Graph Algorithms in DROP

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Spanning Tree

Overview

A *spanning tree* of an undirected graph G is a subgraph that includes all of the vertexes of G, with minimum possible number of edges (Wikipedia (2020)). In general, a graph may have several spanning trees, but a graph that is not connected will not contain a spanning tree. If all of the edges of G are also edges of a spanning tree T of G, then G is a tree and identical to T, that is, a tree has a unique spanning tree and that is itself

Applications

1. Use in Path Finding Algorithms: Several path-finding algorithms, including Dijkstra's algorithm and the A* search algorithm, internally build a spanning tree as an intermediate step in solving the problem.
2. Use in Cost Minimization Problems: In order to minimize the cost of power networks, wiring connections, piping, automatic speech recognition, etc., people often use algorithms that gradually build a spanning tree – or many such trees – as intermediate steps in the process of finding the minimum spanning tree (Graham and Hell (1985)).
3. Use in Link-State Protocols: The internet and many other telecommunications networks have transmission links that connect nodes together in a mesh topology that includes some loops. In order to avoid *bridge loops* and *routing loops*, many protocols design for such networks – including Spanning Tree Protocol, Open Shortest Path First, Link-State Routing Protocol, Augmented Tree-Based Routing, etc. – require each router to remember a spanning tree.
4. Graph Embeddings with Maximum Genus: A special kind of tree, the Xuong tree, is used in topological graph theory to find graph embeddings with maximum genus. A

Xuong tree is a spanning tree such that, in the remaining graph, the number of connected components with an odd number of edges is as small as possible. A Xuong tree and an associated maximum genus embedding can be found in polynomial time (Beineke and Wilson (2009)).

Definitions

A tree is a connected, undirected graph with no cycles. It is a spanning tree of a graph G if it spans G – that is, it includes every vertex of G – and is a subgraph of G, i.e., every edge in the tree belongs to G. A spanning tree of a connected graph G can also be defined as a maximal set of edges G that contains no cycle, or as a minimal set of edges that connect all vertexes.

Fundamental Cycles

Adding just one edge to the spanning tree will create a cycle; such a cycle is called a *fundamental cycle*. There is a distinct fundamental cycle for each edge not in the spanning tree; thus, there is a one-to-one correspondence between fundamental cycles and edges not in the spanning tree. For a connected graph with V vertexes, and spanning tree will have $V - 1$ edges, and thus, a graph of E edges and one of its spanning trees will have $E - V + 1$ fundamental cycles. For any given spanning tree, the set of all $E - V + 1$ fundamental cycles forms a cycle basis, a basis for the cycle space (Kocay and Kreher (2004)).

Fundamental Cut-sets

1. Motivation behind the Fundamental Cut-set: Dual to the notion of a fundamental cycle is the *fundamental cut-set*. By deleting just one edge of the spanning tree, the vertexes are partitioned into two disjoint sets. The fundamental cut-set is defined as the set of edges that must be removed from the graph G to achieve the same partition. Thus, each spanning tree defines a set of $V - 1$ fundamental cut-sets, one for each edge of the spanning tree (Kocay and Kreher (2004)).
2. Duality between Cut-sets and Cycles: The duality between fundamental cut-sets and fundamental cycles is established by noting that the cycle edges not in the spanning tree can only appear in the cut-sets of the other edges of the cycle; and *vice versa*; edges in a cut-set can only appear in those cycles containing the edge corresponding to the cut-set. This duality can be expressed using the theory of matroids, according to which the spanning tree is the base of a graphic matroid; a fundamental cycle is the unique circuit within the set formed by adding one element to the base, and fundamental cut-sets are defined in the same way as the dual matroid (Oxley (2006)).

Spanning Forests

1. Competing Definitions of Spanning Forests: In graphs that are not connected, there can be no spanning tree, and on must consider *spanning forests* instead. Here, there are two competing definitions:
    a. Some authors consider a spanning forest to be the maximal acyclic subgraph of a given graph, or equivalently, a graph consisting of a spanning tree in each connected component of the graph (Bollobas (1998), Mehlhorn (1999)).
    b. For other authors, a spanning forest is a forest that spans all of the vertexes, meaning only that each vertex in the graph is a vertex in the forest. Under this definition, even a connected graph may have a disconnected spanning forest, such as a forest in which each vertex forms a single-vertex tree (Cameron (1994)).

2. Full versus Maximal Spanning Forest: To avoid confusion between these two definitions, Gross and Yellen (2005) suggest the term *full spanning forest* for a spanning forest with the same connectivity as a given graph, while Bondy and Murthy (2008) instead call this kind of forest a maximal spanning forest.

Counting Spanning Trees

The number $t(G)$ of the spanning trees of a connected graph is a well-studied invariant.

In Specific Graphs

1. When G is a Tree: In some cases, it is easy to calculate $t(G)$ directly. If G is a tree itself, then

$$t(G) = 1$$

2. G is a Cycle Graph: When G is a cycle graph with n vertexes, then

$$t(G) = n$$

3. G is Complete with n Vertexes: For a complete graph with n vertexes, Cayley's formula (Aigner and Ziegler (1998)) gives the number of spanning trees as n^{n-2}.
4. G is Complete Bipartite: If G is a complete bipartite graph $K_{p,q}$ then

$$t(G) = p^{q-1}q^{p-1}$$

(Hartsfield and Ringel (2003)).

5. <u>G is an n-dimensional Hyper-cube</u>: For an n-dimensional hyper-cube graph, the number of spanning trees is

$$t(G) = 2^{2^n-n-1}\prod_{k=2}^{n} k^{\binom{n}{k}}$$

(Harary, Hayes, and Wu (1988)).

In Arbitrary Graphs

1. <u>Arbitrary Graph Spanning Tree Count</u>: More generally, for any graph G, the number $t(G)$ can be calculated in polynomial time as a determinant of a matrix derived from the graph, using Kirchoff's matrix-tree theorem.
2. <u>Kirchoff's Matrix-Tree Theorem Method</u>: Specifically, to compute $t(G)$, one constructs a square matrix in which both the rows and the columns are indexed by vertexes of G. The entry in row i and column j is one of three values:
    a. The degree of vertex i if

$$i = j$$

    b. -1 if vertexes i and j are adjoint, OR
    c. 0 if vertexes i and j are different from each other but not adjacent.

    The resulting matrix is singular, so its determinant is zero. However, deleting a row and a column for an arbitrarily chosen vertex leads to a smaller matrix whose determinant is exactly $t(G)$.

Deletion-Contraction

1. The Deletion-Contraction Recurrence Formula: If G is a graph or a multi-graph, and e is an arbitrary edge of G, then the number $t(G)$ of spanning trees of G satisfies the *deletion-contraction recurrence*

$$t(G) = t(G - e) + t(G/e)$$

   where $G - e$ is the multi-graph obtained by deleting e, and G/e is the contraction of G by e (Kocay and Kreher (2004)). The term $G - e$ in the formula counts the number of spanning trees of G that do not use the edge e, and the term $t(G/e)$ counts the spanning trees of G that use the edge e.
2. Retention of Redundant Graph Edges: In the above formula, is the given graph G is a multi-graph, or if a contraction causes two vertexes to be connected to each other by multiple edges, then the redundant edges should not be removed, as that would lead to the wrong total. For instance, a bond graph connecting two edges by k edges has k different spanning trees, each consisting of one of these edges.

Tutte Polynomial

1. Sum over Internal/External Activity: The Tutte polynomial of a graph can be defined as a sum, over the spanning trees of the graph, of terms computed from *internal activity* and *external activity* of the tree. Its value at the arguments $(1, 1)$ is the number of spanning trees, or, in a disconnected graph, the number of maximal spanning forests (Bollobas (1998)).
2. Computational Complexity using Contraction-Deletion Recurrence: The Tutte polynomial can be computed using a deletion-contraction recurrence, but its computational complexity is high: for many values of its arguments, computing it is exactly **#P**-complete, and it is also hard to approximate with a guaranteed approximation ratio. The point $(1, 1)$ at which it can be evaluated using Kirchoff's

theorem, is one of the few exceptions (Jaeger, Vertigan, and Welsh (1990), Goldberg and Jerrum (2008)).

Algorithms – Construction

1. Spanning Tree using BFS/DFS: A single spanning tree of a graph can be found in linear time by either depth-first search or breadth-first search. Bothe of these algorithms explore then given graph, starting from an arbitrary vertex V, by looping through the neighbors of the vertexes they discover and adding each unexplored neighbor to a data structure to be explored later. They differ in whether the data structure is a stack – in the case of depth-first search – or a queue – in the breadth-first search. In either case, one can form a spanning tree by connecting each vertex, other than the root vertex V, to a vertex from which it was discovered. This tree is known as the depth-first search tree or the breadth-first search tree according to the graph exploration algorithm used to construct it (Kozen (1992)). Depth-first search trees are a special case of a class of spanning trees called the Tremaux trees, named after the 19th century discoverer of depth-first search (de Fraysseix and Rosenstiehl (1982)).
2. BFS/DFS in Parallel/Distributed Environments: Spanning trees are important in parallel and distributed computing, as a way of maintaining communications between a set of processors; see, for instance, the spanning tree protocol used by the OSI link-layer devices of the Shout protocol used for distributed computing. However, the breadth-first and the depth-first methods for constructing spanning trees on sequential computes are not well-suited for parallel and distributed computer (Reif (1985)). Instead, researchers have devised more specialized algorithms for finding spanning trees in these models of computation (Gallagher, Humblet, and Spira (1983), Gazit (1991), Bader and Cong (2005)).

