COMP 322: Parallel and Concurrent Programming

Lecture 22: Parallel Graph Algorithms

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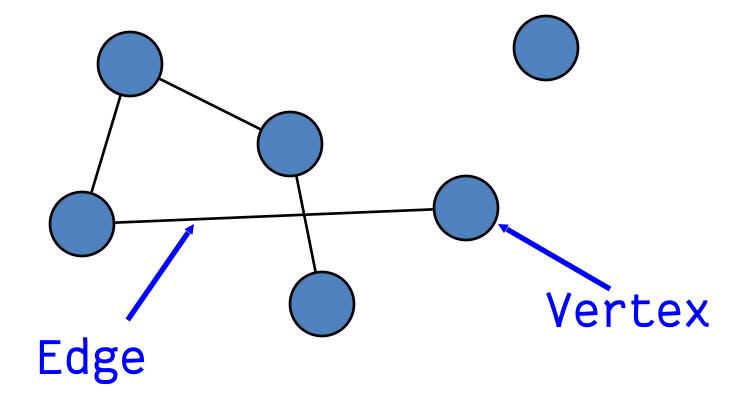
http://comp322.rice.edu

Some slides in this presentation are adopted from Aydin Buluç: "Parallel Graph Algorithms", LBNL, CS267, Spring 2016, Hall Perkins, "Data Structures", CSE 374, University of Washington



Graphs

Graph G = (V,E)
- a set of vertices and a set of
 edges between vertices



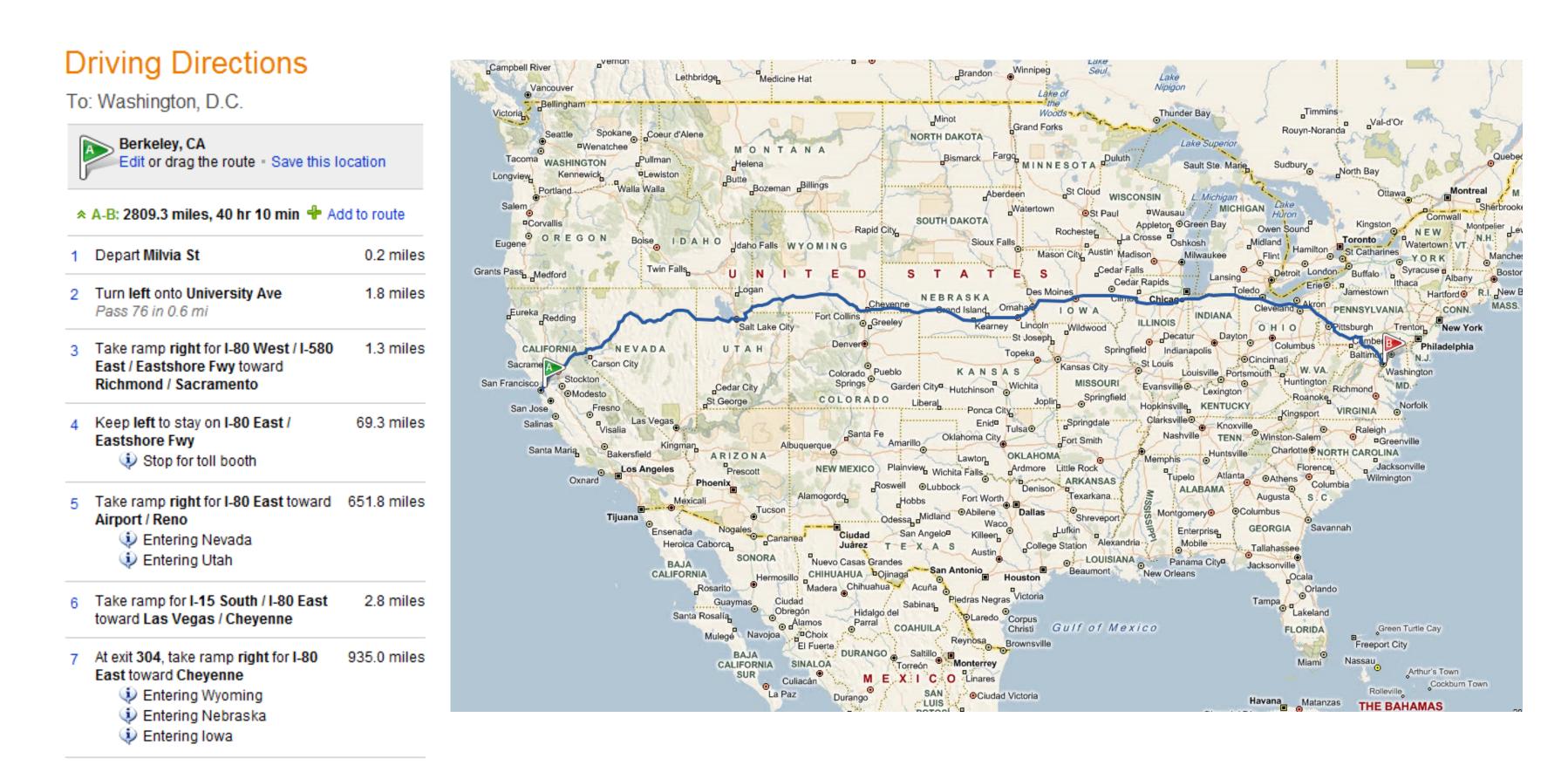
n=|V| (number of vertices) m=|E| (number of edges)

D=diameter (max #hops between any pair of vertices)

- Edges can be directed or undirected, weighted or not.
- They can even have attributes (i.e. semantic graphs)
- Sequences of edges $< u_1, u_2 >$, $< u_2, u_3 >$, ... , $< u_{n-1}, u_n >$ is a **path** from u_1 to u_n . Its **length** is the sum of its weights.



Routing in transportation networks



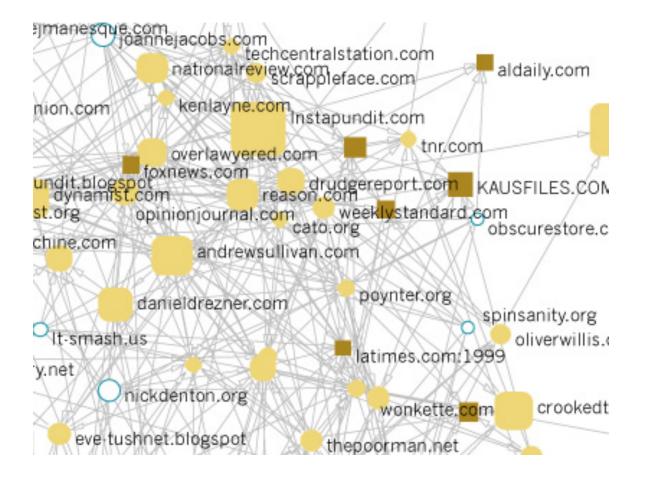
Road networks, Point-to-point shortest paths: 15 seconds (naïve) -> 10 microseconds

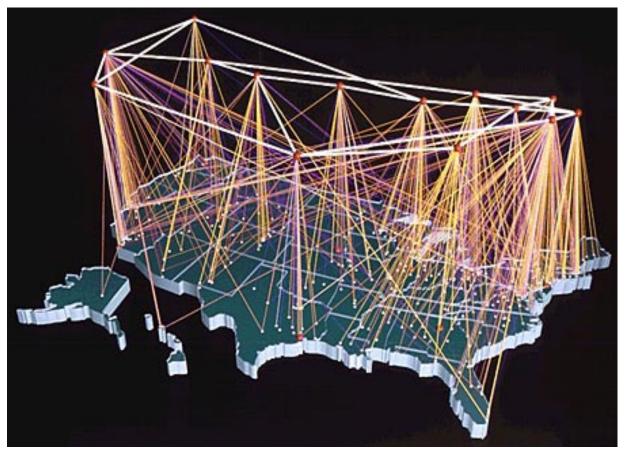
H. Bast et al., "Fast Routing in Road Networks with Transit Nodes", Science 27, 2007.

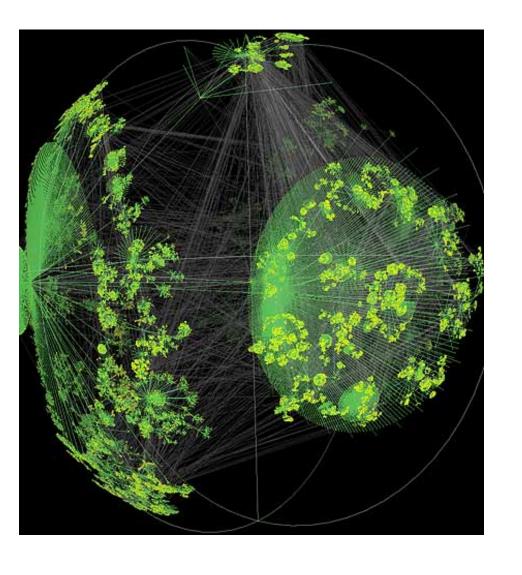


Internet and the WWW

- The world-wide web can be represented as a directed graph
 - Web search and crawl: traversal
 - Link analysis, ranking: Page rank and HITS
 - Document classification and clustering
- Internet topologies (router networks) are naturally modeled as graphs







