Algorithmic Approaches for Biological Data, Lecture #19

Katherine St. John

City University of New York
American Museum of Natural History

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Outline

- More on Dynamic Programming

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- Aligning Sequences

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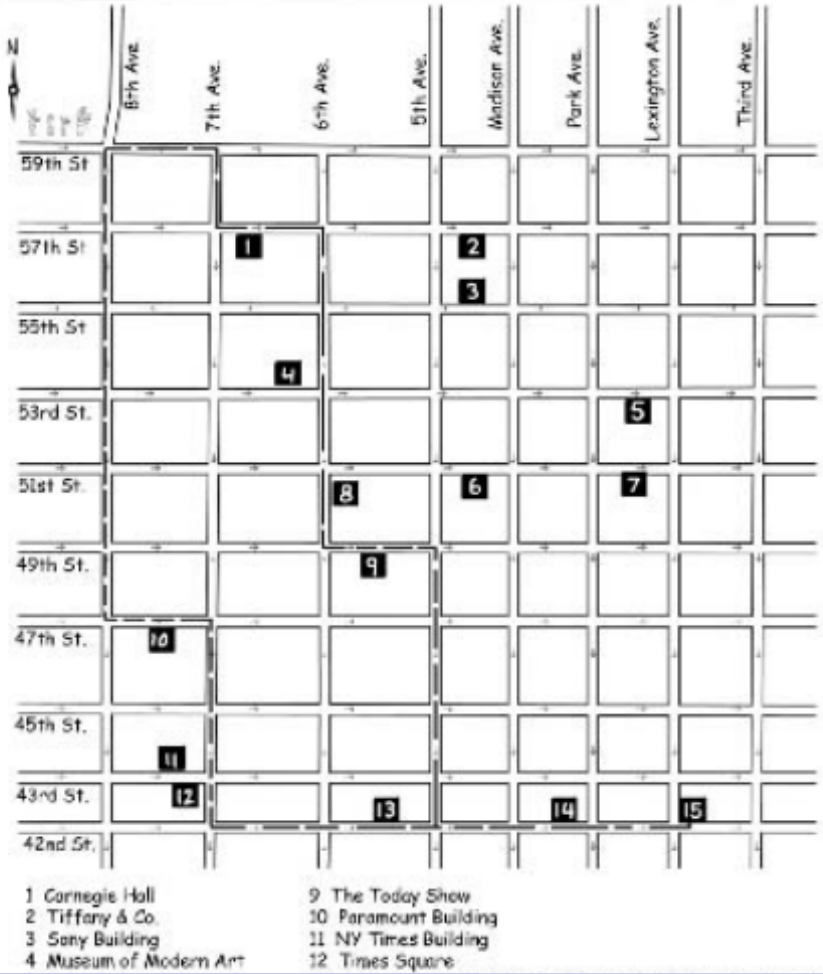
- More on Dynamic Programming
- Aligning Sequences
- Minimal Spanning Trees

Recap: Manhattan Tourist Problem



- In hurry, and want to visit as many landmarks as possible.

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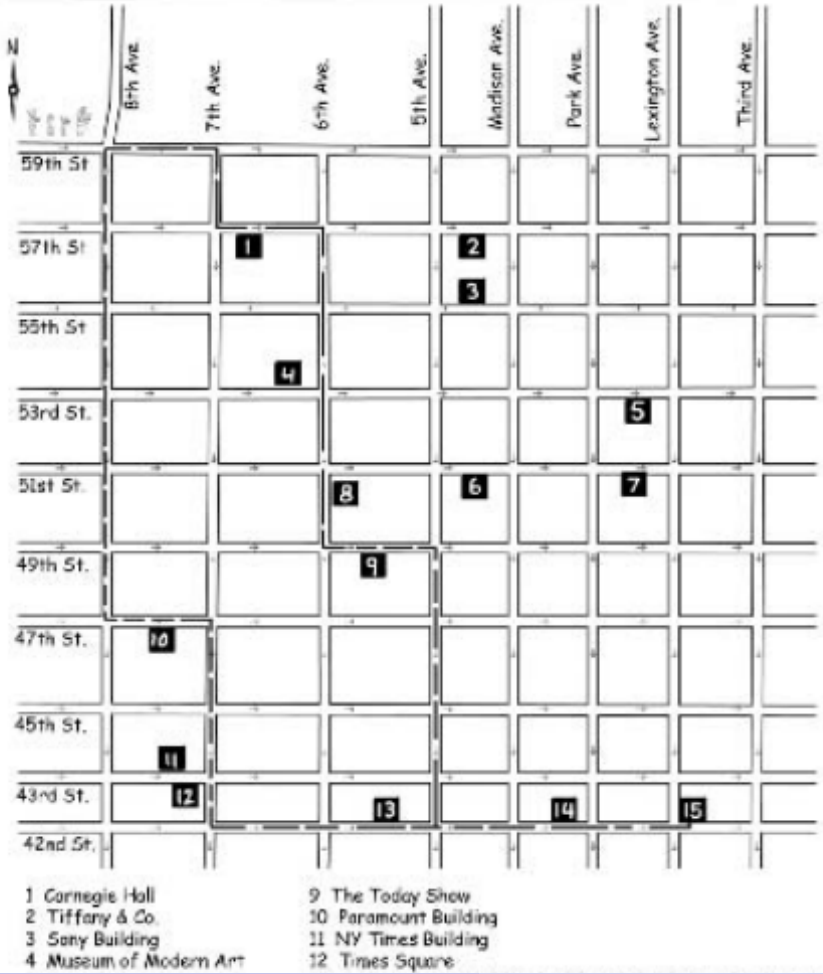

- In hurry, and want to visit as many landmarks as possible.
- Can only walk south and east.

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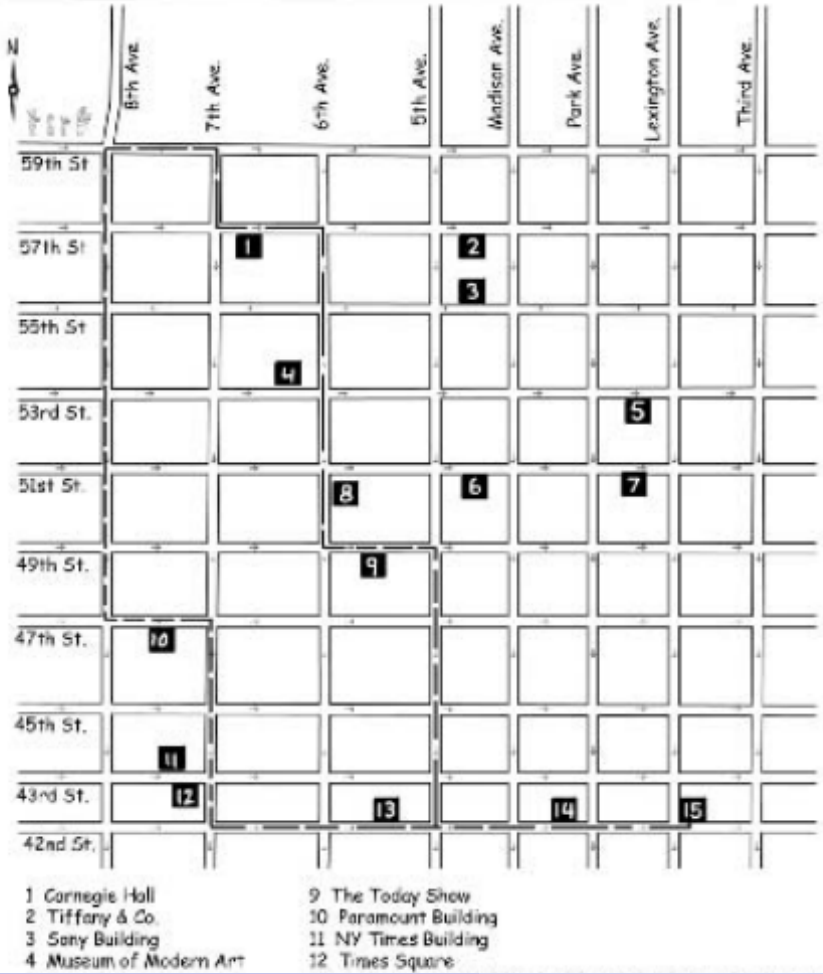
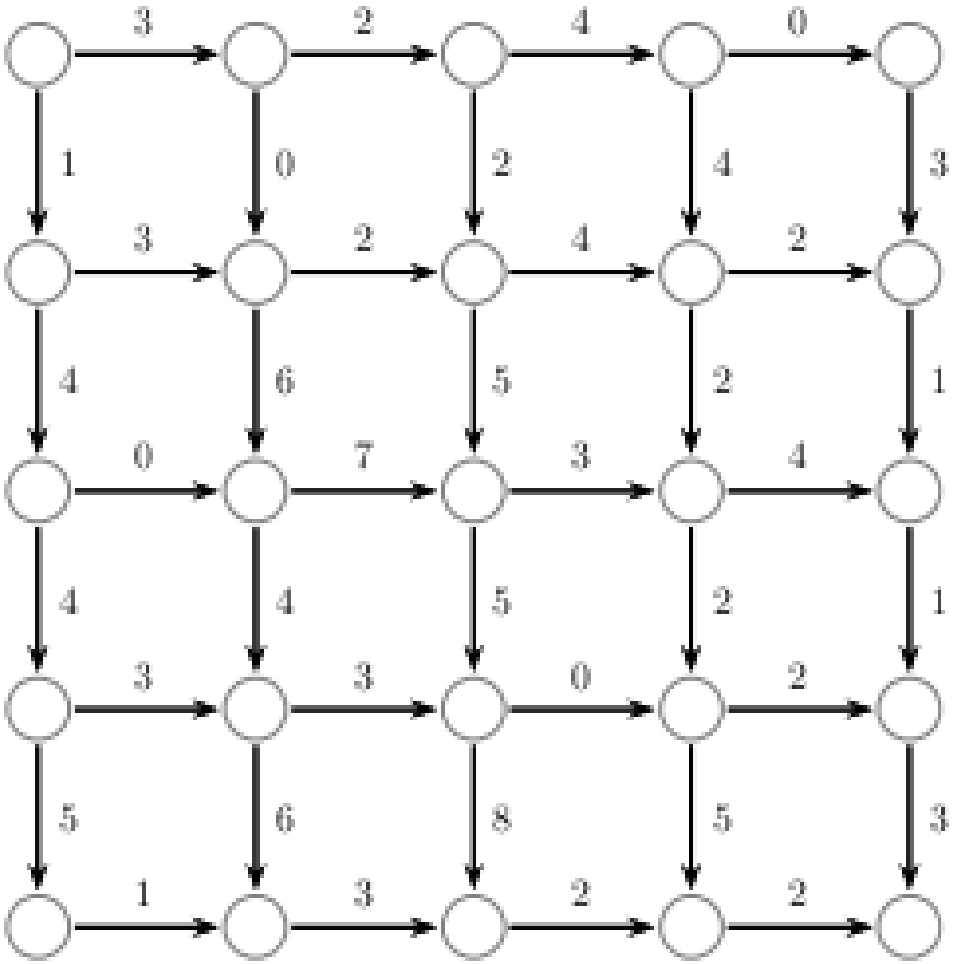


