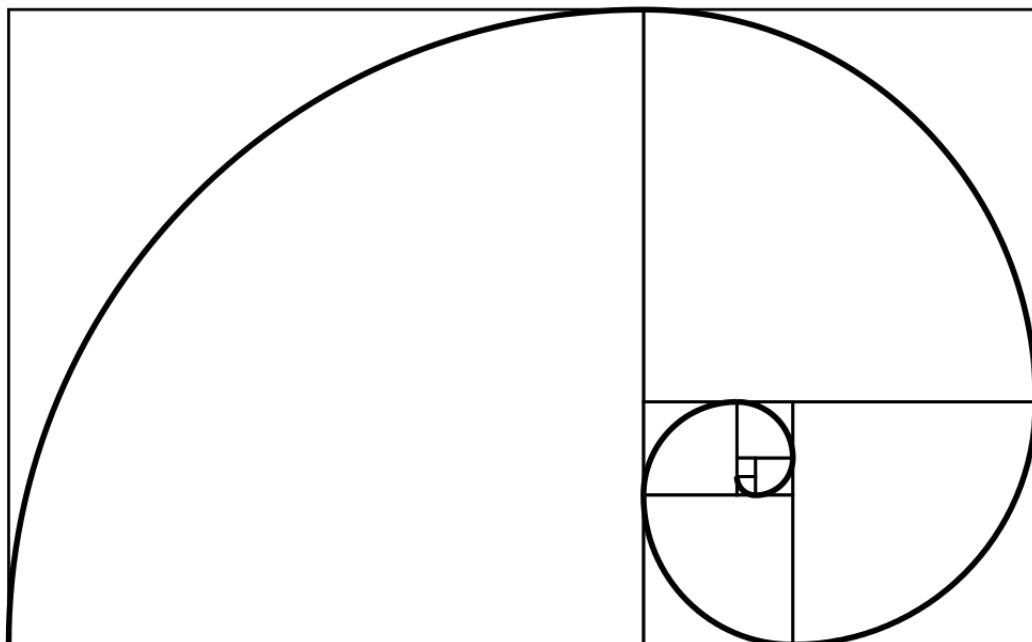


Elementary Algorithms



Xinyu LIU ¹

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¹Xinyu LIU

Version: 0.6180339887498949

Email: liuxinyu95@gmail.com

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Programmers learn elementary algorithms at school. Except for programming contest, code interview, they seldom use algorithms in commercial software development. When talking about algorithms in AI and machine learning, it actually means scientific modeling, but not about data structure or elementary algorithm. Even when programmers need them, they have already been provided in libraries. It seems quite enough to know about how to use the library as a tool but not ‘re-invent the wheel’.

I would say elementary algorithms are critical in solving ‘interesting problems’, the usefulness of the problem set aside. Let’s start with two problems.

0.1 The smallest free number

Richard Bird gives an interesting programming problem to find the minimum number that not appears in a given list(Chapter 1, [?]). It’s common to use a number as the identifier (Id) to index entities. At any time, a number is either occupied or free. When client tries to acquire a new number as index, we want to always allocate the smallest available one. Suppose numbers are non-negative integers and those being occupied are recorded in a list, for example:

[18, 4, 8, 9, 16, 1, 14, 7, 19, 3, 0, 5, 2, 11, 6]

How can we find the smallest free number, which is 10, from the list? It seems quite easy to figure out the solution.

```

1: function MIN-FREE( $A$ )
2:    $x \leftarrow 0$ 
3:   loop
4:     if  $x \notin A$  then
5:       return  $x$ 
6:     else
7:        $x \leftarrow x + 1$ 

```

Where the \notin is realized like below.

```

1: function ‘ $\notin$ ’( $x, X$ )
2:   for  $i \leftarrow 1$  to  $|X|$  do
3:     if  $x = X[i]$  then
4:       return False
5:   return True

```

Some environments have built-in implementation to test if an element is in a list. Below is an example program.

```

def minfree(lst):
    i = 0
    while True:
        if i not in lst:
            return i
        i = i + 1

```

However, when there are millions of numbers being used, this solution performs poor. The time spent is quadratic to the length of the list. In a computer with 2 cores of 2.10 GHz CPU, and 2G RAM, the C implementation takes 5.4s to search the minimum free number among 100,000 numbers, and takes more than 8 minutes to handle a million numbers.

0.1.1 Improvement

The key idea to improve the solution is based on the fact that, for n numbers x_1, x_2, \dots, x_n , if there exists free number, some x_i must be outside the range $[0, n)$; otherwise the list is exactly some permutation of $0, 1, \dots, n - 1$ hence n should be returned as the minimum free number. In summary:

$$\text{minfree}(x_1, x_2, \dots, x_n) \leq n \quad (1)$$

A better solution is to use an array of $n + 1$ flags to mark whether a number in range $[0, n]$ is free.

```

1: function MIN-FREE( $A$ )
2:    $F \leftarrow$  [False, False, ..., False] where  $|F| = n + 1$ 
3:   for  $\forall x \in A$  do
4:     if  $x < n$  then
5:        $F[x] \leftarrow$  True
6:   for  $i \leftarrow [0, n]$  do
7:     if  $F[i] = \text{False}$  then
8:       return  $i$ 

```

Line 2 initializes a flag array all of False values. Then we scan all numbers in A and mark the corresponding flag to True if the value is less than n . Finally, we iterate to find the first False flag. This program takes time proportion to n . It uses $n + 1$ flags to cover the special case that $\text{sorted}(A) = [0, 1, 2, \dots, n - 1]$. This solution is much faster than the brute force one. In the same computer, the Python implementation takes 0.02s when dealing with 100,000 numbers.

Although this solution only takes $O(n)$ time, it needs additional $O(n)$ space to store the flags. We haven't tuned it yet. Each time the program allocates memory to create an array of $n + 1$ flags, then releases it when finish. Such memory allocation and release is expensive and cost a lot of processing time.

To improve it, we can allocate the memory in advance for later reusing, and change to bit-wise flags instead of array. For example as the following C program:

```

#define N 1000000
#define WORD_LENGTH (sizeof(int) * 8)

void setbit(unsigned int* bits, unsigned int i) {
    bits[i / WORD_LENGTH] |= 1 << (i % WORD_LENGTH);
}

int testbit(unsigned int* bits, unsigned int i) {
    return bits[i / WORD_LENGTH] & (1 << (i % WORD_LENGTH));
}

unsigned int bits[N / WORD_LENGTH + 1];

int minfree(int* xs, int n) {
    int i, len = N/WORD_LENGTH + 1;
    for (i = 0; i < len; ++i) {
        bits[i]=0;
    }
    for (i=0; i < n; ++i) {
        if(xs[i] < n) {
            setbit(bits, xs[i]);
        }
    }
    for (i=0; i <= n; ++i) {
        if (!testbit(bits, i)) {
            return i;
        }
    }
}

```

```

}
}
}

```

This program can handle 1 million numbers in 0.023s in the same computer.

0.1.2 Divide and Conquer

The above improvement costs $O(n)$ additional space for flags, can we eliminate it? The divide and conquer strategy is to break the problem into smaller ones, then solve them separately to get the answer.

We can put numbers $x_i \leq \lfloor n/2 \rfloor$ into a sub-list A' and put the rest into another sub-list A'' . According to (1), if the length of A' equals to $\lfloor n/2 \rfloor$, it means A' is 'full'. The minimum free number must be in A'' . We can recursively search in A'' which is shorter the original list. Otherwise, it means the minimum free number is in A' , which again leads to a smaller problem.

When search in A'' , the conditions change a bit. We do not start from 0, but from $\lfloor n/2 \rfloor + 1$ as the new lower bound. We define the algorithm as $search(A, l, u)$, where l is the lower bound and u is the upper bound index. For the empty list as a special case, we return the l as the result.

$$minfree(A) = search(A, 0, |A| - 1)$$

$$\begin{aligned}
 search(\emptyset, l, u) &= l \\
 search(A, l, u) &= \begin{cases} |A'| = m - l + 1 : & search(A'', m + 1, u) \\
 otherwise : & search(A', l, m) \end{cases}
 \end{aligned}$$

where

$$\begin{aligned}
 m &= \lfloor \frac{l + u}{2} \rfloor \\
 A' &= [x | x \in A, x \leq m] \\
 A'' &= [x | x \in A, x > m]
 \end{aligned}$$

This algorithm doesn't need additional space¹. Each recursive call performs $O(|A|)$ comparisons to build A' and A'' . After that the problem scale halves. Therefore, the time is bound to $T(n) = T(n/2) + O(n)$, which reduce to $O(n)$ according to master theorem. Alternatively, observe that the first call takes $O(n)$ to build A' and A'' and the second call takes $O(n/2)$, and $O(n/4)$ for the third... The total time is $O(n + n/2 + n/4 + \dots) = O(2n) = O(n)$. We use $[a | a \in A, p(a)]$ for list. It is different with $\{a | a \in A, p(a)\}$, which is a set.

Below example Haskell program implements this algorithm.

```

minFree xs = bsearch xs 0 (length xs - 1)

bsearch xs l u | xs == [] = l
               | length as == m - l + 1 = bsearch bs (m+1) u
               | otherwise = bsearch as l m

where
  m = (l + u) `div` 2
  (as, bs) = partition (<= m) xs

```

¹The recursion takes $O(\lg n)$ stack spaces, but it can be eliminated through tail recursion optimization

0.1.3 Expressiveness and performance

One may concern the performance of this divide and conquer algorithm. There are $O(\lg n)$ recursive calls, which need additional stack space. If wanted, we can eliminate the recursion:

```

1: function MIN-FREE( $A$ )
2:    $l \leftarrow 0, u \leftarrow |A|$ 
3:   while  $u - l > 0$  do
4:      $m \leftarrow l + \frac{u - l}{2}$ 
5:      $left \leftarrow l$ 
6:     for  $right \leftarrow l$  to  $u - 1$  do
7:       if  $A[right] \leq m$  then
8:          $A[left] \leftrightarrow A[right]$ 
9:          $left \leftarrow left + 1$ 
10:    if  $left < m + 1$  then
11:       $u \leftarrow left$ 
12:    else
13:       $l \leftarrow left$ 

```

As shown in figure 1, this program re-arranges the array such that all elements before $left$ are less than or equal to m ; while those between $left$ and $right$ are greater than m .

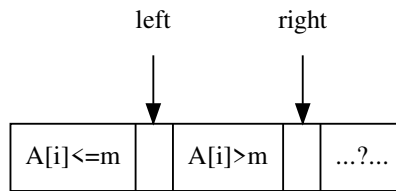


Figure 1: Divide the array, all $A[i] \leq m$ where $0 \leq i < left$; while all $A[i] > m$ where $left \leq i < right$. The rest elements haven't been processed yet.

This solution is fast and needn't extra stack space. However, compare to the previous recursive one, there is some expressiveness drops. Depends on individual taste, one may prefer one over the other.

0.2 Regular number

The second puzzle is to find the 1,500-th number, which only contains factor 2, 3 or 5. Such numbers are called regular number, also known as 5-smooth indicating the greatest prime factor is at most 5, or Hamming numbers named after Richard Hamming in computer science. 2, 3, and 5 are of course regular numbers. $60 = 2^2 3^1 5^1$ is the 25-th number. $21 = 2^0 3^1 7^1$ is not valid because it has a factor 7. We consider $1 = 2^0 3^0 5^0$ be the 0-th regular number. The first 10 regular numbers are:

1, 2, 3, 4, 5, 6, 8, 9, 10, 12, ...

0.2.1 The brute-force solution

The straightforward way is to check numbers one by one from 1, extract all factors of 2, 3 and 5 to see if the left part is 1:

```

1: function REGULAR-NUMBER( $n$ )

```

```

2:  x ← 1
3:  while n > 0 do
4:    x ← x + 1
5:    if VALID?(x) then
6:      n ← n - 1
7:  return x

8:  function VALID?(x)
9:    while x mod 2 = 0 do
10:     x ← ⌊x/2⌋
11:   while x mod 3 = 0 do
12:     x ← ⌊x/3⌋
13:   while x mod 5 = 0 do
14:     x ← ⌊x/5⌋
15:  return x = 1 ?

```

This ‘brute-force’ algorithm works for small n . However, to find the 1500-th regular number (which is 860934420), its C implementation takes 40.39s in above computer. When n increases to 15,000, it can’t terminate after 10 minutes.

0.2.2 Improvement

Modular and divide calculations are very expensive [2]. And they are executed a lot in loops. Instead of checking if a number only contains 2, 3, or 5 as factors, we can construct regular number from these three factors. We can start from 1, multiply it with 2, 3, or 5 to generate the rest numbers. The problem turns to be how to generate regular numbers in order? One method is to utilize the queue data structure.

A queue allows to add element to one end (called enqueue), and delete from the other (called dequeue). The element enqueued first will be dequeued first. This nature is called FIFO (First In First Out). The idea is to add 1 as the first number to the queue. We repeatedly dequeue a number, multiply it with 2, 3, and 5, to generate 3 new numbers; then add them back to the queue in order. A new generated number may already exist in the queue. In such case, we drop the duplicated number. Because the new number may be smaller than the others in the queue, we must put them at the correct position. Figure 2 shows this idea.

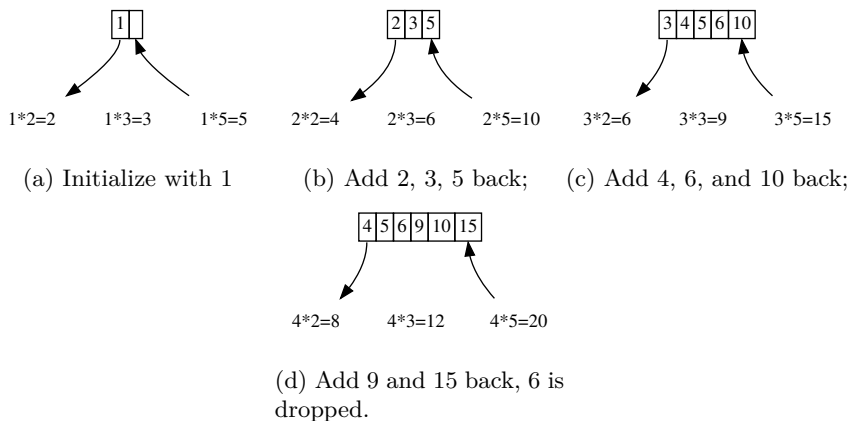


Figure 2: First 4 steps to generate regular numbers.

We can design the algorithm based on this idea:

```

1: function REGULAR-NUMBER( $n$ )
2:    $Q \leftarrow \emptyset$ 
3:    $x \leftarrow 1$ 
4:   ENQUEUE( $Q, x$ )
5:   while  $n > 0$  do
6:      $x \leftarrow$  DEQUEUE( $Q$ )
7:     UNIQUE-ENQUEUE( $Q, 2x$ )
8:     UNIQUE-ENQUEUE( $Q, 3x$ )
9:     UNIQUE-ENQUEUE( $Q, 5x$ )
10:     $n \leftarrow n - 1$ 
11:  return  $x$ 

12: function UNIQUE-ENQUEUE( $Q, x$ )
13:   $i \leftarrow 0, m \leftarrow |Q|$ 
14:  while  $i < m$  and  $Q[i] < x$  do
15:     $i \leftarrow i + 1$ 
16:  if  $i \geq m$  or  $x \neq Q[i]$  then
17:    INSERT( $Q, i, x$ )

```

The INSERT function takes $O(m)$ time to insert a number at proper position, where $m = |Q|$ is the length of the queue. It skips insertion if the number already exists. The length of the queue increases proportion to n (Each time, we dequeue an element, and enqueue 3 new at most. The increase ratio ≤ 2), the total time is $O(1 + 2 + 3 + \dots + n) = O(n^2)$.

Figure3 shows the number of access to the queue against n . It is a quadratic curve, which reflects the $O(n^2)$ performance.

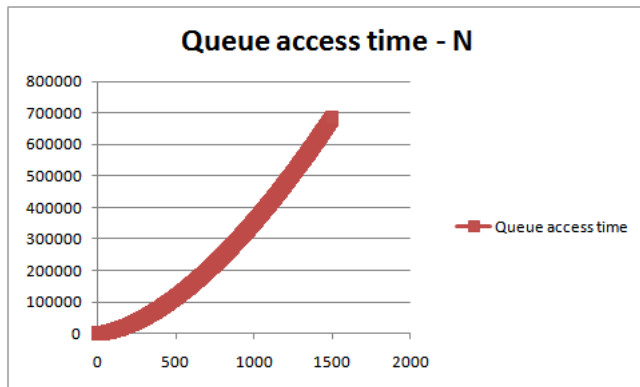


Figure 3: Queue access count - n .

The corresponding C implementation takes 0.016s to output 860934420. It is about 2500 times faster than the naive search solution.

We can also realize this improvement recursively. Suppose X is an infinite list of all regular numbers $[x_1, x_2, x_3, \dots]$. For every number, we multiply it by 2, the result is still a list of regular numbers: $[2x_1, 2x_2, 2x_3, \dots]$. We can also multiply numbers in X by 3 and 5, to generate two new infinite lists. If we merge them together, remove the duplicated numbers, and prepend 1 as the first, then we get X again. In other words, the following equation holds:

$$X = 1 : [2x | \forall x \in X] \cup [3x | \forall x \in X] \cup [5x | \forall x \in X] \quad (2)$$

Where symbol $x : X$ means to link x before list X , such that x becomes the first element. It is called ‘cons’ in Lisp. We link 1 before the rest, as it is the first regular number. To implement infinite lists merge, we define \cup to recursively compare elements in two sorted lists. Let $X = [x_1, x_2, x_3, \dots]$, $Y = [y_1, y_2, y_3, \dots]$ be two such lists, $X' = [x_2, x_3, \dots]$ and $Y' = [y_2, y_3, \dots]$ contain the rest elements except without their heads x_1 and y_1 . We define merge as below:

$$X \cup Y = \begin{cases} x_1 < y_1 : & x_1 : X' \cup Y \\ x_1 = y_1 : & x_1 : X' \cup Y' \\ y_1 < x_1 : & y_1 : X \cup Y' \end{cases}$$

We need not concern about either X or Y is empty, because they are both infinite lists. In functional settings that support lazy evaluation, this algorithm can be implemented as the following example program:

```

ns = 1 : (map (*2) ns) `merge` (map (*3) ns) `merge` (map (*5) ns)

merge (x:xs) (y:ys) | x < y = x : merge xs (y:ys)
                  | x = y = x : merge xs ys
                  | otherwise = y : merge (x:xs) ys

```

The 1500th number 860934420 is given by `ns !! 1500`. In the same computer, it takes about 0.03s to output the answer.

0.2.3 Queues

Although the improved solution is much faster than the original brute-force one, it generates duplicated numbers, and they are eventually dropped. In order to keep numbers ordered, it needs linear time scan and insertion, which degrades the enqueue operation from constant time to $O(|Q|)$. To avoid duplication, we can separate all regular numbers into 3 disjoint buckets: $Q_2 = \{2^i | i > 0\}$, $Q_{23} = \{2^i 3^j | i \geq 0, j > 0\}$, and $Q_{235} = \{2^i 3^j 5^k | i, j \geq 0, k > 0\}$. The constraints that $j \neq 0$ in Q_{23} , and $k \neq 0$ in Q_{235} ensure there is no overlap. The bucket is realized as a queue. They are initialized as $Q_2 = \{2\}$, $Q_{23} = \{3\}$, and $Q_{235} = \{5\}$. Starting from 1, each time we extract the smallest number x from the three queues as the next regular number. Then do the following:

- If x comes from Q_2 , we enqueue $2x$, $3x$, and $5x$ back to Q_2 , Q_{23} , and Q_{235} respectively;
- If x comes from Q_{23} , we only enqueue $3x$ to Q_{23} , and $5x$ to Q_{235} . We should not add $2x$ to Q_2 , because Q_2 cannot hold any numbers divided by 3.
- If x comes from Q_{235} , we only need enqueue $5x$ to Q_{235} . We should not add $2x$ to Q_2 , or $3x$ to Q_{23} because they can't hold numbers divided by 5.

We reach to the answer after repeatedly enqueue the smallest number n times. The following algorithm implements this idea:

```

1: function REGULAR-NUMBER( $n$ )
2:    $x \leftarrow 1$ 
3:    $Q_2 \leftarrow \{2\}$ ,  $Q_{23} \leftarrow \{3\}$ ,  $Q_{235} \leftarrow \{5\}$ 
4:   while  $n > 0$  do
5:      $x \leftarrow \min(\text{HEAD}(Q_2), \text{HEAD}(Q_{23}), \text{HEAD}(Q_{235}))$ 
6:     if  $x = \text{HEAD}(Q_2)$  then
7:       DEQUEUE( $Q_2$ )
8:       ENQUEUE( $Q_2, 2x$ )

```

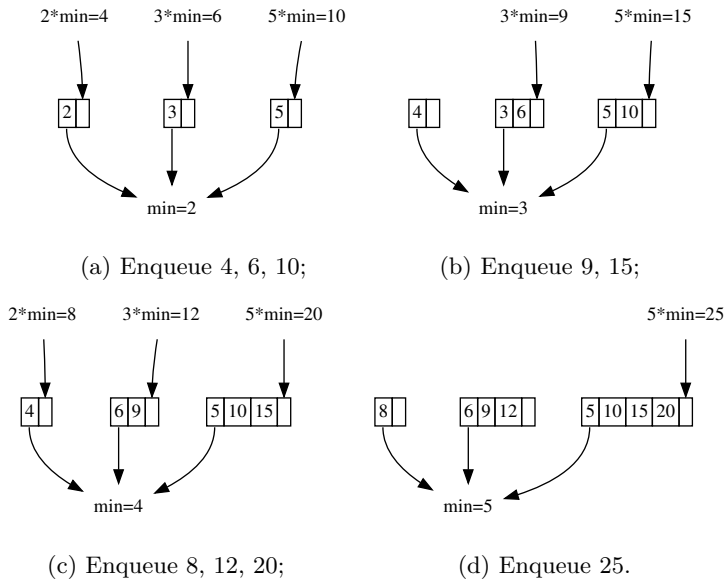


Figure 4: First 4 steps with Q_2 , Q_{23} , and Q_{235} . They were initialize with 2, 3, 5.

```

9:     ENQUEUE( $Q_{23}$ ,  $3x$ )
10:    ENQUEUE( $Q_{235}$ ,  $5x$ )
11:    else if  $x = \text{HEAD}(Q_{23})$  then
12:        DEQUEUE( $Q_{23}$ )
13:        ENQUEUE( $Q_{23}$ ,  $3x$ )
14:        ENQUEUE( $Q_{235}$ ,  $5x$ )
15:    else
16:        DEQUEUE( $Q_{235}$ )
17:        ENQUEUE( $Q_{235}$ ,  $5x$ )
18:     $n \leftarrow n - 1$ 
19:    return  $x$ 

```

This algorithm loops on n . Each time it extracts the minimum number from the head of three queues. This takes constant time. Then it add at most 3 numbers to each queue respectively. This takes constant time too. Therefore the algorithm is bound to $O(n)$.

0.3 Summary

One might think the brute-force solution was sufficient to solve both programming puzzles. However, as the problem scales up, we have to seek for better solutions. There are many interesting problems, which were hard before, but through computer programming, we are able to solve them nowadays. This book aims to provide both functional and imperative definition for the commonly used elementary algorithms and data structures. We referenced many results from Okasaki's work[3] and classic text books(for example [4]). We try to avoid relying on a specific programming language, because it may or may not be familiar with the reader, and programming languages keep changing. Instead, we use pseudo code or mathematics notation to make the algorithm definition generic. When give code examples, the functional ones look more like Haskell, and the imperative ones look like a mix of C, Java, and Python. They are only for illustration purpose, but not guaranteed following any language specification strictly.

Exercise 1

1. For the free number puzzle, since all numbers are not negative, we can leverage the sign as a flag to indicate a number exists. We can scan the number list, for every number $|x| < n$ (where n is the length), negate the number at position $|x|$. Then we run another round of scan to find out the first positive number. It's position is the answer. Write a program to realize this method.
2. There are n numbers $1, 2, \dots, n$. After some processing, they are shuffled, and a number x is altered to y . Suppose $1 \leq y \leq n$, design a solution to find x and y in linear time with constant space.
3. Below example program is a solution for the regular number puzzle. Is it equivalent to the queue based solution?

```
Int regularNum(Int m) {
    nums = Int[m + 1]
    n = 0, i = 0, j = 0, k = 0
    nums[0] = 1
    x2 = 2 * nums[i]
    x3 = 3 * nums[j]
    x5 = 5 * nums[k]
    while (n < m) {
        n = n + 1
        nums[n] = min(x2, x3, x5)
        if (x2 == nums[n]) {
            i = i + 1
            x2 = 2 * nums[i]
        }
        if (x3 == nums[n]) {
            j = j + 1
            x3 = 3 * nums[j]
        }
        if (x5 == nums[n]) {
            k = k + 1
            x5 = 5 * nums[k]
        }
    }
    return nums[m];
}
```


Chapter 1

List

1.1 Introduction

List and array are the preliminary build blocks to create complex data structure. Both can hold multiple elements as a container. Array is trivially implemented as a range of consecutive cells indexed by a number. The number is called address or position. Array is typically bounded. Its size need be determined before using. While list increases on-demand to hold additional elements. One can traverse a list one by one from head to tail. Particularly in functional settings, the list related algorithms play critical roles to control the computation and logic structure¹. Readers already familiar with map, filter, fold algorithms are safe to skip this chapter, and directly start from chapter 2.

1.2 Definition

List, also known as singly linked-list is a data structure recursively defined as below:

- A *list* is either empty, denoted as \emptyset or NIL;
- Or contains an element and linked with a *list*.

Figure 1.1 shows a list of nodes. Each node contains two part, an element called key, and a reference to the sub-list called next. The sub-list reference in the last node is empty, marked as ‘NIL’.

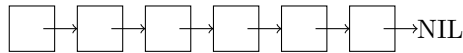


Figure 1.1: A list of nodes

Every node links to the next one or NIL. Linked-list is often defined through compound structure², for example:

```
struct List<A> {  
    A key  
    List<A> next  
}
```

¹In low level, lambda calculus plays the most critical role as one of the computation model equivalent to Turing machine[93], [99].

²In most cases, the data stored in list have the same type. However, there is also heterogeneous list, like the list in Lisp for example.

It needs more clarification for the empty list. Many traditional environments support *null* concept. There are two different ways to represent empty list. One is to use null (or NIL) directly; the other is to construct a list, but put nothing as []. From implementation perspective, null need not allocate any memory, while [] does. In this book, we use \emptyset to represent generic empty list, set, or container.

1.2.1 Access

Given a none empty list L , we need define two functions to access its first element, and the rest sub-list. They are often called $first(L)$, $rest(L)$ or $head(L)$, $tail(L)$ ³. On the other hand, we can construct a list from an element x and another list xs (can be empty), denoted as $x : xs$. It is also called the **cons** operation. We have the following equations hold:

$$\begin{cases} head(x : xs) & = x \\ tail(x : xs) & = xs \end{cases} \quad (1.1)$$

For a none empty list X , we will also use x_1 for the first element, and use X' for the rest sub-list. For example, when $X = [x_1, x_2, x_3, \dots]$, then $X' = [x_2, x_3, \dots]$.

Exercise 1.2

1. For list of type A , suppose we can test if any two elements $x, y \in A$ are equal, define an algorithm to test if two lists are identical.

1.3 Basic operations

From the definition, we can count the length recursively: for empty list, the length is zero, otherwise, it is the length of the sub-list plus one.

$$\begin{aligned} length(\emptyset) &= 0 \\ length(L) &= 1 + length(L') \end{aligned} \quad (1.2)$$

In order to count the length, this algorithm traverses all the elements from head to end, hence it is bound to $O(n)$ time, where n is the number of elements. To avoid repeatedly counting, we can also persist the length in a variable, and update it when mutate (add or delete) the list. Below is the iterative way to count length:

```

1: function LENGTH(L)
2:    $n \leftarrow 0$ 
3:   while  $L \neq \text{NIL}$  do
4:      $n \leftarrow n + 1$ 
5:      $L \leftarrow \text{NEXT}(L)$ 
6:   return  $n$ 

```

We will also use notion $|L|$ for the length of list L when the context is clear.

1.3.1 index

Different from array, which supports random access an element at position i in constant time, we need traverse the list i steps to access the target element.

$$getAt(i, x : xs) = \begin{cases} i = 0 : & x \\ i \neq 0 : & getAt(i - 1, xs) \end{cases} \quad (1.3)$$

³They are named as `car` and `cdr` in Lisp due to the design of machine registers[63].

In order to get the i -th element from a none empty list:

- if i is 0, the result is the first element;
- Otherwise, the result is the $(i - 1)$ -th element in the sub-list.

We intend to leave the empty list not handled. The behavior when pass \emptyset is undefined. As such, the out of bound case also leads to undefined behavior. If $i > |L|$ exceeds the length, we end up the edge case to access the $(i - |L|)$ -th element of the empty list. On the other hand, if $i < 0$, minus it by one makes it even farther away from 0. We finally end up with the same situation that the index is negative, while the list is empty.

This algorithm is bound to $O(i)$ time as it advances the list i steps. Below is the corresponding imperative implementation:

```

1: function GET-AT( $i, L$ )
2:   while  $i \neq 0$  do
3:      $L \leftarrow \text{NEXT}(L)$                                 ▷ Raise error when  $L = \text{NIL}$ 
4:      $i \leftarrow i - 1$ 
5:   return FIRST( $L$ )

```

Exercise 1.3

1. In the iterative GET-AT(i, L) algorithm, what is the behavior when L is empty? what is the behavior when i is out of the bound or negative?

1.3.2 Last

There is a pair of symmetric operations to ‘first/rest’. They are called ‘last/init’. For a none empty list $X = [x_1, x_2, \dots, x_n]$, function *last* returns the last element x_n , while *init* returns the sub-list of $[x_1, x_2, \dots, x_{n-1}]$. Although they are symmetric pairs left to right, ‘last/init’ need linear time, because we need traverse the whole list to tail.

When access the last element of list X :

- If the X contains only one element as $[x_1]$, then x_1 is the last one;
- Otherwise, the result is the last element of the sub-list X' .

$$\begin{aligned} \text{last}([x]) &= x \\ \text{last}(x : xs) &= \text{last}(xs) \end{aligned} \tag{1.4}$$

Similarly, when extract the sub-list of X contains all elements without the last one:

- If X is a singleton $[x_1]$, the result is empty $[\]$;
- Otherwise, we recursively get the initial sub-list for X' , then prepend x_1 to it as the result.

$$\begin{aligned} \text{init}([x]) &= [\] \\ \text{init}(x : xs) &= x : \text{init}(xs) \end{aligned} \tag{1.5}$$

We leave the empty list not handled for both operations. The behavior is undefined if pass \emptyset in. Below are the iterative implementation:

```

1: function LAST( $L$ )
2:    $x \leftarrow \text{NIL}$ 
3:   while  $L \neq \text{NIL}$  do
4:      $x \leftarrow \text{FIRST}(L)$ 

```

```

5:     L ← REST(L)
6:     return x

7: function INIT(L)
8:     L' ← NIL
9:     while REST(L) ≠ NIL do           ▷ Raise error when L is NIL
10:        L' ← CONS(FIRST(L), L')
11:        L ← REST(L)
12:     return REVERSE(L')

```

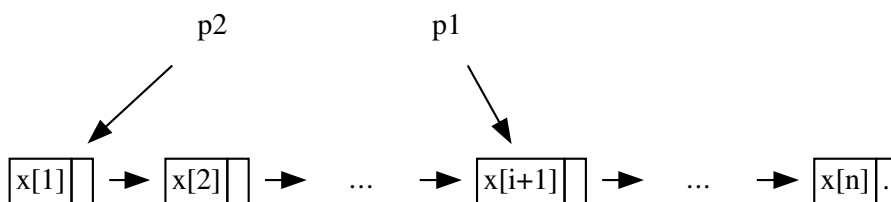
As advancing towards the tail, this algorithm accumulates the ‘init’ result through ‘cons’. However, such result is in the reversed order. We need apply reverse (defined in section 1.4.2) again to return the correct result. There is a question to ask if we can use ‘append’ instead of ‘cons’ in the exercise.

1.3.3 Reverse index

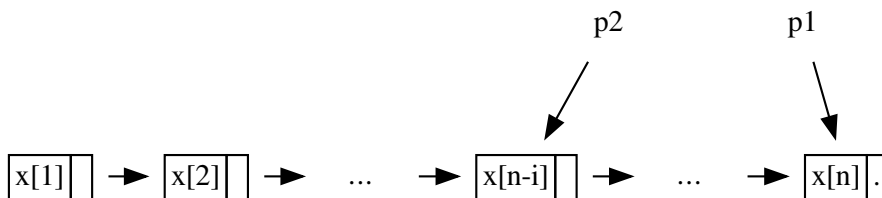
last is a special case of reverse index. The generic case is to find the last i -th element of a given list. The naive implementation takes two rounds of traverse: Determine the length n through the first round; then access the $(n - i - 1)$ -th element through the second round:

$$\text{lastAt}(i, L) = \text{getAt}(|L| - i - 1, L) \quad (1.6)$$

There actually exists better solution. The idea is to keep two pointers p_1, p_2 with the distance i between them. The equation $\text{rest}^i(p_2) = p_1$ holds, where $\text{rest}^i(p_2)$ means repeatedly apply $\text{rest}()$ function i times. When succeed p_2 by i steps gets p_1 . We start by pointing p_2 to the list head, and advance both pointers in parallel till p_1 arrives at tail. At that time point, p_2 exactly points to the i -th element from right. Figure 1.2 shows this idea. As p_1, p_2 form a window, this method is also called ‘sliding window’ solution.



(a) p_2 starts from the head, behind p_1 in i steps.



(b) When p_1 reaches the tail, p_2 points to the i -th element from right.

Figure 1.2: Sliding window formed by two pointers

```

1: function LAST-AT( $i, L$ )

```



```

2:  p ← L
3:  while i > 0 do
4:    L ← REST(L)                                ▷ Raise error if out of bound
5:    i ← i - 1
6:  while REST(L) ≠ NIL do
7:    L ← REST(L)
8:    p ← REST(p)
9:  return FIRST(p)

```

The functional implementation need special consideration as we cannot update pointers directly. Instead, we advance two lists $X = [x_1, x_2, \dots, x_n]$ and $Y = [x_i, x_{i+1}, \dots, x_n]$ simultaneously, where Y is the sub-list without the first $i - 1$ elements.

- If Y is a singleton list, i.e. $[x_n]$, then the last i -th element is the head of X ;
- Otherwise, we drop the first element from both X and Y , then recursively check X' and Y' .

$$\text{lastAt}(i, X) = \text{slide}(X, \text{drop}(i, X)) \quad (1.7)$$

where function $\text{slide}(X, Y)$ drops the heads for both lists:

$$\begin{aligned} \text{slide}(x : xs, [y]) &= x \\ \text{slide}(x : xs, y : ys) &= \text{slide}(xs, ys) \end{aligned} \quad (1.8)$$

Function $\text{drop}(m, X)$ discards the first m elements from list X . It can be implemented by advancing X by m steps:

$$\begin{aligned} \text{drop}(0, X) &= X \\ \text{drop}(m, \emptyset) &= \emptyset \\ \text{drop}(m, x : xs) &= \text{drop}(m - 1, xs) \end{aligned} \quad (1.9)$$

Exercise 1.4

1. In the INIT algorithm, can we use $\text{APPEND}(L', \text{FIRST}(L))$ instead of ‘cons’?
2. How to handle empty list or out of bound index error in LAST-AT algorithm?

1.3.4 Mutate

Mutate operations include append, insert, update, and delete. Some functional environments actually implement mutate by creating a new list, while the original one is persisted for later reuse, or released at sometime (chapter 2 in [3]).

Append

Append is the symmetric operation of *cons*, it adds element on the tail instead of head. Because of this, it is also called ‘snoc’. For linked-list, it means we need traverse to the tail, hence it takes $O(n)$ time, where n is the length. To avoid repeatedly traverse, we can record the tail reference as a variable, and keep updating it upon changes.

$$\begin{aligned} \text{append}(\emptyset, x) &= [x] \\ \text{append}(y : ys, x) &= y : \text{append}(ys, x) \end{aligned} \quad (1.10)$$

- If append x to the empty list, the result is $[x]$;

- Otherwise, we firstly recursive append x to the rest sub-list, then prepend the original head to form the result.

The corresponding iterative implementation is as the following:

```

1: function APPEND( $L, x$ )
2:   if  $L = \text{NIL}$  then
3:     return CONS( $x, \text{NIL}$ )
4:    $H \leftarrow L$  ▷ save the head
5:   while REST( $L$ )  $\neq$  NIL do
6:      $L \leftarrow$  REST( $L$ )
7:   REST( $L$ )  $\leftarrow$  CONS( $x, \text{NIL}$ )
8:   return  $H$ 

```

Update the REST is typically implemented by setting the `next` reference field as shown in below example program.

```

List<A> append(List<A> xs, T x) {
  if (xs == null) {
    return cons(x, null)
  }
  List<A> head = xs
  while (xs.next  $\neq$  null) {
    xs = xs.next
  }
  xs.next = cons(x, null)
  return head
}

```

Exercise 1.5

1. Add a ‘tail’ field in list definition, optimize the append algorithm to constant time.
2. With the additional ‘tail’ field, when need we update the tail variable? How does it affect the performance?

Set value

Similar to `getAt`, we need advance to the target position, then change the element there. To define function `setAt(i, x, L)`:

- If $i = 0$, it means we are changing the first element, the result is $x : L'$;
- Otherwise, we need recursively set the value at position $i - 1$ for the sub-list L' .

$$\begin{aligned}
 \text{setAt}(0, x, y : ys) &= x : ys \\
 \text{setAt}(i, x, y : ys) &= y : \text{setAt}(i - 1, x, ys)
 \end{aligned}
 \tag{1.11}$$

This algorithm is bound to $O(i)$ time, where i is the position to update.

Exercise 1.6

1. Handle the empty list and out of bound error for `setAt`.

insert

There are two different cases about insertion. One is to insert an element at a given position: $insert(i, x, L)$. The algorithm is similar to $setAt$; The other is to insert an element to a sorted list, and keep the order still sorted.

To insert x at position i , we need firstly advance i steps, then construct a new sub-list with x as the head, then concatenate it to the first i elements⁴.

- If $i = 0$, it then turns to be a ‘cons’ operation: $x : L$;
- Otherwise, we recursively insert x to L' at position $i - 1$; then prepend the original head.

$$\begin{aligned} insert(0, x, L) &= x : L \\ insert(i, x, y : ys) &= x : insert(i - 1, x, ys) \end{aligned} \quad (1.12)$$

When i exceeds the list length, we can treat it as to append x . We leave this as an exercise. The following is the corresponding iterative implementation:

```

1: function INSERT( $i, x, L$ )
2:   if  $i = 0$  then
3:     return CONS( $x, L$ )
4:    $H \leftarrow L$ 
5:    $p \leftarrow L$ 
6:   while  $i > 0$  and  $L \neq \text{NIL}$  do
7:      $p \leftarrow L$ 
8:      $L \leftarrow \text{REST}(L)$ 
9:      $i \leftarrow i - 1$ 
10:   $\text{REST}(p) \leftarrow \text{CONS}(x, L)$ 
11:  return  $H$ 

```

If the list $L = [x_1, x_2, \dots, x_n]$ is sorted, i.e. for any position $1 \leq i \leq j \leq n$, then $x_i \leq x_j$ holds. Here \leq is abstract ordering. It can actually mean \geq for descending order, or subset relationship etc. We can design the insert algorithm to maintain the sorted order. To insert element x to a sorted list L :

- If either L is empty or x is not greater than the first element in L , we prepend x to L and returns $x : L$;
- Otherwise, we recursively insert x to the sub-list L' .

$$\begin{aligned} insert(x, \emptyset) &= [x] \\ insert(x, y : ys) &= \begin{cases} x \leq y : & x : y : ys \\ otherwise : & y : insert(x, ys) \end{cases} \end{aligned} \quad (1.13)$$

Since the algorithm need compare elements one by one, it is bound to $O(n)$ time, where n is the length. Below is the corresponding iterative implementation:

```

1: function INSERT( $x, L$ )
2:   if  $L = \text{NIL}$  or  $x < \text{FIRST}(L)$  then
3:     return CONS( $x, L$ )
4:    $H \leftarrow L$ 
5:   while  $\text{REST}(L) \neq \text{NIL}$  and  $\text{FIRST}(\text{REST}(L)) < x$  do
6:      $L \leftarrow \text{REST}(L)$ 

```

⁴ i starts from 0.

```

7:  REST(L) ← CONS(x, REST(L))
8:  return H

```

With this linear time ordered insertion defined, we can further develop the insertion-sort algorithm. The idea is to repeatedly insert elements to the empty list. Since each insert takes linear time, the overall sort is bound to $O(n^2)$.

$$\begin{aligned} \text{sort}(\emptyset) &= \emptyset \\ \text{sort}(x : xs) &= \text{insert}(x, \text{sort}(xs)) \end{aligned} \tag{1.14}$$

This is a recursive algorithm. It firstly sorts the sub-list, then inserts the first element in it. We can eliminate the recursion to develop an iterative implementation. The idea is to scan the list, and one by one insert them:

```

1: function SORT(L)
2:   S ← NIL
3:   while L ≠ NIL do
4:     S ← INSERT(FIRST(L), S)
5:     L ← REST(L)
6:   return S

```

At any time during the loop, the result is sorted. There is a major difference between the recursive and the iterative implementations. The recursive one processes the list from right, while the iterative one is from left. We'll introduce 'tail-recursion' in section 1.3.5 to eliminate this difference. Chapter 3 introduces insertion sort in detail, including performance analysis and optimization.

Exercise 1.7

1. Handle the out-of-bound case in insertion, and treat it as append.
2. Design the insertion algorithm for array. When insert at position i , all elements after i need shift to the end by one.
3. Implement the insertion sort only with less than ($<$) defined.

delete

Symmetric to insert, delete also has two cases. One is to delete the element at a position; the other is to look up, then delete the element of a given value. The first case is defined as $\text{delAt}(i, L)$, the second case is defined as $\text{delete}(x, L)$.

To delete the element at position i , we need advance i steps to the target position, then by pass the element, and link the rest sub-list.

- If L is empty, then the result is empty too;
- If $i = 0$, we are deleting the head, the result is L' ;
- Otherwise, recursively delete the $(i - 1)$ -th element from L' , then prepend the original head as the result.

$$\begin{aligned} \text{delAt}(i, \emptyset) &= \emptyset \\ \text{delAt}(0, x : xs) &= xs \\ \text{delAt}(i, x : xs) &= x : \text{delAt}(i - 1, xs) \end{aligned} \tag{1.15}$$

This algorithm is bound to $O(i)$ as we need advance i steps to perform deleting. Below is the iterative implementation:

```

1: function DEL-AT( $i, L$ )

```

```

2:   S ← CONS(⊥, L)                                ▷ A sentinel node
3:   p ← S
4:   while i > 0 and L ≠ NIL do
5:     i ← i - 1
6:     p ← L
7:     L ← REST(L)
8:   if L ≠ NIL then
9:     REST(p) ← REST(L)
10:  return REST(S)

```

To simplify the implementation, we introduce a sentinel node S , it contains a special value \perp , and its next reference points to L . With S , we are save to cut-off any node in L even for the first one. Finally, we return the list after S as the result, and S itself can be discarded.

For the ‘find and delete’ case, there are two options. We can either find and delete the first occurrence of a value; or remove all the occurrences. The later is more generic, we leave it as an exercise. When delete x from list L :

- If the list is empty, the result is \emptyset ;
- Otherwise, we compare the head and x , if they are equal, then the result is L' ;
- If the head does not equal to x , we keep the head, and recursively delete x in L' .

$$\begin{aligned}
 delete(x, \emptyset) &= \emptyset \\
 delete(x, y : ys) &= \begin{cases} x = y : ys \\ x \neq y : y : delete(x, ys) \end{cases} \quad (1.16)
 \end{aligned}$$

This algorithm is bound to $O(n)$ time, where n is the length, as it need scan the list to find the target element. For the iterative implementation, we also introduce a sentinel node to simplify the logic:

```

1: function DELETE( $x, L$ )
2:   S ← CONS(⊥, L)
3:   p ← L
4:   while L ≠ NIL and FIRST(L) ≠  $x$  do
5:     p ← L
6:     L ← REST(L)
7:   if L ≠ NIL then
8:     REST(p) ← REST(L)
9:   return REST(S)

```

Exercise 1.8

1. Design the algorithm to find and delete all occurrences of a given value.
2. Design the delete algorithm for array, all elements after the delete position need shift to front by one.

concatenate

Append is a special case for concatenation. Append only adds one element, while concatenation adds multiple ones. However, the performance would be quadratic if repeatedly appending as below:

$$\begin{aligned}
 X \# \emptyset &= X \\
 X \# (y : ys) &= append(X, y) \# ys \quad (1.17)
 \end{aligned}$$

In this implementation when concatenate X and Y , each append operation traverses to the tail, and we do this for $|Y|$ times. the total time is bound to $O(|X| + (|X| + 1) + \dots + (|X| + |Y|)) = O(|X||Y| + |Y|^2)$. Consider the link (cons) operation is fast (constant time), we can traverse to the tail of X only once, then link Y to the tail.

- If X is empty, the result is Y ;
- Otherwise, we concatenate the sub-list X' with Y , then prepend the head as the result.

We can further improve it a bit: when Y is empty, we needn't traverse, but directly return X :

$$\begin{aligned} \emptyset \# Y &= Y \\ X \# \emptyset &= X \\ (x : xs) \# Y &= x : (xs \# Y) \end{aligned} \tag{1.18}$$

The modified algorithm only traverse list X , then link its tail to Y , hence it is bound $O(|X|)$ time. In imperative settings, concatenation can be realized in constant time with the additional tail variable. We leave its implementation as exercise. Below is the iterative implementation without using the tail variable:

```

1: function CONCAT( $X, Y$ )
2:   if  $X = \text{NIL}$  then
3:     return  $Y$ 
4:   if  $Y = \text{NIL}$  then
5:     return  $X$ 
6:    $H \leftarrow X$ 
7:   while  $\text{REST}(X) \neq \text{NIL}$  do
8:      $X \leftarrow \text{REST}(X)$ 
9:    $\text{REST}(X) \leftarrow Y$ 
10:  return  $H$ 

```

1.3.5 sum and product

It is common to calculate the sum or product of a list of numbers. They have almost same structure. We will introduce how to abstract them to higher order computation in section 1.6.

Recursive sum and product

To calculate the sum of a list:

- If the list is empty, the result is zero;
- Otherwise, the result is the first element plus the sum of the rest.

$$\begin{aligned} \text{sum}(\emptyset) &= 0 \\ \text{sum}(x : xs) &= x + \text{sum}(xs) \end{aligned} \tag{1.19}$$

We can't merely replace $+$ to \times to obtain product algorithm, because it always returns zero. We need define the product of the empty list as 1.

$$\begin{aligned} \text{product}(\emptyset) &= 1 \\ \text{product}(x : xs) &= x \cdot \text{product}(xs) \end{aligned} \tag{1.20}$$

Both algorithms traverse the list, hence are bound to $O(n)$ time, where n is the length.

Tail call recursion

Both sum and product algorithms calculate from right to left. We can change them to calculate the *accumulated* result from left to right. For sum, it accumulates from 0, then adds element one by one; while for product, it starts from 1, then repeatedly multiplying elements. The accumulate process can be defined as:

- If the list is empty, return the accumulated result;
- Otherwise, accumulate the first element to the result, then go on accumulating.

Below are the accumulated sum and product:

$$\begin{aligned} \text{sum}'(A, \emptyset) &= A & \text{prod}'(A, \emptyset) &= A \\ \text{sum}'(A, x : xs) &= \text{sum}(x + A, xs) & \text{prod}'(A, x : xs) &= \text{prod}'(x \cdot A, xs) \end{aligned} \quad (1.21)$$

Given a list, we can call sum' with 0, and prod' with 1:

$$\text{sum}(X) = \text{sum}'(0, X) \quad \text{product}(X) = \text{prod}'(1, X) \quad (1.22)$$

Or merely simplify it to Curried form:

$$\text{sum} = \text{sum}'(0) \quad \text{product} = \text{prod}'(1)$$

Curried form was introduced by Schönfinkel (1889 - 1942) in 1924, then widely used by Haskell Curry from 1958. It is known as *Currying*[73]. For a function taking 2 parameters $f(x, y)$, when pass one argument x , it ends up to another function of y : $g(y) = f(x, y)$ or $g = f x$. We can further extend it to multiple variables, that $f(x, y, \dots, z)$ can be Curried to a series of functions: $f, f x, f x y, \dots$. No matter how many variables, we can treat them as a series of Curried function, each has only one parameter: $f(x, y, \dots, z) = f(x)(y)\dots(z) = f x y \dots z$.

The accumulated sum does not only calculate the result from left to right, it needn't book keeping any context, state, or intermediate result for recursion. All such states are either passed as argument (i.e. A), or can be dropped (the previous element in the list). Such recursive calls are often optimized as pure loops in practice. We call this kind of function as *tail recursion* (or 'tail call'), and the optimization to eliminate recursion is called 'tail recursion optimization'[61], because the recursion happens at the tail place in the function. The performance of tail call can be greatly improved after optimization, and we can avoid the issue of stack overflow in deep recursions.

In section 1.3.4 about insertion sort, we mentioned the recursive algorithm sorts elements from right. We can also optimize it to tail call:

$$\begin{aligned} \text{sort}'(A, \emptyset) &= A \\ \text{sort}'(A, x : xs) &= \text{sort}'(\text{insert}(x, A), xs) \end{aligned} \quad (1.23)$$

And the sort is defined in Curried form with \emptyset as the start value:

$$\text{sort} = \text{sort}'(\emptyset) \quad (1.24)$$

As a typical tail call problem, let's consider how to compute b^n effectively? (refer to problem 1.16 in [63].) A brute-force solution is to repeatedly multiplying b for n times from 1. This algorithm is bound to $O(n)$:

- 1: **function** POW(b, n)
- 2: $x \leftarrow 1$
- 3: **loop** n times

```

4:     x ← x · b
5:     return x

```

Actually, the solution can be greatly improved. When compute b^8 , after the first 2 loops, we get $x = b^2$. At this stage, we needn't multiply x with b to get b^3 , but directly compute x^2 , which gives b^4 . If do this again, we get $(b^4)^2 = b^8$. Thus we only need loop 3 times, but not 8 times.

Based on this idea, if $n = 2^m$ for some none negative integer m , we can design below algorithm to compute b^n :

$$\begin{aligned} b^1 &= b \\ b^n &= (b^{\frac{n}{2}})^2 \end{aligned}$$

We next extend this divide and conquer method for any none negative integer n :

- If $n = 0$, define $b^0 = 1$;
- If n is even, we halve n , to compute $b^{\frac{n}{2}}$. Then square it;
- Otherwise n is odd. Since $n - 1$ is even, we recursively compute b^{n-1} , the multiply b atop it.

$$\begin{aligned} b^0 &= 1 \\ b^n &= \begin{cases} 2|n : & (b^{\frac{n}{2}})^2 \\ otherwise : & b \cdot b^{n-1} \end{cases} \end{aligned} \quad (1.25)$$

However, the 2nd clause blocks us to turn it tail recursive. Alternatively, we can square the base number, and halve the exponent.

$$\begin{aligned} b^0 &= 1 \\ b^n &= \begin{cases} 2|n : & (b^2)^{\frac{n}{2}} \\ otherwise : & b \cdot b^{n-1} \end{cases} \end{aligned} \quad (1.26)$$

With this change, we can develop a tail recursive algorithm to compute $b^n = \text{pow}(b, n, 1)$.

$$\begin{aligned} \text{pow}(b, 0, A) &= A \\ \text{pow}(b, n, A) &= \begin{cases} 2|n : & \text{pow}(b^2, \frac{n}{2}, A) \\ otherwise : & \text{pow}(b, n-1, b \cdot A) \end{cases} \end{aligned} \quad (1.27)$$

Compare to the brute-force implementation, this one improves to $O(\lg n)$ time. Actually, we can improve it further. If represent n in binary format $n = (a_m a_{m-1} \dots a_1 a_0)_2$, we clearly know that the computation for b^{2^i} is necessary if $a_i = 1$. This is quite similar to the idea of Binomial heap (section 10.2). We can multiplying all of them for bits of 1.

For example, when compute b^{11} , as $11 = (1011)_2 = 2^3 + 2 + 1$, thus $b^{11} = b^{2^3} \times b^2 \times b$. We get the result by these steps:

1. calculate b^1 , which is b ;
2. Square to b^2 from the previous result;
3. Square again to b^{2^2} from step 2;
4. Square to b^{2^3} from step 3.

Finally, we multiply the result of step 1, 2, and 4 to get b^{11} . Summarize this idea, we improve the algorithm as below.

$$\begin{aligned} \text{pow}(b, 0, A) &= A \\ \text{pow}(b, n, A) &= \begin{cases} 2|n : & \text{pow}(b^2, \frac{n}{2}, A) \\ \text{otherwise} : & \text{pow}(b^2, \lfloor \frac{n}{2} \rfloor, b \cdot A) \end{cases} \end{aligned} \quad (1.28)$$

This algorithm essentially shifts n to right 1 bit each time (divide n by 2). If the LSB (Least Significant Bit, the lowest) is 0, n is even. It squares the base and keeps the accumulator A unchanged; If the LSB is 1, n is odd. It squares the base and accumulates it to A ; When n is zero, we exhaust all bits, A is the final result. At any time, the updated base number b' , the shifted exponent number n' , and the accumulator A satisfy the invariant $b^n = A \cdot (b')^{n'}$.

Compare to previous implementation, which minus by one for odd n , this algorithm halves n every time. It exactly runs m rounds, where m is the number of bits. We leave the imperative implementation as exercise.

Back to the sum and product. The iterative implementation applies plus and multiply while traversing:

```

1: function SUM( $L$ )
2:    $s \leftarrow 0$ 
3:   while  $L \neq \text{NIL}$  do
4:      $s \leftarrow s + \text{FIRST}(L)$ 
5:      $L \leftarrow \text{REST}(L)$ 
6:   return  $s$ 

7: function PRODUCT( $L$ )
8:    $p \leftarrow 1$ 
9:   while  $L \neq \text{NIL}$  do
10:     $p \leftarrow p \cdot \text{FIRST}(L)$ 
11:     $L \leftarrow \text{REST}(L)$ 
12:  return  $p$ 

```

One interesting usage of product is to calculate factorial of n as: $n! = \text{product}([1..n])$.

