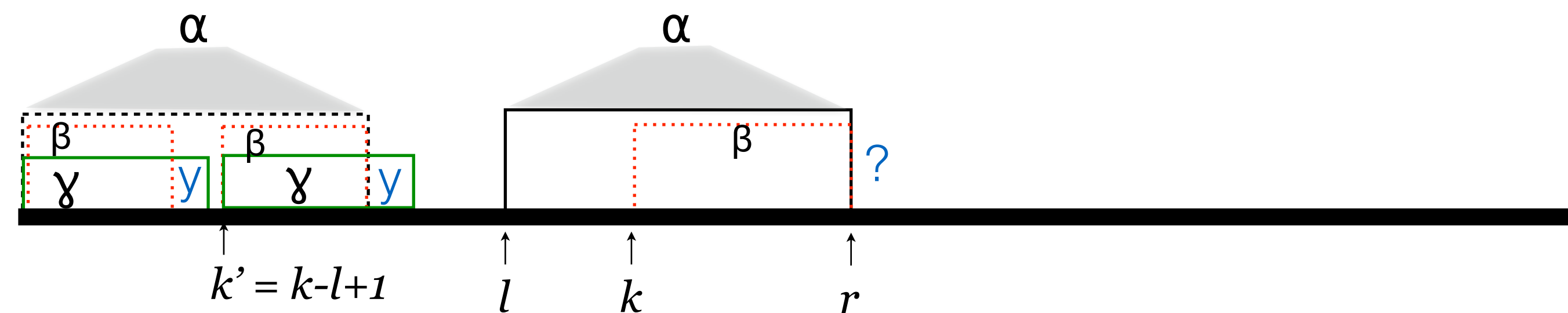
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- Input:  $Z_2 \dots Z_{k-1}$ , and the boundaries  $l, r$  of the rightmost Z-box found starting someplace in  $2 \dots k-1$ .
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If  $k \leq r$ , this is the situation:

Case 2b :  $Z_{k'} > |\beta|$ :

$Z_{k'} > |\beta|$ : Then the  $\gamma$  that starts at  $k'$  matches the  $\gamma$  that starts at the beginning of  $T$ , **but**, it cannot (completely) match the substring starting at  $k \dots$  why?



# Z Algorithm

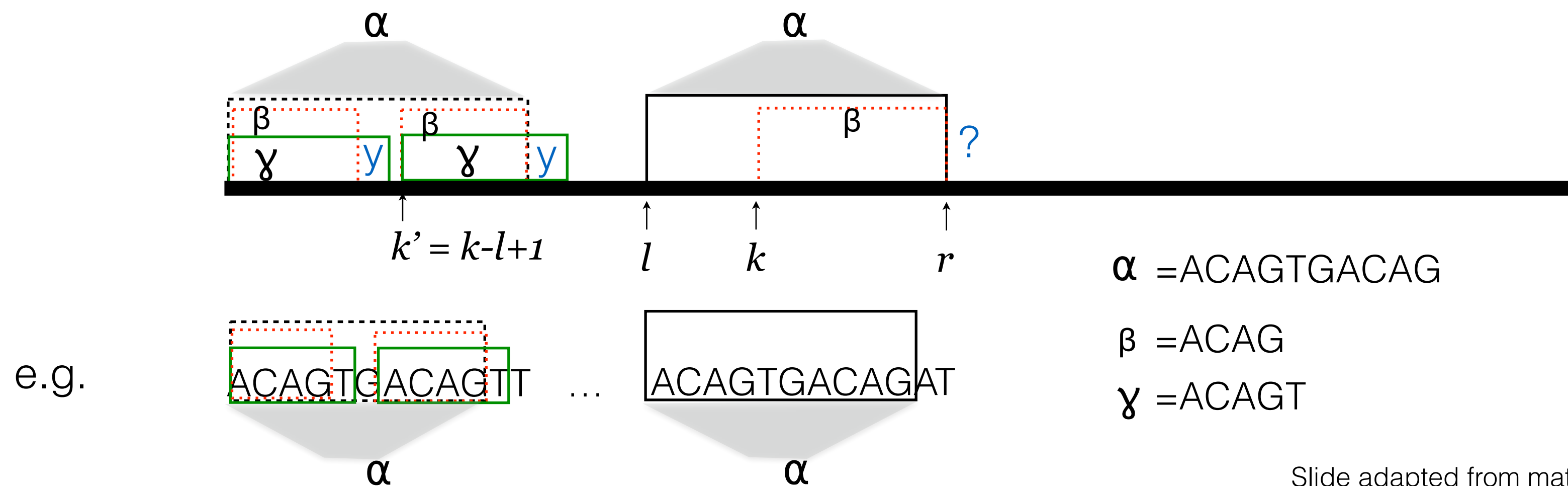
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If  $k \leq r$ , this is the situation:

