Outline: Reachability Query Evaluation

- What is reachability query?
- Reachability query evaluation based on matrix multiplication
- Warren's algorithm (for generating transitive closures)
- Strassen's algorithm (for matrix multiplication)
- Reachability based on tree encoding

Motivation

• Efficient method to evaluate graph reachability queries

Given a directed graph G, check whether a node v is reachable from another node u through a path in G.

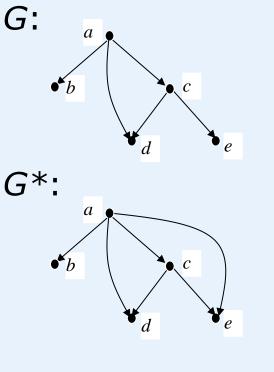
• Application

- XML data processing
- Type checking in object-oriented languages and databases
- Geographical navigation
- Internet routing
- CAD/CAM, CASE, office systems, software management

Motivation

• A simple method

- store a transitive closure as a matrix



The transitive closure G^* of a graph G is a graph such that there is an edge (u, v) in G^* iff there is path from u to v in G.

Matrix Multiplication

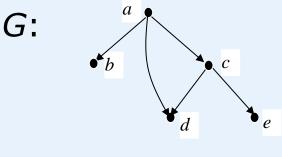
• Definition

- Two matrices *A* and *B* are compatible if the number of columns of *A* equals the number of *B*.
- If $A = (a_{ij})$ is an $m \times n$ matrix and $B = (b_{ij})$ is an $n \times p$ matrix, then their matrix product $C = A \times B$ is an $m \times p$ matrix $C = (c_{ik})$ such that

$$c_{ik} = \sum_{i=1}^{n} a_{ij} b_{jk}$$

for i = 1, 2, ..., m and k = 1, 2, ..., p.

Each entry (i, j) in $M \times M$ represents a path of length 2 from *i* to *j*.



Each entry (i, j) in $M \times M$ represents a path of length 2 from *i* to *j*. Each entry (i, j) in $M \times M \times M$ represents a path of length 3 from *i* to *j*. *k*

Each entry (i, j) in $M \times M \times M \dots \times M$ represents a path of length k from i to j.

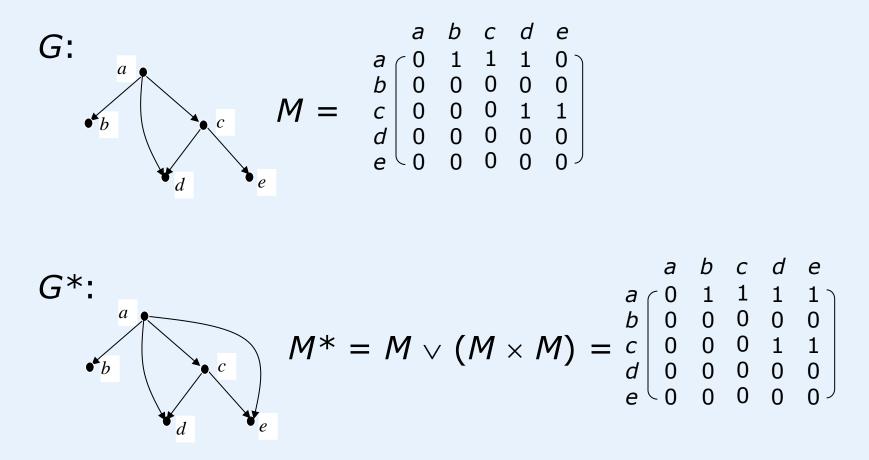
Define:

 $M^* = M^{(1)} \lor M^{(2)} \lor M^{(3)} \dots \lor M^{(n)}$

Each entry (i, j) in M^* represents a path from *i* to *j*.

Time overhead: $O(n^4)$. Space overhead: $O(n^2)$. Query time: O(1).

Example



Each entry (i, j) in P represents a path from i to j.