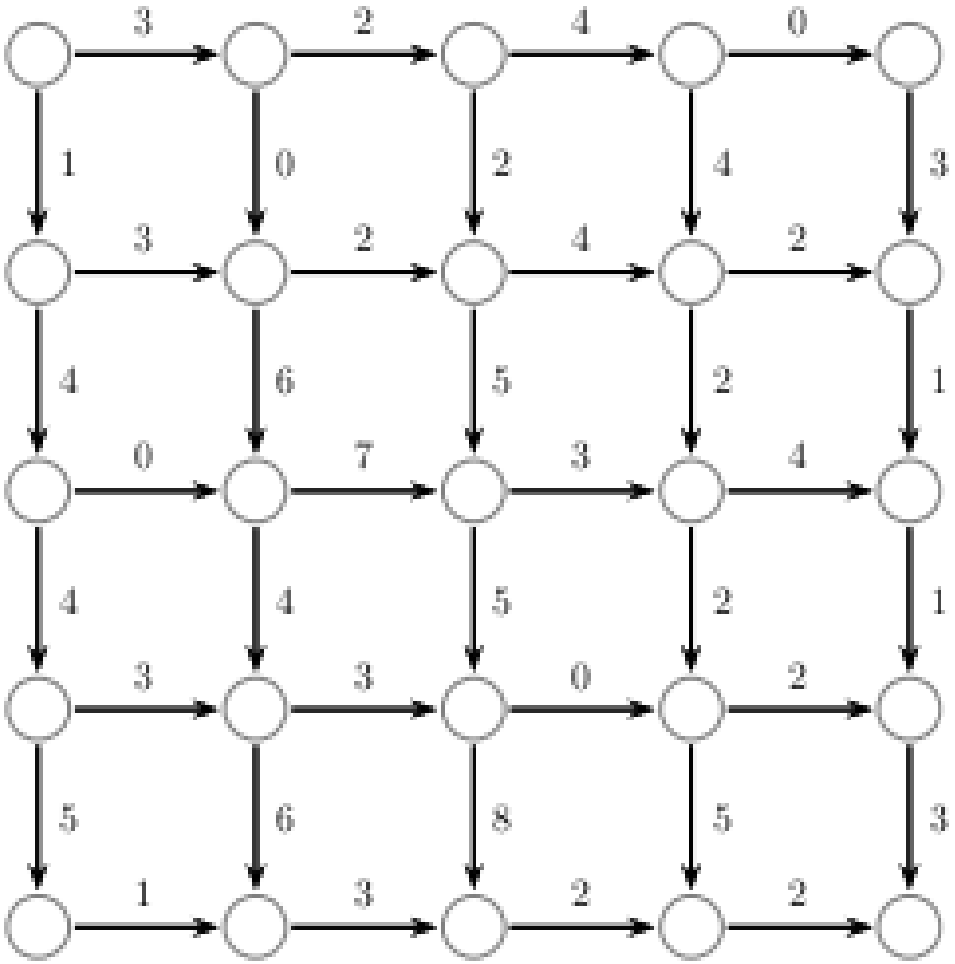
- In hurry, and want to visit as many landmarks as possible.
- Can only walk south and east.
- What's the best route?

In Pairs: Tourists Problems



- In hurry, and want to visit as many landmarks (numbers on edges) as possible.

In Pairs: Tourists Problems



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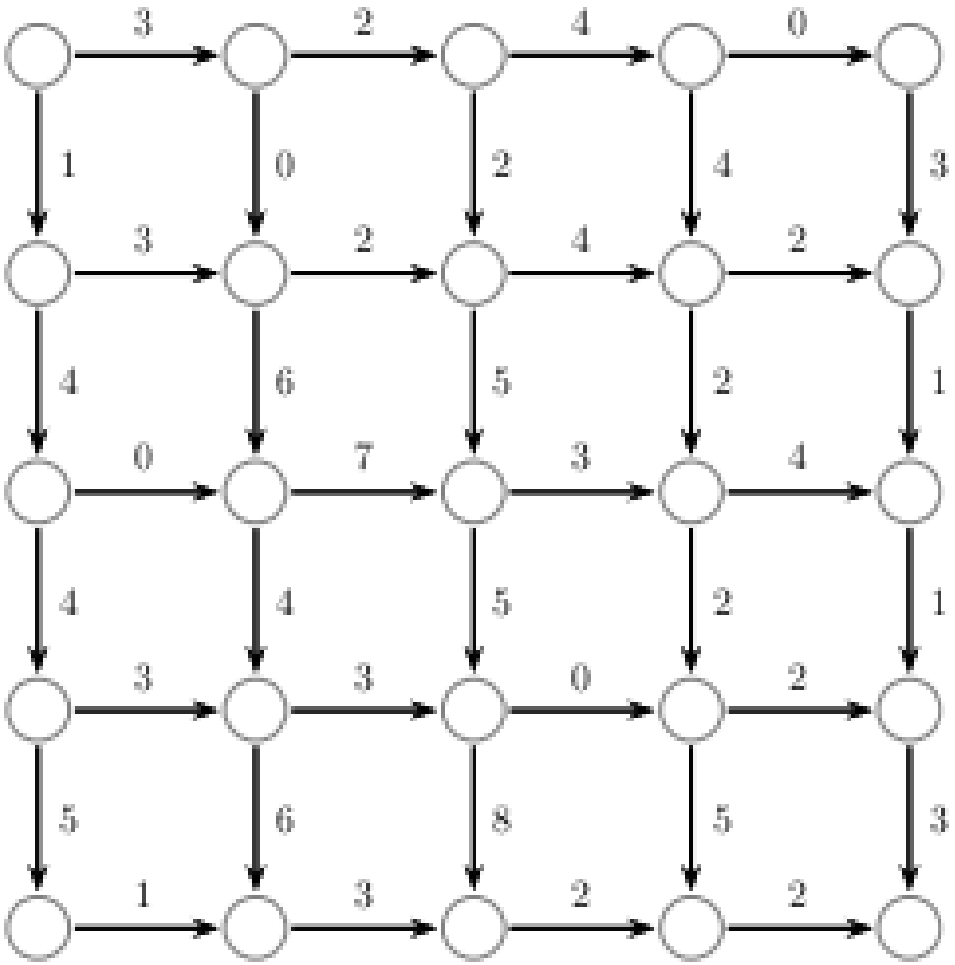

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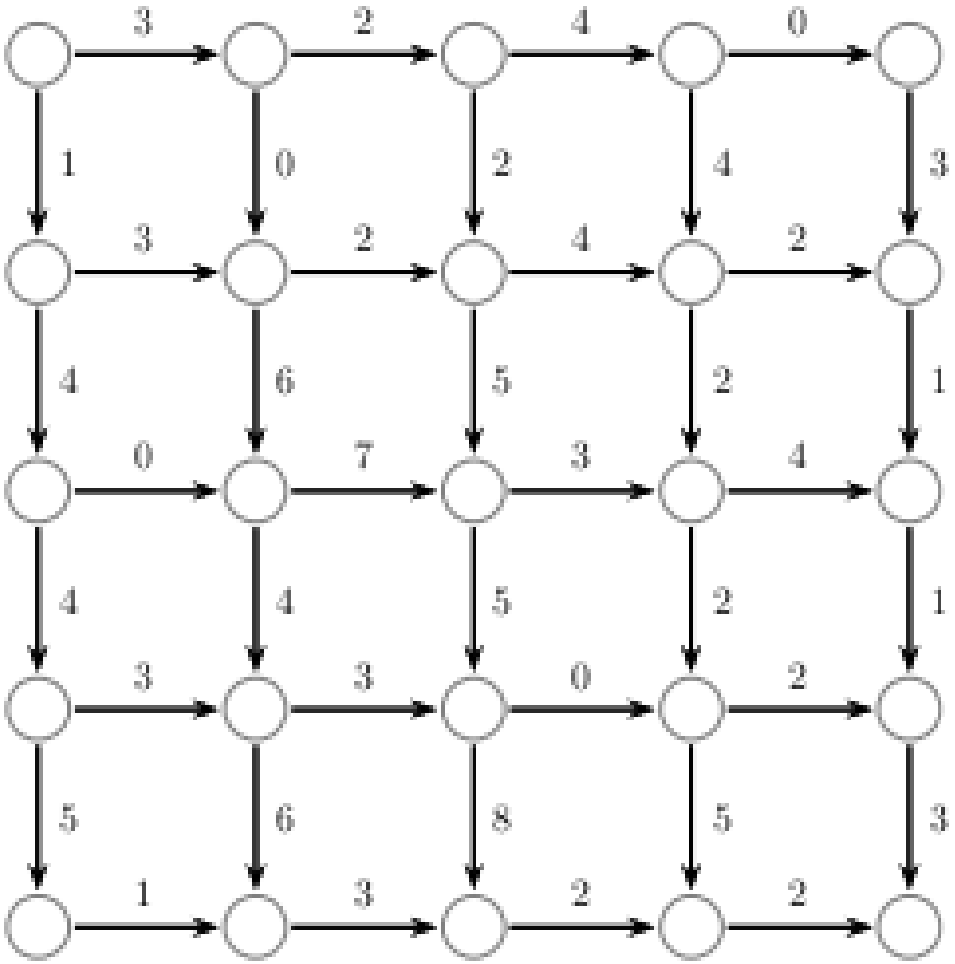
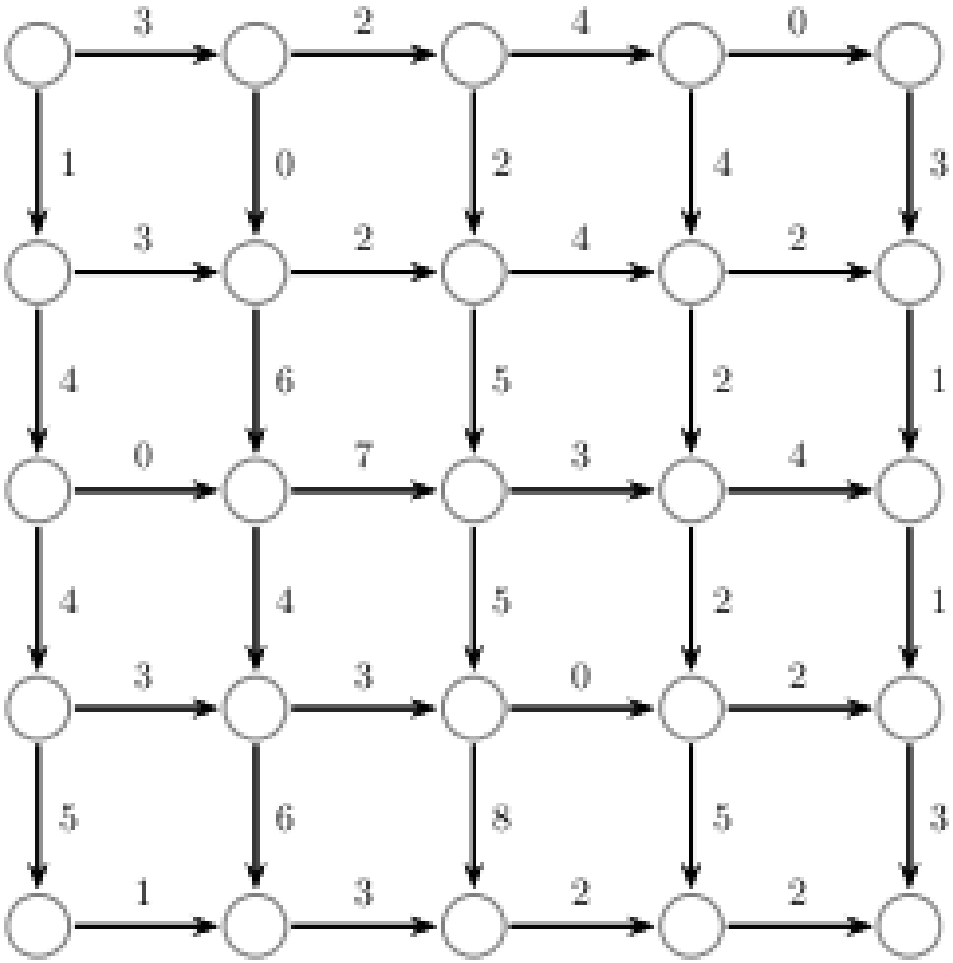
- Can only walk south and east.
- What's the best route found by greedy approach?

