

Algorithm Bank

```
USComputing.makeCheatSheet();
```

contributors

```
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```

category

<algorithm template>

<pseudocode> *// time complexity*

<Description>

Time / Space Complexity

Invariants

[data structure template]

<available implementations>

<Description>

{orders of growth}

Orders of Growth

$T(n)$ refers to the running time on inputs of size n .

$T(n) = O(f(n))$	$\exists c > 0$ and $\exists n_0 > 0$ such that for all $n > n_0$, $T(n) \leq cf(n)$.
------------------	---

$T(n) = \Omega(f(n))$	$\exists c > 0$ and $\exists n_0 > 0$ such that for all $n > n_0$, $T(n) \geq cf(n)$.
-----------------------	---

$T(n) = \theta(f(n))$	$T(n) = O(f(n))$ and $T(n) = \Omega(f(n))$.
-----------------------	--

Rules of Big-O Notation

If $T(n)$ is a polynomial of degree k ,

$$T(n) = O(n^k)$$

If $T(n) = O(f(n))$ and $S(n) = O(g(n))$,

$$T(n) + S(n) = O(f(n) + g(n))$$

$$T(n) \times S(n) = O(f(n) \times g(n))$$

Sterling's Approximation

$$n! \approx \sqrt{2\pi n} \left(\frac{n}{e}\right)^n$$

Algorithm Analysis

Cost of Loops / Nested Loops

$$(\# \text{ iterations}) \times (\text{maximum cost of 1 iteration})$$

Sequential Statements

$$(\text{cost of first}) + (\text{cost of second statement})$$

If / Else Statements

$$\max(\text{cost of first}, \text{cost of second})$$

Recurrences (eg. Fibonacci)

$$T(n) = 1 + T(n-1) + T(n-2) = O(2^n)$$

{solving recurrences}

Useful Summations:

$$\sum_{i=1}^n i^c \in \Theta(n^{c+1})$$

$$\sum_{i=1}^n \frac{1}{i} \in \Theta(\log n)$$

$$\sum_{i=1}^n c^i \in \Theta(c^n)$$

$$\sum_{i=1}^n \log(i)^c \in \Theta(n \cdot \log(n)^c)$$

$$\sum_{i=1}^n \log(i)^c \cdot i^d \in \Theta(n^{d+1} \cdot \log(n)^c)$$

$$\sum_{i=1}^n \log(i)^c \cdot i^d \cdot b^i \in \Theta(n^d \cdot \log(n)^c \cdot b^n)$$

$T(n) = T(n/2) + O(1)$	$O(\log n)$	$1 + 1/2 + \dots + 1/n$ (Harmonic Progression)
$T(n) = T(n-1) + O(1)$	$O(n)$	
$T(n) = 2T(n/2) + O(1)$	$O(n)$	
$T(n) = T(n-1) + O(n)$	$O(n^2)$	$1 + 2 + \dots + n$ (Arithmetic Progression)
$T(n) = 2T(n/2) + O(n)$	$O(n \log n)$	

Master Theorem:

$$\text{If } T(n) \leq aT\left(\frac{n}{b}\right) + O(n^d)$$

then

$$T(n) = \begin{cases} O(n^d \log n) & \text{if } a = b^d \text{ (Case 1)} \\ O(n^d) & \text{if } a < b^d \text{ (Case 2)} \\ O(n^{\log_b a}) & \text{if } a > b^d \text{ (Case 3)} \end{cases}$$

<binary search>

```
binarySearch(A, key, n) //  $O(\log n)$ 
    begin = 0
    end = n-1
    while (begin < end):
        mid = begin + (end-begin)/2;
        if (key <= A[mid]) then
            end = mid
        else begin = mid+1
    return A[begin]
```

From a sorted array $A[1..n]$, returns the element key if it is found in the array.

Loop Invariant: $A[\text{begin}] \leq \text{key} \leq A[\text{end}]$

<peak finding for 1D array>

```
findPeak(A, n) //  $T(n) = O(\log n)$ 
    if (A[n/2] is a peak)
        return n/2
    else if (A[n/2 + 1] > A[n/2])
        findPeak(A[n/2+1..n], n/2) //  $T(n/2)$ 
    else if (A[n/2 - 1] > A[n/2]) then
        findPeak(A[1..n/2-1], n/2)
```

Returns a local maximum element / peak from some array $A[1..n]$. $A[i]$ is a local maximum iff $A[i-1] \leq A[i]$ and $A[i+1] \leq A[i]$.

Loop Invariant: There exists a peak in the range $[\text{begin}, \text{end}]$, and every peak in that range is a valid peak in $[1, n]$.

Key Property: If we recurse on the right half, then there exists a peak in that right half. This can be proven by induction cooker.

<slower peak finding for 2D array>

Given a 2D array $A[1..n, 1..m]$, returns a peak that is not smaller than the (at most) 4 neighbours.

```
findPeak() //  $T(n, m)$ 
    find maximum element of middle column; //  $O(n)$ 
    if (that element is a peak)
        return that element;
    else if (left neighbour is larger)
        recurse on the left half; //  $T(n, m/2)$ 
    else if (right neighbour is larger)
        recurse on the right half;
```

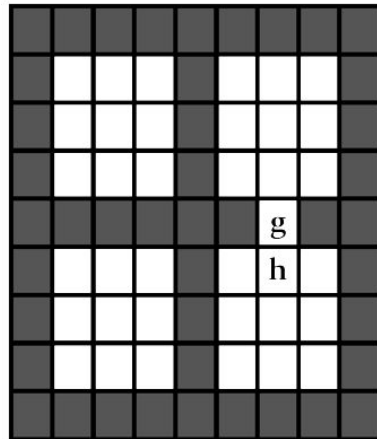
10	8	4	2	1
3	2	2	12	13
17	5	1	11	1
7	4	6	9	4
8	1	1	2	6

Time Complexity: $T(n, m) = T(n, m/2) + O(n) = O(n \log m)$

<faster peak finding for 2D array>

Given a 2D array $A[1..n, 1..m]$, returns a peak that is not smaller than the (at most) 4 neighbours.

```
findPeak() //  $T(n, m)$   
    find max element in the border and cross; //  $O(n + m)$   
    if (that element is a peak)  
        return that element;  
    else //  $T(n/2, m/2)$   
        recurse on the quadrant containing the element bigger than max
```

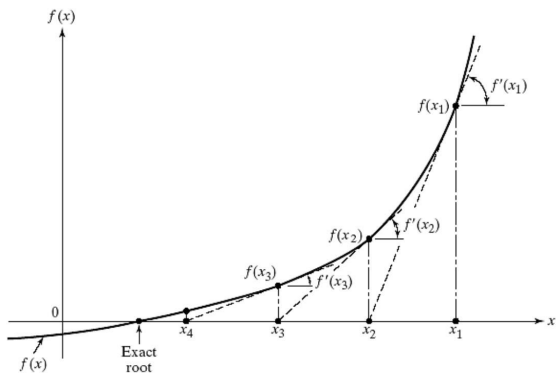


Time Complexity: $T(n, m) = T(n/2, m/2) + cn + cm = O(n + m)$

Proof of Correctness: If we recurse on a quadrant, then the quadrant definitely contains a peak. Every peak in the quadrant is not a peak in the matrix. Recursing in the quadrant would give us a peak at least as large as every element on the boundary.

<newton's method>

```
findRoot(float x, float error)
    diff = error + 1;
    while (diff > error)
        float f = function(x);
        float df = derivative(x);
        float newX = x - (f/df);
        diff = abs(x - newX);
        x = newX;
    return x;
```



This algorithm finds a root of $f(x) = 0$ via successive approximation.

After every iteration i , we update our value of root x to be

$$x_{i+1} = x_i - \frac{f(x_i)}{f'(x_i)}$$

Time Complexity: If we have quadratic convergence, which means that at every iteration, the number of correct digits doubles. So, for d digits of accuracy, we require $O(\log d)$ iterations. However, it has more expensive computation.

Conditions for Quadratic Convergence: The function f must be continuously differentiable, have a non-zero derivative at root, and have a second derivative at root.

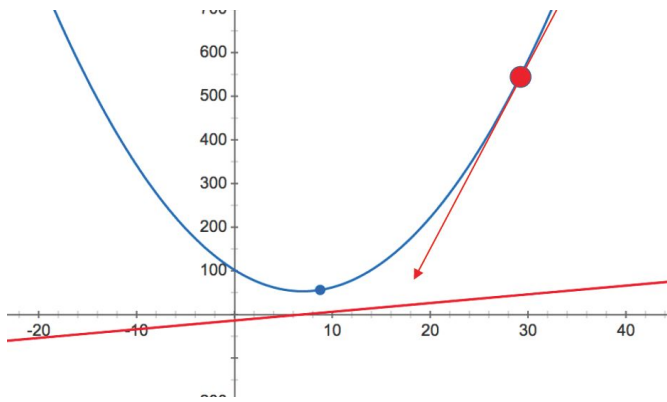
<gradient descent>