Algorithms - Optimization

1. Spanning Trees under Optimal Condition: In certain fields of optimization theory, it is often useful to find a minimum spanning tree of a weighted graph. Other optimization problems in spanning trees have also been studied, including the maximum spanning tree, the maximum tree that spans k vertexes, the spanning tree with the fewest edges per vertex, the spanning tree with the largest number of leaves, the spanning tree with the fewest leaves – closely related to the Hamiltonian path problem, the maximum diameter spanning tree, and the maximum dilation spanning tree (Eppstein (1999), Wu and Cao (2004)).
2. Optimal Spanning Trees in Euclidean Space: Optimal spanning tree problems have also been studied for a finite set of points in a geometric space such as the Euclidean space. For such an input, the spanning tree is again a set of trees that has as its vertexes the given points. The quality of the tree is measured in the same way as in a graph, using the Euclidean distance between pairs of points as the weight for each edge. Thus, for instance, a Euclidean minimum spanning tree is the same as the graph minimum spanning tree in a complete graph with Euclidean edge weights. However, it is not necessary to construct the graph in order to solve the optimization problem; the Euclidean minimum spanning tree problem, for instance, can be solved more efficiently in $\mathcal{O}(n \log n)$ time by constructing Delaunay triangulation and then applying a linear planar graph minimum spanning tree algorithm to the resulting triangulation (Eppstein (1999)).

Randomization

1. Generation of Uniform Spanning Trees: A spanning tree chosen from among all the spanning trees with equal probability is called a uniform spanning tree. Wilson's algorithm can be used to generate uniform spanning trees in polynomial time by a

process of taking a random walk on the given graph and erasing the cycles created by this walk (Wilson (1996)).

2. Generating Random Minimal Spanning Tree: An alternative model for generating spanning trees randomly but not uniformly is the random minimal spanning tree. In this model, the edges of the graph are assigned random weights and then the minimum spanning tree of the weighted graph is constructed (McDiarmid, Johnson, and Stone (1997)).

Enumeration

Because a graph may have exponentially many spanning trees, it is not possible to list them all in polynomial time. However, algorithms are known for listing all spanning trees in polynomial time per tree (Gabow and Myers (1978)).

In Infinite Graphs

1. Infinite Graph – Axiom of Choice: Every finite connected graph has a spanning tree. However, for infinite connected graphs, the existence of spanning trees is equivalent to the axiom of choice. An infinite graph is connected if every pair of its vertexes forms the pair of end-points of a finite path. As with finite graphs, a tree is a connected graph with no finite cycles, and a spanning tree can be defined either as a maximal acyclic set of edges or as a tree that contains every vertex (Serre (2003)).
2. Equivalence to Zorn's Lemma: The trees within a graph may be partially ordered by their subgraph relation, and infinite chain in this partial order has an upper bound, i.e., the union of the trees in the chain. Zorn's lemma, one of many equivalent statements to the axiom of choice, requires that a partial order in which all chains are upper bounded have a maximal element; in the partial order on the trees of the graph, this

maximal element must be a spanning tree. Therefore, if Zorn's lemma is assumed, every infinite connected graph has a spanning tree (Serra (2003)).

3. Spanning Tree as a Choice Function: In the other direction, given a family of sets, it is possible to construct an infinite graph such that every spanning tree of the graph corresponds to a choice function of the family of sets. Therefore, if every infinite graph has a spanning tree, then the axiom of choice is true (Soukup (2008)).

In Directed Multi-graphs

The idea of a spanning tree can be generalized to directed multigraphs (Levine (2011)). Given a vertex v on a directed multi-graph G, an *oriented spanning tree* T rooted at v is an acyclic subgraph of G in which every vertex other than v has an out-degree of 1. This definition is only satisfied when the *branches* of T point towards v.

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Minimum Spanning Tree

Overview

1. Definition of Minimum Spanning Tree: A *minimum spanning tree (MST)* or *minimum weight spanning tree* is the subset of the edges of a connected, edge-weighted, undirected graph that connects all vertexes together, without any cycles and with minimum possible total edge weight. That is, it is a spanning tree whose sum of edges is as small as possible (Wikipedia (2020)).
2. Minimum Spanning Tree vs. Forest: More generally, any edge-weighted undirected graph – not necessarily connected – has a *minimum spanning forest*, which is a union of minimum spanning trees for its connected components.
3. Specialization of the Generic Spanning Tree: A *spanning tree* for that graph would be a subset of those paths that have no cycles but still connects every vertex; there might be several spanning trees possible. A *minimum spanning tree* would be the one with the lowest total cost, representing the least expensive path.

Multiplicity Properties

If there are n vertexes in the graph, then each spanning tree has $n - 1$ edges. There may be several minimum spanning trees of the same weight; in particular, if all the edges of a given graph are the same, then every spanning tree of that graph is a minimum.

Uniqueness Property

1. Statement of the Uniqueness Property: If each edge has a distinct weight, then there will be only one unique, minimum spanning tree. This generalizes to spanning forests as well.
2. Proof of the Uniqueness Property:
    a. Assume the contrary, that there are two different MST's – A and B.
    b. Since A and B differ despite containing the same nodes, there is at least one edge the belongs to one but not the other. Among such edges, let e_1 be the one with least weight; this choice is unique because the edge weights are all distinct. Without loss of generality, assume e_1 is in A.
    c. Since B is an MST, $\{e_1\} \cup B$ must contain a cycle C with e_1.
    d. As a tree, A contains no cycles, therefore C must have an edge e_2 that is not in A.
    e. Since e_1 was chosen as the unique lowest weight edge among those belonging to exactly one of A and B, the weight of e_2 must be greater than the weight of e_1.
    f. As e_1 and e_2 are part of the cycle C, replacing e_2 with e_1 in B therefore yields a spanning tree with smaller weight.
    g. This contradicts the assumption that B is an MST.

    More generally, of the edge weights are all not distinct, then only the multi-set of weights in minimum spanning trees is certain to be unique; it is the same for all minimum spanning trees.

Minimum Cost Subgraph Property

If the weights are *positive*, then a minimum spanning tree is in fact a minimum cost subgraph connecting all vertexes, since subgraphs containing cycles necessarily have more total weight.

Cycle Property

1. Statement of the Cycle Property: For any cycle C in the graph, if the weight of an edge e in C is larger than the individual weights of all other edges of C, then this edge cannot belong to an MST.
2. Proof of the Cycle Property: Assume the contrary, i.e., that e belongs to an MST T_1. Then deleting e will break T_1 into two subtrees with two ends of e in different subtrees. The remainder of C connects the subtrees, hence there is an edge f of C in different subtrees, i.e., it reconnects subtrees into a tree T_2 with weight less than that of T_1, because the weight f is less than that of weight e.

Cut Property

1. Statement of the Cut Property: For any cut C of the graph, if the weight of an edge e in the cut-set C is strictly smaller than the weight of all other edges in the cut-set of C, then this edge belongs to all MST's of the graph.
2. Proof - Case of Single Minimum Edge: Assume that there is an MST T that does not contain e. Adding e to T will produce a cycle that crosses the cut once at e and crosses back another edge e'. Deleting e' produces a spanning tree $T \setminus \{e'\} \cup \{e\}$ of strictly smaller weight than T. This contradicts the assumption that T was an MST.
3. Extension to Multiple Maximum Edges: By a similar argument. If more than one is of the same weight across the cut, then such edge is contained in some minimum spanning tree.

Minimum-Cost Edge Property

1. Statement of the Property: If the minimum cost edge e of a graph is unique, then this edge is included in any MST.
2. Proof of the Statement: If e was not included in the MST, removing any of the larger cost edges in the cycle formed after adding e to the MST would yield a spanning tree of smaller weight.

Contraction Property

If T is a tree of MST edges, then T can be contracted into a single vertex while maintaining the invariant that the MST of the contracted graph plus T gives the MST of the graph before contraction (Pettie and Ramachandran (2002a)).

Algorithms

1. Classical MST Algorithm #1 – Boruvka: The first algorithm for finding a minimum spanning tree was developed by Otakar Boruvka. In each stage, called the *Boruvka step*, it identifies a forest F consisting of the minimum-weight edge incident to each vertex in the graph G, then forms the graph

$$G_1 = G \setminus F$$

as the input to the next step. Here $G \setminus F$ denotes the graph derived from G by contracting edges in F – by the cut property, these edges belong to the MST. Each Boruvka step takes linear time on m. Since the number of vertexes is reduced by at least half in each step, Boruvka's algorithm takes $\mathcal{O}(m \log n)$ time (Pettie and Ramachandran (2002a)).
2. Classical MST Algorithm #2 - Prim: A second algorithm is Prim's algorithm, which grows the MST T one edge at a time. Initially, T contains an arbitrary vertex. In each

step, T is augmented with the least-weight edge (x, y) such that x is in T and y is not in T. By the cut property, all edges added to T are in the MST. Its runtime is either $\mathcal{O}(m \log n)$ or $\mathcal{O}(m + n \log n)$, depending on the structure used.

