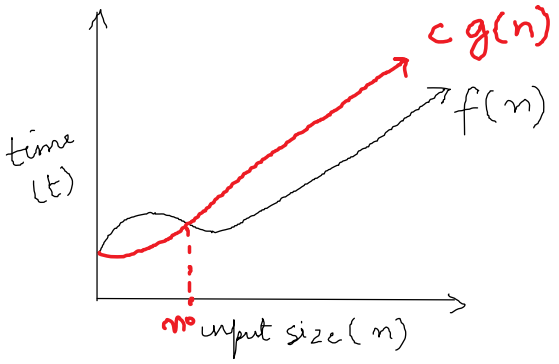
Algorithms: Space and Time Complexity

INTRODUCTION TO ASYMPTOTIC NOTATION

There will be many solutions to a given problem each of which will be given by an algorithm. Now, we want that algorithm which is going to give me the result quickest while consuming not much of the space (memory). Therefore, design and analysis of algorithms is the subject to design the various algorithms for a problem and analyze them for the best possible algorithm to choose.

Before proceeding, we have some notations to understand. These are called asymptotic notations.

Let's say we have a function f(n) and as the n increases the rate of growth of time increases in a certain way.



1. **Big-Oh (O)**: Let's find another function 'cg(n)' (above graph) in such a way that the after it gets an input n_0 the value of this function is always greater than the f(n). Then if:

$$f(n) \leq cg(n)$$
$$n \geq n_0$$
$$c > 0, n \geq 1$$

If the above satisfies, then we can say that

$$f(n) = O(g(n))$$

Which is equivalent to say that f(n) is smaller than g(n).

Let's take an example: f(n) = 3n + 2 and g(n) = n, is f(n) = O(g(n))?

$f(n) = 3n+2$, $g(n) = n$, for $f(n) = O(g(n))$ then

$\Rightarrow f(n) \leq c\,g(n)$

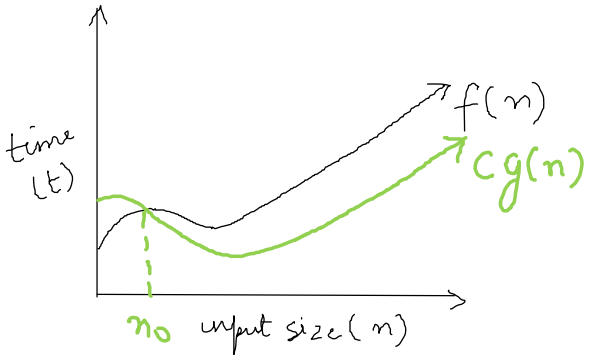
$\Rightarrow 3n+2 \leq cn$

Let $c=4 \Rightarrow 3n+2 \leq 4n \Rightarrow 2 \leq n$ $\therefore c=4$,

$\therefore f(n) = c\,g(n)$

Note: The tightest bound here is 'n'. If f(n) = O(g(n)) then definitely n^2, n^3… will be upper bounds, but we need to see the tightest bound which is 'n' in this case.

2. **Big-Omega(Ω)** :



Let's find another function 'cg(n)' (above graph) in such a way that the after it gets an input n_0 the value of this function is always smaller than the f(n). Then if:

$$f(n) \geq cg(n)$$
$$n \geq n_0$$
$$c > 0, n \geq 1$$

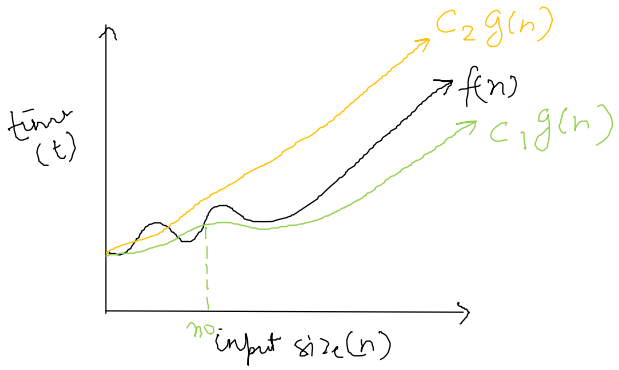
If the above satisfies, then we can say that

$$f(n) = \Omega\big(g(n)\big)$$

Which is equivalent to say that f(n) is greater than g(n).

We will see examples about it.

3. **Big-Theta(Θ):** We say that a function f(n) = Θ(g(n)), if the function f(n) is bounded by both lower and upper bounds. Let's see the graph for same.



Therefore,

$$c_1 g(n) \leq f(n) \leq C_2 g(n)$$

$$C_1, C_2 > 0$$

$$n \geq n_0, n_0 \geq 1$$

If the above is satisfied then we can say f(n) = Θ(g(n))

Example: f(n) = 3n + 2, g(n) = n. Is f(n) = Θ(g(n))?

$f(n) = 3n+2$, $g(n) = n$

(1) $f(n) \le c_1 g(n)$

$3n+2 \le c_1 n$ (for $c_1 = 4$ this is true)

$\therefore 3n+2 \le 4n$ for all $n_0 \ge 1$

$\therefore f(n) = O(g(n))$ — (i)

(2) $f(n) \ge c_2 g(n)$

$3n+2 \ge c_2 n$

$3n+2 \ge n$ $(c_2 = 1)$

$\therefore 3n+2 \ge n$ for all $n_0 \ge 1$

$\Rightarrow f(n) = \Omega(g(n))$ — (ii)

(i) & (ii) $\Rightarrow$ $f(n) = \Theta(g(n))$

Practical significance of the symbols:

Given any algorithm:

- O is going to say "worst case time" or the "upper bound". In other words, if you are giving time complexity in O notation, that will mean "In any case the time will not exceed this".
- Ω is going to say "best case time" which means in any case you can never achieve better than this.
- Θ is giving you the average case

In practicality we worry about the question "What is the worst case time the algorithm will take for any input?"

For some algorithms, the best and worst case will be same. In those scenarios we go for Θ.

We have seen that an algorithm's time complexity is given as a function f(n). This function is an *approximation* of the time taken by the algorithm and NOT the actual time it may take. Now let's see how to find f(n) which means *what is the approximate time taken by the algorithm.* Before we go into that let's understand more about algorithms.

There are two types of algorithms:

1. Iterative
2. Recursive

- It is worth noting that *any program that can be written using iteration can be written using recursion and vice versa.* Therefore, both are equivalent in power.
- For iterative program, you count the number of times the loop is going to get executed to find the time it's going to take. To find the time taken by a recursive program we use recursive equations. This means that they are both same in power but their analysis methods are different.
- ***In case if the algorithm does not contain either iteration or recursion it means that there is no dependency of the running time on the input size which means whatever is the size of the input the running time will be a constant value.***

Let's see some of the iterative programs and how to do complexity analysis of them.

TIME COMPLEXITY ANALYSIS OF ITERATIVE PROGRAMS

Example 1: Do the complexity analysis of the following program.

1)

```
A()
{
  int i,j;
  for(i=1 to n)        <- n times
    for(j=1 to n)      <- n times
      pf("Rahul")      : O(n^2)
}
```

2)

```
1991. A()
{ i=1, s=1;
  while (s<=n)
  { i++;
    s=s+i;
    pf("Rahul");
  }
}
```

Le 'k' be the value that 's' takes before the loop stops.

With each loop:

i=1, 2, 3, 4, … k

s = 1, 3, 6, 10, … n

We see that for every increase in 'i' s is the sum of first 'i' natural numbers. Therefore at when the loop reaches k to halt:

$K(k+1)/2 > n$

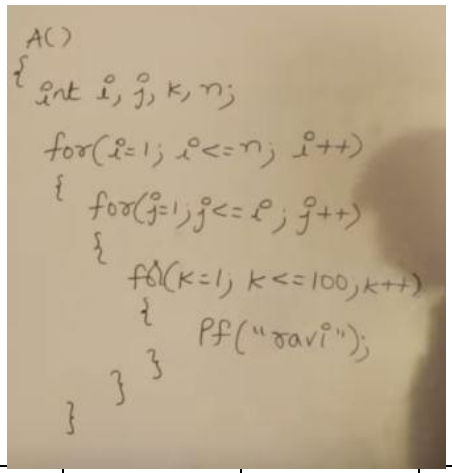
$(K^2 + k)/2 > n$

⇨ $K = O(\sqrt{n})$

3)

```
A()
{ for(i=1; i^2<=n; i++) ≡ for(i=1; i<=√n; i++))
  { pf("Hello");        : O(√n)
  }
}
```

4)



from the following table:

innermost loop will get executed:

100 + 200 + 300 .... nx100 or

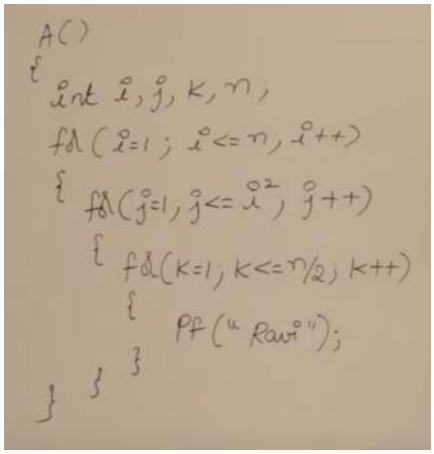
1x100 + 2x100 + 3x100 ... nx100 or

100 (1+2+3...n) or

100 (n(n+1)/2) ⇒ $O(n^2)$

I	1	2	3	4	…	N
J (times)	1	2	3	4	…	N
K(times)	1x100	2x100	3x100	4x100	…	Nx100

5



"Ravi" will get printed:

$n/2 \times 1 + n/2 \times 2 + n/2 \times 9 + n/2 \times 16 \cdots n/2 \times n^2$

$\Rightarrow n/2 \,(1 + 2 + 9 + 16 + n^2)$

$\Rightarrow n/2 \left(\frac{n(n+1)(2n+1)}{6}\right)$

$\Rightarrow \boxed{O(n^4)}$

I	1	2	3	4	…	N
J(times exec)	1	2	9	16	…	N^2
K(times exec)	(N /2)x1	(N /2)x2	(N /2)x9	(N /2)x16	…	(N/2)*N^2

$F(n) = n^k + n^{k-1} + n^{k-2} \ldots = O(n^k)$

6

```
A()
{ for (i=1 ; i<=n; i*=2)
  { print("Rahul"); }
}
```

Analysis:

for loops: $i = 1, 2, 4, \ldots, n$

Let us say it is going to take 'k' iterations by the time we reach 'n'.

∴ iterations: $2^0, 2^1, 2^2, 2^4 \ldots 2^k$

⇒ when program reaches 'n'

$2^k = n \Rightarrow \log(2^k) = \log(n)$

$\Rightarrow k = \log(n)$ ∴ $\boxed{O(\log n)}$

If i was increasing at the rate of 3, 4, 5, 6, instead of 2 in above example:

Then: for I = I * 2 : $O(\log_2 n)$

I = I * 3 : $O(\log_3 n)$ Therefore, for I = I *m complexity will be **$O(\log_m n)$**

I = I * 4 : $O(\log_4 n)$

I = I * 5 : $O(\log_5 n)$

Let's see an example depending on this example.

7

```
A()
{ int i, j, k;
  fo(i=n/2; i<=n; i++)
    fo(j=1; j<=n/2; j++)
      fo(k=1; k<=n; k=k*2)
        Pf("ravi");
}
```

runs → $n/2$ times

runs → $n/2$ times

runs → $\log_2 n$ times (prev example)

$\therefore$ complexity $= n/2 * n/2 * \log_2 n$

$= O(n^2 \log_2 n)$

We don't need to unroll the loops in this example because every loop's conditional statement is independent of the variable of the other loops.

8

```
A()
{ int i, j, k;
  fo(i=n/2; i<=n; i++)
    fo(j=1; j<=n; j=2*j)
      fo(k=1; k<=n; k=k*2)
        Pf(ravi);
}
```

runs → $n/2$ times

runs → $\log_2 n$ times

runs → $\log_2 n$ times

complexity: $n/2 * \log_2 n * \log_2 n$

$= O(n(\log_2 n)^2)$

In this example also the loops are independent of other loops' variables. So, no need to unroll them.

9 assume $n \geq 2$

```
A()
{ while(n>1)
  { n = n/2;
  }
}
```

Case 1: n is power of 2

for $n = 2^1$ while will execute 1 time

for $n = 2^2$ while will execute 2 time

for $n = 2^3$ while will execute 3 times

for $n = 2^k$ while will execute k times

$\therefore$ for n power of 2: $k = \log_2 n$

Case 2: n is not power of 2

let's say $n = 20$

→ 20 → 10 → 5 → 2 → 1 (4 times)

$\lfloor \log_2 20 \rfloor \simeq 4$

$\hookrightarrow O(\lfloor \log_2 n \rfloor)$

For question 9 above, if n was updating like:

N = n/5 then the complexity would be $O(\log_5 n)$

N = n/m then the complexity would be $O(\log_m n)$

Important result

10

```
A()
{
  for(i=1; i<=n; i++)
    for(j=1; j<=n; j=j+i)
      Pf("ravi");
}
```

from the following table:

"ravi" will get printed:

$N + N/2 + N/3 + \dots + N/N$

$= N(1 + 1/2 + 1/3 + \dots + 1/N)$

$= N(\log N) = O(n \log n)$

The inner loop is dependent on the variable of the outer loop. In this example we will have to unroll the loops to see wassup!

For I equals to	1	2	3	4	…	K	N
J will execute	1 to N	1 to N	1 to N	1 to N	…	1 to N	1 to N
J will execute times	N times	N/2 times	N/3 times	N/4 times	…	N/K times	N/N times

11

```
A()
{ int n = 2^k;
  for(i=1; i<=n; i++)
  {
    j=2
    while(j<=n)
    {
      j=j^2;
      Pf("ravi");
    }
  }
}
```

from the table below:

printf("ravi") will run

$n*(k+1)$ times

$n = 2^{2^k} \Rightarrow \log(n) = 2^k$

$\Rightarrow \log(\log(n)) = k$

$\Rightarrow n(\log\log n + 1) = n\log\log n + n = O(n \log\log n)$

At K	1	2	3	K
N will be	4	16	2^8	2^K
J values after each loop	2, 4	2, 4, 16	2, 4, 16, 256	2, 4, 16, …, 2^K
While will execute	N x 2 times	N x 3 times	N x 4 times	N x (K+1) times

TIME COMPLEXITY ANALYSIS OF RECURSIVE ALGORITHMS

Whenever a recursive function is given, the way you analyze the time complexity is different than the way you analyze the time complexity of iterative algorithms mainly because there is nothing to count in them.

To analyze the time taken by the recursive algorithm the first step is to find a recursive equation for the problem given and then proceed with that. Let's see that with the help of an example.

Example 1:

```
A(n)
{ if (n>1)
  return (A(n-1));
}
```

Now, let's suppose that the time taken to execute A(n) is T(n), then:

For the statement *if(n>1)* let's say some constant time 'c' is taken and

For A(n-1) the time will be T(n-1). Then we can say that our recursive equation for

The time complexity will be.

Recursive Equation : T(n) = c + T(n-1)

To solve the recursive equation, there are different ways:

1. Back substitution

   T(n) = c + T(n-1) --- 1
   T(n-1) = c + T(n-2) --- 2
   T(n-2) = c + T(n-3) --- 3

   Substituting 2 in 1 we get: T(n) = c + c + T(n-2) = 2c + T(n-2)
   Substituting 3 in the above equation: T(n) = 2c + c + T(n-3) = 3c + T(n-3)
   …
   T(n) = kc + T(n-k) --- 4

   So when are we going to stop the algorithm? Take a look at the algorithm. Now 1 above is valid only when n>1. Therefore, whenever n = 1 we are going to stop.

   This condition when the recursion will stop is called ***anchor condition, base condition or stopping condition.***

   Now if we want to stop, we need T(1) in the back substitution chain.

   From 4 above, we need n-k =1 to get T(1)
   => k = n-1

   ⇨ T(n) = (n-1)c + T(n-(n-1))
   ⇨ T(n) = (n-1)c + T(1)
   ⇨ T(n) = (n-1)c + c
   ⇨ T(n) = nc
   ⇨ T(n) = O(n)

When using back substitution:

1. Find the recursive equation
2. Back substitute (find the general T(n))
3. Find the stopping condition
4. Solve

Example 2: For the given recursive relation, find the time complexity

T(n) = n + T(n-1), n > 1

1, n = 1

Solution : $T(n) = n + T(n-1)$ — (1)

$T(n-1) = (n-1) + T(n-2)$ — (2)

$T(n-2) = (n-2) + T(n-3)$ — (3)

substituting (2) in (1) we get: $T(n) = n + (n-1) + T(n-2)$ — (4)

substituting (3) in (4) we get: $T(n) = n + (n-1) + (n-2) + T(n-3)$

$\Rightarrow T(n) = n + (n-1) + (n-2) + \dots + (n-k) + T(n-(k+1))$ — (5)

let's eliminate T( ) in (5) according to base condition recursion will stop when n = 1

∴ T(1) will come

so $n-(k+1) = 1$

∴ $n-k-1 = 1$

∴ $k = n-2$

(5) $\Rightarrow T(n) = n + (n-1) + (n-2) + \dots + (n-(n-2)) + T(1)$

$T(n) = n + (n-1) + (n-2) + \dots + 2 + T(1)$

$T(n) = n + (n-1) + (n-2) + \dots + 2 + 1$

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

$T(n) = O(n^2)$

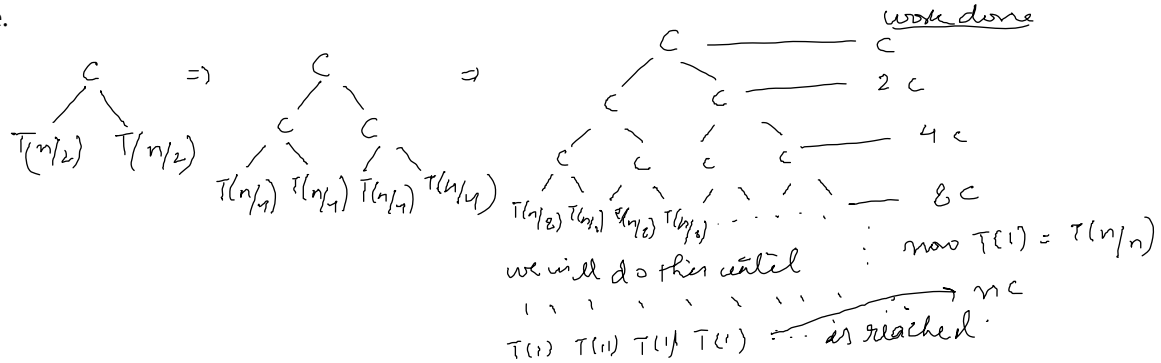
Let's see the next method which is called **RECURSION TREE** method.

Example: T(n) = 2T(n/2) + c, n > 1

1 , n = 1

Here we can think that if I do 'c' amount of work, then I can reduce the problem into two sets that taken T(n/2) time. Therefore.

T(n) =



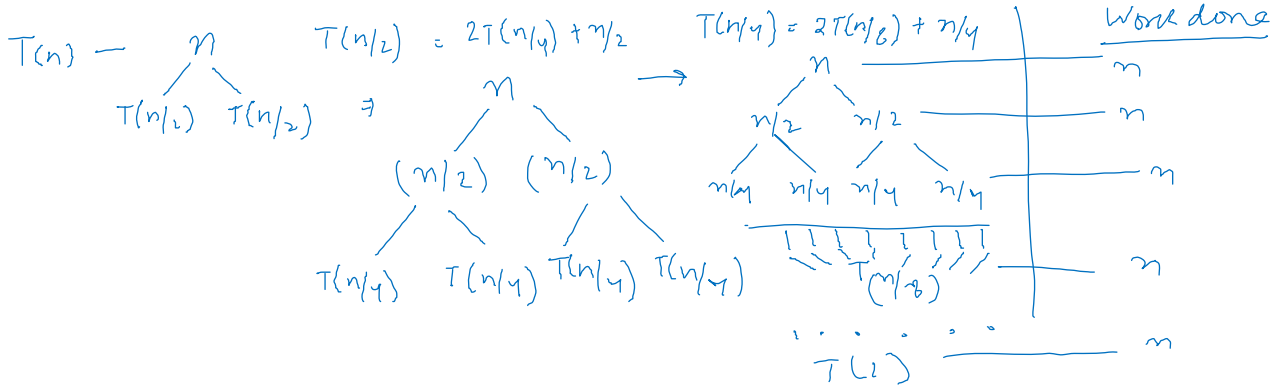
∴ Total work done: c + 2c + 4c + 8c +…+ nc

- ⇨ C(1+2+4+8+…+n) => C(sum of GP)
- ⇨ Let' say $n = 2^k$ => $C\ (\ 1(2^{k+1} -1)/(2-1))$
- ⇨ C(1+2+4+8+…+2^k) => C(2n -1) = O(n)

Example 2: T(n) = 2T(n/2) + n, n > 1

1 , n = 1

In this problem for every 'n' work done we can divide the problem into two halves, the time for which will be n/2



Total work: n + n + n … but how many n's are there?

Total n = n * number of levels, but how many levels are there?

Number of element in each level follow the fashion: 1, 2, 4, 8,… or $2^0, 2^1, 2^2, 2^3, \ldots, 2^k$

Therefore number of levels = K + 1 (0…k)

Number of n's = 2^k

K = logn

- ⇨ Number of levels = logn + 1
- ⇨ Total work done = n(logn + 1)
- ⇨ O(nlogn)

We saw recursion and back substitution methods for finding out time complexity of an algorithm. But, we need not do any of this as we are going to now learn about MASTER's THEOREM.

But before learning about master's theorem, we need to know "*how to compare two functions****" or answering questions like "****given two functions which one is asymptotically larger****".***

COMPARING VARIOUS FUNCTIONS TO ANALYZE TIME COMPLEXITY

If two function f(n) and g(n) are given and we need to know which one is larger.

1. Substitute LARGE values to 'n' and see or
2. Apply logarithm on both sides and then substitute
3. Whenever you cancel out the common terms and constants are remaining then the functions are *asymptotically equal.* Note: constants may not be equal.

Example: n^2 or 2^n. which one is more asymptotically complex?

Let $f(x) = n^2$ and $g(x) = 2^n$
applying log to both functions

$n^2 : 2 \log n \quad 2^n = n \log 2$

now let's substitute large values
let $n = 2^{100}$ then $n \log_2 2 = 2^{100}$
$2 \log_2 (2^{100}) = 2 \times 100 = 200$

$\therefore g(x) = 2^n$ is asymptotically more complex

Example: $f(x) = 3^n \quad g(x) = 2^n$

apply log: $n \log_2 3 \quad n \log_2 2$

remove common: $n \log_2 3 \quad n \log_2 2 \rightarrow \log_2 3 > \log_2 2 \therefore f(x) = 3^n$ is asymptotically more complex.

Example: $f(x) = n^2, \; g(x) = n \log n$

① cancel common terms: $n, \log n \mid n > \log n \therefore f(x) = n^2$ has greater complexity

Example $f(x) = n \quad g(x) = (\log n)^{100}$

applying log: $\log_2 n, \; 100 \log_2 \log_2 n$

let $n = 2^{128}$ $\log_2 2^{128}, \; 100 \log_2 \log_2 2^{128} \Rightarrow 128, 100 \log_2 128$
$\Rightarrow 128, 100 \times 7$
$\Rightarrow 128, 700$

let $n = 2^{1024}$ $\log_2 2^{1024}, \; 100 \log_2 \log_2 2^{1024} \rightarrow 1024, 100 \times \log_2 1024$
$\Rightarrow 1024, 100 * 10$
$\Rightarrow 1024, 1000$

$\therefore n$ is growing more later $\therefore$ its complexity is more!!!

Example $f(x) = n^{\log n} \quad g(x) = n \log n$, is $f(n) = O(g(n))$?

log on both sides we get: $\log n \log n, \; \log n + \log \log n$

substitute: $n = 2^{1024}, \; \frac{1024 \times 1024}{(1024)^2}, \; 1024 + 10, \; \frac{10}{}$ $\therefore n \log n < n^{\log n}$ in asymptotic complexity

Example $f(x) = \sqrt{\log n} \quad g(x) = \log \log n$

log both sides: $\frac{1}{2} \log \log n \quad \log \log \log n \mid n = 2^{2^{10}}$
$\Rightarrow \frac{1}{2} \times 10, \; 3.5$

Example $f(x) = n^{\sqrt{n}}$ $g(x) = n^{\log n}$ is $f(x) = O(g(x))$?

log: $\sqrt{n}\log n$ $\log n \log n$ | $\sqrt{n}$, $\log n$ | $\frac{1}{2}\log n$, $\log\log n$ | $n = 2^{10}$ → $\frac{1}{2} \times 2^{10}$, 10

∴ $n^{\sqrt{n}}$ has higher complexity asymptotically.

Example $f(n) = \begin{cases} n^3, & 0 < n < 10000 \\ n^2, & n \geq 10000 \end{cases}$ $g(n) = \begin{cases} n, & 0 < n < 100 \\ n^3, & n > 100 \end{cases}$

We worry about the large numbers. In this example, let's take the values the functions f(n) and g(n) take when n > 10000. F(n) takes n^2 and g(n) takes n^3. Therefore, in this example f(n) = O(g(n)).