```
findMin(float x, float step, float error)
    diff = error + 1;
    while (diff > error)
        float df = derivative(x);
        float newX = x - (step * df);
        diff = |x - newX|;
        x = newX;
    return x
```

Finds the minimum value of $f(x)$ via successive approximation.

Time Complexity: It has more iterations than Newton's method because it has linear convergence, but it has faster computation.

Conditions for Convergence: This algorithm will converge if f is convex and differentiable, and its gradient is L -Lipschitz, and if step size $\gamma \leq 1/L$.



<bubble sort>

```
bubbleSort(A, n)
  repeat (until no swaps): // Worst: n iterations
    for j ← 1 to n - 1 // O(n)
      if (A[j] > A[j + 1])
        swap(A[j], A[j + 1])
```



Advantages: If you are stuck in a crowded ISB and you need to alight ASAP, all you have to shout is “Eh, eh, BubbleSort me in front”.

Time Complexity

- **Worst and Average:** $O(n^2)$
- **Best:** $O(n)$ when A is already sorted

Loop

At the end of iteration j of the outer loop, the biggest j items are correctly stored in the final j positions of the array.

Invariant

Stable? Yes

In-place? Yes *// $O(1)$ space complexity*

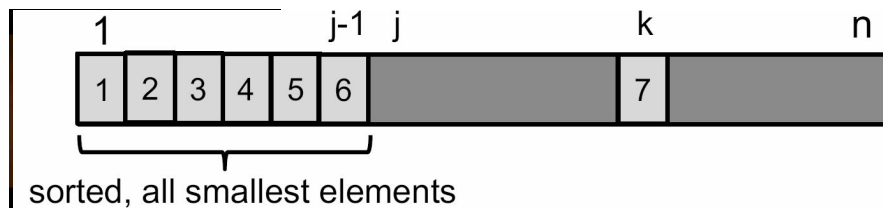
Note: Coefficient is much worse than other $O(n^2)$ algorithms.

<selection sort>

```

selectionSort(A, n) //  $O(n^2)$  and  $\Omega(n^2)$ 
  for j ← 1 to n - 1:
    find minimum element A[j] in A[j..n]; // Time:  $n - j$ 
    swap(A[j], A[k]);

```

**Loop****Invariant**

At the end of iteration j , the smallest j items are correctly stored in the first j positions of the array.

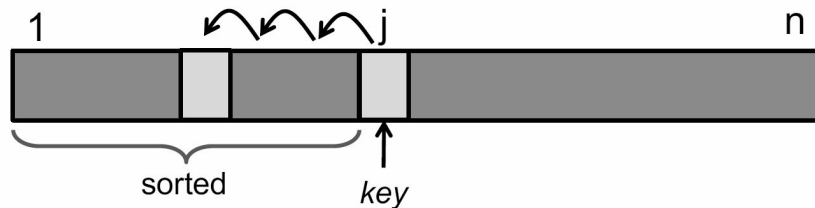
Stable? No

In-place? Yes // $O(1)$ space complexity

Advantages: SelectionSort minimises the number of times data is written (only $2n$ writes needed). Use SelectionSort if you have very large data to sort - comparing is relatively cheap.

<insertion sort>

```
insertionSort(A, n)
  for j ← 2 to n
    key ← A[j]
    // insert key into sorted array A[1..j-1]
    while (i > 0) and (A[i] > key) // at most j times
      A[i + 1] ← A[i]
      i ← i - 1
    A[i + 1] ← key
```



Time Complexity

- **Worst and Average:** $O(n^2)$
- **Best:** $O(n)$ when arr is already sorted

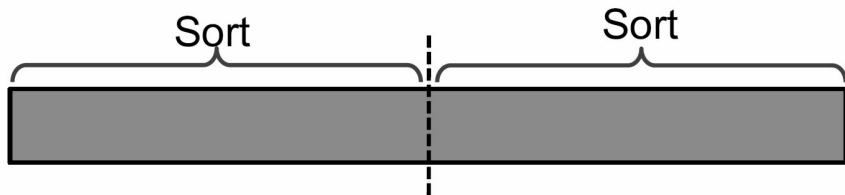
Invariant: $A[1..j-1]$ is sorted, ie. the first few elements are *relatively* sorted.

Stable? Yes

In-place? Yes // $O(1)$ space complexity

<merge sort>

```
mergeSort(A, n) //  $T(n)$ 
  if (n == 1) return; //  $\theta(1)$ 
  else
    x ← mergeSort(A[1..n/2], n/2); //  $T(n/2)$ 
    y ← mergeSort(A[n/2 + 1, n], n/2); //  $T(n/2)$ 
  return merge(x, y, n/2); //  $\theta(n)$ 
```



Time Complexity:

$$T(n) = 2T(n/2) + cn = O(n \log n)$$

Stable? Yes

In-Place? No, as it requires additional temporary arrays // *additional space complexity of $O(n)$*

For implementation of linked lists, however, additional space complexity is $O(\log n)$.

Disadvantages: MergeSort is slow when there are a small number of items to sort. Hence, at a base case of recursion, use a different sort (eg. InsertionSort for $n < 1024$).

<quick sort>

```

paranoidQuickSort(A[1..n], n) //  $T(n)$ 
  if (n == 1) then return;
  else
    repeat // expected: executed max 2 times only
      pIndex = random(1, n);
    until p > (1/10)n and p < (9/10)n

    p = partition(A[1..n], n, pIndex); //  $O(n)$ 
    x = quickSort(A[1..p-1], p-1); //  $T(k)$ 
    y = quickSort(A[p+1..n], n-p); //  $T(n-k)$ 

```

Partition the array into two sub-arrays around a pivot p such that elements in the lower subarray $\leq p \leq$ elements in upper subarray. Then, recursively sort these subarrays.

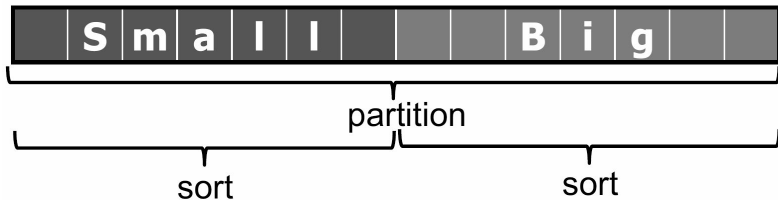
Time Complexity: $O(n \log n)$

Stable? No

In-place? Yes

Choice of Pivot: A pivot is good if it divides the array into two pieces, each of which is size at least $n/10$.

Improvement: Halt recursion early, leaving small arrays unsorted. Perform InsertionSort on entire array.



<partition>

```
partition(A[1..n], n, pIndex)
    pivot = A[pIndex];
    swap(A[1], A[pIndex]); // store pivot in A[1]
    low = 2; high = n+1;
    while (low < high)
        while ((A[low] < pivot) and (low < high)) low++;
        while ((A[high] > pivot) and (low < high)) high--;
        if (low < high) swap(A[low], A[high]);
    swap(A[1], A[low-1]);
    return low-1;
```

Assuming no duplicates in the array A,
and pIndex is the index of the pivot.

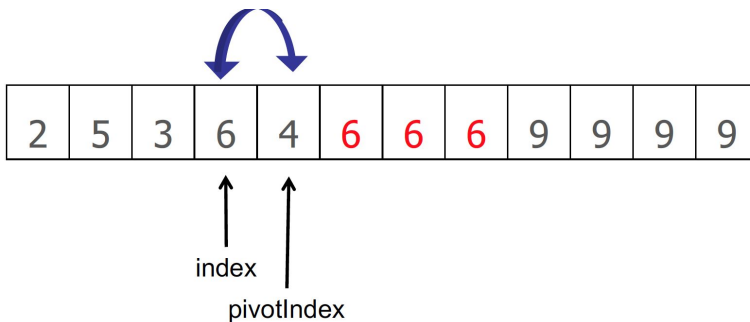
Time Complexity
 $O(n)$

Loop Invariant: At the end of every loop iteration, for all $i > \text{high}$, $A[i] > \text{pivot}$; for all $1 < j < \text{low}$, $A[j] < \text{pivot}$.

<3-way partition>

