Roadmap

Part I: Shortest Paths

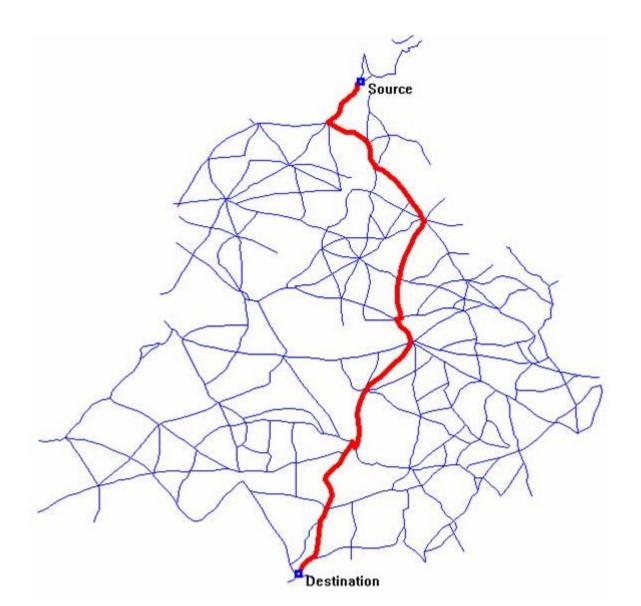
Dijkstra

Part II: Applications of Shortest Paths

- DNA Alignment
- Constraint Systems

SHORTEST PATHS

(ON WEIGHTED GRAPHS)



Shortest Path Problem

Basic question: find the shortest path!

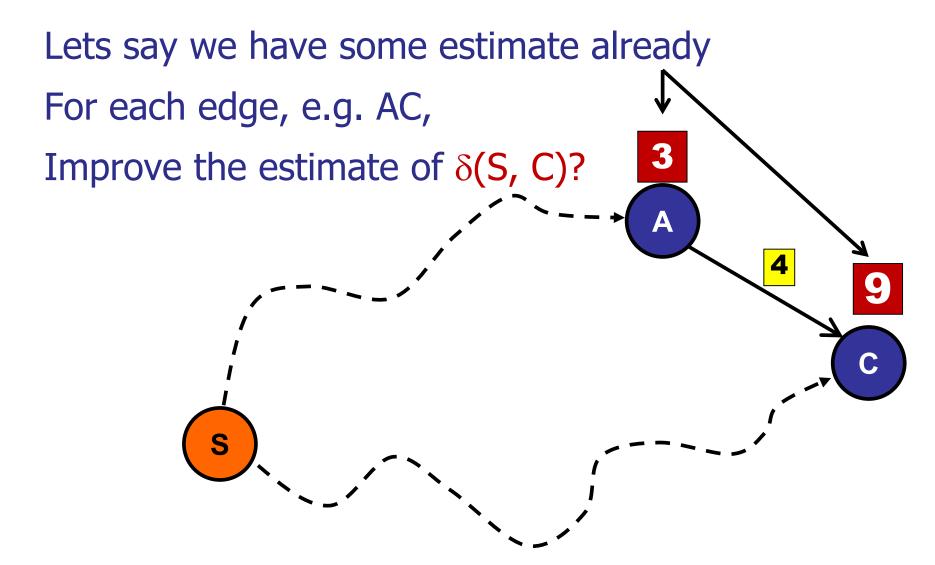
- Source-to-destination: one vertex to another
- Single source: one vertex to every other
- All pairs: between all pairs of vertices

Variants:

- Edge weights: non-negative, arbitrary, Euclidean, ...
- Cycles: cyclic, acyclic, no negative cycles

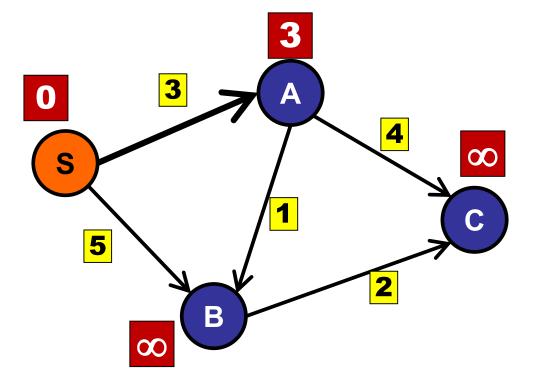
Shortest Paths

Maintain estimate for each distance:



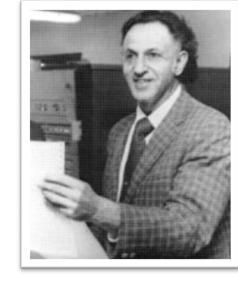
Shortest Paths

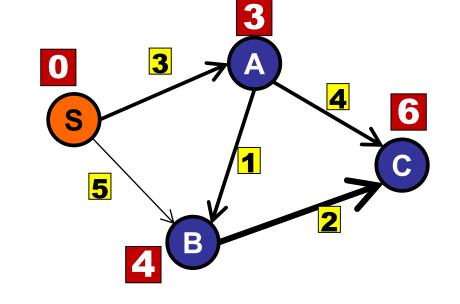
```
relax(int u, int v) {
    if (dist[v] > dist[u] + weight(u,v))
        dist[v] = dist[u] + weight(u,v);
}
```



Bellman-Ford

```
n = V.length;
for (i=0; i<n; i++)
    for (each edge e in the graph)
        relax(e)</pre>
```





Bellman-Ford Summary

Basic idea:

- Repeat |V| times: relax every edge
- Stop when "converges".
- O(VE) time.



Special issues:

- If negative weight-cycle: impossible.
- Use Bellman-Ford to detect negative weight cycle.
- If all weights are the same, use BFS.

Today

Key idea:

Relax the edges in the "right" order.

Only relax each edge once:

O(E) cost (for relaxation step).





Edsger W. Dijkstra

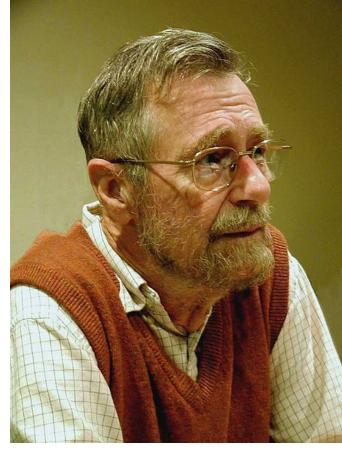
"Computer science is no more about computers than astronomy is about telescopes."

"The question of whether a computer can think is no more interesting than the question of whether a submarine can swim."

"There should be no such thing as boring mathematics."

"Elegance is not a dispensable luxury but a factor that decides between success and failure."

"Simplicity is prerequisite for reliability."



1930-2002

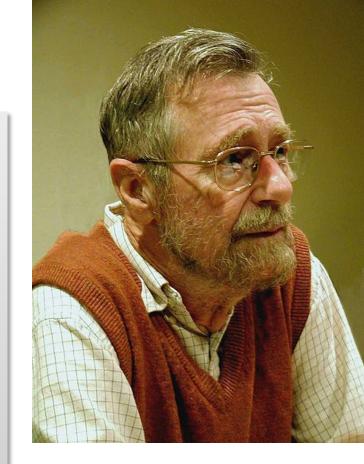
Edsger W. Dijkstra

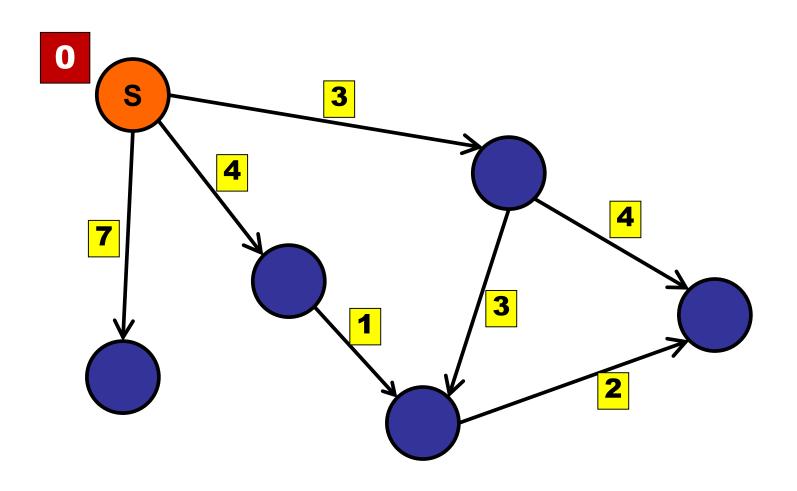
"It is practically impossible to teach good programming to students that have had a prior exposure to BASIC: as potential programmers they are mentally mutilated beyond hope of regeneration."

