

Algorithm Design and Analysis

**CSE
565**

LECTURES 15

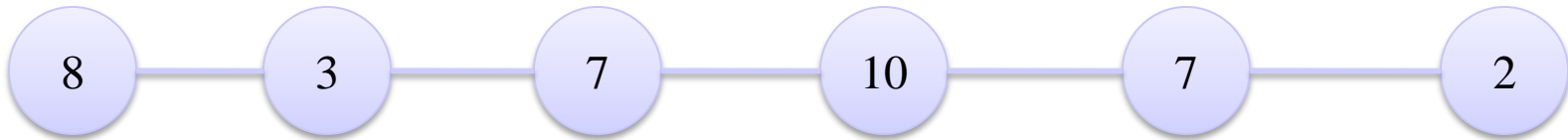
Dynamic Programming

- RNA Secondary Structure
- Shortest Paths: Bellman-Ford

Sofya Raskhodnikova

Review

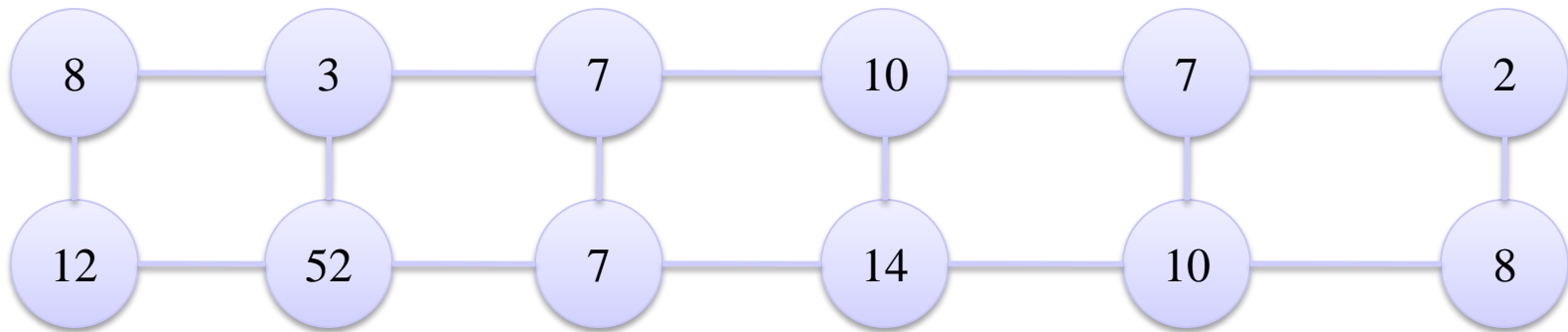
- Weighted independent set on the chain
 - Input: a chain graph of length n with values v_1, \dots, v_n
 - Goal: find a heaviest independent set



- Let $\text{OPT}(j) = ???$
- Write down a recursive formula for OPT
 - How many different subproblems?

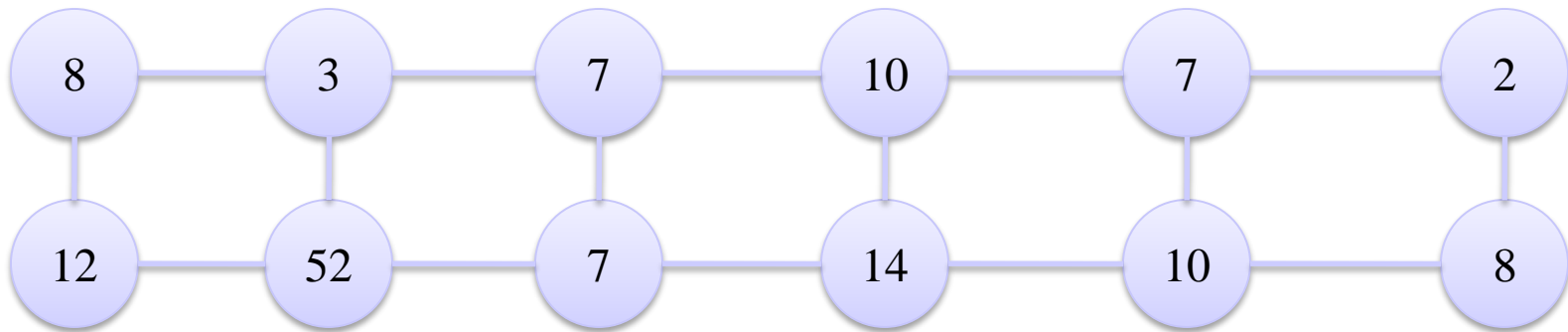
Exercise

- Do the same with a $2 \times n$ grid graph

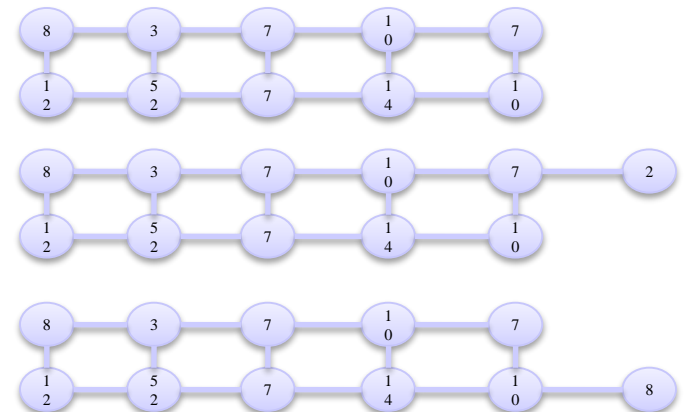


Exercise

- Do the same with a 2 x n grid graph

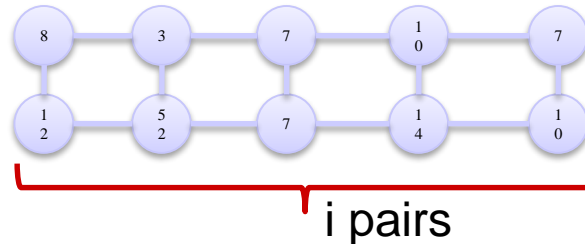


- Three types of subproblems:
 - $\text{grid}(i)$
 - $\text{gridTop}(i)$
 - $\text{gridBottom}(i)$

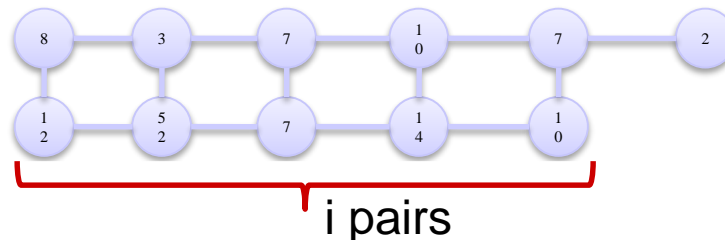


Exercise

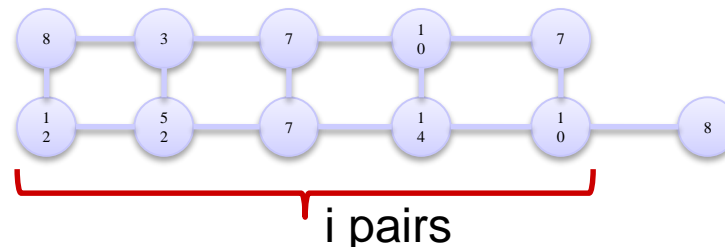
- $\text{grid}(i)$: maximum independent set in the subgraph consisting of only the first i pairs of nodes



- $\text{gridTop}(i)$: maximum independent set in the subgraph consisting of the first i pairs of nodes plus the top node of the $(i+1)$ -st pair



- $\text{gridBottom}(i)$: maximum independent set in the subgraph consisting of the first i pairs of nodes plus the bottom node of the $(i+1)$ -st pair



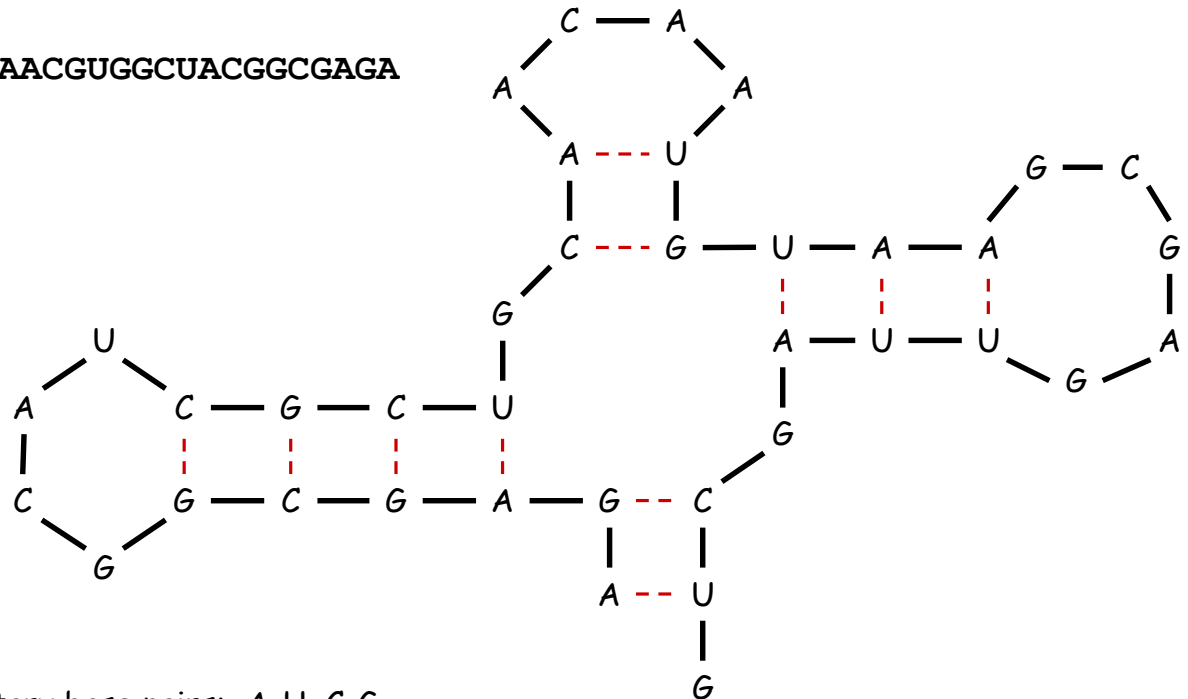
RNA Secondary Structure

RNA Secondary Structure

RNA. String $B = b_1b_2\dots b_n$ over alphabet $\{A, C, G, U\}$.