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Warren's Algorithm

Warren's algorithm is a quite simple way to generate a boolean matrix to represent the transitive closure of a graph *G*. Assume that *G* is represented by a boolean matrix *M* in which M(i, j) = 1 if edge (i, j) is in *G*, and M(i, j) = 0 if (i, j) is not in *G*. Then, the matrix *M*' for the transitive closure of *G* can be computed from *M*, in which M'(i, j) = 1 if there exits a path from *i* to *j* in *G*, and M'(i, j) = 0 if there is no path from *i* to *j* in *G*. Warren's algorithm is given below:

Algorithm *Warren*

for i = 2 to n do for j = 1 to i - 1 do {if M(i, j) = 1 then set $M(i, *) = M(i, *) \lor M(j, *);$ } for i = 1 to n - 1 do for j = i + 1 to n do {if M(i, j) = 1 then set $M(i, *) = M(i, *) \lor M(j, *);$ }

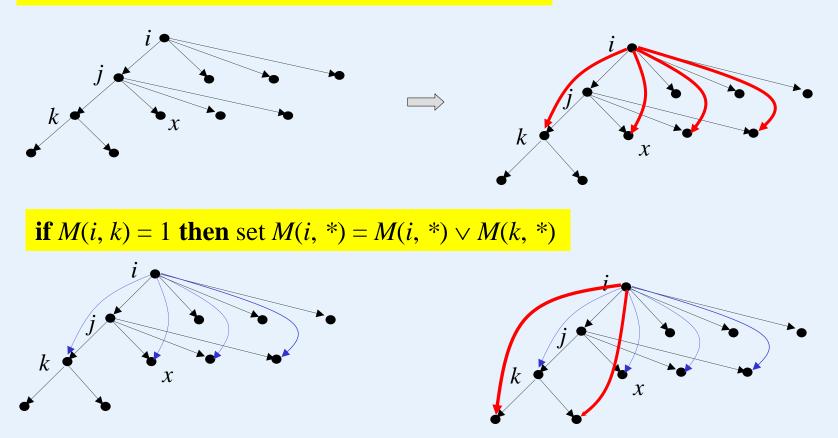


In the algorithm, M(i, *) denotes row *i* of *M*. The theoretic time complexity of Warren's algorithm is $O(n^3)$.

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if M(i, j) = 1 **then** set $M(i, *) = M(i, *) \lor M(j, *)$



S. Warshall, "A Theorem on Boolean Matrices," *JACM*, 9. 1(Jan. 1962), 11 - 12. H.S. Warren, "A Modification of Warshall's Algorithm for the Transitive Closure of Binary Relations," *Commun. ACM* 18, 4 (April 1975), 218 - 220.

Strassen's Algorithm

Strassen's algorithm runs in $O(n^{\lg 7}) = O(n^{2.81})$ time. For sufficiently large values of *n*, it outperforms Warren's algorithm.

• An overview of the algorithm

Strassen's algorithm can be viewed as an application of a familiar design technique: divide and conquer. Consider the computation $C = A \times B$, where *A*, *B*, and *C* are $n \times n$ matrices. Assuming that *n* is an exact power of 2, we divide each of *A*, *B*, and *C* into four $n/2 \times n/2$ matrices, rewriting the equation $C = A \times B$ as follows:

$$\begin{pmatrix} r & s \\ t & u \end{pmatrix} = \begin{pmatrix} a & b \\ c & d \end{pmatrix} \times \begin{pmatrix} e & f \\ g & h \end{pmatrix}$$

$$r = ae + bg$$

$$s = af + bh$$

$$t = ce + dg$$

$$u = af + dh$$

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Each of these four equations specifies two multiplications of $n/2 \times n/2$ matrices and the addition of their $n/2 \times n/2$ products. So the time complexity of the algorithm satisfies the following recursive equation:

 $T(n) = 8T(n/2) + \mathcal{O}(n^2)$

The solution of this equation is $T(n) = O(n^3)$.

