Competitive Programming Algorithms

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Contents

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:

  $$\min(a_l, \ldots, a_r) = \min\left(\min(a_l, \ldots, a_k), \min(a_k, \ldots, a_r)\right) \quad l < k < r$$

  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.

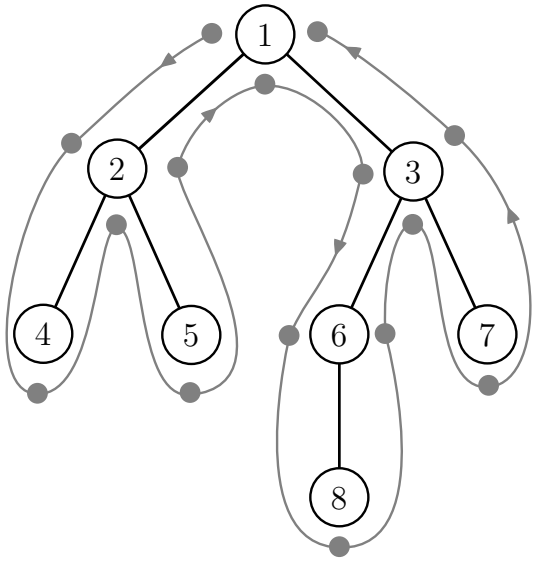
  For instance, the addition, subtraction and xor operations have an inverse (subtraction, addition and xor respectively).

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:

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

Where $E =$ 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.

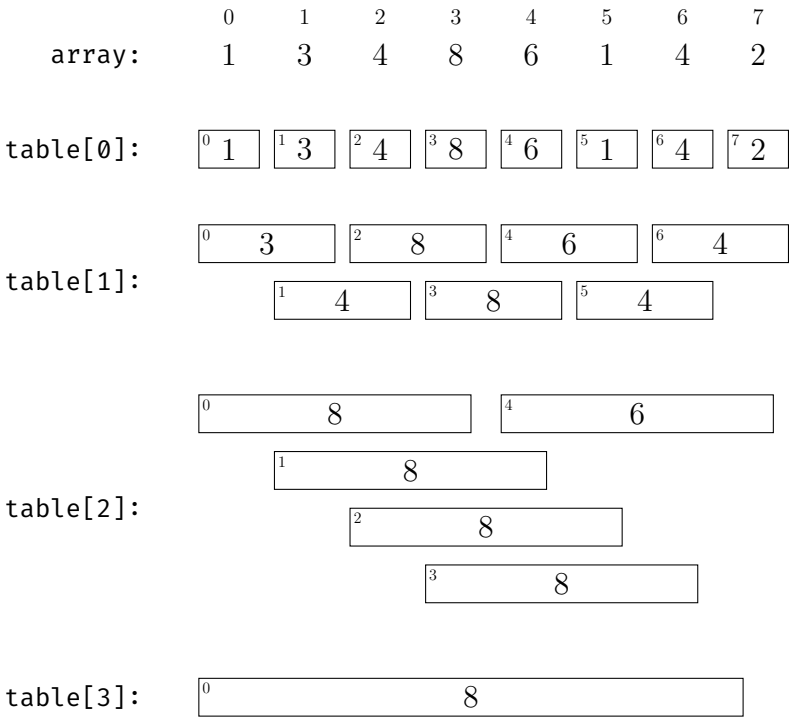
The table consists of $\log n$ rows. Each one of them contains the value of the function in intervals of length 2^j where j is the row index. In particular, $\text{table}[j][i] = f([i, i+2^j])$, where $f(I)$ is the value of f over all the elements in I.

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 where 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.



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: $\max(8, 6) = 8$

```cpp
class SparseTable {
private:
    vl logs;
    vector<vl> table;
    std::function<ll(ll, ll)> f;

public:
    SparseTable(vl &data, std::function<ll(ll, ll)> f) : f(f) {
        int n = data.size();
        table.pb(data);
        for (int j = 1; (1ll << j) <= n; ++j) {
            vl nextRow(n);
            for (int i = 0; i + (1ll << j) <= n; ++i) {
                int otherIndex = i + (1ll << (j - 1));
                nextRow[i] = f(table.back()[i], table.back()[otherIndex]);
            }
            table.push_back(std::move(nextRow));
        }

        logs = vl(n + 1, 0);
        for (int i = 2; i <= n; ++i) {
            logs[i] = logs[i / 2] + 1;
        }
    }

    ll valueInRange(int left, int right) {
        ll j = logs[right - left + 1];
        ll intervalSize = 1ll << j;
        return f(table[j][left], table[j][right - intervalSize + 1]);
    }
};
```

