CMSC423: Bioinformatic Algorithms, Databases and Tools
Lecture 7

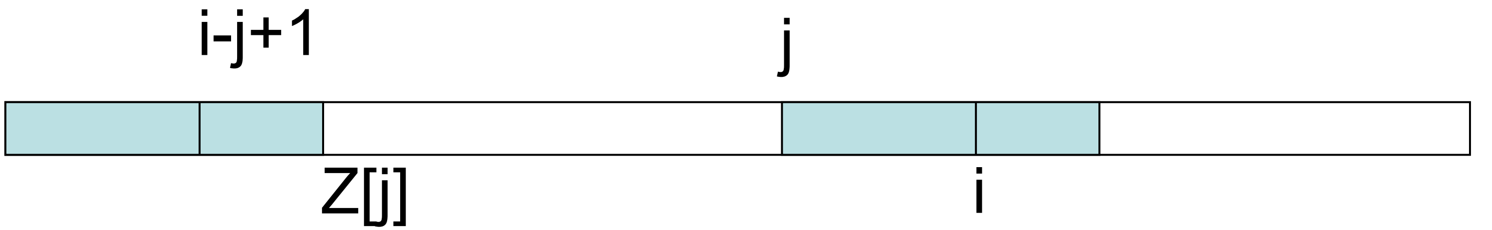
Exact string matching

Suffix trees

Suffix arrays

Basic idea: 1-D dynamic programming

Can Z[i] be computed with the help of Z[j] for j < i?



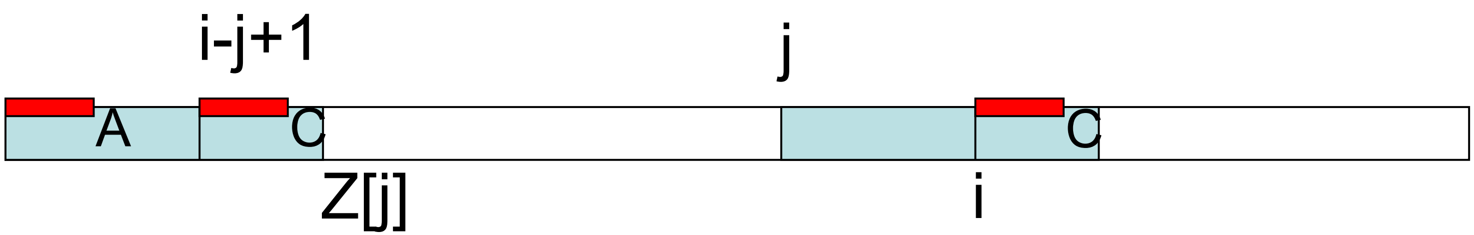
Assume there exists j < i, s.t. j + Z[j] – 1 > i
then Z[i – j + 1] provides information about Z[i]

If there is no such j, simply compare characters T[i..] to T[0..]
since they have not been seen before.

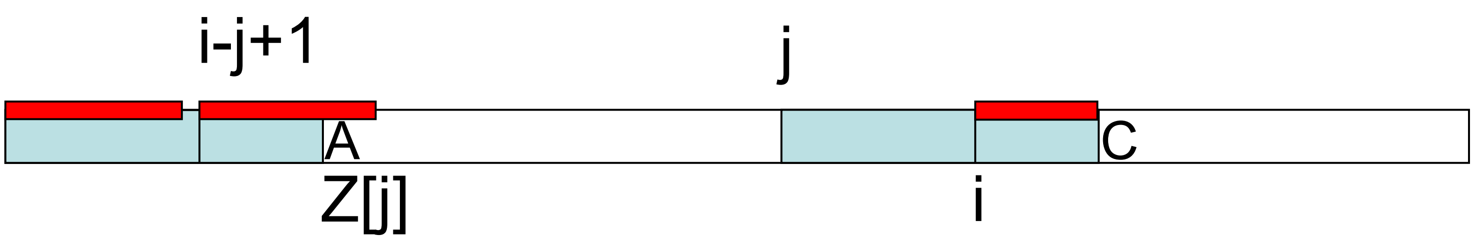
Three cases

Let $j < i$ be the coordinate that maximizes $j + Z[j] – 1$ (intuitively, the $Z[j]$ that extends the furthest)

