Graphs

1. Basic definitions

Graph $G = (V, E)$ where V is a set of **vertices** and E is a set of **edges**. Each edge $e \in E$ is a 2-tuple of the form (v, w) where $v, w \in V$, and e is called an **incident** on v and w.

- An edge may be directed or undirected. \bullet
- An edge may also have a **weight**.

Directed, unweighted

Directed, weighted

- A **path** is a sequence of vertices connected by edges, and represented as a sequence in 2 ways:
	- $(v_0, e_1, v_1, e_2, v_2, ..., v_{n-1}, e_n, v_n)$ -- alternating vertices and edges

 $(v_0, v_1, v_2, ..., v_{n-1}, v_n)$ -- vertices only

A graph is **connected** if, for any vertices v and w, there is a path from v to w.

An unconnected graph

2. Representing Graphs

- Adjacency matrix
	- n by n matrix, where n is number of vertices
	- $\Delta(m,n) = 1$ iff (m,n) is an edge, or 0 otherwise
	- \circ For weighted graph: A(m,n) = w (weight of edge), or positive infinity otherwise

- Adjacency list
	- Each vertex has a linked list of edges
	- Edge stores destination and label
	- Better when adjacency matrix is **sparse**

3. Graph Traversal

Walk through a graph systematically in a predefined order -- Depth-first, or Breadth-first.

3.1 Depth-First Traversal

Follow a path until it ends, or until a cycle. Use a **stack**.

Start vertex $= 0$ Assume vertex with smaller label is visited first.

```
* Depth-first: 0, 1, 3, 4, 2
```
• Algorithm:

Let $G = (V, E)$ is a graph which is represented by an adjacency matrix Adj. Assume that nodes in a graph record visited/unvisited information.

```
procedure DEPTH-FIRST (G)
1. Initialize all vertices as "unvisited".
2. Let S be a stack.
3. Push the root on S.
```

```
4. While S not empty, do
5. begin
6. Let n <- Pop S.
7 If n is marked as "unvisited", then
8. begin
9. Mark n as "visited", and output n to the terminal.
10. For each vertex v in Adj[n], do
11. If v is marked as "unvisited", then // this test is actually redundant
12. push v on S.
13. end
```

```
14. end
```


3.2 Breadth-First Traversal

Visit nodes layer-by-layer. Use a **queue**.

S

G

Start vertex = 0 Assume vertex with smaller label is visited first.

- Breadth-first: 0.1.2.3.4

Algorithm :

```
procedure BREADTH-FIRST (G)
1. Initialize all vertices as "unvisited".
2. Let Q be a queue.
3. Enqueue the root on Q.
4. While Q not empty, do
5. begin
6. n <- Dequeue Q.
7. If n is marked as "unvisited", then
8. begin
9. Mark n as "visited", and output n to the terminal.
10. For each vertex v in Adj[n], do
11. If v is marked "unvisited", then
12. enqueue v on Q.
```
13. **end** 14. **end**

4. Graph Search

- Two search methods corresponding to the two traversal schemes above: Depth-First Search (DFS) and Breadth-First Search (BFS).
- Terminate search/traversal as soon as the item is found.

5. Minimum Spanning Trees (MST)

A minimum spanning tree T of an **undirected** graph G is a subgraph of G that **connects all the vertices** in G at the **lowest total cost**.

Tree for G

 $(total cost = 6)$

- MST is used as one of the most important tools to analyze **computer networks** (e.g. cabling, network load capacity, optimal flow).
- Two algorithms: **Prim's** algorithm and **Kruskal's** algorithm.
- They are both *greedy algorithms*.

6.1 Prim's Algorithm

- Maintains ONE TREE throughout the algorithm, and make it grow by adding edge by edge.
- The idea is to select the next edge
- which is adjacent from any vertex/node in the tree built so far; and
- which has the lowest weight among alternatives (i.e., all edges connected from any vertex/node in the tree built so far).

Algorithm: \bullet

Let $G = (V, E)$ which is represented by an adjacency list Adj . Some support data structures:

- **d** is an array of size |V|. Each d[i] contains the shortest distance for vertex i
- **Q** is a **priority queue** of UNKNOWN vertices.
- **p** is an array of size |V|. Each P[i] contains the **parent** of vertex i.
- **s** is the source vertex.

```
PRIM(G, s)
1. Initialize d[s] with 0, P[s] with 0, and
   all other d[i] (i!=s) with a positive infinity and
            p[i] (i!=s) with \theta.
2. Q <- V // initialize Q with all vertices as UNKNOWN
3. while Q not empty do
4. begin
5. u <- ExtractMin(Q) // Q is modified
6. Mark u as KNOWN // Dequeing u is the same as marking it as KNOWN
7. for each vertex v in Adj[u] do
8. begin
9. if v is UNKNOWN and d[v] > weight(u, v), then do
10. begin
11. d[v] = weight(u, v) // update with shorter weight
12. p[v] = u // update v's parent as v
13. end
14. end
15. end
```
• Example (NOTE: v0 is the source vertex, and d[i] for each vertex i is also indicated in its circle):