1.3.6 maximum and minimum

For a list of comparable elements (we can define order for any two elements), there is the maximum and minimum. The algorithm structure of *max/min* is same. For a none empty list:

- If there is only one element (a singleton) $[x_1]$, the result is x_1 ;
- Otherwise, we recursively find the min/max of the sub-list, then compare it with the first element to determine the result.

$$\begin{aligned} \text{min}([x]) &= x \\ \text{min}(x : xs) &= \begin{cases} x < \text{min}(xs) : & x \\ \text{otherwise} : & \text{min}(xs) \end{cases} \end{aligned} \quad (1.29)$$

and

$$\begin{aligned} \text{max}([x]) &= x \\ \text{max}(x : xs) &= \begin{cases} x > \text{max}(xs) : & x \\ \text{otherwise} : & \text{max}(xs) \end{cases} \end{aligned} \quad (1.30)$$

Both process the list from right to left. We can modify them to tail recursive. It also brings us the ‘on-line’ feature, that at any time, the accumulator is the min/max so far processed. Use *min* for example:

$$\begin{aligned} \min'(a, \emptyset) &= a \\ \min'(a, x : xs) &= \begin{cases} x < a : & \min'(x, xs) \\ \text{otherwise} : & \min'(a, xs) \end{cases} \end{aligned} \quad (1.31)$$

Different from *sum'/prod'*, we can't pass a fixed starting value to the tail recursive *min'/max'*, unless we use $\pm\infty$ in below Curried form:

$$\min = \min'(\infty) \quad \max = \max'(-\infty)$$

Alternatively, we can pass the first element as the accumulator given min/max only takes none empty list:

$$\min(x : xs) = \min'(x, xs) \quad \max(x : xs) = \max'(x, xs) \quad (1.32)$$

The optimized tail recursive algorithm can be further changed to purely iterative implementation. We give the MIN example, and skip MAX.

```

1: function MIN(L)
2:   m ← FIRST(L)
3:   L ← REST(L)
4:   while L ≠ NIL do
5:     if FIRST(L) < m then
6:       m ← FIRST(L)
7:     L ← REST(L)
8:   return m

```

There is a way to realize the tail recursive algorithm without using accumulator explicitly. The idea is to re-use the first element as the accumulator. Every time, we compare the head with the next element; then drop the greater one for *min*, and drop the less one for *max*.

$$\begin{aligned} \min([x]) &= x \\ \min(x_1 : x_2 : xs) &= \begin{cases} x_1 < x_2 : & \min(x_1 : xs) \\ \text{otherwise} : & \min(x_2 : xs) \end{cases} \end{aligned} \quad (1.33)$$

We skip the definition for *max* as it is symmetric.

Exercise 1.9

1. Change the *length* to tail call.
2. Change the insertion sort to tail call.
3. Implement the $O(\lg n)$ algorithm to calculate b^n by represent n in binary.

1.4 Transform

From algebraic perspective, there are two types of transform: one keeps the list structure, but only change the elements; the other alter the list structure, hence the result is not isomorphic to the original list. Particularly, we call the former *map*.

1.4.1 map and for-each

The first example is to convert a list of numbers to their represented strings, like to change [3, 1, 2, 4, 5] to ["three", "one", "two", "four", "five"]

$$\begin{aligned} toStr(\emptyset) &= \emptyset \\ toStr(x : xs) &= str(x) : toStr(xs) \end{aligned} \quad (1.34)$$

For the second example, consider a dictionary, which is a list of words grouped by initial letter. Like:

```
[[a, an, another, ... ],
 [bat, bath, bool, bus, ...],
 ...,
 [zero, zoo, ...]]
```

Next we process a text (*Hamlet* for example), and augment each word with their number of occurrence, like:

```
[[ (a, 1041), (an, 432), (another, 802), ... ],
 [ (bat, 5), (bath, 34), (bool, 11), (bus, 0), ... ],
 ...,
 [ (zero 12), (zoo, 0), ... ]]
```

Now for every initial letter, we want to figure out which word occurs most. How to write a program to do this work? The output is a list of words, that every one has the most occurrences in the group, something like [a, but, can, ...]. We need develop a program that transform **a list of groups of word-number pairs** into **a list of words**.

First, we need define a function. It takes a list of word-number pairs, finds the word paired with the biggest number. Sort is overkill. What we need is a special max function $maxBy(cmp, L)$, where cmp compares two elements abstractly.

$$\begin{aligned} maxBy(cmp, [x]) &= x \\ maxBy(cmp, x_1 : x_2 : xs) &= \begin{cases} cmp(x_1, x_2) : maxBy(cmp, x_2 : xs) \\ otherwise : maxBy(cmp, x_1 : xs) \end{cases} \end{aligned} \quad (1.35)$$

For a pair $p = (a, b)$ we define two access functions:

$$\begin{cases} fst(a, b) = a \\ snd(a, b) = b \end{cases} \quad (1.36)$$

Instead of embedded parenthesis $fst((a, b)) = a$, we omit one layer, and use a space. Generally, we treat $f x = f(x)$ when the context is clear. Then we can define a special compare function for word-count pairs:

$$less(p_1, p_2) = snd(p_1) < snd(p_2) \quad (1.37)$$

Then pass $less$ to $maxBy$ to finalize our definition (in Curried form):

$$max'' = maxBy(less) \quad (1.38)$$

With $max''()$ defined, we can develop the solution to process the whole list.

$$\begin{aligned} solve(\emptyset) &= \emptyset \\ solve(x : xs) &= fst(max''(x)) : solve(xs) \end{aligned} \quad (1.39)$$

Map

The `solve()` and `toStr()` functions reveal the same structure, although they are developed for different problems. We can abstract this common structure as `map`:

$$\begin{aligned} \text{map}(f, \emptyset) &= \emptyset \\ \text{map}(f, x : xs) &= f(x) : \text{map}(f, xs) \end{aligned} \quad (1.40)$$

`map` takes the function f as argument, applies it to every element to form a new list. A function that computes with other functions is called *high-order* function. If the type of f is $A \rightarrow B$, which means it sends an element of A to the result of B , then the type of `map` is:

$$\text{map} :: (A \rightarrow B) \rightarrow [A] \rightarrow [B] \quad (1.41)$$

We read it as: `map` takes a function of $A \rightarrow B$, then convert a list $[A]$ to another list $[B]$. The two examples in previous section can be defined with `map` as (in Curried form):

$$\begin{aligned} \text{toStr} &= \text{map } \text{str} \\ \text{solve} &= \text{map } (\text{fst} \circ \text{max}'') \end{aligned}$$

Where $f \circ g$ means function composite, i.e. first apply g then apply f . $(f \circ g) x = f(g(x))$, Read as f after g . `Map` can also be defined from the domain theory point of view. Function $y = f(x)$ defines the map from x in set X to y in set Y :

$$Y = \{f(x) | x \in X\} \quad (1.42)$$

This type of set definition is called Zermelo-Frankel set abstraction (known as ZF expression) [72]. The different is that the mapping is from a list (but not set) to another: $Y = [f(x) | x \in X]$. There can be duplicated elements. For list, such ZF style expression is called *list comprehension*.

List comprehension is a powerful tool. As an example, let us see how to realize the permutation algorithm. Extend from generating all-permutations as [72] and [94], we define a generic `perm(L, r)`, that permutes r out of the total n elements in the list L .

There are total $P_n^r = \frac{n!}{(n-r)!}$ solutions.

$$\text{perm}(L, r) = \begin{cases} |L| < r \text{ or } r = 0 : & [[]] \\ \text{otherwise} : & [x : ys \mid x \in L, ys \in \text{perm}(\text{delete}(x, L), r - 1)] \end{cases} \quad (1.43)$$

If pick zero element for permutation, or there are too few (less than r), the result is a list of empty list; otherwise, we recursively pick $r - 1$ out of the rest $n - 1$ elements; then prepend x before each. Below Haskell example program utilizes the list comprehension feature:

```
perm xs r | r == 0 || length xs < r = [[]]
          | otherwise = [ x:ys | x <- xs,
                             ys <- perm (delete x xs) (r-1)]
```

For the iterative MAP implementation, below algorithm uses a sentinel node to simplify the logic to handle head reference.

- 1: **function** MAP(f, L)
- 2: $L' \leftarrow \text{CONS}(\perp, \text{NIL})$ ▷ Sentinel node
- 3: $p \leftarrow L'$
- 4: **while** $L \neq \text{NIL}$ **do**

```

5:      $x \leftarrow \text{FIRST}(L)$ 
6:      $L \leftarrow \text{REST}(L)$ 
7:      $\text{REST}(p) \leftarrow \text{CONS}(f(x), \text{NIL})$ 
8:      $p \leftarrow \text{REST}(p)$ 
9:     return  $\text{REST}(L)$ 

```

▷ Drop the sentinel

For each

Sometimes we only need to traverse the list, repeatedly process the elements one by one without building the new list. Here is an example that print every element out:

```

1: function PRINT( $L$ )
2:   while  $L \neq \text{NIL}$  do
3:     print  $\text{FIRST}(L)$ 
4:      $L \leftarrow \text{REST}(L)$ 

```

More generally, we can pass a procedure P , then traverse the list and apply P to each element.

```

1: function FOR-EACH( $P, L$ )
2:   while  $L \neq \text{NIL}$  do
3:      $P(\text{FIRST}(L))$ 
4:      $L \leftarrow \text{REST}(L)$ 

```

Examples

As an example, let's see a “ n -lights puzzle”[96]. There are n lights in a room, all of them are off. We execute the following n rounds:

1. Switch all the lights in the room (all on);
2. Switch lights with number 2, 4, 6, ... , that every other light is switched, if the light is on, it will be off;
3. Switch every third lights, number 3, 6, 9, ... ;
4. ...

And at the last round, only the last light (the n -th light) is switched. The question is how many lights are on in the end?

Let's start with a brute-force solution, then improve it step by step. We represent the state of n lights as a list of 0/1 numbers. 0 is off, 1 is on. The initial state are all zeros: $[0, 0, \dots, 0]$. We label the light from 1 to n , then map them to $(i, \text{on/off})$ pairs:

$$\text{lights} = \text{map}(i \mapsto (i, 0), [1, 2, 3, \dots, n])$$

It binds each number to zero, the result is a list of pairs: $L = [(1, 0), (2, 0), \dots, (n, 0)]$. Next we operate this list of pairs for n rounds. In the i -th round, switch the second value in this pair if its label is divided by i . Consider $1 - 0 = 1$, and $1 - 1 = 0$, we can switch 0/1 value of x by $1 - x$. For light (j, x) , if $i|j$, (i.e. $j \bmod i = 0$), then switch, otherwise leave the light untouched.

$$\text{switch}(i, (j, x)) = \begin{cases} j \bmod i = 0 : & (j, 1 - x) \\ \text{otherwise} : & (j, x) \end{cases} \quad (1.44)$$

The i -th round for all lights can be realized as map:

$$\text{map}(\text{switch}(i), L) \quad (1.45)$$

Here we use the Curried form of *switch*, which is equivalent to:

$$\text{map}((j, x) \mapsto \text{switch}(i, (j, x)), L)$$

Next, we define a function *op*(), which performs above mapping on *L* over and over by *n* rounds. We call this function with *op*([1, 2, ..., *n*], *L*).

$$\begin{aligned} \text{op}(\emptyset, L) &= L \\ \text{op}(i : is, L) &= \text{op}(is, \text{map}(\text{switch}(i), L)) \end{aligned} \quad (1.46)$$

At this stage, we can sum the second value of each pair in list *L* to get the answer.

$$\text{solve}(n) = \text{sum}(\text{map}(\text{snd}, \text{op}([1, 2, \dots, n], \text{lights}))) \quad (1.47)$$

Below is the example Haskell implementation of this brute-force solution:

```

solve = sum ◦ (map snd) ◦ proc where
  lights = map (λi → (i, 0)) [1..n]
  proc n = operate [1..n] lights
  operate [] xs = xs
  operate (i:is) xs = operate is (map (switch i) xs)

switch i (j, x) = if j `mod` i == 0 then (j, 1 - x) else (j, x)

```

Run this program from 1 light to 100 lights, let's see what the answers are (we added line breaks):

```

[1,1,1,
 2,2,2,2,2,
 3,3,3,3,3,3,3,
 4,4,4,4,4,4,4,4,4,
 5,5,5,5,5,5,5,5,5,5,5,
 6,6,6,6,6,6,6,6,6,6,6,6,6,
 7,7,7,7,7,7,7,7,7,7,7,7,7,7,7,
 8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,8,
 9,9,9,9,9,9,9,9,9,9,9,9,9,9,9,9,9,10]

```

This result is interesting:

- the first 3 answers are 1;
- the 4-th to the 8-th answers are 2;
- the 9-th to the 15-th answers are 3;
- ...

It seems that the i^2 -th to the $((i + 1)^2 - 1)$ -th answers are i . Actually, we can prove it:

Proof. Given n lights labeled from 1 to n , consider which lights are on finally. Since the initial states for all lights are off, we can say that, the lights which are manipulated odd times are on. For every light i , it will be switched at the j round if i can be divided by j (denote as $j|i$). Only the lights which have odd number of factors are on in the end.

The key point to solve this puzzle, is to find all numbers which have odd number of factors. For any positive integer n , let S be the set of all factors of n . S is initialized to \emptyset . If p is a factor of n , there must exist a positive integer q such that $n = pq$ holds. It means q is also a factor of n . We add 2 different factors to set S if and only if $p \neq q$, which keeps $|S|$ even all the time unless $p = q$. In such case, n is a square number. We can only add 1 factor to set S , which leads to odd number of factors. \square

At this stage, we can design a fast solution by finding the number of square numbers under n .

$$\text{solve}(n) = \lfloor \sqrt{n} \rfloor \quad (1.48)$$

Below Haskell example program outputs the answer for 1, 2, ..., 100 lights:

```
map (floor ∘ sqrt) [1..100]
```

Map is a generic concept does not limit to list. It can be applied to many complex algebraic structures. The next chapter about binary search tree explains how to map on trees. As long as we can traverse the structure, and the empty is defined, we can use the same mapping idea.

1.4.2 reverse

It's a classic exercise to reverse a singly linked-list with minimum space. One must carefully manipulate the node reference, however, there exists easy method to implement reverse:

1. Write a purely recursive solution;
2. Change it to tail-call;
3. Translate the tail-call solution to imperative operations.

The purely recursive solution is straightforward. To reverse a list L .

- If L is empty, the reversed result is empty;
- Otherwise, recursively reverse sub-list L' , then append the first element to the end.

$$\begin{aligned} \text{reverse}(\emptyset) &= \emptyset \\ \text{reverse}(x : xs) &= \text{append}(\text{reverse}(xs), x) \end{aligned} \quad (1.49)$$

However, the performance is poor. As it need traverse to the end to append, this algorithm is bound to quadratic time. We can optimize it with tail call, use an accumulator to store the reversed part so far. We initialize the accumulator as empty: $\text{reverse} = \text{reverse}'(\emptyset)$.

$$\begin{aligned} \text{reverse}'(A, \emptyset) &= A \\ \text{reverse}'(A, x : xs) &= \text{reverse}'(x : A, xs) \end{aligned} \quad (1.50)$$

Different from appending, $\text{cons}(\cdot)$ is a constant time operation. The idea is to repeatedly take the elements from the head, and prepend them to the accumulator. It essentially likes to store elements in a stack, then pop them out. The overall performance is $O(n)$, where n is the length. Since tail call need not keep the context, we can optimize it to purely iterative loops:

- 1: **function** REVERSE(L)
- 2: $A \leftarrow \text{NIL}$
- 3: **while** $L \neq \text{NIL}$ **do**
- 4: $A \leftarrow \text{CONS}(\text{FIRST}(L), A)$
- 5: $L \leftarrow \text{REST}(L)$
- 6: **return** A

However, this algorithm creates a new reversed list, but not mutate the original one. We need change it to in-place mutate L as the below example program:

```

List<T> reverse(List<T> xs) {
  List<T> p, ys = null
  while (xs ≠ null) {
    p = xs
    xs = xs.next
    p.next = ys
    ys = p
  }
  return ys
}

```

Exercise 1.10

1. Given a number from 0 to 1 billion, write a program to give its English representation. For e.g. 123 is ‘one hundred and twenty three’. What if there is decimal part?
2. Implement the algorithm to find the maximum value in a list of pairs $[(k, v)]$ in tail call.

1.5 Sub-list

Different from array which is capable to slice a continuous segment fast, it typically need linear time to traverse and extract sub-list.

1.5.1 take, drop, and split-at

Taking the first n elements is essentially to slice the list from 1 to n : $sublist(1, n, L)$. If either $n = 0$ or $L = \emptyset$, the sub-list is empty; otherwise, we recursively take the first $n - 1$ elements from the L' , then prepend the first element.

$$\begin{aligned}
 take(0, L) &= \emptyset \\
 take(n, \emptyset) &= \emptyset \\
 take(n, x : xs) &= x : take(n - 1, xs)
 \end{aligned} \tag{1.51}$$

This algorithm handles the out of bound case like this: if $n > |L|$ or n is negative, it ends up to the edge case that L becomes empty, hence returns the whole list as the result.

Drop, on the other hand, discards the first n elements and returns the rest. It is equivalent to slice the sub-list from right: $sublist(n + 1, |L|, L)$, where $|L|$ is the length. Its implementation is symmetric:

$$\begin{aligned}
 drop(0, L) &= L \\
 drop(n, \emptyset) &= \emptyset \\
 drop(n, x : xs) &= drop(n - 1, xs)
 \end{aligned} \tag{1.52}$$

We leave the imperative implementation for $take/drop$ as exercise. As the next step, we can develop a algorithm to extract sub-list at any position for a given length:

$$sublist(from, cnt, L) = take(cnt, drop(from - 1, L)) \tag{1.53}$$

Or slice the list with left and right boundaries:

$$slice(from, to, L) = drop(from - 1, take(to, L)) \tag{1.54}$$

The boundary is defined as $[from, to]$. It includes both ends. We can also split a list at a given position:

$$splitAt(i, L) = (take(i, L), drop(i, L)) \quad (1.55)$$

Exercise 1.11

1. Define *sublist* and *slice* in Curried Form without L as parameter.

conditional take and drop

Instead of specifying number of elements for *take/drop*, one may want to provide a predication. We keep taking or dropping as far as the condition meets. We define such algorithm as *takeWhile/dropWhile*.

takeWhile/dropWhile examine elements one by one against the prediction. They ignore the rest even if some elements satisfy the condition. We'll see this different in the section of filtering.

$$\begin{aligned} takeWhile(p, \emptyset) &= \emptyset \\ takeWhile(p, x : xs) &= \begin{cases} p(x) : & x : takeWhile(p, xs) \\ otherwise : & \emptyset \end{cases} \end{aligned} \quad (1.56)$$

Where p is the prediction. When applied to an element, p returns true or false to indicate the condition is satisfied. *dropWhile* is symmetric:

$$\begin{aligned} dropWhile(p, \emptyset) &= \emptyset \\ dropWhile(p, x : xs) &= \begin{cases} p(x) : & dropWhile(p, xs) \\ otherwise : & x : xs \end{cases} \end{aligned} \quad (1.57)$$

1.5.2 break and group

Break and group are operations to re-arrange a list into multiple sub-lists. They typically perform the re-arrangement while traverse the list to keep the performance linear.

break and span

break/span can be considered as a general form of splitting. Instead of splitting at a given position, *break/span* scans elements with a prediction. It extracts the longest prefix of the list against the condition, and returns it together with the rest as a pair.

There are two different cases. For a given predication, one is to pick the elements satisfied; the other is to pick the elements not satisfied. The former is called *span*, the later is called *break*.

$$\begin{aligned} span(p, \emptyset) &= (\emptyset, \emptyset) \\ span(p, x : xs) &= \begin{cases} p(x) : & (x : A, B) \text{ where } (A, B) = span(p, xs) \\ otherwise : & (\emptyset, x : xs) \end{cases} \end{aligned} \quad (1.58)$$

and we can define *break* with *span* by negating the predication in Curried form:

$$break(p) = span(\neg p) \quad (1.59)$$

Both *span* and *break* find the longest *prefix*. They stop immediately when the condition does not meet and ignores the rest. Below is the iterative implementation for *span*:

```

1: function SPAN( $p, L$ )
2:    $A \leftarrow \text{NIL}$ 
3:   while  $L \neq \text{NIL}$  and  $p(\text{FIRST}(L))$  do
4:      $A \leftarrow \text{CONS}(\text{FIRST}(L), A)$ 
5:      $L \leftarrow \text{REST}(L)$ 
6:   return ( $A, L$ )

```

This algorithm creates a new list to hold the longest prefix, another option is to reuse the original list and break it in-place:

```

1: function SPAN( $p, L$ )
2:    $A \leftarrow L$ 
3:    $tail \leftarrow \text{NIL}$ 
4:   while  $L \neq \text{NIL}$  and  $p(\text{FIRST}(L))$  do
5:      $tail \leftarrow L$ 
6:      $L \leftarrow \text{REST}(L)$ 
7:   if  $tail = \text{NIL}$  then
8:     return ( $\text{NIL}, L$ )
9:    $\text{REST}(tail) \leftarrow \text{NIL}$ 
10:  return ( $A, L$ )

```

group

span breaks list into two parts, group divides list into multiple sub-lists. For example, we can use group to change a long word into small units, each contains consecutive same characters:

```

group ``Mississippi'' = [``M'', ``i'', ``ss'', ``i'',
                          ``ss'', ``i'', ``pp'', ``i'']

```

For another example, given a list of numbers:

$$L = [15, 9, 0, 12, 11, 7, 10, 5, 6, 13, 1, 4, 8, 3, 14, 2]$$

We can divide it into small lists, each one is in descending order:

$$\text{group}(L) = [[15, 9, 0], [12, 11, 7], [10, 5], [6], [13, 1], [4], [8, 3], [14, 2]]$$

These are useful operations. The string groups can be used to build Radix tree, a data structure support fast text search. The number groups can be used to implement nature merge sort algorithm. We'll introduce them in later chapters.

We can abstract the group condition as a relation \sim . It tests whether two consecutive elements x, y are generic 'equivalent': $x \sim y$. We scan and list and compare two elements each time. If they match, we add both to a group; otherwise, only add x to the group, and use y to initialize another group.

$$\begin{aligned}
 \text{group}(\sim, \emptyset) &= [\emptyset] \\
 \text{group}(\sim, [x]) &= [[x]] \\
 \text{group}(\sim, x : y : xs) &= \begin{cases} x \sim y : & (x : ys) : yss \\ \text{otherwise} : & [x] : ys : yss \end{cases} \quad (1.60)
 \end{aligned}$$

where $(ys : yss) = \text{group}(\sim, xs)$. This algorithm is bound to $O(n)$ time, where n is the length. We can also implement the iterative group algorithm. For the none empty list L , we initialize the result groups as $[[x_1]]$, where x_1 is the first element. We scan the list from the second one, append it to the last group if the two consecutive elements are 'equivalent'; otherwise we start a new group.

```

1: function GROUP( $\sim, L$ )
2:   if  $L = \text{NIL}$  then
3:     return [NIL]
4:    $x \leftarrow \text{FIRST}(L)$ 
5:    $L \leftarrow \text{REST}(L)$ 
6:    $g \leftarrow [x]$ 
7:    $G \leftarrow [g]$ 
8:   while  $L \neq \text{NIL}$  do
9:      $y \leftarrow \text{FIRST}(L)$ 
10:    if  $x \sim y$  then
11:       $g \leftarrow \text{APPEND}(g, y)$ 
12:    else
13:       $g \leftarrow [y]$ 
14:       $G \leftarrow \text{APPEND}(G, g)$ 
15:     $x \leftarrow y$ 
16:     $L \leftarrow \text{NEXT}(L)$ 
17:   return  $G$ 

```

However, this program performs in quadratic time if the append isn't optimized with the tail reference. If don't care the order, we can alternatively change append to cons. With the group algorithm defined, we can realize the above 2 cases as below:

$$\text{group}(=, [m, i, s, s, i, s, s, i, p, p, i]) = [[M], [i], [ss], [i], [ss], [i], [pp], [i]]$$

and

$$\begin{aligned} \text{group}(\geq, [15, 9, 0, 12, 11, 7, 10, 5, 6, 13, 1, 4, 8, 3, 14, 2]) \\ = [[15, 9, 0], [12, 11, 7], [10, 5], [6], [13, 1], [4], [8, 3], [14, 2]] \end{aligned}$$

Another method to implement group is to use the *span* function. Given a predication, span breaks the list into two parts: the longest sub-list satisfies the condition, and the rest. We can repeatedly apply span to the rest part till it becomes empty. However, the predication passed to span is an unary function. It takes an element and tests it. While in group, the predication is a binary function. It takes two elements and compares. We can use Currying: to pass and fix the first element in the binary predication, then use the Curried function to test the other.

$$\begin{aligned} \text{group}(\sim, \emptyset) &= [\emptyset] \\ \text{group}(\sim, x : xs) &= (x : A) : \text{group}(\sim, B) \end{aligned} \tag{1.61}$$

Where $(A, B) = \text{span}(y \mapsto x \sim y, xs)$ is the span result applied to the rest sub-list. Although this new group function generates the correct result for string case:

```

group (==) ``Mississippi''
[``m'', ``i'', ``ss'', ``i'', ``ss'', ``i'', ``pp'', ``i'']

```

However, it can't group the list of numbers correctly with \leq relation:

```

group ( $\geq$ ) [15, 9, 0, 12, 11, 7, 10, 5, 6, 13, 1, 4, 8, 3, 14, 2]
[[15,9,0,12,11,7,10,5,6,13,1,4,8,3,14,2]]

```

When the first number 15 is used as the left hand of \geq , it is the maximum value, hence *span* ends with putting all elements to A , and leaves B empty. It is not a defect, but the correct behavior, because group is defined to put equivalent elements together. To be accurate, the equivalent relation (\sim) needs satisfy three things: reflexive, transitive, and symmetric.

1. **Reflexive.** $x \sim x$, any element equals to itself;

2. **Transitive.** $x \sim y, y \sim z \Rightarrow x \sim z$, if two elements equal, and one of them equals to another, then all three equal;
3. **Symmetric.** $x \sim y \Leftrightarrow y \sim x$, the order of comparing two equal elements doesn't affect the result.

When group “Mississippi”, we use the equal (=) operator. It conforms the three rules, and generates the correct result. However, when pass Curried (\geq) predication for numbers, it violets both reflexive and symmetric rules, hence generates unexpected result. The second algorithm using span, limits its use case to strictly equality; while the first algorithm does not. It only tests the predication for every two elements matches, which is weaker than equality relation.

Exercise 1.12

1. Change the *take/drop* algorithm, such that when n is negative, returns \emptyset for take, and the whole list for drop.
2. Implement the in-place imperative *take/drop* algorithms.
3. Implement the iterative ‘take while’ and ‘drop while’ algorithms.
4. Consider the below *span* implementation:

$$\begin{aligned} \text{span}(p, \emptyset) &= (\emptyset, \emptyset) \\ \text{span}(p, x : xs) &= \begin{cases} p(x) : & (x : A, B) \\ \text{otherwise} : & (A, x : B) \end{cases} \end{aligned}$$

where $(A, B) = \text{span}(p, xs)$. What is the difference between this one and the algorithm we defined previously?

1.6 Fold

We've seen most list algorithms share some common structure. This is not by chance. Such commonality is rooted from the recursive nature of list. We can abstract the list algorithms to a higher level concept, fold⁵, which is essentially the initial algebra of all list related computation[99].

1.6.1 fold right

Compare *sum*, *product* and *sort*, we can find the common structure.

$$\begin{aligned} h(\emptyset) &= z \\ h(x : xs) &= x \oplus h(xs) \end{aligned} \tag{1.62}$$

There are two things we can abstract as parameters:

- The result for empty list. It is 0 for sum, 1 for product, and \emptyset for sort.
- The binary operation applies to the head and the recursive result. It is plus for sum, multiply for product, and ordered-insertion for sort.

⁵also known as reduce

We abstract the result for empty list as the *initial value*, denoted as z to mimic the generic zero concept. The binary operation as \oplus . The above definition can be then parameterized as:

$$\begin{aligned} h(\oplus, z, \emptyset) &= z \\ h(\oplus, z, x : xs) &= x \oplus h(\oplus, z, xs) \end{aligned} \quad (1.63)$$

Let's feed it a list $L = [x_1, x_2, \dots, x_n]$, and expand to see how it behaves like:

$$\begin{aligned} &h(\oplus, z, [x_1, x_2, \dots, x_n]) \\ &= x_1 \oplus h(\oplus, z, [x_2, x_3, \dots, x_n]) \\ &= x_1 \oplus (x_2 \oplus h(\oplus, z, [x_3, \dots, x_n])) \\ &\dots \\ &= x_1 \oplus (x_2 \oplus (\dots(x_n \oplus h(\oplus, z, \emptyset))\dots)) \\ &= x_1 \oplus (x_2 \oplus (\dots(x_n \oplus z)\dots)) \end{aligned}$$

We need add the parentheses, because the computation starts from the right-most ($x_n \oplus z$). It repeatedly folds to left towards x_1 . This is quite similar to a fold-fan in figure 1.3. Fold-fan is made of bamboo and paper. Multiple frames stack together with an axis at one end. The arc shape paper is fully expanded by these frames; We can close the fan by folding the paper. It ends up as a stick.



Figure 1.3: Fold fan

We can consider the fold-fan as a list of bamboo frames. The binary operation is to fold a frame to the top of the stack. The initial stack is empty. To fold the fan, we start from one end, repeatedly apply the binary operation, till all the frames are stacked. The sum and product algorithms do the same thing like folding fan.

$$\begin{aligned} \text{sum}([1, 2, 3, 4, 5]) &= 1 + (2 + (3 + (4 + 5))) \\ &= 1 + (2 + (3 + 9)) \\ &= 1 + (2 + 12) \\ &= 1 + 14 \\ &= 15 \\ \\ \text{product}([1, 2, 3, 4, 5]) &= 1 \times (2 \times (3 \times (4 \times 5))) \\ &= 1 \times (2 \times (3 \times 20)) \\ &= 1 \times (2 \times 60) \\ &= 1 \times 120 \\ &= 120 \end{aligned}$$

We name this kind of process fold. Particularly, since the computation starts from the right end, we denote it *foldr*:

$$\begin{aligned} \text{foldr}(f, z, \emptyset) &= z \\ \text{foldr}(f, z, x : xs) &= f(x, \text{foldr}(f, z, xs)) \end{aligned} \quad (1.64)$$

We can define sum and product with *foldr* as below:

$$\begin{aligned} \sum_{i=1}^n x_i &= x_1 + (x_2 + (x_3 + \dots + (x_{n-1} + x_n))\dots) \\ &= \text{foldr}(+, 0, [x_1, x_2, \dots, x_n]) \end{aligned} \quad (1.65)$$

$$\begin{aligned} \prod_{i=1}^n x_i &= x_1 \times (x_2 \times (x_3 \times \dots + (x_{n-1} \times x_n))\dots) \\ &= \text{foldr}(\times, 1, [x_1, x_2, \dots, x_n]) \end{aligned} \quad (1.66)$$

Or in Curried form: *sum* = *foldr*(+, 0), *product* = *foldr*(×, 1). We can also define the insertion sort with *foldr* as:

$$\text{sort} = \text{foldr}(\text{insert}, \emptyset) \quad (1.67)$$

1.6.2 fold left

We can convert *foldr* to tail call. It generates the same result, but computes from left to right. For this reason, we define it as *foldl*:

$$\begin{aligned} \text{foldl}(f, z, \emptyset) &= z \\ \text{foldl}(f, z, x : xs) &= \text{foldl}(f, f(z, x), xs) \end{aligned} \quad (1.68)$$

Use *sum* for example, we can see how the computation is expanded from left to right:

$$\begin{aligned} &\text{foldl}(+, 0, [1, 2, 3, 4, 5]) \\ &= \text{foldl}(+, 0 + 1, [2, 3, 4, 5]) \\ &= \text{foldl}(+, (0 + 1) + 2, [3, 4, 5]) \\ &= \text{foldl}(+, ((0 + 1) + 2) + 3, [4, 5]) \\ &= \text{foldl}(+, (((0 + 1) + 2) + 3) + 4, [5]) \\ &= \text{foldl}(+, ((((0 + 1) + 2) + 3) + 4 + 5, \emptyset) \\ &= 0 + 1 + 2 + 3 + 4 + 5 \end{aligned}$$

Here we delay the evaluation of $f(z, x)$ in every step. This is the behavior for lazy-evaluation. Otherwise, they will be evaluated in sequence of [1, 3, 6, 10, 15] in each call. Generally, we can expand *foldl* as:

$$\text{foldl}(f, z, [x_1, x_2, \dots, x_n]) = f(f(\dots(f(f(z, x_1), x_2), \dots), x_n)) \quad (1.69)$$

Or express as infix:

$$\text{foldl}(\oplus, z, [x_1, x_2, \dots, x_n]) = z \oplus x_1 \oplus x_2 \oplus \dots \oplus x_n \quad (1.70)$$

foldl is tail recursive. We can implement it with loops. We initialize the result as z , then apply the binary operation on top of it with every element. It is typically called REDUCE in most imperative environment.

```

1: function REDUCE( $f, z, L$ )
2:   while  $L \neq \text{NIL}$  do
3:      $z \leftarrow f(z, \text{FIRST}(L))$ 
4:      $L \leftarrow \text{REST}(L)$ 
5:   return  $z$ 

```

Both *foldr* and *foldl* have their own suitable use cases. They are not always exchangeable. For example, some container only allows to add element in one end (like stack). We can define a function *fromList* to build such a container from a list (in Curried form):

$$\text{fromList} = \text{foldr}(\text{add}, \text{empty})$$

Where *empty* is the empty container. The singly linked-list is such a container. It performs well when add element to the head, but poorly when append to tail. *foldr* is a natural choice when duplicate a list while keep the order. But *foldl* will generate a reversed list. As a workaround, to implement the iterative reducing from right, we can first reverse the list, then reduce it:

```
1: function REDUCE-RIGHT(f, z, L)
2:   return REDUCE(f, z, REVERSE(L))
```

One may think *foldl* should be the preferred one as it is optimized with tail call, hence fits for both functional and imperative settings. It is also the online algorithm that always holds the result so far. However, *foldr* plays a critical role when handling infinite list (modeled as stream) with lazy evaluation. For example, below program wraps every natural number to a singleton list, and returns the first 10:

$$\begin{aligned} & \text{take}(10, \text{foldr}((x, xs) \mapsto [x] : xs, \emptyset, [1, 2, \dots])) \\ & \Rightarrow [[1], [2], [3], [4], [5], [6], [7], [8], [9], [10]] \end{aligned}$$

It does not work with *foldl* because the outer most evaluation never ends. We use a unified notation *fold* when either left or right works. In this book, we also use *fold_l* and *fold_r* to emphasis folding over the direction. Although this chapter is about list, the fold concept is generic. It can be applied to other algebraic structures. We can fold a tree (2.6 in [99]), a queue, and many other things as long as they satisfy the following 2 criteria:

- The empty is defined (like the empty tree);
- We can decompose the recursive structure (like decompose tree into sub-trees and key).

People abstract them further with concepts like foldable, monoid, and traversable.

Exercise 1.13

1. To define insertion-sort with *foldr*, we designe the insert function as *insert*(*x*, *L*), such that it can be expressed as *sort* = *foldr*(*insert*, \emptyset). The type for *foldr* is:

$$\text{foldr} :: (A \rightarrow B \rightarrow B) \rightarrow B \rightarrow [A] \rightarrow B$$

Where its first parameter *f* has the type $A \rightarrow B \rightarrow B$, the initial value *z* has the type *B*. It folds on a list of *A*, and builds the result of *B*. How to define the insertion-sort with *foldl*? What is the type signature of *foldl*?

1.6.3 example

As an example, let's see how to implement the *n*-lights puzzle with *fold* and *map*. In the brute-force solution, we create a list of pairs. Each pair (*i*, *s*) has a number *i*, and on/off state *s*. Every round *j*, we scan the lights, toggle the *i*-th switch when the *j* divides the *i*. We can define this process with *fold*:

$$\text{fold}_r(\text{step}, [(1, 0), (2, 0), \dots, (n, 0)], [1, 2, \dots, n])$$

As the initial state, all lights are off. We fold on the list of round numbers from 1 to *n*. Function *step* takes two parameters: the round number *i*, and the list of pairs. It performs switching through *map*:

$$\text{fold}_r((i, L) \mapsto \text{map}(\text{switch}(i), L), [(1, 0), (2, 0), \dots, (n, 0)], [1, 2, \dots, n])$$

The $fold_r$ result is the pairs of final on/off state, we next extract the state from each through map , and count the number with sum :

$$sum(map(snd, fold_r((i, L) \mapsto map(switch(i), L), [(1, 0), (2, 0), \dots, (n, 0)], [1, 2, \dots, n]))) \quad (1.71)$$

concatenate

What if we apply $fold$ on “ $+$ ” (section 1.3.4) for a list of lists? It concatenates them to a long list, just like sum to numbers.

$$concat = fold_r(+, \emptyset) \quad (1.72)$$

This is in Curried form. Its usage is as:

$$concat([[1], [2, 3, 4], [5, 6, 7, 8, 9]]) \Rightarrow [1, 2, 3, 4, 5, 6, 7, 8, 9]$$

Exercise 1.14

1. What’s the performance of $concat$?
2. Design a linear time $concat$ algorithm
3. Define map in $foldr$

1.7 Search and filter

Search and filter are generic concepts apply to a wide range of things. For list, it often takes linear time to find the result, as we need traverse in most cases.

1.7.1 Exist

Given some a of type A , and a list of A , how to test if x is in the list? The idea is to compare every element in the list with a , until either they are equal, or reach to the end:

- If the list is empty, then a does not exist;
- If the first element equals to a , then it exists;
- Otherwise, recursively test if a exists in the rest sub-list.

$$\begin{aligned} a \in \emptyset &= False \\ a \in (b : bs) &= \begin{cases} b = a : True \\ b \neq a : a \in bs \end{cases} \end{aligned} \quad (1.73)$$

This algorithm is also called $elem$. It bounds to $O(n)$ where n is the length. If the list is ordered (ascending for example), one may want to improve the algorithm to logarithm time with the idea of divide and conquer. However, list does not support random access, we can’t apply binary search. See chapter 3 for details.

1.7.2 Look up

Let's extend *elem* a bit. In the *n*-lights puzzle, we use a list of pairs $[(k, v)]$. Every pair contains a key and a value. This kind of list is called 'associate list' (or assoc list). If want to look up a given value in such list, we need extract some part (the value) for comparison.

$$\begin{aligned} \text{lookup}(x, \emptyset) &= \text{Nothing} \\ \text{lookup}(x, (k, v) : kvs) &= \begin{cases} v = x : & \text{Just } (k, v) \\ v \neq x : & \text{lookup}(x, kvs) \end{cases} \end{aligned} \quad (1.74)$$

Different from *elem*, we do not return true/false. Instead, we want to return the pair of key-value when find. However, it is not guaranteed the value always exists. We use an algebraic type called 'Maybe'. A type of **Maybe** *A* has two different kinds of value. It maybe some *a* in *A* or nothing. Denoted as *Just a* or *Nothing*. This is the way to deal with null reference issues(4.2.2 in [99]).

1.7.3 find and filter

We can make 'look up' more generic. Instead of only comparing if the element equals to the given value, we can abstract to find the element that satisfies a specific predicate:

$$\begin{aligned} \text{find}(p, \emptyset) &= \text{Nothing} \\ \text{find}(p, (x : xs)) &= \begin{cases} p(x) : & \text{Just } x \\ \text{otherwise} : & \text{find}(p, xs) \end{cases} \end{aligned} \quad (1.75)$$

Although there can be multiple elements match, the *find* algorithm picks the first. We can expand it to find all elements. It is often called *filter* as demonstrated in figure 1.4.



Figure 1.4: Input: $[x_1, x_2, \dots, x_n]$, Output: $[x'_1, x'_2, \dots, x'_m]$. and $\forall x'_i \Rightarrow p(x'_i)$.

We can define it in ZF expression:

$$\text{filter}(p, X) = [x_i | x_i \in X, p(x_i)] \quad (1.76)$$

Different from *find*, when there is no element satisfies the predicate, *filter* returns the empty list. It scans to examine every element one by one:

$$\begin{aligned} \text{filter}(p, \emptyset) &= \emptyset \\ \text{filter}(p, x : xs) &= \begin{cases} p(x) : & x : \text{filter}(p, xs) \\ \text{otherwise} : & \text{filter}(p, xs) \end{cases} \end{aligned} \quad (1.77)$$

This definition builds the result from right to left. For iterative implementation, if build the result with *append*, it will degrade to $O(n^2)$.

```

1: function FILTER(p, L)
2:   L' ← NIL
3:   while L ≠ NIL do
4:     if p(FIRST(L)) then
5:       L' ← APPEND(L', FIRST(L))

```

▷ Linear time

6: $L \leftarrow \text{REST}(L)$

The right way is to use *cons* instead, however, it builds the result in the reversed order. We can further reverse it within linear time (see the exercise). The nature to build result from right indicates that we can define filter in *foldr*. We need define a function f to test an element against the predicate, if OK, prepend to the result:

$$f(x, A) = \begin{cases} p(x) : & x : A \\ \text{otherwise} : & A \end{cases} \quad (1.78)$$

We also need pass the predicate p to f . There are actually 3 parameters as $f(p, x, A)$. Filter is defined in *foldr* with a Curried form of f :

$$\text{filter}(p) = \text{foldr}((x, A) \mapsto f(p, x, A), \emptyset) \quad (1.79)$$

We can further simplify it (called η -conversion[73]) as:

$$\text{filter}(p) = \text{foldr}(f(p), \emptyset) \quad (1.80)$$

Filter is also a generic concept not only limit to list. We can apply a predicate on any traversable structures to extract the result.

1.7.4 Match

Match is to find a pattern among some structure. Even if we limit to list and string, there are still too many things to cover. We have dedicated chapters about string matching. This section deals with the problem, that given a list A , and test if it exists in another list B . There are two special cases: to test if A is prefix or suffix of B . The *span* algorithm in (1.58) actually finds a prefix under a certain condition. We can do similar things: to compare each element between A and B from left till meet any different one or reach the end of either list. Define $A \subseteq B$ if A is prefix of B :

$$\begin{aligned} \emptyset \subseteq B &= \text{True} \\ (a : as) \subseteq \emptyset &= \text{False} \\ (a : as) \subseteq (b : bs) &= \begin{cases} a \neq b : \text{False} \\ a = b : as \subseteq bs \end{cases} \end{aligned} \quad (1.81)$$

Prefix testing takes linear time as it scans the lists. However, we can not do suffix testing in this way because it is hard to start from the aligned right ends, and scan backwards for lists. This is different from array. Alternatively, we can reverse both lists in linear time, hence change the problem to prefix testing:

$$A \supseteq B = \text{reverse}(A) \subseteq \text{reverse}(B) \quad (1.82)$$

With \subseteq defined, we can test if a list is the sub-list of another one. We call it infix testing. The idea is to scan the target list, and repeatedly applying the prefix testing:

$$\begin{aligned} \text{infix?}(a : as, \emptyset) &= \text{False} \\ \text{infix?}(A, B) &= \begin{cases} A \subseteq B : \text{True} \\ \text{otherwise} : \text{infix?}(A, B') \end{cases} \end{aligned} \quad (1.83)$$

For the edge case that A is empty, we define empty is infix of any list. Because $\emptyset \subseteq B$ is always true, it gives the right result. It also evaluates $\text{infix?}(\emptyset, \emptyset)$ correctly. Below is the corresponding iterative implementation:

```

1: function IS-INFIX(A, B)
2:   if A = NIL then
3:     return TRUE
4:   n ← |A|
5:   while B ≠ NIL and n ≤ |B| do
6:     if A ⊆ B then
7:       return TRUE
8:     B ← REST(B)
9:   return FALSE

```

Because prefix testing runs in linear time, and it is called in the loop of scan. This algorithm is bound to $O(nm)$, where m, n are the length of the two lists respectively. It is an interesting problem to improve this ‘position by position’ scan algorithm to linear time, even when we apply it to arrays. Chapter 13 introduces some smart methods, like the Knuth-Morris-Pratt (KMP) algorithm and Boyer-Moore algorithm. Appendix C introduces another method called suffix-tree.

In a symmetric way, we can enumerate all suffixes of B , and check if A is prefix of any of them:

$$\text{infix?}(A, B) = \exists S \in \text{suffixes}(B), A \subseteq S \quad (1.84)$$

This can be implemented with list comprehension as below example Haskell program:

```
isInfixOf a b = (not o null) [ s | s ← tails(b), a `isPrefixOf` s ]
```

Where function `isPrefixOf` does the prefixing testing, `tails` generates all suffixes of a given list. We left its implementation as an exercise.

Exercise 1.15

1. Implement the linear time existence testing algorithm.
2. Implement the iterative look up algorithm.
3. Implement the linear time filter algorithm through *reverse*.
4. Implement the iterative prefix testing algorithm.
5. Implement the algorithm to enumerate all suffixes of a list.

1.8 zip and unzip

The assoc list of paired values is often used as a light weighted dictionary for small set of data. It is easier to build assoc list than tree or heap based dictionary, although the look up performance of assoc list is linear instead of logarithm. In the ‘ n -lights’ puzzle, we build the assoc list as below:

$$\text{map}(i \mapsto (i, 0), [1, 2, \dots, n])$$

More often, we need ‘zip’ two lists to one. We can define a *zip* function to do that:

$$\begin{aligned} \text{zip}(A, \emptyset) &= \emptyset \\ \text{zip}(\emptyset, B) &= \emptyset \\ \text{zip}(a : as, b : bs) &= (a, b) : \text{zip}(as, bs) \end{aligned} \quad (1.85)$$

This algorithm works even the two lists have different length. The result length equals to the shorter one. We can even use it to zip infinite lists (under lazy evaluation if both are infinite), for example⁶:

⁶In Haskell: `zip (repeat 0) [1..n]`

$$\text{zip}([0, 0, \dots], [1, 2, \dots, n])$$

For a list of words, we can index them with numbers as:

$$\text{zip}([1, 2, \dots], [a, an, another, \dots])$$

zip build the result from right. We can also define it with *fldr*. It is bound to $O(m)$ time, where m is the length of the shorter list. When implement the iterative *zip*, the performance will drop to quadratic if using *append*, unless with the reference to the tail position.

```

1: function ZIP( $A, B$ )
2:    $C \leftarrow \text{NIL}$ 
3:   while  $A \neq \text{NIL}$  and  $B \neq \text{NIL}$  do
4:      $C \leftarrow \text{APPEND}(C, (\text{FIRST}(A), \text{FIRST}(B)))$            ▷ Linear time
5:      $A \leftarrow \text{REST}(A)$ 
6:      $B \leftarrow \text{REST}(B)$ 
7:   return  $C$ 

```

To avoid *append*, we can use 'cons' then reverse the result. However, it can not deal with two infinite lists. In imperative settings, we can also re-use A to store the result (treat it as transform a list of elements to a list of pairs).

We can extend to *zip* multiple lists to one. Some programming libraries provide, `zip`, `zip3`, `zip4`, ..., till `zip7`. Sometimes, we don't want to build a list of pairs, but apply a combinator function. For example, given a list of unit prices [1.00, 0.80, 10.05, ...] for fruits: apple, orange, banana, ... When customer has a list of quantities, like [3, 1, 0, ...], means this customer, buys 3 apples, 1 orange, 0 banana, ... Below program generates a payment list:

$$\begin{aligned} \text{pays}(U, \emptyset) &= \emptyset \\ \text{pays}(\emptyset, Q) &= \emptyset \\ \text{pays}(u : us, q : qs) &= (u \cdot q) : \text{pays}(us, qs) \end{aligned}$$

It is same as the *zip* function except uses multiply but not 'cons' to combine elements. We can abstract the combinator as a function f , and pass it to *zip* to build a generic algorithm:

$$\begin{aligned} \text{zipWith}(f, A, \emptyset) &= \emptyset \\ \text{zipWith}(f, \emptyset, B) &= \emptyset \\ \text{zipWith}(f, a : as, b : bs) &= f(a, b) : \text{zipWith}(f, as, bs) \end{aligned} \tag{1.86}$$

Here is an example that defines the inner-product (or dot-product)[98] through *zipWith*:

$$A \cdot B = \text{sum}(\text{zipWith}(\cdot, A, B)) \tag{1.87}$$

unzip is the inverse operation of *zip*. It converts a list of pairs to two separated lists. Below is its definition with *fldr* in Curried form:

$$\text{unzip} = \text{fldr}((a, b), (A, B) \mapsto (a : A, b : B), (\emptyset, \emptyset)) \tag{1.88}$$

We fold from a pair of empty lists, break a, b from the pairs and prepend them to the two intermediate lists respectively. We can also use *fst* and *snd* explicitly as:

$$(p, P) \mapsto (\text{fst}(p) : \text{fst}(P), \text{snd}(p) : \text{snd}(P))$$

For the fruits example, suppose the unit price is stored in a assoc list: $U = [(apple, 1.00), (orange, 0.80, \dots)]$ for lookup, for example $\text{lookup}(melon, U)$. The purchase quantity is a assoc list: $Q =$

$[(apple, 3), (orange, 1), (banana, 0), \dots]$. How to calculate the total payment? The straight forward way is to extract the unit price and the quantity lists, then compute their inner-product:

$$pay = sum(zipWith(\cdot, snd(unzip(U)), snd(unzip(Q)))) \quad (1.89)$$

As an example, let's see how to use *zipWith* to define infinite Fibonacci numbers with lazy evaluation:

$$F = 0 : 1 : zipWith(+, F, F') \quad (1.90)$$

Where F is the infinite list of Fibonacci numbers, starts from 0 and 1. F' is the rest Fibonacci numbers without the first one. From the third, every Fibonacci number is the sum of numbers from F and F' at the same position. Below example program list the first 15 Fibonacci numbers:

```
fib = 0 : 1 : zipWith (+) fib (tail fib)

take 15 fib
[0,1,1,2,3,5,8,13,21,34,55,89,144,233,377]
```

zip and *unzip* are generic. We can expand to *zip* two trees, where the nodes contain paired elements from both. When traverse a collection of elements, we can also use the generic *zip* and *unzip* to track the path, this is a method to mimic the 'parent' reference in imperative implementation (last chapter of [10]).

Exercise 1.16

1. Design the *iota* (I) algorithm for below usages:
 - $iota(\dots, n) = [1, 2, 3, \dots, n]$;
 - $iota(m, n) = [m, m + 1, m + 2, \dots, n]$, where $m \leq n$;
 - $iota(m, m + a, \dots, n) = [m, m + a, m + 2a, \dots, n]$;
 - $iota(m, m, \dots) = repeat(m) = [m, m, m, \dots]$;
 - $iota(m, \dots) = [m, m + 1, m + 2, \dots]$.

The last two cases are about infinite list. One possible implementation is through streaming and lazy evaluation ([63] and [10]).

2. Implement the linear time imperative *zip* algorithm
3. Define *zip* with *foldr*.
4. For the fruits example, suppose the quantity assoc list only contains the items with none-zero quantity. i.e. instead of

$$Q = [(apple, 3), (banana, 0), (orange, 1), \dots]$$

but

$$Q = [(apple, 3), (orange, 1), \dots]$$

because customer does not buy banana. Design a program to calculate the total payment.

5. Implement *lastAt* with *zip*.

1.9 Further reading

List is the fundamental thing to build more complex data structures and algorithms particularly in functional settings. We introduced elementary algorithms to construct, access, update, and transform list; how to search, filter data, and compute atop list. Although most programming environments provide pre-defined tools and libraries to support list, we should not simply treat them as black-boxes. Rabhi and Lapalme introduce many functional algorithms about list in [72]. Haskell library provides detailed documentation about basic list algorithms. There are materials provide good examples of folding, especially in [1]. It also introduces about the *fold fusion law*.

Exercise 1.17

1. Design algorithm to remove the duplicated elements in a list. For imperative implementation, the elements should be removed in-place. The original element order should be maintained. What is the complexity of this algorithm? How to simplify it with additional data structure?
2. List can represent decimal non-negative integer. For example 1024 as list is $4 \rightarrow 2 \rightarrow 0 \rightarrow 1$. Generally, $n = d_m \dots d_2 d_1$ can be represented as $d_1 \rightarrow d_2 \rightarrow \dots \rightarrow d_m$. Given two numbers a, b in list form. Realize arithmetic operations such as add and subtraction.
3. In imperative settings, a circular linked-list is corrupted, that some node points back to previous one, as shown in figure 1.5. When traverse, it falls into infinite loops. Design an algorithm to detect if a list is circular. On top of that, improve it to find the node where loop starts (the node being pointed by two precedents).

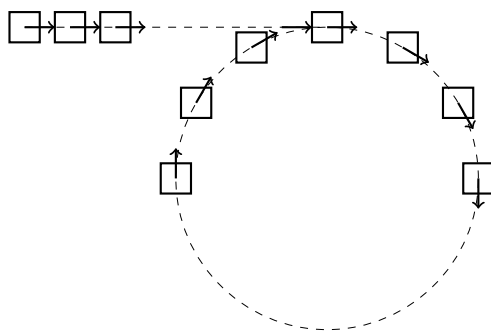


Figure 1.5: A circular linked-list

Chapter 2

Binary Search Tree

2.1 Introduction

Array and list are typically considered the basic data structures. However, we'll see they are not necessarily easy to implement in chapter 12. Upon imperative settings, array is the most elementary data structures. It is possible to implement linked-list using arrays (Equation 3.4). While in functional settings, linked-list acts as the building blocks to create array and other data structures.

We start from Binary Search Trees as the first data structure. Let us see an interesting programming problem given by Bentley in *Programming Pearls*[2]. It is about to count the number of words in text. Here is an example solution:

```
void wordcount(Input in) {
    bst<string, int> map;
    while string w = read(in) {
        map[w] = if map[w] == null then 1 else map[w] + 1
    }
    for var (w, c) in map {
        print(w, ":", c)
    }
}
```

We can run it to count the words in a text file:

```
$ cat bbe.txt | wordcount > wc.txt
```

The map is a binary search tree. Here we use the word as the key, and its occurrence number as the value. This program runs fast, which reflects the power of binary search tree. Before dive into it, let us first see the more generic tree, the binary tree. A binary tree can be defined recursively. It is

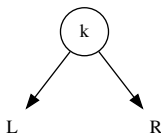
- either empty;
- or contains 3 parts: the element, and two sub-trees called left and right children.

Figure 2.1 shows an example of binary tree.

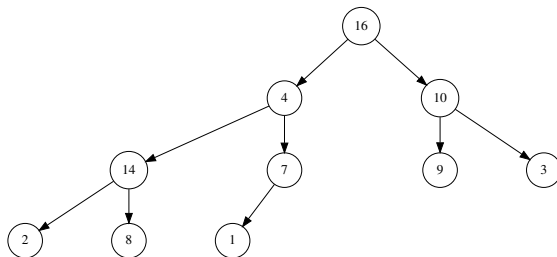
A binary search tree is a special binary tree that its elements are comparable¹, and satisfies the following constraints:

- For any node, all the keys in its left sub-tree are less than the key in this node;

¹It is abstract ordering, not limit to magnitude, but like precedence, subset of etc. the 'less than' (<) is abstract in this chapter.



(a) Binary tree structure



(b) A binary tree

Figure 2.1: Binary tree concept and an example.

- the key in this node is less than any key in its right sub-tree.

Figure 2.2 shows an example of binary search tree. Comparing with Figure 2.1, we can see the differences in keys ordering. To highlight the elements in binary search tree is comparable, we call it as *key*, and name the augmented satellite data as *value*.

2.2 Data Layout

Based on the recursive definition of binary search tree, we can design the data layout as shown in figure 2.3. A node stores the key as a field, it can also store augmented data (known as satellite data). The next two fields are pointers to the left and right sub-trees. To make it easy for backtracking, it can also store a parent field pointed to its ancestor node.