Strassen discovered a different approach that requires only 7 recursive multiplications of $n/2 \times n/2$ matrices and $O(n^2)$ scalar additions and subtractions, yielding the recurrence:

$$T(n) = 7T(n/2) + O(n^2)$$

= $O(n^{\lg 7})$
= $O(n^{2.81}).$

Strassen's algorithm works in four steps:

- 1. Divide the input matrices A and B into $n/2 \times n/2$ matrices.
- 2. Using O(n^2) scalar additions and subtractions, computer 14 matrices $A_1, B_1, A_2, B_2, ..., A_7, B_7$, each of which is $n/2 \times n/2$.
- 3. Recursively compute the seven matrix products $P_i = A_i \times B_i$ for i = 1, 2, ..., 7.
- 4. Computer the desire submatrices r, s, t, u of the result matrix C by adding and/or subtracting various combinations of the P_i matrices, using only $O(n^2)$ scalar additions and subtraction.

$$A_1 = a, A_2 = (a + b), A_3 = (c + d), A_4 = d, A_5 = (a + d), A_6 = (b - d), A_7 = (c - a)$$

 $B_1 = (f - h), B_2 = h, B_3 = e, B_4 = (g - d), B_5 = (e + h), B_6 = (g + h), B_7 = (e + f)$

 $r = ae + bg = P_5 + P_4 - P_2 + P_6, s = af + bh = P_1 + P_2,$ $t = ce + dg = P_3 + P_4, u = af + dh = P_5 + P_1 - P_3 + P_7.$

7 matrix multiplication, 18 matrix additions and subtractions.

Assume that $n = 2^m$. We have

$$T(2^{m}) = 7T(2^{m-1}) + 18(2^{m-1})^{2}.$$

$$A_{m} = 7A_{m-1} + 18(2m-1)^{2}, \qquad A_{1} = 18.$$

$$G(x) = A_{1} + A_{2}x + A_{3}x^{2} + \dots$$

$$= A_{1} + (7A_{1} + 18 \cdot 2^{2})x$$

$$+ (7A_{2} + 18 \cdot 2^{3})x^{2}$$

$$\dots$$

$$= 18 + 7x \ G(x) + 18 \cdot 4x/(1 - 4x)$$

(1 - 7x)G(x) = 18(4x/(1 - 4x) + 1) = 18/(1 - 4x)

$$(1 - 7x)G(x) = 18(4x/(1 - 4x) + 1) = 18/(1 - 4x)$$

$$G(x) = 18/(1 - 4x)(1 - 7x) = 18\left(\frac{-4/3}{1 - 4x} + \frac{7/3}{1 - 7x}\right)$$

$$G(x) = 6\sum_{k=0}^{\infty} (7^{k+1} - 4^{k+1})x^{k}$$

$$\prod_{k=0}^{\infty} A_{m} = 6(7^{m} - 4^{m}), \qquad m = \log_{2}n$$

$$= O(6 \cdot 7^{\log_{2}n})$$

$$= O(6 \cdot n^{\log_{2}7})$$

$$= O(n^{2.81})$$

• Determining the submatrix products

It is not clear exactly how Strassen discovered the submatrix products that are the key to making his algorithm work. Here, we reconstruct one plausible discovery method.

Write $P_i = A_i \times B_i$ = $(\alpha_{i1}a + \alpha_{i2}b + \alpha_{i3}c + \alpha_{i4}d) (\beta_{i2}e + \beta_{i1}f + \beta_{i3}g + \beta_{i4}h)$, where the coefficients α_{ij} , β_{ij} are all drawn from the set {-1, 0, 1}. We guess that each product is computed by adding or subtracting some of the submatrices of *A*, adding or subtracting some of submatrices of *B*, and then multiplying the two results together.