 (0)

$$
Q = (v_0, v_1, v_2, v_3, v_4)
$$

$$
Q = \{v_4,\,v_1,\,v_2,\,v_3\}
$$

(3)
$$
v_0
$$
 v_1
\n $\frac{1}{6}$ $\frac{1}{1}$ $\frac{3}{1}$ v_2
\n v_4 v_3

$$
\begin{array}{|c|cccc|} \hline v & \text{known} & d_v & p_v \\ \hline v_0 & T & 0 & 0 \\ v_1 & F & 1 & v_3 \\ v_2 & F & 3 & v_3 \\ v_3 & T & 1 & v_4 \\ v_4 & T & 1 & v_0 \\ \hline C = (v_1, v_1) & 0 & 0 \\ \hline \end{array}
$$

$$
\mathbf{Q} = (\mathbf{v}_1, \mathbf{v}_2)
$$

 (4) $\mathbf{v_0}$ \mathbf{v}_1 2 0) T 5 \mathbf{v}_2 3) $\,1$ $\mathbf{1}$ б 3 O 1 $\mathbf{1}$ \mathbf{v}_4 \mathbf{v}_3

$$
\begin{array}{c}\n\swarrow = \vee_1, \vee_2 \vee \\
\hline\n\frac{v \text{ known } d_v \text{ p}_v}{v_0 \text{ T}} \\
\frac{v_0 \text{ T}}{v_1 \text{ T}} \text{ 1 } v_3 \\
\frac{v_2 \text{ F}}{v_3 \text{ T}} \text{ 1 } v_4 \\
\frac{v_4 \text{ T}}{v_4 \text{ T}} \text{ 1 } v_0\n\end{array}
$$

$$
Q = \{v_2\}
$$

 (5) $\mathbf{v_0}$ \mathbf{v}_1 \overline{a} $d_{\rm v}$ known $\frac{p_{\nu}}{0}$ 0 5 v ä $\frac{1}{0}$
3
1 $\overline{\mathtt{v}_0}$ 3) \mathbf{v}_2 $\,1\,$ $\begin{bmatrix} v_1 \\ v_2 \end{bmatrix}$ v_3 6 $\mathbf{1}$ \mathbf{v}_3 3 $\bar{v_3}$ Œ 1 v_4 $\mathbf{1}$ $\mathbf{1}$ \mathbf{v}_4 v_0 \mathbf{v}_4 \mathbf{v}_3

 $Q = \{\}$

- The main idea is to
	- start with a set (called **forest**) of singleton trees, and
	- **merge two trees at a time,** unless it creates a cycle in the merged tree, until the forest becomes one tree.
- The algorithm makes use of notions such as forest and **union-find** algorithm. But even without knowing them, you can intuitively understand Kruskal's algorithm quite easily.
- Algorithm:

Let $G = (V, E)$ which is represented by an adjacency list **Adj**. Some support data structures:

- **F** is the forest -- a set of all (partial) trees.
- **MST** is the minimum spanning tree, represented by a **set of edges**.
- **Q** is a **priority queue** of edges.

```
KRUSKAL(G)
1. Let F be a set of singleton set of all vertices in G.
2. MST <- {}
3. Q <- E
4. while Q not empty do
5. (u, v) <- ExtractMin(Q) \qquad // Q is modified
6. if FIND-SET(u) != FIND-SET(v) then // FIND-SET(i) returns the set in F
                                       // which vertex i belongs to.
                                       // This effectively does cycle check.
                                       // If ACCEPTED,
7. begin
8. merge(FIND-SET(u),FIND-SET(v)) in F
9. MST <- MST Union {(u, v)}
10. end
11. return MST.
```
NOTE: In the figure below, a number in a vertex indicates the vertex number (NOT any kind of value).

$$
F = \{ (v_0), (v_1), (v_2), (v_3), (v_4) \}
$$

\nMST = {}
\n
$$
Q = \{ (v_0, v_4), (v_1, v_3), (v_3, v_4), (v_0, v_1), (v_2, v_3), (v_1, v_2), (v_1, v_4) \}
$$

 (2)

$$
Q = \{ (v_3, v_4), (v_2, v_3), (v_1, v_2), (v_1, v_4) \}
$$

 (6)

The algorithm continues until Q becomes empty, but since the forest has become one tree, all remaining edges in Q will be rejected and no no change will happen to MST.