For illustration purpose, we'll skip the augmented data. The appendix of this chapter includes an example definition. In functional settings, it is seldom to use pointers for backtracking. Typically, there is no such need, because the algorithm is usually top-down recursive. Below is the example functional definition:

```

data Tree a = Empty
         | Node (Tree a) a (Tree a)
  
```

2.3 Insertion

When insert a key k (or along with a value) to binary search tree T , we need ensure the key ordering property is always hold:

- If the tree is empty, construct a leaf node with key = k ;

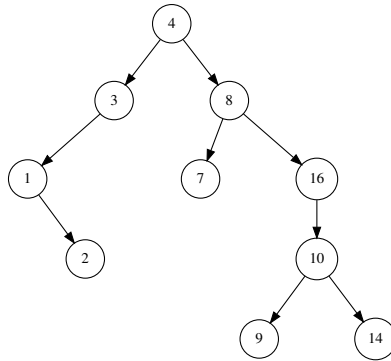


Figure 2.2: A Binary Search Tree

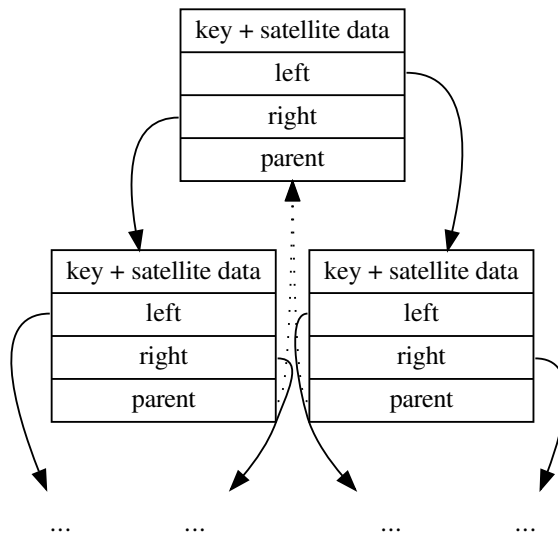


Figure 2.3: Node layout with parent field.

- If k is less than the key of root, insert it to the left sub-tree;
- Otherwise, insert it in the right sub-tree.

There is an exceptional case that k is equal to the key of root. It means k already exists in the tree. We can overwrite it, or append data, or do nothing. We'll skip such case handling. This algorithm is simple and straightforward. We can define it as a recursive function:

$$\begin{aligned} \text{insert}(\emptyset, k) &= \text{Node}(\emptyset, k, \emptyset) \\ \text{insert}(\text{Node}(T_l, k', T_r), k) &= \begin{cases} k < k' : & \text{Node}(\text{insert}(T_l, k), k', T_r) \\ \text{otherwise} : & \text{Node}(T_l, k', \text{insert}(T_r, k)) \end{cases} \quad (2.1) \end{aligned}$$

For the none empty node, T_l denotes the left sub-tree, T_r denotes the right sub-tree, and k' is the key. The function $\text{Node}(l, k, r)$ creates a node from two sub-trees and a key. \emptyset means empty (also known as NIL. This symbol was invented by mathematician André Weil for null set. It came from the Norwegian alphabet). Below is the corresponding example program in Haskell for insertion.

```
insert Empty k = Node Empty k Empty
insert (Node l x r) k | k < x = Node (insert l k) x r
                    | otherwise = Node l x (insert r k)
```

This example program utilizes the *pattern matching* features. The appendix of this chapter provides another example without using this feature. Insertion can also be implemented without recursion. Here is a pure iterative algorithm:

```
1: function INSERT( $T, k$ )
2:    $root \leftarrow T$ 
3:    $x \leftarrow \text{CREATE-LEAF}(k)$ 
4:    $parent \leftarrow \text{NIL}$ 
5:   while  $T \neq \text{NIL}$  do
6:      $parent \leftarrow T$ 
7:     if  $k < \text{KEY}(T)$  then
8:        $T \leftarrow \text{LEFT}(T)$ 
9:     else
10:       $T \leftarrow \text{RIGHT}(T)$ 
11:     $\text{PARENT}(x) \leftarrow parent$ 
12:    if  $parent = \text{NIL}$  then ▷ tree  $T$  is empty
13:      return  $x$ 
14:    else if  $k < \text{KEY}(parent)$  then
15:       $\text{LEFT}(parent) \leftarrow x$ 
16:    else
17:       $\text{RIGHT}(parent) \leftarrow x$ 
18:    return  $root$ 

19: function CREATE-LEAF( $k$ )
20:    $x \leftarrow \text{EMPTY-NODE}$ 
21:    $\text{KEY}(x) \leftarrow k$ 
22:    $\text{LEFT}(x) \leftarrow \text{NIL}$ 
23:    $\text{RIGHT}(x) \leftarrow \text{NIL}$ 
24:    $\text{PARENT}(x) \leftarrow \text{NIL}$ 
25:   return  $x$ 
```

While a bit more complex than the functional one, the iterative implementation runs faster, and it is capable to process very deep tree.

2.4 Traverse

Traverse is to visit every element one by one. There are 3 different ways to walk through a binary tree: (1) pre-order tree walk, (2) in-order tree walk, (3) and post-order tree walk. They are named to highlight the order of visiting key before/after sub-trees.

- pre-order: **key** - left - right;
- in-order: left - **key** - right;
- post-order: left - right - **key**.

Each ‘visit’ operation is recursive, for example in pre-order traverse, when visit the left sub-tree, we recursively traverse it if it is not empty. For the tree shown in figure 2.2, the corresponding visiting orders are as below:

- pre-order: 4, 3, 1, 2, 8, 7, 16, 10, 9, 14
- in-order: 1, 2, 3, 4, 7, 8, 9, 10, 14, 16
- post-order: 2, 1, 3, 7, 9, 14, 10, 16, 8, 4

It is not by accident that the in-order traverse lists the elements one by one increasingly. The definition of the binary search tree ensures it is always true. We leave the proof as an exercise. Specifically, the in-order traverse algorithm is defined as:

- If the tree is empty, stop and return;
- Otherwise, in-order traverse the left sub-tree; then visit the key; finally in-order traverse the right sub-tree.

We can further define a generic *map* to apply any given function *f* to every element in the tree along the in-order traverse. The result is a new tree mapped by *f*.

$$\begin{aligned} \text{map}(f, \emptyset) &= \emptyset \\ \text{map}(f, \text{Node}(T_l, k, T_r)) &= \text{Node}(\text{map}(f, T_l), f(k), \text{map}(f, T_r)) \end{aligned} \quad (2.2)$$

If we only need manipulate keys but not to transform the tree, we can implement this algorithm imperatively.

```

1: function IN-ORDER-TRAVERSE(T, f)
2:   if T ≠ NIL then
3:     IN-ORDER-TRAVERSE(LEFT(T), f)
4:     f(KEY(T))
5:     IN-ORDER-TRAVERSE(RIGHT(T), f)

```

Leverage in-order traverse, we can change the *map* function to convert a binary search tree to a sorted list. Instead building the tree in recursive case, we concatenate the result to a list:

$$\begin{aligned} \text{toList}(\emptyset) &= [] \\ \text{toList}(\text{Node}(T_l, k, T_r)) &= \text{toList}(T_l) \# [k] \# \text{toList}(T_r) \end{aligned} \quad (2.3)$$

We can develop a method to sort a list of elements: first build a binary search tree from the list, then turn it back to list through in-order traversing. This method is called as ‘tree sort’. For a given list $X = [x_1, x_2, x_3, \dots, x_n]$.

$$\text{sort}(X) = \text{toList}(\text{fromList}(X)) \quad (2.4)$$

And we can write it in point-free form[8].

$$\text{sort} = \text{toList} \circ \text{fromList}$$

Where function *fromList* repeatedly inserts elements from a list to a tree. It can be defined to recursively process the list.

$$\begin{aligned} \text{fromList}([\] &= \emptyset \\ \text{fromList}(X) &= \text{insert}(\text{fromList}(X'), x_1) \end{aligned}$$

When the list is empty, the result is an empty tree; otherwise, it inserts the first element x_1 to the tree, then recursively inserts the rests $X' = [x_2, x_3, \dots, x_n]$. By using list folding[7] (see appendix A.6), we can also define *fromList* as the following:

$$\text{fromList}(X) = \text{fold}_l(\text{insert}, \emptyset, X) \quad (2.5)$$

We can also rewrite it in Curried form[9] (also known as partial application) such as to omit parameter X :

$$\text{fromList} = \text{fold}_l \text{ insert } \emptyset$$

Exercise 2.1

1. Given the in-order and pre-order traverse results, re-construct the tree, and output the post-order traverse result. For example:
 - Pre-order: 1, 2, 4, 3, 5, 6;
 - In-order: 4, 2, 1, 5, 3, 6;
 - Post-order: ?
2. Write a program to re-construct the binary tree from the pre-order and in-order traverse lists.
3. For binary search tree, prove that the in-order traverse always visits elements in increase order
4. Consider the performance of tree sort algorithm, what is its complexity for n elements?

2.5 Query

Because the elements stored in binary search tree is well ordered and organized recursively. It supports varies of search effectively. This is one of the reasons people name it as binary search tree. There are mainly three types of querying: (1) look up a key; (2) find the minimum or maximum element; (3) given any node, find its predecessor or successor.

2.5.1 Look up

Because binary search tree is recursive and all elements satisfy the ordering property, we can look up a key k top-down from the root as the following:

- If the tree is empty, terminate. The key does not exist;
- Compare k with the key of root, if equal, we are done. The key is stored in the root;

- If k is less than the key of root, then recursively look up the left sub-tree;
- Otherwise, look up the right sub-tree.

We can define the recursive *lookup* function for this algorithm as below.

$$\begin{aligned} \text{lookup}(\emptyset, x) &= \emptyset \\ \text{lookup}(\text{Node}(T_l, k, T_r), x) &= \begin{cases} k = x : & T \\ x < k : & \text{lookup}(T_l, x) \\ \text{otherwise} : & \text{lookup}(T_r, x) \end{cases} \end{aligned} \quad (2.6)$$

This function returns the tree node being located or empty if not found. One may instead return the value that bound to the key. However, in search implementation, we need consider using *Maybe* type (also known as `Optional<T>`) to handle the not found case, for example:

```

lookup Empty _ = Nothing
lookup t@(Node l k r) x | k == x = Just k
                       | x < k = lookup l x
                       | otherwise = lookup r x

```

If the binary search tree is well balanced, which means almost all branch nodes have both none empty sub-trees except for leaves. This is not the formal definition of balance. We'll define it in chapter 4. For a balanced tree of n elements, the algorithm takes $O(\lg n)$ time to look up a key. If the tree is poor balanced, the worst case is bound to $O(n)$ time. If denote the height of the tree as h , we can represent the performance of look up as $O(h)$.

We can also implement looking up purely iterative without recursion:

```

1: function SEARCH( $T, x$ )
2:   while  $T \neq \text{NIL}$  and  $\text{KEY}(T) \neq x$  do
3:     if  $x < \text{KEY}(T)$  then
4:        $T \leftarrow \text{LEFT}(T)$ 
5:     else
6:        $T \leftarrow \text{RIGHT}(T)$ 
7:   return  $T$ 

```

2.5.2 Minimum and maximum

From the definition, we know that less keys are always on the left. To locate the minimum element, we can keep traversing along the left sub-trees till reach to a node, where its left sub-tree is empty. In a symmetric way, keep traversing along the right sub-trees gives the maximum.

$$\begin{aligned} \min(\text{Node}(\emptyset, k, T_r)) &= k \\ \min(\text{Node}(T_l, k, T_r)) &= \min(T_l) \end{aligned} \quad (2.7)$$

$$\begin{aligned} \max(\text{Node}(T_l, k, \emptyset)) &= k \\ \max(\text{Node}(T_l, k, T_r)) &= \max(T_r) \end{aligned} \quad (2.8)$$

Both functions are bound to $O(h)$ time, where h is the height of the tree.

2.5.3 Successor and predecessor

When treat binary search tree as a generic container (a collection of elements), it is common to traverse it with a bi-directional iterator. Start from the minimum element, one can keep moving forward with the iterator towards the maximum, or go back and forth. Below example program prints elements in sorted order.

```

void printTree (Node<T> t) {
    for (var it = Iterator(t), it.hasNext(); it = it.next()) {
        print(it.get(), ", ");
    }
}

```

Such use cases demand us to design algorithm to find the successor or predecessor of any node. The successor of element x is defined as the smallest element y that satisfies $x < y$. If the node of x has none empty right sub-tree, then minimum element of the right sub-tree is the successor. As shown in figure 2.4, to find the successor of 8, we search the minimum element in its right sub-tree, which is 9. If the right sub-tree of node x is empty, we need back-track along the parent field till the closest ancestor whose left sub-tree is also an ancestor of x . In figure 2.4, since node 2 does not have right sub-tree, we go up to its parent of node 1. However, node 1 does not have left sub-tree, we need go up again, hence reach to node 3. As the left sub-tree of node 3 is also an ancestor of node 2, node 3 is the successor of node 2.

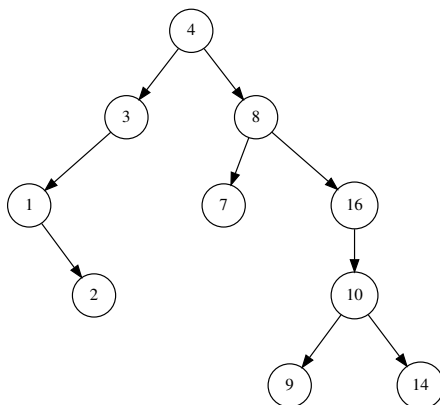


Figure 2.4: The successor of 8, is the minimum one in its right sub-tree, 9; In order to find the successor of 2, we go up to its parent 1, then 3.

If we finally reach to the root when back-track along the parent, but still can not find an ancestor on the right, then the node does not have a successor. Below algorithm finds the successor of a given node x :

```

1: function SUCC( $x$ )
2:   if RIGHT( $x$ )  $\neq$  NIL then
3:     return MIN(RIGHT( $x$ ))
4:   else
5:      $p \leftarrow$  PARENT( $x$ )
6:     while  $p \neq$  NIL and  $x =$  RIGHT( $p$ ) do
7:        $x \leftarrow p$ 
8:        $p \leftarrow$  PARENT( $p$ )
9:   return  $p$ 

```

This algorithm returns NIL when x does not has successor. The predecessor finding algorithm is symmetric:

```

1: function PRED( $x$ )
2:   if LEFT( $x$ )  $\neq$  NIL then

```

```

3:     return MAX(LEFT( $x$ ))
4:   else
5:      $p \leftarrow$  PARENT( $x$ )
6:     while  $p \neq$  NIL and  $x =$  LEFT( $p$ ) do
7:        $x \leftarrow p$ 
8:        $p \leftarrow$  PARENT( $p$ )
9:     return  $p$ 

```

It seems hard to find the purely functional solution, because there is no pointer like field linking to the parent node². One solution is to left ‘breadcrumbs’ when we visit the tree, and use these information to back-track or even re-construct the whole tree. Such data structure, that contains both the tree and ‘breadcrumbs’ is called zipper[?].

Our original purpose to develop *succ* and *pred* functions is ‘to traverse all the elements’ as a generic container. However, in functional settings, we typically traverse the tree in-order through *map*. We’ll meet similar situations in the rest of this book. A problems valid in imperative settings may not be necessarily meaningful in functional settings. For example, to delete an element from red-black tree[5].

Exercise 2.2

1. Use PRED and SUCC to write an iterator to traverse the binary search tree as a generic container. What’s the time complexity to traverse a tree of n elements?
2. One can traverse elements inside a range $[a, b]$ for example:
`for_each (m.lower_bound(12), m.upper_bound(26), f);`
 Write an equivalent functional program for binary search tree.

2.6 Deletion

We need special consideration when delete an element from the binary search tree. This is because we must keep the ordering property, that for any node, all keys in left sub-tree are less than the key of this node, and they are all less than any keys in right sub tree. Blindly deleting a node may break this constraint.

To delete a node x from a binary search tree[6].

- If x has no sub-trees (a leaf) or only one sub-tree, splice x out;
- Otherwise (x has two sub-trees), use the minimum element y of its right sub-tree to replace x , and splice the original y out.

The simplicity comes from the fact that, for the node to be deleted, if the right sub-tree is not empty, then the minimum element is some node in it. It can’t have two none empty children, and end up in the trivial case. Therefore, the node can be directly splice out from the tree.

Figure 2.5, 2.6, and 2.7 illustrate different cases for deletion.

Based on this idea, we can define the *delete* algorithm as below:

$$\begin{aligned}
 delete(\emptyset, x) &= \emptyset \\
 delete(Node(T_l, k, T_r), x) &= \begin{cases} x < k : Node(delete(T_l, x), k, T_r) \\ x > k : Node(T_l, k, delete(T_r, x)) \\ x = k : del(T_l, T_r) \end{cases} \quad (2.9)
 \end{aligned}$$

²There is `ref` in ML and OCaml, we limit to the purely functional settings.

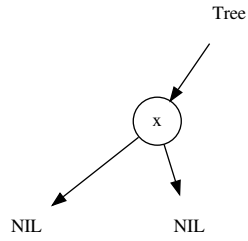
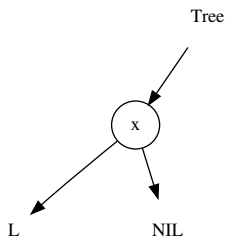
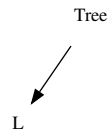
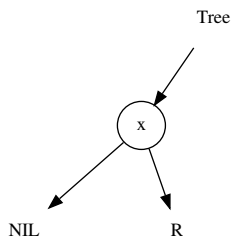
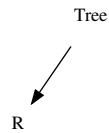
Figure 2.5: x can be spliced out.(a) Before delete x .(b) After delete x , x is spliced out, and replaced by its left child.(c) Before delete x .(d) After delete x , x is spliced out, and replaced by its right sub-tree.

Figure 2.6: Delete a node with only one none empty sub-tree.

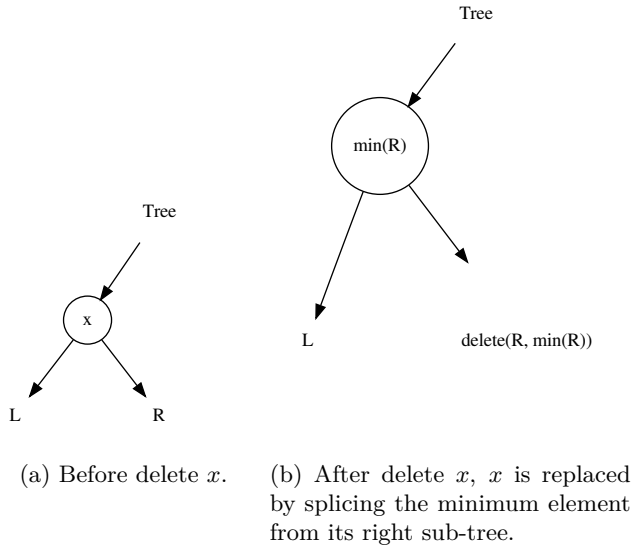


Figure 2.7: Delete a node with two non-empty sub-trees.

Function *del* performs slicing, and mutually call *delete* recursively to cut off the minimum from the right sub-tree.

$$\begin{aligned}
 \text{del}(\emptyset, T_r) &= T_r \\
 \text{del}(T_l, \emptyset) &= T_l \\
 \text{del}(T_l, T_r) &= \text{Node}(T_l, y, \text{delete}(T_r, y))
 \end{aligned} \tag{2.10}$$

Where $y = \text{min}(T_r)$ is the minimum element in the right sub-tree. Here is the corresponding example program:

```

delete Empty _ = Empty
delete (Node l k r) x | x < k = Node (delete l x) k r
                    | x > k = Node l k (delete r x)
                    | otherwise = del l r

where
  del Empty r = r
  del l Empty = l
  del l r = let k' = min r in Node l k' (delete r k')

```

This algorithm firstly looks up the node to be deleted, then executes the deletion. It takes $O(h)$ time where h is the height of the tree.

The imperative deletion algorithm needs set the parent properly in addition. The following one returns the root of the result tree.

```

1: function DELETE( $T, x$ )
2:    $r \leftarrow T$ 
3:    $x' \leftarrow x$  ▷ save  $x$ 
4:    $p \leftarrow \text{PARENT}(x)$ 
5:   if LEFT( $x$ ) = NIL then
6:      $x \leftarrow \text{RIGHT}(x)$ 
7:   else if RIGHT( $x$ ) = NIL then
8:      $x \leftarrow \text{LEFT}(x)$ 
9:   else ▷ neither children is empty
10:     $y \leftarrow \text{MIN}(\text{RIGHT}(x))$ 

```

```

11:     KEY( $x$ )  $\leftarrow$  KEY( $y$ )
12:     Copy other satellite data from  $y$  to  $x$ 
13:     if PARENT( $y$ )  $\neq$   $x$  then                                 $\triangleright$   $y$  does not have left sub-tree
14:         LEFT(PARENT( $y$ ))  $\leftarrow$  RIGHT( $y$ )
15:     else                                                         $\triangleright$   $y$  is the root of the right sub-tree
16:         RIGHT( $x$ )  $\leftarrow$  RIGHT( $y$ )
17:     if RIGHT( $y$ )  $\neq$  NIL then
18:         PARENT(RIGHT( $y$ ))  $\leftarrow$  PARENT( $y$ )
19:     Remove  $y$ 
20:     return  $r$ 
21: if  $x \neq$  NIL then
22:     PARENT( $x$ )  $\leftarrow$   $p$ 
23: if  $p =$  NIL then                                              $\triangleright$  remove the root
24:      $r \leftarrow x$ 
25: else
26:     if LEFT( $p$ ) =  $x'$  then
27:         LEFT( $p$ )  $\leftarrow$   $x$ 
28:     else
29:         RIGHT( $p$ )  $\leftarrow$   $x$ 
30:     Remove  $x'$ 
31:     return  $r$ 

```

We assume the node to be deleted is not empty. This algorithm first records the root, creates copy reference to x , and its parent. If either sub-tree is empty, then we splice x out. Otherwise, the node has two none empty sub-trees. We first located the minimum node y in its right sub-tree, then replace the key of x with the one in y , copy the satellite data, and finally, splice y out. We also need handle the special case, that y is the root of the right sub-tree.

At last, we need reset the stored parent if x has only one none empty sub-tree. If the parent pointer we copied is empty, it means that we are deleting the root. In this case, we need return the new root. After the parent is set properly, we can safely remove x . The deletion algorithm is bound to $O(h)$ time, where h is the height of the tree.

Exercise 2.3

1. There is a symmetric deletion algorithm. When neither sub-tree is empty, we can replace the key by splicing the maximum node off the left sub-tree. Write a program to implement this solution.

2.7 Random build

All binary search tree algorithms we give so far are bound bound to $O(h)$ time. The height h of the tree impacts the performance. For a poor unbalanced tree, $O(h)$ tends to be $O(n)$. It leads to the worst case. While for well balanced tree, $O(h)$ close to $O(\lg n)$. We can gain good performance.

We'll see two well designed solutions to keep the tree balanced in chapter 4 and 5. There exists a simple method, to build the binary search tree randomly[4]. It decreases the possibility of giving a unbalanced binary tree. The idea is to randomly shuffle the elements before building the tree.

Exercise 2.4

1. Write a randomly building algorithm for binary search tree.

2.8 Map

We can use binary search tree to realize the map data structure (also known as associative data structure or dictionary). A finite map is a collection of key-value pairs. The keys are unique, that every key is mapped to a value. For keys of type K , values of type V , the map is $Map\ K\ V$ or $Map<K, V>$. For none empty map, it contains n mappings of $k_1 \mapsto v_1, k_2 \mapsto v_2, \dots, k_n \mapsto v_n$. When use the binary search tree to implement map, we constrain K to be ordered set. Every node stores both key and value. We use the tree insert/update operation to bind a key to a value. Given a key k , we use the tree lookup to find the mapped value, or returns nothing when k does not exist. The red-black tree and AVL tree introduced in later chapters can also be used to implement map.

2.9 Appendix: Example programs

Definition of binary search tree node with parent field.

```

data Node<T> {
  T key
  Node<T> left
  Node<T> right
  Node<T> parent

  Node(T k) = Node(null, k, null)

  Node(Node<T> l, T k, Node<T> r) {
    left = l, key = k, right = r
    if (left  $\neq$  null) then left.parent = this
    if (right  $\neq$  null) then right.parent = this
  }
}

```

Example program of recursive insertion. It does not use pattern matching.

```

Node<T> insert (Node<T> t, T x) {
  if (t == null) {
    return Node(null, x, null)
  } else if (t.key < x) {
    return Node(insert(t.left, x), t.key, t.right)
  } else {
    return Node(t.left, t.key, insert(t.right, x))
  }
}

```

Example program to look up a key. Purely iterative without recursion.

```

Optional<Node<T>> lookup (Node<T> t, T x) {
  while (t  $\neq$  null and t.key  $\neq$  x) {
    if (x < t.key) {
      t = t.left
    } else {
      t = t.right
    }
  }
  return Optional(t);
}

```

Example iterative program to find the minimum of a tree.

```
Optional<Node<T>> min (Node<T> t) {  
    while (t ≠ null and t.left ≠ null) {  
        t = t.left  
    }  
    return Optional(t);  
}
```

Example program to find the successor of a node.

```
Optional<Node<T>> succ (Node<T> x) {  
    if (x == null) {  
        return Optional.None  
    } else if (x.right ≠ null) {  
        return min(x.right)  
    } else {  
        p = x.parent  
        while (p ≠ null and x == p.right) {  
            x = p  
            p = p.parent  
        }  
        return Optional(p);  
    }  
}
```

Chapter 3

Insertion sort

3.1 Introduction

Insertion sort is a straightforward sort algorithm¹. We give its preliminary definition for list in chapter 1. For a collection of comparable elements, we repeatedly pick one, insert them to a list and maintain the ordering. As every insertion takes linear time, its performance is bound to $O(n^2)$ where n is the number of elements. This performance is not as good as the divide and conqueror sort algorithms, like quick sort and merge sort. However, we can still find its application today. For example, a well tuned quick sort implementation falls back to insertion sort for small data set. The idea of insertion sort is similar to sort a deck of a poker cards([4] pp.15). The cards are shuffled. A player takes card one by one. At any time, all cards on hand are sorted. When draws a new card, the player inserts it in proper position according to the order of points as shown in figure 3.1.



Figure 3.1: Insert card 8 to a deck.

Based on this idea, we can implement insertion sort as below:

```
1: function SORT( $A$ )
2:    $S \leftarrow \text{NIL}$ 
3:   for each  $a \in A$  do
4:     INSERT( $a, S$ )
5:   return  $S$ 
```

We store the sorted result in a new array, alternatively, we can change it to in-place:

```
1: function SORT( $A$ )
```

¹We skip the ‘Bubble sort’ method

- ```

2: for $i \leftarrow 2$ to $|A|$ do
3: ordered insert $A[i]$ to $A[1\dots(i-1)]$

```

Where the index  $i$  ranges from 1 to  $n = |A|$ . We start from 2, because the singleton sub-array  $[A[1]]$  is ordered. When process the  $i$ -th element, all elements before  $i$  are sorted. We continuously insert elements till consuming all the unsorted ones, as shown in figure 3.2.

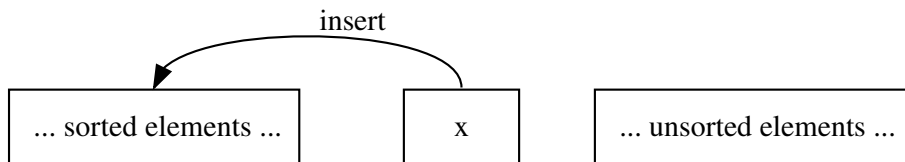


Figure 3.2: Continuously insert elements to the sorted part.

## 3.2 Insertion

In chapter 1, we give the ordered insertion algorithm for list. For array, we also scan it to locate the insert position either from left or right. Below algorithm is from right:

- ```

1: function SORT( $A$ )
2:   for  $i \leftarrow 2$  to  $|A|$  do ▷ Insert  $A[i]$  to  $A[1\dots(i-1)]$ 
3:      $x \leftarrow A[i]$  ▷ Save  $A[i]$  to  $x$ 
4:      $j \leftarrow i - 1$ 
5:     while  $j > 0$  and  $x < A[j]$  do
6:        $A[j + 1] \leftarrow A[j]$ 
7:        $j \leftarrow j - 1$ 
8:      $A[j + 1] \leftarrow x$ 

```

It's expensive to insert at arbitrary position, as array stores elements continuously. When insert x at position i , we need shift all elements after i (i.e. $A[i + 1], A[i + 2], \dots$) one cell to right. After free up the cell at i , we put x in, as shown in figure 3.3.

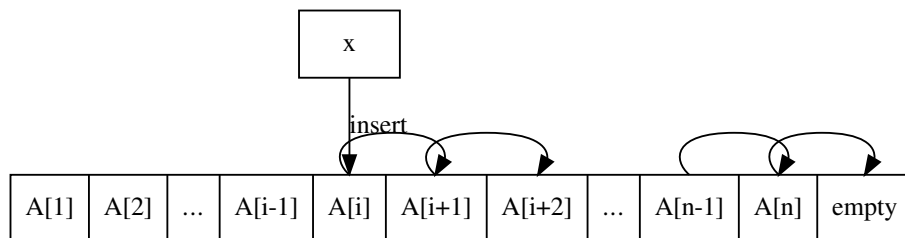


Figure 3.3: Insert x to A at i .

For the array of length n , suppose after comparing x to the first i elements, we located the position to insert. Then we shift the rest $n - i + 1$ elements, and put x in the i -th cell. Overall, we need traverse the whole array if scan from left. On the other hand, if scan from right to left, we examine $n - i + 1$ elements, and perform the same amount of shifts. We can also define a separated INSERT() function, and call it inside the loop. The insertion takes linear time no matter scans from left or right, hence the sort algorithm is bound to $O(n^2)$, where n is the number of elements.

Exercise 3.1

1. Implement the insert to scan from left to right.
2. Define the insert function, and call it from the sort algorithm.

3.3 Binary search

When insert a poker card, human does not scan, but takes a quick glance at the deck to locate the position. We can do this because the deck is sorted. Binary search is such a method that applies to ordered sequence.

```

1: function SORT( $A$ )
2:   for  $i \leftarrow 2$  to  $|A|$  do
3:      $x \leftarrow A[i]$ 
4:      $p \leftarrow$  BINARY-SEARCH( $x, A[1\dots(i-1)]$ )
5:     for  $j \leftarrow i$  down to  $p$  do
6:        $A[j] \leftarrow A[j-1]$ 
7:      $A[p] \leftarrow x$ 

```

Binary search utilize the fact that the slice $A[1\dots(i-1)]$ is ordered. Suppose it is ascending without loss of generality (as we can define \leq abstract). To find the position j that satisfies $A[j-1] \leq x \leq A[j]$, we compare x to the middle element $A[m]$, where $m = \lfloor \frac{i}{2} \rfloor$. If $x < A[m]$, we then recursively apply binary search to the first half; otherwise, we search the second half. As every time, we halve the elements, binary search takes $O(\lg i)$ time to locate the insert position.

```

1: function BINARY-SEARCH( $x, A$ )
2:    $l \leftarrow 1, u \leftarrow 1 + |A|$ 
3:   while  $l < u$  do
4:      $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$ 
5:     if  $A[m] = x$  then
6:       return  $m$  ▷ Duplicated element
7:     else if  $A[m] < x$  then
8:        $l \leftarrow m + 1$ 
9:     else
10:       $u \leftarrow m$ 
11:   return  $l$ 

```

The improved sort algorithm is still bound to $O(n^2)$. The one with scan takes $O(n^2)$ comparisons and $O(n^2)$ shifts; with binary search, it overall takes $O(n \lg n)$ comparisons and $O(n^2)$ shifts.

Exercise 3.2

1. Implement the recursive binary search.

3.4 List

With binary search, the search time improved to $O(n \lg n)$. However, as we need shift array cells when insert, the overall time is still bound to $O(n^2)$. On the other hand, when use list, the insert operation is constant time at a given node reference. In chapter 1, we

define the insertion sort algorithm for list as below:

$$\begin{aligned} \text{sort}(\emptyset) &= \emptyset \\ \text{sort}(x : xs) &= \text{insert}(x, \text{sort}(xs)) \end{aligned} \quad (3.1)$$

Or with fold_l in Curried form:

$$\text{sort} = \text{fold}_l(\text{insert}, \emptyset) \quad (3.2)$$

However, the list insert algorithm still takes linear time, because we need scan to locate the insert position:

$$\begin{aligned} \text{insert}(x, \emptyset) &= [x] \\ \text{insert}(x, y : ys) &= \begin{cases} x \leq y : & x : y : ys \\ \text{otherwise} : & y : \text{insert}(x, ys) \end{cases} \end{aligned} \quad (3.3)$$

Instead of using node reference, we can also realize list through an additional index array. For every element $A[i]$, $\text{Next}[i]$ stores the index to the next element follows $A[i]$, i.e. $A[\text{Next}[i]]$ is the next element of $A[i]$. There are two special indexes: for the tail node $A[m]$, we define $\text{Next}[m] = -1$, indicating it points to NIL; we also define $\text{Next}[0]$ to index the head element. With the index array, we can implement the insertion algorithm as below:

```

1: function INSERT( $A, \text{Next}, i$ )
2:    $j \leftarrow 0$  ▷  $\text{Next}[0]$  for head
3:   while  $\text{Next}[j] \neq -1$  and  $A[\text{Next}[j]] < A[i]$  do
4:      $j \leftarrow \text{Next}[j]$ 
5:    $\text{Next}[i] \leftarrow \text{Next}[j]$ 
6:    $\text{Next}[j] \leftarrow i$ 

7: function SORT( $A$ )
8:    $n \leftarrow |A|$ 
9:    $\text{Next} = [1, 2, \dots, n, -1]$  ▷  $n + 1$  indexes
10:  for  $i \leftarrow 1$  to  $n$  do
11:    INSERT( $A, \text{Next}, i$ )
12:  return  $\text{Next}$ 

```

With list, although the insert operation changes to constant time, we need traverse the list to locate the position. It is still bound to $O(n^2)$ times comparison. Unlike array, list does not support random access, hence we can not use binary search to speed up.

Exercise 3.3

1. For the index array based list, we return the re-arranged index as result. Design an algorithm to re-order the original array A from the index Next .

3.5 Binary search tree

We drive into a corner. We want to improve both comparison and insertion at the same time, or will end up with $O(n^2)$ performance. For comparison, we need binary search to achieve $O(\lg n)$ time; on the other hand, we need change the data structure, because array can not support constant time insertion at a position. We introduce a powerful data structure in chapter 2, the binary search tree. It supports binary search from its definition by nature. At the same time, we can insert a new node in binary search tree fast at the given location.


```
1: function SORT( $A$ )
2:    $T \leftarrow \emptyset$ 
3:   for each  $x \in A$  do
4:      $T \leftarrow$  INSERT-TREE( $T, x$ )
5:   return TO-LIST( $T$ )
```

Where INSERT-TREE() and TO-LIST() are defined in chapter 2. In average case, the performance of tree sort is bound to $O(n \lg n)$, where n is the number of elements. This is the lower limit of comparison based sort([?] pp.180-193). However, in the worst case, if the tree is poor balanced the performance drops to $O(n^2)$.

3.6 Summary

Insertion sort is often used as the first example of sorting. It is straightforward and easy to implement. However its performance is quadratic. Insertion sort does not only appear in textbooks, it has practical use case in the quick sort implementation. It is an engineering practice to fallback to insertion sort when the number of elements is small.

Chapter 4

Red-black tree

4.1 Introduction

As the example in chapter 2, we use the binary search tree as a dictionary to count the word occurrence in text. One may want to feed a address book to a binary search tree, and use it to look up the contact as below example program:

```
void addrBook(Input in) {
    bst<string, string> dict
    while (string name, string addr) = read(in) {
        dict[name] = addr
    }
    loop {
        string name = read(console)
        var addr = dict[name]
        if (addr == null) {
            print("not found")
        } else {
            print("address: ", addr)
        }
    }
}
```

Unlike the word counter program, this one performs poorly, especially when search names like Zara, Zed, Zulu, etc. This is because the address entries are typically listed in lexicographic order, i.e. the names are input in ascending order. If insert numbers 1, 2, 3, ..., n to a binary search tree, it ends up like in figure 4.1. It is an extremely unbalanced binary search tree. The *lookup()* is bound to $O(h)$ time for a tree with height h . When the tree is well balanced, the performance is $O(\lg n)$, where n is the number of elements in the tree. But in this extreme case, the performance downgrades to $O(n)$. It is equivalent to list scan.

Exercise 4.1

1. For a big address entry list in lexicographic order, one may want to speed up building the address book with two concurrent tasks: one reads from the head; while the other reads from the tail, till they meet at some middle point. What does the binary search tree look like? What if split the list into multiple sections to scale the concurrency?
2. Find more cases to exploit a binary search tree, for example in figure 4.2.

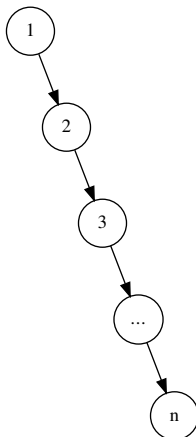


Figure 4.1: unbalanced tree

4.1.1 Balance

To avoid extremely unbalanced case, we can shuffle the input (12.4 in [4]), however, when the input is entered by user interactively, we can not randomize the sequence. People developed solutions to make the tree balanced. They mostly rely on the rotation operation. Rotation changes the tree structure while maintain the elements ordering. This chapter introduces the red-black tree, the widely used self-adjusting balanced binary search tree. Next chapter is about AVL tree, another self-balanced tree. Chapter 8 introduce the splay tree. It adjusts the tree in steps to make it balanced.

4.1.2 Tree rotation

Tree rotation transforms the tree structure while keeping the in-order traverse result unchanged. There are multiple binary search trees generate the same ordered element sequence. Figure 4.3 shows the tree rotation.

Tree rotation can be defined with pattern matching:

$$\begin{aligned} rotate_l((a, x, b), y, c) &= (a, x, (b, y, c)) \\ rotate_l T &= T \end{aligned} \tag{4.1}$$

and

$$\begin{aligned} rotate_r(a, x, (b, y, c)) &= ((a, x, b), y, c) \\ rotate_r T &= T \end{aligned} \tag{4.2}$$

The second row in each equation keeps the tree unchanged if the pattern does not match (for example, both sub-trees are empty). We can also implement tree rotation imperatively. We need re-assign sub-trees and parent node reference. When rotate, we pass both the root T , and the node x as parameters:

- 1: **function** LEFT-ROTATE(T, x)
- 2: $p \leftarrow$ PARENT(x)
- 3: $y \leftarrow$ RIGHT(x) ▷ assume $y \neq$ NIL
- 4: $a \leftarrow$ LEFT(x)
- 5: $b \leftarrow$ LEFT(y)
- 6: $c \leftarrow$ RIGHT(y)
- 7: REPLACE(x, y) ▷ replace node x with y

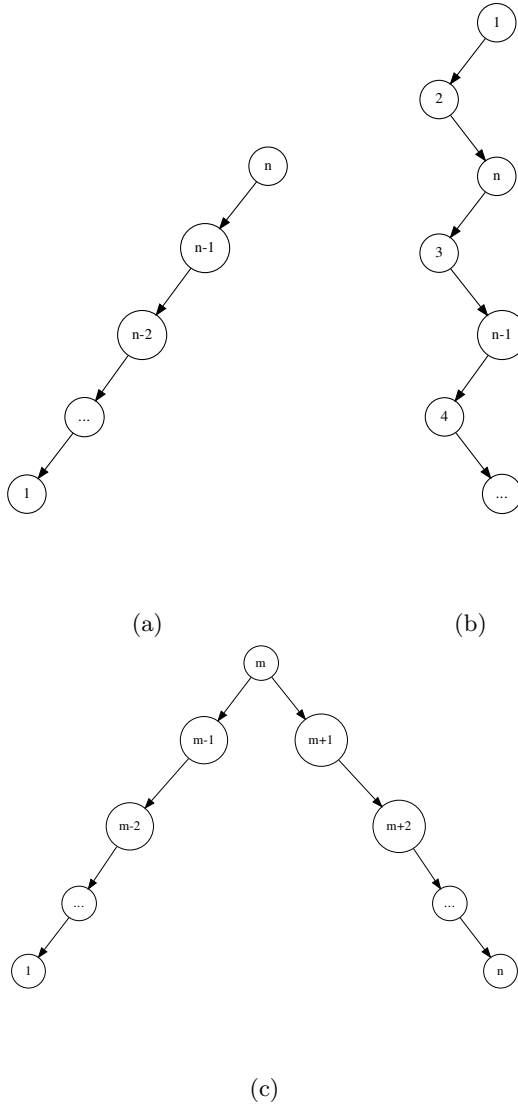


Figure 4.2: Unbalanced trees

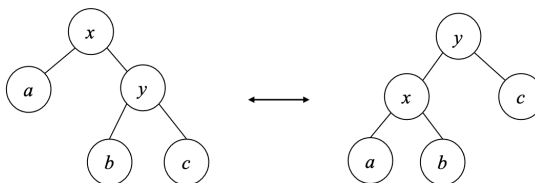


Figure 4.3: 'left rotate' and 'right rotate'.

```

8:   SET-SUBTREES( $x, a, b$ )           ▷ Set  $a, b$  as the sub-trees of  $x$ 
9:   SET-SUBTREES( $y, x, c$ )           ▷ Set  $x, c$  as the sub-trees of  $y$ 
10:  if  $p = \text{NIL}$  then                 ▷  $x$  was the root
11:       $T \leftarrow y$ 
12:  return  $T$ 

```

The RIGHT-ROTATE is symmetric, we leave it as exercise. The REPLACE(x, y) uses node y to replace x :

```

1: function REPLACE( $x, y$ )
2:    $p \leftarrow \text{PARENT}(x)$ 
3:   if  $p = \text{NIL}$  then                 ▷  $x$  is the root
4:       if  $y \neq \text{NIL}$  then  $\text{PARENT}(y) \leftarrow \text{NIL}$ 
5:       else if  $\text{LEFT}(p) = x$  then
6:           SET-LEFT( $p, y$ )
7:       else
8:           SET-RIGHT( $p, y$ )
9:        $\text{PARENT}(x) \leftarrow \text{NIL}$ 

```

Procedure SET-SUBTREES(x, L, R) assigns L as the left, and R as the right sub-trees of x :

```

1: function SET-SUBTREES( $x, L, R$ )
2:   SET-LEFT( $x, L$ )
3:   SET-RIGHT( $x, R$ )

```

It further calls SET-LEFT and SET-RIGHT to set the two sub-trees:

```

1: function SET-LEFT( $x, y$ )
2:    $\text{LEFT}(x) \leftarrow y$ 
3:   if  $y \neq \text{NIL}$  then  $\text{PARENT}(y) \leftarrow x$ 

4: function SET-RIGHT( $x, y$ )
5:    $\text{RIGHT}(x) \leftarrow y$ 
6:   if  $y \neq \text{NIL}$  then  $\text{PARENT}(y) \leftarrow x$ 

```

We can see how pattern matching simplifies the tree rotation. Based on this idea, Okasaki developed the purely functional algorithm for red-black tree in 1995[13].

Exercise 4.2

1. Implement the RIGHT-ROTATE.

4.2 Definition

A red-black tree is a self-balancing binary search tree[14]. It is essentially equivalent to 2-3-4 tree¹. By coloring the node red or black, and performing rotation, red-black tree provides an efficient way to keep the tree balanced. On top of the binary search tree definition, we label the node with a color. We say it is a red-black tree if the coloring satisfies the following 5 rules([4] pp273):

1. Every node is either red or black.
2. The root is black.
3. Every leaf (NIL) is black.

¹Chapter 7, B-tree. For any 2-3-4 tree, there is at least one red-black tree has the same ordered data.

4. If a node is red, then both sub-trees are black.
5. For every node, all paths from it to descendant leaves contain the same number of black nodes.

Why do they keep the red-black tree balanced? The key point is that, the longest path from the root to leaf can not be as 2 times longer than the shortest path. Consider rule 4, there can not be any two adjacent red nodes. Therefore, the shortest path only contains black nodes. Any longer path must have red ones. In addition, rule 5 ensures all paths have the same number of black nodes. So as to the root. It eventually ensures any path is not 2 times longer than others[14]. Figure 4.4 gives an example of red-black tree.

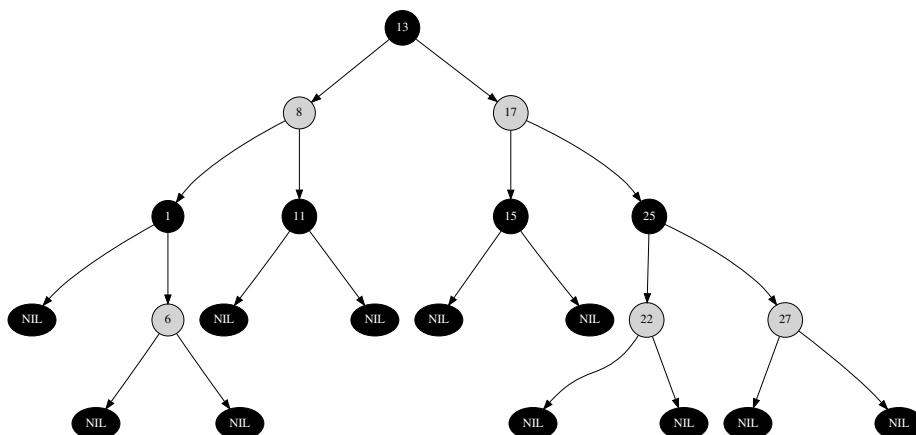


Figure 4.4: A red-black tree

As all NIL nodes are black, we can hide them as shown in figure 4.5. All operations including *lookup*, *min/max*, are same as the binary search tree. However, the *insert* and *delete* are special, as we need maintain the coloring rules.

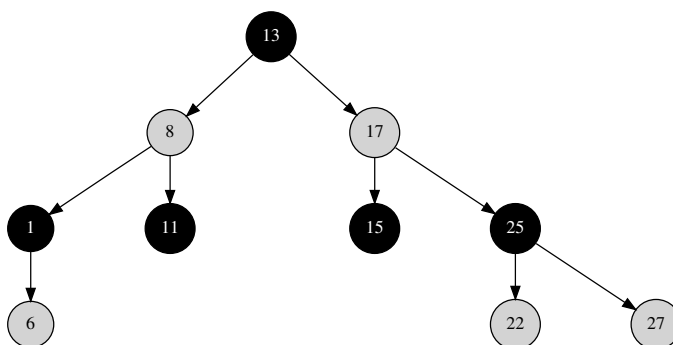


Figure 4.5: Hide the NIL nodes

Below example program adds the color field atop binary search tree definition:

```
data Color = R | B
data RBTREE a = Empty
```

Exercise 4.3

1. Prove the height h of a red-black tree of n nodes is at most $2 \lg(n + 1)$

4.3 Insert

The *insert* algorithm for red-black tree has two steps. The first step is as same as the binary search tree. The tree may become unbalanced after that, we need fix it to resume the red-black tree coloring in the second step. When insert a new element, we always make it red. Unless the new node is the root, we won't break any coloring rules except for the 4-th. Because it may bring two adjacent red nodes. Okasaki finds there are 4 cases violate rule 4. All have two adjacent red nodes. They share a uniformed structure after fixing[13] as shown in figure 4.6.

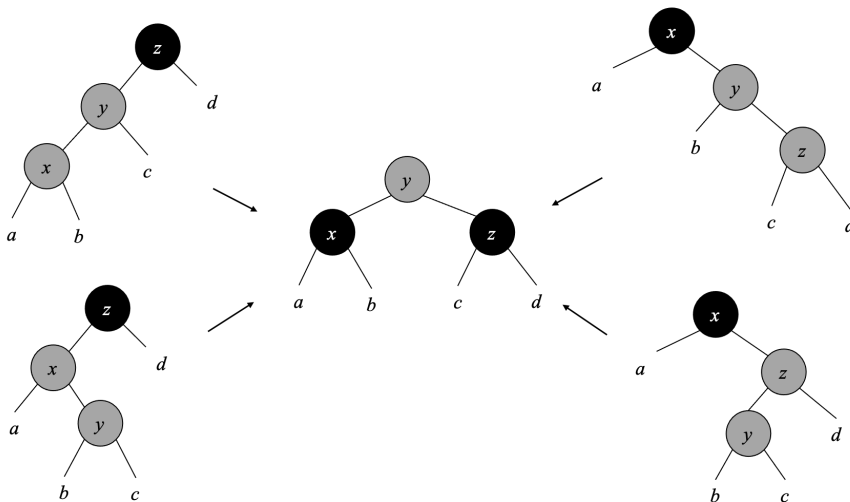


Figure 4.6: Fix 4 cases to the same structure.

All 4 transformations move the redness one level up. When perform bottom-up recursive fixing, it may color the root red. While rule 2 requires the root always be black. We need revert the root back to black finally. With pattern matching, we can define a *balance* function to fix the tree. Denote the color as \mathcal{C} with values black \mathcal{B} , and red \mathcal{R} . A none empty node is in the form of $T = (\mathcal{C}, l, k, r)$, where l, r are the left and right sub-trees, k is the key.

$$\begin{aligned}
 \text{balance } \mathcal{B} (\mathcal{R}, (\mathcal{R}, a, x, b), y, c) z d &= (\mathcal{R}, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{balance } \mathcal{B}, (\mathcal{R}, a, x, (\mathcal{R}, b, y, c)) z d &= (\mathcal{R}, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{balance } \mathcal{B} a x (\mathcal{R}, b, y, (\mathcal{R}, c, z, d)) &= (\mathcal{R}, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{balance } \mathcal{B} a x (\mathcal{R}, (\mathcal{R}, b, y, c), z, d) &= (\mathcal{R}, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{balance } T &= T
 \end{aligned}
 \tag{4.3}$$

The last row says if the tree is not in any 4 patterns, then we leave it unchanged. We define the *insert* algorithm for red-black tree as below:

$$\text{insert } T k = \text{makeBlack } (\text{ins } T k)
 \tag{4.4}$$

where

$$\begin{aligned} \mathit{ins} \ \emptyset \ k &= (\mathcal{R}, \emptyset, k, \emptyset) \\ \mathit{ins} \ (\mathcal{C}, l, k', r) \ k &= \begin{cases} k < k' : \mathit{balance} \ \mathcal{C} \ (\mathit{ins} \ l \ k) \ k' \ r \\ k > k' : \mathit{balance} \ \mathcal{C} \ l \ k' \ (\mathit{ins} \ r \ k) \end{cases} \end{aligned} \quad (4.5)$$

If the tree is empty, we create a red leaf of k ; otherwise, let the sub-trees and the key be l , r , k' , we compare k and k' , then recursively insert k to a sub-tree. After that, we call *balance* to fix the coloring, then force the root to be black finally.

$$\mathit{makeBlack} \ (\mathcal{C}, l, k, r) = (\mathcal{B}, l, k, r) \quad (4.6)$$

Below is the corresponding example program:

```
insert t x = makeBlack $ ins t where
  ins Empty = Node R Empty x Empty
  ins (Node color l k r)
    | x < k    = balance color (ins l) k r
    | otherwise = balance color l k (ins r)
  makeBlack(Node _ l k r) = Node B l k r

balance B (Node R (Node R a x b) y c) z d =
  Node R (Node B a x b) y (Node B c z d)
balance B (Node R a x (Node R b y c)) z d =
  Node R (Node B a x b) y (Node B c z d)
balance B a x (Node R b y (Node R c z d)) =
  Node R (Node B a x b) y (Node B c z d)
balance B a x (Node R (Node R b y c) z d) =
  Node R (Node B a x b) y (Node B c z d)
balance color l k r = Node color l k r
```

We skip to handle the duplicated keys. If the key already exists, we can overwrite, drop, or store the values in a list ([4], pp269). Figure 4.7 shows two red-black trees built from sequence 11, 2, 14, 1, 7, 15, 5, 8, 4 and 1, 2, ..., 8. The second example demonstrates the tree is well balanced even for ordered input.

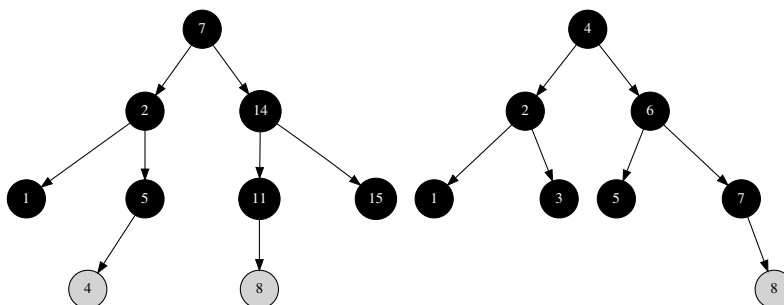


Figure 4.7: Red-black tree examples

The algorithm performs top-down recursive insertion and fixing. It is bound to $O(h)$ time, where h is the height of the tree. As the red-black tree coloring rules are maintained, h is the logarithm to the number of nodes n . The overall performance is $O(\lg n)$.

Exercise 4.4

1. Implement the *insert* algorithm without using pattern matching, but test the 4 cases separately.

4.4 Delete

Delete is more complex than insert. We can also use pattern matching and recursion to simplify the *delete* algorithm for red-black tree². There are alternatives to mimic delete. Sometimes, we build the read-only tree, then use it for frequently looking up[5]. When delete, we mark the deleted node with a flag, and later rebuild the tree if such nodes exceeds 50%. Delete may also violate the red-black tree coloring rules. We use the same idea to apply fixing after delete. The coloring violation only happens when delete a black node according to rule 5. The black nodes along the path decreases by one, hence not all paths contain the same number of black nodes.

To resume the blackness, we introduce a special ‘doubly-black’ node([4], pp290). One such node is counted as 2 black nodes. When delete a black node x , we can move the blackness either up to its parent or down to one sub-tree. Let this node be y that accepts the blackness. If y was red, we turn it black; if y was already black, we make it ‘doubly-black’, denoted as \mathcal{B}^2 . Below example program adds the ‘doubly-black’ support:

```
data Color = R | B | BB
data RBTree a = Empty | BBEmpy
           | Node Color (RBTree a) a (RBTree a)
```

Because all empty leaves are black, when push the blackness down to a leaf, it becomes ‘doubly-black’ empty (**BBEmpy**, or bold \emptyset). The first step is to perform the normal binary search tree delete; then if the cut off node is black, we shift the blackness, and fix the tree coloring.

$$delete = makeBlack \circ del \tag{4.7}$$

This definition is in Curried form. When delete the only element, the tree becomes empty. To cover this case, we modify *makeBlack* as below:

$$\begin{aligned} makeBlack \emptyset &= \emptyset \\ makeBlack (\mathcal{C}, l, k, r) &= (\mathcal{B}, l, k, r) \end{aligned} \tag{4.8}$$

Where *del* accepts the tree and k to be deleted:

$$del \emptyset k = \emptyset$$

$$del (\mathcal{C}, l, k', r) k = \begin{cases} k < k' : & fixB^2(\mathcal{C}, (del \ l \ k), k', r) \\ k > k' : & fixB^2(\mathcal{C}, l, k', (del \ r \ k)) \\ k = k' : & \begin{cases} l = \emptyset : & (\mathcal{C} = \mathcal{B} \mapsto shiftB \ r, r) \\ r = \emptyset : & (\mathcal{C} = \mathcal{B} \mapsto shiftB \ l, l) \\ else : & fixB^2(\mathcal{C}, l, k'', (del \ r \ k'')) \\ & \text{where } k'' = min(r) \end{cases} \end{cases} \tag{4.9}$$

When the tree is empty, the result is \emptyset ; otherwise, we compare the key k' in the tree with k . If $k < k'$, we recursively delete k from the left sub-tree; if $k > k'$ then delete from the right. Because the recursive result may contain doubly-black node, we need apply $fixB^2$ to fix it. When $k = k'$, we need splice it out. If either sub-tree is empty, we replace it with the other, then shift the blackness if the spliced node is black. This is represented with McCarthy form ($p \mapsto a, b$), which is equivalent to ‘(if p then a else b)’. If neither sub-tree is empty, we cut the minimum element $k'' = min(r)$, and use k'' to replace k .