$$P_{i} = A_{i} \times B_{i} = (\alpha_{i1}a + \alpha_{i2}b + \alpha_{i3}c + \alpha_{i4}d) (\beta_{i1}e + \beta_{i2}f + \beta_{i3}g + \beta_{i4}h)$$

$$= (a \ b \ c \ d) \begin{bmatrix} \alpha_{i1} \\ \alpha_{i2} \\ \alpha_{i3} \\ \alpha_{i4} \end{bmatrix} (\beta_{i1} \ \beta_{i2} \ \beta_{i3} \ \beta_{i4}) \begin{bmatrix} e \\ f \\ g \\ h \end{bmatrix}$$

$$= (a \ b \ c \ d) \begin{bmatrix} \alpha_{i1}\beta_{i1} & \alpha_{i1}\beta_{i2} & \alpha_{i1}\beta_{i3} & \alpha_{i1}\beta_{i4} \\ \alpha_{i2}\beta_{i1} & \alpha_{i2}\beta_{i2} & \alpha_{i2}\beta_{i3} & \alpha_{i2}\beta_{i4} \\ \alpha_{i3}\beta_{i1} & \alpha_{i3}\beta_{i2} & \alpha_{i3}\beta_{i3} & \alpha_{i3}\beta_{i4} \\ \alpha_{i4} \ \beta_{i1} & \alpha_{i4}\beta_{i2} & \alpha_{i4}\beta_{i3} & \alpha_{i4}\beta_{i4} \end{bmatrix} \begin{bmatrix} e \\ f \\ g \\ h \end{bmatrix}$$

$$\begin{pmatrix} r & s \\ t & u \end{pmatrix} = \begin{pmatrix} a & b \\ c & d \end{pmatrix} \times \begin{pmatrix} e & f \\ g & h \end{pmatrix}$$

$$r = ae + bg$$

$$s = af + bh$$

$$t = ce + dg$$

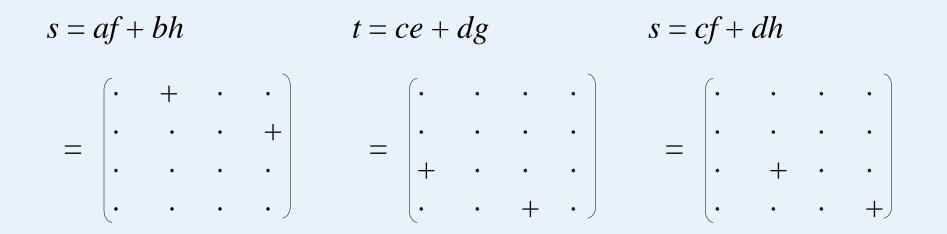
$$u = af + dh$$

r = ae + bg

 $= (a \ b \ c \ d) \begin{pmatrix} +1 \ 0 & 0 & 0 \\ 0 & 0 & +1 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} e \\ f \\ g \\ h \end{pmatrix}$

$$\begin{pmatrix} + & \cdot & \cdot & \cdot \\ \cdot & \cdot & + & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \end{pmatrix}$$

'.' - represents 0.
'+' - represents +1.
'-' - represents -1.



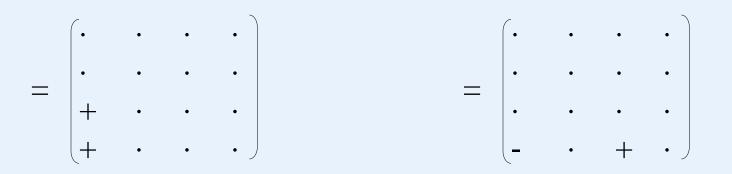
We will create 7 matrices in such a way that the above 4 matrices can be generated by addition and subtraction operations over these 7 matrices. Furthermore, the 7 matrices themselves can be produced by 7 multiplications and some additions and subtractions.

 $P_{1} = A_{1} \cdot B_{1} = a \cdot (f - h) = af - ah \qquad P_{2} = A_{2} \cdot B_{2} = (a + b) \cdot h = ah + bh$ $= \begin{pmatrix} \cdot & + & - \\ \cdot & \cdot & - \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \end{pmatrix} \qquad = \begin{pmatrix} \cdot & \cdot & + \\ \cdot & \cdot & + \\ \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot \end{pmatrix}$

