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## Part I Data Structure

#### **CHAPTER**

### PRIORITY QUEUES AND HEAPS

1

#### Data

- Collection of elements
- Each element x has a priority x.priority

#### Operations

- INSERT(Q, x)Add x to QNote: x.priority can be non-unique
- Max(Q)Return the element with max priority Note: Q is unchanged
- Extract-Max(Q)
  Remove and return the element with the max priority

#### 1.1 Implementation

#### 1.1.1 Attempts

#### Implementation 1: Unsorted Array / Linked List

- Insert takes  $\Theta(1)$  time in the worst case
- Max takes  $\Theta(n)$  time in the worst case
- EXTRACTMAX takes  $\Theta(n)$  time in the worst case

#### Implementation 2: Sorted Array / Linked List

- INSERT takes  $\Theta(n)$  time in the worst case
- Max takes  $\Theta(1)$  time in the worst case
- EXTRACTMAX takes  $\Theta(1)$  time in the worst case

#### 1.1.2 Implementation

We want to combine the advantages of both data structures by having a "partially sorted" ADT – a (binary) *heap*.

There are two kinds of binary heaps: max-heaps and min-heaps. In both kinds, the values in the nodes satisfy a **heap property**, the specifics of which depend on the kind of heap.

- Max heap property: the key of every node x is *larger* than or equal to the keys of its children. The largest element in a max-heap is stored at the root.
- Min heap property: the key of every node x is *smaller* than or equal to the keys of its children. The smallest element in a min-heap is stored at the root,

These are called *heap orders*. There is no ordering between the siblings. A max/min heap is valid if it is a nearly complete binary tree and it satisfies the max/min heap property.

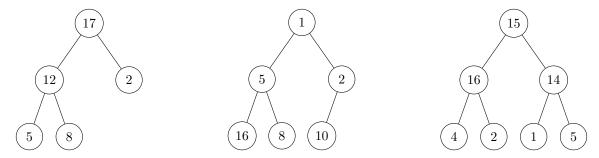


Figure 1.1: A valid max-heap (left), a valid min-heap (middle), and an invalid heap (right)

Although a heap is an almost complete binary tree  $^1$ , in practice, we usually use an array to store the data in memory. An array H that represents a heap is an object with two attributes: H.length, which (as usual) gives the number of elements in the array, and H.heap-size, which represents how many elements in the heap are stored within array H. The root of the tree is H[1], and given the index i of a node, we can compute the indices of its parent, left child, and right child:

• Parent	• Left	• Right
$\textbf{return}  \lfloor i/2 \rfloor$	$\mathbf{return}\ 2i$	<b>return</b> $2i + 1$

<sup>&</sup>lt;sup>1</sup>That is, the tree is completely filled on all levels except possibly the lowest, which is filled from the left up to a point.

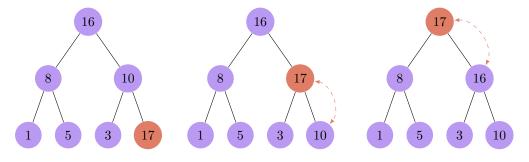
#### 1.2.1 INSERT

To insert element with key p into the heap H,

- Increment H.heap-size and add a new node with key p to the next available position
- Repeatedly swap the new item with its parent until the heap property is satisfied

  This swapping process is called **bubbling up**
- Worst-case runtime:  $\Theta(\lg n)$

For example, consider Insert(H, 17) where H = [16, 8, 10, 1, 5, 3]

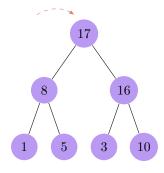


```
\begin{aligned} & \textbf{procedure} \  \, \text{MAX-HEAP-INSERT}(H,\,p) \\ & i \leftarrow H.heap\text{-}size \leftarrow H.heap\text{-}size + 1 \\ & H[i] = p \\ & \textbf{while} \  \, \text{PARENT}(i) > 0 \  \, \textbf{and} \  \, H[i] > H[\text{PARENT}(i)] \  \, \textbf{do} \\ & \text{swap} \  \, H[i] \  \, \textbf{with} \  \, H[\text{PARENT}[i]] \\ & i \leftarrow \text{PARENT}(i) \\ & \textbf{end} \  \, \textbf{while} \\ & \textbf{end procedure} \end{aligned}
```

#### 1.2.2 FIND-MAX

To find the maximum key in the heap H,

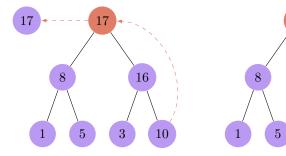
- Simply return the item in the root
- Worst-case runtime:  $\Theta(1)$

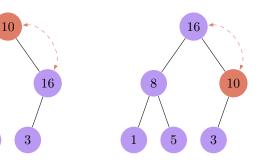


- 1: **procedure** FIND-MAX(H)
- 2: return H[1]
- 3: end procedure

#### 1.2.3 EXTRACT-MAX

- Save the item from the root in a temporary variable
- Replace the root with the rightmost item in the lowest level of the tree and decrement H.heap-size
- Repeatedly swap the item we moved with its largest child until the heap property is restored. This swapping process is called **bubble down**.
- Worst-case runtime:  $\Theta(\lg n)$





- 1: **procedure** Extract-Max(H)
- 2:  $max \leftarrow H[1]$
- 3:  $H[1] \leftarrow H[H.heap\text{-}size]$
- 4:  $H.heap\text{-}size \leftarrow H.heap\text{-}size 1$
- 5: MAX-HEAPIFY(H, 1)
- 6: **return** max
- 7: end procedure

```
1: procedure MAX-HEAPIFY(H, i)
        l \leftarrow \text{Left}(i)
        r \leftarrow \text{Right}(i)
 3:
 4:
        if l \leq H.heap\text{-}size and H[l] > H[i] then
             largest \leftarrow l
 5:
 6:
        else
             largest \leftarrow i
 7:
 8:
        end if
        if r \leq H.heap\text{-}size and H[r] > H[largest] then
 9:
             largest \leftarrow r
10:
        end if
11:
        if largest \neq i then
12:
            swap H[i] with H[largest]
13:
14:
             Max-Heapify(H, largest)
        end if
16: end procedure
```

#### 1.2.4 BUILD-MAX-HEAP

- Takes an array A of length n and builds a max-heap H from it.
- Worst-case runtime:  $\Theta(n)$

```
1: procedure BUILD-MAX-HEAP(A)
2: H.heap\text{-}size \leftarrow A.length
3: for i = \lfloor \frac{A.length}{2} \rfloor downto 1 do
4: MAX-HEAPIFY(H, i)
5: end for
6: end procedure
```

#### DICTIONARIES

#### Data

- $\bullet$  A set S
- Each element x has a **unique** key x.key

#### Operations

- Search(S, k)Return x in S with x.key = k (or NIL).
- INSERT(S, x)Add x to S – if S contains y with y.key = x.key, then  $replace\ y$  with x.
- Delete $(S,x)^{a}$

Remove element x from S.

 $<sup>^</sup>a\mathrm{If}$  we are given the key k instead of the element x, we could do  $\mathsf{Delete}(S,\mathsf{Search}(S,\,\mathbf{k}))$ 

	Search	Insert	Delete#
unsorted array	n	n	1
sorted* array	$\lg n$	n	n
unsorted linked list	n	n	1
sorted* linked list	n	n	1
direct access table	1	1	1
hash table	n	n	n
binary search tree	height of the BST	height of the BST	height of the BST
balanced search tree	$\lg n$	$\lg n$	$\lg n$

<sup>\*:</sup> these require the keys to be ordered

<sup>#</sup>: here we are only doing deletion (without having to search for x)

A binary search tree is a binary tree with the binary-search-tree property:

Let x be a node in a binary search tree. If y is a node in the left subtree of x, then  $y.key \le x.key$ . If y is a node in the right subtree of x, then  $y.key \ge x.key$ .

