

# Chapter 4

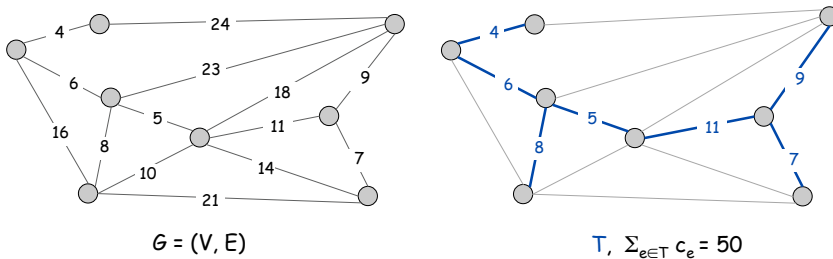
## Greedy Algorithms

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 Slides by Kevin Wayne.  
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## 4.5 Minimum Spanning Tree

### Minimum Spanning Tree

**Minimum spanning tree.** Given a connected graph  $G = (V, E)$  with real-valued edge weights  $c_e$ , an MST is a subset of the edges  $T \subseteq E$  such that  $T$  is a spanning tree whose sum of edge weights is minimized.



**Cayley's Theorem.** There are  $n^{n-2}$  spanning trees of  $K_n$ .

↑  
 can't solve by brute force

### Applications

MST is fundamental problem with diverse applications.

- Network design.
  - telephone, electrical, hydraulic, TV cable, computer, road
- Approximation algorithms for NP-hard problems.
  - traveling salesperson problem, Steiner tree
- Indirect applications.
  - max bottleneck paths
  - LDPC codes for error correction
  - image registration with Renyi entropy
  - learning salient features for real-time face verification
  - reducing data storage in sequencing amino acids in a protein
  - model locality of particle interactions in turbulent fluid flows
  - autoconfig protocol for Ethernet bridging to avoid cycles in a network
- Cluster analysis.

## Greedy Algorithms

**Kruskal's algorithm.** Start with  $T = \phi$ . Consider edges in ascending order of cost. Insert edge  $e$  in  $T$  unless doing so would create a cycle.

**Reverse-Delete algorithm.** Start with  $T = E$ . Consider edges in descending order of cost. Delete edge  $e$  from  $T$  unless doing so would disconnect  $T$ .

**Prim's algorithm.** Start with some root node  $s$  and greedily grow a tree  $T$  from  $s$  outward. At each step, add the cheapest edge  $e$  to  $T$  that has exactly one endpoint in  $T$ .

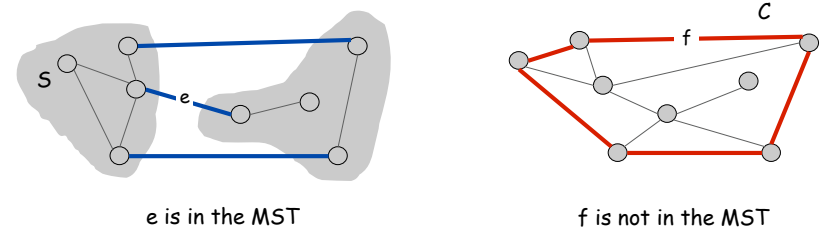
**Remark.** All three algorithms produce an MST.

## Greedy Algorithms

**Simplifying assumption.** All edge costs  $c_e$  are distinct.

**Cut property.** Let  $S$  be any subset of nodes, and let  $e$  be the min cost edge with exactly one endpoint in  $S$ . Then the MST contains  $e$ .

**Cycle property.** Let  $C$  be any cycle, and let  $f$  be the max cost edge belonging to  $C$ . Then the MST does not contain  $f$ .