Secondary structure. RNA is single-stranded so it tends to loop back and form base pairs with itself. This structure is essential for understanding behavior of molecule.

Ex: GUCGAUUGAGCGAAUGUAACAACGUGGCUACGGCGAGA



complementary base pairs: A-U, C-G

RNA Secondary Structure

Secondary structure. A set of pairs $S = \{ (b_i, b_j) \}$ that satisfy:

- [Watson-Crick.] S is a matching and each pair in S is a Watson-Crick complement: $A-U$, $U-A$, $C-G$, or $G-C$.
- [No sharp turns.] The ends of each pair are separated by at least 4 intervening bases. If $(b_i, b_j) \in S$, then $i < j - 4$.
- [Non-crossing.] If (b_i, b_j) and (b_k, b_l) are two pairs in S , then we cannot have $i < k < j < l$.

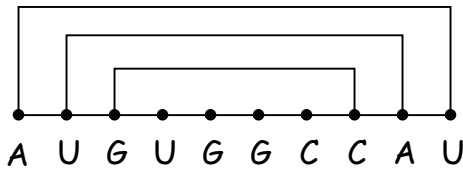
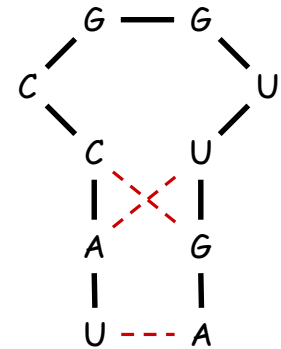
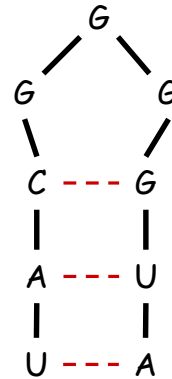
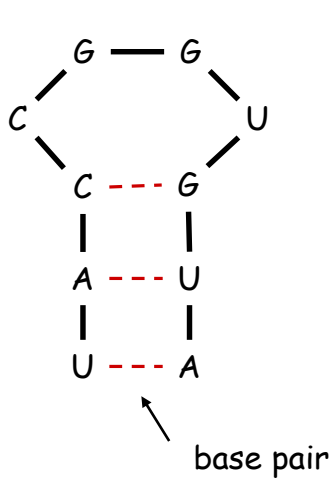
Free energy. Usual hypothesis is that an RNA molecule will form the secondary structure with the optimum total free energy.

↑
approximate by number of base pairs

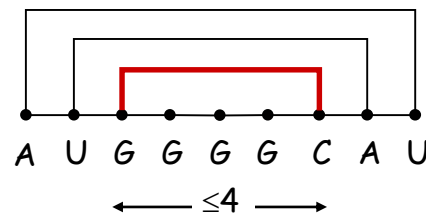
Goal. Given an RNA molecule $B = b_1b_2\dots b_n$, find a secondary structure S that maximizes the number of base pairs.

RNA Secondary Structure: Examples

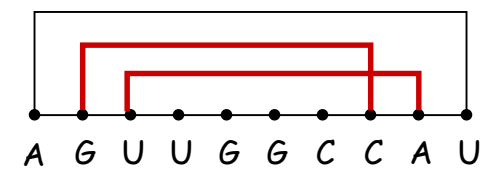
Examples.



ok



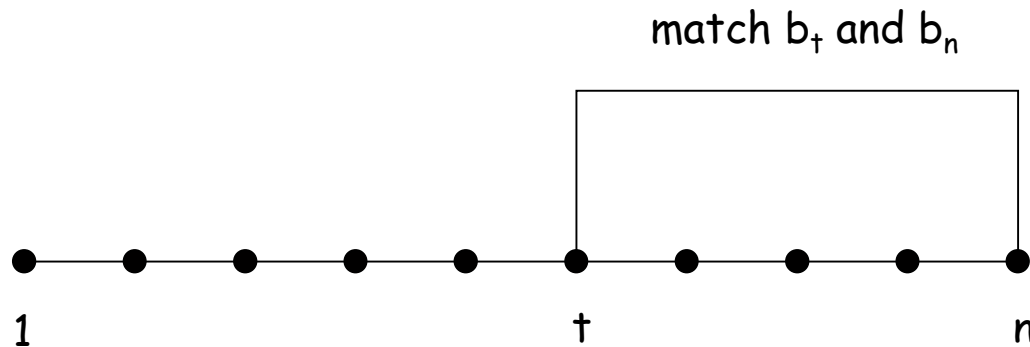
sharp turn



crossing

RNA Secondary Structure: Subproblems

First attempt. $OPT(j)$ = maximum number of base pairs in a secondary structure of the substring $b_1b_2\dots b_j$.



Difficulty. Results in two sub-problems.

- Finding secondary structure in: $b_1b_2\dots b_{t-1}$. ← $OPT(t-1)$
- Finding secondary structure in: $b_{t+1}b_{t+2}\dots b_{n-1}$. ← need more sub-problems

Dynamic Programming Over Intervals

Notation. $OPT(i, j)$ = maximum number of base pairs in a secondary structure of the substring $b_i b_{i+1} \dots b_j$.

- Case 1. $i \geq j - 4$.
 - $OPT(i, j) = 0$ by no-sharp turns condition.
- Case 2. Base b_j is not involved in a pair.
 - $OPT(i, j) = OPT(i, j-1)$
- Case 3. Base b_j pairs with b_t for some $i \leq t < j - 4$.
 - non-crossing constraint decouples resulting sub-problems
 - $OPT(i, j) = 1 + \max_t \{ OPT(i, t-1) + OPT(t+1, j-1) \}$

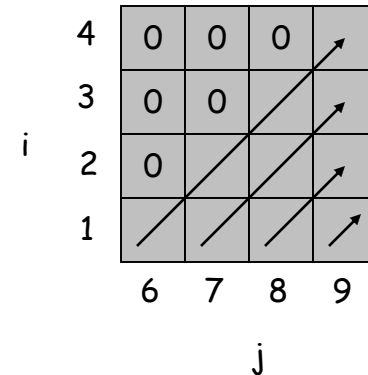
↑
take max over t such that $i \leq t < j-4$ and
 b_t and b_j are Watson-Crick complements

Bottom Up Dynamic Programming Over Intervals

Q. In what order should we solve the subproblems?

A. Do shortest intervals first.


```
RNA( $b_1, \dots, b_n$ ) {  
  for  $k = 5, 6, \dots, n-1$   
    for  $i = 1, 2, \dots, n-k$   
       $j = i + k$   
      Compute  $M[i, j]$   
  
  return  $M[1, n]$  ← using recurrence  
}
```




Running time. $O(n^3)$.


Dynamic Programming Summary

Recipe.

- Decide which subproblems to use (define $OPT(???)$).  If it fails, try again.
- Recursively define **value** of optimal solution.
- Compute value of optimal solution (bottom up or via memoization).
- Construct optimal solution from computed information.

Dynamic programming techniques.

- Binary choice: weighted interval scheduling.
- Multi-way choice: segmented least squares.  Viterbi algorithm for Hidden Markov Models also uses DP to optimize a maximum likelihood tradeoff between parsimony and accuracy
- Adding a new variable: knapsack.
- Dynamic programming over intervals: RNA secondary structure.

 parsing algorithm for context-free grammars has similar structure

Top-down vs. bottom-up: different people have different intuition.

Bellman-Ford: Shortest paths via dynamic programming

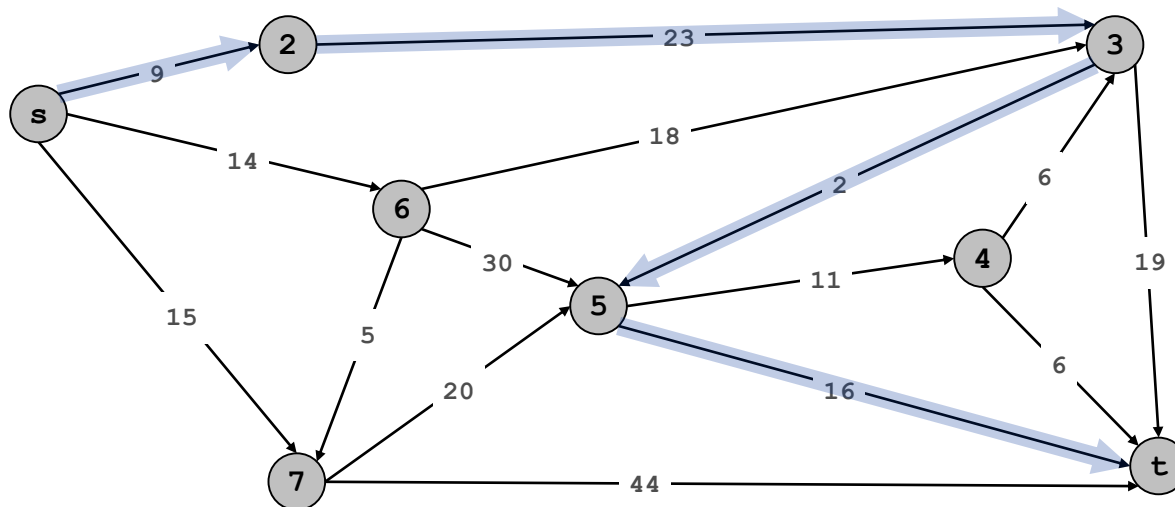
For consistency with book: shortest
paths from all vertices
to a destination t

Single-source Shortest Path Problem

- **Input:**

- Directed graph $G = (V, E)$.
- Source node s , destination node t .
- for each edge e , length $\ell(e)$ = length of e .
- length path = sum of edge lengths

- **Find:** shortest directed path from s to t .



