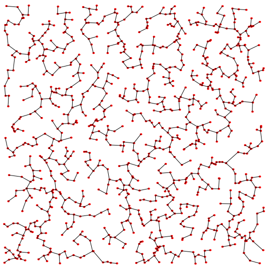
Algorithms and Analysis

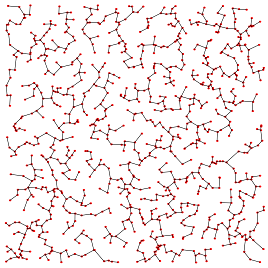
Lesson 21: *Know Your Graph Algorithms*



Weighted graph algorithms, Minimum spanning tree, Prim, Kruskal, shortest path, Dijkstra

Outline

1. **Minimum Spanning Tree**
2. Prim's Algorithm
3. Kruskal's Algorithm
4. Union Find
5. Shortest Path

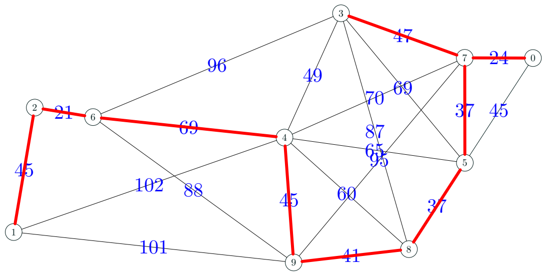


Graph Algorithms

- We consider a graph algorithm to be **efficient** if it can solve a graph problem in $O(n^a)$ time for some fixed a
- That is, an efficient algorithm runs in polynomial time
- A problem is **hard** if there is no known efficient algorithm
- This does **not** mean the best we can do is to look through all possible solutions—see later lectures
- In this lecture we are going to look at some efficient graph algorithms for weighted graphs

Minimum spanning tree

- A minimal spanning tree is the shortest tree which spans the entire graph

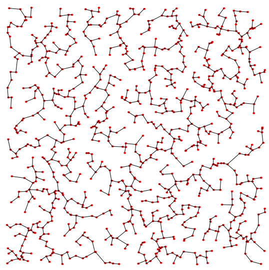


Greedy Strategy

- We consider two algorithms for solving the problem
  - Prim's algorithm (discovered 1957)
  - Kruskal's algorithm (discovered 1956)
- Both algorithms use a **greedy strategy**
- Generally greedy strategies are not guaranteed to give globally optimal solutions
- There exists a class of problems with a **matroid** structure where greedy algorithms lead to globally optimal solutions
- Minimum spanning trees, Huffman codes and shortest path problems are matroids

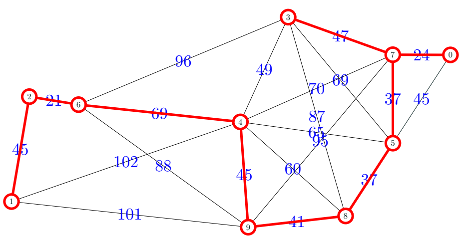
Outline

1. Minimum Spanning Tree
2. **Prim's Algorithm**
3. Kruskal's Algorithm
4. Union Find
5. Shortest Path



Prim's Algorithm

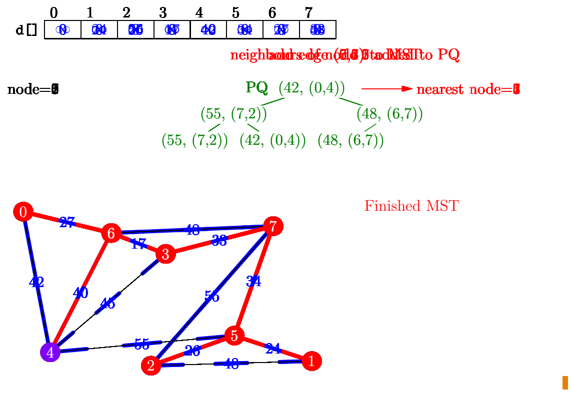
- Prim's algorithm grows a subtree greedily
- Start at an arbitrary node
- Add the shortest edge to a node not in the tree



Pseudo Code

```
PRIM(G = (V, E, w)) {
  for i←1 to |V|
    d_i ←∞            \\ Minimum 'distance' to subtree
  endfor
  E_T ←∅              \\ Set of edges in subtree
  PQ.initialise()     \\ initialise an empty priority queue
  node ← v_1          \\ where v_1 ∈ V  is arbitrary
  for i←1 to |V| − 1
    d_node ←0
    for k ∈ {v ∈ V|(node, v) ∈ E} \\ k  is a neighbours of node
      if ( w_node,k < d_k  )
        d_k ←w_node,k
        PQ.add( (d_k, (node,k)) )
      endif
    endfor
    do
      (a_node, next_node) ←PQ.getMin()
    until (d_next_node > 0)
    E_T ←E_T ∪ {(a_node, next_node)}
    node ←next_node
  endfor
  return E_T
}
```