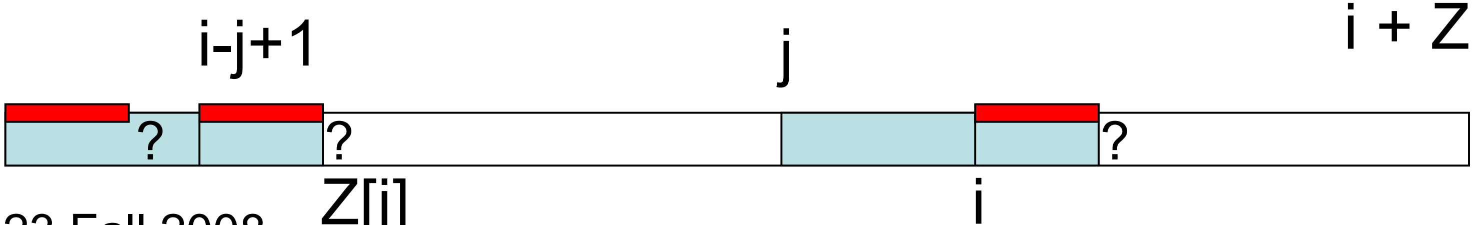
I. $Z[i – j + 1] < Z[j] – i + j – 1 \Rightarrow Z[i] = Z[i – j + 1]$



II. $Z[i – j + 1] > Z[j] – i + j – 1 \Rightarrow Z[i] = Z[j] –i + j - 1$



III. $Z[i – j + 1] = Z[j] – i + j – 1 \Rightarrow Z[i] =$??, compare from $i + Z[i – j + 1]$



Time complexity analysis

- Why do these tricks save us time?

1. Cases I and II take constant time per Z-value computed – total time spent in these cases is O(n)
2. Case III might involve 1 or more comparisons per Z-value

   however:

   - every successful comparison (match) shifts the rightmost character that has been visited
   - every unsuccessful comparison terminates the “round” and algorithm moves on to the next Z-value

   total time spent in III cannot be more than # of characters in the text

Overall running time is O(n)

Space complexity?

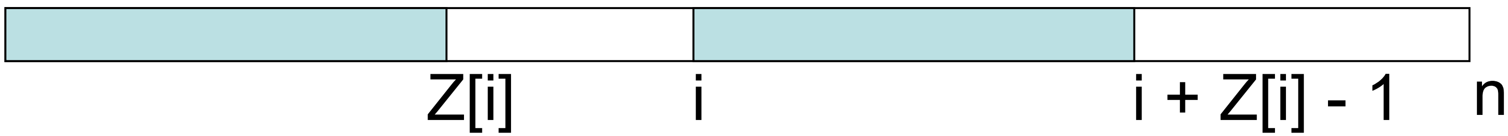
- If using Z algorithm for matching, how many Z values do we need to store?

  PPPPPPPPPP$TTTTTTTTTTTTTTTTTTTTTTTT

- Only need to remember Z-values for pattern and the “farthest reaching Z-value” (Z[j] in what we discussed before)

Z algorithm, not just for matching

- Lempel-Ziv compression (e.g. gzip)