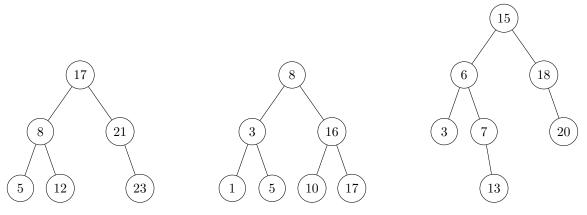


Figure 2.1: Examples of binary search trees

class BST\_Node: class Dictionary: class Item: key: Any item: Item root: BST\_Node

left: BST\_Node right: BST\_Node

#### 2.1.1INSERT

value: Any

```
1: procedure Insert(S, x)
      S.root \leftarrow BST-INSERT(S.root, x)
```

```
3: end procedure
```

```
1: procedure BST-INSERT(root, x)
 2:
        # Insert x into stubree at root; return new
    root
        if root = NIL then
 3:
            root \leftarrow \text{BST} \quad \text{Node}(x) \text{ # Add } x
 4:
        else if x.key < root.item.key then
 5:
            root.left \leftarrow \text{BST-Insert}(root.left, x)
 6:
 7:
        else if x.key > root.item.key then
            root.right \leftarrow BST-Insert(root.right, x)
 8:
        else # x.key = root.item.key
 9:
            root.item \leftarrow x \text{ # replace with } x
10:
        end if
11:
12:
        return root
13: end procedure
```

#### 2.1.2 SEARCH

```
1: procedure SEARCH(S, k)

2: node \leftarrow BST-SEARCH(S.root, k)

3: if node = NIL then

4: return NIL

5: end if

6: return node.item

7: end procedure
```

```
1: procedure BST-SEARCH(root, k)
       # Return node under root with key k (or NIL)
2:
       if root = NIL then
3:
           pass # k not in tree
4:
       else if k < root.item.key then
5:
           root \leftarrow BST\text{-}Search(root.left, k)
6:
       else if k > root.item.key then
7:
           root \leftarrow BST\text{-}Search(root.right, k)
8:
       else # k = root.item.key
9:
           pass
10:
       end if
11:
       return root
12:
13: end procedure
```

#### 2.1.3 Delete

```
1: procedure DELETE(S, k)
2: S.root \leftarrow BST-DELETE(S.root, k)
3: end procedure
```

```
1: procedure BST-DELETE(root, x)
       # Delete x from stubree at root; return new root
3:
       if root = NIL then pass # x not in tree
       else if x < root.item.key then
4:
           root.left \leftarrow BST-Delete(root.left, x)
5:
       else if x > root.item.key then
6:
           root.right \leftarrow \text{BST-Delete}(root.right, x)
7:
8:
       else # x.key = root.item.key
           if root.left = NIL then
9:
               root \leftarrow root.right \# could be NIL
10:
           else if root.right = NIL then
11:
               root \leftarrow root.left
12:
13:
           else # Replace root.item with its successor
               root.item, root.right \leftarrow \text{BST-Del-Min}(root.right)
14:
           end if
15:
       end if
16:
       return root
18: end procedure
```

```
1: procedure BST-DEL-MIN(root)
2: # Remove element with smallest key under root; return item and root of resulting subtree

Require: root ≠ NIL
3: if root.left = NIL then
4: return root.item, root.right
5: else
6: item, root.left ← BST-DEL-MIN(root.left)
7: return item, root
8: end if
9: end procedure
```

#### 2.2 Balanced Search trees

Despite the simplicity of the BST, it is not a very efficient data structure. The worst-case running time of the BST operations is proportional to the height of the tree, which is  $\Theta(n)$ , where n is the number of elements in the tree. The shape of a BST is determined by the order in which keys are inserted. If the keys are inserted in sorted order, the BST degenerates into a linked list.

We can improve the performance of the BST by making it more balanced. A balanced BST (also known as an AVL tree – Adelson-Velsky, Landis Tree) is one in which the heights of the two subtrees of any node differ by at most one. The height of a balanced BST is  $\Theta(\log n)$ , where n is the number of elements in the tree.

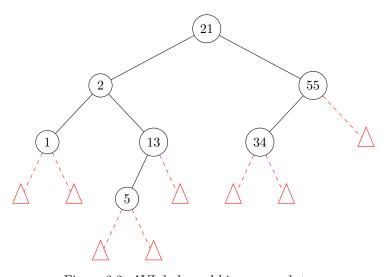


Figure 2.2: AVL balanced binary search tree

To implement an AVL tree, we need a mechanism to detect imbalance in the tree, and a way to restore balance. We will use the following definition of  $balance\ factor$  of a node x in a BST:

#### Definition 2.2.1 Balance Factor

An AVL balanced node x has a balance factor of -1, 0, or 1. If the height of its left subtree is  $h_L$ , and the height of its right subtree is  $h_R$ , then x has a balance factor of  $h_L - h_R$ .

- If  $h_R h_L = 0$ , then x is balanced.
- If  $h_R h_L = 1$ , then x is right-heavy.
- If  $h_R h_L = -1$ , then x is left-heavy.

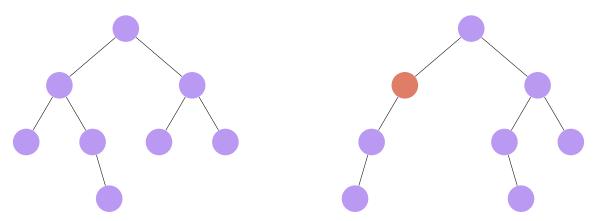


Figure 2.3: AVL balanced tree (left) and unbalanced tree (right)

#### Rotations

To restore balance, we need to perform a *rotation* on the tree. There are four types of rotations, depending on the balance factor of the node and its children. The following figure shows the four types of rotations.

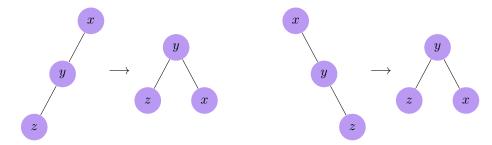


Figure 2.4: Single Left Rotation

Figure 2.5: Single Left Rotation

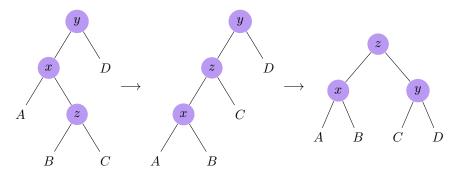


Figure 2.6: Double Left-Right Rotation

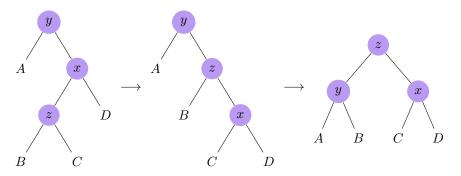


Figure 2.7: Double Right-Left Rotation

#### 2.2.1 INSERT

```
1: procedure AVL-INSERT(root, x)
         # Insert x into the tree at root, return new root
2:
        \mathbf{if} \ \mathit{root} = \mathrm{NIL} \ \mathbf{then}
3:
             root \leftarrow AVL \quad Node(x) \# add x
 4:
        else if x.key < root.item.key then
5:
             root.left \leftarrow AVL-Insert(root.left, x)
6:
             root \leftarrow \text{AVL-Balance-Right}(root)
 7:
        else if x.key > root.item.key then
8:
             root.right \leftarrow \text{AVL-Insert}(root.right, x)
9:
             root \leftarrow AVL-BALANCE-LEFT(root)
10:
11:
        \mathbf{else} \# \ x.key = root.item.key
             root.item \leftarrow x \text{ # replace with } x
12:
        end if
13:
        return \ root
14:
15: end procedure
```

#### 2.2.2 **Delete**

```
procedure AVL-DELETE(root, x)
   # Delete x from the tree at root, return new root
   if root = NIL then
       pass # x not in tree
   else if x.key < root.item.key then
       root.left \leftarrow AVL-Delete(root.left, x)
       root \leftarrow AVL-BALANCE-LEFT(root)
   else if x.key > root.item.key then
       root.right \leftarrow AVL-Delete(root.right, x)
       root \leftarrow AVL-BALANCE-RIGHT(root)
   else \# x.key = root.item.key
       if root.left = NIL then
           root \leftarrow root.right \# could be NIL
       else if root.right = NIL then
           root \leftarrow root.left
       else
           if root.left.height > root.right.height then
               root.item, root.left \leftarrow \text{AVL-Delete-Max}(root.left)
           else
               root.item, root.right \leftarrow \text{AVL-Delete-Min}(root.right)
           end if
       end if
       root.height \leftarrow 1 + Max(root.left.height, root.right.height)
   end if
   return root
end procedure
```

```
procedure AVL-Del-Max(root)

# Delete the maximum item from the tree at root, return new root and deleted item

Require: root ≠ NIL

if root.right = NIL then

return root.item, root.left

else

item, root.right ← AVL-Delete-Max(root.right)

root ← AVL-Balance-Right(root)

return item, root

end if
end procedure
```

