CSEP 521
Applied Algorithms
Spring 2005

Dynamic Programming

Contiguous Ordering - PQ Trees

Reading

- Chapter 15

Outline for the Evening

- DNA
- Approximate String Matching
- Approximate String Searching
- Dynamic Progamming
- Longest Common Subsequence
- DNA reconstruction
- Contiguous Ordering and PQ-trees

DNA

- DNA is a large molecule that can be abstractly defined as a sequence of symbols from the set, A, C, G, T, called nucleotides.
- The human genome has about 3 billion nucleotides.
  - A huge percentage of the genome is shared by all humans.
  - Some of the variation makes us different.
  - Some of the variation is inconsequential.
  - The human genome is still being discovered.

Approximate Matching

- Two DNA sequences approximately match if one can be transformed into the other by a short sequence of replacements and insertions of gaps.
- Example:
  - S = AGCATG
  - T = AGATCGT
- Approximate matching
  - S′ = A G - - C A T G
  - T′ = A G A T C G T -

- is a gap

Applications of Approximate Matching

- DNA string alignment.
  - Given two similar DNA sequences find the best way to align them to the same length.
- DNA database searching.
  - Find DNA sequences that are similar to the query.
- Approximate text matching for searching.
  - agrep in unix
- Spell checking
  - Find the words that most closely match the misspelled word.

Scoring an Approximate Matching

- We need a way of scoring the quality of an approximate matching.
- A scoring function is a mapping σ from $\{A, C, G, T, -\}^2$ to integers.
  - The quantity $\sigma(x,y)$ is the score of a pair of symbols, x and y.
- Example:
  - $\sigma(x,y) = +2$ if x=y and x in {A,C,G,T}
  - $\sigma(x,y) = -1$ otherwise

Scoring Example

- Example:
  - S′ = A G - - C A T G
  - T′ = A G A T C G T -
- Score = 4 x 2 + 4 x(-1) = 4
- Is this the best match between the two strings with this scoring function?
  - S = AGCATG
  - T = AGATCGT

Approximate String Matching Problem

- Input: Two strings S and T in an alphabet Σ and a scoring function σ.
- Output: Two strings S' and T' in the alphabet $\Sigma' = \Sigma$ union {-} with the properties:
  - S = S' with the -'s removed.
  - T = T' with the -'s removed.
  - |S'| = |T'|
  - The score $\sum_{i=1}^{|S'|} \sigma(S'[i], T'[i])$ is maximized.

Algorithms for Approximate String Matching

- O(mn) time and storage algorithm (using dynamic programming) invented by Needleman and Wunch, 1970.
- Fischer and Paterson, 1974, invented a very similar algorithm for computing the minimum edit distance between two strings.

Dynamic Programming for Approximate String Matching

- Assume S has length m and T has length n.
- For all i and j, $0 \leq i \leq m$ and $0 \leq j \leq n$, we find the maximum score for the sequences S[1..i] and T[1..j].
- The "dynamic program" fills in a (m+1)x(n+1) matrix M in increasing order of i and j with these maximum values.
- Once the dynamic program has completed we can recover the optimal string S' and T' from the matrix M.

Max Score Recurrence

- Define M[i,j] = maximum score for a match between S[1..i] and T[1..j].

$$M[i,0] = \sum_{k=1}^{i} \sigma(S[k],-)$$ match of S[1..i] with empty string

$$M[0,j] = \sum_{k=1}^{j} \sigma(-,T[k])$$ match of T[1..j] with empty string

$$M[i,j] = \max\{$$
$$M[i-1,j-1] + \sigma(S[i],T[j]),$$
$$M[i-1,j] + \sigma(S[i],-),$$
$$M[i,j-1] + \sigma(-,T[j])\}$$

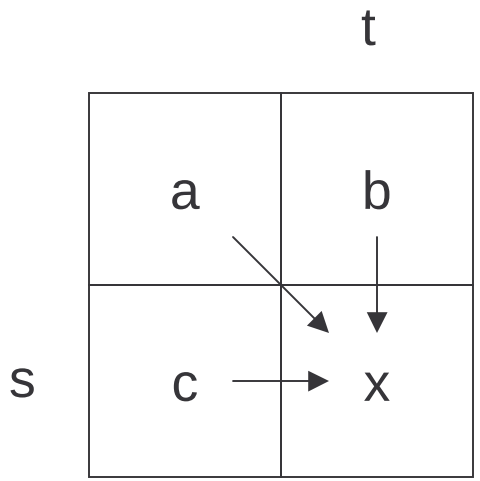
Dynamic Program Initialization

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1							
2	G	-2							
3	C	-3							
4	A	-4							
5	T	-5							
6	G	-6							

The Dynamic Programming Pattern



d = a + 2 if s = t
  = a - 1 otherwise

h = c - 1

v = b - 1

x = max(d, h, v)

Dynamic Program Example (1)

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2						
2	G	-2							
3	C	-3							
4	A	-4							
5	T	-5							
6	G	-6							

Dynamic Program Example (2)

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1					
2	G	-2	1						
3	C	-3							
4	A	-4							
5	T	-5							
6	G	-6							

Dynamic Program Example (3)

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0				
2	G	-2	1	4					
3	C	-3	0						
4	A	-4							
5	T	-5							
6	G	-6							

Dynamic Program Example (4)

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0	-1	-2	-3	-4
2	G	-2	1	4	3	2	1	0	-1
3	C	-3	0	3	3	2	4	3	2
4	A	-4	-1	2	5	4	3	3	2
5	T	-5	-2	1	4	7	6	5	
6	G	-6	-3	0	3	6	6		

Dynamic Program Example (5)

S = AGCATG
T = AGATCGT

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0	-1	-2	-3	-4
2	G	-2	1	4	3	2	1	0	-1
3	C	-3	0	3	3	2	4	3	2
4	A	-4	-1	2	5	4	3	3	2
5	T	-5	-2	1	4	7	6	5	5
6	G	-6	-3	0	3	6	6	8	7

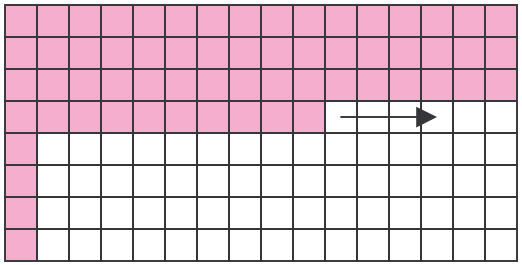
Max score for any matching

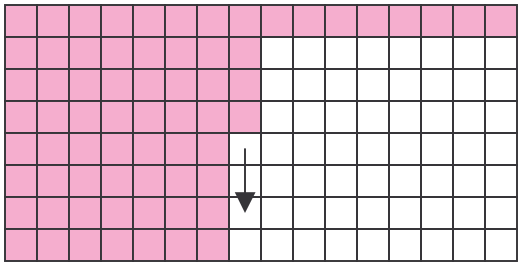
Dynamic Programming Order

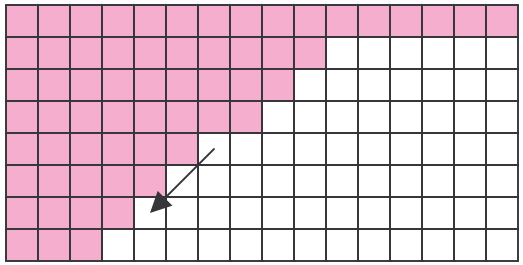
```
By row
for i = 1 to m do
    for j = 1 to n do
        M[i,j] :=  ...
```

```
By column
for j = 1 to n do
    for i = 1 to m do
        M[i,j] := ...
```

By diagonal



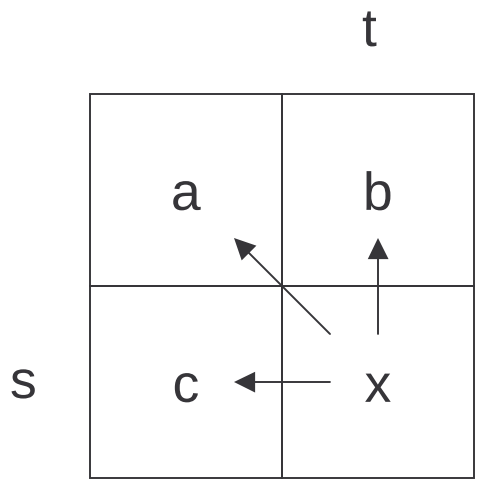




Which order is best?

How to Find the Matching

- To find S' and T' we build a matching graph.



x = a + 2 if s = t
= a - 1 otherwise ?

x = c - 1 ?

x = b - 1 ?

If the answer is yes,
include the corresponding edge.

Computing the Matching Graph (1)

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0	-1	-2	-3	-4
2	G	-2	1	4	3	2	1	0	-1
3	C	-3	0	3	3	2	4	3	2
4	A	-4	-1	2	5	4	3	3	2
5	T	-5	-2	1	4	7	6	5	5
6	G	-6	-3	0	3	6	6	8	7

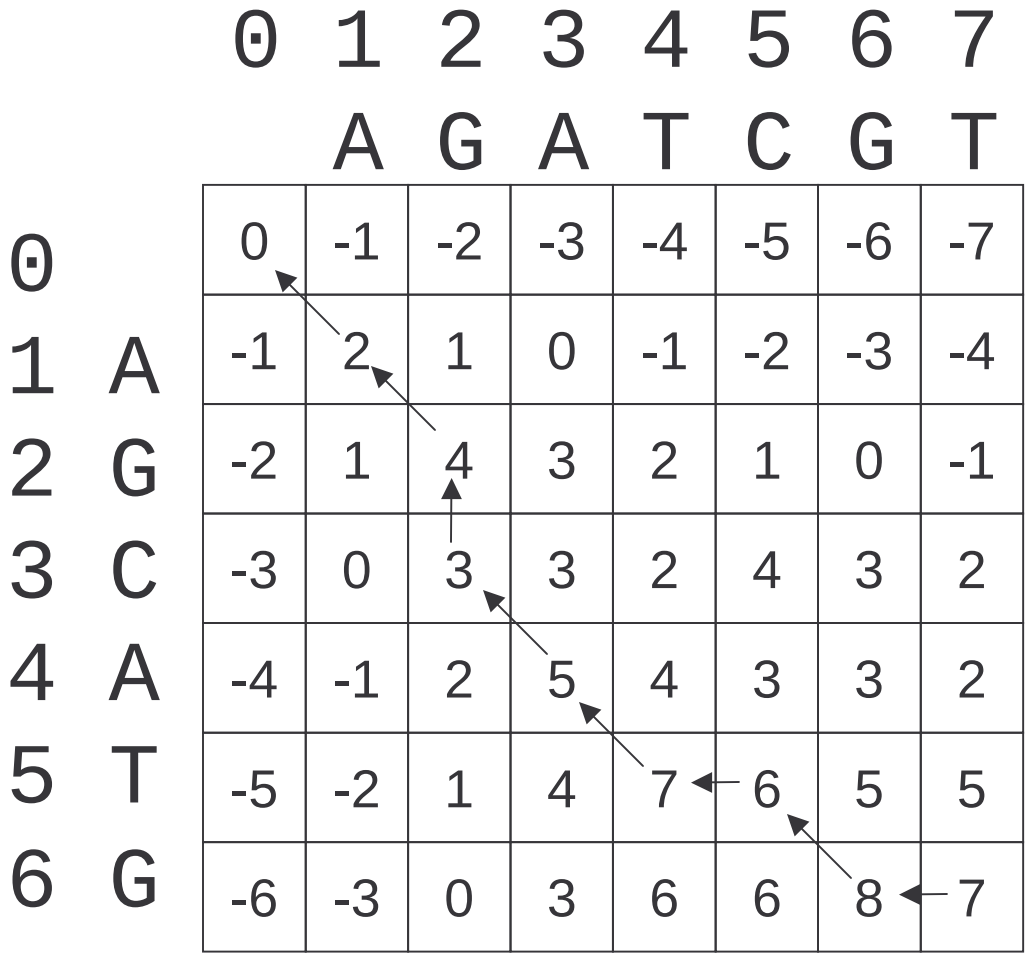
Computing the Matching Graph (2)

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0	-1	-2	-3	-4
2	G	-2	1	4	3	2	1	0	-1
3	C	-3	0	3	3	2	4	3	2
4	A	-4	-1	2	5	4	3	3	2
5	T	-5	-2	1	4	7	6	5	5
6	G	-6	-3	0	3	6	6	8	7

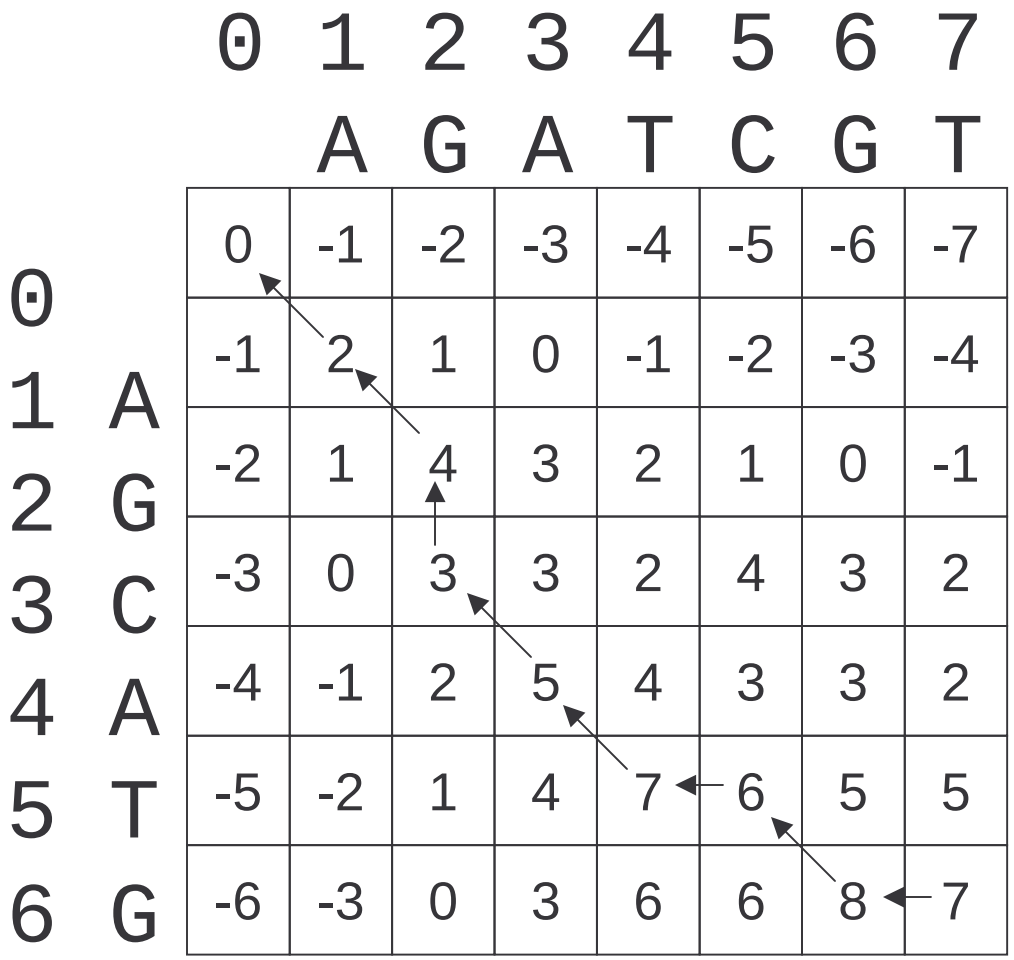
Computing the Matching Graph (3)