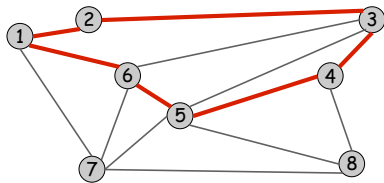


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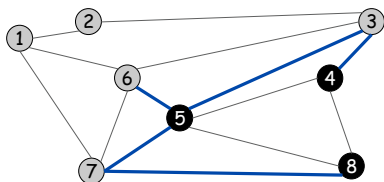
## Cycles and Cuts

**Cycle.** Set of edges the form  $a-b, b-c, c-d, \dots, y-z, z-a$ .



Cycle  $C = 1-2, 2-3, 3-4, 4-5, 5-6, 6-1$

**Cutset.** A cut is a subset of nodes  $S$ . The corresponding cutset  $D$  is the subset of edges with exactly one endpoint in  $S$ .

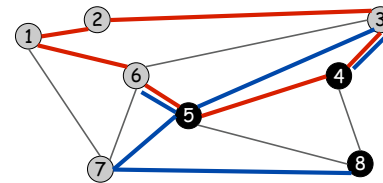


Cut  $S = \{4, 5, 8\}$   
Cutset  $D = 5-6, 5-7, 3-4, 3-5, 7-8$

7

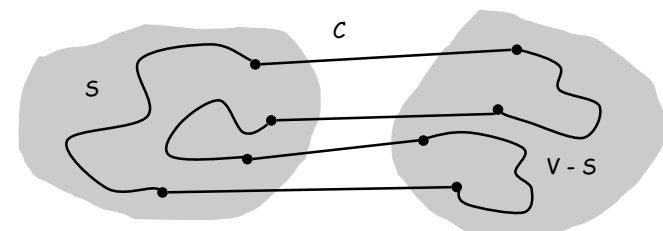
## Cycle-Cut Intersection

**Claim.** A cycle and a cutset intersect in an even number of edges.



Cycle  $C = 1-2, 2-3, 3-4, 4-5, 5-6, 6-1$   
Cutset  $D = 3-4, 3-5, 5-6, 5-7, 7-8$   
Intersection =  $3-4, 5-6$

**Pf.** (by picture)



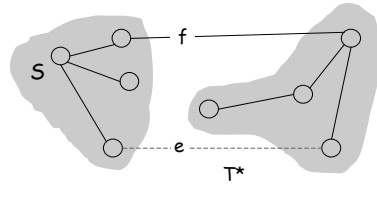
8

**Simplifying assumption.** All edge costs  $c_e$  are distinct.

**Cut property.** Let  $S$  be any subset of nodes, and let  $e$  be the min cost edge with exactly one endpoint in  $S$ . Then the MST  $T^*$  contains  $e$ .

Pf. (exchange argument)

- Suppose  $e$  does not belong to  $T^*$ , and let's see what happens.
- Adding  $e$  to  $T^*$  creates a cycle  $C$  in  $T^*$ .
- Edge  $e$  is both in the cycle  $C$  and in the cutset  $D$  corresponding to  $S$   
 $\Rightarrow$  there exists another edge, say  $f$ , that is in both  $C$  and  $D$ .
- $T' = T^* \cup \{e\} - \{f\}$  is also a spanning tree.
- Since  $c_e < c_f$ ,  $\text{cost}(T') < \text{cost}(T^*)$ .
- This is a contradiction. ▀



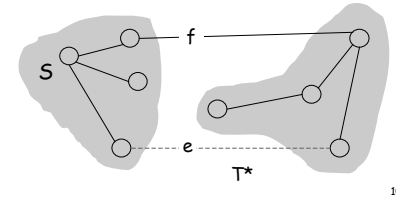
9

**Simplifying assumption.** All edge costs  $c_e$  are distinct.

**Cycle property.** Let  $C$  be any cycle in  $G$ , and let  $f$  be the max cost edge belonging to  $C$ . Then the MST  $T^*$  does not contain  $f$ .