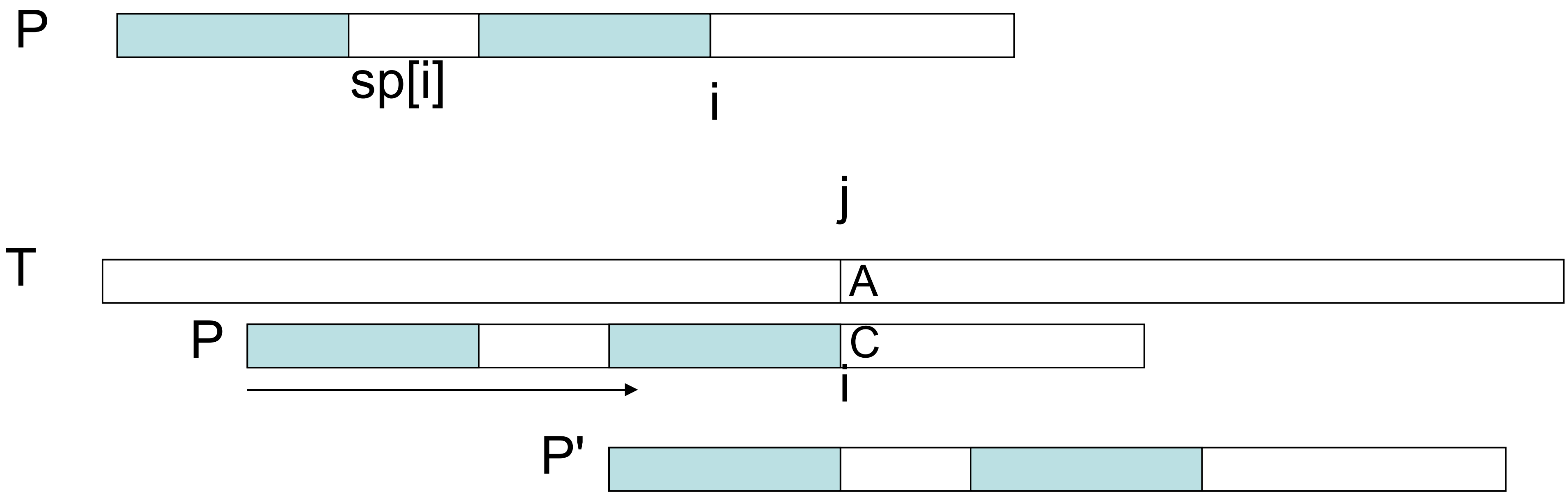


if Z[i] = 0, just send/store the character T[i], otherwise, instead of sending T[i..i+Z[i] – 1] (Z[i] – 1 characters/bytes) simply send Z[i] (one number)

- Note: other exact matching algorithms used for data compression (e.g. Burrows-Wheeler transform relates to suffix arrays)

Knuth-Morris-Pratt algorithm

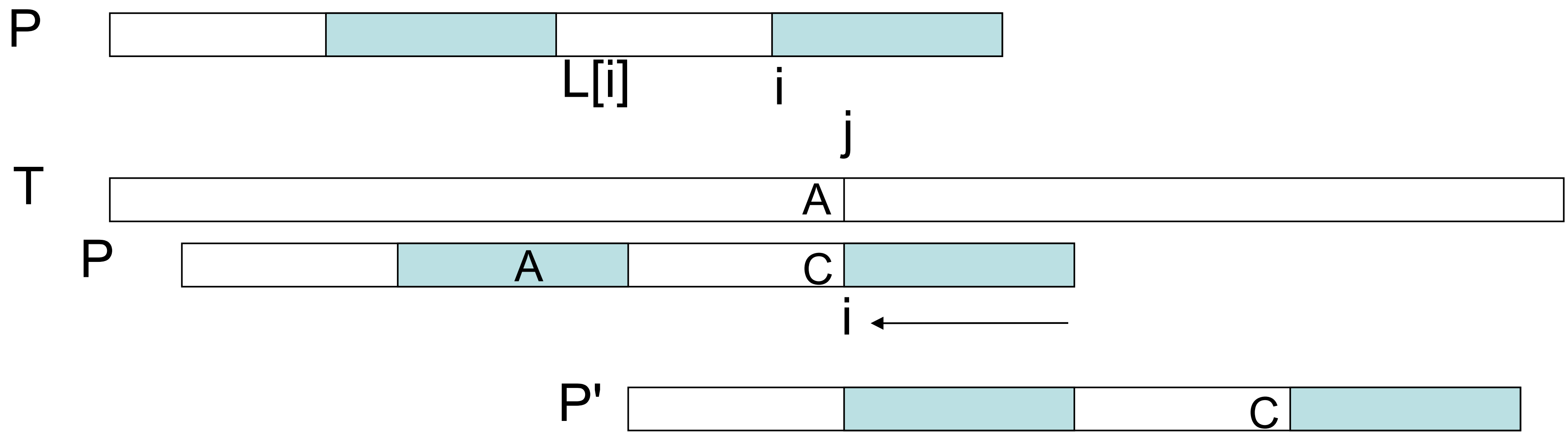
Given a Pattern and a Text, preprocess the Pattern to compute sp[i] = length of longest prefix of P that matches a suffix of P[0..i]