Prim's Algorithm in Detail



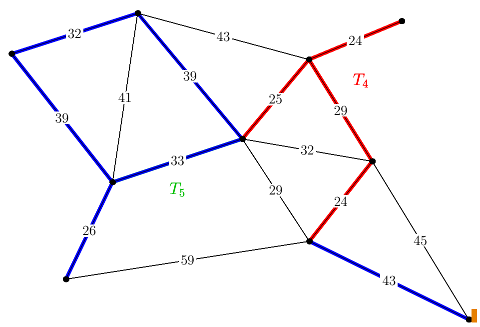
Why Does This Work?

- Clearly Prim's algorithm produces a spanning tree
  - It is a tree because we always choose an edge to a node not in the tree
  - It is a spanning tree because it has $|\mathcal{V}| - 1$ edges
- Why is this a minimum spanning tree?
- Once again we look for a proof by induction

Proof by induction

- We want to show that each subtree, T_i, for $i = 1, 2, \cdots, n$ is part of (a subgraph) of some minimum spanning tree
- In the base case, T_1 consists of a tree with no edges, but this has to be part of the minimum spanning tree
- To prove the inductive case we assume that T_i is part of the minimum spanning tree
- We want to prove that T_{i+1} formed by adding the shortest edge is also part of the minimum spanning tree
- We perform the proof by contradiction—we assume that this added edge isn't part of the minimum spanning tree

Contrariwise



Loop Counting

```
PRIM(G = (V, E, w)) {
  for i←0 to |V|
     d_i ←∞
  endfor
  E_T ←∅
  PQ.initialise()
  node ← v_1
  for i←1 to |V| − 1                      // loop 1  O(|V|)
     d_node ←0
     for k ∈ {v ∈ V|(node, v) ∈ E}  // inner loop O(|E|/|V|)
        if ( w_node,k < d_k )
           d_k ←w_node,k
           PQ.add( (d_k, (node,k)) )     // O(log(|E|))
        endif
     endfor
     do
        (a_node, next_node) ←PQ.getMin()
     until (d_next_node > 0)
     E_T ←E_T ∪ {(node, next_node)}
     node ←next_node
  endfor
  return E_T
}
```

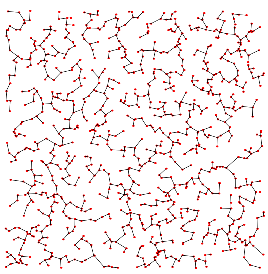

Run Time

- The worst time is

$$O(|\mathcal{V}|) \times O\left(\frac{|\mathcal{E}|}{|\mathcal{V}|}\right) \times O\big(\log(|\mathcal{E}|)\big) = O\left(|\mathcal{E}| \log(|\mathcal{E}|)\right)$$

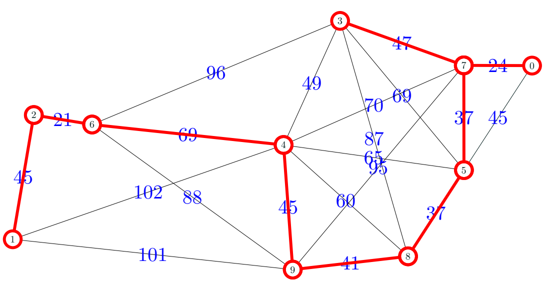
- Note that $|\mathcal{E}| < |\mathcal{V}|^2$
- Thus, $\log(|\mathcal{E}|) < 2\log(|\mathcal{V}|) = O\left(\log(|\mathcal{V}|)\right)$
- Thus the worst case time complexity is $|\mathcal{E}| \log(|\mathcal{V}|)$

Outline



Kruskal's Algorithm

- Kruskal's algorithm works by choosing the shortest edges which don't form a loop



Pseudo Code

```
KRUSKAL(G = (𝒱, ℰ, w))
{
  PQ.initialise()
  for edge ∈ |ℰ|
    PQ.add( (w_edge, edge) )
  endfor

  ℰ_T ← ∅
  noEdgesAccepted ←0

  while (noEdgesAccepted < |𝒱| − 1)
    edge ←PQ.getMin()
    if ℰ_T ∪ {edge} is acyclic
      ℰ_T ←ℰ_T ∪ {edge}
      noEdgesAccepted ←noEdgesAccepted +1
    endif
  endwhile

  return ℰ_T
}
```