²Actually, the tree is rebuilt in purely functional setting, although the common part is reused. This feature is called ‘persist’

To reserve the blackness, $shiftB$ makes a black node doubly-black, and forces it black for other cases. It flips doubly-black to normal black when applied twice.

$$\begin{aligned}
 shiftB (\mathcal{B}, l, k, r) &= (\mathcal{B}^2, l, k, r) \\
 shiftB (\mathcal{C}, l, k, r) &= (\mathcal{B}, l, k, r) \\
 shiftB \emptyset &= \emptyset \\
 shiftB \emptyset &= \emptyset
 \end{aligned}
 \tag{4.10}$$

Below is the example program (except the doubly-black fixing part).

```

delete :: (Ord a) => RBTree a -> a -> RBTree a
delete t k = makeBlack $ del t k where
  del Empty _ = Empty
  del (Node color l k' r) k
    | k < k' = fixDB color (del l k) k' r
    | k > k' = fixDB color l k' (del r k)
    | isEmpty l = if color == B then shiftBlack r else r
    | isEmpty r = if color == B then shiftBlack l else l
    | otherwise = fixDB color l k' (del r k') where k' = min r
  makeBlack (Node _ l k r) = Node B l k r
  makeBlack _ = Empty

shiftBlack (Node B l k r) = Node BB l k r
shiftBlack (Node _ l k r) = Node B l k r
shiftBlack Empty = BEmpty
shiftBlack BEmpty = Empty

```

The $fixB^2$ function eliminates the doubly-black node by rotation and re-coloring. The doubly-black node can be branch node or empty \emptyset . There are three cases:

Case 1. *The sibling of the doubly-black node is black, and it has a red sub-tree.* We can fix this case with a rotation. There are 4 sub-cases, all can be transformed to a uniformed pattern, as shown in figure A.1.

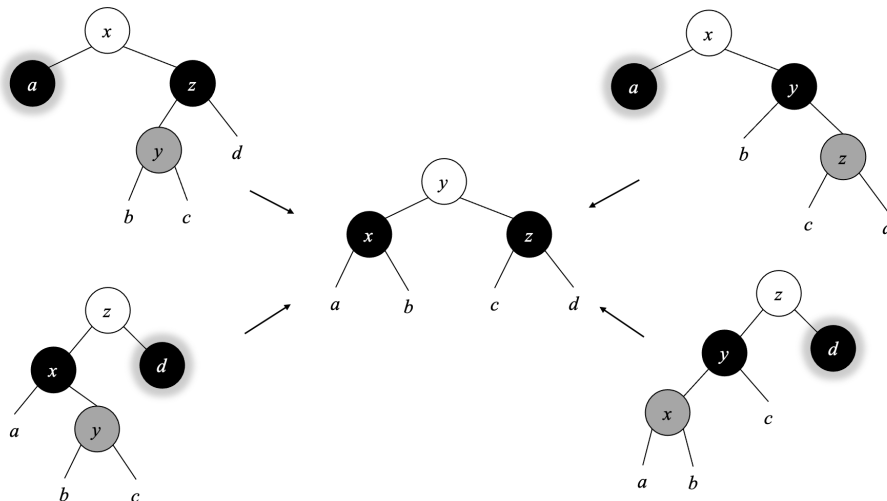


Figure 4.8: 4 sub-cases share the uniformed fixing pattern

The fixing for these 4 sub-cases can be realized with pattern matching.

$$\begin{aligned}
 \text{fix}B^2 C a_{\mathcal{B}^2} x (\mathcal{B}, (\mathcal{R}, b, y, c), z, d) &= (C, (\mathcal{B}, \text{shift}B(a), x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{fix}B^2 C a_{\mathcal{B}^2} x (\mathcal{B}, b, y, (\mathcal{R}, c, z, d)) &= (C, (\mathcal{B}, \text{shift}B(a), x, b), y, (\mathcal{B}, c, z, d)) \\
 \text{fix}B^2 C (\mathcal{B}, a, x, (\mathcal{R}, b, y, c)) z d_{\mathcal{B}^2} &= (C, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, \text{shift}B(d))) \\
 \text{fix}B^2 C (\mathcal{B}, (\mathcal{R}, a, x, b), y, c) z d_{\mathcal{B}^2} &= (C, (\mathcal{B}, a, x, b), y, (\mathcal{B}, c, z, \text{shift}B(d)))
 \end{aligned} \tag{4.11}$$

Where $a_{\mathcal{B}^2}$ means node a is doubly-black, it can be branch or \emptyset .

Case 2. *The sibling of the doubly-black is red.* We can rotate the tree to turn it into case 1 or 3, as shown in figure A.2.

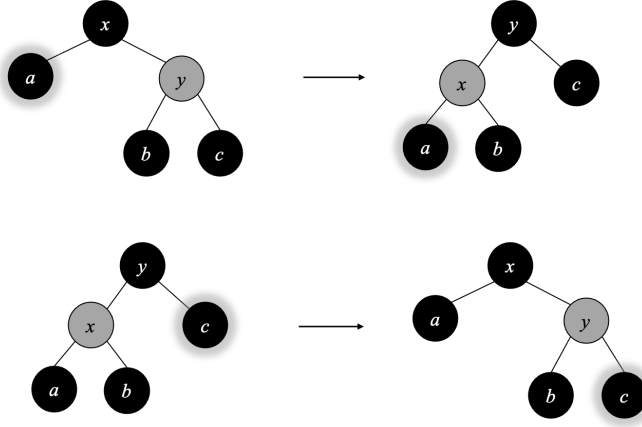


Figure 4.9: The sibling of the doubly-black is red.

We add this fixing as additional 2 rows in equation (4.11):

$$\begin{aligned}
 \text{fix}B^2 \mathcal{B} a_{\mathcal{B}^2} x (\mathcal{R}, b, y, c) &= \text{fix}B^2 \mathcal{B} (\text{fix}B^2 \mathcal{R} a x b) y c \\
 \text{fix}B^2 \mathcal{B} (\mathcal{R}, a, x, b) y c_{\mathcal{B}^2} &= \text{fix}B^2 \mathcal{B} a x (\text{fix}B^2 \mathcal{R} b y c)
 \end{aligned} \tag{4.12}$$

Case 3. *The sibling of the doubly-black node, and its two sub-trees are all black.* In this case, we change the sibling to red, flip the doubly-black node to black, and propagate the doubly-blackness a level up to parent as shown in figure A.3.

There are two symmetric sub-cases. For the upper case, x was either red or black. x changes to black if it was red, otherwise changes to doubly-black; Same coloring changes to y in the lower case. We add this fixing to equation (4.12):

$$\begin{aligned}
 \text{fix}B^2 C a_{\mathcal{B}^2} x (\mathcal{B}, b, y, c) &= \text{shift}B (C, (\text{shift}B a), x, (\mathcal{R}, b, y, c)) \\
 \text{fix}B^2 C (\mathcal{B}, a, x, b) y c_{\mathcal{B}^2} &= \text{fix}B^2 \mathcal{B} a x (\text{fix}B^2 \mathcal{R} b y c) \\
 \text{fix}B^2 C l k r &= (C, l, k, r)
 \end{aligned} \tag{4.13}$$

If none of the patterns match, the last row keeps the node unchanged. The doubly-black fixing is recursive. It terminates in two ways: One is **Case 1**, the doubly-black node is eliminated. Otherwise the blackness may move up till the root. Finally the we force the root be black. Below example program puts all three cases together:

```

— the sibling is black, and has a red sub-tree
fixDB color a@(Node BB _ _ ) x (Node B (Node R b y c) z d)
  = Node color (Node B (shiftBlack a) x b) y (Node B c z d)

```

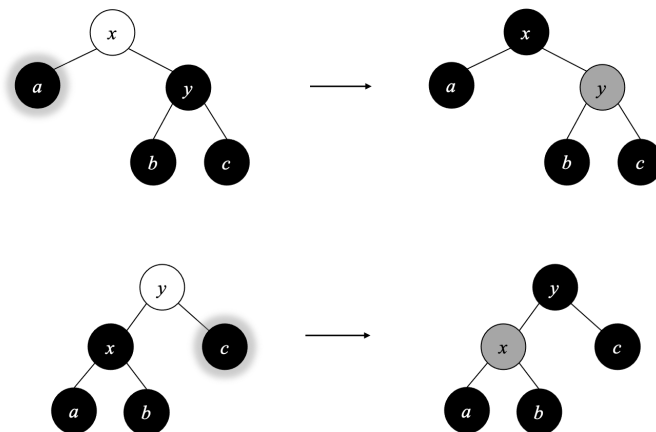


Figure 4.10: move the blackness up.

```

fixDB color BBEEmpty x (Node B (Node R b y c) z d)
  = Node color (Node B Empty x b) y (Node B c z d)
fixDB color a@(Node BB _ _ _) x (Node B b y (Node R c z d))
  = Node color (Node B (shiftBlack a) x b) y (Node B c z d)
fixDB color BBEEmpty x (Node B b y (Node R c z d))
  = Node color (Node B Empty x b) y (Node B c z d)
fixDB color (Node B a x (Node R b y c)) z d@(Node BB _ _ _)
  = Node color (Node B a x b) y (Node B c z (shiftBlack d))
fixDB color (Node B a x (Node R b y c)) z BBEEmpty
  = Node color (Node B a x b) y (Node B c z Empty)
fixDB color (Node B (Node R a x b) y c) z d@(Node BB _ _ _)
  = Node color (Node B a x b) y (Node B c z (shiftBlack d))
fixDB color (Node B (Node R a x b) y c) z BBEEmpty
  = Node color (Node B a x b) y (Node B c z Empty)
— the sibling is red
fixDB B a@(Node BB _ _ _) x (Node R b y c)
  = fixDB B (fixDB R a x b) y c
fixDB B a@BBEmpty x (Node R b y c)
  = fixDB B (fixDB R a x b) y c
fixDB B (Node R a x b) y c@(Node BB _ _ _)
  = fixDB B a x (fixDB R b y c)
fixDB B (Node R a x b) y c@BBEmpty
  = fixDB B a x (fixDB R b y c)
— the sibling and its 2 children are all black, move the blackness up
fixDB color a@(Node BB _ _ _) x (Node B b y c)
  = shiftBlack (Node color (shiftBlack a) x (Node R b y c))
fixDB color BBEEmpty x (Node B b y c)
  = shiftBlack (Node color Empty x (Node R b y c))
fixDB color (Node B a x b) y c@(Node BB _ _ _)
  = shiftBlack (Node color (Node R a x b) y (shiftBlack c))
fixDB color (Node B a x b) y BBEEmpty
  = shiftBlack (Node color (Node R a x b) y Empty)
— otherwise
fixDB color l k r = Node color l k r

```

The delete algorithm is bound to $O(h)$ time, where h is the height of the tree. As red-black tree maintains the balance, $h = O(\lg n)$ for n nodes.

Exercise 4.5

1. Implement the alternative delete algorithm: mark the node as deleted without actually removing it. When the marked nodes exceed 50%, re-build the tree.

4.5 Imperative red-black tree algorithm \star

We simplify the red-black tree implementation with pattern matching. In this section, we give the imperative algorithm for completeness. When insert, the first step is as same as the binary search tree, then as the second step, we fix the balance through tree rotations.

```

1: function INSERT( $T, k$ )
2:    $root \leftarrow T$ 
3:    $x \leftarrow$  CREATE-LEAF( $k$ )
4:   COLOR( $x$ )  $\leftarrow$  RED
5:    $p \leftarrow$  NIL
6:   while  $T \neq$  NIL do
7:      $p \leftarrow T$ 
8:     if  $k <$  KEY( $T$ ) then
9:        $T \leftarrow$  LEFT( $T$ )
10:    else
11:       $T \leftarrow$  RIGHT( $T$ )
12:   PARENT( $x$ )  $\leftarrow$   $p$ 
13:   if  $p =$  NIL then ▷ tree  $T$  is empty
14:     return  $x$ 
15:   else if  $k <$  KEY( $p$ ) then
16:     LEFT( $p$ )  $\leftarrow$   $x$ 
17:   else
18:     RIGHT( $p$ )  $\leftarrow$   $x$ 
19:   return INSERT-FIX( $root, x$ )

```

We make the new node red, and then perform fixing before return. There are 3 basic cases, each one has a symmetric case, hence there are total 6 cases. Among them, we can merge two cases, because both have a red ‘uncle’ node. We change the parent and uncle to black, and set grand parent to red:

```

1: function INSERT-FIX( $T, x$ )
2:   while PARENT( $x$ )  $\neq$  NIL and COLOR(PARENT( $x$ )) = RED do
3:     if COLOR(UNCLE( $x$ )) = RED then ▷ Case 1,  $x$ 's uncle is red
4:       COLOR(PARENT( $x$ ))  $\leftarrow$  BLACK
5:       COLOR(GRAND-PARENT( $x$ ))  $\leftarrow$  RED
6:       COLOR(UNCLE( $x$ ))  $\leftarrow$  BLACK
7:        $x \leftarrow$  GRAND-PARENT( $x$ )
8:     else ▷  $x$ 's uncle is black
9:       if PARENT( $x$ ) = LEFT(GRAND-PARENT( $x$ )) then
10:        if  $x =$  RIGHT(PARENT( $x$ )) then ▷ Case 2,  $x$  is on the right
11:           $x \leftarrow$  PARENT( $x$ )
12:           $T \leftarrow$  LEFT-ROTATE( $T, x$ ) ▷ Case 3,  $x$  is on the left
13:          COLOR(PARENT( $x$ ))  $\leftarrow$  BLACK
14:          COLOR(GRAND-PARENT( $x$ ))  $\leftarrow$  RED
15:           $T \leftarrow$  RIGHT-ROTATE( $T, GRAND-PARENT(x)$ )
16:        else
17:          if  $x =$  LEFT(PARENT( $x$ )) then ▷ Case 2, Symmetric
18:             $x \leftarrow$  PARENT( $x$ )
19:             $T \leftarrow$  RIGHT-ROTATE( $T, x$ ) ▷ Case 3, Symmetric
20:          COLOR(PARENT( $x$ ))  $\leftarrow$  BLACK
21:          COLOR(GRAND-PARENT( $x$ ))  $\leftarrow$  RED

```

```

22:         T ← LEFT-ROTATE(T, GRAND-PARENT(x))
23:     COLOR(T) ← BLACK
24:     return T

```

This algorithm takes $O(\lg n)$ time to insert a key, where n is the number of nodes. Compare to the *balance* function defined previously, they have different logic. Even input the same sequence of keys, they build different red-black trees. Figure 4.11 shows the result when input the same sequence of keys to the imperative algorithm. We can see the difference from figure 4.7. There is a bit performance overhead in the pattern matching algorithm. Okasaki discussed the difference in detail in [13].

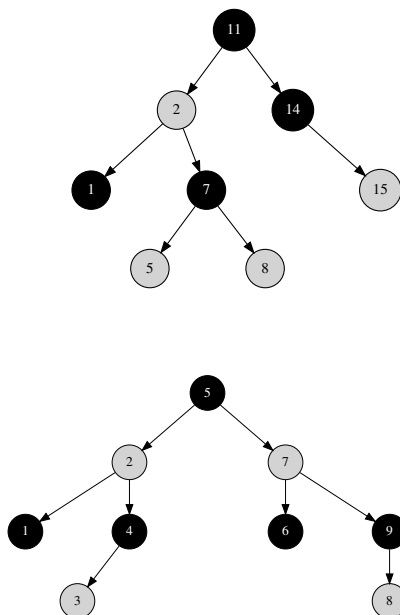


Figure 4.11: Red-black trees created by imperative algorithm.

We provide the imperative delete algorithm in Appendix A of this book.

4.6 Summary

Red-black tree is a popular implementation of balanced binary search tree. We introduce another one, called AVL tree in the next chapter. Red-black tree is a good start for more data structures. If extend the number of children from 2 to k , and maintain the balance, it leads to B-tree; If store the data along with the edge but not inside node, it leads to Radix tree. To maintain the balance, we need handle multiple cases. Okasaki's developed a method that makes the red-black tree easy to implement. There are many implementations based on this idea[16]. We also provide AVL tree and Splay tree implementation based on pattern matching in this book.

4.7 Appendix: Example programs

Definition of red-black tree node with parent field. When not explicitly defined, the color of the new node is red by default.

```

data Node<T> {
  T key
  Color color
  Node<T> left
  Node<T> right
  Node<T> parent

  Node(T x) = Node(null, x, null, Color.RED)

  Node(Node<T> l, T k, Node<T> r, Color c) {
    left = l, key = k, right = r, color = c
    if left  $\neq$  null then left.parent = this
    if right  $\neq$  null then right.parent = this
  }

  Self setLeft(l) {
    left = l
    if l  $\neq$  null then l.parent = this
  }

  Self setRight(r) {
    right = r
    if r  $\neq$  null then r.parent = this
  }

  Node<T> sibling() = if parent.left == this then parent.right
                   else parent.left

  Node<T> uncle() = parent.sibling()

  Node<T> grandparent() = parent.parent
}

```

Insert a key to red-black tree:

```

Node<T> insert(Node<T> t, T key) {
  root = t
  x = Node(key)
  parent = null
  while (t  $\neq$  null) {
    parent = t
    t = if (key < t.key) then t.left else t.right
  }
  if (parent == null) { //tree is empty
    root = x
  } else if (key < parent.key) {
    parent.setLeft(x)
  } else {
    parent.setRight(x)
  }
  return insertFix(root, x)
}

```

Fix the balance:

```

// Fix the red→red violation
Node<T> insertFix(Node<T> t, Node<T> x) {
  while (x.parent  $\neq$  null and x.parent.color == Color.RED) {
    if (x.uncle().color == Color.RED) {
      // case 1: ((a:R x:R b) y:B c:R)  $\implies$  ((a:R x:B b) y:R c:B)

```



```

    x.parent.color = Color.BLACK
    x.grandparent().color = Color.RED
    x.uncle().color = Color.BLACK
    x = x.grandparent()
} else {
    if (x.parent == x.grandparent().left) {
        if (x == x.parent.right) {
            // case 2: ((a x:R b:R) y:B c) ==> case 3
            x = x.parent
            t = leftRotate(t, x)
        }
        // case 3: ((a:R x:R b) y:B c) ==> (a:R x:B (b y:R c))
        x.parent.color = Color.BLACK
        x.grandparent().color = Color.RED
        t = rightRotate(t, x.grandparent())
    } else {
        if (x == x.parent.left) {
            // case 2': (a x:B (b:R y:R c)) ==> case 3'
            x = x.parent
            t = rightRotate(t, x)
        }
        // case 3': (a x:B (b y:R c:R)) ==> ((a x:R b) y:B c:R)
        x.parent.color = Color.BLACK
        x.grandparent().color = Color.RED
        t = leftRotate(t, x.grandparent())
    }
}
t.color = Color.BLACK
return t
}

```


Chapter 5

AVL tree

5.1 Introduction

The idea of red-black tree is to limit the number nodes along a path within a range. AVL tree takes a direct approach: quantify the difference between branches. For a node T , define:

$$\delta(T) = |r| - |l| \tag{5.1}$$

Where $|T|$ is the height of tree T , l and r are the left and right sub-trees. Define $\delta(\emptyset) = 0$ for the empty tree. If $\delta(T) = 0$ for every node T , the tree is definitely balanced. For example, a complete binary tree has $n = 2^h - 1$ nodes for height h . There are not any empty branches unless the leaves. The less absolute value of $\delta(T)$, the more balanced between the sub-trees. We call $\delta(T)$ the *balance factor* of a binary tree.

5.2 Definition

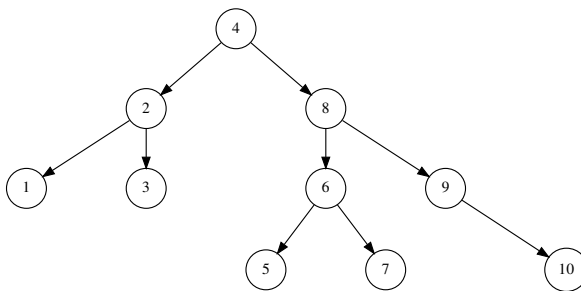


Figure 5.1: an AVL tree

A binary search tree is an AVL tree if every sub-tree T satisfies:

$$|\delta(T)| \leq 1 \tag{5.2}$$

There are three valid values for $\delta(T)$: ± 1 , and 0. Figure 5.1 shows an AVL tree. This definition ensures the tree height $h = O(\lg n)$, where n is the number of nodes in the tree.

Let's prove it. For an AVL tree of height h , the number of nodes varies. There are at most $2^h - 1$ nodes for a complete binary tree case. We are interesting in how many nodes at least. Let the minimum number be $N(h)$. We have the following result:

- Empty tree \emptyset : $h = 0$, $N(0) = 0$;
- Singleton tree: $h = 1$, $N(1) = 1$;

Figure 5.2 shows an AVL tree T of height h . It contains three parts, the key k , and two sub-trees l , r . We have the following equation:

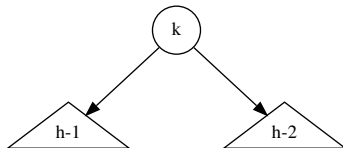


Figure 5.2: An AVL tree of height h . The height of one sub-tree is $h - 1$, the other is no less than $h - 2$.

$$h = \max(|l|, |r|) + 1 \quad (5.3)$$

There must be a sub-tree of height $h - 1$. From the definition, we have $||l| - |r|| \leq 1$ holds. Hence the height of the other tree can not be lower than $h - 2$. The total number of the nodes in T is the sum of both sub-trees plus 1 (for the root):

$$N(h) = N(h - 1) + N(h - 2) + 1 \quad (5.4)$$

This recursive equation is similar to Fibonacci numbers. Actually we can transform it to Fibonacci numbers through $N'(h) = N(h) + 1$. Equation (5.4) then changes to:

$$N'(h) = N'(h - 1) + N'(h - 2) \quad (5.5)$$

Lemma 5.2.1. *Let $N(h)$ be the minimum number of nodes for an AVL tree of height h , and $N'(h) = N(h) + 1$, then*

$$N'(h) \geq \phi^h \quad (5.6)$$

Where $\phi = \frac{\sqrt{5} + 1}{2}$ is the golden ratio.

Proof. When $h = 0$ or 1 , we have:

- $h = 0$: $N'(0) = 1 \geq \phi^0 = 1$
- $h = 1$: $N'(1) = 2 \geq \phi^1 = 1.618\dots$

For the induction case, assume $N'(h) \geq \phi^h$.

$$\begin{aligned} N'(h + 1) &= N'(h) + N'(h - 1) \quad \{\text{Fibonacci}\} \\ &\geq \phi^h + \phi^{h-1} \\ &= \phi^{h-1}(\phi + 1) \quad \left\{ \phi + 1 = \phi^2 = \frac{\sqrt{5} + 3}{2} \right\} \\ &= \phi^{h+1} \end{aligned}$$

□

From Lemma 5.2.1, we immediately obtain:

$$h \leq \log_{\phi}(n+1) = \log_{\phi} 2 \cdot \lg(n+1) \approx 1.44 \lg(n+1) \quad (5.7)$$

We prove the height of AVL tree is proportion to $O(\lg n)$, indicating AVL tree is balanced.

When insert or delete, the balance factor may exceed the valid value range, we need fix to resume $|\delta| < 1$. Traditionally, the fixing is through tree rotations. We give the simplified implementation based on pattern matching. The idea is similar to the functional red-black tree(Okasaki, [13]). Because of this ‘modify-fix’ approach, AVL tree is also self-balanced binary search tree. We can re-use the binary search tree definition. Although the balance factor δ can be computed recursively, we record it inside each node as $T = (l, k, r, \delta)$, and update it when mutate the tree¹. Below example program adds δ as an **Int**:

```
data AVLTree a = Empty
    | Br (AVLTree a) a (AVLTree a) Int
```

For AVL tree, *lookup*, *max*, *min* are as same as the binary search tree. We focus on *insert* and *delete* algorithms.

5.3 Insert

When insert a new element, $|\delta(T)|$ may exceed 1. We can use pattern matching similar to red-black tree to develop a simplified solution. After insert element x , for those sub-trees which are the ancestors of x , the height may increase at most by 1. We need recursively update the balance factor along the path of insertion. Define the insert result as a pair $(T', \Delta H)$, where T' is the updated tree and ΔH is the increment of height. We modify the binary search tree *insert* function as below:

$$insert = fst \circ ins \quad (5.8)$$

Where $fst(a, b) = a$ returns the first element in a pair. $ins(T, k)$ does the actual work to insert element k into tree T :

$$\begin{aligned} ins \ \emptyset \ k &= ((\emptyset, k, \emptyset, 0), 1) \\ ins \ (l, k', r, \delta) \ k &= \begin{cases} k < k' : tree \ (ins \ l \ k) \ k' \ (r, 0) \ \delta \\ k > k' : tree \ (l, 0) \ k' \ (ins \ r, k) \ \delta \end{cases} \end{aligned} \quad (5.9)$$

If the tree is empty \emptyset , the result is a leaf of k with balance factor 0. The height increases to 1. Otherwise let $T = (l, k', r, \delta)$. We compare the new element k with k' . If $k < k'$, we recursively insert k it to the left sub-tree l , otherwise insert to r . As the recursive insert result is a pair of $(l', \Delta l)$ or $(r', \Delta r)$, we need adjust the balance factor and update tree height through function *tree*, it takes 4 parameters: $(l', \Delta l)$, k' , $(r', \Delta r)$, and δ . The result is $(T', \Delta H)$, where T' is the new tree, and ΔH is defined as:

$$\Delta H = |T'| - |T| \quad (5.10)$$

We can further break it down into 4 cases:

$$\begin{aligned} \Delta H &= |T'| - |T| \\ &= 1 + \max(|r'|, |l'|) - (1 + \max(|r|, |l|)) \\ &= \max(|r'|, |l'|) - \max(|r|, |l|) \\ &= \begin{cases} \delta \geq 0, \delta' \geq 0 : \ \Delta r \\ \delta \leq 0, \delta' \geq 0 : \ \delta + \Delta r \\ \delta \geq 0, \delta' \leq 0 : \ \Delta l - \delta \\ otherwise : \ \Delta l \end{cases} \end{aligned} \quad (5.11)$$

¹Alternatively, we can record the height instead of δ [20].

Where $\delta' = \delta(T') = |r'| - |l'|$, is the updated balance factor. Appendix B provides the proof for it. We need determine δ' before balance adjustment.

$$\begin{aligned}
 \delta' &= |r'| - |l'| \\
 &= |r| + \Delta r - (|l| + \Delta l) \\
 &= |r| - |l| + \Delta r - \Delta l \\
 &= \delta + \Delta r - \Delta l
 \end{aligned}
 \tag{5.12}$$

With the changes in height and balance factor, we can define the *tree* function in (5.9):

$$\text{tree } (l', \Delta l) \ k \ (r', \Delta r) \ \delta = \text{balance } (l', k, r', \delta') \ \Delta H
 \tag{5.13}$$

Below example programs implements what we deduced so far:

```

insert t x = fst $ ins t where
  ins Empty = (Br Empty x Empty 0, 1)
  ins (Br l k r d)
    | x < k = tree (ins l) k (r, 0) d
    | x > k = tree (l, 0) k (ins r) d

tree (l, dl) k (r, dr) d = balance (Br l k r d') deltaH where
  d' = d + dr - dl
  deltaH | d >= 0 && d' >= 0 = dr
         | d <= 0 && d' >= 0 = d+dr
         | d >= 0 && d' <= 0 = dl - d
         | otherwise = dl
    
```

5.3.1 Balance

There are 4 cases need fix as shown in figure 5.3. The balance factor is ± 2 , exceeds the range of $[-1, 1]$. We adjust them to a uniformed structure in the center, with the $\delta(y) = 0$.

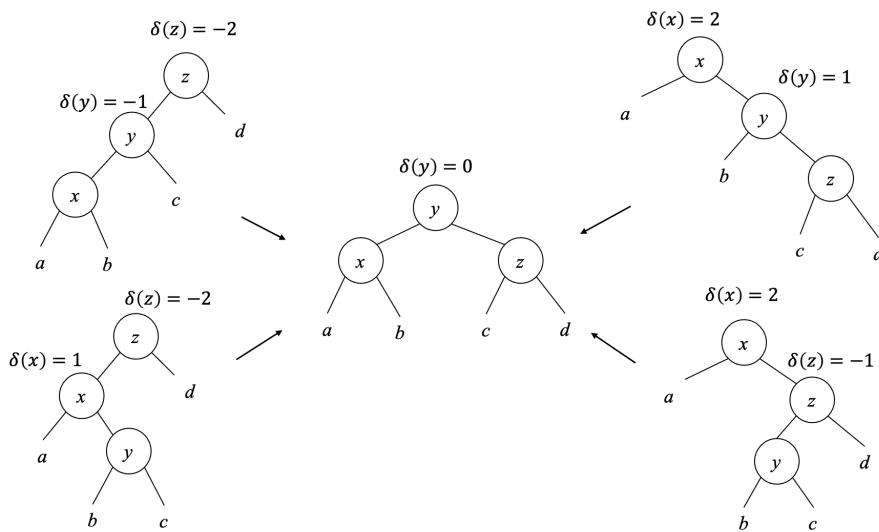


Figure 5.3: Fix 4 cases to the same structure

We call the 4 cases: left-left, right-right, right-left, and left-right. Denote the balance factors before fixing as $\delta(x), \delta(y)$, and $\delta(z)$; after fixing, they change to $\delta'(x), \delta'(y) = 0$,

and $\delta'(z)$ respectively. The values of $\delta'(x)$ and $\delta'(z)$ can be given as below. Appendix B gives the proof.

Left-left:

$$\begin{aligned}\delta'(x) &= \delta(x) \\ \delta'(y) &= 0 \\ \delta'(z) &= 0\end{aligned}\tag{5.14}$$

Right-right:

$$\begin{aligned}\delta'(x) &= 0 \\ \delta'(y) &= 0 \\ \delta'(z) &= \delta(z)\end{aligned}\tag{5.15}$$

Right-left and Left-right:

$$\begin{aligned}\delta'(x) &= \begin{cases} \delta(y) = 1 : & -1 \\ \text{otherwise} : & 0 \end{cases} \\ \delta'(y) &= 0 \\ \delta'(z) &= \begin{cases} \delta(y) = -1 : & 1 \\ \text{otherwise} : & 0 \end{cases}\end{aligned}\tag{5.16}$$

Based on this, we can implement the pattern matching fix as below:

$$\begin{aligned}\text{balance } ((a, x, b, \delta(x)), y, c, -1), z, d, -2) \Delta H &= ((a, x, b, \delta(x)), y, (c, z, d, 0), 0, \Delta H - 1) \\ \text{balance } (a, x, (b, y, c, z, d, \delta(z)), 1), 2) \Delta H &= ((a, x, b, 0), y, (c, z, d, \delta(z)), 0, \Delta H - 1) \\ \text{balance } ((a, x, (b, y, c, \delta(y)), 1), z, d, -2) \Delta H &= ((a, x, b, \delta'(x)), y, (c, z, d, \delta'(z)), 0, \Delta H - 1) \\ \text{balance } (a, x, ((b, y, c, \delta(y)), z, d, -1), 2) \Delta H &= ((a, x, b, \delta'(x)), y, (c, z, d, \delta'(z)), 0, \Delta H - 1) \\ \text{balance } T \Delta H &= (T, \Delta H)\end{aligned}\tag{5.17}$$

Where $\delta'(x)$ and $\delta'(z)$ are defined in (B.17). If none of the pattern matches, the last row keeps the tree unchanged. Below is the example program implements *balance*:

```
balance (Br (Br (Br a x b dx) y c (-1)) z d (-2)) dH =
    (Br (Br a x b dx) y (Br c z d 0) 0, dH-1)
balance (Br a x (Br b y (Br c z d dz) 1) 2) dH =
    (Br (Br a x b 0) y (Br c z d dz) 0, dH-1)
balance (Br (Br a x (Br b y c dy) 1) z d (-2)) dH =
    (Br (Br a x b dx') y (Br c z d dz') 0, dH-1) where
    dx' = if dy == 1 then -1 else 0
    dz' = if dy == -1 then 1 else 0
balance (Br a x (Br (Br b y c dy) z d (-1)) 2) dH =
    (Br (Br a x b dx') y (Br c z d dz') 0, dH-1) where
    dx' = if dy == 1 then -1 else 0
    dz' = if dy == -1 then 1 else 0
balance t d = (t, d)
```

The performance of *insert* is proportion to the height of the tree. From (5.7), it is bound to is $O(\lg n)$ where n is the number of elements in the tree.

Verification

To test an AVL tree, we need verify two things: It is a binary search tree; and for every sub-tree T , equation (5.2): $\delta(T) \leq 1$ holds. Below function examines the height difference between the two sub-trees recursively:

$$\begin{aligned}\text{avl? } \emptyset &= \text{True} \\ \text{avl? } T &= \text{avl? } l \wedge \text{avl? } r \wedge ||r| - |l|| \leq 1\end{aligned}\tag{5.18}$$

Where l , r are the left and right sub-trees. The height is calculated recursively:

$$\begin{aligned} |\emptyset| &= 0 \\ |T| &= 1 + \max(|r|, |l|) \end{aligned} \tag{5.19}$$

Below example program implements AVL tree height verification:

```

isAVL Empty = True
isAVL (Br l _ r _) = isAVL l && isAVL r && abs (height r - height l) ≤ 1

height Empty = 0
height (Br l _ r _) = 1 + max (height l) (height r)

```

Exercise 5.1

1. We only give the algorithm to test AVL height. Complete the program to test if a binary tree is AVL tree.

5.4 Imperative AVL tree algorithm ★

This section gives the imperative algorithm for completeness. Similar to the red-black tree algorithm, we first re-use the binary search tree insert, then fix the balance through tree rotations.

```

1: function INSERT( $T, k$ )
2:    $root \leftarrow T$ 
3:    $x \leftarrow \text{CREATE-LEAF}(k)$ 
4:    $\delta(x) \leftarrow 0$ 
5:    $parent \leftarrow \text{NIL}$ 
6:   while  $T \neq \text{NIL}$  do
7:      $parent \leftarrow T$ 
8:     if  $k < \text{KEY}(T)$  then
9:        $T \leftarrow \text{LEFT}(T)$ 
10:    else
11:       $T \leftarrow \text{RIGHT}(T)$ 
12:     $\text{PARENT}(x) \leftarrow parent$ 
13:    if  $parent = \text{NIL}$  then ▷ tree  $T$  is empty
14:      return  $x$ 
15:    else if  $k < \text{KEY}(parent)$  then
16:       $\text{LEFT}(parent) \leftarrow x$ 
17:    else
18:       $\text{RIGHT}(parent) \leftarrow x$ 
19:    return AVL-INSERT-FIX( $root, x$ )

```

After insert, the balance factor δ may change because of the tree growth. Insert to the right may increase δ by 1, while insert to the left may decrease it. We perform bottom-up fixing from x to root. Denote the new balance factor as δ' , there are 3 cases:

- $|\delta| = 1, |\delta'| = 0$. The new node makes the tree well balanced. The height of the parent keeps unchanged.
- $|\delta| = 0, |\delta'| = 1$. Either the left or the right sub-tree increases its height. We need go on checking the upper level.
- $|\delta| = 1, |\delta'| = 2$. We need rotate the tree to fix the balance factor.


```

1: function AVL-INSERT-FIX( $T, x$ )
2:   while PARENT( $x$ )  $\neq$  NIL do
3:      $P \leftarrow$  PARENT( $x$ )
4:      $L \leftarrow$  LEFT( $x$ )
5:      $R \leftarrow$  RIGHT( $x$ )
6:      $\delta \leftarrow \delta(P)$ 
7:     if  $x =$  LEFT( $P$ ) then
8:        $\delta' \leftarrow \delta - 1$ 
9:     else
10:       $\delta' \leftarrow \delta + 1$ 
11:       $\delta(P) \leftarrow \delta'$ 
12:      if  $|\delta| = 1$  and  $|\delta'| = 0$  then ▷ Height unchanged
13:        return  $T$ 
14:      else if  $|\delta| = 0$  and  $|\delta'| = 1$  then ▷ Go on bottom-up update
15:         $x \leftarrow P$ 
16:      else if  $|\delta| = 1$  and  $|\delta'| = 2$  then
17:        if  $\delta' = 2$  then
18:          if  $\delta(R) = 1$  then ▷ Right-right
19:             $\delta(P) \leftarrow 0$  ▷ By (B.6)
20:             $\delta(R) \leftarrow 0$ 
21:             $T \leftarrow$  LEFT-ROTATE( $T, P$ )
22:          if  $\delta(R) = -1$  then ▷ Right-left
23:             $\delta_y \leftarrow \delta(\text{LEFT}(R))$  ▷ By (B.17)
24:            if  $\delta_y = 1$  then
25:               $\delta(P) \leftarrow -1$ 
26:            else
27:               $\delta(P) \leftarrow 0$ 
28:               $\delta(\text{LEFT}(R)) \leftarrow 0$ 
29:              if  $\delta_y = -1$  then
30:                 $\delta(R) \leftarrow 1$ 
31:              else
32:                 $\delta(R) \leftarrow 0$ 
33:               $T \leftarrow$  RIGHT-ROTATE( $T, R$ )
34:               $T \leftarrow$  LEFT-ROTATE( $T, P$ )
35:          if  $\delta' = -2$  then
36:            if  $\delta(L) = -1$  then ▷ Left-left
37:               $\delta(P) \leftarrow 0$ 
38:               $\delta(L) \leftarrow 0$ 
39:              RIGHT-ROTATE( $T, P$ )
40:            else ▷ Left-Right
41:               $\delta_y \leftarrow \delta(\text{RIGHT}(L))$ 
42:              if  $\delta_y = 1$  then
43:                 $\delta(L) \leftarrow -1$ 
44:              else
45:                 $\delta(L) \leftarrow 0$ 
46:                 $\delta(\text{RIGHT}(L)) \leftarrow 0$ 
47:                if  $\delta_y = -1$  then
48:                   $\delta(P) \leftarrow 1$ 
49:                else
50:                   $\delta(P) \leftarrow 0$ 
51:                LEFT-ROTATE( $T, L$ )

```

```

52:             RIGHT-ROTATE( $T, P$ )
53:         break
54:     return  $T$ 

```

Besides rotation, we also need update δ for the impacted nodes. The right-right and left-left cases need one rotation, while the right-left and left-right case need two rotations. We skip the AVL tree delete algorithm in this chapter. Appendix B provides the delete implementation.

5.5 Summary

AVL tree was developed in 1962 by Adelson-Velskii and Landis[18], [19]. It is named after the two authors. AVL tree was developed earlier than the red-black tree. Both are self-balance binary search trees. Most tree operations are bound $O(\lg n)$ time. From (5.7), AVL tree is more rigidly balanced, and performs faster than red-black tree in looking up intensive applications [18]. However, red-black tree performs better in frequently insertion and removal cases. Many popular self-balance binary search tree libraries are implemented on top of red-black tree. AVL tree also provides the intuitive and effective solution to the balance problem.

5.6 Appendix: Example programs

Definition of AVL tree node.

```

data Node< $T$ > {
    int delta
     $T$  key
    Node< $T$ > left
    Node< $T$ > right
    Node< $T$ > parent
}

```

Fix the balance:

```

Node< $T$ > insertFix(Node< $T$ > t, Node< $T$ > x) {
    while (x.parent  $\neq$  null) {
        var (p, l, r) = (x.parent, x.parent.left, x.parent.right)
        var d1 = p.delta
        var d2 = if x == parent.left then d1 - 1 else d1 + 1
        p.delta = d2

        if abs(d1) == 1 and abs(d2) == 0 {
            return t
        } else if abs(d1) == 0 and abs(d2) == 1 {
            x = p
        } else if abs(d1) == 1 and abs(d2) == 2 {
            if d2 == 2 {
                if r.delta == 1 { //Right-right
                    p.delta = 0
                    r.delta = 0
                    t = rotateLeft(t, p)
                } else if r.delta == -1 { //Right-Left
                    var dy = r.left.delta
                    p.delta = if dy == 1 then -1 else 0
                    r.left.delta = 0
                    r.delta = if dy == -1 then 1 else 0
                    t = rotateRight(t, r)
                    t = rotateLeft(t, p)
                }
            }
        }
    }
}

```

```
    } else if d2 == -2 {
        if l.delta == -1 { //Left-left
            p.delta = 0
            l.delta = 0
            t = rotateRight(t, p)
        } else if l.delta == 1 { //Left-right
            var dy = l.right.delta
            l.delta = if dy == 1 then -1 else 0
            l.right.delta = 0
            p.delta = if dy == -1 then 1 else 0
            t = rotateLeft(t, l)
            t = rotateRight(t, p)
        }
    }
    break
}
}
return t
}
```


Chapter 6

Radix tree

Binary search tree stores data in nodes. Can we use the edges to carry information? Radix trees, including trie, prefix tree, and suffix tree are the data structures developed based on this idea in 1960s. They are widely used in compiler design[21], and bio-information processing, like DNA pattern matching [23].

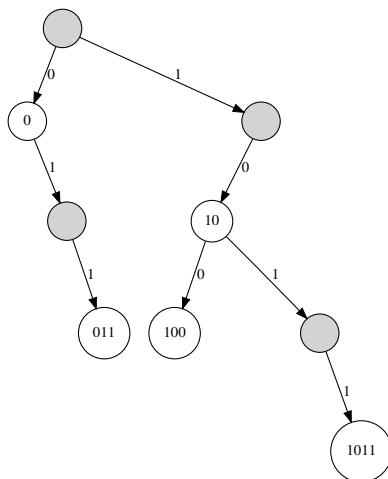


Figure 6.1: Radix tree.

Figure 6.1 shows a Radix tree. It contains bits 1011, 10, 011, 100 and 0. When lookup a key $k = (b_0b_1\dots b_n)_2$, we take the first bit b_0 (MSB from left), check whether it is 0 or 1. For 0, turn left, else turn right. Then take the second bit and repeat looking up till either reach a leaf node or consume all the n bits. We needn't store keys in Radix tree node. The information is represented by edges. The nodes labelled with key in figure 6.1 are for illustration purpose. If the keys are integers, we can represent them in binary format, and implement lookup with bit-wise manipulations.

6.1 Integer trie

We call the data structure in figure 6.1 *binary trie*. Trie was developed by Edward Fredkin in 1960. It comes from “retrieval”, pronounce as /'tri:/ by Fredkin, while others pronounce it as /'traɪ/ “try”[24]. Although it's also called prefix tree in some context, we treat trie and prefix tree different in this chapter. A binary trie is a special

binary tree in which the placement of each key is controlled by its bits, each 0 means ‘go left’ and each 1 means ‘go right’[21]. Consider the binary trie in figure 6.2. The three keys are different bit strings of “11”, “011”, and “0011” although they are all equal to 3.

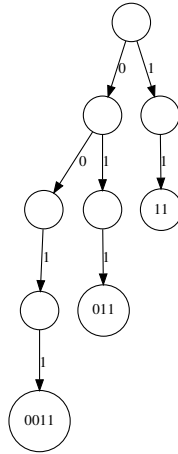


Figure 6.2: A big-endian trie.

It is inefficient to treat the prefix zeros as valid bits. For 32 bits integers, we need a tree of 32 levels to insert number 1. Okasaki suggested to use little-endian integers instead[21]. 1 is represented as bits $(1)_2$, 2 as $(01)_2$, and 3 is $(11)_2$, ...

6.1.1 Definition

We can re-use binary tree structure to define the little-endian binary trie. A node is either empty, or a branch containing the left, right sub-trees, and an optional value. The left sub-tree is encoded as 0 and the right sub-tree is encoded as 1.

```
data IntTrie a = Empty
             | Branch (IntTrie a) (Maybe a) (IntTrie a)
```

Given a node in the binary trie, the integer key bound to it is uniquely determined through its position. That is the reason we need not save the key, but only the value in the node. The type of the key is always integer, we call the tree *IntTrie A* if the value is of type *A*.

6.1.2 Insert

When insert an integer key k and a value v , we convert k into binary form. If k is even, the lowest bit is 0, we recursively insert to the left sub-tree; otherwise if k is odd, the lowest bit is 1, we recursively insert to the right. We next divide k by 2 to remove the lowest bit. For none empty trie $T = (l, v', r)$, where l, r are the left and right sub-trees, and v' is the optional value, function *insert* can be defined as below:

$$\begin{aligned}
 \text{insert } \emptyset k v &= \text{insert}(\emptyset, \text{Nothing}, \emptyset) k v \\
 \text{insert } (l, v', r) 0 v &= (l, \text{Just } v, r) \\
 \text{insert } (l, v', r) k v &= \begin{cases} \text{even}(k) : (\text{insert } l \frac{k}{2} v, v', r) \\ \text{odd}(k) : (l, v', \text{insert } r \lfloor \frac{k}{2} \rfloor v) \end{cases} \quad (6.1)
 \end{aligned}$$

If $k = 0$, we put v in the node. When $T = \emptyset$, it becomes $(\emptyset, \text{Just } v, \emptyset)$. As far as $k \neq 0$, we goes down along the tree based on the parity of k . We create empty leaf $(\emptyset, \text{Nothing}, \emptyset)$ whenever meet \emptyset node. This algorithm overrides the value if k already exists. Alternatively, we can store a list, and append v to it. Figure 6.3 shows an example trie, generated by inserting the key-value pairs of $\{1 \rightarrow a, 4 \rightarrow b, 5 \rightarrow c, 9 \rightarrow d\}$. Below is the example program implements *insert*:

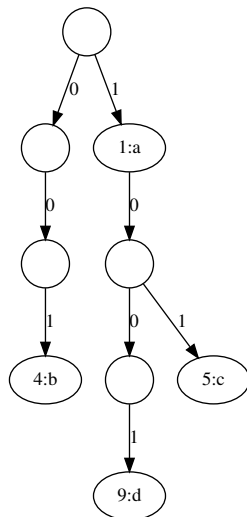


Figure 6.3: A little-endian integer binary trie of $\{1 \rightarrow a, 4 \rightarrow b, 5 \rightarrow c, 9 \rightarrow d\}$.

```

insert Empty k x = insert (Branch Empty Nothing Empty) k x
insert (Branch l v r) 0 x = Branch l (Just x) r
insert (Branch l v r) k x | even k    = Branch (insert l (k `div` 2) x) v r
                          | otherwise = Branch l v (insert r (k `div` 2) x)

```

We can define the even/odd testing by modular 2, and check if the remainder is 0 or not: $\text{even}(k) = (k \bmod 2 = 0)$. Or use bit-wise operation in some environment, like $(k \ \& \ 0x1) == 0$. We can eliminate the recursion through loops to realize an iterative implementation as below:

```

1: function INSERT( $T, k, v$ )
2:   if  $T = \text{NIL}$  then
3:      $T \leftarrow \text{EMPTY-NODE}$  ▷ (NIL, Nothing, NIL)
4:    $p \leftarrow T$ 
5:   while  $k \neq 0$  do
6:     if EVEN?( $k$ ) then
7:       if LEFT( $p$ ) = NIL then
8:         LEFT( $p$ )  $\leftarrow$  EMPTY-NODE
9:        $p \leftarrow$  LEFT( $p$ )
10:    else
11:      if RIGHT( $p$ ) = NIL then
12:        RIGHT( $p$ )  $\leftarrow$  EMPTY-NODE
13:       $p \leftarrow$  RIGHT( $p$ )
14:     $k \leftarrow \lfloor k/2 \rfloor$ 
15:  VALUE( $p$ )  $\leftarrow$   $v$ 
16:  return  $T$ 

```

INSERT takes, a trie T , a key k , and a value v . For integer k with m bits in binary, it goes into m levels of the trie. The performance is bound to $O(m)$.

6.1.3 Look up

When look up key k in a none empty integer trie, if $k = 0$, then the root node is the target. Otherwise, we check the lowest bit, then recursively look up the left or right sub-tree accordingly.

$$\begin{aligned}
 \text{lookup } \emptyset k &= \text{Nothing} \\
 \text{lookup } (l, v, r) 0 &= v \\
 \text{lookup } (l, v, r) k &= \begin{cases} \text{even}(k) : \text{lookup } l \lfloor \frac{k}{2} \rfloor \\ \text{odd}(k) : \text{lookup } r \lfloor \frac{k}{2} \rfloor \end{cases} \quad (6.2)
 \end{aligned}$$

Below example program implements the *lookup* function:

```

lookup Empty _ = Nothing
lookup (Branch _ v _) 0 = v
lookup (Branch l _ r) k | even k    = lookup l (k `div` 2)
                        | otherwise = lookup r (k `div` 2)

```

We can eliminate the recursion to implement the iterative *lookup* as the following:

```

1: function LOOKUP( $T, k$ )
2:   while  $k \neq 0$  and  $T \neq \text{NIL}$  do
3:     if  $\text{EVEN?}(k)$  then
4:        $T \leftarrow \text{LEFT}(T)$ 
5:     else
6:        $T \leftarrow \text{RIGHT}(T)$ 
7:      $k \leftarrow \lfloor k/2 \rfloor$ 
8:   if  $T \neq \text{NIL}$  then
9:     return  $\text{VALUE}(T)$ 
10:  else
11:    return  $\text{NIL}$ 

```

The *lookup* function is bound to $O(m)$ time, where m is the number of bits of k .

Exercise 6.1

1. Can we change the definition from `Branch (IntTrie a) (Maybe a) (IntTrie a)` to `Branch (IntTrie a) a (IntTrie a)`, and return *Nothing* if the value does not exist, and *Just v* otherwise?

6.2 Integer prefix tree

Trie is not space efficient. As shown in figure 6.3, there are only 4 nodes with value, while the rest 5 are empty. The space usage is less than 50%. To improve the efficiency, we can consolidate the chained nodes to one. Integer prefix tree is such a data structure developed by Donald R. Morrison in 1968. He named it as 'Patricia', standing for **P**RACTICAL **A**LGORITHM **T**O **R**ETRIEVE **I**NFORMATION **C**ODED **I**N **A**LPHANUMERIC[22]. When the keys are integer, we call it integer prefix tree or simply integer tree when the context is clear. Okasaki provided the implementation in [21]. Consolidate the chained nodes in figure 6.3, we obtained an integer tree as shown in figure 6.4.

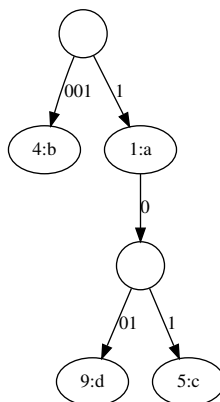


Figure 6.4: Little endian integer tree for the map $\{1 \rightarrow a, 4 \rightarrow b, 5 \rightarrow c, 9 \rightarrow d\}$.

The key to the branch node is the longest common prefix for its descendant trees. In other words, the sibling sub-trees branch out at the bit where ends at their longest prefix. As the result, integer tree eliminates the redundant spaces in trie.

6.2.1 Definition

Integer prefix tree is a special binary tree. It is either empty or a node of:

- A leaf contains an integer key k and a value v ;
- Or a branch with the left and right sub-trees, that share the **longest common prefix** bits for their keys. For the left sub-tree, the next bit is 0, for the right, it is 1.

Below example program defines the integer prefix tree. The branch node contains 4 components: The longest prefix, a mask integer indicating from which bit the sub-trees branch out, the left and right sub-trees. The mask is $m = 2^n$ for some integer $n \geq 0$. All bits that are lower than n do not belong to the common prefix.

```

data IntTree a = Empty
                | Leaf Int a
                | Branch Int Int (IntTree a) (IntTree a)

```

6.2.2 Insert

When insert integer y to tree T , if T is empty, we create a leaf of y ; If T is a singleton leaf of x , besides the new leaf of y , we need create a branch node, set x and y as the two sub-trees. To determine whether y is on the left or right, we need find the longest common prefix p of x and y . For example if $x = 12 = (1100)_2$, $y = 15 = (1111)_2$, then $p = (1100)_2$, where o denotes the bits we don't care. We can use another integer m to mask those bits. In this example, $m = 4 = (100)_2$. The next bit after p presents 2^1 . It is 0 in x , 1 in y . Hence, we set x as the left sub-tree and y as the right, as shown in figure 6.5.

If T is neither empty nor a leaf, we firstly check if y matches the longest common prefix p in the root, then recursively insert it to the sub-tree according to the next bit after p . For example, when insert $y = 14 = (1110)_2$ to the tree shown in figure 6.5, since $p = (1100)_2$ and the next bit (the bit of 2^1) is 1, we recursively insert y to the right

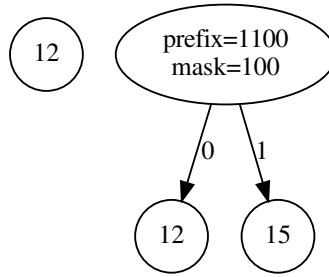
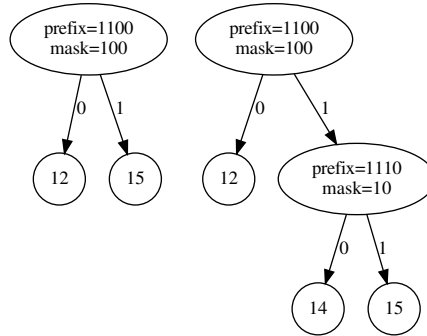
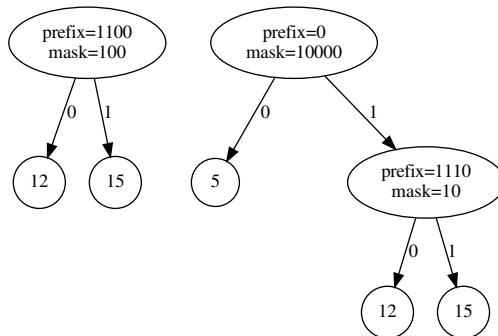


Figure 6.5: Left: T is a leaf of 12; Right: After insert 15.

sub-tree. If y does not match p in the root, we need branch a new leaf as shown in figure 6.6.



(a) Insert $14 = (1110)_2$, which matches $p = (1100)_2$. It is inserted to the right.



(b) Insert $5 = (101)_2$, which does not match $p = (1100)_2$. Branch out a new leaf.

Figure 6.6: The tree is a branch node.

