

Competitive Programming Algorithms

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Chapter 1

Basic range queries

1.1 Types of range queries

Depending on the type of function whose value we have to calculate over the given range:

- *Idempotent functions.* These functions fulfill the following condition $f(f(x)) = f(x)$. For instance, the maximum and minimum of a list of values are idempotent. Furthermore, since the GCD and LCM can be seen as the “maximum” and the “minimum” of the exponents in the prime factorization, it is only natural that they fulfill the same property.

The most important property of these functions for range queries is that we can evaluate the elements of the range several times without affecting the result. For instance:

$$\min(a_l, \dots, a_r) = \min(\min(a_l, \dots, a_k), \min(a_k, \dots, a_r)) \quad l < k < r$$

even though the union of the intervals includes a_k twice. This is the property in which sparse tables are based.

- *Reversible functions.* Functions that have an inverse also have advantages in range queries. That is because we can easily remove elements from any range to obtain a smaller one. In these cases we can obtain the final range by adding and subtracting ranges that have been precalculated.

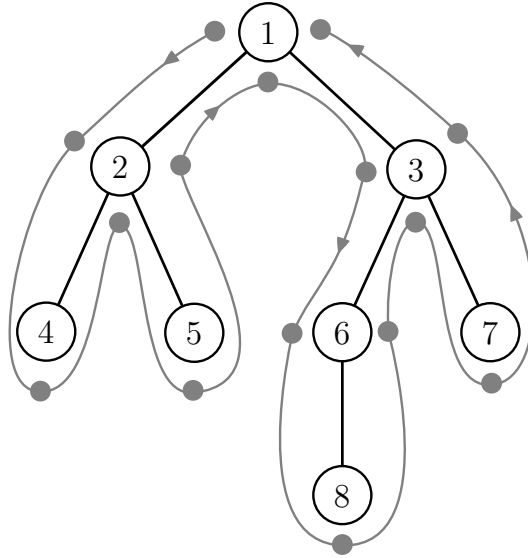
For instance, the addition, subtraction and xor operations have an inverse (subtraction, addition and xor respectively).

There are also other problems that can be transformed into a range query easily.

1.1.1 LCA using RMQ

To use this algorithm we need a rooted tree with undirected edges where the nodes are labeled in a particular order. Specifically, nodes at a greater depth have to be labeled with a greater value. Furthermore, the algorithm could be extended to process a forest (instead of a single tree) but this version cannot process forests.

We can traverse the tree using dfs and store in an array each node that we encounter. If we also keep track of the time at which each node was found for the first time, the LCA can be converted into calculating the minimum in an array of length $E + V$.



After running a DFS in the tree, we would get the following array of values and discovery times:

0	1	2	3	4	5	6	7	8	9	10	11	12	13	14
1	2	4	2	5	2	1	3	6	8	6	3	7	3	1

Node	Time	Node	Time
1	0	5	4
2	1	6	8
3	7	7	12
4	2	8	9

Now if we want to get the LCA between nodes 5 and 6, we have to obtain the minimum value in the range $[4, 8]$. As we can see, the result is obviously 1.

If we compare this approach to binary lifting, we observe that we have a considerably more expensive precalculation phase but, afterwards, answering any queries takes constant time instead of logarithmic time. In particular, the complexities for this method are:

- Precompute the values: $\mathcal{O}(E \log(E))$
- Calculate the LCA of a node: $\mathcal{O}(1)$
- Memory usage: $\mathcal{O}(E \log(E))$

Where $E = \text{edges}$.

1.2 Sparse table

The sparse table is a data structure that calculates the value of a function over a range of immutable elements with the following complexity:

- $\mathcal{O}(n \log n)$ to build the data structure
- $\mathcal{O}(1)$ to answer queries on a range.
- $\mathcal{O}(n \log n)$ memory

Furthermore, the function must be **idempotent**. This allows the use of overlapped intervals in the calculations. A Sparse Table can be adapted to answer queries with more general functions. However, it would lose the constant time query capabilities and would be no more efficient than a segment tree or a BIT.

On the other hand, the data structure is rather simple and its implementation is considerable shorter than any other alternatives.

The table consists of $\log n$ rows. Each one of them contains the value of the function in intervals of length 2^j where j is the row index. In particular, $\text{table}[j][i] = f([i, i + 2^j])$, where $f(I)$ is the value of f over all the elements in I .

To construct the table we take advantage of the fact that the intervals of each row are the exact union of two intervals of the previous row. Additionally, we have to create a lookup table for logarithms so that the queries can be processed fast enough. It is important to notice that if many sparse tables were to be constructed, it would be advisable to share the log array among them by populating it with all the values that might be needed initially or using a DP recursive approach.

1.2.1 Example

One of the best applications of the sparse table is to calculate the maximum of any range in an array of elements. The following illustration displays all the intervals that will be included in the sparse table. To avoid intersections, intervals that belong to the same level of the table may be displayed above or below each other.

In each interval, we can see both the index (top left corner) and the value of the maximum in that interval. It can also be seen that all intervals can be calculated using the values obtained in the previous level.

	0	1	2	3	4	5	6	7
array:	1	3	4	8	6	1	4	2
table[0]:	⁰ 1	¹ 3	² 4	³ 8	⁴ 6	⁵ 1	⁶ 4	⁷ 2
table[1]:	⁰ 3	² 8	⁴ 6	⁶ 4				
		¹ 4	³ 8	⁵ 4				
	⁰ 8			⁴ 6				
table[2]:		¹ 8						
			² 8					
				³ 8				
table[3]:	⁰ 8							

Now, if we want to calculate the maximum between indices 2 and 7 we will:

1. Calculate the length of the interval. In this case, $7 - 2 + 1 = 6$
2. Calculate the maximum value of k such that $2^k < 6$. In this case, $k = 2$.
3. Pick the interval that starts on 2 with length $2^k = 4$ and the interval that starts on $7 - 2^k + 1$ with the same length. That is to say, intervals 2 and 4 from level 2 of the table.

As we can see these intervals cover the entire range, albeit they overlap. However, the overlap does not affect the result of the maximum.

4. Take the maximum between the values of the two intervals selected: $\max(8, 6) = 8$

```

20 class SparseTable {
21 private:
22     vl logs;
23     vector<vl> table;
24     std::function<ll(ll, ll)> f;
25
26 public:
27     SparseTable(vl &data, std::function<ll(ll, ll)> f) : f(f) {
28         int n = data.size();
29         table.pb(data);
30         for (int j = 1; (1ll << j) ≤ n; ++j) {
31             vl nextRow(n);
32             for (int i = 0; i + (1ll << j) ≤ n; ++i) {
33                 int otherIndex = i + (1ll << (j - 1));
34                 nextRow[i] = f(table.back()[i], table.back()[otherIndex]);
35             }
36             table.push_back(std::move(nextRow));
37         }
38
39         logs = vl(n + 1, 0);
40         for (int i = 2; i ≤ n; ++i) {
41             logs[i] = logs[i / 2] + 1;
42         }
43     }
44
45     ll valueInRange(int left, int right) {
46         ll j = logs[right - left + 1];
47         ll intervalSize = 1ll << j;
48         return f(table[j][left], table[j][right - intervalSize + 1]);
49     }
50 };

```


1.2.2 Sparse Table (sort of) with $\mathcal{O}(n)$ memory

This variant of the sparse table is only capable of answering very specific queries. In particular, the operation must meet the following constraints:

- It is idempotent (as in a normal Sparse Table)
- The result of the operation over a range is an element in that range

Therefore, this data structure will mostly only be used for querying the maximum or the minimum over a range. On the other hand, we obtain a data structure that uses significantly less memory and can be built in considerably less time, albeit with slower queries.

Explanation

With that goal in mind, we will group the elements of the array in blocks. These blocks should be of size $\log(n)$. However, since n will never be larger than 2^{30} , we can set their size to 30. Now we will build two data structures:

- A Sparse Table where each element is a block of the array. In order to simplify this task, in the Sparse Table we will store the index of the result of applying the operation to the range instead of the result itself.