Example $f_1 = 2^n$, $f_2 = n^{3/2}$, $f_3 = n\log n$ $f_4 = n^{\log n}$

For this problem to solve. You have to compare all of the functions with each other. Pick a function which looks complex (like f_1) and then compare it with others. Proceed this with others also.

Answer: f1 > f4 > f2 > f3

MASTERS THEOREM

This theorem is used to solve the recursive equations and find out the time complexity in terms of asymptotic notations.

If the recursive equation is of the form:

$$T(n) = aT(n / b) + \Theta(n^K \log^p n)$$

$$a \geq 1, b > 1, k \geq 0 \text{ and p is a real number}$$

Then:

1. If $a > b^k$, then $T(n) = \Theta(n^{\log_b a})$
2. If $a = b^k$
    a. If $p > -1$, then $T(n) = \Theta(n^{\log_b a} \log^{p+1} n)$
    b. If $p = -1$, then $T(n) = \Theta(n^{\log_b a} \log\log n)$
    c. If $p < -1$, then $T(n) = \Theta(n^{\log_b a})$
3. If $a < b^k$
    a. If $p >= 0$, then $T(n) = \Theta(n^k \log^p n)$
    b. If $p < 0$, then $T(n) = \Theta(n^k)$

Master's theorem is used to find the time complexity of the recursive relations given. For a given recursive equation:

1. Find out what is a, b, k and p
2. Compare 'a' with 'b^k'
3. Follow the results on the comparison in step 2.

Let's see some examples.

Example 1: $T(n) = 3T(n/2) + n^2$

Here a = 3, b = 2, k = 2, p = 0
$b^k = 4$, => $a < b^k$
and p>= 0 => $T(n) = \Theta(n^k \log^p n) = \mathbf{\Theta(n^2)}$

Example 2: $T(n) = 3T(n/2) + n^2$

Here a = 4, b = 2, k = 2, p = 0
$b^k = 4 \Rightarrow a = b^k$
and p > -1, then $T(n) = \Theta(n^{\log_b a} \log^{p+1} n)$
⇨ $T(n) = \Theta(n^{\log_2 4} \log^{0+1} n) = \mathbf{\Theta(n^2 logn)}$

Example 3: $T(n) = T(n/2) + n^2$

Here a = 1, b = 2, k = 2, p = 0
$b^k = 4 \Rightarrow a < b^k$
and p >= 0, then $T(n) = \Theta(n^k \log^p n)$
⇨ $T(n) = \Theta(n^2 \log^0 n) = \mathbf{\Theta(n^2)}$

Example 4: $T(n) = 2^nT(n/2) + n^n$
Here $a = 2^n$ which is not a constant, therefore Master's Theorem can't be applied for this problem. ***We will see how to convert the problems for which master's theorem can't be applied into one where it can be applied.***

Example 5: $T(n) = 16T(n/4) + n$
Here a = 16, b = 4, k = 1, p = 0
$b^k = 4 \Rightarrow a > b^k$
⇨ $T(n) = \Theta(n^{\log_b a}) = \Theta(n^{\log_4 16})$
⇨ $T(n) = \mathbf{\Theta(n^2)}$

Example 6: $T(n) = 2T(n/2) + nlogn$
Here a = 2, b = 2, k = 1, p = 1
$b^k = 2 \Rightarrow a = b^k$
and p > -1, then $T(n) = \Theta(n^{\log_b a} \log^{p+1} n)$
⇨ $T(n) = \Theta(n^{\log_2 2} \log^{1+1} n) = \mathbf{\Theta(nlog^2 n)}$

Example 7: $T(n) = 2T(n/2) + n/logn$
Or $T(n) = 2T(n/2) + nlog^{-1}n$
Here a = 2, b = 2, k = 1, p = -1
$b^k = 2 \Rightarrow a = b^k$
and p = -1, then $T(n) = \Theta(n^{\log_b a} loglogn)$
⇨ $T(n) = \Theta(n^{\log_2 2} loglogn)$
⇨ $T(n) = \mathbf{\Theta(nloglogn)}$

Example 8: $T(n) = 2T(n/4) + n^{0.51}$
Here a = 2, b = 4, k = 0.51, p = 0
$b^k = 4^{0.51} \Rightarrow a < b^k$
and p >= 0, then $T(n) = \Theta(n^k \log^p n)$
⇨ $T(n) = \Theta(n^{0.51} \log^0 n)$
⇨ $T(n) = \mathbf{\Theta(n^{0.51})}$

Example 9: $T(n) = 0.5T(n/2) + 1/n$
Here a = 0.5, b = 2, k = -1
Not valid for master's theorem as 'a' and 'k' values are not valid.

Example 10: $T(n) = 6T(n/3) + n^2logn$
Here a = 6, b = 3, k = 2, p = 1
$b^k = 9 \Rightarrow a < b^k$
and p >= 0, then $T(n) = \Theta(n^k \log^p n)$
⇨ $T(n) = \Theta(n^2 \log^1 n)$
⇨ **$T(n) = \Theta(n^2 logn)$**

Example 11: $T(n) = 64T(n/8) - n^2logn$
Here we have '-' instead of a +. This says that whenever we **don't do n^2logn work** the problem is going to divide itself into 64 parts. Therefore, this question is not valid for Master's theorem.

Example 12: $T(n) = 7T(n/3) + n^2$
Here a = 7, b = 3, k = 2, p = 0
$b^k = 9 \Rightarrow a < b^k$
p >= 0, then $T(n) = \Theta(n^k \log^p n)$
⇨ $T(n) = \Theta(n^2 \log^0 n)$
⇨ $T(n) = \mathbf{\Theta(n^2)}$
⇨

Example 13: $T(n) = 4T(n/2) + logn$
Here a = 4, b = 2, k = 0, p = 1
$b^k = 1 \Rightarrow a > b^k$

Example 14: $T(n) = \sqrt{2}T(n/2) + logn$
Here $a = \sqrt{2}$, b = 2, k = 0, p = 1
$b^k = 1 \Rightarrow a > b^k$

Therefore, $T(n) = \Theta(n^{\log_b a})$
⇨ $T(n) = \Theta(n^{\log_2 4})$
⇨ $T(n) = \mathbf{\Theta(n^2)}$

then $T(n) = \Theta(n^{\log_b a})$ => $T(n) = \Theta(n^{\log_2 root2})$
⇨ $T(n) = \mathbf{\Theta(\sqrt{n})}$

Example 15: $T(n) = 2T(n/2) + \sqrt{n}$
Here a = 2, b = 2, k = 1/2, p = 0
$b^k = \sqrt{2}$ => $a > b^k$
Therefore, $T(n) = \Theta(n^{\log_b a})$
⇨ $T(n) = \Theta(n^{\log_2 2})$
⇨ $T(n) = \mathbf{\Theta(n)}$

OTHER REMAINING EXAMPLES ARE NOT WRITTEN DUE TO THEIR SIMPLICITY.

Now that we have seen the Master's Algorithm and Time Complexity of algorithms, let's move on to the analysis of Space Complexity of the algorithms.

ANALYZING SPACE COMPLEXITY OF ITERATIVE AND RECURSIVE ALGORITHMS

So what is space?

Space: Given a program, how many memory cells are required to finish running it.

Space has to be analyzed in terms of given input size. This means if given the size of input as 'n' what is the total space required in relation to this input size.

Intuition:

If I need 'n' extra cells to run this program, space complexity will be O(n)
If I need '10' extra cells to run a program, space complexity will be O(1)
If I need 'n^2' extra cells to run a program, the space complexity will be O(n^2)

Note: Most of the times there is a tradeoff between the space and time complexity. It can be said that these two complexities are inversely proportional to each other.

Let's start with how to analyze the algorithm and answer what will be the total space required by the algorithm.

SPACE COMPLEXITY OF ITERATIVE ALGORITHMS

The space complexity of the algorithm is calculated using the "extra space" required to run the algorithm "apart from the input size given". Let's understand with the help of some examples.

Example 1

```
Algo(A[],l,n)
{ int i,j=10;
  for(i=1 to j)
     A[i]=0;
}
```

Apart from the space taken by the input, This algorithm is not taking any extra space. Therefore space complexity is O(1).

Example 2

```
Algo(A[],l,n)
{ int i;
  create B[n];
  for(i=1 to n)
     B[i]=A[i];
}
```

extra

Apart from space taken by the input, we have another array B which takes space of size n.
∴ int i → 1 space
B[n] → n space
Total space = 1+n or O(n)

Example 3

```
Algo(A[],l,n)
{ create B[n,n]
  int i,j
  for(i=1 to n)
    for(j=1 to n)
      B[i,j]=A[i]
}
```

n^2 space
2 spaces
Total = (n^2+2) or $O(n^2)$
computation so NO SPACES

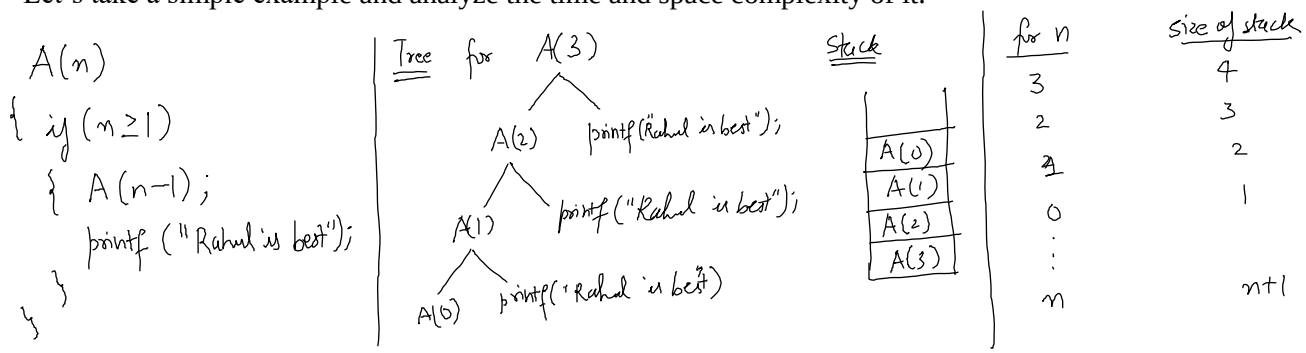
Finding the space complexity of an iterative program is quite easy. The process of finding the space complexity of a recursive program is quite complex. Let's see how it is done.

SPACE COMPLEXITY OF RECURSIVE ALGORITHMS

There are various ways to analyze the recursion algoirthms' space complexity.

*Note: Whenever the size of the program is small, use **Tree Method.** (3-4 lines)*
*Whenever the size of the program is big, use **Stack Method.** (lot of lines)*

Let's take a simple example and analyze the time and space complexity of it.



Points to know before we do anything.

1. ***Every function call is given a space in the stack memory (RAM).***
2. ***The calls of the recursive functions are stored in the stack until the halting/anchor condition is reached.***
3. ***The space taken by that stack is the space complexity of the recursive algorithm. For each call we can assume that the stack allocates 'k' units of space.***

As seen above, you can use the tree or stack method to see the size of the memory which will be required by the recursive algorithm. Now let's say that 'k' is the size of each stack cell.

Therefore, total memory required for input size of 'n' = (n+1)k or **O(kn)** or **O(n)**

Let's also analyze the time complexity of this algorithm.

Assume that the time taken by A(n) to run is T(n). Therefore, for A(n-1) time will be T(n-1).

⇨ Recursive equation: T(n) = T(n-1) + c (*for printing)* ---(1)

Since this equation does not follow the rules required for Master's Theorem, therefore it can't be applied here. Let's do the back substitution.

T(n-1) = T(n-2) + c --- (2)
T(n-2) = T(n-3) + c --- (3)

Substituting (2) in (1) we get: T(n) = T(n-2) + 2c --- (4)
Substituting (3) in (4) we get: T(n) = T(n-3) + 3c

Therefore: T(n) = T(n-k) + kc

for halting condition n >=1. T(n-k) will become T(0) when n-k = 0or k = n

- ⇨ T(n) = T(n-n) + nc
- ⇨ T(n) = c + nc
- ⇨ T(n) = (n+1)c or **O(n)**

IMPORTANT

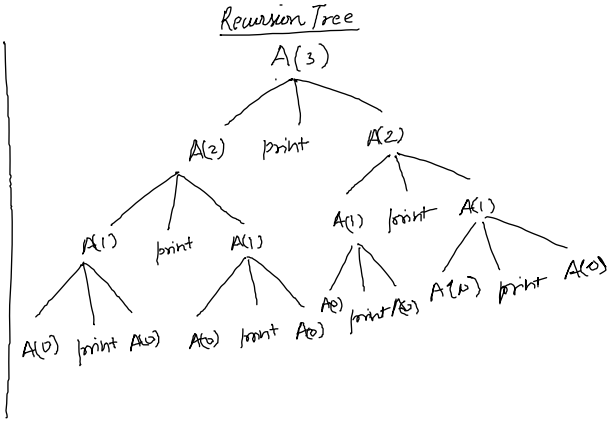
Questions that can be asked:

1. ***How many times the recursive function A(n) is called***
2. ***What is the space complexity?***
3. ***What is the time complexity?***

Let's see one more example

Example 2:

```
A(n)
{  if (n>1)
   {  A(n-1);
      printf(" Rahul is great! ");
      A(n-1);
   }
}
```



N	Number of calls for A(n)
3	$15 = 2^{3+1} - 1$
2	$7 = 2^{2+1} - 1$
1	$3 = 2^{1+1} - 1$
N	$2^{N+1} - 1$

Note: The number of recursive calls to a function does not define the amount of space taken by the program. Though it looks like this algorithm's space complexity is O(2^n), that is not the case. Let's see how.

The interesting thing is that the stack for the program does not take more than 4 cells to deal with all of the recursive calls for n = 3. This is because for every leaf node reached in the recursion tree, it gets popped out of the stack. Thus the pushing of non-leaf nodes from left-bottom-right mechanism and popping off is a constant process which doesn't take more than 4 cells of stack for n = 3.

Therefore, for this algorithm for an input size of 'n' the stack will take n+1 cells. If each cell is of size k.

Space complexity = O((n+1)k) or simply O(n).

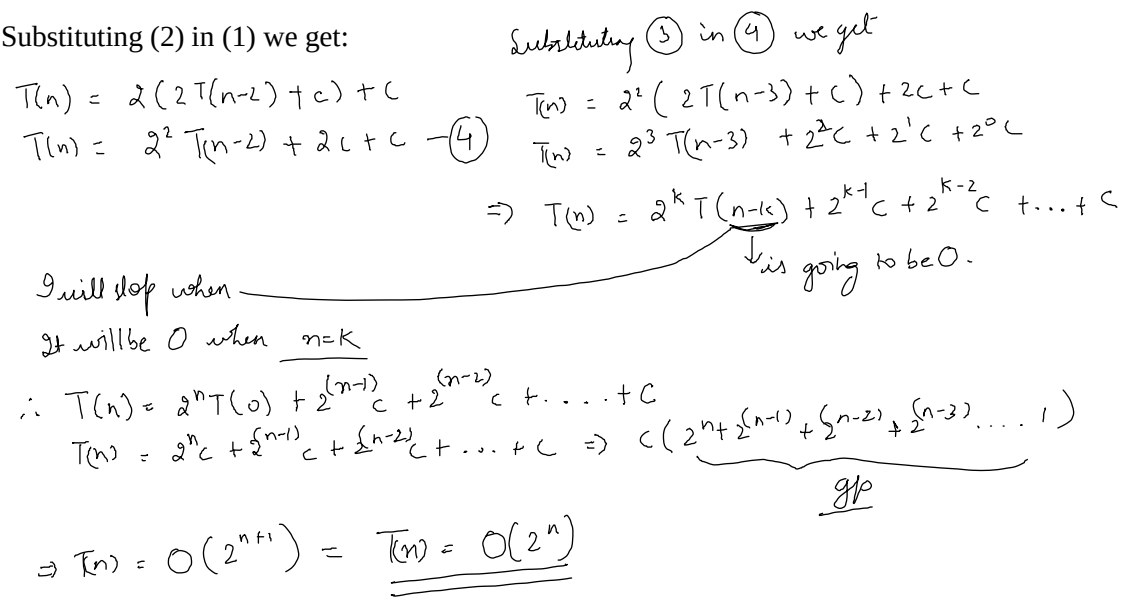
Let's see the time complexity of this algorithm.

T(n) = T(n-1) + T(n-1) + c or T(n) = 2T(n-1) + c (not eligible for Master's theorem). --- (1)

Let's use back substitution method.

T(n-1) = 2T(n-2) + c --- (2)
T(n-2) = 2T(n-3) + c --- (3)

Substituting (2) in (1) we get:



The space complexity of the algorithm is O(n) and the time complexity is $O(2^n)$. This is an exponential time complexity. This can be reduced by application **of *dynamic programming*** where we can decide dynamically using lookup table (where the previous calculation results are already saved) to not run another recursive call which has already happened.

Thank you for reading my notes. I hope they help you. Next up is Sorting Algorithms which is in a different file. Please go to that file for the continuation of the notes. <3

Algorithms: Sorting Algorithms

Given a sequence of numbers, you have to arrange them in the ascending or descending order. This is called sorting. Sorting algorithms can be iterative or recursive.

Let's learn about the different sorting algorithms and analyze their space and time complexity. First we are going to start with the iterative Insertion Sort.

INSERTION SORT ALGORITHM AND ANALYSIS

"Insertion sort", the name suggests that there is an insertion happening. Understand it with an example where you want to arrange the playing cards which are placed on a table, face down.

1. Take the first card in your left hand.
2. Take the second card in your right hand, compare it with the left hand card

   If smaller then keep this card in the most left side on the left hand
   If larger then keep this card in the right most side on the left hand

3. Repeat step 2 over again.

At every new picking of the card, your left hand will always have sorted cards. Let us right the algorithm in the context of an array containing integers which we will sort using **Insertion Sort.**

```
Insertion_Sort(A)

{

        for( j = 2 to A.length)
        {
                key = A[ j ];
                //insert A[ j ] into sorted sequence A[1 … j-1]
                i = j – 1;
                while( i > 0 and A[ i ] > key)
                        A[i+1] = A[i];
                        i = i - 1;

                A[i+1] = key;

        }

}
```

Let array = 9, 6, 5, 0, 8, 2, 7, 1, 3 (please follow the algorithm above to sort the list).

Time complexity:

The worst case time complexity for insertion sort can be calculated as below. For worst case to happen, the elements should be already in descending order in the array for which we have to do ascending order sorting using Insertion Sort.

For j	Comparison	Movements	Total Operations
2	1	1	2
3	2	2	4
4	3	3	6
…	…	…	…
N	n-1	n-1	2(n-1)

Therefore, total operations done: $2 + 4 + 6 + \ldots + 2(n-1)$

Or: $2(2-1) + 2(3-1) + 2(4-1) + \ldots + 2(n-1)$

Or: $2(1) + 2(2) + 2(3) + \ldots + 2(n-1)$

Or: $2 (1 + 2 + 3 + \ldots + n-1)$

- ⇨ $2(n(n-1))/2$
- ⇨ **$O(n^2)$**

The best case time complexity for Insertion Sort can be calculated as below. For best case to happen, the array should already have the sorted elements inside it.

For j	Comparison	Movements	Total Operations
2	1	0	1
3	1	0	1
4	1	0	1
…	…	…	…
N	1	0	N - 1

Total operations for best case time complexity: $1 + 1 + 1 + \ldots + N-1$

When the array is already sorted you will just compare the element in you right hand (card analogy) with the rightmost element in the left hand only once for each element in the array.

Therefore, best case time complexity = Ω(n)

<u>Space Complexity of Insertion Sort:</u>

Apart from the input array A[], I only need three variables ‘key’, ‘i’ and ‘j’. So, whatever is the size of the input, I only need 3 extra variables for Insertion sort to work.

Therefore, the space complexity for Insertion Sort is **O(1)** or constant space.

Note: Whenever a sorting algorithm executes in constant space, we call such a sorting algorithm INPLACE algorithm

In Insertion Sort, we saw that the time complexity depends on the number of comparisons involved and the number of movements involved. So how can we decrease this complexity? Let's try some methods.

1. Using Binary Search instead of sequential search in the sorted list

Comparisons using Binary Search	Movements using Binary Search	Total complexity
O(logn)	O(n) (no reduction)	O(nx(n-1) elements)) = $O(n^2)$

Using binary search will not reduce the time complexity of the Insertion Sort algorithm.

2. Using Linked List for insertion

Comparisons using Linked List	Movements using Linked List	Total complexity
O(n) (no reduction)	O(1) (direct insertion)	O(nx(n-1 elements)) = $O(n^2)$

Using linked list will also not reduce the time complexity of the Insertion Sort Algorithm.

Time and Space complexity for Insertion Sort

Time Complexity	**Best Case**	**Worst Case**	**Average Case**
	$\Omega(n)$	**$O(n^2)$**	**$\Theta(n^2)$**

Space Complexity	**O(1)**

Let's move on to the next sorting algorithm which is going to work better than Insertion Sort in terms of time complexity. This algorithm is called Merge sort.

MERGE SORT ALGORITHM AND ANALYSIS

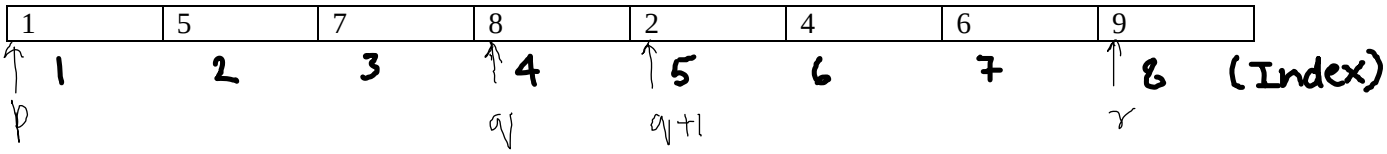
Merge sort falls under the Divide-and-conquer algorithms. It simply means you divide the problem into smaller steps and tackle the problem of sorting using bottom-up approach.

Before we go into the algorithm and analysis of it, let's understand the heart of the algorithm, which is a procedure called Merging. For clarity, here is the algorithm

```
MERGE(A, p, q, r)
{
        n1 = q-p+1
        n2 = r – q
        Let L[1…n1+1] and R[1 … n2 + 1] be new arrays
        for( i=1 to n1)
                L[i] = A[p + i-1]
        for( j=1 to n2)
                R[j] = A[q + j]
        L[n1 + 1] = ∞
        R[n2 + 1] = ∞
        for(k = p to r)
                if(L[i] <= R[j]
                        A[k] = L[i]
                        i=i+1
                else A[k] = R[j]
                        j=j + 1
}
```

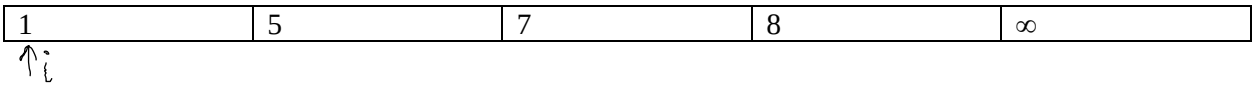
Working of MERGE:

We have a list of elements where left half and right half are sorted.

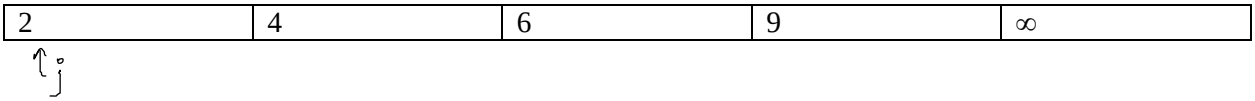


We divide the list above into two lists L and R containing the first half sorted elements and the second half sorted elements.

L = An array of size q-p+1 where last element is a very big number denoted by ∞ here.



R = An array of size r-q where last element is a very big number denoted by ∞ here.



Now, we compare the elements of L and R and arrange them in the ascending order in the final array. The final array looks like below.

A =

1	2	4	5	6	7	8	9

For merge sort to work we need to copy the elements from the input which takes ‘n’ extra space other than the input. And to compare the two sorted lists it takes one comparison per input, therefore it will take ‘n’ comparisons.

Time Complexity = O(n)

Space Complexity = O(n)

If the size of list L and R is ‘n’ and ‘m’ respectively, the time and space complexity will be O(n+m). The lists L and R should have sorted elements in them.

Note: We add ∞ in the end of the two lists for proper comparison. If L = 10,20,30,40, ∞ and R = 1,2,3,4, ∞ then A = 1,2,3,4.. initially but to enter the elements of L we need some element to compare it to, so the fifth element in R is compared with the elements of L to add them to the sorted list A. Then A will become 1, 2, 3, 4, 10, 20, 30, 40

Now that we have seen how the MERGE method is working. Let’s use it to create Merge Sort algorithm.