Length of path $(s, 2, 3, 5, t)$ is $9 + 23 + 2 + 16 = 50$.

When is there a shortest path?

Under which conditions do shortest paths

- Always exist?
 - Sometimes exist and sometimes not exist?
 - Never exist?
-
- In a directed graph with nonnegative edge lengths?

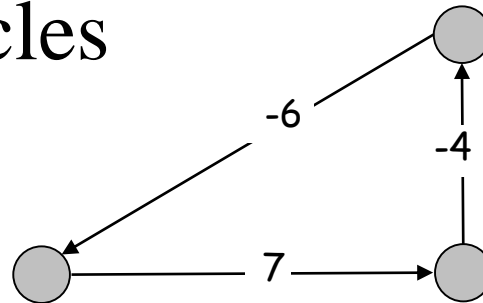
 - In a directed graph with negative edges lengths?

When is there a shortest path?

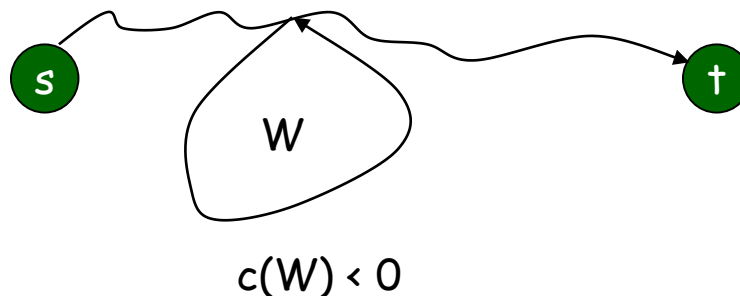
- Edge weights nonnegative:
 - shortest path always exists
- Negative weight edges:
 - shortest path **may** exist or not
 - If *no negative cycles in G* , then shortest path exists
 - If *negative cycles in G* , then no shortest path

Shortest Paths: Negative-Cost Cycles

Negative cost cycles



Observation. If some path from s to t contains a negative cost cycle, there does not exist a shortest s - t path; otherwise, there exists one that is simple.



Shortest Paths: Dynamic Programming

Def. $OPT(i, v)$ = length of shortest v - t path P using at most i edges.

- Case 1: P uses at most $i-1$ edges.
 - $OPT(i, v) = OPT(i-1, v)$
- Case 2: P uses exactly i edges.
 - if (v, w) is first edge, then OPT uses (v, w) , and then selects best w - t path using at most $i-1$ edges

$$OPT(i, v) = \begin{cases} 0 & \text{if } i=0 \\ \min \left\{ OPT(i-1, v), \min_{(v, w) \in E} \{ OPT(i-1, w) + c_{vw} \} \right\} & \text{otherwise} \end{cases}$$

Remark. By previous observation, if no negative cycles, then $OPT(n-1, v)$ = length of shortest v - t path.

Shortest Paths: Implementation

```
Shortest-Path(G, t) {  
  foreach node v ∈ V  
    M[0, v] ← ∞  
  M[0, t] ← 0  
  
  for i = 1 to n-1  
    foreach node v ∈ V  
      M[i, v] ← M[i-1, v]  
      foreach edge (v, w) ∈ E  
        M[i, v] ← min { M[i, v], M[i-1, w] + cvw }  
}
```

Analysis. $\Theta(mn)$ time, $\Theta(n^2)$ space.

Finding the shortest paths. Maintain a "successor" for each table entry.

Shortest Paths: Improvements

- Maintain one array $M[v]$ = length of shortest v - t path found so far.
- No need to check edges of the form (v, w) unless $M[w]$ changed in previous iteration.

Theorem. Throughout the algorithm,

- $M[v]$ is length of some v - t path, and
- For every i : after i rounds of updates, the value $M[v]$ is no larger than the length of shortest v - t path using $\leq i$ edges.

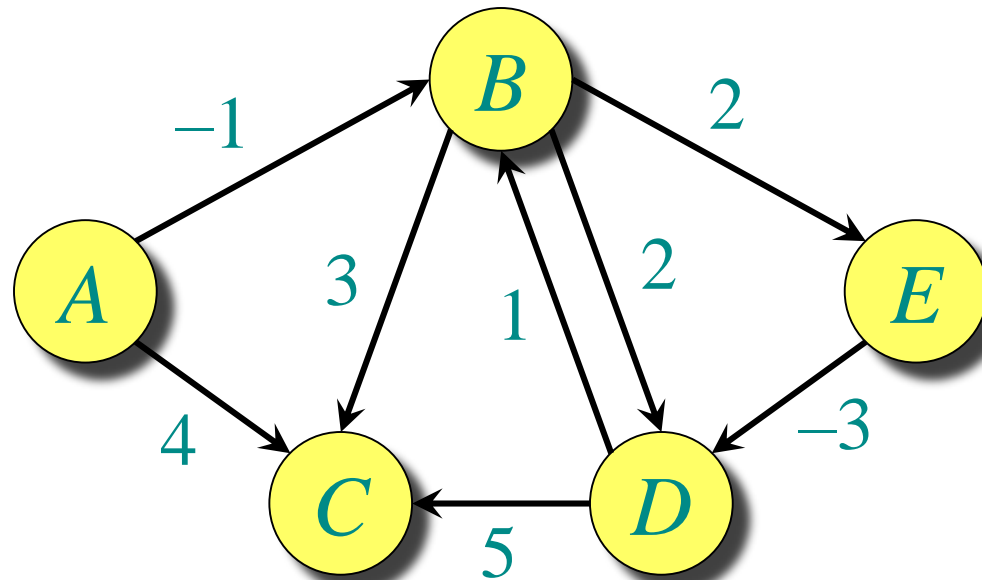
Space and time complexity.

- Memory: $O(m + n)$.
- Running time: $O(mn)$ worst case, but substantially faster in practice.

Belman-Ford: Efficient Implementation

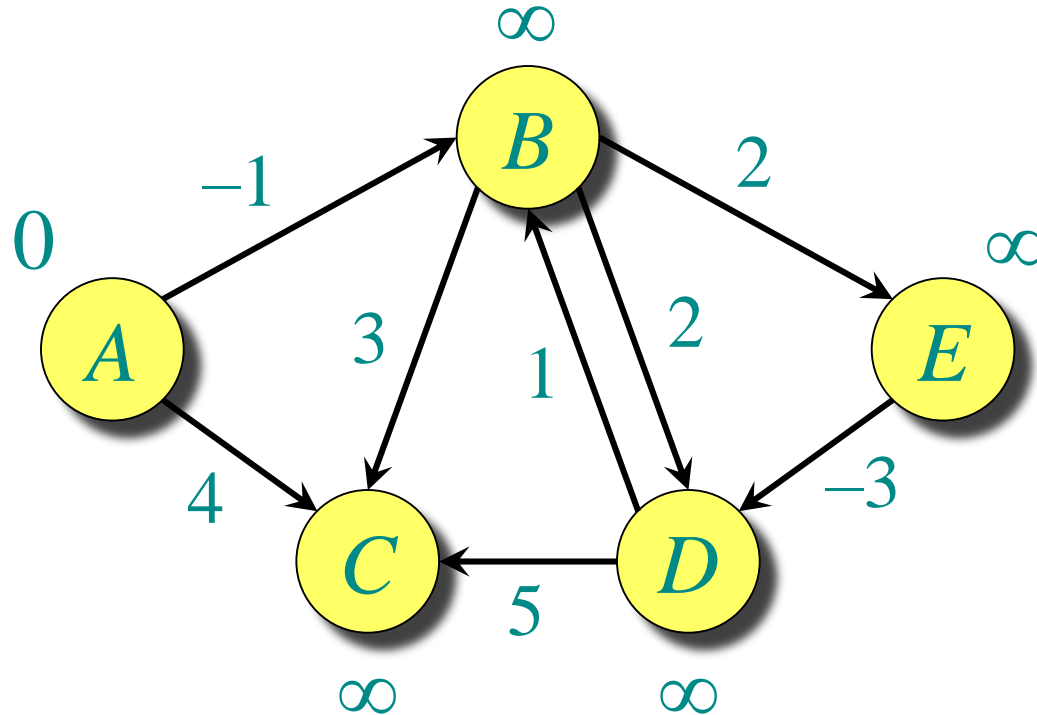
```
Bellman-Ford-Shortest-Path( $G, s, t$ ) {  
  foreach node  $v \in V$  {  
     $M[v] \leftarrow \infty$   
    successor[ $v$ ]  $\leftarrow \phi$   
  }  
  
   $M[t] = 0$   
  for  $i = 1$  to  $n-1$  {  
    foreach node  $w \in V$  {  
      if ( $M[w]$  has been updated in previous iteration) {  
        foreach node  $v$  such that  $(v, w) \in E$  {  
          if ( $M[v] > M[w] + c_{vw}$ ) {  
             $M[v] \leftarrow M[w] + c_{vw}$   
            successor[ $v$ ]  $\leftarrow w$   
          }  
        }  
      }  
    }  
    If no  $M[w]$  value changed in iteration  $i$ , stop.  
  }  
}
```