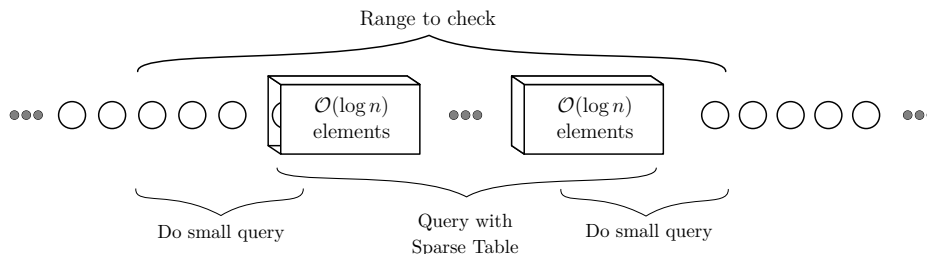
Therefore, the elements in the first row of the table will be the index of the result of applying the operation to each block of the array while the elements in the following layers will represent applying the operation to 2, 4, 8 ... blocks.

- A structure that stores the result for every range of 30 contiguous elements in the array.

If we have these two data structures we can split the (large) query into three subqueries that will most likely overlap. In particular, we will split the range $[l, r]$ into:

- A range of size 30 starting at l .
- The blocks that are fully contained within the interval.
- A range of size 30 that ends at r .

The middle range will be processed using the Sparse Table of blocks while the other two must be calculated using the new data structure.



In order to answer the small queries, we will use a bitmask for every position. That is to say, a vector of n integers where each of them is a bitmask for that position. Let's look at the bitmask of position r . The bit $r - k$, ($k < 30$) will be one iff that element is the result in the range $[r - k, r]$. For instance, at position 6 of this example array the bitmask would be: This bitmask approach is particularly useful because the vector of bitmasks can

	0	1	2	3	4	5	6
array:	1	4	2	6	7	4	5
mask:	1	0	1	0	0	1	1

be built in linear time. If we look at the code below (`build_mask()`), the `while` loop will only be executed at most once for every element while the `for` loop iterates through all elements exactly once.

```

20 class rmq {
21     vl data;
22     int n, rowSize;
23     vi mask, sparseTable;
24     static const int blockSize = 30;
25     std::function<ll(ll, ll)> f;
26
27 public:
28     rmq(const vl &v, decltype(f) function)
29         : data(v), n(v.size()), mask(n), sparseTable(n), f(function) {
30         rowSize = n / blockSize;
31         build_mask();
32         build_sparse_table();
33     }
34
35     ll query(int l, int r) {
36         // Small query
37         if (r - l + 1 ≤ blockSize) {
38             return data[small_query_index(r, r - l + 1)];
39         }
40
41         // Get the result for the endpoints
42         int ans =
43             op(small_query_index(l + blockSize - 1), small_query_index(r));
44
45         // Query the sparse table
46         int x = l / blockSize + 1, y = r / blockSize - 1;
47
48         if (x ≤ y) {
49             // Row to query
50             int j = msb_index(y - x + 1);
51

```

```

52         ans = op(ans, op(sparseTable[rowSize * j + x],
53                           sparseTable[rowSize * j + y - (1 << j) + 1]));
54     }
55     return data[ans];
56 }
57
58 private:
59     static int lsb(int x) { return x & -x; }
60     static int msb_index(int x) { return __builtin_clz(1) - __builtin_clz(x); }
61
62     // Get the index that contains the answer for the small query
63     int small_query_index(int r, int size = blockSize) {
64         int dist_from_r = msb_index(mask[r] & ((1 << size) - 1));
65
66         return r - dist_from_r;
67     }
68
69     // Return the index that contains the result of the operation
70     int op(int index1, int index2) {
71         return f(data[index1], data[index2]) = data[index1] ? index1 : index2;
72     }
73
74     void build_mask() {
75         int current_mask = 0;
76         // We use this mask so that we only keep track of the at most
77         // the size of the block bits
78         int discard_mask = (1 << blockSize) - 1;
79         for (int i = 0; i < n; ++i) {
80             current_mask = (current_mask << 1) & discard_mask;
81
82             while (current_mask > 0 &&
83                    op(i, i - msb_index(lsb(current_mask))) == i) {
84                 // Current value is smaller than the value represented by the
85                 // last 1 in curr_mask, so that bit should be off
86                 current_mask ^= lsb(current_mask);
87             }
88             current_mask |= 1;
89             mask[i] = current_mask;
90         }
91     }
92
93     void build_sparse_table() {
94         // Fill first row
95         for (int i = 0; i < rowSize; ++i) {
96             sparseTable[i] = small_query_index(blockSize * (i + 1) - 1);
97         }
98         for (int j = 1; (1 << j) <= rowSize; ++j) {
99             for (int i = 0; i + (1 << j) <= rowSize; ++i) {

```

```

99         int previousStep = 1 << (j - 1);
100         sparseTable[rowSize * j + i] =
101             op(sparseTable[rowSize * (j - 1) + i],
102               sparseTable[rowSize * (j - 1) + i + previousStep]);
103     }
104 }
105 }
106 };

```

1.3 Fenwick tree (BIT)

A Fenwick tree or binary indexed tree (BIT) can be used to calculate the value of a **reversible** function F over a range of values. Given an array of elements A of size N :

- Given a range $[l, r]$, the value $F(a_l, \dots, a_r)$ can be calculated in $\mathcal{O}(\log n)$
- Updating one of the values of the array takes $\mathcal{O}(\log n)$
- Requires the same amount of memory as the array A

To do so, we create a new array `ft` where each element represents the value of the function over a particular range. Let $\text{LSOne}(i)$ be the result of setting to 0 all bits of i except for the least significant one. For instance, $\text{LSOne}(0110) = 0010$. Then, the i -th element of `ft` contains the value $F(a_{i-\text{LSOne}(i)+1}, \dots, a_i)$.

In most cases, F will be the sum of all elements $F(a_l, \dots, a_r) = \sum_l^r a_i$. In that case, `ft[i]` contains the sum of all the elements from position $i - \text{LSOne}(i)$ (excluded) to position i (included).

It is also important to note that this BIT is **1-indexed internally** to simplify slightly the implementation. However, the interface automatically subtracts one to all index parameters given.

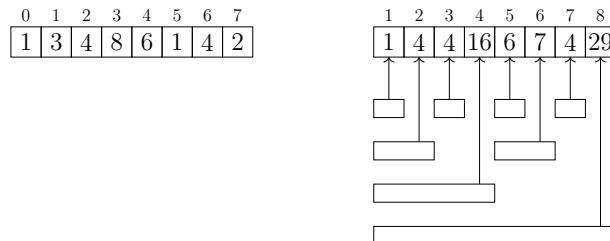
Range Update and Point Query

The standard BIT allows point update and range query. Using a difference array, we can transform them into range update and point query. If B is the difference array of A , the elements of B are defined as: $b_i = a_i - a_{i-1}$ and $b_1 = a_1$. Therefore:

- $\sum_1^i b_j = a_i$, converting the range query into a point query
- To update the elements in the range $[l, r]$ by d , we can add d to the l -th element and subtract d from the r -th element. In doing so, queries that reach until a point between l and r will be increased by d but queries that reach further will not be affected. Therefore we have converted two point updates into a range update.

Example

For instance, if we use the addition operation, array on the left would be processed into the BIT tree displayed on the right. Each box under the BIT tree represents the elements that are added to get the value of that position.



```

20 // Return lsb
21 int LSONe(int a) {
22     return a & (-a);
23 }
24
25 template <typename T>
26 class FenwickTree {
27 private:
28     vector<T> ft;
29
30 public:
31     FenwickTree(const vector<T> &data)
32         : ft(data.size() + 1, 0) {
33         for (int i = 0; i < data.size(); ++i) {
34             adjust(i, data[i]);
35         }
36     }
37
38     //RSQ in range [0, index]
39     T rsq(int index) {
40         index++;
41         T sum = 0;
42         while (index != 0) {
43             sum += ft[index];
44             index -= LSONe(index); // Delete the lsb
45         }
46         return sum;
47     }
48     //RSQ in range [begin, end]
49     T rsq(int begin, int end) {
50         return begin == 0 ? rsq(end) : rsq(end) - rsq(begin - 1);
51     }
52
53     // Add the delta to the index element
54     void adjust(int index, T delta) {
55         index++;
56         while (index < ft.size()) {
57             ft[index] += delta;
58             index += LSONe(index);
59         }
60     }
61 };

```

Chapter 2

Graphs

2.1 Dijkstra's

Shortest path from `orig` node to `dest` (or to every node) in a graph that does not contain negative edges. It chooses the best path greedily in each iteration and, therefore, it only works on graphs without negative weights.

```
20 int dijkstra(int orig, int dest, vector<vector<pii>> &graph) {
21     vi dists(graph.size(), INT_MAX / 10);
22     priority_queue<pii, vector<pii>, greater<pii>> q;
23
24     q.push({0, orig});
25     dists[orig] = 0;
26     while (!q.empty()) {
27         auto a = q.top();
28         q.pop();
29         if (a.se == dest) { // If we already reached the destination
30             return a.fi;
31         }
32         if (dists[a.se] != a.fi) { // If we have found a better option
33             continue;
34         }
35         for (auto b : graph[a.se]) { // Else iterate through the edges
36             if (dists[b.fi] > dists[a.se] + b.se) {
37                 dists[b.fi] = dists[a.se] + b.se;
38                 q.push({dists[b.fi], b.fi});
39             }
40         }
41     }
42     return dists[dest];
43 }
```

Running time: $\mathcal{O}(E + V \log V)$
(V = vertices, E = edges)

Remarks

- If we ignore the check in line 30, we can return the distances vector, which will contain the shortest distance from `dist` to every other node.
- If we are doing some kind of pruning it is imperative that we prune as many branches as possible in the main loop. That is to say, we should introduce as many `if` statements in line 36 to make sure that we run the `for` loop as few times as possible.