In Pairs: Tourists Problems



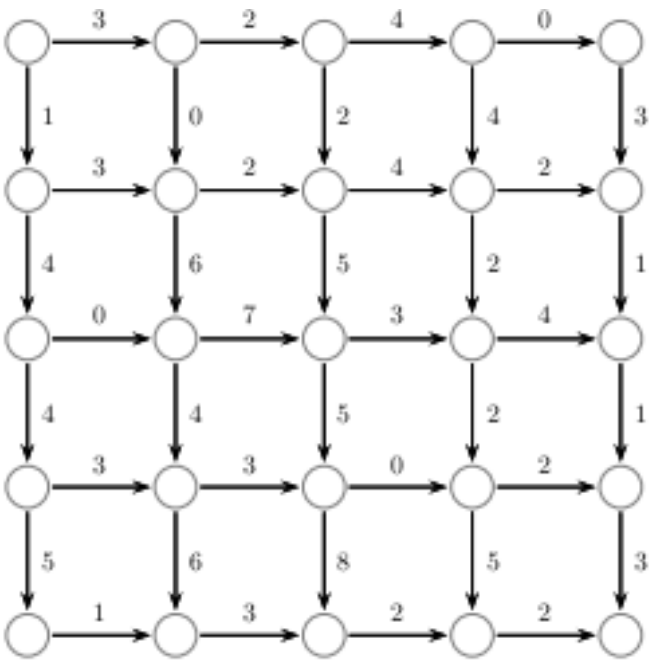
- In hurry, and want to visit as many landmarks (numbers on edges) as possible.
- Can only walk south and east.
- What's the best route found by greedy approach?
- What's the best overall?

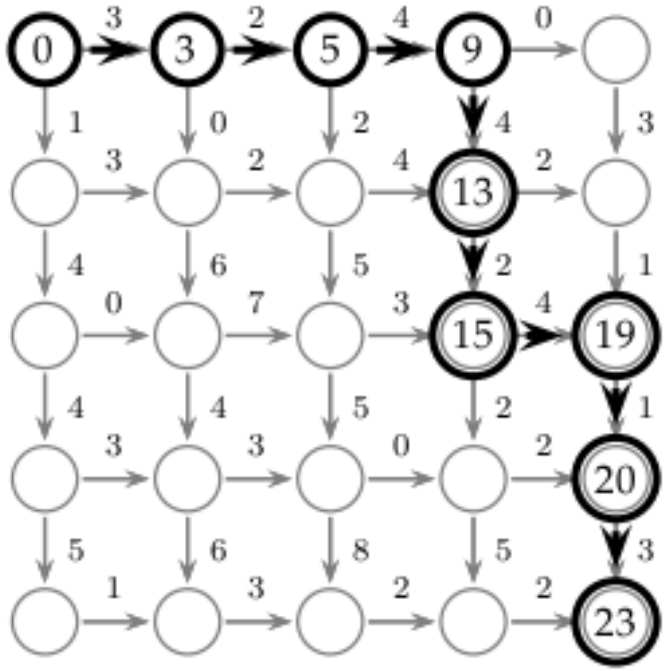
In Pairs: Tourists Problems



Greedy Algorithm: Do the best at the each step.

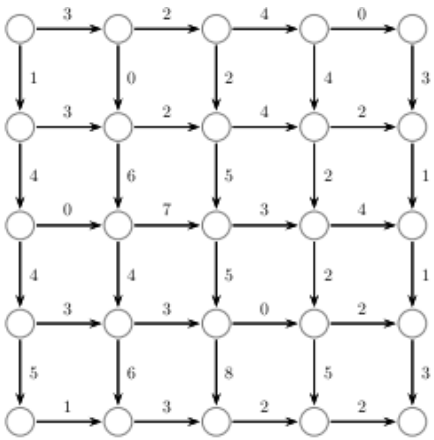
Greedy Approach: Tourists Problems





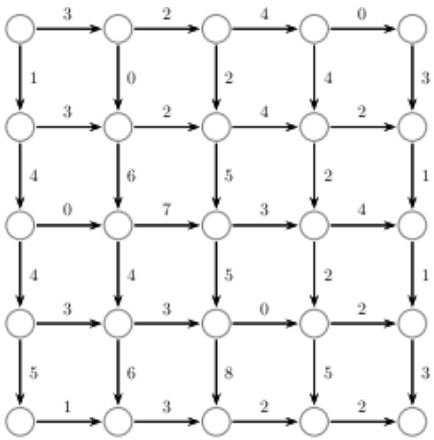
Greedy Algorithm: Do the best at the each step.

Dynamic Programming



- The best path is the larger of the best path going south and the best going east.

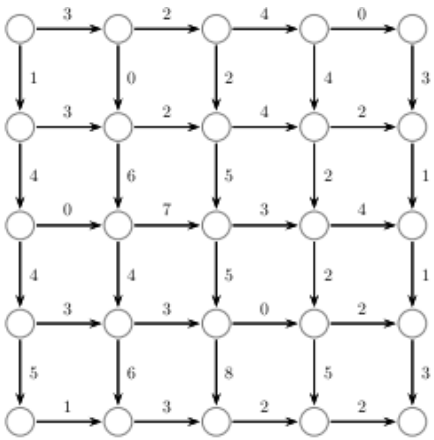
Dynamic Programming



- The best path is the larger of the best path going south and the best going east.

$$s_{i,j} = \max \begin{cases} s_{i-1,j} + \text{ weight of the edge between } (i-1,j) \text{ and } (i,j) \\ s_{i,j-1} + \text{ weight of the edge between } (i,j-1) \text{ and } (i,j) \end{cases}$$

Dynamic Programming



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- Compute the best for each subproblem and save it for future computations.

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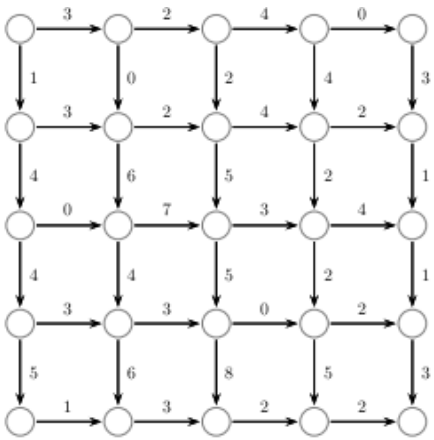

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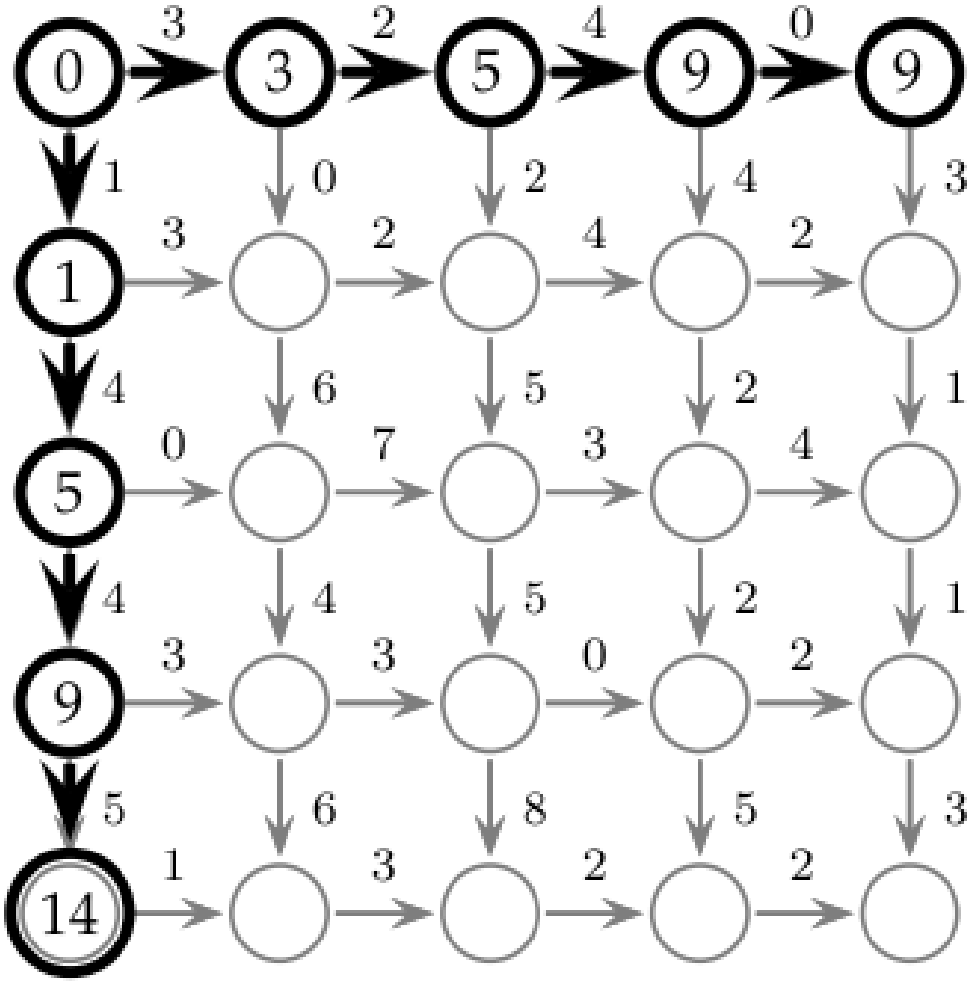
- Compute the best for each subproblem and save it for future computations.
- Store the answers in an array.

