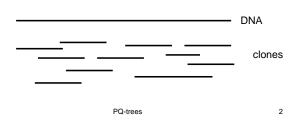
CSE 421 Introduction to Algorithms

Contiguous Ordering - PQ Trees

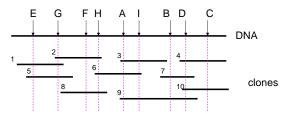
DNA Sequence Reconstruction

- DNA can only be sequenced in relatively small pieces, up to about 1,000 nucleotides.
- By chemistry a much longer DNA sequence can be broken up into overlapping sequences called clones.
 Clones are 10's of thousands of nucleotides long.



Tagging the Clones

• By chemistry the clones can be tagged by identifying a region of the DNA uniquely.

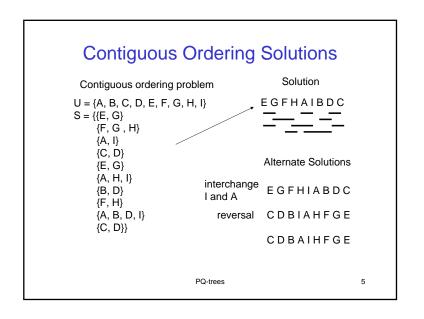


• Each clone is then tagged correspondingly.

PQ-trees

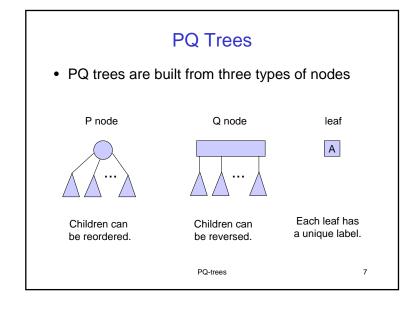
Problem to Solve

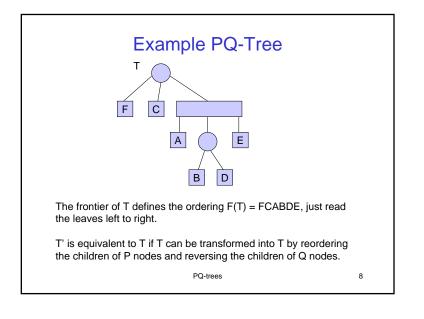
 Given a set of tagged clones, find a consistent ordering of the tags that determines a possible ordering of the DNA molecule.

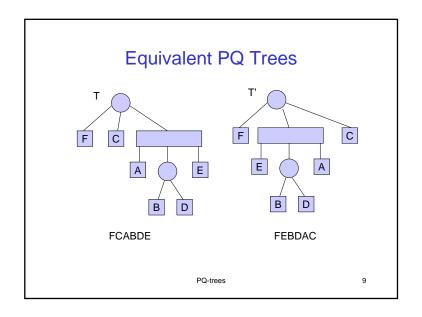


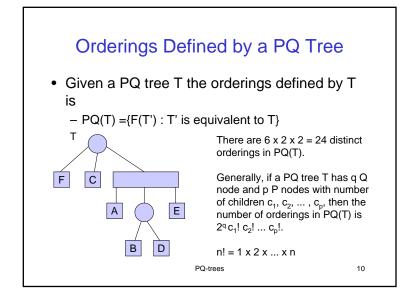
Linear Time Algorithm

- Booth and Lueker, 1976, designed an algorithm that runs in time O(n+m+s).
 - n is the size of the universe, m is the number of sets, and s is the sum of the sizes of the sets.
- It requires a novel data structure called the PQ tree that represents a set of orderings.
- PQ trees can also be used to test whether an undirected graph is planar.









PQ Tree Solution for the Contiguous Ordering Problem

- Input: A universe U and a set S = {S₁, S₂, ..., S_m} of subsets of U.
- Output: A PQ tree T with leaves U with the property that PQ(T) is the set of all orderings of U where each set in S is contiguous in the ordering.

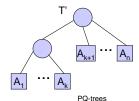
PQ-trees

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Example Solution U = {A,B,C,D,E,F} S = {{A,C,E}, {A,C,F}, {B,D,E}} There are 8 orderings that are possible in keeping each of these sets contiguous.

PQ Tree Restriction

- Let U = {A₁,A₂,...,A_n}, S = {A₁,A₂,...,A_k}, and T a PQ tree.
- We will define a function Restrict with the following properties:
 - Restrict(T,S) is a PQ tree.
 - PQ(Restrict(T,S)) = PQ(T) intersect PQ(T') where



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High Level PQ tree Algorithm

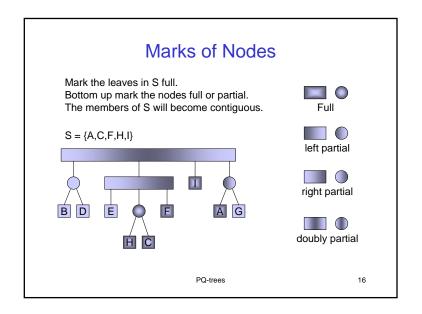
- Input is $U = \{A_1, A_2, ..., A_n\}$, and subsets $S_1, S_2, ..., S_m$ of U.
- Initialization:
 - -T = P node with children $A_1, A_2, ..., A_n$
- Calculate m restrictions:
 - for j = 1 to m do T := Restrict(T,S_i)
- At the end of iteration k:
 - PQ(T) = the set of ordering of U where each set S_1 , S_2 , ..., S_k are contiguous.