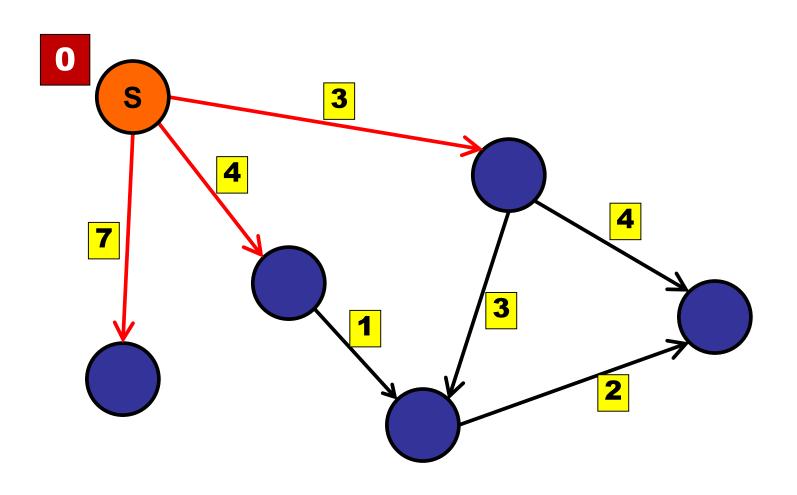
"The use of COBOL cripples the mind; its teaching should, therefore, be regarded as a criminal offense."

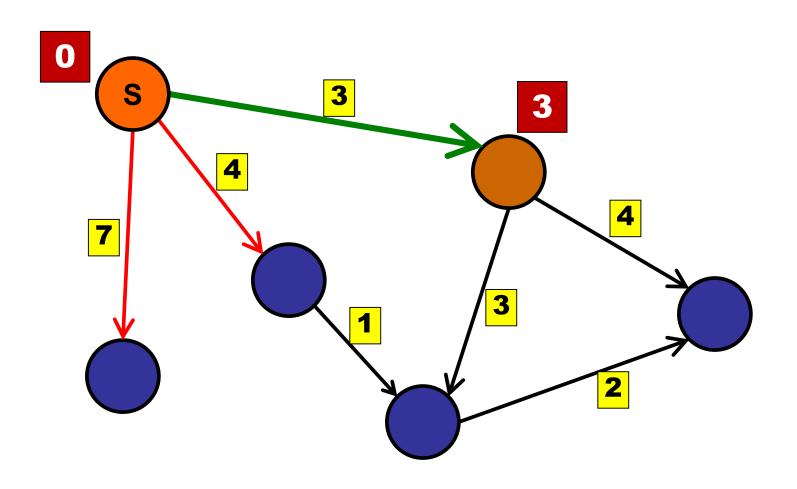
"APL is a mistake, carried through to perfection. It is the language of the future for the programming techniques of the past: it creates a new generation of coding bums."

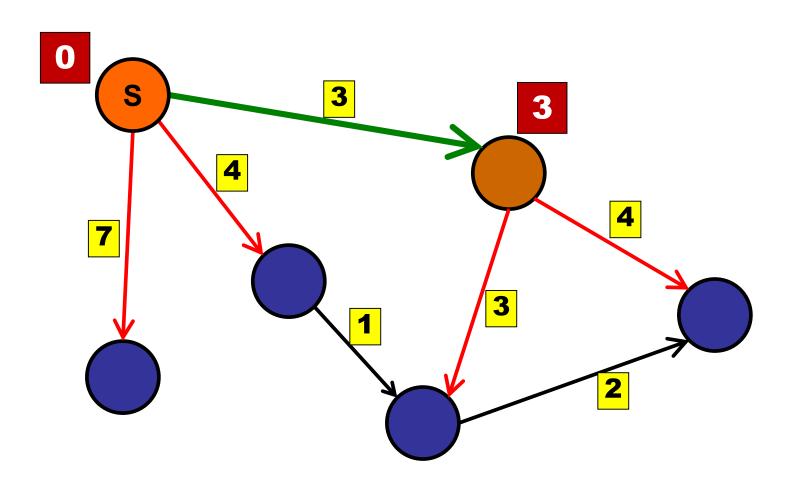
"Object-oriented programming is an exceptionally bad idea which could only have originated in California."



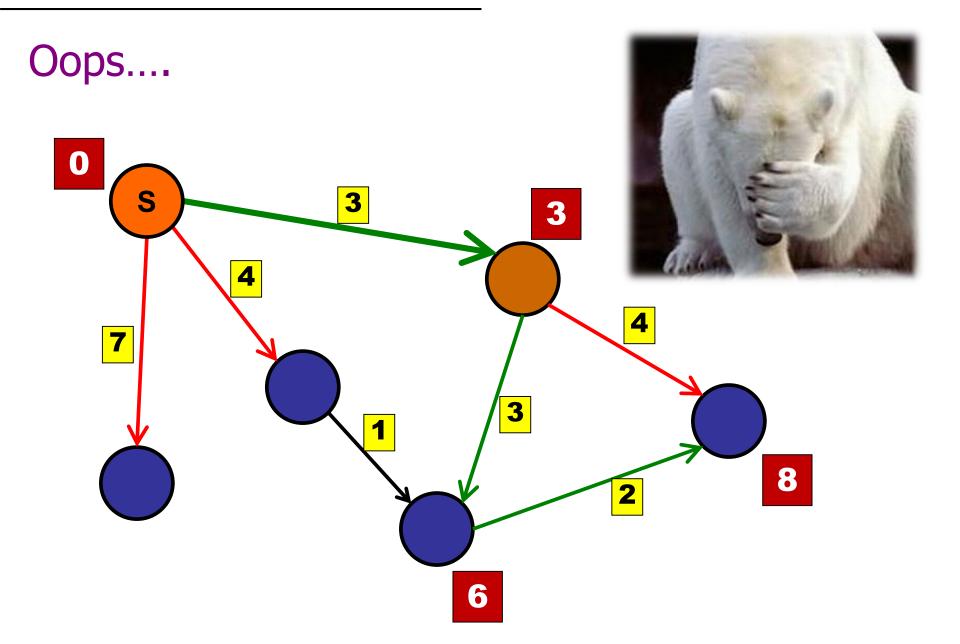






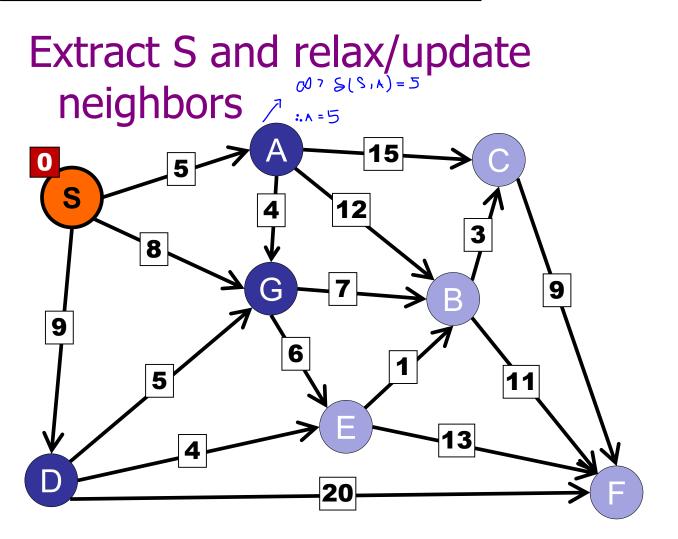


Dijkstra's Algorithm (Failed Try)



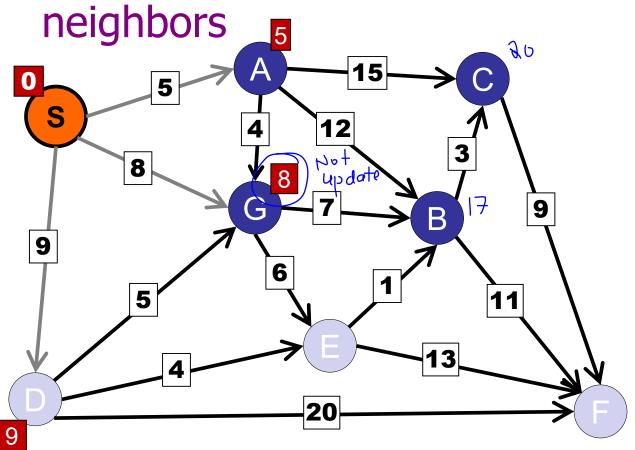
Basic idea:

- Initialize:
 - Put all vertices into a priority queue
 - Set all priorities to estimated distances as infinity
 - Set the starting vertex estimated distance as 0
- Repeat until the priority is empty:
 - Extract the vertex v in the priority queue with the shortest estimated distance
 - Relax all the neighbors of v in the priority queue and update their estimated distance



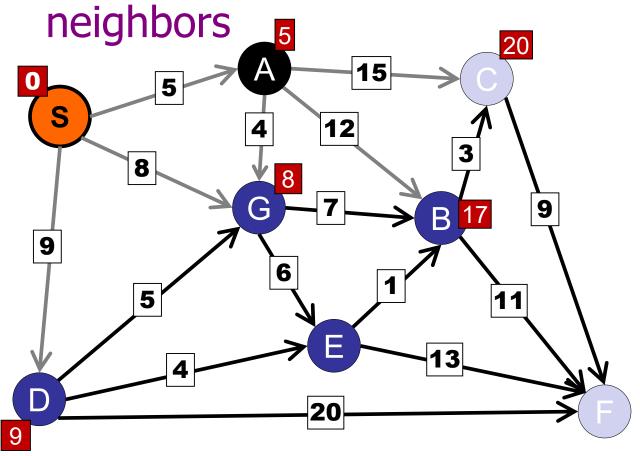
Vertex	Dist.	
S	0	
A	S	
G	∞	
<u> </u>	00	
B	∞0	
	\	
(Not sh	(Not showing	
vertices with		
distance =		
infinity)		