Dynamic Programming



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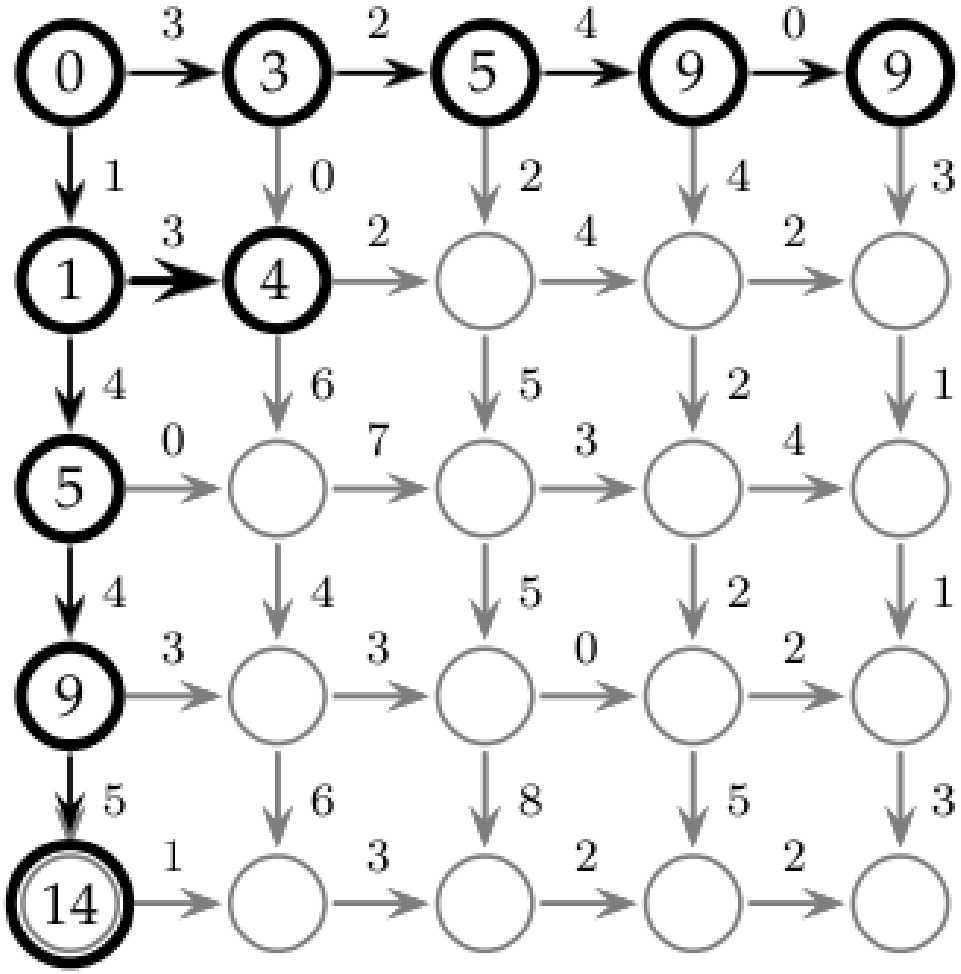

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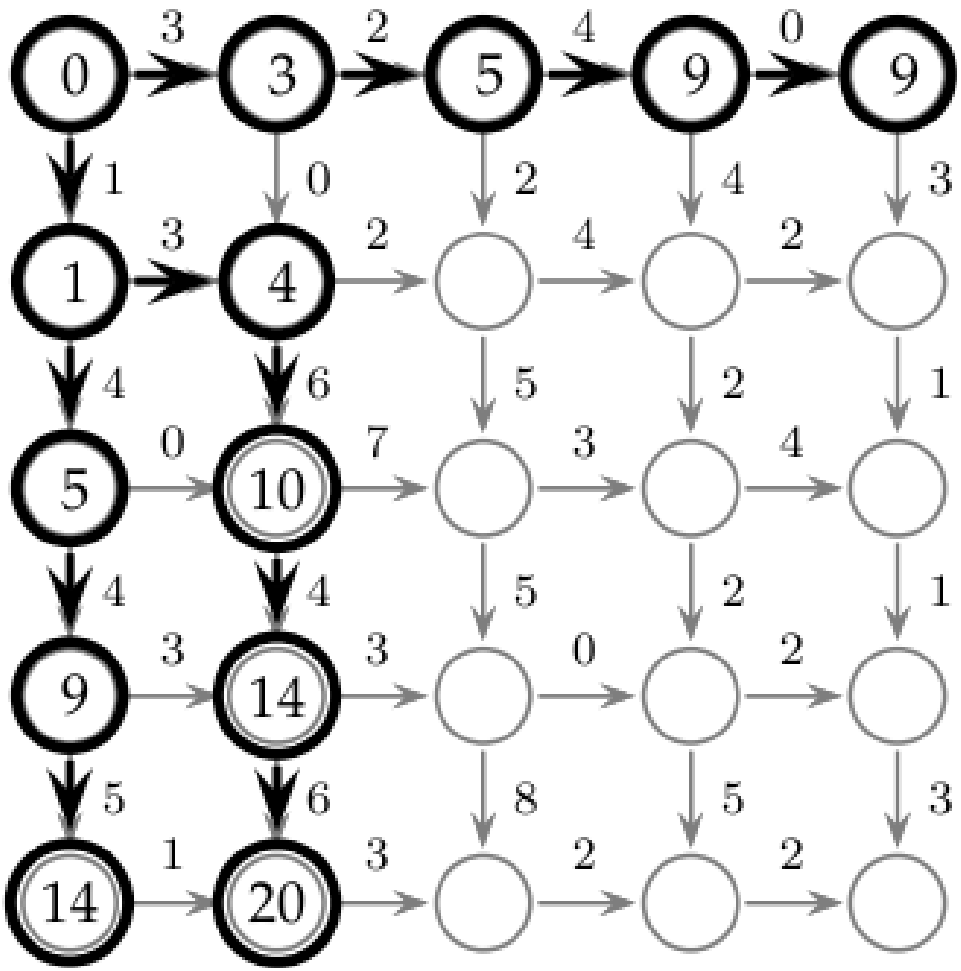

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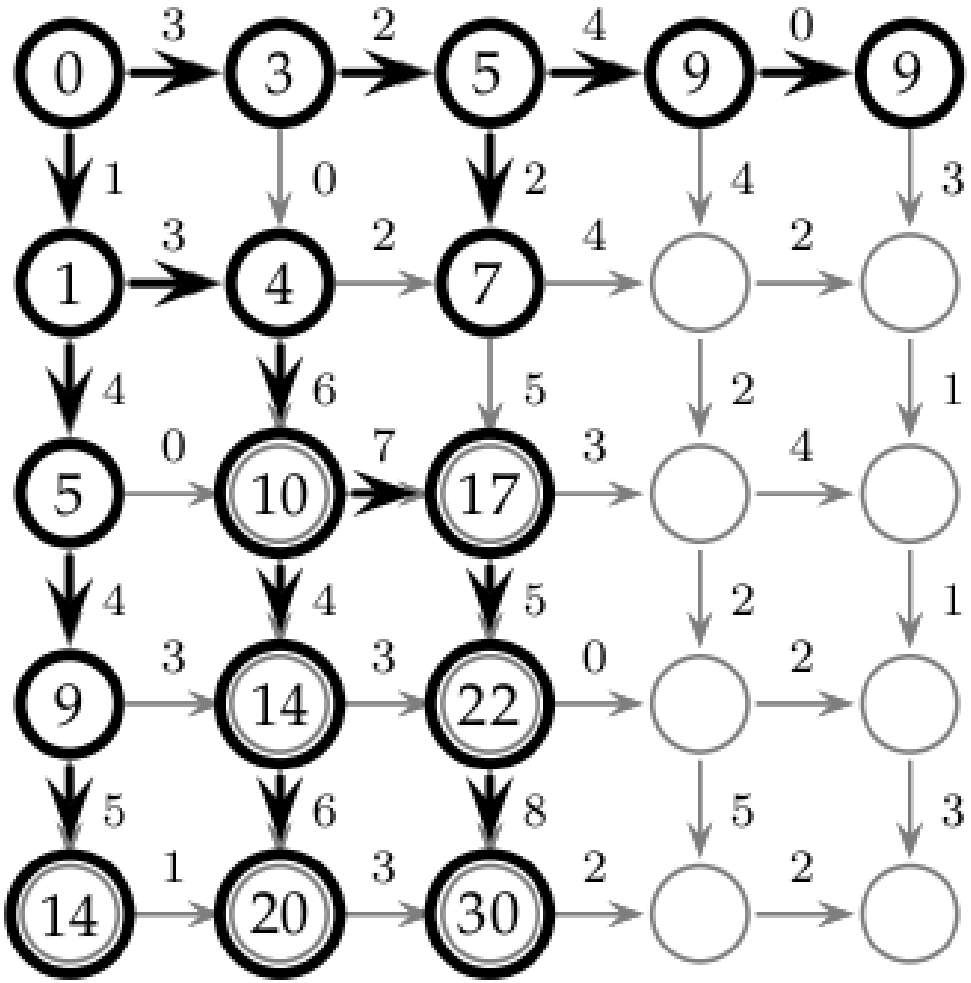