		0	1	2	3	4	5	6	7
			A	G	A	T	C	G	T
0		0	-1	-2	-3	-4	-5	-6	-7
1	A	-1	2	1	0	-1	-2	-3	-4
2	G	-2	1	4	3	2	1	0	-1
3	C	-3	0	3	3	2	4	3	2
4	A	-4	-1	2	5	4	3	3	2
5	T	-5	-2	1	4	7	6	5	5
6	G	-6	-3	0	3	6	6	8	7

Computing the Matching Graph



Computing the Matching Path



Matching Path
(0,0)
(1,1)
(2,2)
(3,2)
(4,3)
(5,4)
(5,5)
(6,6)
(6,7)

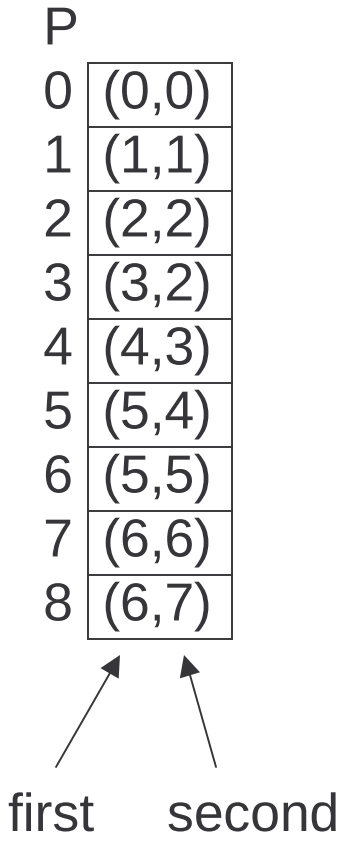
There can be multiple paths

Algorithm to find Matching

- Follow any path in the matching graph starting at (m,n).
- The path will end up at (0,0).
- Output each pair (i,j) visited to make a list of pairs forming a matching path.

Computing the Matching

```
p = length of the matching path P
i :=1;
j := 1;
for k = 1 to p do
    if P[k].first = P[k-1].first then
       S'[k] := - ;
    else
       S'[k] :=  S[i];
        i := i + 1;
    if P[k].second = P[k-1].second then
       T'[k] := - ;
    else
       T'[k] :=  T[j];
        j := j + 1;
```



Creating the Matching

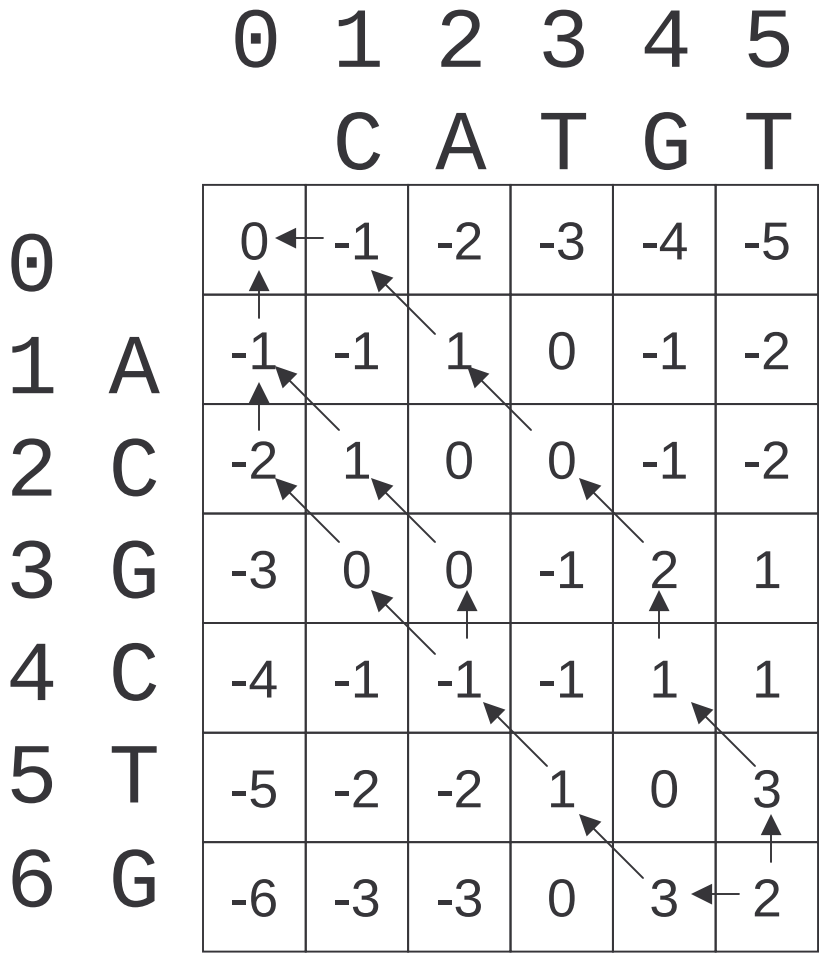
P	
0	(0,0)
1	(1,1)
2	(2,2)
3	(3,2)
4	(4,3)
5	(5,4)
6	(5,5)
7	(6,6)
8	(6,7)

```
     1 2 3 4 5 6
S =  A G C A T G
T =  A G A T C G T

S'=  A G C A T - G -
T'=  A G - A T C G T
```

Score = 5 x 2 + 3 x (-1) = 7

Example of Multiple Paths



Multiple matching with same score

```
- A C G C T G
C A T G - T -

A C G C T G -
- C A - T G T

A C G C T G -
- - C A T G T
```

score = 3 x 2 + 4 x (-1)
= 2

Exercise

- Find an optimal approximate matching for
  - A G T T C
  - A C T A T C

		0	1	2	3	4	5	6
			A	C	T	A	T	C
0		0	-1	-2	-3	-4	-5	-6
1	A	-1						
2	G	-2						
3	T	-3						
4	T	-4						
5	C	-5						

Approximate String Searching

- Input: Query string Q and target string T in an alphabet Σ and a scoring function σ, and a minimum score r.
- Output: The set of k such that for some $i \leq k$ $score(Q,T[i..k]) \geq r$. That is, an approximate match of some substring of T that ends at index k has a score of at least r.
  - score(X,Y) is the maximum score for all matchings between X and Y.

Search Algorithm

- We change the previous dynamic program slightly.

$$M[i,0] = \sum_{k=1}^{i} \sigma(Q[k],-)$$

$$M[0,j] = 0$$

We don't care where the match begins in T

$$M[i,j] = \max\{$$

$$M[i-1,j-1] + \sigma(Q[i],T[j]),$$

$$M[i-1,j] + \sigma(Q[i],-),$$

$$M[i,j-1] + \sigma(-,T[j])\}$$

Choose all k such that $M[m,k] \geq r$ where m is the length of Q.

Example of Approximate Matching

Q = AGTA
T = AGATCGTAGT

r = 5

scoring function
+2 for exact match
-1 otherwise

		0	1	2	3	4	5	6	7	8	9	10
			A	G	A	T	C	G	T	A	G	T
0		0	0	0	0	0	0	0	0	0	0	0
1	A	-1	2	1	2	1	0	-1	-1	2	1	0
2	G	-2	1	4	3	2	1	2	1	1	4	3
3	T	-3	0	3	3	5	4	3	4	3	3	6
4	A	-4	-1	2	5	4	4	3	3	6	5	5

output is 3, 8, 9, 10

Recovering the Matchings

Q = AGTA
T = AGATCGTAGT

		0	1	2	3	4	5	6	7	8	9	10
			A	G	A	T	C	G	T	A	G	T
0		0	0	0	0	0	0	0	0	0	0	0
1	A	-1	2	1	2	1	0	-1	-1	2	1	0
2	G	-2	1	4	3	2	1	2	1	1	4	3
3	T	-3	0	3	3	5	4	3	4	3	3	6
4	A	-4	-1	2	5	4	4	3	3	6	5	5

```
Q  AGTA
T  AG-A 1-3

Q  A--GTA
T  ATCGTA 3-8
```

```
Q  A--GTA-
T  ATCGTAG 3-9

Q  AGTA
T  AGT- 8-10
```

Notes on Approximate Matching

- Time complexity O(mn)
- Storage complexity O(mn)
  - Storage in the dynamic program can be reduced to O(m+n) by just keeping the frontier.
  - Recovering the matching can be done in time O(m+n) cleverly.

FASTA and BLAST

- Two of best known approximate search algorithms for DNA database searching
- Both use the idea of exclusion search
  - Parameter k for number of possible errors
  - Exact search on k+1 substrings. At least one must succeed

k = 4 search string

1. Find all the exact matches for at least one of the strings
2. For each such match do an approximate matching

Example

k = 2

AGTTATGCC ⟶ AGT TAT GCC

Dynamic Programming O(mn)
Exclusion Search $O(sm^2 + n)$

m search string length
n database length
s number of successes in exact search

Dynamic Programming

- A strategy for designing algorithms.
- A technique, not an algorithm.
- The word “programming” is historical and predates computer programming.
- Ideal when the problem breaks down into recurring small sub-problems.

Longest Common Subsequence

- Longest common subsequence (LCS) problem:
  - Given two sequences x[1..m] and y[1..n], find the longest subsequence which occurs in both (not necessarily contiguous).
  - Example: x = A B C B D A B , y = B D C A B A
  - B C and A A are both subsequences of both
    - What is the LCS? BCAB, BCBA
  - Brute-force algorithm: For every subsequence of x, check if it's a subsequence of y
    - How many subsequences of x are there?
    - What will be the running time of the brute-force alg?

LCS Algorithm

- Brute-force algorithm: 2^m subsequences of x each takes O(n) to search in y: O($n\ 2^m$)
- We can do better: for now, let's only worry about the problem of finding the *length* of the LCS
  - When finished we will see how to backtrack from this solution back to the actual LCS.
- Notice LCS problem has optimal substructure
  - Subproblems: LCS of pairs of *prefixes* of x and y

Finding LCS Length

- Define c[i,j] to be the length of the LCS of X_i =x[1..i] and Y_j=y[1..j]
  - What is the length of LCS of x and y?

$$c[m,n]$$

- Theorem:

$$c[i,j] = \begin{cases} c[i-1,j-1]+1 & \text{if } x[i] = y[j], \\ \max(c[i,j-1], c[i-1,j]) & \text{otherwise} \end{cases}$$

LCS Recurrence

$$c[i,j] = \begin{cases} c[i-1,j-1]+1 & \text{if } x[i] = y[j], \\ \max(c[i,j-1], c[i-1,j]) & \text{otherwise} \end{cases}$$

Proof: When calculating c[i,j], there are two cases to consider:

- **First case:** x[i]=y[j]: one more symbol in strings X and Y matches, so the length of LCS X_i and Y_j equals to the length of LCS of smaller strings X_{i-1} and Y_{i-1} , plus 1.

LCS Recurrence

$$c[i,j] = \begin{cases} c[i-1,j-1]+1 & \text{if } x[i] = y[j], \\ \max(c[i,j-1], c[i-1,j]) & \text{otherwise} \end{cases}$$

- **Second case:** $x[i] \neq y[j]$
- As symbols don't match, our solution is not improved, and the length of $LCS(X_i, Y_j)$ is the maximum of $LCS(X_i, Y_{j-1})$ and $LCS(X_{i-1}, Y_j)$

Why not just take the length of $LCS(X_{i-1}, Y_{j-1})$?

LCS recursive solution

$$c[i,j] = \begin{cases} c[i-1,j-1]+1 & \text{if } x[i] = y[j], \\ \max(c[i,j-1], c[i-1,j]) & \text{otherwise} \end{cases}$$

Why not just take the length of LCS(X_{i-1}, Y_{j-1}) ?

Answer: Let x=abc y=db

c[3,2]=max(c[3,1], c[2,2])=max(0,1)=1

c[3,2]≠ c[2,1]=0

Exercise: Write the Program

1. m = length(X) // # of symbols in X
2. n = length(Y) // # of symbols in Y
3. for i = 1 to m c[i,0] = 0 // special case: Y_0
4. for j = 1 to n c[0,j] = 0 // special case: X_0

Finish it

Exercise: Create a Dynamic Program

- Design a dynamic program for knapsack problem.
- Input: $(s_1,c_1), (s_2,c_2),\ldots, (s_n,c_n), \ S$
- Output: find a subset X of {1,2,…,n} such that

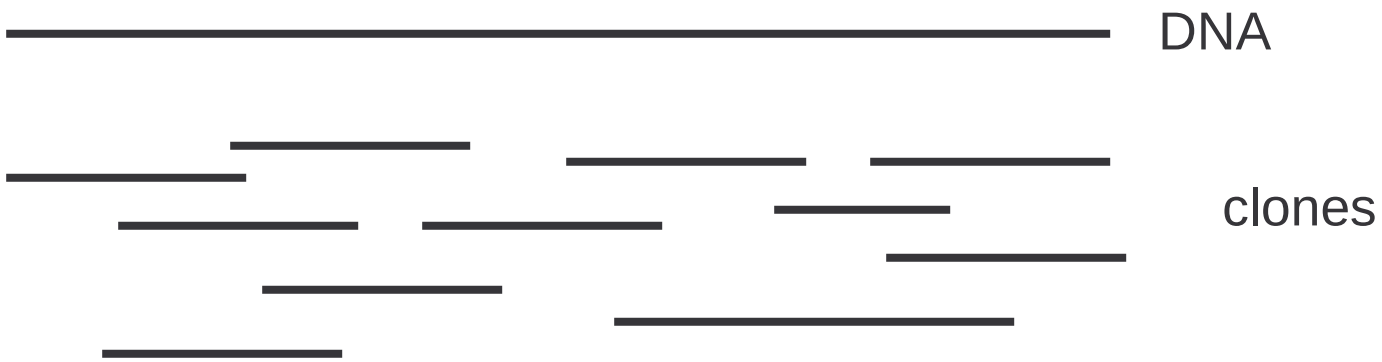
$$\sum_{i\in X} s_i \le S \ \text{ and } \sum_{i\in X} c_i \text{ is maximized}$$