Extract A and relax/update



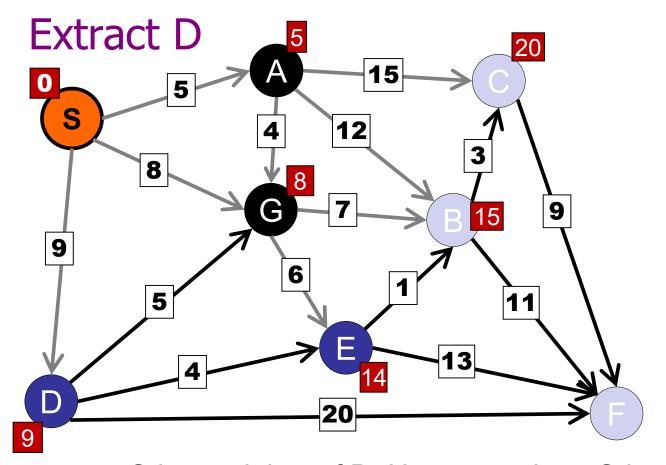
Vertex	Dist.
A	5
G	8
D	9

Extract G and relax/update



Vertex	Dist.
G	8
D	9
В	17
С	20

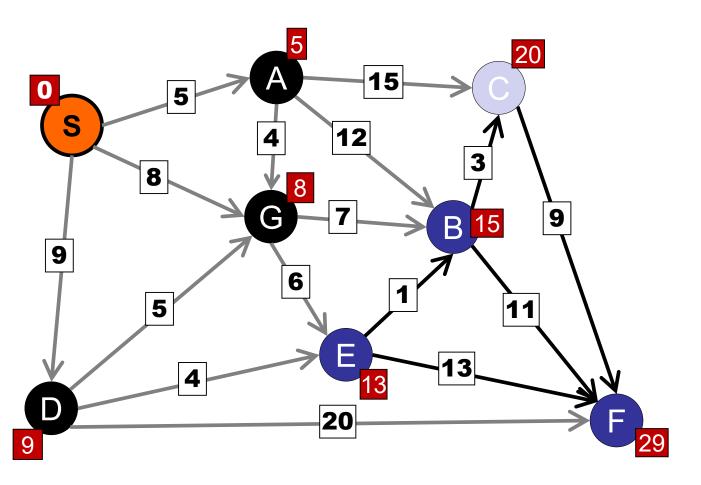
Dist. of B updated to 15



Vertex	Dist.
D	9
E	14
В	15
С	20

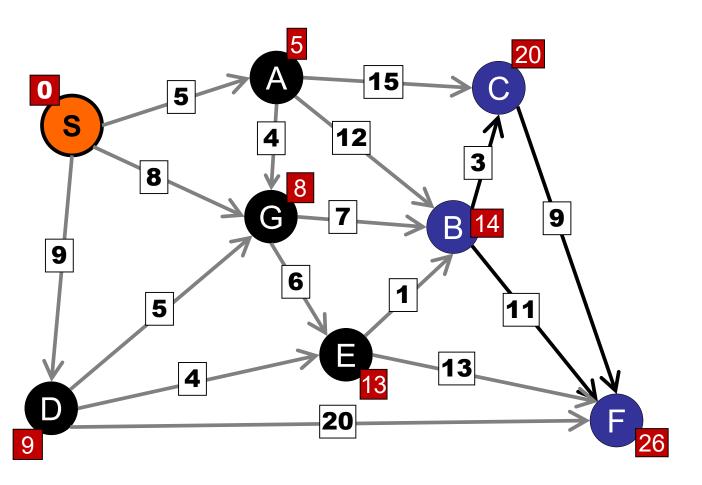
G is a neigbor of D. However, since G is already "dequeued", G won't be added back to the PQ anymore

Extract E



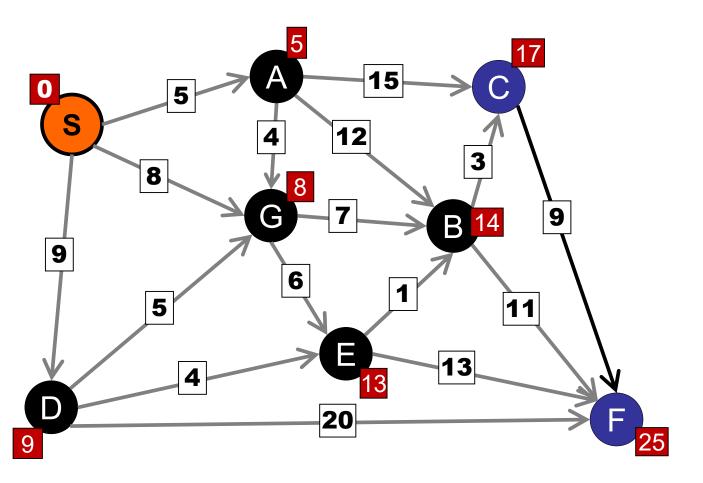
Vertex	Dist.
E	13
В	15
С	20
F	29

Extract B



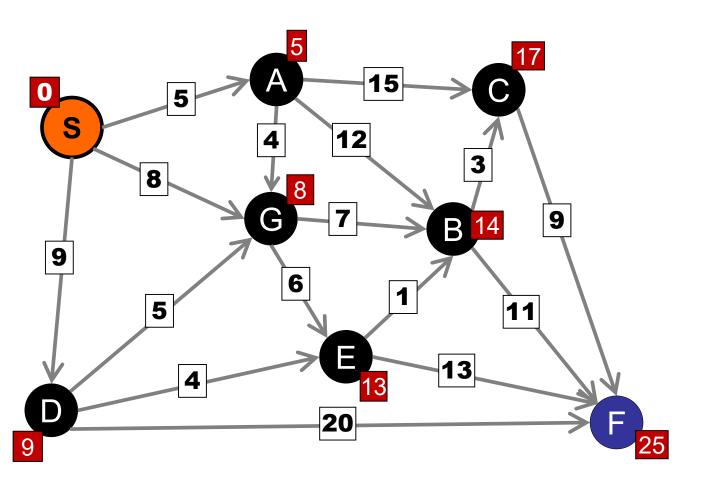
Vertex	Dist.
В	14
С	20
F	26

Extract C



Vertex	Dist.
С	20 17
F	25

Extract F

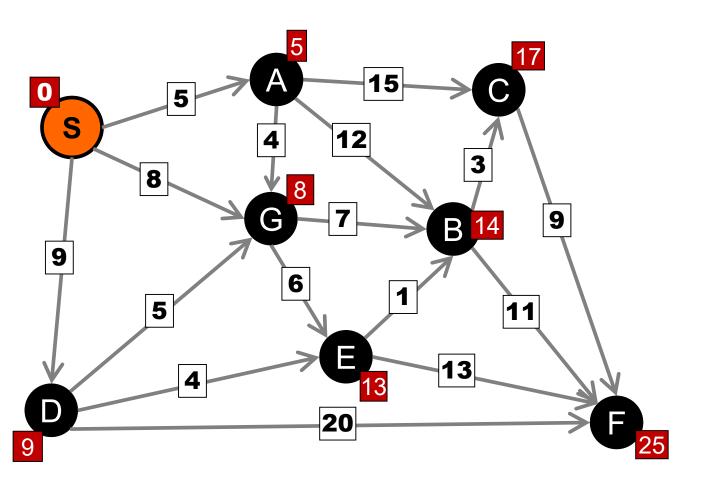


Vertex	Dist.
F	25

Vertex

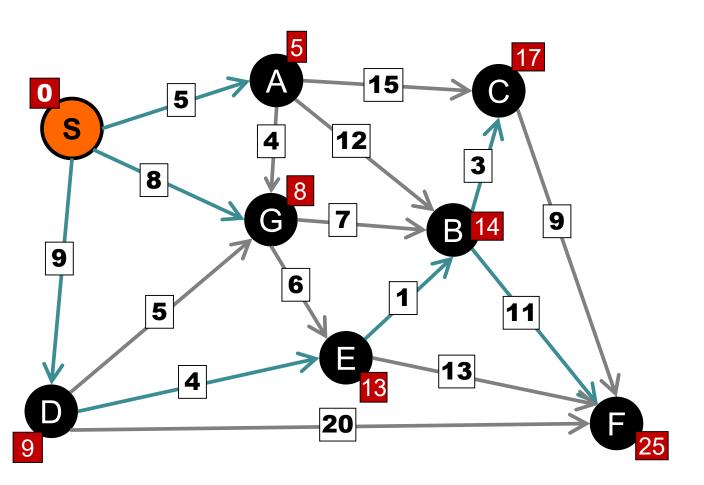
Dist.