Compare P with T until finding a mis-match (at coordinate i + 1 in P and j + 1 in T). Shift P such that first sp[i] characters match T[j – sp[i] + 1 .. j]. Continue matching from T[i+1], P[sp[i]+1]

Boyer-Moore algorithm

Preprocess the pattern, computing, for every i, L[i] = largest coordinate < n, s.t. P[i..n] matches a suffix of P[1..L[i]] (inverted Z function)



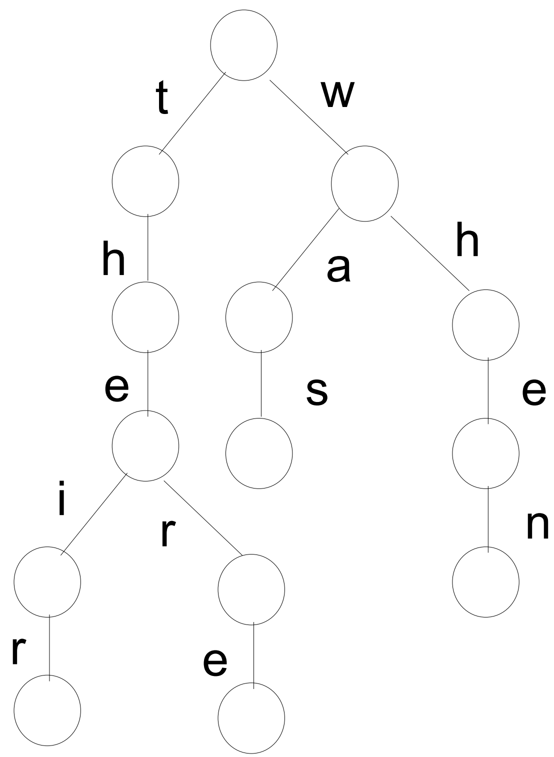
Match the pattern backwards (starting at the right) until mismatch.
Shift the pattern such that P[L[i] – n + i + 1] matches at T[j]
Repeat.

Bad character rule: find character T[j – 1] in P and shift until it matches. Choose the longest shift (btwn. suffix & char. rules)

Suffix trees

Intro to suffix trees

- Used in fast exact matching
- Basic idea: extend a trie – structure for storing multiple strings