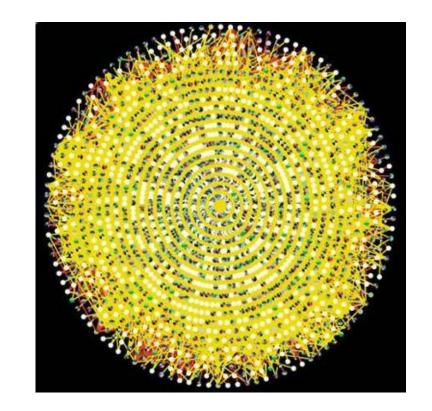


Large-scale data analysis

- Graph abstractions are very useful to analyze complex data sets.
- Sources of data: simulations, experimental devices, the Internet, sensor networks
- Challenges: data size, heterogeneity, uncertainty, data quality

Astrophysics: massive datasets, temporal variations

Bioinformatics: data quality, heterogeneity



Social Informatics: new analytics challenges, data uncertainty

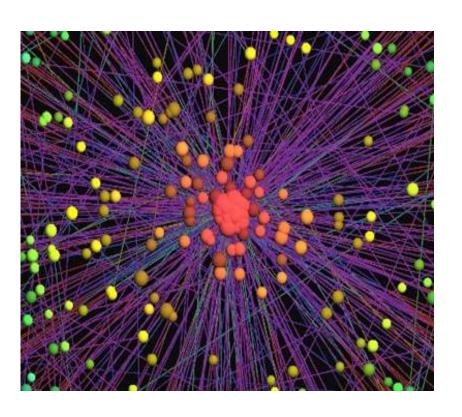
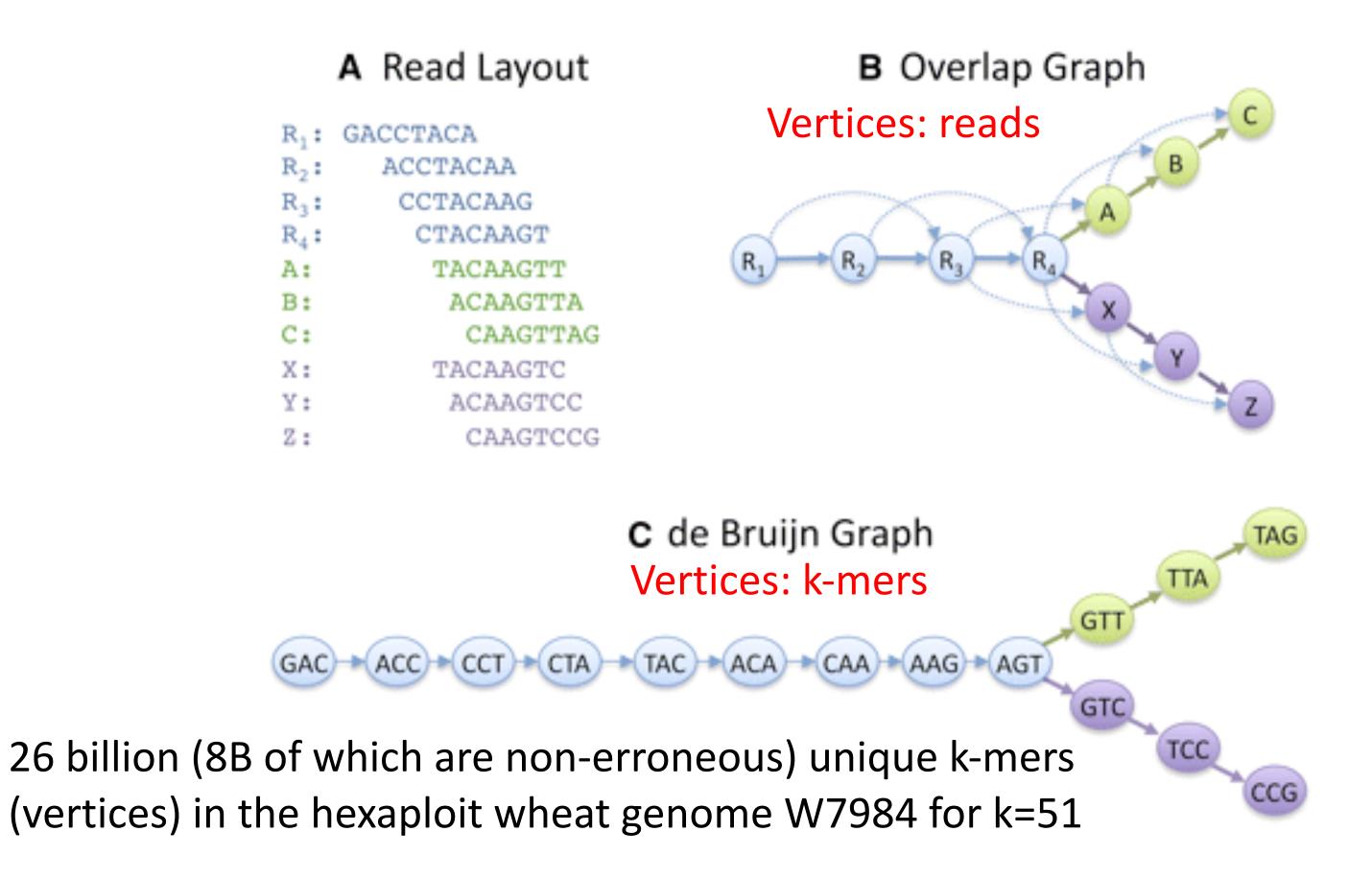


Image sources: (1) http://physics.nmt.edu/images/astro/hst_starfield.jpg (2,3) www.visualComplexity.com



Large Graphs in Biology

Whole genome assembly

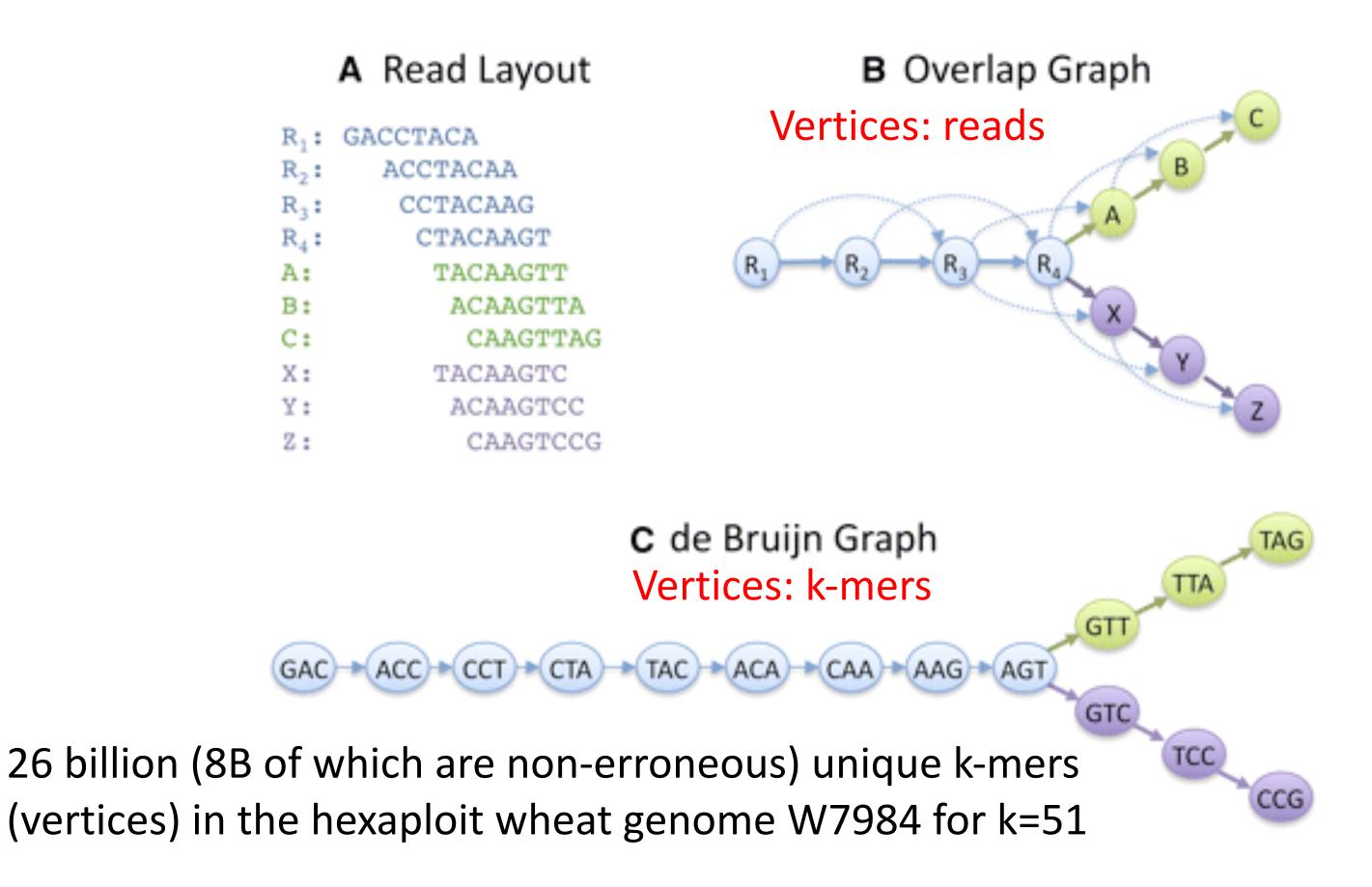


Schatz et al. (2010) Perspective: Assembly of Large Genomes w/2nd-Gen Seq. Genome Res. (figure reference)