#### 2.2.3 Rebalancing

```
1: procedure AVL-BALANCE-LEFT(root)
Require: root \neq NIL
       # First, recalculate height
       root.height \leftarrow 1 + \text{Max}(root.left.height, root.right.height)
3:
4:
        # Then, rebalance the left, if necessary
       if root.right.height > root.left.height + 1 then
5:
           # Check for double rotation
6:
           if root.right.left.height > root.right.right.height then
 7:
               root.right \leftarrow AVL-Rotate-Right(root.right)
8:
9:
10:
           root \leftarrow \text{AVL-Rotate-left}(root)
        end if
11:
       {f return}\ root
12:
13: end procedure
```

```
1: procedure AVL-ROTATE-LEFT(parent)
Require: parent \neq NIL, parent.right \neq NIL
        # Rearrange references
 2:
        child \leftarrow parent.right
 3:
 4:
        parent.right \leftarrow child.left
        child.left \leftarrow parent
 5:
        # Update heights; parent first because it is now deeper
 6:
        parent.height \leftarrow 1 + \text{Max}(parent.left.height, parent.right.height)
 7:
        child.height \leftarrow 1 + \text{Max}(\textit{child.left.height}, \textit{child.right.height})
 8:
 9:
        # Return new parent
        return child
10:
11: end procedure
```

#### 2.3 Hashing

• Universe U

The set of all keys. We assume that |U| is very large.

 $\bullet$  Hash Table T

An array of fixed size m. Each location T[i] is called a bucket.

• Hash Function h

The hash function  $h: U \to \{0, 1, \dots, m-1\}$  maps each key in U to an index in  $\{0, 1, \dots, m-1\}$ . For each key  $k \in U$ , h(k) is called the *home bucket* of k.

To access item with key k, examine T[h(k)].

A hash table is an effective data structure for implementing dictionaries. Although SEARCH for an element in a hes table can take as long as searching for an element in a linked list –  $\Theta(n)$  time in the worst case – in practice, hashing preforms extremely well. Under reasonable assumptions, the average time to search for an element in a hash table is  $\mathcal{O}(1)$ .

#### 2.3.1 Direct Access Tables

Direct addressing is a simple technique that works well when the universe U of keys is reasonably small. If U is small, then we can use an array T of size |U| to implement a dictionary, called a direct access table. The key k is used as an index into T to access the item with key k.

#### 2.3.2 Hash Tables

The downside of direct addressing is apparent: if the universe U is large or infinite. storing a table T of size |U| is impractical, and the set K of keys *actually stored* may be so small relative to Y that most of the space allocated for T would be wasted. Instead, we use a hash table.

However, when  $m \ll |U|$ , collisions are unavoidable. A *collision* occurs when two keys  $k_1$  and  $k_2$  (with  $k_1 \neq k_2$ ) are mapped to the same bucket  $h(k_1) = h(k_2)$ . There are two ways to handle collisions: *open addressing* and *closed addressing* / *chaining*.

#### Open Addressing

In open addressing, if T[h(k)] is occupied, then we search for the next available location in T to store the item with key k. We call the original hash function  $h_1$  the *primary hash function*, such that  $h_1(k)$  is the home bucket of k. We use the *probe sequence* h(k,i) to determine the bucket to try after i collisions.

• Linear Probing

$$h(k,i) = (h_1(k) + i) \mod m$$

Note that long clusters of occupied buckets can occur.

• Quadratic Probing

$$h(k,i) = (h_1(k) + c_1i + c_2i^2) \mod m$$

 $c_1$  and  $c_2$  are constants dependent on m.

• Double Hashing

 $h(k,i) = (h_i(k) + i \cdot (h_2(k))) \mod m$ , where  $h_2(k)$  is a secondary hash function.

#### Close Addressing / Chaining

In close addressing, we use a linked list to store the items in each bucket. Each nonempty slot points to a linked list, and all the elements that hash to the same slot go into that slot's linked list.

The average-case performance of the hash table depends on how evenly the hash function h distributes the keys across the buckets in the table. The <u>simple uniform hashing assumption</u>(SUHA)

states that any given key is equally likely to hash into any of the m slots of the table, independently of where any other elements has hashed to. Under this assumption, the expected number of keys in each bucket is the same.

The expected number of keys in a bucket is  $\frac{n}{m}$ , where n is the number of items in the table and m is the size of the table. This ratio is called the *load factor* of the hash table, and we denote it by  $\alpha$ .

#### DYNAMIC ARRAY

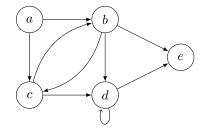
C styled arrays are static, meaning that they have a fixed size. In this chapter, we will learn how to implement a dynamic array, which is a data structure that can grow and shrink in size.

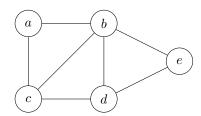
```
class DynamicArray {
    capacity: integer # room for elements
    size: integer # actual number of elements
};
```

```
1: procedure Insert(A, x)
                                                   1: procedure Resize(A)
                                                          B \leftarrow \text{DynamicArray}(2 \times A.capacity)
      if A.size = A.capacity then
          A \leftarrow \text{Resize}(A)
                                                          for i = 1 to A.size do
3:
                                                   3:
      end if
                                                             INSERT(B, A[i])
4:
                                                   4:
      A.size \leftarrow A.size + 1
                                                          end for
                                                   5:
      A[A.size] \leftarrow x
                                                          return B
                                                   6:
                                                   7: end procedure
7: end procedure
```

To analyze the running time of the above algorithm, see this example using accounting method for amortized analysis. The amortized running time of the above algorithm is  $\Theta(1)$ .

#### GRAPHS





#### 4.1

#### Graphs

#### 4.1.1 Graphs

Define a graph  $G = \{V, E\}$ 

#### Representations

• Adjacency matrix

	a	b	c	d	e
$\overline{a}$	0	1	1	0	0
b	1	0	1	1	1
c	1	1	0	1	0
d	0	1	1	0	1
e	0 1 1 0 0	1	0	1	0

Complexity: let n = |V| and m = |E|

• Space:  $O(n^2)$ 

• Edge query:  $\Theta(1)$  time

• Adjacency list

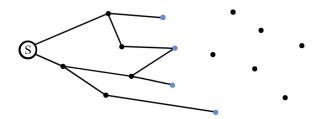
Complexity: let n = |V| and m = |E|

• Space:  $\Theta(n+m)$ 

• Edge query:  $\Theta(n)$  in worst-case time

#### 4.1.2 Breadth-First Search

In breadth first search, we start at a source  $s \in V$ , and explore every vertex reachable from a, using only edges.



We assign each vertex  $v \in V$  a color, which can be one of the following:

- ullet White: v has not been discovered
- Gray: v has been discovered, but not explored
- ullet Black: v has been discovered and explored

Define  $\pi[v]$  to be the predecessor of v in the breadth-first search tree.

Define d[v] to be the distance from s to v in the breadth-first search tree.

We use a queue to keep track of the vertices that we have discovered, but not yet explored.

```
1: procedure BFS(G, s)
         # Initialize tracking info for all vertices
 3:
         for v \in G.V do
 4:
              colour[v] = white
              \pi[v] \leftarrow \text{NIL}
 5:
              d[v] \leftarrow \infty
 6:
         end for
 7:
 8:
         # Initialize empty queue and source vertex tracking info
         Q \leftarrow \text{Make-queue}()
 9:
         \operatorname{colour}[s] \leftarrow \operatorname{gray}
10:
         \pi[s] \leftarrow \text{NIL}
11:
         d[s] \leftarrow 0
12:
13:
         ENQUEUE(Q, s)
         # Main loop. Loop Invariant: Q contains all (and only) gery vertices
14:
         while Q \neq \text{Empty-queue do}
15:
              u \leftarrow \text{Dequeue}()
16:
              for v \in G.Adj[u] do
17:
                   if \operatorname{colour}[v] \leftarrow \text{white then}
18:
                       \operatorname{colour}[v] \leftarrow \operatorname{gray}
19:
                       \pi[v] \leftarrow u
20:
                       d[v] \leftarrow d[u] + 1
21:
                       ENQUEUE(Q, v)
22:
                   end if
23:
              end for
24:
              colour[u] = black
25:
         end while
26:
27: end procedure
```

In breath first search,

- Each vertex is enqueued at most once
- Each vertex is dequeued at most once
- Each adjacent list is examined at most once
- The time complexity is  $\Theta(n+m)$

#### **BFS Finds Shortest Paths**

Define  $\delta(s, v)$  to be the length of the shortest path from vertex s to vertex v (i.e. the smallest number of edges in any path from s to v). If there is no path from s to v, then  $\delta(s, v) = \infty$ . Note that this definition will change when we consider weighted graphs.

```
Theorem 4.1.1 Let G = \{V, E\} be a graph, and let s \in V. Then, after BFS(G, s), \forall v \in V, \delta(s, v) = d[v]
```

To prove this theorem, we will need to prove the following lemmas first.

