Sum of Integers 1 through N

What is 1 + 2 + ... + n? Let's figure it out by pairing up low values with high values.

If n is even, we pair 1 with n, 2 with n - 1, and so on. We will have $\frac{n}{2}$ pairs each with sum n + 1.

If n is odd, we pair 0 with n, 1 with n - 1, and so on. We will have $\frac{n+1}{2}$ pairs with sum n.

n is even			
pair #	a	b	a + b
1	1	n	n + 1
2	2	n - 1	n + 1
3	3	n - 2	n + 1
4	4	n - 3	n + 1
...	...	...	...
$\frac{n}{2}$	$\frac{n}{2}$	$\frac{n}{2}$ + 1	n + 1
total:	$\frac{n}{2} * (n+1)$		

n is odd			
pair #	a	b	a + b
1	0	n	n
2	1	n - 1	n
3	2	n - 2	n
4	3	n - 3	n
...	...	...	...
$\frac{n+1}{2}$	$\frac{n-1}{2}$	$\frac{n+1}{2}$	n
total:	$\frac{n+1}{2} * n$		

In either case, the sum is $\frac{n(n+1)}{2}$.

This reasoning comes up a lot in nested loops. For example, consider the following code:

```
1  for (int i = 0; i < n; i++) {
2    for (int j = i + 1; j < n; j++) {
3      System.out.println(i + j);
4    }
5  }
```

On the first iteration of the outer for loop, the inner for loop iterates n - 1 times. On the second iteration of the outer for loop, the inner for loop iterates n-2 times. Next, n - 3, then n - 4, and so on. There are $\frac{n(n-1)}{2}$ total iterations of the inner for loop. Therefore, this code takes $O(n^2)$ time.

Sum of Powers of 2

Consider this sequence: $2^0 + 2^1 + 2^2 + ... + 2^n$. What is its result?

A nice way to see this is by looking at these values in binary.

	Power	Binary	Decimal
	2^0	00001	1
	2^1	00010	2
	2^2	00100	4
	2^3	01000	8
	2^4	10000	16
sum:	2^5-1	11111	32 - 1 = 31

Therefore, the sum of $2^0 + 2^1 + 2^2 + ... + 2^n$ would, in base 2, be a sequence of (n + 1) 1s. This is $2^{n+1} - 1$.

Takeaway: The sum of a sequence of powers of two is roughly equal to the *next* value in the sequence.

Bases of Logs

Suppose we have something in $\log_2$ (log base 2). How do we convert that to $\log_{10}$? That is, what's the relationship between $\log_b k$ and $\log_x k$?

Let's do some math. Assume $c = \log_b k$ and $y = \log_x k$.

```
log_b k = c --> b^c = k          // This is the definition of log.
log_x(b^c) = log_x k             // Take log of both sides of b^c = k.
c log_x b = log_x k              // Rules of logs. You can move out the exponents.
c = log_b k = log_x k / log_x b  // Dividing above expression and substituting c.
```

Therefore, if we want to convert $\log_2 p$ to $\log_{10}$, we just do this:

$$\log_{10} p = \frac{\log_2 p}{\log_2 10}$$

Takeaway: Logs of different bases are only off by a constant factor. For this reason, we largely ignore what the base of a log within a big O expression. It doesn't matter since we drop constants anyway.

Permutations

How many ways are there of rearranging a string of n unique characters? Well, you have n options for what to put in the first characters, then n - 1 options for what to put in the second slot (one option is taken), then n - 2 options for what to put in the third slot, and so on. Therefore, the total number of strings is n!.

$$n! = n * (n - 1) * (n - 2) * (n - 3) * \ldots * 1$$

What if you were forming a k-length string (with all unique characters) from n total unique characters? You can follow similar logic, but you'd just stop your selection/multiplication earlier.

$$\frac{n!}{(n-k)!} = n * (n - 1) * (n - 2) * (n - 3) * \ldots * (n - k + 1)$$

Combinations

Suppose you have a set of n distinct characters. How many ways are there of selecting k characters into a new set (where order doesn't matter)? That is, how many k-sized subsets are there out of n distinct elements? This is what the expression n-choose-k means, which is often written $\binom{n}{k}$.

Imagine we made a list of all the sets by first writing all k-length substrings and then taking out the duplicates.

From the above *Permutations* section, we'd have $n!/(n-k)!$ k-length substrings.