An example of this approach is problem [UVA-11635](#). In that problem, we add a lot of branches to the queue (we may run the `for` loop twice in some nodes) but we prune them in the main loop. Thus the running time is still acceptable.

- However, pruning the branches with a higher cost can be quite complicated when we have to optimize several factors (see section 2.1.1). Therefore, we will omit the check in line 33 if we think it might discard relevant options.

2.1.1 Dijkstra with cost and distance

In this problem we are going to define two values for each edge, cost and distance:

- *Cost*. This is the number that we want to minimize. It is the equivalent to the usual cost in a normal Dijkstra problem
- *Distance*. We define the distance of a path as the sum of the distances of the edges in it. And the distance of the path from source to destination cannot exceed a given limit (B)

This problem can be solved with a slightly modified version of Dijkstra's:

```
20 int B;
21 using pii = pair<int, pii>;
22 vector<vector<pii>> adyList; //destination, cost, distance
23 ll dijkstra(int orig, int dest) {
24     vi distances(adyList.size(), iinf);
25     priority_queue<pii, vector<pii>, greater<pii>> q; //cost,node,dist
26
27     distances[orig] = 0;
28     q.push({orig, {0, 0}});
29
30     while (!q.empty()) {
31         auto a = q.top();
32         q.pop();
33
34         if (a.se.fi == dest) {
35             return a.fi;
36         }
37         distances[a.se.fi] = a.se.se;
38
39         for (auto b : adyList[a.se.fi]) {
40             if ((a.se.se + b.se.se < distances[b.fi]) ) {
41                 q.push({a.fi + b.se.fi, {b.fi, a.se.se + b.se.se}});
42             }
43         }
44     }
45     return -1;
46 }
```

Running time: $\mathcal{O}(B \cdot (V + E \log E))$

(V = vertices, E = edges, B = max_distance)

In this algorithm, we will process each node at most B times. Furthermore, if we process a node with a cost c and a distance d , we know that this is the best possible cost for that distance d since all the nodes in the queue have a higher cost already. Therefore, we can close the node for that particular distance value (line 37).

An example of this algorithm is [SWERC-19_20-A](#)

2.2 Bellman Ford's

Shortest path from `orig` to every other node. It is slower than Dijkstra but it works on graphs with negative weights.

This algorithm works by trying to relax every edge $V - 1$ times. If there are no negative cycles, after $V - 1$ iterations, we must have found the minimum distance to every node. Therefore if after these iterations, we run another iteration and the distance to a node decreases, we must have a negative cycle.

```
20 vi bellmanFord(int orig, vector<pair<pii, int>> edges, int n) {
21     vi dist(n, INT_MAX / 10);
22     dist[orig] = 0;
23     for (int i = 0; i < n - 1; ++i) {
24         for (auto e : edges) {
25             dist[e.fi.se] = min(dist[e.fi.se], dist[e.fi.fi] + e.se);
26         }
27     }
28     // dist[i] contains the shortest path from 0 to i
29
30     //We can now check for a negative cycle
31     bool negativeCycle = false;
32     for (auto e : edges) {
33         if (dist[e.fi.se] > min(dist[e.fi.se], dist[e.fi.fi] + e.se)) {
34             negativeCycle = true;
35         }
36     }
37     return dist;
38 }
```

Running time: $\mathcal{O}(VE)$

(V = vertices, E = edges)

Remarks

- If we keep track of the distance that decrease when we check for a negative cycle, we will get at least one node of every negative cycle present in the graph.

We can use this, for instance, to check if we can reach a node with a cost smaller than a given bound. If it is connected to a node in a negative cycle, it's distance will be as small as we want it to be (by looping in the cycle).

This can be seen at play in [UVA-10557](#)

- If we modify slightly the main loop, iteration i will be the result of considering paths of at most $i + 1$ edges:

```

1  for (int i = 0; i < n - 1; ++i) {
2      for (auto e : edges) {
3          dists2[e.fi.se] = min(dists2[e.fi.se], dists[e.fi.fi] + e.se);
4      }
5      dists = dists2;
6  }

```

This can be seen at play in UVA-11280

2.3 Warshall's

Warshall's algorithm solves the APSP (All pairs shortest path) using DP. Each iteration of the outer loop tries to add a node (the k -th node in particular) to the path between all pairs of nodes. We can think of the comparison as:

Is the path from i to j shorter if we first move from i to k and, then, from k to j ?

It is important to note that we must use an adjacency matrix in this implementation.

```

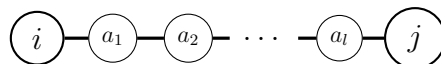
20 void warshall(int n) {
21     for (int k = 0; k < n; ++k) {
22         for (int i = 0; i < n; ++i) {
23             for (int j = 0; j < n; ++j) {
24                 adyMat[i][j] = min(adyMat[i][j], adyMat[i][k] + adyMat[k][j]);
25             }
26         }
27     }
28 }

```

Running time: $\mathcal{O}(V^3)$
(V = vertices, E = edges)

Obtaining the path

To get the explicit path, we will store the last vertex in the path that the algorithm found to go from i to j . That is to say, after a given iteration the optimal path from i to j is: Then



we should store that the last node in the path that goes from i to j is a_j . The code to do so is the following:

```

20 ll lastInPath[lim][lim];
21
22 void warshall(int n) {
23     for (int k = 0; k < n; ++k) {
24         for (int i = 0; i < n; ++i) {
25             for (int j = 0; j < n; ++j) {
26                 if (adList[i][j] > adList[i][k] + adList[k][j]) {
27                     adList[i][j] = adList[i][k] + adList[k][j];
28                     lastInPath[i][j] = lastInPath[k][j];
29                 }
30             }
31         }
32     }
33 }
34
35 // Give an empty vector
36 void getPath(int i, int j, vector<int> &path) {
37     if (i != j) {
38         getPath(i, lastInPath[i][j], path);
39         path.push_back(j);
40     }
41 }

```

2.4 DFS

2.4.1 Articulation points and bridges

These algorithms can be used in undirected graphs, and we will use the following definitions:

- **Articulation point.** A node whose removal would increase the number of connected components of the graph. That is to say that it “splits” a connected component.
- **Bridge.** An edge whose removal increases the number of connected components in the graph.

We will use a modified version of DFS to solve this problem. We mainly introduce two new properties for every node:

- **num.** Time at which the node was first explored by DFS
- **low.** Earliest node that can be found in the DFS spanning tree that starts from this node

When we visit a node, for every edge, there are two options:

- **Tree edge.** This edge points to a node that has not been discovered yet. As such we explore it (calling `dfs`) and, we update the value of `low` for the current node.
After the update, we can now process the child since we will not visit it again and its DFS tree has been fully explored
- **Back edge.** This edge points to a node that has already been visited. Therefore, it will have a relatively low `num` and we use it to update the `low` value of the current node

```

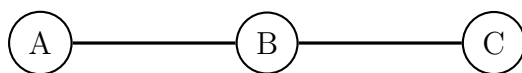
20 vector<vi> adyList; // Graph
21 vi num, low;      // num and low for DFS
22 int cnt;          // Counter for DFS
23 int root, rchild; // Root and number of (DFS) children
24 vi artic;         // Contains the articulation points at the end
25 set<pii> bridges; // Contains the bridges at the end
26
27 void dfs(int nparent, int nnode) {
28     num[nnode] = low[nnode] = cnt++;
29     rchild += (nparent == root);
30
31     for (auto a : adyList[nnode]) {
32         if (num[a] == -1) { // Tree edge
33             dfs(nnode, a);
34             low[nnode] = min(low[nnode], low[a]);
35
36             if (low[a] ≥ num[nnode]) {
37                 artic[nnode] = true;
38             }
39
40             if (low[a] > num[nnode]) {
41                 bridges.insert((nnode < a) ? mp(nnode, a) : mp(a, nnode));
42             }
43         } else if (a ≠ nparent) { // Back edge
44             low[nnode] = min(low[nnode], num[a]);
45         }
46     }
47 }
48 void findArticulations(int n) {
49     cnt = 0;
50     low = num = vi(n, -1);
51     artic = vi(n, 0);
52     bridges.clear();
53
54     for (int i = 0; i < n; ++i) {
55         if (num[i] ≠ -1) {
56             continue;
57         }
58         root = i;
59         rchild = 0;
60         dfs(-1, i);
61         artic[root] = rchild > 1; //Special case
62     }
63 }