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 we will build two data structures:

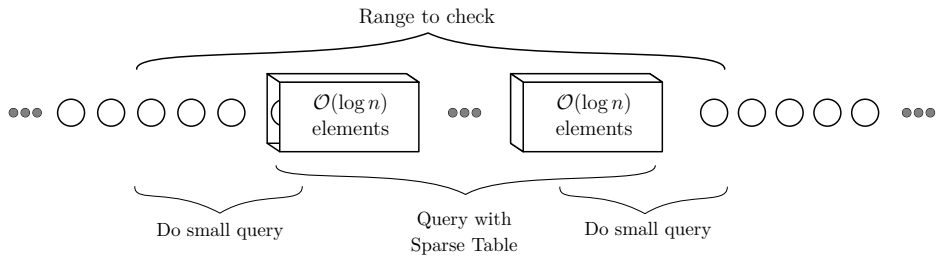
- A Sparse Table where each element is a block of the array. In order to simplify this task, in the Sparse Table we will store the index of the result of applying the operation to the range instead of the result itself.

  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
```

```
            ans = op(ans, op(sparseTable[rowSize * j + x],
                             sparseTable[rowSize * j + y - (1 << j) + 1]));
        }
        return data[ans];
    }

private:
    static int lsb(int x) { return x & -x; }
    static int msb_index(int x) { return __builtin_clz(1) - __builtin_clz(x); }

    // Get the index that contains the answer for the small query
    int small_query_index(int r, int size = blockSize) {
        int dist_from_r = msb_index(mask[r] & ((1 << size) - 1));

        return r - dist_from_r;
    }

    // Return the index that contins the result of the operation
    int op(int index1, int index2) {
        return f(data[index1], data[index2]) == data[index1] ? index1 : index2;
    }

    void build_mask() {
        int current_mask = 0;
        // We use this mask so that we only keep track of the at most
        // the size of the block bits
        int discard_mask = (1 << blockSize) - 1;
        for (int i = 0; i < n; ++i) {
            current_mask = (current_mask << 1) & discard_mask;

            while (current_mask > 0 &&
                   op(i, i - msb_index(lsb(current_mask))) == i) {
                // Current value is smaller than the value represented by the
                // last 1 in curr_mask, so that bit should be off
                current_mask ^= lsb(current_mask);
            }
            current_mask |= 1;
            mask[i] = current_mask;
        }
    }
    void build_sparse_table() {
        // Fill first row
        for (int i = 0; i < rowSize; ++i) {
            sparseTable[i] = small_query_index(blockSize * (i + 1) - 1);
        }
        for (int j = 1; (1 << j) <= rowSize; ++j) {
            for (int i = 0; i + (1 << j) <= rowSize; ++i) {
```

```
                int previousStep = 1 << (j - 1);
                sparseTable[rowSize * j + i] =
                    op(sparseTable[rowSize * (j - 1) + i],
                       sparseTable[rowSize * (j - 1) + i + previousStep]);
            }
        }
    }
};
```

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 $F(a_l, \ldots, a_r)$ can be calculated in $\boldsymbol{\mathcal{O}(\log n)}$
- Updating one of the values of the array takes $\boldsymbol{\mathcal{O}(\log n)}$
- Requires the same amout 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 LSOne(i) be the result of setting to 0 all bits of i except for the least significant one. For instance, LSOne(0110) = 0010. Then, the i-th element of `ft` contains the value $F(a_{i-\text{LSOne}(i)+1}, \ldots, a_i)$.

In most cases, F will be the sum of all elements $F(a_l, \ldots, a_r) = \sum_l^r a_i$. 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 interally** to simplify slightly the implementation. However, the interface automatically subtracts one to all index parameters given.

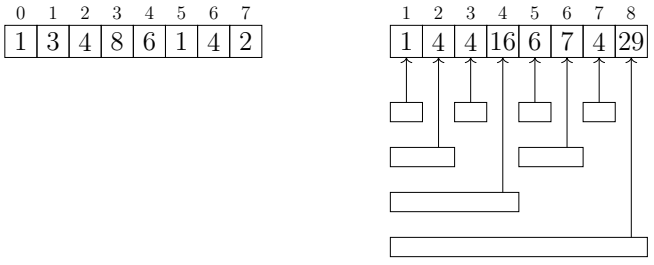
Range Update and Point Query

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.