Since each k-sized subset can be rearranged k! unique ways into a string, each subset will be duplicated k! times in this list of substrings. Therefore, we need to divide by k! to take out these duplicates.

$$\binom{n}{k} = \frac{1}{k!} * \frac{n!}{(n-k)!} = \frac{n!}{k!(n-k)!}$$

Proof by Induction

Induction is a way of proving something to be true. It is closely related to recursion. It takes the following form.

Task: Prove statement P(k) is true for all k >= b.

- Base Case: Prove the statement is true for P(b). This is usually just a matter of plugging in numbers.
- Assumption: Assume the statement is true for P(n).
- Inductive Step: Prove that *if* the statement is true for P(n), then it's true for P(n+1).

This is like dominoes. If the first domino falls, and one domino always knocks over the next one, then all the dominoes must fall.

Let's use this to prove that there are 2^n subsets of an n-element set.

- Definitions: let $S = \{a_1, a_2, a_3, \ldots, a_n\}$ be the n-element set.

- Base case: Prove there are 2^0 subsets of {}. This is true, since the only subset of {} is {}.
- Assume that there are 2^n subsets of $\{a_1, a_2, a_3, \ldots, a_n\}$.
- Prove that there are 2^{n+1} subsets of $\{a_1, a_2, a_3, \ldots, a_{n+1}\}$.

  Consider the subsets of $\{a_1, a_2, a_3, \ldots, a_{n+1}\}$. Exactly half will contain a_{n+1} and half will not.

  The subsets that do not contain a_{n+1} are just the subsets of $\{a_1, a_2, a_3, \ldots, a_n\}$. We assumed there are 2^n of those.

  Since we have the same number of subsets with x as without x, there are 2^n subsets with a_{n+1}.

  Therefore, we have $2^n + 2^n$ subsets, which is 2^{n+1}.

Many recursive algorithms can be proved valid with induction.

Topological Sort

A topological sort of a directed graph is a way of ordering the list of nodes such that if `(a, b)` is an edge in the graph then a will appear before b in the list. If a graph has cycles or is not directed, then there is no topological sort.

There are a number of applications for this. For example, suppose the graph represents parts on an assembly line. The edge (Handle, Door) indicates that you need to assemble the handle before the door. The topological sort would offer a valid ordering for the assembly line.

We can construct a topological sort with the following approach.

1. Identify all nodes with no incoming edges and add those nodes to our topological sort.
   - » We know those nodes are safe to add first since they have nothing that needs to come before them. Might as well get them over with!
   - » We know that such a node must exist if there's no cycle. After all, if we picked an arbitrary node we could just walk edges backwards arbitrarily. We'll either stop at some point (in which case we've found a node with no incoming edges) or we'll return to a prior node (in which case there is a cycle).
2. When we do the above, remove each node's outbound edges from the graph.
   - » Those nodes have already been added to the topological sort, so they're basically irrelevant. We can't violate those edges anymore.
3. Repeat the above, adding nodes with no incoming edges and removing their outbound edges. When all the nodes have been added to the topological sort, then we are done.

More formally, the algorithm is this:

1. Create a queue `order`, which will eventually store the valid topological sort. It is currently empty.
2. Create a queue `processNext`. This queue will store the next nodes to process.
3. Count the number of incoming edges of each node and set a class variable `node.inbound`. Nodes typically only store their outgoing edges. However, you can count the inbound edges by walking through each node `n` and, for each of its outgoing edges `(n, x)`, incrementing `x.inbound`.
4. Walk through the nodes again and add to `processNext` any node where `x.inbound == 0`.
5. While `processNext` is not empty, do the following:
   - » Remove first node n from `processNext`.

- » For each edge (n, x), decrement x.inbound. If x.inbound == 0, append x to processNext.
- » Append n to order.

6. If order contains all the nodes, then it has succeeded. Otherwise, the topological sort has failed due to a cycle.

This algorithm does sometimes come up in interview questions. Your interviewer probably wouldn't expect you to know it offhand. However, it would be reasonable to have you derive it even if you've never seen it before.

▸ Dijkstra's Algorithm

In some graphs, we might want to have edges with weights. If the graph represented cities, each edge might represent a road and its weight might represent the travel time. In this case, we might want to ask, just as your GPS mapping system does, what's the shortest path from your current location to another point p? This is where Dijksta's algorithm comes in.