```

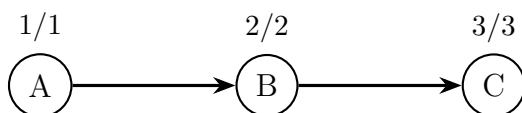
Running time: $\mathcal{O}(V + E)$
(V = vertices, E = edges)

Explanation

The first graph that we will consider is the following: After applying DFS on A we get the



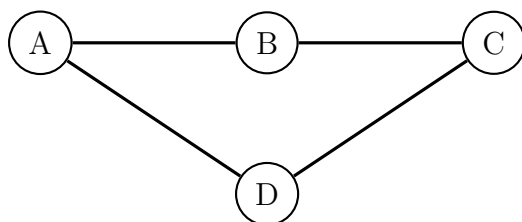
following DFS spanning tree. Above every node, we have included num / low .



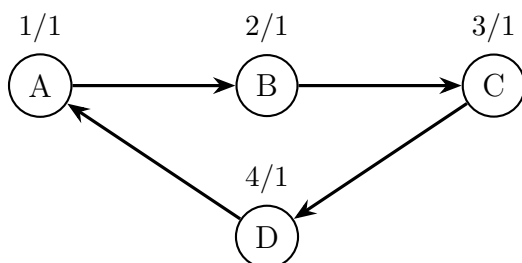
This is a rather simple graph and its only articulation point is B . This is because it has a child whose low value is greater than or equal to B 's num value. Therefore, there is no connection from that child (namely C) to a node explored before B that does not go through B .

However, we can already see that the root has to be treated as a separate case. The root will be an articulation point iff it has more than one child in its DFS tree. It is important to note that the children of the DFS tree need not be the same as the children of the root in the initial graph.

Let's look at another example



As before, we show the DFS spanning tree:



Now we have no articulation point since there is no node that has a child with a low greater than or equal than the parent's num . This difference is caused by the fact that now there is an edge that makes C accessible through a path that does not involve traversing B .

In this case, we can see how the root has only one child in the spanning tree but two in the initial graph. This reflects the fact that those numbers need not coincide.

Finally, the condition for a bridge is: $\text{low}[\text{child}] > \text{num}[\text{parent}]$. This is equivalent to stating that the child has no other way of reaching either the parent or a node that was explored before the parent

2.4.2 Trajan's algorithm for strongly connected components

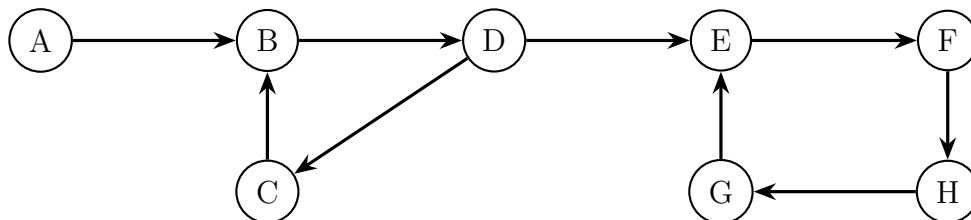
In a directed graph, we say that a subset of vertices comprises a strongly connected component if every vertex is reachable from every other vertex in this subset.

We will now present an algorithm that divides the graph into strongly connected parts that are as large as possible. It will use some of the same concepts as in the previous section.

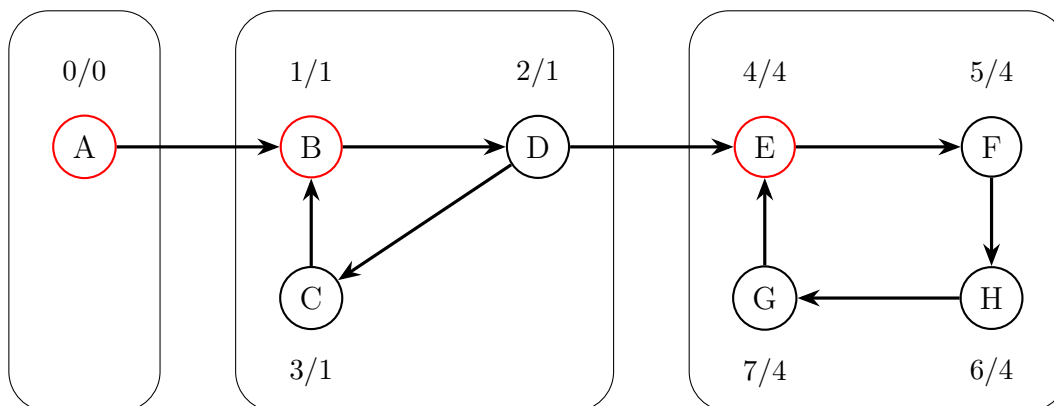
Explanation

The main idea is the following: if when we are done with a node, we have not been able to reach a node that was further back, this one is the root of a SCC.

Let's explain this reasoning with an example:



And, after running DFS, we would get the following spanning tree with three SCCs.



Let's look at the moment in which we close node F . As we can see the low value is lower than the num . Therefore, there is a connection from F to another node that was visited before and it will be a part of the SCC "generated" by that node.

However, when we close E , we can see that the low and the num are equal. As a result, there is no way to get to a node that has a number lower than E 's through the spanning tree of E . Therefore, there is no way to have a bigger SCC that contains E .

To get the nodes that are part of the SCC, we need to get all the nodes in the stack before the one that "generates" the SCC (g). This is because the stack only contains the

nodes that belong to the spanning tree of g and do not belong to any other SCC. Therefore, they must belong to the one generated by g .

Furthermore, all those nodes will have the same `low` value since the `low` any node with a higher value must have been processed before. Therefore, g is accessible from all those nodes and, clearly, all those nodes are accessible from g . Thus, they fulfill the definition of an SCC.

```

20 vector<vi> adyList; // Graph
21 vi low, num;      // num and low for DF
22 int cnt;          // Counter for DFS
23 stack<int> st;
24 vi inStack;       // Position in the stack + 1
25 vector<vi> sccs; // Contains the SCCs at the end
26
27 void dfs(int u) {
28     low[u] = num[u] = cnt++;
29     st.push(u);
30     inStack[u] = st.size();
31     for (auto a : adyList[u]) {
32         if (num[a] == -1) {
33             dfs(a);
34         }
35         if (inStack[a]) {
36             low[u] = min(low[u], low[a]);
37         }
38     }
39     if (low[u] == num[u]) { // Root of a SCC
40         vi v;
41         // Add all the nodes till u (included)
42         int lim = inStack[u];
43         while (st.size() && st.size() >= lim) {
44             v.push_back(st.top());
45             inStack[st.top()] = false;
46             st.pop();
47         }
48         sccs.push_back(v);
49     }
50 }
51 void TarjanSCC(int n) {
52     low = num = vi(n, -1);
53     inStack = vi(n, 0);
54     st = stack<int>();
55     cnt = 0;
56     sccs = vector<vi>();
57
58     for (int i = 0; i < n; ++i) {
59         if (num[i] == -1) {
60             dfs(i);
61         }
62     }
63 }

```

Running time: $\mathcal{O}(V + E)$
(V = vertices, E = edges)