```cpp
// Return lsb
int LSOne(int a) {
    return a & (-a);
}

template <typename T>
class FenwickTree {
private:
    vector<T> ft;

public:
    FenwickTree(const vector<T> &data)
        : ft(data.size() + 1, 0) {
        for (int i = 0; i < data.size(); ++i) {
            adjust(i, data[i]);
        }
    }

    //RSQ in range [0, index]
    T rsq(int index) {
        index++;
        T sum = 0;
        while (index != 0) {
            sum += ft[index];
            index -= LSOne(index); // Delete the lsb
        }
        return sum;
    }
    //RSQ in range [begin, end]
    T rsq(int begin, int end) {
        return begin == 0 ? rsq(end) : rsq(end) - rsq(begin - 1);
    }

    // Add the delta to the index element
    void adjust(int index, T delta) {
        index++;
        while (index < ft.size()) {
            ft[index] += delta;
            index += LSOne(index);
        }
    }
};
```

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 pipii = pair<int, pii>;
22 vector<vector<pipii>> adyList; //destination, cost, distance
23 ll dijkstra(int orig, int dest) {
24     vi distances(adyList.size(), iinf);
25     priority_queue<pipii, vector<pipii>, greater<pipii>> 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: $\mathcal{O}\big(B \cdot (V + E \log E)\big)$
(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 parth 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:

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

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?

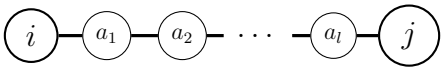
It is important to note that we must use an adjacency matrix in this implementation.

```
void warshall(int n) {
    for (int k = 0; k < n; ++k) {
        for (int i = 0; i < n; ++i) {
            for (int j = 0; j < n; ++j) {
                adyMat[i][j] = min(adyMat[i][j], adyMat[i][k] + adyMat[k][j]);
            }
        }
    }
}
```

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:

```cpp
ll lastInPath[lim][lim];

void warshall(int n) {
    for (int k = 0; k < n; ++k) {
        for (int i = 0; i < n; ++i) {
            for (int j = 0; j < n; ++j) {
                if (adyList[i][j] > adyList[i][k] + adyList[k][j]) {
                    adyList[i][j] = adyList[i][k] + adyList[k][j];
                    lastInPath[i][j] = lastInPath[k][j];
                }
            }
        }
    }
}

// Give an empty vector
void getPath(int i, int j, vector<int> &path) {
    if (i != j) {
        getPath(i, lastInPath[i][j], path);
        path.push_back(j);
    }
}
```

2.4 DFS

2.4.1 Articulation points and bridges

These algorightms 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 point 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 it's 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

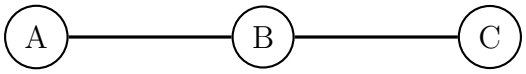
```cpp
vector<vi> adyList; // Graph
vi num, low;        // num and low for DFS
int cnt;            // Counter for DFS
int root, rchild;   // Root and number of (DFS) children
vi artic;           // Contains the articulation points at the end
set<pii> bridges;   // Contains the bridges at the end

void dfs(int nparent, int nnode) {
    num[nnode] = low[nnode] = cnt++;
    rchild += (nparent == root);

    for (auto a : adyList[nnode]) {
        if (num[a] == -1) { // Tree edge
            dfs(nnode, a);
            low[nnode] = min(low[nnode], low[a]);

            if (low[a] >= num[nnode]) {
                artic[nnode] = true;
            }

            if (low[a] > num[nnode]) {
                bridges.insert((nnode < a) ? mp(nnode, a) : mp(a, nnode));
            }
        } else if (a != nparent) { // Back edge
            low[nnode] = min(low[nnode], num[a]);
        }
    }
}
void findArticulations(int n) {
    cnt = 0;
    low = num = vi(n, -1);
    artic = vi(n, 0);
    bridges.clear();