#### **Lemma 4.1.1** $\forall (u, v) \in E, \ \delta(s, v) \leq \delta(s, u) + 1$

Proof. (idea)

If  $\delta(s, u) = \infty$ , then the claim holds trivially.

If  $\delta(s, u) \neq \infty$ , then u is reachable from s.

Thus, v is also reachable from s.

Thus, the shortest path from s to v is no longer than the shortest path from s to u, plus the edge (u, v).

Hence,  $\delta(s, v) \leq \delta(s, u) + 1$ .

#### Lemma 4.1.2 At ant point during BFS, $\forall v \in V, d[v] \geq \delta(s, v)$

Proof. (idea)

Use induction on the number of ENQUEUE operations.

Immediately after we do the first ENQUEUE operation, d[s] = 0, and  $\delta(s, s) = 0$ .

We also have  $d[v] = \infty$ , and  $\delta(s, v) = \infty$  for all  $v \in V - \{s\}$ .

Now, consider some vertex v that is first discovered while visiting a vertex u.

By the IH, we have  $d[u] \geq \delta(s, u)$ .

Hence,  $d[v] = d[u] + 1 \ge \delta(s, u) + 1$  by Lemma 4.2.1.

Then v is painted grey and d[v] is not changed for the rest of the algorithm.

**Lemma 4.1.3** If 
$$Q = \langle v_1, \dots, v_r \rangle$$
, then  $d[v_i] \leq d[v_{i+1}]$  for all  $i \in \{1, \dots, r-1\}$  and  $d[v_r] \leq d[v_1] + 1$ 

Proof. (sketch)

Use induction on the number of Dequeue / Enqueue operations.

When  $Q = \langle s \rangle$ , the claim holds trivially.

To prove the inductive step, we need to show that the lemma hold after applying DEQUEUE / ENQUEUE to  $Q = \langle v_1, \dots, v_3 \rangle$ .

• Case 1

If we perform a DEQUEUE operation, then  $Q = \langle v_2, \dots, v_3 \rangle$  afterwards.

By the IH,  $d[v_r] \le d[v_1] + 1$  and  $d[v_1] \le d[v_2]$ .

Hence,  $d[v_r] \le d[v_2] + 1$ .

All other inequalities are unaffected.

• Case 2

If we perform a ENQUEUE operation, then  $Q = \langle v_1, \dots, v_{r+1} \rangle$  afterwards.

We discover  $v_{r+1}$  while visiting some vertex u, so  $d[v_{r+1}] = d[u] + 1$ .

Vertex u must have been the previous vertex dequeued from the queue.

Hence, either  $v_1$  was discovered while visiting u, in which case  $[v_1] = d[u] + 1$ , or Q was equal to  $\langle u_2, v_1, \ldots \rangle$  at some prior point, in which case  $d[u] \leq d[v_1]$  by IH.

Hence, 
$$d[v_{r+1}] = d[u] + 1 \le d[v_1] + 1$$
.

Otherwise,  $d[v_r] \leq d[u] + 1 = d[v_{r+1}]$  by the IH.

Now, we can prove the theorem.

*Proof.* To derive a contradiction, suppose  $d[v] \neq \delta(s, v)$  for some vertex  $v \in V$ .

Suppose v is a vertex with minimal  $\delta(s, v)$  for which this is satisfied.

By Lemma 4.1.2, we have  $d[v] > \delta(s, v)$ .

Because we chose v with minimal  $\delta(s, v)$ , we have  $d[u] = \delta(s, u)$ .

Hence,  $d[v] > \delta(s, v) = \delta(s, u) + 1 = d[u] + 1$ .

Consider the colour of v when we first dequeue u from Q.

- If v is painted white, then we set d[v] = d[u] + 1, which is a contradiction.
- If v is painted **black**, then v was in the queue before u. By Lemma 4.1.3, we have  $d[v] \leq d[u]$ , which is a contradiction.
- If v is painted **grey**, then v was discovered while visiting some vertex w that was dequeued earlier than u. Hence, d[v] = d[w] + 1, and by Lemma 4.1.3 we have  $d[w] \le d[u]$ . So  $d[v] \le d[u] + 1$ , which is a contradiction.

#### Time complexity of BFS

- Initialization (painting vertices white, setting entries of d to  $\infty$  and entries of  $\pi$  to NIL) takes  $\Theta(|V|)$  time.
- After initialization, we never paint a vertex white.
- Thus, each vertex is enqueued/dequeued at most once.
- Hence, we spend  $\mathcal{O}(|V|)$  time doing queue operations.
- Every time we dequeue a vertex, we scan its out-neighbourhood to discover its neighbours:
  - With an **adjacency list**, we consider each edge at most once (or at most twice in an undirected graph), so in total we need at most  $\mathcal{O}(|E|)$  time to consider all of the edges.
  - With an adjacency matrix, we scan each row of the matrix at most once, so in total we need at most  $\mathcal{O}(|V|^2)$  time to consider all of the edges.

Using adjacency list:  $\mathcal{O}(|V| + |E|)$  Using adjacency matrix:  $\mathcal{O}(|V|^2)$ 

#### 4.1.3 Depth-First Search

- In DFS, we walk through the graph as far as possible until we hit a dead end when this happens, we backtrack to an undiscovered vertex.
- Similar to BFS, we paint vertices as we go:
  - Painted white: undiscovered
  - Painted grey: discovered but not yet visited
  - Painted black: visited
- Instead of storing distances/depths, we store timestamps:
- disc[v] = time at which v is first discovered
  - vis[v] = time at which we finish visiting v
- One approach is to simply replace the *queue* from the BFS algorithm with a *stack*. This gives us an **iterative** DFS algorithm.
- However, it is more natural to write DFS as a recursive algorithm.

```
1: procedure DFS(G)
                                                                   1: procedure DFS-VISIT(G, v)
         # Initialization
                                                                           # Discovered (colour[v] = grey)
                                                                   2:
 3:
         for each v \in G.V do
                                                                   3:
                                                                           d[v] \leftarrow \text{time} \leftarrow \text{time} + 1
             d[v] \leftarrow f[v] \leftarrow \infty
                                                                           # Do something with v, if desired
 4:
                                                                   4:
             \pi[v] \leftarrow \text{NIL}
                                                                           # Explore v's adjacency list
 5:
                                                                   5:
         end for
                                                                           for each u \in G.adi[v] do
 6:
                                                                   6:
         time \leftarrow 0 \# global
                                                                               if d[u] = \infty then
 7:
                                                                   7:
 8:
         # Main loop
                                                                   8:
                                                                                    \# \operatorname{colour}[u] = \operatorname{white}
         for each v \in G.V do
                                                                                    \pi[u] = v
 9:
                                                                   9:
             if d[v] = \infty then
                                                                                    DFS-Visit(G, u)
10:
                                                                  10:
                 \# \operatorname{colour}[v] = \operatorname{white}
                                                                               end if
11:
                                                                  11:
                  DFS-Visit(G, v)
                                                                           end for
12:
                                                                  12:
             end if
                                                                           # Finished (colour[v] = black)
13:
                                                                  13:
         end for
                                                                           f[v] \leftarrow \text{time} \leftarrow \text{time} + 1
14:
                                                                  14:
15: end procedure
                                                                  15: end procedure
```

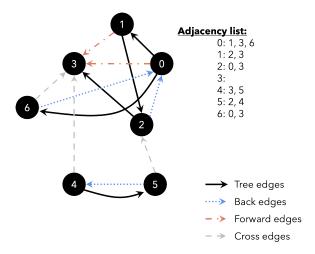
#### **DFS Forests**

We classify each edge (u, v) based on the colour of v when we consider this edge:

- Tree edges are the edges  $u, v \in E$  that form the DFS forest stored by  $\pi$ The vertex v is painted white when (u, v) is considered
- Back edges are the edges  $(u, v) \in E$  such that v is an ancestor of u in the DFS forest. The vertex v is painted **grey** when (u, v) is considered

- Forward edges are the edges  $(u, v) \in E$  such that v is a descendant of u in the DFS forest The vertex v is painted black when (u, v) is considered
- Cross edges are all other edges  $(u, v) \in E$  that are not part of the DFS forest (i.e. v is neither an ancestor nor a descendant of u)

The vertex v is painted **black** when (u, v) is considered



Note that for undirected graphs, there are NO forward edges and NO cross edges.