- Hint: For $i \le n$ and $k \le S$ recursively define

$$c(i,k) = \max\{\sum_{j\in X} c_j : X \subseteq \{1,2,\ldots,i\} \text{ and } \sum_{j\in X} s_j = k\}$$

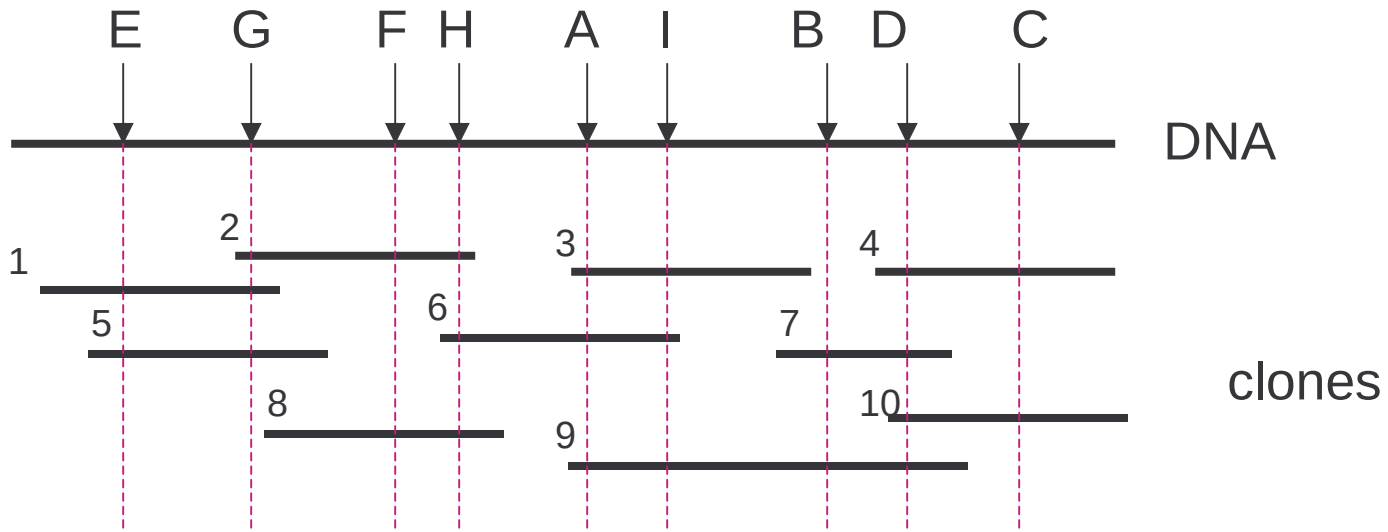
DNA Sequence Reconstruction

- 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.

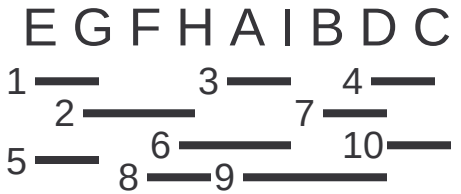
Problem to Solve

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

input

clone	tag
1.	{E, G}
2.	{F, G , H}
3.	{A, I}
4.	{C, D}
5.	{E, G}
6.	{A, H, I}
7.	{B, D}
8.	{F, H}
9.	{A, B, D, I}
10.	{C, D}

output



Contiguous Ordering Solutions

Contiguous ordering problem

U = {A, B, C, D, E, F, G, H, I}
S = {{E, G}
{F, G , H}
{A, I}
{C, D}
{E, G}
{A, H, I}
{B, D}
{F, H}
{A, B, D, I}
{C, D}}

Solution

E G F H A I B D C

Alternate Solutions

interchange I and A: E G F H I A B D C

reversal: C D B I A H F G E

C D B A I H F G E

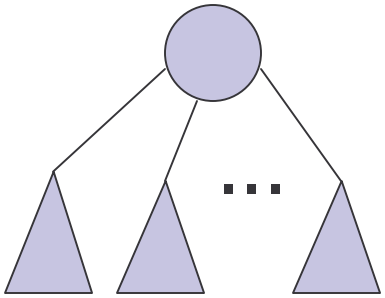
Linear Time Algorithm

- 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 Trees

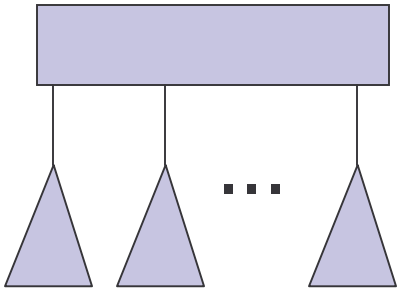
- PQ trees are built from three types of nodes

P node



Children can be reordered.

Q node

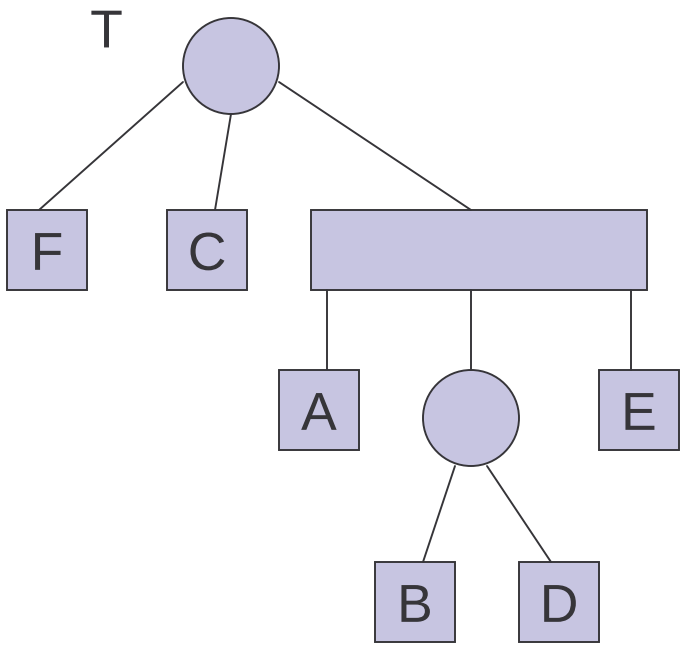


Children can be reversed.

leaf

Each leaf has a unique label.

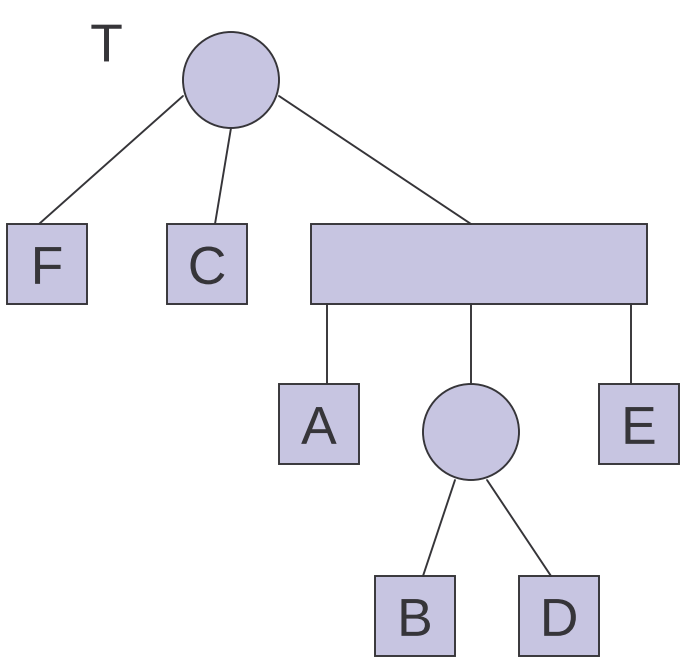
Example PQ-Tree



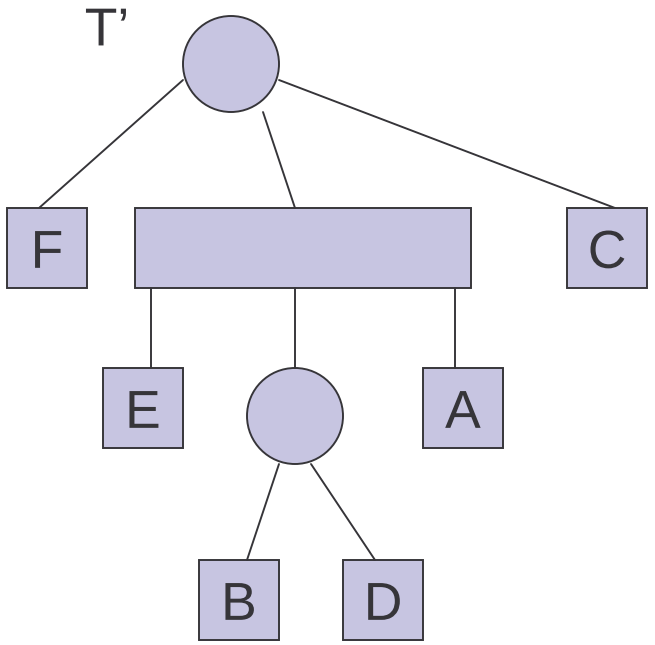
The frontier of T defines the ordering F(T) = FCABDE, just read the leaves left to right.

T' is equivalent to T if T can be transformed into T by reordering the children of P nodes and reversing the children of Q nodes.

Equivalent PQ Trees



FCABDE

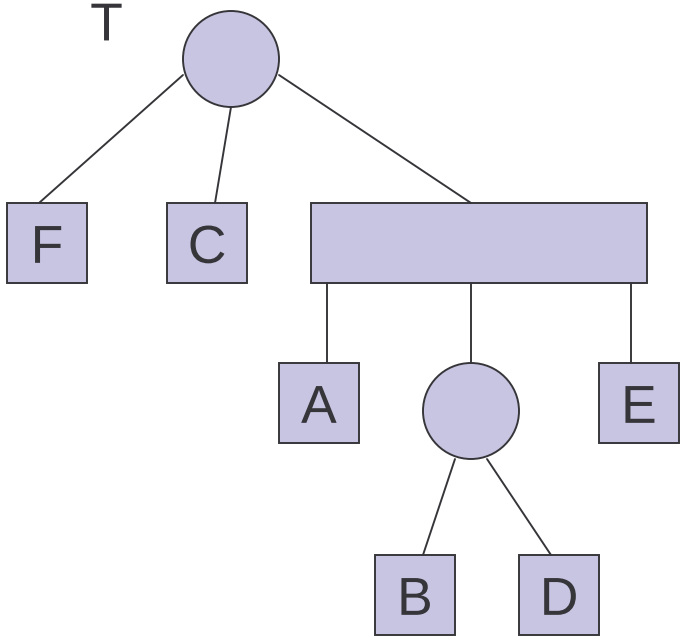


FEBDAC

Orderings Defined by a PQ Tree

- Given a PQ tree T the orderings defined by T is
  - PQ(T) ={F(T') : T' is equivalent to T}

T



There are 6 x 2 x 2 = 24 distinct orderings in PQ(T).

Generally, if a PQ tree T has q Q node and p P nodes with number of children c_1, c_2, ... , c_p, then the number of orderings in PQ(T) is $2^q\, c_1!\, c_2! \ldots c_p!$.

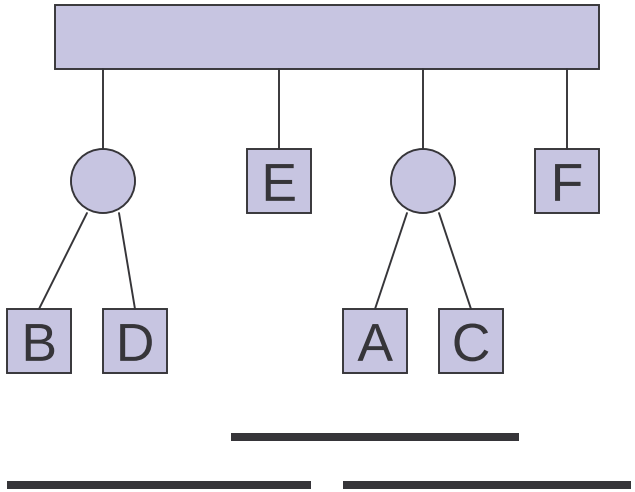
n! = 1 x 2 x ... x n

PQ Tree Solution for the Contiguous Ordering Problem

- Input: A universe U and a set $S = \{S_1, S_2, ..., S_m\}$ 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.

Example Solution

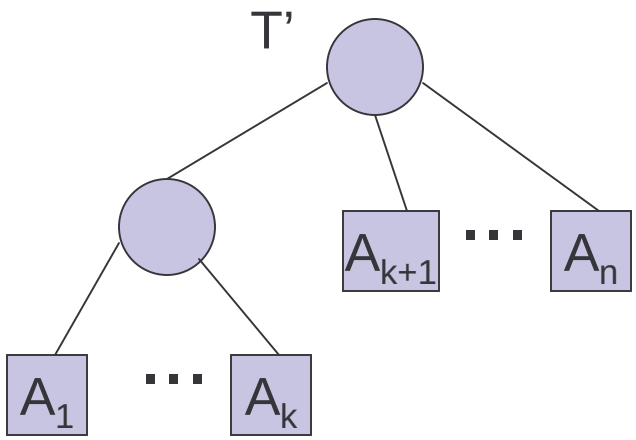
U = {A,B,C,D,E,F}
S = {{A,C,E}, {A,C,F}, {B,D,E}}



There are 8 orderings that are possible in keeping each of these sets contiguous.

PQ Tree Restriction

- Let U = {A_1,A_2,...,A_n}, S = {A_1,A_2,...,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



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_j)
- 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.

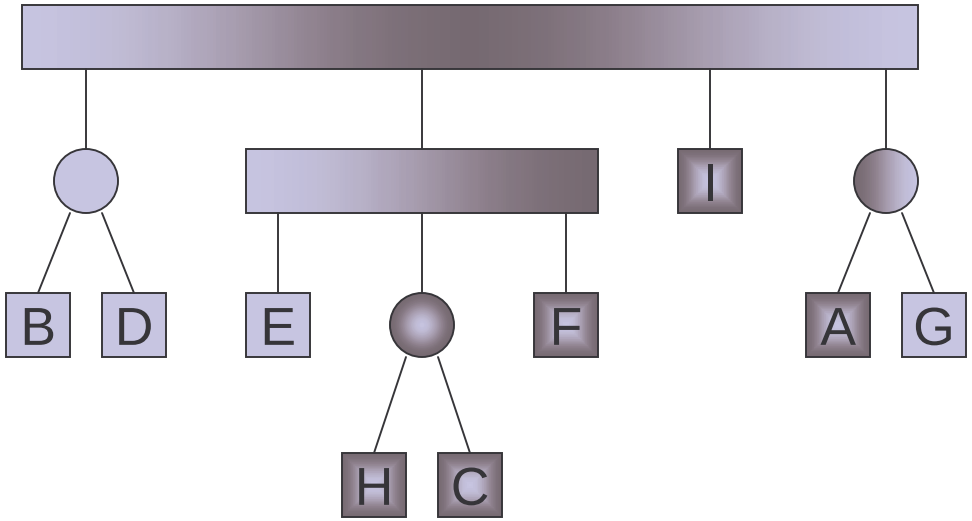
Marking Nodes

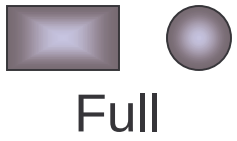
- Given a set S and PQ tree T we can mark nodes either full or partial.
  - A leaf is full if it is a member of S.
  - A node is full if all its children are full.
  - A node is partial if either it has both full and non-full children or it has a partial child.
  - A node is doubly partial if it has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

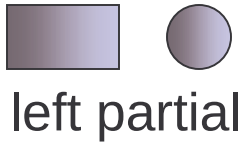
Marks of Nodes

Mark the leaves in S full.
Bottom up mark the nodes full or partial.
The members of S will become contiguous.