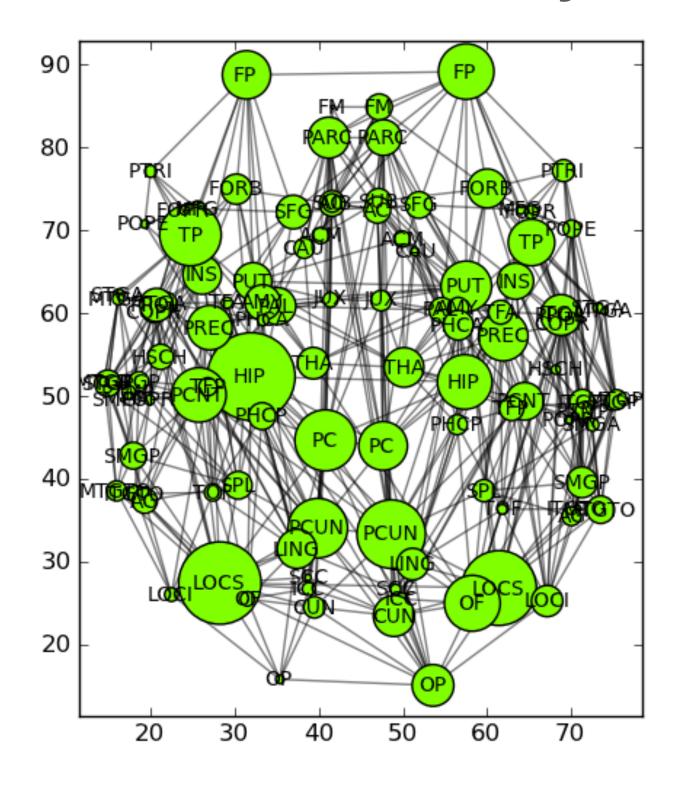
Large Graphs in Biology

Whole genome assembly



Schatz et al. (2010) Perspective: Assembly of Large Genomes w/2nd-Gen Seq. Genome Res. (figure reference)

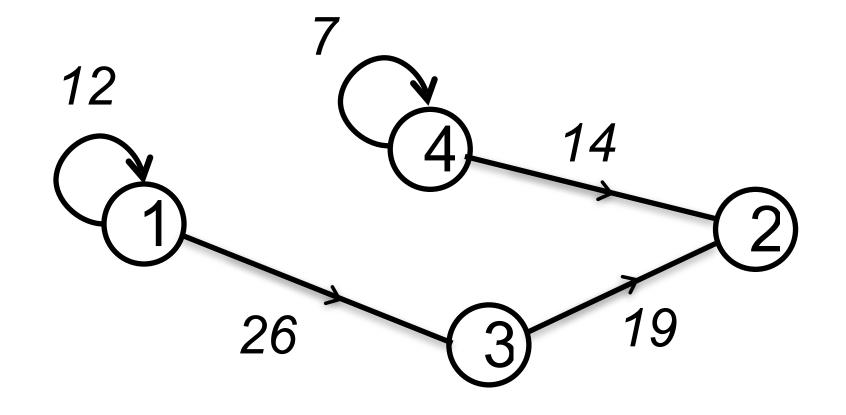
Graph Theoretical analysis of Brain Connectivity

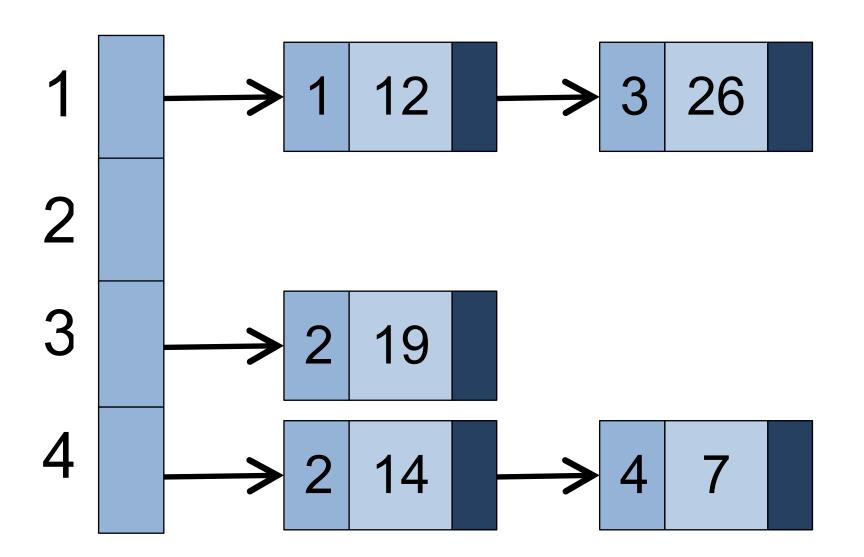


Potentially millions of neurons and billions of edges with developing technologies



Adjacency List graph representation







Graph Algorithms

- Traversals
 - DFS, BFS
- Finding paths
 - Single-source shortest paths (Dijkstra, Bellman-Ford)
 - All-pairs shortest-paths (Floyd-Warshall)
- Maximal independent sets
- Decomposition (connected components, strongly connected components)
- Maximum cardinality matching
- Connecting
 - Minimum spanning tree



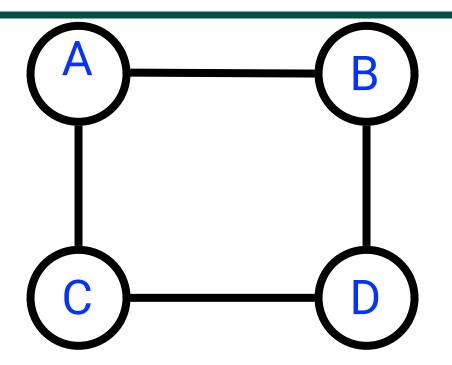
Spanning Tree Definition

- A spanning tree, T, of a connected undirected graph G is
 - rooted at some vertex of G
 - defined by a parent map for each vertex
 - contains all the vertices of G, i.e. spans all vertices
 - contains exactly |v| 1 edges
 - adding any other edge will create a cycle
 - contains no cycles (a tree!)
- The edges involved in T are a subset of the edges in G

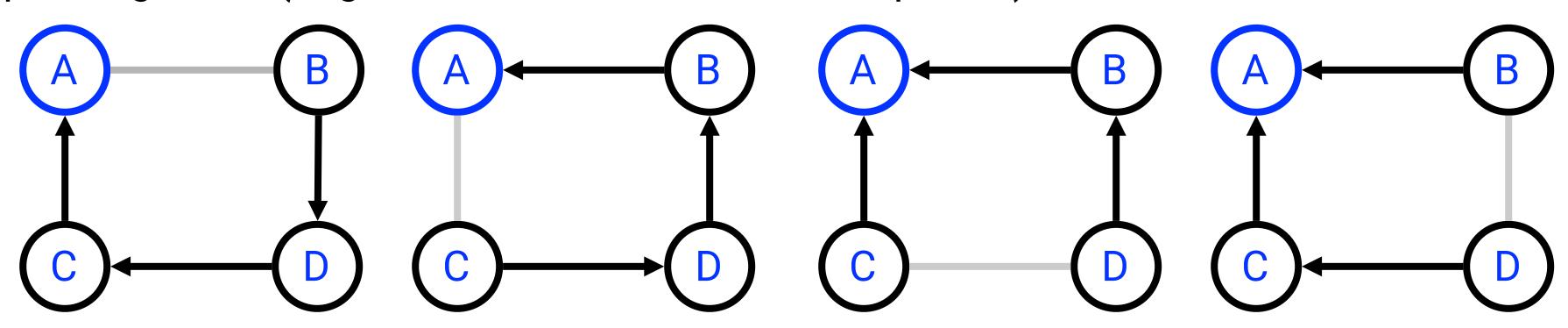


An Example Graph with 4 possible spanning trees rooted at vertex A

Example Undirected Graph:



Spanning Trees (edges are directed from child to parent):



Vertex	Parent
Α	null
В	D
С	Α
D	С

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Vertex	Parent
Α	null
В	Α
С	D
D	В

Vertex	Parent
Α	null
В	Α
С	Α
D	В

Vertex	Parent
Α	null
В	Α
С	Α
D	С



Sequential Spanning Tree Algorithm

```
1. class V {
      V [] neighbors; // adjacency list for input graph
3.
      V parent; // output value of parent in spanning tree
      boolean makeParent(V n) {
4.
       if (parent = null) { parent = n; return true; }
5.
        else return false; // return true if n became parent
6.
7.
      } // makeParent
8.
      void compute() {
        for (int i=0; i<neighbors.length; i++) {</pre>
         final V child = neighbors[i];
10.
         if (child.makeParent(this))
11.
            child.compute(); // recursive call
12.
13.
14. } // compute
15. } // class V
16. . . // main program
17. root.parent = root; // Use self-cycle to identify root
18. root.compute();
19. . . .
```



Exercise: Parallel Spanning Tree Algorithm using object-based isolated construct

```
1. class V {
     V [] neighbors; // adjacency list for input graph
3.
     V parent; // output value of parent in spanning tree
      boolean makeParent(V n) {
4.
       if (parent = null) { parent = n; return true; }
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        else return false; // return true if n became parent
6.
7.
      } // makeParent
     void compute() {
8.
        for (int i=0; i<neighbors.length; i++) {</pre>
         final V child = neighbors[i];
10.
         if (child.makeParent(this))
11.
           child.compute(); // recursive call
12.
13.
14. } // compute
15. } // class V
16. . . // main program
17. root.parent = root; // Use self-cycle to identify root
18. root.compute();
19. . . .
```