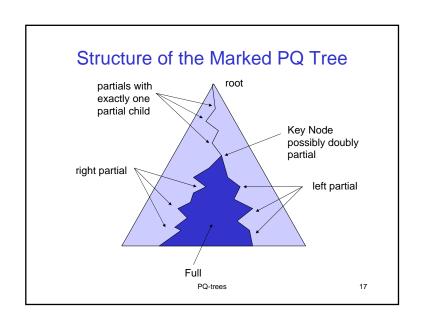
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Marking Nodes

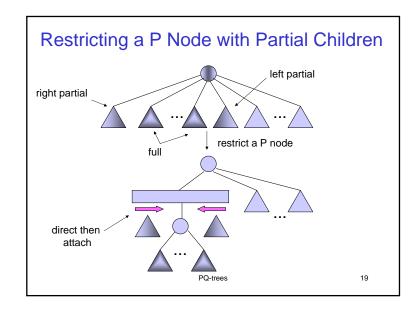
- Given a set S and PQ tree T we can mark nodes either full or partial.
 - A leaf is full if it is a member of S.
 - A node is full if all its children are full.
 - A node is partial if either it has both full and nonfull children or it has a partial child.
 - A node is doubly partial if it has two partial children.

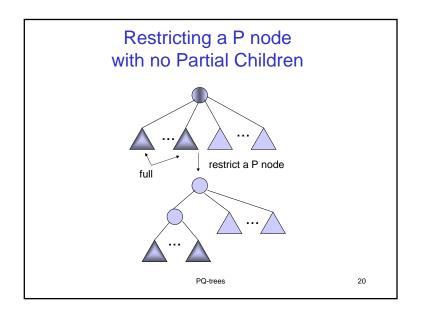


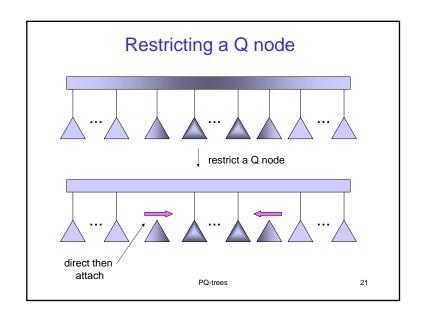


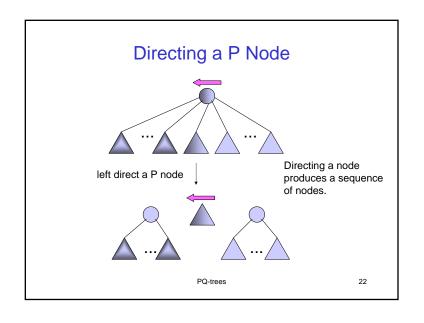
Restrict(T,S)

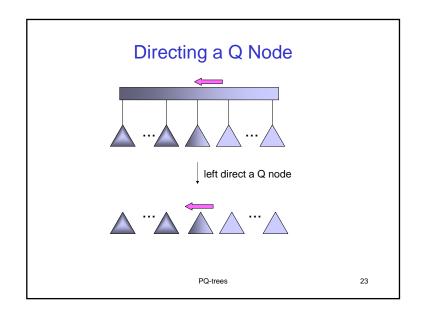
- Mark the full and partial nodes from the bottom up.
 - In the process the marked leaves become contiguous.
- Locate the key node.
 - Deepest node with the property that all the full leaves are descendents of the node.
- Restrict the key node.
 - In the process of restricting the key node we will have to recursively direct partial nodes.
 - Directing a node returns a sequence of nodes.