Dijkstra's algorithm is a way to find the shortest path between two points in a weighted directed graph (which might have cycles). All edges must have positive values.

Rather than just stating what Dijkstra's algorithm is, let's try to derive it. Consider the earlier described graph. We could find the shortest path from s to t by literally taking all possible routes using actual time. (Oh, and we'll need a machine to clone ourselves.)

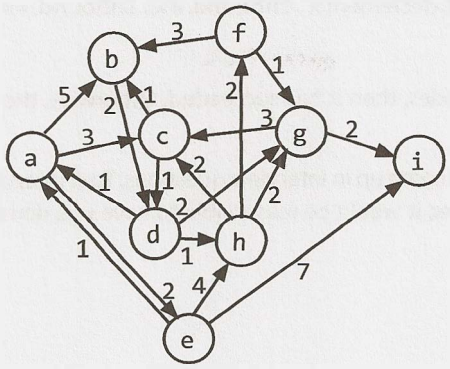
1. Start off at s.
2. For each of s's outbound edges, clone ourselves and start walking. If the edge (s, x) has weight 5, we should actually take 5 minutes to get there.
3. Each time we get to a node, check if anyone's been there before. If so, then just stop. We're automatically not as fast as another path since someone beat us here from s. If no one has been here before, then clone ourselves and head out in all possible directions.
4. The first one to get to t wins.

This works just fine. But, of course, in the real algorithm we don't want to literally use a timer to find the shortest path.

Imagine that each clone could jump immediately from one node to its adjacent nodes (regardless of the edge weight), but it kept a time_so_far log of how long its path would have taken if it did walk at the "true" speed. Additionally, only one person moves at a time, and it's always the one with the lowest time_so_far. This is sort of how Dijkstra's algorithm works.

Dijkstra's algorithm finds the minimum weight path from a start node s to *every* node on the graph.

Consider the following graph.



Assume we are trying to find the shortest path from a to i. We'll use Dijkstra's algorithm to find the shortest path from a to all other nodes, from which we will clearly have the shortest path from a to i.

We first initialize several variables:

- path_weight[node]: maps from each node to the total weight of the shortest path. All values are initialized to infinity, except for path_weight[a] which is initialized to 0.
- previous[node]: maps from each node to the previous node in the (current) shortest path.
- remaining: a priority queue of all nodes in the graph, where each node's priority is defined by its path_weight.

Once we've initialized these values, we can start adjusting the values of path_weight.

> A (min) **priority queue** is an abstract data type that—at least in this case—supports insertion of an object and key, removing the object with the minimum key, and decreasing a key. (Think of it like a typical queue, except that, instead of removing the oldest item, it removes the item with the lowest or highest priority.) It is an abstract data type because it is defined by its behavior (its operations). Its underlying implementation can vary. You could implement a priority queue with an array or a min (or max) heap (or many other data structures).

We iterate through the nodes in remaining (until remaining is empty), doing the following:

1. Select the node in remaining with the lowest value in path_weight. Call this node n.
2. For each adjacent node, compare path_weight[x] (which is the weight of the current shortest path from a to x) to path_weight[n] + edge_weight[(n, x)]. That is, could we get a path from a to x with lower weight by going through n instead of our current path? If so, update path_weight and previous.
3. Remove n from remaining.

When remaining is empty, then path_weight stores the weight of the current shortest path from a to each node. We can reconstruct this path by tracing through previous.

Let's walk through this on the above graph.

1. The first value of n is a. We look at its adjacent nodes (b, c, and e), update the values of path_weight (to 5, 3, and 2) and previous (to a) and then remove a from remaining.
2. Then, we go to the next smallest node, which is e. We previously updated path_weight[e] to be 2. Its adjacent nodes are h and i, so we update path_weight (to 6 and 9) and previous for both of those.

Observe that 6 is `path_weight[e]` (which is 2) + the weight of the edge `(e, h)` (which is 4).

3. The next smallest node is `c`, which has `path_weight` 3. Its adjacent nodes are b and d. The value of `path_weight[d]` is infinity, so we update it to 4 (which is `path_weight[c] + weight(edge c, d)`. The value of `path_weight[b]` has been previously set to 5. However, since `path_weight[c] + weight(edge c, b)` (which is 3 + 1 = 4) is less than 5, we update `path_weight[b]` to 4 and `previous` to `c`. This indicates that we would improve the path from a to b by going through `c`.