#### Time Complexity

The run-time of DFS is similar to BFS.

Using adjacency list:  $\mathcal{O}(|V| + |E|)$  Using adjacency matrix:  $\mathcal{O}(|V|^2)$ 

#### Parenthesis theorem

Theorem 4.1.2 After performing  $\mathbf{DFS}(G=(V,E))$ , for any two vertices u,  $v \in V$ , exactly one of the following statements holds:

- 1 The intervals [disc[u], vis[u]] and [disc[v], vis[v]] are disjoint, and neither u nor v is a descendant of the other in the DFS forest.
- 2 The interval [disc[u], vis[u]] is contained entirely in the interval [disc[v], vis[v]], and u is a descendant of v in the DFS forest.
- 3 The interval [disc[v], vis[v]] is contained entirely in the interval [disc[u], vis[u]], and v is a descendant of u in the DFS forest.

Proof. (sketch)

Suppose that disc[u] < disc[v].

• Case 1: disc[v] < vis[u]



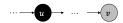
v is first discovered while u is painted grey.

So v is a descendant of u.

We don't backtrack to u until we have finished visiting v.

Therefore, we paint v black and set vis[v] before backtracking to u. Hence, vis[v] < vis[u].

• Case 2: vis[u] < disc[v]



v is first discovered while u is painted black.

So v is not a descendant of u.

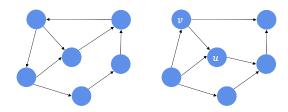
Since disc[u] < dics[v], u is not a descendant of v.

Since disc[u] < vis[u] and disc[v] < vis[v], we have disc[u] < vis[u] < disc[v] < vis[v].

When disc[v] < disc[u], proof is symmetric.

#### 4.1.4 Strongly connected

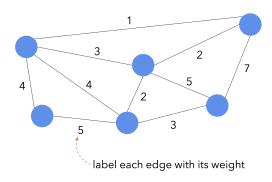
Recall that an undirected graph is connected if and only if there is a path of edges between any pair of vertices in V. What about directed graphs? A directed graph G = (V, E) is strongly connected if and only if, for all  $u, v \in V$ , there is a path of edges from u to v in G.



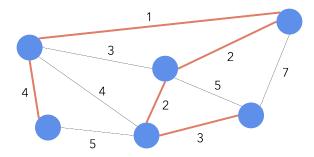
A strongly connected graph (left) and a non-strongly connected graph (right, where v is not reachable from u)

- Run DFS on the **transpose** of G (reverse edge direction of all edges in G)
- Reorder vertices in decreasing order of finish time (in G.V and within each adjacency list) Run DFS on G using the new ordering of vertices
- Each DFS tree is one strongly connected component

In a weighted graph G = (V, E), each edge  $e \in E$  has a weight w(e)



A minimum spanning tree (MST) T of a weighted, undirected, connected graph G = (v, E) is an acyclic subset of E that connects all of the vertices in V and whose total weight  $\sum_{\{u,v\}\in T} w(\{u,v\})$  is minimized.



Above, we define an MST as a set of edges. We also often call the graph M=(V,T) an MST of G.

The graph M=(V,T) belongs to a special class of graphs called **trees**, which can be defined in many ways.

#### 4.2.1 Prim's Algorithm

In Prim's Algorithm, we start with an empty tree T, add edges one at a time to T until we have an MST. At each step, pick the **smallest** edge that connects some vertex in T to a vertex outside T.



```
procedure PRIM(G, w : E \to \mathbb{R}, r \in G.V)
   # Initialization
   T = \varnothing
   Q = \text{Make-Queue}(G.V)
   # Place all vertices in the queue
   for v \in G.V do
       pri[v] = \infty
       \pi[v] = \text{NIL}
       Q.Insert(v)
   end for
   # Now, set r as the root
   pri[r] = 0
   Q.Decrease-Key(r)
   # Main loop
   while not Q.Empty() do
       # Connect a vertex with minimum priority (edge weight)
       u = Q.\text{Extract-Min}()
       if \pi[u] \neq NIL then T = T \cup \{\pi[u], u\}
       end if
       # Update priorities of neighbors of u
       for v \in G.Adj[u] do
          if v \in Q and w(u, v) < pri[v] then
              \pi[v] = u
              pri[v] = w(u, v)
              Q.Decrease-Key(v)
          end if
       end for
   end while
   {\bf return}\ T
end procedure
```

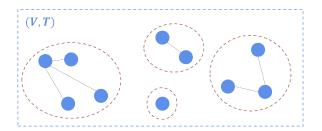
#### Runtime

- Initialization:  $\Theta(n)$
- Main loop: n iterations; one Extract-Min each time  $\Theta(n \lg n)$
- Inner loop: examine each edge twice; at most Decrease-Key per edge  $\Theta(m\lg n)$
- Overall:  $\Theta((m+n)\lg n)$

Note that to make Decrease-Key efficient, we need to track index[v] – the position of v in the min-heap – and update the index values during each swap.

#### 4.2.2 Kruskal's algorithm

In Kruskal's algorithm, we repeatedly pick the **cheapest edge** of the graph G that **does not create a cycle** in the current set of edges.



```
1: procedure Kruskal(G, w)
        # Sort edges: w(e_1) \le w(e_2) \le \cdots \le w(e_m)
        T = \varnothing
3:
        for each e_i = e_1, e_2, ..., e_m do
4:
           let (u_i, v_i) = e_i
5:
            if u_i, v_i are not already connected by an edge in T then
6:
                T = T \cup \{e_i\}
7:
            end if
8:
9:
        end for
        {\bf return}\ T
10:
11: end procedure
```

To determine if  $u_i, v_i$  are already connected, we can use BFS / DFS, which takes  $\Theta(n)$  time <sup>1</sup>. The overall run-time would be  $\Theta(m \cdot n)$ .

To make this algorithm more efficient, we can use disjoint sets.

<sup>&</sup>lt;sup>1</sup>BFS / DFS takes  $\Theta(m+n)$  time. Since  $m \le n-1$ , this step takes  $\Theta(n)$  time.

```
1: procedure Kruskal(G, w)
        # Sort edges: w(e_1) \le w(e_2) \le \cdots \le w(e_m)
3:
        T = \varnothing
        for \mathbf{do}v \in G.V
 4:
            Make-Set(v)
 5:
        end for
6:
        for each e_i = e_1, e_2, ..., e_m do
7:
8:
            let (u_i, v_i) = e_i
            if FIND-SET(u_i) \neq FIND-SET(v_i) then
9:
                T = T \cup \{e_i\}
10:
                Union(u_i, v_i)
11:
            end if
12:
        end for
13:
14:
        return T
15: end procedure
```

#### 4.3

#### Disjoint Sets

#### Data

 A collection {S,...,S} of disjoint, dynamic sets where S<sub>i</sub> ≠ Ø
 Each set in this collection contains a single representative

#### Operations

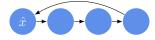
- Make-Set(x) Precondition:  $x \in U, x \notin S_1, ..., x \notin S_n$ Create a new set  $S_x = \{x\}$ , add  $S_x$  to the collection
- FIND-SET(x)

Return the representative element for set S s.t.  $x \in S$ , or NIL if x no such S exists

To check if two elements belong to the same set, we can simply check if they have the same representative. Note that we cannot ask for all t he elements of a given set, or for the number of elements in a set.

#### 4.3.1 Implementation

Implementation 1: Circular Linked List, Boolean rep



We use a .rep field to indicate whether a node is a representative. .rep is set to true for the representative of each set, and false for all other nodes.