S = {A,C,F,H,I}



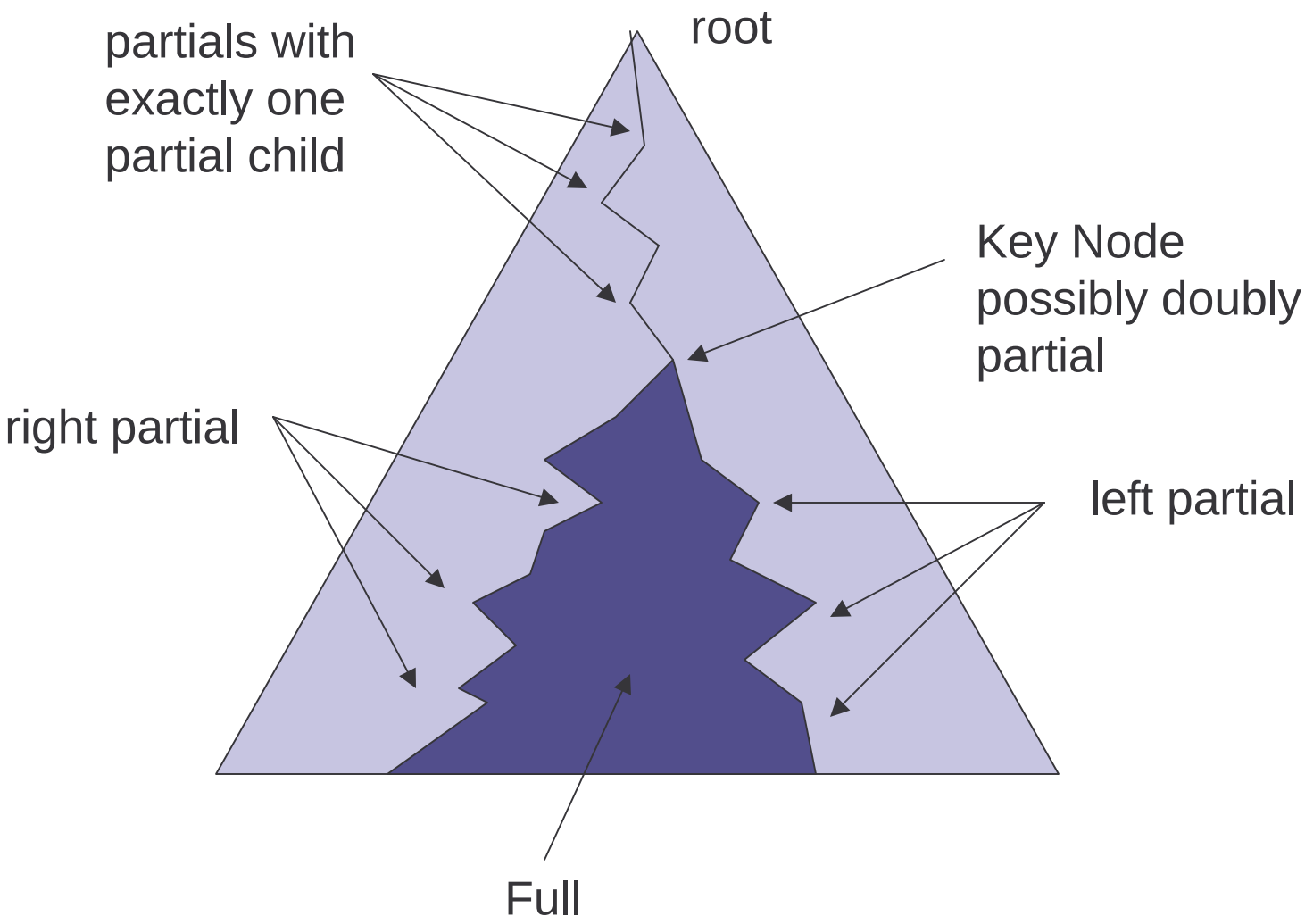

Full


left partial


right partial


doubly partial

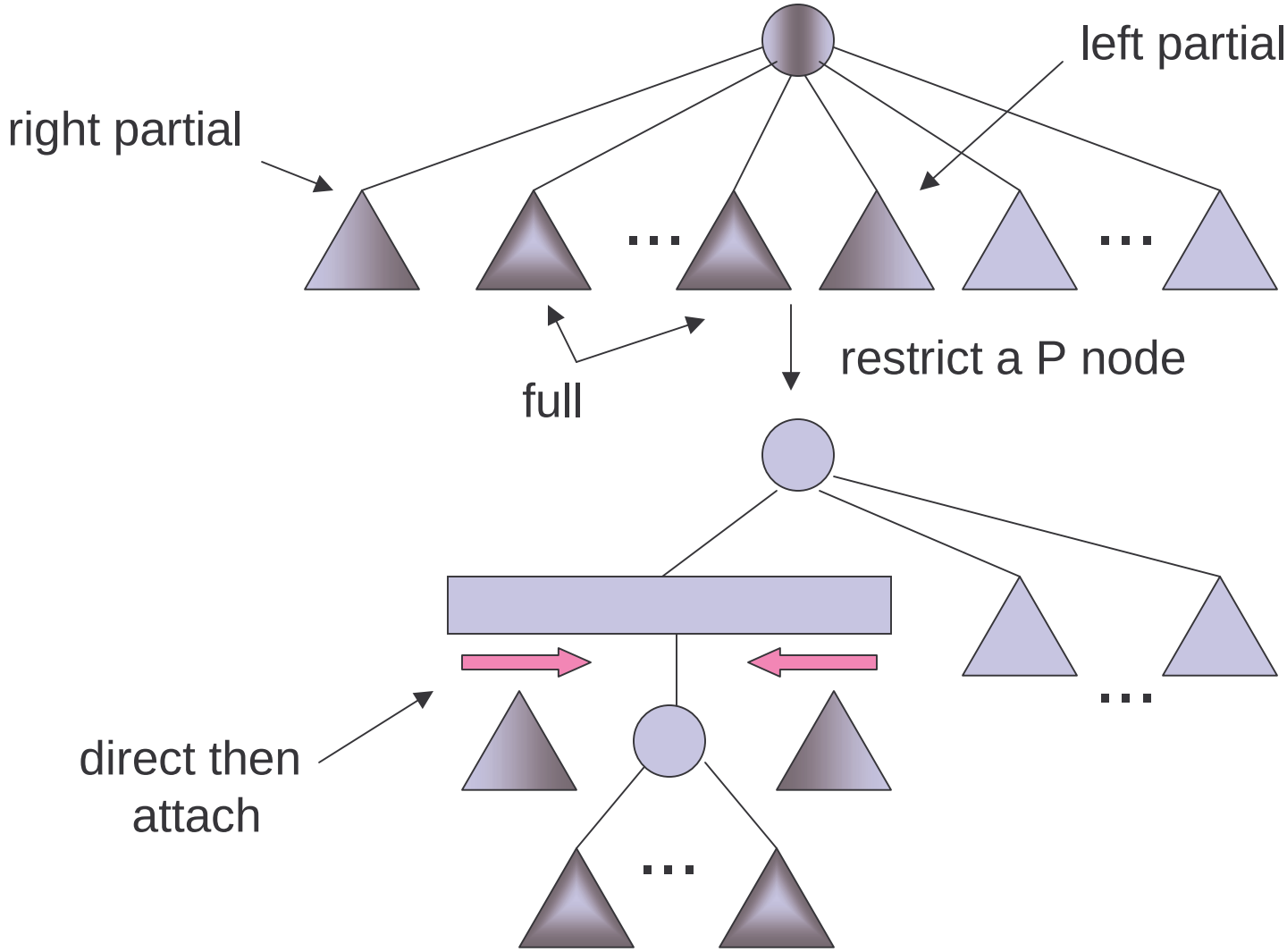
Structure of the Marked PQ Tree



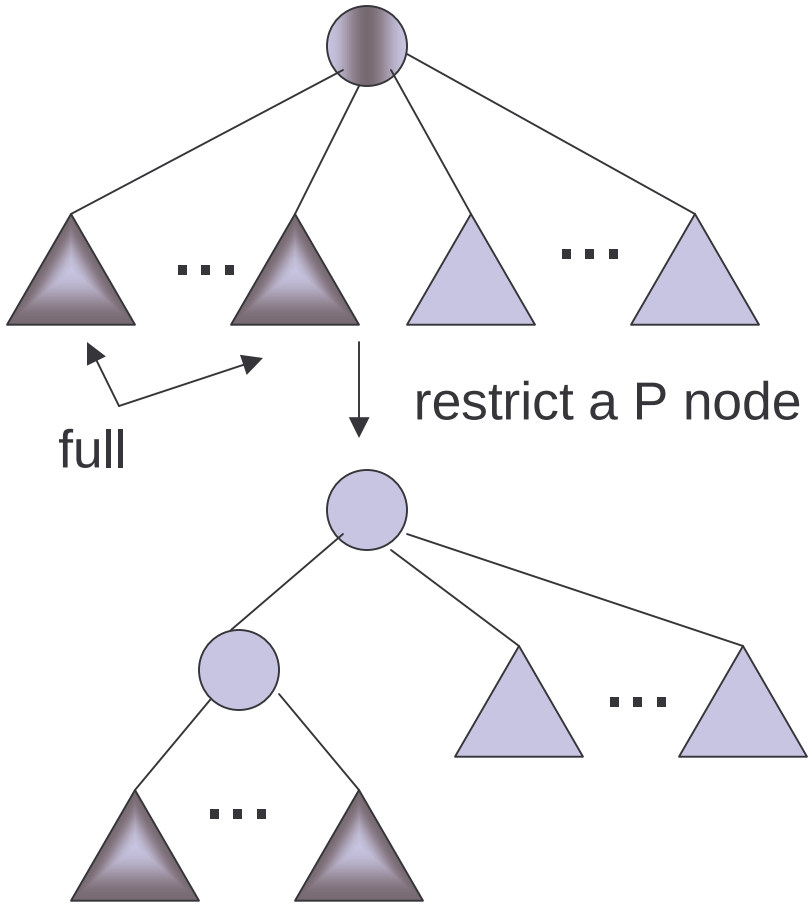
Restrict(T,S)

- 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.

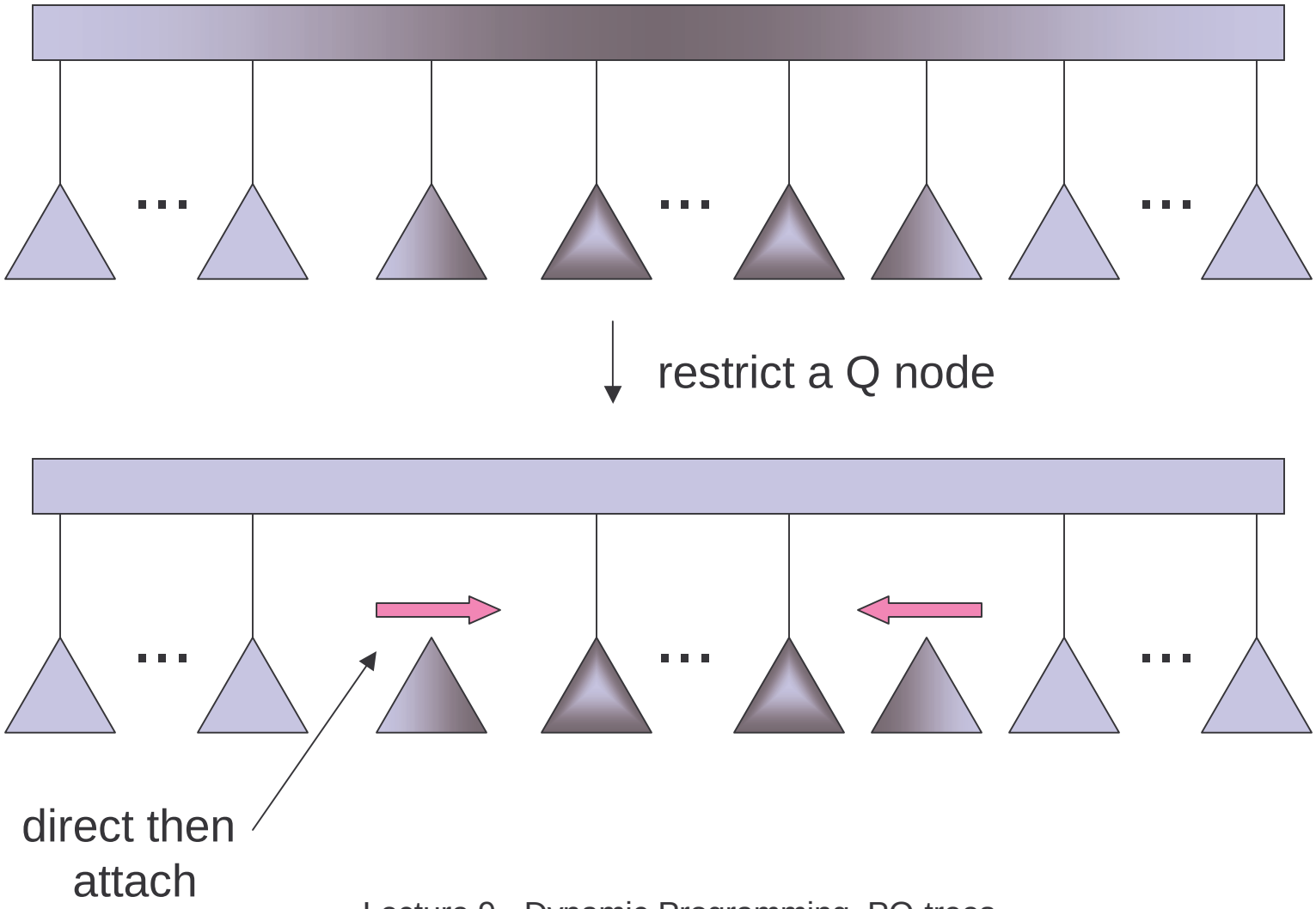
Restricting a P Node with Partial Children