We continue doing this until `remaining` is empty. The following diagram shows the changes to the `path_weight` (left) and `previous` (right) at each step. The topmost row shows the current value for n (the node we are removing from `remaining`). We black out a row after it has been removed from `remaining`.

	INITIAL		n = a		n = e		n = c		n = b		n = d		n = h		n = g		n = f		FINAL	
	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr	wt	pr
a	0	-	removed																0	-
b	∞	-	5	a			4	c	removed										4	c
c	∞	-	3	a			removed												3	a
d	∞	-					4	c			removed								4	c
e	∞	-	2	a	removed														2	a
f	∞	-											7	h			removed		7	h
g	∞	-									6	d			removed				6	d
h	∞	-			6	e					5	d	removed						5	d
i	∞	-	∞	-	9	e									8	g			8	g

Once we're done, we can follow this chart backwards, starting at `i` to find the actual path. In this case, the smallest weight path has weight 8 and is `a -> c -> d -> g -> i`.

Priority Queue and Runtime

As mentioned earlier, our algorithm used a priority queue, but this data structure can be implemented in different ways.

The runtime of this algorithm depends heavily on the implementation of the priority queue. Assume you have v vertices and e nodes.

- If you implemented the priority queue with an array, then you would call `remove_min` up to v times. Each operation would take $O(v)$ time, so you'd spend $O(v^2)$ time in the `remove_min` calls. Additionally, you would update the values of `path_weight` and `previous` at most once per edge, so that's $O(e)$ time doing those updates. Observe that e must be less than of equal to v^2 since you can't have more edges than there are pairs of vertices. Therefore, the total runtime is $O(v^2)$.
- If you implemented the priority queue with a min heap, then the `remove_min` calls will each take $O(\log v)$ time (as will inserting and updating a key). We will do one `remove_min` call for each vertex, so that's $O(v \log v)$ (v vertices at $O(\log v)$ time each). Additionally, on each edge, we might call one update key or insert operation, so that's $O(e \log v)$. The total runtime is $O((v + e) \log v)$.

Which one is better? Well, that depends. If the graph has a lot of edges, then v^2 will be close to e. In this case, you might be better off with the array implementation, as $O(v^2)$ is better than $O((v + v^2) \log v)$. However, if the graph is sparse, then e is much less than v^2. In this case, the min heap implementation may be better.

Hash Table Collision Resolution

Essentially any hash table can have collisions. There are a number of ways of handling this.

Chaining with Linked Lists

With this approach (which is the most common), the hash table's array maps to a linked list of items. We just add items to this linked list. As long as the number of collisions is fairly small, this will be quite efficient.

In the worst case, lookup is `O(n)`, where `n` is the number of elements in the hash table. This would only happen with either some very strange data or a very poor hash function (or both).

Chaining with Binary Search Trees

Rather than storing collisions in a linked list, we could store collisions in a binary search tree. This will bring the worst-case runtime to `O(log n)`.

In practice, we would rarely take this approach unless we expected an extremely nonuniform distribution.

Open Addressing with Linear Probing

In this approach, when a collision occurs (there is already an item stored at the designated index), we just move on to the next index in the array until we find an open spot. (Or, sometimes, some other fixed distance, like the `index + 5`.)

If the number of collisions is low, this is a very fast and space-efficient solution.

One obvious drawback of this is that the total number of entries in the hash table is limited by the size of the array. This is not the case with chaining.

There's another issue here. Consider a hash table with an underlying array of size 100 where indexes 20 through 29 are filled (and nothing else). What are the odds of the next insertion going to index 30? The odds are 10% because an item mapped to any index between 20 and 30 will wind up at index 30. This causes an issue called *clustering*.

Quadratic Probing and Double Hashing

The distance between probes does not need to be linear. You could, for example, increase the probe distance quadratically. Or, you could use a second hash function to determine the probe distance.

Rabin-Karp Substring Search

The brute force way to search for a substring S in a larger string B takes `O(s(b-s))` time, where `s` is the length of S and b is the length of B. We do this by searching through the first `b - s + 1` characters in B and, for each, checking if the next `s` characters match S.

The Rabin-Karp algorithm optimizes this with a little trick: if two strings are the same, they must have the same hash value. (The converse, however, is not true. Two different strings can have the same hash value.)