MAKE-Set(x): Θ(1)
 We only need to create a linked list with a single node

• FIND-SET(x):  $\Theta(n)$ 

We need to traverse all list nodes to find x and then the representative

• Union(x,y):  $\Theta(n_1+n_2)$ 

We need to first identify the two representatives.<sup>2</sup>

- If x and y share the same representative, do nothing;
- Otherwise, merge the two circular liked lists via changing the *next* attribute for two nodes (conveniently, we choose the representatives, but any two nodes would work), then pick a new representative for the merged set.

We should consider the total amortized complexity of m operations.

• Upper Bound

Given m operations, we know that each list has size  $\leq m$ . Then, each operations takes time  $\mathcal{O}(m)$ . In total, the amortized complexity is  $\mathcal{O}(m^2)$ .

• Lower Bound

Consider  $\frac{m}{3}$  Make-Set operations,  $\frac{m}{3}$  Union operations, and  $\frac{m}{3}$  Find-Set operations.

The Make-Set and Union operations take  $\Omega(m)$  time. The Find-Set operations take  $\Omega\left(\frac{m^2}{9}\right)$  time.

Thus, the total time is  $\Omega(m^2)$ .

Thus, we can conclude that the amortized complexity of m operations is  $\Theta(m^2)$ .

#### Implementation 2: Circular Linked List, Pointer to rep

This is similar to implementation 1, except that we use a pointer to the representative instead of a boolean rep field.

Now, FIND-SET takes  $\Theta(1)$  time, and UNION takes  $\Theta(n_1)$  time since the .rep field needs to be updates for one of the to-be-merged sets.

• Upper Bound

This is the same as implementation 1.

• Lower Bound

Consider  $\frac{m}{2}$  Make-Set operations and  $\frac{m}{2}$  Union operations.

Then Union operations would take  $\sum_{i=1}^{\frac{m}{2}-1} i \in \Omega(m^2)$ 

<sup>&</sup>lt;sup>2</sup>If the representatives are given, Union(x, y) is  $\Theta(1)$ .

#### Implementation 3: Circular Linked List, Pointer to rep, with size

In this implementation, we add a *size* field to *rep* to keep track of the number of elements in the set. During Union, we merge the smaller set into the larger set, so there will be less updates to the *rep* field. We then update the *size* field for the representative of the merged set.

#### • Upper Bound

For any sequence of m operations, let n be the number of MAKE-SET operations. Then, the total time for all UNION operations is less than or equal to the total number of updates to the rep field, for all nodes.

For each element x, x.rep is updated exactly when the set that contains x is smaller (or the same size) than the other set. Thus, this set must at least double in size after the UNION operation. Since there are n Make-Set operations, there can be at most  $\log n$  updates to the rep attribute for every set.

In total, the amortized complexity is in  $\mathcal{O}(n \log n + m) \in \text{$\updownarrow$} \log \text{$\backslash$}$ .

• Lower Bound

#### Implementation 4: Inverted Trees

Each node has parent attribute, and representative is the root of the tree (root.parent = root). These trees do not have to be binary trees.

• Make-Set(x):  $\Theta(1)$ 

We only need to create a tree with a single node

• FIND-SET(x):  $\Theta(n)$ 

We need to fallow *parent* pointers to find the representative. The time depends on how deep the chain / tree is.

• Union(x, y):  $\Theta(n)$ 

We need to find the two representatives first via FIND-SET, change one of their *parent* pointer to point to the other representative (one more level is added to the chain/tree).

Overall, the total worst case of m operations is  $\Theta(m^2)$ , as it is possible for us to generate a single chain.

#### Implementation 5: Inverted Trees, with size

We are using the same *union by weight* idea as implementation 3, Overall, the total worst case running time is  $\Theta(m \log m)$ .

#### Implementation 6: Inverted Trees Path Compression

The problem is not the total size but rather the height, we want to keep things as close to the root as possible.

FIND-SET(x) would follow the pointers, as before, but also add constant-time work to edit the nodes it visits on its way to all point to the root directly as their *parent* attribute. Then, we just need to perform FIND-SET(x) on the bottom of every long chain formed to compress.

#### Implementation 7: Inverted Trees Path Compression, with rank

This is a "union-by-rank" idea where rank is an upper bound on height. For MAKE-SET and UNION, the rank can be treated as the same as the height. However, due to path compression, the height may get smaller (we don't want to keep track of/compute that).

During Union, make the root with smaller rank a child of the other tree.

- If  $r_2 < r_1$ , make tree with rank  $r_2$  a child of tree with rank  $r_1$ .  $r_1$  does not change.
- If  $r_1 = r_2$ , make tree with rank  $r_2$  a child of tree with rank  $r_1$ , and increment  $r_1$  by 1.

Overall, the total worst case run-time of m operations if  $\Theta(m \log^* m)$ , where  $\log^* m$  is the iterated logarithm <sup>3</sup>.

<sup>&</sup>lt;sup>3</sup>Intuitively, the iterated logarithm represents the number of times the logarithm function must be iteratively applied before the result is less than or equal to 1. For example,  $\log^* 2 = 1$ ,  $\log^* 2^2 = \log^* 4 = 1$ ,  $\log^* 16 = 3$ ,  $\log^* 2^{16} = 1 + \log^* 16 = 4$ ,  $\log^* 2^{65536} = 1 + \log^* 65536 = 1 + \log^* 2^{16} = 5$ 

# Part II Algorithms

#### **CHAPTER**

## SORTING

#### 5.1 Heap Sort

#### Implementation 1:

- Run Build-Max-Heap(A)
- Run Extract-Max(A) for n-1 times

#### Implementation 2:

• We modify the EXTRACT-MAX algorithm to swap the root with the last item

#### 5.2 Quick Sort

```
1: procedure QuickSort(A)
2: if thenLen(A) \leq 1
3: return A
4: end if
5: L, p, G \leftarrow PARTITION(A)
6: return QuickSort(L) + [p] + QuickSort(G)
7: end procedure
```

### 5.2.1 Deterministic Quick Sort

In deterministic quick sort, we choose the pivot to be a certain index in the array. We can choose the pivot to be the first element, the last element, or the middle element.

- Run-time depends on input ordering
- Bad ordering would yield bad run-time, while random ordering would generally yield better run-time

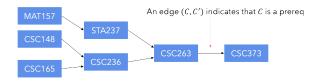
#### 5.2.2 Randomized Quick Sort

In randomized quick sort, we choose the pivot to be a random index in the array. Intuitively, the expected run-time would be the same as deterministic quick sort  $-\Theta(n \lg n)$  – but the worst case run-time would be much better.

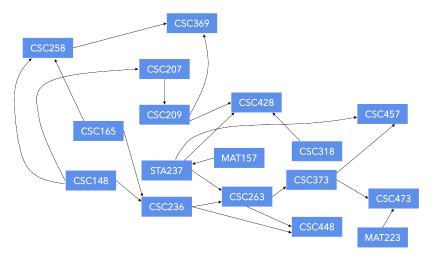
### 5.3 Topology Sort

Example. We wish to determine the sequence of courses to take during our undergraduate program

- $\bullet$  A university course C may have a set of prerequisite courses that must be completed before C
- How can we determine a valid sequence of courses to take?

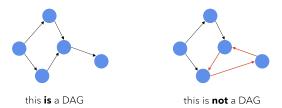


When we add more nodes/edges, things become less clear



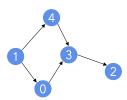
#### 5.3.1 Directed Acyclic Graphs

A directed acyclic graph (or DAG) is a directed graph with no cycles



#### 5.3.2 Topological Sort

A topological sort/ordering of a DAG G = (V, E) is a sequence of its vertices such that, if  $(u, v) \in E$ , then u appears before v in the sequence



1, 0, 4, 3, 2 is a topological ordering of these vertices

Given a DAG G = (V, E), how can we efficiently compute a topological ordering of G?

- Claim: if we perform DFS on a DAG G, the resulting DFS forest contains no back edges.
- Claim: every out-neighbour of every vertex v has an earlier 'visited' time than v.
  - If (v, u) is a tree / forward edge, then u is a descendant of v. By the Parenthesis Theorem, [disc[u], vis[u]] is contained in [disc[v], vis[v]]. Hence, vis[u] < vis[v].
  - If (v, u) is a cross edge, then u was already visited by the time we finish visiting v. Hence, vis[u] < vis[v].