Example of Bellman-Ford



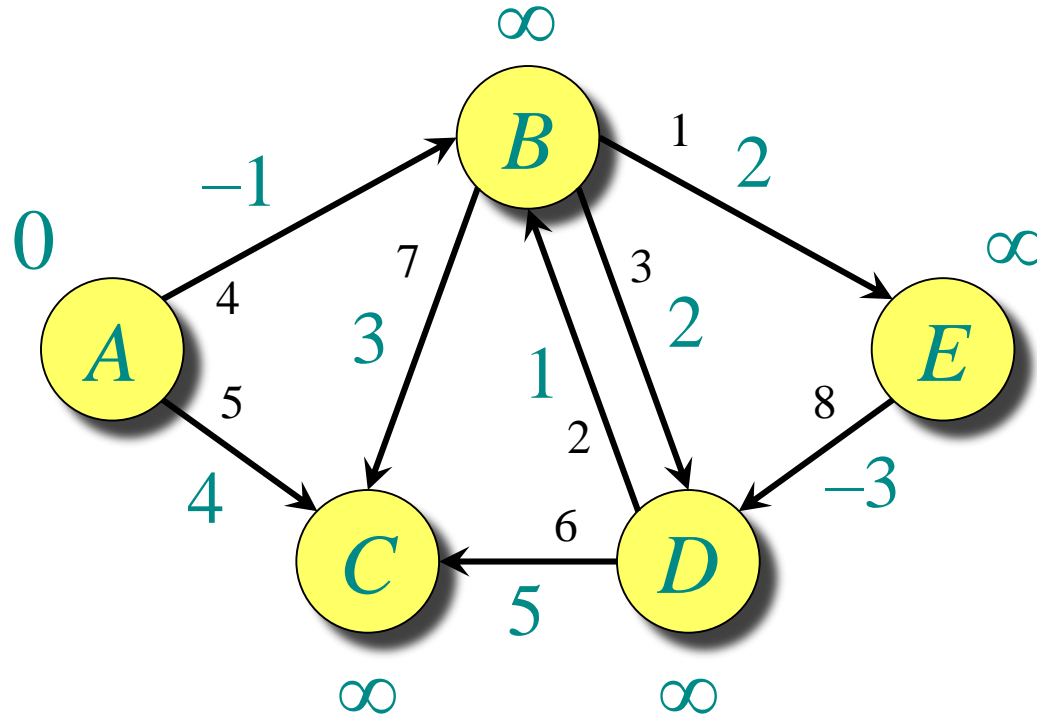
The demonstration is for a slightly different version of the algorithm (see CLRS) that computes distances from the source node rather than distances to the destination node.

Example of Bellman-Ford



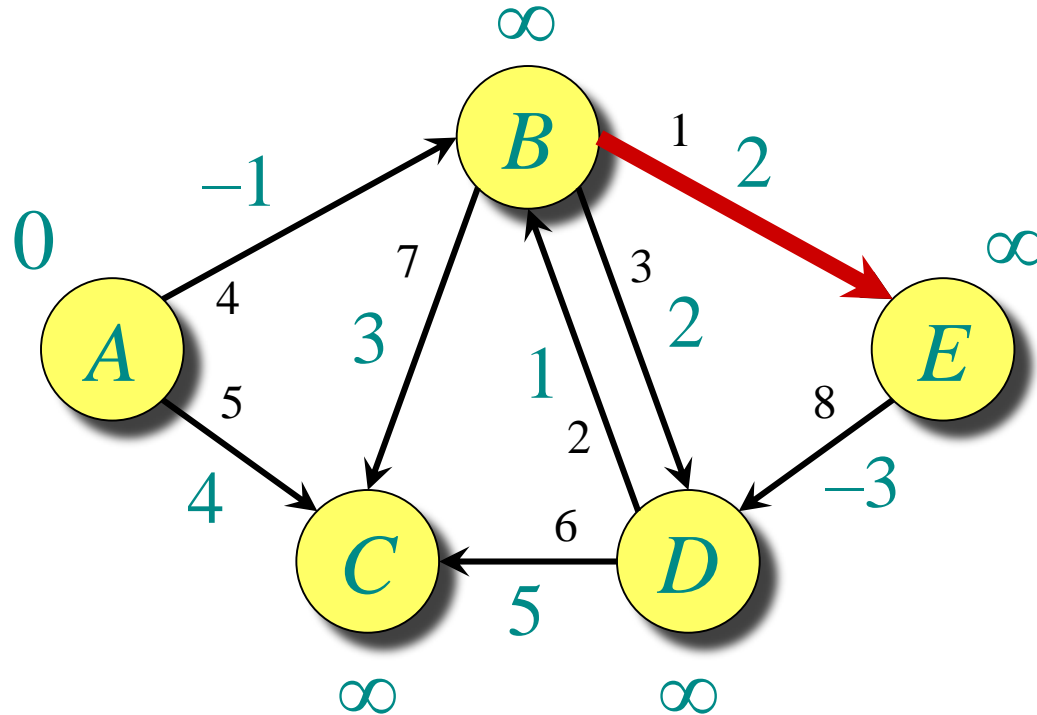
Initialization.

Example of Bellman-Ford

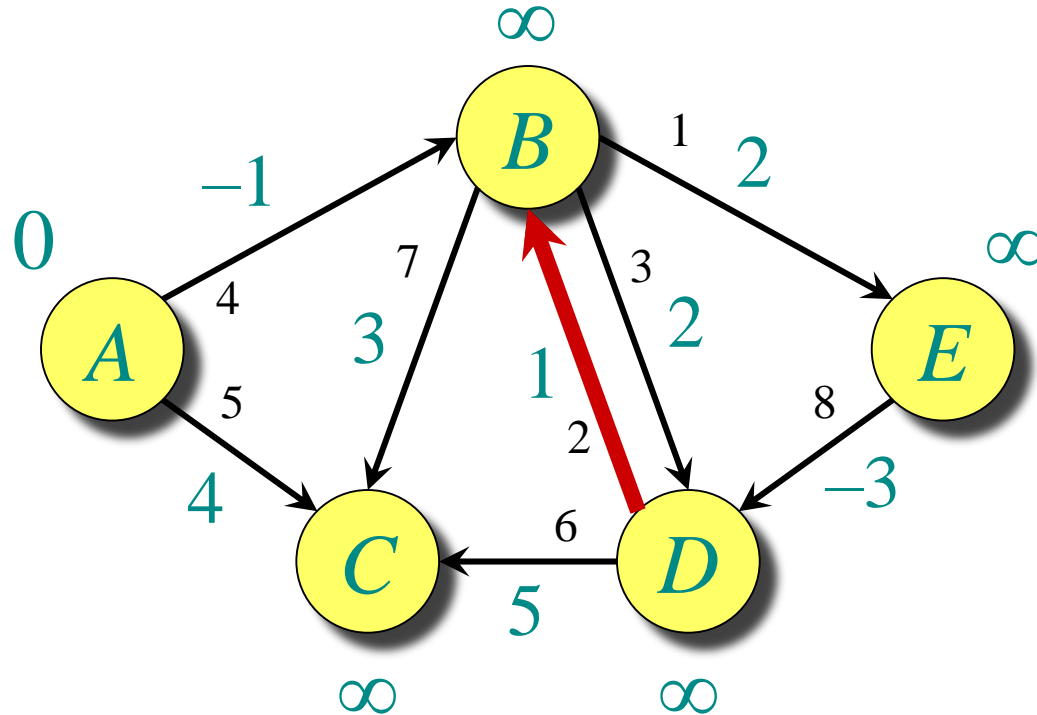


Order of edge relaxation.