Working of MERGE SORT

```
Merge_sort(A, p, r)
{
        if p < r
                q = floor[(p+r)/2]
                Merge_sort(A, p, q)
                Merge_sort(A, q+1, r)
                MERGE(A,p,q,r)
}
```

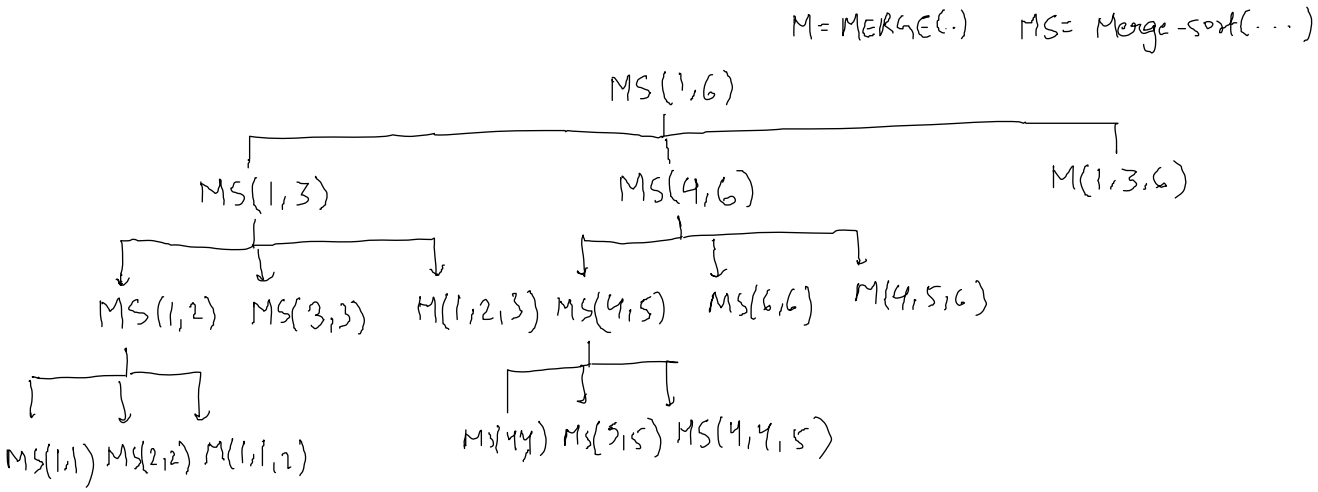
As said earlier, Mege Sort falls under the category of Divide and Conquer algorithms. In this sorting technique we divide the array to be sorted into single element array (single element array is already sorted) and move up from there to give us the final sorted array.

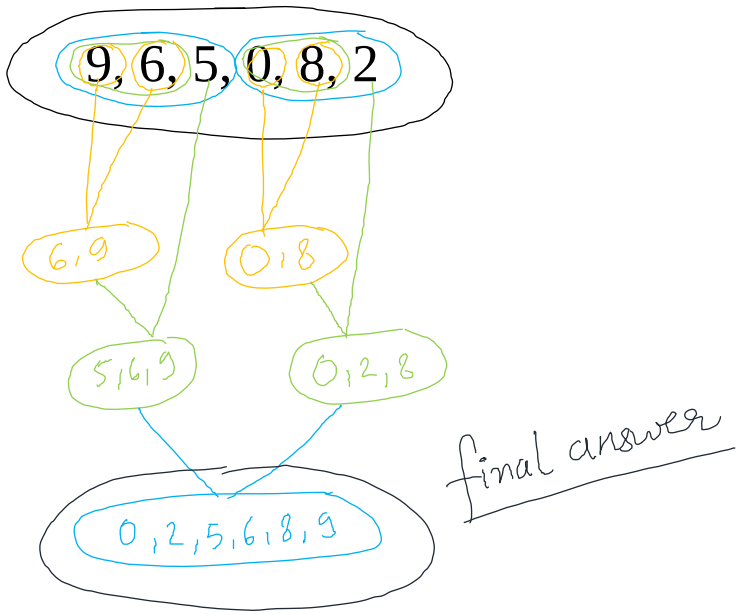
This is a recursive algorithm where each function call is going to call three functions:

Merge_sort(A, p, q)
Merge_sort(A, q+1, r)
MERGE(A,p,q,r) Let’s see how it is doing the work using an example.

Sort the array A = [9, 6, 5, 0, 8, 2] using merge sort.

Recursion tree for Merge Sort.





Space Complexity Analysis:

We know that the extra space required for the Merge Operation is O(n).

We need extra space in the stack for function calling. To analyze this, we need

1. Total number of function calls made
2. The order in which they are made
3. The height of the stack that is needed for this.

Total number of function calls made for above example: 16 so do we really need a stack of size 16 for this? Let's see.

That is indeed not the case: The height of the stack is equal to the height of the recursion tree made by the merge sort algorithm.

Note: All the function calls in a level will be carried out in the stack memory of same level. Level 3 calls will be made on the third memory cell of the stack. (Interesting).

The height of the recursion tree for an input size of n = ceil(logn) + 1. For every level we need a cell in the stack which let's say occupies 'k' space units.

Therefore, for stack we need k(logn + 1) space.

- ⇨ **Space complexity for stack: O(k(logn+1)) or O(logn)**
- ⇨ **For merge procedure space required is of O(n)**

Total space complexity = O(n + logn) or O(n) for merge sort.

Now let us analyze the time complexity of the merge sort algorithm

Time Complexity Analysis:

Let us say we are sorting an array of size n.

Let's say that the time taken by merge sort on array of size n = T(n)

```
Merge_sort(A, p, r)          → T(n)
{
        if p < r
                q = floor[(p+r)/2]
                Merge_sort(A, p, q)      → T(n/2)
                Merge_sort(A, q+1, r)    → T(n/2)
                MERGE(A,p,q,r)           → O(n)
}
```

$\therefore T(n) = 2T(n/2) + O(n)$

Using Master's Theorem

$a = 2 \quad b = 2 \quad k = 1 \quad p = 0$

$a = b^k \; \& \; p > -1$

$\therefore T(n) = \Theta(n^{\log_b a} \log^{p+1} n)$

$T(n) = \Theta(n^{\log_2 2} \log^{0+1} n)$

$T(n) = \Theta(n \log n)$

Time and Space complexity for Merge Sort

Time Complexity	Best Case	Worst Case	Average Case
	Ω(nlogn)	**O(nlogn)**	**Θ(nlogn)**

Space Complexity	O(n)

Let's see some questions on Merge Sort.

Q1. Given "logn" sorted list each of size "n/logn". What is the total time required to merge them into one list?

Total number of sorted lists = logn

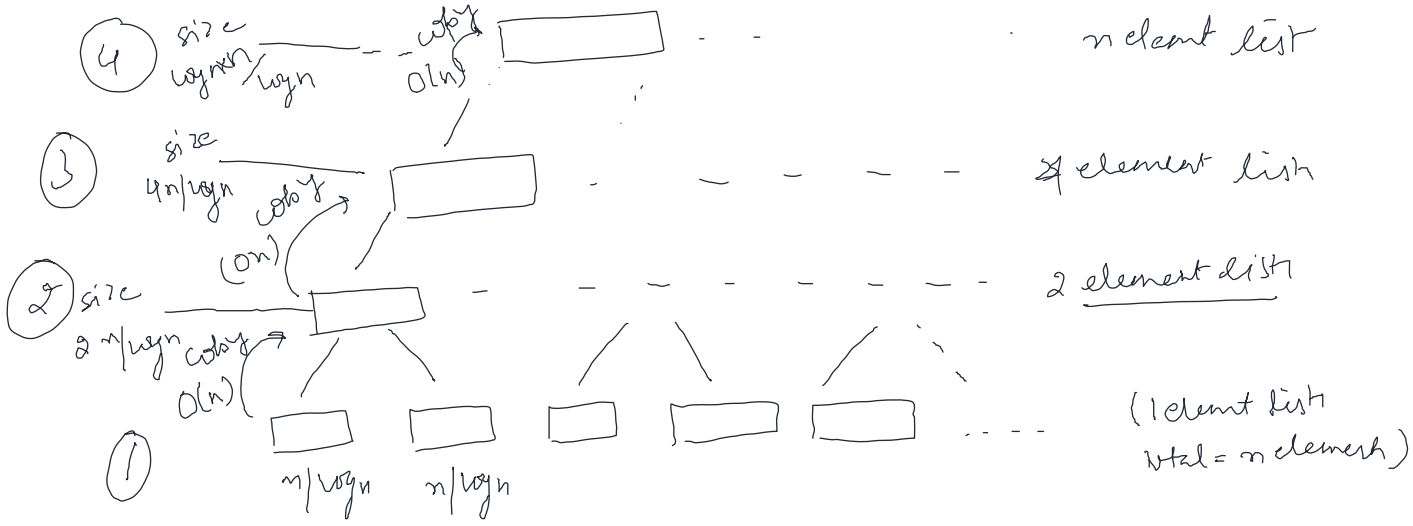
Each list is of size: n/logn

Total number of elements : logn x n/logn = n

For copying the elements in level of the recursion tree =O(n)

This copying has to be done for the height of the tree= loglogn

Total time complexity : O(nloglogn)



total complexity = O(n) X no. of climbings I have to do to reach last level of tree

from (1) to (2) climbings = log 2 (or 1 climb)

" (2) to (3) " = log 4 (or 2 climbs)

from 1 to last (top of tree) climbings = log (log n) (or log n climbings)

∴ complexity = O(n log log n)

Q2. "n" strings each of length "n" are given then what is the time taken to sort them?

If two strings are of length n, then the time taken to compare them will be O(n)

At the bottom level we are given n string each of length n.

For one comparison time taken = O(n)

For n comparisons time taken = $O(n^2)$

For copying in the next level time taken = n strings of size n = $O(n^2)$

Total time taken for comparison + copying in **one level** = $2.O(n^2)$ or $O(n^2)$

This has to be repeated until we reach the top level. So how many levels we are going to traverse for that?

To go from bottom to (bottom -1) level we take one step or log2 steps or ***log(size of array at bottom-1 level)***

From bottom to (bottom -2) level we take two steps or log4 steps or ***log(size of array at bottom -2 level)***

We know the size of array at the top level has to be 'n'.

Therefore to reach the top level, we have to take log(size of top array) or logn steps.

Total time complexity : (number of steps taken) X (time complexity for copying and comparison on each level)

- ⇨ **Total complexity = $O(n^2 logn)$**

POINTS ON MERGE SORT

1. Merge sort uses divide and conquer paradigm
2. The time complexity for two lists of size m and n to merge is O(m+n)
3. Questions can be asked like "What is the order of the array (given in question) in the second pass of two-way merge sort?"

LET'S MOVE ON TO OUR NEXT SORTING ALGORITHM

QUICK SORT ALGOIRTHM AND ANALYSIS

Just as we saw that the heart of the merge sort algorithm was the MERGE procedure, the heart of the quick sort algorithm is the PARTITION procedure. The name is given "quick sort" because for small values of n (100 etc.) quick sort has lesser time complexity than the merge sort. This algorithm also falls under "Divide and Conquer" category.

Before we jump to the sorting algorithm, let's see the PARTITION function first.

```
PARTITION(A, p, r)

        x = A[r]
        i = p -1

        for(j = p to r-1)

        {
                if(A[j] <= x)
                        i = i+1
                        exchange A[i] with A[j]

        }

        Exchange A[i+1] with A[r]

        Return i+1

}
```

The partition function is quite easy to understand.

1. We take the last element of the array to be sorted in a variable (x) (*you can take any element; it doesn't need to be the last element of the array*)
2. The partition method is going to check from index p(first) to r-1(second last) and compare the elements on those index of the array with x
3. We take two pointers 'i' and 'j' pointing at index (p-1) and 'p' initially.
4. With each increment of 'j' the array element at A[j] will be compared with the element x
    a. If A[j] is bigger than x: We don't do anything
    b. If A[j] <= x:
        i. Increment i by 1 (i+1)
        ii. Replace A[i+1] with A[j]
5. Replace A[i+1] with x

This will repeat until the last but one index is reached by the pointer j. The essence is that, after the partition method completes its execution, all the elements to the left of x will be smaller than x and all the elements to the right of x will be greater than x.
The element x is already sorted now.

This procedure will be repeated recursively for the two new arrays (Array containing elements <= x and array containing elements > x).

The partition method runs for n-1 elements in the array, therefore the time complexity of it is O(n-1) or O(n).

This is pretty simple, now let's see the Quick Sort algorithm.

The heart of the Quick Sort algorithm is the PARTITION method.

Quick Sort Algorithm

```
QUICKSORT(A,p,r)
{
        if(p < r)
        {
                q = PARTITION(A,p,r)
                QUICKSORT(A, p, q-1)
                QUICKSORT(A, q+1, r)
        }
}
```

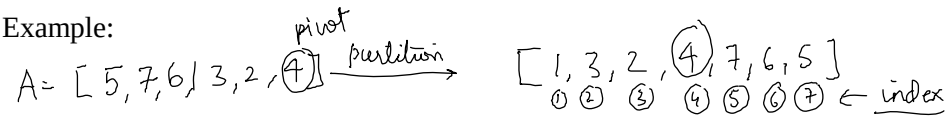
The index of the sorted element by the PARTITION algorithm is returned as q in the above algorithm.

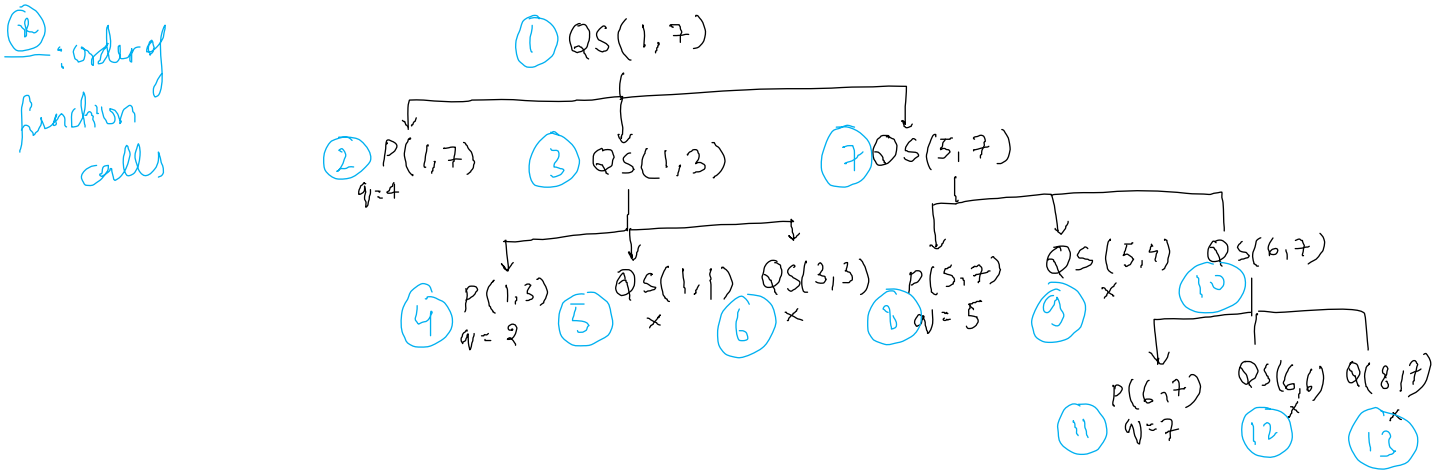
Note: In the merge sort algorithm, the arrays were divided into halves. In the quick sort algorithm the sub arrays can have different lengths depending on the value of 'q' returned by the PARTITION algorithm.

The element around which the partitioning is happening is called the PIVOT.

Let's take an example and elaborate the recursion tree.

Example:





Space Complexity of Quick Sort:

1. Determine the total number of function calls
2. Determine the order of function calls

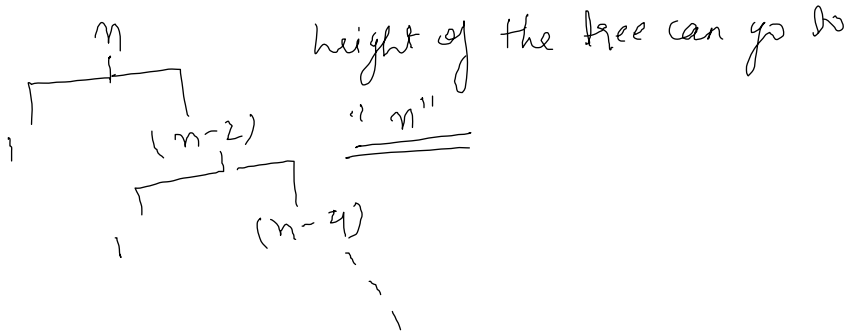
3. Use stack to evaluate the calls.

Total function calls = 13

This is not the size of the stack we require. **Infact the size of the stack will be the number of levels in the recursion tree.**

Case 1: If the input is divided into two equal halves, the height of tree will be logn and the space complexity will be O(logn) (best case)

Case 2: In case the input is divided into unbalanced arrays.



In this case the stack size can go to the size of the array, therefore in the **worst case** the space complexity will be O(n).

In **average case** the space complexity will be O(logn).

Time complexity of Quick Sort Algorithm:

```
QUICKSORT(A,p,r)
{
        if(p < r)
        {
                q = PARTITION(A,p,r)
                QUICKSORT(A, p, q-1)
                QUICKSORT(A, q+1, r)
        }
}
```

Let us assume that the time taken to sort 'n' elements is T(n). Let is consider the "Best Case" where the partition method is going to give the pivot element in the middle of the array every time. Then (look left)

$\Rightarrow T(n) = 2 * T(n/2) + O(n)$

$\Rightarrow$ through Master's theorem : $O(n \log n)$ "best case"

For the worst case:

```
QUICKSORT(A,p,r)
{
        if(p < r)
        {
                q = PARTITION(A,p,r)
                QUICKSORT(A, p, q-1)
                QUICKSORT(A, q+1, r)
        }
}
```

$T(n)$

$O(n)$

$T(0)$

$T(n-1)$

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

$T(n) = T(n-1) + cn$

back substitution

$= T(n-2) + c(n-1) + cn$

$= T(n-3) + c(n-2) + c(n-1) + cn$

$= c + c2 + c3 + \dots + cn$

$= O(n^2)$

Time and Space complexity for Quick Sort

Time Complexity	Best Case	Worst Case	Average Case
	Ω(nlogn)	**O(n^2)**	**Θ(nlogn)**

Space Complexity	Best Case	Worst Case	Average Case
	O(logn)	**O(n)**	**Θ(logn)**

Let's see some examples on quick sort.

1. If the input is in ascending order

$A = 1, 2, 3, 4, 5, 6$

pivot

$((1, 2, 3, 4), 5)$ (6) pivot

$\therefore T(n) = O(n) + T(n-1)$

↑ partition ↑ for array size $(n-1)$

$\Rightarrow T(n) = O(n^2)$

2. If the input is in descending order

$A = \{6, 5, 4, 3, 2, 1\}$

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

$= O(n^2)$

3. If the array contains same elements

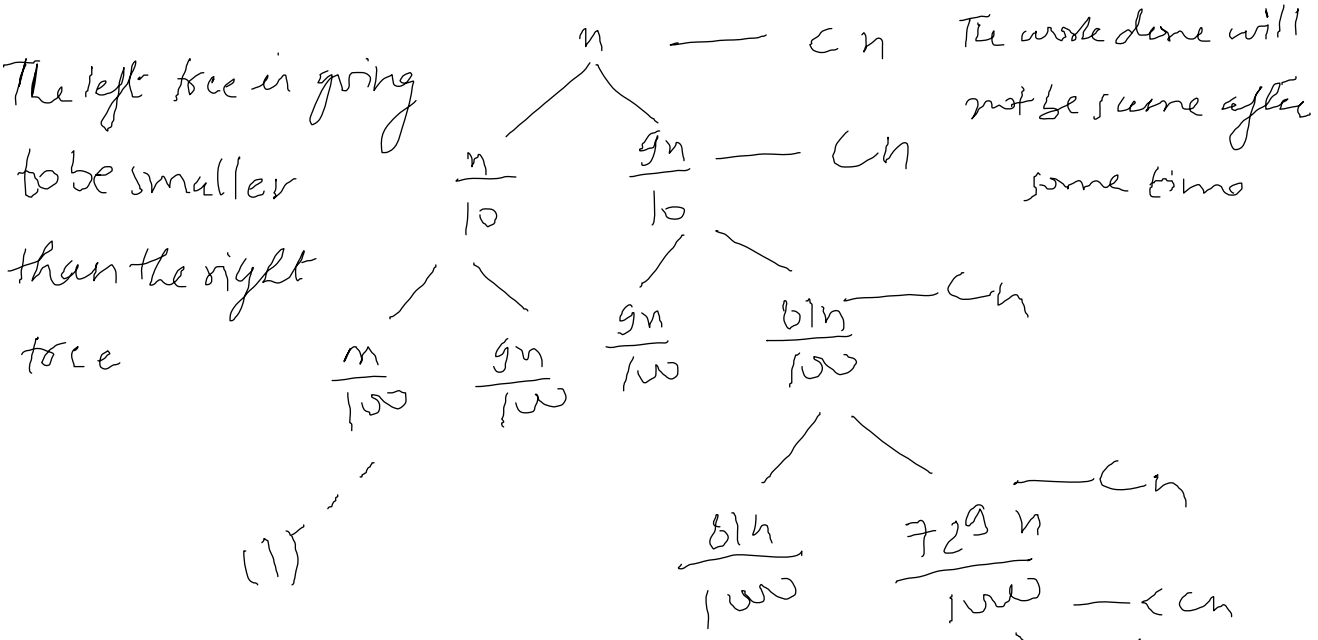
A = {2, 2, 2, 2, 2, 2}

Again: $T(n) = O(n) + T(n-1)$

$= O(n^2)$

Note: If the array is in ascending order/descending order/contains same elements, the time complexity is going to be worst case time complexity which is $O(n^2)$.

4. When the array is split in a ratio. Let's split the array in a ratio of 1:9



The size of the array decreases as in each level like this

$n \to \frac{n}{(10/9)} \to \frac{n}{(10/9)^2}$ ---- 1 ∴ in the tree levels will be $\log_{10/9} n$

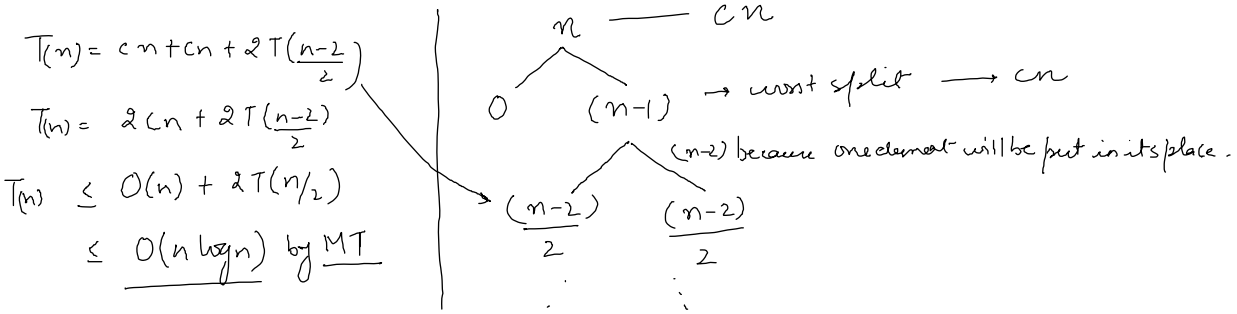
or $\log_{10/9} n = \Theta(\log_2 n)$ & each level has "cn" (roughly) work

∴ time complexity = $\Theta(n \log_2 n)$

Therefore, even if the split is 1:9 we got the best case time complexity.

We can see that in quick sort, if the split is of 1:9, 1:99, 1:999, even then the best case time complexity Ω(nlogn) will be reached.

5. When the worst case and best case splitting is alternating

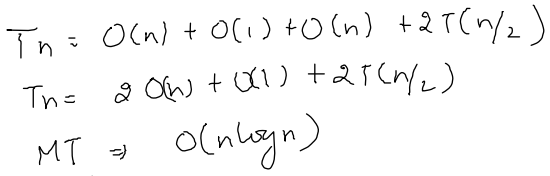


Therefore, even if the split is alternating between the one that produces best case and the one that produces worst case, we get the best case time complexity.

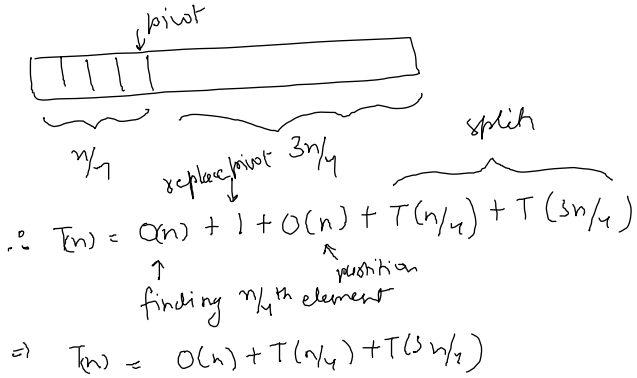
Let's see some questions on Quick Sort

Q1. The median of 'n' elements can be found in O(n) time. Which of the following is correct about the complexity of quick sort, in which median is selected as pivot?

1. Finding the median takes O(n)
2. For median to be pivot, I'm going to put it at the end of the array in the partition function. This takes O(1) time.
3. Now since the median is going to be at the center of the sorted array, we are essentially going to split the array in approximately two equal halves. For this we know the complexity is Θ(nlogn).
4. And we know that the partition algorithm takes O(n) time.

