Manual do Programador Competitivo

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Sumário

Prefácio

O objetivo deste livro é oferecer uma introdução completa à programação competitiva. É necessário que você já conheça os conceitos básicos de programação, mas não é preciso ter experiência prévia com programação competitiva.

O livro é especialmente destinado a estudantes que desejam aprender algoritmos e, possivelmente, participar da *International Olympiad in Informatics* (IOI) ou do *International Collegiate Programming Contest* (ICPC). No Brasil, a Olimpíada Brasileira de Informática (OBI) classifica para a IOI, e a Maratona de Programação da Sociedade Brasileira de Computação é a fase regional do ICPC. É claro que o livro também é adequado para qualquer pessoa interessada em programação competitiva.

Leva muito tempo para se tornar um bom programador competitivo, mas também é uma oportunidade para aprender muito. Você pode ter certeza de que o seu entendimento geral sobre algoritmos ficará muito melhor se dedicar um tempo para ler este livro, resolver problemas e participar de competições.

Esta tradução e o livro em si estão em constante desenvolvimento. Você pode enviar seu *feedback* da versão original do livro para `ahslaaks@cs.helsinki.fi`, ou enviar um *pull request* diretamente para fazer correções na tradução do livro.

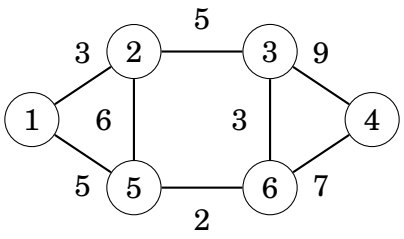
Helsinki, agosto de 2019
Antti Laaksonen

Capítulo 1

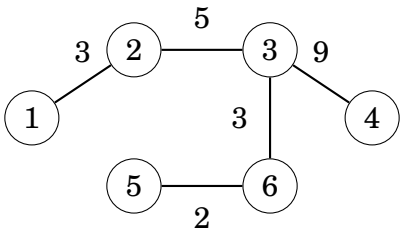
Árvores geradoras

Uma **árvore geradora** de um grafo é composta por todos os nós do grafo e por algumas de suas arestas, de forma que haja um caminho entre quaisquer dois nós. Assim como as árvores em geral, as árvores geradoras são conectadas e acíclicas. Normalmente, existem várias maneiras de construir uma árvore geradora.

Por exemplo, considere o seguinte grafo:

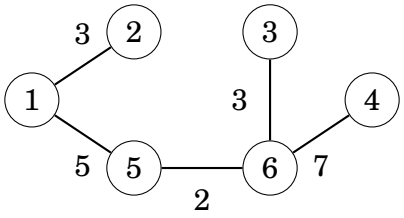


Uma árvore geradora para o grafo é a seguinte:

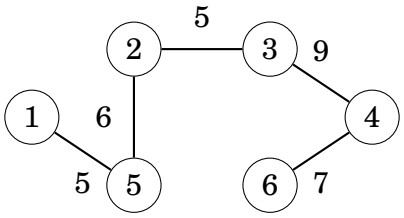


O peso de uma árvore geradora é a soma dos pesos de suas arestas. Por exemplo, o peso da árvore geradora acima é $3+5+9+3+2=22$.

A **minimum spanning tree** is a spanning tree whose weight is as small as possible. The weight of a minimum spanning tree for the example graph is 20, and such a tree can be constructed as follows:



In a similar way, a **maximum spanning tree** is a spanning tree whose weight is as large as possible. The weight of a maximum spanning tree for the example graph is 32:



Note that a graph may have several minimum and maximum spanning trees, so the trees are not unique.

It turns out that several greedy methods can be used to construct minimum and maximum spanning trees. In this chapter, we discuss two algorithms that process the edges of the graph ordered by their weights. We focus on finding minimum spanning trees, but the same algorithms can find maximum spanning trees by processing the edges in reverse order.

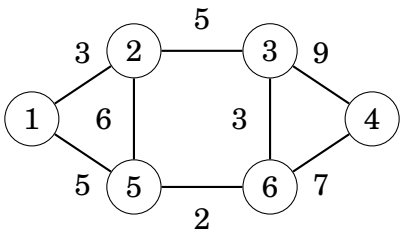
1.1 Kruskal's algorithm

In **Kruskal's algorithm**[1], the initial spanning tree only contains the nodes of the graph and does not contain any edges. Then the algorithm goes through the edges ordered by their weights, and always adds an edge to the tree if it does not create a cycle.