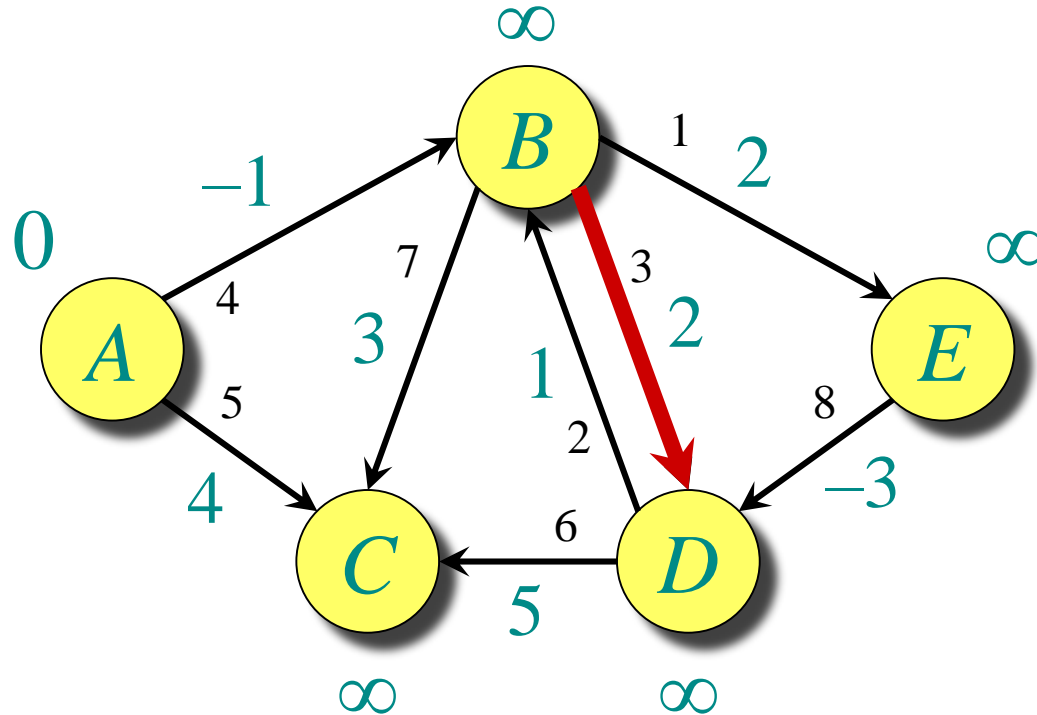
Example of Bellman-Ford



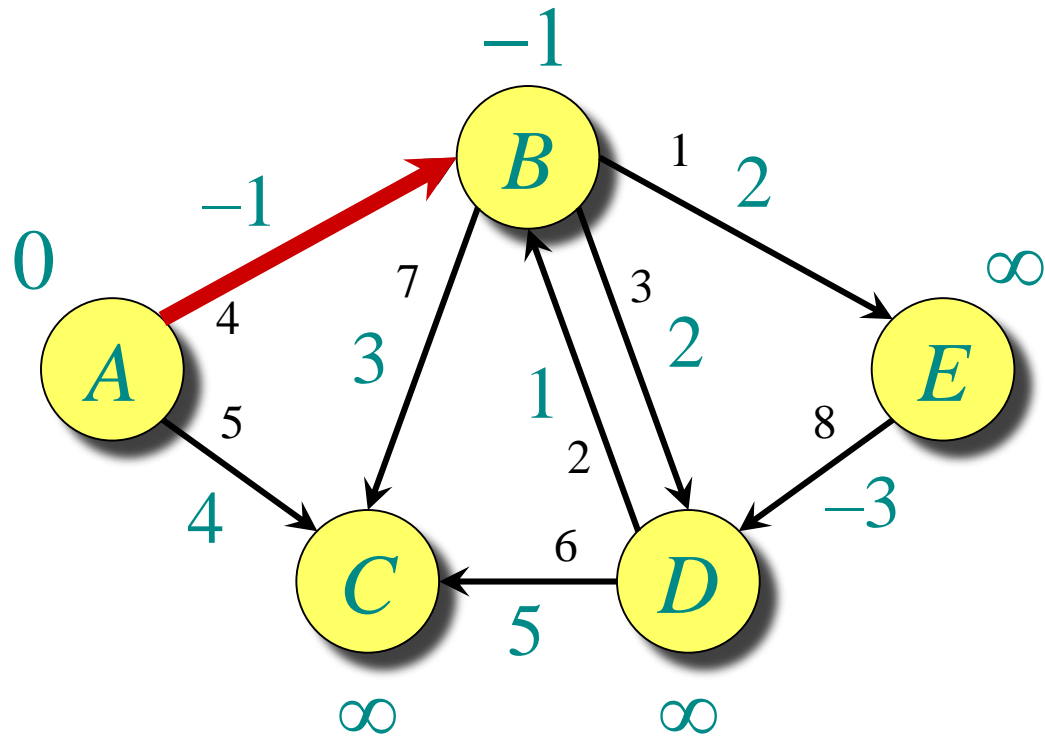
Example of Bellman-Ford



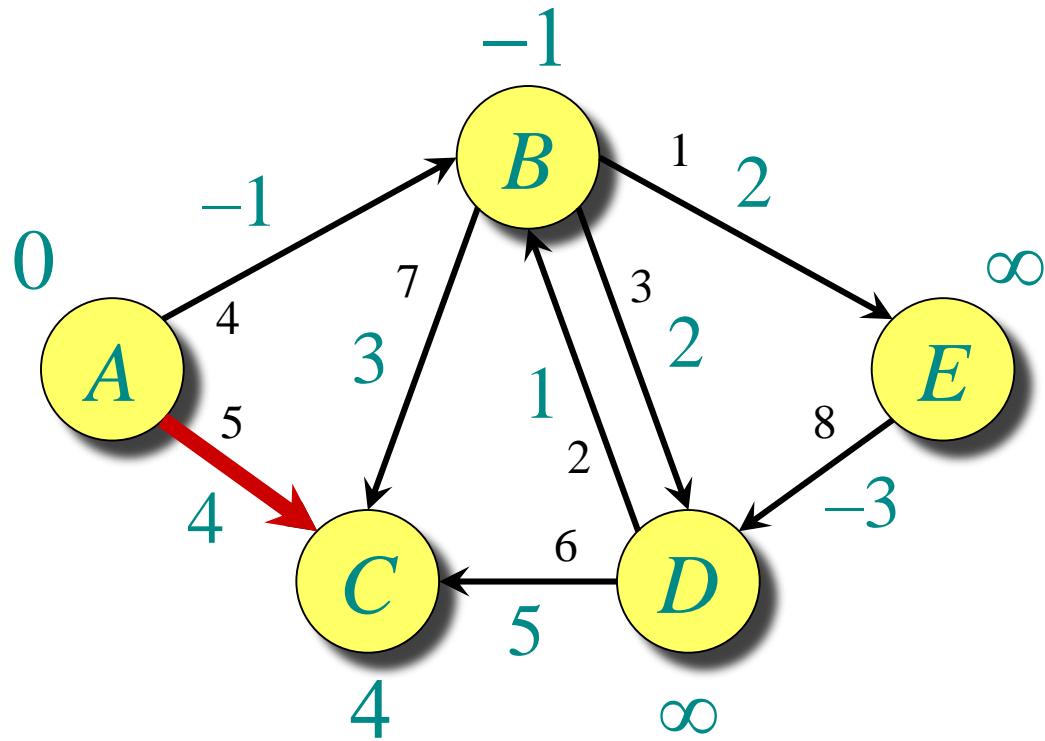
Example of Bellman-Ford



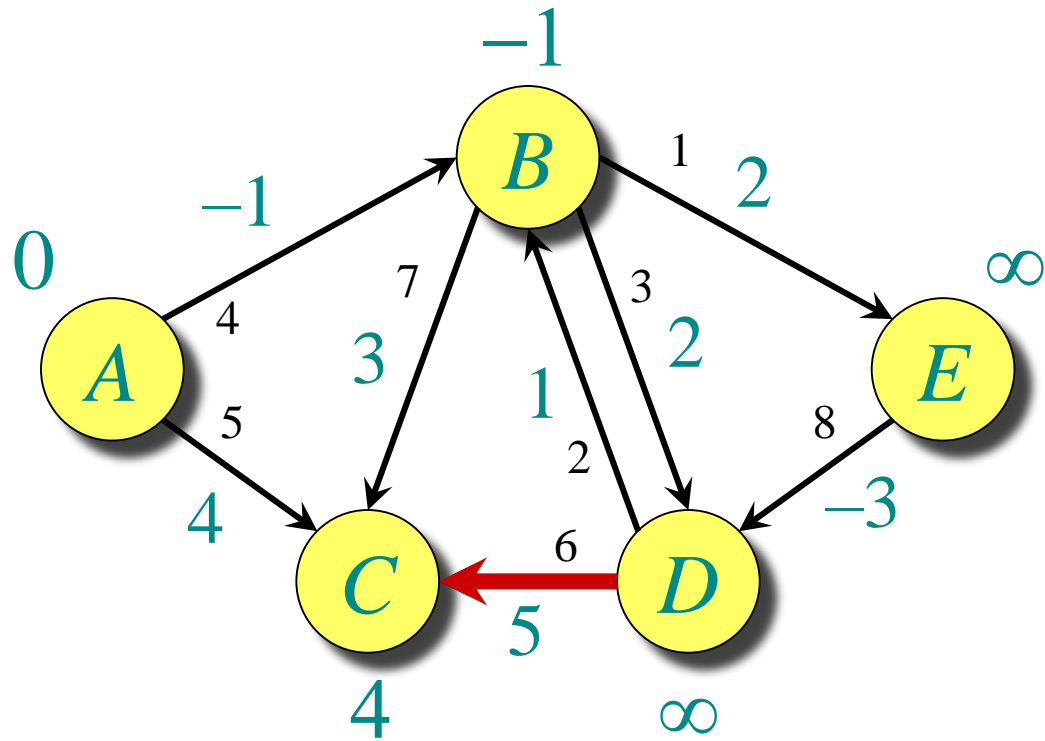
Example of Bellman-Ford



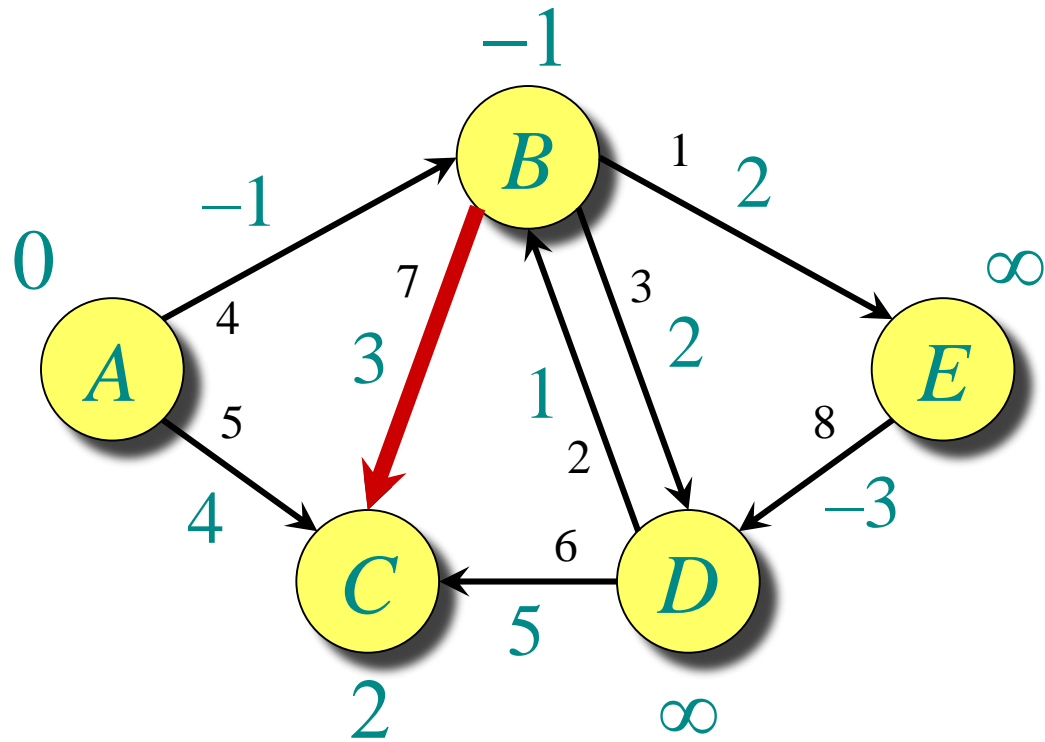