Pf. (exchange argument)

- Suppose  $f$  belongs to  $T^*$ , and let's see what happens.
- Deleting  $f$  from  $T^*$  creates a cut  $S$  in  $T^*$ .
- Edge  $f$  is both in the cycle  $C$  and in the cutset  $D$  corresponding to  $S$   
 $\Rightarrow$  there exists another edge, say  $e$ , that is in both  $C$  and  $D$ .
- $T' = T^* \cup \{e\} - \{f\}$  is also a spanning tree.
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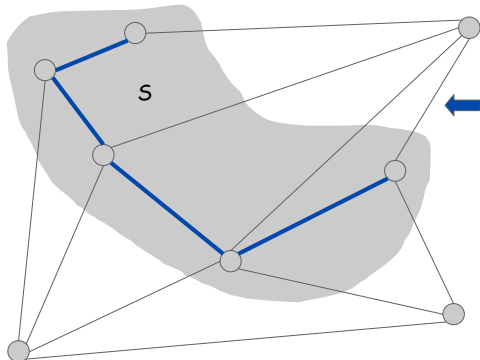


10

### Prim's Algorithm: Proof of Correctness

**Prim's algorithm.** [Jarník 1930, Dijkstra 1957, Prim 1959]

- Initialize  $S =$  any node.
- Apply cut property to  $S$ .
- Add min cost edge in cutset corresponding to  $S$  to  $T$ , and add one new explored node  $u$  to  $S$ .



11

### Implementation: Prim's Algorithm

**Implementation.** Use a priority queue ala Dijkstra.

- Maintain set of explored nodes  $S$ .
- For each unexplored node  $v$ , maintain attachment cost  $a[v] =$  cost of cheapest edge  $v$  to a node in  $S$ .
- $O(n^2)$  with an array;  $O(m \log n)$  with a binary heap.

```

Prim(G, c) {
  foreach (v ∈ V) a[v] ← ∞
  Initialize an empty priority queue Q
  foreach (v ∈ V) insert v onto Q
  Initialize set of explored nodes S ← ∅

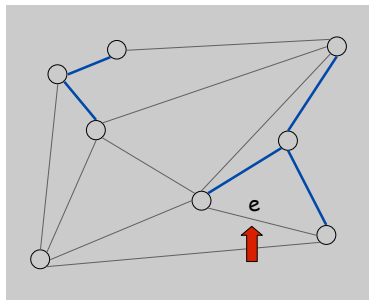
  while (Q is not empty) {
    u ← delete min element from Q
    S ← S ∪ { u }
    foreach (edge e = (u, v) incident to u)
      if ((v ∉ S) and (c_e < a[v]))
        decrease priority a[v] to c_e
  }
}

```

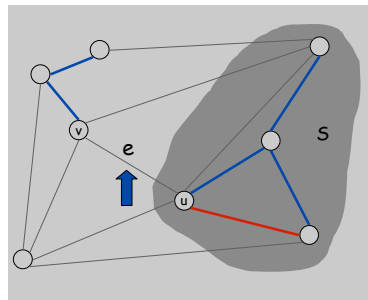
12

**Kruskal's algorithm.** [Kruskal, 1956]

- Consider edges in ascending order of weight.
- Case 1: If adding  $e$  to  $T$  creates a cycle, discard  $e$  according to cycle property.
- Case 2: Otherwise, insert  $e = (u, v)$  into  $T$  according to cut property where  $S =$  set of nodes in  $u$ 's connected component.



Case 1



Case 2

**Implementation.** Use the **union-find** data structure.

- Build set  $T$  of edges in the MST.
- Maintain set for each connected component.
- $O(m \log n)$  for sorting and  $O(m \alpha(m, n))$  for union-find.

$m \leq n^2 \Rightarrow \log m$  is  $O(\log n)$        $\alpha(m, n)$  essentially a constant

```

Kruskal(G, c) {
  Sort edges weights so that  $c_1 \leq c_2 \leq \dots \leq c_m$ .
  T ←  $\phi$ 

  foreach (u ∈ V) make a set containing singleton u

  for i = 1 to m
    (u,v) =  $e_i$ 
    if (u and v are in different sets) {
      T ← T ∪ { $e_i$ }
      merge the sets containing u and v
    }
  return T
}
    
```

Lexicographic Tiebreaking

To remove the assumption that all edge costs are distinct: perturb all edge costs by tiny amounts to break any ties.