```
twoPassPartitioning()  
  do a regular partition;  
  pack duplicates;
```

Three-way partitioning is used when there are duplicate pivots.



<multi pivot quicksort>

```
multiPivotQuickSort(A) //  $T(n)$ 
    choose k pivots at random;
    sort the pivots; //  $O(k \log k)$ 
    for each item in the array: //  $n$  items
        use binary search to identify the right bucket  $O(\log k)$ 
        place item in the right bucket;
    for all the buckets: //  $k$  buckets
        multiPivotQuickSort(bucket) //  $T(n/k)$ 
```

For QuickSort algorithm with k pivots and n items to sort, where $n > k$.

Time

$$T(n) = kT(n/k) + O(n \log k) = O(n \log n)$$

Complexity

Although multi-pivot quicksort runtime gives no improvement at all, in reality, 2 and 3 pivot QuickSort is actually faster than regular QuickSort.

<quick select>

```
quickSelect(A[1..n], n, k)
  if (n == 1) return A[1];
  else
    choose random pivot index pIndex;
    p = partition(A[1..n], n, pIndex);
    if (k == p) return A[p];
    else if (k < p) return quickSelect(A[1..p-1], k);
    else return quickSelect(A[p+1..n], k-p);
```

From an array A of n elements, returns the kth smallest element.

Time Complexity: $O(n)$

Key Point: Only recurses once. Take note that recursing left and right are not exactly the same. But dominated by the $O(n)$ operation that is partition.

<finding minimum using queues>

We will use a Queue ADT which contains pointers which indicate “valleys” in the queue. A valley is an item that is smaller than everything in the queue after it.

Maintain a secondary linked list between these valleys: each element has a pointer to the previous valley and next valley. The pointer to the first valley is minimum.

```
dequeue()
    if (dequeuing the current minimum)
        minimum = next valley;
        minimum.previous = null;
        remove node from queue;
    else dequeue normally;
```

```
enqueue(x)
    add x to head of the queue; // it instantly becomes a valley
    traverse all previous valleys from the tail of list:
        remove all pointers from the nodes we just traversed;
        if (found valley smaller than x):
            stop and update the next pointer of the node we stopped at to x;

findMin() { return first valley }
```

<knuth shuffle>

```
KnuthShuffle(A[1..n]) //  $O(n \log n)$   
  for i = 2 to n do  
    r = random(1, i)  
    swap(A, i, r)
```

Generates a random permutation of an array. It does so by iterating through an array, creating a random prefix.

<height>

```
height()
    leftHeight = -1;
    rightHeight = -1;
    if (m_leftTree != null)
        leftHeight = m_leftTree.height();
    if (m_rightTree != null)
        rightHeight = m_rightTree.height();
    return max(leftHeight, rightHeight)+1;
```

The height of a tree is the number of edges on the longest path from the root to the leaf.

```
h(null) = -1;
h(v) = 0 if v is a leaf;
h(v) = max(h(v.left), h(v.right)) + 1;
```

The largest possible height h is $\theta(n)$.

Balance:

A BST is balanced if $h = O(\log n)$. All operations on such a tree will run in $O(\log n)$ time.

<search>

```
search(queryKey) // O(h)
    if (queryKey.compareTo(key) < 0)
        if (leftTree != null)
            return leftTree.search(queryKey);
        else return null;
    else if (queryKey.compareTo(key) > 0)
        if (rightTree != null)
            return rightTree.search(queryKey);
        else return null;
    else return this;
```

```
searchMax()
    if (rightTree != null)
        return rightTree.searchMax();
    else return this;

searchMin()
    if (leftTree != null) {
        return leftTree.searchMin();
    }
    else return this;
```


<successor>

```
successor()
    if (this.right != null)
        return this.right.searchMin();
    else
        parent = this.parent;
        child = this;
        while ((parent != null) && (child == parent.right))
            child = parent;
            parent = child.parent;
        return parent;
```

<traversal>

```
inOrderTraversal() //  $O(n)$ 
    if (leftTree != null) leftTree.inOrderTraversal();
    visit(this);
    if (rightTree != null) rightTree.inOrderTraversal();

preOrderTraversal()
    visit(this);
    if (leftTree != null) leftTree.preOrderTraversal();
    if (rightTree != null) rightTree.preOrderTraversal();

postOrderTraversal()
    if (leftTree != null) leftTree.postOrderTraversal();
    if (rightTree != null) rightTree.postOrderTraversal();
    visit(this);
```

<insertion>

```
insert(x)
    if (x < key) left.insert(x);
    else right.insert(x);
    height = max(left.height, right.height) + 1;
    walk up tree and for every step
        check for balance;
        if out of balance, use rotations to rebalance;
```

For an AVL tree, after every insertion, you will have to update the height and rebalance the tree.

In the worst case, only **two** rotations are required.

<deletion>

```
delete(v)
    if (v has no children)
        remove(v);
    else if (v has only one child)
        remove (v);
        connect(child(v), parent(v))
    else if (v has two children)
        x = successor(v);
        swap(v, x);
        delete v which is in the original position of the successor;
    update heights up to the root;
    for every ancestor of the deleted node:
        if it is not height-balanced, perform a rotation;
```

For an AVL tree, deletion can take up to $\log n$ rotations.

<rotate>

```

rightRotate(node) // left != null
    oldParent = node.parent;
    newParent = node.left;
    grandChild = newParent.right;

    connect(newParent, node);
    connect(team, grandChild);
    connect(oldParent, newParent);

```

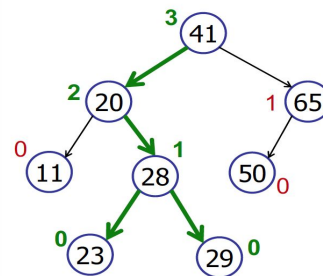
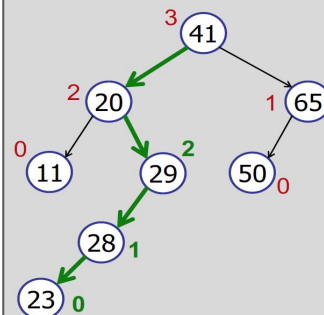
```

leftRotate(node) // right != null
    oldParent = node.parent;
    newParent = node.right;
    grandchild = newParent.left;

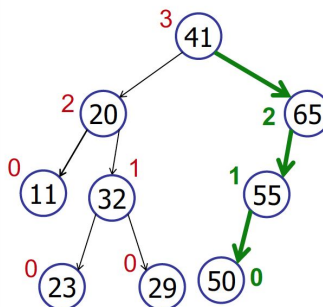
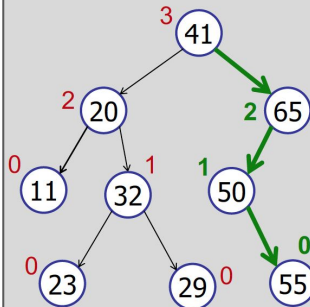
    connect(newParent, team);
    connect(team, grandchild);
    connect(oldParent, newParent);

```

right-rotate(29)



left-rotate(50)



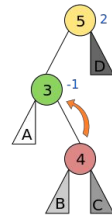
<rebalance node>

```

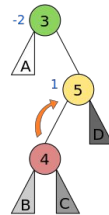
rebalance(node)
  if (node is right-heavy):
    if (node.right is balanced
        || node.right is right-heavy)
      leftRotate(node);
    else if (node.right is left-heavy):
      rightRotate(node.right); leftRotate(node);
  else if (node is left-heavy):
    if (node.left is balanced
        || node.left is left-heavy):
      rightRotate(node);
    else if (node.left is right-heavy):
      leftRotate(node.left); rightRotate(node);

```

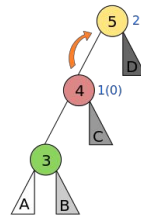
Left Right Case



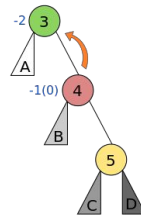
Right Left Case



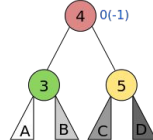
Left Left Case



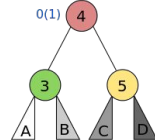
Right Right Case



Balanced



Balanced



[tries]

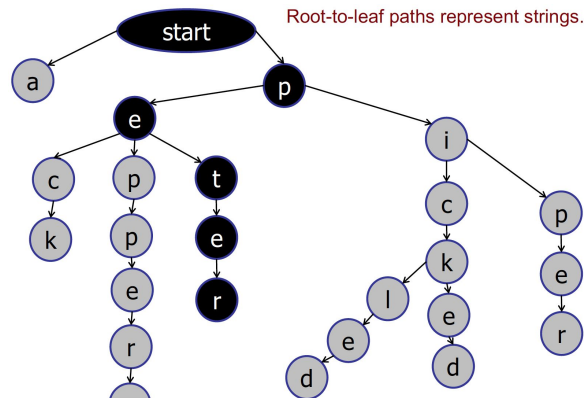
In a trie, one letter is stored in each node.
Root-to-leaf paths represent strings.

