Paper: Analysis & Design of Algorithms

Chapter 1: Introduction to Algorithm

Concept of algorithm

An algorithm is a set of rules for carrying out calculation that transform the input to the output.

A common man's belief is that a computer can do anything and everything that he imagines. It is very difficult to make people realize that it is not really the computer but the man behind computer who does everything.

In the modern internet world man feels that just by entering what he wants to search into the computers he can get information as desired by him. He believes that, this is done by computer. A common man seldom understands that a man made procedure called search has done the entire job and the only support provided by the computer is the executional speed and organized storage of information.

In the above instance, a designer of the information system should know what one frequently searches for. He should make a structured organization of all those details to store in memory of the computer. Based on the requirement, the right information is brought out. This is accomplished through a set of instructions created by the designer of the information system to search the right information matching the requirement of the user. This set of instructions is termed as program. It should be evident by now that it is not the computer, which generates automatically the program but it is the designer of the information system who has created this.

Thus, the program is the one, which through the medium of the computer executes to perform all the activities as desired by a user. This implies that programming a computer is more important than the computer itself while solving a problem using a computer and this part of programming has got to be done by the man behind the computer. Even at this stage, one should not quickly jump to a conclusion that coding is programming. Coding is perhaps the last stage in the process of programming. Programming involves various activities form the stage of conceiving the problem upto the stage of creating a model to solve the problem. The formal representation of this model as a sequence of instructions is called an algorithm and coded algorithm in a specific computer language is called a program.

One can now experience that the focus is shifted from computer to computer programming and then to creating an algorithm. This is algorithm design, heart of problem solving.

Characteristics of an algorithm

Every algorithm should have the following five characteristic feature

1. Input

2. Output
3. Definiteness
4. Effectiveness
5. Finiteness

Therefore, an algorithm can be defined as a sequence of definite and effective instructions, which terminates with the production of correct output from the given input.
In other words, viewed little more formally, an algorithm is a step by step formalization of a mapping function to map input set onto an output set.

The problem of writing down the correct algorithm for the above problem of brushing the teeth is left to the reader.

For the purpose of clarity in understanding, let us consider the following examples.

Example 1:

Problem : finding the largest value among n>=1 numbers.

Input : the value of n and n numbers

Output : the largest value

Steps :

1. Let the value of the first be the largest value denoted by BIG
2. Let R denote the number of remaining numbers. R=n-1
3. If R != 0 then it is implied that the list is still not exhausted. Therefore look the next number called NEW.
4. Now R becomes R-1
5. If NEW is greater than BIG then replace BIG by the value of NEW
6. Repeat steps 3 to 5 until R becomes zero.
7. Print BIG
8. Stop

End of algorithm

- **Analyze the algorithm**
  - Time Complexity : time needed to execute the algorithm
    - Worse case, best case, average case.
    - For some algorithms, worst case occurs often, average case is often roughly as bad as the worst case. So generally, worse case running time.
  - Space Complexity: space needed to execute the algorithm

- Worst case
  - Provides an upper bound on running time
  - An absolute guarantee
- Average case
  - Provides the expected running time
- Best case
  - Provides an lower bound on running time

Asymptotic notation

O-notation (upper bounds):

We write $f(n) = O(g(n))$ if there exist constants $c > 0$, $n_0 > 0$ such that $0 \leq f(n) \leq cg(n)$ for all $n \geq n_0$.

EXAMPLE: $2n^2 = O(n^3)$ $(c = 1, n_0 = 2)$

functions, not values

Definition

$O(g(n)) = \{ f(n) :$ there exist constants $c > 0$, $n_0 > 0$ such that $0 \leq f(n) \leq cg(n)$ for all $n \geq n_0 \}$

Convention: A set in a formula represents an anonymous function in the set.

EXAMPLE: $f(n) = n^3 + O(n^2)$
means
$f(n) = n^3 + h(n)$
for some $h(n) \in O(n^2)$.

EXAMPLE: $n^2 + O(n) = O(n^2)$
means
for any $f(n) \in O(n)$:
$n^2 + f(n) = h(n)$
for some $h(n) \in O(n^2)$.

Ω-notation (lower bounds)

O-notation is an *upper-bound* notation. It makes no sense to say $f(n)$ is at least $O(n^2)$.

$\Omega(g(n)) = \{ f(n) :$ there exist constants $c > 0, n_0 > 0$ such that $0 \le cg(n) \le f(n)$ for all $n \ge n_0 \}$

Θ-notation (tight bounds)

$$\Theta(g(n)) = O(g(n)) \cap \Omega(g(n))$$

EXAMPLE: $\frac{1}{2}n^2 - 2n = \Theta(n^2)$

o-notation and ω-notation

O-notation and Ω-notation are like $\le$ and $\ge$.
o-notation and ω-notation are like $<$ and $>$.

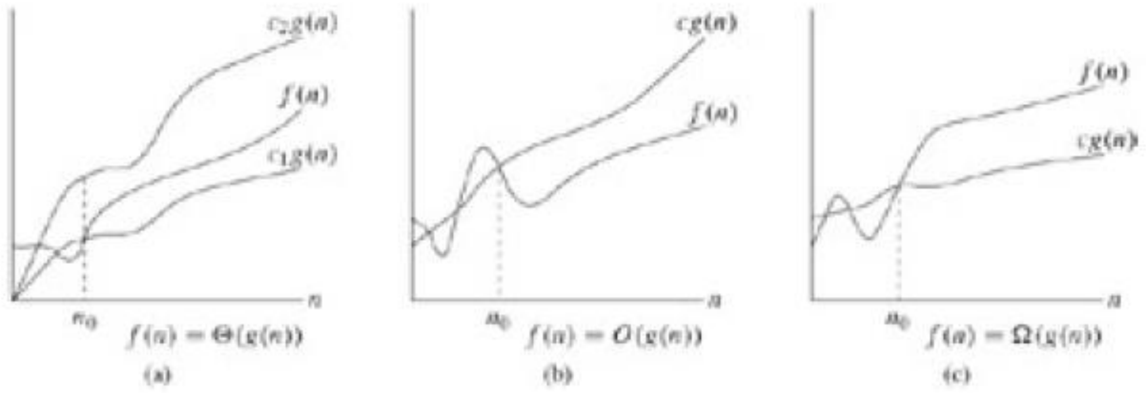
$o(g(n)) = \{ f(n) :$ for any constant $c > 0$,
there is a constant $n_0 > 0$
such that $0 \le f(n) < cg(n)$
for all $n \ge n_0 \}$

EXAMPLE: $2n^2 = o(n^3)$ $(n_0 = 2/c)$

O-notation and Ω-notation are like $\leq$ and $\geq$.
o-notation and ω-notation are like $<$ and $>$.

$\omega(g(n)) = \{ f(n)$: for any constant $c > 0$,
there is a constant $n_0 > 0$
such that $0 \leq cg(n) < f(n)$
for all $n \geq n_0$ $\}$

EXAMPLE: $\sqrt{n} = \omega(\lg n) \quad (n_0 = 1 + 1/c)$



Transitivity:

-

$$f(n) = \Theta(g(n)) \text{ and } g(n) = \Theta(h(n)) \text{ imply } f(n) = \Theta(h(n)),$$
$$f(n) = O(g(n)) \text{ and } g(n) = O(h(n)) \text{ imply } f(n) = O(h(n)),$$
$$f(n) = \Omega(g(n)) \text{ and } g(n) = \Omega(h(n)) \text{ imply } f(n) = \Omega(h(n)),$$
$$f(n) = o(g(n)) \text{ and } g(n) = o(h(n)) \text{ imply } f(n) = o(h(n)),$$
$$f(n) = \omega(g(n)) \text{ and } g(n) = \omega(h(n)) \text{ imply } f(n) = \omega(h(n)).$$

Reflexivity:

-

$$f(n) = \Theta(f(n)),$$
$$f(n) = O(f(n)),$$
$$f(n) = \Omega(f(n)).$$

Symmetry:

$$f(n) = \Theta(g(n)) \text{ if and only if } g(n) = \Theta(f(n)).$$

Transpose symmetry:

•

$$f(n) = O(g(n)) \text{ if and only if } g(n) = \Omega(f(n)),$$
$$f(n) = o(g(n)) \text{ if and only if } g(n) = \omega(f(n)).$$

Example: $2n^2 = O(n^3)$, with $c = 1$ and $n0 = 2$.
Examples of functions in $O(n^2)$:
n^2
$n^2 + n$
$n^2 + 1000n$
$1000n^2 + 1000n$
Also,
n
$n/1000$
$n^{1.99999}$
$n^2/ \lg \lg \lg n$

***A recurrence** is a function is deÞned in terms of*
• one or more base cases, and
• itself, with smaller arguments.

Substitution method
1. Guess the solution.
2. Use induction to Þnd the constants and show that the solution works.

Recursion trees
Use to generate a guess. Then verify by substitution method.

