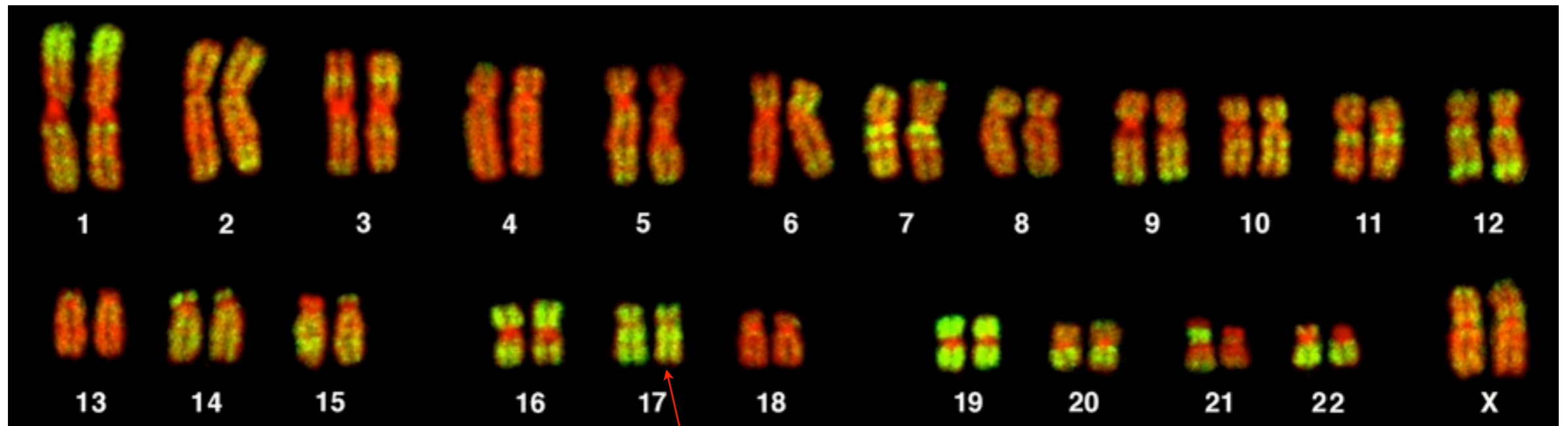


String Matching Z

(Following Gusfield Chapter 2)

Exact String Search

Microscopy of chromosomes of a human female (karyotype):



Bolzer et al, PLoS Biol. 2005

ggccgggcccctgtgaccacagtccacatcacaccaggacacagaggaagggccgggcccctgtgaccacagtccacatcacaccaggacacagaggaagggccgggcccctcatgaccacagt
gtccacatcaca

Where does this string occur in the genome?

Exact String Matching

Exact String Matching Problem. Given a (long) string T and a shorter string P , find all occurrences of P in T . Occurrences of P are allowed to overlap.

- Motivation is obvious:
 - search for words in long documents, webpages, etc.
 - find subsequences of DNA, proteins that are known to be important.
- We'll see 4 efficient algorithms for this problem.

The Simple (Slow) Algorithm

```
SimpMatch(T, P):  
  for i = 1..|T|:  
    j = 1  
    while j ≤ |P| and T[i+j-1] == P[j]:  
      j += 1  
    if j == |P|+1: print "Occurs at", i
```

- Runs in $O(|T| \times |P|)$ time.
- Information gathered in **while** loop at iteration i is ignored in iteration $i+1$.
- Key idea for speeding it up: use what we learned about T in the **while** loop to increment i by more than 1 in the **outer loop**.

Exploiting Patterns in P

i
↓
All this happened, more or less.
happy
happy

- After comparing “happy” to “happe” at iteration i ,
 - we know that $T[i..i+3] = \text{“happ”} = P[1..4]$
 - we can deduce that there can be no match at $i+1$ because $T[i+1] = P[2] = \text{“a”}$ but $P[1] = \text{“h”}$
 - in fact, since “h” does not appear in $T[i..i+3] = P[1..4]$, we could set $i = i + 4$

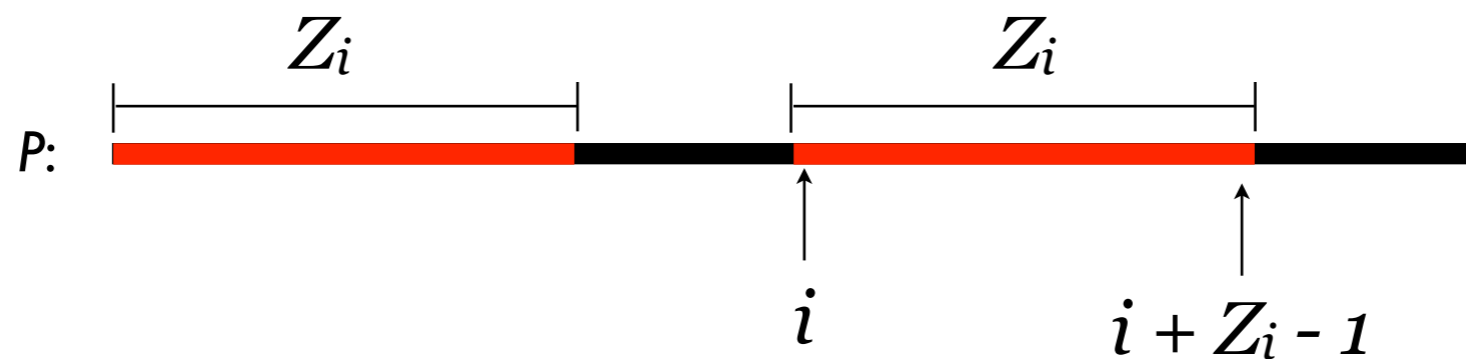
- Since T will have matched some part of P , it is the similarities between various parts of P that allow us to make these deductions.