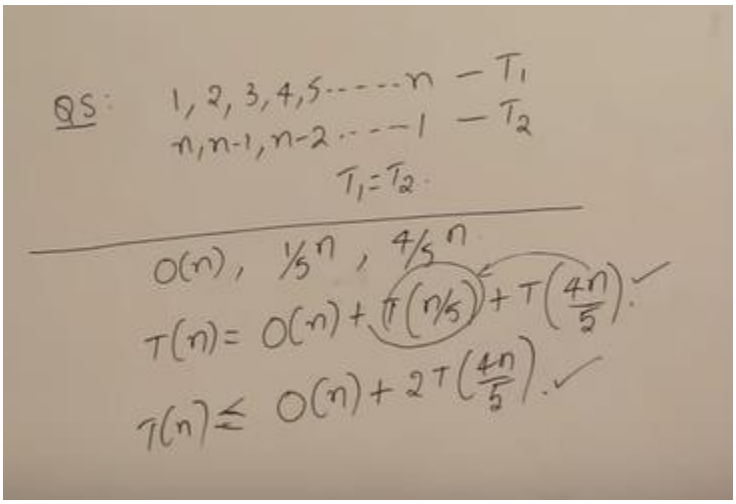


Q2. In quick sort, for sorting 'n' elements, the $(n/4)^{th}$ smallest element is selected as pivot using O(n) time algorithm. What is the worst case time complexity of quick sort?



This is essentially partitioning of the array in the ratio of 1:3. We have already seen that 1:9, 1:99, 1:999 has the time complexity of Θ(nlogn), so for a split of 1:3 also we are going to get the time complexity of

Θ(nlogn).



Let's move on to our next segment.

INTRODUCTION TO HEAPS

Now we have seen some algorithms. Now all algorithms take an input and give some output. The way in which the input is given makes a lot of difference in the way the algorithm will take space or time. So depending on how the input is, the running time of the algorithm will change.

Let's elaborate more with an example.

Let's take a data structure as input to various algorithms. Then the time complexities for various operations is given in the table below.

Data structure	**Insertion complexity**	**Search complexity**	**Find minimum complexity**	**Delete minimum complexity**
Unsorted array	O(1)	O(n) (linear)	O(n)	O(n)
Ascending order Sorted array	O(n)	O(logn)(binary)	O(1)	O(n)
Unsorted Linked List	O(1)	O(n)	O(n)	O(n)

Now some of the algorithms need Insertion, finding minimum and delete minimum operations. We can see above that at least one of the operations in the array or linked list has a complexity of O(n).

This is where the data structure **Heap** comes in. This data structure is optimized for the operations: Insertion, finding minimum and deleting the minimum entity in it. Heaps are of two types: **max** and **min** heap. Let's see their complexity for the same operations given in the above table.

Note: Depending on what kind of operations you want, choose the data structure.

Data structure	Insertion complexity	Search complexity	Find minimum complexity	Delete minimum complexity
Min Heap	O(logn)	O(n) (linear)	O(1)	O(logn)

Let's take a deeper look into heaps.

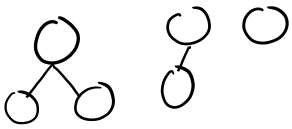
HEAP

Heaps can be implemented as a binary tree, 3-ary tree or in general an n-art tree.

For now let's talk about the binary tree, later we will go to ternary or even n-ary tree implementation

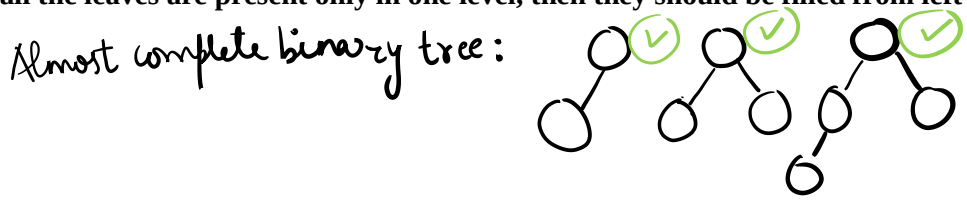
Property of binary tree:

1. Every node can have at most two children

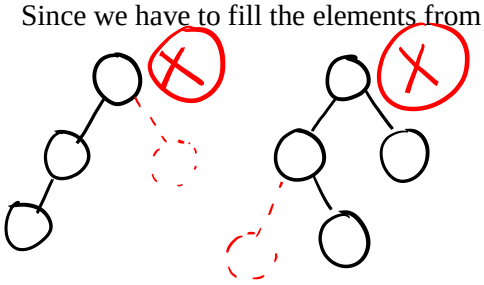


Every heap is an almost-complete binary tree. A complete binary tree is a binary tree where all of the nodes except the leaf nodes have 2-childrens. Now we said that heap is an almost complete binary tree.

Almost complete means that the leaves should be present only at the last level and last but one level. If all the leaves are present only in one level, then they should be filled from left to right.



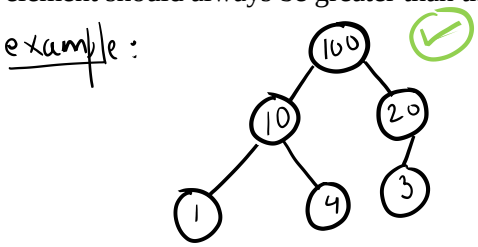
Since we have to fill the elements from left to right, the following binary trees can't be used as heaps.



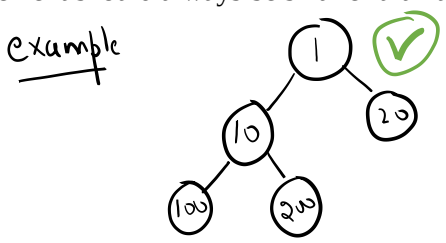
Since before going to the next level the previous level has to Be completely filled from L-to-R, and then the last level also Has to be filled from L-to-R, the Binary Trees on the Left can't be used as heaps.

Let's see examples of Heap.

1. **Max heap:** A max heap is a complete binary tree or almost-complete binary tree where the root element should always be greater than the elements in their child sub-trees.



1. **Min heap:** A min heap is a complete binary tree or almost-complete binary tree where the root element should always be smaller than the elements in their child sub-trees.



Properties:
Max Heap Property: Maximum element should be at the root
Min Heap Property: Minimum element should be at the root

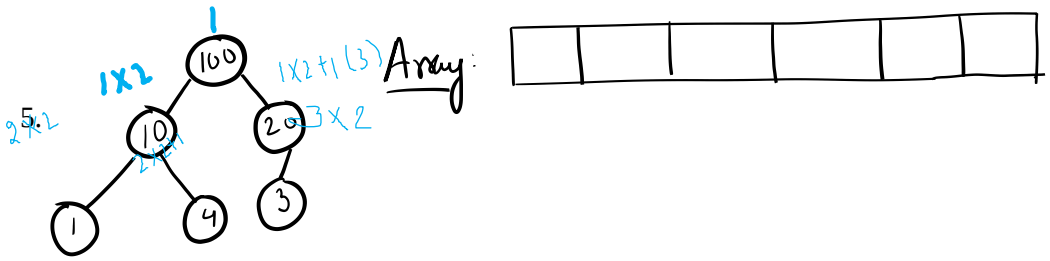
Now let's see how we are going to implement the heap.

<u>Implementing Heap</u>

Instead of making the linked list and then implement the binary tree which takes more space, we can implement the tree using an array. We are interpreting the tree as an array.

To fill the array with the elements of the tree:

1. First element will be the root of the entire tree
2. The index of left side will be calculated as (index of current root x 2)
3. The index of right side will be calculated as (index of current root x 2 + 1)
4. Example:



So any complete binary tree could be placed inside an array which is completely filled without any gaps. *This is the main reason we need complete or almost complete binary trees.* If the tree is not almost complete, we might end up getting an array which has a lot of gaps in between.

If we are at a node, to find the parent of it just divide the index of the node with 2 and ceil it.

Parent of the node = ceil(index of the node/2).

If i is a node: Left child of i = $2i$

Right child of i = $2i + 1$

Parent of i = $\lfloor i \ / \ 2 \rfloor$

Multiplying i with 2 is: i << 2
Dividing i by 2 is: i >> 2

This is how you can put a binary tree in an array.

Now the questions that arise can be:

1. Given a max heap in the tree form what is the array representation of it?
2. Given an array, is the array a max heap or not?
3. If the array is not heap, till what element it is heap?

Before answering questions, we need to keep in mind:

1. Every leaf element is a heap
2. The length of the array is the total number of elements in the array. (A.length)
3. The heap size of the array is the number of elements till which array is heap. (A.heapsize)
4. If the array is in **asc** or **desc** order, then it is already in **min heap** and **max heap** respectively.

Let's use them in an example:

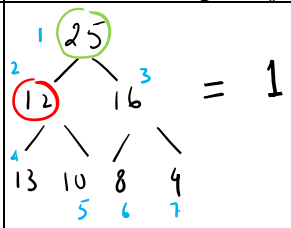
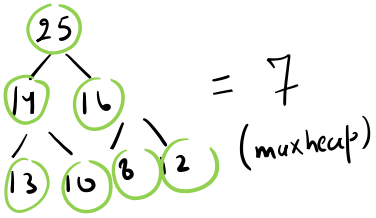
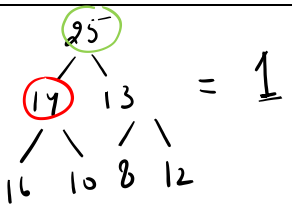
Example:

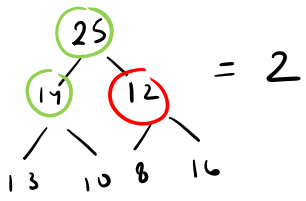
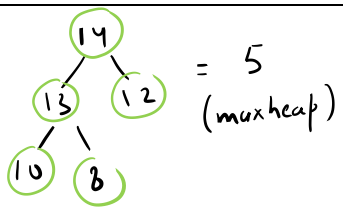
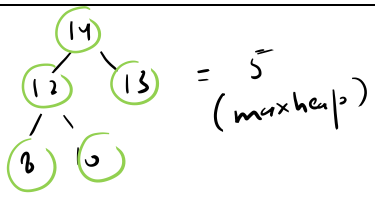
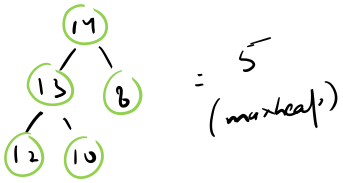
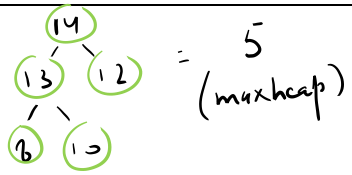
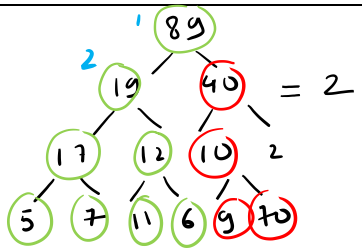
Q.1 Is the array given a max heap?

Q.2 If it is not max heap, till what elements it is heap? (heapsize)

Hint: If heapzise = index of last element in the array, then it is max heap.

For a given array, to get the almost complete binary tree, fill up the array with level order traversal.

Array A	**A.length()**	**A.heapsize()**
25, 12, 16, 13, 10, 8, 14	7	
25, 14, 16, 13, 10, 8, 12	7	
25, 14, 13, 16, 10, 8, 12	7	

25, 14, 12, 13, 10, 8, 16	7	
14, 13, 12, 10, 8	5	
14, 12, 13, 8, 10	5	
14, 13, 8, 12, 10	5	
14, 13, 12, 8, 10 ⇒ given a set of numbers the heap can have various forms. (it may not be unique)	5	
89, 19, 40, 17, 12, 10, 2, 5, 7, 11, 6, 9, 70	13	

One may say that to make a max heap, the given elements should be sorted in decreasing order first then heap can be constructed. But, the sorting will take O(nlogn) time and that will be more as max heaps can be constructed in O(n), (we will see the algorithm later).

Now let's go to the algorithms to construct a heap, insert an element in a heap, delete an element in a heap and finally heap sort.

MAX HEAPIFY ALGORITHM AND COMPLETE BINARY TREE

Before going on to the algorithms, let's see the properties of **complete binary tree**.

1. Height of the node: The number of the edges on any path from that node to the leaf node such that the number of edges is maximum.
2. Height of the tree: The height of the root is the height of the tree
3. Given a height 'h', the **maximum number of nodes** in a complete binary tree: $2^{h+1} - 1$
4. Given the height 'h', the **maximum number of nodes** in a complete 3-ary tree: $\frac{3^{h+1}-1}{2}$
5. Given the height 'h', the **maximum number of nodes** in a complete n-ary tree: $\frac{n^{h+1}-1}{n-1}$
6. Given any complete or almost complete binary tree with 'n' nodes, the height of the tree: $\lfloor \log n \rfloor$
   Therefore, we can say height of any heap = Θ(logn)

Let's make our max heap now.

MAX HEAP CREATION FROM A GIVEN ARRAY (MAX-HEAPIFY FUNCTION)

Here we are working in the context of max heap. For min heap, the algorithm will have to be just reversed.

Now given an array, if I want to create a max heap, one thing I can do is:

1. Sort the array: An array sorted in descending order is already a max heap. Here the time taken will be O(nlogn)
2. Can we do something better to reduce the time complexity?

Before we answer the question, let's see some more properties of complete/almost complete binary trees.

1. Where will the leaves start in a tree?
   a. In a complete binary tree, the last level will all have leaves, therefore, if leaves are starting from an index 'i' then all the indices after 'i' will be leaves. This property is also followed in almost complete binary tree.
2. In a complete/almost complete binary tree, the nodes from $\lfloor n \,/\, 2 \rfloor + 1 \; to \; n$ will all be leaves.

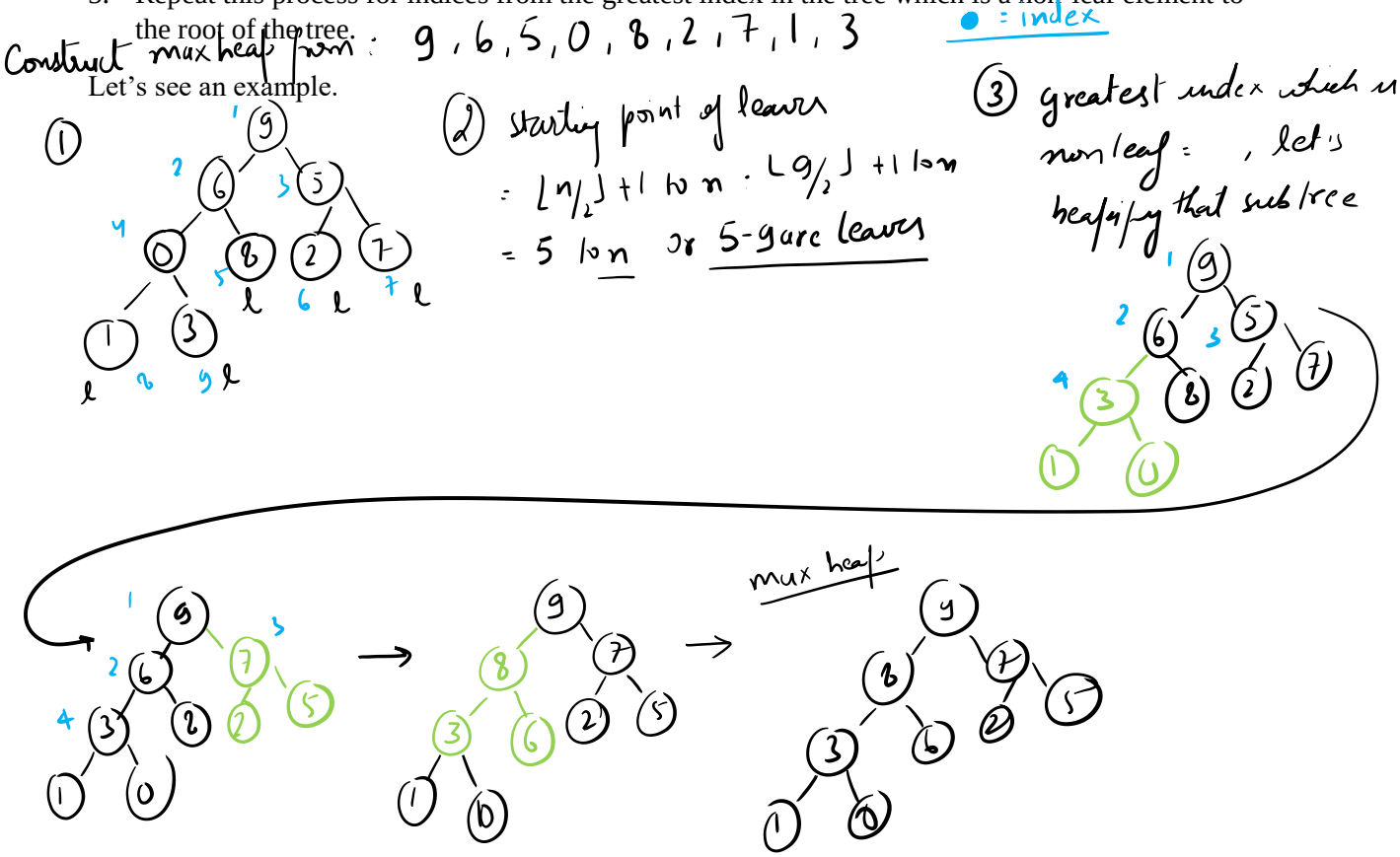
Let's construct our max heap.

Working of MAX_HEAPIFY

1. From the given array create a complete or non-complete binary tree in level order traversal.
2. Find out the elements who are the leaves ($\lfloor n \,/\, 2 \rfloor + 1 \; to \; n$). *All leaves are already max heap*

3. Find the greatest index in the tree which has a non-leaf element.
4. At this greatest index, check the children, if they contain the max number in its subtree, replace it with that number so that the root of this subtree has greatest number to become a max-heap.
5. Repeat this process for indices from the greatest index in the tree which is a non-leaf element to the root of the tree.

Let's see an example.



This is the way to construct a max-heap. The entire idea of creating a max heap is:

"Given an array A with an index i, if the left subtree (can also be the leaf element) and the right sub tree are max heaps, then make the root node also a max heap".

Let's see the algorithm.

```
MAX_HEAPIFY(A, i)

{

        l = 2i;
        r = 2i+1;
        if(l<= A.heapsize and A[l]>A[i])
                largest = l;
        else largest = i;

        if(r <= A.heapsize and A[r] > A[largest]
            largest = r;

        if(largest ≠ i)
            exchange A[i] with A[largest]
            MAX_HEAPIFY(A, largest)

}
```

Time complexity for max-heapify:

For worst case, we may need to get the root element to the bottom of the tree (height of tree), therefore, to get to the bottom of the tree complexity = O(logn)

Space complexity for max-heapify: Since we are not using any extra space for running the algorithm that depends on the input size, the only extra space will be taken by the stack for storing recursion calls. In the worst case space complexity will the height of the tree.

Therefore, space complexity = O(logn)

Note: 'n' is the number of nodes in the subtree for which 'i' is the root.

Let's see the BUILD_MAX_HEAP function and complete the creation of our max heap.

MAX HEAP CREATION FROM A GIVEN ARRAY (BUILD_MAX_HEAP FUNCTION)

```
BUILD_MAX_HEAP(A)

{

        A.heap_size = A.length;
        for(i = ⌊A. length/2⌋ down to 1)
                MAX_HEAPIFY(A, i)

}
```

The condition for the "for" loop is from A.length/2 to 1 is because we want to run the max_heapify algorithm only on the nodes which are not heaps and that too in descending order of the nodes which are not heaps (the leaf nodes are all heaps already, therefore, they will be A.length/2 + 1 to A.length).

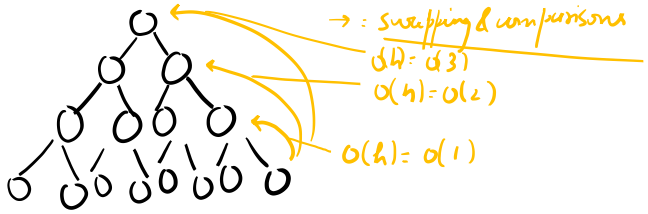
Let's talk about another property of Complete Binary Tree:

Q. How many nodes of height "h" can be present in a complete binary tree?

A. If we have 'n' nodes in the tree, then at height "h" we have $\left\lceil \frac{n}{2^{h+1}} \right\rceil$ nodes at height "h"

Let's now understand the time taken by the algorithm which makes the heap from an array. This is a bit complex so pay attention.

If I have a complete binary tree like this and applying MAX_HEAPIFY:



In general, if I apply Max Heapify on any Node the time taken will be O(h) or O(height of that node).

Let's say we are applying max_heapify on all the nodes including leaves, then the total work done at a particular height will be

Work done at height h = number of nodes in that height x O(h)

Number of nodes in height h = $\left\lceil \frac{n}{2^{h+1}} \right\rceil$

Work done for all the nodes in the tree = $\sum_{h=0}^{\log n} \left\lceil \frac{n}{2^{h+1}} \right\rceil . O(h) = \sum_{h=0}^{\log n} \left\lceil \frac{n}{2^{h}.2} \right\rceil . O(h)$

Now O(h) can be written as: 'c.h'

n, c and h are constants, then we can write: $\frac{Cn}{2} \cdot \sum_{h=0}^{\log n} \left\lceil \frac{h}{2^h} \right\rceil <= O\left(\frac{Cn}{2} \cdot \sum_{h=0}^{\infty} \left\lceil \frac{h}{2^h} \right\rceil\right)$

Now $\sum_{h=0}^{\infty} \left\lceil \frac{h}{2^h} \right\rceil = 2$, Therefore $O\left(\frac{Cn}{2} \cdot \sum_{h=0}^{\infty} \left\lceil \frac{h}{2^h} \right\rceil\right) = \boldsymbol{O(n)}$

Therefore, the time taken to build a max heap is O(n) if the entire array is not at all in heap.

Space Complexity of BUILD_MAX_HEAP

When looking at the algorithm above, the extra space is only taken by the MAX_HEAPIFY algorithm which is O(logn), therefore, Space Complexity of BUILD_MAX_HEAP is O(logn) where n is the root of the entire tree.

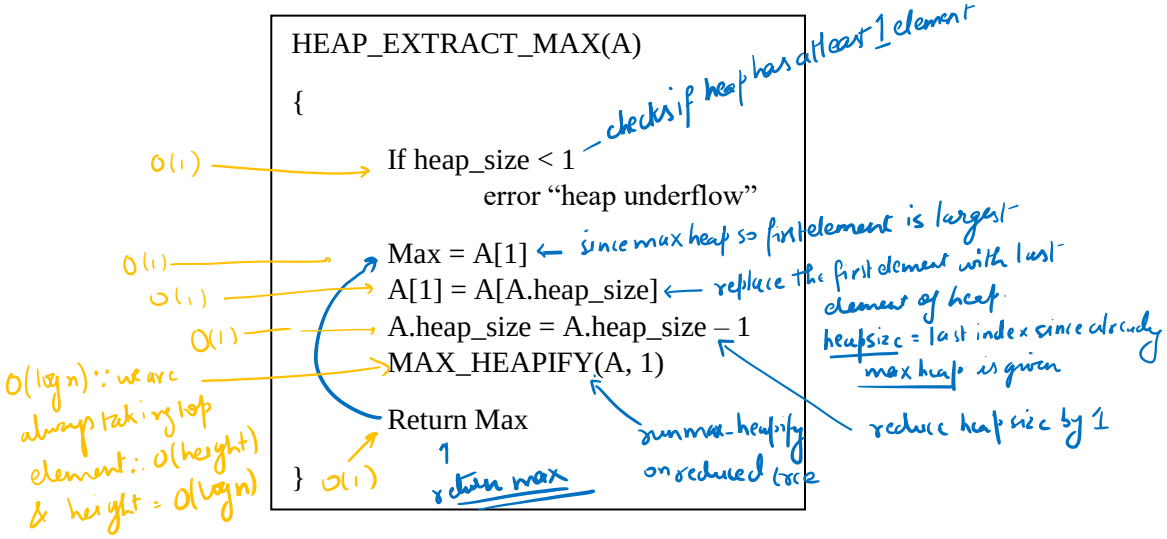
Now, let's see how we are going to apply this heap data structure in order to do the *heap sort.*

HEAP SORT (preliminaries)

Before we jump to sorting, let's see some operations on heap.

1. **Delete the max element from max heap**
   - **a.** Take the first element as the max, delete it
   - **b.** Now there is a space to fill, so take the last element from the heap and put in the first position
   - **c.** Check if the new tree (almost complete binary tree) is a max heap or not,
   - **d.** If not, start the MAX_HEAPIFY routine

   The algorithm looks like below



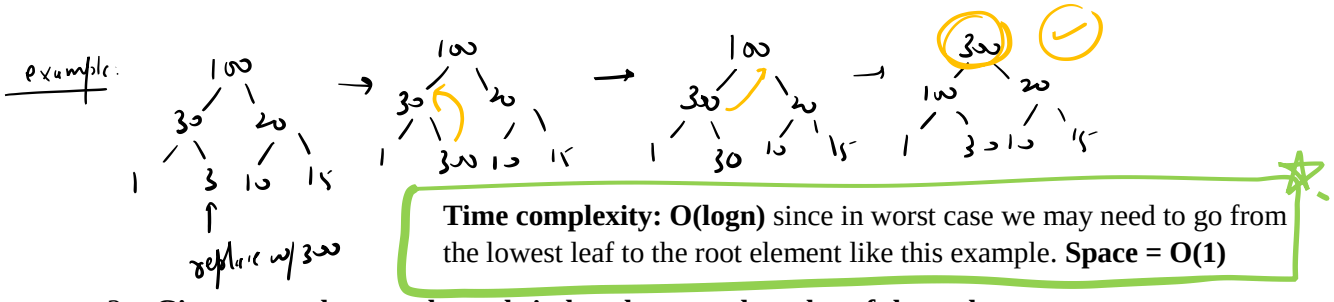
Time complexity = O(logn)

Space Complexity = O(logn)

2. **Given a max heap and a node index, increment the value of the node.**
   - a. Replace the key (the new value) with the element on the index
   - b. Check if the subtree is in max heap
   - c. If not, replace the elements and move up to the root until the tree is in max heap.