```
search(string); //  $O(L)$ 
```

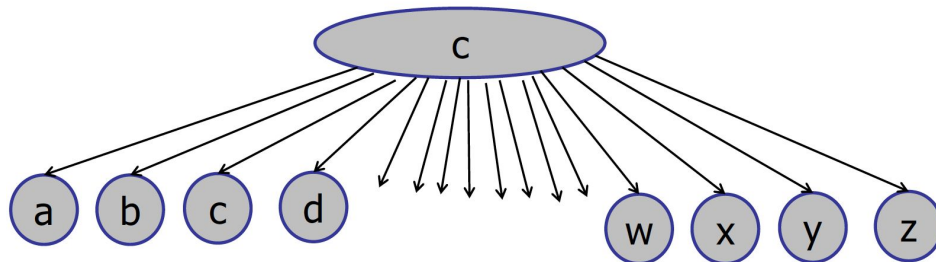
```
insert(string);
```

Space Complexity:

Storing a trie: $O(\text{size of text} * \text{overhead})$



```
TrieNode children[] = new TrieNode[256];
```



[skip lists]

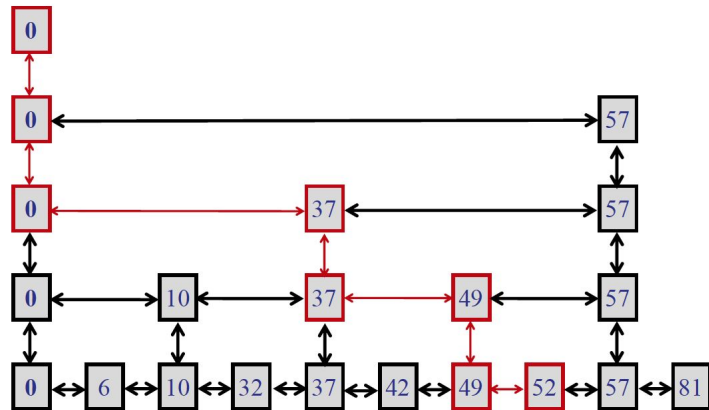
```
search(key) //  $O(\log n)$ 
    node = root
    while (node.key < key) and (node.level > 1):
        while (node.next.key < key):
            node = node.next
        node = node.down
    while (node.next.key < key):
        node = node.next
    return node.key == key ? node : null
```

```
insert(key) //  $O(\log n)$ 
    k = 0
    while (!done):
        flip a fair coin:
            with probability  $\frac{1}{2}$  : done = true
            with probability  $\frac{1}{2}$  : k++
```

Every search and insert operation completes in $O(\log n)$ time with high probability of at least $1 - 1/n$.

In a **skip list** with two lists, the express list skips \sqrt{n} elements per stop, and search takes $O(\sqrt{n})$. A proper skip list has $\log n$ levels.

Invariant: The bottom list contains every element, and about half of the elements in level j gets promoted to level $j + 1$.

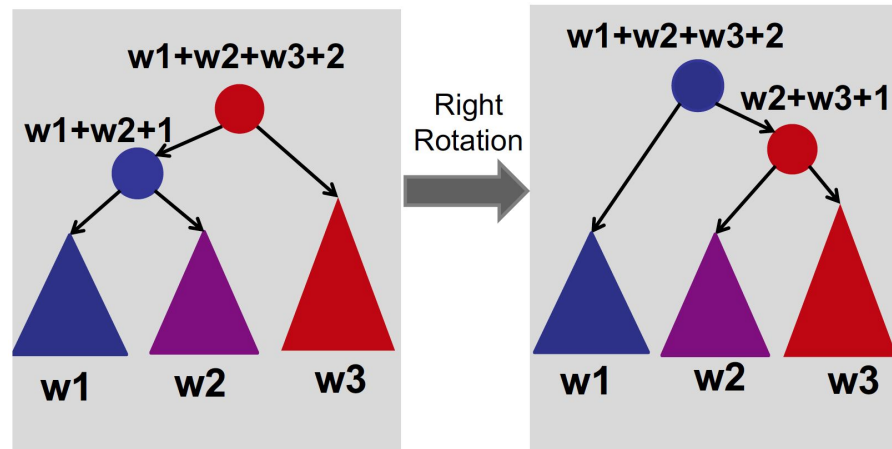


[order statistics trees]

In an **Order Statistics Tree**, we also store the **size** of the subtree in every node. The **weight** of a node is the size of the tree rooted at that node.

$$w(\text{leaf}) = 1;$$
$$w(v) = w(v.\text{left}) + w(v.\text{right}) + 1;$$

This weight attribute must be maintained whenever a rotation occurs.

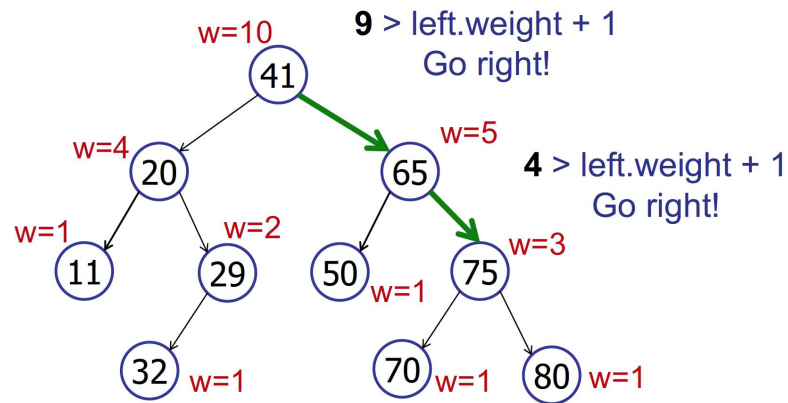


<select>

```
select(k)
  rank = m_left.weight + 1;
  if (k == rank) then
    return v;
  else if (k < rank) then
    return m_left.select(k);
  else if (k > rank) then
    return m_right.select(k - rank);
```

Finds the node of rank k within the tree.

select(9)

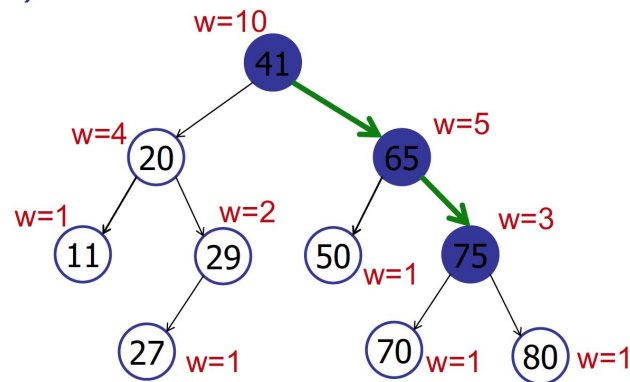


<rank>