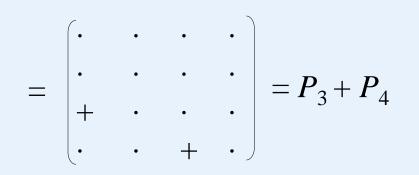
s = af + bh

$$= \begin{pmatrix} \cdot & + & \cdot & \cdot \\ \cdot & \cdot & \cdot & + \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \end{pmatrix} = P_1 + P_2$$



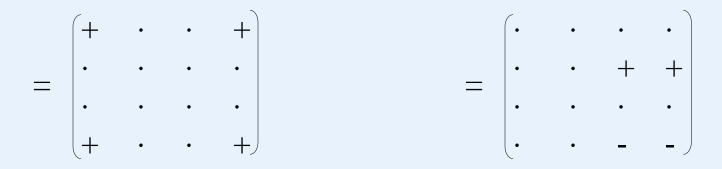


t = ce + dg



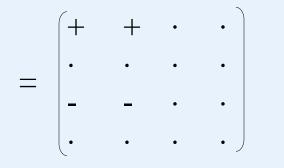
$$P_5 = A_5 \cdot B_5 = (a+d) \cdot (e+h)$$
$$= ae + ah + de + dh$$

$$\begin{aligned} P_6 &= A_6 \cdot B_6 = (b-d) \cdot (g+h) \\ &= bg + bh - dg - dh \end{aligned}$$



r = ae + bg

$$P_7 = A_7 \cdot B_7 = (a - c) \cdot (e + f)$$
$$= ae + af - ce - cf$$



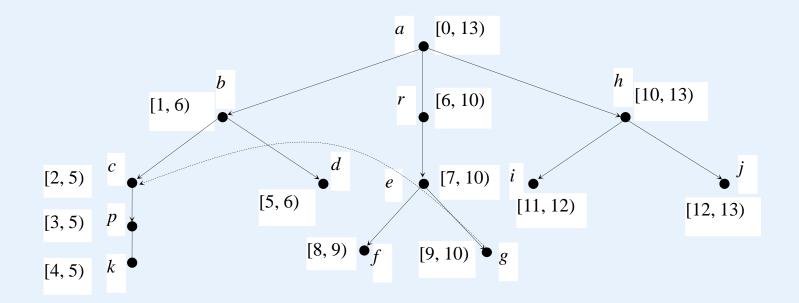
$$u = cf + dh$$

$$= \begin{pmatrix} \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot \\ \cdot & + & \cdot & \cdot \\ \cdot & \cdot & \cdot & + \end{pmatrix} = P_5 + P_1 - P_3 - P_7$$

First kind of tree encoding

- Definition
 - We can assign each node *v* in a tree *T* an interval $[\alpha_v, \beta_v)$, where α_v is *v*'s preorder number (denoted *pre*(*v*)) and $\beta_v - 1$ is equal to the largest preorder number among all the nodes in *T*[*v*] (subtree rooted at *v*).
 - So another node *u* labeled $[\alpha_u, \beta_u)$ is a descendant of *v* (with respect to *T*) iff $\alpha_u \in [\alpha_v, \beta_v)$.
 - If $\alpha_u \in [\alpha_v, \beta_v)$, we say, $[\alpha_u, \beta_u)$ is subsumed by $[\alpha_v, \beta_v)$. This method is called the *tree labeling*.

Example:



For a directed graph, the intervals cannot be used to check reachability. The containment is just a sufficient condition, not a necessary condition.

Reachability checking based on tree encoding

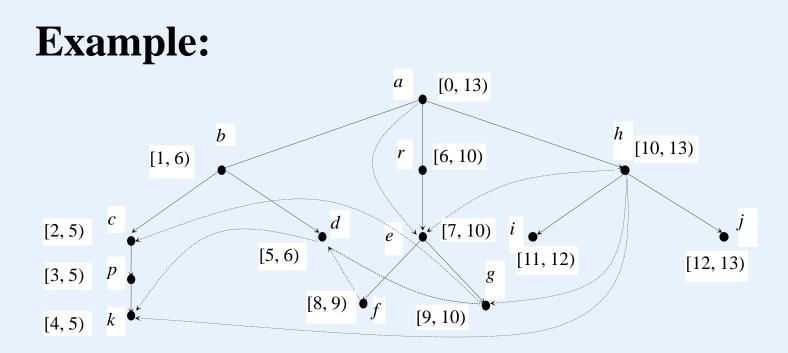
Directed acyclic graphs (DAGs)

- Find a spanning tree *T* of *G*, and assign each node *v* an interval.
- Examine all the nodes in *G* in reverse topological order and do the following:

For every edge (p, q), add all the intervals associated with the node q to the intervals associated with the node p.