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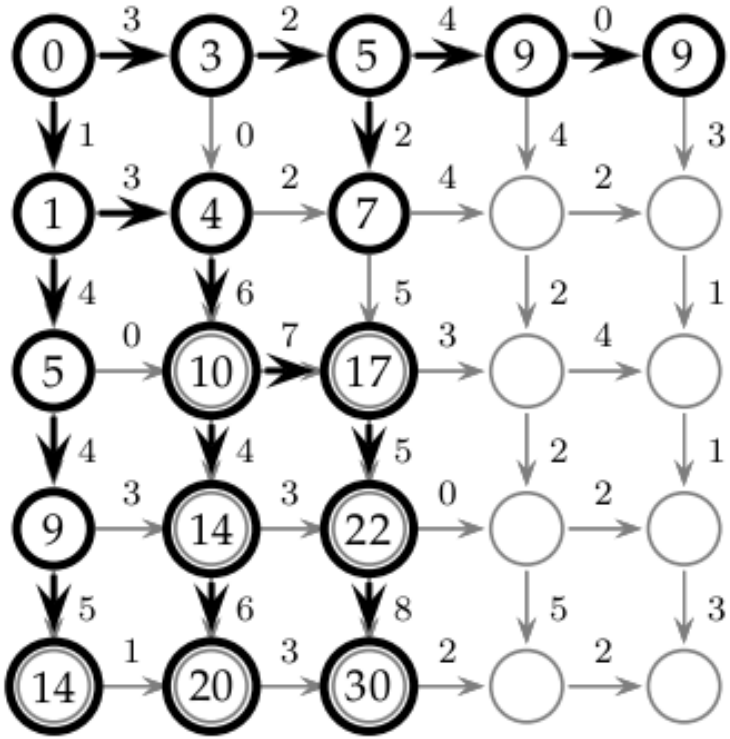

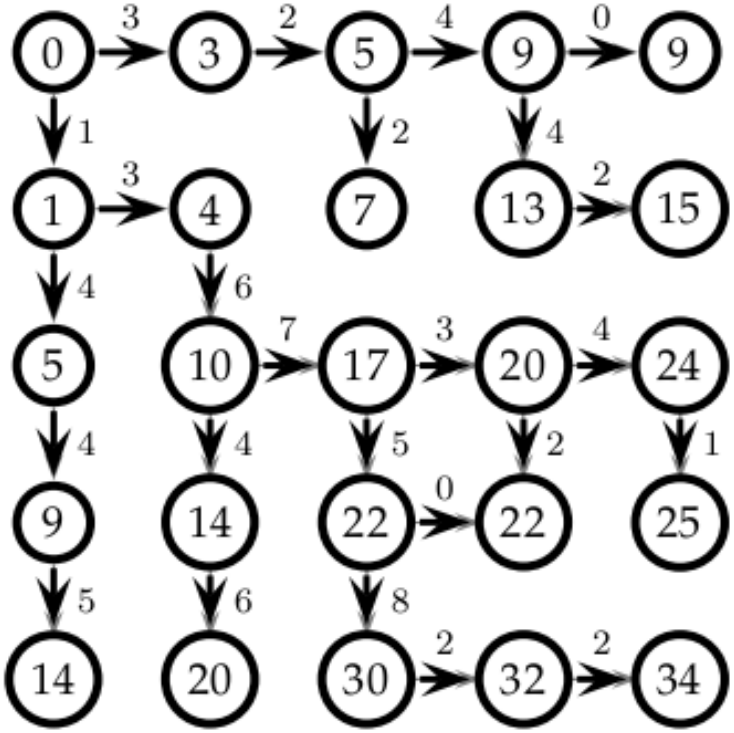

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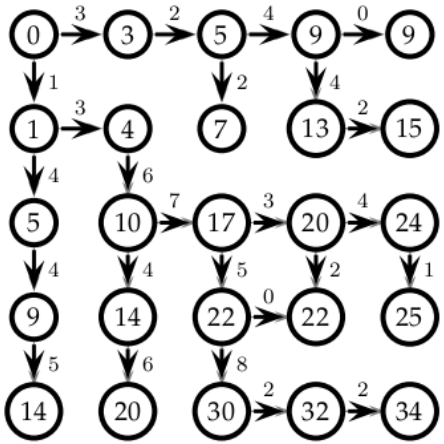
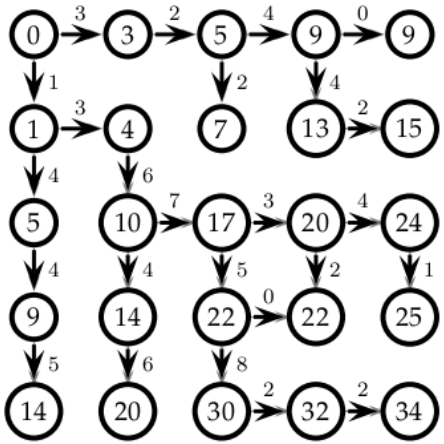
Dynamic Programming



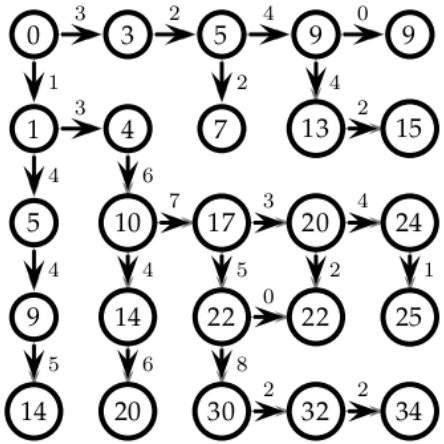
- How do you code this?

Dynamic Programming



- How do you code this?
  - What are the inputs?

Dynamic Programming



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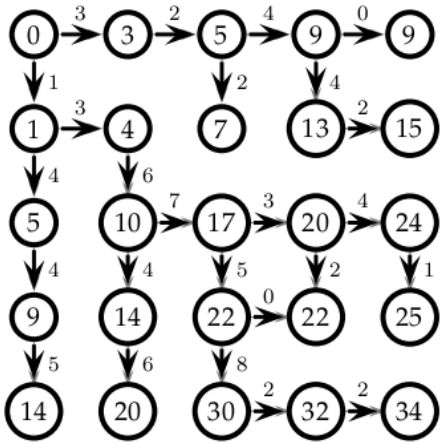
Dynamic Programming



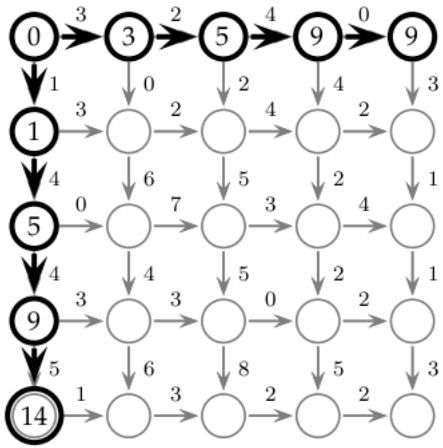
- How do you code this?
  - What are the inputs?

    Graph with weighted edges
  - What are the outputs?

    Final score (could also give path)

Dynamic Programming

- How do you code this?



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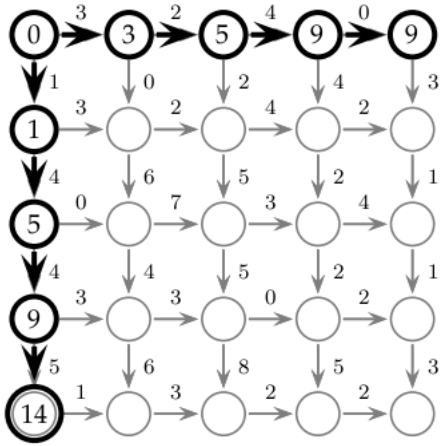
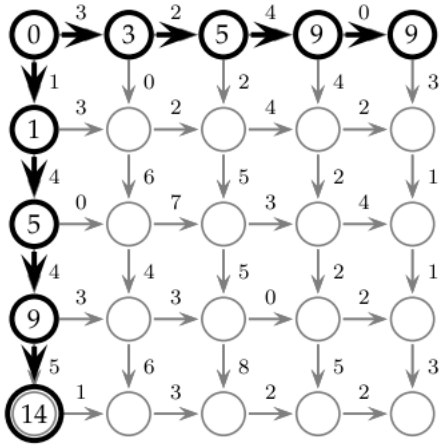


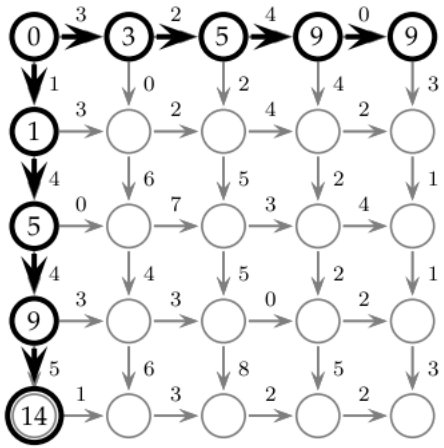
- How do you code this?
  1. Fill in the edge values.

Dynamic Programming



- How do you code this?
  1. Fill in the edge values.
  2. Fill in the second column, using the first.

Dynamic Programming



- How do you code this?
  1. Fill in the edge values.
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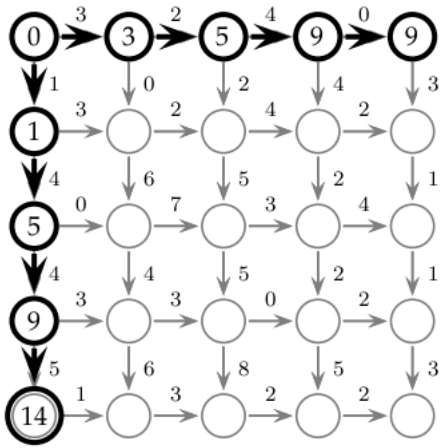
Dynamic Programming



- How do you code this?
  1. Fill in the edge values.
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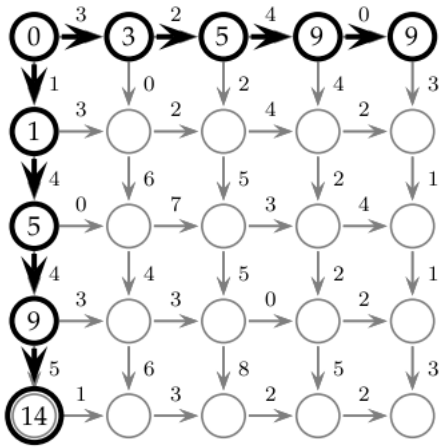
  4. Keep repeating until entire array is filled.