   The algorithm looks like below:

```
HEAP_INCREASE_KEY(A, i, key)
{
        If key < A[i]
                error
        A[i] = key
        while(i>1 and A[i/2] < A[i])
                exchange A[i] and A[i/2]
                i = i/2
}
```



Time complexity: O(logn) since in worst case we may need to go from the lowest leaf to the root element like this example. **Space = O(1)**

3. **Given a max heap and a node index, decrease the value of the node.**
    a. Replace the key (the new value) with the element on the index
    b. Now the left and right subtrees to this node will be max heaps so,
    c. Run MAX_HEAPIFY function from this node to max heapify it.

    Time complexity = Time to run max_heapify

    In worst case, we may need to run max heapify from the top element in the complete binary tree.
    Therefore, **Time complexity = O(logn)** and **Space Complexity = O(logn)**

    Note: In a max heap if you decrement an element, it is equivalent to calling Max_Heapify fuction so the complexity is judged by max_heapify function.

    Let's see how to insert an element in the max heap.

4. **Insert an element in max heap:** Whenever we want to insert an element, we insert it in the last position which is available in the heap.
    a. Insert the element in the last position of the heap
    b. Compare it with the parent
    c. If it is bigger than the parent, replace the parent with this element
    d. Repeat b and c until the tree is max heap

    Time complexity: In the worst case the element might have to travel from the leaf to the root.

⇨ Time complexity = **O(logn)**
⇨ Space complexity = **O(1)** (no extra space is taken)

SUMMARY OF OPERATIONS AND THEIR COMPLEXITY

We learnt about heap because for problems which require insertion, finding max and stuff, heap is a good data structure. Well it will not work for all of the operations (for ex. For deleting a random element). Let's see where heap will be a good data structure and where we may need to analyze other algorithms than heap.

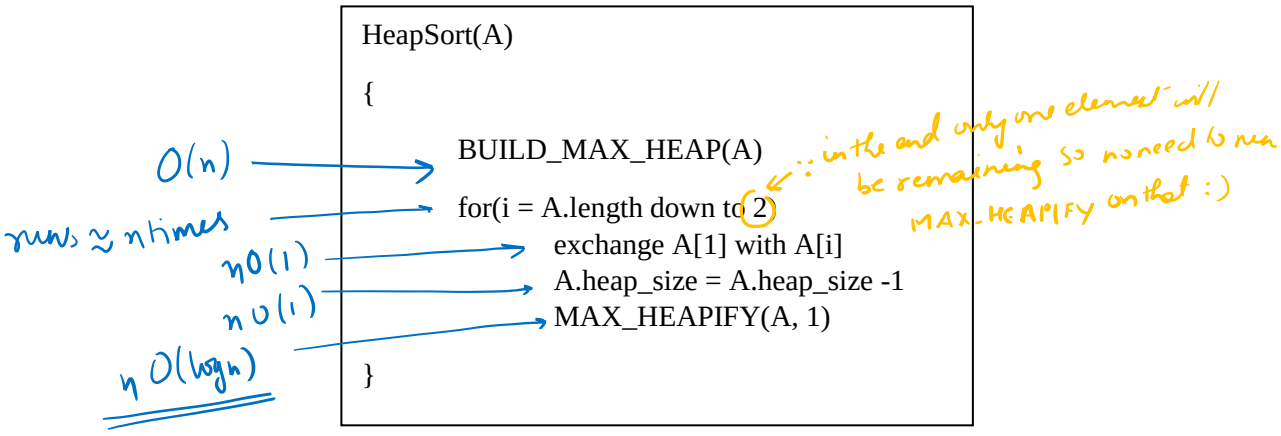
Green means heap is optimal for such problems

Red means heap is not optimal for such problems

Problem:	Find max	Delete max	Insert an element	Increase key	Decrease Key	Find min	Search Random	Delete Random
Complexity of Max Heap:	O(1)	O(logn)	O(logn)	O(logn)	O(logn)	O(n)	O(n)	O(n)

Now, let's see how to implement a sorting algorithm using heap data structure.

HEAP SORT ALGORITHM AND ANALYSIS



The gist is that, "At every point we are going to take the largest element in the heap and write it in the end, then we are not going to see that element for the remaining part of the algorithm. Then we construct the heap from the remaining elements and repeat this process."

Time Complexity: We are running the for loop ~ n times and MAX_HEAPIFY function is taking O(logn) time.

Therefore, **Time complexity for heap sort = O(nlogn)**

One can argue that the MAX_HEAPIFY will run on a smaller tree every time, but until one entire level is not removed the function will run O(number of leaves x logn) = O(n/2 x logn)= O(nlogn). This is not

same as that of BUILD_MAX_HEAP where the complexity depends on the height of the node. Therefore the complexity can't be O(n).

QUESTIONS ON HEAP

Question 1. In a heap with 'n' elements with the smallest element at the root, the 7th smallest element can be found in time:

a. O(nlogn)
b. O(n)
c. O(logn)
d. O(1)

Answer 1: Since we are not taking smallest but 7th smallest element, therefore time can't be O(1).

To solve this we will have to extract first six elements from the heap which will take 6 x O(logn) time.

Find the 7th element will take O(1) time

Putting back 6 extracted elements will take 6xO(logn)

Total time complexity = 6O(logn) + O(1) + 6O(logn) = **O(logn) Therefore option (c) is the correct choice.**

Question 2: In a binary max heap containing 'n' numbers, the smallest element can be found in what time?

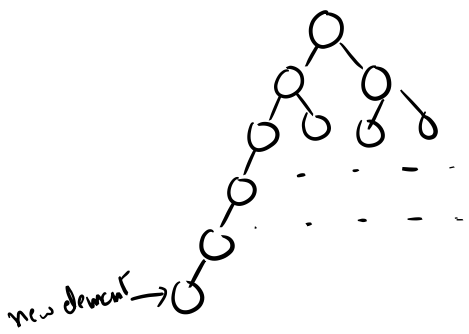
a. O(loglogn)
b. O(n)
c. O(logn)
d. O(1)

Answer 2: The minimum element will be present in the leaf nodes. In these leaf nodes we need to search for the smallest element.

Time complexity = Search for smallest element from $\left\lfloor \frac{n}{2} \right\rfloor + 1 \; to \; n$ which will take **O(n/2)** or **O(n)** time.

Question 3: Consider the process of inserting an element into a max heap. If we perform a binary search on the path from new leaf to root to find the position of newly inserted element, the number of comparisons performed are?

Let's say the tree is like this:



To find the position of newly inserted element we need to apply binary search on the path from new leaf to root.

Path from leaf to root will have **log(n)** elements.

Binary search on **n** elements takes **O(logn)** time
Binary search on logn elements will take O(loglogn) time.

Therefore answer will be : O(loglogn)

If in the question it was asked “the element will be inserted in what time?”. Then O(loglogn) will not be the answer as for insertion we need to run max_heapify. In that case the time complexity would have been

O(logn)

Question 4: We have a binary heap on ‘n’ elements and wish to insert ‘n’ more elements (not necessarily one after another) into this heap. The total time required for this is:

a. O(logn)
b. O(n)
c. O(nlogn)
d. $O(n^2)$

We know that inserting an element in a max heap taken O(logn) time and if we are inserting ‘n’ elements it will take O(nlogn) time.

The above will only happen if we insert elements in an order of ONE AFTER THE OTHER.

The question says that one after the other order is not necessary, so I can consider the already make heap that it is not in heap and add n elements at the end of the array.

The extended array will have **2n** elements.

I will run BUILD_MAX_HEAP on this array which will do the job in O(2n) time.

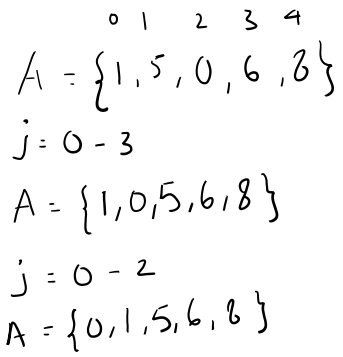
⇨ **The correct choice is (b) O(n)**

Let’s move on to the next sorting algorithm.

BUBBLE SORT

Let's see the algorithm for Bubble sort.

```
BUBBLE_SORT(int a[], n)
{
        int swapped, i, j;
        for(i = 0, i<n, i++)
        {
                swapped = 0;
                for(j=0;j<n-i-1;j++)
                {
                        If(a[j] > a[j+1]
                                swap(a[j], a[j+1]);
                                swapped = 1;
                }
        }
        if(swapped == 0)
                break;
}
```



Analysis of Bubble sort:

Now we can look at the complexity of the algorithm by looking at the number of swaps required, or even the number of comparisons required.

Worst case:

In the worst case scenario for an array which contains 'n' elements we have to do:

(n-1) + (n-2) + (n-3) + … + 1 comparisons (**worst case input will be an array sorted in descending order).**

This sum = (n-1)(n-2)/2 = **$O(n^2)$**

Best Case:

In the best case, the array will already be sorted and thus after the first iterations only (n-1) comparisons will be required.

Therefore, best case time complexity = Ω(n-1) or **Ω(n)**

If we are stopping in the middle:

Suppose we found that the array is sorted after 2 iterations doing (n-1) and (n-2) comparisons respectively in each iteration. Then the time complexity = O(n-2+n-2) = O(n) again. So, we can say that the time complexity will be O(kn) for all the middle cases. For the worst case, k becomes 'n' giving $O(n^2)$ complexity.

Summary for Bubble Sort:

Time Complexity	Best Case	Worst Case	Average Case
	$\Omega(n)$	**$O(n^2)$**	**$\Theta(n^2)$**

Let's look at another sorting algorithm

BUCKET SORT

Bucket sort is applied for problems like below:

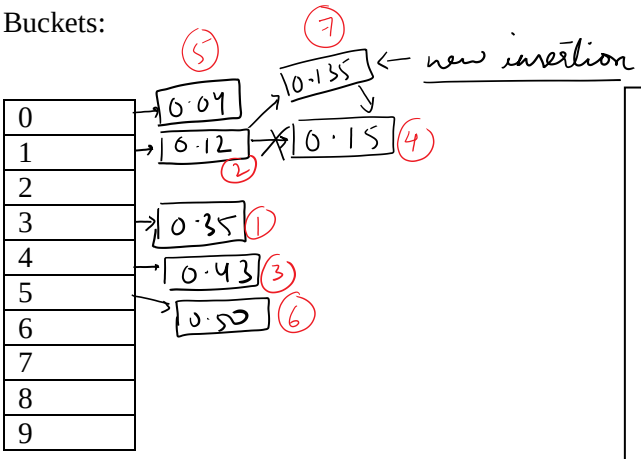
Sort a large set of floating point numbers which are in the range 0.0 to 1.0 and are uniformly distributed across the range.

Let's take the numbers: 0.35, 0.12, 0.43, 0.15, 0.04, 0.50, 0.132

1. We take 10 "buckets" determined by the radix of the number.
2. Put the numbers to be sorted in the correct bucket (determined by radix)
3. If there are more than one numbers in a bucket to be inserted, use insertion sort for the correct placement
4. Read the bucket from top to bottom to get the sorted elements.

Let's take a look at the sorting problem above.

Buckets:



Best case:

If all of the elements are uniformly distributed, then we may just need to add them to the bucket and then take them out of the bucket (no insertion sort because no two elements are in the same bucket). Time complexity will be O(n) + O(n) = O(n) for best case. Space complexity = O(buckets + elements) = O(k+n)

Worst case:

All the buckets may get n/k elements and in these elements we may have to apply insertion sort. Therefore, worst case time complexity = $O((n/k) * n) = O(n^2)$

Summary for Bucket Sort:

Time Complexity	**Best Case**	**Worst Case**	**Average Case**
	$\Omega(n)$	**$O(n^2)$**	**$\Theta(n^2)$**

Space Complexity = O(n+k) where k is the number of buckets and n is the number of elements to be sorted.

Let's see our next sorting algorithm

COUNTING SORT

There is a restriction with counting sort. It can't be applied like other sorting algorithms. The restriction is that *the keys or the numbers we have to sort, should always occur in a particular range.*

The restriction should be pre-defines.
Example: The numbers we have to sort is always between 1-5 or 10-1000 etc.

Let's sort: 2, 2, 3, 4, 1, 5, 1, 5 Range: 1-5

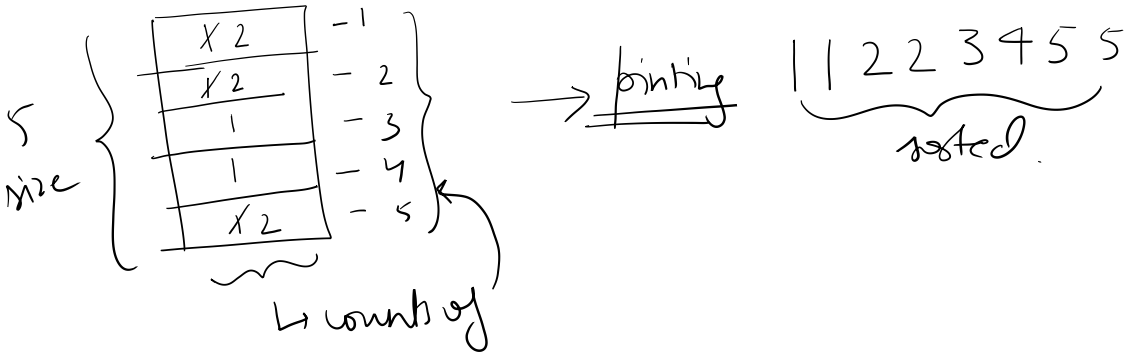
Here the keys are: 1, 2, 3, 4, and 5.

The gist is to use any data structure to store the 'count' of these keys.

1. Initialize a data structure (array or dictionary) with the size of number of keys
2. Traverse through the given list of numbers to be sorted
3. For each number seen, increment the count of it in the data structure we initialized until the list in question is completely traversed
4. Print each key the number of times it was seen to get the sorted elements.

Above question solution:

Since the keys range from 1-5 I am initializing an array to store their counts.



Analysis of counting sort:

Let's say the number of keys to be sorted = n

The range of these keys = k

We have to scan both of these lists one time, therefore **time complexity = O(n+k)**

Space Complexity: The extra space required is for the new data structure we are initializing to hold the counts. This space complexity will depend on the range of the keys

Therefore, **space complexity = O(k)**

Disadvantages:

1. *The restriction itself is a disadvantage*
2. *The space complexity will increase with an increased range.*
    a. *If we want to sort 1, 1000, 2, 4 these four elements the space of the data structure will be at least 1000 or O(1000)to store the count.*

RADIX SORT

Let's understand radix sort with an example and then move on to the algorithm. Let's say the numbers we have to sort is like this:

804
26
5
64
52
1

We are using base 10 here (which is decimal).

1. Determine the number of the digits in the largest number in the given list to be sorted, let's say it is 'm' digits
2. Convert all the numbers into 'm' digit number (in this example 1 will be written as 001)
3. Form the least significant digit to the most significant apply any stable sorting algorithm.
    a. Take the units place and arrange numbers according to the result. If two numbers are same, then arrange them in the way they occurred in the original sequence.
    b. Take the elements sorted by units place in point a. above and sort them using the tens place.
    c. Repeat this process until you end up sorting the numbers using most significant digit.
4. You'll get your sorted elements after doing this procedure.

Let's sort the elements:
804
26
5
64
52
1

Original Sequence	Conversion to max digits	Units place sorting	Tens place sorting	Hundreds place sorting
804	804	001	001	001
26	026	052	804	005
5	005	804	005	026
64	064	064	026	052
52	052	005	052	064
1	001	026	064	804

final sorted elements

RADIX SORT ALGORITHM

```
RADIX_SORT(A, d)
{
        //Each key in A[1…n]is a d-digit integer
        //Digits are numbered 1 to d from right to left

        For i=1 to d do:

                Use a stable sorting algorithm to sort A on digit i
}
```

A = the array containing the elements to be sorted, d= the maximum number of digits.

Analysis of Radix Sort

The intuition for the algorithm:

1. When we do the sorting based on the unit's digit, all the elements which have only 1 digits get sorted in their correct position.
2. When we do the sorting based on the tens digit, all the elements which have 2 digits (in the original sequence) get sorted in their correct position.
3. When we do the sorting based on the hundreds digit, all the elements which have 3 digits(in the original sequence before appending zeros) get sorted in their correct position.

Time complexity: The time complexity depends on the for loop that we have at the heart of the algorithm.

We will repeat the for loop depending on the number of digits present in every number.

In any number system of base b the maximum digits that you can have is b. Therefore, at any place (units, tens or hundreds) in the base 10 system we can have only 10 possible digits (0-9). Therefore, counting sort can be used as the stable sorting algorithm here.

Now, counting sort has to be applied 'd' times.

Complexity = d*O(n+b) where n is the number of keys in the input and b is the range of the input.

Now d is the number of digits in the largest number present in our input. Let's say that the largest number present in the input is *l.*

Therefore, $d = \log_b l$

Time complexity = $\log_b l$.O(n+b)

Let's assume that the largest number is of the order of n^k.

Then time complexity = $\log_b n^K\ (O.(n+b)) = k \log_b n\,.\,(O(n+k))$

K is a constant, so time complexity = O($n \log_b n$) (worst case).

For the algorithm to give O(n) time complexity, the b and n should be same.

Space complexity: The extra space will be required by the counting sort algorithm to store the count of the numbers. This extra space depends on the base of the numbers.

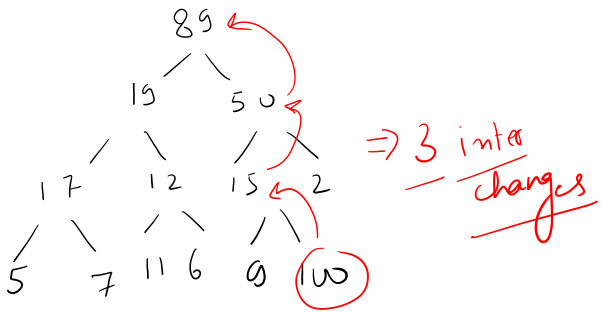
Therefore, **space complexity = O(b).**

QUESTIONS

Gate - 2015

Consider the following array of elements
< 89, 19, 50, 17, 12, 15, 2, 5, 7, 11, 6, 9, 100 >
The minimum number of interchanges needed to convert it into a maxheap is.

a) 4 b) 5 c) 2 d) 3



Algorithms – Searching, Greedy Algorithms

SEARCHING ALGORITHMS

In computer science, a search algorithm is an algorithm that retrieves information stored within some data structure. Here we are going to look at linear search and binary search.

Linear Search

The name itself says that we are going to go in a linear fashion. This algorithm is also called **sequential search.**

It sequentially checks each element of the list for a target value until a match is found or until all the elements have been searched.

It works on both sorted and unsorted data.

Problem Statement: Given a list L of n elements with values or records $L_0 \ldots L_{n-1}$ and target value T, the following subroutine uses linear search to find the index of the target T in L.

Basic algorithm:

1. Set i to 0
2. If L_i = T, the search terminates successfully; return i
3. Increase i by 1
4. If i < n, go to step 2. Otherwise, the search terminates unsuccessfully

Time complexity

1. **Approach 1**
    a. **Best case:** number of iterations = 1
    b. **Worst case:** number of iterations = n+1 (we didn't find the element at all)
    c. **Average case :** number of iterations = best + worst / 2 = O(n+2/2) = O(n)
2. **Approach 2: Using recurrence relation**

    T(n) = T(n-1) + 1 if n > 1

    T(1) = 1

    Then by back substitution T(n) = O(n)

Implementation of linear search on a linked list or array is going to give the same worst case time which is O(n)

Let's see the next searching algorithm called Binary Search

Binary Search

Binary search can be only applied when:

1. *The data is stored in an array*
2. *The data is sorted*

Binary search cannot be applied when:

1. *The data is stored in a linked list and sorted*
2. *The data is unsorted*

Binary search, also known as **half-interval search** or **logarithmic search,** is a search algorithm that finds the position of a target value within a sorted array. It does not work on unsorted array.

- Binary search works on the sorted arrays, it begins by comparing the middle element of the array to the target value
- If target value matches the middle element, its position in the array is returned
- If the target value is less than the middle element, then, the search is continued on the left half of the array otherwise the search is continued on the right half of the array

Problem Statement: Given an array A of n elements with values or records $A_0 \dots A_{n-1}$, sorted such that $A_0 \leq \cdots \leq A_{n-1}$, and target value T, the following subroutine uses binary search to find the index of T in A.

Algorithm:

1. Set L to 0 and R to n-1
2. If L > R, the search terminates as unsuccessful
3. Set m (the position of the middle element) to the floor (the largest previous integer) of (L+R)/2
4. If T = A_m, the search is done; return m
5. If T > A_m set L to m+1 and go to step 2
6. If T < A_m set R to m-1 and go to step 2

Time complexity:

Recurrence relation: T(n) = T(n/2) + 1 if n > 1

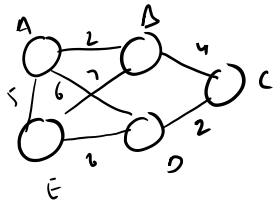
T(n) = 1 if n = 1

⇨ **T(n) = O($\log_2 n$)**

GREEDY ALGORITHMS

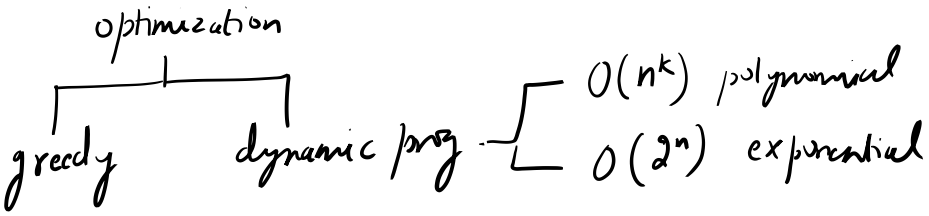
There are problems where we need to optimize some property like; “minimum cost”, “minimum spanning tree”, “maximize profit”, “maximize the reliability”, “minimize risk” etc. Where we want to maximize or minimize, basically we say that these problems are optimization problems.

There are various ways to solve such problems. Let’s understand with an example. Let’s say I have a graph like below. And we want to find out the smallest path from A to C.



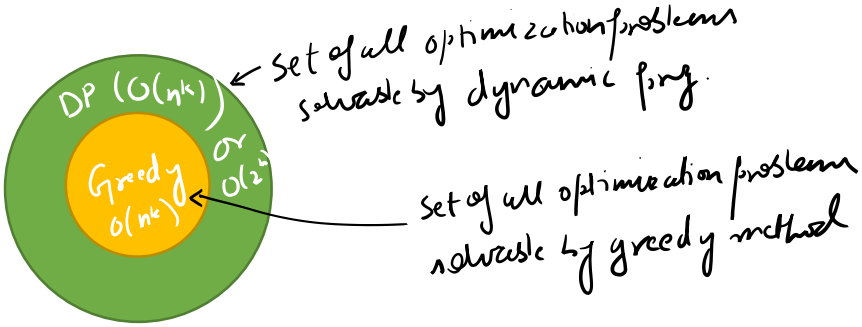
One way to do this is to use **exhaustive search** which means find out all the paths possible and select the minimum from those paths. This is going to be an exponential time or $O(2^n)$ algorithm and we don't want that. We want to see if we can do something better than this.

To solve such optimization problems, we found that there are two programming paradigms.



Using greedy method, we will not be able to solve all the optimization problems. The problem should have some properties then only we can apply greedy method.

We will be able to solve all the optimization problems using dynamic programming, but some programs even after applying DP will give result in exponential time. Therefore, we use dynamic programming where we can get result in polynomial time otherwise it is as good as applying exhaustive search.



Let's see the problems for which greedy algorithms and dynamic programming can be applied to understand them better.

KNAPSACK PROBLEM (Greedy)

Knapsack means a bag. The problem statement is like this.

Problem Statement: We are given a bag that has a holding capacity of 20 units. We are given three objects, ob1, ob2 and ob3. Every object has got some profit provided that you sell respective units of that object. What are the objects you will place in the knapsack to get the maximum profit?

	Ob1	**Ob2**	**Ob3**
Profit	25	24	15
Weight	18	15	10

M (capacity of the bag) = 20 units

1. If we try to put all the objects in the bag, we can't clearly because the maximum capacity is 20.

2. So what I can do next is that I will try to be ***greedy about profits.*** In this way I will try to add those objects first which will give me the maximum profits and move to the next maximum profit making object. Object 1 is giving me the maximum profit after that object 2 is giving me maximum profit, so I am taking all the Object 1 and will fill the remaining space in the knapsack with the object2.