Done!



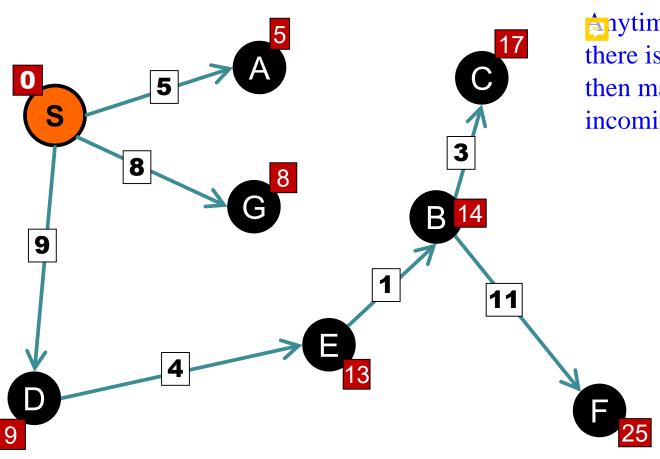
Vertex Dist.

Done



Vertex Dist.

Shortest Path Tree



incoming vertex

Abstract Data Type

Priority Queue

```
void
        insert (Key k, Priority p)
                                         insert k with
                                         priority p
   Data extractMin()
                                         remove key with
                                         minimum priority
   void
        decreaseKey(Key k, Priority p)
                                         reduce the priority of
                                         key k to priority p
boolean contains (Key k)
                                         does the priority
                                         queue contain key k?
boolean isEmpty()
                                         is the priority queue
                                         empty?
```

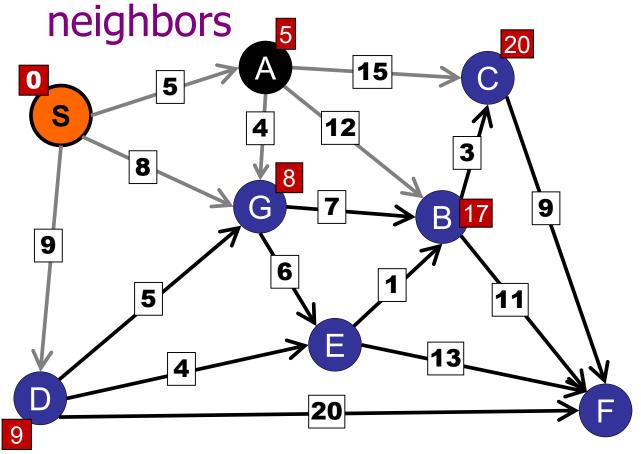
Notes:

Assume data items are unique.

```
relax(Edge e) {
    int v = e.from();
    int w = e.to();
    double weight = e.weight();
    if (distTo[w] > distTo[v] + weight) {
         distTo[w] = distTo[v] + weight;
         \exists v;
         pq.decreaseKey(w, distTo[w]);
```

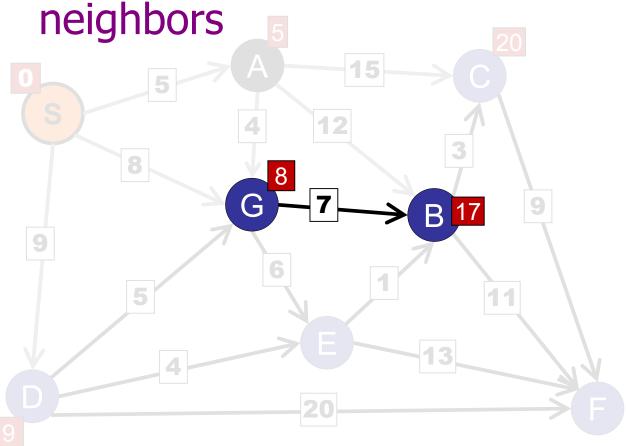
```
relax(Edge e) {
    int v = e.from();
    int w = e.to();
    double weight = e.weight();
    if (distTo[w] > distTo[v] + weight) {
          distTo[w] = distTo[v] + weight;
          parent[w] = v;
          pq.decreaseKey(w, distTo[w]);
```

Remove G and relax/update



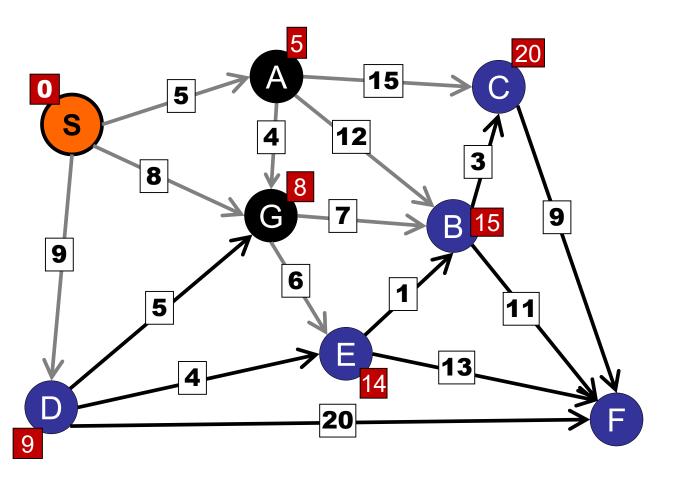
Vertex	Dist.
G	8
D	9
В	17
С	20

Remove G and relax/update



Vertex	Dist.
G	8
D	9
В	17
С	20

Remove G and relax.



Vertex	Dist.
D	9
E	14
В	15
C	20

```
relax(Edge e) {
    int v = e.from();
    int w = e.to();
    double weight = e.weight();
    if (distTo[w] > distTo[v] + weight) {
          distTo[w] = distTo[v] + weight;
          parent[w] = v;
          pq.decreaseKey(w, distTo[w]);
```

Since every edge is only relaxed 1 time (since only will travel the edge once since only extract each vertex 1 time relax (Edge e) {

```
int v = e.from();
int w = e.to();
double weight = e.weight();
if (distTo[w] > distTo[v] + weight) {
     distTo[w] = distTo[v] + weight;
     parent[w] = v;
     pq.decreaseKey(w, distTo[w]);
```

Analysis:

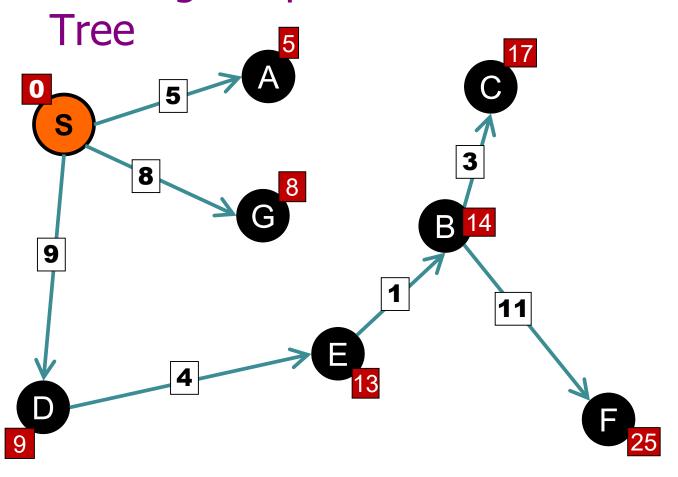
- deleteMin: |V| times each
 - Each node is added to the priority queue once.

- relax / decreaseKey: |E| times
 - Each edge is relaxed once.

Priority queue operations: O(log V)

- Total: $O((V+E)\log V) = O(E \log V)$

Following the parents: Yields the Shortest Path



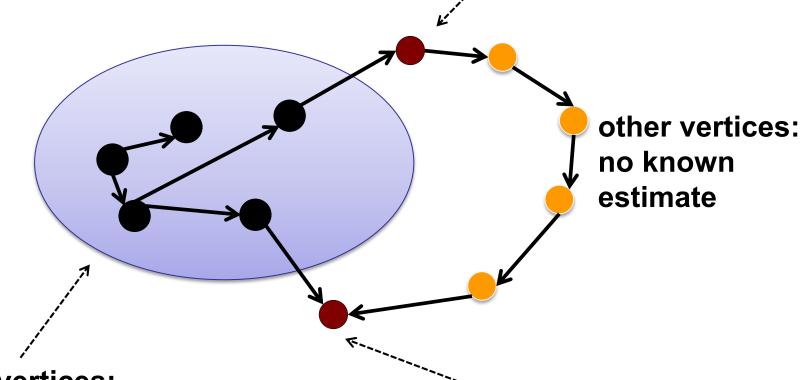
Why does it work?

Proof by induction:

- Every "finished" (dequeued) vertex has a correct estimate.
 - Namely, shortest path is found for that vertex
- Initially: only "finished" vertex is start.

fringe vertices: neighbor of a finished vertex.

Every edge crossing the boundary has been relaxed.



finished vertices: distance is accurate.

fringe vertices: top in priority queue neighbor of a finished vertex.