For integer key k and value v , let (k, v) be the leaf. For branch node, denote it as (p, m, l, r) , where p is the longest common prefix, m is the mask, l and r are the left and

right sub-trees. Below *insert* function defines the above 3 cases:

$$\begin{aligned}
 \text{insert } \emptyset k v &= (k, v) \\
 \text{insert } (k, v') k v &= (k, v) \\
 \text{insert } (k', v') k v &= \text{join } k (k, v) k' (k', v') \\
 \text{insert } (p, m, l, r) k v &= \begin{cases} \text{match}(k, p, m) : & \begin{cases} \text{zero}(k, m) : & (p, m, \text{insert } l k v) \\ \text{otherwise} : & (p, m, \text{insert } r k v) \end{cases} \\ \text{otherwise} : & \text{join } k (k, v) p (p, m, l, r) \end{cases}
 \end{aligned} \tag{6.3}$$

The first clause creates a leaf when $T = \emptyset$; the second clause overrides the value for the same key. Function $\text{match}(k, p, m)$ tests if integer k and prefix p have the same bits after masked with m through: $\text{mask}(k, m) = p$, where $\text{mask}(k, m) = \overline{m-1} \& k$. It applies bit-wise not to $m-1$, then does bit-wise and with k . $\text{zero}(k, m)$ tests the next bit in k masked with m is 0 or not. We shift m one bit to right, then do bit-wise and with k :

$$\text{zero}(k, m) = x \& (m \gg 1) \tag{6.4}$$

Function $\text{join}(p_1, T_1, p_2, T_2)$ takes two different prefixes and trees. It extracts the longest common prefix of p_1 and p_2 as $(p, m) = \text{LCP}(p_1, p_2)$, creates a new branch node, then set T_1 and T_2 as the two sub-trees:

$$\text{join}(p_1, T_1, p_2, T_2) = \begin{cases} \text{zero}(p_1, m) : & (p, m, T_1, T_2) \\ \text{otherwise} : & (p, m, T_2, T_1) \end{cases} \tag{6.5}$$

To calculate the longest common prefix, we can firstly compute bit-wise exclusive-or for p_1 and p_2 , then count the highest bit $\text{highest}(\text{xor}(p_1, p_2))$ as:

$$\begin{aligned}
 \text{highest}(0) &= 0 \\
 \text{highest}(n) &= 1 + \text{highest}(n \gg 1)
 \end{aligned}$$

Then generate a mask $m = 2^{\text{highest}(\text{xor}(p_1, p_2))}$. The longest common prefix p can be given by masking the bits with m for either p_1 or p_2 , like $p = \text{mask}(p_1, m)$. The following example program implements the *insert* function:

```

insert t k x
= case t of
  Empty → Leaf k x
  Leaf k' x' → if k == k' then Leaf k x
               else join k (Leaf k x) k' t
  Branch p m l r
    | match k p m → if zero k m
                    then Branch p m (insert l k x) r
                    else Branch p m l (insert r k x)
    | otherwise → join k (Leaf k x) p t

join p1 t1 p2 t2 = if zero p1 m then Branch p m t1 t2
                  else Branch p m t2 t1

where
  (p, m) = lcp p1 p2

lcp p1 p2 = (p, m) where
  m = bit (highestBit (p1 `xor` p2))
  p = mask p1 m

highestBit x = if x == 0 then 0 else 1 + highestBit (shiftR x 1)

mask x m = x .&. complement (m - 1)

```

```

zero x m = x .&. (shiftR m 1) == 0
match k p m = (mask k m) == p

```

We can also implement *insert* imperatively:

```

1: function INSERT( $T, k, v$ )
2:   if  $T = \text{NIL}$  then
3:     return CREATE-LEAF( $k, v$ )
4:    $y \leftarrow T$ 
5:    $p \leftarrow \text{NIL}$ 
6:   while  $y$  is not leaf, and MATCH( $k, \text{PREFIX}(y), \text{MASK}(y)$ ) do
7:      $p \leftarrow y$ 
8:     if ZERO?( $k, \text{MASK}(y)$ ) then
9:        $y \leftarrow \text{LEFT}(y)$ 
10:    else
11:       $y \leftarrow \text{RIGHT}(y)$ 
12:   if  $y$  is leaf, and  $k = \text{KEY}(y)$  then
13:     VALUE( $y$ )  $\leftarrow v$ 
14:   else
15:      $z \leftarrow \text{BRANCH}(y, \text{CREATE-LEAF}(k, v))$ 
16:     if  $p = \text{NIL}$  then
17:        $T \leftarrow z$ 
18:     else
19:       if LEFT( $p$ ) =  $y$  then
20:         LEFT( $p$ )  $\leftarrow z$ 
21:       else
22:         RIGHT( $p$ )  $\leftarrow z$ 
23:   return  $T$ 

```

Where BRANCH(T_1, T_2) creates a new branch node, extracts the longest common prefix, then sets T_1 and T_2 as the two sub-trees.

```

1: function BRANCH( $T_1, T_2$ )
2:    $T \leftarrow \text{EMPTY-NODE}$ 
3:   (PREFIX( $T$ ), MASK( $T$ ))  $\leftarrow \text{LCP}(\text{PREFIX}(T_1), \text{PREFIX}(T_2))$ 
4:   if ZERO?(PREFIX( $T_1$ ), MASK( $T$ )) then
5:     LEFT( $T$ )  $\leftarrow T_1$ 
6:     RIGHT( $T$ )  $\leftarrow T_2$ 
7:   else
8:     LEFT( $T$ )  $\leftarrow T_2$ 
9:     RIGHT( $T$ )  $\leftarrow T_1$ 
10:  return  $T$ 

```

```

11: function ZERO?( $x, m$ )
12:  return ( $x \& \lfloor \frac{m}{2} \rfloor$ ) = 0

```

Function LCP find the longest bit prefix from two integers:

```

1: function LCP( $a, b$ )
2:    $d \leftarrow \text{xor}(a, b)$ 
3:    $m \leftarrow 1$ 
4:   while  $d \neq 0$  do
5:      $d \leftarrow \lfloor \frac{d}{2} \rfloor$ 

```

```

6:      $m \leftarrow 2m$ 
7:     return (MASKBIT( $a, m$ ),  $m$ )

8: function MASKBIT( $x, m$ )
9:     return  $x \& \overline{m-1}$ 

```

Figure 6.7 gives an example integer tree created from the *insert* algorithm. Although integer prefix tree consolidates the chained nodes, the operation to extract the longest common prefix need linear scan the bits. For integer of m bits, the insert is bound to $O(m)$.

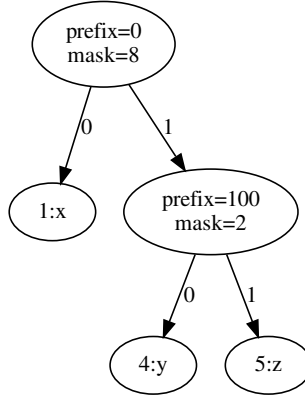


Figure 6.7: Insert $\{1 \rightarrow x, 4 \rightarrow y, 5 \rightarrow z\}$ to the big-endian integer tree.

6.2.3 Lookup

When lookup key k , if the integer tree $T = \emptyset$ or it is a leaf of $T = (k', v)$ with different key, then k does not exist; if $k = k'$, then v is the result; if $T = (p, m, l, r)$ is a branch node, we need check if the common prefix p matches k under the mask m , then recursively lookup the sub-tree l or r upon next bit. If fails to match the common prefix p , then k does not exist.

$$\begin{aligned}
 \text{lookup } \emptyset k &= \text{Nothing} \\
 \text{lookup } (k', v) k &= \begin{cases} k = k' : & \text{Just } v \\ \text{otherwise} : & \text{Nothing} \end{cases} \\
 \text{lookup } (p, m, l, r) k &= \begin{cases} \text{match}(k, p, m) : & \begin{cases} \text{zero}(k, m) : & \text{lookup } l k \\ \text{otherwise} : & \text{lookup } r k \end{cases} \\ \text{otherwise} : & \text{Nothing} \end{cases}
 \end{aligned} \tag{6.6}$$

We can also eliminate the recursion to implement the iterative lookup algorithm.

```

1: function LOOK-UP( $T, k$ )
2:   if  $T = \text{NIL}$  then
3:     return NIL
4:   while  $T$  is not leaf, and MATCH( $k, \text{PREFIX}(T), \text{MASK}(T)$ ) do
5:     if ZERO?( $k, \text{MASK}(T)$ ) then
6:        $T \leftarrow \text{LEFT}(T)$ 
7:     else
8:        $T \leftarrow \text{RIGHT}(T)$ 

```

```

9:   if  $T$  is leaf, and  $\text{KEY}(T) = k$  then
10:      return  $\text{VALUE}(T)$ 
11:   else
12:      return NIL

```

The *lookup* algorithm is bound to $O(m)$, where m is the number of bits in the key.

Exercise 6.2

1. Write a program to implement the *lookup* function.
2. Implement the pre-order traverse for both integer trie and integer tree. Only output the keys when the nodes store values. What pattern does the result follow?

6.3 Trie

From integer trie and tree, we can extend the key to a list of elements. Particularly the trie and tree with key in alphabetic string are powerful tools for text manipulation.

6.3.1 Definition

When extend the key type from 0/1 bits to generic list, the tree structure changes from binary tree to multiple sub-trees. Taking English characters for example, there are up to 26 sub-trees when ignore the case as shown in figure 6.8.

Not all the 26 sub-trees contain data. In figure 6.8, there are only three none empty sub-trees bound to 'a', 'b', and 'z'. Other sub-trees, such as for 'c', are empty. We can hide them in the figure. When it is case sensitive, or extent the key from alphabetic string to generic list, we can adopt collection types, like map to define trie.

A trie is either empty or a node of 2 kinds:

1. A leaf of value v without any sub-trees;
2. A branch, containing a value v and multiple sub-trees. Each sub-tree is bound to an element k of type K .

Let the type of value be V , we denote the trie as $\text{Trie } K V$. Below example program defines trie.

```

data Trie k v = Trie { value :: Maybe v
                      , subTrees :: [(k, Trie k v)]}

```

The empty trie is in form of $(\text{Nothing}, \emptyset)$.

6.3.2 Insert

When insert a pair of key and value to the trie, where the key is a list of elements. Let the trie be $T = (v, ts)$, where v is the value stored in the trie, and $ts = \{c_1 \mapsto T_1, c_2 \mapsto T_2, \dots, c_m \mapsto T_m\}$ contains mappings between elements and sub-trees. Element c_i is mapped to sub-tree T_i . We can either implement the mapping through associated list: $[(c_1, T_1), (c_2, T_2), \dots, (c_m, T_m)]$, or through self-balanced tree map (Chapter 4 or 5).

$$\begin{aligned}
 \text{insert } (v, ts) \ \emptyset \ v' &= (v', ts) \\
 \text{insert } (v, ts) \ (k : ks) \ v' &= (v, \text{ins } ts)
 \end{aligned} \tag{6.7}$$

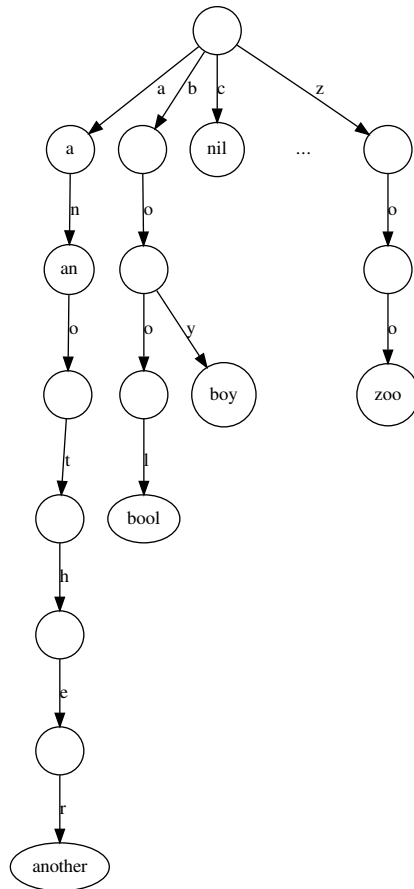


Figure 6.8: A trie of 26 branches, containing key 'a', 'an', 'another', 'bool', 'boy', and 'zoo'.

When the key is empty, we override the value; otherwise, we extract the first element k , check if there is a map among the sub-trees for k , and recursively insert ks and v' :

$$\begin{aligned} \text{ins } \emptyset &= [k \mapsto \text{insert } (\text{Nothing}, \emptyset) \text{ ks } v'] \\ \text{ins } ((c \mapsto t) : ts) &= \begin{cases} c = k : & (k \mapsto \text{insert } t \text{ ks } v') : ts \\ \text{otherwise} : & (c \mapsto t) : (\text{ins } ts) \end{cases} \end{aligned} \quad (6.8)$$

If there is no sub-tree in the node, we create a mapping from k to an empty trie node $t = (\text{Nothing}, \emptyset)$; otherwise, we located the sub-tree t mapped to k , then recursively insert ks and v' to t . Below is the example program implement *insert*, it's based on associated list to manage sub-tree mappings.

```

insert (Trie _ ts) [] x = Trie (Just x) ts
insert (Trie v ts) (k:ks) x = Trie v (ins ts) where
  ins [] = [(k, insert empty ks x)]
  ins ((c, t) : ts) = if c == k then (k, insert t ks x) : ts
                    else (c, t) : (ins ts)

empty = Trie Nothing []

```

We can also eliminate the recursion to implement *insert* iteratively.

```

1: function INSERT( $T, k, v$ )
2:   if  $T = \text{NIL}$  then
3:      $T \leftarrow \text{EMPTY-NODE}$ 
4:    $p \leftarrow T$ 
5:   for each  $c$  in  $k$  do
6:     if SUB-TREES( $p$ )[ $c$ ] = NIL then
7:       SUB-TREES( $p$ )[ $c$ ]  $\leftarrow$  EMPTY-NODE
8:      $p \leftarrow$  SUB-TREES( $p$ )[ $c$ ]
9:   VALUE( $p$ )  $\leftarrow v$ 
10:  return  $T$ 

```

For the key type $[K]$ (list of K), if K is finite set of m elements, and the length of the key is n , then the insert algorithm is bound to $O(mn)$. When the key is lower case English strings, then $m = 26$, the insert operation is proportion to the length of key string.

6.3.3 Look up

When look up a none empty key ($k : ks$) from trie $T = (v, ts)$, starting from the first element k , if there exists sub-tree T' mapped to k , we then recursively lookup ks in T' . When the key is empty, then return the value as result:

$$\begin{aligned} \text{lookup } \emptyset (v, ts) &= v \\ \text{lookup } (k : ks) (v, ts) &= \begin{cases} \text{lookup}_l k \text{ ts} = \text{Nothing} : & \text{Nothing} \\ \text{lookup}_l k \text{ ts} = \text{Just } t : & \text{lookup } ks \text{ t} \end{cases} \end{aligned} \quad (6.9)$$

Where function lookup_l is defined in chapter 1. It looks up if a key exists in an assoc list. Below is the corresponding iterative implementation:

```

1: function LOOK-UP( $T, key$ )
2:   if  $T = \text{NIL}$  then
3:     return Nothing
4:   for each  $c$  in  $key$  do
5:     if SUB-TREES( $T$ )[ $c$ ] = NIL then
6:       return Nothing

```



```

7:     T ← SUB-TREES(T)[c]
8:     return VALUE(T)

```

The lookup algorithm is bound to $O(mn)$, where n is the length of the key, and m is the size of the element set.

Exercise 6.3

1. Use the self-balance binary tree, like red-black tree or AVL tree to implement a *map* data structure, and manage the sub-trees with *map*. We call such implementation *MapTrie* and *MapTree* respectively. What are the performance of *insert* and *lookup* for map based tree and trie?

6.4 Prefix tree

Trie is not space efficient. We can consolidate the chained nodes to obtain the prefix tree.

6.4.1 Definition

A prefix tree node t contains two parts: an optional value v ; zero or multiple sub prefix trees, each t_i is bound to a list s_i . The sub-trees and their mappings are denoted as $[s_i \mapsto t_i]$. These lists share the longest common prefix s bound to the node t . i.e. s is the longest common prefix of $s \# s_1, s \# s_2, \dots$. For any $i \neq j$, list s_i and s_j don't have none empty common prefix. Consolidate the chained nodes in figure 6.8, we obtain the corresponding prefix tree in figure 6.9.

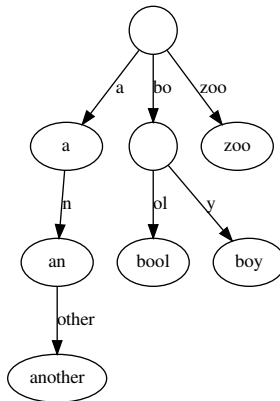


Figure 6.9: A prefix tree with keys: 'a', 'an', 'another', 'bool', 'boy', 'zoo'.

Below example program defines the prefix tree:

```

data PrefixTree k v = PrefixTree { value :: Maybe v
                                   , subTrees :: [[k], PrefixTree k v]}

```

We denote prefix tree $t = (v, ts)$. Particularly, $(Nothing, \emptyset)$ is the empty node, and $(Just v, \emptyset)$ is a leaf node of value v .

6.4.2 Insert

When insert key s , if the prefix tree is empty, we create a leaf node of s as figure 6.10 (a); otherwise, if there exists common prefix between s and s_i , where s_i is bound to some

sub-tree t_i , we branch out a new leaf t_j , extract the common prefix, and map it to a new internal branch node t' , then put t_i and t_j as two sub-trees of t' . Figure 6.10 (b) shows this case. There are two special cases: s is the prefix of s_i as shown in figure 6.10 (c) \rightarrow (e); or s_i is the prefix of s as shown in figure 6.10 (d) \rightarrow (e).

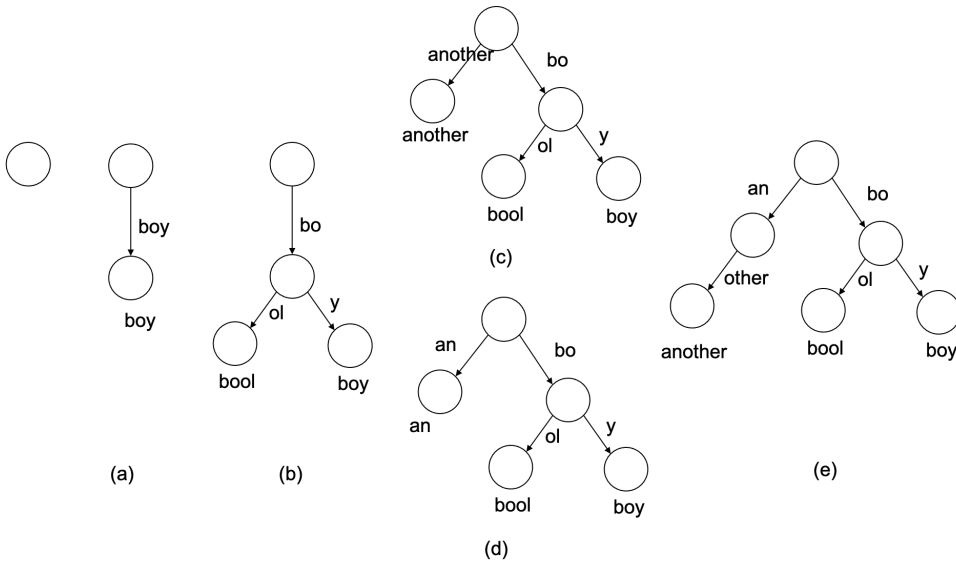


Figure 6.10: (a) insert ‘boy’ to empty tree; (b) insert ‘bool’, branch a new node out; (c) insert ‘another’ to (b); (d) insert ‘an’ to (b); (e) insert ‘an’ to (c), same result as insert ‘another’ to (d)

Below function inserts key s and value v to the prefix tree $t = (v', ts)$:

$$\begin{aligned} \text{insert } (v', ts) \ \emptyset \ v &= (\text{Just } v, ts) \\ \text{insert } (v', ts) \ s \ v &= (v', \text{ins } ts) \end{aligned} \quad (6.10)$$

If the key s is empty, we overwrite the value to v ; otherwise, we call ins to examine the sub-trees and their prefixes.

$$\begin{aligned} \text{ins } \emptyset &= [s \mapsto (\text{Just } v, \emptyset)] \\ \text{ins } (s' \mapsto t) : ts' &= \begin{cases} \text{match } s \ s' : (\text{branch } s \ v \ s' \ t) : ts' \\ \text{otherwise} : (s' \mapsto t) : \text{ins } ts' \end{cases} \end{aligned} \quad (6.11)$$

If there is no sub-tree in the node, then we create a leaf of v as the single sub-tree, and map s to it; otherwise, for each sub-tree mapping $s' \mapsto t$, we compare s' with s . If they have common prefix (tested by the match function), then we *branch* out new sub-tree. We define two lists matching if they have common prefix:

$$\begin{aligned} \text{match } \emptyset \ B &= \text{True} \\ \text{match } A \ \emptyset &= \text{True} \\ \text{match } (a : as) \ (b : bs) &= a = b \end{aligned} \quad (6.12)$$

To extract the longest common prefix of two lists A and B , we define a function $(C, A', B') = \text{lcp } A \ B$, where $C \# A' = A$ and $C \# B' = B$ hold. If either A or B is empty, or their first elements are different, then the common prefix $C = \emptyset$; otherwise, we

recursively extract the longest common prefix from the rest lists, and prepend the head element:

$$\begin{aligned}
 lcp \ \emptyset \ B &= (\emptyset, \emptyset, B) \\
 lcp \ A \ \emptyset &= (\emptyset, A, \emptyset) \\
 lcp \ (a : as) \ (b : bs) &= \begin{cases} a \neq b : & (\emptyset, a : as, b : bs) \\ \textit{otherwise} : & (a : cs, as', bs') \end{cases} \quad (6.13)
 \end{aligned}$$

where $(cs, as', bs') = lcp \ as \ bs$ in the recursive case. Function *branch* $A \ v \ B \ t$ takes two keys A, B , a value v , and a tree t . It extracts the longest common prefix C from A and B , maps it to a new branch node, and assign sub-trees:

$$\begin{aligned}
 \textit{branch} \ A \ v \ B \ t &= \\
 lcp \ A \ B &= \begin{cases} (C, \emptyset, B') : & (C, (\textit{Just} \ v, [B' \mapsto t])) \\ (C, A', \emptyset) : & (C, \textit{insert} \ t \ A' \ v) \\ (C, A', B') : & (C, (\textit{Nothing}, [A' \mapsto (\textit{Just} \ v, \emptyset), B' \mapsto t])) \end{cases} \quad (6.14)
 \end{aligned}$$

If A is the prefix of B , then A is mapped to the node of v , and the remaining list is re-mapped to t , which is the single sub-tree in the branch; if B is the prefix of A , then we recursively insert the remaining list and the value to t ; otherwise, we create a leaf node of v put it together with t as the two sub-trees of the branch. The following example program implements the *insert* algorithm:

```

insert (PrefixTree _ ts) [] v = PrefixTree (Just v) ts
insert (PrefixTree v' ts) k v = PrefixTree v' (ins ts) where
  ins [] = [(k, leaf v)]
  ins ((k', t) : ts) | match k k' = (branch k v k' t) : ts
                    | otherwise = (k', t) : ins ts

leaf v = PrefixTree (Just v) []

match [] _ = True
match _ [] = True
match (a:_) (b:_) = a == b

branch a v b t = case lcp a b of
  (c, [], b') → (c, PrefixTree (Just v) [(b', t)])
  (c, a', []) → (c, insert t a' v)
  (c, a', b') → (c, PrefixTree Nothing [(a', leaf v), (b', t)])

lcp [] bs = ([], [], bs)
lcp as [] = ([], as, [])
lcp (a:as) (b:bs) | a ≠ b = ([], a:as, b:bs)
                  | otherwise = (a:cs, as', bs') where
                    (cs, as', bs') = lcp as bs

```

We can eliminate the recursion to implement the *insert* algorithm in loops.

```

1: function INSERT( $T, k, v$ )
2:   if  $T = \text{NIL}$  then
3:      $T \leftarrow \text{EMPTY-NODE}$ 
4:    $p \leftarrow T$ 
5:   loop
6:      $\textit{match} \leftarrow \text{FALSE}$ 
7:     for each  $s_i \mapsto T_i$  in SUB-TREES( $p$ ) do
8:       if  $k = s_i$  then
9:         VALUE( $T_i$ )  $\leftarrow v$ 
10:      return  $T$ 

```

▷ Overwrite

```

11:       $c \leftarrow \text{LCP}(k, s_i)$ 
12:       $k_1 \leftarrow k - c, k_2 \leftarrow s_i - c$ 
13:      if  $c \neq \text{NIL}$  then
14:           $match \leftarrow \text{TRUE}$ 
15:          if  $k_2 = \text{NIL}$  then ▷  $s_i$  is prefix of  $k$ 
16:               $p \leftarrow T_i, k \leftarrow k_1$ 
17:              break
18:          else ▷ Branch out a new leaf
19:               $\text{ADD}(\text{SUB-TREES}(p), c \mapsto \text{BRANCH}(k_1, \text{LEAF}(v), k_2, T_i))$ 
20:               $\text{DELETE}(\text{SUB-TREES}(p), s_i \mapsto T_i)$ 
21:              return  $T$ 
22:      if not  $match$  then ▷ Add a new leaf
23:           $\text{ADD}(\text{SUB-TREES}(p), k \mapsto \text{LEAF}(v))$ 
24:          break
25:      return  $T$ 

```

Function LCP extracts the longest common prefix from two lists.

```

1: function LCP( $A, B$ )
2:    $i \leftarrow 1$ 
3:   while  $i \leq |A|$  and  $i \leq |B|$  and  $A[i] = B[i]$  do
4:        $i \leftarrow i + 1$ 
5:   return  $A[1..i - 1]$ 

```

There is a special case in $\text{BRANCH}(s_1, T_1, s_2, T_2)$. If s_1 is empty, the key to be insert is some prefix. We set T_2 as the sub-tree of T_1 . Otherwise, we create a new branch node and set T_1 and T_2 as the two sub-trees.

```

1: function BRANCH( $s_1, T_1, s_2, T_2$ )
2:   if  $s_1 = \text{NIL}$  then
3:        $\text{ADD}(\text{SUB-TREES}(T_1), s_2 \mapsto T_2)$ 
4:       return  $T_1$ 
5:    $T \leftarrow \text{EMPTY-NODE}$ 
6:    $\text{SUB-TREES}(T) \leftarrow \{s_1 \mapsto T_1, s_2 \mapsto T_2\}$ 
7:   return  $T$ 

```

Although the prefix tree improves the space efficiency of trie, it is still bound to $O(mn)$, where n is the length of the key, and m is the size of the element set.

6.4.3 Look up

When look up a key k , we start from the root. If $k = \emptyset$ is empty, then return the root value as the result; otherwise, we examine the sub-tree mappings, locate the one $s_i \mapsto t_i$, such that s_i is some prefix of k , then recursively look up $k - s_i$ in sub-tree t_i . If there does not exist s_i as the prefix of k , then there is no such key in the prefix tree.

$$\begin{aligned}
 \text{lookup } \emptyset (v, ts) &= v \\
 \text{lookup } k (v, ts) &= \text{find } ((s, t) \mapsto s \sqsubseteq k) ts = \\
 &\quad \begin{cases} \text{Nothing} : & \text{Nothing} \\ \text{Just } (s, t) : & \text{lookup } (k - s) t \end{cases} \quad (6.15)
 \end{aligned}$$

Where $A \sqsubseteq B$ means list A is prefix of B . Function *find* is defined in chapter 1, which searches element in a list with a given predication. Below example program implements the look up algorithm.

```

lookup [] (PrefixTree v _) = v
lookup ks (PrefixTree v ts) =

```

```

case find ( $\lambda(s, t) \rightarrow s \text{ `isPrefixOf` } ks$ ) ts of
  Nothing  $\rightarrow$  Nothing
  Just ( $s, t$ )  $\rightarrow$  lookup (drop (length  $s$ )  $ks$ )  $t$ 

```

The prefix testing is linear to the length of the list, the *lookup* algorithm is bound to $O(mn)$ time, where m is the size of the element set, and n is the length of the key. We skip the imperative implementation, and leave it as the exercise.

Exercise 6.4

1. Eliminate the recursion to implement the prefix tree *lookup* purely with loops

6.5 Applications of trie and prefix tree

We can use trie and prefix tree to solve many interesting problems, like implement a dictionary, populate candidate inputs, and realize the textonym input method. Different from the industry implementation, we give the examples to illustrate the ideas of trie and prefix tree.

6.5.1 Dictionary and input completion

As shown in figure 6.11, when user enters some characters, the dictionary application searches the library, populates a list of candidate words or phrases that start from what input.

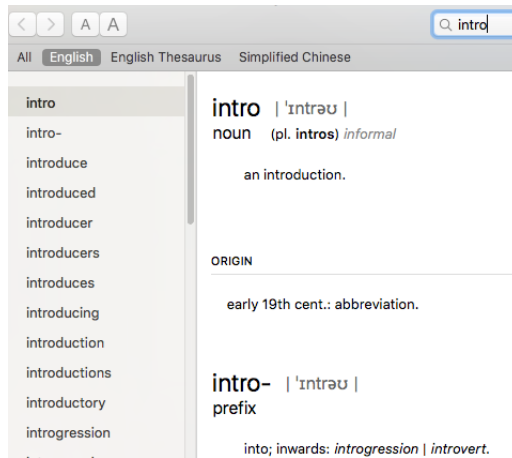


Figure 6.11: A dictionary application

A dictionary can contain hundreds of thousands words. It's expensive to perform a complete search. Commercial dictionaries adopt varies engineering approach, like caching, indexing to speed up search. Similarly, figure 6.12 shows a smart text input component. When type some characters, it populates a candidate lists, with all items starting with the input string.

Both examples give the 'auto-completion' functionality. We can implement it with prefix tree. For illustration purpose, we limit to English characters, and set a upper bound n for the number of candidates. A dictionary stores key-value pairs, where the key is English word or phrase, the value is the corresponding meaning and explanation. When user input string s , we look up the prefix tree for all keys start with s . If s is empty

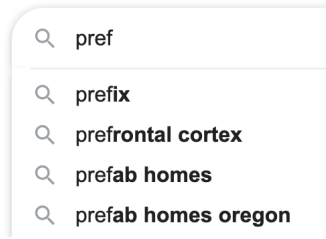


Figure 6.12: A smart text input component

we expand all sub-trees till reach to n candidates; otherwise, we locate the sub-tree from the mapped key, and look up recursively. In the environment supports lazy evaluation, we can expand all candidates, and take the first n on demand: $take\ n\ (startsWith\ s\ t)$, where t is the prefix tree.

$$\begin{aligned}
 startsWith\ \emptyset\ (Nothing, ts) &= enum\ ts \\
 startsWith\ \emptyset\ (Just\ x, ts) &= (\emptyset, x) : enum\ ts \\
 startsWith\ s\ (v, ts) &= find\ ((k, t) \mapsto s \sqsubseteq k\ \text{or}\ k \sqsubseteq s)\ ts = \\
 &\begin{cases} Nothing : & \emptyset \\ Just\ (k, t) : & [(k \# a, b) | (a, b) \in startsWith\ (s - k)\ t] \end{cases} \quad (6.16)
 \end{aligned}$$

Given a prefix s , function $startsWith$ searches all candidates in the prefix tree starts with s . If s is empty, it enumerates all sub-trees, and prepend (\emptyset, x) for none empty value x in the root. Function $enum\ ts$ is defined as:

$$enum = concatMap\ (k, t) \mapsto [(k \# a, b) | (a, b) \in startsWith\ \emptyset\ t] \quad (6.17)$$

Where $concatMap$ (also known as $flatMap$) is an important concept for list computation. Literally, it results like firstly map on each element, then concatenate the result together. It's typically realized with 'build-foldr' fusion law to eliminate the intermediate list overhead. (see chapter 5 in my book *Isomorphism – mathematics of programming*) If the input prefix s is not empty, we examine the sub-tree mappings, for each list and sub-tree pair (k, t) , if either s is prefix of k or vice versa, we recursively expand t and prepend k to each result key; otherwise, s does not match any sub-trees, hence the result is empty. Below example program implements this algorithm.

```

startsWith [] (PrefixTree Nothing ts) = enum ts
startsWith [] (PrefixTree (Just v) ts) = ([], v) : enum ts
startsWith k (PrefixTree _ ts) =
  case find (\(s, t) -> s `isPrefixOf` k || k `isPrefixOf` s) ts of
    Nothing -> []
    Just (s, t) -> [(s # a, b) |
                    (a, b) <- startsWith (drop (length s) k) t]
enum = concatMap (\(k, t) -> [(k # a, b) | (a, b) <- startsWith [] t])

```

We can also realize the algorithm $STARTS-WITH(T, k, n)$ imperatively. From the root, we loop on every sub-tree mapping $k_i \mapsto T_i$. If k is the prefix for any sub-tree T_i , we expand all things in it up to n items; if k_i is the prefix of k , we then drop that prefix, update the key to $k - k_i$, then search T_i for this new key.

- 1: **function** $STARTS-WITH(T, k, n)$
- 2: **if** $T = NIL$ **then**
- 3: **return** NIL
- 4: $s \leftarrow NIL$

```

5:  repeat
6:      match ← FALSE
7:      for  $k_i \mapsto T_i$  in SUB-TREES( $T$ ) do
8:          if  $k$  is prefix of  $k_i$  then
9:              return EXPAND( $s \# k_i, T_i, n$ )
10:         if  $k_i$  is prefix of  $k$  then
11:             match ← TRUE
12:              $k \leftarrow k - k_i$                                 ▷ drop the prefix
13:              $T \leftarrow T_i$ 
14:              $s \leftarrow s \# k_i$ 
15:             break
16:     until not match
17:     return NIL

```

Where function EXPAND(s, T, n) populates n results from T and prepand s to each key. We implement it with ‘breadth first search’ method (see section 14.3):

```

1:  function EXPAND( $s, T, n$ )
2:       $R \leftarrow \text{NIL}$ 
3:       $Q \leftarrow [(s, T)]$ 
4:      while  $|R| < n$  and  $Q \neq \text{NIL}$  do
5:          ( $k, T$ ) ← POP( $Q$ )
6:           $v \leftarrow \text{VALUE}(T)$ 
7:          if  $v \neq \text{NIL}$  then
8:              INSERT( $R, (k, v)$ )
9:          for  $k_i \mapsto T_i$  in SUB-TREES( $T$ ) do
10:             PUSH( $Q, (k \# k_i, T_i)$ )

```

6.5.2 Predictive text input

Before 2010, most mobile phones had a small keypad as shown in 6.13, called ITU-T keypad. It maps a digit to 3 - 4 characters. For example, when input word ‘home’, one can press keys in below sequence:



Figure 6.13: The mobile phone ITU-T keypad.

1. Press key ‘4’ twice to enter ‘h’;
2. Press key ‘6’ three times to enter ‘o’;
3. Press key ‘6’ to enter ‘m’;
4. Press key ‘3’ twice to enter ‘e’;

A smarter input method allows to press less keys:

1. Press key sequence ‘4’, ‘6’, ‘6’, ‘3’, the word ‘home’ appears as a candidate;
2. Press key ‘*’ to change to next candidate, word ‘good’ appears;
3. Press key ‘*’ again for another candidate, word ‘gone’ appears;
4. ...

This is called predictive input, or abbreviated as ‘T9’[25], [26]. We can realize it by storing the word dictionary in a prefix tree. The commercial implementations uses multiple layers of caches/index in both memory and file system. We simplify it as an example of prefix tree application. First, we need define the digit key mappings:

$$M_{T9} = \left\{ \begin{array}{l} 2 \mapsto \text{"abc"}, 3 \mapsto \text{"def"}, 4 \mapsto \text{"ghi"}, \\ 5 \mapsto \text{"jkl"}, 6 \mapsto \text{"mno"}, 7 \mapsto \text{"pqrs"}, \\ 8 \mapsto \text{"tuv"}, 9 \mapsto \text{"wxyz"} \end{array} \right\} \quad (6.18)$$

$M_{T9}[i]$ gives the corresponding characters for digit i . We can also define the reversed mapping from a character back to digit.

$$M_{T9}^{-1} = \text{concatMap } ((d, s) \mapsto [(c, d) | c \in s]) M_{T9} \quad (6.19)$$

Given a string, we can convert it to a sequence of digits by looking up M_{T9}^{-1} .

$$\text{digits}(s) = [M_{T9}^{-1}[c] | c \in s] \quad (6.20)$$

For any character does not belong [a..z], we map it to a special key '#' as fallback. Below example program defines the above two mappings.

```
mapT9 = Map.fromList [( '2', "abc"), ( '3', "def"), ( '4', "ghi"),
                    ( '5', "jkl"), ( '6', "mno"), ( '7', "pqrs"),
                    ( '8', "tuv"), ( '9', "wxyz")]

rmapT9 = Map.fromList $ concatMap (\(d, s) -> [(c, d) | c <- s]) $
  Map.toList mapT9

digits = map (\c -> Map.findWithDefault '#' c rmapT9)
```

Suppose we already build the prefix tree (v, ts) from all words in a dictionary. We need change the above auto completion algorithm to process digit string ds . For every sub-tree mappings $(s \mapsto t) \in ts$, we convert the prefix s to $\text{digits}(s)$, check if it matches to ds (either one is the prefix of the other). There can be multiple sub-trees match ds as:

$$\begin{aligned} pfx &= [(s, t) | (s \mapsto t) \in ts, \text{digits}(s) \sqsubseteq ds \text{ or } ds \sqsubseteq \text{digits}(s)] \\ \text{find}_{T9} t \ \emptyset &= [\emptyset] \\ \text{find}_{T9} (v, ts) ds &= \text{concatMap find pfx} \end{aligned} \quad (6.21)$$

For each mapping (s, t) in pfx , function find recursively lookup the remaining digits ds' in t , where $ds' = \text{drop } |s| \ ds$, then prepend s to every candidate. However, the length may exceeds the number of digits, we need cut and only take $n = |ds|$ characters:

$$\text{find } (s, t) = [\text{take } n \ (s \# s_i) | s_i \in \text{find}_{T9} t \ ds'] \quad (6.22)$$

The following example program implements the predictive input look up algorithm:


```

findT9 _ [] = [[]]
findT9 (PrefixTree _ ts) k = concatMap find pfx where
  find (s, t) = map (take (length k) ◦ (s++)) $ findT9 t (drop (length s) k)
  pfx = [(s, t) | (s, t) ← ts, let ds = digits s in
         ds `isPrefixOf` k || k `isPrefixOf` ds]

```

To realize the predictive text input imperatively, we can perform breadth first search with a queue Q of tuples $(prefix, D, t)$. Every tuple records the possible *prefix* searched so far; the remaining digits D to be searched; and the sub-tree t we are going to search. Q is initialized with the empty prefix, the whole digits sequence, and the root. We repeatedly pop the tuple from the queue, and examine the sub-tree mappings. for every mapping $(s \mapsto T')$, we convert s to $digits(s)$. If D is prefix of it, then we find a candidate. We append s to *prefix*, and record it in the result. If $digits(s)$ is prefix of D , we need further search the sub-tree T' . We create a new tuple of $(prefix \# s, D', T')$, where D' is the remaining digits to be searched. Then push this new tuple back to the queue.

```

1: function LOOK-UP-T9( $T, D$ )
2:    $R \leftarrow \text{NIL}$ 
3:   if  $T = \text{NIL}$  or  $D = \text{NIL}$  then
4:     return  $R$ 
5:    $n \leftarrow |D|$ 
6:    $Q \leftarrow \{(\text{NIL}, D, T)\}$ 
7:   while  $Q \neq \text{NIL}$  do
8:      $(prefix, D, T) \leftarrow \text{POP}(Q)$ 
9:     for  $(s \mapsto T') \in \text{SUB-TREES}(T)$  do
10:       $D' \leftarrow \text{DIGITS}(s)$ 
11:      if  $D' \sqsubset D$  then ▷  $D'$  is prefix of  $D$ 
12:        APPEND( $R, (prefix \# s)[1..n]$ ) ▷ limit the length to  $n$ 
13:      else if  $D \sqsubset D'$  then
14:        PUSH( $Q, (prefix \# s, D - D', T')$ )
15:   return  $R$ 

```

Exercise 6.5

1. Implement the auto-completion and predictive text input with trie.
2. How to ensure the candidates in lexicographic order in the auto-completion and predictive text input program? What's the performance change accordingly?
3. In the environment without lazy evaluation support, how to return the first n candidates on-demand?

6.6 Summary

We start from integer trie and prefix tree. By turning the integer key to binary format, we re-used binary tree to realize the integer based map data structure. Then extend the key from integer to generic list, and limit the list element to finite set. Particularly for alphabetic strings, the generic trie and prefix tree can be used as tools to manipulate the text information. We give example applications about auto-completion and predictive text input. as another instance of radix tree, the suffix tree is closely related to trie and prefix tree used in text, and DNA processing.

6.7 Appendix: Example programs

Definition of integer binary trie:

```

data IntTrie<T> {
  IntTrie<T> left = null
  IntTrie<T> right = null
  Optional<T> value = Optional.None
}

```

The following example *insert* program uses bit-wise operation to test even/odd, and shift the bit to right:

```

IntTrie<T> insert(IntTrie<T> t, Int key,
  Optional<T> value = Optional.None) {
  if t == null then t = IntTrie<T>()
  p = t
  while key ≠ 0 {
    if key & 1 == 0 {
      p = if p.left == null then IntTrie<T>() else p.left
    } else {
      p = if p.right == null then IntTrie<T>() else p.right
    }
    key = key >> 1
  }
  p.value = Optional.of(value)
  return t
}

```

Definition of integer prefix tree:

```

data IntTree<T> {
  Int key
  T value
  Int prefix
  Int mask = 1
  IntTree<T> left = null
  IntTree<T> right = null

  IntTree(Int k, T v) {
    key = k, value = v, prefix = k
  }

  bool isLeaf = (left == null and right == null)

  Self replace(IntTree<T> x, IntTree<T> y) {
    if left == x then left = y else right = y
  }

  bool match(Int k) = maskbit(k, mask) == prefix
}

Int maskbit(Int x, Int mask) = x & (~(mask - 1))

```

Insert key-value to integer prefix tree.

```

IntTree<T> insert(IntTree<T> t, Int key, T value) {
  if t == null then return IntTree(key, value)
  node = t
  Node<T> parent = null
  while (not node.isLeaf()) and node.match(key) {
    parent = node
    node = if zero(key, node.mask) then node.left else node.right
  }
  if node.isleaf() and key == node.key {

```

```

        node.value = value
    } else {
        p = branch(node, IntTree(key, value))
        if parent == null then return p
        parent.replace(node, p)
    }
    return t
}

IntTree<T> branch(IntTree<T> t1, IntTree<T> t2) {
    var t = IntTree<T>()
    (t.prefix, t.mask) = lcp(t1.prefix, t2.prefix)
    (t.left, t.right) = if zero(t1.prefix, t.mask) then (t1, t2)
                       else (t2, t1)
    return t
}

bool zero(int x, int mask) = (x & (mask >> 1) == 0)

Int lcp(Int p1, Int p2) {
    Int diff = p1 ^ p2
    Int mask = 1
    while diff ≠ 0 {
        diff = diff >> 1
        mask = mask << 1
    }
    return (maskbit(p1, mask), mask)
}

```

Definition of trie and the insert program:

```

data Trie<K, V> {
    Optional<V> value = Optional.None
    Map<K, Trie<K, V>> subTrees = Map.empty()
}

Trie<K, V> insert(Trie<K, V> t, [K] key, V value) {
    if t == null then t = Trie<K, V>()
    var p = t
    for c in key {
        if p.subTrees[c] == null then p.subTrees[c] = Trie<K, V>()
        p = p.subTrees[c]
    }
    p.value = Optional.of(value)
    return t
}

```

Definition of Prefix Tree and insert program:

```

data PrefixTree<K, V> {
    Optional<V> value = Optional.None
    Map<[K], PrefixTree<K, V>> subTrees = Map.empty()

    Self PrefixTree(V v) {
        value = Optional.of(v)
    }
}

PrefixTree<K, V> insert(PrefixTree<K, V> t, [K] key, V value) {
    if t == null then t = PrefixTree()
    var node = t
    loop {
        bool match = false
        for var (k, tr) in node.subtrees {
            if key == k {
                tr.value = value
            }
        }
    }
}

```

```

        return t
    }
    prefix, k1, k2 = lcp(key, k)
    if prefix ≠ [] {
        match = true
        if k2 == [] {
            node = tr
            key = k1
            break
        } else {
            node.subtrees[prefix] = branch(k1, PrefixTree(value),
                                           k2, tr)
            node.subtrees.delete(k)
            return t
        }
    }
}
if !match {
    node.subtrees[key] = PrefixTree(value)
    break
}
return t
}
}

```

The longest common prefix `lcp` and `branch` example programs.

```

([K], [K], [K]) lcp([K] s1, [K] s2) {
    j = 0
    while j < length(s1) and j < length(s2) and s1[j] == s2[j] {
        j = j + 1
    }
    return (s1[0..j-1], s1[j..], s2[j..])
}

PrefixTree<K, V> branch([K] key1, PrefixTree<K, V> tree1,
                        [K] key2, PrefixTree<K, V> tree2) {
    if key1 == []:
        tree1.subtrees[key2] = tree2
        return tree1
    t = PrefixTree()
    t.subtrees[key1] = tree1
    t.subtrees[key2] = tree2
    return t
}

```

Populate multiple candidates, they share the common prefix

```

[([K], V)] startsWith(PrefixTree<K, V> t, [K] key, Int n) {
    if t == null then return []
    [T] s = []
    repeat {
        bool match = false
        for var (k, tr) in t.subtrees {
            if key.isPrefixOf(k) {
                return expand(s ++ k, tr, n)
            } else if k.isPrefixOf(key) {
                match = true
                key = key[length(k)..]
                t = tr
                s = s ++ k
                break
            }
        }
    }
    return []
}

```

```

}

[[[K], V]] expand([[K] s, PrefixTree<K, V> t, Int n) {
  [[[K], V]] r = []
  var q = Queue([s, t])
  while length(r) < n and !q.isEmpty() {
    var (s, t) = q.pop()
    v = t.value
    if v.isPresent() then r.append((s, v.get()))
    for k, tr in t.subtrees {
      q.push((s ++ k, tr))
    }
  }
  return r
}

```

Predictive text input lookup

```

var T9MAP={ '2':"abc", '3':"def", '4':"ghi", '5':"jkl", \
  '6':"mno", '7':"pqrs", '8':"tuv", '9':"xyz"}

var T9RMAP = { c : d for var (d, cs) in T9MAP for var c in cs }

string digits(string w) = ''.join([T9RMAP[c] for c in w])

[string] lookupT9(PrefixTree<char, V> t, string key) {
  if t == null or key == "" then return []
  res = []
  n = length(key)
  q = Queue("", key, t)
  while not q.isEmpty() {
    (prefix, key, t) = q.pop()
    for var (k, tr) in t.subtrees {
      ds = digits(k)
      if key.isPrefixOf(ds) {
        res.append((prefix ++ k)[:n])
      } else if ds.isPrefixOf(key) {
        q.append((prefix ++ k, key[length(k)..], tr))
      }
    }
  }
  return res
}

```


Chapter 7

B-Tree

7.1 Introduction

The integer prefix tree in previous chapter gives a way to encode the information in the edge of the binary tree. Another way to extend the binary search tree is to increase the sub-trees from 2 to k . B-tree is such a data structure, that can be considered as a generic form of k -ary search tree. It is also developed to be self-balanced[39]. B-tree is widely used in computer file system (some are based on B+ tree, an extension of B-tree) and database system. Figure 7.1 gives an example B-tree, we can find the difference and similarity between B-tree and binary search tree.

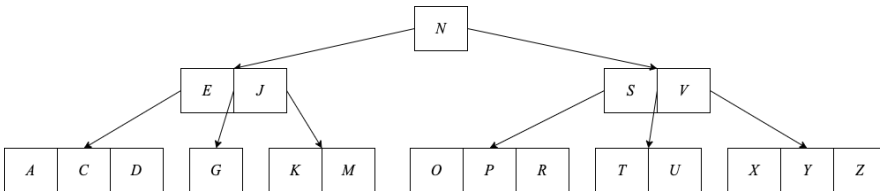


Figure 7.1: A B-Tree

A binary search tree is either empty or contains a key k and two sub-trees l and r . Every key in l is less than k , while k is less than every key in r :

$$\forall x \in l, y \in r \Rightarrow x < k < y \tag{7.1}$$

Extend to multiple keys and sub-trees, we obtain the B-tree. A B-tree is either empty or contains n keys and $n + 1$ sub-trees, each sub-tree is also a B-Tree. We denote these keys and sub-trees as k_1, k_2, \dots, k_n and $t_1, t_2, \dots, t_n, t_{n+1}$, as shown in figure 7.2.

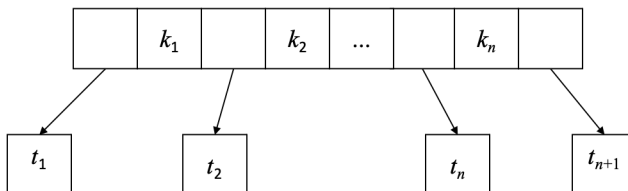


Figure 7.2: A B-Tree node

For every node, the keys and sub-trees satisfy the following rules:

- Keys are in ascending order: $k_1 < k_2 < \dots < k_n$;
- For every key k_i , all keys in sub-tree t_i are less than it, while k_i is less than every key in sub-tree t_{i+1} :

$$\forall x_i \in t_i, i = 0, 1, \dots, n \Rightarrow x_1 < k_1 < x_2 < k_2 < \dots < x_n < k_n < x_{n+1} \quad (7.2)$$

Leaf node has no sub-tree. There can be optional values bound to the keys in B-tree node. We skip the values for simplicity. Let the type of keys be K , the type of the B-tree is $BTree\ K$, or denoted as $BTree<K>$. On top of it, we also need define a set of self-balance rules:

1. All leaves have the same depth;
2. Let d be the *minimum degree* number of a B-tree, such that each node:
 - has at most $2d - 1$ keys;
 - has at least $d - 1$ keys, except for the root;

In summary:

$$d - 1 \leq |keys(t)| \leq 2d - 1 \quad (7.3)$$

We next prove that a B-tree satisfying these rules is always balanced.

Proof. Consider a B-tree of n keys. The minimum degree $d \geq 2$. Let the height be h . All the nodes have at least $d - 1$ keys except for the root. The root contains at least 1 key. There are at least 2 nodes at depth 1, at least $2d$ nodes at depth 2, at least $2d^2$ nodes at depth 3, ..., at least $2d^{h-1}$ nodes at depth h . Multiply all nodes with $d - 1$ except for the root, the total number of keys satisfies the following:

$$\begin{aligned} n &\geq 1 + (d - 1)(2 + 2d + 2d^2 + \dots + 2d^{h-1}) \\ &= 1 + 2(d - 1) \sum_{k=0}^{h-1} d^k \\ &= 1 + 2(d - 1) \frac{d^h - 1}{d - 1} \\ &= 2d^h - 1 \end{aligned} \quad (7.4)$$

It limits the tree height with logarithm of the number of keys.

$$h \leq \log_d \frac{n + 1}{2} \quad (7.5)$$

□

Hence B-tree is balanced. The simplest B-tree is called 2-3-4 tree, where $d = 2$. Every node except for the root contains 2, 3, or 4 sub-trees. Essentially, a red-black tree can be mapped to a 2-3-4 tree. For a none empty B-tree of degree d , we denote it as $(d, (ks, ts))$, where ks are the keys, ts are the sub-trees. Below example program defines the B-tree.

```
data BTree a = BTree [a] [BTree a]
```

The empty node is in the form of (\emptyset, \emptyset) or `BTree [] []`. Instead of storing d in every node, we pass it together with B-tree t as a pair (d, t) .

7.2 Insert

The idea is similar to the binary search tree. While we need deal with multiple keys and sub-trees. When insert key x to B-tree t , starting from the root, we examine the keys in the node to locate a position¹ where all keys on the left are less than x , while the rest keys on the right are greater than x . If the node is a leaf, and it is not full ($|keys(t)| < 2d - 1$), we insert x at this position. Otherwise, this position points to a sub-tree t' , we recursively insert x to t' .

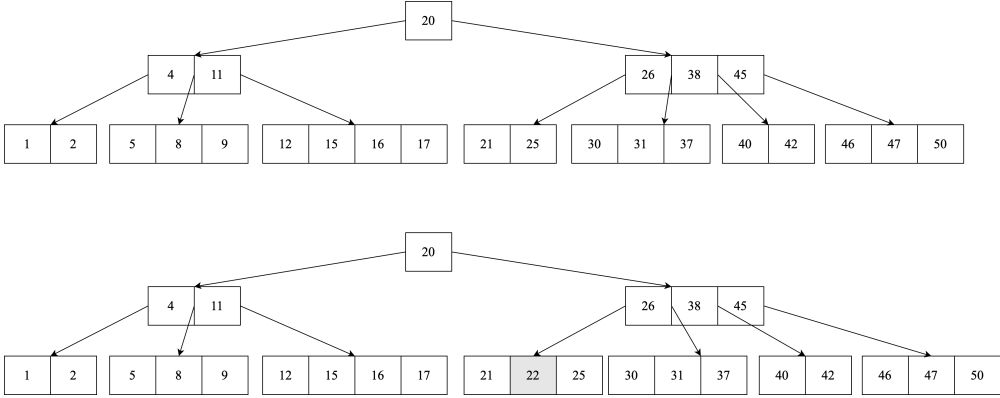


Figure 7.3: Insert 22 to a 2-3-4 tree. $22 > 20$, go to the right sub-tree; next as $22 < 26$, go to the first sub-tree; finally, $21 < 22 < 25$, and the leaf is not full.

As an example, consider the 2-3-4 tree in figure 7.3. when insert $x = 22$, because $20 < 22$, we next examine the sub-tree on the right, which contains 26, 38, 45. Since $22 < 26$, we next go to the first sub-tree containing 21 and 25. This is a leaf, and it is not full. Hence we insert 22 to this node.

However, if there are $2d - 1$ keys in the leaf, we will break the B-tree rules after insert x , as the node will be too 'full'. For the same B-tree in figure 7.3, we'll meet this issue when insert 18. There are two solutions: insert then split, and split before insert.

7.2.1 Insert then split

We can adopt the similar 'insert then fix' method for the red-black tree. First, we insert the key to the proper ordering position without considering the B-tree balance rules. As the next step, if the new tree violates the balance rules, we perform a recursive bottom-up fixing by splitting the overly full node. We need define the function to test whether a given node satisfies the minimum degree constraint or not.