3. <u>Classical MST Algorithm #3 - Kruskal</u>: The third algorithm commonly in use is the Kruskal's algorithm, which also takes $\mathcal{O}(m \log n)$ time.
4. <u>Classical MST Algorithm – Reverse-Delete</u>: A fourth algorithm, not as commonly used, is the reverse-delete algorithm, which is the reverse of the Kruskal's algorithm. Its runtime is $\mathcal{O}(m \log n\, [\log \log n]^3)$
5. <u>Greedy Algorithms with Polynomial Runtime</u>: All these four are greedy algorithm. Since they run in polynomial time, the problem of finding such trees is in **FP**, and related decision problems such as finding whether an edge is in the MST or determining if the total minimum weight exceeds a certain value are in **P**.

Faster Algorithms

1. <u>Hybrid Linear-Time Randomized Algorithm</u>: In a comparison model, in which only allowed operations on edge-weights are pair-wise comparisons, Karger, Klein, and Tarjan (1995) found a linear time randomized algorithm based on a combination of the Boruvka's algorithm and the reverse-delete algorithm (Pettie and Ramachandran (2002b)).
2. <u>Non-Randomized Comparison Based Algorithm</u>: The fastest randomized comparison-based algorithm with known complexity, by Chazelle (2000a, 2000b), is based on soft-heap, and approximate priority queue. It's running time is $\mathcal{O}\big(E\ \alpha(E, V)\big)$ where $\alpha(E, V)$ is the classical functional inverse of the Ackermann function. The function $\alpha(E, V)$ grows extremely slowly, so that for all practical purposes it may be considered a constant no greater than 4, thus Chazelle's algorithm takes very close to linear time.

Linear-Time Algorithms in Special Cases – Dense Graphs

If the graph is dense, i.e.,

$$\frac{m}{n} \geq \log \log \log n$$

then a deterministic algorithm by Fredman and Tarjan (1987) finds the MAST in time $\mathcal{O}(m)$. The algorithm executes in a number of phases. Each phase executes Prim's algorithm many times, each for a limited number of steps. The runtime for each phase is $\mathcal{O}(m + n)$. If the number of vertexes before a phase is n', then the number of phases remaining after a phase is at most $\frac{n'}{2^{\frac{m}{n'}}}$. Hence, at most $\log n$ phases are needed, which gives a linear runtime for dense graphs (Pettie and Ramachandran (2002a)). There are other algorithms that work in linear-time on dense graphs (Gabow, Galil, Spencer, and Tarjan (1986), Chazelle (2000b)).

Linear Time Algorithm – Integer Weights

If the edge weights are integers represented in binary, then deterministic algorithms are known that solve the problem in $\mathcal{O}(m + n)$ integer operations (Fredman and Willard (1994)). Whether the problem can be solved *deterministically* for a *general graph* in *linear time* by a comparison-based algorithm remains an open question.

Decision Trees

1. <u>Idea behind the Decision Tree</u>: Given graph G where the nodes and the edges are fixed but the weights are unknown, it is possible to construct a binary decision tree (DT) for calculating the MST for any permutation of weights. Each internal node of a

DT contains a comparison between two edges, i.e., “is the weight of the edge between x and y larger than that between w and z?” The two children of the node correspond to the two possible answers “yes” and “no”. In each leaf of the DT, there is a list of edges from G that correspond to an MST. The runtime complexity of the DT is the largest number of queries required to find the MST, which is just the depth of the DT. A DT for a graph G is called *optimal* if it has the smallest depth of all correct DT’s for G.

2. Steps for Determining Optimal Decision Trees: For every integer r, it is possible to find the optimal decision trees for all graphs on r vertexes by brute-force search. This search proceeds in two steps:
    a. Generate all potential DT’s
    b. Identify the correct DT’s
3. Generating all Potential DT’s:
    a. There are $2^{\binom{r}{2}}$ different graphs on r vertexes.
    b. For each graph an MST can always be found using $r(r-1)$ comparisons, e.g., by using Prim’s algorithm.
    c. Hence, the depth of an optimal DT is less than r^2.
    d. Hence, the number of internal nodes in an optimal DT is less than 2^{r^2}
    e. Every internal node compares two edges. The number of edges is at most r^2, so the different number of comparisons is at most r^4.
    f. Hence, the number of potential DT’s is less than

$$(r^4)^{2^{r^2}} = r^{2^{r^2+2}}$$

4. Identifying the correct Decision Trees: To check if a DT is correct, it must be checked on all possible permutations of the edge weights.
    a. The number of such permutations is at most $(r^2)!$
    b. For each permutation, the MST problem is solved on a given graph using any existing algorithm, and the result is compared to the answer given by the DT

c. The running time of any MST algorithm is at most r^2, so the total time required to check all permutations is at most $(r^2 + 1)!$

Hence the total time required for finding an optimal DT for *all* graphs with r vertexes is:

$$2^{\binom{r}{2}} \cdot r^{2^{r^2+2}} \cdot (r^2 + 1)! = 2^{2^{r^2+O(r)}}$$

(Pettie and Ramachandran (2002a)).

Optimal Algorithm

1. Provably Optimal Deterministic Comparison based MST: Pettie and Ramachandran (2002a) have constructed a provably optimal deterministic comparison based minimum spanning tree algorithm. The following is a simplified description of the algorithm steps:
2. Optimal Decision Trees on r Vertexes: Let

$$r = \log\log\log n$$

where n is the number of vertexes. Find all optimal decision trees on r vertexes. This can be done in $O(n)$ using the Decision Trees above.

3. Graph Partition - r Vertexes per Component: Partition the graph into components with at most r vertexes per each component. This partition uses a *soft heap*, which *corrupts* a small number of edges of the graph.
4. MST using DT in each Component: Use the optimal decision trees to find an MST for the uncorrupted subgraph within each component.
5. Contraction of the Connected Components: Contract each component spanned by the MST's to a single vertex, and apply any algorithm that works on dense graphs in time $O(m)$ to the contraction of the uncorrupted subgraph.

6. Adding back the Corrupted Edges: Add back the corrupted edges to the resulting forest to form the subgraph guaranteed to contain the minimum spanning tree, and smaller by a smaller factor than the starting graph. Apply the optimal algorithm recursively to this graph.
7. Runtime of the Algorithm: The runtime of all steps in the algorithm is $O(m)$, *except for the step of using decision trees*. The runtime of this step is not known, but is known to be optimal – no algorithm can do better than the optimal decision tree. Thus, this algorithm has a peculiar property that it is *provably optimal* although its runtime complexity is *unknown*.

Parallel and Distributed Algorithms

1. $O(\log n)$ Runtime in Parallel Environments: Research has also considered parallel algorithms for the MST problem. With a linear number of processors, it is possible to solve the problem in $O(\log n)$ time (Chong, Han, Tak (2001), Pettie and Ramachandran (2002c)). Bader and Cong (2006) demonstrate an algorithm that can compute the MST's 5 times faster on 8 processors than an optimized sequential algorithm.
2. Specialized Algorithms for Large Graphs: Other specialized algorithms have been designed for computing MST's of a graph so large that it must be stored on disk at all times. These *external storage* algorithms, for example described by Dementiev, Sanders, Schultes, and Sibeyn (2004), can operate, by the author's claims, as little as 2 to 5 times slower than a traditional in-memory algorithm. These rely on efficient external storage sorting algorithms and graph contraction techniques for reducing the graph's size efficiently.
3. Distributed Approaches for Calculating the MST: The problem can also be approached in a distributed manner. If each node is considered a computer and no node knows anything except its own connected links, one can still calculate the distributed MST.

MST on Complete Graphs

1. Complete Graphs with i.i.d. Weights: Alan M. Frieze showed that given a complete graph on n vertexes, with edge weights that are i.i.d. random variables with a distribution function F satisfying $F'(0) > 0$ then as n approaches $+\infty$ the expected weight of the MST approaches $\frac{\zeta(3)}{F\prime(0)}$, where ζ is Riemann Zeta function – more specifically, $\zeta(3)$ is the Apery's constant. Frieze and Steele also proved convergence in probability. Svante Janson proved a CLT for the weight of the MST.
2. MST Sizes for $U[0,1]$ Weights: For uniform random weights in $[0,1]$, the exact expected size of the MAST has been computed for small complete graphs (Steele (2002)).