When adding an interval [i, j) to the interval sequence associated with a node, if an interval [i', j'] is subsumed by [i, j), it will be discarded from the sequence. In other words: if $i' \in [i, j)$, then discard [i', j']. On the other hand, if an interval [i', j'] is equal to [i, j) or subsumes [i, j). [i, j) will not be added to the sequence. Otherwise, [i, j) will be inserted.

Topological order of a directed acyclic graph: Linear ordering of the vertices of *G* such that if $(u, v) \in E$, then *u* appears somewhere before *v*.

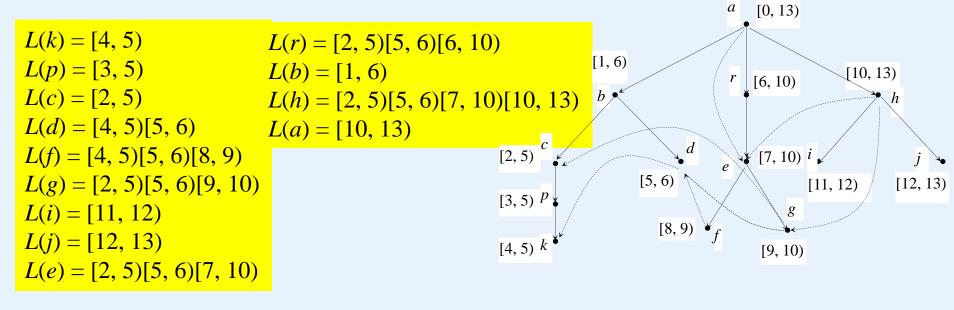


Topological order: a, b, r, h, e, f, g, d, c, p, k, i, j

Reverse topological order:

A sequence of the nodes of *G* such that for any edge (*u*, *v*) *v* appears before *u* in the sequence.

Reverse topological order



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Generation of interval sequences

- Create interval sequences for all the nodes along the reverse topological order
- •First of all, we notice that each leaf node is exactly associated with one interval, which is trivially sorted.
- •Let $v_1, ..., v_l$ be the child nodes of v, associated with the interval sequences $L_1, ..., L_l$, respectively.
- •Assume that the intervals in each L_i are sorted according to the first element in each interval. We will merge all L_i 's into the interval sequence associated L with v as follows.
- Let $[a_1, b_1)$ (from *L*) and $[a_2, b_2)$ (from L_i) be the interval encountered. We will perform the following checkings:

 $L = \dots [a_1, b_1) \dots$ $L_i = \dots [a_2, b_2) \dots$

-If $a_2 >= a_1$ then {if $a_2 \in [a_1, b_1)$ then go to the interval next to $[a_2, b_2)$ and compare it with $[a_1, b_1)$ in a next step else go to the interval next to $[a_1, b_1)$ and compare it with $[a_2, b_2)$ in a next step.}

-If $a_1 > a_2$ **then**

{if $a_1 \in [a_2, b_2)$ then remove $[a_1, b_1)$ from *L* and compare the interval next to $[a_1, b_1)$ with $[a_2, b_2)$ in a next step else insert $[a_2, b_2)$ into *L* before $[a_1, b_1)$.}

Obviously, $|L| \le b$ (the number of the leaf nodes in the spanning tree *T*) and the intervals in *L* are sorted. The time spent on this process is $O(d_v b)$, where d_v represents the outdegree of *v*. So the whole cost is bounded by

$$O(\sum_{v} d_{v}b) = O(be).$$

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Reachability checking for DAGs

- Let *u* and *v* be two nodes of *G*.
- *u* is a descendant of *v* iff there exists an interval $[\alpha, \beta)$ in L(v) such that $\alpha_u \in [\alpha, \beta)$.