Dynamic Programming



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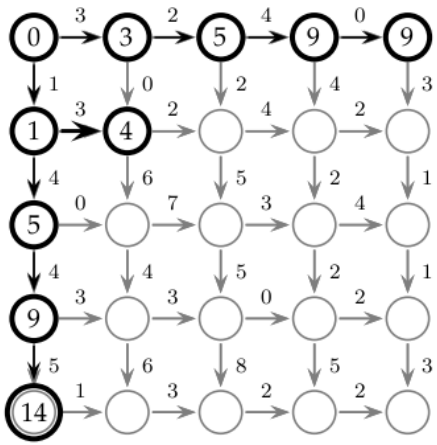
- What data structures do you need?

Dynamic Programming



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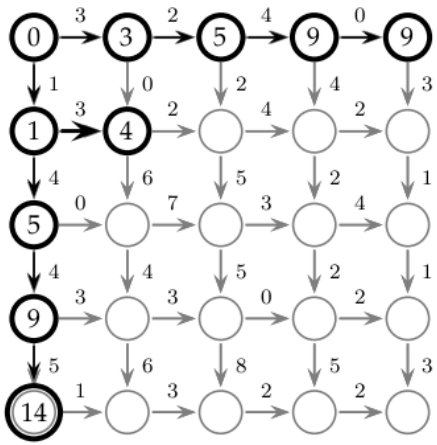
- What data structures do you need?
  - *Grid (array) to store the best subproblems answers.*

Dynamic Programming



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- What data structures do you need?
  - *Grid (array) to store the best subproblems answers.*
  - *The path, or could 'read' if off grid.*

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

Dynamic Programming & Sequence Alignment

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

- How do you (globally) align two sequences?

Dynamic Programming & Sequence Alignment

A C G T C C T C

A C G C C T A C

- How do you (globally) align two sequences?
- Needleman-Wunsch Algorithm: use dynamic programming.

Pairwise Sequence Alignment

- Look at smaller example: `AGG` and `AGAG`.

		A	G	A	G
	0				
A					
G					
G					

Pairwise Sequence Alignment

		A	G	A	G
	0				
A					
G					
G					

- Look at smaller example: `AGG` and `AGAG`.
- Same basic set up as a 'grid'.

Pairwise Sequence Alignment

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- Scoring:

Pairwise Sequence Alignment

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- Scoring:
  - +1 for a match

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- Same basic set up as a 'grid'.
- Add an extra row and column to allow for a gap at the beginning of sequence.
- Start the grid with `0`.
- Scoring:
  - +1 for a match
  - −1 for a mismatch
- Now allowed to go 'diagonally' (match the elements)

Pairwise Sequence Alignment

		A	G	A	G
	0				
A	-1				
G					
G					

- Look at smaller example of `AGG` vs `AGAG`.
- Same basic set up as a 'grid'.
- Add an extra row and column to allow for a gap at the beginning of sequence.
- Start the grid with `0`.
- Scoring:
  - +1 for a match.
  - −1 for a mismatch.
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Pairwise Sequence Alignment

		A	G	A	G
	0				
A	-1				
G	-2				
G					

- Look at smaller example of `AGG` vs `AGAG`.
- Same basic set up as a 'grid'.
- Add an extra row and column to allow for a gap at the beginning of sequence.
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Pairwise Sequence Alignment

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- Same basic set up as a 'grid'.
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Pairwise Sequence Alignment

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Pairwise Sequence Alignment

		A	G	A	G
	0	-1	-2	-3	-4
A	-1				
G	-2				
G	-3				

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- Same basic set up as a 'grid'.
- Add an extra row and column to allow for a gap at the beginning of sequence.
- Start the grid with `0`.
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  - +1 for a match.
  - −1 for a mismatch.
- Now allowed to go 'diagonally' (match the elements).

Pairwise Sequence Alignment

- For each, we take the best of:

		A	G	A	G
	0	-1	-2	-3	-4
A	-1	1			
G	-2				
G	-3				

Pairwise Sequence Alignment

		A	G	A	G
	0	-1	-2	-3	-4
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  - matching elements $(+1)$.

Pairwise Sequence Alignment

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G	-2				
G	-3				

- For each, we take the best of:
  - matching elements $(+1)$.
  - adding a gap to first sequence (-1).

Pairwise Sequence Alignment

		A	G	A	G
	0	-1	-2	-3	-4
A	-1	1			
G	-2				
G	-3				

- For each, we take the best of:
  - matching elements $(+1)$.
  - adding a gap to first sequence (-1).
  - adding a gap to second sequence (-1).

Pairwise Sequence Alignment

		A	G	A	G
	0	-1	-2	-3	-4
A	-1	1			
G	-2				
G	-3				

- For each, we take the best of:
  - matching elements $(+1)$.
  - adding a gap to first sequence (-1).
  - adding a gap to second sequence (-1).
- Pictorially:

Pairwise Sequence Alignment

		A	G	A	G
	0	-1	-2	-3	-4
A	-1	1			
G	-2				
G	-3				

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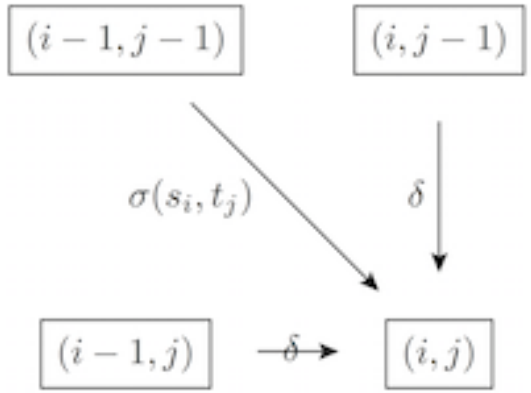

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3. What happens if we score +5 for match and -4 for mismatch (NCBI's `blastn`)?
4. What happens if σ scores pairs differently?

$$\sigma(s,t) = \begin{cases} 2 & \text{if } s = t \\ -1 & \text{if } s \neq t, s, t \in \{A, G\} \\ -1 & \text{if } s \neq t, s, t \in \{C, T\} \\ -2 & \text{otherwise} \end{cases}$$

(Weighing transversions and transitions differently.)

First Example

		A	G	A	G
	0	-1	-2	-3	-4
A	-1	1	0	-1	-2
G	-2	-1	2	1	0
G	-3	-1	1	1	2

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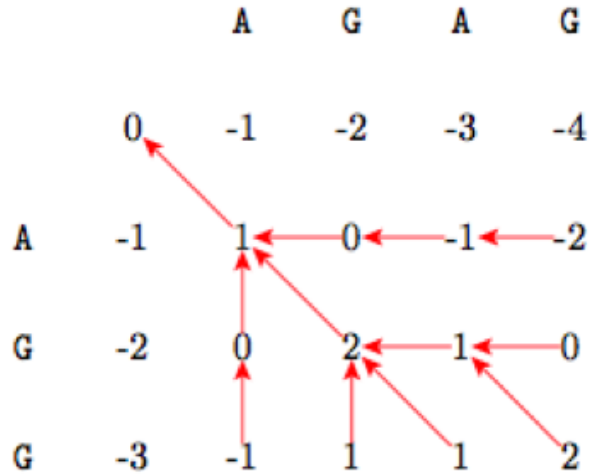

Recap: In Pairs

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	0				
A					
G					
G					

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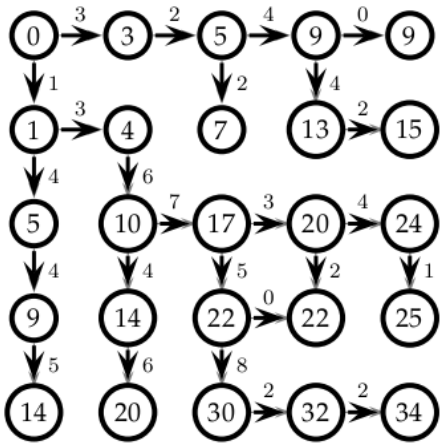
(Transversions with twice the weight as transitions.)

Variations on the Theme



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  - Locally aligning sections of the sequences (Smith-Waterman).

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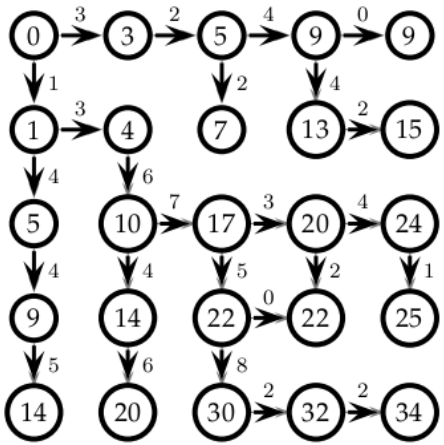

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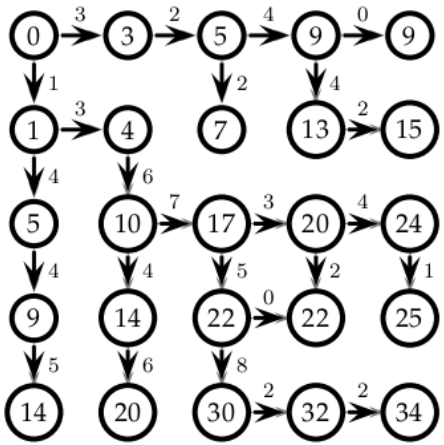

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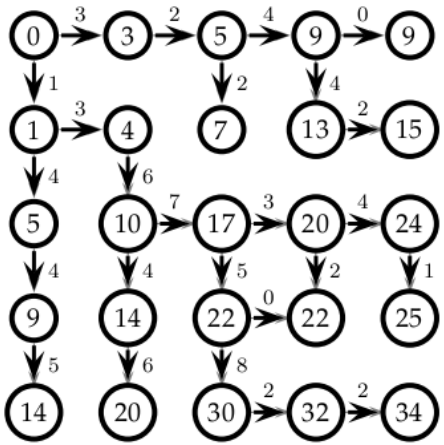

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Pairwise vs. Multiple Sequence Alignment

- While pairwise alignment can be done efficiently, multiple sequence alignment is hard.