Master method
Used for many divide-and-conquer recurrences of the form
T (n) = aT (n/b) + f (n) , where $a \geq 1$, $b > 1$, and $f (n) > 0$.

The details are :

Substitution Method

The most general method:

1. ***Guess*** the form of the solution.
2. ***Verify*** by induction.
3. ***Solve*** for constants.

EXAMPLE: $T(n) = 4T(n/2) + n$

- [Assume that $T(1) = \Theta(1)$.]
- Guess $O(n^3)$. (Prove O and Ω separately.)
- Assume that $T(k) \le ck^3$ for $k < n$.
- Prove $T(n) \le cn^3$ by induction.

Example of Substitution

$$\begin{aligned} T(n) &= 4T(n/2) + n \\ &\le 4c(n/2)^3 + n \\ &= (c/2)n^3 + n \\ &= cn^3 - ((c/2)n^3 - n) \longleftarrow \textit{desired} - \textit{residual} \\ &\le cn^3 \longleftarrow \textit{desired} \end{aligned}$$

whenever $(c/2)n^3 - n \ge 0$, for example, if $c \ge 2$ and $n \ge 1$.

residual

- We must also handle the initial conditions, that is, ground the induction with base cases.
- ***Base:*** $T(n) = \Theta(1)$ for all $n < n_0$, where n_0 is a suitable constant.
- For $1 \le n < n_0$, we have "$\Theta(1)$" $\le cn^3$, if we pick c big enough.

A tight bound

We shall prove that $T(n) = O(n^2)$.

Assume that $T(k) \le ck^2$ for $k < n$:

$$\begin{aligned}
T(n) &= 4T(n/2) + n \\
&\le 4c(n/2)^2 + n \\
&= cn^2 + n \\
&= \cancel{O(n^2)} \quad \textbf{\textit{Wrong!}} \text{ We must prove the I.H.} \\
&= cn^2 - (-n) \quad [\text{ desired} - \text{residual }] \\
&\le cn^2 \quad \text{for } \textbf{\textit{no}} \text{ choice of } c > 0. \text{ Lose!}
\end{aligned}$$

IDEA: Strengthen the inductive hypothesis.

- ***Subtract*** a low-order term.

Inductive hypothesis: $T(k) \le c_1k^2 - c_2k$ for $k < n$.

$$\begin{aligned}
T(n) &= 4T(n/2) + n \\
&= 4(c_1(n/2)^2 - c_2(n/2)) + n \\
&= c_1n^2 - 2c_2n + n \\
&= c_1n^2 - c_2n - (c_2n - n) \\
&\le c_1n^2 - c_2n \quad \text{if } c_2 \ge 1.
\end{aligned}$$

Pick c_1 big enough to handle the initial conditions.

Recursive Tree Method

- A recursion tree models the costs (time) of a recursive execution of an algorithm.
- The recursion-tree method can be unreliable, just like any method that uses ellipses (…).
- The recursion-tree method promotes intuition, however.
- The recursion tree method is good for generating guesses for the substitution method.

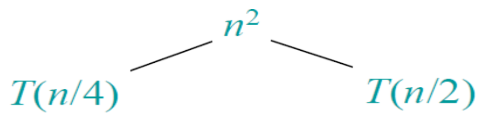
EXAMPLE SOLVED:

Solve $T(n) = T(n/4) + T(n/2) + n^2$:

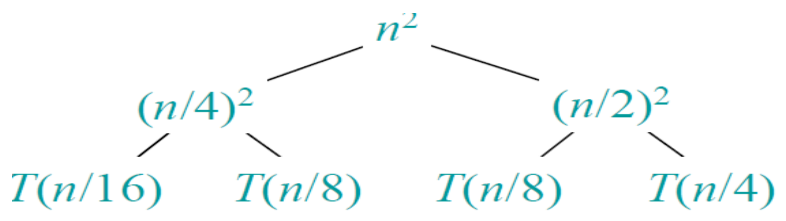
Step 1:

$$T(n)$$

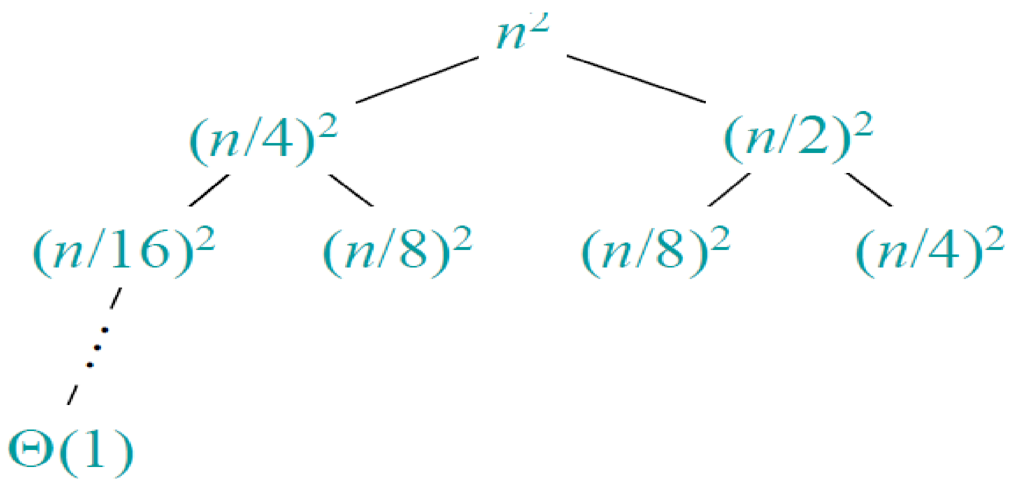
Step 2:



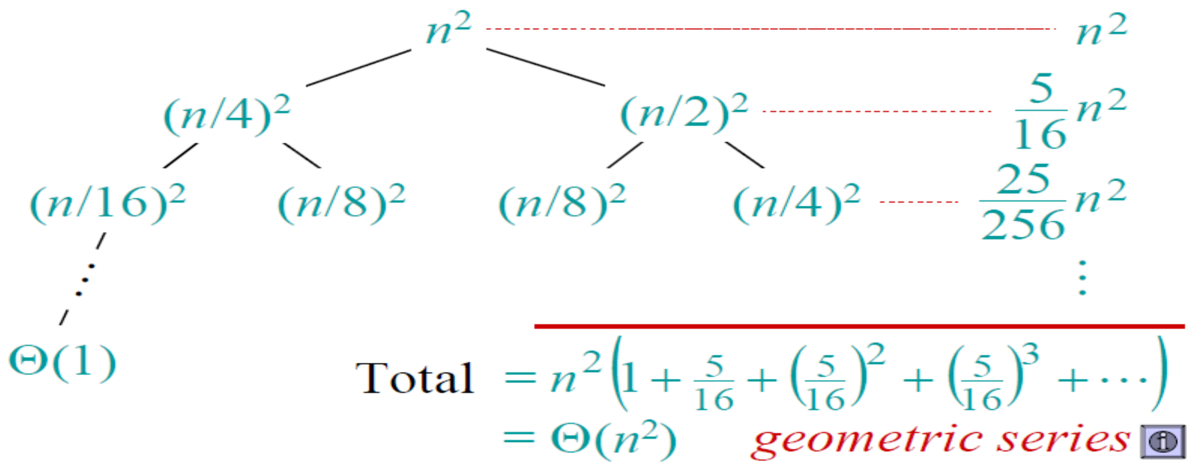
Step 3:



Step 4:



Step 5:



Master Method

The master method applies to recurrences of the form

$$T(n) = a\,T(n/b) + f(n)\ ,$$

where $a \geq 1$, $b > 1$, and f is asymptotically positive.

Three Common Cases

Compare $f(n)$ with $n^{\log_b a}$:

1. $f(n) = O(n^{\log_b a - \varepsilon})$ for some constant $\varepsilon > 0$.
   - $f(n)$ grows polynomially slower than $n^{\log_b a}$ (by an n^{ε} factor).

   Solution: $T(n) = \Theta(n^{\log_b a})$.

2. $f(n) = \Theta(n^{\log_b a} \lg^k n)$ for some constant $k \geq 0$.
   - $f(n)$ and $n^{\log_b a}$ grow at similar rates.

   Solution: $T(n) = \Theta(n^{\log_b a} \lg^{k+1} n)$.

3. $f(n) = \Omega(n^{\log_b a + \varepsilon})$ for some constant $\varepsilon > 0$.
   - $f(n)$ grows polynomially faster than $n^{\log_b a}$ (by an n^{ε} factor),

   and $f(n)$ satisfies the ***regularity condition*** that $af(n/b) \leq cf(n)$ for some constant $c < 1$.

   Solution: $T(n) = \Theta(f(n))$.