Example of Bellman-Ford



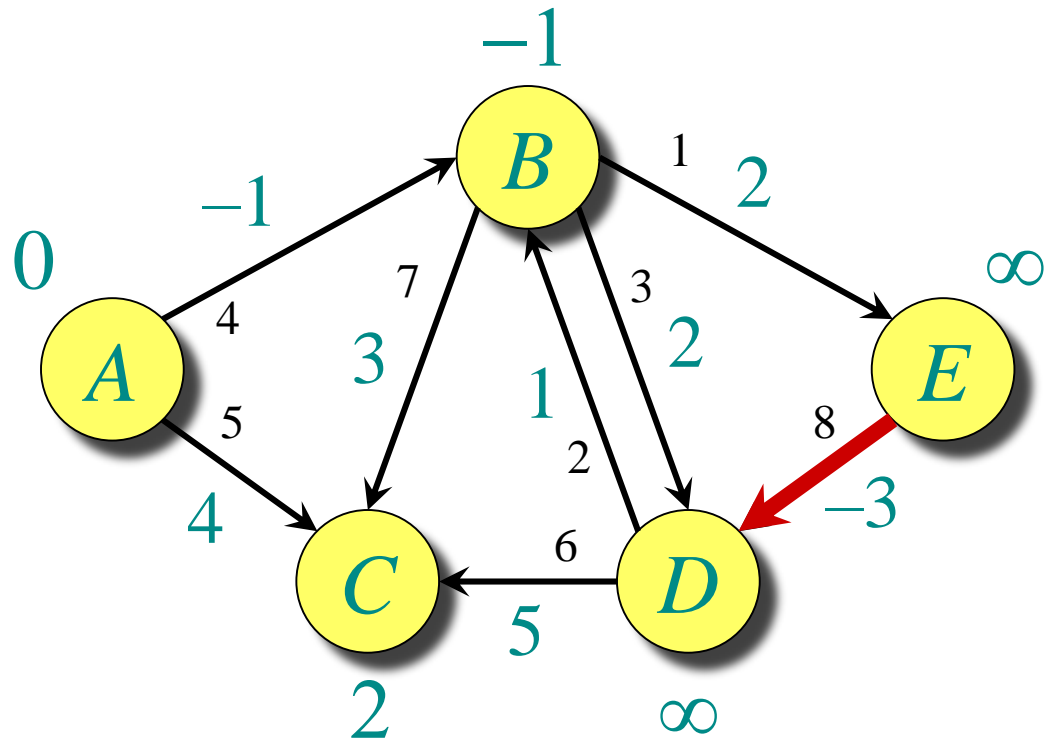
Example of Bellman-Ford



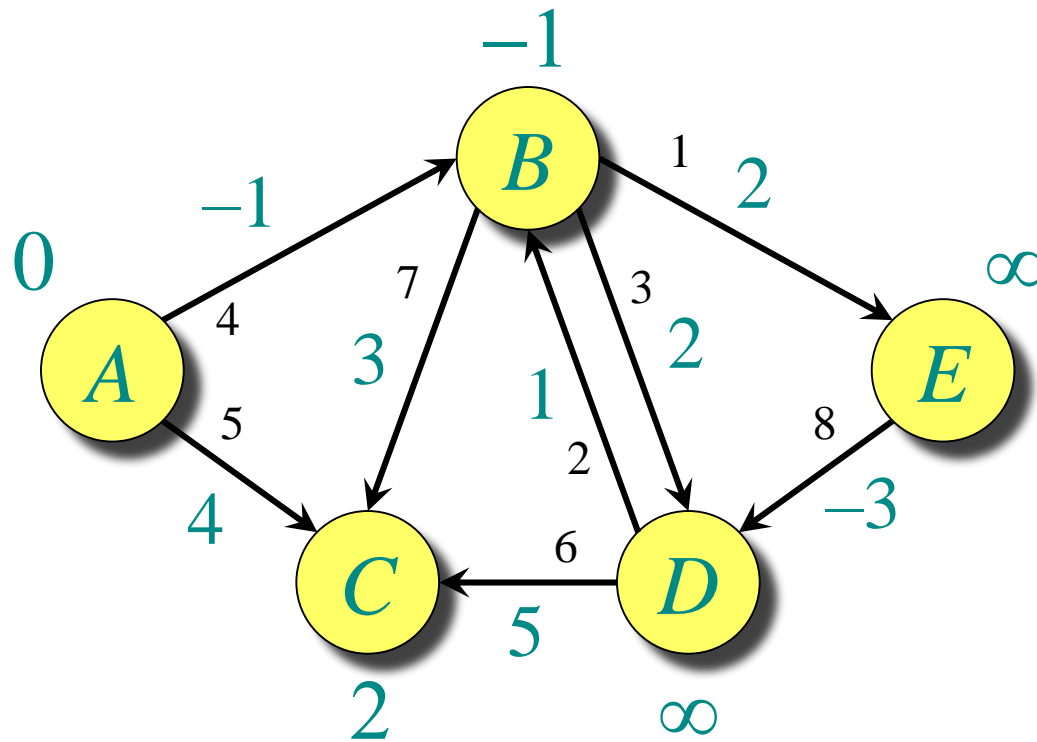
Example of Bellman-Ford



Example of Bellman-Ford

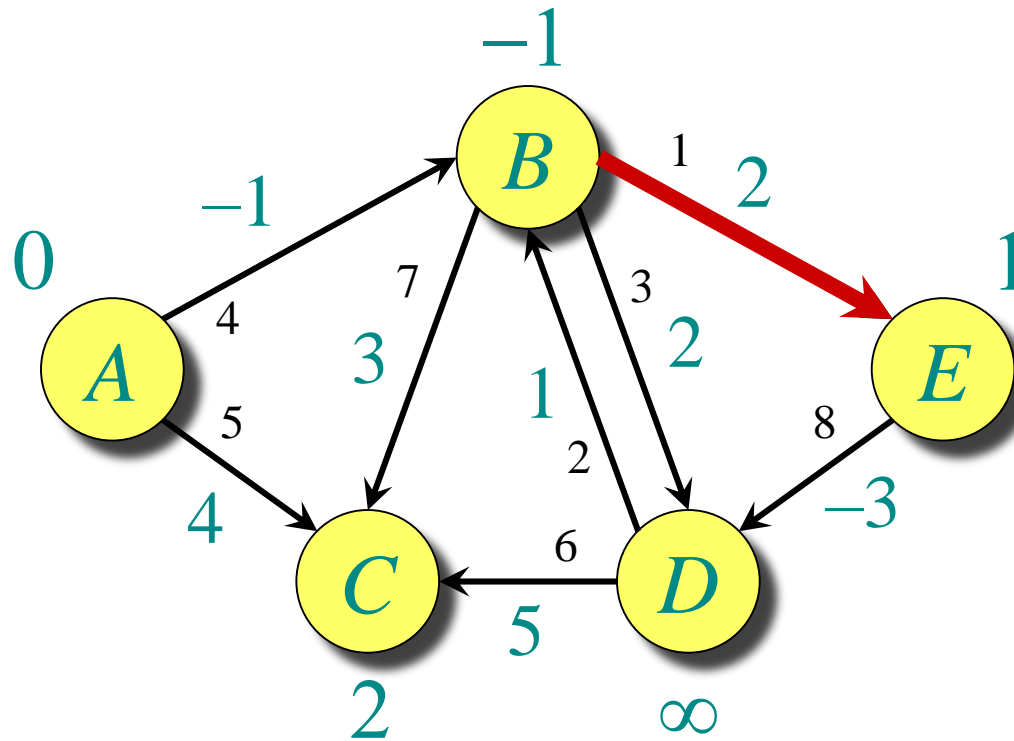


Example of Bellman-Ford

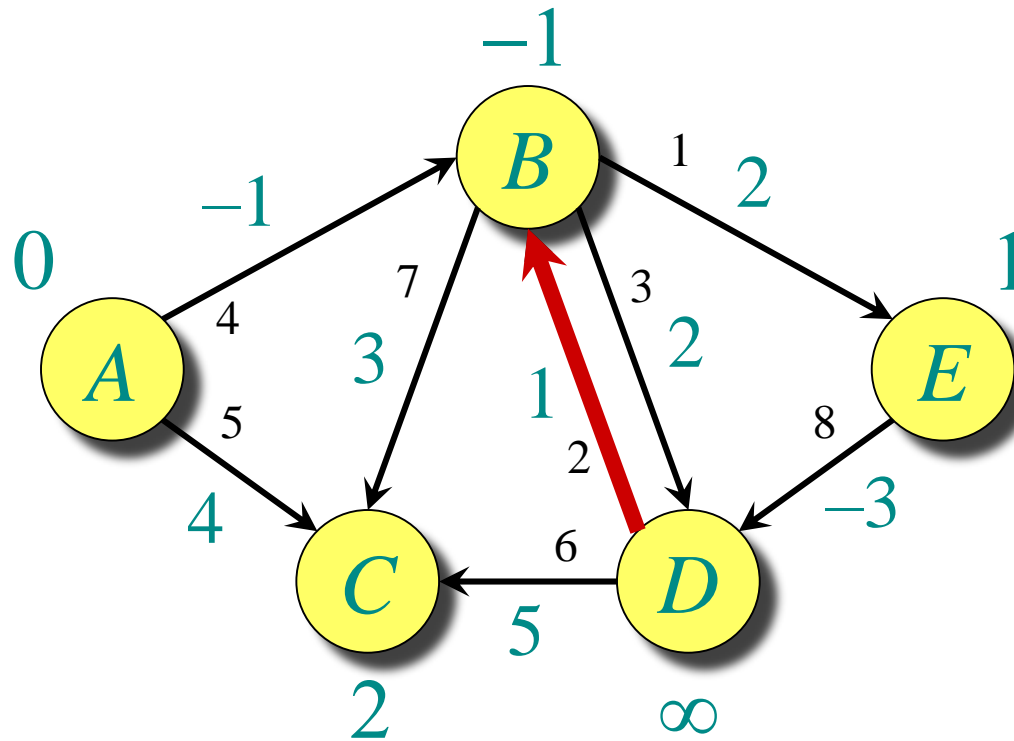


End of pass 1.