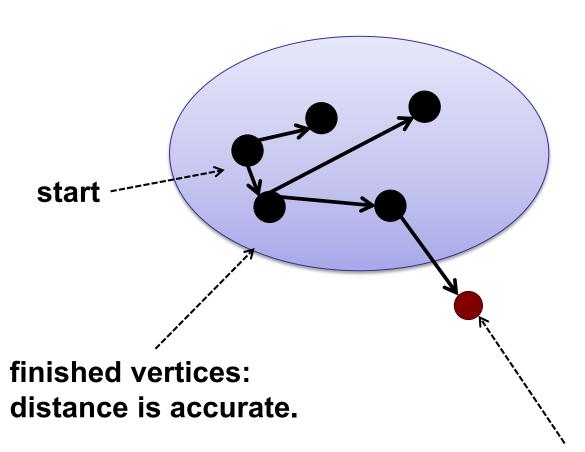
Proof by induction:

- Every "finished" vertex has correct estimate.
- Initially: only "finished" vertex is start.

Proof by induction:

- Every "finished" vertex has correct estimate.
- Initially: only "finished" vertex is start.

- Inductive step:
 - Remove vertex from priority queue.
 - Relax its edges.
 - Add it to finished.
 - Claim: it has a correct estimate.

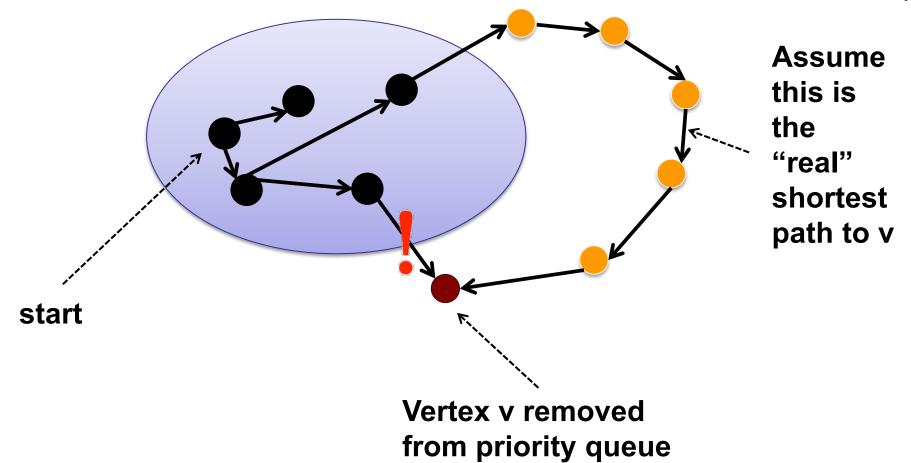


Let this distance of v be d_v

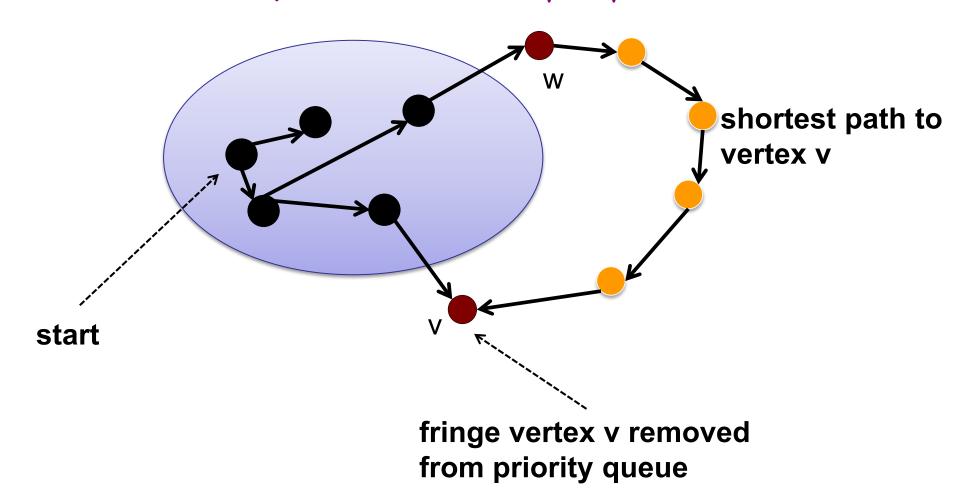
Vertex v going to be removed from priority queue next. Thus, with minimum distance amount the unfinished

trying to prove by contradiction

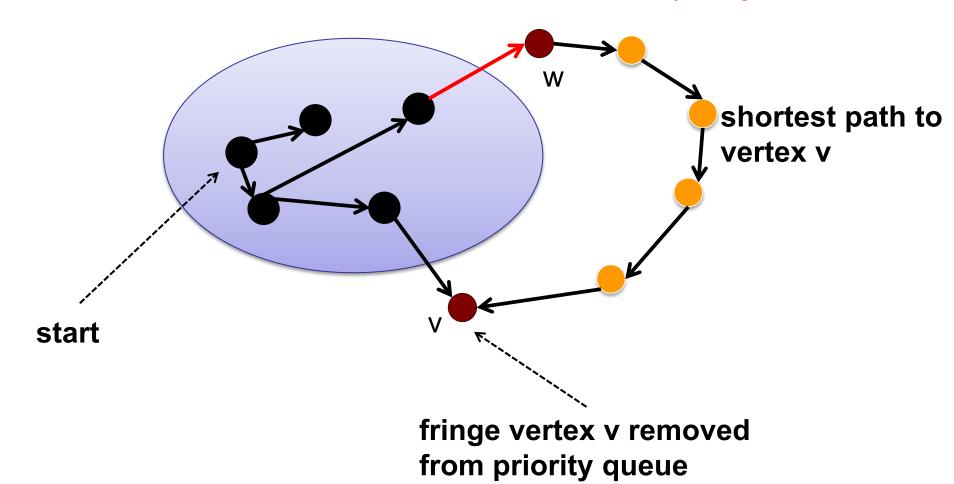
Assume NOT. The current estimate is not the shortest path. And the new path has dist. < d_v



There must be a vertex w in the current PQ on this "real" path. And let this "real" path has distance $r_v < d_v$



If P is shortest path to v, then prefix of P is shortest path to w. Then distTo[w] is accurate. And $distTo[w] < r_v < d_v = distTo[v]$



But distTo[w] >= distTo[v] according to PQ! Contradiction! Because v is the min in PQ! vertex w This "real" path must be longer! start vertex v

Vertex v going to be removed from priority queue next. Thus, with minimum distance amount the unfinished

Proof by induction:

- Every "finished" vertex has correct estimate.
- Initially: only "finished" vertex is start.

- Inductive step:
 - Remove vertex from priority queue.
 - Relax its edges.
 - Add it to finished.
 - Claim: it has a correct estimate.

```
relax(Edge e) {
    int v = e.from();
    int w = e.to();
    double weight = e.weight();
    if (distTo[w] > distTo[v] + weight) {
          distTo[w] = distTo[v] + weight;
          parent[w] = v;
          pq.decreaseKey(w, distTo[w]);
```

Analysis:

- insert / deleteMin: |V| times each
 - Each node is added to the priority queue **once**.

- decreaseKey: |E| times
 - Each edge is relaxed once.

Priority queue operations: O(log V)

- Total: $O((V+E)\log V) = O(E \log V)$

Source-to-Destination:

– What if you stop the first time you dequeue the destination?

– Recall:

- a vertex is "finished" when it is dequeued
- if the destination is finished, then stop

Dijkstra Summary

Basic idea:

- Maintain distance estimates.
- Repeat:
 - Find unfinished vertex with smallest estimate.
 - Relax all outgoing edges.
 - Mark vertex finished.

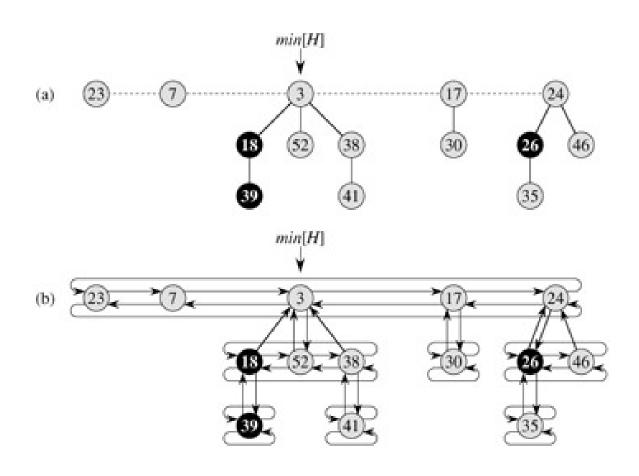
O(E log V) time

Dijkstra's Performance

PQ Implementation	insert	deleteMin	decreaseKey	Total
Array	1	V	1	O(V ²)
AVL Tree	log V	log V	log V	O(E log V)
d-way Heap	dlog _d V	dlog _d V	log _d V	O(Elog _{E/V} V)
Fibonacci Heap	1	log V	1	O(E + V log V)

Fibonacci Heap

Not in this course

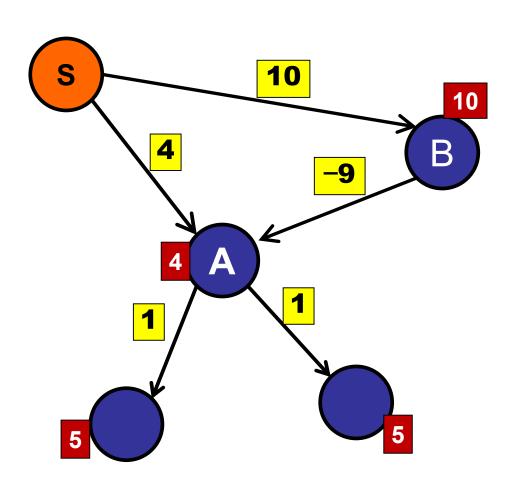


Dijkstra Summary

Edges with negative weights?