Ex. $T(n) = 4T(n/2) + n$
$a = 4,\ b = 2 \Rightarrow n^{\log_b a} = n^2;\ f(n) = n.$
CASE 1: $f(n) = O(n^{2-\varepsilon})$ for $\varepsilon = 1$.
$\therefore\ T(n) = \Theta(n^2).$

Ex. $T(n) = 4T(n/2) + n^2$
$a = 4,\ b = 2 \Rightarrow n^{\log_b a} = n^2;\ f(n) = n^2.$
CASE 2: $f(n) = \Theta(n^2 \lg^0 n)$, that is, $k = 0$.
$\therefore\ T(n) = \Theta(n^2 \lg n).$

Ex. $T(n) = 4T(n/2) + n^3$
$a = 4, b = 2 \Rightarrow n^{\log_b a} = n^2; f(n) = n^3.$
CASE 3: $f(n) = \Omega(n^{2+\varepsilon})$ for $\varepsilon = 1$
and $4(n/2)^3 \le cn^3$ (reg. cond.) for $c = 1/2$.
$\therefore\ T(n) = \Theta(n^3)$.

Ex. $T(n) = 4T(n/2) + n^2/\lg n$
$a = 4, b = 2 \Rightarrow n^{\log_b a} = n^2; f(n) = n^2/\lg n.$
Master method does not apply. In particular, for every constant $\varepsilon > 0$, we have $n^{\varepsilon} = \omega(\lg n)$.

Chapter 2: Divide-and-conquer

Divide-and-conquer is a top-down technique for designing algorithms that consists of dividing the problem into smaller sub problems hoping that the solutions of the sub problems are easier to find and then composing the partial solutions into the solution of the original problem.

Little more formally, divide-and-conquer paradigm consists of following major phases:

- **Divide** : divide the problem into several sub-problems that are similar to the original problem but smaller in size,
- Solve the sub-problem recursively (successively and independently), If sub problem is small enough, solve it in a straightforward manner (base case).
- **Combine:** Combine these solutions to sub problems to create a solution to the original problem.

Divide and Conquer Examples

Binary Search
Heap Construction
Tower of Hanoi
Quick Sort
Merge Sort
Multiplying large Integers
Exponentiation
Matrix Multiplication (Strassen’s way)

Binary Search (simplest application of divide-and-conquer)

Binary Search is an extremely well-known instance of divide-and-conquer paradigm. Given an ordered array of n elements, the basic idea of binary search is that for a given element we "probe" the middle element of the array. We continue in either the lower or upper segment of the array, depending on the outcome of the probe until we reached the required (given) element.

Problem Let $A[1 \ . \ . \ . \ n]$ be an array of non-decreasing sorted order; that is $A\ [i] \leq A\ [j]$ whenever $1 \leq i \leq j \leq n$. Let *'q'* be the query point. The problem consist of finding *'q'* in the array *A*. If *q* is not in *A*, then find the position where *'q'* might be inserted.

Formally, find the index i such that $1 \leq i \leq n+1$ and $A[i\text{-}1] < x \leq A[i]$.

Binary Search

Look for *'q'* either in the first half or in the second half of the array *A*. Compare *'q'* to an element in the middle, $\lceil n/2 \rceil$, of the array. Let $k = \lceil n/2 \rceil$. If $q \leq A[k]$, then search in the $A[1 \ . \ . \ . \ k]$; otherwise search $T[k+1 \ . \ . \ n]$ for *'q'*. Binary search for q in subarray $A[i \ . \ . \ j]$ with the promise that

```
$A[i-1] < x \leq A[j]$
If $i = j$ then
    return $i$ (index)
$k = (i + j)/2$
if $q \leq A\ [k]$
```

```
    then return Binary Search [$A$ [$i$-$k$], $q$]
    else return Binary Search [$A$[$k$+$1$ . . $j$], $q$]
```

Analysis

Binary Search can be accomplished in logarithmic time in the worst case , i.e., $T(n) = \theta(log\ n)$. This version of the binary search takes logarithmic time in the best case.

Quick Sort

The basic version of quick sort algorithm was invented by C. A. R. Hoare in 1960 and formally introduced quick sort in 1962. It is used on the principle of divide-and-conquer. Quick sort is an algorithm of choice in many situations because it is not difficult to implement, it is a good "general purpose" sort and it consumes relatively fewer resources during execution.

Good points

- It is in-place since it uses only a small auxiliary stack.
- It requires only n log(n) time to sort n items.
- It has an extremely short inner loop
- This algorithm has been subjected to a thorough mathematical analysis, a very precise statement can be made about performance issues.

Bad Points

- It is recursive. Especially if recursion is not available, the implementation is extremely complicated.
- It requires quadratic (*i.e.*, n^2) time in the worst-case.
- It is fragile i.e., a simple mistake in the implementation can go unnoticed and cause it to perform badly.

Quick sort works by partitioning a given array $A[p\ .\ .\ r]$ into two non-empty sub array $A[p\ .\ .\ q]$ and $A[q+1\ .\ .\ r]$ such that every key in $A[p\ .\ .\ q]$ is less than or equal to every key in $A[q+1\ .\ .\ r]$. Then the two subarrays are sorted by recursive calls to Quick sort. The exact position of the partition depends on the given array and index q is computed as a part of the partitioning procedure.

QuickSort

```
1. If $p < r$ then
2.     $q$ Partition ($A$, $p$, $r$)
3.     Recursive call to Quick Sort ($A$, $p$, $q$)
4.     Recursive call to Quick Sort ($A$, $q + r$, $r$)
```

Note that to sort entire array, the initial call Quick Sort (A, 1, length[A])

As a first step, Quick Sort chooses as pivot one of the items in the array to be sorted. Then array is then partitioned on either side of the pivot. Elements that are less than or equal to pivot will move toward the left and elements that are greater than or equal to pivot will move toward the right.

Partitioning the Array

Partitioning procedure rearranges the subarrays in-place.

PARTITION (A, p, r)

```
1.  $x \leftarrow A[p]$
2.  $i \leftarrow p-1$
3.  $j \leftarrow r+1$
4.  while TRUE do
5.      Repeat $j \leftarrow j-1$
6.      until $A[j] \leq x$
7.      Repeat $i \leftarrow i+1$
8.      until $A[i] \geq x$
9.      if $i < j$
10.         then exchange $A[i] \leftrightarrow A[j]$
11.         else return $j$
```

Partition selects the first key, $A[p]$ as a pivot key about which the array will partitioned:
Keys $\leq A[p]$ will be moved towards the left .
Keys $\geq A[p]$ will be moved towards the right.
The running time of the partition procedure is $\Theta(n)$ where $n = r - p + 1$ which is the number of keys in the array.
Another argument that running time of PARTITION on a subarray of size $\Theta(n)$ is as follows: Pointer i and pointer j start at each end and move towards each other, conveying somewhere in the middle. The total number of times that i can be incremented and j can be decremented is therefore O(n). Associated with each increment or decrement there are O(1) comparisons and swaps. Hence, the total time is O(n).

Array of Same Elements

Since all the elements are equal, the "less than or equal" teat in lines 6 and 8 in the PARTITION (A, p, r) will always be true. this simply means that repeat loop all stop at once. Intuitively, the first repeat loop moves j to the left; the second repeat loop moves i to the right. In this case, when all elements are equal, each repeat loop moves i and j towards the middle one space. They meet in the middle, so $q = Floor(p+r/2)$. Therefore, when all elements in the array $A[p \,.\,.\, r]$ have the same value equal to $Floor(p+r/2)$.

Performance of Quick Sort

The running time of quick sort depends on whether partition is balanced or unbalanced, which in turn depends on which elements of an array to be sorted are used for partitioning.
A very good partition splits an array up into two equal sized arrays. A bad partition, on other hand, splits an array up into two arrays of very different sizes. The worst partition puts only one element in one array and all other elements in the other array. If the partitioning is balanced, the Quick sort runs asymptotically as fast as merge sort. On the other hand, if partitioning is unbalanced, the Quick sort runs asymptotically as slow as insertion sort.