Exercise: Parallel Spanning Tree Algorithm using object-based isolated construct

```
1. class V {
      V [] neighbors; // adjacency list for input graph
      V parent; // output value of parent in spanning tree
      boolean makeParent(final V n) {
        return <u>isolatedWithReturn(this,</u> () \rightarrow {
5.
          if (parent = null) { parent = n; return true; }
          else return false; // return true if n became parent
        });
8.
      } // makeParent
      void compute() {
10.
        for (int i=0; i<neighbors.length; i++) {</pre>
11.
          final V child = neighbors[i];
12.
          if (child.makeParent(this))
13.
            \underline{async}(() \rightarrow \{ child.compute(); \});
14.
15.
16. } // compute
17. } // class V
18. . . .
19. root.parent = root; // Use self-cycle to identify root
20. finish(() \rightarrow \{ root.compute(); \});
21.
```



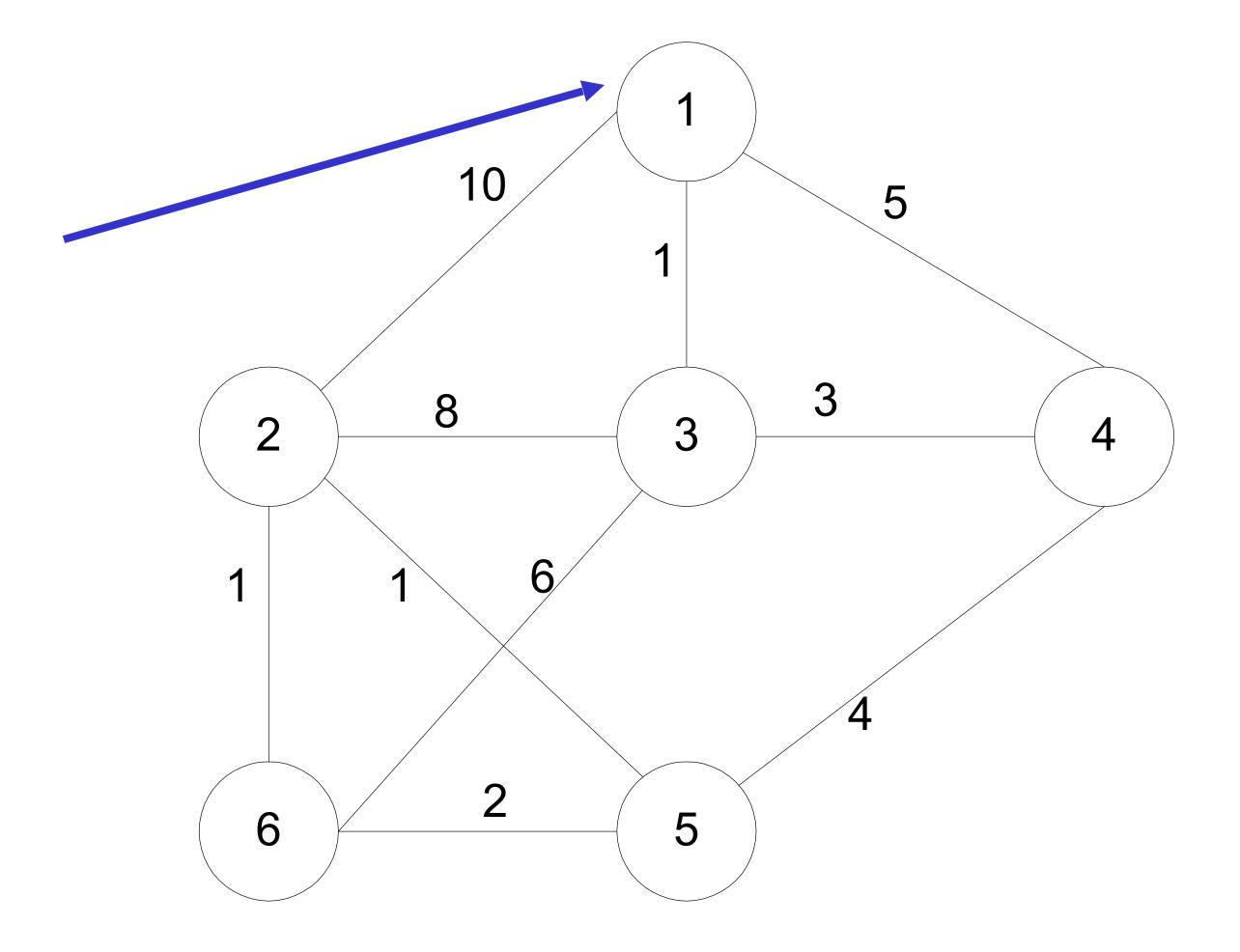
Minimum Spanning Tree

- For graphs that have edge weights
- Spanning tree with a minimum weight
- Sequential algorithms:
 - Prim's algorithm: greedy, grow a single tree by adding nodes closest to it
 - Kruskal's algorithm: greedy, add lightest edges that don't create a cycle
 - Boruvka's algorithm: combination of Prim's and Kruskal's
 - Can be parallelized



Starting from empty T, choose a vertex at random and initialize

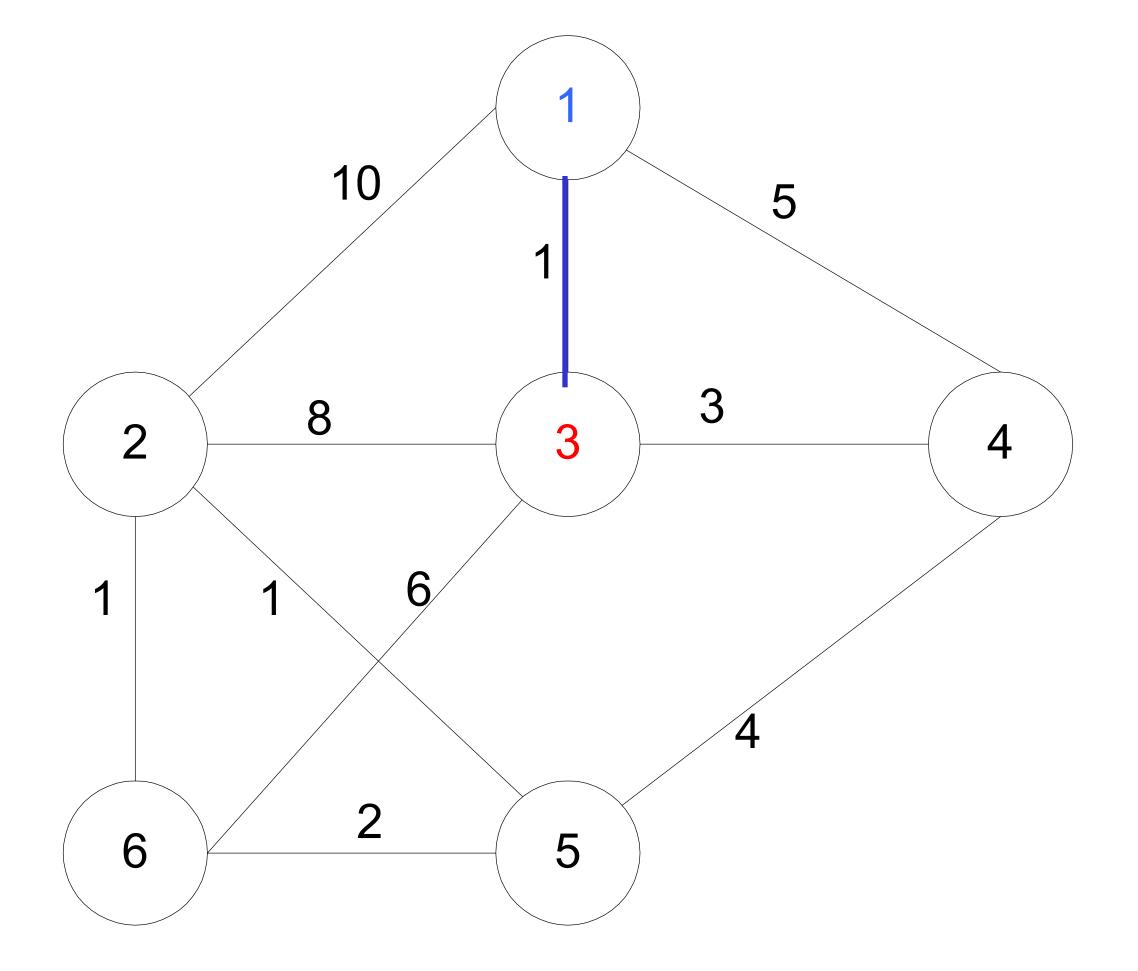
$$V = \{1\}, E' = \{\}$$





Choose the vertex u not in V such that edge weight from u to a vertex in V is minimal (greedy!)

$$V=\{1,3\} E'=\{(1,3)\}$$





Repeat until all vertices have been chosen

Choose the vertex u not in V such that edge weight from v to a vertex in V is minimal (greedy!)