```
rank(node)
  rank = node.left.weight + 1;
  while (node != root)
    if (node is left child)
      do nothing;
    else if (node is right child)
      rank += node.parent.left.weight + 1;
      node = node.parent;
  return rank;
```

Computes the rank of a node v.

rank(75)

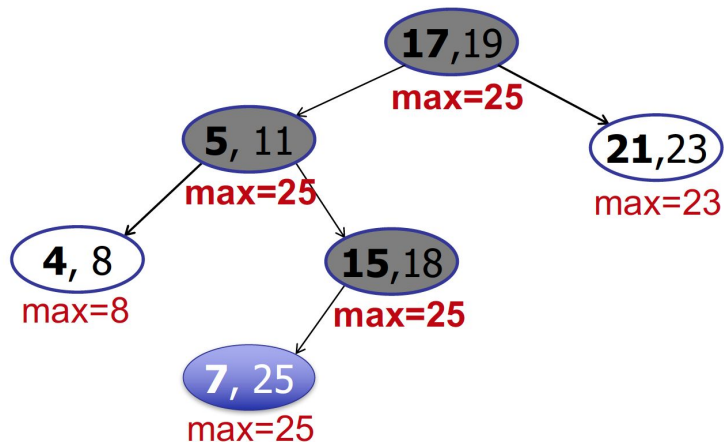


$$\text{rank} = 2 + 2 + 5 = 9$$

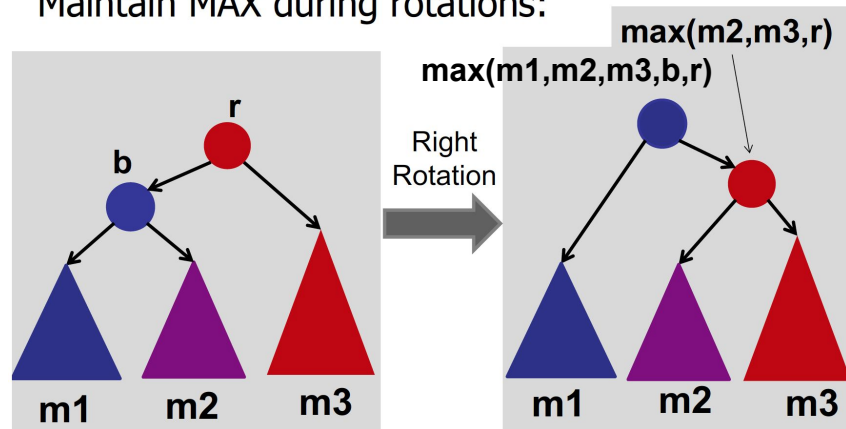
[interval trees]

An **interval tree** is an AVL tree where each node is an interval (low, high) and contains the maximum endpoint max in its subtree. It is sorted by left endpoint.

For every insertion, the max has to be updated every node along the path from the inserted node to the root.



Maintain MAX during rotations:



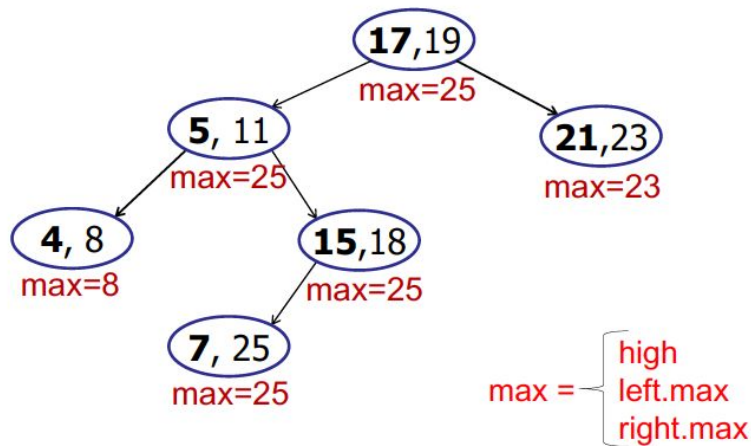
<interval search>

```
intervalSearch(x) //  $O(\log n)$   
  c = root;  
  while (c != null and x is not in c.interval)  
    if (c.left == null)  
      c = c.right;  
    else if (x > c.left.max)  
      c = c.right;  
    else  
      c = c.left;  
  return c.interval;
```

Correctness: If the search goes right, then there is no overlap in the left subtree \rightarrow either search finds key in the right subtree or it is not in the tree.

If the search goes left, and there is no overlap in the left subtree \rightarrow there is no overlap in the right subtree either.

Finds an interval that contains x.



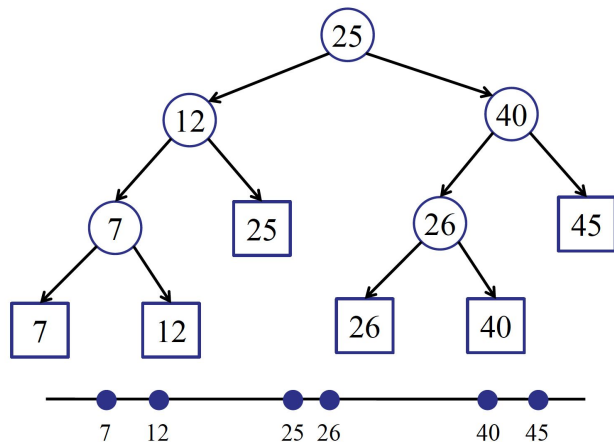
<all overlaps>

```
allOverlaps(x) //  $O(k \log n)$   
  repeat until no more intervals:  
    search for an interval containing x;  
    add that interval to list;  
    delete that interval;  
  repeat for all intervals in list:  
    add the interval back in tree;
```

Lists all the intervals that overlap with point x .
The time complexity if there are k overlapping intervals is $O(k \log n)$, although the best known solution has a time complexity of $O(k + \log n)$.

[range trees]

In a **Range Tree**, we store all points in the leaves, whereas internal nodes only store copies. Each internal node v stores the maximum of any leaf in its left subtree.



Preprocessing Time Complexity: $O(n \log n)$

Space Complexity: $O(n)$

A one-dimensional range query, **query**(low, high), will return all the points in the tree that fall between the range of low and high.

```
rangeQuery(low, high)
    v = findSplit(low, high); //  $O(\log n)$ 
    LeftTraversal(v.left, low, high);
    RightTraversal(v.right, low, high);
```

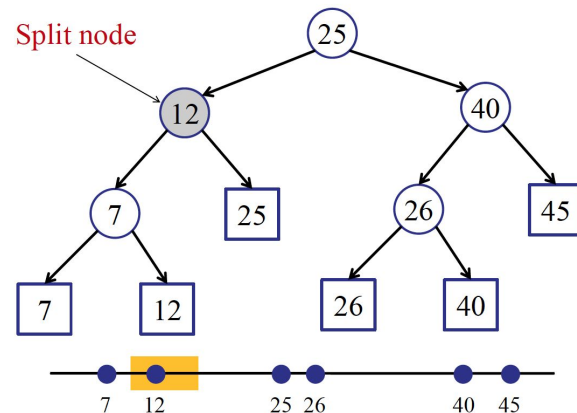
Time Complexity: $O(k + \log n)$, where k is the number of points found.

<find split>

```
findSplit(low, high) //  $O(\log n)$   
  v = root;  
  done = false;  
  while (!done)  
    if (high <= v.key) then v=v.left;  
    else if (low > v.key) then v=v.right;  
    else done = true;  
  return v;
```

A **split node** is the first node from the root in which its point value is between the range query.

Example: query(8, 20)



<range traversal>

```
LeftTraversal(v, low, high)
    if (low <= v.key)
        all-leaf-traversal(v.right);
        LeftTraversal(v.left, low, high);
    else
        LeftTraversal(v.right, low, high);
```

```
RightTraversal(v, low, high)
    if (v.key <= high)
        all-leaf-traversal(v.left);
        RightTraversal(v.right, low, high);
    else
        RightTraversal(v.left, low, high);
```

For the left traversal, we either
→ output all in the right subtree and recurse left
→ *or* recurse right.

For the right traversal, we either
→ output all in the left subtree and recurse right
→ *or* recurse left.

Time

Traversal algorithm recurses at most $O(\log n)$ times. Outputting all in a subtree has a cost of $O(k)$ where k is the number of items found.

Complexity:

<number of points in range>

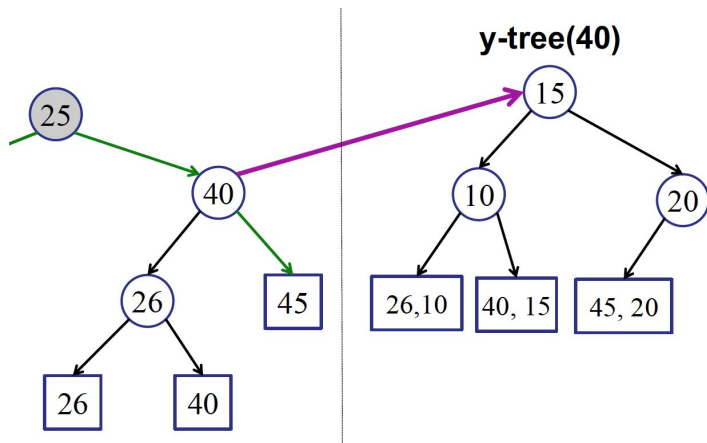
```
LeftTraversal(v, low, high)
    if (low <= v.key)
        total += v.right.count;
        LeftTraversal(v.left, low, high);
    else
        LeftTraversal(v.right, low, high);
```

To just find out the number of points in the range, just keep a count of the number of nodes in each subtree.

[two-dimensional range trees]

For a **two-dimensional range tree**,

1. Create a 1D-range tree (using only x-coordinates) of the points (ie. the x-nodes).
2. Store a y-tree (using only y-coordinates) at each x-node containing all the points in the x-node's subtree.



Space Complexity: $O(n \log n)$
Each point in the x-tree appears at most $O(\log n)$ y-trees (ie. at most one y-tree per level). The rest of the x-tree takes $O(n)$ space.

BuildTree Time Complexity: $O(n \log n)$

Inserting / Deleting Nodes: $O(n)$
On every insertion / deletion, you will have to do a rotation, and every rotation requires us to entirely rebuild the y-trees for the rotated nodes.

<two-dimensional range queries>