Vertexes	Expected Size	Approximate Expected Size
2	$\frac{1}{2}$	0.5000000
3	$\frac{3}{4}$	0.7500000
4	$\frac{31}{35}$	0.8857143
5	$\frac{893}{924}$	0.9664502
6	$\frac{278}{273}$	1.0183151
7	$\frac{30739}{29172}$	1.0537160
8	$\frac{199462271}{184848378}$	1.0790588
9	$\frac{126510063932}{115228853025}$	1.0979027

Applications

1. Use in Network/Algorithm Construction: MST's have direct applications in the design of networks, including computer networks, telecommunication networks, transportation networks, water supply networks and electrical grids – which they were first invented for, as indicated above (Graham and Hell (1985)). They are invoked as sub-routines in algorithms for other problems, including the Christofides algorithm for approximating the traveling salesman problem (Christofides (1976)), approximating the multi-terminal minimum cut problem – which is equivalent in the single terminal case to the maximum flow problem (Dahlhaus, Johnson, Papadimitriou, Seymour, and Yannakakis (1994)), and approximating the minimum-cost weighted perfect matching (Supowit, Plaistead, and Reingold (1980)).
2. Practical Use of MSTs:
    a. Taxonomy (Sneath (1957))
    b. Cluster Analysis: Clustering points in the plane (Asano, Bhattacharya, Kiel, and Yao (1988)), single-linkage clustering – a method of hierarchical clustering (Gower and Ross (1969)), and clustering gene expression data (Paivinen (2005)).
    c. Constructing trees for broadcasting in computer networks (Dalal and Metcalfe (1978))
    d. Image Registration (Ma, Hero, Gorman, and Michel (2000)), and Segmentation (Felzenszwalb and Huttenlocher (2004))
    e. Curvilinear feature extraction in computer vision (Suk and Song (1984))
    f. Hand-writing Recognition of Mathematical Expressions (Tapia and Rojas (2004))
    g. Circuit Design – Implementing Efficient Multiple Constant Multiplications, as used in Finite Impulse Response Filters (Ohlsson (2004))

h. Regionalization of socio-geographic areas, the grouping of areas into homogenous, contiguous regions (Assuncao, Neves, Camara, and Da Costa Freitas (2006))
i. Comparing eco-toxicology data (Devillers and Doro (1989))
j. Topological Observability in Power Systems (Mori and Tsuzuki (1991))
k. Measuring Homogeneity of Two-dimensional Materials (Filliben, Kafadar, and Shier (1983))
l. Minimax Process Control (Kalaba (1963))
m. Minimum spanning trees can also be used to describe financial markets (Mantegna (1999), Djauhari and Gan (2015)). A correlation matrix can be created by calculating a coefficient of correlation between any two stocks. This matrix can be represented topologically as a complex network and an MST can be constructed to visualize relationships.

Related Problems

1. Subset Vertexes Steiner Tree: The problem of finding a Steiner tree of a subset of vertexes, that is, the minimum tree that spans a given subset, is known to be **NP**-complete (Garey and Johnson (1979)).
2. k-Minimum Spanning Tree: A related problem is the k minimum spanning tree (k-MST), which is the tree that spans some subset of k vertexes in a graph with minimum weight.
3. k Smallest Spanning Trees: A set of k *smallest spanning trees* is a subset of k spanning trees such that no spanning tree outside the subset has a smaller weight (Gabow (1997), Eppstein (1992), Frederickson (1997)). Note that this problem is unrelated to k minimum spanning tree.
4. Euclidean Minimum Spanning Tree: The Euclidean minimum spanning tree is a spanning tree of a graph with edge weights corresponding to the Euclidean distance between vertexes which are points in the plane – or space.

5. Rectilinear Minimum Spanning Tree: The rectilinear minimum spanning tree is a spanning tree of a graph with edge weights corresponding to the rectilinear distance between vertexes which are points in the plane – or space.
6. Distributed Minimum Spanning Tree: In the distributed model where each node is considered a computer and no node knows anything except its own connected links, one can consider distributed minimum spanning tree. The mathematical definition of the problem is the same, but there are different approaches for a solution.
7. Capacitated Minimum Spanning Tree: The capacitated minimum spanning tree is a tree that a marked node – origin, or root – and each of the subtrees attached to the node contains no more than c nodes. c is called the tree capacity. Solving the CMST optimally is **NP**-hard (Jothi and Raghavachari (2005)), but good heuristics such as Esau-Williams and Sharma produce solutions close to optimal in polynomial time.
8. Degree Constrained Minimum Spanning Tree: The degree constrained minimum spanning tress is a spanning tree in which each of the vertexes is connected to no more than d other vertexes for some given number d. The case $d = 2$ is a special case of traveling salesman problem, so the degree-constrained minimum spanning tree is **NP**-hard in general.
9. Directed Graph Minimum Spanning Tree: For directed graphs, the minimum spanning tree problem is called the Arboresence problem and can be solved in quadratic time using the Chu-Liu/Edmonds algorithm.
10. Maximum Spanning Tree: A *maximum spanning tree* is a spanning tree with weight greater than or equal to the weight of every other spanning tree. Such a tree can be found with algorithms such as Prim's or Kruskal's after multiplying the edge weights by -1 and solving the MST problem on the new graph. A path in the minimum spanning tree is the widest path in the graph between its two end-points; among all the possible paths, it maximizes the weight of the minimum-weight edge (Hu (1961)). Maximum spanning trees find applications in parsing algorithms for natural languages (McDonald, Pereira, Ribarov, and Hajic (2005)) and in training algorithms for conditional random fields.

11. Dynamic Minimum Spanning Tree: The *dynamic MST* problem concerns the update of a previously computed MST after an edge weight change in the original graph of the insertion/deletion of a vertex (Spira and Pan (1975), Chin and Houck (1978), Holm, de Lichtenberg, and Thorup (2001)).
12. Minimum Labeling Spanning Tree: The minimum labeling spanning tree problem is to find a spanning tree with the least type of labels if each edge in a graph is associated with a label from a finite label set instead of a weight (Chang and Leu (1997)).
13. Minimum Bottleneck Spanning Trees: A bottleneck is the highest weight edge in a spanning tree. A spanning tree is a *minimum bottleneck spanning tree* – or *MBST* – if the graph does not contain a spanning tree with a smaller bottleneck edge weight. An MST is necessarily an MBST – provable by the cut property – but an MBST is not necessarily an MST.

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Prim's Algorithm

Overview

1. Purpose of the Prim's Algorithm: Prim's algorithm – also known as Jarnik's algorithm – is a greedy algorithm that finds the minimum spanning tree for a weighted, undirected graph. This means that it finds the subset of the edges that form a tree that includes every vertex, where the total weight of all the edges in the tree is minimized. The algorithm operates by building this tree one vertex at a time, from an arbitrary starting vertex, at each step adding the cheapest possible connection from the tree to another vertex (Wikipedia (2019)).
2. Developers of the Algorithm: The algorithm was developed by the Czech mathematician Jarnik (1930) and later re-discovered and re-published by Prim (1957) and Dijkstra (1959). Therefore, it is also sometimes called the *Jarnik's algorithm* (Sedgewick and Wayne (2011)), *Prim-Dijkstra algorithm* (Cheriton and Tarjan (1976)), *Prim-Jarnik algorithm* (Rosen (2011)), or the *DJP algorithm* (Pettie and Ramachandran (2002)).
3. Comparison with Kruskal's and Boruvska's Algorithms: Other well-known algorithms for this problem include Kruskal's algorithm and Boruvska's algorithm (Tarjan (1983)). These algorithms find a minimum spanning forest in a possibly disconnected graph; in contrast, the most basic form of the Prim's algorithm only finds minimum spanning trees in connected graphs. However, by running Prim's algorithm separately for each connected component of the graph, it can also be used to find the minimum spanning forest (Kepner and Gilbert (2011)). In terms of their asymptotic time complexity, these three algorithms are equally fast for sparse graphs, but slower than other more sophisticated algorithms (Cheriton and Tarjan (1976), Pettie and Ramachandran (2002)). However, for graphs that are sufficiently dense,

Prim's algorithm can be made to run in linear time, meeting or improving the time bounds for other algorithms (Tarjan (1983)).

Description

1. Overview of the Algorithm Steps: The algorithm may be informally described as performing the following steps:
    a. Initialize a tree with a single vertex, chosen arbitrarily from the graph.
    b. Grow the tree by one edge. Of the edges that connect the tree to vertices not yet in the tree, find the minimum weight edge, and transfer it to the tree.
    c. Repeat the previous step until all the vertices are in the tree.

    In more detail, it may be implemented following the pseudocode below.
2. Initialization of Edges and Costs: Associate each vertex v of the graph with a number $C[v]$ - the cheapest cost of connection to v - and an edge $E[v]$ - the edge providing the cheapest connection. To initialize these values, set all values of $C[v]$ to $+\infty$ - or to any number larger than the maximum edge weight – and set each $E[v]$ to a special flag indicating that there is no edge connecting v to earlier vertices.
3. Initializing the Forest and the Vertices: Initialize an empty forest F and a set Q of vertices that have not yet been included in F – initially all vertices.
4. Iteration over the Queue Elements: Repeat the following steps until the Q is empty:
    a. Find and remove a vertex v from the Q having the minimum possible value of $C[v]$
    b. Add v to F and, if $E[v]$ is not the special flag value, also add $E[v]$ to F
    c. Loop over the edges vw connecting v to other vertices w. For each such edge, if w still belongs to Q and vw has a smaller weight than $C[w]$, perform the following steps:
        i. Set $C[w]$ to the cost of edge vw
        ii. Set $C[w]$ to point to edge vw
5. Retrieve the Forest containing the MST's: Return F

6. Starting Vertex for the Algorithm: As described above, the starting vertex for the algorithm will be chosen arbitrarily, because the first iteration of the main loop will have a set of vertices in Q that all the same weight, and the algorithm will automatically start a new tree in $F$when it completes the spanning tree of each connected component of the input graph. The algorithm may be modified to start with any particular vertex s by setting $C[s]$ to be a number smaller than other values of C – for instance, zero – and it may be modified to find only a single spanning tree rather than an entire spanning forest – matching more closest the informal description – by stopping whenever it encounters another vertex flagged as having no associated edge.
7. Choices for implementing the Queue: Different variations of the algorithm differ from each other in how the object Q is implemented: as a simple linked-list, as an array of vertexes, or as a more complicated priority queue data structure. The choices lead to differences in time complexity of the algorithm. In general, a priority queue will be much quicker at finding the vertex v with minimum cost, but will entail more expensive updates when the value of $C[v]$ changes.