Best Case

The best thing that could happen in Quick sort would be that each partitioning stage divides the array exactly in half. In other words, the best to be a median of the keys in A[p . . r] every time procedure 'Partition' is called. The procedure 'Partition' always split the array to be sorted into two equal sized arrays.
If the procedure 'Partition' produces two regions of size n/2. the recurrence relation is then
$T(n) = T(n/2) + T(n/2) + \Theta(n) \quad = 2T(n/2) + \Theta(n)$

And from case 2 of Master theorem

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

Worst case

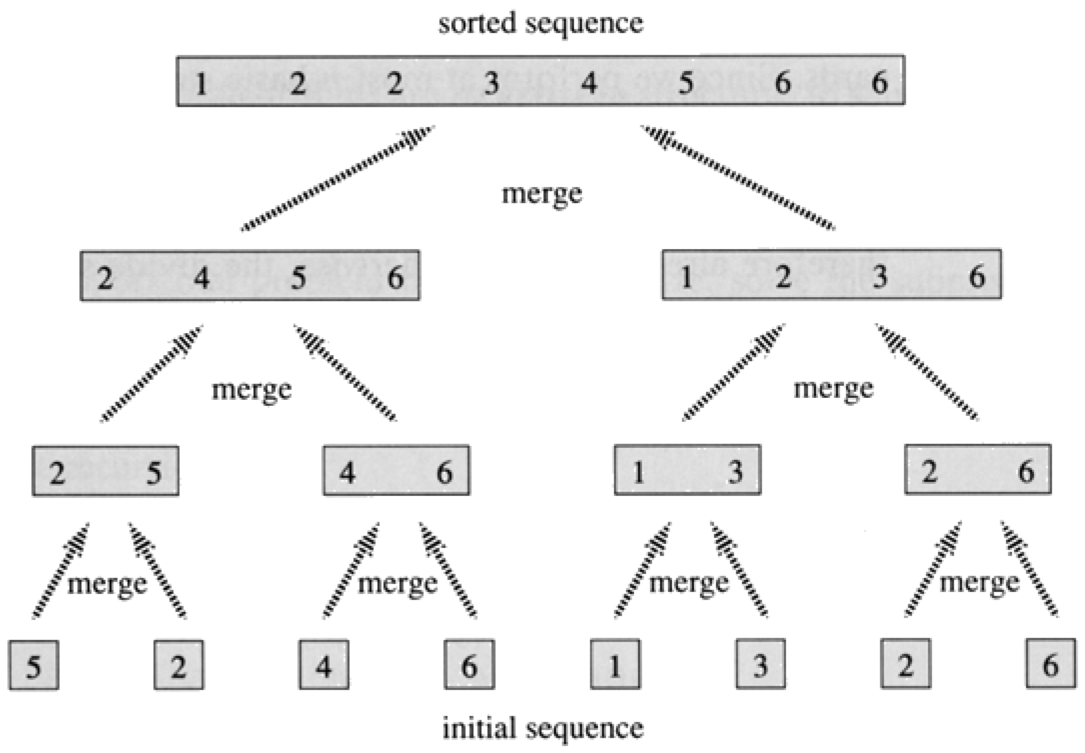
The worst-case occurs if given array A[1 . . n] is already sorted. The PARTITION (A, p, r) call always return p so successive calls to partition will split arrays of length n, n-1, n-2, . . . , 2 and running time proportional to $n + (n-1) + (n-2) + \ldots + 2 = [(n+2)(n-1)]/2 = \Theta(n^2)$. The worst-case also occurs if A[1 . . n] starts out in reverse order.

Merge Sort

Merge-sort is based on the divide-and-conquer paradigm. The Merge-sort algorithm can be described in general terms as consisting of the following three steps:

1. **Divide Step**
   If given array A has zero or one element, return S; it is already sorted. Otherwise, divide A into two arrays, A_1 and A_2, each containing about half of the elements of A.
2. **Recursion Step**
   Recursively sort array A_1 and A_2.
3. Conquer Step
   Combine the elements back in A by merging the sorted arrays A_1 and A_2 into a sorted sequence.

We can visualize Merge-sort by means of binary tree where each node of the tree represents a recursive call and each external nodes represent individual elements of given array A. Such a tree is called Merge-sort tree. The heart of the Merge-sort algorithm is conquer step, which merge two sorted sequences into a single sorted sequence.



To begin, suppose that we have two sorted arrays $A_1[1], A_1[2], \dots, A_1[M]$ and $A_2[1], A_2[2], \dots, A_2[N]$. The following is a direct algorithm of the obvious strategy of successively choosing the smallest remaining elements from A_1 to A_2 and putting it in A.

MERGE (A_1, A_2, A)

```
i.← j 1
A₁[m+1], A₂[n+1] ← INT_MAX
For k ←1 to m + n do
   if A₁[i] < A₂[j]
      then A[k] ← A₁[i]
         i ← i +1
      else
         A[k] ← A₂[j]
            j ← j + 1
```

Merge Sort Algorithm

MERGE_SORT (A)

```
$A_1[1 \,..\, \lfloor n/2 \rfloor] \leftarrow A[1 \,..\, \lfloor n/2 \rfloor]$
$A_2[1 \,..\, \lfloor n/2 \rfloor] \leftarrow A[1 + \lfloor n/2 \rfloor \,..\, n]$
Merge Sort ($A_1$)
Merge Sort ($A_1$)
Merge Sort ($A_1$, $A_2$, A)
```

Analysis

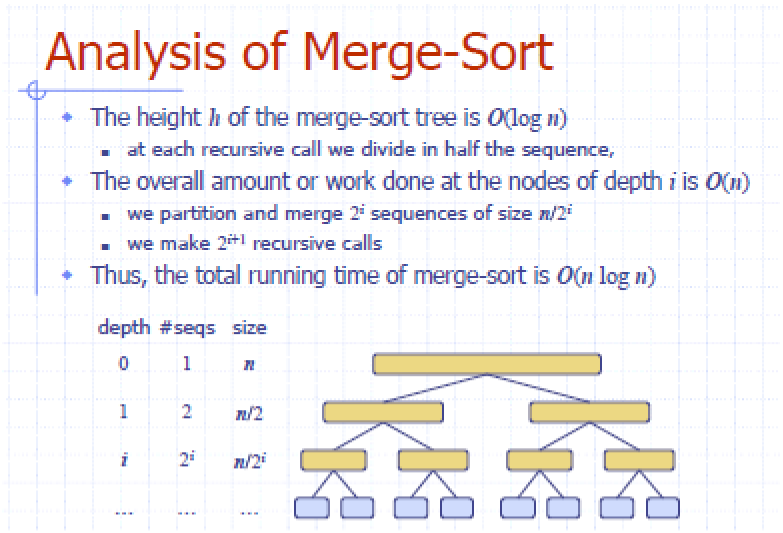
Let T(n) be the time taken by this algorithm to sort an array of n elements dividing A into subarrays A_1 and A_2 takes linear time. It is easy to see that the Merge (A_1, A_2, A) also takes the linear time. Consequently,

$$T(n) = T(\lfloor n/2 \rfloor) + T(\lfloor n/2 \rfloor) + \theta(n)$$

for simplicity

$$T(n) = 2T(n/2) + \theta(n)$$

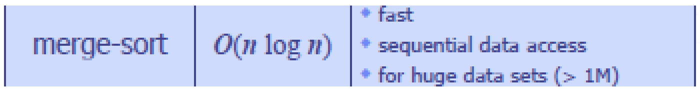
The total running time of Merge sort algorithm is O(n lg n), which is asymptotically optimal like Heap sort, Merge sort has a guaranteed n lg n running time. Merge sort required Θ(n) extra space. Merge is not in-place algorithm. The only known ways to merge in-place (without any extra space) are too complex to be reduced to practical program.



Analysis of Merge-Sort

- The height h of the merge-sort tree is $O(\log n)$
  - at each recursive call we divide in half the sequence,
- The overall amount or work done at the nodes of depth i is $O(n)$
  - we partition and merge 2^i sequences of size $n/2^i$
  - we make 2^{i+1} recursive calls
- Thus, the total running time of merge-sort is $O(n \log n)$

depth	#seqs	size
0	1	n
1	2	$n/2$
i	2^i	$n/2^i$
…	…	…



merge-sort	$O(n \log n)$	• fast • sequential data access • for huge data sets (> 1M)

Chapter 3: Greedy Algorithm

Greedy algorithm make a *locally optimal choice* in hope of getting a *globally optimal solution*.
Greedy-choice property
A globally optimal solution can be arrived at by making a locally optimal (greedy) choice.

Difference between greedy and dynamic programming:
Dynamic programming:
• Make a choice at each step.
• Choice depends on knowing optimal solutions to subproblems. Solve subproblems first.
• Solve bottom-up.
Greedy:
• Make a choice at each step.
• Make the choice before solving the subproblems.
• Solve top-down.

Typically show the greedy-choice property by what we did for activity selection:
• Look at a globally optimal solution.
• If it includes the greedy choice, done.
• Else, modify it to include the greedy choice, yielding another solution that's just as good.

Can get efficiency gains from greedy-choice property.
• Preprocess input to put it into greedy order.
• Or, if dynamic data, use a priority queue.

The knapsack problem is a good example of the difference.
0-1 knapsack problem:
· *n* items.
· Item *i* is worth $\$v_i$, weighs w_i pounds.
· Find a most valuable subset of items with total weight $\leq W$.
· Have to either take an item or not take it.can.t take part of it.
Fractional knapsack problem: Like the 0-1 knapsack problem, but can take fraction of an item.
Both have optimal substructure.
But the fractional knapsack problem has the greedy-choice property, and the 0-1 knapsack problem does not.
To solve the fractional problem, rank items by value/weight: v_i/w_i .