	Weights	Profits
Object 1	18	25
Object 2	2	24*2/15
Total	**20**	**28.2**

But, is this the maximum profit? To answer this, we can go to the next stage.

3. I can now be ***greedy about weights***. Here I will add those objects first which have the least weight and then go to the next object which has the second least weight.

	Weights	Profits
Object 3	10	15
Object 2	10	24 * 10/15
Total	**20**	**31**

I found that if I am being greedy about weights, I am getting more profit. But is this the maximum profit again?

4. Next I can go with ***how much profit I am getting per object/weight.*** This way I can go about the **Profit/Weight ratio**

	Ob1	**Ob2**	**Ob3**
Profit	25	24	15
Weight	18	15	10
Profit/Weight	25/18 = 1.4	24/15 = 1.6	15/10 = 1.5

Intuitively, I will put Object 2 first because I am getting maximum profit per object in this category.

	Weights	Profits
Object 2	15	15*1.6 = 24
Object 3	5	5 * 1.5 = 7.5
Total	**20**	**31.5**

So I found out that neither by being greedy about profit or weights I am getting the maximum profit. I get the maximum profit by using the per weight profit of all the objects and then putting them in the decreasing order of profit.

Let’s see the algorithm and analyze it.

Greedy knapsack algorithm

```
Greedy Knapsack
{
        For i = 1 to n:                                   O(n)
                compute pi/wi
        Sort objects in non-increasing order of p/w       O(nlogn) best complexity I used sorting (merge sort)

        for i=1 to n from sorted list                     O(n)
                if(m > 0 && wi <=m)
                        m = m – wi
                        P = P + pi
                else
                        break;

        if (m>0)                                          O(1)
                P = P + pi(m/wi)
}
```

Time complexity: T(n) = O(n) + O(n) + O(nlogn) + O(1)

T(n) = O(nlogn) (worst case time)

I can also use heap in this problem but **for the worst case** the time complexity will still be O(nlogn).

For using heap sort, we will first make the max heap which takes O(n) and then delete or extract the max from the heap which takes O(logn) time. And this deletion in **worst case** may happen n times.

One can argue that after deletion the depth of the tree may reduce. Yes, that can indeed be the case in which the time complexity may be O(nlog(n-k)) but since we are talking about the **worst case time complexity,** the max heap may be a complete binary tree or almost complete binary tree with (n/2) leaf elements.

Therefore, the complexity = O(n/2 log(n)) which is still **O(nlogn)**

Example for knapsack:

Question: Find the maximum profit.

M = 15, N = 5

Objects	1	2	3	4	5
Profit	2	28	25	18	9
Weight	1	4	5	3	3

The p/w is

Object	1	2	3	4	5
Profit/weight	2	7	5	6	3

Objects sorted by profit/weight = {2, 4, 3, 5, 1}

Now, M = 15

Knapsack = all object2 + all object4 + all object3 + all object5

Profit = 28 + 18 + 25 + 9 = 80

Special case of knapsack: If all of the weights are same, we need not sort them by profit/weight ratio. We can sort them by the profits then and that will be enough

Let's move on to our next greedy method which is called Huffman Coding.

HUFFMAN CODING (Greedy)

Let's say we have a file and we want to store some characters in it. Now these characters are going to take space, obviously. If the characters are "abcd" in the entire file with nothing more than that and I give the two bit representation for each character like:

a = 00 then "abcd" will be 00011011 in the file
b = 01
c = 10
d = 11

Now, if the file has 100 characters, then the number of bits required to represent all of these characters will be: 100 x 2 = 200 bits

Now if the distribution of the characters is not even (number of characters in the file are not same) then we can use Huffman Codes to reduce the size of the file or reduce the number of bits all the characters in the file will take collectively.

To do this:

1. Count the number of characters grouped by character type in the file
   Let's say:
   A = 50
   B = 40
   C = 5
   D = 5
2. The character which has the highest frequency, represent it using the least number of bits.
   A = 0 C = 110
   B = 10 D = 111

We are using codes which are un-equal in the size. This is also called **un-equal sized encoding/different sized encoding/variable sized encoding**.

Now when we use this encoding, we need to make sure that proper decoding is possible. Therefore, each encoding will be unique for each character. For example, if A's encoding is 0 then, any other character's encoding can't start from 0.
Technically we are using **prefix codes** here, which means that if I am using a pattern to denote a character, then that pattern should not be a *prefix* of any other pattern.

Are we getting any gain from such an encoding?

Character	Frequency	Bit Representation	Space taken
A	50	0	50x1 bit = 50 bits
B	40	10	40x2 bits = 80 bits
C	5	110	5x3 bits = 15 bits
D	5	111	5x3 bits = 15 bits
Total	**100**	**-**	**160 bits**

Clearly we are getting a gain of 40 bits. So we are being greedy about the allocation of space for characters here.

Therefore, in most of the problems where the frequency of characters in a file is different, Huffman coding is going to give us better results in terms of storage. Therefore, Huffman coding is an algorithm which is used to find the codes which will help us reduce the size of the data.

Let's see the algorithm for Huffman codes.

```
HUFFMAN(C)
{
        N = |c|
        make a min-heap Q with 'c'

        For i = 1 to n-1
                allocate a new node 'z'
                z.left = x = Extract_min(Q)
                z.right = y = Extract_min(Q)
                z.freq = x.freq + y.freq
                INSERT(Q,z)

        Return (Extract_min(Q))
}
```

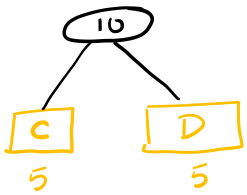
Let us understand this with the help of an example.

Let's say I have a file with 100 characters and their frequency is:

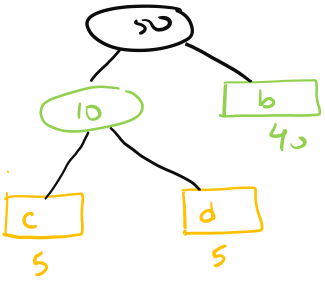
A= 50, B = 40, C = 5 and D = 5, and N(number of distinct characters) = 4

Then, the following are the steps to get the Huffman code for the characters.

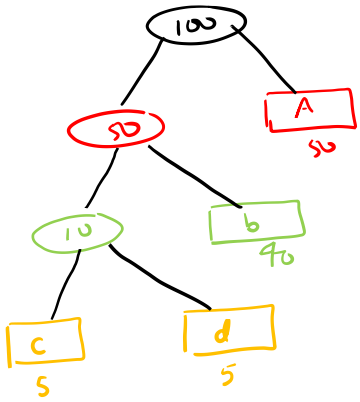
1. Take the first two characters having the least frequency and make them the children of a root in a tree. Here C and D are the characters with least frequencies, the tree will look like.



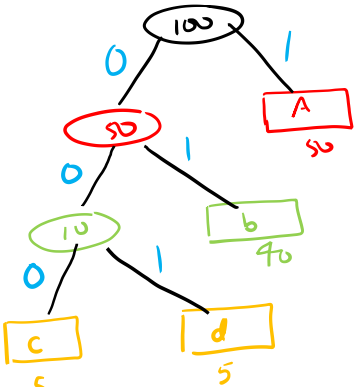
2. Now take this new node and the next character apart from C and D with the least frequency. That will be B with a frequency of 40. Combine these two in a new root node. Least one is the left child.



3. Now take this new node and the next character apart from B, C and D with the least frequency. That will be A with a frequency of 50. Combine these two in a new root node.



4. Now each side of the root node is given either 0 or 1. Let's give the left size 0 and right side 1.



5. Traverse through the tree from the root node to get the Huffman code.
   A = 1
   B = 01
   C = 000
   D = 001

(*steps 2 and 3 should be repeated until we have represented all the characters in the given problem)*

Total bits used without Huffman code = 200

Total bits used with Huffman coding = 160

Bits per character before Huffman coding = 200/100 = 2 bits/character

Bits per character after Huffman coding = 160/100 = 1.6 bits/character

We can also get the number of bits used by a character by calculating **Weighted external path length.** This is calculated as below:

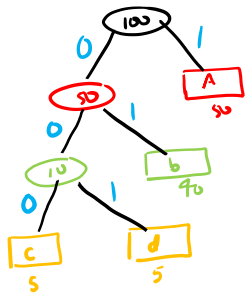
For C: "what is the length of this leaf from the root" = 3

For D: "what is the length of this leaf from the root" = 3

For B: "what is the length of this leaf from the root" = 2

For A: "what is the length of this leaf from the root" = 1

(refer the tree on the right hand side)



Then for each **weighted external path length** you can then multiply with the frequency of the character to get the total bits consumed by this file.

50x1 + 40x2 + 5x3 + 5x3 = 160 bits.

"How can we build a tree so that we can decrease the weight of the external path length? *This is also equivalent to making a tree for the Huffman coding, this way also a question can be asked.*

Let's take another example:

A = 40 D = 5

B = 30 E = 3

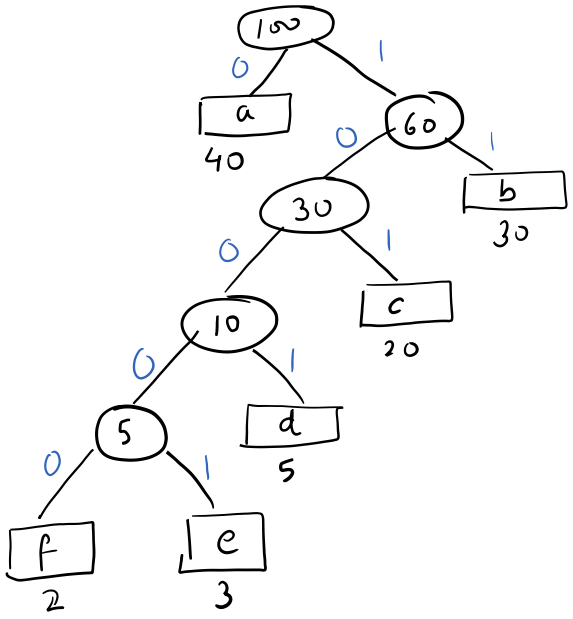
C = 20 F = 2

Let's store them in a data structure:

40	30	20	5	3	2

Take the two most minimum and create the nodes, keeping the minimum one at the left side.

In the next step, these two nodes will be replaced by one node (3, 2) will become (5) and then take the next minimum element from the data structure and repeat this process as we did earlier. We will get the following tree out of it. REMEMBER TO PUT THE SMALLER CHILD ON THE LEFT AND BIGGER CHILD ON THE RIGHT. Then put 0 and 1 on left-right or right-left. I'll put 0 on left and 1 on right.



a = 0 — 1 bit × 40 = 40

b = 11 — 2 bits × 30 = 60

c = 101 — 3 bits × 20 = 60

d = 1001 — 4 bits × 5 = 20

e = 10001 — 5 bits × 3 = 15

f = 10000 — 5 bits × 2 = 10

Total = 100 characters

= 205 bits

We are going to get the prefix code for each character because in the tree each character is a leaf and thus has no children.

Let's see the time complexity of the algorithm. Let's see step by step what has happened.

```
HUFFMAN(C)
{
        N = |c|                                  ← O(1)
        make a min-heap Q with 'c'               ← O(n)
        For i = 1 to n-1                         ← n-1 times
                allocate a new node 'z'
                z.left = x = Extract_min(Q)      ← O(log n)
                z.right = y = Extract_min(Q)     ← O(log n)
                z.freq = x.freq + y.freq
                INSERT(Q,z)                      ← O(log n)
        Return (Extract_min(Q))                  ← O(1)
}
```

$T(n) = 2O(1) + O(n) + 2(n-1)O(\log n) + (n-1)O(\log n)$

$= O(n) + 3(n-1)O(\log n)$

$= O(n) + O(n \log n)$

$= O(n \log n)$

Huffman Coding takes O(nlogn) time.

Space Complexity: We are going to represent the data using the tree. The space required will be ~ O(n)

Therefore, space complexity will be **O(n).**

Question: Instead of using heap why can't I sort the elements to get the minimum?

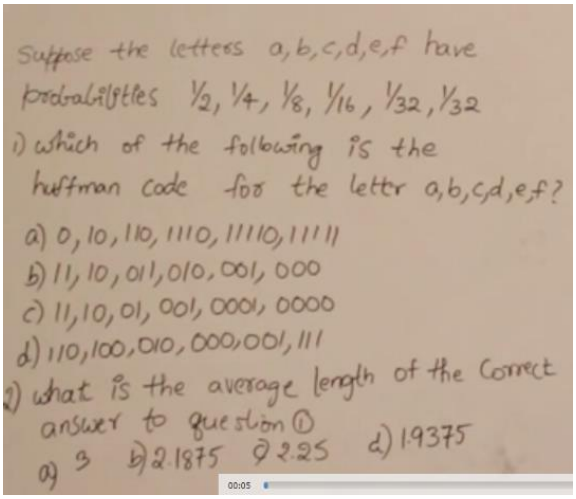
1. Sorting will take O(nlogn) time
2. After deletion, elements have to be inserted in the array, that insertion can take O(n) time.
3. **O(n) times insertion will be done (n-1) time for loop iteration. Therefore if sorting is taken into picture the time complexity will be $O(n^2)$ and we don't want that.**

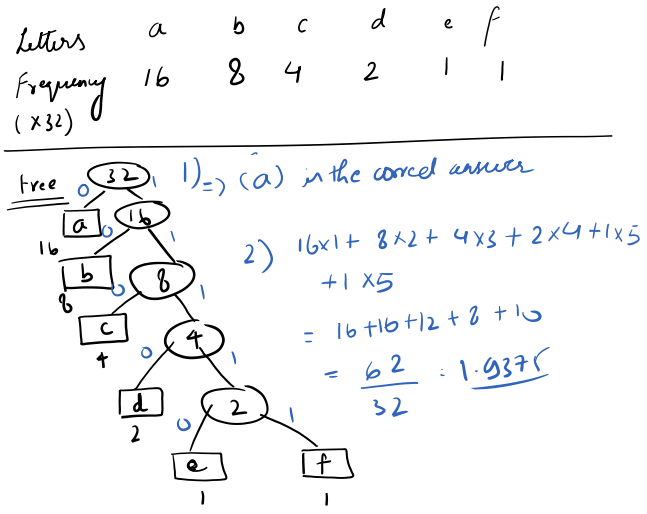
Question: So when should I use sorting and when should I use heaps?

Answer: When there is no requirement of putting an element, heaps can be replaced by sorting algorithms. Otherwise, heaps will be useful.

Let's see some questions on Huffman coding.

Question1:





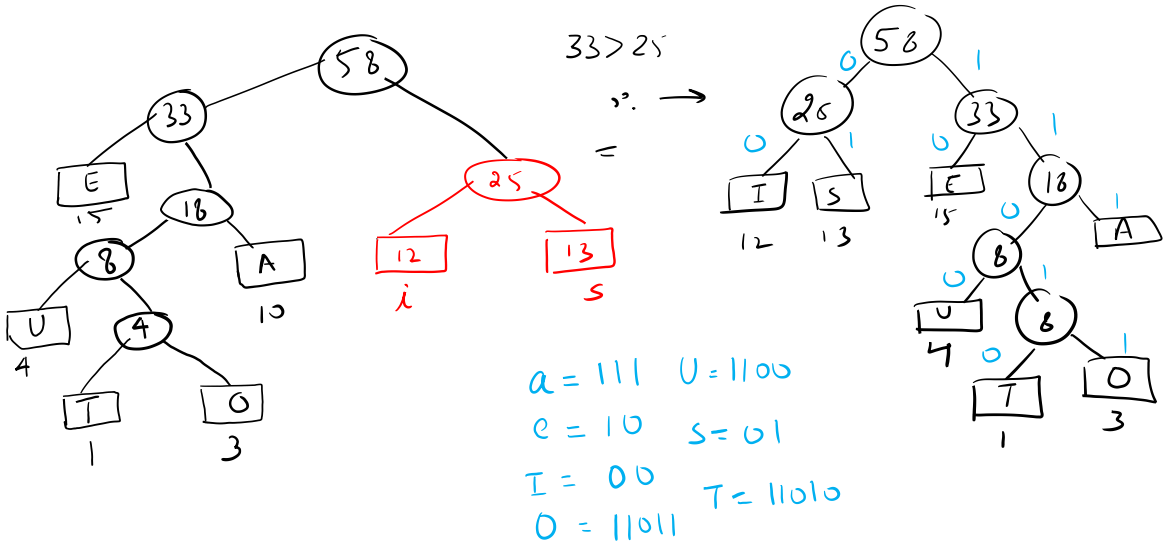
Sometimes it happens that the newly created node need not be chosen immediately after its creation. Let's see and example on that.

Question 2:

A	E	I	O	U	S	T
10	15	12	3	4	13	1

The tree for the given question can be seen below.

A	E	I	O	U	S	T
10	15	12	3	4	13	1



Let's see another greedy algorithm

JOB SEQUENCING WITH DEADLINES(Greedy)

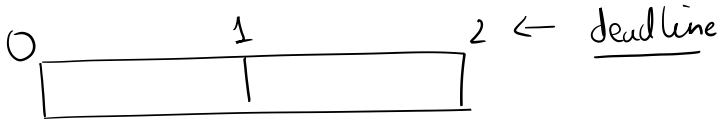
In the job sequencing with deadlines the problem is as follows:

Problem: There are some jobs given and the profit associated with them. The jobs will give those profits if the job is completed within a given deadline. If every job takes one unit of time what is the maximum profit that we can get?

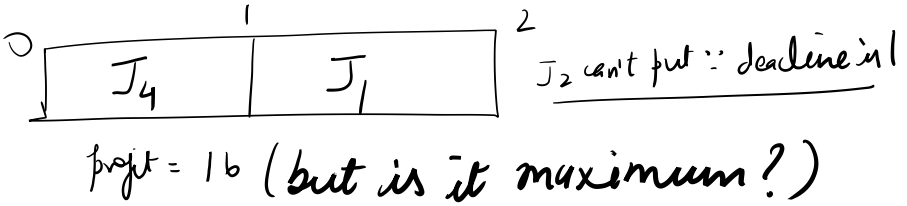
Let's say the jobs, profits and deadlines are given as below.

Jobs	J1	J2	J3	J4
Deadlines	2	1	1	2
Profits	6	8	5	10

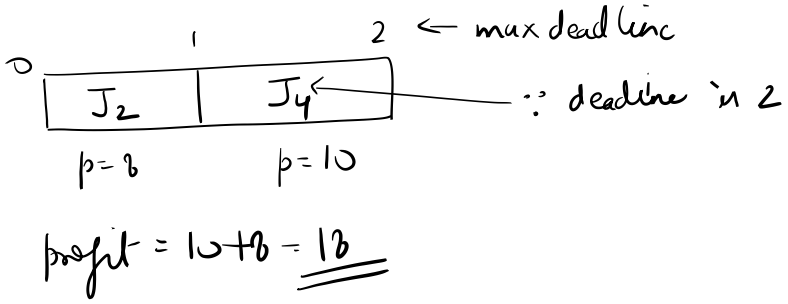
What I want to do is to do jobs in such a way that I get the maximum profits but the jobs should be done within their deadlines. Every job will take 1 unit of time to get completed.



Way 1: To solve this problem I can select the jobs which have their profits arranged in decreasing order.



Way 2: I can select the jobs according to the maximum profits and then place them as far away as possible according to their deadlines.



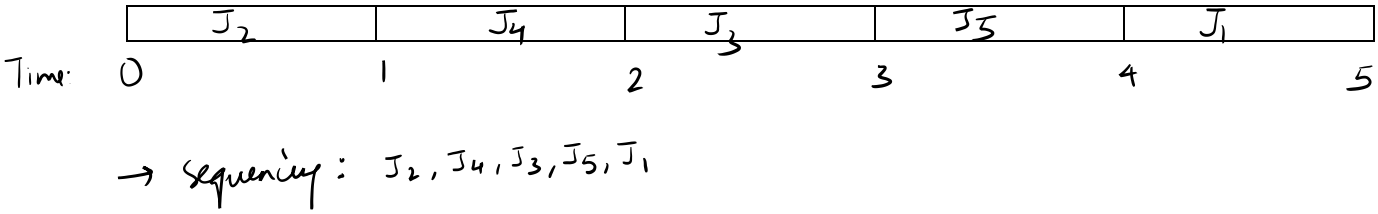
Second way of solving this problem is going to produce the MAXIMUM PROFIT

Let's see another example

Example 2: The jobs, profits and deadlines are given below. Schedule the jobs to get the maximum profit.

Jobs	J1	J2	J3	J4	J5	J6
Deadline	5	3	3	2	4	2
Profits	200	180	190	300	120	100

Max deadline = 5, therefore I can have max of 5 jobs in the sequencing table.



Steps to follow and their complexity analysis:

1. Create the Job Sequencing array with *number of elements = max deadline/max number of jobs.* **If the deadline is given very high and jobs are small, we don't need that big of an array. So be careful when deadlines are very high given <3**
2. Sort out the jobs in the decreasing order of their profit. **[O(nlogn)]**
3. Take each job and then start from the point where its deadline is given and search for an empty location to the left of that deadline. This searching can take O(n) time and for n such jobs, the complexity can be **$O(n^2)$**
4. Place the jobs in the empty position available. If empty position is not available, the job can't be placed.
5. Do this until the job sequencing array is full.

Time complexity = O(nlogn) + $O(n^2)$ = $O(n^2)$

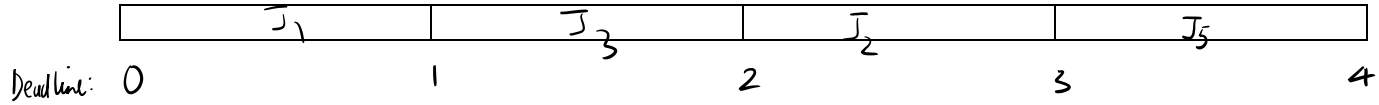
Let's see some more examples

Example 3: The jobs, profits and deadlines are given below. Schedule the jobs to get the maximum profit.

Jobs	J1	J2	J3	J4	J5
Profits	2	4	3	1	10
Deadlines	3	3	3	4	4

Answer: max deadline = 4

Job sequencing array:



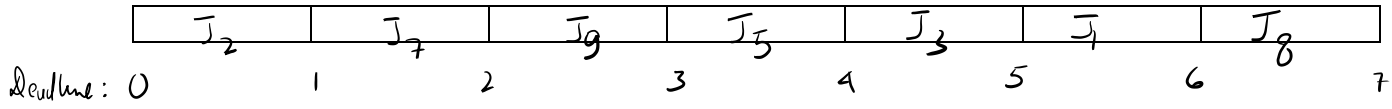
Sequencing = J_1, J_2, J_3, J_5 Profit = 2 + 3 + 4 + 10 = 19

Example 4: The jobs, profits and deadlines are given below. Schedule the jobs to get the maximum profit.

Jobs	J1	J2	J3	J4	J5	J6	J7	J8	J9
Profit	15	20	30	18	18	10	23	16	25
Deadline	7	2	5	3	4	5	2	7	3

Max deadline = 7 Jobs in descending order of profit: J3, J9, J7, J2, J4, J5, J8, J1, J6

Sequencing array



Sequencing = $J_2, J_7, J_9, J_5, J_3, J_1, J_8$ Profit = 20 + 15 + 30 + 18 + 23 + 16 + 25 = 157

Let's see our next greedy optimization problem.

OPTIMAL MERGE PATTERNS (Greedy)

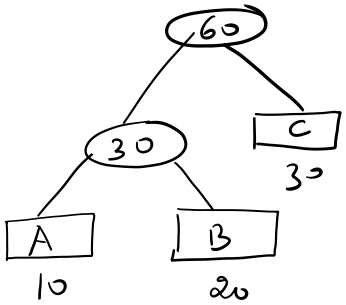
In optimal merge patterns, we have some files with some non-uniform records that we want to merge together. All the files have some data which is in the sorted format, now what we want to do is that we want to merge all of them into a one file. The catch is that this merging should happen with the least number of record movements.

If you recall, merging of records can be done using the MERGE operation of merge sort algorithm. However, we are concerned about the minimum record movement here when the merge operation is done.

Let's understand with an example.

FILES	A	B	C
NO. of RECORDS	10	20	30

Let's do the merging like below:



The movements of the records is like this.

All the 10 records of the file A have been moved once in the parent node of the tree and all the 20 records of the file B have been moved once to the parent node.

This parent node and the records in C have moved their 30 records each once to the final root node of the tree which is the new file size.

Therefore, total movements = 10x1 + 20x1 + 30x1 + 30x1 = 90

BUT IS THIS THE LEAST NUMBER OF MOVEMENTS?

The way in which this tree has been created to get the least number of movements (yes, 90 is the least number of movements needed for optimal merging in this question) has already been seen by us when we were creating HUFFMAN CODES.

The only difference between optimal merging and Huffman code tree creation is that in optimal merging we don't need to worry about the lesser of the nodes being on the left or right position because we want to just count in this problem.

Since this problem is similar to Huffman code creation, the algorithm is also going to be the same. So I am not elaborating much here. Let's see the time complexity.