Time Complexity

1. Determinants of the Time Complexity: The time complexity for the Prim's algorithm depends on the data structures used for the graphs and for ordering the edges by weight, which can be done using a priority queue. The table below shows the typical choices.
2. Table Time Complexity by Algorithm:

Minimum Edge Weight Data Structure	**Total Time Complexity**
Adjacency Matrix, Searching	$\mathcal{O}(\lvert V\rvert^2)$
Binary Heap and Adjacency List	$\mathcal{O}([\lvert V\rvert + \lvert E\rvert] \log\lvert V\rvert) = \mathcal{O}(\lvert E\rvert \log\lvert V\rvert)$
Fibonacci Heap and Adjacency List	$\mathcal{O}([\lvert E\rvert + \lvert V\rvert] \log\lvert V\rvert)$

3. Implementation using Adjacency Matrix/List: A simple implementation of Prim's, using an adjacency matrix or an adjacency list graph representation and linearly using an array of weights to find the minimum weight edge to add, requires $\mathcal{O}(|V|^2)$ running time. However, this running time can be greatly improved further by using heaps to implement finding minimum weight edges in the algorithm's inner loop.
4. Heap Based Edge Weight Ordering: A first improved version uses a heap to store all edges of the input graph, ordered by their weight. This leads to an $\mathcal{O}(|E|\log|E|)$ worst-case running time. But storing vertexes instead of edges can improve it still further. The heap should order their vertexes by their smallest edge weight that connects them to any vertex in a partially constructed minimum spanning tree (MST) – or ∞ if no such edge exists. Every time a vertex v is chosen and added to the MST, a decrease-key operation is performed on all vertexes w, setting the key to the minimum of its previous value and the edge cost of (v, w).
5. Impact of Denseness and Queue Implementation: Using a simple binary heap data structure, Prim's algorithm can be shown to run in time $\mathcal{O}(|E|\log|V|)$ where $|E|$ is the number of edges and $|V|$ is the number of vertexes. Using a more sophisticated Fibonacci heap, this can be brought down to $\mathcal{O}([|E| + |V|]\log|V|)$ which is asymptotically faster when the graph is dense enough that $|E|$ is $\omega(|V|)$, and linear time when is at least $\mathcal{O}(|V|\log|V|)$. For graphs of even greater density, having at least $|V|^c$ edges for some

$$c > 1$$

Prim's algorithm can be made to run in linear time even more simply, by using a d-ary heap in place of a Fibonacci heap (Johnson (1975), Tarjan (1983)).

Proof of Correctness

1. Basic Thrust of the Algorithm: Let $\boldsymbol{P}$ be a connected, weighted graph. At every iteration of Prim's algorithm, an edge must be found that connects a vertex in the subgraph to a vertex outside the subgraph. Since $\boldsymbol{P}$ is connected, there will always be a path to every vertex. The output Y of Prim's algorithm is a tree, because the edge and the vertex added to Y are connected.
2. An Alternate Minimum Spanning Tree: Let Y_1 be a minimum spanning tree of the graph $\boldsymbol{P}$. If

$$Y_1 = Y$$

   then Y is a minimum spanning tree. Otherwise, let e be the first edge added during the construction of tree Y that is not in Y_1, and let V be the set of vertexes connected by edges added before edge e. Then one endpoint of edge e is in set V and the other is not.
3. Differences between the Current and the Alternate MSTs: Since tree Y_1 is a spanning graph of $\boldsymbol{P}$, there is a path in tree Y_1 joining the two endpoints. As one travels along the path, one encounters an edge f joining as vertex in set V to one that is not in V. Now, at the iteration where edge e was added to tree Y, edge f could have also been added, and it would have been added instead of edge e if its weight was less than e. Since it was not added, it may be concluded that

$$w(f) \geq w(e)$$

4. Reconstructing Current from Alternate MST: Let tree Y_2 be a graph obtained by removing edge f and adding edge e to the tree Y_1. It is easy to show that tree Y_2 is connected, has the same number of edges as tree Y_1, and the total weight of its edges is not larger than that of tree Y_1, therefore it is also a minimum spanning tree of graph $\boldsymbol{P}$, and it contains e and all the edges added to before it during the construction of set V.

5. Metrics Comparison between the MSTs: On repeating the steps above, eventually a minimum spanning tree of graph $\boldsymbol{P}$ that is identical to tree Y is obtained. This shows that Y is a minimum spanning tree. The minimum spanning allows for the first subset of the first subregion to be expanded into a smaller subset X, which is assumed to be minimum.

Parallel Algorithm

1. Parallelizable Component of the Prim's Algorithm: The main loop pf the Prim's algorithm is inherently sequential and thus not parallelizable. However, the inner loop, which determines the next edge of the minimum weight that does not form a cycle, can be parallelized by dividing the vertexes and edges between the available processors (Grama, Gupta, Karypis, and Kumar (2003)). The pseudocode below demonstrates this.
2. Partition the Vertexes among the Processors: Assign each processor P_i a set V_i of consecutive vertexes of length $\frac{|V|}{|P|}$.
3. Dividing the Edges among the Processors: Create C, E, F, and Q as in the sequential algorithm above and divide C and E as well as the graph between all the processors such that each processor holds the incoming edges to its set of vertexes. Let C_i, E_i denote the parts of C and E stored on processor P_i.
4. Local Minimum Vertexes and their Eventual Union: Repeat the following steps until Q is empty:
    a. On every processor, find the vertex v_i having the minimum value in $C_i[v_i]$ - the local solution.
    b. Min-reduce the local solution to find the vertex v having the minimum possible value of $C[v]$ – the global solution.
    c. Broadcast the selected node to every processor.
    d. Add v to F, and if $E[v]$ is not special value flag, add $E[v]$ to F.

    e. On every processor, update C_i and E_i as in the sequential algorithm.

5. <u>Return the Forest containing the MSTs</u>: Return F.
6. <u>Performance of the Parallelized Version</u>: This algorithm can generally be implemented on a distributed machine (Grama, Gupta, Karypis, and Kumar (2003)) as well as on shared memory machines (Quinn and Deo (1984)). It has also been implemented in graphical processing units (GPUs) (Wang, Huang, and Guo (2011)). The running time is $\mathcal{O}\left(\frac{|V|^2}{|P|}\right) + \mathcal{O}(|V| \log|P|)$, assuming that the *reduce* and the *broadcast* operations can be performed in $\mathcal{O}(\log|P|)$ (Grama, Gupta, Karypis, and Kumar (2003)). A variant of the Prim's algorithm for shared memory machines, in which Prim's sequential algorithm is being run in parallel, starting from different vertexes, has also been explored (Setia, Nedunchezhian, and Balachandran (2015)). It should, however, be noted that more sophisticated algorithms exist to solve the distributed minimum spanning tree problem in a more efficient manner.

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Kruskal's Algorithm

Introduction

1. <u>Principal Idea behind Kruskal's Algorithm</u>: *Kruskal's algorithm* (Kruskal (1956), Wikipedia (2020)) is a minimum spanning tree algorithm which finds an edge of the least possible weight that connects any two trees in the forest (Cormen, Leiserson, Rivest, and Stein (2009)).It is a greedy algorithm in graph theory as it finds a minimum spanning tree for a connected, weighted graph adding increasing cost arc at each step. This means that it finds the subset of edges that forms a tree that includes every vertex, where the total weight of all the edges in the tree is minimized. If the graph is not connected, then it finds a *minimum spanning forest* – a minimum spanning tree for each component.
2. <u>Alternate Algorithms for Extracting MSFs</u>: Other algorithms for this problem include Prim's algorithm, reverse-delete algorithm, and Boruvka's algorithm.

The Algorithm

1. <u>Forest with Vertexes Per Tree</u>: Create a forest F - a set of trees – where each vertex in the graph is a separate tree.
2. <u>Set of all Graph Edges</u>: Create a set S containing all the edges in the graph.
3. <u>Edge-Based Processing and Tree Update</u>: While S is not empty and F is not yet spanning:
    a. Remove and edge with minimum weight from S
    b. If the removed edge connects two different trees, then add it to the forest F, combining the two trees into a single tree.

4. Minimum Spanning Tree and Forest: At the termination of the algorithm, the forest forms a set of minimum spanning trees of the graph. If the graph is connected, the forest has a single component, and forms a minimum spanning tree.