The algorithm maintains the components of the tree. Initially, each node of the graph belongs to a separate component. Always when an edge is added to the tree, two components are joined. Finally, all nodes belong to the same component, and a minimum spanning tree has been found.

Example

Let us consider how Kruskal's algorithm processes the following graph:



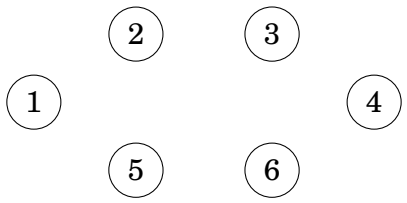
The first step of the algorithm is to sort the edges in increasing order of their weights. The result is the following list:

[1]The algorithm was published in 1956 by J. B. Kruskal [48].

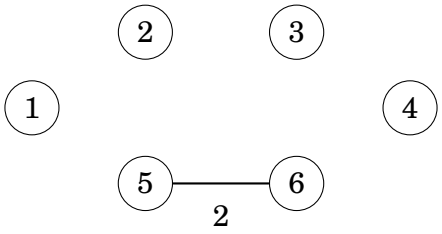
edge	weight
5–6	2
1–2	3
3–6	3
1–5	5
2–3	5
2–5	6
4–6	7
3–4	9

After this, the algorithm goes through the list and adds each edge to the tree if it joins two separate components.

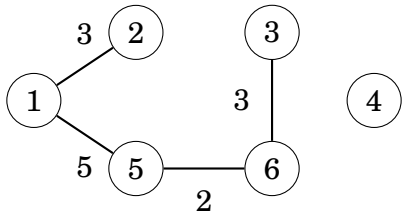
Initially, each node is in its own component:



The first edge to be added to the tree is the edge 5–6 that creates a component $\{5,6\}$ by joining the components $\{5\}$ and $\{6\}$:



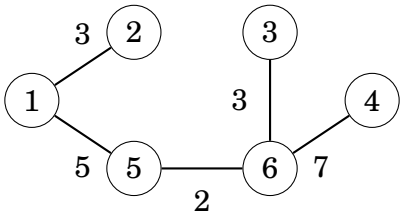
After this, the edges 1–2, 3–6 and 1–5 are added in a similar way:



After those steps, most components have been joined and there are two components in the tree: $\{1,2,3,5,6\}$ and $\{4\}$.

The next edge in the list is the edge 2–3, but it will not be included in the tree, because nodes 2 and 3 are already in the same component. For the same reason, the edge 2–5 will not be included in the tree.

Finally, the edge 4–6 will be included in the tree:

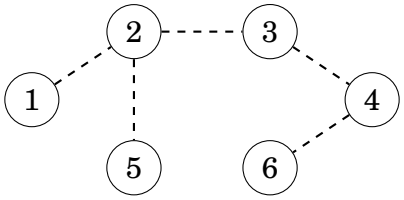


After this, the algorithm will not add any new edges, because the graph is connected and there is a path between any two nodes. The resulting graph is a minimum spanning tree with weight $2+3+3+5+7=20$.

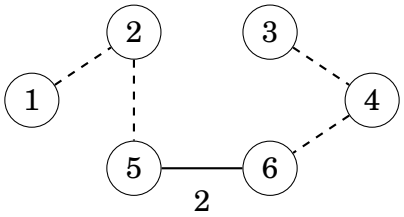
Why does this work?

It is a good question why Kruskal's algorithm works. Why does the greedy strategy guarantee that we will find a minimum spanning tree?

Let us see what happens if the minimum weight edge of the graph is *not* included in the spanning tree. For example, suppose that a spanning tree for the previous graph would not contain the minimum weight edge 5–6. We do not know the exact structure of such a spanning tree, but in any case it has to contain some edges. Assume that the tree would be as follows:



However, it is not possible that the above tree would be a minimum spanning tree for the graph. The reason for this is that we can remove an edge from the tree and replace it with the minimum weight edge 5–6. This produces a spanning tree whose weight is *smaller*:



For this reason, it is always optimal to include the minimum weight edge in the tree to produce a minimum spanning tree. Using a similar argument, we can show that it is also optimal to add the next edge in weight order to the tree, and so on. Hence, Kruskal's algorithm works correctly and always produces a minimum spanning tree.