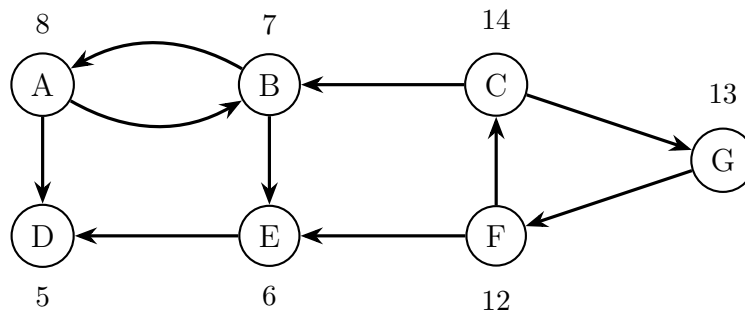
2.5 Kosaraju's

Kosaraju's algorithm is a slightly simpler method for finding the SCC of a graph. On the other hand, it is also somewhat slower than Trajan's approach since it will require running DFS on the graph twice. The algorithm follow this procedure:

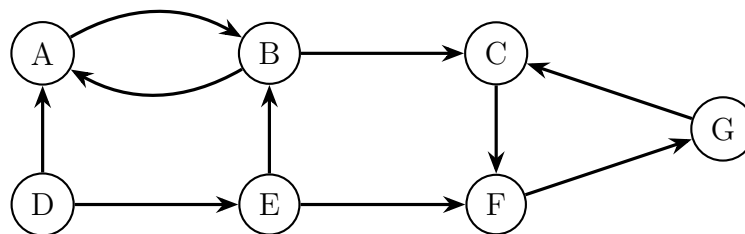
1. Run DFS on the graph and store the vertices in postorder in a list called **postorder**.
2. Reverse the graph
3. Loop through the nodes in **postorder** starting from the one that was closed the last. For each of them check if it has already been added to a SCC (visited). If it hasn't, run DFS from that node and create a SCC with all the nodes that this DFS visits and hadn't been visited before.

Example

Let's look at an example graph where we have run DFS starting first in node *A* and, since it didn't explore the entire graph, we also run it from node *C*. We have included the time at which each node was closed:



Now we reverse the graph and we get the following:



Finally, we can loop through the nodes in postorder, starting with the node that was close the last:

$$\text{postorder} = \{C, G, F, A, B, E, D\}$$

1. We run DFS on node C and we get the SCC:

$$s_1 = \{C, F, G\}$$

2. We skip nodes G and F in the list since they are already in a SCC and we run DFS on node A , getting the SCC:

$$s_2 = \{A, B\}$$

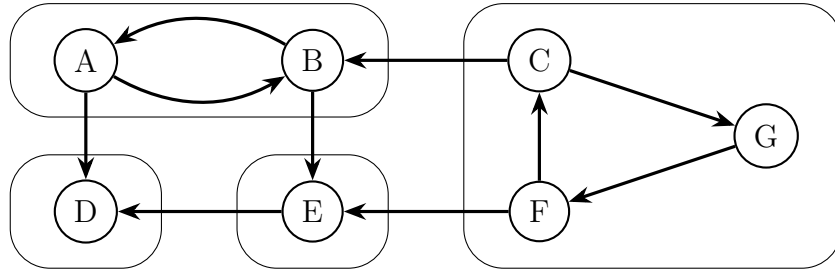
3. We skip node B since it is already in a SCC and we run DFS on node E , getting the SCC:

$$s_3 = \{E\}$$

4. We finally run DFS on node D , and we get the last SCC:

$$s_4 = \{D\}$$

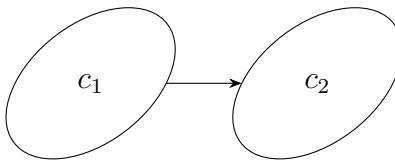
Now, returning to the initial graph, we have found the following SCCs:



Explanation

Let's look at why this algorithm works.

Firstly, we have to take into account that the SCCs of a graph G are preserved when we reverse all the edges and get G^t . The only relevant issue is the order in which we process the SCCs. Let's assume we have a graph that has two SCC's: We have three options:



- *They are not connected.* In this case, it does not matter whether we explore one or the other first since DFS will not “leak” from one of them to the other
- *They are connected only in one direction.* This is the case that the figure shows and it is the most important one. If we explore c_2 before exploring c_1 , DFS will first explore the entirety of c_2 and then, when it is exploring c_1 it will not “leak” to c_2 because those nodes are already marked as visited.
- *They are connected in both directions.* This can never happen since, if they were to be connected bidirectionally, they would form a single SCC, not two.

Therefore, the correctness of this algorithm simply depends on exploring the SCCs in the right order.

Let's demonstrate the following claim:

In the previous setting, the maximum closing time of the nodes in c_1 will be greater than the maximum closing time of the nodes in c_2

We just have to distinguish two cases:

- If we started exploring c_2 before c_1 , there is no way to get to c_1 from c_2 . Therefore, we will start exploring c_1 when we have already closed c_2 , which means that all nodes in c_2 will be closed before the nodes in c_1 are even “opened”.
- If we started exploring c_1 before c_2 , at some point, DFS will leak to c_2 and it will explore it entirely before returning to c_1 . Therefore, the closing time of every node in c_2 will be lower than the closing time of the node where DFS was started in c_1 .

This completes the proof of that statement. Let's now apply it to check the correctness of this algorithm using induction.

- *Base case:*

After reversing the graph, we start with the node that was closed the last (a). Let's call it's SCC s_1 . Let's assume that there is an edge from s_1 to another SCC (s_α) in G^t , which would make DFS leak to that SCC. However, if that was the case, there would be an edge from s_α to s_1 in G and, therefore, we can apply the previous claim.

In that scenario, the maximum closing time of s_α would be greater than the maximum closing time of s_1 . This is a contradiction because we have stated that $a \in s_1$ is the node that was closed the last.

Therefore, there cannot be any edge from s_1 to another SCC.

- *Inductive step:*

Let's now assume that we have already processed n SCCs. We now choose a node b , which is the node with the highest closing time such that $b \notin s_i$, $i = 1, \dots, n$.

We will call the SCC of this node s_{n+1} . As before, we want to prove that s_{n+1} is not connected to any s_β that hasn't been explored yet in G^t .

We will assume that there is an edge from s_{n+1} to a $s_\beta \notin \{s_1 \dots s_n\}$. Therefore, in G , there is an edge from s_β to s_{n+1} , which implies that the maximum closing time of s_β is higher than the maximum closing time of s_{n+1} .

Let's define $x_\beta :=$ (the node with the maximum closing time of s_β). We just stated that the closing time of x_β is greater than the closing time of b (there cannot be a node with a greater closing time in s_{n+1}).

However, this is a contradiction. Therefore, s_{n+1} cannot be connected to an SCC that has not been explored and, thus, DFS will not leak.

□

```

20 vector<vi> adyList; // Graph
21 vector<int> visited; // Visited for DFS
22 vector<vi> sccs; // Contains the SCCs at the end
23
24 void dfs(int nnode, vector<int> &v, vector<vi> &adyList) {
25     if (visited[nnode]) {
26         return;
27     }
28     visited[nnode] = true;
29     for (auto a : adyList[nnode]) {
30         dfs(a, v, adyList);
31     }
32     v.push_back(nnode);
33 }
34
35 void Kosaraju(int n) {
36     visited = vi(n, 0);
37     stack<int> s = stack<int>();
38     sccs = vector<vi>();
39
40     vector<int> postorder;
41     for (int i = 0; i < n; ++i) {
42         dfs(i, postorder, adyList);
43     }
44     reverse(all(postorder));
45
46     vector<vi> rAdyList = vector<vi>(n, vi());
47     for (int i = 0; i < n; ++i) {
48         for (auto v : adyList[i]) {
49             rAdyList[v].push_back(i);
50         }
51     }
52
53     visited = vi(n, 0);
54     vi data;
55     for (auto a : postorder) {
56         if (!visited[a]) {
57             data = vi();
58             dfs(a, data, rAdyList);
59             if (!data.empty())
60                 sccs.pb(data);
61         }
62     }
63 }

```

Running time: $\mathcal{O}(V + E)$
(V = vertices, E = edges)

Remarks

- The SCCs of any graph form a DAG

2.6 Kruskal's

Kruskal's algorithm finds a minimum spanning forest of the given graph. To do so, it uses UFDS to keep track of which nodes are already connected.