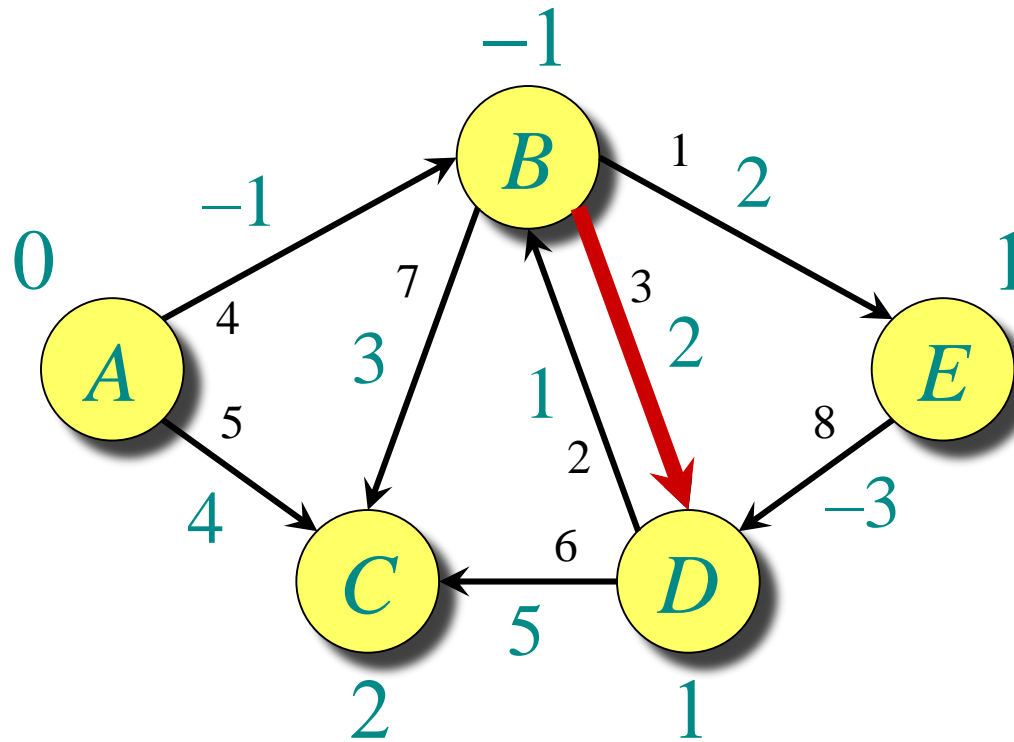
Example of Bellman-Ford



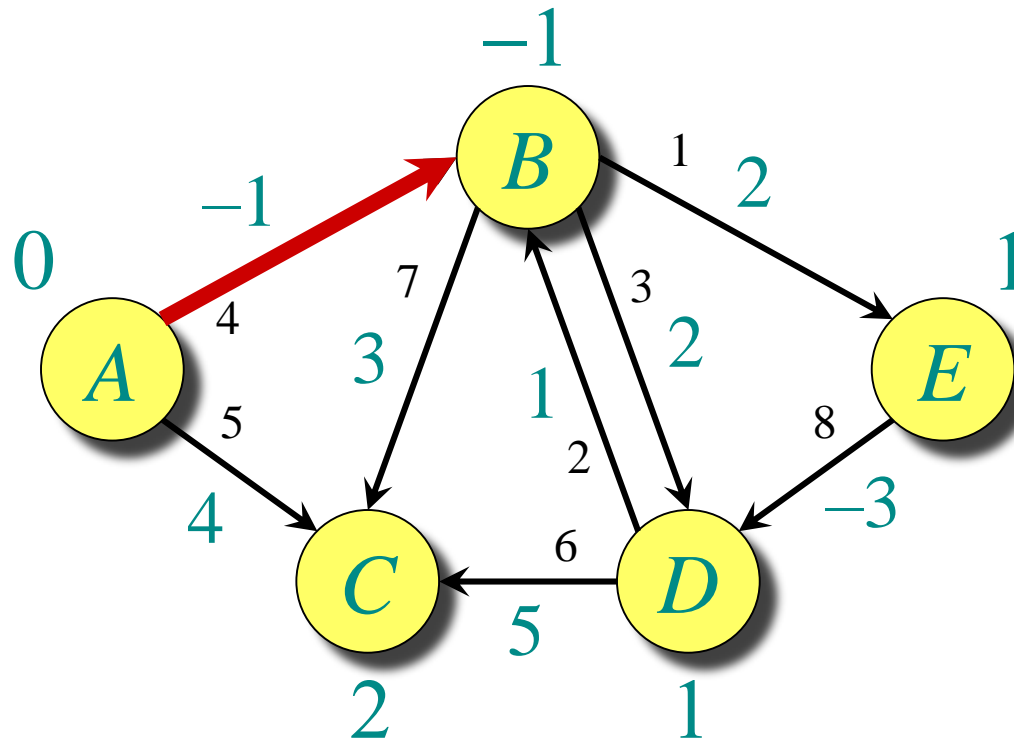
Example of Bellman-Ford



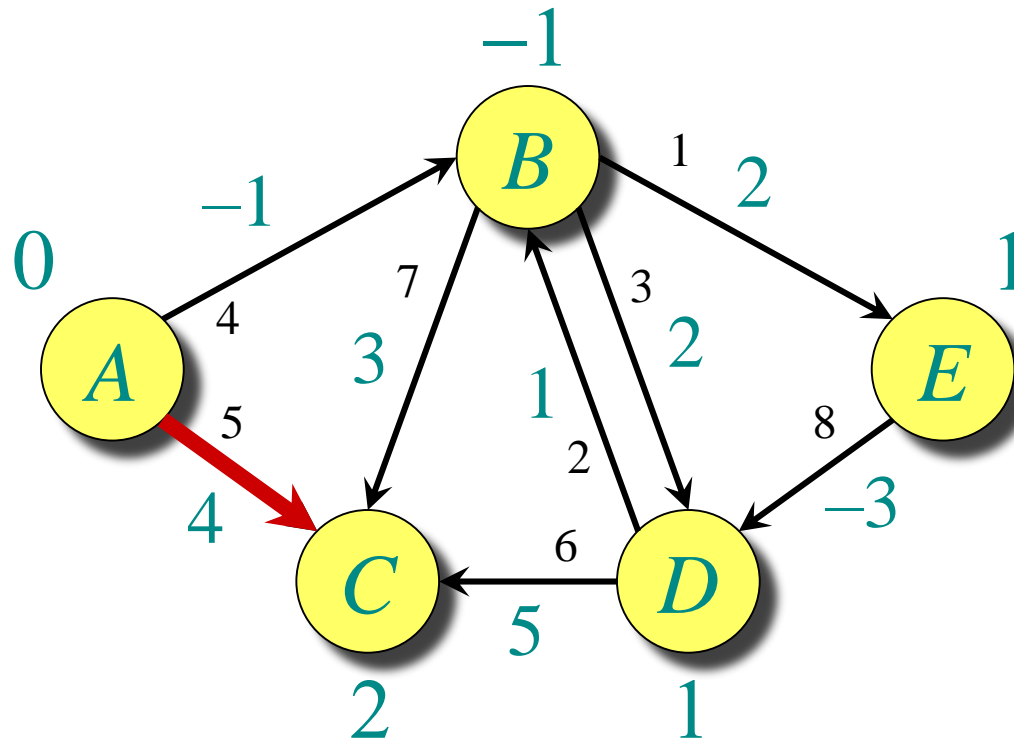
Example of Bellman-Ford



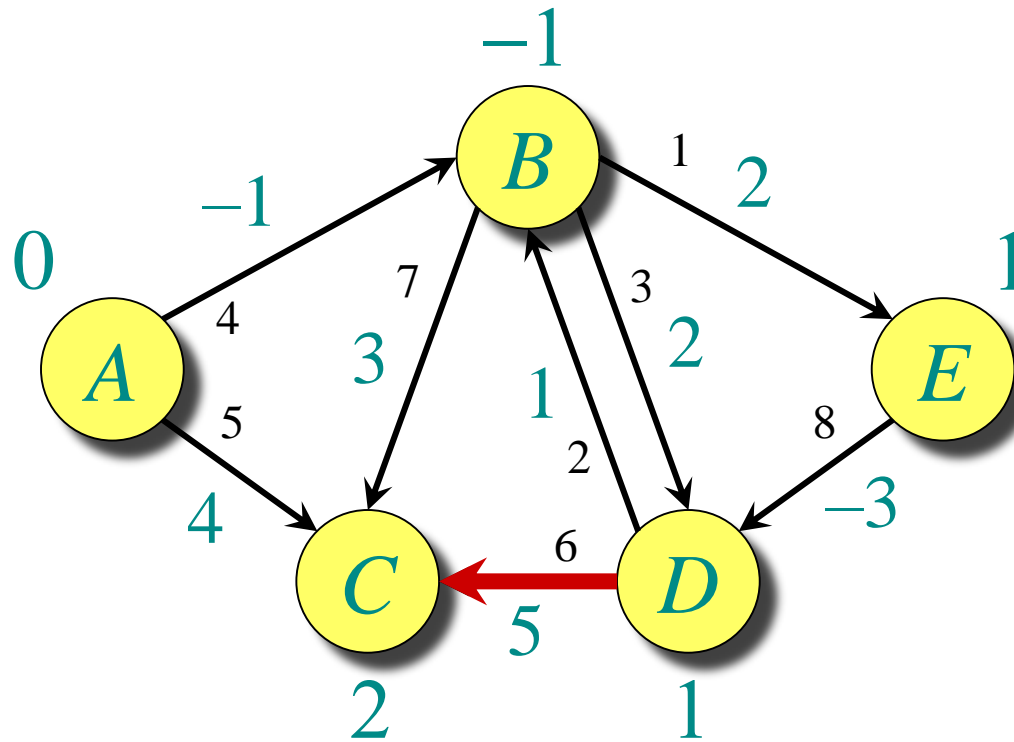
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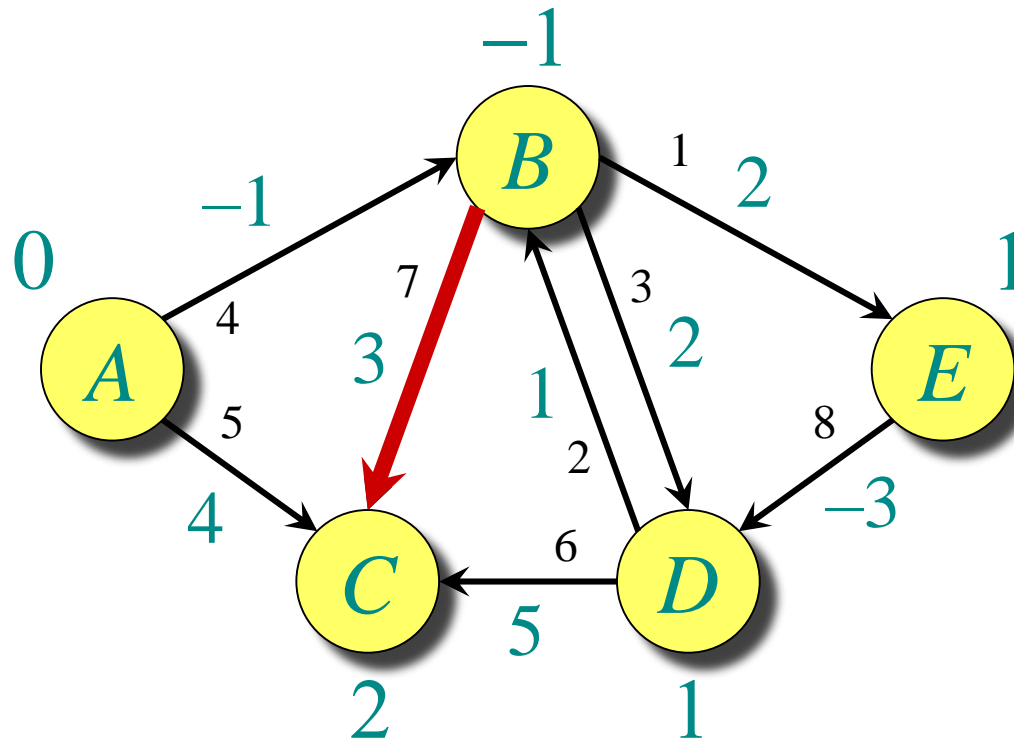