Complexity

1. Asymptotic Bounds Using $|E|/|V|$: Kruskal's algorithm can be shown to run in $\mathcal{O}(|E| \log|E|)$ or equivalently, in $\mathcal{O}(|E| \log|V|)$, where $|E|$ is the number of edges in the graph and $|V|$ is the number of vertexes, all using simple data structures. These running times are equivalent because:
    a. $|E|$ is at most $|V|^2$ and

    $$\log|V|^2 = 2\log|V|$$

    is $\mathcal{O}(\log|V|)$
    b. Each isolated vertex is a separate component of the minimum spanning forest. If one ignores isolated vertexes, one obtains

    $$|V| \le 2|E|$$

    so $\log|V|$ is $\mathcal{O}(\log|E|)$.
2. Rationale behind the Bound Estimate: This bound may be achieved as follows. First, sort the edges by weight using a comparison sort in $\mathcal{O}(|E| \log|E|)$ time; this allows the step that removes an edge with minimum weight from S to operate in constant time. Next, a disjoint-set data structure is used to keep track of which vertexes are in which components. This needs $\mathcal{O}(|V|)$ operations; since in each iteration where a vertex is connected to a spanning tree, two *find* operations and possibly one union for each edge are needed. Even a simple disjoint-set data structure such as disjoint set

forests with union by rank can perform $\mathcal{O}(|V|)$ operations in $\mathcal{O}(|V|\log|V|)$ time. Thus, the total time is

$$\mathcal{O}(|E|\log|E|) = \mathcal{O}(|E|\log|V|)$$

3. Sophisticated Disjoint Sets and Sorters: Provided that the edges are already sorted or can be sorted in linear time – for example, with counting sort or radix sort, the algorithm can use a more disjoint set data structure to run in $\mathcal{O}\big(|E|\alpha(|V|)\big)$, where α is an extremely slowly growing inverse of the single-valued Ackermann function.

Proof of Correctness

The proof consists of two parts. First, it is proved that the algorithm produces a spanning tree. Second, it is proved that the constructed tree is of minimal weight.

Spanning Tree

Let G be a connected, weighted graph, and Y be a subgraph produced by the algorithm. Y cannot have a cycle, being within one subtree and not between two different trees. Y cannot be disconnected, since the first encountered edge that joins the two components of Y would have been added by the algorithm. Thus Y is a spanning tree of G.

Minimality

1. Proposition: Existence of an MST: It may be shown, using induction, that the following proposition $\boldsymbol{P}$ by induction is true; if F is the set of edges at any stage in the algorithm, then there is some minimum spanning tree that contains F.

2. <u>Induction Proof - Validity at Start</u>: Clearly $\boldsymbol{P}$ is tree at the beginning when F is empty; any spanning tree will do, and there exists one, because a connected weighted graph always has a minimum spanning tree.
3. <u>Inductive Proof - Intermediate Stage Validity</u>: Now assume that $\boldsymbol{P}$ is true for some non-final edge state F and let T be a minimum spanning tree that contains F.
    a. If the next chosen edge e is also in T, then $\boldsymbol{P}$ is true for $F + e$.
    b. Otherwise, if e is not in T, then $T + e$ has a cycle C. This cycle contains edges that do not belong to F, since E does not form a cycle when added to F but does in T. Let f be an edge which is in C but not in $F + e$. Note that F also belongs to T, and by $\boldsymbol{P}$ has not been considered by the algorithm. f must therefore haver a weight at least a large as e. Then $T - f + e$ is a tree, and it has the same or less weight as T. So $T - f + e$ is a minimum spanning tree containing $F + e$ and again $\boldsymbol{P}$ holds.
4. <u>Completing the Inductive Proof</u>: Therefore, by the principle of induction, $\boldsymbol{P}$ holds when F has become a spanning tree, which is only possible if F is a minimum spanning tree itself.

Parallel Algorithm

1. <u>Strategies for Parallelizing the Algorithm</u>: Kruskal's algorithm is inherently sequential and hard to parallelize. It is, however, possible to perform the initial sorting of the edges in parallel, or alternatively, to use a parallel implementation of the binary heap to extract the minimum-weight edge in every iteration (Quinn and Deo (1984)). As parallel sorting is possible in time $\mathcal{O}(n)$ on $\mathcal{O}(\log n)$ processors (Grama, Gupta, Karypis, and Kumar (2003)), the runtime of the Kruskal's algorithm can be reduced to $\mathcal{O}\big(|E|\alpha(|V|)\big)$, where α is again the inverse of the single-valued Ackermann function.
2. <u>The Filter-Kruskal Parallel Version</u>: The variant of Kruskal's algorithm, named Filter-Kruskal, has been described by Osipov, Sanders, and Singler (2009) and is

better suited for parallelization. The basic idea behind Filter-Kruskal is to partition the edges in a way similar to quicksort and to filter out the edges that connect the vertexes of the same tree to reduce the cost of sorting.

3. Advantages of the Filter-Kruskal Scheme: Filter-Kruskal lends itself better for parallelization as sorting, filtering, and partitioning can be performed easily by distributing the edges between the processors (Osipov, Sanders, and Singler (2009)).
4. Other Approaches to Kruskal Parallelization: Finally, other variants of a parallel implementation of Kruskal's algorithm have been explored. Examples include a scheme to that uses helper threads to remove edges that are definitely not part of the MST in the background (Katsigiannis, Anastopoulos, Konstantinos, and Koziris (2012)), and a variant that runs the sequential algorithm in *p* subgraphs, and then merges those subgraphs until only one, the final MST, remains (Loncar, Skrbic, and Balaz (2014)).

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Boruvka’s Algorithm

Overview

1. Definition of Boruvka’s Algorithm: Boruvka’s algorithm is a greedy algorithm for finding a minimum spanning tree in a graph for which all edge weights are distinct, or a minimum spanning forest in case of a graph that is not connected (Wikipedia (2019)).
2. Principal Steps behind the Algorithm: The algorithm begins by finding the minimum-weight edge incident to each vertex of the graph, and adding all of the edges to the forest. Then, it repeats a similar process of finding the minimum-weight edges from each tree constructed so far to a different tree, and adding all of these edges to the forest. Each repetition of this process reduces the number of trees, within each connected component of the graph, to at most half of the former value, so after logarithmically many repetitions the process finishes. When it does, the set of edges it has added forms the minimum spanning forest.

Special Cases

If the edges do not have distinct weights, a consistent tie-breaking rule, i.e., breaking ties by the object identifiers of the edge, can be used. An optimization is to remove G from each edge that is found to connect two vertexes in the same component as each other.

Complexity

Boruvka's algorithm can be shown to take $O(\log V)$ iterations of the outer loop until it terminates, and therefore to run in time $O(E \log V)$. In planar graphs, and more generally in families of graphs closed under graph minor operations, it can be made to run in linear time, by removing all but the cheapest edge between each pair of components after each stage of the algorithm (Eppstein (1999), Mares (2004)).

Other Algorithms

1. Prim's and Kruskal's MST Algorithms: Other algorithms for this problem include Prim's algorithm and Kruskal's algorithm. Fast parallel algorithms can be obtained by combining Prim's algorithm with Boruvka's (Bader and Cong (2006)).
2. Fast Randomized and Deterministic Algorithms: A faster randomized MST algorithm based in part on Boruvka's algorithm dur to Karger, Klein, and Tarjan (1995) runs in $O(E)$ time. The best known minimum spanning tree algorithm by Chazelle (2000) is also based in part on Boruvka's and runs in $O\big(E\ \alpha(E, V)\big)$ time, where α is the inverse of the Ackermann's function. These randomized and deterministic algorithms combine steps of the Boruvka's algorithm, reducing the number of components that need to be connected, with steps of a different type that reduce the number of edges between pairs of components.

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Reverse-Delete Algorithm

Overview

1. Purpose of the Reverse-Delete Algorithm: The reverse-delete algorithm is an algorithm in graph theory used to obtain a minimum spanning tree from a given connected, edge-weighted graph. It first appeared in Kruskal (1956), but it should not be confused with the Kruskal algorithm, which appears in the same publication. If the graph is disconnected, the algorithm will find a minimum spanning tree for each disconnected part of the graph. The set of these minimum spanning trees is called a minimum spanning forest, which contains every vertex in the graph Wikipedia (2019)).
2. Greedy Nature of the Algorithm: The algorithm is a greedy algorithm. choosing the best choice given any situation. It is the reverse of Kruskal's algorithm, which is another greedy algorithm to find a minimum spanning tree. Kruskal's algorithm starts with an empty graph and adds edges while the reverse-delete algorithm starts from an empty graph and deletes edges from it.
3. Steps in Reverse-Delete Algorithm:
    a. Start with a graph G, which contains a list of edges E.
    b. Go through E in decreasing order of edge weights.
    c. For each edge, check if deleting the edges will further disconnect the graph.
    d. Perform any deletion that does not lead to additional disconnection.

Running Time

The algorithm can be shown to run in $\mathcal{O}(E \log V\,[\log\log V]^3)$ using the big-$\mathcal{O}$ notation, where E is then number of edges and V is the number of vertexes. This bound is achieved as follows:

a. Sorting the edges by weight using comparison sort takes $\mathcal{O}(E \log E)$ time, which can be simplified to $\mathcal{O}(E \log V)$ using the fact that the largest E can be is V^2.
b. There are E iterations in the loop.
c. Deleting an edge, checking the continuity in the resulting graph, and, if it is disconnected, re-inserting the edge, can be done in $\mathcal{O}(\log V\,[\log\log V]^3)$ time per operation (Thorup (2000)).