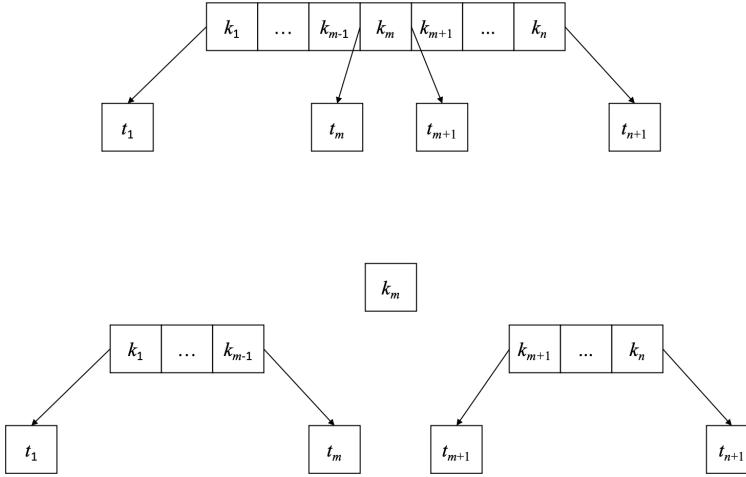
$$\begin{cases} \text{full } d(k_s, t_s) & = |k_s| > 2d - 1 \\ \text{low } d(k_s, t_s) & = |k_s| < d - 1 \end{cases} \quad (7.6)$$

When the node contains too many keys and sub-trees, we define *split* function to break it into 3 parts at a given position m as shown in figure 7.4:

$$\text{split } m(k_s, t_s) = ((k_{s_l}, t_{s_l}), k, (k_{s_r}, t_{s_r})) \quad (7.7)$$

We reuse the list *splitAt* function defined in chapter 1 (Equation 1.55) to realize it.

¹In fact, it is sufficient to only support less-than and equality. See exercise 1.

Figure 7.4: Split the node into 3 parts at m

$$\begin{cases} (ks_l, (k : ks_r)) & = \text{splitAt } (m-1) \text{ } ks \\ (ts_l, ts_r) & = \text{splitAt } m \text{ } ts \end{cases}$$

We can define the reversed operation *unsplit* to combine the 3 parts back into a B-tree node.

$$\text{unsplit } (ks_l, ts_l) \ k \ (ks_r, ts_r) = (ks_l \# [k] \# ks_r, ts_l \# ts_r) \quad (7.8)$$

Below function first inserts x to the tree t , then calls *fix* to resume the B-tree balance rules with the given degree d .

$$\text{insert } x \ (d, t) = \text{fix } (d, \text{ins } t) \quad (7.9)$$

After *ins*, if the root contains too many keys, function *fix* calls *split* to break it and build a new root.

$$\text{fix } (d, t) = \begin{cases} \text{full } d \ t : & (d, ([k], [l, r])), \text{ where } (l, k, r) = \text{split } d \ t \\ \text{otherwise} : & (d, t) \end{cases} \quad (7.10)$$

ins need handle two cases: for leaf node, we can reuse the list ordered *insert* function defined in chapter 1 (Equation 1.13); otherwise, we need find the position to recursively insert to sub-tree. To do that, we define a *partition* function as:

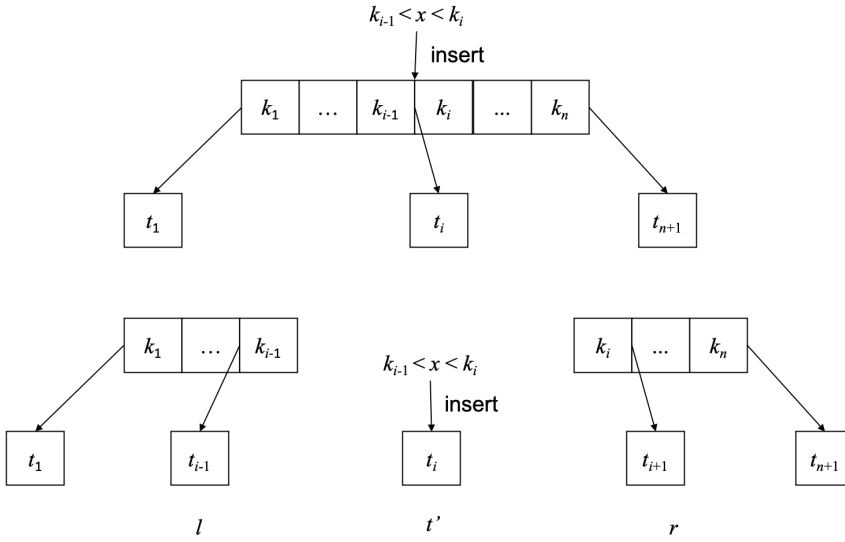
$$\text{partition } x \ (ks, ts) = (l, t', r) \quad (7.11)$$

Where $l = (ks_l, ts_l)$ and $r = (ks_r, ts_r)$. It further uses the list partition function *span* defined in chapter 1 (Equation 1.58):

$$\begin{cases} (ks_l, ks_r) & = \text{span } (< x) \ ks \\ (ts_l, (t' : ts_r)) & = \text{splitAt } |ks_l| \ ts \end{cases}$$

As such, we separate all the keys and sub-trees less than x on the left as l , and those greater than x on the right as r . The last sub-tree that less than x is extracted as t' . We then recursively insert x to t' , as shown in figure 7.5.

$$\begin{aligned} \text{ins } (ks, \emptyset) &= (\text{insert}_L \ x \ ks, \emptyset) && \text{list insert for leaf} \\ \text{ins } (ks, ts) &= \text{balance } d \ l \ (\text{ins } t') \ r && \text{where } (l, t', r) = \text{partition } x \ t \end{aligned} \quad (7.12)$$

Figure 7.5: partition a node with x

After insert x to t' , it may contains too many keys that violates B-tree rules. We define function *balance* to recursively recover B-tree rules by splitting sub-tree.

$$\text{balance } d (ks_l, ts_l) t (ks_r, ts_r) = \begin{cases} \text{full } d t : \text{fix}_f \\ \text{otherwise} : (ks_l \# ks_r, ts_l \# [t] \# ts_r) \end{cases} \quad (7.13)$$

where fix_f splits sub-tree t with degree d as $(t_1, k, t_2) = \text{split } d t$, then combine them to a new B-tree node:

$$\text{fix}_f = (ks_l \# [k] \# ks_r, ts_l \# [t_1, t_2] \# ts_r) \quad (7.14)$$

The following example program implements *insert* for B-tree.

```

partition x (BTree ks ts) = (l, t, r) where
  l = (ks1, ts1)
  r = (ks2, ts2)
  (ks1, ks2) = span (< x) ks
  (ts1, (t:ts2)) = splitAt (length ks1) ts

split d (BTree ks ts) = (BTree ks1 ts1, k, BTree ks2 ts2) where
  (ks1, k:ks2) = splitAt (d - 1) ks
  (ts1, ts2) = splitAt d ts

insert x (d, t) = fixRoot (d, ins t) where
  ins (BTree ks []) = BTree (List.insert x ks) []
  ins t = balance d l (ins t') r where (l, t', r) = partition x t

fixRoot (d, t) | full d t = let (t1, k, t2) = split d t in
  (d, BTree [k] [t1, t2])
  | otherwise = (d, t)

balance d (ks1, ts1) t (ks2, ts2)
  | full d t = fixFull
  | otherwise = BTree (ks1 # ks2) (ts1 # [t] # ts2)
where
  fixFull = let (t1, k, t2) = split d t in
  BTree (ks1 # [k] # ks2) (ts1 # [t1, t2] # ts2)

```

Figure 7.6 shows the example B-trees built by repeatedly insert elements from list “GMPXACDEJKNORSTUVYZ”.

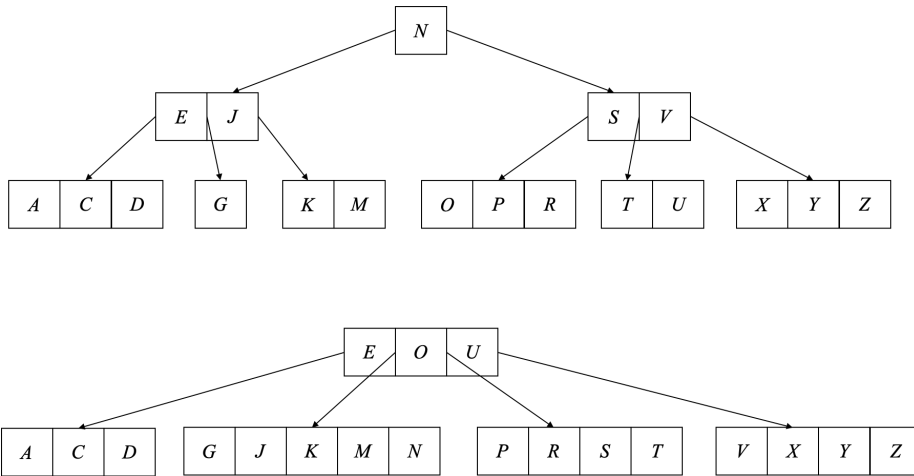


Figure 7.6: Repeatedly insert elements from “GMPXACDEJKNORSTUVYZ”. above: $d = 2$ (2-3-4 tree), below: $d = 3$

7.2.2 Split before insert

The second method is to split a node before insertion to prevent it becoming overly full. We often see this method in imperative implementations. When perform top-down recursive insert, if we reach to a node with $2d - 1$ keys, we divide it into 3 parts as shown in figure 7.4, such that each new node has $d - 1$ keys. They will be valid B-tree node after insertion. For node x , let $K(x)$ be the keys, $T(x)$ be the sub-trees. Denote the i -th key of x as $k_i(x)$, the j -th sub-tree as $t_j(x)$. Below algorithm splits the i -th sub-tree of node z :

- 1: **procedure** SPLIT(z, i)
- 2: $d \leftarrow \text{DEG}(z)$
- 3: $x \leftarrow t_i(z)$
- 4: $y \leftarrow \text{CREATE-NODE}$
- 5: $K(y) \leftarrow [k_{d+1}(x), k_{d+2}(x), \dots, k_{2d-1}(x)]$
- 6: $K(x) \leftarrow [k_1(x), k_2(x), \dots, k_{d-1}(x)]$
- 7: **if** x is not leaf **then**
- 8: $T(y) \leftarrow [t_{d+1}(x), t_{d+2}(x), \dots, t_{2d}(x)]$
- 9: $T(x) \leftarrow [t_1(x), t_2(x), \dots, t_d(x)]$
- 10: INSERT-AT($K(z), i, k_d(x)$)
- 11: INSERT-AT($T(z), i + 1, y$)

When split the node $x = t_i(z)$, we push the d -th key $k_d(x)$ up to the parent node z . If z is already full, the pushing will break B-tree rules. To solve this problem, we need do the top-down check from the root along the path when insert. Split any node with $2d - 1$ keys. Since all parent nodes are processed to be not full, they can accept the additional key pushed up. This method needs one single pass down the tree without any back-tracking. If the root is full, we create a new node, and put the root as it singleton sub-tree. Below is the insert algorithm:

- 1: **function** INSERT(t, k)
- 2: $r \leftarrow t$

```

3:   if  $r$  is full then                                     ▷ root is full
4:      $s \leftarrow$  CREATE-NODE
5:      $T(s) \leftarrow [r]$ 
6:     SPLIT( $s, 1$ )
7:      $r \leftarrow s$ 
8:   return INSERT-NONFULL( $r, k$ )

```

Where INSERT-NONFULL assumes the node r passed in is not full. If r is a leaf, we insert k to the keys based on order (Exercise 3 asks to realize the ordered insert with binary search); otherwise, we locate the position, where $k_i(r) < k < k_{i+1}(r)$. Split the sub-tree $t_i(r)$ if it is full, and go on insert to this sub-tree.

```

1: function INSERT-NONFULL( $r, k$ )
2:    $n \leftarrow |K(r)|$ 
3:   if  $r$  is leaf then
4:      $i \leftarrow 1$ 
5:     while  $i \leq n$  and  $k > k_i(r)$  do
6:        $i \leftarrow i + 1$ 
7:     INSERT-AT( $K(r), i, k$ )
8:   else
9:      $i \leftarrow n$ 
10:    while  $i > 1$  and  $k < k_i(r)$  do
11:       $i \leftarrow i - 1$ 
12:    if  $t_i(r)$  is full then
13:      SPLIT( $r, i$ )
14:      if  $k > k_i(r)$  then
15:         $i \leftarrow i + 1$ 
16:    INSERT-NONFULL( $t_i(r), k$ )
17:   return  $r$ 

```

This algorithm is recursive. Exercise 2 asks to eliminate the recursion with pure loops. Figure 7.7 gives the result with the same input of “GMPXACDEJKNORSTUVYZ”.

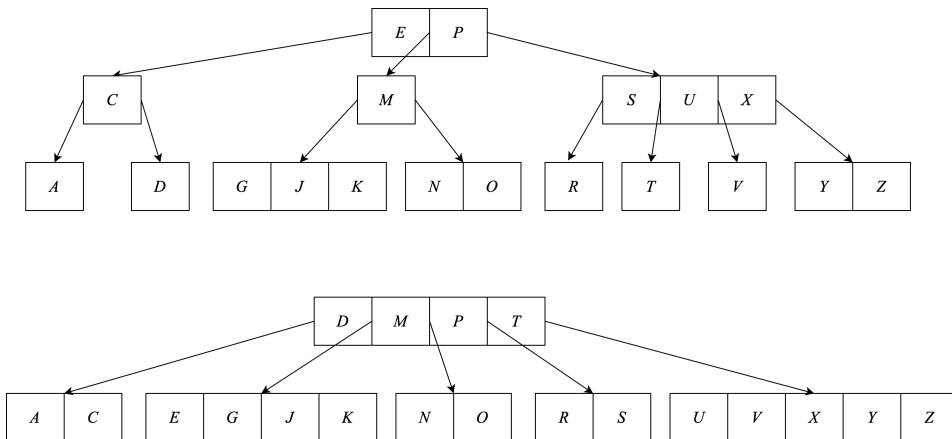


Figure 7.7: Insert from “GMPXACDEJKNORSTUVYZ”. up: $d = 2$, 2-3-4 tree; bottom: $d = 3$.

7.2.3 Paired lists

When use list to store ordered keys, we always start from the first key, and scan the list to find the insert position. If the keys are stored in array, we can improve it with binary search. Can we start somewhere in the node, go left or right depending on the order of keys? One idea is to separate the B-tree node into three parts: left l , a sub-tree t' , and right r . Where left and right are lists of pairs, each pair contains a key and a sub-tree: (k_i, t_i) . However, l is reversed. In other words, l and r are head-to-head connected by t' as a U-shape shown in figure 7.8. We can move forward and backward both in constant time.

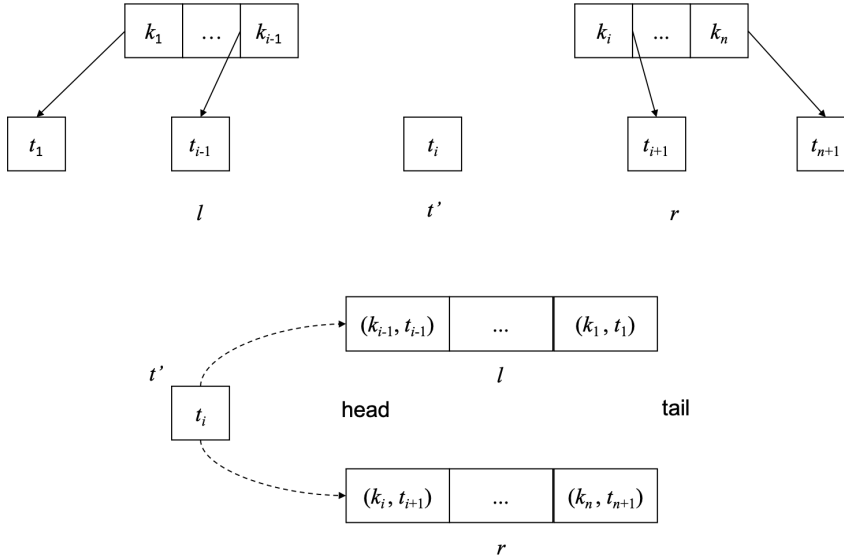


Figure 7.8: Define the B-tree node with a sub-tree and paired lists

Below example program defines B-tree node. It's either empty, or contains 3 parts: the left (key, sub-tree) list in reversed order, a sub-tree, and the right (key, sub-tree) list. We denoted the none empty node as (l, t', r) .

```
data BTree a = Empty
           | BTree [(a, BTree a)] (BTree a) [(a, BTree a)]
```

When move to right by a step, we take the first pair (k, t) from r , then form another pair (k, t') in front of l , and replace t' with t . When move to left a step, it is symmetric. Both operations take constant time.

$$\begin{aligned} \text{step}_l ((k, t) : l, t', r) &= (l, t, (k, t') : r) \\ \text{step}_r (l, t', (k, t) : r) &= ((k, t') : l, t, r) \end{aligned} \quad (7.15)$$

With the left/right moves, we can implement a generic partition function *partition p t*, that separates the tree t with a given predicate p into 3 parts: left, middle, right: (l, m, r) , such that all sub-trees in l and m satisfy p , while the sub-trees in r do not. Let the function

$hd = fst \circ head$, which picks the first pair (a, b) from a list, then extracts a out.

$$\begin{aligned}
 \text{partition } p (\emptyset, m, r) &= \begin{cases} p(\text{hd}(r)) : & \text{partition } p (\text{step}_r t) \\ \text{otherwise} : & (\emptyset, m, r) \end{cases} \\
 \text{partition } p (l, m, \emptyset) &= \begin{cases} (\text{not} \circ p)(\text{hd}(l)) : & \text{partition } p (\text{step}_l t) \\ \text{otherwise} : & (l, m, \emptyset) \end{cases} \\
 \text{partition } p (l, m, r) &= \begin{cases} p(\text{hd}(l)) \text{ and } (\text{not} \circ p)(\text{hd}(r)) : & (l, m, r) \\ p(\text{hd}(r)) : & \text{partition } p (\text{step}_r t) \\ (\text{not} \circ p)(\text{hd}(l)) : & \text{partition } p (\text{step}_l t) \end{cases}
 \end{aligned} \tag{7.16}$$

For example, $\text{partition } (< k) t$ moves all keys and sub-trees in t less than k out of the right part. Below example program implements the partition function:

```

partition p t@(BTree [] m r)
  | p (hd r) = partition p (stepR t)
  | otherwise = ([], m, r)
partition p t@(BTree l m [])
  | (not ∘ p) (hd l) = partition p (stepL t)
  | otherwise = (l, m, [])
partition p t@(BTree l m r)
  | p (hd l) && (not ∘ p) (hd r) = (l, m, r)
  | p (hd r) = partition p (stepR t)
  | (not ∘ p) (hd l) = partition p (stepL t)

```

We can also use $\text{step}_l/\text{step}_r$ to split a B-tree at position d when it becomes overly full. Let $n = |l|$ be the number of keys/sub-trees of the left part. $f^n(x)$ means repeatedly apply function f to x for n times.

$$\text{split } d t = \begin{cases} n < d : & sp(\text{step}_r^{d-n}(t)) \\ n > d : & sp(\text{step}_r^{n-d}(t)) \\ \text{otherwise} : & sp(t) \end{cases} \tag{7.17}$$

Where sp does the separation work as below:

$$sp (l, t, (k, t') : r) = ((l, t, \emptyset), k, (\emptyset, t', r)) \tag{7.18}$$

With partition and split defined, we can define B-tree insert algorithm for the paired lists implementation. Firstly, we need modify the low/full testing to count both left and right parts:

$$\begin{aligned}
 \text{full } d \emptyset &= \text{False} \\
 \text{full } d (l, t', r) &= |l| + |r| > 2d - 1
 \end{aligned} \tag{7.19}$$

and

$$\begin{aligned}
 \text{low } d \emptyset &= \text{False} \\
 \text{low } d (l, t', r) &= |l| + |r| < d - 1
 \end{aligned} \tag{7.20}$$

When insert key x to B-tree t of degree d , we do the recursive insertion, then fix the root if it gets overly full:

$$\text{insert } x (d, t) = \text{fix } (d, \text{ins } t) \tag{7.21}$$

Where fix splits the root at d if needed:

$$\text{fix } (d, t) = \begin{cases} \text{full } d t : & (d, (\emptyset, t_1, [(k, t_2)]) \text{ where } (t_1, k, t_2) = \text{split } d t \\ \text{otherwise} : & (d, t) \end{cases} \tag{7.22}$$

Function *ins* need handle both $t = \emptyset$, and $t \neq \emptyset$ cases. For empty case, we create a singleton leaf; otherwise, we call $(l, t', r) = \text{partition} (< x) t$ to locate the position for recursive insert:

$$\begin{aligned} \text{ins } \emptyset &= (\emptyset, \emptyset, [(x, \emptyset)]) \\ \text{ins } t &= \begin{cases} t' = \emptyset : \text{balance } d \text{ l } \emptyset ((x, \emptyset) : r) \\ t' \neq \emptyset : \text{balance } d \text{ l } (\text{ins } t') r \end{cases} \end{aligned} \quad (7.23)$$

Function *balance* examines if the sub-tree t contains too many keys, and splits it.

$$\text{balance } d \text{ l } t \text{ r} = \begin{cases} \text{full } d \text{ t} : & \text{fixFull} \\ \text{otherwise} : & (l, t, r) \end{cases} \quad (7.24)$$

Where $\text{fixFull} = (l, t_1, ((k, t_2) : r))$, and $(t_1, k, t_2) = \text{split } d \text{ t}$. Below example program implements the insert algorithm:

```

insert x (d, t) = fixRoot (d, ins t) where
  ins Empty = BTree [] Empty [(x, Empty)]
  ins t = let (l, t', r) = partition (< x) t in
    case t' of
      Empty → balance d l Empty ((x, Empty):r)
      _     → balance d l (ins t') r

fixRoot (d, t) | full d t = let (t1, k, t2) = split d t in
  (d, BTree [] t1 [(k, t2)])
  | otherwise = (d, t)

balance d l t r | full d t = fixFull
  | otherwise = BTree l t r

where
  fixFull = let (t1, k, t2) = split d t in BTree l t1 ((k, t2):r)

split d t@(BTree l _ _) | n < d = sp $ iterate stepR t !! (d - n)
  | n > d = sp $ iterate stepL t !! (n - d)
  | otherwise = sp t

where
  n = length l
  sp (BTree l t ((k, t'):r)) = (BTree l t [], k, BTree [] t' r)

```

Exercise 7.1

1. Can we use \leq to support duplicated keys in B-Tree?
2. For the 'split then insert' algorithm, eliminate the recursion with loops.
3. We use linear search among keys to find the proper insert position. Improve the imperative implementation with binary search. Is the big-O performance improved?

7.3 Look up

For look up, we can extend from the binary search tree to multiple branches, and obtain the generic B-tree look up solution. There are only two directions when look up the binary search tree: left and right, while, there are multiple ways in B-tree. Consider look up k in B-tree $t = (ks, ts)$, if t is a leaf (ts is empty), then the problem becomes list look up; otherwise, we partition the t with k into three parts: $l = (ks_l, ts_l), t', r = (ks_r, ts_r)$, where all keys in l and sub-tree t' are less than k , and the remaining ($\geq k$) is in r . If

the first key in ks_r equals k , then we find the answer; otherwise, we recursive look up in sub-tree t' .

$$\begin{aligned} \text{lookup } k (ks, \emptyset) &= \begin{cases} k \in ks : & \text{Just } (ks, \emptyset) \\ \text{otherwise} : & \text{Nothing} \end{cases} \\ \text{lookup } k (ks, ts) &= \begin{cases} \text{Just } k = \text{safeHd } ks_r : & \text{Just } (ks, ts) \\ \text{otherwise} : & \text{lookup } k t' \end{cases} \end{aligned} \quad (7.25)$$

Where $((ks_l, ts_l), t', (ks_r, ts_r)) = \text{partition } k t$, and

$$\begin{aligned} \text{safeHd } [] &= \text{Nothing} \\ \text{safeHd } (x : xs) &= \text{Just } x \end{aligned}$$

Below example program² implements *lookup*.

```
lookup k t@(BTree ks []) = if k `elem` ks then Just t else Nothing
lookup k t = if (Just k) == safeHd ks then Just t
           else lookup k t' where
  (_, t', (ks, _)) = partition k t
```

For the paired list implementation, the idea is similar. If the tree is not empty, we partition it with the predicate ' $< k$ '. Then check if the first key in the right part equals to k , or recursively look up the partitioned sub-tree:

$$\begin{aligned} \text{lookup } k \emptyset &= \text{Nothing} \\ \text{lookup } k t &= \begin{cases} \text{Just } k = \text{safeFst } (\text{safeHd } r) : & \text{Just } (l, t', r) \\ \text{otherwise} : & \text{lookup } k t' \end{cases} \end{aligned} \quad (7.26)$$

Where $(l, t', r) = \text{partition } (< k) t$ for the none empty tree case. *safeFst* applies *fst* function to a 'Maybe' value. Below example program utilizes *fmap* to do this:

```
lookup x Empty = Nothing
lookup x t = let (l, t', r) = partition (< x) t in
  if (Just x) == fmap fst (safeHd r) then Just (BTree l t' r)
  else lookup x t'
```

For the imperative implementation, we start from the root r , find a position i among the keys, such that $k_i(r) \leq k < k_{i+1}(r)$. If $k_i(r) = k$ then return the node r and i as a pair; otherwise, move to sub-tree $t_i(r)$ to go on looking up. If r is a leaf and k is not in the keys, the return nothing. It means k does not exit in the tree.

```
1: function LOOK-UP( $r, k$ )
2:   loop
3:      $i \leftarrow 1, n \leftarrow |K(r)|$ 
4:     while  $i \leq n$  and  $k > k_i(r)$  do
5:        $i \leftarrow i + 1$ 
6:     if  $i \leq n$  and  $k = k_i(r)$  then
7:       return ( $r, i$ )
8:     if  $r$  is leaf then
9:       return Nothing ▷  $k$  does not exist
10:    else
11:       $r \leftarrow t_i(r)$  ▷ go to the  $i$ -th sub-tree
```

Exercise 7.2

1. Improve the imperative look up with binary search among keys.

²safeHd is provided as listToMaybe in some library.

7.4 Delete

After delete a key, the number of keys may be too few to be a valid B-tree node. Except the root, the number of keys should not be less than $d - 1$, where d is the minimum degree. There are two methods symmetric to insert: we can either delete then fix, or merge before delete.

7.4.1 Delete and fix

We first extend the *delete* algorithm for binary search tree to multiple branches, then fix the B-tree balance rules. The main delete program is defined with these two steps:

$$\text{delete } x (d, t) = \text{fix}(d, \text{del } x t) \quad (7.27)$$

Where function *del* is the one we extend to support multiple branches. If t is a leaf, we merely delete x from the keys; otherwise, we partition the tree with x into 3 parts: (l, t', r) . Where all the keys in l and sub-tree t' are less than x , and the rest in r are great than or equal (\geq) to x . When r isn't empty, we pick the first key k_i from it. If the key equals to x , ($k_i = x$), we next replace it with the maximum key k' of sub-tree t' ($k' = \max(t')$), and recursively delete k' from t' as shown in figure 7.9. Otherwise (either r is empty, or $k_i \neq x$), we recursively delete x from sub-tree t' .

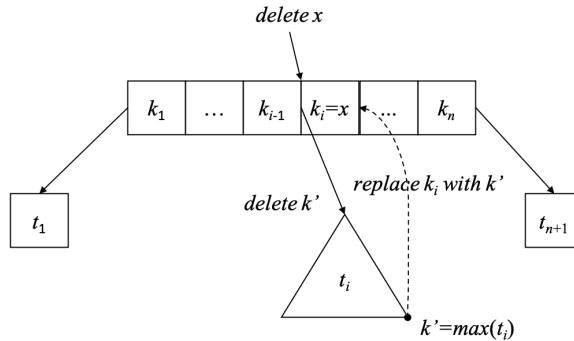


Figure 7.9: Replace k_i with $k' = \max(t')$, then recursively delete k' from t' .

$$\begin{aligned} \text{del } x (ks, \emptyset) &= (\text{delete}_l x ks, \emptyset) \\ \text{del } x t &= \begin{cases} \text{Just } x = \text{safeHd } ks' : \text{balance } d l (\text{del } k' t') (k' : (\text{tail } ks'), ts') \\ \text{otherwise} : \text{balance } d l (\text{del } x t') (ks', ts') \end{cases} \end{aligned} \quad (7.28)$$

Where $(l, t', (ks', ts')) = \text{partition } x t$, are the 3 parts partitioned by x . On top of it, we extract the maximum key k' from t' . The *max* function is defined as:

$$\begin{aligned} \text{max } (ks, \emptyset) &= \text{last } ks \\ \text{max } (ks, ts) &= \text{max } (\text{last } ts) \end{aligned} \quad (7.29)$$

Function *last* returns the last element from a list (Equation 1.4 in chapter 1). *delete_l* is the list delete algorithm (Equation 1.16 in chapter 1). *tail* drops the first element from a list and returns the rest (Equation 1.1). We need modify the *balance* function, which

we defined for *insert* before, with the additional logic to merge the node if it contains too less keys.

$$\text{balance } d (ks_l, ts_l) t (ks_r, ts_r) = \begin{cases} \text{full } d t : \text{fix}_f \\ \text{low } d t : \text{fix}_l \\ \text{otherwise} : (ks_l \# ks_r, ts_l \# [t] \# ts_r) \end{cases} \quad (7.30)$$

If t is overly low ($< d - 1$ keys), we call fix_l to merge it with the left part (ks_l, ts_l) or right part (ks_r, ts_r) depends on which side of keys is not empty. Use the left part for example: we extract the last element from ks_l and ts_l respectively, say k_m and t_m . Then call *unsplit* (defined in Equation 7.8) to merge them with t as *unsplit* $t_m k_m t$. It forms a new sub-tree with more keys. Finally we call *balance* again to build the result B-tree.

$$\text{fix}_l = \begin{cases} ks_l \neq \emptyset : \text{balance } d (\text{init } ks_l, \text{init } ts_l) (\text{unsplit } t_m k_m t) (ks_r, ts_r) \\ ks_r \neq \emptyset : \text{balance } d (ks_l, ts_l) (\text{unsplit } t k_1 t_1) (\text{tail } ks_r, \text{tail } ts_r) \\ \text{otherwise} : t \end{cases} \quad (7.31)$$

The last case (otherwise) means $ks_l = ks_r = \emptyset$, both sides are empty. The tree is a singleton leaf hence need not fixing. k_1 and t_1 are the first element in ks_r and ts_r respectively. Finally, we need modify the *fix* function defined for *insert*, add new logic for *delete*:

$$\begin{aligned} \text{fix } (d, (\emptyset, [t])) &= (d, t) \\ \text{fix } (d, t) &= \begin{cases} \text{full } d t : (d, ([k], [l, r])), \text{ where } (l, k, r) = \text{split } d t \\ \text{otherwise} : (d, t) \end{cases} \end{aligned} \quad (7.32)$$

What we add is the first case. After delete, if the root contains nothing but a sub-tree, we can shrink the height, pull the single sub-tree as the new root. The following example program implements the *delete* algorithm.

```

delete x (d, t) = fixRoot (d, del x t) where
  del x (BTree ks []) = BTree (List.delete x ks) []
  del x t = if (Just x) == safeHd ks' then
    let k' = max t' in
      balance d l (del k' t') (k':(tail ks'), ts')
    else balance d l (del x t') r
  where
    (l, t', r@(ks', ts')) = partition x t

fixRoot (d, BTree [] [t]) = (d, t)
fixRoot (d, t) | full d t = let (t1, k, t2) = split d t in
  (d, BTree [k] [t1, t2])
  | otherwise = (d, t)

balance d (ks1, ts1) t (ks2, ts2)
  | full d t = fixFull
  | low d t = fixLow
  | otherwise = BTree (ks1 # ks2) (ts1 # [t] # ts2)
where
  fixFull = let (t1, k, t2) = split d t in
    BTree (ks1 # [k] # ks2) (ts1 # [t1, t2] # ts2)
  fixLow | not $ null ks1 = balance d (init ks1, init ts1)
    (unsplit (last ts1) (last ks1) t)
    (ks2, ts2)
  | not $ null ks2 = balance d (ks1, ts1)
    (unsplit t (head ks2) (head ts2))
    (tail ks2, tail ts2)
  | otherwise = t

```

We leave the *delete* function for the 'paired list' implementation as an exercise. Figure 7.10, 7.11, and 7.12 give examples of delete.

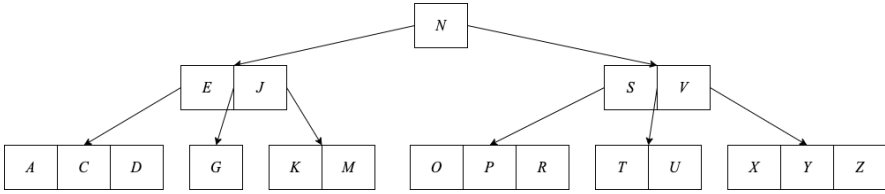


Figure 7.10: Before delete

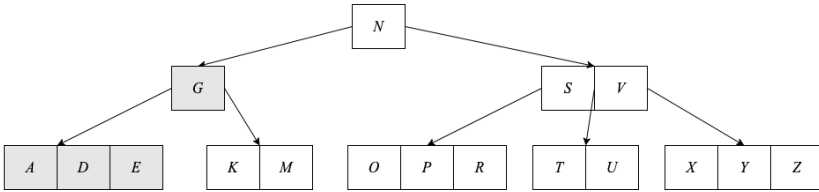
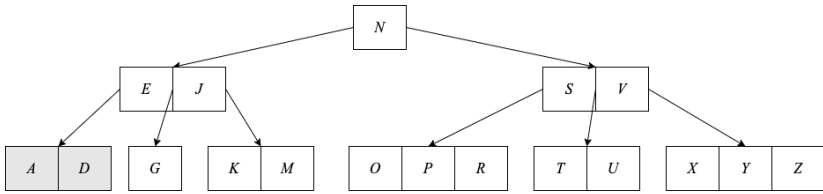


Figure 7.11: Delete 'C', then delete 'J'

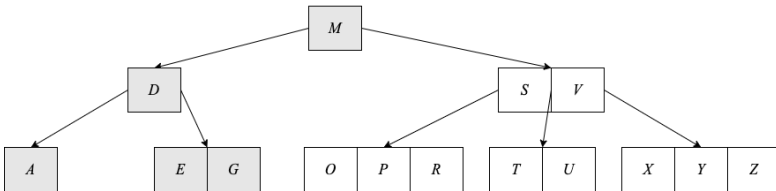
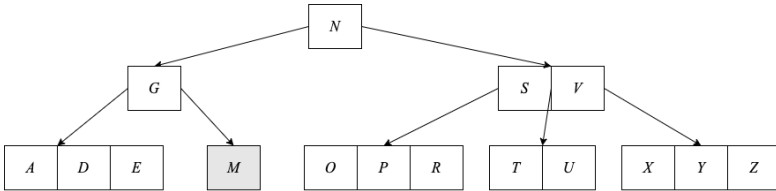


Figure 7.12: Delete 'K', then delete 'N'

7.4.2 Merge before delete

The other way is to merge the nodes before delete if there are too few keys. Consider delete key x from the tree t , let us start from the easy case.

Case 1. If x exists in node t , and t is a leaf, we can directly remove x from t . If t is the singleton node in the tree (root), we needn't worry about too few keys.

Case 2. If x exists in node t , but t is not a leaf. There are three sub-cases:

Case 2a. As shown in figure 7.9, let the predecessor of $k_i = x$ be k' , where $k' = \max(t_i)$. If t_i has sufficient keys ($\geq d$), we replace k_i with k' , then recursively delete k' from t_i .

Case 2b. If t_i does not have enough keys, but the sub-tree t_{i+1} does ($\geq d$). Symmetrically, we replace k_i with its successor k'' , where $k'' = \min(t_{i+1})$, then recursively delete k'' from t_{i+1} , as shown in figure 7.13.

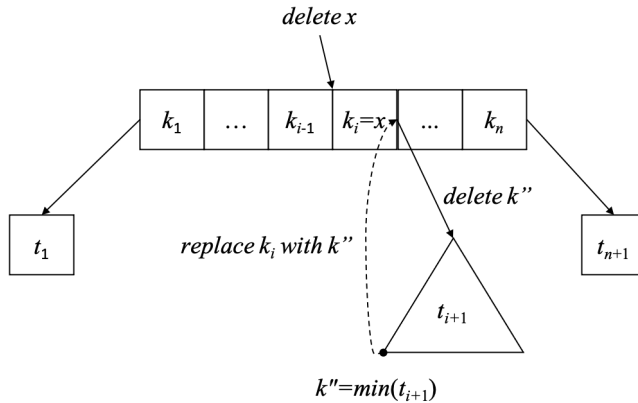


Figure 7.13: Replace k_i with $k'' = \min(t_{i+1})$, then delete k'' from t_{i+1} .

Case 2c. If neither t_i nor t_{i+1} contains sufficient keys ($|t_i| = |t_{i+1}| = d - 1$), we merge t_i, x, t_{i+1} to a new node. This new node has $2d - 1$ keys, we can safely perform delete on it as shown in figure 7.14.

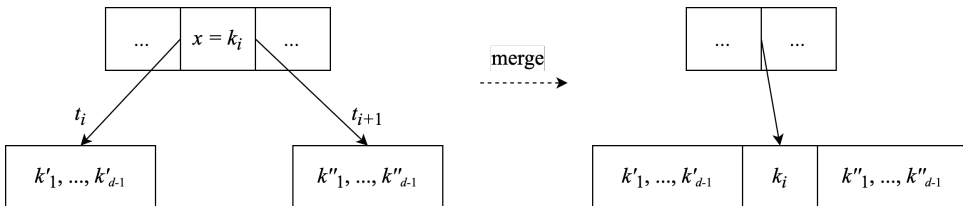


Figure 7.14: Merge before delete

Merge pushes a key k_i to the sub-tree. After that, if node t becomes empty, it means k_i is the only key in t , and t_i, t_{i+1} are the only two sub-trees. We need shrink the tree height as shown in figure 7.15.

Case 3. If node t does not contain x , we need recursively delete x from a sub-tree t_i . There are two sub-cases if there are too few keys in t_i :

Case 3a. Among the two siblings t_{i-1}, t_{i+1} , if either one has enough keys ($\geq d$), we move a key from t to t_i , then move a key from the sibling up to t , and move the corresponding sub-tree from the sibling to t_i . As shown in figure 7.16, t_i received one more key. We next recursively delete x from t_i .

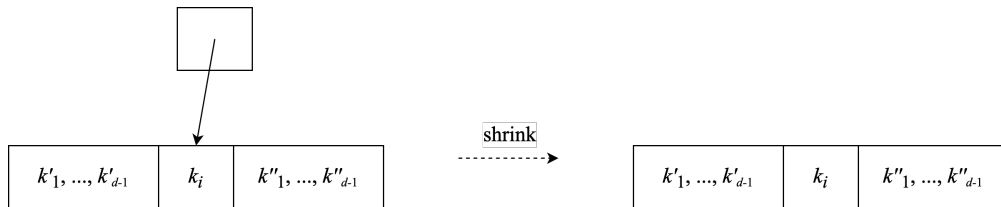


Figure 7.15: Shrink

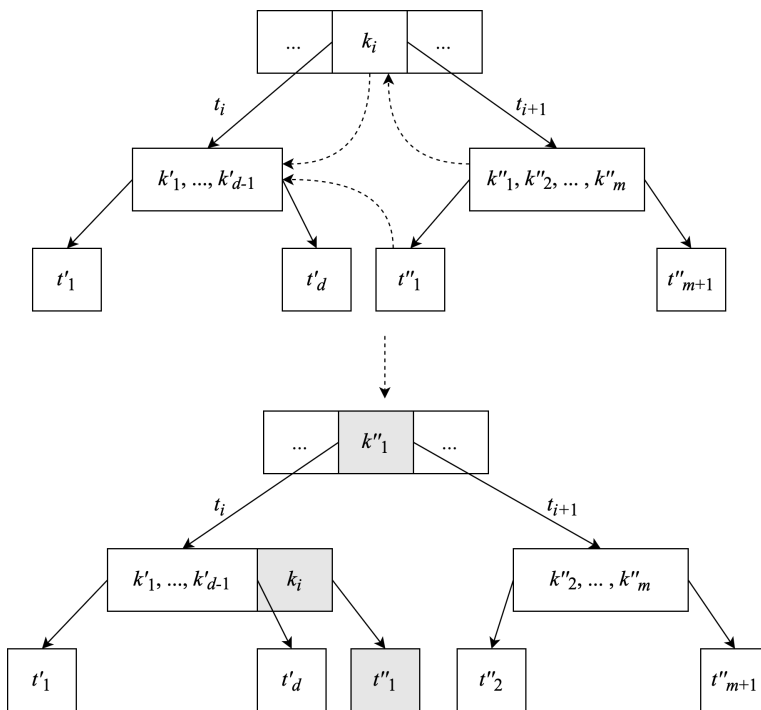


Figure 7.16: Borrow from the right sibling.

Case 3b. If neither sibling has sufficient keys ($|t_{i-1}| = |t_{i+1}| = d - 1$), we merge t_i , a key from t , and either sibling into a new node, as shown in figure 7.17. Then recursively delete x from it.

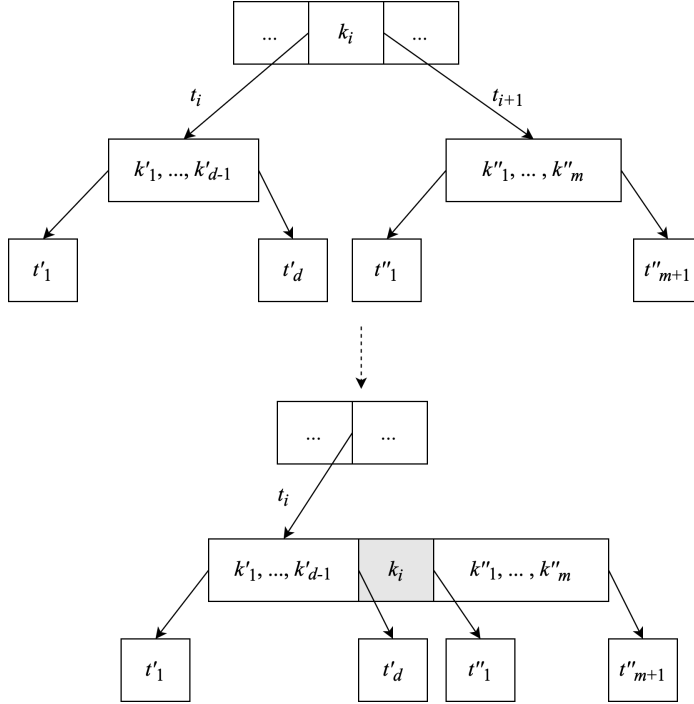


Figure 7.17: Merge t_i , k , t_{i+1}

Below DELETE algorithm implements the ‘merge then delete’ method:

```

1: function DELETE( $t, k$ )
2:   if  $t$  is empty then
3:     return  $t$ 
4:    $i \leftarrow 1, n \leftarrow |K(t)|$ 
5:   while  $i \leq n$  and  $k > k_i(t)$  do
6:      $i \leftarrow i + 1$ 
7:   if  $k = k_i(t)$  then
8:     if  $t$  is leaf then ▷ case 1
9:       REMOVE( $K(t), k$ )
10:    else ▷ case 2
11:      if  $|K(t_i(t))| \geq d$  then ▷ case 2a
12:         $k_i(t) \leftarrow \text{MAX}(t_i(t))$ 
13:        DELETE( $t_i(t), k_i(t)$ )
14:      else if  $|K(t_{i+1}(t))| \geq d$  then ▷ case 2b
15:         $k_i(t) \leftarrow \text{MIN}(t_{i+1}(t))$ 
16:        DELETE( $t_{i+1}(t), k_i(t)$ )
17:      else ▷ case 2c
18:        MERGE-AT( $t, i$ )
19:        DELETE( $t_i(t), k$ )
20:        if  $K(T)$  is empty then
21:           $t \leftarrow t_i(t)$  ▷ Shrinks height
22:    return  $t$ 

```

```

23:   if  $t$  is not leaf then
24:     if  $k > k_n(t)$  then
25:        $i \leftarrow i + 1$ 
26:     if  $|K(t_i(t))| < d$  then ▷ case 3
27:       if  $i > 1$  and  $|K(t_{i-1}(t))| \geq d$  then ▷ case 3a: left
28:         INSERT( $K(t_i(t)), k_{i-1}(t)$ )
29:          $k_{i-1}(t) \leftarrow$  POP-LAST( $K(t_{i-1}(t))$ )
30:         if  $t_i(t)$  is not leaf then
31:           INSERT( $T(t_i(t)),$  POP-BACK( $T(t_{i-1}(t))$ ))
32:         else if  $i \leq n$  and  $|K(t_{i+1}(t))| \geq d$  then ▷ case 3a: right
33:           APPEND( $K(t_i(t)), k_i(t)$ )
34:            $k_i(t) \leftarrow$  POP-FIRST( $K(t_{i+1}(t))$ )
35:           if  $t_i(t)$  is not leaf then
36:             APPEND( $T(t_i(t)),$  POP-FIRST( $T(t_{i+1}(t))$ ))
37:         else ▷ case 3b
38:           if  $i = n + 1$  then
39:              $i \leftarrow i - 1$ 
40:             MERGE-AT( $t, i$ )
41:           DELETE( $t_i(t), k$ )
42:           if  $K(t)$  is empty then ▷ Shrinks height
43:              $t \leftarrow t_1(t)$ 
44:   return  $t$ 

```

Where MERGE-AT(t, i) merges sub-tree $t_i(t)$, key $k_i(t)$, and $t_{i+1}(t)$ into one sub-tree.

```

1: procedure MERGE-AT( $t, i$ )
2:    $x \leftarrow t_i(t)$ 
3:    $y \leftarrow t_{i+1}(t)$ 
4:    $K(x) \leftarrow K(x) \# [k_i(t)] \# K(y)$ 
5:    $T(x) \leftarrow T(x) \# T(y)$ 
6:   REMOVE-AT( $K(t), i$ )
7:   REMOVE-AT( $T(t), i + 1$ )

```

Exercise 7.3

1. When delete a key k from the branch node, we use the maximum key from the predecessor sub-tree $k' = \max(t')$ to replace k , then recursively delete k' from t' . There is a symmetric method, to replace k with the minimum key from the successor sub-tree. Implement this solution.
2. Define the *delete* function for the ‘paired list’ implementation.

7.5 Summary

We extend the binary search tree to multiple branches, then constrain the branches within a range to develop the B-tree. B-tree is used as a tool to control the magnetic disk access (chapter 18, [4]). Because all B-tree nodes store keys in a range, not too few or too many. B-tree is balanced. Most of the tree operations are proportion to the height. The performance is bound to $O(\lg n)$ time, where n is the number of keys in B-tree.

7.6 Appendix: Example programs

Definition of B-tree:

```

data BTree<K, Int deg> {
    [K] keys
    [BTree<K>] subStrees;
}

```

Split node

```

void split(BTree<K, deg> z, Int i) {
    var d = deg
    var x = z.subTrees[i]
    var y = BTree<K, deg>()
    y.keys = x.keys[d ...]
    x.keys = x.keys[ ... d - 1]
    if not isLeaf(x) {
        y.subTrees = x.subTrees[d ... ]
        x.subTrees = x.subTrees[... d]
    }
    z.keys.insert(i, x.keys[d - 1])
    z.subTrees.insert(i + 1, y)
}

```

```

Bool isLeaf(BTree<K, deg> t) = t.subTrees == []

```

Insert a key to B-tree:

```

BTree<K, deg> insert(BTree<K, deg> tr, K key) {
    var root = tr
    if isFull(root) {
        var s = BTree<K, deg>()
        s.subTrees.insert(0, root)
        split(s, 0)
        root = s
    }
    return insertNonfull(root, key)
}

```

Insert a key to a non-full node.

```

BTree<K, deg> insertNonfull(BTree<K, deg> tr, K key) {
    if isLeaf(tr) {
        orderedInsert(tr.keys, key)
    } else {
        Int i = length(tr.keys)
        while i > 0 and key < tr.keys[i - 1] {
            i = i - 1
        }
        if isFull(tr.subTrees[i]) {
            split(tr, i)
            if key > tr.keys[i] then i = i + 1
        }
        insertNonfull(tr.subTree[i], key)
    }
    return tr
}

```

Where `orderedInsert` inserts an element to an ordered list.

```

void orderedInsert([K] lst, K x) {
    Int i = length(lst)
    lst.append(x)
    while i > 0 and lst[i] < lst[i-1] {

```

```

        (lst[i-1], lst[i]) = (lst[i], lst[i-1])
        i = i - 1
    }
}

Bool isFull(BTree<K, deg> x) = length(x.keys) ≥ 2 * deg - 1
Bool isLow(BTree<K, deg> x) = length(x.keys) ≤ deg - 1

```

Iterative look up:

```

Optional<(BTree<K, deg>, Int)> lookup(BTree<K, deg> tr, K key) {
    loop {
        Int i = 0, n = length(tr.keys)
        while i < n and key > tr.keys[i] {
            i = i + 1
        }
        if i < n and key == tr.keys[i] then return Optional((tr, i))
        if isLeaf(tr) {
            return Optional.None
        } else {
            tr = tr.subTrees[i]
        }
    }
}

```

Imperative merge before delete:

```

BTree<K, deg> delete(BTree<K, deg> t, K x) {
    if empty(t.keys) then return t
    Int i = 0, n = length(t.keys)
    while i < n and x > t.keys[i] { i = i + 1 }
    if x == t.keys[i] {
        if isLeaf(t) { // case 1
            removeAt(t.keys, i)
        } else {
            var tl = t.subtrees[i]
            var tr = t.subtrees[i + 1]
            if not low(tl) { // case 2a
                t.keys[i] = max(tl)
                delete(tl, t.keys[i])
            } else if not low(tr) { // case 2b
                t.keys[i] = min(tr)
                delete(tr, t.keys[i])
            } else { // case 2c
                mergeSubtrees(t, i)
                delete(d, tl, x)
                if empty(t.keys) then t = tl // shrink height
            }
        }
        return t
    }
    if not isLeaf(t) {
        if x > t.keys[n - 1] then i = i + 1
        if low(t.subtrees[i]) {
            var tl = if i == 0 then null else t.subtrees[i - 1]
            var tr = if i == n then null else t.subtrees[i + 1]
            if tl ≠ null and (not low(tl)) { // case 3a, left
                insert(t.subtrees[i].keys, 0, t.keys[i - 1])
                t.keys[i - 1] = popLast(tl.keys)
                if not isLeaf(tl) {
                    insert(t.subtrees[i].subtrees, 0, popLast(tl.subtrees))
                }
            } else if tr ≠ null and (not low(tr)) { // case 3a, right
                append(t.subtrees[i].keys, t.keys[i])
                t.keys[i] = popFirst(tr.keys)
                if not isLeaf(tr) {
                    append(t.subtrees[i].subtrees, popFirst(tr.subtrees))
                }
            }
        }
    }
}

```

```

        }
    } else { // case 3b
        mergeSubtrees(t, if i < n then i else (i - 1))
        if i == n then i = i - 1
    }
    delete(t.subtrees[i], x)
    if empty(t.keys) then t = t.subtrees[0] // shrink height
}
return t
}

```

merge sub-trees, find the min/max key from a B-tree.

```

void mergeSubtrees(BTree<K, deg>, Int i) {
    t.subtrees[i].keys += [t.keys[i]] + t.subtrees[i + 1].keys
    t.subtrees[i].subtrees += t.subtrees[i + 1].subtrees
    removeAt(t.keys, i)
    removeAt(t.subtrees, i + 1)
}

K max(BTree<K, deg> t) {
    while not empty(t.subtrees) {
        t = last(t.subtrees)
    }
    return last(t.keys)
}

K min(BTree<K, deg> t) {
    while not empty(t.subtrees) {
        t = t.subtrees[0]
    }
    return t.keys[0]
}

```


Chapter 8

Binary Heaps

8.1 Introduction

Heaps are one of the most widely used data structures—used to solve practical problems such as sorting, prioritized scheduling and in implementing graph algorithms, to name a few[40].

Most popular implementations of heaps use a kind of implicit binary heap using arrays, which is described in [4]. Examples include C++/STL heap and Python heapq. The most efficient heap sort algorithm is also realized with binary heap as proposed by R. W. Floyd [41] [42].

However, heaps can be general and realized with varies of other data structures besides array. In this chapter, explicit binary tree is used. It leads to Leftist heaps, Skew heaps, and Splay heaps, which are suitable for purely functional implementation as shown by Okasaki[3].

A heap is a data structure that satisfies the following *heap property*.

- Top operation always returns the minimum (maximum) element;
- Pop operation removes the top element from the heap while the heap property should be kept, so that the new top element is still the minimum (maximum) one;
- Insert a new element to heap should keep the heap property. That the new top is still the minimum (maximum) element;
- Other operations including merge etc should all keep the heap property.

This is a kind of recursive definition, while it doesn't limit the under ground data structure.

We call the heap with the minimum element on top as *min-heap*, while if the top keeps the maximum element, we call it *max-heap*.

8.2 Implicit binary heap by array

Considering the heap definition in previous section, one option to implement heap is by using trees. A straightforward solution is to store the minimum (maximum) element in the root of the tree, so for 'top' operation, we simply return the root as the result. And for 'pop' operation, we can remove the root and rebuild the tree from the children.

If binary tree is used to implement the heap, we can call it *binary heap*. This chapter explains three different realizations for binary heap.

8.2.1 Definition

The first one is implicit binary tree. Consider the problem how to represent a complete binary tree with array. (For example, try to represent a complete binary tree in the programming language doesn't support structure or record data type. Only array can be used). One solution is to pack all elements from top level (root) down to bottom level (leaves).

Figure 8.1 shows a complete binary tree and its corresponding array representation.

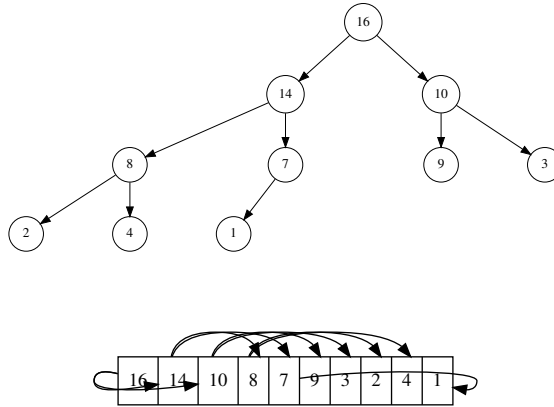


Figure 8.1: Mapping between a complete binary tree and array

This mapping between tree and array can be defined as the following equations (The array index starts from 1).

- 1: **function** PARENT(i)
- 2: **return** $\lfloor \frac{i}{2} \rfloor$

- 3: **function** LEFT(i)
- 4: **return** $2i$

- 5: **function** RIGHT(i)
- 6: **return** $2i + 1$

For a given tree node which is represented as the i -th element of the array, since the tree is complete, we can easily find its parent node as the $\lfloor i/2 \rfloor$ -th element; Its left child with index of $2i$ and right child of $2i + 1$. If the index of the child exceeds the length of the array, it means this node does not have such a child (leaf for example).

In real implementation, this mapping can be calculated fast with bit-wise operation like the following example ANSI C code. Note that, the array index starts from zero in C like languages.

```
#define PARENT(i) (((i) + 1) >> 1) - 1)
#define LEFT(i) (((i) << 1) + 1)
#define RIGHT(i) (((i) + 1) << 1)
```

8.2.2 Heapify

The most important thing for heap algorithm is to maintain the heap property, that the top element should be the minimum (maximum) one.