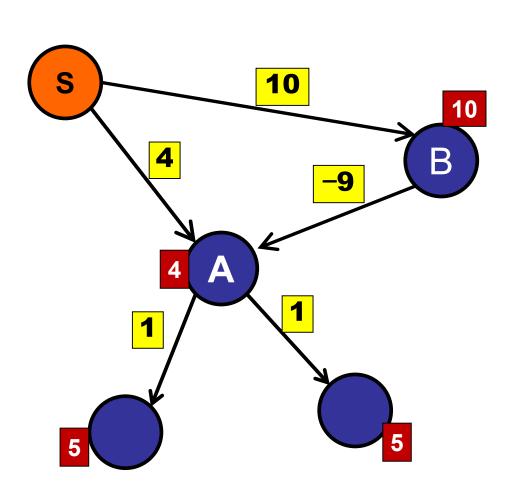
shortest path to What goes wrong with negative weights? fringe vertex v vertex w start vertex v fringe vertex v removed from priority queue

Edges with negative weights?



Step 1: Remove A.
Relax A.
Mark A done.

Edges with negative weights?



Step 1: Remove A. Relax A. Mark A done.

. . .

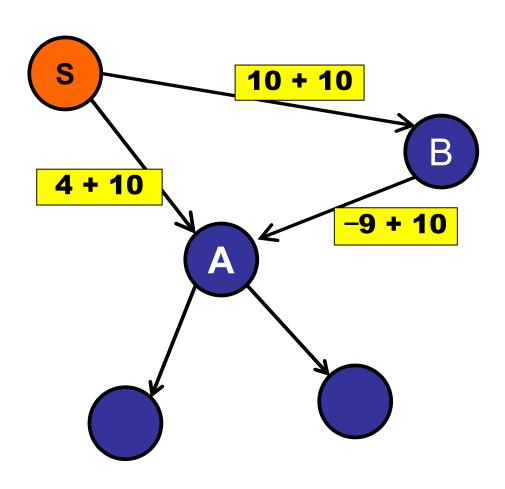
Step 4: Remove B.
Relax B.
Mark B done.

Oops: We need to update A.

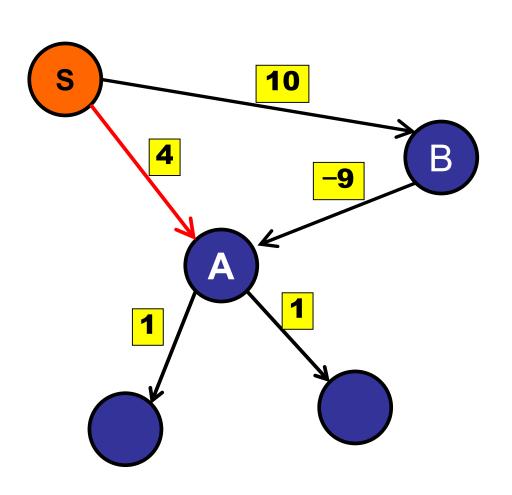
shortest path to What goes wrong with negative weights? fringe vertex v vertex w start vertex v fringe vertex v removed from priority queue

Can we reweight?

e.g.: weight
$$+= 10$$



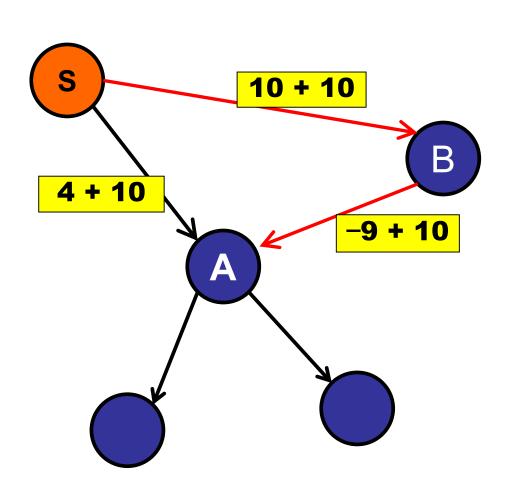
Can we reweight?



Path S-B-A: 1

Path S-A:

Can we reweight?



Path S-B-A: 21

Path S-A: 14

Dijkstra Summary

Basic idea:

- Maintain distance estimates.
- Repeat:
 - Find unfinished vertex with smallest estimate.
 - Relax all outgoing edges.
 - Mark vertex finished.

O(E log V) time (with AVL tree Priority Queue).

No negative weight edges!

Dijkstra Comparison

Same algorithm:

- Maintain a set of explored vertices.
- Add vertices to the explored set by following edges that go from a vertex in the explored set to a vertex outside the explored set.

- BFS: Take edge from vertex that was discovered least recently.
- DFS: Take edge from vertex that was discovered most recently.
- Dijkstra's: Take edge from vertex that is **closest** to source.

Dijkstra Comparison

Same algorithm:

- Maintain a set of explored vertices.
- Add vertices to the explored set by following edges that go from a vertex in the explored set to a vertex outside the explored set.

BFS: Use queue.

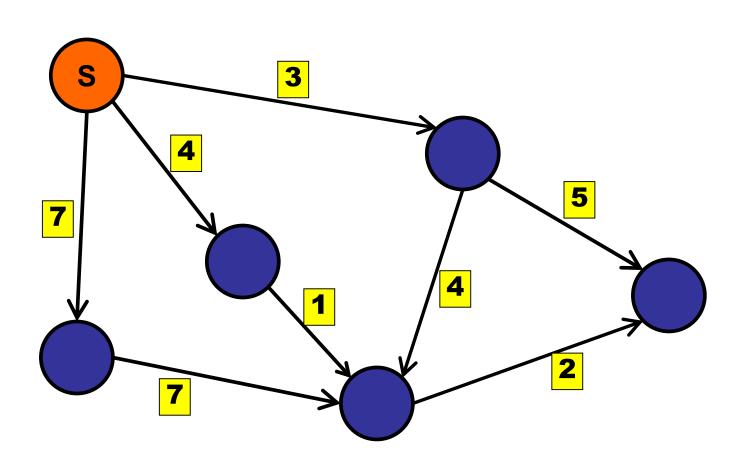
DFS: Use stack.

Dijkstra's: Use priority queue.



Longest Paths

Any ideas?

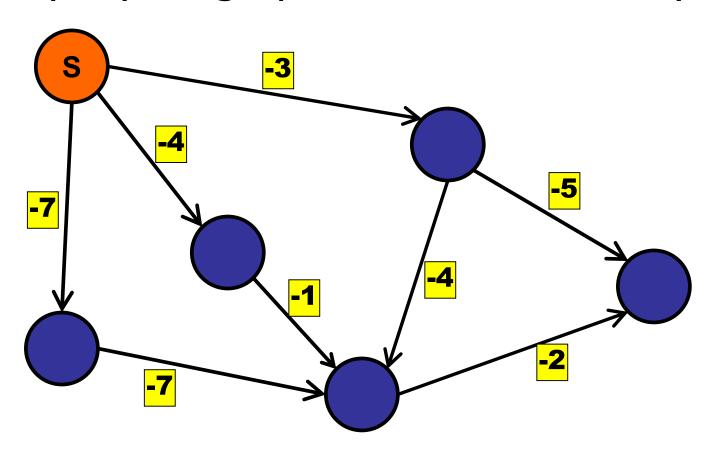


Longest Paths

Negate the edges?

Using BF not Dijkstras

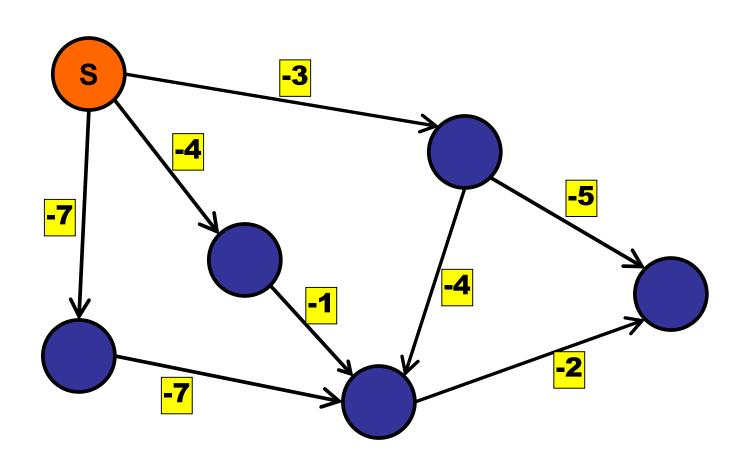
Only if your graph does not have a cycle!