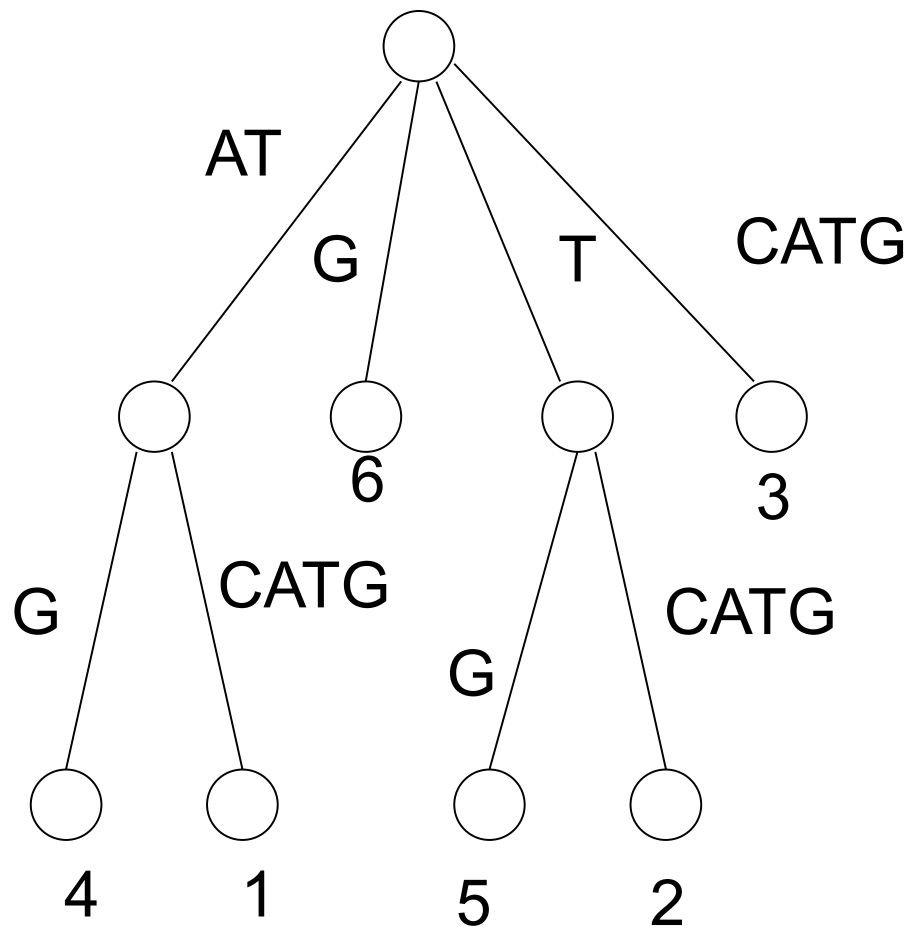


their
there
was
when

Suffix tree

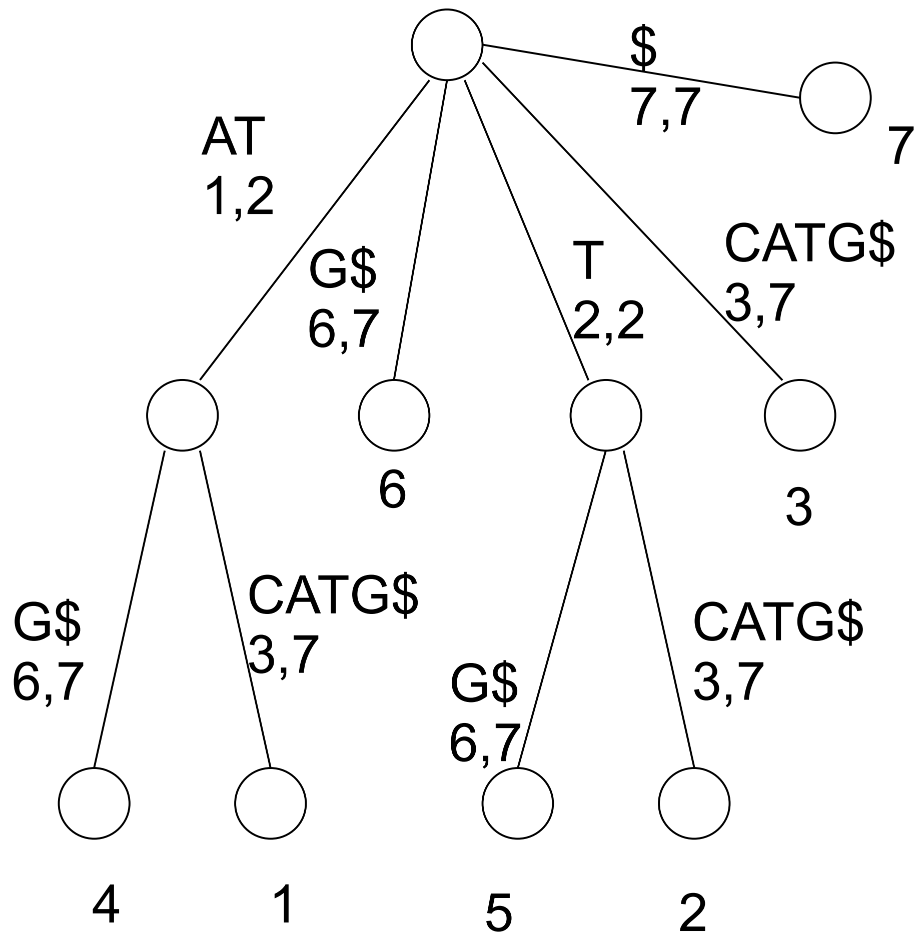
- Extends trie of all suffixes of a string