Example:

Reachability checking for cyclic graphs

- Using the Tarjan's algorithm to recognize all the *strongly connected components (SCCs)*. In each SCC, any two nodes are reachable from each other.
- Collapse each SCC to a single node. In this way, any cyclic graph *G* is transformed to a DAG *G*'.
- Let *u* and *v* be to two nodes in *G*. Check their reachability according to two cases:
 - *u* and *v* are in two different SCC.
 - *u* and *v* are in the same SCC.

Second kind of tree encoding: Using tree encoding as a filter

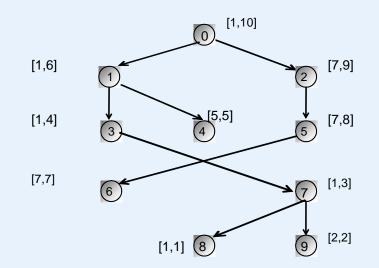
• Each node *v* in a tree *T* is labeled with a with a range

$$I_v = [r_x, r_v],$$

where r_v is the postorder number of v (the postorder numbers are assumed to begin at 1) and r_x is the lowest postorder number of any node x in the subtree rooted at v (i.e., including v).

- This approach guarantees that the containment between intervals is equivalent to the reachability relationship between the nodes, since the postorder traversal enters a node before all of its descendants have been visited.
- In other words, $u \sim v \Leftrightarrow I_v \subseteq I_u$.

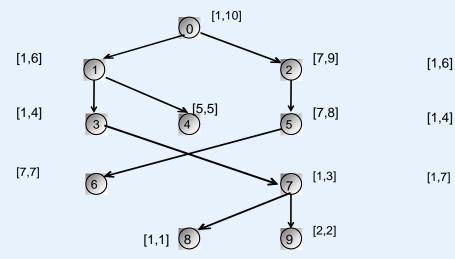
Example:

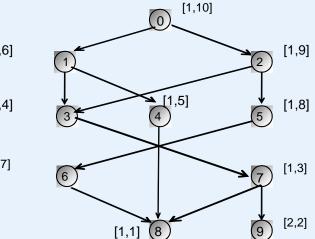


The above figure shows the interval labeling on a tree, assuming that the children are ordered from left to right. It is easy to see that reachability can be answered by interval containment. For example, $1 \sim 9$, since $I_9 = [2, 2] \subset [1, 6] = I_1$, but $2 \sim 7$, since $I_7 = [1, 3] \not\subset [7, 9] = I_2$.

Using tree encoding as a filter

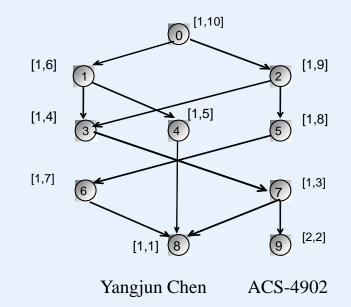
To generalize the interval labeling to a DAG G, we have to ensure that a node is not visited more than once, and a node will keep the postorder number r_v of its first visit. Its r_x is now the lowest postorder number in the sub-graph rooted at v.



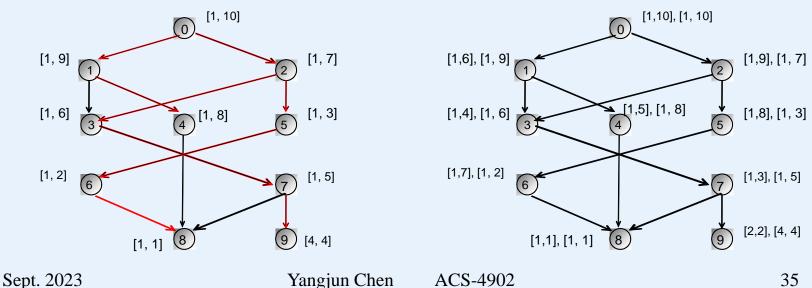


The above shows an interval labeling on a DAG, assuming a left to right ordering of the children. As one can see, interval containment of nodes in a DAG is not exactly equivalent to reachability.