⇒ Preprocess P to find these similarities.

Z-Algorithm

Fundamental Preprocessing

Def. $Z_i(P)$ = the length of the longest substring of P that starts at $i > 1$ and matches a prefix of P .



- $P = \text{"aardvark"}: Z_2 = 1, Z_6 = 1$
- $P = \text{"alfalfa"}: Z_4 = 4$
- $P = \text{"photophosphorescent"}: Z_6 = Z_{10} = 3$

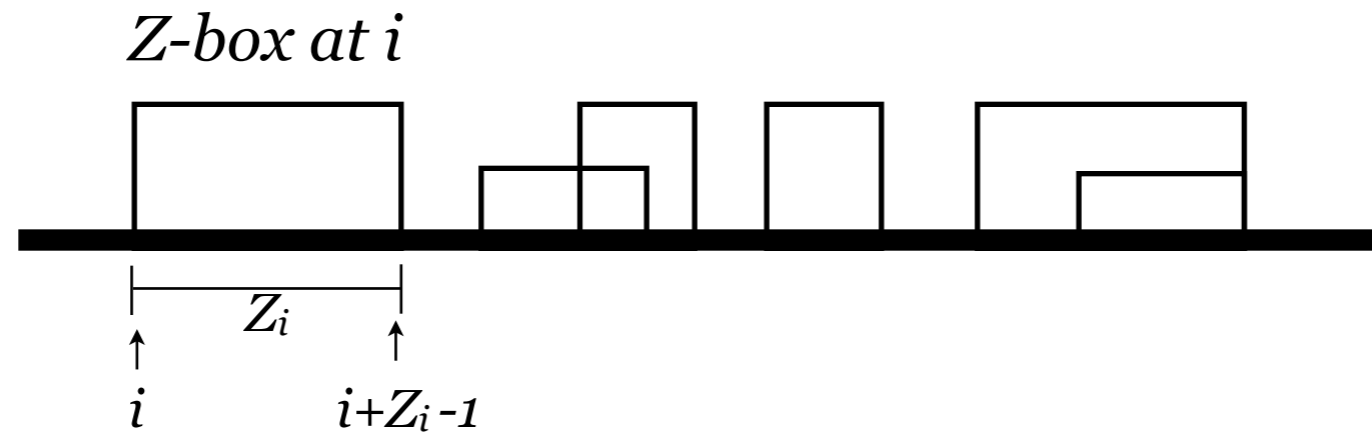
String Search With Z_i

```
ZMatch(T, P):  
  S = P$T  
  Compute all  $Z_i$  for S  
  return all  $i - |P| - 1$  such that  $Z_i = |P|$   
      ↑  
  (map indices of S to indices of T)
```

Why does this work?

- $Z_i(S) = |P|$ if and only if the string starting at i in S matches P .
- Running time is $O(|P| + |T| + Z_S)$, where Z_S is the time to compute the Z_i for S .
- **Next:** an $O(|P| + |T|)$ algorithm for computing the Z_i .

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 $2 \dots k-1$.

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



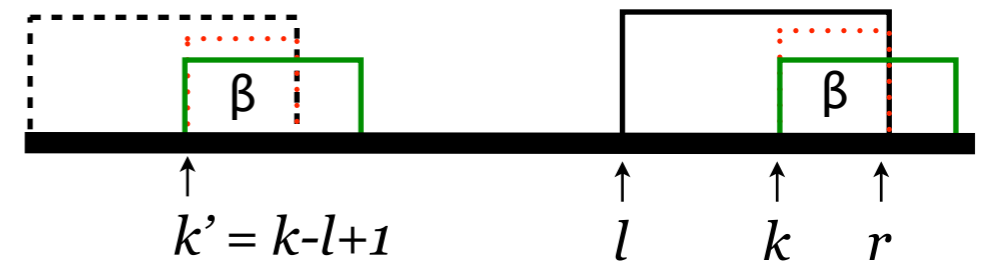
Two subcases:

$Z_{k'} < \beta$:



Set $Z_k = Z_{k'}$ and leave l, r unchanged.

$Z_{k'} \geq \beta$:



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.
- Runs in $O(|S|)$ time:
 - only match characters covered by a Z-box once, so there are $O(|S|)$ matches.
 - every iteration contains at most one mismatch, so there are $O(|S|)$ 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.