    for (int i = 0; i < n; ++i) {
        if (num[i] != -1) {
            continue;
        }
        root = i;
        rchild = 0;
        dfs(-1, i);
        artic[root] = rchild > 1; //Special case
    }
}
```

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

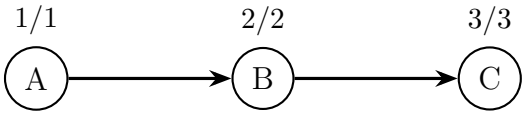
(V = vertices, E = edges)

Explanation

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



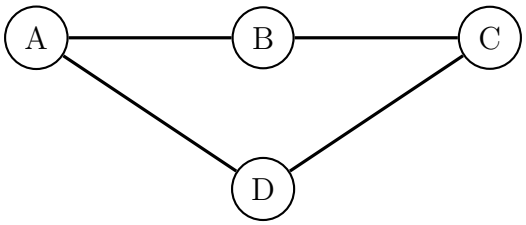
following DFS spanning tree. Above every node, we have included `num / low`.



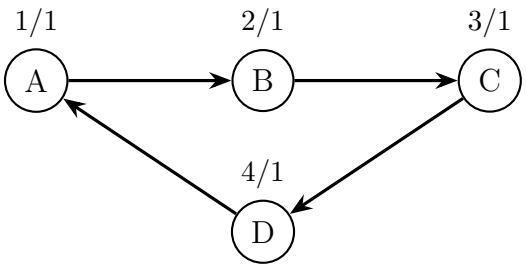
This is a rather simple graph and it's only articulation point is B. This is because it has a child whose `low` value is greater than or equal to B's `num` value. Therefore, there is no connection from that child (namely C) to a node explored before B that does not go through B.

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: `low[child]>num[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

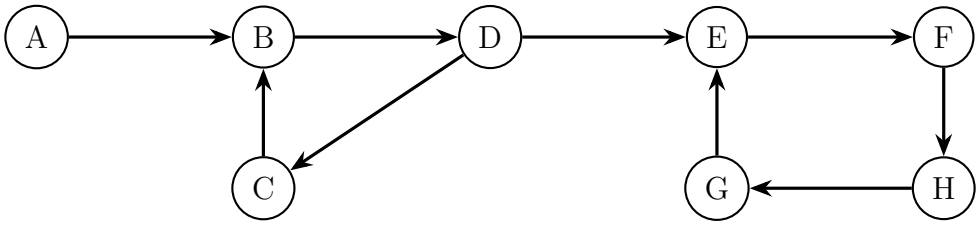
In a directed graph, we say that a subset of vertices comprises a strongly connected component if every vertex is reachable from every other vertex in this subset.

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.

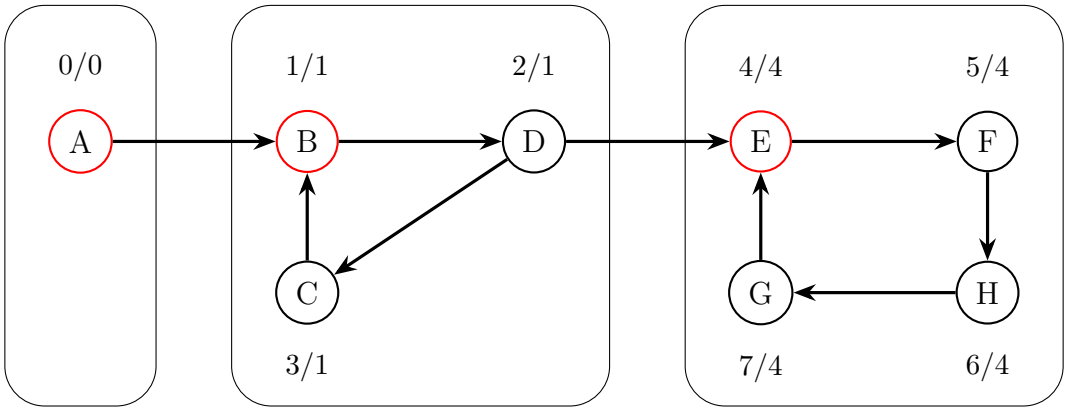
Explanation

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.