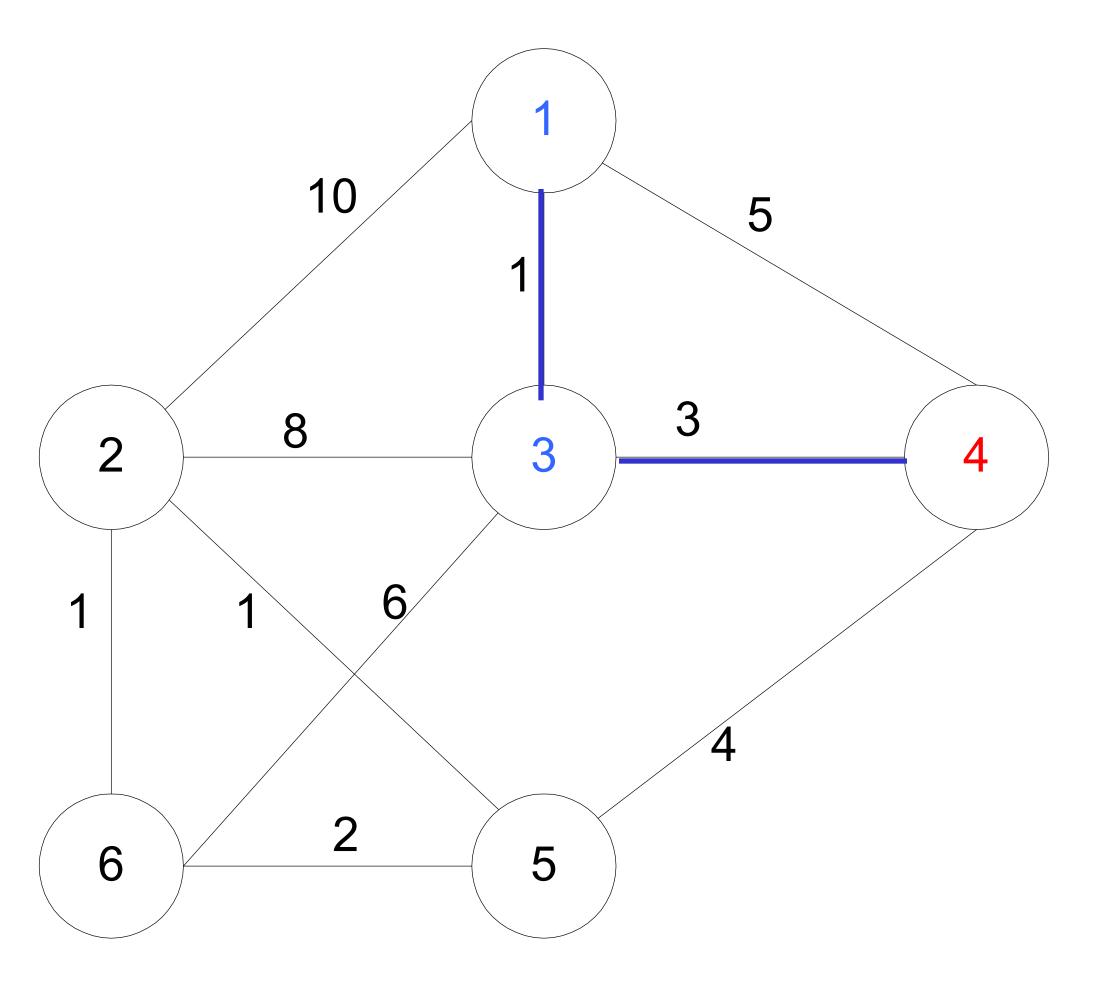
$$V = \{1,3,4\} E' = \{(1,3),(3,4)\}$$

$$V = \{1,3,4,5\} E' = \{(1,3),(3,4),(4,5)\}$$

. . . .