1 ATCATG
2 TCATG
3 CATG
4 ATG
5 TG
6 G



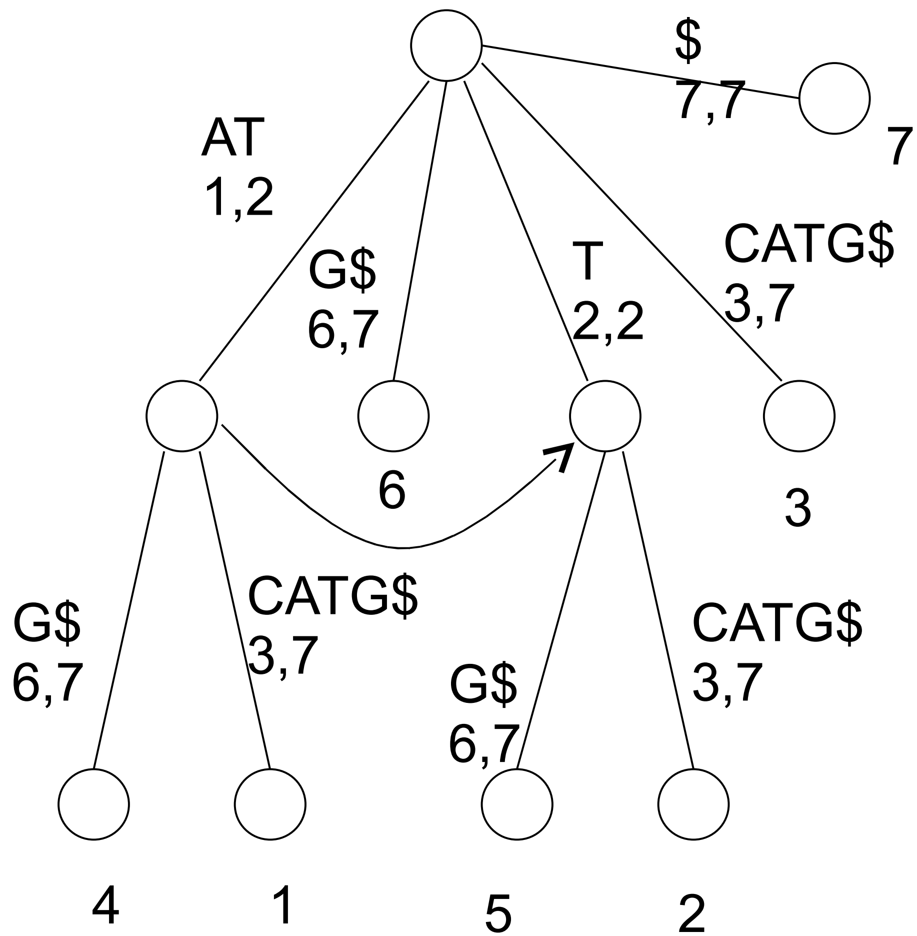
Suffix tree ...cont

- To store in linear time – just store range in sequence instead of string
- To ensure suffixes end at leaves, add $ char at end of string
- ATCATG$