2.6.1 UFDS

UFDS (Union-find data structure) is a data structure that stores a partition of the vertices into sets such that all vertices in the same set are connected. Each node u will have two properties:

- *Parent*. It is the representative of the partition that contains u .
- *Rank*. It is an upper bound of the height of the “tree” that starts on u .

```
20  const int lim = 200000;
21  int parent[lim];
22  int rankk[lim];
23
24  void initialize(int n) {
25      for (int i = 0; i < n; ++i) {
26          rankk[i] = 0;
27          parent[i] = i;
28      }
29  }
30  int find(int x) {
31      if (parent[x] == x)
32          return x;
33      else
34          return parent[x] = find(parent[x]);
35  }
36
37  void Union(int a, int b) {
38      int pa = find(a);
39      int pb = find(b);
40      if (pa == pb) {
41          return;
42      }
43      if (rankk[pa] > rankk[pb]) {
44          parent[pb] = pa;
45      } else if (rankk[pa] < rankk[pb]) {
46          parent[pa] = pb;
47      } else {
48          parent[pa] = pb;
49          rankk[pb]++;
50      }
51  }
```


Running time: $\mathcal{O}(E \log V)$

(V = vertices, E = edges)

Explanation

There are two main optimizations that are applied in this implementation:

- *Union by rank.* When we join two partitions, we have to choose a node to represent the new partition. In order to choose between the two parents, we use their rank.

Our goal is to minimize the height of the trees that start at every node. Therefore, we pick the node with the highest rank as the parent. This choice ensures that the rank of both parents will not increase.

However, if both parents have the same rank, we can choose either of them.

- *Path shortening.* The find function updates the value of the parent of each node so that it does not point to its “immediate” parent but to the highest possible ancestor. This difference increases the efficiency of subsequent executions of the find routine.

2.6.2 Kruskal’s

Using UFDS, the implementation of Kruskal is trivial. We just edges that connect vertices that are not connected already until all vertices are connected.

```
20 ll kruskal(vector<pair<pii, int>> &edgeList) {
21     int cost = 0;
22
23     auto cmp = [](pair<pii, int> a, pair<pii, int> b) { return a.se < b.se; };
24     sort(all(edgeList), cmp);
25
26     for (auto a : edgeList) {
27         if (find(a.fi.fi) != find(a.fi.se)) {
28             //Not connected already → connect them
29             Union(a.fi.fi, a.fi.se);
30             cost += a.se;
31         }
32     }
33     return cost;
34 }
```

Running time: $\mathcal{O}(\max\{E, V\} \log(\max\{E, V\}))$

(V = vertices, E = edges)

2.7 Flows and cuts

In this section we will consider graphs as networks of pipes and the “weights” of the edges will be their capacity.

2.7.1 Edmonds-Karp’s (Max Flow)

The first problem that we have to consider is how to find the maximum flow from one source node to a sink node. Edmonds-Karp’s is an implementation of Ford-Fulkerson’s that solves this problem.

This algorithm has some major caveats: it requires the use of an adjacency matrix and it is not as fast as other options.

To improve its running time, this implementation uses both an adjacency matrix and adjacency list. However, we have to be careful when creating the adjacency list since for every forward edge, we need a backward edge that will start with a capacity of 0 but its capacity may increase.

Therefore, the code for adding edges would be the following:

```
1 // Add a directed edge
2 void addedgeUni(int orig, int dest, ll flow) {
3     adjList[orig].pb(dest);
4     adjMat[orig][dest] = flow;
5     adjList[dest].pb(orig); //Add edge for residual flow
6 }
7 // Add a bidirectional edge
8 void addEdgeBi(int orig, int dest, ll flow) {
9     adjList[orig].pb(dest);
10    adjList[dest].pb(orig);
11    adjMat[orig][dest] = flow;
12    adjMat[dest][orig] = flow;
13 }
```

```

20 vector<vector<ll>> adjList;
21 vector<vector<ll>> adjMat;
22
23 void initialize(int n) {
24     adjList = decltype(adjList)(n);
25     adjMat = decltype(adjMat)(n, vector<ll>(n, 0));
26 }
27
28 map<int, int> p;
29 bool bfs(int source, int sink) {
30     queue<int> q;
31     vi visited(adjList.size(), 0);
32     q.push(source);
33     visited[source] = 1;
34     while (!q.empty()) {
35         int u = q.front();
36         q.pop();
37         if (u == sink)
38             return true;
39         for (auto v : adjList[u]) {
40             if (adjMat[u][v] > 0 && !visited[v]) {
41                 visited[v] = true;
42                 q.push(v);
43                 p[v] = u;
44             }
45         }
46     }
47     return false;
48 }
49 int max_flow(int source, int sink) {
50     ll max_flow = 0;
51     while (bfs(source, sink)) {
52         ll flow = inf;
53         for (int v = sink; v != source; v = p[v]) {
54             flow = min(flow, adjMat[p[v]][v]);
55         }
56         for (int v = sink; v != source; v = p[v]) {
57             adjMat[p[v]][v] -= flow; // Decrease capacity forward edge
58             adjMat[v][p[v]] += flow; // Increase capacity backward edge
59         }
60         max_flow += flow;
61     }
62     return max_flow;
63 }

```

Running time: $\mathcal{O}(VE^2)$
(V = vertices, E = edges)

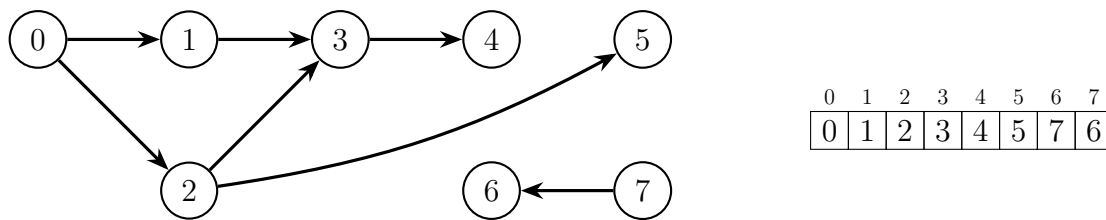
Remarks

- If we have multiple sources s_1, \dots, s_n and multiple sinks t_1, \dots, t_n , we can use the same algorithm. We just have to create a source s that connects to s_i with edges of infinite capacity and a sink t such that s_i is connected to t with edges of infinite capacity.
- If we have vertex capacities, we can split the vertex v into two vertices: v_{in} and v_{out} , connected with an edge that has the vertex capacity as a capacity. Then we connect the incoming edges to v_{in} and the out-coming edges to v_{out}

2.8 Directed Acyclic Graphs (DAG)

2.8.1 Topological sort

A topological sort of a directed graph is a linear ordering of its vertices such that for every directed edge $u \rightarrow v$, u comes before v in the ordering. A topological sorting is possible if and only if the graph has no directed cycles, that is, it has to be a DAG. As an example:



Regarding the algorithm to obtain the topological sorting, there are two alternatives:

- A modified version of DFS
- Kahn's algorithm

Using DFS

The key observation is:

When DFS closes a node, all nodes that are accessed from that node are already closed

Therefore if we order the vertices regarding the DFS closing time, we can be sure that if there exists an edge $u \rightarrow v$, v will be placed before u since it must have been closed before u was closed. Now we should realize that to get the topological sorting, we only need to reverse this ordering.

```
20 vi topoSort;
21 vi visited;
22 vector<vi> adyList;
23 void dfs(int node) {
24     if (visited[node]) {
25         return;
26     }
27     visited[node] = true;
28     for (auto a : adyList[node]) {
29         dfs(a);
30     }
31     topoSort.push_back(node);
32 }
33 void topologicalSort() {
34     int n = adyList.size();
35
36     visited = vi(n, 0);
37     topoSort.clear();
38
39     for (int i = 0; i < n; ++i) {
40         if (!visited[i]) {
41             dfs(i);
42         }
43     }
44     reverse(all(topoSort));
45 }
```

Running time: $\mathcal{O}(E + V)$

(V = vertices, E = edges)

Kahn's algorithm

Kahn's algorithm is a very simple algorithm. It simply keeps track of the in-degree of every vertex and only adds to the topological sort list vertices that do not have any incident edges.

Furthermore, this algorithm can be easily adapted to store all possible topological orderings by using a recursive function and running through all possibilities at each step

```
20 vi topoSort;
21 vi visited;
22 vector<vi> adyList;
23 void dfs(int node) {
24     if (visited[node]) {
25         return;
26     }
27     visited[node] = true;
28     for (auto a : adyList[node]) {
29         dfs(a);
30     }
31     topoSort.push_back(node);
32 }
33 void topologicalSort() {
34     int n = adyList.size();
35
36     visited = vi(n, 0);
37     topoSort.clear();
38
39     for (int i = 0; i < n; ++i) {
40         if (!visited[i]) {
41             dfs(i);
42         }
43     }
44     reverse(all(topoSort));
45 }
```

Running time: $\mathcal{O}(E + V)$

(V = vertices, E = edges)

2.9 Bipartite Graphs

A graph is bipartite if its vertices can be split into two different so that no two nodes in the same set are connected by an edge.