```
2DRangeQuery(low, high)
    v = findSplit(low, high); // O(log n)
    2DLeftTraversal(v, low, high);
    2DRightTraversal(v, low, high);
```

```
2DLeftTraversal(v, low, high)
    if (v.key.x >= low.x)
        ytree.search(low.y, high.y); // O(log n)
        2DLeftTraversal(v.left, low, high);
    else
        2DLeftTraversal(v.right, low, high);
```

Given a 2D array of points, searches for all the points that fall within a rectangular box.

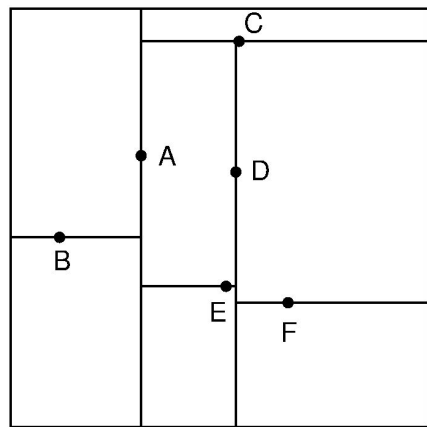
Time Complexity:
O(log n) to find split node
O(log n) recursing steps
O(log n) y-tree searches of O(log n)
O(k) enumerating output

Curse of Dimensionality:
For d-dimensional range trees, recursively construct a (d-1)-dimensional range tree in each node of a 1D-range tree.

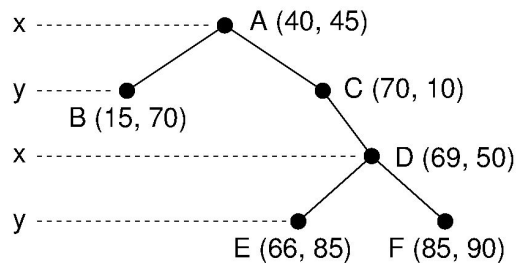
- **Query cost:** $O(\log^d n + k)$
- **buildTree cost:** $O(n \log^{(d-1)} n)$
- **Space:** $O(n \log^{(d-1)} n)$

[kd-trees]

In a **kd-tree**, each alternate level in the tree divides the points on a plane into half either vertically or horizontally.



(a)



(b)

Query Cost: Worst case $O(\sqrt{n})$, but it sometimes works better in practice for most queries.

Advantages over 2D range trees: Easier to update dynamically and good for nearest-neighbour queries.

[hash tables with separate chaining]

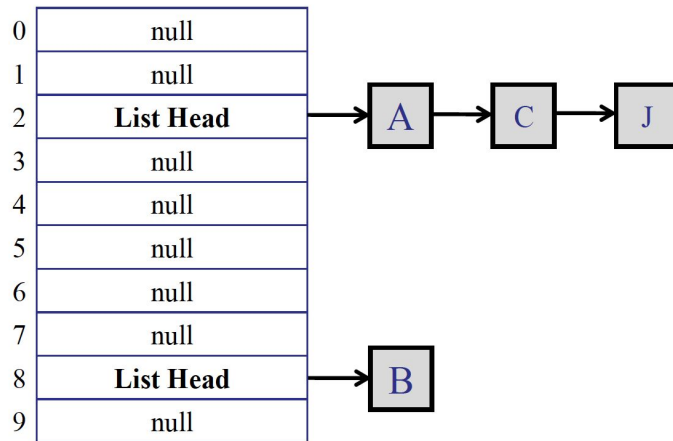
```
insert(key, value)    // Worst: O(1)
    calculate h(key);
    lookup h(key) in hash table;
    add h(key) to linked list;

search(key) // Worst: O(n), Expected: O(1)
    calculate h(key);
    search for (key,value) in linked list

delete(key) // O(1 + n/m)
    calculate h(key);
    search for (key,value) in linked list
    delete item from linked list
```

Given n items, a hash table of these entries would have m buckets, each bucket containing a linked list of items to store multiple keys.

Space Complexity: $O(m + n)$



<open addressing>

```
insert(key, value) // Average  $\leq 1 / (1 - \alpha)$ 
    int num_collisions = 1;
    while (num_collisions <= m)
        int bucket = h(key, num_collisions);
        if (T[bucket] == null){
            T[bucket] = {key, value};
            return success;
        }
        num_collisions++;
    throw new TableFullException();

delete(key)
    find key to delete;
    remove it from the table;
    set bucket to DELETED;
```

When you insert items, on collision, probe a sequence of buckets in the hash table until you find an empty one.

The **hash function** is redefined as $h(\text{key}, \text{num_collisions})$.

Load α of a hash table is the average #items per bucket, i.e. $\alpha = n/m$.

<hash functions>

Linear Probing:

$$h(\text{key}, i) = (h(\text{key}) + i) \% m$$

Modified Linear Probing:

$$h(\text{key}, i) = (h(\text{key}) + i*d) \% m$$

where $d > 1$ and is coprime to m .

Quadratic Probing:

$$h(\text{key}, i) = (h(\text{key}) + i^2) \% m$$

Double Hashing:

$$h(\text{key}, i) = (f(\text{key}) + i*g(\text{key})) \% m$$

A **hash function** stores a key k into a bucket $h(k)$. A good **hash function** $h(\text{key}, i)$, where i is the number of collisions, should enumerate all possible buckets and follow the Simple Uniform Hashing Assumption.

Simple Uniform Hashing Assumption: Every key is equally likely to map to every bucket, and keys are mapped independently.

If table is $\frac{1}{4}$ full, there will be clusters of size $\theta(\log n)$, but may still be fast due to caching - it is cheap to access nearby cells.

If $g(k)$ is relatively prime to m , then $h(k,i)$ hits all the buckets.

<resizing>

```
growTable
```

```
    if (n == m) then m = 2m;
```

```
shrinkTable
```

```
    if (n < m/4) then m = m/2;
```

Amortized

Operation has amortized cost $T(n)$ if **for every integer k** , the cost of k operations is $\leq k T(n)$.

Analysis:

Time

Inserting k elements into a hash table takes time $O(k)$. Hence, the insert operation has amortized cost $O(1)$.

Complexity:

[fingerprint hash table]

A **fingerprint hash table** (of size m with n elements) implements a Set ADT that maintains a vector of 0/1 bits.

```
insert(key)
    m_table[hash(key)] = 1;

lookup(key)
    return (m_table[hash(key)] == 1);
```

For a **lookup**(key),

$$\begin{aligned} P(\text{no false positive}) &= P(\text{no collision}) = (1 - 1/m)^n \approx (1/e)^{(n/m)} \\ P(\text{false positive}) &= 1 - (1/e)^{(n/m)} \end{aligned}$$

Insert operation:

`hash("www.microsoft.com")`

Lookup operation:

`hash("www.rugby.com")`

Even if the URL is NOT in the set,
it may *sometimes* report **true**.
(False positives.)

0	0
1	0
2	0
3	1
4	0
5	0
6	1
7	0
8	1
9	0

[bloom filter]

A **bloom filter** is a fingerprint hash table that makes use of more than one hash functions. For the case of just 2 hash functions below:

```
insert(URL)
    k1 = hash1(URL); k2 = hash2(URL);
    T[k1] = 1; T[k2] = 1;

query(URL) // requires 2 collisions for false +ve
    k1 = hash1(URL); k2 = hash2(URL);
    if (T[k1] && T[k2]) return true;
    else return false
```

Use k hash functions!

hash("www.gmail.com")

0	0
1	0
2	1
3	1
4	0
5	0
6	1
7	0
8	1
9	0

For a bloom filter with k hash functions, assuming (bogus) fact that each table slot is independent,

$$P(\text{a given bit is } 0) = (1 - 1/m)^{kn} \approx e^{(-kn/m)}$$
$$P(\text{false positive}) = P(\text{collision at all } k \text{ spots}) = (1 - (1/e)^{(kn/m)})^k$$

Optimal number for k is $(m/n) \ln 2$.

[adjacency matrix]