$$V=\{1,3,4,5,2,6\}$$

$$E'=\{(1,3),(3,4),(4,5),(5,2),(2,6)\}$$



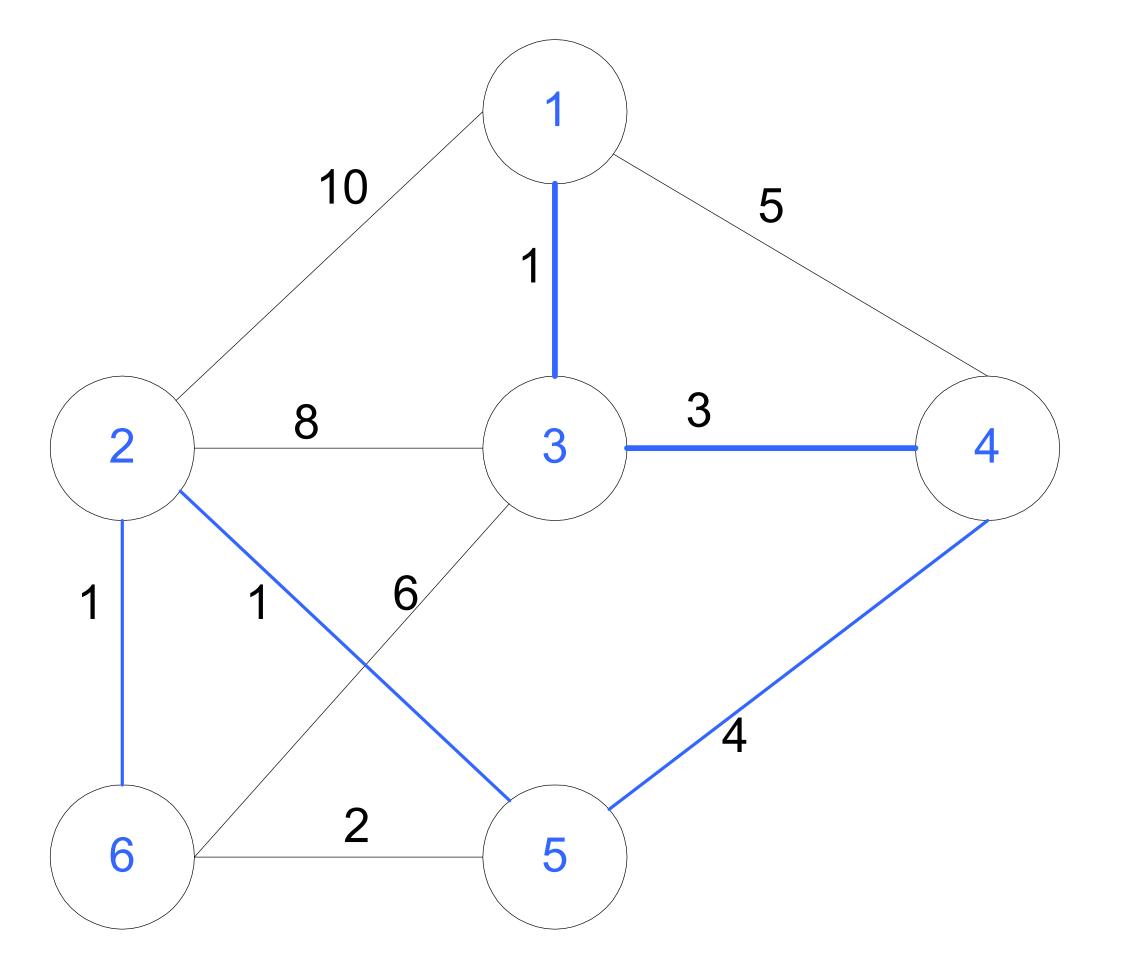


Repeat until all vertices have been chosen

$$V=\{1,3,4,5,2,6\}$$

E'=\{(1,3),(3,4),(4,5),(5,2),(2,6)\}

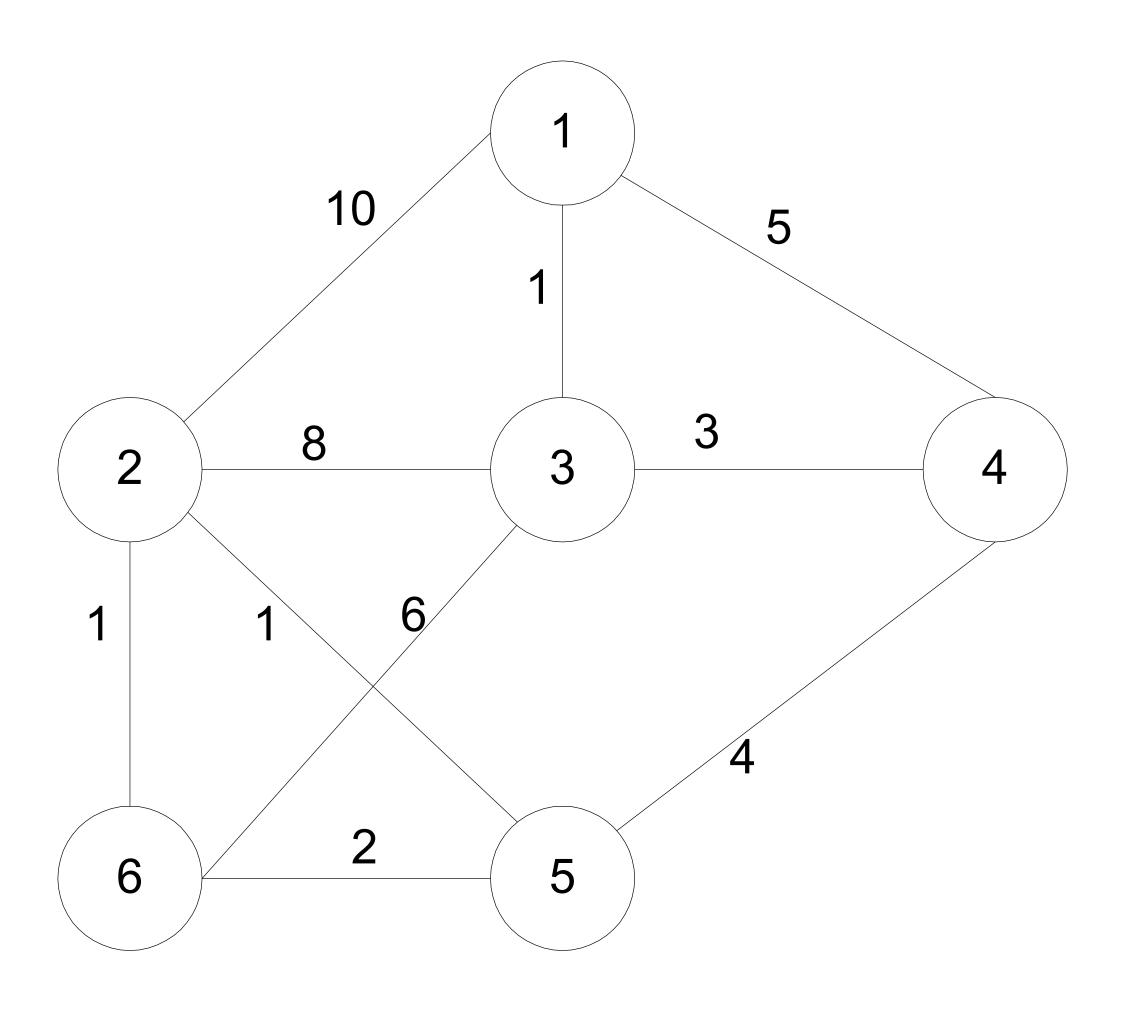
Final Cost: 1 + 3 + 4 + 1 + 1 = 10



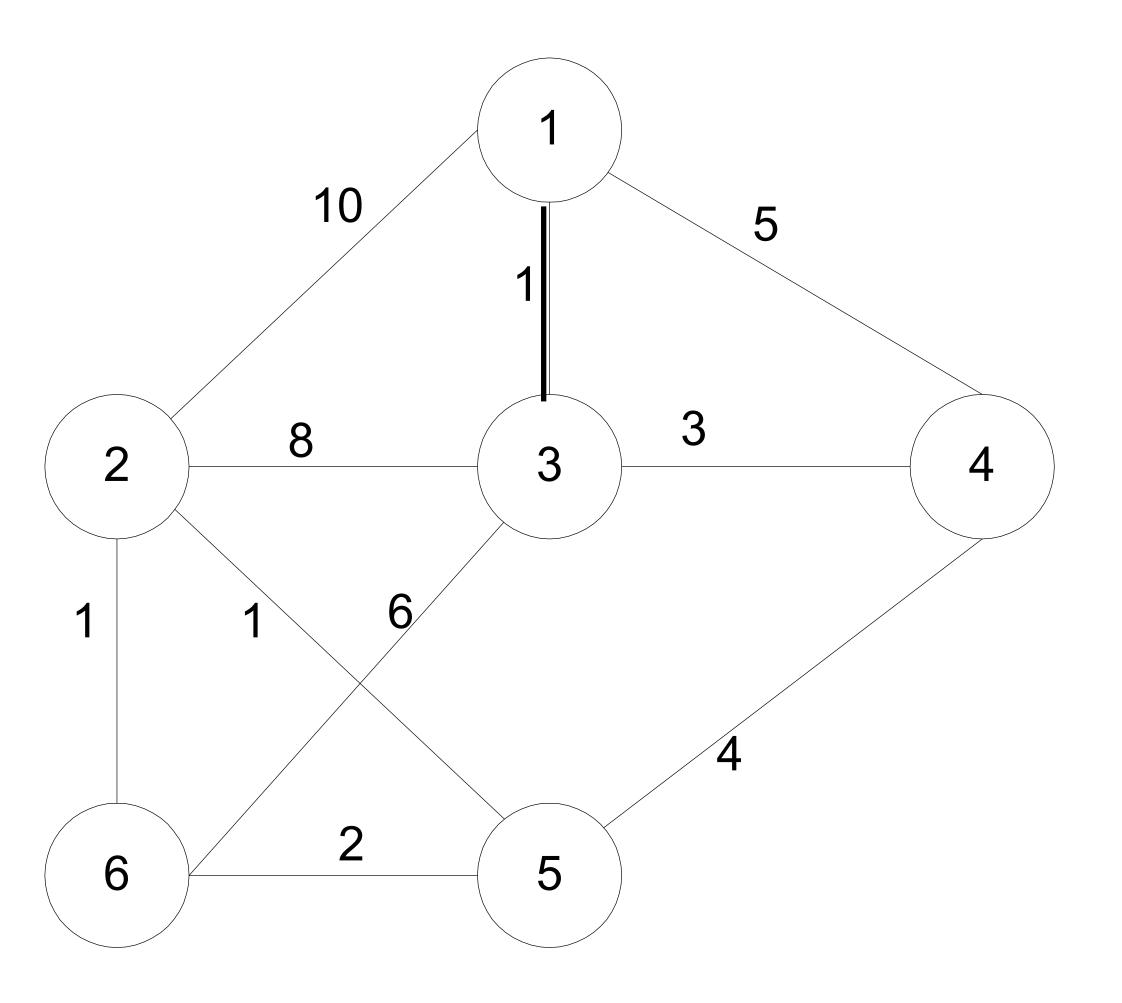


- Select edges in order of increasing cost
- Accept an edge to expand tree or forest only if it does not cause a cycle
- Implementation using adjacency list, priority queues and disjoint sets