Definitions

It is important to note that in this section a path (unless specified otherwise) will be a simple path (not containing repeated vertices or edges).

- *Matching*. Set of pairwise non-adjacent edges in a graph. That is to say, no more than one edge from the set should be incident to any vertex of the graph.
- *Saturated* (a vertex with respect to some matching). A saturated vertex is a vertex that is an endpoint of an edge contained in the matching.
- *Alternating path* (with respect to some matching). Path in which the edges alternately belong / do not belong to the matching.
- *Augmenting path* (with respect to some matching M). Alternating path whose initial and final vertices are unsaturated (they do not belong to the matching). That is to say, if we represent the edges already included in M as I and the new ones as U , it follows this pattern:

$$U - I - U - \dots - U - I - U$$

We can also notice that there will be $\left\lfloor \frac{|P|}{2} \right\rfloor$ edges already included and $\left\lceil \frac{|P|}{2} \right\rceil$ new edges.

- *Independent set*. Set of vertices in which no two vertices represent an edge in the original graph.
- *Vertex coverage*. Set of vertices C that fulfills the following property: Every vertex of G is incident on, at least, one vertex of C .

From these definitions, we can derive the following features in a bipartite graph:

- *Maximum cardinality bipartite matching (MCBM)*. Matching that contains the maximum number of edges.
- *Maximum independent set (MIS)*. Independent set that fulfills that if any other vertex was to be added to it, there would be an edge between two of the vertices of the set.
- *Minimum vertex coverage (MVC)*. Vertex coverage with the minimum number of vertices.

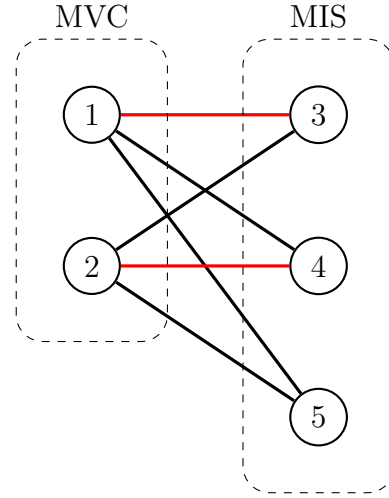
Furthermore, it can be proved that even though these “sets” may not be unique, their cardinality is. Additionally, they are closely related among them:

$$|MIS| = |V| - |MCBM| \qquad |MCBM| = |MVC|$$

Example

In this example we have a bipartite graph where nodes 1 and 2 belong to the first set of vertices and nodes 3, 4 and 5 to the second set.

- Since there are only two vertices in the first set, the MCBM has to be at most two. We have found a matching of size two (in red), so that must be the solution.
- The MIS has to be one of the two sets of vertices since all vertices from one set are connected to all vertices from the second set. We pick the maximum one.
- Finally, the MVC has to be the smallest set for the same reasons.



Finally, we can also notice how the MCBM is not unique even though its cardinality is unique.

Berge's lemma

A matching M is maximum \iff there is no augmenting path relative to the matching M

Proof

We can prove it by contradiction:

\implies Let there be an augmenting path P relative to M . This path will necessarily be of odd length (it has one more edge not in M than in M). We can now create a new matching $M' = M \oplus P = (M \setminus P) \cup (P \setminus M)$.

Now we have to see that this matching is valid. In order for it not to be valid, there must be a vertex such that two edges in M' are adjacent to. Furthermore, one of those edges must belong to $P \setminus M$ while the other one belongs to M . However, the second one must then also belong to P (P alternates edges) and will not be in $M \setminus P$. Therefore, it cannot be in M' and we reached a contradiction

Finally, we can see that there are $|M| + 1$ edges in M' since:

- By subtracting P from M we delete $\left\lfloor \frac{|P|}{2} \right\rfloor$ edges
- By adding $P \setminus M$, we add $\left\lceil \frac{|P|}{2} \right\rceil$ edges

Therefore, M could not be a maximum matching

\Leftarrow Let there be a matching M' of greater cardinality than M . We can consider the subgraph $Q = M \oplus M'$. Any vertex in this subgraph has a maximum degree of 2, which means that all connected components in it are either:

- An isolated vertex
- a (simple)path whose edges are alternate from M and M'
- A cycle of even length whose edges are alternate from M and M'

However, since there are more edges from M' than from M , there must be at least one component with more edges from M' than from M . Since such path must be alternating, it will have initial and final vertices unsaturated by M , making it an augmenting path for M .

□

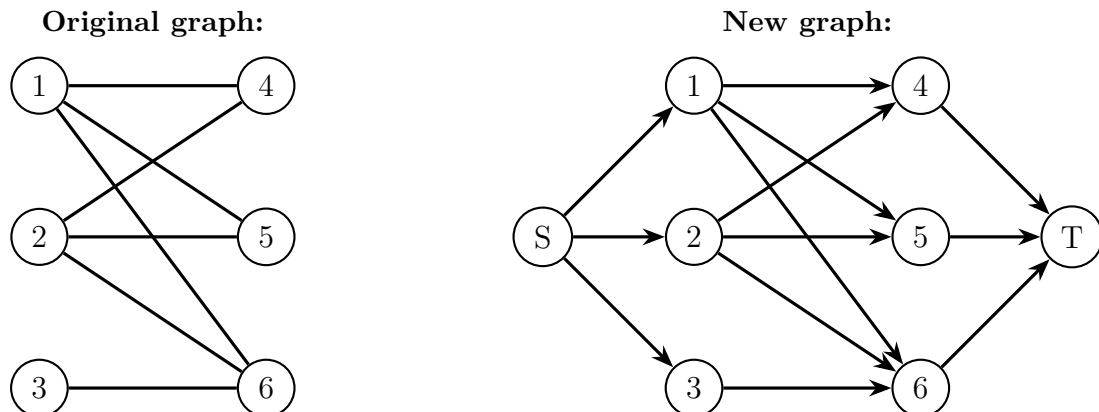
2.9.1 Algorithms to find MCBM

Reduce to Max-Flow

The bipartite matching problem can be easily reduced to a max-flow problem. We only have to:

- Make the edges between the two components directed from the first component to the second (all edges must go in the same direction)
- Connect the source to all nodes in the first component.
- Connect the nodes in the second component to the sink.
- Set the capacities of all edges to 1.

For instance:



After this process, we can run the normal max-flow algorithm and the maximum flow between the source and the sink will be the result. This will have a time complexity of $\mathcal{O}(VE^2)$ using Edmonds-Karp's or $\mathcal{O}(V^2E)$ using Dinic's

Kuhn's Algorithm

On a high level, the algorithm implements the following pseudocode (where M is the matching):

```
M ← ∅
while (able to find augmenting path P){
    M ← P ⊕ M
}
```

This is a direct application of Berge's lemma; however, if we were to implement it naïvely, we could end up with a time complexity of $\mathcal{O}(V^2E)$ since there will be at most V augmenting paths and to find each of them, we would need to check for paths that start on each node and then run DFS to find the actual path. To make it faster, it can be implemented using the following pseudocode (where n_1 is the size of the first set in the graph):

```
M ← ∅
for (i = 0 ... n1){
    P ← augmenting path that starts on i
    if(P ≠ ∅){
        M ← P ⊕ M
    }
}
```

To understand why this implementation should work, it is necessary to make a few observations:

- The augmenting path found in each iteration starts on a vertex in the first set, then traverses some number of vertices that are already saturated and it ends on a vertex of the second set that is not saturated.
- When we update M with the new P , no vertices that were saturated before will be unsaturated now. Since all saturated vertices in P are connected by two adjacent edges, one of them will still be present in $P \oplus M$ since it could not be present on M before.
- If there is no augmenting path that starts from i in the current iteration, it will be impossible to find one in a some future iteration. This is because no vertex can go from being saturated to being unsaturated in this process.

With all of this in mind, we can obtain a c++ implementation that runs on $\mathcal{O}(EV)$. Furthermore, if we make sure that the first set of the bipartite graph is the one with less elements, the runtime will be faster since the iterations of the outer loop will decrease.