Knapsack Problem

There are *n* items in a store. For i =1,2, . . . , n, item i has weight $w_i > 0$ and worth $v_i > 0$. Thief can carry a maximum weight of *W* pounds in a knapsack. In this version of a problem the items can be broken into smaller piece, so the thief may decide to carry only a fraction x_i of object *i*, where $0 \leq x_i \leq 1$. Item *i* contributes x_iw_i to the total weight in the knapsack, and x_iv_i to the value of the load.

In Symbol, the fraction knapsack problem can be stated as follows.
maximize ${}^{n}\mathbf{S}_{i=1}\, x_iv_i$ subject to constraint ${}^{n}\mathbf{S}_{i=1}\, x_iw_i \leq W$

It is clear that an optimal solution must fill the knapsack exactly, for otherwise we could add a fraction of one of the remaining objects and increase the value of the load. Thus in an optimal solution $^{n}\mathbf{S}_{i=1}\, x_i w_i = W.$

knapsack (*w, v, W*)

```
FOR $i$ =1 to $n$
   do $x[i]$ =0
weight = 0
while weight < $W$
   do $i$ = best remaining item
      IF weight + $w[i] \leq W$
         then $x[i]$ = 1
            weight = weight + $w[i]$
         else
            $x[i]$ = ($w$ - weight) / $w[i]$
            weight = $W$
return $x$
```

Analysis

If the items are already sorted into decreasing order of $v_i / w_i,$ then the while-loop takes a time in $O(n)$
Therefore, the total time including the sort is in $O(n \log n)$.

Minimum Spanning Tree Kruskal's Algorithm:

1. Kruskal's Algorithm is a greedy algorithm because at each step it adds to the forest

   an edge of least possible weight.

2. It uses disjoint set data structures to maintain several disjoint elements. Each set

   Contains the vertices in a tree of the current forest.

3. Using FINDSET we determine whether two vertices u and v belong to the same tree

   The combining of two trees is done by UNION.

4. With each node 'x' we maintain the integer rank[x] which is an upper bound on the

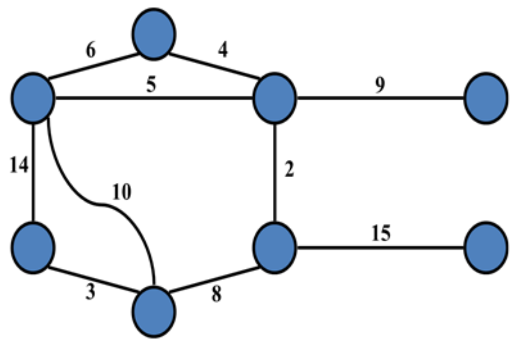
   Height x[the number of edges in the longest path between a descendent leaf and x].

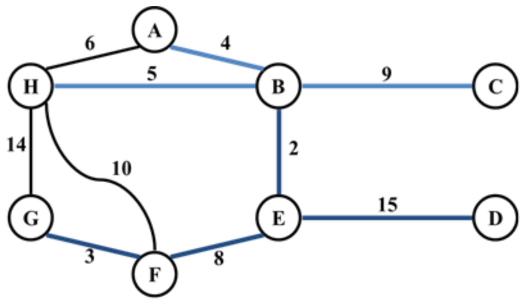
5. **Algorithm**:

```
MST-KRUSKAL(G, w)
1   A ← Ø
2    for each vertex v _ V[G]
3        do MAKE-SET(v)
4    sort the edges of E into nondecreasing order by weight w
5    for each edge (u, v) _ E, taken in nondecreasing order by weight
6        do if FIND-SET(u) ≠ FIND-SET(v)
7              then A ← A _ {(u, v)}
8                   UNION(u, v)
9   return A
```

Working:

Lines 1-3 initialize the set *A* to the empty set and create |*V*| trees, one containing each vertex. The edges in *E* are sorted into nondecreasing order by weight in line 4. The **for** loop in lines 5-8 checks, for each edge (*u*, *v*), whether the endpoints *u* and *v* belong to the same tree. If they do, then the edge (*u*, *v*) cannot be added to the forest without creating a cycle, and the edge is discarded. Otherwise, the two vertices belong to different trees. In this case, the edge (*u*, *v*) is added to *A* in line 7, and the vertices in the two trees are merged in line 8.





Minimum Spanning Tree Prim's Algorithm:

1. This strategy is greedy since the tree is augmented at each step with an edge that contributes the minimum amount possible to the tree's weight. The key to implement Prim's Algorithm efficiently is to make it easy to select a new edge to be added to the tree formed by the edges in A.

2. The tree starts from an arbitrary root vertex *r* and grows until the tree spans all the vertices in *V*. At each step, a light edge is added to the tree *A* that connects *A* to an isolated vertex of $G_A = (V, A)$.

3. **Algorithm:**

```
    MST-PRIM(G, w, r)
1    for each u _ V [G]
2         do key[u] ← ∞
3             π[u] ← NIL
4    key[r] ← 0
5     Q ← V [G]
6     while Q ≠ Ø
7         do u ← EXTRACT-MIN(Q)
8             for each v _ Adj[u]
9                  do if v _ Q and w(u, v) < key[v]
10                         then π[v] ← u
11                               key[v] ← w(u, v)
```

Working:

Lines 1-5 set the key of each vertex to ∞ (except for the root r, whose key is set to 0 so that it will be the first vertex processed), set the parent of each vertex to NIL, and initialize the min-priority queue Q to contain all the vertices. The algorithm maintains the following three-part loop invariant:

Prior to each iteration of the while loop of lines 6-11,
1. A = {(v, π[v]) : v _ V - {r} - Q}.
2. The vertices already placed into the minimum spanning tree are those in V - Q.
3. For all vertices v _ Q, if π[v] ≠ NIL, then key[v] < ∞ and key[v] is the weight of a light edge (v, π[v]) connecting v to some vertex already placed into the minimum spanning tree.

Line 7 identifies a vertex u _ Q incident on a light edge crossing the cut (V -Q, Q) (with the exception of the first iteration, in which u = r due to line 4). Removing u from the set Q adds it to the set V - Q of vertices in the tree, thus adding (u, π[u]) to A. The for loop of lines 8-11 update the key and π fields of every vertex v adjacent to u but not in the tree. The updating maintains the third part of the loop invariant.

Dijkstra's algorithm: Dijkstra's algorithm solves the single-source shortest-path problem when all edges have non-negative weights. It is a greedy algorithm and similar to Prim's algorithm. Algorithm starts at the source vertex, s, it grows a tree, T, that ultimately spans all vertices reachable from S. Vertices are added to T in order of distance i.e., first S, then the vertex closest to S, then the next closest, and so on. Following implementation assumes that graph G is represented by adjacency lists.

DIJKSTRA (G, w, s)

```
1.  INITIALIZE SINGLE-SOURCE (G, s)
2.  S ← { }     // S will ultimately contains vertices of final shortest-
    path weights from s
3.  Initialize priority queue Q i.e., Q ← V[G]
4.  while priority queue Q  is not empty do
5.      u ← EXTRACT_MIN(Q)    // Pull out new vertex
6.      S ← S È {u}
        // Perform relaxation for each vertex v adjacent to u
7.      for each vertex v in Adj[u] do
8.          Relax (u, v, w)
```

Analysis

Like Prim's algorithm, Dijkstra's algorithm runs in O(|E|lg|V|) time.

All pair shortest path problem by Floyd’s algorithm

Chapter 4 : Dynamic Programming

1. Dynamic programming, like the divide-and-conquer method, solves problems by combining the solutions to subproblems.

2. divide-and-conquer algorithms partition the problem into independent subproblems, solve the subproblems recursively, and then combine their solutions to solve the original problem. In contrast, dynamic programming is applicable when the subproblems are not independent, that is, when subproblems share subsubproblems.

3. A dynamic-programming algorithm solves every subsubproblem just once and then saves its answer in a table, thereby avoiding the work of recomputing the answer every time the subsubproblem is encountered.

4. Dynamic programming is typically applied to ***optimization problems***. In such Problems there can be many possible solutions. Each solution has a value, and we wish to find a solution with the optimal (minimum or maximum) value. We call such a solution *an* optimal solution to the problem, as opposed to *the* optimal solution, since there may be several solutions that achieve the optimal value.

5. The development of a dynamic-programming algorithm can be broken into a Sequence of four steps.

1. Characterize the structure of an optimal solution.
2. Recursively define the value of an optimal solution.
3. Compute the value of an optimal solution in a bottom-up fashion.
4. Construct an optimal solution from computed information.

6. Steps 1-3 form the basis of a dynamic-programming solution to a problem. Step 4 can be omitted if only the value of an optimal solution is required. When we do perform step 4, we sometimes maintain additional information during the computation in step 3 to ease the construction of an optimal solution.