**Impact.** Kruskal and Prim only interact with costs via pairwise comparisons. If perturbations are sufficiently small, MST with perturbed costs is MST with original costs.

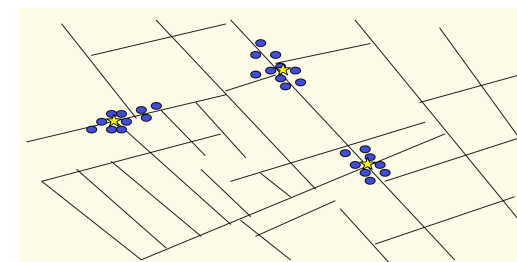
↑  
e.g., if all edge costs are integers, perturbing cost of edge  $e_i$  by  $i / n^2$

**Implementation.** Can handle arbitrarily small perturbations implicitly by breaking ties lexicographically, according to index.

```

boolean less(i, j) {
  if (cost( $e_i$ ) < cost( $e_j$ )) return true
  else if (cost( $e_i$ ) > cost( $e_j$ )) return false
  else if (i < j) return true
  else return false
}
    
```

## 4.7 Clustering



Outbreak of cholera deaths in London in 1850s. Reference: Nina Mishra, HP Labs

## Clustering

**Clustering.** Given a set  $U$  of  $n$  objects labeled  $p_1, \dots, p_n$ , classify into coherent groups.

↑  
photos, documents, micro-organisms

**Distance function.** Numeric value specifying "closeness" of two objects.

↑  
number of corresponding pixels whose intensities differ by some threshold

**Fundamental problem.** Divide into clusters so that points in different clusters are far apart.

- Routing in mobile ad hoc networks.
- Identify patterns in gene expression.
- Document categorization for web search.
- Similarity searching in medical image databases
- Skycat: cluster  $10^9$  sky objects into stars, quasars, galaxies.

## Clustering of Maximum Spacing

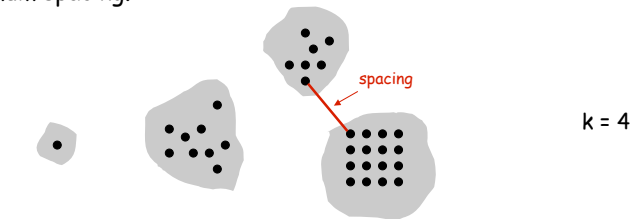
**k-clustering.** Divide objects into  $k$  non-empty groups.

**Distance function.** Assume it satisfies several natural properties.

- $d(p_i, p_j) = 0$  iff  $p_i = p_j$  (identity of indiscernibles)
- $d(p_i, p_j) \geq 0$  (nonnegativity)
- $d(p_i, p_j) = d(p_j, p_i)$  (symmetry)

**Spacing.** Min distance between any pair of points in different clusters.

**Clustering of maximum spacing.** Given an integer  $k$ , find a  $k$ -clustering of maximum spacing.



17

18

## Greedy Clustering Algorithm

**Single-link k-clustering algorithm.**

- Form a graph on the vertex set  $U$ , corresponding to  $n$  clusters.
- Find the closest pair of objects such that each object is in a different cluster, and add an edge between them.
- Repeat  $n-k$  times until there are exactly  $k$  clusters.

**Key observation.** This procedure is precisely Kruskal's algorithm (except we stop when there are  $k$  connected components).

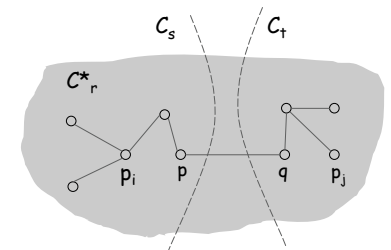
**Remark.** Equivalent to finding an MST and deleting the  $k-1$  most expensive edges.

## Greedy Clustering Algorithm: Analysis

**Theorem.** Let  $C^*$  denote the clustering  $C_1^*, \dots, C_k^*$  formed by deleting the  $k-1$  most expensive edges of a MST.  $C^*$  is a  $k$ -clustering of max spacing.