As we can see, the search for an augmenting path from a node will try all options to pair that node to a node in the second set. For each one of them, if they are already matched to some node in the first set, it will try to create an augmenting path from there. The algorithm will stop when it finds an unsaturated vertex or runs out of vertex to check.

```

20 // List of vertices in the 2nd component connected to
21 // the i-th vertex in the first component
22 vector<vi> adyList;
23
24 // Index of the vertex in 1st component connected to the
25 // i-th vertex in the second component
26 vector<int> match;
27 vector<bool> used;
28 bool augmentPath(int current) {
29     if (used[current]) {
30         return false;
31     }
32     used[current] = 1;
33     for (int to : adyList[current]) {
34         if (match[to] == -1 || augmentPath(match[to])) {
35             match[to] = current;
36             return true;
37         }
38     }
39     return false;
40 }
41 int calculateMCBM(int n1, int n2) {
42     match = vi(n2, -1);
43     int res = 0;
44     for (int i = 0; i < n1; ++i) {
45         used.assign(n1, false);
46         res += augmentPath(i);
47     }
48     return res;
49 }

```

Running time: $\mathcal{O}(EV)$
(V = vertices, E = edges)

Chapter 3

Mathematics

3.1 General calculations

3.1.1 Binary exponentiation

Binary exponentiation calculates a power in logarithmic time. Furthermore, it can be used for modular arithmetic:

```
20 ll power(ll base, ll exp) {
21     if (exp == 0) {
22         return 1;
23     }
24     ll res = power(base, exp / 2);
25     res = (res * res) % mod;
26     if (exp % 2) {
27         res *= base;
28     }
29     return res % mod;
30 }
```

Running time: $\mathcal{O}(\log(\text{exp}))$

3.2 Modular arithmetic

3.2.1 Inverses

To calculate a modular inverse, we will use Fermat's little theorem:

$$a^{p-1} \equiv 1 \pmod{p} \implies a^{p-2} \equiv a^{-1} \pmod{p}$$

If we combine this fact with binary exponentiation, we can obtain the modular inverse in logarithmic time:

```

1 ll inverse(ll num) {
2     return power(num, mod - 2);
3 }
```

Running time: $\mathcal{O}(\log(\text{mod}))$

3.3 Catalan numbers

We define the n th Catalan number as:

$$C_n = \frac{1}{n+1} \binom{2n}{n} = \frac{1}{n+1} \frac{(2n)!}{n! n!}$$

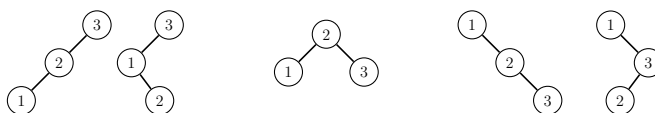
We can also define them recursively:

$$C_0 = 1 \quad C_{n+1} = \sum_{i=0}^n (C_i C_{n-i})$$

They can be used to solve many different problems. For instance:

- Number of different binary trees of n nodes. We can look at the specific case $n = 3$. As we can see in the figure below, $C_3 = 5$. Furthermore, we can clearly identify the recursive relationship:

$$C_3 = (3 \text{ is root}) + (2 \text{ is root}) + (1 \text{ is root}) = C_2 \cdot C_0 + C_1 \cdot C_1 + C_0 \cdot C_2$$



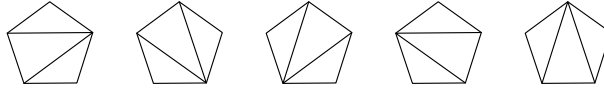
- Number of expressions that contain n pairs of parenthesis correctly paired. For instance, for $n = 3$, there only $C_3 = 5$ valid arrangements are:

$()()() \quad ()(()) \quad (())() \quad ((())) \quad (()())$

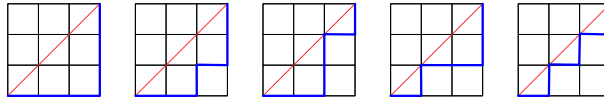
- Number of different ways of arranging $n + 1$ factors in parenthesis In the case of $n = 3$, we can use the factors a, b, c, d . Then, we will have the following options:

$$(ab)(cd) \quad a(b(cd)) \quad ((ab)c)d \quad (a(bc))d \quad a((bc)d)$$

- Number of ways to split a convex polygon of $n + 2$ sides into triangles.



- Number of paths from the bottom-left corner to the top-right corner of a $n \times n$ grid moving only up or right at every point and while not reaching the diagonal.



3.4 Permutations

3.4.1 Converting one permutation into another

In this problem we are given two permutations of the same size and we are tasked with converting one of them into the other. In order to do so, we will swap the elements at two positions in the permutation zero or more times.

$$\begin{array}{r} \begin{array}{cccccc} 0 & 1 & 2 & 3 & 4 & 5 & 6 \\ \hline 1 & 2 & 3 & 4 & 5 & 5 & 6 \end{array} \\ \text{A} = \\ \begin{array}{cccccc} 0 & 1 & 2 & 3 & 4 & 5 & 6 \\ \hline 1 & 3 & 2 & 4 & 5 & 5 & 6 \end{array} \\ \text{B} = \end{array}$$

In this case, the most efficient way is to swap positions 1 and 2 of permutation B to get permutation A. From these examples, we can deduce the following observations:

- One swap will fix at most two numbers out of place.
- We will need at most $n - 1$ swaps to change one permutation into the other. Note that we can “skip” the swap that corresponds to the last element since, at that point, by the Pigeon Principle, all elements must be in the correct position.

To solve the problem, we shall change the representation to a graph where the edge $a \rightarrow b$ represents that there exists j such that $A[j]=a$, $B[j]=b$. When draw these edges, we notice that all edges form cycles (possibly of length 1). Furthermore, the cost of fixing all the positions that comprise each cycle will be the length of the cycle minus 1.

Finally, since the graph is made out of cycles, we know that in this graph connectivity and strong connectivity are equivalent and we can ignore the direction of the edges. This reduces the problem to counting the number of connected components and the result is:

$$\# \text{ Swaps} = n - \# \text{ Components}$$

This can be simply implemented using UFDS:

```
55 int swapsPermutation(vi perm1, vi perm2) {
56     int n = perm1.size();
57     UFDS::initialize(n + 1);
58     int components = n;
59     for (int i = 0; i < n; ++i) {
60         if (UFDS::find(perm1[i]) != UFDS::find(perm2[i])) {
61             components--;
62             UFDS::Union(perm1[i], perm2[i]);
63         }
64     }
65     return n - components;
66 }
```

Chapter 4

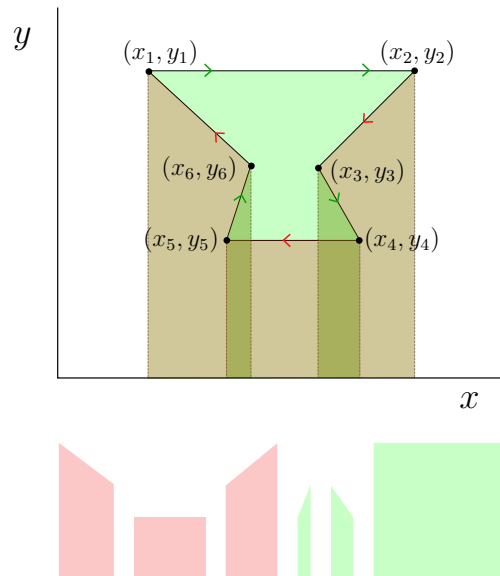
Geometry

4.1 Area of polygon

In this problem, we are given a polygon expressed as a list of vertices. We are tasked with calculating the area of the polygon.

For now, we will assume that the points are ordered in a clock-wise fashion and we will consider three different scenarios for each segment:

- $\Delta x = 0$. It does not add any area to the polygon.
- $\Delta x \neq 0$. It has an area associated with it that is equal to the area between the segment and the x axis
 - $\Delta x > 0$. We consider this area positive (green on the figure)
 - $\Delta x < 0$. We consider this area negative (red on the figure)



Now we add all the areas associated with each segment and we get a total area. If the vertices were ordered in a counter-clock-wise fashion, this total area will be negative. Therefore, we will only consider the absolute value of the result.

```
20
21 double calcAreaSegment(pii a1, pii a2) {
22     if (a1.fi == a2.fi)
23         return 0;
24
25     return (a2.fi - a1.fi) * (max(a1.se, a2.se) - abs(a1.se - a2.se) / 2.0);
26 }
```



```

27 double calcAreaPolygon(vector<pii> points) {
28     double ans = 0;
29     for (int i = 1; i < points.size(); ++i) {
30         ans += calcAreaSegment(points[i - 1], points[i]);
31     }
32     ans += calcAreaSegment(points.back(), points[0]);
33     return abs(ans);
34 }

```

Running time: $\mathcal{O}(n)$

(n = vertices)

Chapter 5

Ad-hoc

The algorithms in this chapter do not fall into standard categories, so they ended up here.