7. Elements of Dynamic Programming

* Optimal Substructure

*Overlapping Subproblems

8. A problem exhibits ***optimal substructure*** if an optimal solution to the problem contains within it optimal solutions to subproblems. Whenever a problem exhibits optimal substructure, it is a good clue that dynamic programming might apply.

9. Optimal substructure varies across problem domains in two ways:

1. How many subproblems are used in an optimal solution to the original problem, and
2. How many choices we have in determining which subproblem(s) to use in an optimal solution.

10. Overlapping subproblems **:**

The second ingredient that an optimization problem must have for dynamic programming to be applicable is that the space of subproblems must be "small" in the sense that a recursive algorithm for the problem solves the same subproblems over and over, rather than always generating new subproblems. Typically, the total number of distinct subproblems is a polynomial in the input size. When a recursive algorithm revisits the same problem over and over again, we say that the optimization problem has ***overlapping subproblems.***

Optimal Matrix Chain Multiplication

We are given a sequence of matrices to multiply:

$$A_1 A_2 A_3 \ldots A_n$$

Matrix multiplication is associative, so

$$A_1 (A_2 A_3) = (A_1 A_2) A_3$$

that is, we can can generate the product in two ways.

The cost of multiplying an nxm by an mxp one is O(nmp) (or O(n^3) for two nxn ones). A poor choice of parenthesisation can be expensive: eg if we have

Matrix	Rows	Columns
A_1	10	100
A_2	100	5
A_3	5	50

the cost for (A_1 A_2) A_3 is

A_1A_2	10x100x5 = 5000	=> A_1 A_2 (10x5)
(A_1A_2) A_3	10x5x50 = 2500	=> $A_1A_2A_3$ (10x50)
Total	7500	

but for A_1 (A_2 A_3)

A_2A_3	100x5x50 = 25000	=> A_2A_3 (100x50)
A_1(A_2A_3)	10x100x50 = 50000	=> $A_1A_2A_3$ (10x50)
Total	75000	

Clearly demonstrating the benefit of calculating the optimum order before commencing the product calculation!

Optimal Sub-structure

As with the optimal binary search tree, we can observe that if we divide a chain of matrices to be multiplied into two optimal sub-chains:

$$(A_1 A_2 A_3 \ldots A_j) (A_{j+1} \ldots A_n)$$

then the optimal parenthesisations of the sub-chains must be composed of optimal chains. If they were not, then we could replace them with cheaper parenthesisations.

This property, known as optimal sub-structure is a hallmark of dynamic algorithms: it enables us to solve the small problems (the sub-structure) and use those solutions to generate solutions to larger problems.

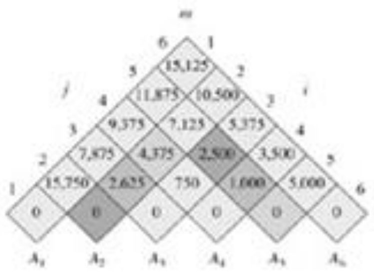
For matrix chain multiplication, the procedure is now almost identical to that used for constructing an optimal binary search tree. We gradually fill in two matrices,

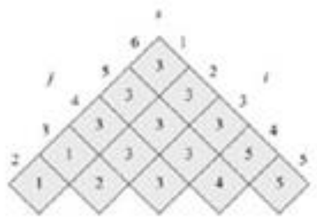
- one containing the costs of multiplying all the sub-chains. The diagonal below the main diagonal contains the costs of all pair-wise multiplications: cost[1,2] contains the cost of generating product A_1A_2, etc. The diagonal below that contains the costs of triple products: eg cost[1,3] contains the cost of generating product $A_1A_2A_3$, which we derived from comparing cost[1,2] and cost[2,3], etc.
- one containing the index of last array in the left parenthesisation (similar to the root of the optimal sub-tree in the optimal binary search tree, but there's no root here - the chain is divided into left and right sub-products), so that best[1,3] might contain 2 to indicate that the left sub-chain contains A_1A_2 and the right one is A_3 in the optimal parenthesisation of $A_1A_2A_3$.

Algorithm:

```
MATRIX-CHAIN-ORDER(p)
 1 n ← length[p] - 1
 2 for i ← 1 to n
 3        do m[i, i] ← 0
 4 for l ← 2 to n                ▹l is the chain length.
 5        do for i ← 1 to n - l + 1
 6                 do j ← i + l - 1
 7                    m[i, j] ← ∞
 8                    for k ← i to j - 1
 9                        do q ← m[i, k] + m[k + 1, j] + $p_{i-1} p_k p_j$
10                           if q < m[i, j]
11                              then m[i, j] ← q
12                                   s[i, j] ← k
13 return m and s
```

The algorithm first computes m[i, i] ← 0 for i = 1, 2, ..., n (the minimum costsfor chains of length 1) in lines 2-3. It then uses recurrence (15.12) to compute m[i, i + 1] for i = 1, 2, ..., n -1 (the minimum costs for chains of length l = 2) during the first execution of the loop in lines 4-12. The second time through the loop, it computes m[i, i + 2] for i = 1, 2, ..., n - 2 (the minimum costs for chains of length l = 3), and so forth. At each step, the m[i, j] cost computed in lines 9-12 depends only on table entries m[i, k] and m[k + 1, j] already computed.





```
PRINT-OPTIMAL-PARENS(s, i, j)
 if i = j
         then print "A"$_i$
         else print "("
                   PRINT-OPTIMAL-PARENS(s, i, s[i, j])
                   PRINT-OPTIMAL-PARENS(s, s[i, j] + 1, j)
                   print ")"
```

The above algorithms are used to find optimal solution for the matrix.

Optimal binary search trees

we are given a sequence $K = k_1, k_2, ..., k_n$_ of n distinct keys in sorted order (so that $k_1 < k_2 < \cdots < k_n$), and we wish to build a binary search tree from these keys. For each key k_i, we have a probability p_i that a search will be for k_i. Some searches may be for values not in K, and so we also have $n + 1$ "dummy keys" $d_0, d_1, d_2, ..., d_n$ representing values not in K. In particular, d_0 represents all values less than k_1, d_n represents all values greater than k_n, and for $i = 1, 2, ..., n -1$, the dummy key d_i represents all values between k_i and k_{i+1}. For each dummy key d_i, we have a probability q_i that a search will correspond to d_i.

- Problem
  - Given sequence $K = k_1 < k_2 < \cdots < k_n$ of n sorted keys,with a search probability p_i for each key k_i.
  - Want to build a binary search tree (BST) with minimum expected search cost.
  - Actual cost of items examined.
  - For key k_i, cost = depth$_T(k_i)$+1, where depth$_T(k_i)$ = depth of k_i in BST T .

- Expected Cost

$E[\text{search cost in } T]$

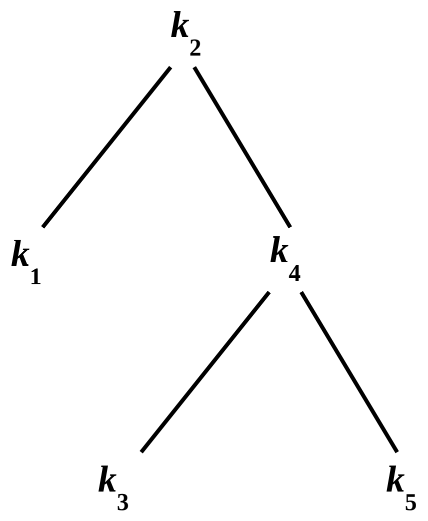
$$= \sum_{i=1}^{n} (\text{depth}_T(k_i) + 1) \cdot p_i$$

$$= \sum_{i=1}^{n} \text{depth}_T(k_i) \cdot p_i + \sum_{i=1}^{n} p_i \longleftarrow \boxed{\text{Sum of probabilities is 1.}}$$

$$= 1 + \sum_{i=1}^{n} \text{depth}_T(k_i) \cdot p_i$$

Example

- Consider 5 keys with these search probabilities: $p_1 = 0.25$, $p_2 = 0.2$, $p_3 = 0.05$, $p_4 = 0.2$, $p_5 = 0.3$.

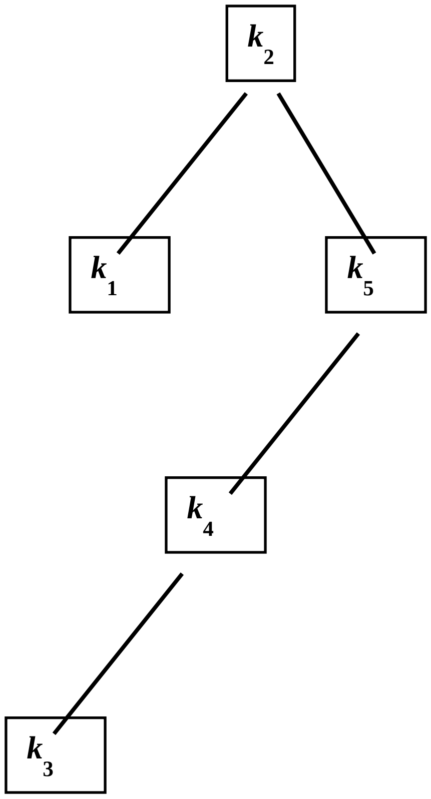


i	$\text{depth}_T(k_i)$	$\text{depth}_T(k_i) \cdot p_i$
1	1	0.25
2	0	0
3	2	0.1
4	1	0.2
5	2	0.6
		1.15

Therefore, E [search cost] = 2.15.

