Lecture 25: Graph Algorithms: Dijkstra

BT 3051 - Data Structures and Algorithms for Biology

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Dijkstra's algorithm

- ► How to find the shortest path from u to v in a graph?
- Different algorithms exist for
 - Negative weights (Bellman–Ford)
 - All pairs shortest paths (Floyd–Warshall dynamic programming)
- BFS works when all weights are unity!

Dijkstra's algorithm Algorithm Design

- ► Applying the greedy method to the single-source, shortest-path problem, results in an algorithm known as *Dijkstra's algorithm*
- Main idea: applying the greedy method to perform a weighted BFS starting at the source vertex s
- Greedy method: iteratively grows a *cloud* of vertices out of s, with the vertices entering the cloud in order of their distances from s
- ► In each iteration, the next vertex chosen is the vertex outside the cloud that is closest to s, and we perform an *edge relaxation*
- ► Algorithm terminates when no more vertices are outside the cloud*
- ► We then have a shortest path from s to every vertex of G that is reachable from s

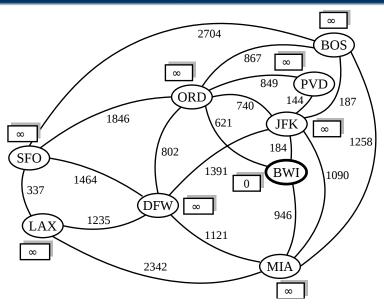
Dijkstra's algorithm Edge Relaxation

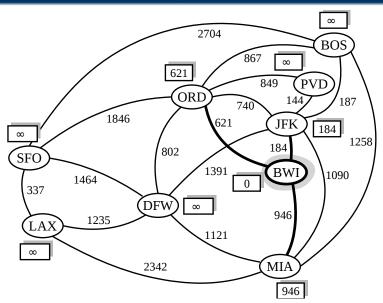
For all v, dist[v] is the length of some path (best path so far) from s to v

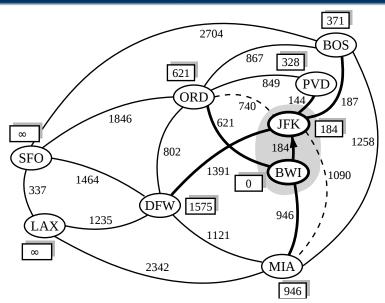
Relaxation along edge e from v to w

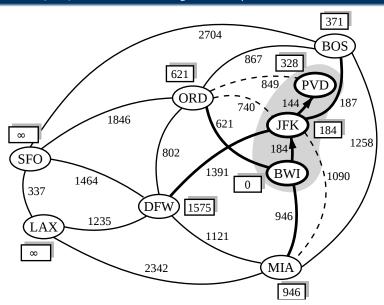
- ▶ dist[v] is length of some path from s to v
- ▶ dist[w] is length of some path from s to w
- ▶ if $v \rightarrow w$ gives a shorter path to w through v, update dist[w] and pred[w]

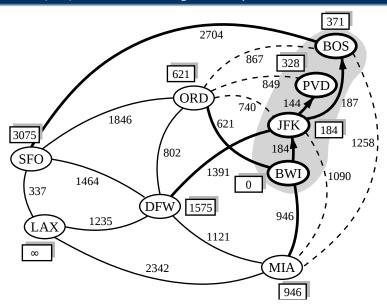
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if dist[u] + edge_weight(u,v) < dist[v]:
    dist[v] = dist[u] + edge_weight(u,v)</pre>
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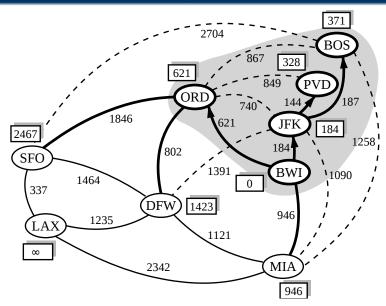


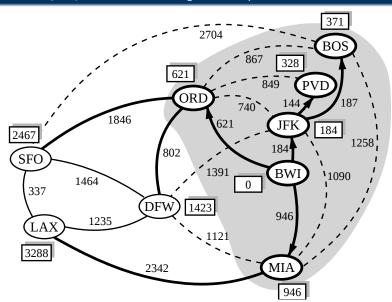


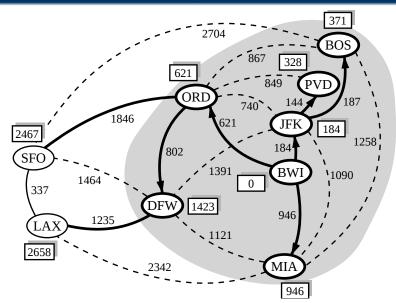


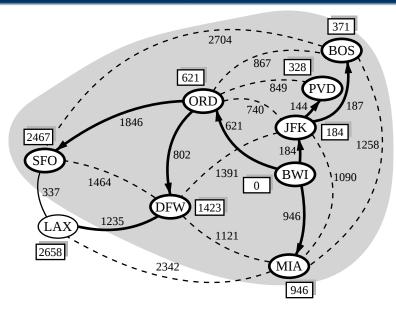


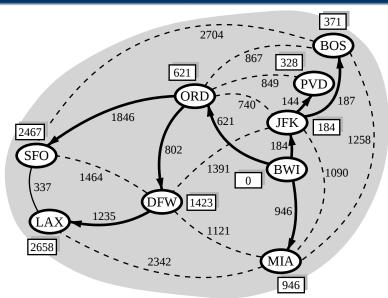












Dijkstra's Shortest Path Algorithm

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