Longest Paths

Acyclic Graph:

shortest path in negated=longest path in regular



Longest Path

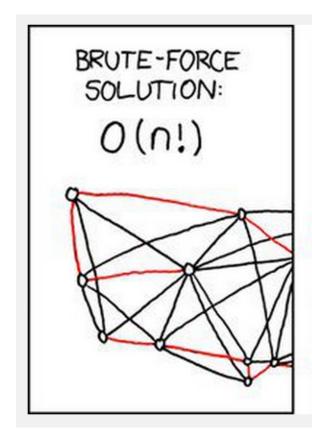
Directed Acyclic Graph:

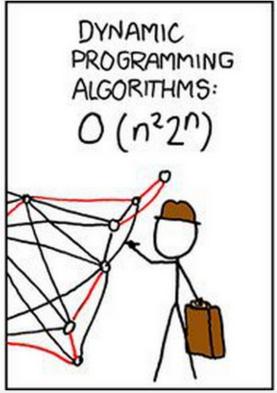
Solvable efficiently using topological sort

General (cyclic) Graphs:

- NP-Hard
- Reduction from Hamiltonian Path:
 - If you could find the longest simple path, then you could decide if there is a path that visits every vertex.
 - Any polynomial time algorithm for longest path thus implies a polynomial time algorithm for HAMPATH.

Also called the Travelling Salemans Problem

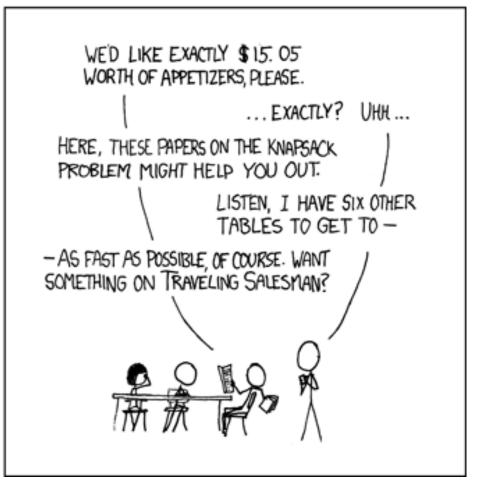






MY HOBBY: EMBEDDING NP-COMPLETE PROBLEMS IN RESTAURANT ORDERS

~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~				
[CHOTCHKIES RESTAURANT]				
~ APPETIZERS ~				
MIXED FRUIT	2.15			
FRENCH FRIES	2.75			
SIDE SALAD	3.35			
HOT WINGS	3.55			
MOZZARELLA STICKS	4.20			
SAMPLER PLATE	5.80			
→ SANDWICHES ~				
RARRECUE	6 55			



#### Roadmap

Part I: Shortest Paths

Part II: Applications of Shortest Paths

- DNA Alignment
- Constraint Systems

### Input: two DNA strings:

- AGGAACCGTA
- AGAATCCGAA

### How similar are they?

Metric: edit distance

How many operations to transform one DNA string into another?

### Input: two DNA strings:

- AGGAACCGTA ← delete G, delete T
- AGAATCCGA ← add T

### Three operations:

- Delete a character
- Add a character
- Transform a character

### Input: two DNA strings:

- AGGAACCGTA ← delete G, delete T
- AGAATCCGA ← add T

### Three operations:

- Delete a character cost = d
- Add a character cost = a
- Transform a character cost = t

OR: minimum *cost* to transform A to B?

#### Model question as a directed graph:

- For each character i, character j:
  - Create a node in the graph N(i,j)
  - N(i,j) represents adapting position i of the old string to match position j of the new string.

- For node N(i,j), three outgoing edges:
  - insert character j+1 from new string after position i
  - delete character i+1 from old string
  - transform character i+1 to character j+1

Transform: CG to AGT

start ACG AGCG CG AGTCG G AG AGG AGTG AG A **AGT** 

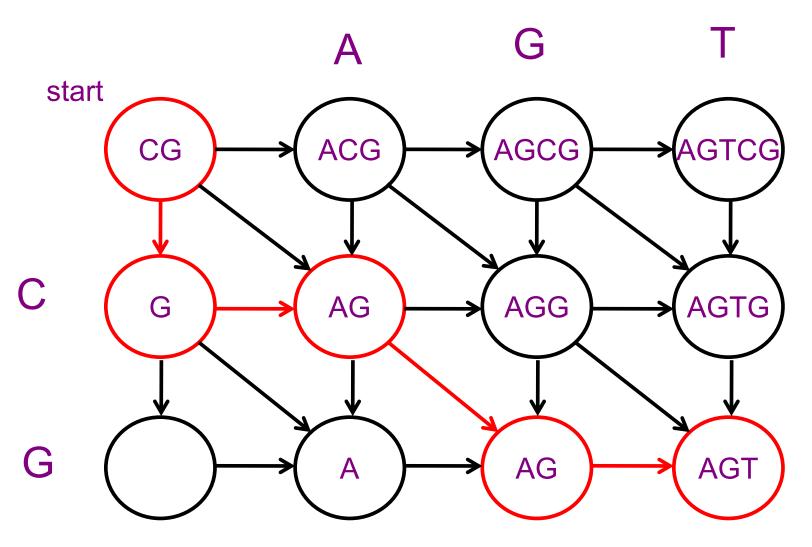
Vertical: delete character

Horizontal: add character

Diagonal: transform character

### CG to AGT

Delete C, Add A, Leave G, Add T:



Vertical: delete character

Horizontal: add character

Diagonal: transform character

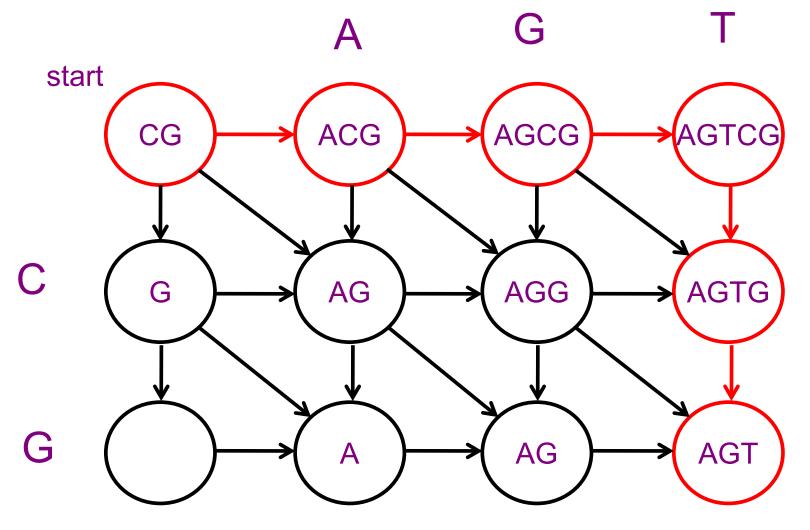
### CG to AGT

Vertical: delete character

Add A, Add G, Add T, Delete C, Delete G:

Horizontal: add character

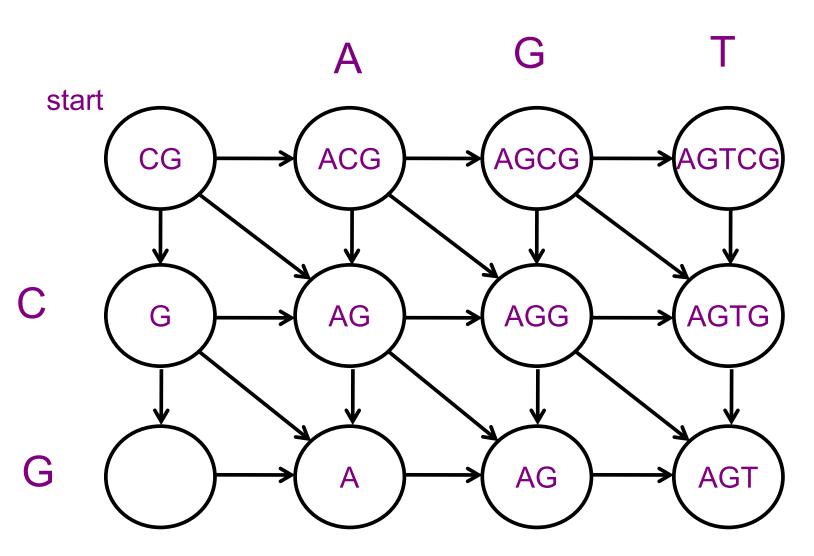
Diagonal: transform character



#### Model question as a directed graph:

- For node N(i,j):
  - The first i letters of the old string have been replaced with the first j letters of the new string.
  - The shortest path to N(i,j) is the shortest set of changes to change the first i letters of the old string to the first j letters of the new string.