```
Int[][] adjMatrix = new int[n][n];
```

Format:

Undirected, unweighted: $A[v][w] = 1$ iff $(v,w) \in E$

Undirected, weighted: $A[v][w]$ and $A[w][v] = \text{weight}(v,w)$ else 0

Directed, weighted: $A[v][w] = \text{weight}(v,w)$ else 0

Good for: Dense graph, $|E| = \theta(V^2)$

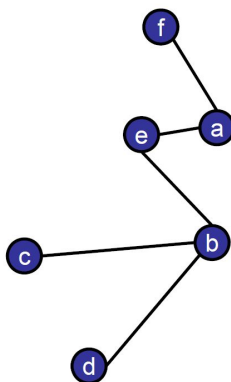
Space Complexity: $O(V^2)$

Find neighbours of v: Slow

Enumerate neighbours: Slow

Are v and w neighbours: Fast

	a	b	c	d	e	f
a	0	0	0	0	1	1
b	0	0	1	1	1	0
c	0	1	0	0	0	0
d	0	1	0	0	0	0
e	1	1	0	0	0	0
f	1	0	0	0	0	0



[adjacency list]

<implementations>

Format: 1D array of **V** lists, one for each vertex. For each vertex **i**, **AdjList[i]** stores list of **i** neighbours.

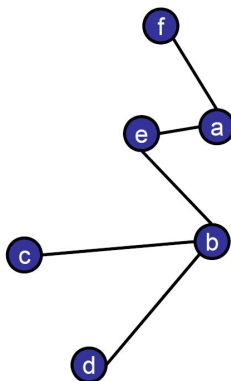
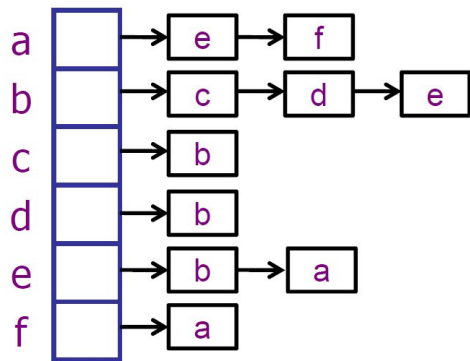
Good for: Sparse graph, $|E| < \theta(V^2)$

Space Complexity: $O(V+E)$

Find neighbours of v: Fast

Enumerate neighbours: Fast

Are v and w neighbours: Slow



[edge list]

<implementations>

Format: ArrayList EdgeList of E edges. For each edge i, EdgeList[i] stores an integer triple {u,v,w(u,v)}

Space Complexity: $O(E)$

<breadth-first search>

```
BFS(G, s, f)
    Queue.add(s)
    while not Queue.empty()
        curr = Queue.dequeue()
        if curr == f
            return curr
        for each neighbor u of curr
            if u is not visited
                visit(u)
                Queue.enqueue(u)
    return null
```

Explores the graph level by level, advancing a frontier.

Works best with adjacency list. Visits every node and every vertex, but not every path.

Capable of finding shortest path in tree and unweighted graph.

Time / Space Complexity

Time: $O(V+E)$

<depth-first search>

```
DFS(G, s, f)
  Stack.push(s)
  while not Stack.empty()
    curr = Stack.pop()
    if curr == f
      return curr
    for each neighbor u of curr
      if u is not visited
        visit(u)
        Stack.push(u)
  return null
```

Follow path until you get stuck. Backtrack until you find a new edge. Recursively explore it, don't repeat a vertex. This implementation uses a stack to recurse.

Works best with adjacency list. Visits every node and every vertex, but not every path.

Capable of finding shortest path in tree.

Time / Space Complexity

Time: $O(V+E)$

<recursive depth-first search>

```
DFS(G, v, f)
  visit(v)
  if v == f
    return v
  for each neighbor u of v
    if u is not visited
      w = DFS(G, u, f)
      if w is not null
        return w
  return null
```

Follow path until you get stuck. Backtrack until you find a new edge. Recursively explore it, don't repeat a vertex. This implementation uses recursion.

Works best with adjacency list. Visits every node and every vertex, but not every path.

Capable of finding shortest path in tree.

Time / Space Complexity

Time: $O(V+E)$

<floyd-warshall's>

```
D[i][j] = 0 if no edge
```

```
for k in V
  for i in V
    for j in V
      D[i][j] = foo(D[i][j],
                    bar(D[i][k], D[k][j]))
```

Slow/costly preprocessing algorithm but enables all subsequent queries to be handled in $O(1)$.

Time / Space Complexity

$O(V^3)$ due to 3 nested loops

Use Case	foo	bar
APSP	min	sum
Minimax	min	max
Maximin	max	min

<relaxation>

```
relax(int u, int v)
    if dist[v] > dist[u]+weight(u,v) // if SP can be shortened
        dist[v] ← dist[u]+weight(u,v) // relax this edge
        predecessor[v] ← u // remember/update the predecessor
        // if necessary, update some data structure
```

Key operation in all SSSP algorithms.
“Updates” the estimated shortest-path
distance of a vertex from the source.

<bellman-ford's>

BellmanFord(G)

```
for each  $v \in V$ 
   $D[v] \leftarrow \text{INF}$ 
   $p[v] \leftarrow -1$  // to represent NULL
   $D[s] \leftarrow 0$ 
for  $i = 1$  to  $|V|-1$  //  $O(V)$ 
  for each edge  $(u, v) \in E$  //  $O(E)$ 
    relax( $u, v$ ) //  $O(1)$ 
```

Seth format**BellmanFord(G)**

```
 $n = V.\text{length};$ 
for ( $i=0$ ;  $i<n$ ;  $i++$ )
  for (Edge  $e$  : graph)
    relax( $e$ )
```

Inefficient but guaranteed-to-work method of finding shortest path. Works if graph has negative weight edges.

Uses an Edge List.

Time / Space Complexity

Time: $O(VE)$

Invariants

<one-pass bellman-ford's>

```
DAGBellmanFord(V, E)
  toposort(V) //  $O(V+E)$ 
  for each  $v \in V$ 
     $D[v] \leftarrow \text{INF}$ 
     $p[v] \leftarrow -1$  // to represent NULL
     $D[s] \leftarrow 0$ 
  for each vertex  $u$  in toposort(V) //  $O(E)$ 
    for each neighbour  $v$ 
      relax( $u, v, w(u,v)$ ) //  $O(1)$ 
```

Perform topological sort on vertices first in $O(V+E)$. Then, in that order, relax outgoing edges of vertices.

Time / Space Complexity

Time: $O(V+E)$

Use Case

Directed Acyclic Graph

<dijkstra's algorithm>

```
searchPath(int start) {
    pq.insert(start, 0.0);
    distTo = new double[G.size()];
    Arrays.fill(distTo, INFTY);
    distTo[start] = 0;
    while (!pq.isEmpty()) {
        int w = pq.deleteMin(); // |V| times
        for (Edge e : G[w].nbrList) relax(e); // |E| times
    }
    relax(Edge e) {
        int v = e.from(); int w = e.to();
        double weight = e.weight();
        if (distTo[w] > distTo[v] + weight) {
            distTo[w] = distTo[v] + weight;
            parent[w] = v;
            if (pq.contains(w))
                pq.decreaseKey(w, distTo[w]); // |E| times
            else pq.insert(w, distTo[w]); // |V| times
        }
    }
}
```

Can be thought of as a specialised case of BFS where the queue (FIFO to advance frontier) is replaced by a PQ (to greedily find shortest edge)

Time / Space Complexity

Insert/DeleteMin $|V|$ times
Relax/decreaseKey $|E|$ times
PQ is $O(\log V)$
Total $O((V+E)\log V)$

Use Case

No negative weight edge

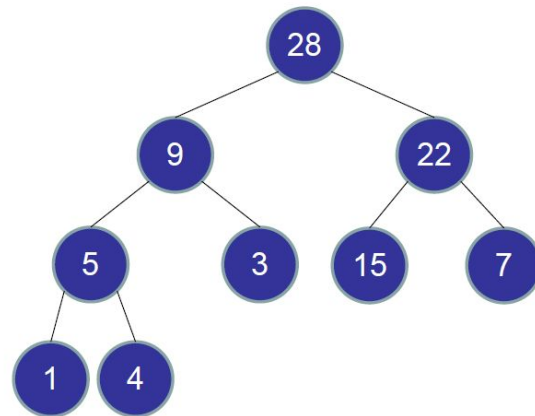
[binary heap]