For the implicit binary heap by array, it means for a given node, which is represented as the i -th index, we can develop a method to check if both its two children are not less than the parent. In case there is violation, we need swap the parent and child recursively [4]. Note that here we assume both the two sub-trees are the valid heaps.

Below algorithm shows the iterative solution to enforce the min-heap property from a given index of the array.

```

1: function HEAPIFY( $A, i$ )
2:    $n \leftarrow |A|$ 
3:   loop
4:      $l \leftarrow \text{LEFT}(i)$ 
5:      $r \leftarrow \text{RIGHT}(i)$ 
6:      $smallest \leftarrow i$ 
7:     if  $l < n \wedge A[l] < A[i]$  then
8:        $smallest \leftarrow l$ 
9:     if  $r < n \wedge A[r] < A[smallest]$  then
10:       $smallest \leftarrow r$ 
11:    if  $smallest \neq i$  then
12:      EXCHANGE  $A[i] \leftrightarrow A[smallest]$ 
13:       $i \leftarrow smallest$ 
14:    else
15:      return

```

For array A and the given index i , None its children should be less than $A[i]$, in case there is violation, we pick the smallest element as $A[i]$, and swap the previous $A[i]$ to child. The algorithm traverses the tree top-down to fix the heap property until either reach a leaf or there is no heap property violation.

The HEAPIFY algorithm takes $O(\lg n)$ time, where n is the number of elements. This is because the loop time is proportion to the height of the complete binary tree.

When implement this algorithm, the comparison method can be passed as a parameter, so that both min-heap and max-heap can be supported. The following ANSI C example code uses this approach.

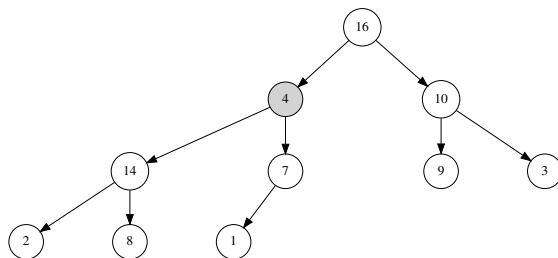
```

typedef int (*Less)(Key, Key);
int less(Key x, Key y) { return x < y; }
int notless(Key x, Key y) { return !less(x, y); }

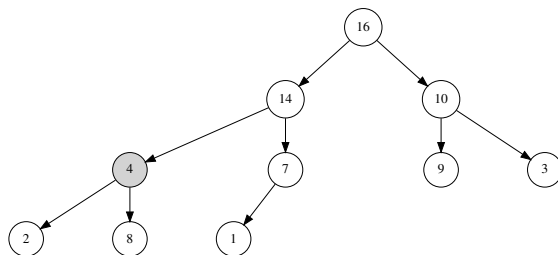
void heapify(Key* a, int i, int n, Less lt) {
  int l, r, m;
  while (1) {
    l = LEFT(i);
    r = RIGHT(i);
    m = i;
    if (l < n && lt(a[l], a[i]))
      m = l;
    if (r < n && lt(a[r], a[m]))
      m = r;
    if (m  $\neq$  i) {
      swap(a, i, m);
      i = m;
    } else
      break;
  }
}

```

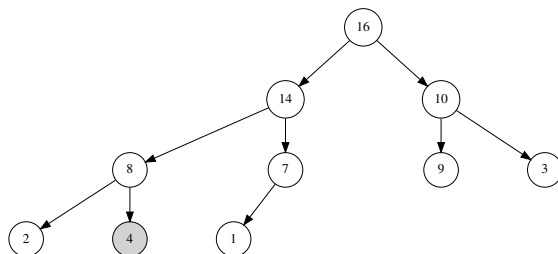
Figure 8.2 illustrates the steps when HEAPIFY processing the array $\{16, 4, 10, 14, 7, 9, 3, 2, 8, 1\}$ from the second index. The array changes to $\{16, 14, 10, 8, 7, 9, 3, 2, 4, 1\}$ as a max-heap.



(a) Step 1, 14 is the biggest element among 4, 14, and 7. Swap 4 with the left child;



(b) Step 2, 8 is the biggest element among 2, 4, and 8. Swap 4 with the right child;



(c) 4 is the leaf node. It hasn't any children. Process terminates.

Figure 8.2: Heapify example, a max-heap case.

8.2.3 Build a heap

With HEAPIFY algorithm defined, it is easy to build a heap from an arbitrary array. Observe that the numbers of nodes in a complete binary tree for each level is a list like below:

$$1, 2, 4, 8, \dots, 2^i, \dots$$

The only exception is the last level. Since the tree may not full (note that complete binary tree doesn't mean full binary tree), the last level contains at most 2^{p-1} nodes, where $2^p + 1 \leq n$ and n is the length of the array.

The HEAPIFY algorithm doesn't have any effect on leave node. We can skip applying HEAPIFY for all leaves. In other words, all leaf nodes have already satisfied the heap property. We only need start checking and maintain the heap property from the last branch node. the index of the last branch node is no greater than $\lfloor n/2 \rfloor$.

Based on this fact, we can build a heap with the following algorithm. (Assume the heap is min-heap).

```

1: function BUILD-HEAP( $A$ )
2:    $n \leftarrow |A|$ 
3:   for  $i \leftarrow \lfloor n/2 \rfloor$  down to 1 do
4:     HEAPIFY( $A, i$ )

```

Although the complexity of HEAPIFY is $O(\lg n)$, the running time of BUILD-HEAP is not bound to $O(n \lg n)$ but $O(n)$. It is a linear time algorithm. This can be deduced as the following:

The heap is built by skipping all leaves. Given n nodes, there are at most $n/4$ nodes being compared and moved down 1 time; at most $n/8$ nodes being compared and moved down 2 times; at most $n/16$ nodes being compared and moved down 3 times,... Thus the upper bound of total comparison and moving time is:

$$S = n\left(\frac{1}{4} + 2\frac{1}{8} + 3\frac{1}{16} + \dots\right) \quad (8.1)$$

Times by 2 for both sides, we have:

$$2S = n\left(\frac{1}{2} + 2\frac{1}{4} + 3\frac{1}{8} + \dots\right) \quad (8.2)$$

Subtract equation (8.1) from (8.2):

$$S = n\left(\frac{1}{2} + \frac{1}{4} + \frac{1}{8} + \dots\right) = n$$

Below ANSI C example program implements this heap building function.

```

void build_heap(Key* a, int n, Less lt) {
  int i;
  for (i = (n-1) >> 1; i >= 0; --i)
    heapify(a, i, n, lt);
}

```

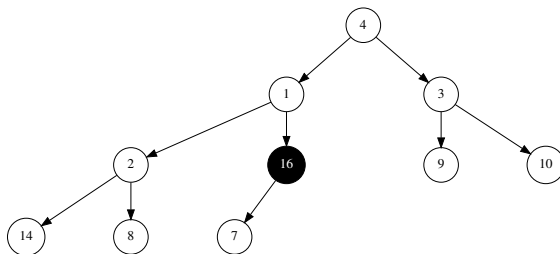
Figure 8.3, 8.4 and 8.5 show the steps when building a max-heap from array $\{4, 1, 3, 2, 16, 9, 10, 14, 8\}$. The node in black color is the one where HEAPIFY being applied, the nodes in gray color are swapped in order to keep the heap property.

8.2.4 Basic heap operations

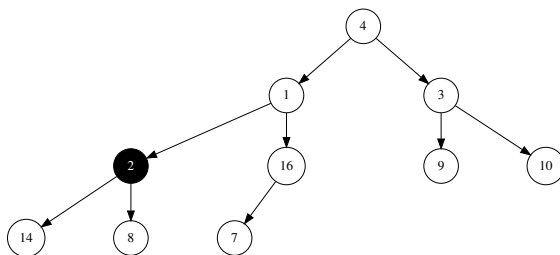
The generic definition of heap (not necessarily the binary heap) demands us to provide basic operations for accessing and modifying data.

4	1	3	2	16	9	10	14	8	7
---	---	---	---	----	---	----	----	---	---

(a) An array in arbitrary order before heap building process;

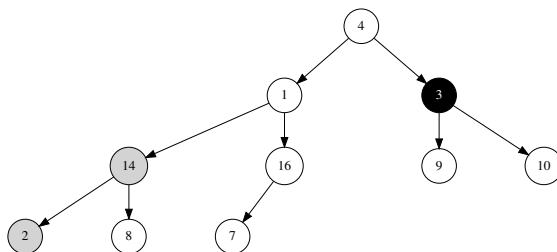


(b) Step 1, The array is mapped to binary tree. The first branch node, which is 16 is examined;

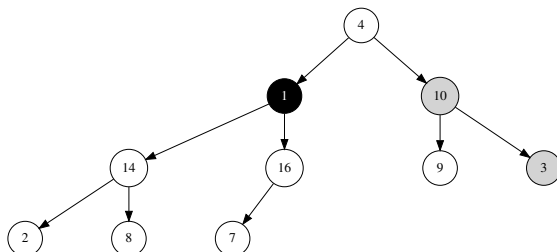


(c) Step 2, 16 is the largest element in current sub tree, next is to check node with value 2;

Figure 8.3: Build a heap from the arbitrary array. Gray nodes are changed in each step, black node will be processed next step.

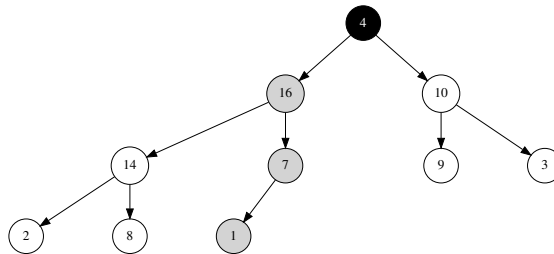


(a) Step 3, 14 is the largest value in the sub-tree, swap 14 and 2; next is to check node with value 3;

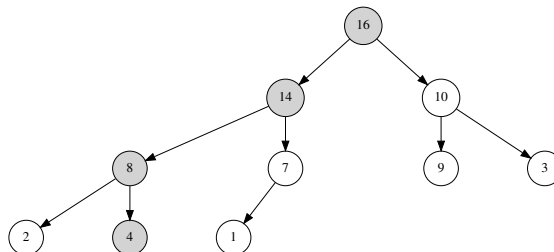


(b) Step 4, 10 is the largest value in the sub-tree, swap 10 and 3; next is to check node with value 1;

Figure 8.4: Build a heap from the arbitrary array. Gray nodes are changed in each step, black node will be processed next step.



(a) Step 5, 16 is the largest value in current sub-tree, swap 16 and 1 first; then similarly, swap 1 and 7; next is to check the root node with value 4;



(b) Step 6, Swap 4 and 16, then swap 4 and 14, and then swap 4 and 8; And the whole build process finish.

Figure 8.5: Build a heap from the arbitrary array. Gray nodes are changed in each step, black node will be processed next step.

The most important operations include accessing the top element (find the minimum or maximum one), popping the top element from the heap, finding the top k elements, decreasing a key (for min-heap. It is increasing a key for max-heap), and insertion.

For the binary tree, most of operations are bound to $O(\lg n)$ in worst-case, some of them, such as top is $O(1)$ constant time.

Access the top element

For the binary tree realization, it is the root stores the minimum (maximum) value. This is the first element in the array.

```
1: function TOP( $A$ )
2:   return  $A[1]$ 
```

This operation is trivial. It takes $O(1)$ time. Here we skip the error handling for empty case. If the heap is empty, one option is to raise an error.

Heap Pop

Pop operation is more complex than accessing the top, because the heap property has to be maintained after the top element is removed.

The solution is to apply HEAPIFY algorithm to the next element after the root is removed.

One simple but slow method based on this idea looks like the following.

```
1: function POP-SLOW( $A$ )
2:    $x \leftarrow$  TOP( $A$ )
3:   REMOVE( $A$ , 1)
4:   if  $A$  is not empty then
5:     HEAPIFY( $A$ , 1)
6:   return  $x$ 
```

This algorithm firstly records the top element in x , then it removes the first element from the array, the size of this array is reduced by one. After that if the array isn't empty, HEAPIFY will applied to the new array from the first element (It was previously the second one).

Removing the first element from array takes $O(n)$ time, where n is the length of the array. This is because we need shift all the rest elements one by one. This bottle neck slows the whole algorithm to linear time.

In order to solve this problem, one alternative is to swap the first element with the last one in the array, then shrink the array size by one.

```
1: function POP( $A$ )
2:    $x \leftarrow$  TOP( $A$ )
3:    $n \leftarrow$  HEAP-SIZE( $A$ )
4:   EXCHANGE  $A[1] \leftrightarrow A[n]$ 
5:   REMOVE( $A$ ,  $n$ )
6:   if  $A$  is not empty then
7:     HEAPIFY( $A$ , 1)
8:   return  $x$ 
```

Removing the last element from the array takes only constant $O(1)$ time, and HEAPIFY is bound to $O(\lg n)$. Thus the whole algorithm performs in $O(\lg n)$ time. The following example ANSI C program implements this algorithm¹.

¹This program does not actually remove the last element, it reuse the last cell to store the popped result

```

Key pop(Key* a, int n, Less lt) {
    swap(a, 0, --n);
    heapify(a, 0, n, lt);
    return a[n];
}

```

Find the top k elements

With pop defined, it is easy to find the top k elements from array. we can build a max-heap from the array, then perform pop operation k times.

```

1: function TOP-K( $A, k$ )
2:    $R \leftarrow \phi$ 
3:   BUILD-HEAP( $A$ )
4:   for  $i \leftarrow 1$  to MIN( $k, |A|$ ) do
5:     APPEND( $R, \text{POP}(A)$ )
6:   return  $R$ 

```

If k is greater than the length of the array, we need return the whole array as the result. That's why it calls the MIN function to determine the number of loops.

Below example Python program implements the top- k algorithm.

```

def top_k(x, k, less_p = MIN_HEAP):
    build_heap(x, less_p)
    return [heap_pop(x, less_p) for _ in range(min(k, len(x)))]

```

Decrease key

Heap can be used to implement priority queue. It is important to support key modification in heap. One typical operation is to increase the priority of a tasks so that it can be performed earlier.

Here we present the decrease key operation for a min-heap. The corresponding operation is increase key for max-heap. Figure 8.6 and 8.7 illustrate such a case for a max-heap. The key of the 9-th node is increased from 4 to 15.

Once a key is decreased in a min-heap, it may make the node conflict with the heap property, that the key may be less than some ancestor. In order to maintain the invariant, the following auxiliary algorithm is defined to resume the heap property.

```

1: function HEAP-FIX( $A, i$ )
2:   while  $i > 1 \wedge A[i] < A[\text{PARENT}(i)]$  do
3:     EXCHANGE  $A[i] \leftrightarrow A[\text{PARENT}(i)]$ 
4:      $i \leftarrow \text{PARENT}(i)$ 

```

This algorithm repeatedly compares the keys of parent node and current node. It swap the nodes if the parent contains the smaller key. This process is performed from the current node towards the root node till it finds that the parent node holds the smaller key.

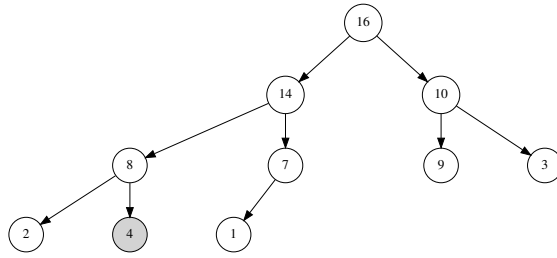
With this auxiliary algorithm, decrease key can be realized as below.

```

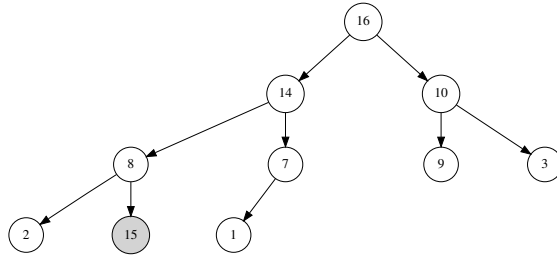
1: function DECREASE-KEY( $A, i, k$ )
2:   if  $k < A[i]$  then
3:      $A[i] \leftarrow k$ 
4:     HEAP-FIX( $A, i$ )

```

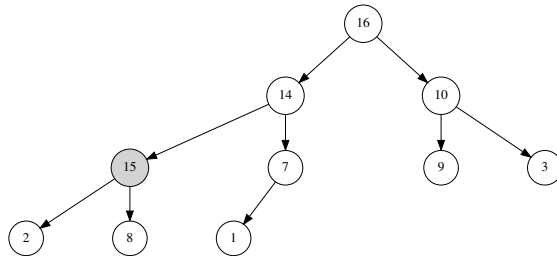
This algorithm is only triggered when the new key is less than the original key. The performance is bound to $O(\lg n)$. Below example ANSI C program implements the algorithm.



(a) The 9-th node with key 4 will be modified;

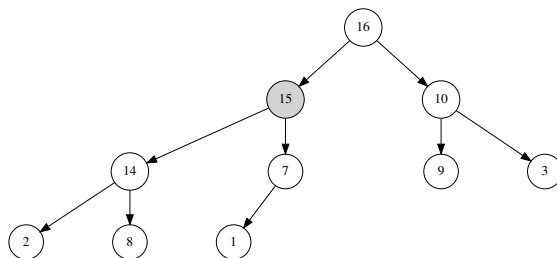


(b) The key is modified to 15, which is greater than its parent;



(c) According the max-heap property, 8 and 15 are swapped.

Figure 8.6: Example process when increase a key in a max-heap.



(a) Since 15 is greater than its parent 14, they are swapped. After that, because 15 is less than 16, the process terminates.

Figure 8.7: Example process when increase a key in a max-heap.

```

void heap_fix(Key* a, int i, Less lt) {
    while (i > 0 && lt(a[i], a[PARENT(i)])) {
        swap(a, i, PARENT(i));
        i = PARENT(i);
    }
}

void decrease_key(Key* a, int i, Key k, Less lt) {
    if (lt(k, a[i])) {
        a[i] = k;
        heap_fix(a, i, lt);
    }
}

```

Insertion

Insertion can be implemented by using DECREASE-KEY [4]. A new node with ∞ as key is created. According to the min-heap property, it should be the last element in the under ground array. After that, the key is decreased to the value to be inserted, and DECREASE-KEY is called to fix any violation to the heap property.

Alternatively, we can reuse HEAP-FIX to implement insertion. The new key is directly appended at the end of the array, and the HEAP-FIX is applied to this new node.

- 1: **function** HEAP-PUSH(A, k)
- 2: APPEND(A, k)
- 3: HEAP-FIX($A, |A|$)

The following example Python program implements the heap insertion algorithm.

```

def heap_insert(x, key, less_p = MIN_HEAP):
    i = len(x)
    x.append(key)
    heap_fix(x, i, less_p)

```

8.2.5 Heap sort

Heap sort is interesting application of heap. According to the heap property, the min(max) element can be easily accessed by from the top of the heap. A straightforward way to sort a list of values is to build a heap from them, then continuously pop the smallest element till the heap is empty.

The algorithm based on this idea can be defined like below.

- 1: **function** HEAP-SORT(A)
- 2: $R \leftarrow \phi$
- 3: BUILD-HEAP(A)
- 4: **while** $A \neq \phi$ **do**
- 5: APPEND($R, \text{HEAP-POP}(A)$)
- 6: **return** R

The following Python example program implements this definition.

```

def heap_sort(x, less_p = MIN_HEAP):
    res = []
    build_heap(x, less_p)
    while x != []:
        res.append(heap_pop(x, less_p))
    return res

```


When sort n elements, the BUILD-HEAP is bound to $O(n)$. Since pop is $O(\lg n)$, and it is called n times, so the overall sorting takes $O(n \lg n)$ time to run. Because we use another list to hold the result, the space requirement is $O(n)$.

Robert. W. Floyd found a fast implementation of heap sort. The idea is to build a max-heap instead of min-heap, so the first element is the biggest one. Then the biggest element is swapped with the last element in the array, so that it is in the right position after sorting. As the last element becomes the new top, it may violate the heap property. We can shrink the heap size by one and perform HEAPIFY to resume the heap property. This process is repeated till there is only one element left in the heap.

```

1: function HEAP-SORT( $A$ )
2:   BUILD-MAX-HEAP( $A$ )
3:   while  $|A| > 1$  do
4:     EXCHANGE  $A[1] \leftrightarrow A[n]$ 
5:      $|A| \leftarrow |A| - 1$ 
6:     HEAPIFY( $A, 1$ )

```

This is in-place algorithm, it needn't any extra spaces to hold the result. The following ANSI C example code implements this algorithm.

```

void heap_sort(Key* a, int n) {
    build_heap(a, n, notless);
    while(n > 1) {
        swap(a, 0, --n);
        heapify(a, 0, n, notless);
    }
}

```

Exercise 8.1

- Somebody considers one alternative to realize in-place heap sort. Take sorting the array in ascending order as example, the first step is to build the array as a minimum heap A , but not the maximum heap like the Floyd's method. After that the first element a_1 is in the correct place. Next, treat the rest $\{a_2, a_3, \dots, a_n\}$ as a new heap, and perform HEAPIFY to them from a_2 for these $n - 1$ elements. Repeating this advance and HEAPIFY step from left to right would sort the array. The following example ANSI C code illustrates this idea. Is this solution correct? If yes, prove it; if not, why?

```

void heap_sort(Key* a, int n) {
    build_heap(a, n, less);
    while(--n)
        heapify(++a, 0, n, less);
}

```

- Because of the same reason, can we perform HEAPIFY from left to right k times to realize in-place top- k algorithm like below ANSI C code?

```

int tops(int k, Key* a, int n, Less lt) {
    build_heap(a, n, lt);
    for (k = MIN(k, n) - 1; k; --k)
        heapify(++a, 0, --n, lt);
    return k;
}

```

8.3 Leftist heap and Skew heap, the explicit binary heaps

Instead of using implicit binary tree by array, it is natural to consider why we can't use explicit binary tree to realize heap?

There are some problems must be solved if we turn into explicit binary tree as the under ground data structure.

The first problem is about the HEAP-POP or DELETE-MIN operation. Consider the binary tree is represented in form of left, key, and right as (L, k, R) , which is shown in figure 8.8

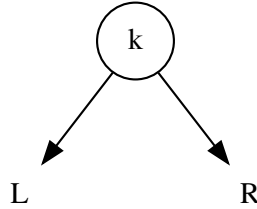


Figure 8.8: A binary tree, all elements in children are not less than k .

If k is the top element, all elements in left and right children are not less than k in a min-heap. After k is popped, only left and right children are left. They have to be merged to a new tree. Since heap property should be maintained after merge, the new root is still the smallest element.

Because both left and right children are binary trees conforming heap property, the two trivial cases can be defined immediately.

$$\text{merge}(H_1, H_2) = \begin{cases} H_2 & : H_1 = \phi \\ H_1 & : H_2 = \phi \\ ? & : \text{otherwise} \end{cases}$$

Where ϕ means empty heap.

If neither left nor right child is empty, because they all fit heap property, the top elements of them are all the minimum respectively. We can compare these two roots, and select the smaller as the new root of the merged heap.

For instance, let $L = (A, x, B)$ and $R = (A', y, B')$, where $A, A', B,$ and B' are all sub trees. If $x < y$, x will be the new root. We can either keep A , and recursively merge B and R ; or keep B , and merge A and R , so the new heap can be one of the following.

- $(\text{merge}(A, R), x, B)$
- $(A, x, \text{merge}(B, R))$

Both are correct. One simplified solution is to only merge the right sub tree. *Leftist* tree provides a systematically approach based on this idea.

8.3.1 Definition

The heap implemented by Leftist tree is called Leftist heap. Leftist tree is first introduced by C. A. Crane in 1972[43].

Rank (S-value)

In Leftist tree, a rank value (or S value) is defined for each node. Rank is the distance to the nearest external node. Where external node is the NIL concept extended from the leaf node.

For example, in figure 8.9, the rank of NIL is defined 0, consider the root node 4, The nearest external node is the child of node 8. So the rank of root node 4 is 2. Because node 6 and node 8 both only contain NIL, so their rank values are 1. Although node 5 has non-NIL left child, However, since the right child is NIL, so the rank value, which is the minimum distance to NIL is still 1.

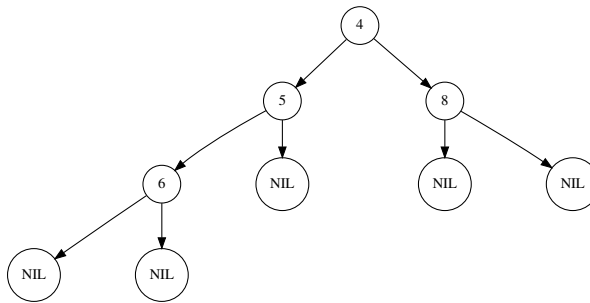


Figure 8.9: $rank(4) = 2$, $rank(6) = rank(8) = rank(5) = 1$.

Leftist property

With rank defined, we can create a strategy when merging.

- Every time when merging, we always merge to right child; Denote the rank of the new right sub tree as r_r ;
- Compare the ranks of the left and right children, if the rank of left sub tree is r_l and $r_l < r_r$, we swap the left and the right children.

We call this ‘Leftist property’. In general, a Leftist tree always has the shortest path to some external node on the right.

Leftist tree tends to be very unbalanced, However, it ensures important property as specified in the following theorem.

Theorem 8.3.1. *If a Leftist tree T contains n internal nodes, the path from root to the rightmost external node contains at most $\lfloor \log(n + 1) \rfloor$ nodes.*

We skip the proof here, readers can refer to [44] and [51] for more information. With this theorem, algorithms operate along this path are all bound to $O(\lg n)$.

We can reuse the binary tree definition, and augment with a rank field to define the Leftist tree, for example in form of (r, k, L, R) for non-empty case. Below Haskell code defines the Leftist tree.

```

data LHeap a = E — Empty
           | Node Int a (LHeap a) (LHeap a) — rank, element, left, right

```

For empty tree, the rank is defined as zero. Otherwise, it's the value of the augmented field. A $rank(H)$ function can be given to cover both cases.

$$rank(H) = \begin{cases} 0 & : H = \phi \\ r & : otherwise, H = (r, k, L, R) \end{cases} \quad (8.3)$$

Here is the example Haskell rank function.

```

rank E = 0
rank (Node r _ _ _) = r

```

In the rest of this section, we denote $rank(H)$ as r_H

8.3.2 Merge

In order to realize 'merge', we need develop the auxiliary algorithm to compare the ranks and swap the children if necessary.

$$mk(k, A, B) = \begin{cases} (r_A + 1, k, B, A) & : r_A < r_B \\ (r_B + 1, k, A, B) & : otherwise \end{cases} \quad (8.4)$$

This function takes three arguments, a key and two sub trees A , and B . if the rank of A is smaller, it builds a bigger tree with B as the left child, and A as the right child. It increment the rank of A by 1 as the rank of the new tree; Otherwise if B holds the smaller rank, then A is set as the left child, and B becomes the right. The resulting rank is $r_b + 1$.

The reason why rank need be increased by one is because there is a new key added on top of the tree. It causes the rank increasing.

Denote the key, the left and right children for H_1 and H_2 as k_1, L_1, R_1 , and k_2, L_2, R_2 respectively. The $merge(H_1, H_2)$ function can be completed by using this auxiliary tool as below

$$merge(H_1, H_2) = \begin{cases} H_2 & : H_1 = \phi \\ H_1 & : H_2 = \phi \\ mk(k_1, L_1, merge(R_1, H_2)) & : k_1 < k_2 \\ mk(k_2, L_2, merge(H_1, R_2)) & : otherwise \end{cases} \quad (8.5)$$

The $merge$ function is always recursively called on the right side, and the Leftist property is maintained. These facts ensure the performance being bound to $O(\lg n)$.

The following Haskell example code implements the merge program.

```

merge E h = h
merge h E = h
merge h1@(Node _ x l r) h2@(Node _ y l' r') =
  if x < y then makeNode x l (merge r h2)
  else makeNode y l' (merge h1 r')

makeNode x a b = if rank a < rank b then Node (rank a + 1) x b a
                 else Node (rank b + 1) x a b

```

Merge operation in implicit binary heap by array

Implicit binary heap by array performs very fast in most cases, and it fits modern computer with cache technology well. However, merge is the algorithm bounds to $O(n)$ time. The typical realization is to concatenate two arrays together and make a heap for this array [50].

```
1: function MERGE-HEAP( $A, B$ )
2:    $C \leftarrow \text{CONCAT}(A, B)$ 
3:   BUILD-HEAP( $C$ )
```

8.3.3 Basic heap operations

Most of the basic heap operations can be implemented with *merge* algorithm defined above.

Top and pop

Because the smallest element is always held in root, it's trivial to find the minimum value. It's constant $O(1)$ operation. Below equation extracts the root from non-empty heap $H = (r, k, L, R)$. The error handling for empty case is skipped here.

$$\text{top}(H) = k \quad (8.6)$$

For pop operation, firstly, the top element is removed, then left and right children are merged to a new heap.

$$\text{pop}(H) = \text{merge}(L, R) \quad (8.7)$$

Because it calls *merge* directly, the pop operation on Leftist heap is bound to $O(\lg n)$.

Insertion

To insert a new element, one solution is to create a single leaf node with the element, and then merge this leaf node to the existing Leftist tree.

$$\text{insert}(H, k) = \text{merge}(H, (1, k, \phi, \phi)) \quad (8.8)$$

It is $O(\lg n)$ algorithm since insertion also calls *merge* directly.

There is a convenient way to build the Leftist heap from a list. We can continuously insert the elements one by one to the empty heap. This can be realized by folding.

$$\text{build}(L) = \text{fold}(\text{insert}, \phi, L) \quad (8.9)$$

Figure 8.10 shows one example Leftist tree built in this way.

The following example Haskell code gives reference implementation for the Leftist tree operations.

```
insert h x = merge (Node 1 x E E) h
findMin (Node _ x _ _) = x
deleteMin (Node _ _ l r) = merge l r
fromList = foldl insert E
```

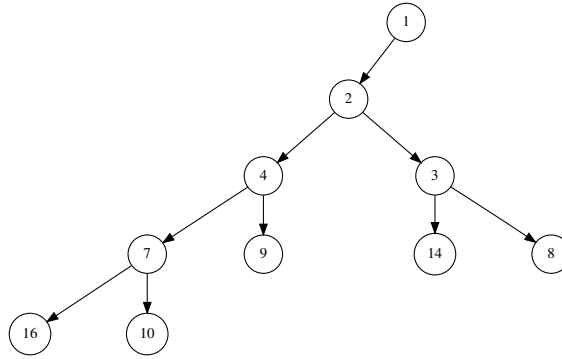


Figure 8.10: A Leftist tree built from list $\{9, 4, 16, 7, 10, 2, 14, 3, 8, 1\}$.

8.3.4 Heap sort by Leftist Heap

With all the basic operations defined, it's straightforward to implement heap sort. We can firstly turn the list into a Leftist heap, then continuously extract the minimum element from it.

$$\text{sort}(L) = \text{heapSort}(\text{build}(L)) \quad (8.10)$$

$$\text{heapSort}(H) = \begin{cases} \phi & : H = \phi \\ \{\text{top}(H)\} \cup \text{heapSort}(\text{pop}(H)) & : \text{otherwise} \end{cases} \quad (8.11)$$

Because pop is logarithm operation, and it is recursively called n times, this algorithm takes $O(n \lg n)$ time in total. The following Haskell example program implements heap sort with Leftist tree.

```

heapSort = hsort o fromList where
  hsort E = []
  hsort h = (findMin h):(hsort $ deleteMin h)

```

8.3.5 Skew heaps

Leftist heap leads to quite unbalanced structure sometimes. Figure 8.11 shows one example. The Leftist tree is built by folding on list $\{16, 14, 10, 8, 7, 9, 3, 2, 4, 1\}$.

Skew heap (or *self-adjusting heap*) simplifies Leftist heap realization and intends to solve the balance issue[46] [47].

When construct the Leftist heap, we swap the left and right children during merge if the rank on left side is less than the right side. This comparison-and-swap strategy doesn't work when either sub tree has only one child. Because in such case, the rank of the sub tree is always 1 no matter how big it is. A 'Brute-force' approach is to swap the left and right children every time when merge. This idea leads to Skew heap.

Definition of Skew heap

Skew heap is the heap realized with Skew tree. Skew tree is a special binary tree. The minimum element is stored in root. Every sub tree is also a skew tree.

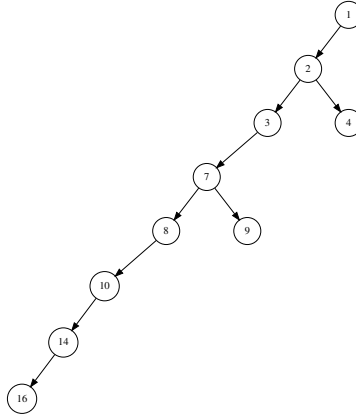


Figure 8.11: A very unbalanced Leftist tree build from list {16, 14, 10, 8, 7, 9, 3, 2, 4, 1}.

It needn't keep the rank (or S -value) field. We can reuse the binary tree definition for Skew heap. The tree is either empty, or in a pre-order form (k, L, R) . Below Haskell code defines Skew heap like this.

```
data SHeap a = E — Empty
           | Node a (SHeap a) (SHeap a) — element, left, right
```

Merge

The merge algorithm tends to be very simple. When merge two non-empty Skew trees, we compare the roots, and pick the smaller one as the new root, then the other tree contains the bigger element is merged onto one sub tree, finally, the two children are swapped. Denote $H_1 = (k_1, L_1, R_1)$ and $H_2 = (k_2, L_2, R_2)$ if they are not empty. if $k_1 < k_2$ for instance, select k_1 as the new root. We can either merge H_2 to L_1 , or merge H_2 to R_1 . Without loss of generality, let's merge to R_1 . And after swapping the two children, the final result is $(k_1, merge(R_1, H_2), L_1)$. Take account of edge cases, the merge algorithm is defined as the following.

$$merge(H_1, H_2) = \begin{cases} H_1 & : H_2 = \phi \\ H_2 & : H_1 = \phi \\ (k_1, merge(R_1, H_2), L_1) & : k_1 < k_2 \\ (k_2, merge(H_1, R_2), L_2) & : otherwise \end{cases} \quad (8.12)$$

All the rest operations, including insert, top and pop are all realized as same as the Leftist heap by using merge, except that we needn't the rank any more.

Translating the above algorithm into Haskell yields the following example program.

```
merge E h = h
merge h E = h
merge h1@(Node x l r) h2@(Node y l' r') =
  if x < y then Node x (merge r h2) l
  else Node y (merge h1 r') l'

insert h x = merge (Node x E E) h

findMin (Node x _ _) = x
```

```
deleteMin (Node _ l r) = merge l r
```

Different from the Leftist heap, if we feed ordered list to Skew heap, it can build a fairly balanced binary tree as illustrated in figure 8.12.

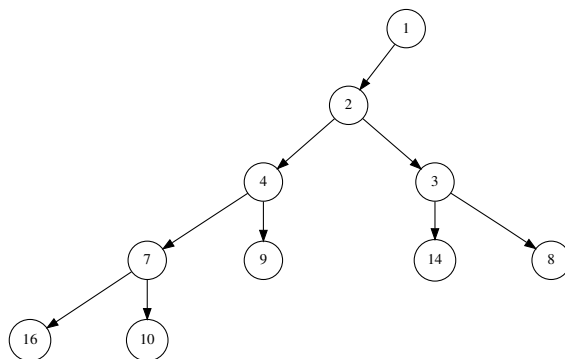


Figure 8.12: Skew tree is still balanced even the input is an ordered list $\{1, 2, \dots, 10\}$.

8.4 Splay heap

The Leftist heap and Skew heap show the fact that it's quite possible to realize heap data structure with explicit binary tree. Skew heap gives one method to solve the tree balance problem. Splay heap on the other hand, use another method to keep the tree balanced.

The binary trees used in Leftist heap and Skew heap are not Binary Search tree (BST). If we turn the underground data structure to binary search tree, the minimum(or maximum) element is not root any more. It takes $O(\lg n)$ time to find the minimum(or maximum) element.

Binary search tree becomes inefficient if it isn't well balanced. Most operations degrade to $O(n)$ in the worst case. Although red-black tree can be used to realize binary heap, it's overkill. Splay tree provides a light weight implementation with acceptable dynamic balancing result.

8.4.1 Definition

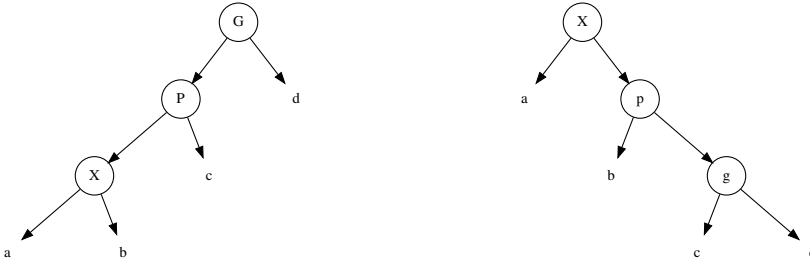
Splay tree uses cache-like approach. It keeps rotating the current access node close to the top, so that the node can be accessed fast next time. It defines such kinds of operation as "Splay". For the unbalanced binary search tree, after several splay operations, the tree tends to be more and more balanced. Most basic operations of Splay tree perform in amortized $O(\lg n)$ time. Splay tree was invented by Daniel Dominic Sleator and Robert Endre Tarjan in 1985[48] [49].

Splaying

There are two methods to do splaying. The first one need deal with many different cases, but can be implemented fairly easy with pattern matching. The second one has a uniformed form, but the implementation is complex.

Denote the node currently being accessed as X , the parent node as P , and the grand parent node as G (If there are). There are 3 steps for splaying. Each step contains 2 symmetric cases. For illustration purpose, only one case is shown for each step.

- *Zig-zig step.* As shown in figure 8.13, in this case, X and P are children on the same side of G , either both on left or right. By rotating 2 times, X becomes the new root.



(a) X and P are both left children or both right children. (b) X becomes new root after rotating 2 times.

Figure 8.13: Zig-zig case.

- *Zig-zag step.* As shown in figure 8.14, in this case, X and P are children on different sides. X is on the left, P is on the right. Or X is on the right, P is on the left. After rotation, X becomes the new root, P and G are siblings.
- *Zig step.* As shown in figure 8.15, in this case, P is the root, we rotate the tree, so that X becomes new root. This is the last step in splay operation.

Although there are 6 different cases, they can be handled in the environments support pattern matching. Denote the non-empty binary tree in form $T = (L, k, R)$, when access key Y in tree T , the splay operation can be defined as below.

$$\text{splay}(T, X) = \begin{cases} (a, X, (b, P, (c, G, d))) & : T = ((a, X, b), P, c), G, d, X = Y \\ ((a, G, b), P, c), X, d & : T = (a, G, (b, P, (c, X, d))), X = Y \\ ((a, P, b), X, (c, G, d)) & : T = (a, P, (b, X, c), G, d), X = Y \\ ((a, G, b), X, (c, P, d)) & : T = (a, G, ((b, X, c), P, d)), X = Y \\ (a, X, (b, P, c)) & : T = ((a, X, b), P, c), X = Y \\ ((a, P, b), X, c) & : T = (a, P, (b, X, c)), X = Y \\ T & : \text{otherwise} \end{cases} \quad (8.13)$$

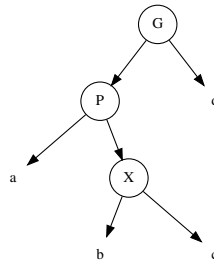
The first two clauses handle the 'zig-zig' cases; the next two clauses handle the 'zig-zag' cases; the last two clauses handle the zig cases. The tree aren't changed for all other situations.

The following Haskell program implements this splay function.

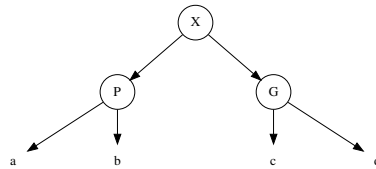
```

data STree a = E — Empty
           | Node (STree a) a (STree a) — left, key, right
— zig-zig
splay t@(Node (Node (Node a x b) p c) g d) y =
  if x == y then Node a x (Node b p (Node c g d)) else t

```



(a) X and P are children on different sides.



(b) X becomes new root. P and G are siblings.

Figure 8.14: Zig-zag case.



(a) P is the root.

(b) Rotate the tree to make X be new root.

Figure 8.15: Zig case.

```

splay t@(Node a g (Node b p (Node c x d))) y =
  if x == y then Node (Node (Node a g b) p c) x d else t
— zig-zag
splay t@(Node (Node a p (Node b x c)) g d) y =
  if x == y then Node (Node a p b) x (Node c g d) else t
splay t@(Node a g (Node (Node b x c) p d)) y =
  if x == y then Node (Node a g b) x (Node c p d) else t
— zig
splay t@(Node (Node a x b) p c) y = if x == y then Node a x (Node b p c) else t
splay t@(Node a p (Node b x c)) y = if x == y then Node (Node a p b) x c else t
— otherwise
splay t _ = t

```

With splay operation defined, every time when insert a new key, we call the splay function to adjust the tree. If the tree is empty, the result is a leaf; otherwise we compare this key with the root, if it is less than the root, we recursively insert it into the left child, and perform splaying after that; else the key is inserted into the right child.

$$\text{insert}(T, x) = \begin{cases} (\phi, x, \phi) & : T = \phi \\ \text{splay}((\text{insert}(L, x), k, R), x) & : T = (L, k, R), x < k \\ \text{splay}(L, k, \text{insert}(R, x)) & : \text{otherwise} \end{cases} \quad (8.14)$$

The following Haskell program implements this insertion algorithm.

```

insert E y = Node E y E
insert (Node l x r) y
  | x > y    = splay (Node (insert l y) x r) y
  | otherwise = splay (Node l x (insert r y)) y

```

Figure 8.16 shows the result of using this function. It inserts the ordered elements $\{1, 2, \dots, 10\}$ one by one to the empty tree. This would build a very poor result which downgrade to linked-list with normal binary search tree. The splay method creates more balanced result.

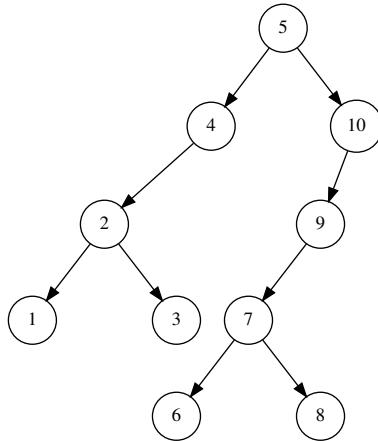


Figure 8.16: Splaying helps improving the balance.

Okasaki found a simple rule for Splaying [3]. Whenever we follow two left branches, or two right branches continuously, we rotate the two nodes.

Based on this rule, splaying can be realized in such a way. When we access node for a key x (can be during the process of inserting a node, or looking up a node, or deleting a node), if we traverse two left branches or two right branches, we partition the tree in two parts L and R , where L contains all nodes smaller than x , and R contains all the

rest. We can then create a new tree (for instance in insertion), with x as the root, L as the left child, and R being the right child. The partition process is recursive, because it will splay its children as well.

$$\text{partition}(T, p) = \left\{ \begin{array}{l}
 (\phi, \phi) : T = \phi \\
 (T, \phi) : T = (L, k, R) \wedge R = \phi \\
 \\
 ((L, k, L'), k', A, B) : \begin{array}{l} T = (L, k, (L', k', R')) \\ k < p, k' < p \\ (A, B) = \text{partition}(R', p) \end{array} \\
 \\
 ((L, k, A), (B, k', R')) : \begin{array}{l} T = (L, k, (L', k', R')) \\ k < p \leq k' \\ (A, B) = \text{partition}(L', p) \end{array} \\
 \\
 (\phi, T) : T = (L, k, R) \wedge L = \phi \\
 \\
 (A, (L', k', (R', k, R))) : \begin{array}{l} T = ((L', k', R'), k, R) \\ p \leq k, p \leq k' \\ (A, B) = \text{partition}(L', p) \end{array} \\
 \\
 ((L', k', A), (B, k, R)) : \begin{array}{l} T = ((L', k', R'), k, R) \\ k' \leq p \leq k \\ (A, B) = \text{partition}(R', p) \end{array}
 \end{array} \right. \quad (8.15)$$

Function $\text{partition}(T, p)$ takes a tree T , and a pivot p as arguments. The first clause is edge case. The partition result for empty is a pair of empty left and right trees. Otherwise, denote the tree as (L, k, R) . we need compare the pivot p and the root k . If $k < p$, there are two sub-cases. one is trivial case that R is empty. According to the property of binary search tree, All elements are less than p , so the result pair is (T, ϕ) ; For the other case, $R = (L', k', R')$, we need further compare k' with the pivot p . If $k' < p$ is also true, we recursively partition R' with the pivot, all the elements less than p in R' is held in tree A , and the rest is in tree B . The result pair can be composed with two trees, one is $((L, k, L'), k', A)$; the other is B . If the key of the right sub tree is not less than the pivot, we recursively partition L' with the pivot to give the intermediate pair (A, B) , the final pair trees can be composed with (L, k, A) and (B, k', R') . There are symmetric cases for $p \leq k$. They are handled in the last three clauses.

Translating the above algorithm into Haskell yields the following partition program.

```

partition E _ = (E, E)
partition t@(Node l x r) y
  | x < y =
    case r of
      E → (t, E)
      Node l' x' r' →
        if x' < y then
          let (small, big) = partition r' y in
            (Node (Node l x l') x' small, big)
        else
          let (small, big) = partition l' y in
            (Node l x small, Node big x' r')
  | otherwise =
    case l of
      E → (E, t)
      Node l' x' r' →
        if y < x' then
          let (small, big) = partition l' y in

```

```

      (small, Node l' x' (Node r' x r))
    else
      let (small, big) = partition r' y in
      (Node l' x' small, Node big x r)

```

Alternatively, insertion can be realized with *partition* algorithm. When insert a new element k into the splay heap T , we can first partition the heap into two trees, L and R . Where L contains all nodes smaller than k , and R contains the rest. We then construct a new node, with k as the root and L, R as the children.

$$\text{insert}(T, k) = (L, k, R), (L, R) = \text{partition}(T, k) \quad (8.16)$$

The corresponding Haskell example program is as the following.

```

insert t x = Node small x big where (small, big) = partition t x

```

Top and pop

Since splay tree is just a special binary search tree, the minimum element is stored in the left most node. We need keep traversing the left child to realize the top operation. Denote the none empty tree $T = (L, k, R)$, the $\text{top}(T)$ function can be defined as below.

$$\text{top}(T) = \begin{cases} k & : L = \phi \\ \text{top}(L) & : \textit{otherwise} \end{cases} \quad (8.17)$$

This is exactly the $\text{min}(T)$ algorithm for binary search tree.

For pop operation, the algorithm need remove the minimum element from the tree. Whenever there are two left nodes traversed, the splaying operation should be performed.

$$\text{pop}(T) = \begin{cases} R & : T = (\phi, k, R) \\ (R', k, R) & : T = ((\phi, k', R'), k, R) \\ (\text{pop}(L'), k', (R', k, R)) & : T = ((L', k', R'), k, R) \end{cases} \quad (8.18)$$

Note that the third clause performs splaying without explicitly call the *partition* function. It utilizes the property of binary search tree directly.

Both the top and pop algorithms are bound to $O(\lg n)$ time because the splay tree is balanced.

The following Haskell example programs implement the top and pop operations.

```

findMin (Node E x _) = x
findMin (Node l x _) = findMin l

deleteMin (Node E x r) = r
deleteMin (Node (Node E x' r') x r) = Node r' x r
deleteMin (Node (Node l' x' r') x r) = Node (deleteMin l') x' (Node r' x r)

```

Merge

Merge is another basic operation for heaps as it is widely used in Graph algorithms. By using the *partition* algorithm, merge can be realized in $O(\lg n)$ time.

When merging two splay trees, for non-trivial case, we can take the root of the first tree as the new root, then partition the second tree with this new root as the pivot. After that we recursively merge the children of the first tree to the partition result. This algorithm is defined as the following.

$$\text{merge}(T_1, T_2) = \begin{cases} T_2 & : T_1 = \phi \\ (\text{merge}(L, A), k, \text{merge}(R, B)) & : T_1 = (L, k, R), (A, B) = \text{partition}(T_2, k) \end{cases} \quad (8.19)$$

If the first heap is empty, the result is definitely the second heap. Otherwise, denote the first splay heap as (L, k, R) , we partition T_2 with k as the pivot to yield (A, B) , where A contains all the elements in T_2 which are less than k , and B holds the rest. We next recursively merge A with L ; and merge B with R as the new children for T_1 .

Translating the definition to Haskell gives the following example program.

```
merge E t = t
merge (Node l x r) t = Node (merge l l') x (merge r r')
  where (l', r') = partition t x
```

8.4.2 Heap sort

Since the internal implementation of the Splay heap is completely transparent to the heap interface, the heap sort algorithm can be reused. It means that the heap sort algorithm is generic no matter what the underground data structure is.

8.5 Notes and short summary

In this chapter, we define binary heap more general so that as long as the heap property is maintained, all binary representation of data structures can be used to implement binary heap.

This definition doesn't limit to the popular array based binary heap, but also extends to the explicit binary heaps including Leftist heap, Skew heap and Splay heap. The array based binary heap is particularly convenient for the imperative implementation because it intensely uses random index access which can be mapped to a completely binary tree. It's hard to find directly functional counterpart in this way.

However, by using explicit binary tree, functional implementation can be achieved, most of them have $O(\lg n)$ worst case performance, and some of them even reach $O(1)$ amortize time. Okasaki in [3] shows detailed analysis of these data structures.

In this chapter, only purely functional realization for Leftist heap, Skew heap, and Splay heap are explained, they can all be realized in imperative approaches.

It's very natural to extend the concept from binary tree to k -ary (k -way) tree, which leads to other useful heaps such as Binomial heap, Fibonacci heap and pairing heap. They are introduced in the following chapters.

Exercise 8.2

- Realize the imperative Leftist heap, Skew heap, and Splay heap.

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Chapter 9

From grape to the world cup, the evolution of selection sort

9.1 Introduction

We have introduced the ‘hello world’ sorting algorithm, insertion sort. In this short chapter, we explain another straightforward sorting method, selection sort. The basic version of selection sort doesn’t perform as good as the divide and conqueror methods, e.g. quick sort and merge sort. We’ll use the same approaches in the chapter of insertion sort, to analyze why it’s slow, and try to improve it by varies of attempts till reach the best bound of comparison based sorting, $O(n \lg n)$, by evolving to heap sort.

The idea of selection sort can be illustrated by a real life story. Consider a kid eating a bunch of grapes. There are two types of children according to my observation. One is optimistic type, that the kid always eats the biggest grape he/she can ever find; the other is pessimistic, that he/she always eats the smallest one.

The first type of kids actually eat the grape in an order that the size decreases monotonically; while the other eat in a increase order. The kid *sorts* the grapes in order of size in fact, and the method used here is selection sort.



Figure 9.1: Always picking the smallest grape.

Based on this idea, the algorithm of selection sort can be directly described as the following.

In order to sort a series of elements:

- The trivial case, if the series is empty, then we are done, the result is also empty;
- Otherwise, we find the smallest element, and append it to the tail of the result;

Note that this algorithm sorts the elements in increase order; It's easy to sort in decrease order by picking the biggest element instead; We'll introduce about passing a comparator as a parameter later on.

This description can be formalized to a equation.

$$\text{sort}(A) = \begin{cases} \phi & : A = \phi \\ \{m\} \cup \text{sort}(A') & : \text{otherwise} \end{cases} \quad (9.1)$$

Where m is the minimum element among collection A , and A' is all the rest elements except m :

$$\begin{aligned} m &= \text{min}(A) \\ A' &= A - \{m\} \end{aligned}$$

We don't limit the data structure of the collection here. Typically, A is an array in imperative environment, and a list (singly linked-list particularly) in functional environment, and it can even be other data structure which will be introduced later.

The algorithm can also be given in imperative manner.

```

function SORT( $A$ )
   $X \leftarrow \phi$ 
  while  $A \neq \phi$  do
     $x \leftarrow \text{MIN}(A)$ 
     $A \leftarrow \text{DEL}(A, x)$ 
     $X \leftarrow \text{APPEND}(X, x)$ 
  return  $X$ 

```

Figure 9.2 depicts the process of this algorithm.

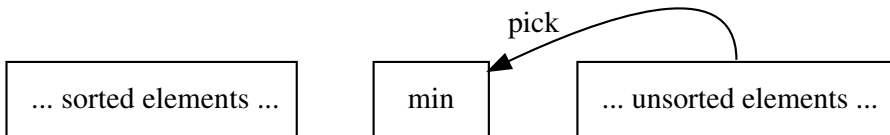


Figure 9.2: The left part is sorted data, continuously pick the minimum element in the rest and append it to the result.

We just translate the very original idea of ‘eating grapes’ line by line without considering any expense of time and space. This realization stores the result in X , and when an selected element is appended to X , we delete the same element from A . This indicates that we can change it to ‘in-place’ sorting to reuse the spaces in A .

The idea is to store the minimum element in the first cell in A (we use term ‘cell’ if A is an array, and say ‘node’ if A is a list); then store the second minimum element in the next cell, then the third cell, ...

One solution to realize this sorting strategy is swapping. When we select the i -th minimum element, we swap it with the element in the i -th cell:

```

function SORT( $A$ )
  for  $i \leftarrow 1$  to  $|A|$  do
     $m \leftarrow \text{MIN}(A[i\dots])$ 
    EXCHANGE  $A[i] \leftrightarrow m$ 

```

Denote $A = \{a_1, a_2, \dots, a_n\}$. At any time, when we process the i -th element, all elements before i , as $\{a_1, a_2, \dots, a_{i-1}\}$ have already been sorted. We locate the minimum element among the $\{a_i, a_{i+1}, \dots, a_n\}$, and exchange it with a_i , so that the i -th cell contains the right value. The process is repeatedly executed until we arrived at the last element.

This idea can be illustrated by figure 9.3.

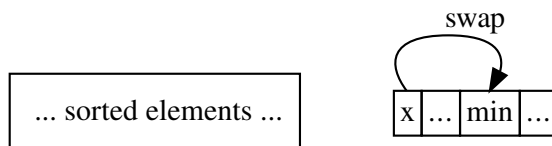


Figure 9.3: The left part is sorted data, continuously pick the minimum element in the rest and put it to the right position.

9.2 Finding the minimum

We haven't completely realized the selection sort, because we take the operation of finding the minimum (or the maximum) element as a black box. It's a puzzle how does a kid locate the biggest or the smallest grape. And this is an interesting topic for computer algorithms.

The easiest but not so fast way to find the minimum in a collection is to perform a scan. There are several ways to interpret this scan process. Consider that we want to pick the biggest grape. We start from any grape, compare it with another one, and pick the bigger one; then we take a next grape and compare it with the one we selected so far, pick the bigger one and go on the take-and-compare process, until there are not any grapes we haven't compared.

It's easy to get loss in real practice if we don't mark which grape has been compared. There are two ways to solve this problem, which are suitable for different data-structures respectively.