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A  C  G  C  C  T  A  C
C  G  C  C  T  A  C  C
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Pairwise vs. Multiple Sequence Alignment

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- Often use a guess at which species are most closely related ('guide tree'):

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  - Repeat.
- Other approaches build the tree and alignment simultaneously.

Finding Trees in Graphs

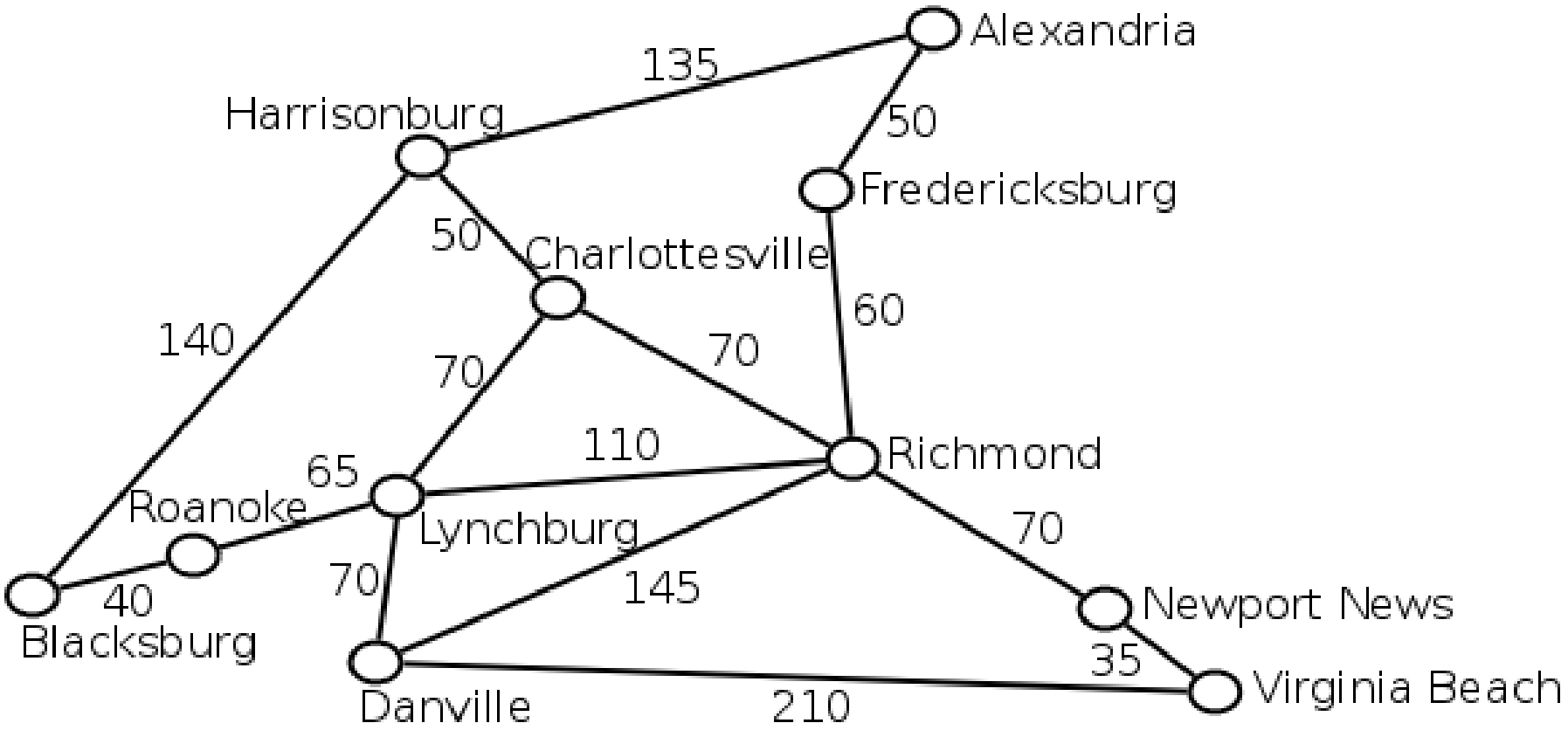
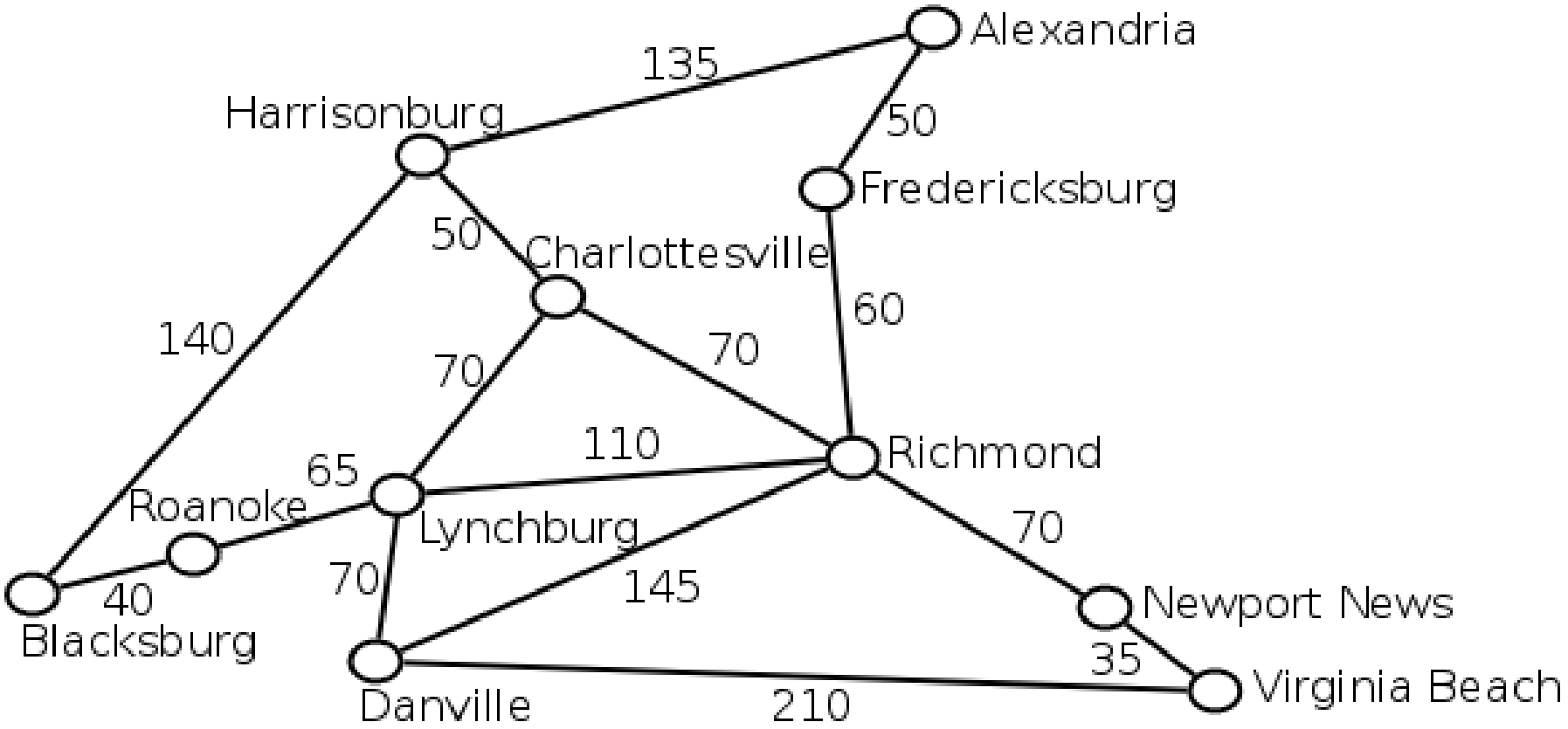


Image from Iam Finlayson (U. Mary Washington).

Finding Trees in Graphs



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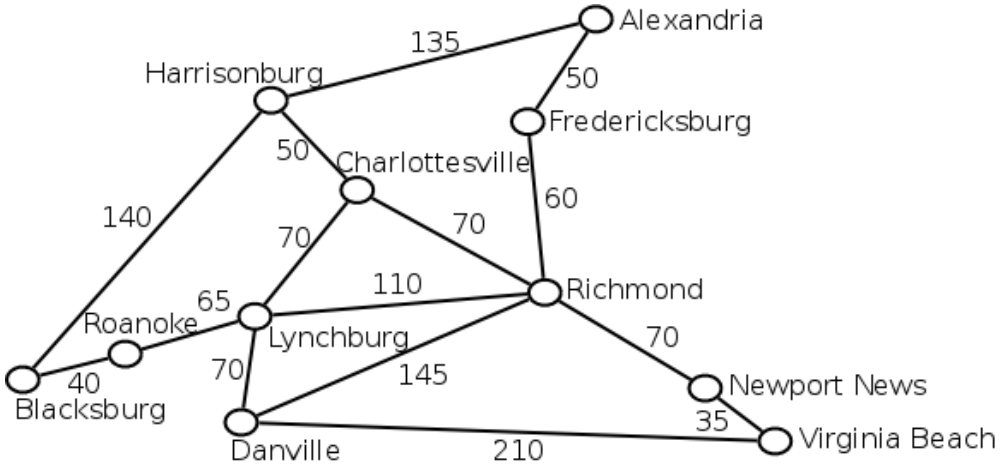
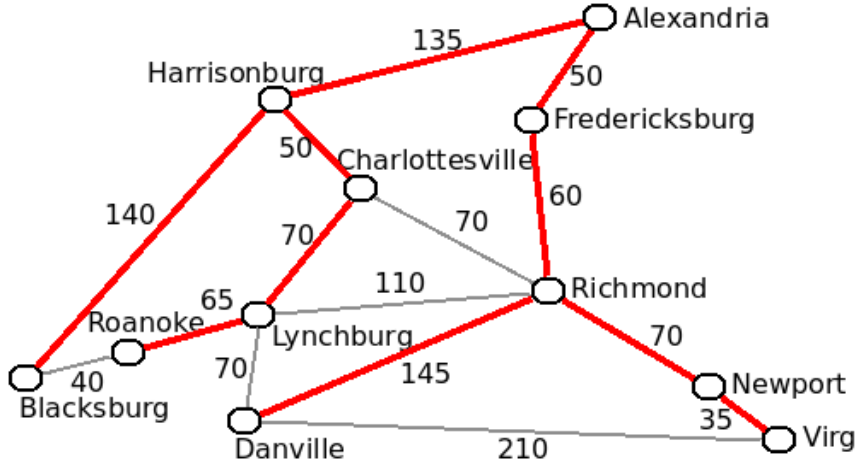
What is the shortest way to connect all the cities?