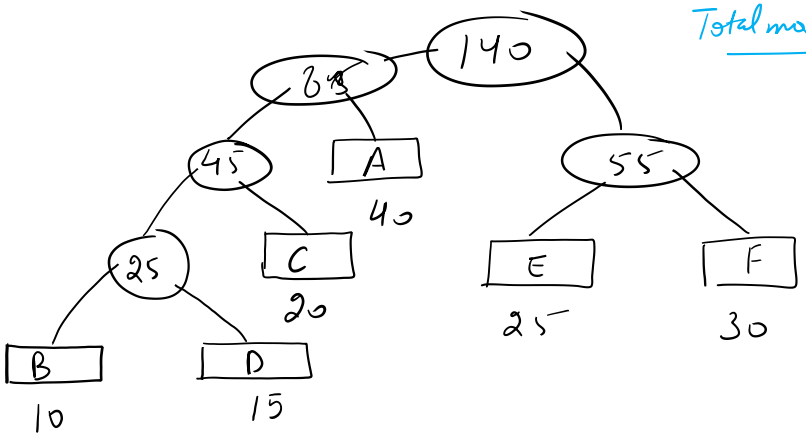
Time complexity

1. Given 'n' files first create a minimum heap (takes O(n) time)
2. Take the two minimums and merge them. To take two minimum, the time taken will be O(logn).
3. We then merge them together and put it back. Time to insert is O(logn)
4. Step 2 and 3 happen (n-1) time. Therefore:

Final time complexity: O(n) + (n-1)O(logn) + (n-1)O(logn) = O(n) + 2(n-1)O(logn) = **O(nlogn)**

Example: What is the optimal merge pattern for the files given below?

File	A	B	C	D	E	F
Records	40	10	20	15	25	30



Total moves: $10 \times 4 + 15 \times 4 + 20 \times 3 + 40 \times 2 + 25 \times 2 + 30 \times 2$

$= 40 + 60 + 60 + 80 + 50 + 60$

$= 340$ moves

Let's move on to the next greedy algorithm which will be on graphs.
Note: the topic of graphs will be discussed in detail in either graph theory or data structures. We will see here some theory of graph required for the respective greedy algorithm on graph.

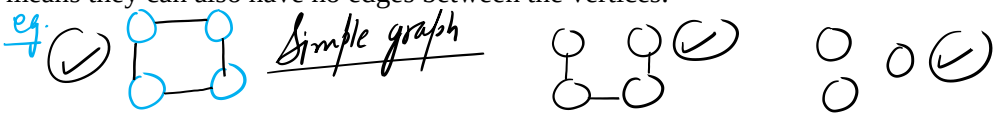
SPANNING TREES AND KIRCHOFF THEOREM

Before moving on to the algorithms, let's clear the theory required to understand the algorithms.

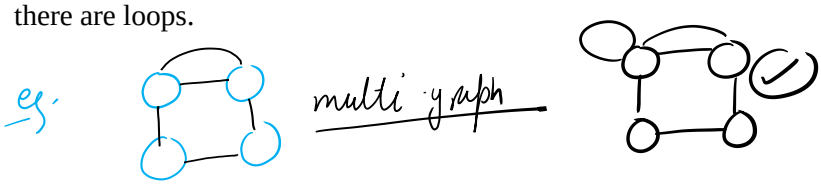
Graph: A graph is a collection of vertices and edges given as an ordered pair (V,E).

Types of graphs can be:

1. **Simple graph:** A graph is a simple graph if between two vertices there is at most one edge. This means they can also have no edges between the vertices.



2. **Multi graph:** A graph is a multi-graph if between any two vertices there is more than one edge or there are loops.

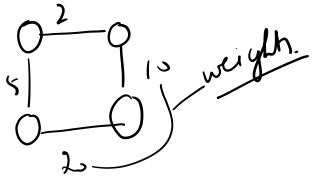


In this topic we care about simple graph.

Properties of simple graphs

1. The minimum number of edges present in a graph = 0
2. The maximum number of edges present in a graph = give all possible edges = $n_{C_2} = \frac{n(n-1)}{2}$ where n is the number of vertices
3. In worst case I can say that
   E = O(n(n-1)/2) = O(n^2) = O(v^2) where v the number of edges
   If I take log on both sides
   v = O(logE) in the worst case.

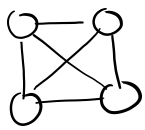
3. **Simple Weighted Graphs**
   In the simple weighted graphs, the edges are given some weights. These meaning of these weights depends on the context.



4. **Simple Unweighted graphs:** The simple graphs which do not have the weights associated with the edges.
5. **Simple Labeled graph:** If all the vertices of a graph are labeled with a name
6. **Simple Unlabeled graph:** If all the vertices of a simple graph are not labeled with anything
7. **Simple Complete graph:** If all the vertices are connected to all the other vertices in a graph with at most one edge, that graph is called a simple complete graph. It is denoted by **K_n** where n is the number of nodes.

SPANNING TREE

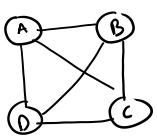
An interesting question that can be asked is *"Given a simple graph what is the minimum number of edges to connect all of the vertices?"*



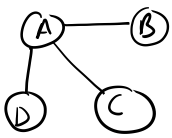
there are 6 edges but do we need all of them to connect all the vertices?

If I answer this question, the result is going to be a **SPANNING TREE.**

A spanning tree is the graph which has minimum number of edges in it such that all the vertices/nodes are connected and any node can be reached from any other node by traveling on a single edge or more than one edge.



spanning tree ⟹



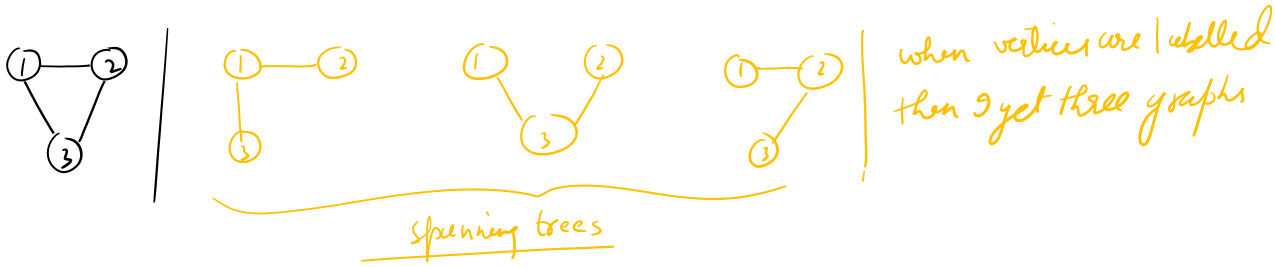
minimum edges = 3

THE MINIMUM NUMBER OF EDGES REQUIED TO CONNECT "n" NODES IN A GRAPH IS "n-1"

Now we know that if a graph contains V vertices then it need a minimum of (V-1) edges to connect all the vertices.

A **spanning tree is also a subgraph of the given graph** from which the spanning tree has been made.

So if I have V vertices in a graph, then how many spanning trees are possible?



In case if the vertices are not labeled, all these spanning trees will be isomorphic.

For K_3 graph number of spanning trees = 3

For K_4 graph number of spanning trees = 4

…

For K_n graph, number of spanning trees = n^{n-2}

What if the graph is not complete?

If the graph is not complete, then the maximum number of spanning trees can't be determined by n^{n-2} because there will be at least one edge missing.

To find out the maximum number of spanning trees for a graph which is not complete we use the **Kirchhoff's Theorem**

KIRCHHOFF'S THEOREM

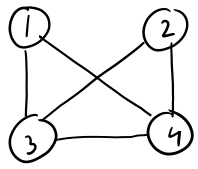
To find out the maximum number of spanning trees we use Kirchhoff's theorem. Here are the steps to do that.

1. Find out the adjacency matrix of the given graph. This graph will be (VxV). Let's call it A.
2. **Theorem**
    a. **Replace all the diagonal 0's elements in A with the degree of the vertex**
    b. **Replace all the non-diagonal 1's with -1**
    c. **Keep all non-diagonal zeros as zeros.**

3. In this modified matrix A, find out the Cofactor of any one of the element.
    a. Cofactor of element A_{11} is calculated as follows
        i. Ignore the row 1 and column 1
        ii. Find the determinant of the remaining matrix
4. The value of the cofactor is the number of spanning trees possible.

Let's take some examples:

Example 1: How many spanning trees are possible for the graph given below



① Adjacency matrix

A	1	2	3	4
1	0	0	1	1
2	0	0	1	1
3	1	1	0	1
4	1	1	1	0

② Theorem application

A	1	2	3	4
1	2	0	-1	-1
2	0	2	-1	-1
3	-1	-1	3	-1
4	-1	-1	-1	3

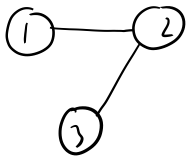
③ Cofactor of A_{11}

$= 2(9-1) - (-1)(-3-1) + (-1)(1+3)$

$= 16 - 2 - 4 = 10$

Therefore, for this graph, 10 spanning trees are possible.

Example 2: How many spanning trees are possible for the graph given below



① Adjacency matrix

A	1	2	3
1	0	1	0
2	1	0	1
3	0	1	0

② Theorem

A	1	2	3
1	1	-1	0
2	-1	2	-1
3	0	-1	1

③ Cofactors

Let us take Cof. of A_{11}

$(2-1) = 1$

Let's understand some more about the spanning trees. Now we know what spanning trees are and now we can see some applications of spanning trees and other algorithms. One of the applications of spanning tree is whenever we want to build something like a network topology we may want to connect all the computers with the least number of wires. But if the problem is like: I want to connect the computers with the minimum total length of the wire (the length of the wire is given for each edge of the tree) then I need to find out **Minimum Spanning Tree.** This means the problem finally translates to finding a minimum spanning tree in a ***weighted graph.*** Let's see how it can be done.

MINIMUM COST SPANNING TREE

Finding a minimum cost spanning tree is not as straightforward as finding the spanning tree because now we want to find out from all the possible spanning trees of a graph, which one will have the minimum cost.

Revision: For a K_n graph the number of spanning trees = n^{n-2}

Therefore, this problem is of $O(n^{n-2})$ which is exponential. We are lucky that there are two algorithms that tackle the problem statement ***"Given a weighted graph what is the minimum spanning tree".***

1. Prim's algorithm
2. Kruskal's algorithm

Let's see Prim's first.

PRIM'S ALGORITHM FOR FINDING OUT MINIMUM COST SPANNING TREE(Greedy)

The informal steps to apply prim's algorithm are:

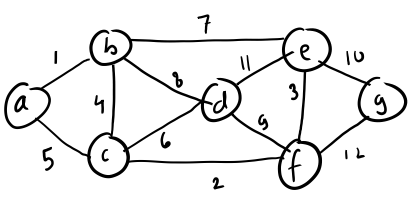
1. Make the skeleton graph meaning draw the graph in the question without its edges.
2. Take the edge which has the minimum weight and join the two nodes containing that edge
3. Look at the connections of these two nodes and add a new node based on the minimum weight
4. The new graph obtained will be a tree with 3 nodes, repeat this process until all the nodes are added in the final graph.

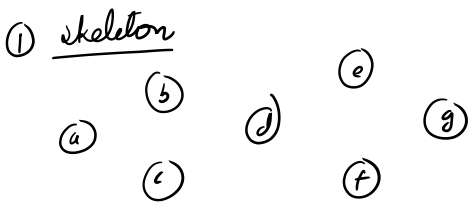
Important things to note:

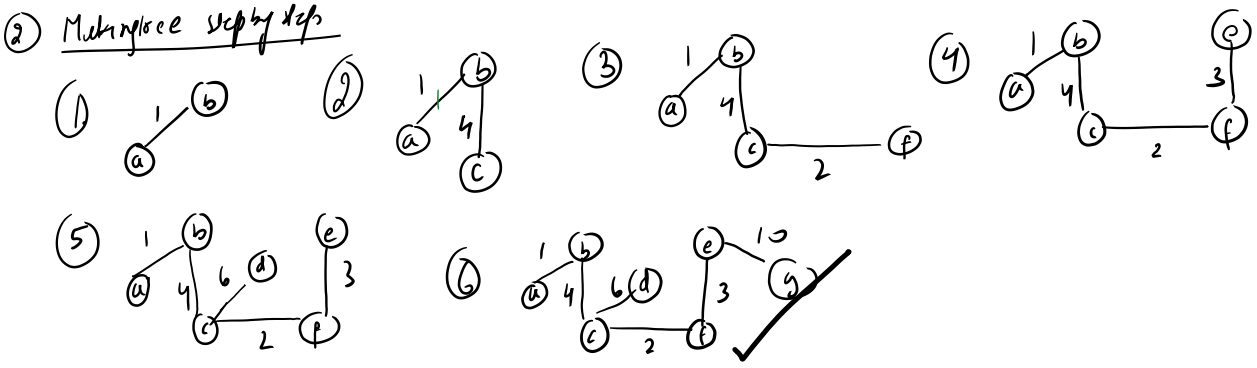
a. At any time of addition of the node a tree is obtained
b. There will be no cycles in this tree because it IS A TREE

Let's take some examples and then we will write the formal algorithm.

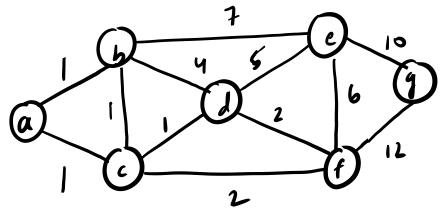
Example 1: Find the minimum cost spanning tree for the graph given below



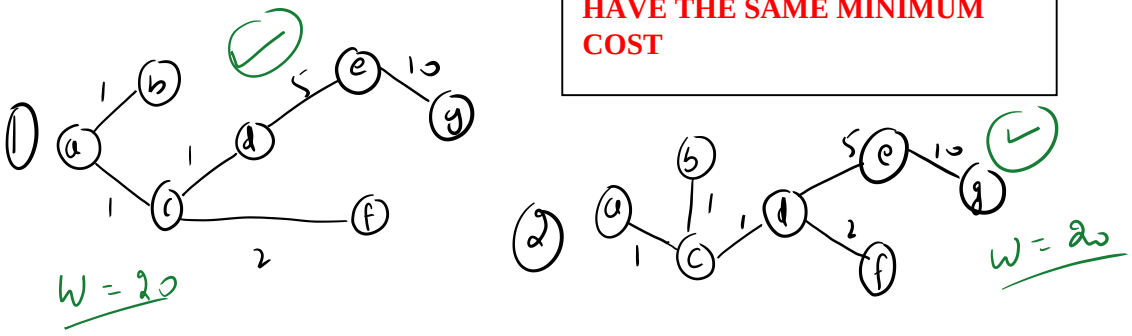




Example 2: An example where all the edge weights are not distinct.

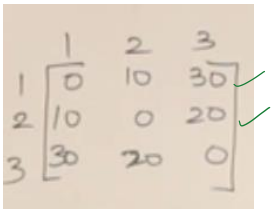


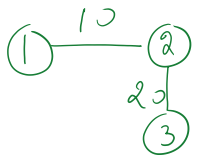
WHENEVER WE HAVE SAME WEIGHTS FOR SOME EDGES THEN THERE IS A CHANCE THAT WE MAY GET MORE THAN ONE MINIMUM SPANNING TREE BUT WILL HAVE THE SAME MINIMUM COST

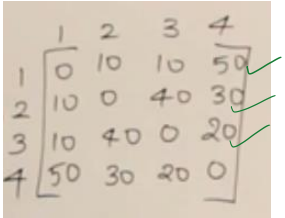


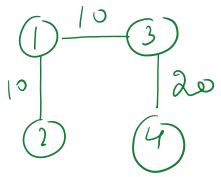
Stop making the graph once the count of the edges is reached (n-1) where n is the number of nodes.

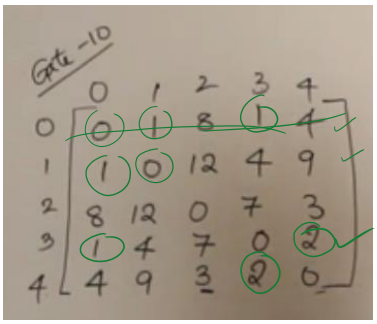
In GATE they are not going to give such simple graphs. They will give the graph in the form of the cost matrix. Let's kick its ass too.





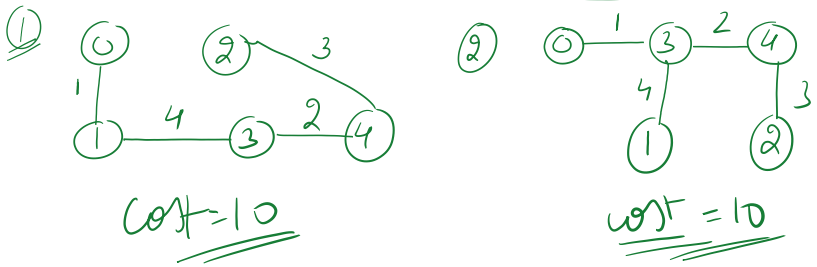






Find the minimum spanning tree such that the node 0 is a leaf

means that 0 can't have more than one connection



Prim's algorithm implementation without minimum heap (Greedy)

This is not necessary for GATE but learning will not hurt. Let's go to the algorithm

```
ALGORITM_PRIMS(E, cost, n, t)

//E is the set of edges. Cost is (nxn) adjacency matrix
//MST is computed and stored in array t[1:n-1, 1:2]

{
    1. Let (k, l) be an edge of min cost in E;
    2. mincost = cost[k, l]
    3. t[1, 1] = k, t[1, 2] = l
    4. for(i = 1to n)
           a. if(cost[i, l] < cost[i, k] then near[i] = l;
           b. else near[i] = k
    5. near[k] = near[l] = 0
    6. for (i=2 to n-1)
           a. let j be an index such that near[j] ≠ 0
              cost[j, near[j]] is minimum;
           b. t[i, 1] = j; t[i,2] = near[j];
           c. mincost = mincost + cost[j, near[j]];
           d. near[j] = 0
           e. for k = 1 to n do
                  i. if((near[k] ≠ 0) and (cost [k, near[k]] > cost[k, j]))
                         1. then near[k] = j

}
```

The prim's algorithm without min heap is going to take $O(n^2)$ time where n = no. of vertices.

So $O(v^2)$ time.

Let's see a second way to implement prim's algorithm which uses min-heap.

Prim's algorithm implementation using min-heap (Greedy)

```
MST_PRIMS(G, cost, r) //using min heap
{
        For each vertex u ϵ G.vertices
                u.key = ∞
                u.π = NIL

        r.key = 0
        Q = G.vertices
        while(Q ≠ ϕ)
                u = EXTRACT_MIN(Q)
                for each vertec 'v' adjacent to 'u'
                        if vϵQ and cost(u,v} <v.key
                                v.parent = u
                                v.key = w(u,v)
}
```

Total time taken for extract_min = O(vlogv)

Total time taken for build heap = O(v)

Total time taken for Decrease key = O(v.vlogv) = O(v^2logv)

This is actually not correct time taken by decrease key because the method will be called based on the number of edges that a particular node has. And in the end, in the worst case the number of calls to Decrease_Key will be nearly the number of edges.

According to aggregate analysis: Time taken by decrease key = O(ElogV)

Total time = O(VlogV + ElogV + V) = O(ElogV)

Which one is better? O(ElogV) or O(V^2)?

It turns out that for dense graphs, E = O(V^2) so Elogv = O(V^2logV)

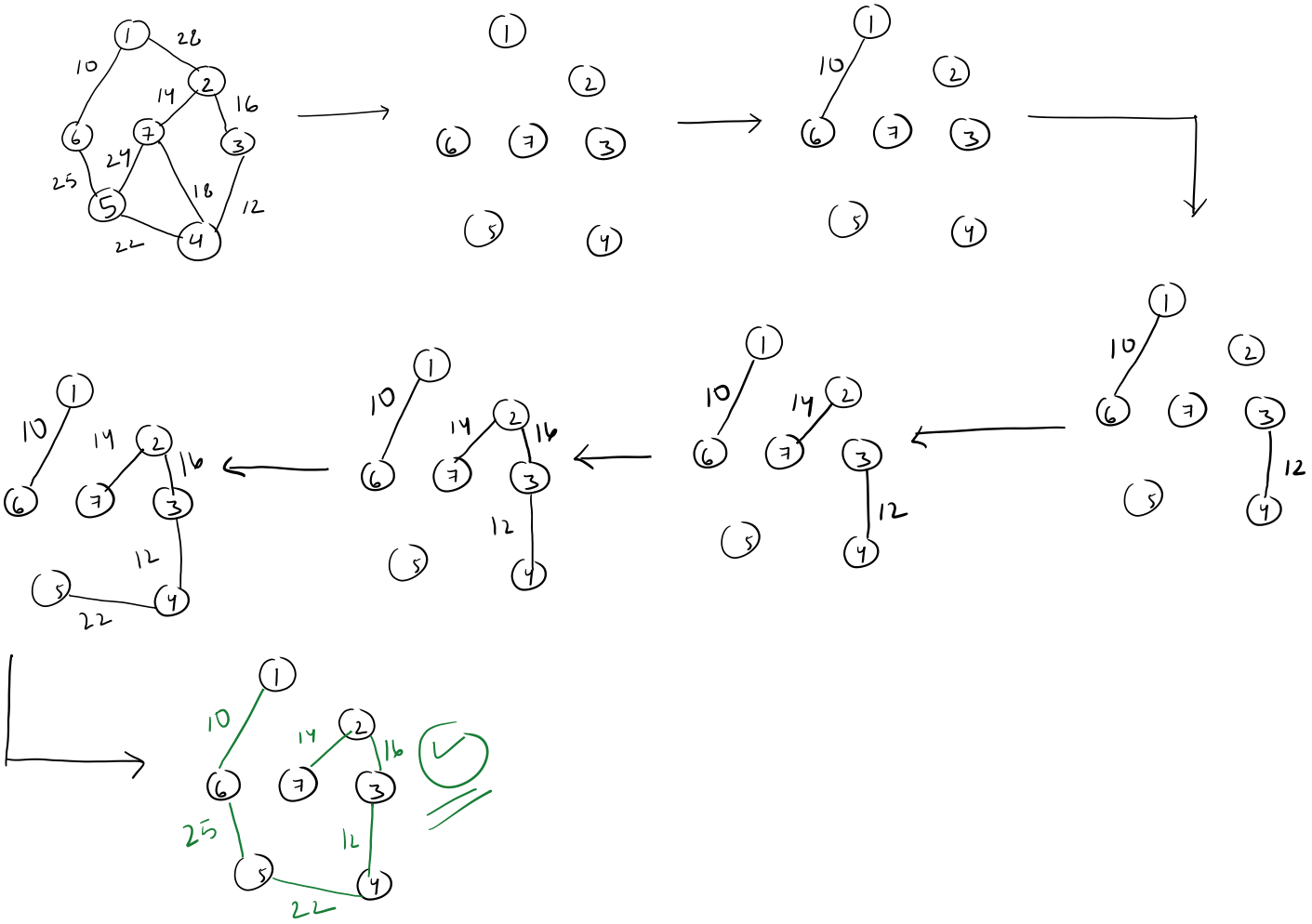
In sparse graph O(ElogV) = O(VlogV).

So for dense graphs, Prim's algorithm without heap is going to be more efficient and in case of sparse graphs Prim's algorithm with heap is going to be efficient.

Let's move on to the next greedy method for solving MST problem: Kruskal's algorithm.

KRUSKAL'S ALGORITHM FOR MINIMUM SPANNING TREE (Greedy)

Let's see an example before we jump to the algorithm.



Steps to make MST using Kruskal's algorithm

1. Get the edge which has minimum weight. Connect the two nodes that have this edge. This step is same as in the Prim's algorithm
2. Now, see which is the next edge which has the minimum weight. Connect the nodes having that edge.
3. Make sure no cycles are formed.
4. Repeat step 2 and 3 until all the vertices have been added.

How Prim's and Kruskal's algorithms are different?

1. In prim's you are building only one tree in each step. In Kruskal's there can be a forest.
2. In prim's you add the vertex/node as the algorithm proceeds. In Kruskal's all the nodes are already present, you are adding the edges in each step.

3. In prim's since it is only one tree and you are adding nodes, a cycle can never be formed. In Kruskal's because you are adding edges, you need to make sure that the cycles are not forming.
4. Applying Prim's and Kruskal's algorithm will give the same minimum spanning tree if all the weights are distinct in the tree. However, if the weights are repeating, you may get different spanning trees but the total weight of all the edges in the respective minimum spanning trees will be **EXACTLY SAME.**
5. **Note: You can find out spanning trees for the graphs which are connected.**

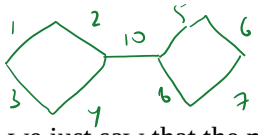
Let's see some more examples.

Gate 2000: Important question since we can explain many concepts in it.