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*Note: Here, we are not necessarily saying that the “Z-box” starting at 0 (ill-defined anyway) is of length  $|\alpha|$ ; Rather  $\alpha$  is defined by  $Z_l$*



# Z Algorithm

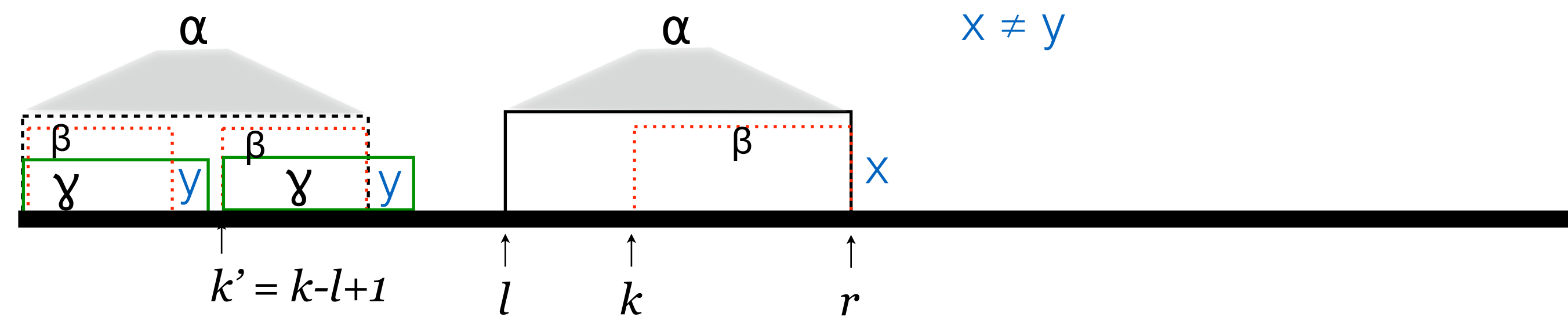
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If it did, then the z-box starting at position  $l$ , would be longer (extend past  $r$ ), contradicting the fact that  $Z_l$  is the *longest* substring starting at  $l$  that matches a prefix of  $T$ .



Set  $Z_k = |\beta|$  and leave  $l, r$  unchanged.



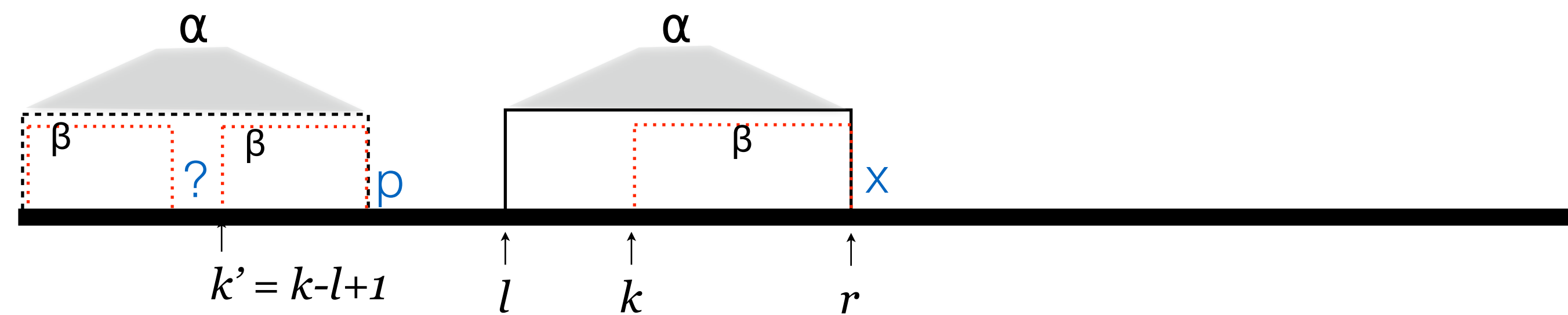
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- Output:  $Z_k$ , and updated  $l, r$