Finding Trees in Graphs





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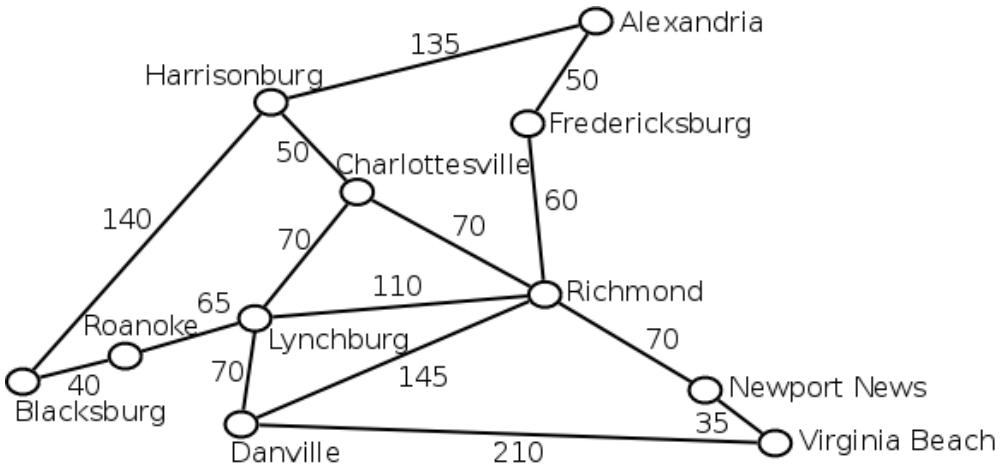

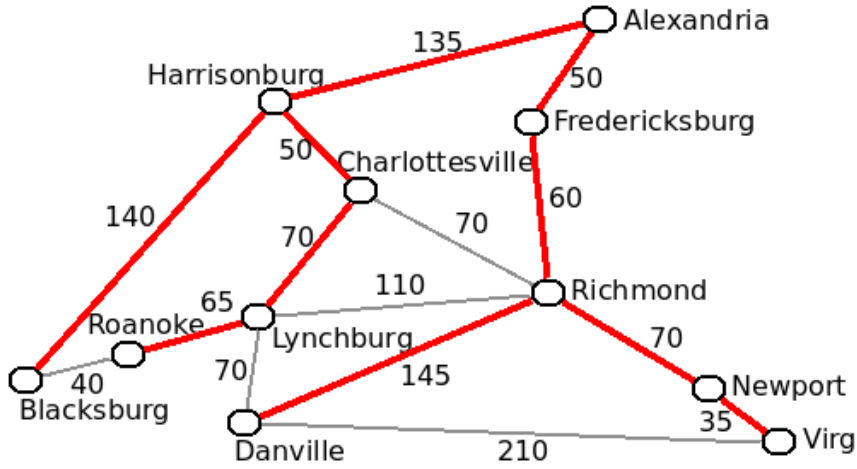

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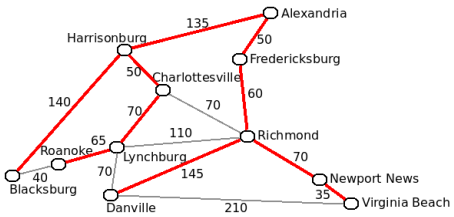
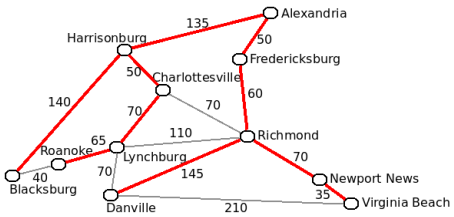


- Given a weighted graph, a minimum spanning tree (MST) is a tree on a subset of the edges that has minimum weight.

Finding Trees in Graphs



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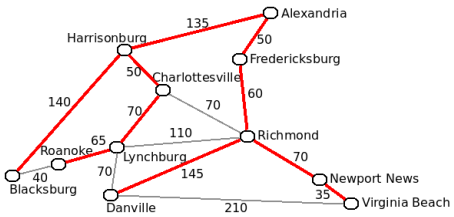
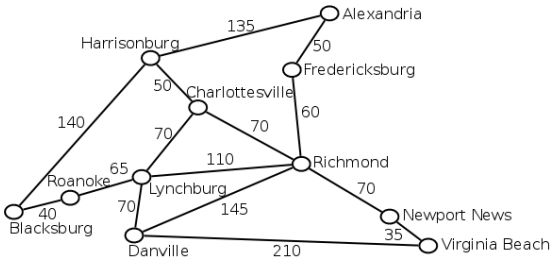
Finding Trees in Graphs



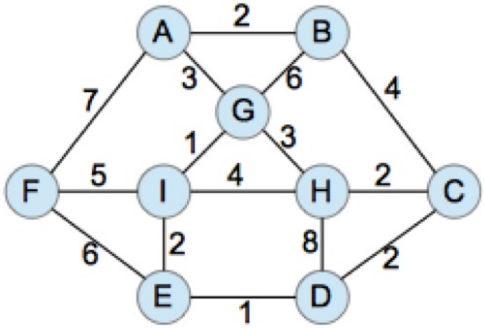
- Given a weighted graph, a minimum spanning tree (MST) is a tree on a subset of the edges that has minimum weight.
- Different than phylogenetic trees: MSTs can only use nodes given; does not add in hypothetical ancestors.
- MST's can be computed quickly and very common.

In Pairs

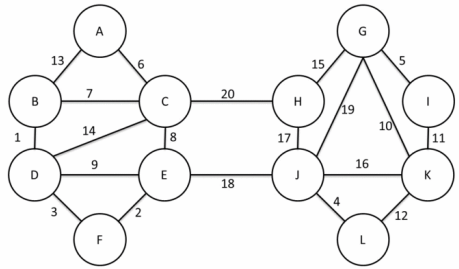
Find a minimum spanning tree (MST) for each:



(Ian Finlayson)

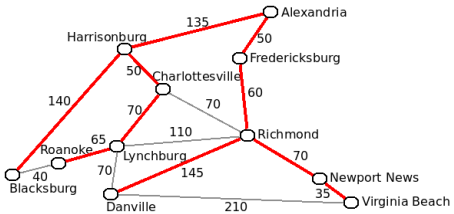


Chegg



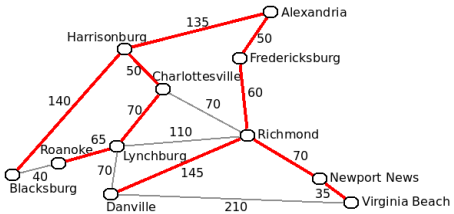
Aliesaraj (wiki)

Kruskal's & Prim's Algorithms



- Kruskal: Sort edges, add in lowest weight remaining edge that does not make a cycle.

Kruskal's & Prim's Algorithms



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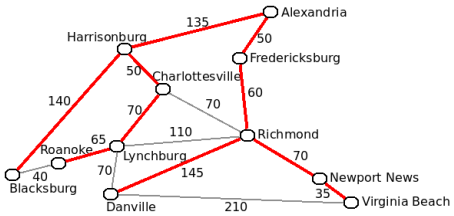
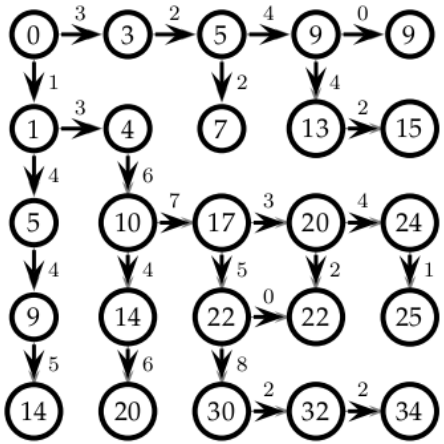
Kruskal's & Prim's Algorithms



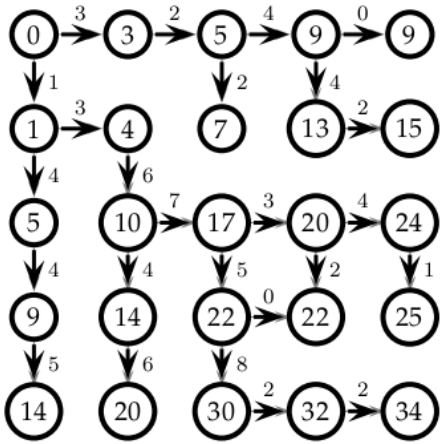
- Kruskal: Sort edges, add in lowest weight remaining edge that does not make a cycle.
- Prim: Build tree by adding next connected edge that does not make a cycle.
- Both are fast: if n is the number of vertices:
  - Kruskal: $O(n^2 \log n)$.
  - Prim: $O(n^2)$ with adjacency matrix.
  - Both can be made faster with fancier ways to store possible edges.

Recap



- Dynamic Programming: very useful tool when problems can be broken down into well structured parts.

Recap



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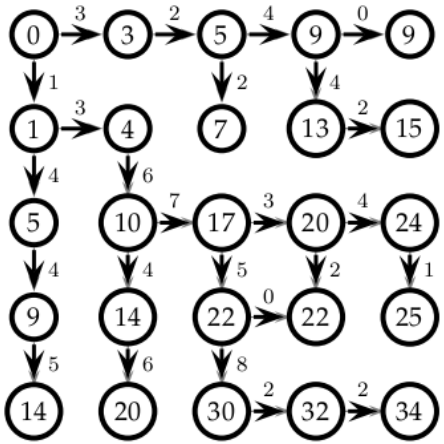

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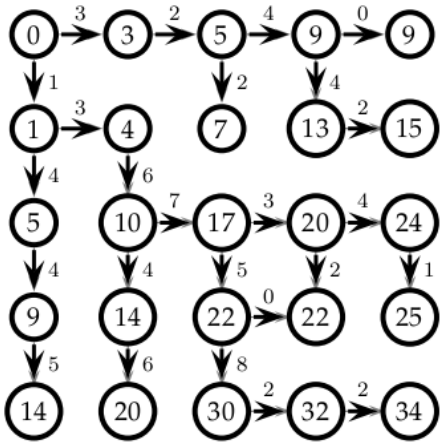
- Email lab reports to `kstjohn@amnh.org`.

Recap



- Dynamic Programming: very useful tool when problems can be broken down into well structured parts.
- Minimum Spanning Trees: fast way to extract a tree from a graph (different from phylo trees since no new ancestor nodes).
- Email lab reports to `kstjohn@amnh.org`.
- Challenges available at `rosalind.info`.