**Pf.** Let  $C$  denote some other clustering  $C_1, \dots, C_k$ .

- The spacing of  $C^*$  is the length  $d^*$  of the  $(k-1)^{\text{st}}$  most expensive edge.
- Let  $p_i, p_j$  be in the same cluster in  $C^*$ , say  $C_r^*$ , but different clusters in  $C$ , say  $C_s$  and  $C_t$ .
- Some edge  $(p, q)$  on  $p_i$ - $p_j$  path in  $C_r^*$  spans two different clusters in  $C$ .
- All edges on  $p_i$ - $p_j$  path have length  $\leq d^*$  since Kruskal chose them.
- Spacing of  $C$  is  $\leq d^*$  since  $p$  and  $q$  are in different clusters. ■



19

20

## Extra Slides

### Deterministic comparison based algorithms.

- $O(m \log n)$  [Jarník, Prim, Dijkstra, Kruskal, Boruvka]
- $O(m \log \log n)$ . [Cheriton-Tarjan 1976, Yao 1975]
- $O(m \beta(m, n))$ . [Fredman-Tarjan 1987]
- $O(m \log \beta(m, n))$ . [Gabow-Galil-Spencer-Tarjan 1986]
- $O(m \alpha(m, n))$ . [Chazelle 2000]

Holy grail.  $O(m)$ .

### Notable.

- $O(m)$  randomized. [Karger-Klein-Tarjan 1995]
- $O(m)$  verification. [Dixon-Rauch-Tarjan 1992]

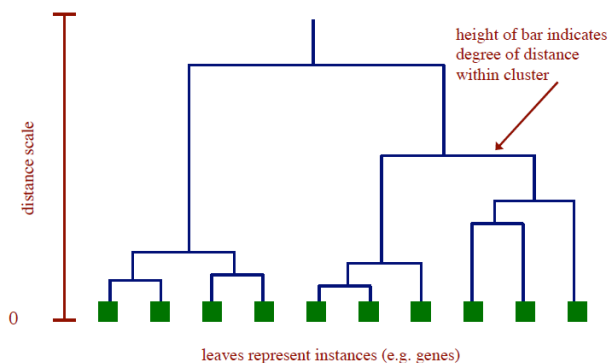
### Euclidean.

- 2-d:  $O(n \log n)$ . compute MST of edges in Delaunay
- k-d:  $O(k n^2)$ . dense Prim

## Dendrogram

**Dendrogram.** Scientific visualization of hypothetical sequence of evolutionary events.

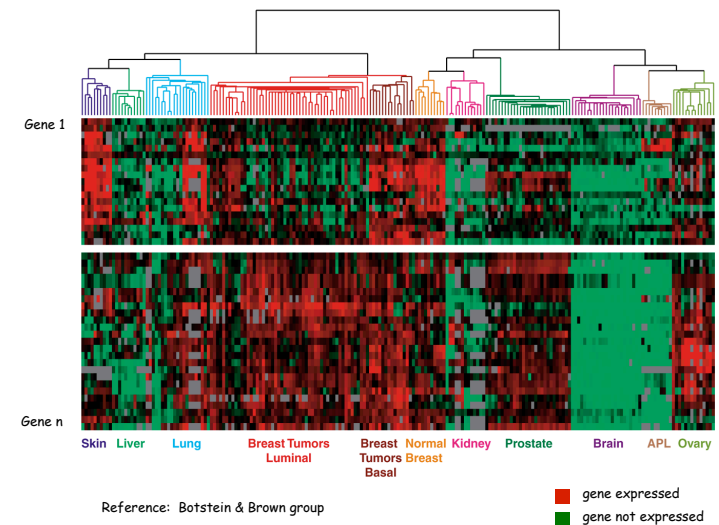
- Leaves = genes.
- Internal nodes = hypothetical ancestors.



Reference: <http://www.biostat.wisc.edu/bmi576/fall-2003/lecture13.pdf>

## Dendrogram of Cancers in Human

Tumors in similar tissues cluster together.



Reference: Botstein & Brown group