If  $k \leq r$ , this is the situation:

Case 2c :  $Z_{k'} = |\beta|$ :

$Z_{k'} = |\beta|$ : Then the character following the z-box of  $Z_{k'}$ , cannot be the same as the character following the length  $\beta$  prefix of the string ... why?



# Z Algorithm

- Input:  $Z_2 \dots Z_{k-1}$ , and the boundaries  $l, r$  of the rightmost Z-box found starting someplace in  $2 \dots k-1$ .
- Output:  $Z_k$ , and updated  $l, r$

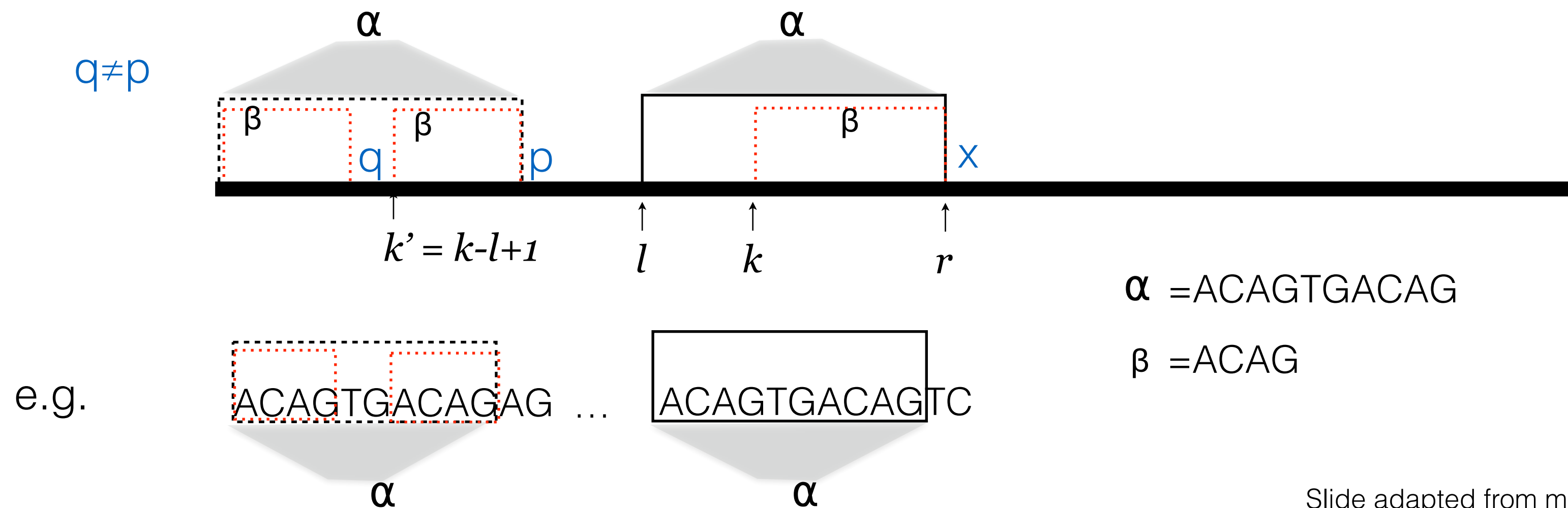
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If  $q = p$ , then  $Z_{k'}$  would have length  $> |\beta|$

What do we know about  $x \dots x \neq p$ . Is  $x = q$ ?