Therefore, if we efficiently precompute a hash value for each sequence of `s` characters within B, we can find the locations of S in `O(b)` time. We then just need to validate that those locations really do match S.

For example, imagine our hash function was simply the sum of each character (where space = 0, a = 1, b = 2, and so on). If S is `ear` and B = `doe are hearing me`, we'd then just be looking for sequences where the sum is 24 (e + a + r). This happens three times. For each of those locations, we'd check if the string really is `ear`.

char:	d	o	e		a	r	e		h	e	a	r	i	n	g		m	e
code:	4	15	5	0	1	18	5	0	8	5	1	18	9	14	7	0	13	5
sum of next 3:	24	20	6	19	24	23	13	13	14	24	28	41	30	21	20	18		

If we computed these sums by doing `hash('doe')`, then `hash('oe ')`, then `hash('e a')`, and so on, we would still be at `O(s(b-s))` time.

Instead, we compute the hash values by recognizing that `hash('oe ') = hash('doe') - code('d') + code(' ')`. This takes `O(b)` time to compute all the hashes.

You might argue that, still, in the worst case this will take `O(s(b-s))` time since many of the hash values could match. That's absolutely true—for this hash function.

In practice, we would use a better *rolling hash function*, such as the Rabin fingerprint. This essentially treats a string like doe as a base 128 (or however many characters are in our alphabet) number.

$$\text{hash('doe')} = \text{code('d')} * 128^2 + \text{code('o')} * 128^1 + \text{code('e')} * 128^0$$

This hash function will allow us to remove the d, shift the o and e, and then add in the space.

$$\text{hash('oe ')} = (\text{hash('doe')} - \text{code('d')} * 128^2) * 128 + \text{code(' ')}$$

This will considerably cut down on the number of false matches. Using a good hash function like this will give us expected time complexity of `O(s + b)`, although the worst case is `O(sb)`.

Usage of this algorithm comes up fairly frequently in interviews, so it's useful to know that you can identify substrings in linear time.

▸ AVL Trees

An AVL tree is one of two common ways to implement tree balancing. We will only discuss insertions here, but you can look up deletions separately if you're interested.

Properties

An AVL tree stores in each node the height of the subtrees rooted at this node. Then, for any node, we can check if it is height balanced: that the height of the left subtree and the height of the right subtree differ by no more than one. This prevents situations where the tree gets too lopsided.

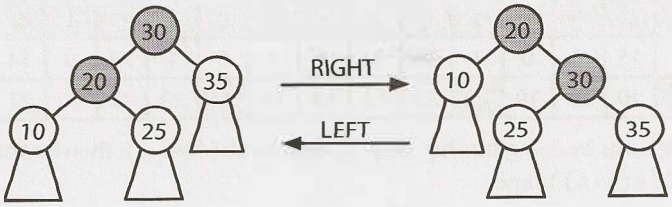
```
balance(n) = n.left.height - n.right.height

-1 <= balance(n) <= 1
```

Inserts

When you insert a node, the balance of some nodes might change to -2 or 2. Therefore, when we "unwind" the recursive stack, we check and fix the balance at each node. We do this through a series of rotations.

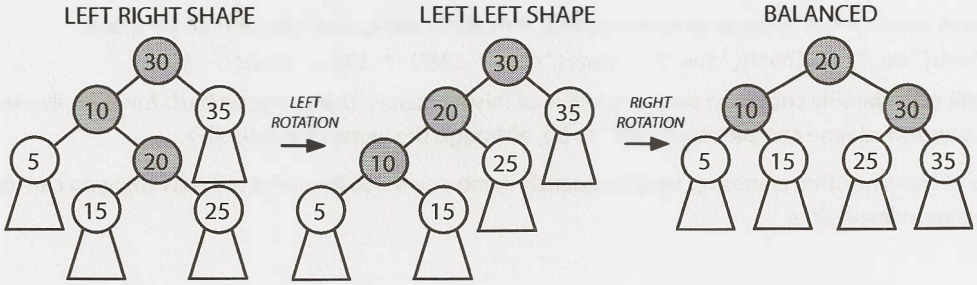
Rotations can be either left or right rotations. The right rotation is an inverse of the left rotation.



Depending on the balance and where the imbalance occurs, we fix it in a different way.