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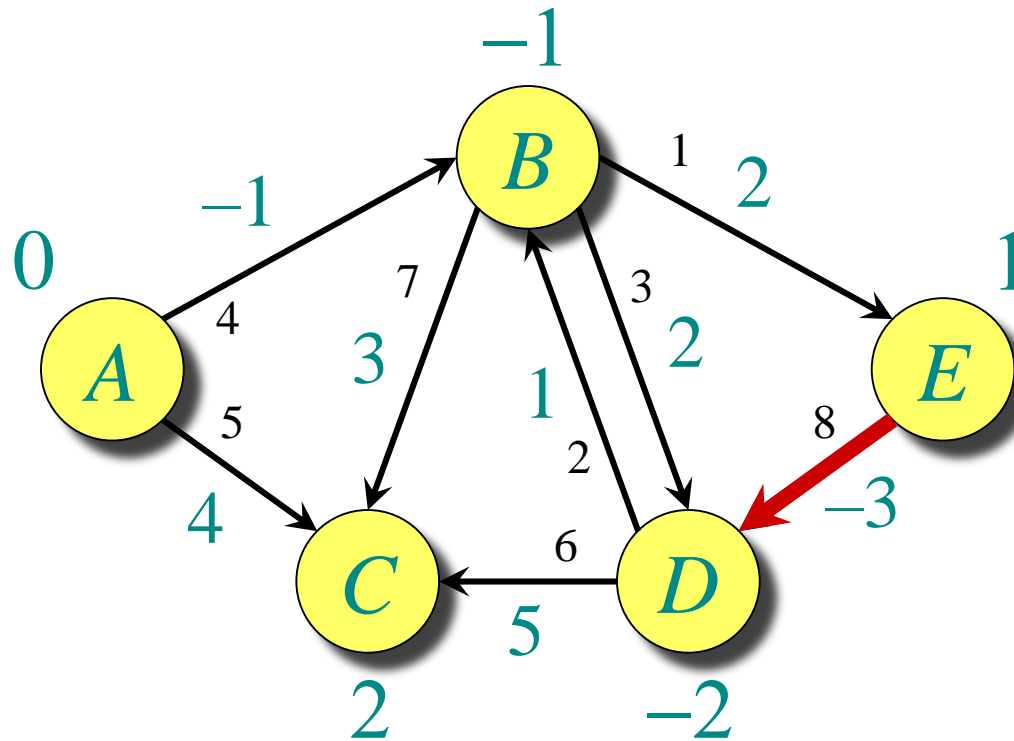
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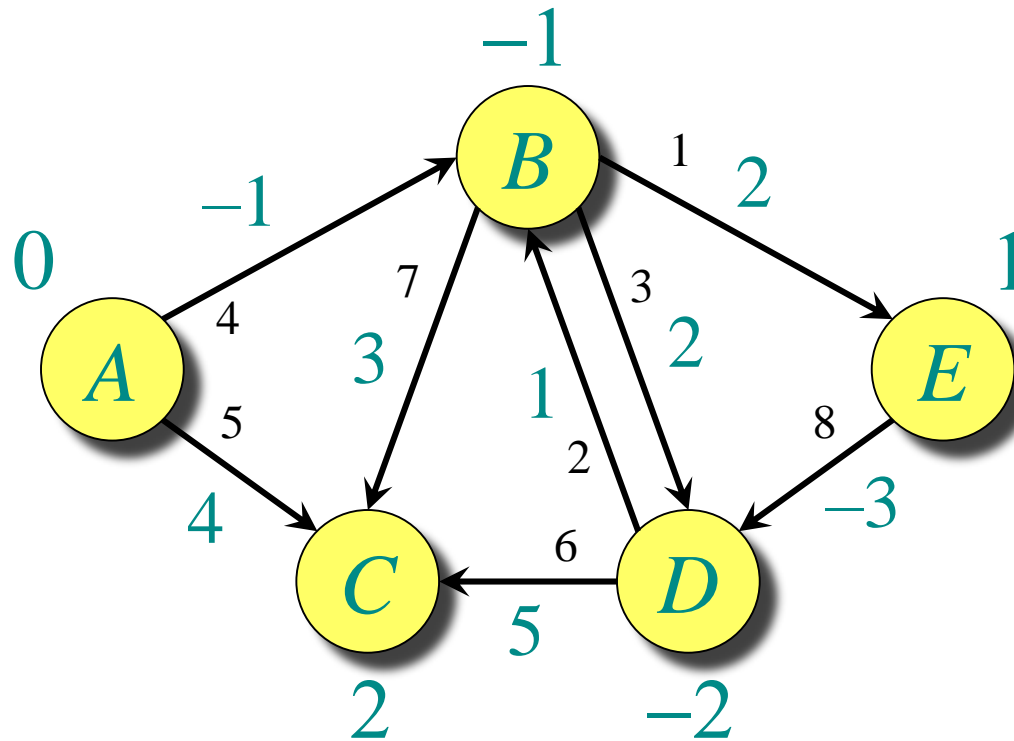
Example of Bellman-Ford



Example of Bellman-Ford



Example of Bellman-Ford



End of pass 2 (and 3 and 4).