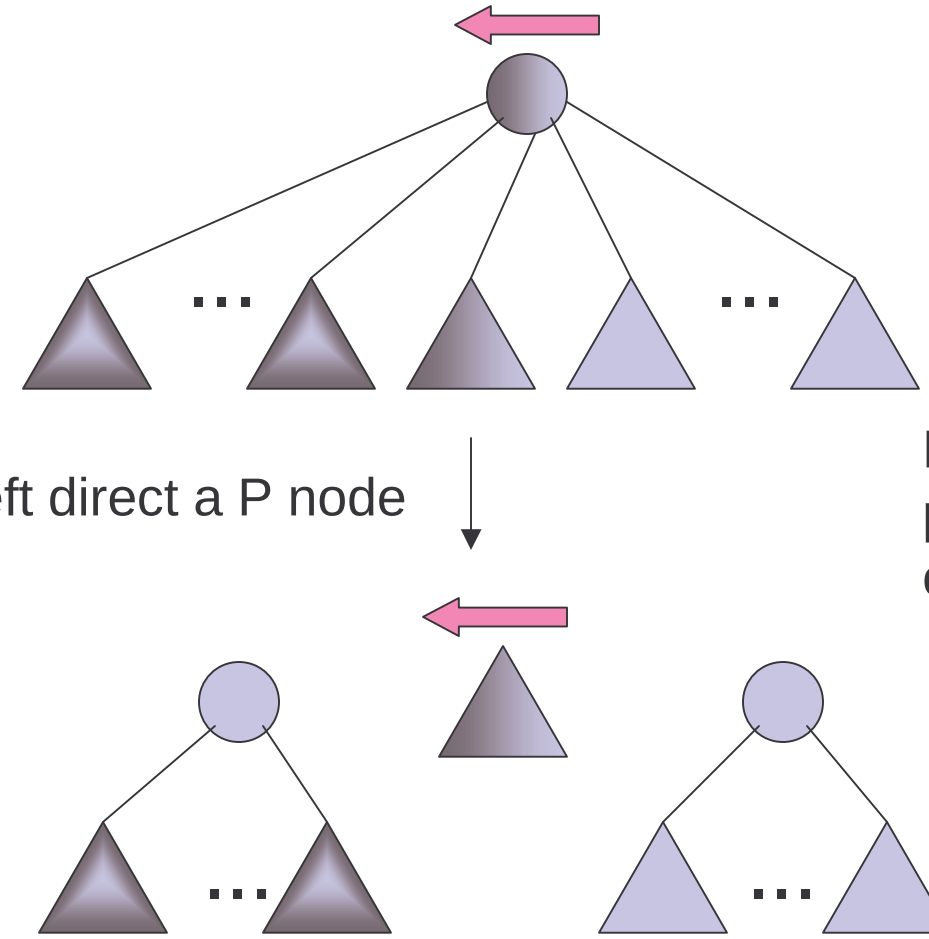
Restricting a P node with no Partial Children



Restricting a Q node



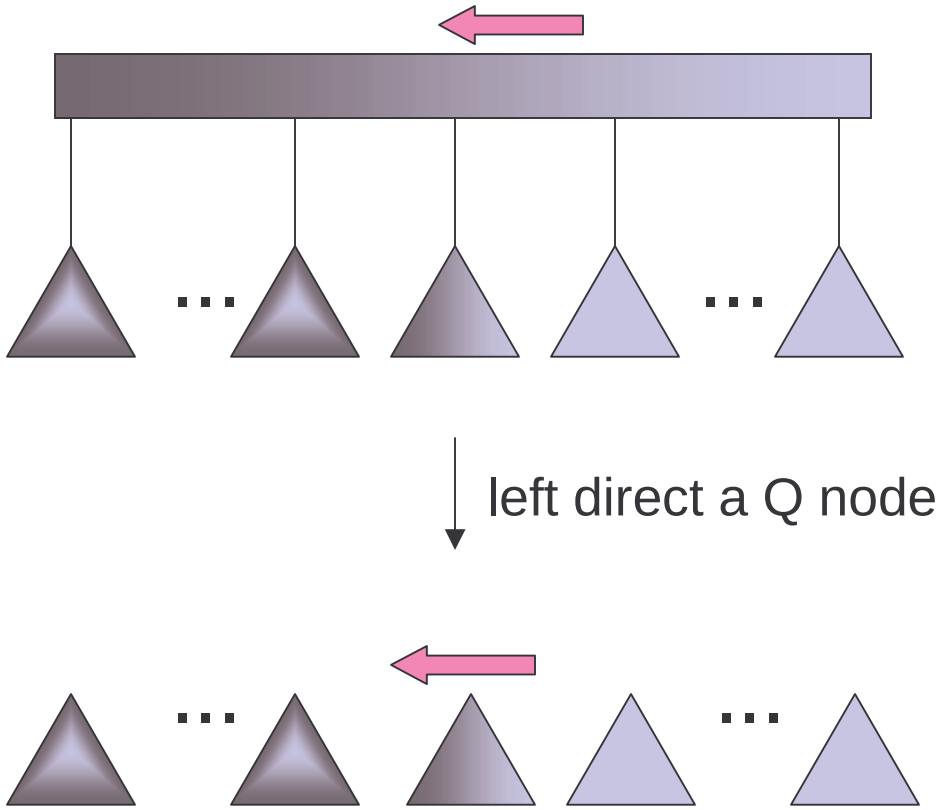
Directing a P Node



left direct a P node

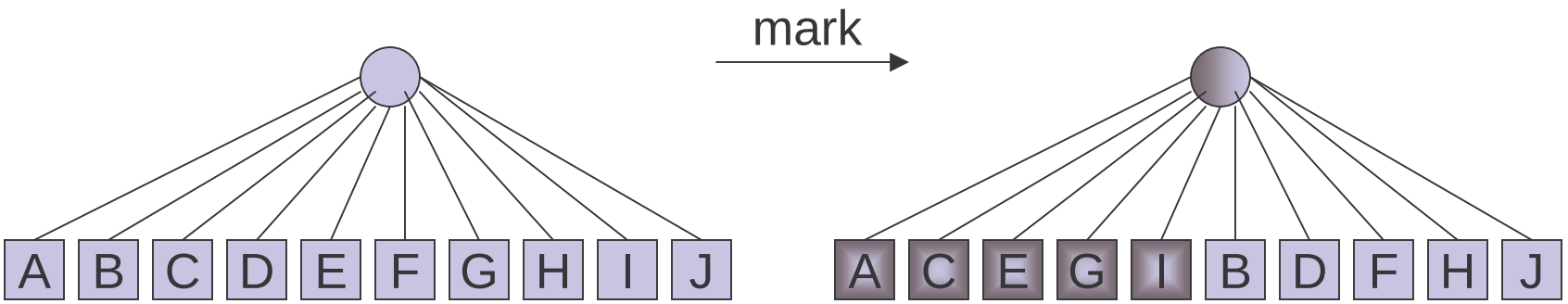
Directing a node produces a sequence of nodes.

Directing a Q Node



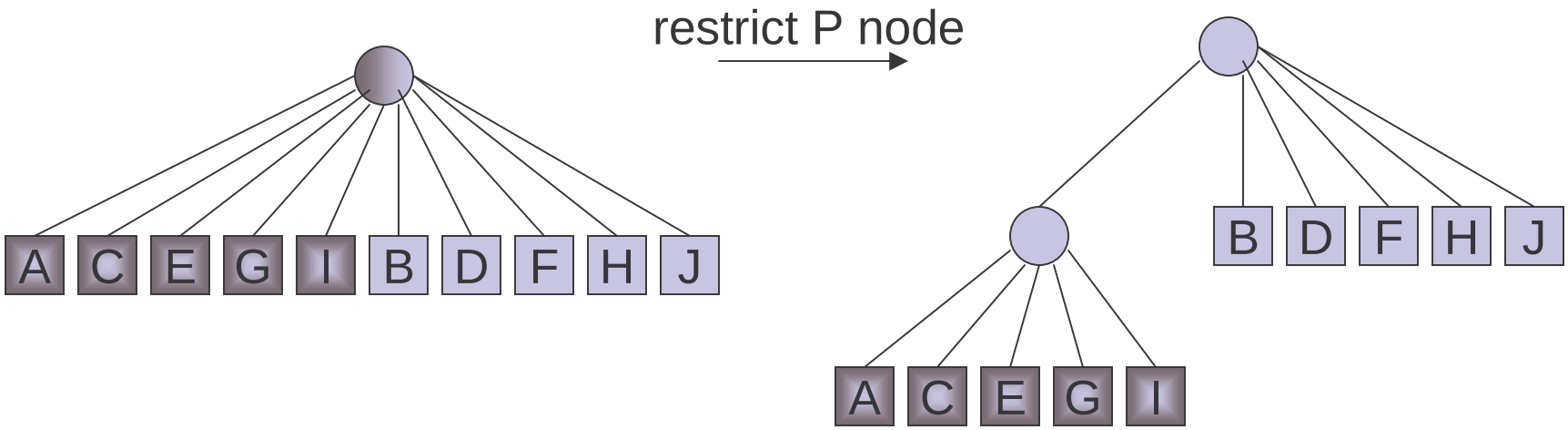
Example (1)

U = {A,B,C,D,E,F,G,H,I,J}
S_1 = {A,C,E,G,I}



Example (2)

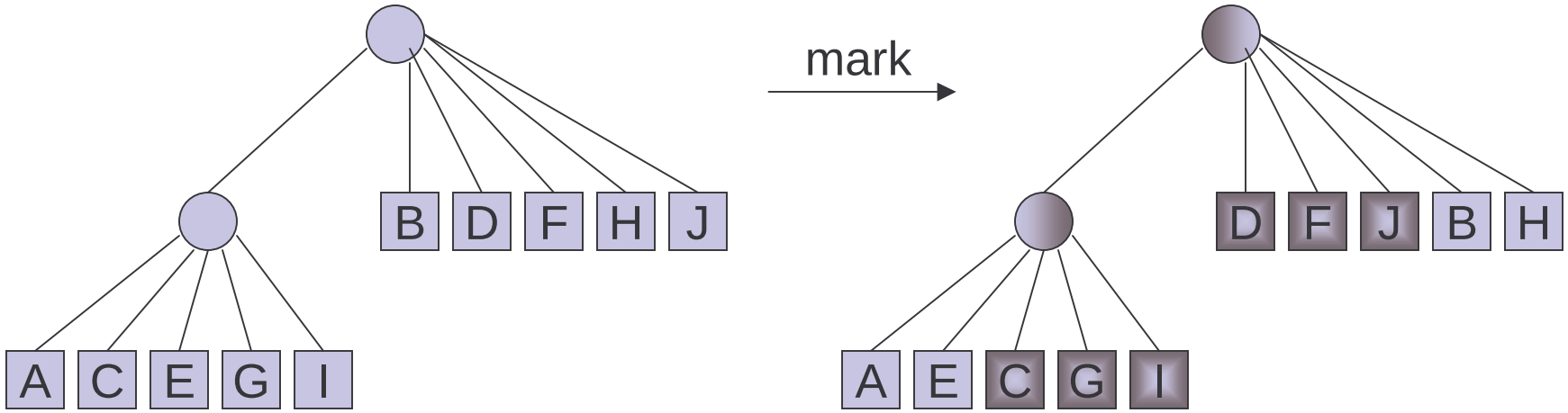
U = {A,B,C,D,E,F,G,H,I,J}
S_1 = {A,C,E,G,I}



special case because
no partial child.

Example (3)

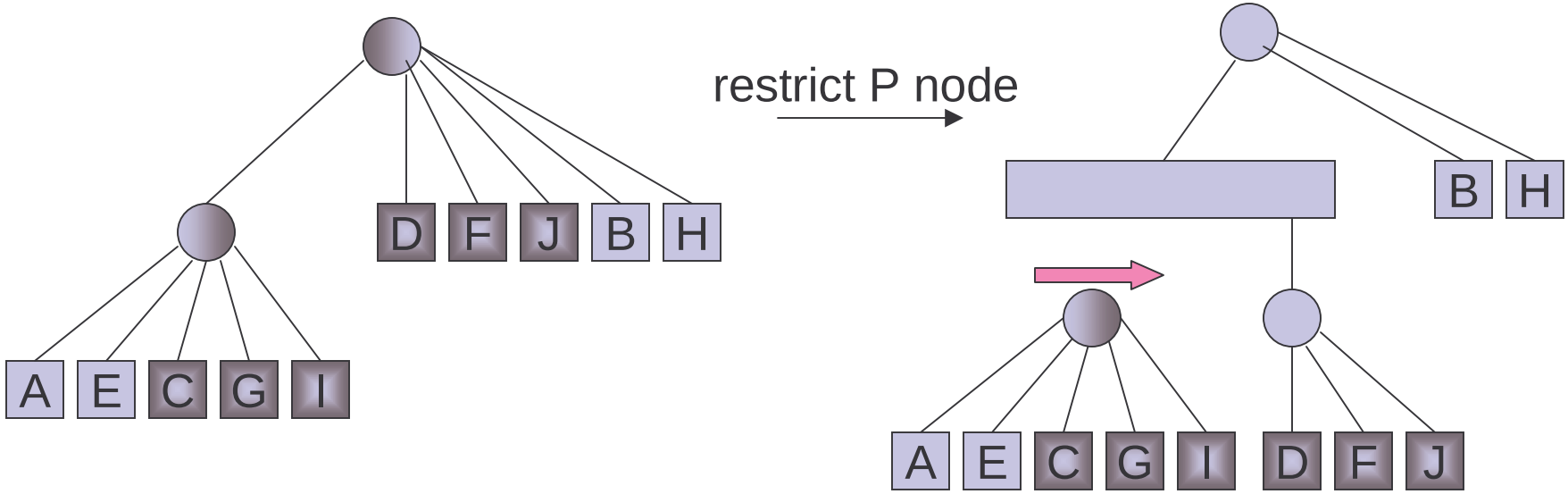
U = {A,B,C,D,E,F,G,H,I,J}
S_2 = {C,D,F,G,I,J}



Example (4)