Example

$p_1 = 0.25, p_2 = 0.2, p_3 = 0.05, p_4 = 0.2, p_5 = 0.3.$



i	$\text{depth}_T(k_i)$	$\text{depth}_T(k_i)\cdot p_i$
1	1	0.25
2	0	0
3	3	0.15
4	2	0.4
5	1	0.3
		1.10

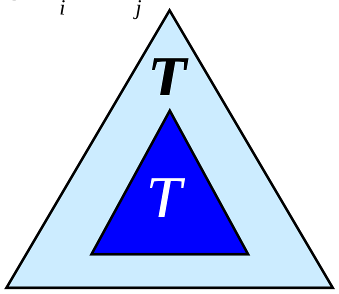
Therefore, E[search cost] = 2.10.

This tree turns out to be optimal for this set of keys.

- **Observations:**
  - » Optimal BST may not have smallest height.
  - » Optimal BST may not have highest-probability key at root.
- Build by exhaustive checking?
  - » Construct each *n*-node BST.
  - » For each, assign keys and compute expected search cost.
  - » But there are $\Omega(4^n/n^{3/2})$ different BSTs with n nodes.

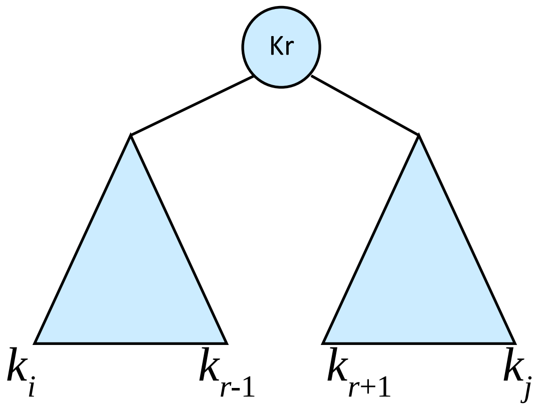
Optimal Substructure

- Any subtree of a BST contains keys in a contiguous range k_i, ..., k_j for some $1 \le i \le j \le n$.
- If T is an optimal BST and
  T contains subtree T' with keys k_i, ... ,k_j ,
  then T' must be an optimal BST for keys k_i, ..., k_j.
- Proof : cut and paste



Optimal Substructure

- One of the keys in $k_i, \ldots, k_j$, say k_r, where $i \le r \le j$, must be the root of an optimal subtree for these keys.
- Left subtree of k_r contains $k_i, \ldots, k_{r-1}$.
- Right subtree of k_r contains $k_r+1, \ldots, k_j$.
- To find an optimal BST:
  - » Examine all candidate roots k_r, for $i \le r \le j$
  - » Determine all optimal BSTs containing $k_i, \ldots, k_{r-1}$ and containing $\ldots, k_j$



Recursive Solution

- Find optimal BST for $k_i, \ldots, k_j$, where $i \ge 1$, $j \le n$, $j \ge i-1$. When $j = i-1$, the tree is empty.
- Define $e[i, j]$ = expected search cost of optimal BST for $k_i, \ldots, k_j$.
- If $j = i-1$, then $e[i, j] = 0$.
- If $j \ge i$,
  - » Select a root k_r, for some $i \le r \le j$.
  - » Recursively make an optimal BSTs
    - for $k_i, \ldots, k_{r-1}$ as the left subtree, and
    - for $k_{r+1}, \ldots, k_j$ as the right subtree.

Recursive Solution

- When the OPT subtree becomes a subtree of a node:
  - » Depth of every node in OPT subtree goes up by 1.
  - » Expected search cost increases by

$$\boxed{w(i,j) = \sum_{l=i}^{j} p_l}$$

- If k_r is the root of an optimal BST for $k_i,..,k_j$:
  - » $e[i, j] = p_r + (e[i, r-1] + w(i, r-1)) + (e[r+1, j] + w(r+1, j))$

    $= e[i, r-1] + e[r+1, j] + w(i, j)$.
- But, we don't know k_r. Hence,

(Because $w(i, j)=w(i,r-1) + p_r + w(r + 1, j)$)

$$\boxed{e[i,j] = \begin{cases} 0 & \text{if } j = i-1 \\ \min_{i \le r \le j} \{e[i,r-1] + e[r+1,j] + w(i,j)\} & \text{if } i \le j \end{cases}}$$

Computing an Optimal Solution

For each subproblem (i,j), store:

- expected search cost in a table $e[1..n+1, 0..n]$
  - » Will use only entries $e[i, j]$, where $j \ge i-1$.
- root$[i, j]$ = root of subtree with keys $k_i,..,k_j$, for $1 \le i \le j \le n$.
- $w[1..n+1, 0..n]$ = sum of probabilities
  - » $w[i, i-1] = 0$ for $1 \le i \le n$.
  - » $w[i, j] = w[i, j-1] + p_j$ for $1 \le i \le j \le n$.

```
OPTIMAL-BST(p, q, n)
1.  for $i \leftarrow 1$ to $n + 1$
2.      do $e[i, i-1] \leftarrow 0$
3.         $w[i, i-1] \leftarrow 0$
4.  for $l \leftarrow 1$ to $n$                              Consider all trees with l keys.
5.      do for $i \leftarrow 1$ to $n - l + 1$                Fix the first key.
6.         do $j \leftarrow i + l - 1$                        Fix the last key
7.            $e[i, j] \leftarrow \infty$
8.            $w[i, j] \leftarrow w[i, j-1] + p_j$
9.            for $r \leftarrow i$ to $j$
10.               do $t \leftarrow e[i, r-1] + e[r + 1, j] + w[i, j]$     Determine the root of the optimal
11.                  if $t < e[i, j]$                                     (sub) tree
12.                     then $e[i, j] \leftarrow t$
13.                          $root[i, j] \leftarrow r$
14. return e and root
```

Time: $O(n^3)$

Chapter 5 Backtracking Algorithm

Backtracking is one of the design techniques used for solving such problems which deal with searching for a set of solutions or which ask for an optimal solution satisfying some constraints can be solved using the backtracking formulation. In backtracking method, the desired solution is expressible as an n-tuple (x1,x2,….xn) where the xi are chosen from some finite set si often the problem to be solved calls for finding one vector that maximizes(or minimizes or satisfies) a criterion function P(x1,x2,…..xn). Sometimes it seeks all vectors that satisfy P. Many of the problems we solve using backtracking require that all the solution using backtracking require that all the solution satisfy a complex set of constraints. These constraints are divided into two categories, for any problem. The constraints may be explicit or implicit.
Explicit constraints are rules, which restrict each vector element to be chosen from the given set.

Implicit constraints are rules, which determine which of the tuples in the solution space, actually satisfy the criterion function.

Explicit constraint are rules that restrict each xi to take on values only from a given set. Some examples that are common for explicit constraints are:
xi >= 0 or Si = {all non negative real numbers}
xi = 0 or 1 or Si = {0,1}
li <= xi <= ui or Si = { ai li <= a <= ui}

The explicit constraints depend on the particular instance depend on the particular instance l if a particular instance l of a particular being solved. All tuples that satisfy the explicit constraints define a possible solution space for 1.The implicit constraints are rules that determine which of the tuples in the solution space of I satisfy the criterion function. Thus implicit constraints describe the way in which the xi must relate to each other.

The major advantage of this algorithm is that if it is realized that the partial vector generated does not lead to an optimal solution then that vector may be ignored.

Backtracking algorithm determine the solution by systematically searching the solution space for the given problem. This search is accomplished by using a free organization. Backtracking is a depth first search with some bounding function.

Applications of Back Tracking:
The most widespread application of backtracking is the execution of back tracking is the execution of regular expression. For Example, the simple pattern "a*a" will fail to match the sequence "aa" without backtracking (because on the first pass, both a's are eaten by "*" leaving nothing behind for the remaining "a" to match. Another common use of backtracking is in path finding algorithms where the function traces over a graph of nodes and backtracks until it finds the least cost path. Backtracking is used in the implementation of programming languages and

other areas such as text parsing. Backtracking is also utilized in the difference engine for the mediawiki software.

8 queen problem

The 8 queen problem can be stated as follows. Consider a chessboard of order 8X8. The problem is to place 8 queens on this board such that no two queens are can attack each other.