Suffix links

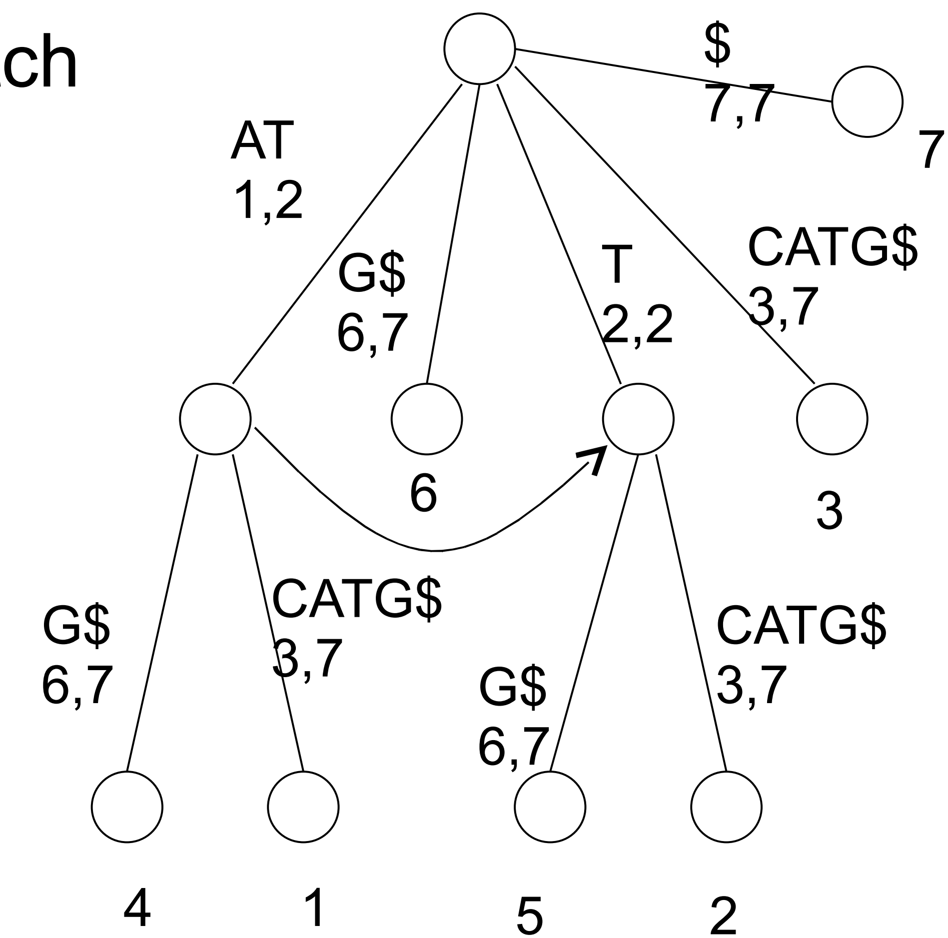
- Link every node labeled aS for some string S to node labeled S (note – it always exists)



Suffix trees for matching

- Suffix trees use O(n) space
- Suffix trees can be constructed in O(n) time
- Is CAT part of ATCATG ?
- Match from root, char by char
- If run out of query – found match
- otherwise, there is no match

- intuition: CAT is the prefix of some suffix



Suffix links – useful for substring matches

- Does any part of AGATG match string AGCAGT?