Analysis

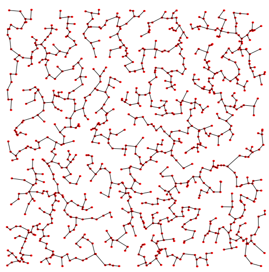
- Kruskal's algorithm looks much simpler than Prim's
- The sorting takes most of the time, thus Prim's algorithms is $O\big(|\mathcal{E}|\log(|\mathcal{E}|)\big) = O\big(|\mathcal{E}|\log(|\mathcal{V}|)\big)$
- We can sort the edges however we want—we could use quick sort rather than heap sort using a priority queue
- But we haven't specified how we determine if the added edge would produce a cycle

Cycling

- For a path to be a cycle the edge has to join two nodes representing the same subtree
- To compute this we need to quickly **find** which subtree a node has been assigned to
- Initially all nodes are assigned to a separate subtree
- When two subtrees are combined by an edge we have to perform the **union** of the two subtrees
- This is a tricky but standard operation known as **union-find**

Outline

1. Minimum Spanning Tree
2. Prim's Algorithm
3. Kruskal's Algorithm
4. **Union Find**
5. Shortest Path



Union-Find

- In the union-find algorithm we have a set of objects $x \in \mathcal{S}$ which are to be grouped into subsets $\mathcal{S}_1$, $\mathcal{S}_2$, . . .
- Initially each object is in its individual subset (no relationships)
- We want to make the **union** of two subsets (add relationship between elements)
- We also want to **find** the subset given an element
- This is a common problem for which we will write a class `DisjointSets` to perform fast `union`s and `find`s

DisjointSets

- We want to create a class

```
class DisjointSets
{
    DisjointSets(int numElements) {/* Constructor */}
    int find(int x) {/* Find root */}
    void union(int root1, int root2) {/* Union */}

    private:
      int[] s;
}
```

- Where `find(x)` returns a unique identifier for the subset which element `x` belongs to
- The array `s` contains labelling information to implement `find(x)`

The Union-Find Dilemma

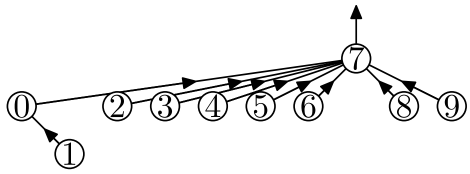
- A natural algorithm to perform finds is to maintain an array returning a subset label for each element—this makes `find` fast
- However, every time we combine two subset we have to change all the labels in this array (taking $O(n)$ operations)
- If we are unlucky the cost of performing n unions is $\Theta(n^2)$
- If we ensure that we relabel the smaller subset then the time complexity is $\Theta(n\log(n))$
- Fast *finds* seems to give slow(ish) *unions*
- What about the other way around?

Fast Union

- To achieve fast unions we can represent our disjoint sets as a forest (many disjoint trees)
- Every time we perform a union we make one of the trees point to the head of the other tree
- The cost of `find` depends on the depth of the tree
- To make unions efficient we make the shallow tree a subtree of the deeper tree

Putting it Together

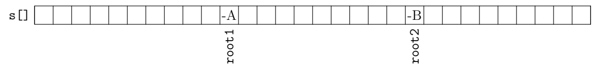
`find(6)=7`



0	1	2	3	4	5	6	7	8	9
7	0	7	7	7	7	7	-3	7	7

Smart Union

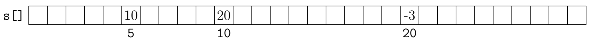
```
DisjointSets::DisjointSets(int numElements)
{
    s = new int[numElements];
    for(int i=0; i<s.length; i++)
        s[i] = -1;                    // roots are negative number
}

void DisjointSets::union(int root1, int root2)
{
    if (s[root2]<s[root1]) {          // root2 is deeper
        s[root1] = root2;             // make root2 the root
    } else {
        if (s[root1]==s[root2])
            s[root1]--;               // update height if same
        s[root2] = root1;             // make root1 new root
    }
}
```



Path Compression

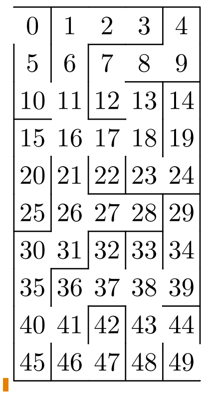
- To speed up `find` we relabel all nodes we visit during `find` by the root label

```
public int DisjointSets::find(int index)
{
    if (s[index]<0)
        return index;
    else
        return s[index] = find(s[index]);
}
```