```
insert(Priority p, Key k) {  
    Node v = m_completeTree.insert(p,k);  
    bubbleUp(v);  
}
```

delete(Help why the slide don't have)

A **binary heap** is an implementation of a Max/Min priority queue ADT that is a complete binary tree.

Every level is full, except possibly the last. All nodes are as far left as possible.



<bubble-up>

```
bubbleUp(Node v) {  
    while (v != null) {  
        if (priority(v) > priority(parent(v)))  
            swap(v, parent(v));  
        else return;  
        v = parent(v);  
    }  
}
```

<Description>

Time / Space Complexity

Invariants

<bubble-down>

```
bubbleDown(Node v)
    while (!leaf(v)) {
        leftP = priority(left(v));
        rightP = priority(right(v));
        maxP = max(leftP, rightP, priority(v));
        if (leftP == max) {
            swap(v, left(v));
            v = left(v); }
        else if (rightP == max) {
            swap(v, right(v));
            v = right(v); }
    else return;
}
```

<Description>

Time / Space Complexity

Invariants

[union-find disjoint set]

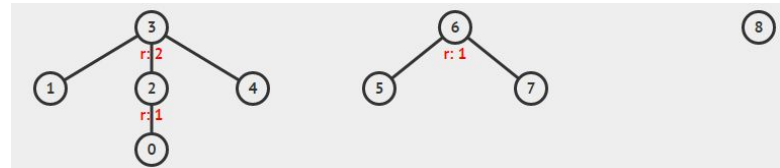
```
union(int p, int q) {
    while (parent[p] != p) p = parent[p];
    while (parent[q] != q) q = parent[q];
    if (size[p] > size[q]):
        parent[q] = p; // Link q to p
        size[p] = size[p] + size[q];
    else:
        parent[p] = q; // Link p to q
        size[q] = size[p] + size[q];

findRoot(int p) {
    root = p
    while (parent[root] != root) root = parent[root];
    while (parent[p] != p) {
        temp = parent[p];
        parent[p] = root;
        p = temp;
    }
    return root;
```

A **UFDS** is used to determine which set an item belongs to, test if two items belong to the same set, and union two disjoint sets into one.

With both **path compression** and **union-by-rank** heuristic applied, UFDS operations run in **near $O(1)$** time.

p	2	3	3	3	3	6	6	6	8
idx	0	1	2	3	4	5	6	7	8



<kruskal's algorithm>

```
sort the set of E edges by increasing weight
//  $O(E \log E)$ 
T={}
while there are unprocessed edges left //  $O(E)$ 
    pick unprocessed edge e with min cost //  $O(1)$ 
    if adding e to T does not form a cycle //  $O(1)$ 
        add e to T //  $O(1)$ 
T is an MST
```

Consider the a set of 1-vertex trees. Remove smallest edge from set of edges and add it to graph if it does not form a cycle.

Uses a UFDS to check for cycle formation by observing if two edges are already in the same tree.

<prim's algorithm>

```
T = {s}
enqueue edges connected to s into PQ
while unprocessed edges in PQ
    poll topmost edge e
    if vertex v linked with edge e is not taken yet
        T = T U v
    enqueue edges adjacent to v not in T into PQ
T is an MST
```

Initially, tree consists of source vertex. Repeatedly find minimum weight edge on the “cut” between tree and rest of graph by extracting from PQ.

Uses a PQ

Time / Space Complexity

We only process each edge once (enqueue and dequeue it), $O(E)$

Each time, we enqueue/dequeue from a PQ in $O(\log E)$

As $E = O(V^2)$, we have $O(\log E) = O(\log V^2) = O(2 \log V) = O(\log V)$

Total time $O(E) * O(\log V) = O(E \log V)$

DS	Operations	Big-O	Main point
Array List	1.Get 2.Add 3.AddBack 4.Remove 5.RemoveBack	1.O(1) 2.O(N) 3.O(1) 4.O(N) 5.O(1)	1.Good for accessing, not good for adding/removing 2.Can be made circular to reduce the need to double the array
Linked List	1.Get 2.Add 3.AddFront 4.Remove 5.RemoveFront	1.O(N) 2.O(N) 3.O(1) 4.O(N) 5.O(1N)	1.Good for adding and removing 2.Tailed Linked List has RemoveBack in O(1) 3.DoublyLinkedList has slightly faster search, average O(n/2) 4.Implement ListNode class
HashMap	1.Find 2.Insert 3.Delete	1.O(1) 2.O(1) 3.O(1)	1.Linear Probing $(\text{hash}(\text{key}) + k) \% m$ 2.Modified $(\text{hash}(\text{key}) + k * d) \% m$; d,m coprime 3.Quadratic $(\text{hash}(\text{key}) + k^2) \% m$ 4.Double: $(\text{hash}(\text{key}) + 3 * \text{hash2}(\text{key})) \% m$

DS	Operations	Big-O	Main point
BST/AVL	1.Insert 2.Delete 3.Search 4.findMin/Max 5.Pred/Succ 6.Inorder 7.Select 8.Rank	1.O(h) 2.O(h) 3.O(h) 4.O(h) 5.O(h) 6.O(N) 7.O(h) 8.O(h)	1.y.key< x.key if y is in left subtree of x 2.y.key ≥ x.key if y is in right subtree of x 3.For AVL tree, $h=\log N$, $h < 2\log_2 n$ 4.AVL Tree A node v is height-balanced if: $ v.\text{left.height} - v.\text{right.height} \leq 1$ 5.Made of nodes/vertices 6.Traversal is O(N) – can use to sort/transfer to another data structure
UFDS	1.findSet(i) 2.isSameSet(i,j) 3.unionSet(i,j) 4.Construct(N)	All O($\alpha(N)$), basically O(1)	1.Union by rank: tree with higher height becomes root when union 2.Path compression: findset compresses path by making root into parent 3.Used in MST Kruskal's to check for cycle
Binary Max Heap	1.ShiftUp/Swim 2.ShiftDown/Sink 3.Insert 4.ExtractMax/Min 5.Fast Create	1.O(log N) 2.O(log N) 3.O(log N) 4.O(log N) 5.O(log N)	1.Implementation for PriorityQueue ADT 2.Binary tree height log N 3.Use compact array 4.ExtractRoot replaces with successor, then sink if need 5.Fast create by pretending array is already heap, then fixing

Algorithm	Complexity	When to Use	Characteristics
Bellman-Ford's	$O(VE)$	General	Relax all edges in $V-1$ passes. Optimise by stopping if any pass finishes without relaxation. Without optimisation, bound is $O(VE)$ cannot do better (input insensitive).
BFS	$O(V+E)$	Unweighted	Replace visited array with distance array, initialise all INF and then replace with counter $D[v]=D[u]+1$
BFS/DFS	$O(V+E)=O(V)$	Tree	Replace visited array with distance array, initialise all INF and then replace with counter $D[v]=D[u]+1$
Dijkstra's	$O((V+E)\log V)$	No neg weight	Greedily extract vertex with lowest $D[u]$ estimate and relax edges out of it – when given undirected/unweighted graph, is a BFS
Modified Dijkstra's	$O((V+E)\log V)$	No neg cycle	Do not delete inferior copy of $D[u]$, at the cost of possibly longer runtime with –ve edges present (but correct answer)
1-Pass Bellman-Ford	$O(V+E)$	DAG	Literally 1-pass Bellman Ford relaxing edges in topological order of source vertex
Prim's	$O(E\log V)$	MST	Start from source vertex and greedily add vertex with smallest weight across the cut. Need PQ to choose edges.
Kruskal's	$O(E\log V)$ from sorting	MST	Sort edges. Add edges as long as they don't form a cycle. Need UFDS to check for cycle forming.

BST Property:

All in left subtree $<$ node $<$ all in right subtree

Successor is minimum of right subtree if right subtree exists

Binary Max Heap Property:

$A[\text{parent}(i)] > A[i]$, binary tree is complete (all levels filled except last)

A larger int can be at a lower level than a smaller int

Tree Property:

Tree is smallest connected graph and has $V-1$ edges

Only one path from any vertex to another

MST and SSSPT are same

MST: If all edge weights are distinct, MST is unique

“Can we run algo faster” yes if we change the data structure first. No constraint saying cannot change edge list to adj list for example \leftarrow watch out chongkf likes to sike ppl