Proof of Correctness: Approach

The proof consists of two parts. First, it is proved that the edges that remain after the algorithm is applied form a spanning tree. Second, it is proved that the spanning tree is of minimal weight.

Proof of Correctness: Part One

The remaining subgraph g produced by the algorithm is not disconnected since the algorithm checks for that. The result subgraph cannot contain a cycle, since if it does, a move along the edges would encounter the maximum edge in the cycle and that would be deleted. Thus, g must be a spanning tree of the main graph G.

Proof of Correctness: Part Two

1. Inductive Proof for the Algorithm: This part shows that the following proposition $\boldsymbol{P}$ is true by induction; if F is the set of edges that remain at the end of the edge-removal loop, then there is some minimum spanning tree with edges that are a subset of F.
2. Starting Point for the Induction: Clearly $\boldsymbol{P}$ holds before the start of the edge-removal loop. Since a weighted, connected graph always has a minimum spanning tree, and since F contains all the edges of the graph, the minimum spanning tree must be a subset of F.
3. Validity for an Intermediate Edge Set: Assume $\boldsymbol{P}$ is true for some non-final edge set F and let T be a minimum spanning tree that is contained in F. It needs to be shown that, after deleting the edge e in the algorithm, there exists some - possible different – spanning tree T' that is a subset of F.
4. Edge not a Member of T: If the next deleted edge e does not belong to T, then

$$T = T'$$

   is a subset of F, and $\boldsymbol{P}$ continues to hold.
5. Edge a Member of T: Otherwise e belongs to T; first, note that the algorithm only removes edges that do not cause a disconnected ness in F. Thus, e does not cause disconnectedness. However, since e is a member of T, deleting e causes a disconnectedness in T. Assume that e separates T into subgraphs T_1 and T_2. Since the whole graph is connected after deleting e, there must exist another path between T_1 and T_2, there must exist a cycle C in F before removing e. There must be another edge in this cycle – call it f – that is not in T but is in F, since if all the cycle edges were in T, it would not be a tree anymore. The next step is to show that

$$T' = T - e + f$$

   is a minimum spanning tree that is a subset of F.
6. Proof that T' is Spanning: First, it is shown that T' is a *spanning tree*. It is clear that deleting an edge in the tree and adding another one does not cause a cycle, but instead

another tree with the same vertexes. Since T was a spanning tree, T' must also be a *spanning tree*, as adding f does not cause any cycles when e is removed.

7. Proof that T' is an MST: Second, it is shown that T' is a *minimum* spanning tree. In the treatment below, w is the weight function. There are three cases for the comparison between the weights of e and f.
    a. The case

    $$w(e) < w(f)$$

    is impossible, since this causes the weight of T' to be less than that of T, as it contradicts the notion that T is a minimum spanning tree.

    b. Likewise, it is impossible to have

    $$w(e) > w(f)$$

    since going through the edges in decreasing order of the edge weights would result in f being seen first. Since there is a cycle C, removing f would not cause any disconnectedness in F, so the algorithm would have removed it from F earlier. This would imply that f does not exist in F, which is a contradiction, since it has been proved earlier that f exists.

    c. Therefore,

    $$w(e) = w(f)$$

    so T' is also a *minimum* spanning tree, so $\boldsymbol{P}$ holds again.

8. Final Step of the Inductive Proof: As a result, $\boldsymbol{P}$ holds when the edge removal loop is completed, i.e., all the edges have been seen, proving that at the end F becomes a *spanning tree*. Since F must have a *minimum* spanning tree as its subset, F must be a *minimum spanning tree* itself.

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Breadth-first Search

Overview

1. Algorithm for Traversing a Graph: *Breadth-first search (BFS)* is an algorithm for traversing or searching a tree or a graph data structure. It starts at the tree root – or some arbitrary vertex of a graph, referred to as the search key – and explores all neighboring nodes at the present depth prior to moving onto the vertexes at the next depth level (Wikipedia (2020)).
2. Comparison to Depth-first Search: It uses the opposite strategy as depth-first search, which instead explores the vertexes as far as possible before being forced to backtrack and expand other nodes (Cormen, Leiserson, Rivest, and Stein (2009)).
3. Characteristics of the Algorithm:

Class	Search Algorithm
Data Structure	Graph
Worst-case Performance	$\mathcal{O}(\|V\| + \|E\|) = \mathcal{O}(b^d)$
Worst-case Space Complexity	$\mathcal{O}(\|V\|) = \mathcal{O}(b^d)$

Objective

1. Input: A *graph* and a *starting vertex root* of the graph
2. Output: The goal state. The *parent* link traces the shortest path back to the *root*.

Implementation

1. Similarity to Non-recursive DFS: This non-recursive implementation is similar to the non-recursive implementation of depth-first search, but differs from it in two ways:
    a. It uses a queue – First In First Out – instead of a stack, and
    b. It checks whether a vertex has been discovered before enqueueing the vertex rather than delaying this check until the vertex is dequeued from the queue.

    The queue contains the frontier along which the algorithm is currently searching.
2. Labeling Mechanism for Discovered Vertexes: Vertexes can be labeled as having been discovered by storing them in a set, or by an attribute in each vertex, depending on the implementation.
3. Parent Attribute of each Vertex: The *parent* attribute for each vertex is useful for accessing the vertexes in the shortest path, for example, by backtracking from the destination vertex up to the starting vertex once the BFS has been run, and the predecessor vertexes have been set.
4. Constructing the Breadth-first Tree: Breadth-first search produces a so-called *breadth-first tree*.

Time and Space Complexity Analysis

1. Time-complexity incurred by BFS: The time complexity can be expressed as $O(|V| + |E|)$, since every vertex and every edge will be explored in the worst-case. $|V|$ is the number of vertexes and $|E|$ is the number of edges in the graph. Note that $O(|E|)$ may vary between $O(1)$ and $O(|V|^2)$, depending upon how sparse the input is.
2. Space Complexity of BFS: When the number of vertexes in the graph is known ahead of time, and additional data structures have been used to determine which data structures have been already added to the queue, the space complexity can be expressed as $O(|V|)$ where $|V|$ is the cardinality of the set of vertexes. This is in

addition to the space required for the graph itself, which may vary depending on the graph representation used by an implementation of the algorithm.

3. Space Time Complexity for Large Graphs: When working with graphs that are too large to store explicitly – or infinite – it is more practical to describe the complexity of the breadth-first search in different terms; to find the number of vertexes d from the starting vertex – measured in terms of the number of edge traversals – BFS takes $\mathcal{O}(b^{d+1})$ time and memory, where b is the *branching factor* of the graph, the average out-degree (Russell and Norvig (1995)).

Completeness Analysis

1. Completeness in Infinite Graphs: In the analysis of the algorithm, the input to the BFS is assumed to be a finite graph, represented explicitly using an adjacency list or a similar representation. However, in application of graph traversal methods in artificial intelligence, the input may be an implicit representation of an infinite graph. In this context, a search method is described as being complete f it is guaranteed to find a goal state if one exists.
2. Completeness in BFS vs. DFS: Breadth-first search is complete, but depth-first search is not. When applied to infinite graphs represented implicitly, breadth-first search will eventually find the goal state, but depth first search may get lost in parts of the graph that have no goal state and never return (Coppin (2004)).

BFS Ordering

1. Enumeration of BFS Ordered Vertexes: An enumeration of the vertexes of a graph is said to be a BFS ordering if it is the possible output of the application of BFS to the graph.
2. Symbology for BFS Ordering Statement: Let

$$G = (V, E)$$

be a graph with n vertexes. Let $N(v)$ be the neighbors of v. Let

$$\sigma = (v_1, \cdots, v_m)$$

be a list of distinct elements of V. For

$$v \in V \setminus \{v_1, \cdots, v_m\}$$

let $\nu_\sigma(v)$ be the least i such that v_i is a neighbor of v, if such an i exists, and ∞ otherwise.

3. Formal Statement of BFS Enumeration: Let

$$\sigma = (v_1, \cdots, v_n)$$

be an enumeration of the vertexes of V. The enumeration σ is said to be a BFS ordering – with source v_1 – if, for all

$$1 < i \leq n$$

v_i is the vertex

$$w \in V \setminus \{v_1, \cdots, v_{i-1}\}$$

such that $\nu_{(v_1, \cdots, v_{i-1})}(w)$ is minimal. Equivalently, σ is a BFS ordering if, for all

$$1 \leq i < j < k \leq n$$

with

$$v_i \in N(v_k) \setminus N(v_j)$$

there exists a neighbor v_m of v_j such that

$$m < i$$

Applications

Breadth-first search can be used to solve many problems in graph theory, for example:

a. Copying garbage collection, Cheney's algorithm
b. Finding the shortest path between nodes v and u, with path length measured by the number of edges – an advantage over DFS (Aziz and Prakash (2010))
c. Reverse Cuthill-McKee mesh numbering
d. Ford-Fulkerson method for computing maximum flow in a flow network
e. Serialization/de-serialization of a binary tree vs. serialization in sorted order, allows the tree to be re-constructed in an efficient manner
f. Construction of the *failure function* of the Aho-Corasick pattern matcher
g. Testing bipartiteness of a graph

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Depth-first Search

Overview

1. Description of Depth-first Search: *Depth-first Search (DFS)* is an algorithm for searching tree or graph data structures. The algorithm starts at the root vertex – selecting some arbitrary vertex as a root vertex in the case of a graph – and explores as far as possible in each branch before backtracking (Wikipedia (2020)).
2. Tremaux Trees for Solving Mazes: A version of depth-first search was investigated by Charles Tremaux as a strategy for solving mazes (Sedgewick (2002), Even (2011)).