```cpp
vector<vi> adyList; // Graph
vi low, num;        // num and low for DF
int cnt;            // Counter for DFS
stack<int> st;
vi inStack;      // Position in the stack + 1
vector<vi> sccs; // Contains the SCCs at the end

void dfs(int u) {
    low[u] = num[u] = cnt++;
    st.push(u);
    inStack[u] = st.size();
    for (auto a : adyList[u]) {
        if (num[a] == -1) {
            dfs(a);
        }
        if (inStack[a]) {
            low[u] = min(low[u], low[a]);
        }
    }
    if (low[u] == num[u]) { // Root of a SCC
        vi v;
        // Add all the nodes till u (included)
        int lim = inStack[u];
        while (st.size() && st.size() >= lim) {
            v.push_back(st.top());
            inStack[st.top()] = false;
            st.pop();
        }
        sccs.push_back(v);
    }
}
void TarjanSCC(int n) {
    low = num = vi(n, -1);
    inStack = vi(n, 0);
    st = stack<int>();
    cnt = 0;
    sccs = vector<vi>();

    for (int i = 0; i < n; ++i) {
        if (num[i] == -1) {
            dfs(i);
        }
    }
}
```

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

(V = vertices, E = edges)

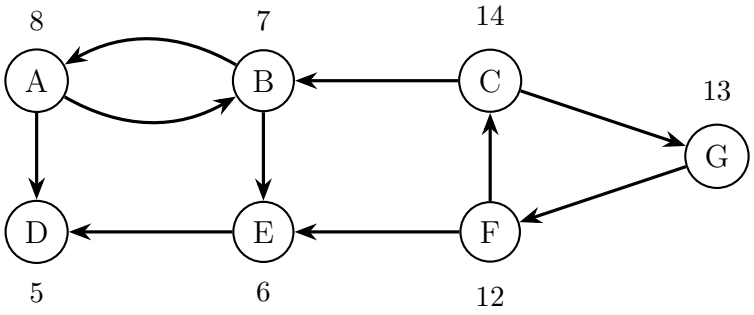
2.5 Kosaraju's

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:

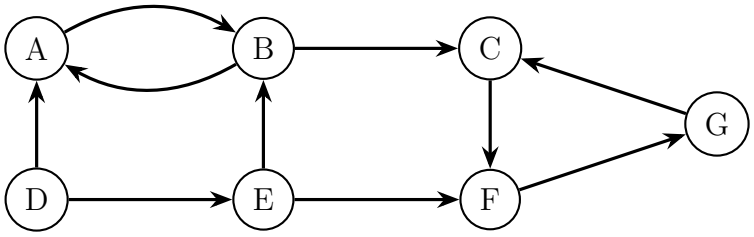
1. Run DFS on the graph and store the vertices in postorder in a list called `postorder`.
2. Reverse the graph
3. Loop through the nodes in `postorder` starting from the one that was closed the last. For each of them check if it has already been added to a SCC (visited). If it hasn't, run DFS from that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

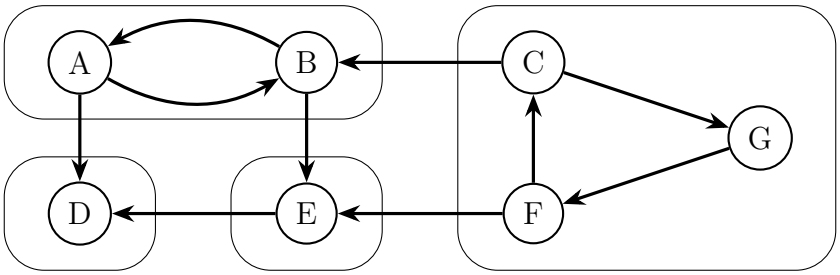


Finally, we can loop through the nodes in postorder, starting with the node that was close the last:

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

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:
$$s_4 = \{D\}$$

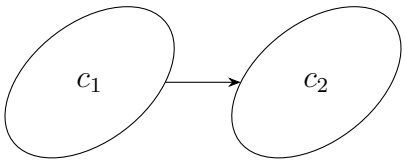
Now, returning to the initial graph, we have found the following SCCs:



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.

□

```cpp
vector<vi> adyList;  // Graph
vector<int> visited; // Visited for DFS
vector<vi> sccs;     // Contains the SCCs at the end

void dfs(int nnode, vector<int> &v, vector<vi> &adyList) {
    if (visited[nnode]) {
        return;
    }
    visited[nnode] = true;
    for (auto a : adyList[nnode]) {
        dfs(a, v, adyList);
    }
    v.push_back(nnode);
}

void Kosaraju(int n) {
    visited = vi(n, 0);
    stack<int> s = stack<int>();
    sccs = vector<vi>();

    vector<int> postorder;
    for (int i = 0; i < n; ++i) {
        dfs(i, postorder, adyList);
    }
    reverse(all(postorder));

    vector<vi> rAdyList = vector<vi>(n, vi());
    for (int i = 0; i < n; ++i) {
        for (auto v : adyList[i]) {
            rAdyList[v].push_back(i);
        }
    }

    visited = vi(n, 0);
    vi data;
    for (auto a : postorder) {
        if (!visited[a]) {
            data = vi();
            dfs(a, data, rAdyList);
            if (!data.empty())
                sccs.pb(data);
        }
    }
}
```

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 it's "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:

```
// Add a directed edge
void addedgeUni(int orig, int dest, ll flow) {
    adjList[orig].pb(dest);
    adjMat[orig][dest] = flow;
    adjList[dest].pb(orig);   //Add edge for residual flow
}
// Add a bidirectional edge
void addEdgeBi(int orig, int dest, ll flow) {
    adjList[orig].pb(dest);
    adjList[dest].pb(orig);
    adjMat[orig][dest] = flow;
    adjMat[dest][orig] = flow;
}
```

```cpp
vector<vector<ll>> adjList;
vector<vector<ll>> adjMat;

void initialize(int n) {
    adjList = decltype(adjList)(n);
    adjMat = decltype(adjMat)(n, vector<ll>(n, 0));
}

map<int, int> p;
bool bfs(int source, int sink) {
    queue<int> q;
    vi visited(adjList.size(), 0);
    q.push(source);
    visited[source] = 1;
    while (!q.empty()) {
        int u = q.front();
        q.pop();
        if (u == sink)
            return true;
        for (auto v : adjList[u]) {
            if (adjMat[u][v] > 0 && !visited[v]) {
                visited[v] = true;
                q.push(v);
                p[v] = u;
            }
        }
    }
    return false;
}
int max_flow(int source, int sink) {
    ll max_flow = 0;
    while (bfs(source, sink)) {
        ll flow = inf;
        for (int v = sink; v != source; v = p[v]) {
            flow = min(flow, adjMat[p[v]][v]);
        }
        for (int v = sink; v != source; v = p[v]) {
            adjMat[p[v]][v] -= flow; // Decrease capacity forward edge
            adjMat[v][p[v]] += flow; // Increase capacity backward edge
        }
        max_flow += flow;
    }
    return max_flow;
}
```

Running time: $\mathcal{O}(VE^2)$

(V = vertices, E = edges)

Remarks

- If we have multiple sources $s_1, \ldots, s_n$ and multiple sinks $t_1, \ldots t_n$, 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}

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:

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

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

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

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

3.3 Catalan numbers

We define the nth Catalan number as:

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

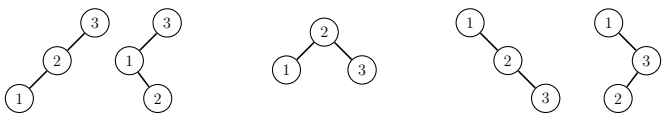
We can also define them recursively:

$$C_0 = 1 \qquad C_{n+1} = \sum_{i=0}^{n} \left(C_i\, C_{n-i}\right)$$

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:

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



Chapter 4

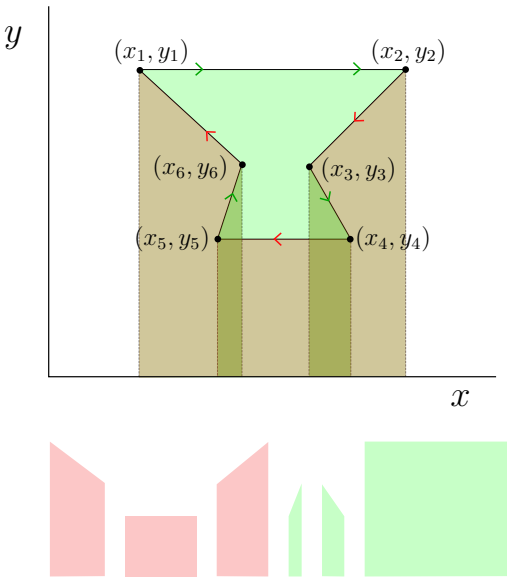
Geometry

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  }
```

```cpp
double calcAreaPolygon(vector<pii> points) {
    double ans = 0;
    for (int i = 1; i < points.size(); ++i) {
        ans += calcAreaSegment(points[i - 1], points[i]);
    }
    ans += calcAreaSegment(points.back(), points[0]);
    return abs(ans);
}
```

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