We claim that a directed graph G can be topologically sorted iff G contains no cycles iff DFS finds no back edges.

- 1 Maintain a linked list L while performing DFS on G = (V, E)
- 2 When we finish visiting a node v (by setting vis[v] and painting v black), add v to the head of the linked list L
- 3 Once DFS terminates, L contains a list of all vertices in V sorted in decreasing order by their 'visited' times

Part III

Analysis

## AVERAGE CASE ANALYSIS

In *average case analysis*, we are interested in the average performance of an algorithm. we take the average, or the expected value, over the distribution of the possible inputs.

For each n, define  $S_n = \{\text{all inputs of size } n\}$ , and if we consider the inputs to be random, then  $S_n$  is the sample space. For each  $x \in S_n$ , define P(x) to be the probability that x will be chosen as the input. Define t(x) as the number of steps preformed on input x. t is the random variable.

Then, the average case running time is defined as

$$T(n) = E[t]$$

$$= \sum_{x \in S_n} P(x) \cdot t(x)$$

**Example.** Consider the linear search algorithm on a linked list L.

```
1: procedure LinSearch(L, x)
2: z \leftarrow L.head
3: while z \neq \text{NIL} and z.data! = x do
4: z \leftarrow z.next
5: end while
6: return z
7: end procedure
```

Let  $S_n$  be the sample space of all linked lists of size n. Let P(x) be the probability that x is chosen as the input. Let t(x) be the number of steps performed on input x.

• We need to know  $S_n$  with probability

Consider the inputs  $\mathtt{input}_1 = ([1, 2, 3], 2)$  and  $\mathtt{input}_2 = (["a", "b", "c"], "b")$ , note that they will take the same steps. We only need one input for each possible value of t.

Define 
$$S_n = \{([1, 2, \dots, n], 1), ([1, 2, \dots, n], 2), \dots, ([1, 2, \dots, n], n), ([1, 2, \dots, n], 0)\}.$$

- We assume all the inputs happen equally likely, then  $P(x) = \frac{1}{n+1}$ .
- We need an exact formula for t(x).

In practice, we choose some "key operations" s.t. counting **only** these operations is within a constant factor of total time – then set t(x) = number of key operations.

Here, we choose line 3,  $z.data \neq x$ , as the key operation.

Then, we have 
$$T(n) = \sum_{(L,i) \in S_n} t(L,i) \cdot P(L,i)$$
  

$$= \frac{1}{n+1} \sum_{i=0}^n t([1,2,\ldots,n],i)$$

$$= \frac{1}{n+1} \left( t([1,2,\ldots,n],0) + \sum_{i=1}^n i \right)$$

$$= \frac{1}{n+1} \left( n + \frac{n(n+1)}{2} \right)$$

$$= \frac{n}{n+1} + \frac{n}{2}$$

**Example.** Consider Search(T, k) on a hash table T for a key k.

Assume t has m slots, and uses chaining to resolve collisions. Assume that prior to applying the textscSearch algorithm, the hash table contains n keys.

Assume the key k is samples uniformly at random from U.

Let N(k) be the number of keys examined during search for k. N(k) is the key operation.

$$E[N(k)] = \sum_{k \in U} P[k] \cdot N(k)$$

$$= \sum_{i=0}^{m-1} \sum_{\substack{k \in U \\ h(k)=i}} P[k] \cdot N(k)$$
regroup terms
$$\leq \sum_{i=0}^{m-1} \sum_{\substack{k \in U \\ h(k)=i}} P[k] \cdot L_i \qquad \text{since } N(k) \leq L_i \text{ when } h(k) = i$$

$$= \sum_{i=0}^{m-1} L_i \cdot \sum_{\substack{k \in U \\ h(k)=i}} P[k]$$

$$= \sum_{i=0}^{m-1} L_i \cdot P[h(k) = i]$$

$$= \sum_{i=0}^{m-1} L_i \cdot \frac{1}{m}$$
$$= \frac{1}{m} \sum_{i=0}^{m-1} L_i$$
$$= \frac{n}{m}$$

**Example.** Consider QUICKSORT on an array A of size n.

Let  $S_n = \{\text{all permutations of } [1, 2, dots, n]\}$ 

We assume an uniform distribution of the inputs, then  $P(x) = \frac{1}{n!}$ . Let the random variable T(A) be the total number of comparisons between elements of A.

Define 
$$X_{i,j} = \begin{cases} 1 & \text{if } i \text{ is compared to } j \\ 0 & \text{otherwise} \end{cases}$$
 for  $1 \le i < j \le n$ .

Then, 
$$T(A) = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} X_{i,j}$$
.

The probability  $P(X_{i,j} = 1) = P(i \text{ or } j \text{ appear in } A \text{ before all other values in range } [i...j])$ 

$$= \frac{1}{j-i+1} + \frac{1}{j-i+1}$$
$$= \frac{2}{j-i+1}$$

Then, 
$$E[T(A)] = \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} E[X_{i,j}]$$

$$= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} P(X_{i,j} = 1)$$

$$= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \frac{2}{j-i+1}$$

$$= \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \frac{2}{\alpha+1}$$
 substitute  $j-i$  with  $\alpha$ 

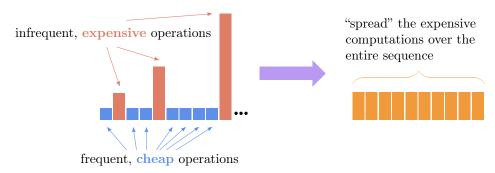
$$< \sum_{i=1}^{n-1} \sum_{j=i+1}^{n} \frac{2}{k}$$

$$= \sum_{i=1}^{n-1} \Theta(\lg n)$$

$$= \Theta(n \lg n)$$

## AMORTIZED ANALYSIS

In amortized analysis, we analyze the cost of a sequence of operations, not just a single operation. The amortized cost of a sequence of operations is the average cost per operation.



- The worst-case sequence complexicy of a sequence S of k operations is the maximum possible total steps performed by S (taken over all possible inputs to the operations in S).
- The worst-case sequence complexity is **at most**  $k \times$  the worst-case complexity of any individual operation in S.
- Suppose that the worst-case sequence complexity of a sequence of k operations is T(k). Then the (worst-case) amortized complexity per operation of this sequence is  $\frac{T(k)}{k}$ .
- With amortized analysis, we take the average of the costs of multiple operations (as opposed to average-case analysis, where we calculate the cost of a single operation by averaging over the input distribution)

In the <u>aggregated method</u>, we determine the upper bound T(n) on the total cost of a sequence of N operations, then calculate the average cost per operation as  $\frac{T(n)}{n}$ .

**Example.** Consider when we insert into an array. We increase the size of the array by 4 when it is  $\frac{3}{4}$  full.

For simplicity, suppose that each insert with no resizing requires c steps, for some constant  $c \in \mathbb{N}^+$  (so each insert with resizing requires  $c \cdot n + c$  steps, where n is the number of items in the array prior to resizing).

Operation Number	$\operatorname{Cost}$
1	c
2	c
3	c
4	4c
5	c
6	c
7	c
8	7c
9	c
10	10c
÷	:

Within a sequence of k insertions, we need to resize  $\lfloor \frac{k-1}{3} \rfloor$  times. For all k insert operations, the total cost is

$$T(k) = c \cdot \sum_{i=1}^{\left\lfloor \frac{k-1}{3} \right\rfloor} (3i+1) + c \cdot \left(k - \left\lfloor \frac{k-1}{3} \right\rfloor\right)$$

Note that 
$$c \cdot \sum_{i=1}^{\left \lfloor \frac{k-1}{3} \right \rfloor} (3i+1) = c \cdot \sum_{i=1}^{\left \lfloor \frac{k-1}{3} \right \rfloor} 3i + \sum_{i=1}^{\left \lfloor \frac{k-1}{3} \right \rfloor} 1$$

$$= 3c \cdot \sum_{i=1}^{\left \lfloor \frac{k-1}{3} \right \rfloor} i + c \cdot \left \lfloor \frac{k-1}{3} \right \rfloor$$

$$= \frac{3}{2}c \cdot \left \lfloor \frac{k-1}{3} \right \rfloor \cdot \left( \left \lfloor \frac{k-1}{3} \right \rfloor + 1 \right) + c \cdot \left \lfloor \frac{k-1}{3} \right \rfloor \in \Theta(k^2)$$

Thus, T(k) is  $\Theta(k^2)$ . The amortized cost per operation is  $\frac{T(k)}{k} = \Theta(k)$ .