# Z Algorithm

- Input:  $Z_2 \dots Z_{k-1}$ , and the boundaries  $l, r$  of the rightmost Z-box found starting someplace in  $2 \dots k-1$ .
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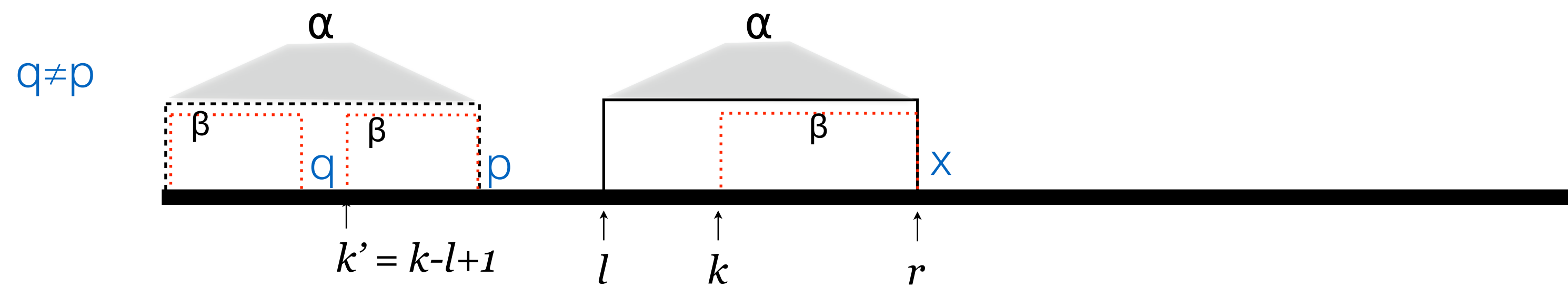
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If  $q = p$ , then  $Z_{k'}$  would have length  $> |\beta|$

What do we know about  $x \dots x \neq p$ . Is  $x = q$ ? We don't know! Must check.



Explicitly compare after  $r$  to set  $Z_k$ .  $l = k$ ,  $r =$  point where comparison failed

# Analysis

- Correctness follows by induction and the arguments we made in the description of the algorithm.
  - If you follow all of the sub-cases, the correctness of z-alg is implied
- Runs in  $O(|P| + |T|)$  time:
  - only match characters covered by a Z-box once, so there are  $O(|P| + |T|)$  matches.
  - every iteration contains at most one mismatch, so there are  $O(|P| + |T|)$  mismatches.
- Immediately gives an  $O(|P| + |T|)$ -time algorithm for string matching as described a few slides ago.
  - $O(|P| + |T|)$  is the best possible worst-case running time, since you might have to look at the whole input.
  - But better algorithms exist in practice that, for real instances, have expected sublinear runtime.

# Summary

The pattern matching problem seeks to find all occurrences of a pattern  $P$  in a text  $T$

The naive algorithm for the problem takes  $O(MN)$  time

By exploiting structure in the *pattern*, we reduce the worst case runtime to  $O(M+N)$

# Example

AGACTT\$ACACGAGACATTATAGAGACTTAGATTAGGC

A	G	A	C	T	T	\$	A	C	A	C	G	A	G	A	C	A	T	T	A	T	A	G	A	G	A	C	T	T	A	G	A	T	T	A	G	G	C
[38,	0,	1,	0,	0,	0,	0,	1,	0,	1,	0,	0,	4,	0,	1,	0,	1,	0,	0,	1,	0,	3,	0,	6,	0,	1,	0,	0,	0,	3,	0,	1,	0,	0,	2,	0,	0,	0]

The Z-algorithm was *not* the first linear time exact pattern matching algorithm, but, in a sense, unifies the ideas behind existing algorithms.

If you explore other exact pattern matching algorithms (Knuth Morris Pratt), one can view the pattern matching table (pm) as a special case of applying the Z-algorithm.