Implementation

When implementing Kruskal's algorithm, it is convenient to use the edge list representation of the graph. The first phase of the algorithm sorts the edges in the list in $O(m \log m)$ time. After this, the second phase of the algorithm builds the minimum spanning tree as follows:

```
for (...) {
  if (!same(a,b)) unite(a,b);
}
```

The loop goes through the edges in the list and always processes an edge a–b where a and b are two nodes. Two functions are needed: the function `same` determines if a and b are in the same component, and the function `unite` joins the components that contain a and b.

The problem is how to efficiently implement the functions `same` and `unite`. One possibility is to implement the function `same` as a graph traversal and check if we can get from node a to node b. However, the time complexity of such a function would be $O(n+m)$ and the resulting algorithm would be slow, because the function `same` will be called for each edge in the graph.

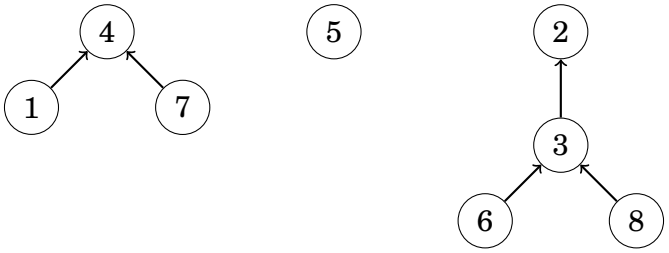
We will solve the problem using a union-find structure that implements both functions in $O(\log n)$ time. Thus, the time complexity of Kruskal's algorithm will be $O(m \log n)$ after sorting the edge list.

1.2 Union-find structure

A **union-find structure** maintains a collection of sets. The sets are disjoint, so no element belongs to more than one set. Two $O(\log n)$ time operations are supported: the `unite` operation joins two sets, and the `find` operation finds the representative of the set that contains a given element[2].

Structure

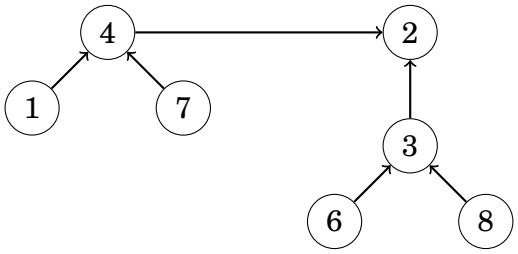
In a union-find structure, one element in each set is the representative of the set, and there is a chain from any other element of the set to the representative. For example, assume that the sets are $\{1,4,7\}$, $\{5\}$ and $\{2,3,6,8\}$:



[2]The structure presented here was introduced in 1971 by J. D. Hopcroft and J. D. Ullman [38]. Later, in 1975, R. E. Tarjan studied a more sophisticated variant of the structure [64] that is discussed in many algorithm textbooks nowadays.

In this case the representatives of the sets are 4, 5 and 2. We can find the representative of any element by following the chain that begins at the element. For example, the element 2 is the representative for the element 6, because we follow the chain $6 \rightarrow 3 \rightarrow 2$. Two elements belong to the same set exactly when their representatives are the same.

Two sets can be joined by connecting the representative of one set to the representative of the other set. For example, the sets $\{1,4,7\}$ and $\{2,3,6,8\}$ can be joined as follows:



The resulting set contains the elements $\{1,2,3,4,6,7,8\}$. From this on, the element 2 is the representative for the entire set and the old representative 4 points to the element 2.

The efficiency of the union-find structure depends on how the sets are joined. It turns out that we can follow a simple strategy: always connect the representative of the *smaller* set to the representative of the *larger* set (or if the sets are of equal size, we can make an arbitrary choice). Using this strategy, the length of any chain will be $O(\log n)$, so we can find the representative of any element efficiently by following the corresponding chain.

Implementation

The union-find structure can be implemented using arrays. In the following implementation, the array `link` contains for each element the next element in the chain or the element itself if it is a representative, and the array `size` indicates for each representative the size of the corresponding set.