U = {A,B,C,D,E,F,G,H,I,J}

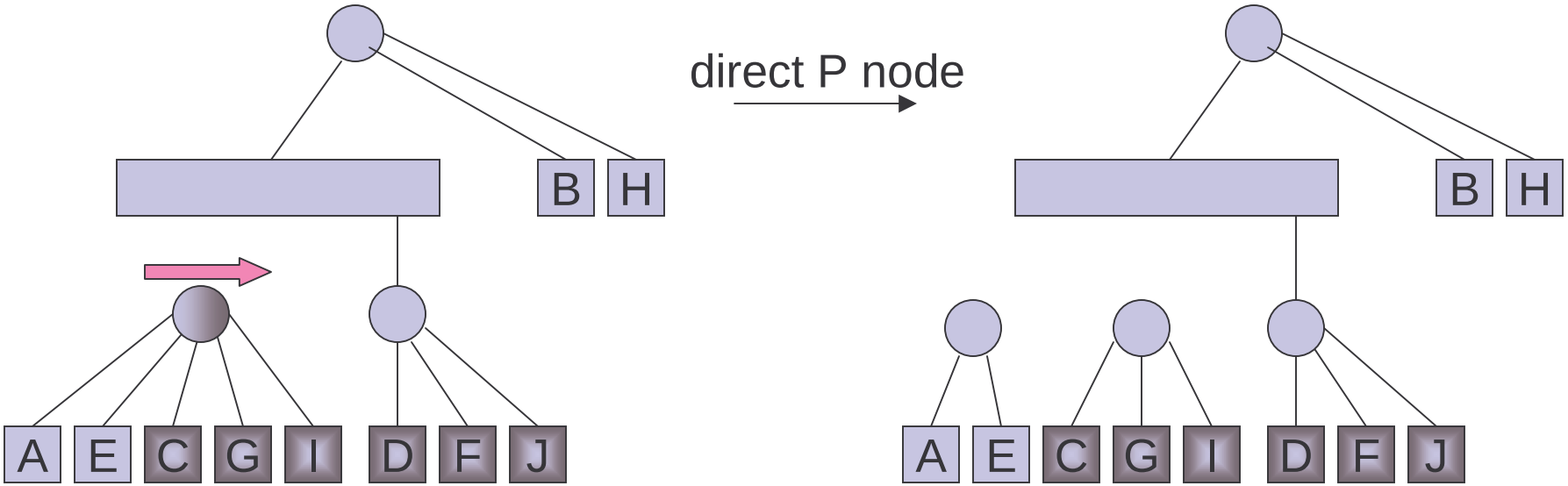
S_2 = {C,D,F,G,I,J}



Example (5)

U = {A,B,C,D,E,F,G,H,I,J}

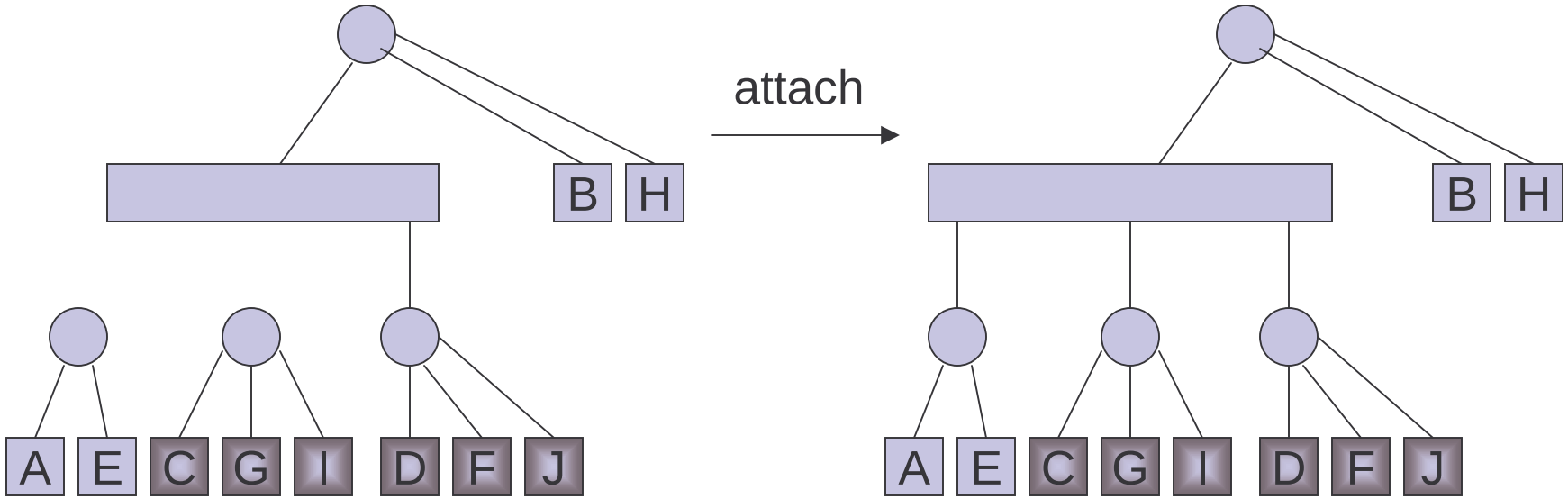
S_2 = {C,D,F,G,I,J}



Example (6)

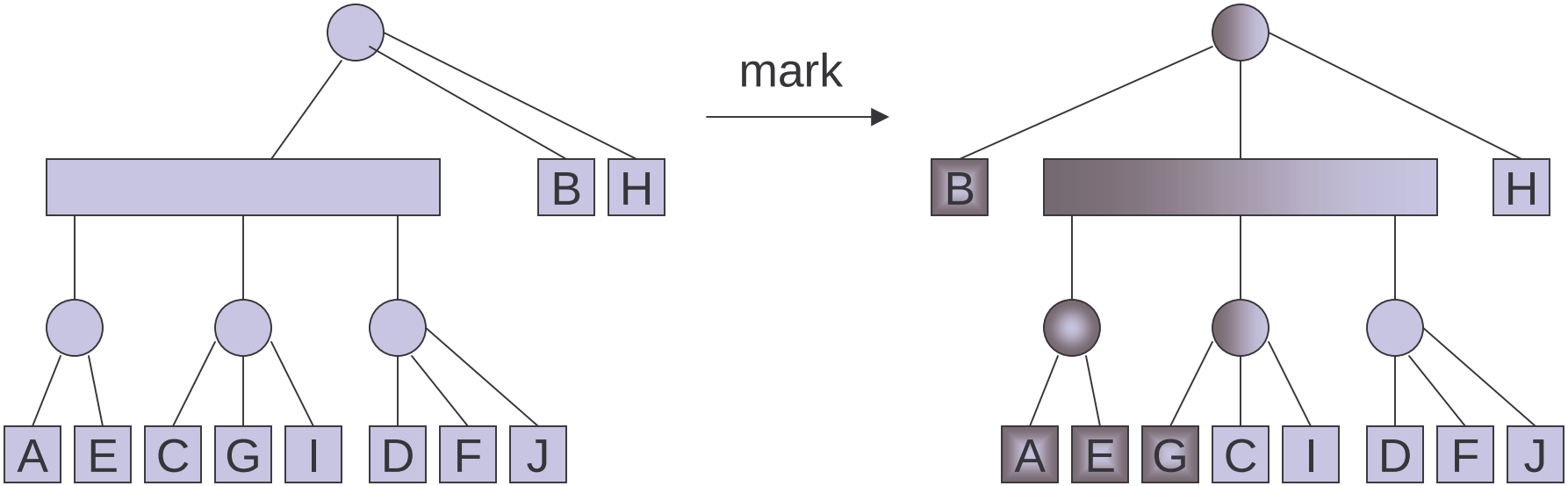
U = {A,B,C,D,E,F,G,H,I,J}

S_2 = {C,D,F,G,I,J}



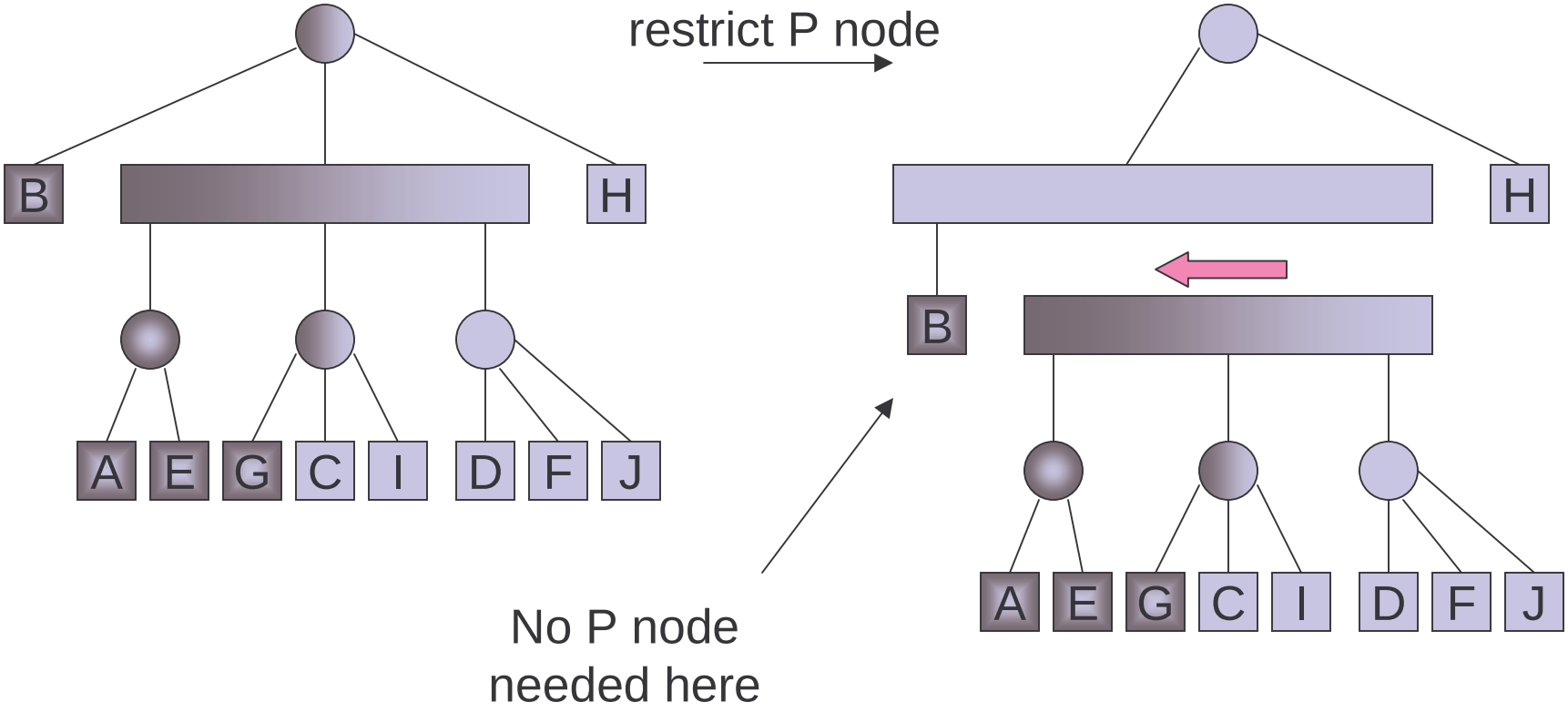
Example (7)

U = {A,B,C,D,E,F,G,H,I,J}
S_3 = {A,B,E,G}



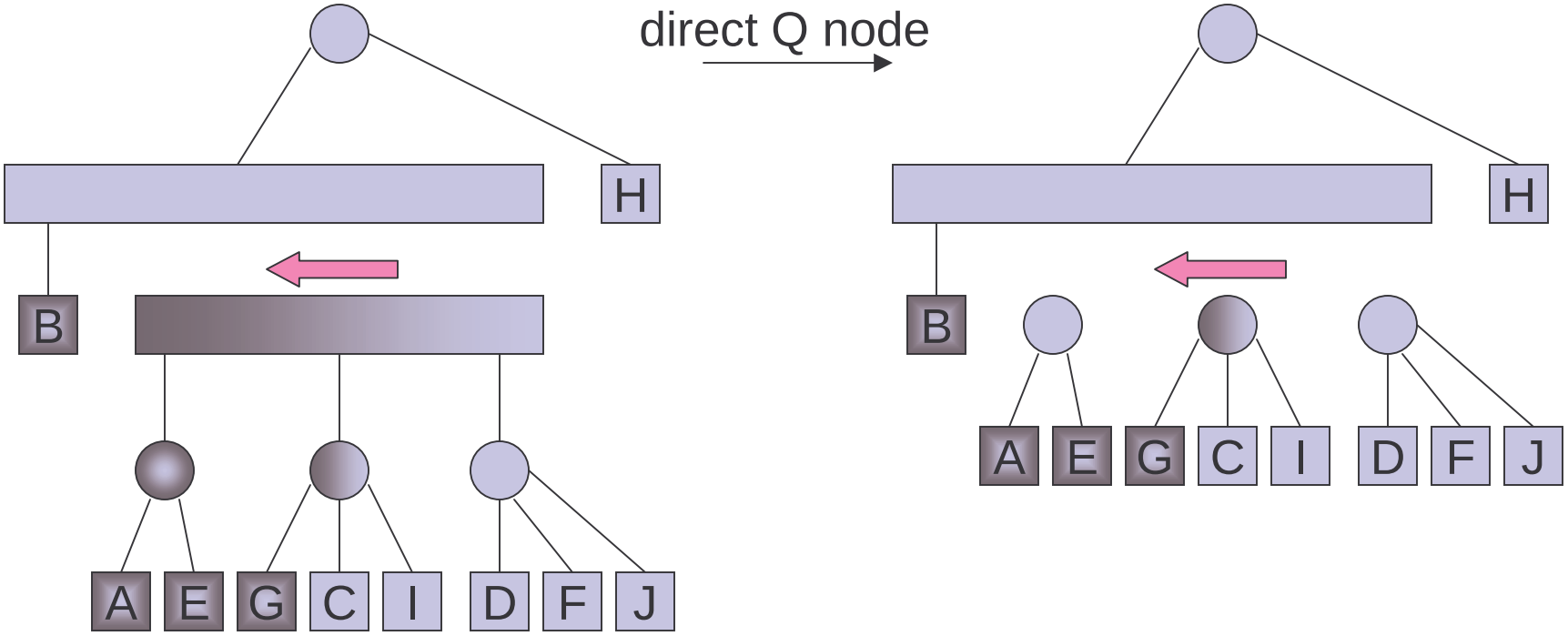
Example (8)