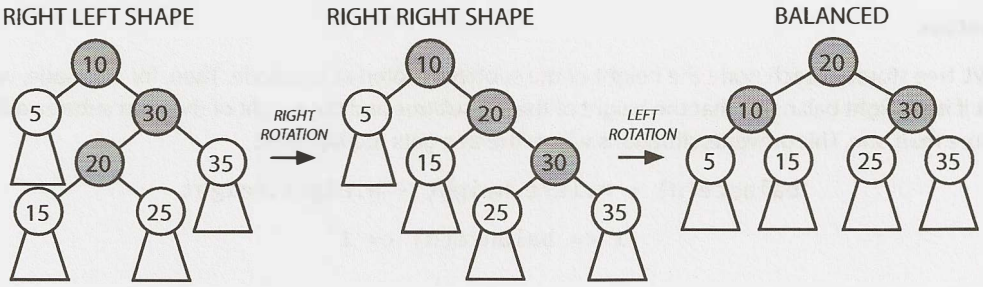
- *Case 1: Balance is 2.*

  In this case, the left's height is two bigger than the right's height. If the left side is larger, the left subtree's extra nodes must be hanging to the left (as in LEFT LEFT SHAPE) or hanging to the right (as in LEFT RIGHT SHAPE). If it looks like the LEFT RIGHT SHAPE, transform it with the rotations below into the LEFT LEFT SHAPE then into BALANCED. If it looks like the LEFT LEFT SHAPE already, just transform it into BALANCED.



- *Case 2: Balance is -2.*

  This case is the mirror image of the prior case. The tree will look like either the RIGHT LEFT SHAPE or the RIGHT RIGHT SHAPE. Perform the rotations below to transform it into BALANCED.



In both cases, "balanced" just means that the `balance` of the tree is between -1 and 1. It does not mean that the `balance` is 0.

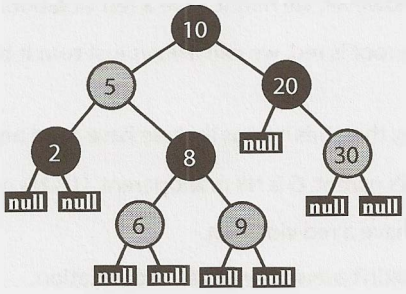
We recurse up the tree, fixing any imbalances. If we ever achieve a balance of 0 on a subtree, then we know that we have completed all the balances. This portion of the tree will not cause another, higher subtree to have a balance of -2 or 2. If we were doing this non-recursively, then we could break from the loop.

Red-Black Trees

Red-black trees (a type of self-balancing binary search tree) do not ensure quite as strict balancing, but the balancing is still good enough to ensure `O(log N)` insertions, deletions, and retrievals. They require a bit less memory and can rebalance faster (which means faster insertions and removals), so they are often used in situations where the tree will be modified frequently.

Red-black trees operate by enforcing a quasi-alternating red and black coloring (under certain rules, described below) and then requiring every path from a node to its leaves to have the same number of black nodes. Doing so leads to a reasonably balanced tree.

The tree below is a red-black tree (where the red nodes are indicated with gray):



Properties

1. Every node is either red or black.
2. The root is black.
3. The leaves, which are NULL nodes, are considered black.
4. Every red node must have two black children. That is, a red node cannot have red children (although a black node can have black children).
5. Every path from a node to its leaves must have the same number of black children.

Why It Balances

Property #4 means that two red nodes cannot be adjacent in a path (e.g., parent and child). Therefore, no more than half the nodes in a path can be red.

Consider two paths from a node (say, the root) to its leaves. The paths must have the same number of black nodes (property #5), so let's assume that their red node counts are as different as possible: one path contains the minimum number of red nodes and the other one contains the maximum number.

- Path 1 (Min Red): The minimum number of red nodes is zero. Therefore, path 1 has b nodes total.
- Path 2 (Max Red): The maximum number of red nodes is b, since red nodes must have black children and there are b black nodes. Therefore, path 2 has 2b nodes total.

Therefore, even in the most extreme case, the lengths of paths cannot differ by more than a factor of two. That's good enough to ensure an `O(log N)` find and insert runtime.

If we can maintain these properties, we'll have a (sufficiently) balanced tree—good enough to ensure `O(log N)` insert and find, anyway. The question then is how to maintain these properties efficiently. We'll only discuss insertion here, but you can look up deletion on your own.