Transform: CG to AGT



Vertical: delete character

Horizontal: add character

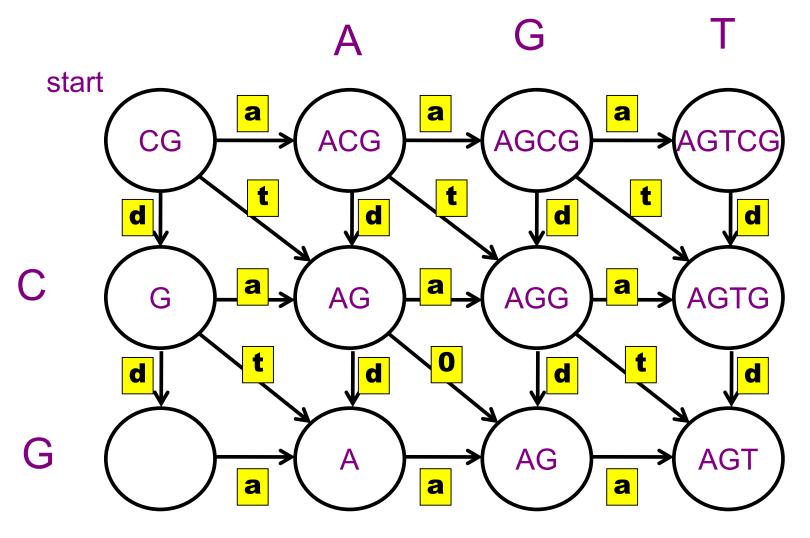
Diagonal: transform character

### CG to AGT

Vertical: delete character

### Edge costs:

Horizontal: add character



Diagonal: transform character

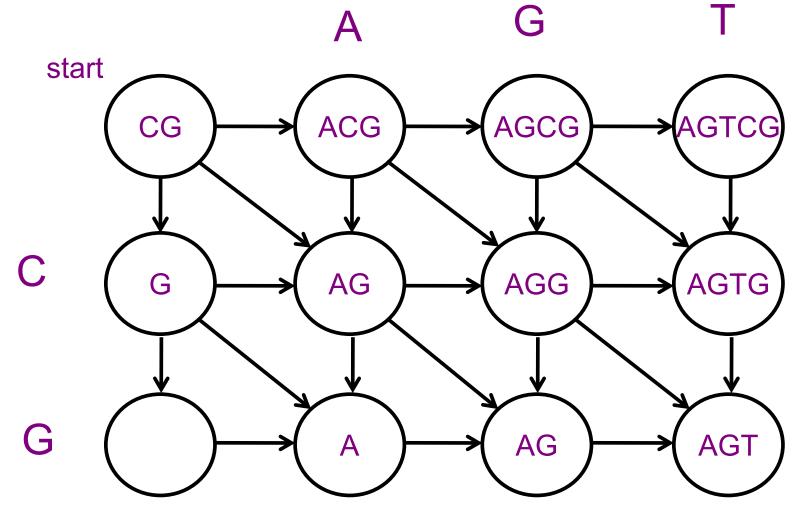
Vertical: delete character

Transform: CG to AGT

Horizontal: add character

Diagonal: transform character

N^2 algo



## Roadmap

Part I: Shortest Paths

Part II: Applications of Shortest Paths

- DNA Alignment
- Constraint Systems

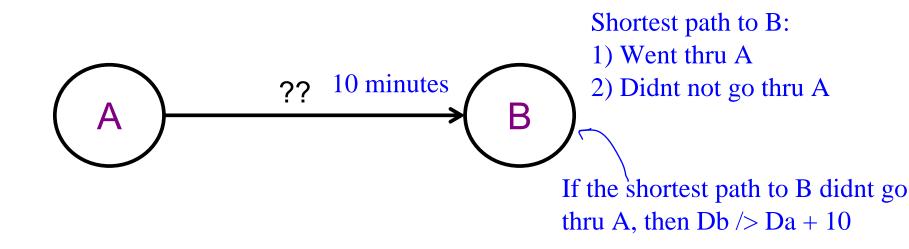
### Input:

- Set of tasks: A, B, C, D, E, F
- Constraints:
  - A must be done at least 10 minutes before C
  - D must be done at most 20 minutes after E
  - B must be done after F

### Output:

- Feasible?
- Schedule?

B must be executed at least 10 minutes after A

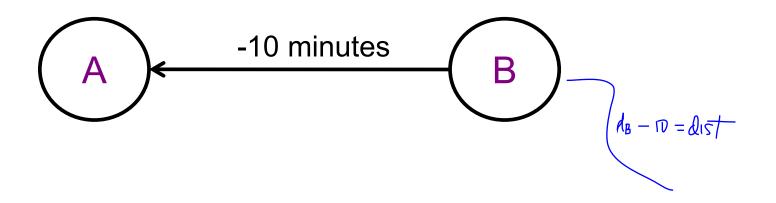


Shortest path = schedule time

$$Db \le Da + 10$$

triangle inequality: shortest path to B is at most 10 longer than shortest path to A

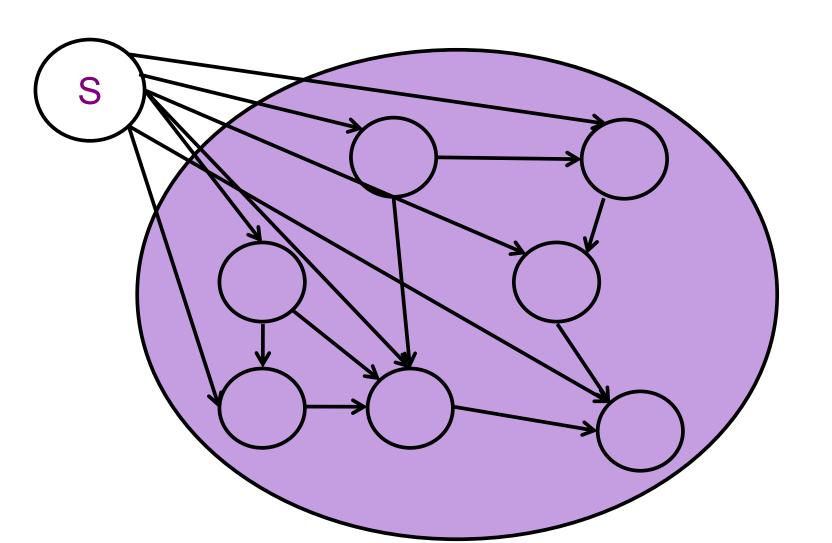
B must be executed at least 10 minutes after A



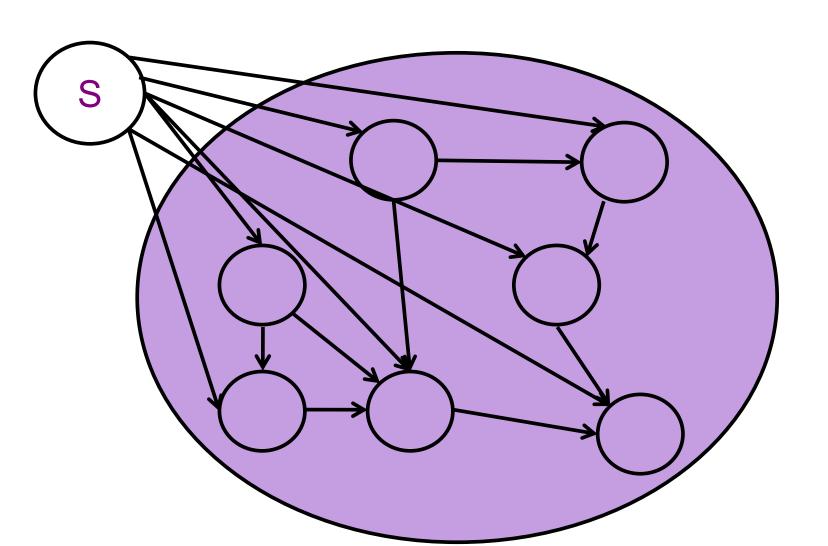
Shortest path = schedule time

triangle inequality: shortest path to B is at least 10 longer than shortest path to A

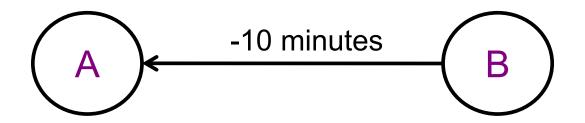
Add source S connected by 0 weight edges to all.



Solve shortest paths.



B must be executed at least 10 minutes after A



Negative edges: use Bellman-Ford!

Running time: O(nm)

### Input:

- Set of tasks: A, B, C, D, E, F
- Constraints:
  - A must be done at least 10 minutes before C
  - D must be done at most 20 minutes after E
  - B must be done after F

### Output:

- Shortest path guarantees constraints are met.
- Shortest path finishes all tasks in minimum time.

## Roadmap

Part I: Shortest Paths

Part II: Applications of Shortest Paths

- DNA Alignment
- Constraint Systems