Question: Let 'G' be an undirected connected graph with distinct edge weights. Let max_e be the edge with maximum weight and min_e be the edge with minimum weight. Which of the following is false?

a. Every minimum spanning tree of 'G' must contain min_e
b. If max_e is in a minimum spanning tree, then its removal must disconnect 'G'
c. No minimum spanning tree contains max_e
d. 'G' has a unique minimum spanning tree

Answer: **a. is true** because we always start with the edge with least weight
b. is also true because if we have worst case tree like below, we will have to add the edge with max weight so that the tree remains connected, otherwise it will be disconnected.



c.is false because we just saw that the max_e can be added to MST in worst case.

d.is true because all the weights are distinct

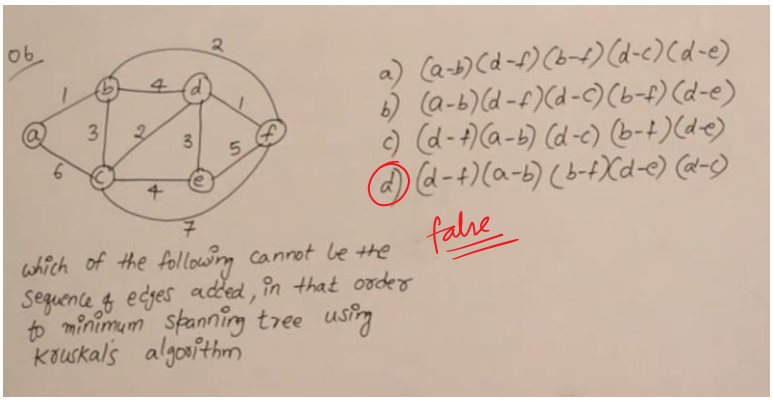
Answer : C.

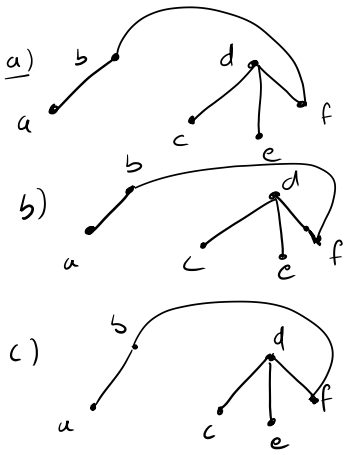
If the question is modified where we are not given if the tree has distinct weight for all edges then (A) and (B) are true and (C) and (D) are false.

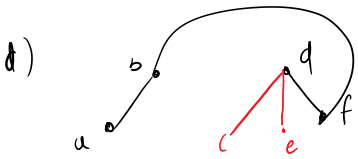
Gate 2007: Let 'w' be the minimum weight among all weights in an undirected connected graph. Let 'e' be a specific edge of weight 'w'. Which of the following is FALSE?

a. There is a minimum spanning tree containing 'e' ← true
b. If 'e' is not in a minimum spanning tree 'T', then in the cycle formed by adding 'e' to 'T', all edges have the same weight ← true
c. Every minimum spanning tree has an edge weight of 'w' ← true
d. 'e' is present in every minimum spanning tree ← false

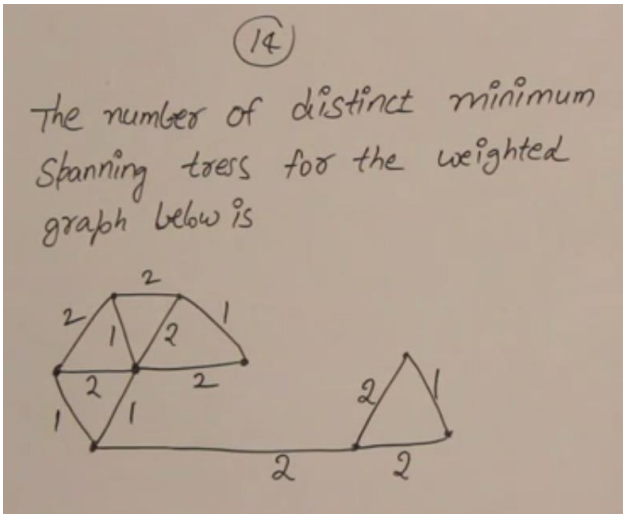
Gate 2006:





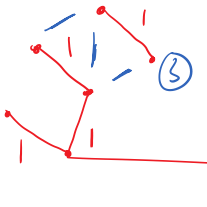


Gate 2014:



① all 1's will be added (there are no cycles)

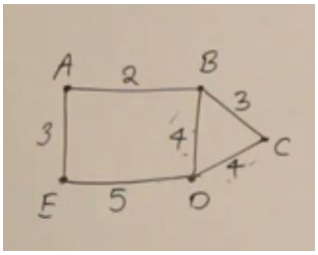
• → choices



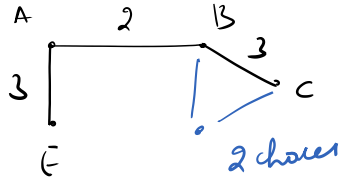
total choices = 3×2 = 6

6 graphs MST

has to be added so the graph is not disconnected



Kruskal's

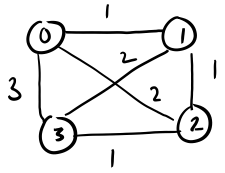


2 choices

∴ total spanning trees possible = 2

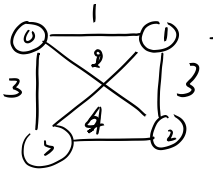
4) A complete, undirected, weighted graph 'G' is given on the vertex {0,1,...n-1} for any fixed 'n'. Draw the minimum spanning tree of G if
a) the weight of the edge (u,v) is |u-v|
b) The weight of the edge (u,v) is (u+v)

a) n=4 → 0 —1— 1 —1— 2 - - - n-1

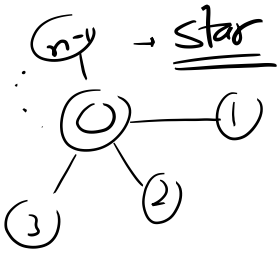


linear

b)



→



star

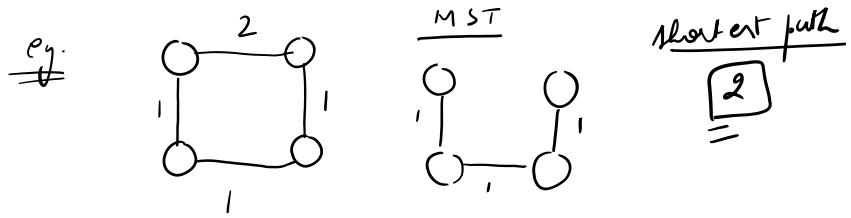
FINDING THE SHORTEST PATH IN A DIRECTED GRAPH (Greedy)

DIJKSTRA'S ALGORITHM or SINGLE SOURCE SHORTEST PATH ALGORITHM

Finding a shortest path is different than finding the minimum spanning tree.

In minimum cost spanning tree:

1. There is no concept of source and destination but in shortest path problem we have a source from where we will start and reach the destination using the shortest path
2. Minimum cost spanning tree is not going to solve the shortest path problem. They may give you shortest path but that will be purely coincidental.



Problem: There will be a graph which will be weighted and directed and a source and a destination are given. We need to reach the destination from the source using the shortest path.

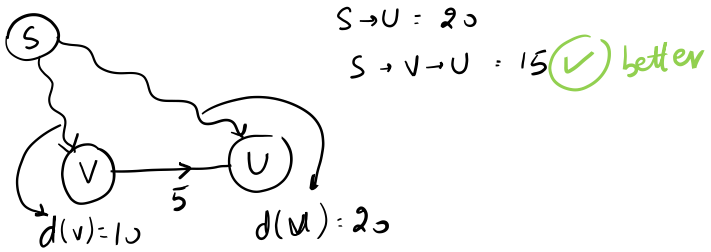
This is also called *Single source shortest path* problem. Here we find out the shortest path from one source to all the other nodes. ☺

Let's build the algorithm in parts.

One of the operations that we use is called **RELAXING AN EDGE.**

Relaxing an edge

We are in the algorithm until some phase and during this we found out that from S to reach V the total distance taken is d(V) = 10 and from S to reach U the total distance taken is d(U) = 20. Let's say there is an edge between V and U with a weight of 5. Then relaxing this edge will mean: in case if I use this V -> U edge in the calculation of minimum path from S to U or V to U then is there going to be any better result?



We will use the relax operation:

$$if\ d(u) > d(v) + c(u,v)\ then,$$

$$d(a) = d(v) + c(v,u)$$

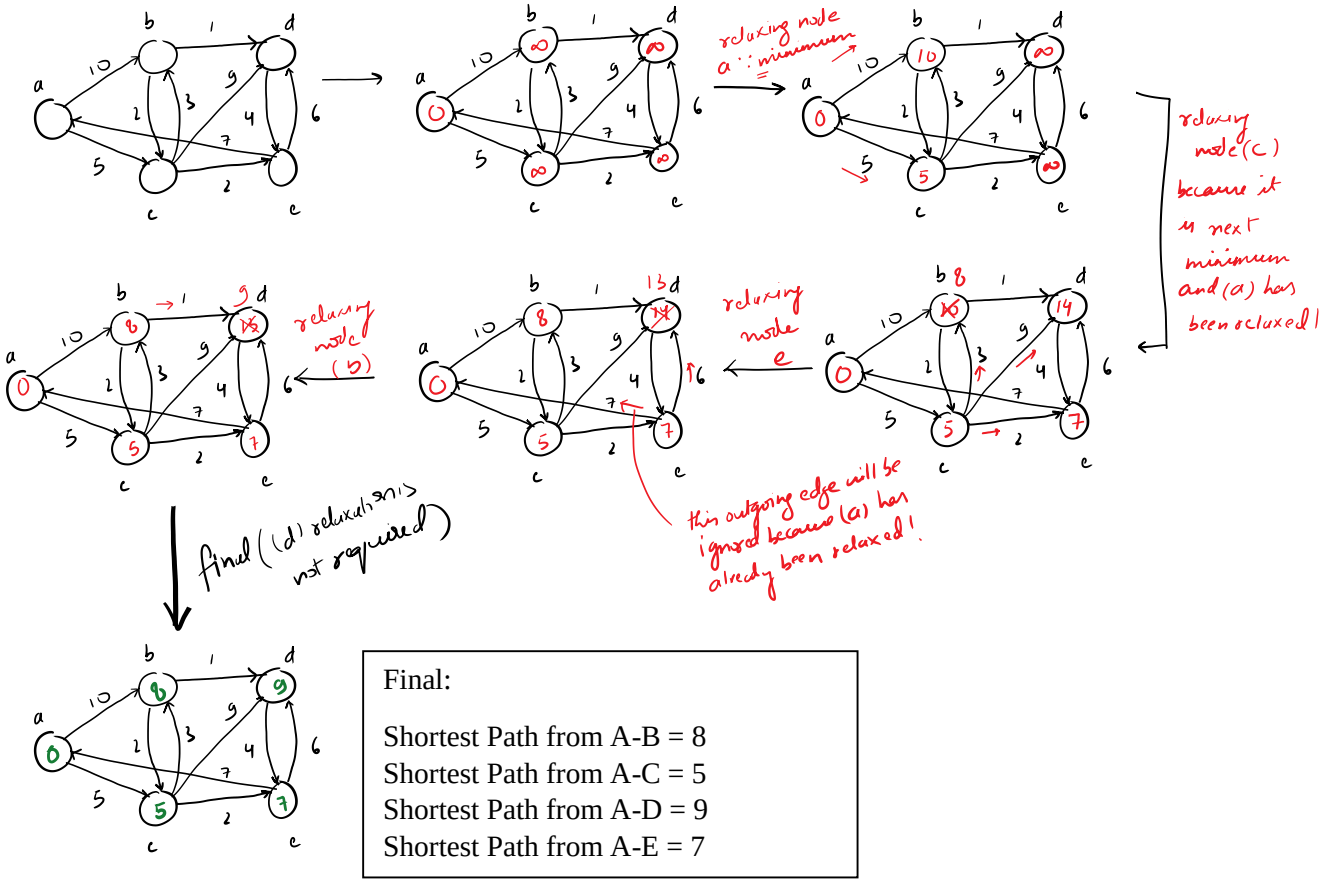
Dijkstra's algorithm should not be used when the edge weights are negative

Steps for Dijkstra's algorithm

1. Make sure there are no edges with negative weights
2. Take source node, the distance of the source node to itself is going to be 0
3. Take all the nodes and make the distance from source to all of them as ∞
4. From the source node, see what outgoing edges are there and relax them.
5. Take the next node which has the minimum of all the current path and has not been calculate the relaxation before.
6. Repeat step 4 until all the outgoing edges of all the nodes have been relaxed.
7. Constantly ask question: "If I relax this node will the distance get better (better means lesser)."

Let's understand with and example.

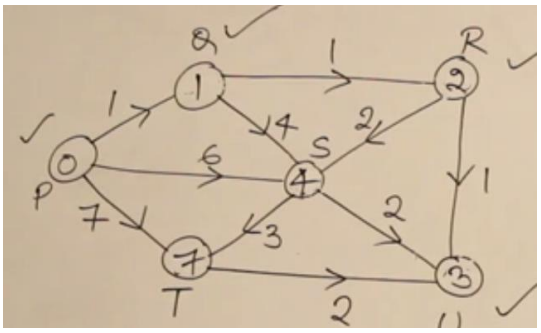
Example: Calculate single source shortest path in the following graph



Final:

Shortest Path from A-B = 8
Shortest Path from A-C = 5
Shortest Path from A-D = 9
Shortest Path from A-E = 7

Example 2: What is the order of relaxation?



Order: P,Q,R,U,S,T

DIJKSTRA'S ALGORITHM

Let's write the Dijkstra's Algorithm, but before let's see some points

1. Since we are extracting the minimum for relaxation, heap sounds like a good data structure to implement Dijkstra's algorithm.
2. Relaxing operation is nothing but the *decrease_key* operation in the heap.

DIJKSTRA(G, W, S)

1. Initialize_single_source(G,S) ← O(V)
2. S = ϕ
3. Q = G.V ← Build heap = O(V)
4. While Q ≠ ϕ runs V times
   a. U = Extract_Min(Q) ← O(logV)
   b. S = $S \cup \{Q\}$
   c. For each vertex $v \epsilon G \cdot Adj(U)$
      i. Relax(u, r,w) ← O(logV)

S = set of all vertices whose shortest path has been decided

Relax() is run on each edge at most one and every call to Relax() runs Decrease_Key() in heap.

→ Extract_min = O(VlogV) will run

→ Relax( ) will run = O(ElogV)

why?

∴ Time complexity is defined below

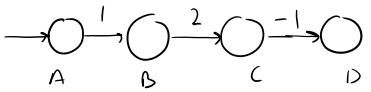
Time complexity for Dijkstra's algorithm = O(V + V + VlogV + ElogV) (using aggregate analysis)

⇨ **O(ElogV) (WORST CASE SCENARIO)**

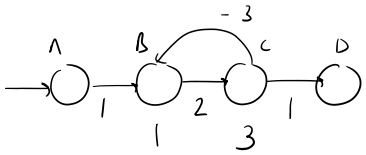
NEGATIVE WEIGHT EDGES AND DIJKSTRA'S ALGORITHM

Shortest paths will not be found when:

1. The graph is disconnected
2. If the graph has negative weight cycles



A-D : 2 ✓ Dijkstra's applicable



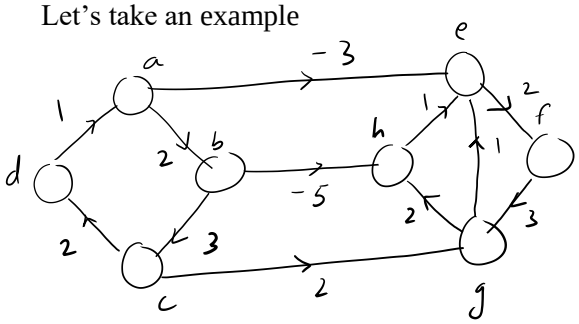
Dijkstra's not applicable

1 3
0 2
-1 1
-2 0
-3 -1

Important note: *If we give Dijkstra's algorithm* ***graphs with negative weight cycles*** *then* ***it is will only work in some cases and find the shortest path.*** *However, if there are graphs with only* ***negative edges and no negative weight cycles****, the algorithm* ***will be able to find shortest path****.*

This is because Dijkstra's algorithm doesn't have the power to differentiate if the graph has negative cycles or not. If an algorithm has this power, then we can find the shortest paths in graphs with negative cycles too. ***Therefore, if there is a cycle with negative weights, then Dijkstra's will not be able to decrease the value of the key as the key has already been deleted from the heap. So Dijkstra's algorithm will fail whenever we delete a note and then for the same node later on we have to decrease the value.***

Let's take an example



Gate 2008

Let's understand with the table

Nodes	A	B	C	D	E	F	G	H
Initialization	**0**	∞	∞	∞	∞	∞	∞	∞
Delete A		2	∞	∞	**-3**	∞	∞	∞
Delete E		2	∞	∞		**-1**	∞	∞
Delete F		**2**	∞	∞			2	∞
Delete B			5	∞			2	**-3**
Delete H			5	∞			**2**	
Delete G			**5**	∞				
Delete C				**7**				
Delete D								

Order: AEFBHGCD
Shortest distances:

A-A = 0	A-E = -3
A-B = 2	A-F = -1
A-C = 5	A-G = 2
A-D = 7	A-H = -3

Now let’s talk about the algorithm that has the capability to find out whether a given graph has any negative weight cycles in it or not.

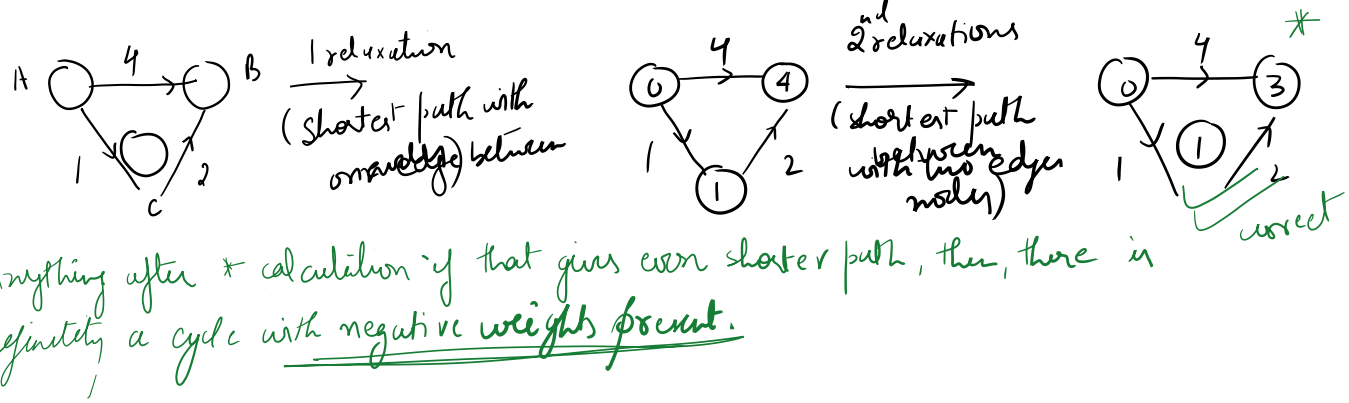
BELLMAN FORD ALGORITHM

This algorithm can say that "No I can't find the shortest path because the negative weight cycle is present" and also it can find out the shortest path when the negative weight cycle is not present. Such a power doesn't come cheap.

Compared to Dijkstra's algorithm, Bellman Ford algorithm is a bit slower so its complexity is more compared to Dijkstra's.

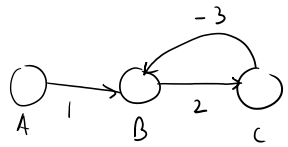
***Bellman Ford works on this**: If you have a graph with 'n' nodes then the shortest path in the graph will never contain more than "n-1" edges. If it is more than n-1 and the shortest path already calculated for the node is decreasing, then there is definitely a cycle with negative weights present.*

This is the basic algorithm which tells about the negative cycles in the graph.

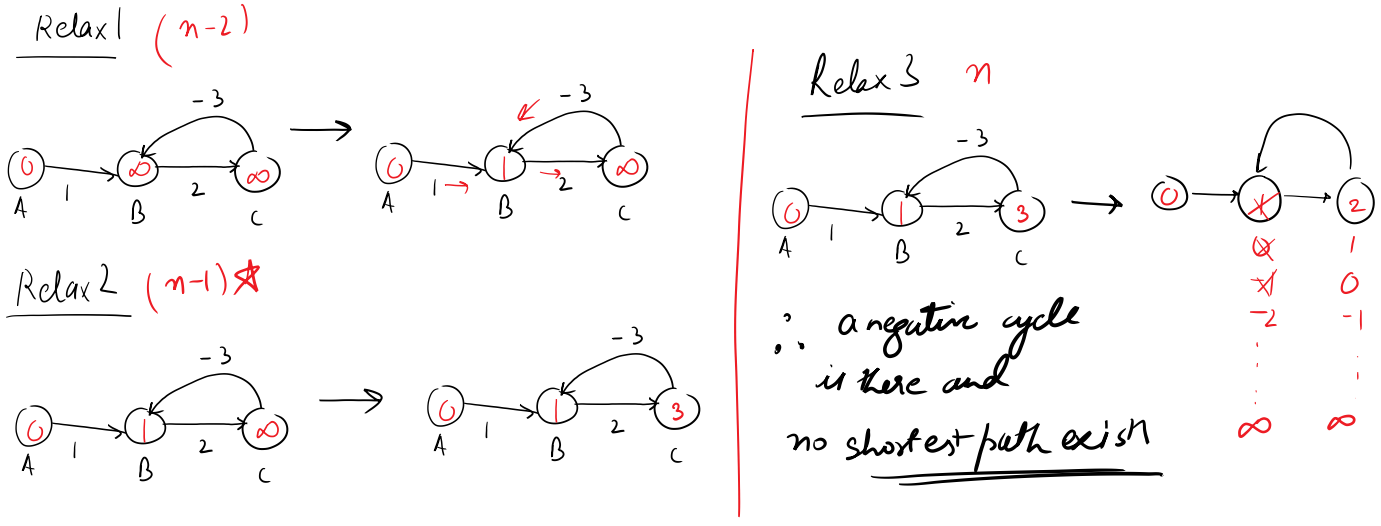


Let's see with an example how Bellman Ford algorithm is going to tell if the negative weight cycle is present or not.

Example:



Number of nodes = 3, so Number of times each edge should be relaxed = 3 – 1 = 2 times.
Bellman Ford algorithm will run : (V-1) + 1 (check the negative cycle) = V times.



Total number of relax operations by Bellman Ford is:

((V+1) -1) x E = VE x (Relax()) times. **Therefore, the time complexity = O(VE)**

Here Relax() will be in an array instead of a heap because for Bellman Ford we don't need a heap as there is no **decrease_key** or **Extract_min** operation. This relax can be done is O(1) or constant time. Therefore, total complexity is O(VE) which is higher than the Dijkstra's algorithm.

Let's take a look at the formal algorithm.

```
BELLMAN_FORD(G, w, S)
{
    1. Initialize_single_source(G, S)
    2. For i=1 to |G.V| -1
        a. For each edge (u, v) ϵ G.E
            i. RELAX(u, v, w)
    3. For each edge (u, v) ϵ G.E
        a. If(v.d > u.d + w(u, v))
            i. Return FALSE
    4. Return TRUE
}
```

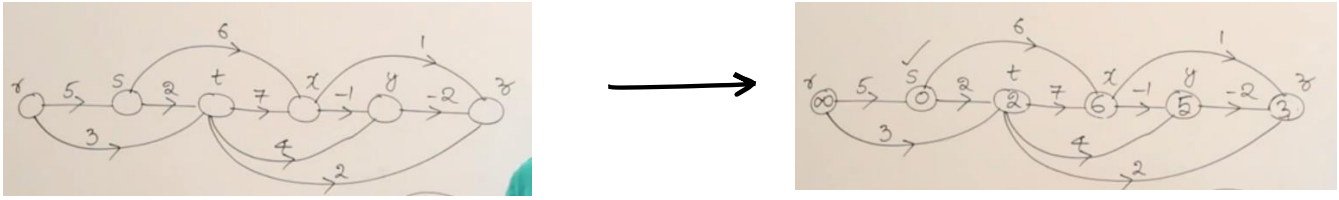
Complexity:
$O(V + VE + E) = O(VE)$

DIRECTED ACYCLIC GRAPH

As the name suggests, it is a directed graph where there are no cycles.

To find the shortest path in Directed acyclic graphs or DAGs

1. Make sure that the graph is topologically sorted (covered in data structure) which take O(V+E) time. After topologically sorting the graph, all the edges will move from left to right.
2. Take each vertex one by one and relax all the edges outgoing from that edge



Analysis:

1. For topological sorting time: O(V+E)
2. For relaxing all the edges outgoing from all the vertices (basically means relaxing all the edges once) = O(E)
3. **Time complexity = O(V+E)**

SHORTEST PATH IN DIRECTED ACYCLIC GRAPHS

DAG_SHORTEST_PATHS(G, W, S)

1. Topologically sort the vertices of 'G' ← O(V+E)
2. Initialize_Single_Source(G, S) ← O(V)
3. For each vertex u, taken in topologically sorted order
    a. For each vertex v ϵ G.adj[u]
        i. Relax(u, v, W)

} O(E)

because array implementation of data structure

Note: ***Don't assume that the fastest shortest path algorithm is DAG one because that will work only in specific cases. So we have seen:***

Dijkstra's Algorithm: O(ElogV)

Bellman Ford Algorithm: O(VE)

DAG Shortest Path: O(V+E)

Use DAG Shortest path algorithm only when you are sure that you don't have any cycles in your graph. Therefore, this will work also when we have negative weights.

This concludes our discussion on optimization with GEEDY ALGORITHMS. Next up is Dynamic Pogramming.