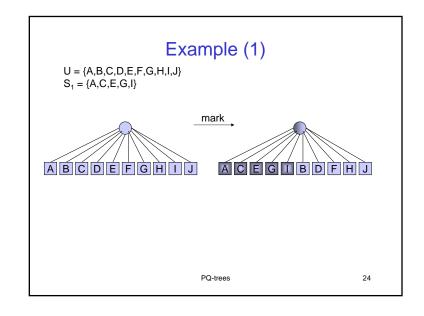


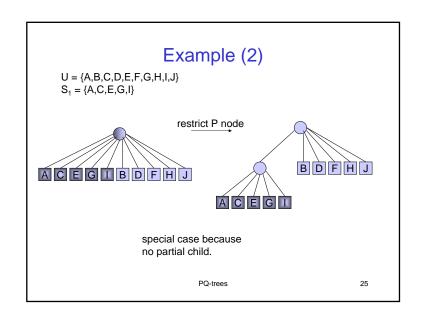


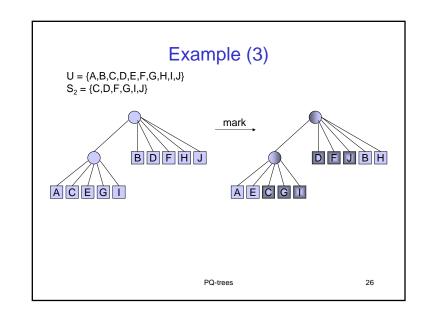


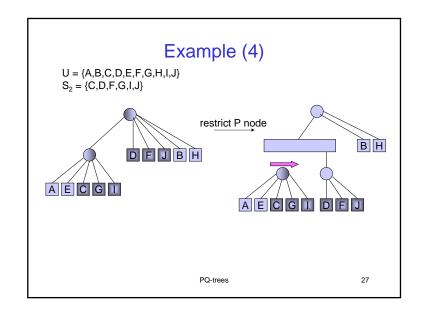


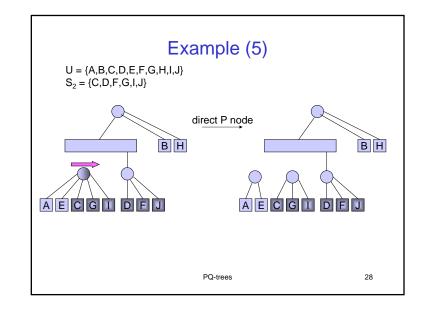


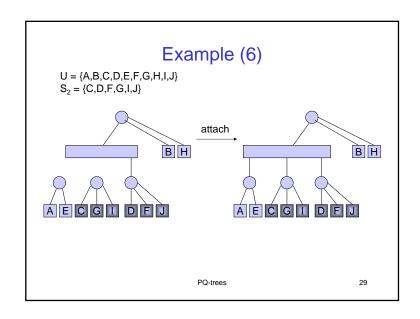


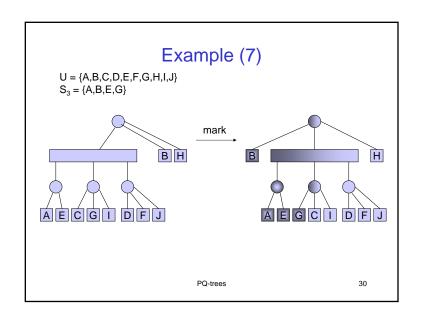


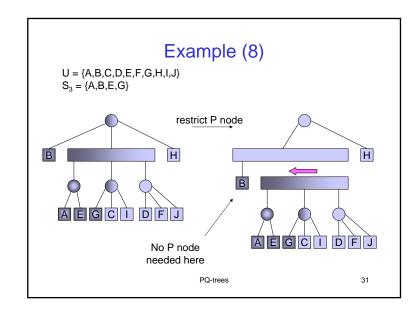


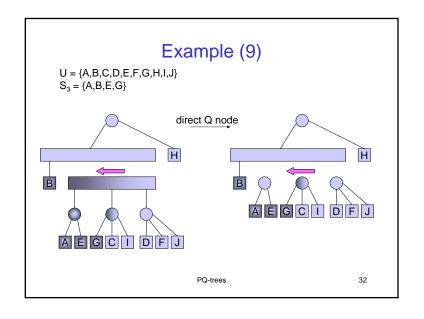


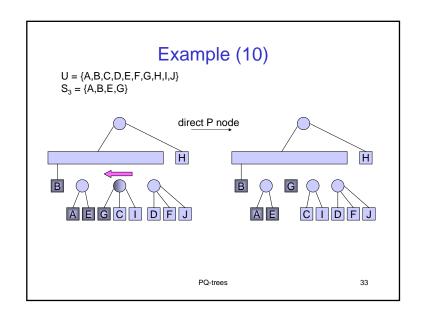


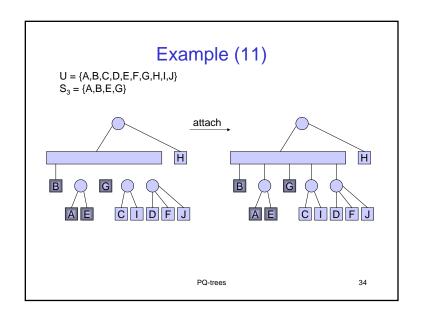


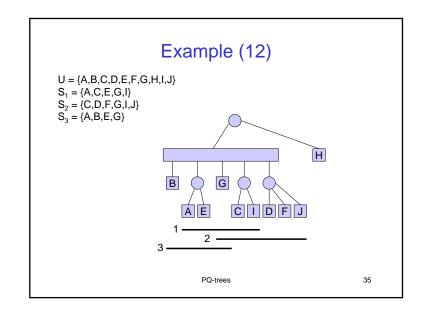


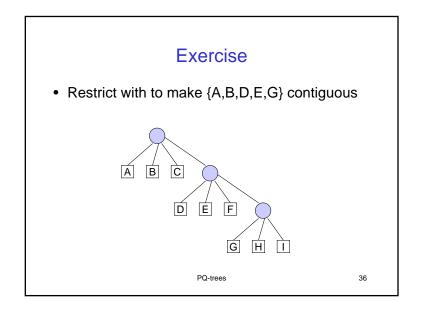








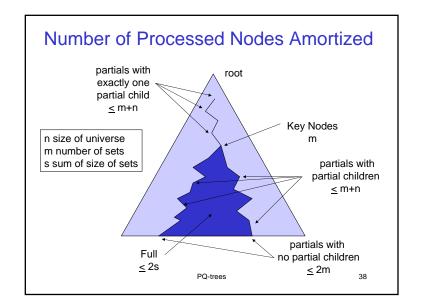




Linear Number of Nodes Processed

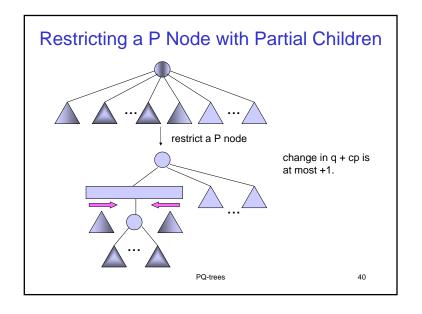
- Let n be the size of the universe, m the number of sets, and s the sum of the sizes of the sets.
 - Number of full nodes processed < 2s.
 - Number of key nodes processed = m.
 - Number of partial nodes with partial children processed below the key node < m + n.
 - Number of partial nodes with no partial children
 2m.
 - Number of partial nodes processed above the key node < m + n.