**Example.** Consider a k digit binary counter.

In this problem, we count the total number of bits changed in the counter. We can do this by counting the number of times each bit changes.

Bit Number	Number of Changes
0	$\overline{m}$
1	$\approx \frac{m}{2}$
2	$pprox rac{m}{2} \ pprox rac{m}{4}$
:	<u>:</u>
i	$pprox rac{m}{2^i}$
:	:

Then, 
$$T = \sum_{i=0}^{(\lg m)-1} \frac{m}{2^i}$$
$$= m \cdot \sum_{i=0}^{(\lg m)} \frac{1}{2^i}$$
$$< m \sum_{i=0}^{\infty} \frac{1}{2^i}$$
$$= 2m$$

#### 7.2 Accounting Method

The accounting method is a form of aggregate analysis which assigns to each operation an amortized cost which may differ from its actual cost. Early operations have an amortized cost higher than their actual cost, which accumulates a saved "credit" that pays for later operations having an amortized cost lower than their actual cost. Because the credit begins at zero, the actual cost of a sequence of operations equals the amortized cost minus the accumulated credit. Because the credit is required to be non-negative, the amortized cost is an upper bound on the actual cost. Usually, many short-running operations accumulate such credit in small increments, while rare long-running operations decrease it drastically.

**Example.** Consider a sequence of m Insert for dynamic array.

Recall that the "cost" is the actual run-time, while the "charge" is the estimated amortized time. Note that for  $k = 2^n + 1$ , we need  $2^n = k - 1$  for reading and  $2^n + 1 = k$  for writing. Thus, the cost is 2k + 1.

Then, we know that 
$$cost(INSERT(k)) = \begin{cases} 2k+1 & \text{if } k=2^n+1\\ 1 & \text{otherwise} \end{cases}$$

Define charge(Insert(k)) = \$5. We need \$1 for writing the new element, and save \$4 as credit. We need to prove our credit invariant: every element in the second half of the array has \$4 credit.

*Proof.* Proof by induction on the number of operations done.

- init: 0 elements, 0 credits
- Consider one Insert Assuming credit invariant holds

- If the array does not grow, then the new element gets \$4 credit. The credit invariant holds.
- If the array does grow, it must be full, the total credits is  $\$4 \cdot \frac{n}{2} = \$2n$ , enough toi cover copying n elements. The new element gets \$4 credit. The credit invariant holds.

Thus, Amortized 
$$\leq \frac{\text{WCSC}}{m} = \frac{\text{total cost}}{m}$$

$$\leq \frac{\text{total charge}}{m} \quad \text{because of credit invariant}$$

$$= \frac{5m}{m}$$

$$= 5$$

## LOWER BOUNDS

For upper bound U(n) on problem complexity, we just need ONE algorithm with worst-case time  $\Theta(U(n))$ . For instance, the sorting has problem complexity  $\mathcal{O}(n \log n)$  because heap sort takes time  $\Theta(n \log n)$ .

For lower bound L(n) on problem complexity, we need a general argument that **every** algorithm takes worst-case time  $\Omega(L(n))$ . The goal is to prove that every algorithm that solves problem P requires time  $\Omega(g(n))$  for some function g(n). In contrast to upper bounds, we want our lower bounds g(n) to be as large as possible.

Our algorithm is optimal with respect to worst-case time complexity when the bounds match. Lower bounds are usually proven only for a certain class of algorithms.

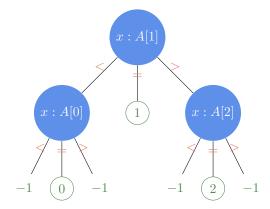
#### 8.1 Comparison-Based Algorithms

A comparison-based algorithm is an algorithm that uses comparisons (for example, >,  $\geq$ , <,  $\leq$ , =,  $\neq$ , 3-way comparisons) on the input values with each other to solve a problem. For example, sorting is a comparison-based algorithm because it uses comparisons to determine the order of elements. These algorithms can be represented in the form of *comparison trees*.

It is conventional to use the same comparison operator in every node when possible. A single comparison tree can only represent the behaviour of an algorithm for a fixed input size. Each input size corresponds to a different tree (with a common structure). Then, an algorithm would lead to a family of comparison trees (one for each input size). For any specific input, the execution of the algorithm can be traced in the decision tree as a path from the root to a leaf node.

- Internal nodes (nodes with children) represent comparisons made by the algorithm: the root is the first comparison, its children the next comparison (depends on the result of the first), and so on.
- Edges show the outcome/result of each comparison

• External nodes (leaves) show the output of the algorithm (different nodes can have the same value since the algorithm can arrive at the same output in different ways).



The number of comparisons performed by the algorithm on any innput is equal to the length of its execution path.

- The worst-case time complexity is proportional to the height of the tree
- The average-case time complexity is proportional to the average depth of the leaves

For any problem that has at least K different outcomes, every decision tree for the algorithm contains at least K leaves (at least 1 leaf for each outcome). In any tree with K leaves and fixed branching factor has height  $\Omega(\log K)$ .

**Example.** Consider searching a sorted list.

Let  $P_1$  be such problem.

- Input: a sorted list A, a value x
- Output: index i such that A[i] = x or -1 if x is not in A

Every comparison tree has at least 1 leaf for each outcome ( $\geq n+1$  since n elements and x could be not in the list)

Then, the worst-case run-time is  $\Omega(\text{height}) = \Omega(\log(\text{number of leaves})) = \Omega(\log(n+1))$ .

**Example.** Consider sorting a list.

Let  $P_2$  be such problem.

- Input: a list A of n elements
- Outcome: permutation of [0, 1, ..., n-1], such that A[i] represents the position of A[i] in the sorted list

The number of leaves  $\geq$  the number of permutations = n!.

The height of the comparison tree  $\geq \log(n!)$ .

Then, the worst-case run-time is  $\Omega(\log(n!)) = \Omega(n \log n)$ .

worst-case runtime = height of comparison tree

- $\geq \log(\text{number of leaves})$
- $\geq \log(\text{number of possible outcomes})$
- $\geq \log(\text{number of outputs})$

**Example.** Consider searching an unsroted list.

Let  $P_3$  be such problem.

- Input: an unsorted list A, a value x
- Output: index i such that A[i] = x or -1 if x is not in A

By applying information theory lower bound, since the comparison tree has st least n+1 leaves (one for each possible output), we have worst case runtime  $\geq \log(n+1)$ 

#### 8.3 Adversary / Adversarial Arguments

The goal is to show that every correct algorithm has a worst-case running time  $\geq L(n)$ . In practice, we often show the contrapositive: if there is an algorithm with running time  $\leq L(n)$ , then the algorithm is incorrect.

runtime = count key operations to use correct, exact lower bounds.

**Example.** Consider searching an unsorted list.

We count the number of comparisons  $(x \stackrel{?}{=} A[j])$ 

Try L(n) = n because we know how to solve within n comparisons. We prove all algorithms that makes < n comparisons are incorrect.

Consider one such algorithm. We work through the comparison tree.

- For each comparison  $x \stackrel{?}{=} A[j]$ , set  $A[j] \neq x$ , go down the False branch
- When we reach the leaf, there are at most n-1 elements set in A. There is at least one element A[i] whose value is not set.
  - If the algorithm returns i, let  $A[i] = 0 \neq x$
  - If the algorithm returns -1, let A[i] = 1 = x

In either case, this algorithm is incorrect.

**Example.** Consider Finding the maximum element in au unsorted list.

- Input: an unsorted list A of n elements
- Output: index i such that  $A[i] \ge A[j]$  for all  $i \in \{0, 1, ..., n-1\}$

By applying the information theory lower bound, we have worst-case runtime  $\geq \Omega(\log(n))$ For the adversary argument, the algorithm requires less than n-1 comparisons to find the maximum element.

We start at the root and traverse the comparison tree.

- Every comparison  $A[i] \stackrel{?}{<} A[j]$  eliminates one possible location for the max.
- There is at most n-2 comparisons, so at most n-2 positions eliminated. There is at least two potential positions for the maximum

No matter which index is output, there is at least one index that makes it incorrect.

# Part IV Appendices

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