U = {A,B,C,D,E,F,G,H,I,J}
S_3 = {A,B,E,G}



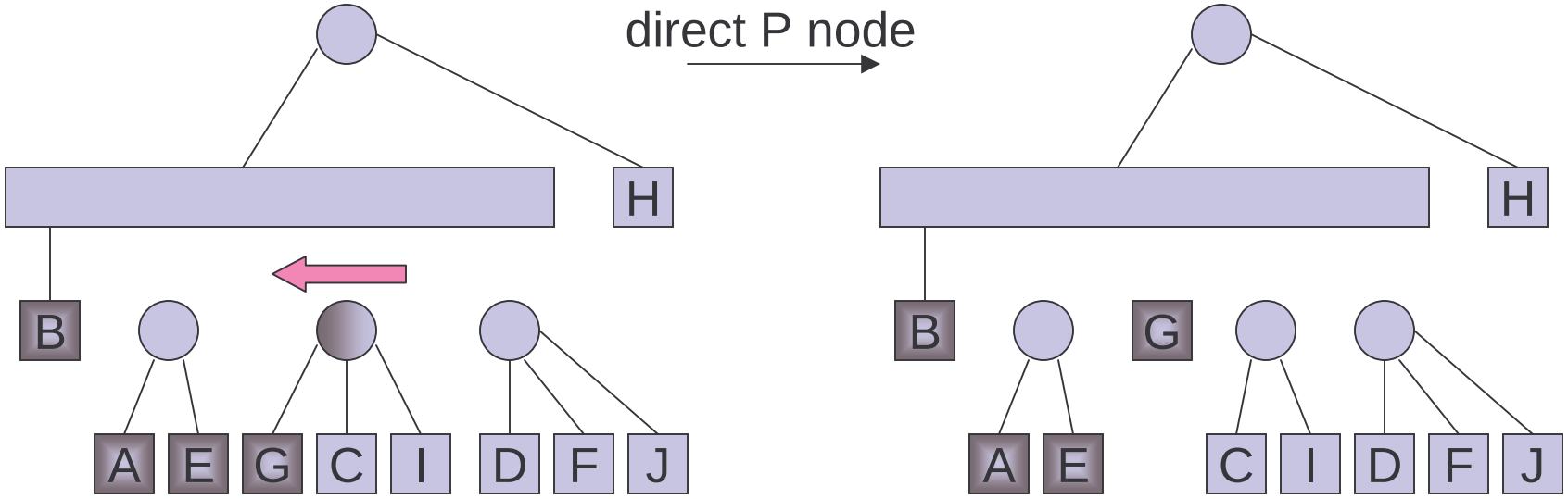
Example (9)

U = {A,B,C,D,E,F,G,H,I,J}
S_3 = {A,B,E,G}



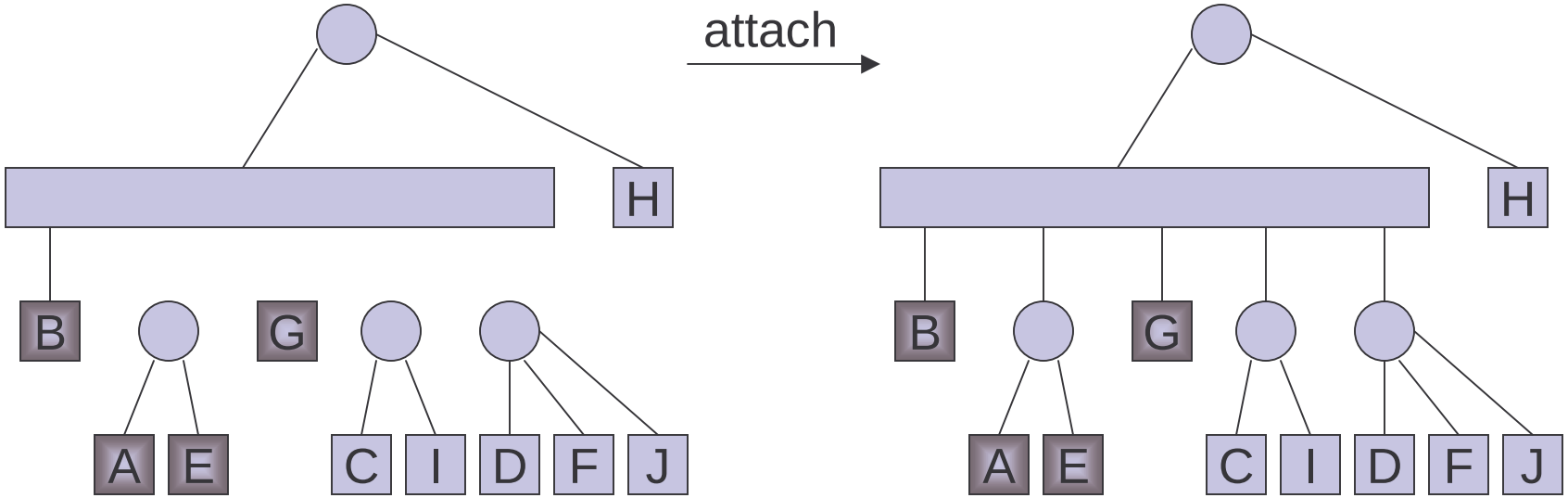
Example (10)

U = {A,B,C,D,E,F,G,H,I,J}
S_3 = {A,B,E,G}



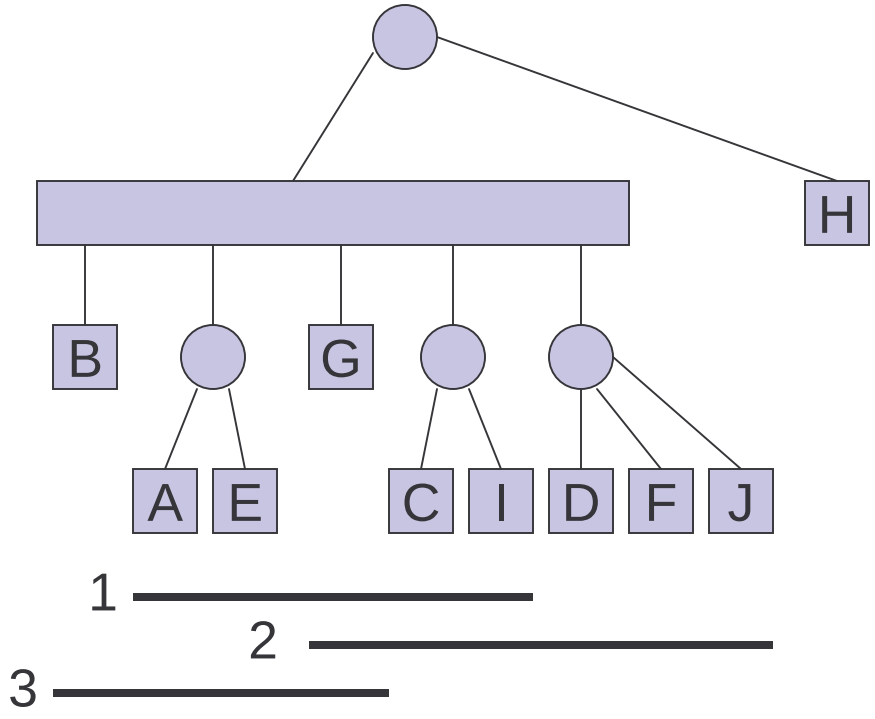
Example (11)

U = {A,B,C,D,E,F,G,H,I,J}
S_3 = {A,B,E,G}



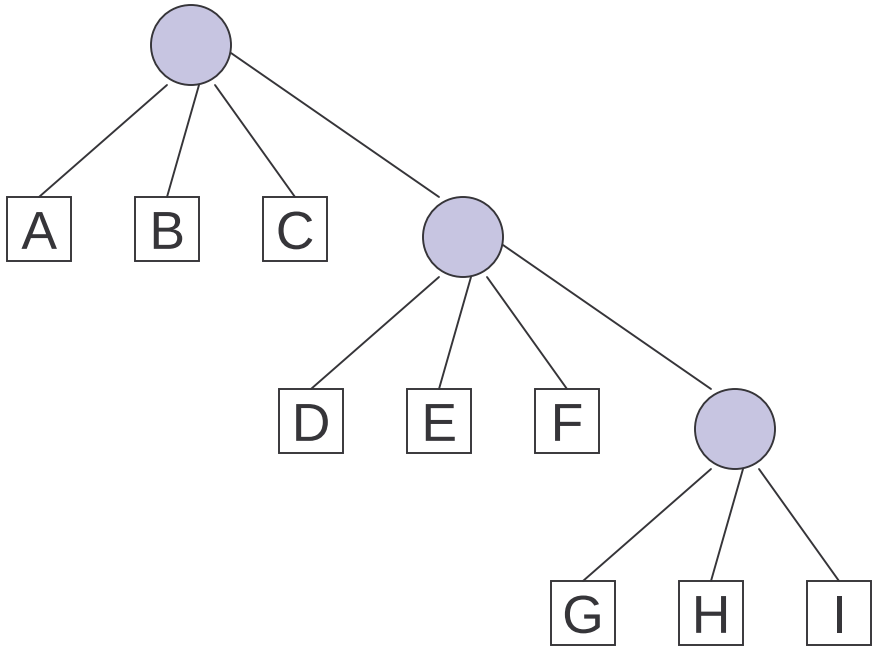
Example (12)

U = {A,B,C,D,E,F,G,H,I,J}
S_1 = {A,C,E,G,I}
S_2 = {C,D,F,G,I,J}
S_3 = {A,B,E,G}



Exercise

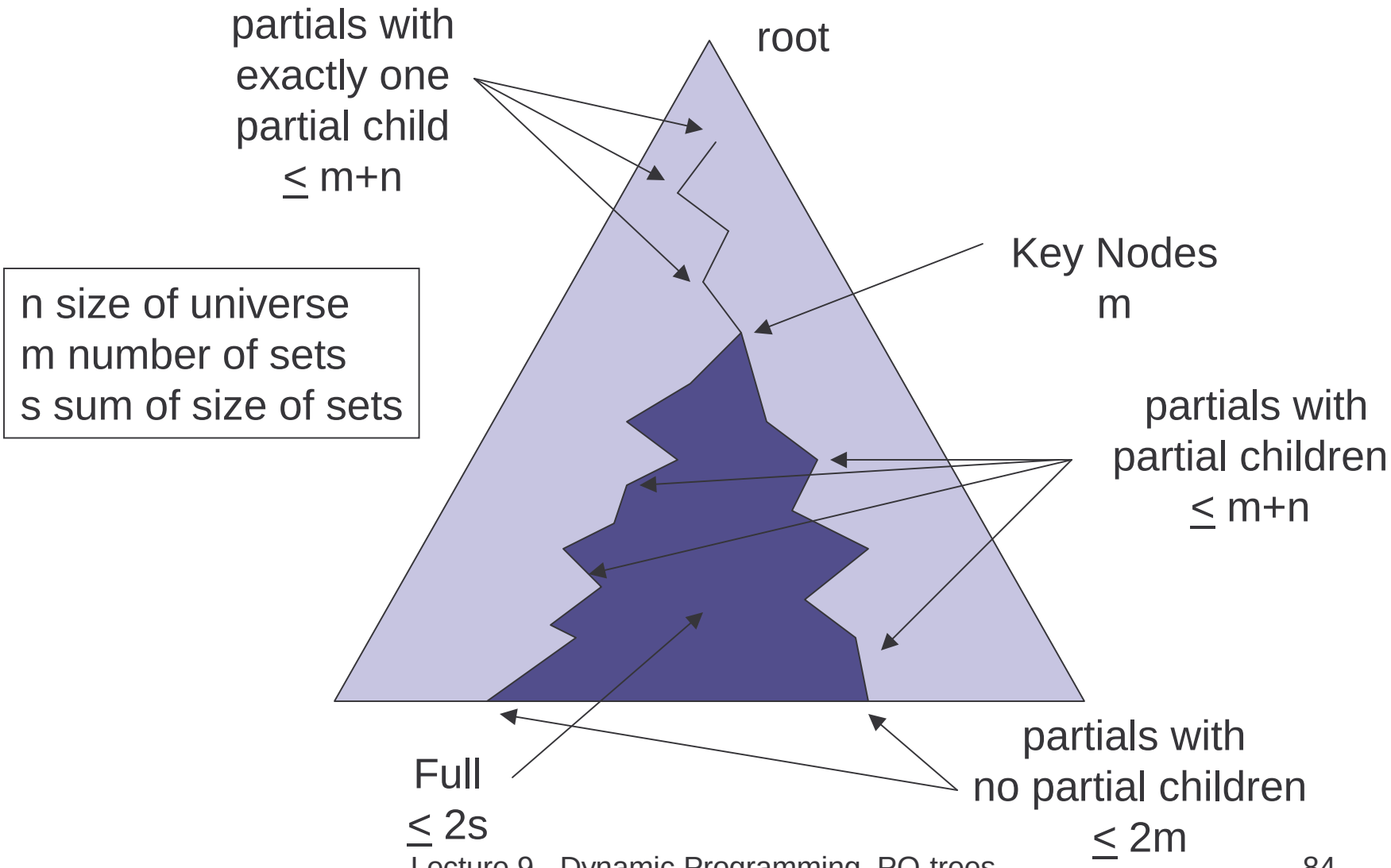
- Restrict with to make {A,B,D,E,G} contiguous



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 $\leq$ 2s.
  - Number of key nodes processed = m.
  - Number of partial nodes with partial children processed below the key node $\leq$ m + n.
  - Number of partial nodes with no partial children $\leq$ 2m.
  - Number of partial nodes processed above the key node $\leq$ m + n.