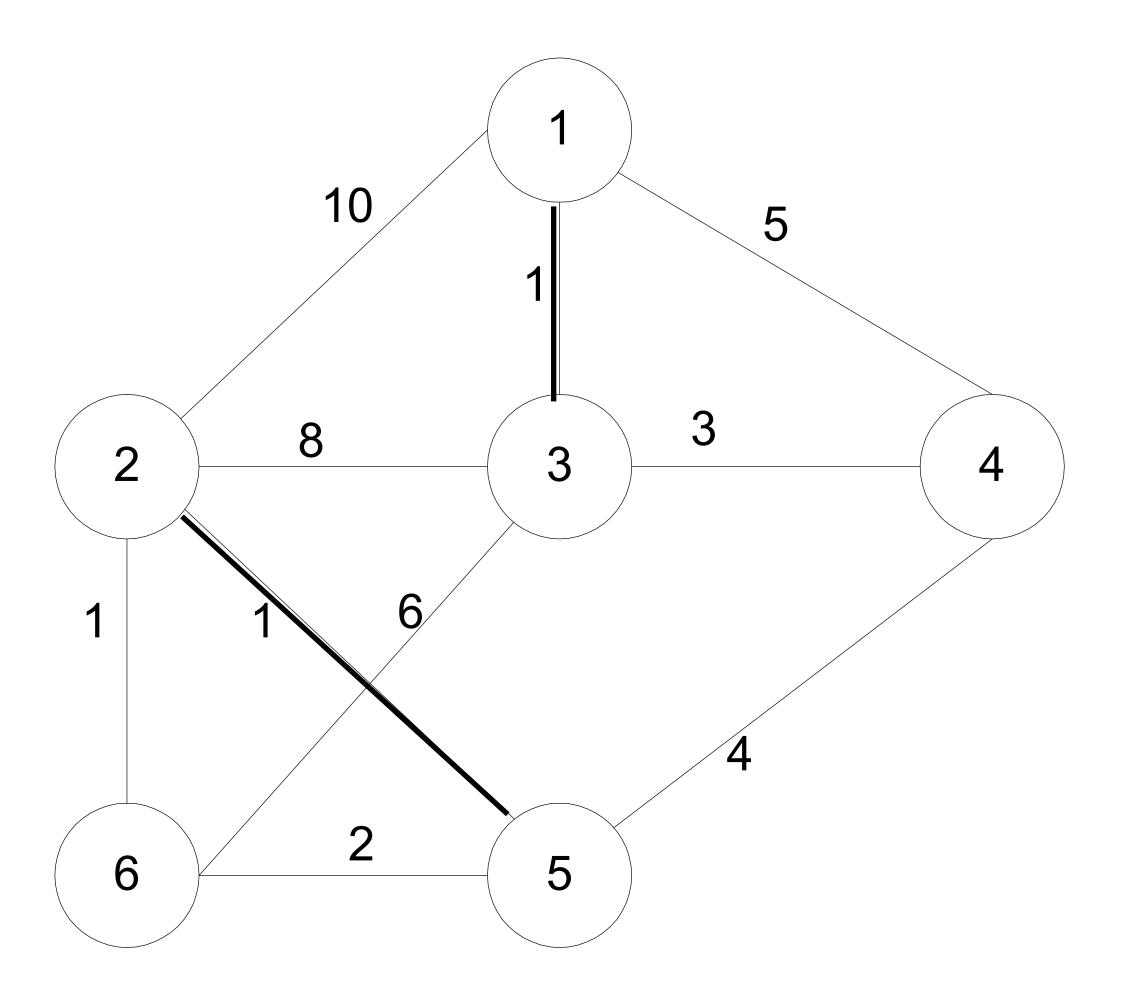






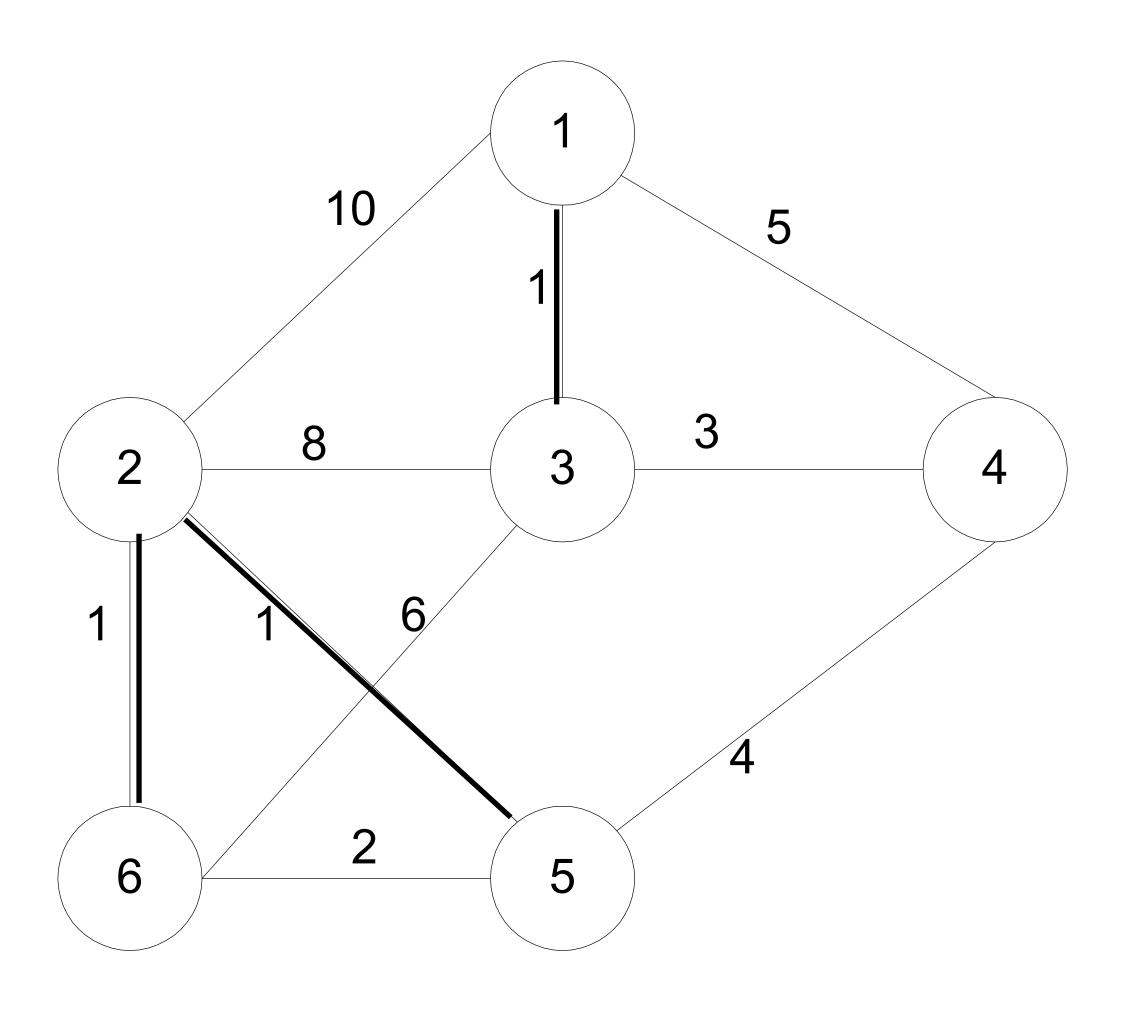




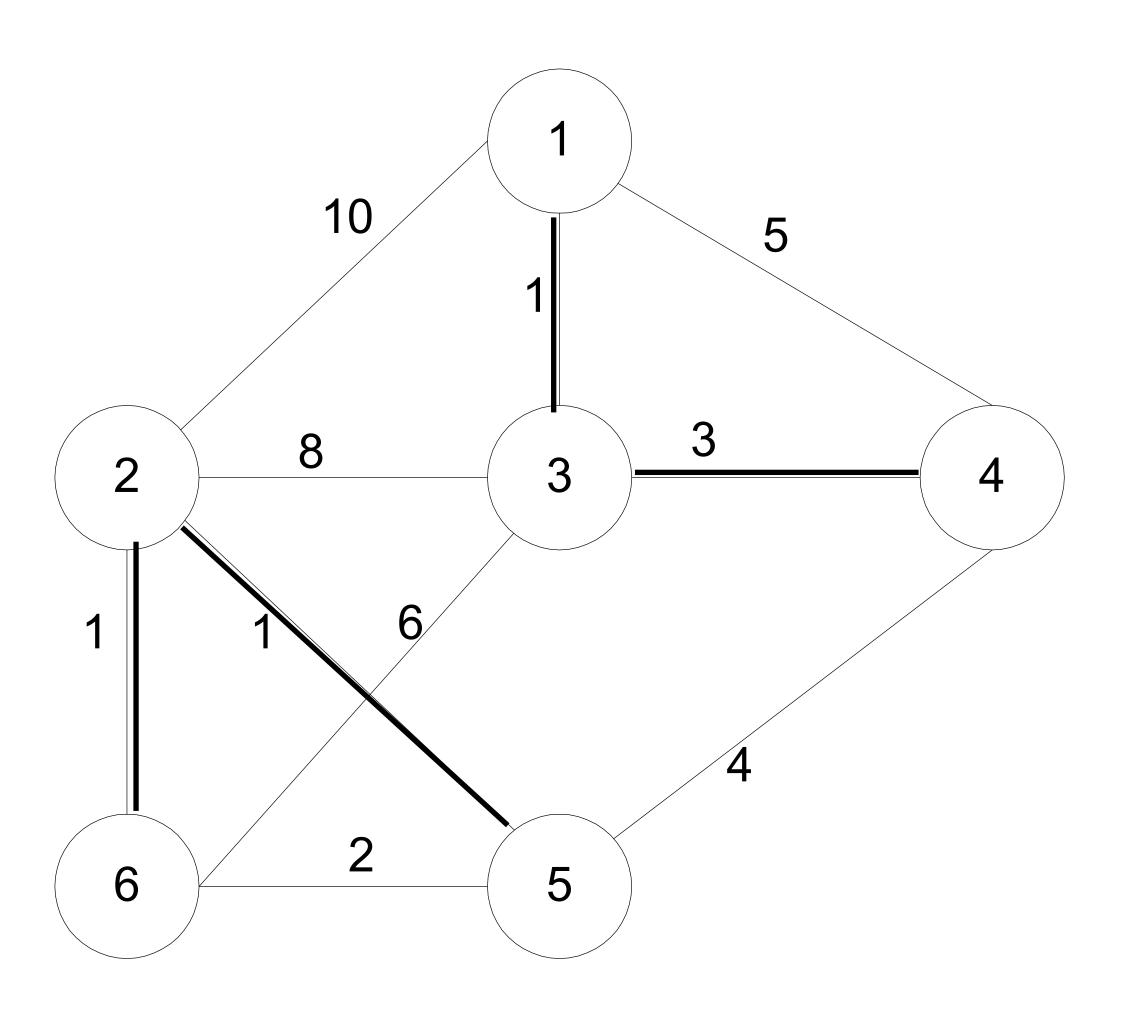




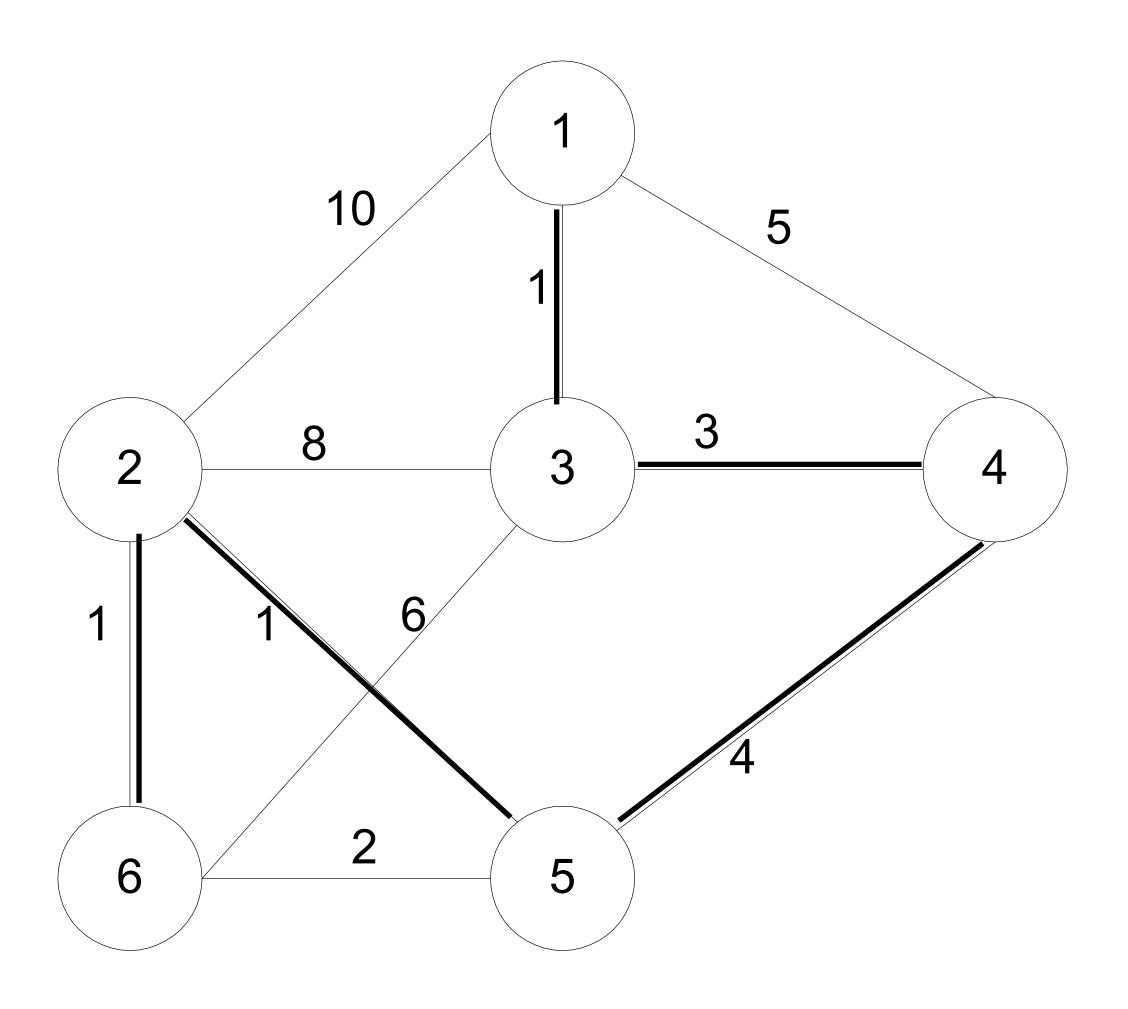
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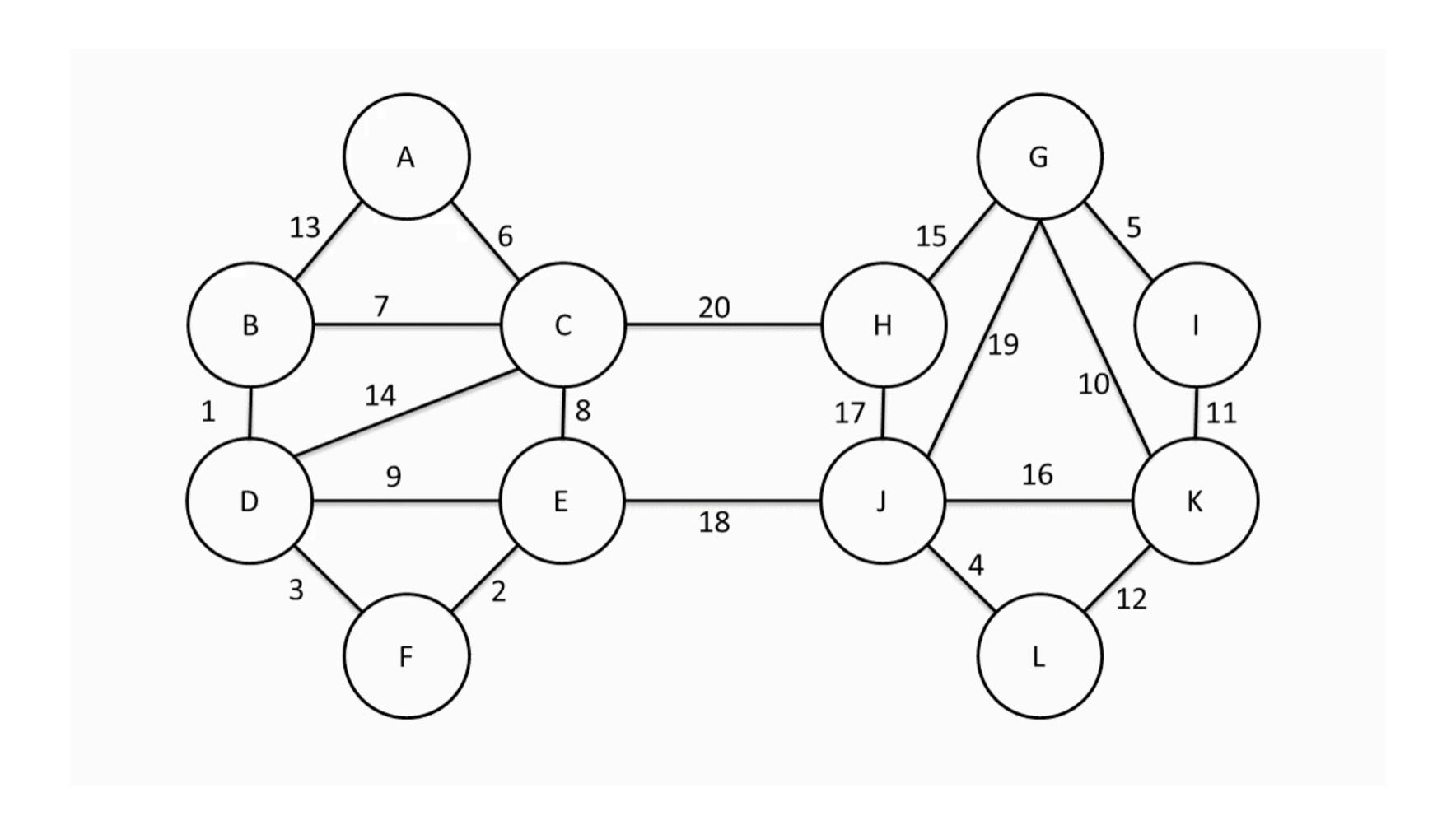


Boruvka's Algorithm

- Combination of Prim's and Kruskal's
- Grow a tree (component) by picking the lightest edge connected to it, just like Prim
- Connect the trees when the lightest edge is between them, just like Kruskal
- Growing of each tree can be done in parallel
- Component contraction
 - Each component represented by a single node
 - When connecting two components, contract the edge and make a single node to represent the two