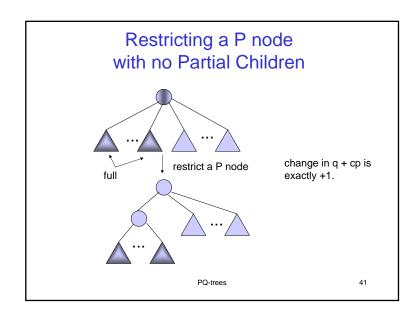
PQ-trees 3

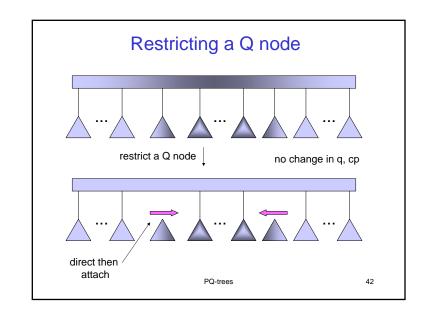


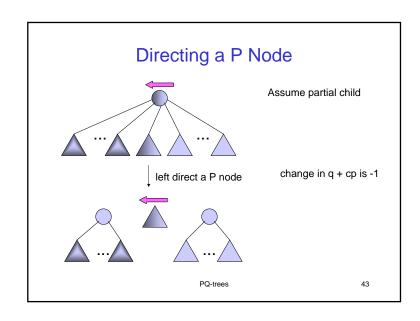
Partials with Partial Children Below the Key Node

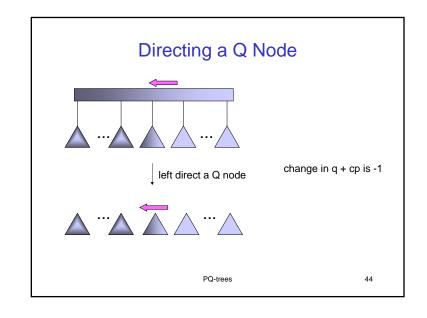
- Amortized complexity argument.
- Consider the quantities:
 - q = number of Q nodes,cp = number of children of P nodes.
 - We examine the quantity x = q + cp
 - x is initially n and never negative.
 - Each restrict of a key node increases x by at most 1.
 - Each direct of a partial node with a partial child decreases x by at least 1.
 - Since there are m restricts of a key node then there are most n + m directs of partials with partial children.











PQ Tree Notes

- In algorithmic design only a linear number of nodes are ever processed.
- Designing the data structures to make the linear time processing a reality is very tricky.
- PQ trees solve the idealized DNA ordering problem.
- In reality, because of errors, the DNA ordering problem is NP-hard and other techniques are used.