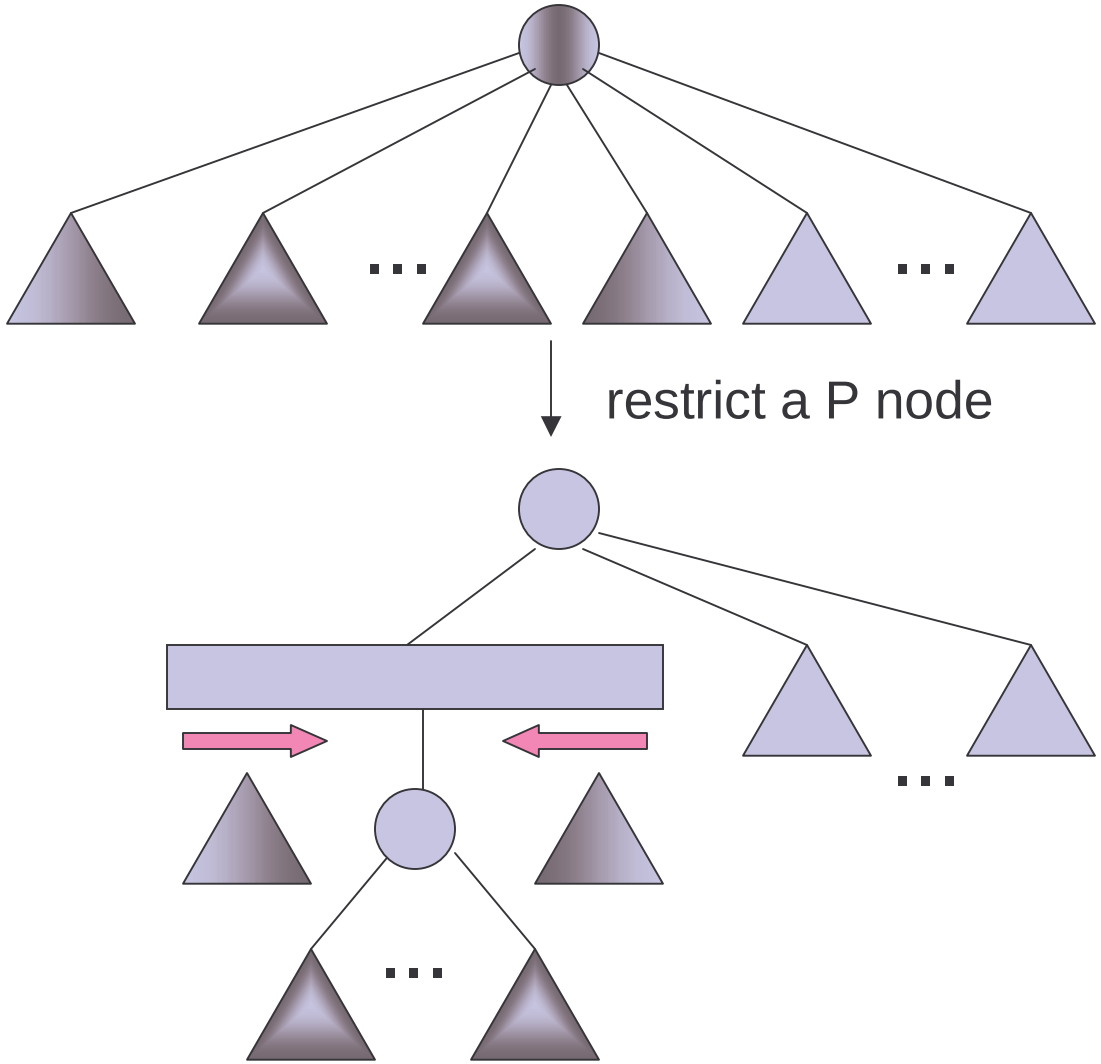
Number of Processed Nodes Amortized



Partials with Partial Children Below the Key Node

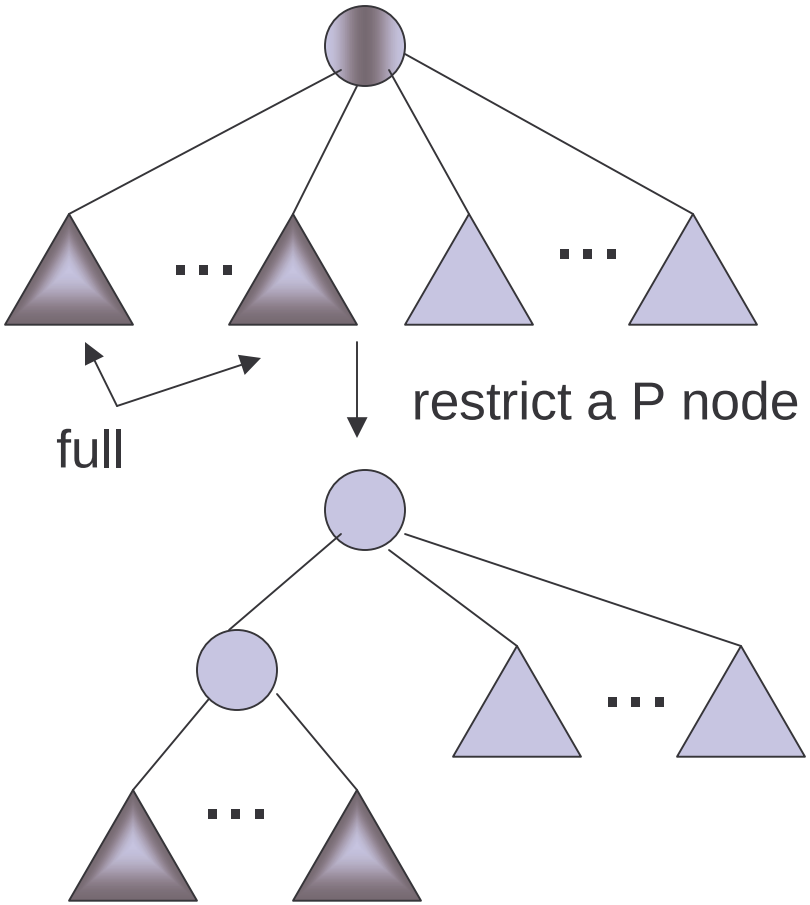
- Amortized complexity argument.
- Consider the quantities:
  - q = number of Q nodes,
    cp = number of children of P nodes.
  - We examine the quantity x = q + cp
  - x is initially n and never negative.
  - Each restrict of a key node increases x by at most 1.
  - Each direct of a partial node with 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.

Restricting a P Node with Partial Children



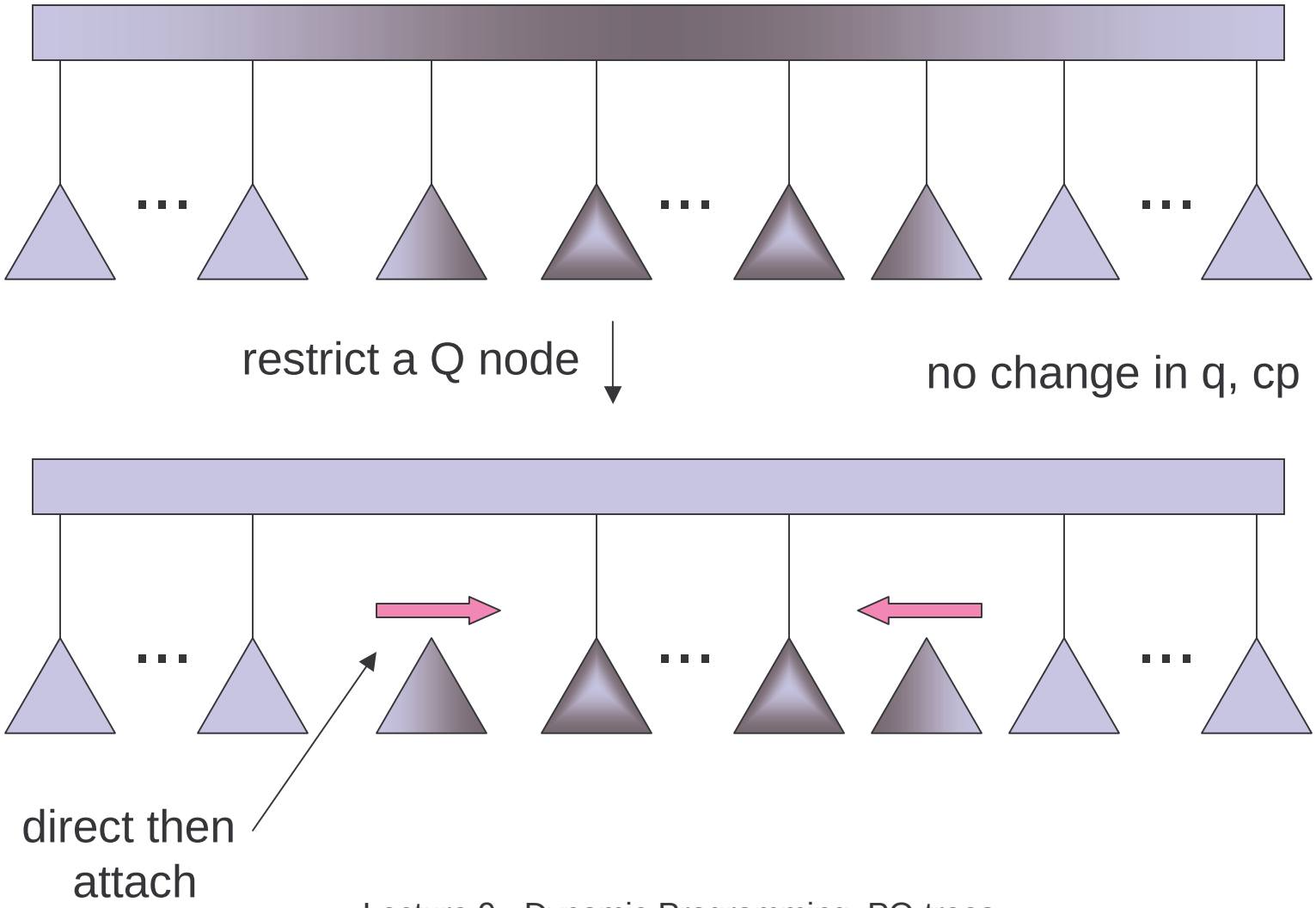
change in q + cp is at most +1.

Restricting a P node with no Partial Children

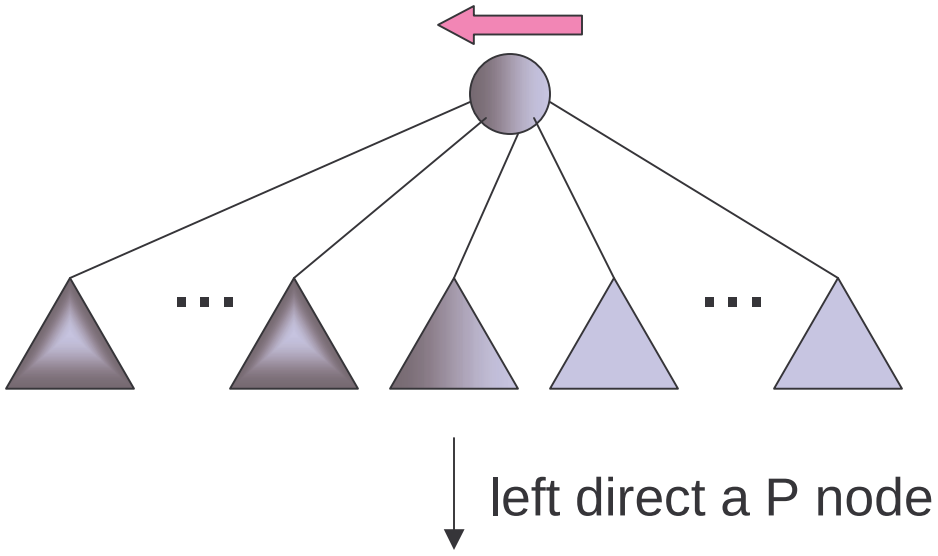


change in q + cp is exactly +1.

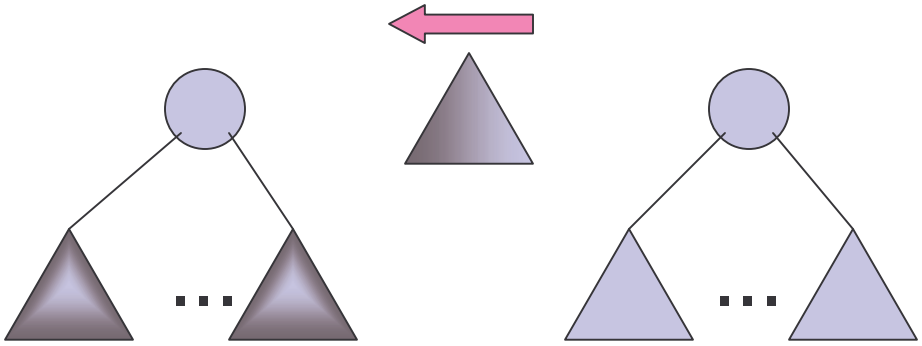
Restricting a Q node



Directing a P Node



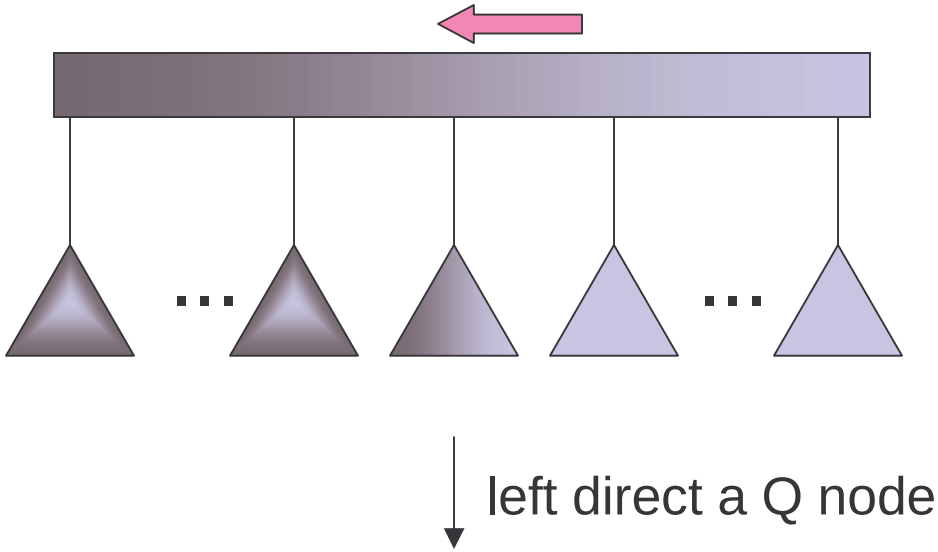
left direct a P node



Assume partial child

change in q + cp is -1

Directing a Q Node



left direct a Q node

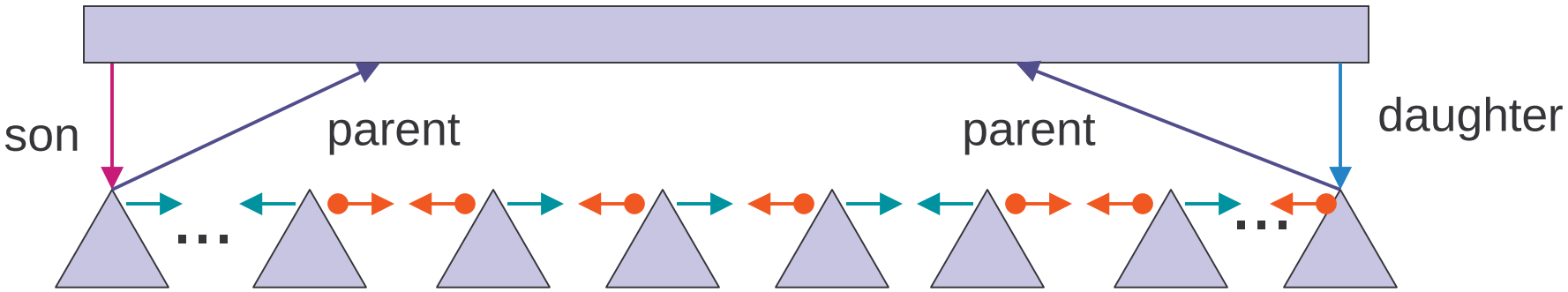
change in q + cp is -1

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.

Example of Data Structure Trick

- Linking the children of a Q node



brother

sister

Linking of siblings can be in any order.
Middle children don't know parents.
End children know parents.