1. If the remainder from dividing *N* by 6 is not 2 or 3 then the list is simply all even numbers followed by all odd numbers ≤ N
2. Otherwise, write separate lists of even and odd numbers (i.e. 2,4,6,8 - 1,3,5,7)
3. If the remainder is 2, swap 1 and 3 in odd list and move 5 to the end (i.e. **3,1**,7,**5**)
4. If the remainder is 3, move 2 to the end of even list and 1,3 to the end of odd list (i.e. 4,6,8,**2** - 5,7,**1,3**)
5. Append odd list to the even list and place queens in the rows given by these numbers, from left to right (i.e. a2, b4, c6, d8, e3, f1, g7, h5)

For *N* = 8 this results in the solution shown above.

GRAPH COLORING

A coloring of a graph is an assignment of a color to each vertex of the graph so that no two vertices connected by an edge have the same color. It is not hard to see that our problem is one of coloring the graph of incompatible turns using as few colors as possible.

The problem of coloring graphs has been studied for many decades, and the theory of algorithms tells us a lot about this problem. Unfortunately, coloring an arbitrary graph with as few colors as possible is one of a large class of problems called "NP-complete problems," for which all known solutions are essentially of the type "try all possibilities."

A k-coloring of an undirected graph $G = (V, E)$ is a function $c : V \rightarrow \{1, 2,..., k\}$ such that $c(u) \neq c(v)$ for every edge (u, v) E. In other words, the numbers 1, 2,..., k represent the k colors, and adjacent vertices must have different colors. The graph-coloring problem is to determine the minimum number of colors needed to color a given graph.

Hamiltonian cycle

A Hamiltonian cycle is a cycle in a graph passing through all the vertices once

Chapter 6 Branch and Bound

The term branch and bound refer to all state space search methods in which all possible branches are derived before any other node can become the E-node. In other words the exploration of a new node cannot begin until the current node is completely explored.

Branch and bound (**BB** or **B&B**) is an algorithm design paradigm for discrete and combinatorial optimization problems. A branch-and-bound algorithm consists of a systematic enumeration of candidate solutions by means of state space search: the set of candidate solutions is thought of as forming a rooted tree with the full set at the root. The algorithm explores *branches* of this tree, which represent subsets of the solution set. Before enumerating the candidate solutions of a branch, the branch is checked against upper and lower estimated *bounds* on the optimal solution, and is discarded if it cannot produce a better solution than the best one found so far by the algorithm.

The method was first proposed by A. H. Land and A. G. Doig in 1960 for discrete programming, and has become the most commonly used tool for solving NP-hard optimization problems.[2] The name "branch and bound" first occurred in the work of Little *et al.* on the traveling salesman problem

In order to facilitate a concrete description, we assume that the goal is to find the *minimum* value of a function $f(x)$, where x ranges over some set S of *admissible* or *candidate solutions* (the *search space* or *feasible region*). Note that one can find the *maximum* value of $f(x)$ by finding the minimum of $g(x) = -f(x)$. (For example, S could be the set of all possible trip schedules for a bus fleet, and $f(x)$ could be the expected revenue for schedule x.)

A branch-and-bound procedure requires two tools. The first one is a *splitting* procedure that, given a set S of candidates, returns two or more smaller sets $S_1, S_2, \ldots$ whose union covers S. Note that the minimum of $f(x)$ over S is $\min\{v_1, v_2, \ldots\}$, where each v_i is the minimum of $f(x)$ within S_i. This step is called **branching**, since its recursive application defines a *search tree* whose *nodes* are the subsets of S.

The second tool is a procedure that computes upper and lower bounds for the minimum value of $f(x)$ within a given subset of S. This step is called **bounding**.

The key idea of the BB algorithm is: if the *lower* bound for some tree node (set of candidates) A is greater than the *upper* bound for some other node B, then A may be safely discarded from the search. This step is called **pruning**, and is usually implemented by maintaining a global variable m (shared among all nodes of the tree) that records the minimum upper bound seen among all subregions examined so far. Any node whose lower bound is greater than m can be discarded.

The recursion stops when the current candidate set S is reduced to a single element, or when the upper bound for set S matches the lower bound. Either way, any element of Swill be a minimum of the function within S.

When $\mathbf{x}$ is a vector of $\mathbb{R}^n$, branch and bound algorithms can be combined with interval analysis and contractor techniques in order to provide guaranteed enclosures of the global minimum.

Generic pseudocode

The following pseudocode is a skeleton branch and bound algorithm for minimizing an objective function *f*. A bounding function *g* is used to compute lower bounds of *f* on nodes of the search tree.

- Using a heuristic, find a solution x_h to the optimization problem. Store its value, $B = f(x_h)$. (If no heuristic is available, set *B* to infinity.) *B* will denote the best solution found so far, and will be used as an upper bound on candidate solutions.
- Initialize a queue to hold a partial solution with none of the variables of the problem assigned.
- Loop until the queue is empty:

    - Take a node *N* off the queue.
    - If *N* represents a single candidate solution *x* and $f(x) < B$, then *x* is the best solution so far. Record it and set $B \leftarrow f(x)$.
    - Else, *branch* on *N* to produce new nodes N_i. For each of these:

        - If $g(N_i) > B$, do nothing; since the lower bound on this node is greater than the upper bound of the problem, it will never lead to the optimal solution, and can be discarded.
        - Else, store N_i on the queue.

  Several different queue data structures can be used. A stack (LIFO queue) will yield a depth-first algorithm. A best-first branch and bound algorithm can be obtained by using apriority queue that sorts nodes on their *g*-value

Applications

This approach is used for a number of NP-hard problems

- Integer programming
- Nonlinear programming

- Travelling salesman problem (TSP)[3][8]
- Quadratic assignment problem (QAP)
- Maximum satisfiability problem (MAX-SAT)
- Nearest neighbor search (NNS)
- Cutting stock problem
- False noise analysis (FNA)
- Computational phylogenetics
- Set inversion
- Parameter estimation
- 0/1 knapsack problem
- Structured prediction in computer vision[9]:267–276

Branch-and-bound may also be a base of various heuristics. For example, one may wish to stop branching when the gap between the upper and lower bounds becomes smaller than a certain threshold. This is used when the solution is "good enough for practical purposes" and can greatly reduce the computations required. This type of solution is particularly applicable when the cost function used is *noisy* or is the result of statistical estimates and so is not known precisely but rather only known to lie within a range of values with a specific probability. An example of its application here is in biology when performing cladistic analysis to evaluate evolutionary relationships between organisms, where the data sets are often impractically large without heuristics

Travelling salesman problem (**TSP**) asks the following question: Given a list of cities and the distances between each pair of cities, what is the shortest possible route that visits each city exactly once and returns to the origin city? It is an NP-hard problem in combinatorial optimization, important in operations research and theoretical computer science.

TSP is a special case of the travelling purchaser problem.

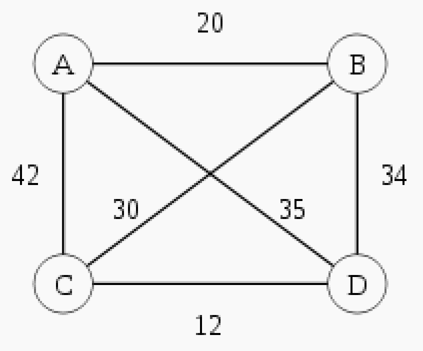
In the theory of computational complexity, the decision version of the TSP (where, given a length *L*, the task is to decide whether the graph has any tour shorter than *L*) belongs to the class of NP-complete problems. Thus, it is possible that the worst-case running time for any algorithm for the TSP increases superpolynomially (or perhaps exponentially) with the number of cities.

The problem was first formulated in 1930 and is one of the most intensively studied problems in optimization. It is used as a benchmark for many optimization methods. Even though the problem is computationally difficult, a large number of heuristics and exact methods are known, so that some instances with tens of thousands of cities can be solved completely and even problems with millions of cities can be approximated within a small fraction of 1%.[1]

The TSP has several applications even in its purest formulation, such as planning, logistics, and the manufacture of microchips. Slightly modified, it appears as a sub-problem in many areas, such as DNA sequencing. In these applications, the concept *city* represents, for example, customers, soldering points, or DNA fragments, and the concept *distance* represents travelling times or cost, or a similarity measure between DNA fragments. In many applications, additional constraints such as limited resources or time windows may be imposed.

Description

As a graph problem



TSP can be modelled as an undirected weighted graph, such that cities are the graph's vertices, paths are the graph's edges, and a path's distance is the edge's length. It is a minimization problem starting and finishing at a specified vertex after having visited each other vertex exactly once. Often, the model is a complete graph (*i.e.* each pair of vertices is connected by an edge). If no path exists between two cities, adding an arbitrarily long edge will complete the graph without affecting the optimal tour.

Note: the above contents are taken from the following books and internet

1. Introduction to Algorithms by Cormen.
2. Design and Analysis of Algorithms by Nitin Upadhyay.
3. Design and Analysis of Algorithms by Udit Agarwal