For example, $5 \not\sim 4$, but $I_4 = [1, 5] \subseteq [1, 8] = I_5$. In other words, $I_v \subseteq I_u$ does not imply that $u \not\sim v$. On the other hand, one can show that $I_v \not\subset I_u \Rightarrow u \not\sim v$. (So the containment is a necessary condition, not a sufficient condition.)



- Instead of using a single interval, one can employs multiple intervals that are obtained via random graph traversals.
- We use the symbol *d* to denote the number of intervals to keep per node, which also corresponds to the number of graph traversals used to obtain the label.
- The following figure shows a DAG labeling using 2 intervals (the first interval assumes a left-to-right ordering of the children, whereas the second interval assumes a right-to-left ordering).



Index construction

An interval I_u^i is denoted as

 $I_u^{\ i} = [I_u^{\ i}[1], I_u^{\ i}[2]] = [r_x, r_u]$

Algorithm 1: Randomized Intervals

RandomizedLabeling(*G*, *d*):

1 **foreach** $i \leftarrow 1$ to d **do** l/d – number of intervals for each node

 $r \leftarrow 1$ // global variable: postorder number of node

```
3 Roots \leftarrow \{n : n \in roots(G)\}
```

4 **foreach** $x \in Roots$ in random order **do**

```
Call RandomizedVisit(x, i, G)
```

RandomizedVisit(*x*, *i*, G) :

6 **if** *x visited before* **then return**

```
7 foreach y \in Children(x) in random order do
```

8 Call **RandomizedVisit**(*y*, *i*, *G*)

9
$$r_c^* \leftarrow min\{I_c^i[1] : c \in Children(x)$$

10
$$I_x^i \leftarrow [min(r, r_c^*), r]$$

11
$$r \leftarrow r + 1$$

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2

5

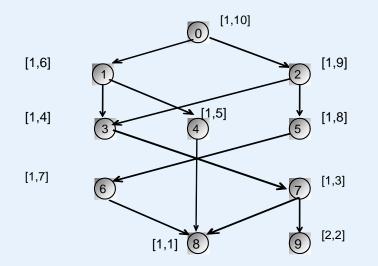
- Assume that each node is associated with an single interval.
- To answer reachability queries between two nodes, u and v, we will first check whether $I_v \not\subset I_u$. If so, we can immediately conclude that $u \not\sim v$.
- On the other hand, if *I_v* ⊆ *I_u*, nothing can be concluded immediately since we know that the index can have false positives, i.e., exceptions. In this case, a DFS (depth-first search) is conducted, with recursive containment check based pruning, to answer queries. In the worst case, it needs O(*n*) time. Another way is to check the exception lists associated with the nodes:

 $E_x = \{y : (x, y) \text{ is an exception, i.e., } I_y \subseteq I_x \text{ and } x \not \sim y\}.$

DFS with prunning

Algorithm 2: Reachability Testing (*for the case of only one interval*) **Reachable**(*u*, *v*, *G*):

| 1 | if $I_v \not\subset I_u$ then |
|----|----------------------------------------------------------------------------|
| 2 | return False // u 🖘 v |
| 3 | else if use exception lists then |
| 4 | if $v \in E_u$ then return False // $u \not\sim v$ |
| 5 | else return <i>True</i> // <i>u</i> ∽ v |
| 6 | else // DFS with pruning |
| 7 | foreach $c \in Children(u)$ such that $I_v \subseteq I_c$ do |
| 8 | if Reachable (c, v, G) then |
| 9 | return <i>True</i> // <i>u</i> ∽ v |
| 10 | return <i>False</i> // <i>u</i> ≁ v |



Exception lists:

 $E_{2} = \{1, 4\}$ $E_{4} = \{3, 7, 9\}$ $E_{5} = \{1, 3, 4, 7, 9\}$ $E_{6} = \{1, 3, 4, 7, 9\}$