Initially, each element belongs to a separate set:

```
for (int i = 1; i <= n; i++) link[i] = i;
for (int i = 1; i <= n; i++) size[i] = 1;
```

The function `find` returns the representative for an element x. The representative can be found by following the chain that begins at x.

```
int find(int x) {
    while (x != link[x]) x = link[x];
    return x;
}
```

The function `same` checks whether elements a and b belong to the same set. This can easily be done by using the function `find`:

```
bool same(int a, int b) {
    return find(a) == find(b);
}
```

The function `unite` joins the sets that contain elements a and b (the elements have to be in different sets). The function first finds the representatives of the sets and then connects the smaller set to the larger set.

```
void unite(int a, int b) {
    a = find(a);
    b = find(b);
    if (size[a] < size[b]) swap(a,b);
    size[a] += size[b];
    link[b] = a;
}
```

The time complexity of the function `find` is $O(\log n)$ assuming that the length of each chain is $O(\log n)$. In this case, the functions `same` and `unite` also work in $O(\log n)$ time. The function `unite` makes sure that the length of each chain is $O(\log n)$ by connecting the smaller set to the larger set.

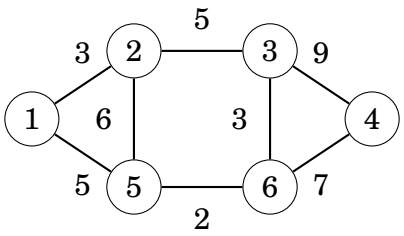
1.3 Prim's algorithm

Prim's algorithm[3] is an alternative method for finding a minimum spanning tree. The algorithm first adds an arbitrary node to the tree. After this, the algorithm always chooses a minimum-weight edge that adds a new node to the tree. Finally, all nodes have been added to the tree and a minimum spanning tree has been found.

Prim's algorithm resembles Dijkstra's algorithm. The difference is that Dijkstra's algorithm always selects an edge whose distance from the starting node is minimum, but Prim's algorithm simply selects the minimum weight edge that adds a new node to the tree.

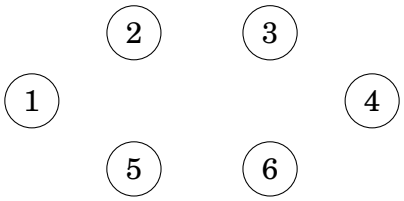
Example

Let us consider how Prim's algorithm works in the following graph:

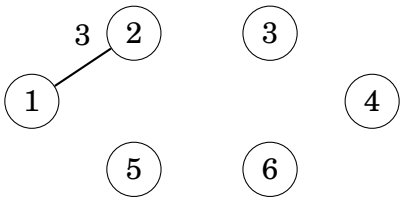


[3]The algorithm is named after R. C. Prim who published it in 1957 [54]. However, the same algorithm was discovered already in 1930 by V. Jarník.

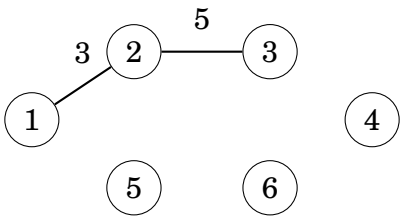
Initially, there are no edges between the nodes:



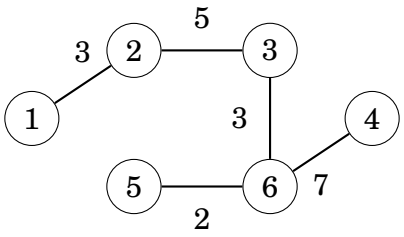
An arbitrary node can be the starting node, so let us choose node 1. First, we add node 2 that is connected by an edge of weight 3:



After this, there are two edges with weight 5, so we can add either node 3 or node 5 to the tree. Let us add node 3 first:



The process continues until all nodes have been included in the tree:



Implementation

Like Dijkstra's algorithm, Prim's algorithm can be efficiently implemented using a priority queue. The priority queue should contain all nodes that can be connected to the current component using a single edge, in increasing order of the weights of the corresponding edges.

The time complexity of Prim's algorithm is $O(n+m \log m)$ that equals the time complexity of Dijkstra's algorithm. In practice, Prim's and Kruskal's algorithms are both efficient, and the choice of the algorithm is a matter of taste. Still, most competitive programmers use Kruskal's algorithm.

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Índice Remissivo