Mazes

- Union-Find is a data structure which can occur in very different applications
- One application is building a maze
- Start from a complete lattice
- Remove a randomly chosen edge if it connects two unconnected regions
- Stop when the start and end cell are connected
- Or better after all cells are connected



Time Complexity of Union-Find

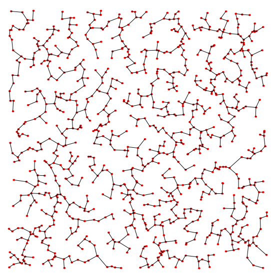
- If we perform M finds and N unions then the time complexity is $O(M \log_2^*(N))$
- Where $\log_2^*(N)$ is the number of times you need to apply the logarithm function before you get a number less than 1
- In practice $\log_2^*(N) \leq 5$ for all conceivable N

$$\log_2(\log_2(\log_2(\log_2(\log_2(1000000))))) = 0.8\ldots$$

- The proof of this time complexity is rather involved

Outline

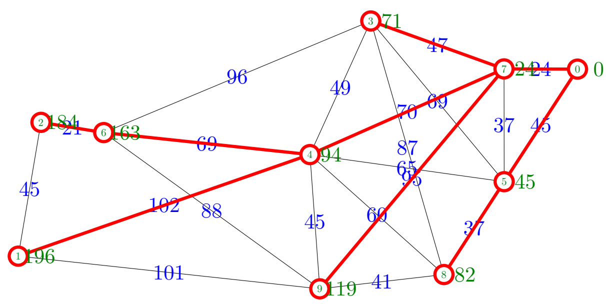
1. Minimum Spanning Tree
2. Prim's Algorithm
3. Kruskal's Algorithm
4. Union Find
5. **Shortest Path**



Shortest path

- We can efficiently compute the shortest path from one vertex to any other vertex
- This defines a spanning tree, but where the optimisation criteria is that we choose the vertex that are closest to the *source*
- To find this spanning tree we use Dijkstra's algorithm where we successively add the nearest node to the source which is connected to the subtree built so far
- This is very close to Prim's algorithm and has the same complexity

Dijkstra's Algorithm



Pseudo Code

```
DIJKSTRA(G = (V, E, w), source) {
  for i←0 to |V|
    d_i ←∞          \\ Minimum 'distance' to source
  endfor
  E_T ←∅            \\ Set of edges in subtree
  PQ.initialise()   \\ initialise an empty priority queue
  node ←source
  d_node ←0
  for i←1 to |V| − 1
    for k ∈ {v ∈ V|(node, v) ∈ E}
      if ( w_node,k + d_node < d_k )
        d_k ←w_node,k + d_node
        PQ.add( (d_k, (node, k)) )
      endif
    endfor
    do
      (a_node, next_node) ←PQ.getMin()
    while next_node not in subtree
    E_T ←E_T ∪ {(a_node, next_node)}
    node ←next_node
  endfor
  return E_T
}
```


Compare to Prim's Algorithm

```
PRIM(G = (V, E, w)) {
  for i←1 to |V|
    d_i ←∞          \\ Minimum 'distance' to subtree
  endfor
  E_T ←∅            \\ Set of edges in subtree
  PQ.initialise()   \\ initialise an empty priority queue
  node ← v_1        \\ where v_1 ∈ V is arbitrary
  for i←1 to |V| − 1
    d_node ←0
    for k ∈ {v ∈ V|(node, v) ∈ E}
      if ( w_node,k < d_k )
        d_k ←w_node,k
        PQ.add( (d_k, (node,k)) )
      endif
    endfor
    do
      (a_node, next_node) ←PQ.getMin()
    until (d_next_node > 0)
    E_T ←E_T ∪ {(a_node, next_node)}
    node ←next_node
  endfor
  return E_T
}
```


Dijkstra Details

- Dijkstra is very similar to Prim's (it differs in the distances that are used)
- It has the same time complexity
- It can be viewed as using a greedy strategy
- It can also be viewed as using the dynamic programming strategy (see lecture 22)

Lessons

- There are many efficient (i.e. polynomial $O(n^a)$) graph algorithms
- Some of the most efficient ones are based on the Greedy strategy
- These are easily implemented using priority queues
- Minimum spanning trees are useful because they are easy to compute
- Dijkstra's algorithm is one of the classics