Properties

1. Characteristics of Depth-first Search:

Class	Search Algorithm
Data Structure	Graph
Worst-case Performance	$\mathcal{O}(\|V\| + \|E\|)$ for explicit graphs traversed without repetition, $\mathcal{O}(b^d)$ for implicit graphs with branching factor b searched to a depth d
Worst-case Space Complexity	$\mathcal{O}(\|V\|)$ if the entire graph is traversed without repetition $\mathcal{O}(Longest\ Path\ Length\ Searched) = \mathcal{O}(bd)$

	for implicit graphs without elimination of duplicate values

2. <u>Time/Space Analysis of DFS</u>: The time and the space analysis of DFS differs according to its application area. In theoretical computer science, DFS is typically used to traverse and entire graph, and takes time $\mathcal{O}(|V| + |E|)$ (Cormen, Leiserson, Rivest, and Stein (2009)); linear in the size of the graph. In these applications, it also uses space $\mathcal{O}(|V|)$ in the worst case to store the stack of vertexes in the current search path as well as the set of already visited vertexes. Thus, in this setting, the time and the space bound are the same as that for breadth-first search and the choice of which of these two algorithms to use depends less on their complexity and more on the different properties of the vertex orderings the two algorithms produce.
3. <u>Case of Large/Infinite Graphs</u>: For applications of DFS in relation to specific domains, such as searching for solutions in artificial intelligence or web crawling, the graph to be traversed is often either too large to be visited in its entirety, or infinite; DFS may suffer from non-termination. In such cases, the search is performed only to a limited depth; due to limited resources such as memory or disk space, one typically does not use data structures to keep track of the set of all previously visited vertexes.
4. <u>Limited Depth-Search Complexity Analysis</u>: When search is performed to a limited depth, the time is still linear in terms of the number of expanded vertexes and edges – although this number is not the same as the size of the entire graph because some vertexes may be searched more than once and the others not at all – but the space complexity for this version of DFS is only proportional to depth limit, and as a result, is much smaller than the space needed for searching to the same depth using breadth-first search. For such applications, DFS also lends itself much better to heuristic methods for choosing a likely-looking branch.
5. <u>Iterative Deepening Depth-first Search</u>: When an appropriate depth limit is not known a priori, iterative deepening depth-first search applies a DFS repeatedly with a sequence of increasing limits. In the artificial intelligence model of analysis, with a branching factor greater than one, iterative deepening increases the running time only

by a constant factor over the case in which the correct depth is known due to the geometric growth in the number of vertexes per level.

DFS Traversal

1. Output Search Tree from DFS: DFS may also be used to collect a sample of graph vertexes. However, incomplete DFS, similar to incomplete BFS, is biased towards vertexes of high degree.
2. Tremaux Tree and Iterative Deepening: The edges traversed from a DFS search form a Tremaux tree, a structure with important applications in graph theory. Performing the search without remembering previously remembered vertexes results in a cycle. Iterative deepening is one technique to avoid infinite loop and to reach all nodes.

Edges from a DFS Output

A convenient description of a DFS of a graph is in terms of the spanning tree of vertexes reached during the search. Based on this spanning tree, the edges from the original graph can be divided into three classes; *forward edges*, which point from the vertex of a tree to one of its descendants, *back edges*, which point from a vertex to one of the ancestors, and *cross edges*, which do neither. Sometimes *tree edges*, which belong to the spanning tree itself, are classified separately from forward edges. If the original graph is undirected, then all of its edges are tree edges or back edges.

Ordering of the DFS Output

1. Enumeration of the DFS Vertexes: An enumeration of the vertexes of a graph is said to be a DFS ordering if it is the possible output of the application of DFS to the graph.

2. <u>Symbology for BFS Ordering Statement</u>: Let

$$G = (V, E)$$

be a graph with n vertexes. Let

$$\sigma = (v_1, \cdots, v_m)$$

be a list of distinct elements of V. For

$$v \in V \setminus \{v_1, \cdots, v_m\}$$

let $\nu_\sigma(v)$ be the greatest i such that v_i is a neighbor of v, if such an i exists, and 0 otherwise.

3. <u>Formal Statement of BFS Enumeration</u>: Let

$$\sigma = (v_1, \cdots, v_n)$$

be an enumeration of the vertexes of V. The enumeration σ is said to be a DFS ordering – with source v_1 – if, for all

$$1 < i \leq n$$

v_i is the vertex

$$w \in V \setminus \{v_1, \cdots, v_{i-1}\}$$

such that $\nu_{(v_1, \cdots, v_{i-1})}(w)$ is maximal. Let $N(v)$ be the neighbors of v. Equivalently, σ is a BFS ordering if, for all

$$1 \leq i < j < k \leq n$$

with

$$v_i \in N(v_k) \setminus N(v_j)$$

there exists a neighbor v_m of v_j such that

$$i < m < j$$

Vertex Orderings

1. DFS Run Linear Vertex Ordering: It is possible to use depth-first search to linearly order the vertexes of a graph or tree. There are four possible ways of doing this.
2. Pre-Ordering: A *pre-ordering* is a list of vertexes in the order in which they were first visited by the DFS algorithm. This is a compact and a natural way of describing the progress of the search. A pre-ordering of an expression tree is the expression in Polish notation.
3. Post-Ordering: A *post-ordering* is a list of vertexes in the order that they were *last* visited by the algorithm. A post-ordering of an expression tree is the expression in reverse Polish notation.
4. Reverse Pre-ordering: A *reverse pre-ordering* is the reverse of a pre-ordering, i.e., a list of vertexes in the opposite order of their first visit. Reverse pre-ordering is not the same as post-ordering.
5. Reverse Post-ordering: A *reverse post-ordering* is the reverse of a post-ordering, i.e., a list of vertexes in the opposite order of their last visit. Reverse post-ordering is not the same as pre-ordering.
6. DFS Ordering for Binary Trees: For binary trees, there is additionally *in-ordering* and *reverse in-ordering*.

7. Topological Sorting of a DAG: Reverse post-ordering produces a topological sorting of any directed acyclic graph. The ordering is also useful in control-flow analysis as it often represents a natural linearization of the control flows.

Implementation

1. Input and Outputs of DFS:
    a. Input => A graph G and a vertex v of G
    b. Output => All vertexes reachable from v are labeled as discovered
2. Recursive and Non-recursive Implementations: The order in which the vertexes are discovered in the recursive DFS is called the lexicographic order (Goodrich and Tamassia (2001), Cormen, Leiserson, Rivest, and Stein (2009)). An example of non-recursive implementation of DFS with worst-case space complexity of $\mathcal{O}(|E|)$ is shown in Kleinberg and Tardos (2006).
3. Order of the Neighbors Processed: The recursive and the non-recursive variations of the DFS visit the neighbors of each vertex in the opposite order from each other: the first neighbor of v visited by the recursive variation is the first one in the list of adjacent edges, while in the non-recursive variation, the first visited neighbor is the last one in the list of adjacent edges.
4. Comparison between Non-recursive DFS and BFS: The non-recursive implementation is similar to BFS, but it differs from it in two ways:
    a. It uses a stack instead of a queue.
    b. It delays checking whether a vertex has been discovered until the vertex is popped from the stack rather than making this check before adding the vertex.

Applications

Applications the use DFS as a building block include:

a. Finding connected components.
b. Topological sorting.
c. Finding components connected by 2 edges or 2 vertexes.
d. Finding components connected by 3 edges or 3 vertexes.
e. Finding the bridges of a graph.
f. Generating the words in order to plot the limit set of a group.
g. Finding strongly connected components.
h. Planarity Testing (Hopcroft and Tarjan (1974), de Fraysseix, de Mendez, and Rosenstiehl (2006)).
i. Solving puzzles with only one solution, such as mazes. DFS can be adapted to find all solutions to a maze by including only vertexes in the current path in the visited set.
j. Maze generation using randomized DFS.
k. Finding bi-connectivity in graphs.

Complexity

1. Parallelizability of Recursive Lexicographic DFS: Given a graph G, let

$$O = (v_1, \cdots, v_n)$$

   be the ordering computed by the standard recursive DFS algorithm. Reif (1985) considered the complexity of computing this lexicographic depth-first search ordering from the graph, given a source. A decision version of the problem, i.e., testing whether some vertex u occurs before some vertex v in this order, is **P**-complete, meaning that it is a *nightmare for parallel processing* (Mehlhorn and Sanders (2008)).
2. DFS Parallelization using Randomization Algorithms: A depth-first search ordering – not necessarily the lexicographic one – can be computed by a randomized parallel

algorithm in the complexity class RNC (Aggarwal and Anderson (1988)). Until recently, it has remained unknown whether a DFS traversal could be constructed by a deterministic parallel algorithm, in the complexity class NC (Karger and Motwani (1997)).

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