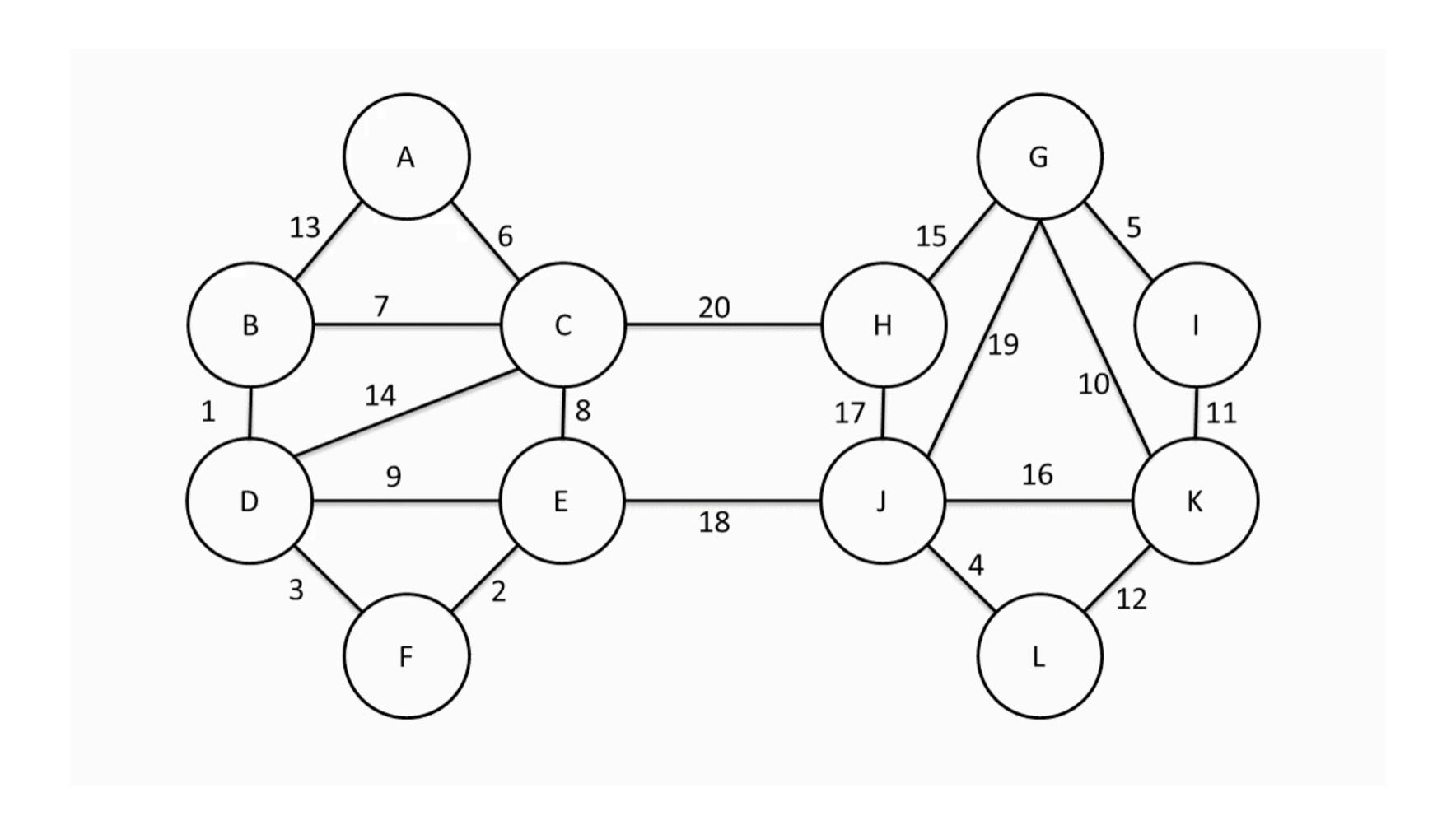
Boruvka's Algorithm



Animation: Randy Cornell, Texas State University



Boruvka's Algorithm



Animation: Randy Cornell, Texas State University



Parallel Boruvka's Algorithm

- Java threads or async tasks picking up components off the worklist
 - You don't want too many threads of tasks, tune for the machine
 - Worklist has to allow concurrent access
- Grow components in parallel
- When inspecting the closest node to expand the component, have to synchronize
 - Other thread or task could be also accessing it
 - Careful not to introduce deadlock
- When contracting an edge, have to synchronize
- When there's only a single component left, you are done