9.2.1 Labeling

Method 1 is to label each grape with a number: $\{1, 2, \dots, n\}$, and we systematically perform the comparison in the order of this sequence of labels. That we first compare grape number 1 and grape number 2, pick the bigger one; then we take grape number 3, and do the comparison, ... We repeat this process until arrive at grape number n . This is quite suitable for elements stored in an array.

```

function MIN( $A$ )
   $m \leftarrow A[1]$ 
  for  $i \leftarrow 2$  to  $|A|$  do
    if  $A[i] < m$  then
       $m \leftarrow A[i]$ 
  return  $m$ 

```

With MIN defined, we can complete the basic version of selection sort (or naive version without any optimization in terms of time and space).

However, this algorithm returns the value of the minimum element instead of its location (or the label of the grape), which needs a bit tweaking for the in-place version. Some languages such as ISO C++, support returning the reference as result, so that the swap can be achieved directly as below.

```

template<typename T>
T& min(T* from, T* to) {
    T* m;
    for (m = from++; from ≠ to; ++from)
        if (*from < *m)
            m = from;
    return *m;
}

template<typename T>
void ssort(T* xs, int n) {
    for (int i = 0; i < n; ++i)
        std::swap(xs[i], min(xs+i, xs+n));
}

```

In environments without reference semantics, the solution is to return the location of the minimum element instead of the value:

```

function MIN-AT( $A$ )
     $m \leftarrow$  FIRST-INDEX( $A$ )
    for  $i \leftarrow m + 1$  to  $|A|$  do
        if  $A[i] < A[m]$  then
             $m \leftarrow i$ 
    return  $m$ 

```

Note that since we pass $A[i\dots]$ to MIN-AT as the argument, we assume the first element $A[i]$ as the smallest one, and examine all elements $A[i+1]$, $A[i+2]$, ... one by one. Function FIRST-INDEX() is used to retrieve i from the input parameter.

The following Python example program, for example, completes the basic in-place selection sort algorithm based on this idea. It explicitly passes the range information to the function of finding the minimum location.

```

def ssort(xs):
    n = len(xs)
    for i in range(n):
        m = min_at(xs, i, n)
        (xs[i], xs[m]) = (xs[m], xs[i])
    return xs

def min_at(xs, i, n):
    m = i;
    for j in range(i+1, n):
        if xs[j] < xs[m]:
            m = j
    return m

```

9.2.2 Grouping

Another method is to group all grapes in two parts: the group we have examined, and the rest we haven't. We denote these two groups as A and B ; All the elements (grapes) as L . At the beginning, we haven't examine any grapes at all, thus A is empty (ϕ), and B contains all grapes. We can select arbitrary two grapes from B , compare them, and put the loser (the smaller one for example) to A . After that, we repeat this process by continuously picking arbitrary grapes from B , and compare with the winner of the previous time until B becomes empty. At this time being, the final winner is the minimum element. And A turns to be $L - \{min(L)\}$, which can be used for the next time minimum finding.

There is an invariant of this method, that at any time, we have $L = A \cup \{m\} \cup B$, where m is the winner so far we hold.

This approach doesn't need the collection of grapes being indexed (as being labeled in method 1). It's suitable for any traversable data structures, including linked-list etc. Suppose b_1 is an arbitrary element in B if B isn't empty, and B' is the rest of elements with b_1 being removed, this method can be formalized as the below auxiliary function.

$$\text{min}'(A, m, B) = \begin{cases} (m, A) & : B = \phi \\ \text{min}'(A \cup \{m\}, b_1, B') & : b_1 < m \\ \text{min}'(A \cup \{b_1\}, m, B') & : \textit{otherwise} \end{cases} \quad (9.2)$$

In order to pick the minimum element, we call this auxiliary function by passing an empty A , and use an arbitrary element (for instance, the first one) to initialize m :

$$\text{extractMin}(L) = \text{min}'(\phi, l_1, L') \quad (9.3)$$

Where L' is all elements in L except for the first one l_1 . The algorithm *extractMin* doesn't not only find the minimum element, but also returns the updated collection which doesn't contain this minimum. Summarize this minimum extracting algorithm up to the basic selection sort definition, we can create a complete functional sorting program, for example as this Haskell code snippet.

```

sort [] = []
sort xs = x : sort xs' where
  (x, xs') = extractMin xs

extractMin (x:xs) = min' [] x xs where
  min' ys m [] = (m, ys)
  min' ys m (x:xs) = if m < x then min' (x:ys) m xs else min' (m:ys) x xs

```

The first line handles the trivial edge case that the sorting result for empty list is obvious empty; The second clause ensures that, there is at least one element, that's why the `extractMin` function needn't other pattern-matching.

One may think the second clause of `min'` function should be written like below:

```

min' ys m (x:xs) = if m < x then min' ys ++ [x] m xs
                  else min' ys ++ [m] x xs

```

Or it will produce the updated list in reverse order. Actually, it's necessary to use 'cons' instead of appending here. This is because appending is linear operation which is proportion to the length of part A , while 'cons' is constant $O(1)$ time operation. In fact, we needn't keep the relative order of the list to be sorted, as it will be re-arranged anyway during sorting.

It's quite possible to keep the relative order during sorting¹, while ensure the performance of finding the minimum element not degrade to quadratic. The following equation defines a solution.

$$\text{extractMin}(L) = \begin{cases} (l_1, \phi) & : |L| = 1 \\ (l_1, L') & : l_1 < m, (m, L'') = \text{extractMin}(L') \\ (m, l_1 \cup L'') & : \textit{otherwise} \end{cases} \quad (9.4)$$

If L is a singleton, the minimum is the only element it contains. Otherwise, denote l_1 as the first element in L , and L' contains the rest elements except for l_1 , that $L' = \{l_2, l_3, \dots\}$. The algorithm recursively finding the minimum element in L' , which yields the intermediate result as (m, L'') , that m is the minimum element in L' , and L'' contains all rest elements except for m . Comparing l_1 with m , we can determine which of them is the final minimum result.

The following Haskell program implements this version of selection sort.

¹known as stable sort.

```

sort [] = []
sort xs = x : sort xs' where
  (x, xs') = extractMin xs

extractMin [x] = (x, [])
extractMin (x:xs) = if x < m then (x, xs) else (m, x:xs') where
  (m, xs') = extractMin xs

```

Note that only ‘cons’ operation is used, we needn’t appending at all because the algorithm actually examines the list from right to left. However, it’s not free, as this program need book-keeping the context (via call stack typically). The relative order is ensured by the nature of recursion. Please refer to the appendix about tail recursion call for detailed discussion.

9.2.3 performance of the basic selection sorting

Both the labeling method, and the grouping method need examine all the elements to pick the minimum in every round; and we totally pick up the minimum element n times. Thus the performance is around $n + (n - 1) + (n - 2) + \dots + 1$ times comparison, which is $\frac{n(n+1)}{2}$. Selection sort is a quadratic algorithm bound to $O(n^2)$ time.

Compare to the insertion sort, which we introduced previously, selection sort performs same in its best case, worst case and average case. While insertion sort performs well in best case (that the list has been reverse ordered, and it is stored in linked-list) as $O(n)$, and the worst performance is $O(n^2)$.

In the next sections, we’ll examine, why selection sort performs poor, and try to improve it step by step.

Exercise 9.1

- Implement the basic imperative selection sort algorithm (the none in-place version) in your favorite programming language. Compare it with the in-place version, and analyze the time and space effectiveness.

9.3 Minor Improvement

9.3.1 Parameterize the comparator

Before any improvement in terms of performance, let’s make the selection sort algorithm general enough to handle different sorting criteria.

We’ve seen two opposite examples so far, that one may need sort the elements in ascending order or descending order. For the former case, we need repeatedly finding the minimum, while for the later, we need find the maximum instead. They are just two special cases. In real world practice, one may want to sort things in varies criteria, e.g. in terms of size, weight, age, ...

One solution to handle them all is to passing the criteria as a compare function to the basic selection sort algorithms. For example:

$$\text{sort}(c, L) = \begin{cases} \phi & : L = \phi \\ m \cup \text{sort}(c, L'') & : \text{otherwise}, (m, L'') = \text{extract}(c, L') \end{cases} \quad (9.5)$$

And the algorithm $\text{extract}(c, L)$ is defined as below.

$$\text{extract}(c, L) = \begin{cases} (l_1, \phi) & : |L| = 1 \\ (l_1, L') & : c(l_1, m), (m, L'') = \text{extract}(c, L') \\ (m, \{l_1\} \cup L'') & : \neg c(l_1, m) \end{cases} \quad (9.6)$$

Where c is a comparator function, it takes two elements, compare them and returns the result of which one is preceding of the other. Passing ‘less than’ operator ($<$) turns this algorithm to be the version we introduced in previous section.

Some environments require to pass the total ordering comparator, which returns result among ‘less than’, ‘equal’, and ‘greater than’. We needn’t such strong condition here, that c only tests if ‘less than’ is satisfied. However, as the minimum requirement, the comparator should meet the strict weak ordering as following [52]:

- Irreflexivity, for all x , it’s not the case that $x < x$;
- Asymmetric, For all x and y , if $x < y$, then it’s not the case $y < x$;
- Transitivity, For all x , y , and z , if $x < y$, and $y < z$, then $x < z$;

The following Scheme/Lisp program translates this generic selection sorting algorithm. The reason why we choose Scheme/Lisp here is because the lexical scope can simplify the needs to pass the ‘less than’ comparator for every function calls.

```
(define (sel-sort-by ltp? lst)
  (define (ssort lst)
    (if (null? lst)
        lst
        (let ((p (extract-min lst)))
          (cons (car p) (ssort (cdr p))))))
  (define (extract-min lst)
    (if (null? (cdr lst))
        lst
        (let ((p (extract-min (cdr lst)))
              (if (ltp? (car lst) (car p))
                  lst
                  (cons (car p) (cons (car lst) (cdr p))))))
        (ssort lst)))
```

Note that, both `ssort` and `extract-min` are inner functions, so that the ‘less than’ comparator `ltp?` is available to them. Passing ‘ $<$ ’ to this function yields the normal sorting in ascending order:

```
(sel-sort-by < '(3 1 2 4 5 10 9))
;Value 16: (1 2 3 4 5 9 10)
```

It’s possible to pass varies of comparator to imperative selection sort as well. This is left as an exercise to the reader.

For the sake of brevity, we only consider sorting elements in ascending order in the rest of this chapter. And we’ll not pass comparator as a parameter unless it’s necessary.

9.3.2 Trivial fine tune

The basic in-place imperative selection sorting algorithm iterates all elements, and picking the minimum by traversing as well. It can be written in a compact way, that we inline the minimum finding part as an inner loop.

```
procedure SORT( $A$ )
  for  $i \leftarrow 1$  to  $|A|$  do
     $m \leftarrow i$ 
    for  $j \leftarrow i + 1$  to  $|A|$  do
      if  $A[i] < A[m]$  then
         $m \leftarrow j$ 
    EXCHANGE  $A[i] \leftrightarrow A[m]$ 
```

Observe that, when we are sorting n elements, after the first $n - 1$ minimum ones are selected, the left only one, is definitely the n -th big element, so that we need NOT find the minimum if there is only one element in the list. This indicates that the outer loop can iterate to $n - 1$ instead of n .

Another place we can fine tune, is that we needn't swap the elements if the i -th minimum one is just $A[i]$. The algorithm can be modified accordingly as below:

```

procedure SORT( $A$ )
  for  $i \leftarrow 1$  to  $|A| - 1$  do
     $m \leftarrow i$ 
    for  $j \leftarrow i + 1$  to  $|A|$  do
      if  $A[j] < A[m]$  then
         $m \leftarrow j$ 
    if  $m \neq i$  then
      EXCHANGE  $A[i] \leftrightarrow A[m]$ 

```

Definitely, these modifications won't affect the performance in terms of big-O.

9.3.3 Cock-tail sort

Knuth gave an alternative realization of selection sort in [51]. Instead of selecting the minimum each time, we can select the maximum element, and put it to the last position. This method can be illustrated by the following algorithm.

```

procedure SORT'( $A$ )
  for  $i \leftarrow |A|$  down-to 2 do
     $m \leftarrow i$ 
    for  $j \leftarrow 1$  to  $i - 1$  do
      if  $A[j] > A[m]$  then
         $m \leftarrow j$ 
    EXCHANGE  $A[i] \leftrightarrow A[m]$ 

```

As shown in figure 13.1, at any time, the elements on right most side are sorted. The algorithm scans all unsorted ones, and locate the maximum. Then, put it to the tail of the unsorted range by swapping.

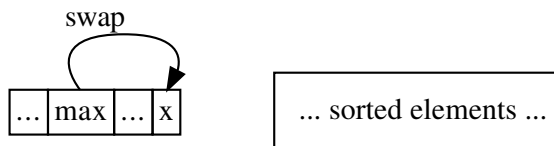


Figure 9.4: Select the maximum every time and put it to the end.

This version reveals the fact that, selecting the maximum element can sort the element in ascending order as well. What's more, we can find both the minimum and the maximum elements in one pass of traversing, putting the minimum at the first location, while putting the maximum at the last position. This approach can speed up the sorting slightly (halve the times of the outer loop). This method is called 'cock-tail sort'.

```

procedure SORT( $A$ )
  for  $i \leftarrow 1$  to  $\lfloor \frac{|A|}{2} \rfloor$  do
     $min \leftarrow i$ 
     $max \leftarrow |A| + 1 - i$ 
    if  $A[max] < A[min]$  then
      EXCHANGE  $A[min] \leftrightarrow A[max]$ 

```



```

for  $j \leftarrow i + 1$  to  $|A| - i$  do
  if  $A[j] < A[\text{min}]$  then
     $\text{min} \leftarrow j$ 
  if  $A[\text{max}] < A[j]$  then
     $\text{max} \leftarrow j$ 
  EXCHANGE  $A[i] \leftrightarrow A[\text{min}]$ 
  EXCHANGE  $A[|A| + 1 - i] \leftrightarrow A[\text{max}]$ 

```

This algorithm can be illustrated as in figure 9.5, at any time, the left most and right most parts contain sorted elements so far. That the smaller sorted ones are on the left, while the bigger sorted ones are on the right. The algorithm scans the unsorted ranges, located both the minimum and the maximum positions, then put them to the head and the tail position of the unsorted ranges by swapping.

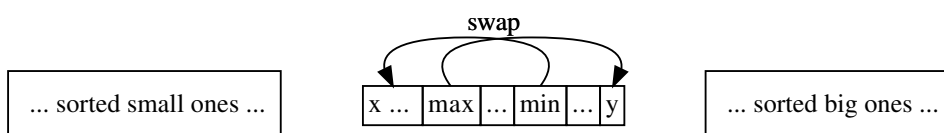


Figure 9.5: Select both the minimum and maximum in one pass, and put them to the proper positions.

Note that it's necessary to swap the left most and right most elements before the inner loop if they are not in correct order. This is because we scan the range excluding these two elements. Another method is to initialize the first element of the unsorted range as both the maximum and minimum before the inner loop. However, since we need two swapping operations after the scan, it's possible that the first swapping moves the maximum or the minimum from the position we just found, which leads the second swapping malfunctioned. How to solve this problem is left as exercise to the reader.

The following Python example program implements this cock-tail sort algorithm.

```

def cocktail_sort(xs):
    n = len(xs)
    for i in range(n // 2):
        (mi, ma) = (i, n - 1 - i)
        if xs[ma] < xs[mi]:
            (xs[mi], xs[ma]) = (xs[ma], xs[mi])
        for j in range(i+1, n - 1 - i):
            if xs[j] < xs[mi]:
                mi = j
            if xs[ma] < xs[j]:
                ma = j
        (xs[i], xs[mi]) = (xs[mi], xs[i])
        (xs[n - 1 - i], xs[ma]) = (xs[ma], xs[n - 1 - i])
    return xs

```

It's possible to realize cock-tail sort in functional approach as well. An intuitive recursive description can be given like this:

- Trivial edge case: If the list is empty, or there is only one element in the list, the sorted result is obviously the origin list;
- Otherwise, we select the minimum and the maximum, put them in the head and tail positions, then recursively sort the rest elements.

This algorithm description can be formalized by the following equation.

$$\text{sort}(L) = \begin{cases} L & : |L| \leq 1 \\ \{l_{\min}\} \cup \text{sort}(L'') \cup \{l_{\max}\} & : \text{otherwise} \end{cases} \quad (9.7)$$

Where the minimum and the maximum are extracted from L by a function $\text{select}(L)$.

$$(l_{\min}, L'', l_{\max}) = \text{select}(L)$$

Note that, the minimum is actually linked to the front of the recursive sort result. Its semantic is a constant $O(1)$ time ‘cons’ (refer to the appendix of this book for detail). While the maximum is appending to the tail. This is typically a linear $O(n)$ time expensive operation. We’ll optimize it later.

Function $\text{select}(L)$ scans the whole list to find both the minimum and the maximum. It can be defined as below:

$$\text{select}(L) = \begin{cases} (\min(l_1, l_2), \max(l_1, l_2)) & : L = \{l_1, l_2\} \\ (l_1, \{l_{\min}\} \cup L'', l_{\max}) & : l_1 < l_{\min} \\ (l_{\min}, \{l_{\max}\} \cup L'', l_1) & : l_{\max} < l_1 \\ (l_{\min}, \{l_1\} \cup L'', l_{\max}) & : \text{otherwise} \end{cases} \quad (9.8)$$

Where $(l_{\min}, L'', l_{\max}) = \text{select}(L')$ and L' is the rest of the list except for the first element l_1 . If there are only two elements in the list, we pick the smaller as the minimum, and the bigger as the maximum. After extract them, the list becomes empty. This is the trivial edge case; Otherwise, we take the first element l_1 out, then recursively perform selection on the rest of the list. After that, we compare if l_1 is less then the minimum or greater than the maximum candidates, so that we can finalize the result.

Note that for all the cases, there is no appending operation to form the result. However, since selection must scan all the element to determine the minimum and the maximum, it is bound to $O(n)$ linear time.

The complete example Haskell program is given as the following.

```

csort [] = []
csort [x] = [x]
csort xs = mi : csort xs' ++ [ma] where
    (mi, xs', ma) = extractMinMax xs

extractMinMax [x, y] = (min x y, [], max x y)
extractMinMax (x:xs) | x < mi = (x, mi:xs', ma)
                    | ma < x = (mi, ma:xs', x)
                    | otherwise = (mi, x:xs', ma)
where (mi, xs', ma) = extractMinMax xs

```

We mentioned that the appending operation is expensive in this intuitive version. It can be improved. This can be achieved in two steps. The first step is to convert the cock-tail sort into tail-recursive call. Denote the sorted small ones as A , and sorted big ones as B in figure 9.5. We use A and B as accumulators. The new cock-tail sort is defined as the following.

$$\text{sort}'(A, L, B) = \begin{cases} A \cup L \cup B & : L = \phi \vee |L| = 1 \\ \text{sort}'(A \cup \{l_{\min}\}, L'', \{l_{\max}\} \cup B) & : \text{otherwise} \end{cases} \quad (9.9)$$

Where l_{\min} , l_{\max} and L'' are defined as same as before. And we start sorting by passing empty A and B : $\text{sort}(L) = \text{sort}'(\phi, L, \phi)$.

Besides the edge case, observing that the appending operation only happens on $A \cup \{l_{\min}\}$; while l_{\max} is only linked to the head of B . This appending occurs in every recursive call. To eliminate it, we can store A in reverse order as \overleftarrow{A} , so that l_{\max} can be

‘cons’ to the head instead of appending. Denote $cons(x, L) = \{x\} \cup L$ and $append(L, x) = L \cup \{x\}$, we have the below equation.

$$\begin{aligned} append(L, x) &= reverse(cons(x, reverse(L))) \\ &= reverse(cons(x, \overleftarrow{L})) \end{aligned} \quad (9.10)$$

Finally, we perform a reverse to turn \overleftarrow{A} back to A . Based on this idea, the algorithm can be improved one more step as the following.

$$sort'(A, L, B) = \begin{cases} reverse(A) \cup B & : L = \phi \\ reverse(\{l_1\} \cup A) \cup B & : |L| = 1 \\ sort'(\{l_{min}\} \cup A, L'', \{l_{max}\} \cup B) & : \end{cases} \quad (9.11)$$

This algorithm can be implemented by Haskell as below.

```
csort' xs = cocktail [] xs [] where
  cocktail as [] bs = reverse as ++ bs
  cocktail as [x] bs = reverse (x:as) ++ bs
  cocktail as xs bs = let (mi, xs', ma) = extractMinMax xs
                       in cocktail (mi:as) xs' (ma:bs)
```

Exercise 9.2

- Realize the imperative basic selection sort algorithm, which can take a comparator as a parameter. Please try both dynamic typed language and static typed language. How to annotate the type of the comparator as general as possible in a static typed language?
- Implement Knuth’s version of selection sort in your favorite programming language.
- An alternative to realize cock-tail sort is to assume the i -th element both the minimum and the maximum, after the inner loop, the minimum and maximum are found, then we can swap the the minimum to the i -th position, and the maximum to position $|A| + 1 - i$. Implement this solution in your favorite imperative language. Please note that there are several special edge cases should be handled correctly:

- $A = \{max, min, \dots\}$;
- $A = \{\dots, max, min\}$;
- $A = \{max, \dots, min\}$.

Please don’t refer to the example source code along with this chapter before you try to solve this problem.

- Realize the function $select(L)$ by folding.

9.4 Major improvement

Although cock-tail sort halves the numbers of loop, the performance is still bound to quadratic time. It means that, the method we developed so far handles big data poorly compare to other divide and conquer sorting solutions.

To improve selection based sort essentially, we must analyze where is the bottleneck. In order to sort the elements by comparison, we must examine all the elements for ordering. Thus the outer loop of selection sort is necessary. However, must it scan all the

elements every time to select the minimum? Note that when we pick the smallest one at the first time, we actually traverse the whole collection, so that we know which ones are relative big, and which ones are relative small partially.

The problem is that, when we select the further minimum elements, instead of re-using the ordering information we obtained previously, we drop them all, and blindly start a new traverse.

So the key point to improve selection based sort is to re-use the previous result. There are several approaches, we'll adopt an intuitive idea inspired by football match in this chapter.

9.4.1 Tournament knock out

The football world cup is held every four years. There are 32 teams from different continent play the final games. Before 1982, there were 16 teams compete for the tournament finals[53].

For simplification purpose, let's go back to 1978 and imagine a way to determine the champion: In the first round, the teams are grouped into 8 pairs to play the game; After that, there will be 8 winner, and 8 teams will be out. Then in the second round, these 8 teams are grouped into 4 pairs. This time there will be 4 winners after the second round of games; Then the top 4 teams are divided into 2 pairs, so that there will be only two teams left for the final game.

The champion is determined after the total 4 rounds of games. And there are actually $8 + 4 + 2 + 1 = 16$ games. Now we have the world cup champion, however, the world cup game won't finish at this stage, we need to determine which is the silver medal team.

Readers may argue that isn't the team beaten by the champion at the final game the second best? This is true according to the real world cup rule. However, it isn't fair enough in some sense.

We often heard about the so called 'group of death', Let's suppose that Brazil team is grouped with Deutch team at the very beginning. Although both teams are quite strong, one of them must be knocked out. It's quite possible that even the team loss that game can beat all the other teams except for the champion. Figure 9.6 illustrates such case.

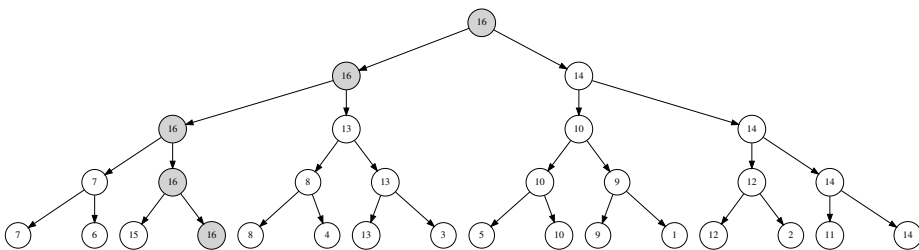


Figure 9.6: The element 15 is knocked out in the first round.

Imagine that every team has a number. The bigger the number, the stronger the team. Suppose that the stronger team always beats the team with smaller number, although this is not true in real world. But this simplification is fair enough for us to develop the tournament knock out solution. This maximum number which represents the champion is 16. Definitely, team with number 14 isn't the second best according to our rules. It should be 15, which is knocked out at the first round of comparison.

The key question here is to find an effective way to locate the second maximum number in this tournament tree. After that, what we need is to apply the same method to select the third, the fourth, ..., to accomplish the selection based sort.

One idea is to assign the champion a very small number (for instance, $-\infty$), so that it won't be selected next time, and the second best one, becomes the new champion. However, suppose there are 2^m teams for some natural number m , it still takes $2^{m-1} + 2^{m-2} + \dots + 2 + 1 = 2^m$ times of comparison to determine the new champion. Which is as slow as the first time.

Actually, we needn't perform a bottom-up comparison at all since the tournament tree stores plenty of ordering information. Observe that, the second best team must be beaten by the champion at sometime, or it will be the final winner. So we can track the path from the root of the tournament tree to the leaf of the champion, examine all the teams along with this path to find the second best team.

In figure 9.6, this path is marked in gray color, the elements to be examined are $\{14, 13, 7, 15\}$. Based on this idea, we refine the algorithm like below.

1. Build a tournament tree from the elements to be sorted, so that the champion (the maximum) becomes the root;
2. Extract the root from the tree, perform a top-down pass and replace the maximum with $-\infty$;
3. Perform a bottom-up back-track along the path, determine the new champion and make it as the new root;
4. Repeat step 2 until all elements have been extracted.

Figure 9.7, 9.8, and 9.9 show the steps of applying this strategy.

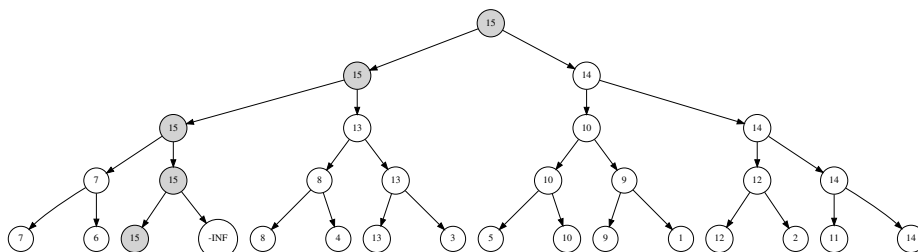


Figure 9.7: Extract 16, replace it with $-\infty$, 15 sifts up to root.

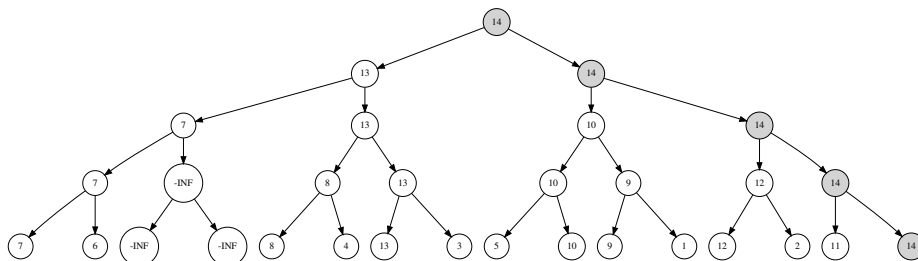
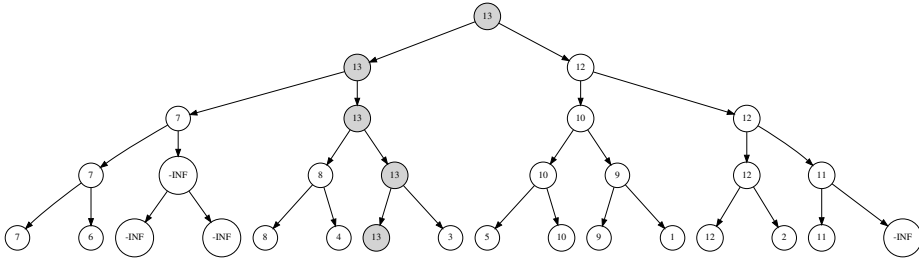


Figure 9.8: Extract 15, replace it with $-\infty$, 14 sifts up to root.

We can reuse the binary tree definition given in the first chapter of this book to represent tournament tree. In order to back-track from leaf to the root, every node should hold a reference to its parent (concept of pointer in some environment such as ANSI C):

Figure 9.9: Extract 14, replace it with $-\infty$, 13 sifts up to root.

```

struct Node {
    Key key;
    struct Node *left, *right, *parent;
};

```

To build a tournament tree from a list of elements (suppose the number of elements are 2^m for some m), we can first wrap each element as a leaf, so that we obtain a list of binary trees. We take every two trees from this list, compare their keys, and form a new binary tree with the bigger key as the root; the two trees are set as the left and right children of this new binary tree. Repeat this operation to build a new list of trees. The height of each tree is increased by 1. Note that the size of the tree list halves after such a pass, so that we can keep reducing the list until there is only one tree left. And this tree is the finally built tournament tree.

function BUILD-TREE(A)

$T \leftarrow \phi$

for each $x \in A$ **do**

$t \leftarrow \text{CREATE-NODE}$

KEY(t) $\leftarrow x$

APPEND(T, t)

while $|T| > 1$ **do**

$T' \leftarrow \phi$

for every $t_1, t_2 \in T$ **do**

$t \leftarrow \text{CREATE-NODE}$

KEY(t) $\leftarrow \text{MAX}(\text{KEY}(t_1), \text{KEY}(t_2))$

LEFT(t) $\leftarrow t_1$

RIGHT(t) $\leftarrow t_2$

PARENT(t_1) $\leftarrow t$

PARENT(t_2) $\leftarrow t$

APPEND(T', t)

$T \leftarrow T'$

return $T[1]$

Suppose the length of the list A is n , this algorithm firstly traverses the list to build tree, which is linear to n time. Then it repeatedly compares pairs, which loops proportion to $n + \frac{n}{2} + \frac{n}{4} + \dots + 2 = 2n$. So the total performance is bound to $O(n)$ time.

The following ANSI C program implements this tournament tree building algorithm.

```

struct Node* build(const Key* xs, int n) {
    int i;
    struct Node *t, **ts = (struct Node**) malloc(sizeof(struct Node*) * n);
    for (i = 0; i < n; ++i)
        ts[i] = leaf(xs[i]);
}

```

```

for (; n > 1; n /= 2)
    for (i = 0; i < n; i += 2)
        ts[i/2] = branch(max(ts[i]→key, ts[i+1]→key), ts[i], ts[i+1]);
t = ts[0];
free(ts);
return t;
}

```

The type of key can be defined somewhere, for example:

```
typedef int Key;
```

Function `leaf(x)` creates a leaf node, with value `x` as key, and sets all its fields, left, right and parent to `NIL`. While function `branch(key, left, right)` creates a branch node, and links the new created node as parent of its two children if they are not empty. For the sake of brevity, we skip the detail of them. They are left as exercise to the reader, and the complete program can be downloaded along with this book.

Some programming environments, such as Python provides tool to iterate every two elements at a time, for example:

```
for x, y in zip(*[iter(ts)]*2):
```

We skip such language specific feature, readers can refer to the Python example program along with this book for details.

When the maximum element is extracted from the tournament tree, we replace it with $-\infty$, and repeatedly replace all these values from the root to the leaf. Next, we back-track to root through the parent field, and determine the new maximum element.

function EXTRACT-MAX(T)

$m \leftarrow \text{KEY}(T)$

$\text{KEY}(T) \leftarrow -\infty$

while $\neg \text{LEAF?}(T)$ **do**

▷ The top down pass

if $\text{KEY}(\text{LEFT}(T)) = m$ **then**

$T \leftarrow \text{LEFT}(T)$

else

$T \leftarrow \text{RIGHT}(T)$

$\text{KEY}(T) \leftarrow -\infty$

while $\text{PARENT}(T) \neq \phi$ **do**

▷ The bottom up pass

$T \leftarrow \text{PARENT}(T)$

$\text{KEY}(T) \leftarrow \text{MAX}(\text{KEY}(\text{LEFT}(T)), \text{KEY}(\text{RIGHT}(T)))$

return m

This algorithm returns the extracted maximum element, and modifies the tournament tree in-place. Because we can't represent $-\infty$ in real program by limited length of word, one approach is to define a relative negative big number, which is less than all the elements in the tournament tree, for example, suppose all the elements are greater than -65535, we can define negative infinity as below:

```
#define N_INF -65535
```

We can implements this algorithm as the following ANSI C example program.

```

Key pop(struct Node* t) {
    Key x = t→key;
    t→key = N_INF;
    while (!isleaf(t)) {
        t = t→left→key == x ? t→left : t→right;
        t→key = N_INF;
    }
}

```

```

while (t→parent) {
    t = t→parent;
    t→key = max(t→left→key, t→right→key);
}
return x;
}

```

The behavior of EXTRACT-MAX is quite similar to the pop operation for some data structures, such as queue, and heap, thus we name it as **pop** in this code snippet.

Algorithm EXTRACT-MAX process the tree in two passes, one is top-down, then a bottom-up along the path that the ‘champion team wins the world cup’. Because the tournament tree is well balanced, the length of this path, which is the height of the tree, is bound to $O(\lg n)$, where n is the number of the elements to be sorted (which are equal to the number of leaves). Thus the performance of this algorithm is $O(\lg n)$.

It’s possible to realize the tournament knock out sort now. We build a tournament tree from the elements to be sorted, then continuously extract the maximum. If we want to sort in monotonically increase order, we put the first extracted one to the right most, then insert the further extracted elements one by one to left; Otherwise if we want to sort in decrease order, we can just append the extracted elements to the result. Below is the algorithm sorts elements in ascending order.

```

procedure SORT( $A$ )
     $T \leftarrow$  BUILD-TREE( $A$ )
    for  $i \leftarrow |A|$  down to 1 do
         $A[i] \leftarrow$  EXTRACT-MAX( $T$ )

```

Translating it to ANSI C example program is straightforward.

```

void tsort(Key* xs, int n) {
    struct Node* t = build(xs, n);
    while(n)
        xs[--n] = pop(t);
    release(t);
}

```

This algorithm firstly takes $O(n)$ time to build the tournament tree, then performs n pops to select the maximum elements so far left in the tree. Since each pop operation is bound to $O(\lg n)$, thus the total performance of tournament knock out sorting is $O(n \lg n)$.

Refine the tournament knock out

It’s possible to design the tournament knock out algorithm in purely functional approach. And we’ll see that the two passes (first top-down replace the champion with $-\infty$, then bottom-up determine the new champion) in pop operation can be combined in recursive manner, so that we needn’t the parent field any more. We can re-use the functional binary tree definition as the following example Haskell code.

```

data Tr a = Empty | Br (Tr a) a (Tr a)

```

Thus a binary tree is either empty or a branch node contains a key, a left sub tree and a right sub tree. Both children are again binary trees.

We’ve use hard coded big negative number to represents $-\infty$. However, this solution is ad-hoc, and it forces all elements to be sorted are greater than this pre-defined magic number. Some programming environments support algebraic type, so that we can define negative infinity explicitly. For instance, the below Haskell program setups the concept of infinity ².

²The order of the definition of ‘NegInf’, regular number, and ‘Inf’ is significant if we want to derive


```
data Infinite a = NegInf | Only a | Inf deriving (Eq, Ord)
```

From now on, we switch back to use the $\min()$ function to determine the winner, so that the tournament selects the minimum instead of the maximum as the champion.

Denote function $\text{key}(T)$ returns the key of the tree rooted at T . Function $\text{wrap}(x)$ wraps the element x into a leaf node. Function $\text{tree}(l, k, r)$ creates a branch node, with k as the key, l and r as the two children respectively.

The knock out process, can be represented as comparing two trees, picking the smaller key as the new key, and setting these two trees as children:

$$\text{branch}(T_1, T_2) = \text{tree}(T_1, \min(\text{key}(T_1), \text{key}(T_2)), T_2) \quad (9.12)$$

This can be implemented in Haskell word by word:

```
branch t1 t2 = Br t1 (min (key t1) (key t2)) t2
```

There is limitation in our tournament sorting algorithm so far. It only accepts collection of elements with size of 2^m , or we can't build a complete binary tree. This can be actually solved in the tree building process. Remind that we pick two trees every time, compare and pick the winner. This is perfect if there are always even number of trees. Considering a case in football match, that one team is absent for some reason (sever flight delay or whatever), so that there left one team without a challenger. One option is to make this team the winner, so that it will attend the further games. Actually, we can use the similar approach.

To build the tournament tree from a list of elements, we wrap every element into a leaf, then start the building process.

$$\text{build}(L) = \text{build}'(\{\text{wrap}(x) | x \in L\}) \quad (9.13)$$

The $\text{build}'(\mathbb{T})$ function terminates when there is only one tree left in \mathbb{T} , which is the champion. This is the trivial edge case. Otherwise, it groups every two trees in a pair to determine the winners. When there are odd numbers of trees, it just makes the last tree as the winner to attend the next level of tournament and recursively repeats the building process.

$$\text{build}'(\mathbb{T}) = \begin{cases} \mathbb{T} & : |\mathbb{T}| \leq 1 \\ \text{build}'(\text{pair}(\mathbb{T})) & : \textit{otherwise} \end{cases} \quad (9.14)$$

Note that this algorithm actually handles another special cases, that the list to be sort is empty. The result is obviously empty.

Denote $\mathbb{T} = \{T_1, T_2, \dots\}$ if there are at least two trees, and \mathbb{T}' represents the left trees by removing the first two. Function $\text{pair}(\mathbb{T})$ is defined as the following.

$$\text{pair}(\mathbb{T}) = \begin{cases} \{\text{branch}(T_1, T_2)\} \cup \text{pair}(\mathbb{T}') & : |\mathbb{T}| \geq 2 \\ \mathbb{T} & : \textit{otherwise} \end{cases} \quad (9.15)$$

The complete tournament tree building algorithm can be implemented as the below example Haskell program.

```
fromList :: (Ord a) => [a] -> Tr (Infinite a)
fromList = build o (map wrap) where
  build [] = Empty
  build [t] = t
  build ts = build $ pair ts
  pair (t1:t2:ts) = (branch t1 t2):pair ts
  pair ts = ts
```

the default, correct comparing behavior of 'Ord'. Anyway, it's possible to specify the detailed order by make it as an instance of 'Ord'. However, this is Language specific feature which is out of the scope of this book. Please refer to other textbook about Haskell.

When extracting the champion (the minimum) from the tournament tree, we need examine either the left child sub-tree or the right one has the same key as the root, and recursively extract on that tree until arrive at the leaf node. Denote the left sub-tree of T as L , right sub-tree as R , and K as its key. We can define this popping algorithm as the following.

$$\text{pop}(T) = \begin{cases} \text{tree}(\phi, \infty, \phi) & : L = \phi \wedge R = \phi \\ \text{tree}(L', \min(\text{key}(L'), \text{key}(R)), R) & : K = \text{key}(L), L' = \text{pop}(L) \\ \text{tree}(L, \min(\text{key}(L), \text{key}(R')), R') & : K = \text{key}(R), R' = \text{pop}(R) \end{cases} \quad (9.16)$$

It's straightforward to translate this algorithm into example Haskell code.

```
pop (Br Empty _ Empty) = Br Empty Inf Empty
pop (Br l k r) | k == key l = let l' = pop l in Br l' (min (key l') (key r)) r
               | k == key r = let r' = pop r in Br l (min (key l) (key r')) r'
```

Note that this algorithm only removes the current champion without returning it. So it's necessary to define a function to get the champion at the root node.

$$\text{top}(T) = \text{key}(T) \quad (9.17)$$

With these functions defined, tournament knock out sorting can be formalized by using them.

$$\text{sort}(L) = \text{sort}'(\text{build}(L)) \quad (9.18)$$

Where $\text{sort}'(T)$ continuously pops the minimum element to form a result tree

$$\text{sort}'(T) = \begin{cases} \phi & : T = \phi \vee \text{key}(T) = \infty \\ \{ \text{top}(T) \} \cup \text{sort}'(\text{pop}(T)) & : \text{otherwise} \end{cases} \quad (9.19)$$

The rest of the Haskell code is given below to complete the implementation.

```
top = only ◦ key
tsort :: (Ord a) => [a] -> [a]
tsort = sort' ◦ fromList where
  sort' Empty = []
  sort' (Br _ Inf _) = []
  sort' t = (top t) : (sort' $ pop t)
```

And the auxiliary function `only`, `key`, `wrap` accomplished with explicit infinity support are list as the following.

```
only (Only x) = x
key (Br _ k _) = k
wrap x = Br Empty (Only x) Empty
```

Exercise 9.3

- Implement the helper function `leaf()`, `branch`, `max()` `lsleaf()`, and `release()` to complete the imperative tournament tree program.
- Implement the imperative tournament tree in a programming language support GC (garbage collection).
- Why can our tournament tree knock out sort algorithm handle duplicated elements (elements with same value)? We say a sorting algorithm stable, if it keeps the original order of elements with same value. Is the tournament tree knock out sorting stable?

- Design an imperative tournament tree knock out sort algorithm, which satisfies the following:
 - Can handle arbitrary number of elements;
 - Without using hard coded negative infinity, so that it can take elements with any value.
- Compare the tournament tree knock out sort algorithm and binary tree sort algorithm, analyze efficiency both in time and space.
- Compare the heap sort algorithm and binary tree sort algorithm, and do same analysis for them.

9.4.2 Final improvement by using heap sort

We manage improving the performance of selection based sorting to $O(n \lg n)$ by using tournament knock out. This is the limit of comparison based sort according to [51]. However, there are still rooms for improvement. After sorting, there lefts a complete binary tree with all leaves and branches hold useless infinite values. This isn't space efficient at all. Can we release the nodes when popping?

Another observation is that if there are n elements to be sorted, we actually allocate about $2n$ tree nodes. n for leaves and n for branches. Is there any better way to halve the space usage?

The final sorting structure described in equation 9.19 can be easily uniformed to a more general one if we treat the case that the tree is empty if its root holds infinity as key:

$$sort'(T) = \begin{cases} \phi & : T = \phi \\ \{top(T)\} \cup sort'(pop(T)) & : otherwise \end{cases} \quad (9.20)$$

This is exactly as same as the one of heap sort we gave in previous chapter. Heap always keeps the minimum (or the maximum) on the top, and provides fast pop operation. The binary heap by implicit array encodes the tree structure in array index, so there aren't any extra spaces allocated except for the n array cells. The functional heaps, such as leftist heap and splay heap allocate n nodes as well. We'll introduce more heaps in next chapter which perform well in many aspects.

9.5 Short summary

In this chapter, we present the evolution process of selection based sort. selection sort is easy and commonly used as example to teach students about embedded looping. It has simple and straightforward structure, but the performance is quadratic. In this chapter, we do see that there exists ways to improve it not only by some fine tuning, but also fundamentally change the data structure, which leads to tournament knock out and heap sort.

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Chapter 10

Binomial heap, Fibonacci heap, and pairing heap

10.1 Introduction

In previous chapter, we mentioned that heaps can be generalized and implemented with varies of data structures. However, only binary heaps are focused so far no matter by explicit binary trees or implicit array.

It's quite natural to extend the binary tree to K-ary [54] tree. In this chapter, we first show Binomial heaps which is actually consist of forest of K-ary trees. Binomial heaps gain the performance for all operations to $O(\lg n)$, as well as keeping the finding minimum element to $O(1)$ time.

If we delay some operations in Binomial heaps by using lazy strategy, it turns to be Fibonacci heap.

All binary heaps we have shown perform no less than $O(\lg n)$ time for merging, we'll show it's possible to improve it to $O(1)$ with Fibonacci heap, which is quite helpful to graph algorithms. Actually, Fibonacci heap achieves almost all operations to good amortized time bound as $O(1)$, and left the heap pop to $O(\lg n)$.

Finally, we'll introduce about the pairing heaps. It has the best performance in practice although the proof of it is still a conjecture for the time being.

10.2 Binomial Heaps

10.2.1 Definition

Binomial heap is more complex than most of the binary heaps. However, it has excellent merge performance which bound to $O(\lg n)$ time. A binomial heap is consist of a list of binomial trees.

Binomial tree

In order to explain why the name of the tree is 'binomial', let's review the famous Pascal's triangle (Also know as the Jia Xian's triangle to memorize the Chinese methematican Jia Xian (1010-1070).) [55].

1
1 1

1 2 1
 1 3 3 1
 1 4 6 4 1
 ...

In each row, the numbers are all binomial coefficients. There are many ways to gain a series of binomial coefficient numbers. One of them is by using recursive composition. Binomial trees, as well, can be defined in this way as the following.

- A binomial tree of rank 0 has only a node as the root;
- A binomial tree of rank n is consist of two rank $n - 1$ binomial trees, Among these 2 sub trees, the one has the bigger root element is linked as the leftmost child of the other.

We denote a binomial tree of rank 0 as B_0 , and the binomial tree of rank n as B_n . Figure 10.1 shows a B_0 tree and how to link 2 B_{n-1} trees to a B_n tree.

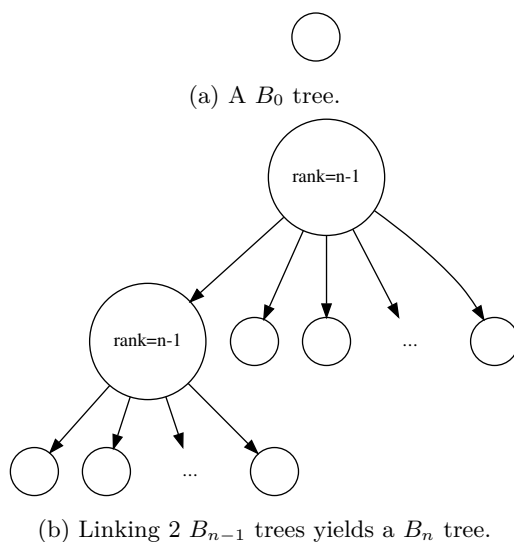


Figure 10.1: Recursive definition of binomial trees

With this recursive definition, it easy to draw the form of binomial trees of rank 0, 1, 2, ..., as shown in figure 10.2

Observing the binomial trees reveals some interesting properties. For each rank n binomial tree, if counting the number of nodes in each row, it can be found that it is the binomial number.

For instance for rank 4 binomial tree, there is 1 node as the root; and in the second level next to root, there are 4 nodes; and in 3rd level, there are 6 nodes; and in 4-th level, there are 4 nodes; and the 5-th level, there is 1 node. They are exactly 1, 4, 6, 4, 1 which is the 5th row in Pascal's triangle. That's why we call it binomial tree.

Another interesting property is that the total number of node for a binomial tree with rank n is 2^n . This can be proved either by binomial theory or the recursive definition directly.

Binomial heap

With binomial tree defined, we can introduce the definition of binomial heap. A binomial heap is a set of binomial trees (or a forest of binomial trees) that satisfied the following

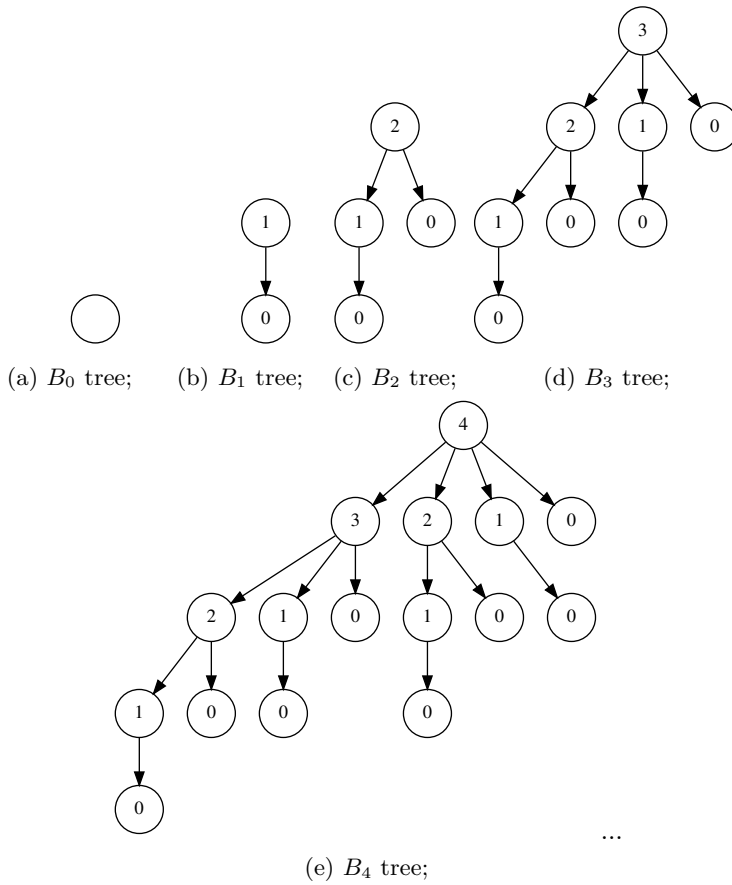


Figure 10.2: Forms of binomial trees with rank = 0, 1, 2, 3, 4, ...

properties.

- Each binomial tree in the heap conforms to *heap property*, that the key of a node is equal or greater than the key of its parent. Here the heap is actually min-heap, for max-heap, it changes to ‘equal or less than’. In this chapter, we only discuss about min-heap, and max-heap can be equally applied by changing the comparison condition.
- There is at most one binomial tree which has the rank r . In other words, there are no two binomial trees have the same rank.

This definition leads to an important result that for a binomial heap contains n elements, and if convert n to binary format yields $a_0, a_1, a_2, \dots, a_m$, where a_0 is the LSB and a_m is the MSB, then for each $0 \leq i \leq m$, if $a_i = 0$, there is no binomial tree of rank i and if $a_i = 1$, there must be a binomial tree of rank i .

For example, if a binomial heap contains 5 element, as 5 is ‘(LSB)101(MSB)’, then there are 2 binomial trees in this heap, one tree has rank 0, the other has rank 2.

Figure 10.3 shows a binomial heap which have 19 nodes, as 19 is ‘(LSB)11001(MSB)’ in binary format, so there is a B_0 tree, a B_1 tree and a B_4 tree.

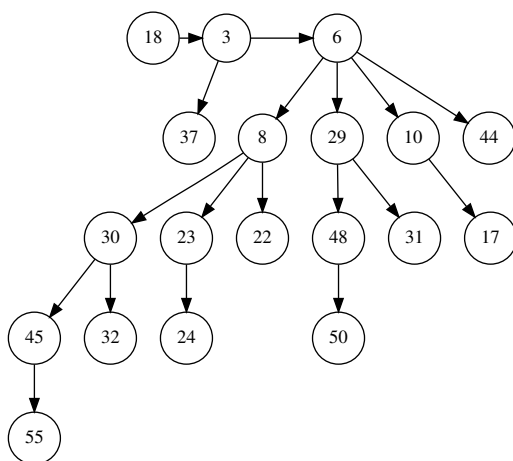


Figure 10.3: A binomial heap with 19 elements

Data layout

There are two ways to define K-ary trees imperatively. One is by using ‘left-child, right-sibling’ approach[4]. It is compatible with the typical binary tree structure. For each node, it has two fields, left field and right field. We use the left field to point to the first child of this node, and use the right field to point to the sibling node of this node. All siblings are represented as a single directional linked list. Figure 10.4 shows an example tree represented in this way.

The other way is to use the library defined collection container, such as array or list to represent all children of a node.

Since the rank of a tree plays very important role, we also defined it as a field.

For ‘left-child, right-sibling’ method, we defined the binomial tree as the following.¹

¹C programs are also provided along with this book.

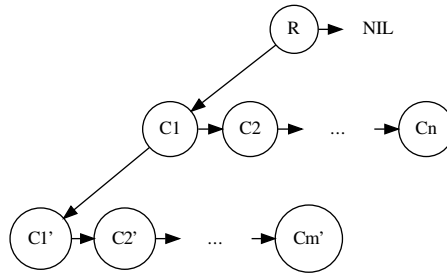


Figure 10.4: Example tree represented in ‘left-child, right-sibling’ way. R is the root node, it has no sibling, so its right side is pointed to NIL . C_1, C_2, \dots, C_n are children of R . C_1 is linked from the left side of R , other siblings of C_1 are linked one next to each other on the right side of C_1 . C'_1, \dots, C'_m are children of C_1 .

```
class BinomialTree:
    def __init__(self, x = None):
        self.rank = 0
        self.key = x
        self.parent = None
        self.child = None
        self.sibling = None
```

When initialize a tree with a key, we create a leaf node, set its rank as zero and all other fields are set as NIL .

It quite nature to utilize pre-defined list to represent multiple children as below.

```
class BinomialTree:
    def __init__(self, x = None):
        self.rank = 0
        self.key = x
        self.parent = None
        self.children = []
```

For purely functional settings, such as in Haskell language, binomial tree are defined as the following.

```
data BiTree a = Node { rank :: Int
                    , root :: a
                    , children :: [BiTree a]}
```

While binomial heap are defined as a list of binomial trees (a forest) with ranks in monotonically increase order. And as another implicit constraint, there are no two binomial trees have the same rank.

```
type BiHeap a = [BiTree a]
```

10.2.2 Basic heap operations

Linking trees

Before dive into the basic heap operations such as pop and insert, We'll first realize how to link two binomial trees with same rank into a bigger one. According to the definition of binomial tree and heap property that the root always contains the minimum key, we firstly compare the two root values, select the smaller one as the new root, and insert the other tree as the first child in front of all other children. Suppose function

$Key(T)$, $Children(T)$, and $Rank(T)$ access the key, children and rank of a binomial tree respectively.

$$link(T_1, T_2) = \begin{cases} node(r+1, x, \{T_2\} \cup C_1) & : x < y \\ node(r+1, y, \{T_1\} \cup C_2) & : otherwise \end{cases} \quad (10.1)$$

Where

$$\begin{aligned} x &= Key(T_1) \\ y &= Key(T_2) \\ r &= Rank(T_1) = Rank(T_2) \\ C_1 &= Children(T_1) \\ C_2 &= Children(T_2) \end{aligned}$$

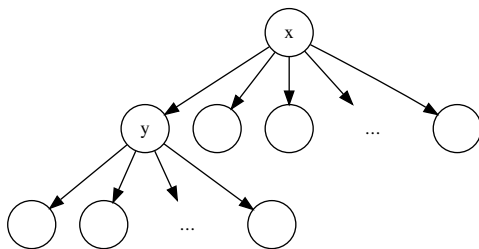


Figure 10.5: Suppose $x < y$, insert y as the first child of x .

Note that the link operation is bound to $O(1)$ time if the \cup is a constant time operation. It's easy to translate the link function to Haskell program as the following.

```
link t1@(Node r x c1) t2@(Node _ y c2) =
  if x < y then Node (r+1) x (t2:c1)
  else Node (r+1) y (t1:c2)
```

It's possible to realize the link operation in imperative way. If we use 'left child, right sibling' approach, we just link the tree which has the bigger key to the left side of the other's key, and link the children of it to the right side as sibling. Figure 10.6 shows the result of one case.

```
1: function LINK( $T_1, T_2$ )
2:   if KEY( $T_2$ ) < KEY( $T_1$ ) then
3:     Exchange  $T_1 \leftrightarrow T_2$ 
4:   SIBLING( $T_2$ ) ← CHILD( $T_1$ )
5:   CHILD( $T_1$ ) ←  $T_2$ 
6:   PARENT( $T_2$ ) ←  $T_1$ 
7:   RANK( $T_1$ ) ← RANK( $T_1$ ) + 1
8:   return  $T_1$ 
```

And if we use a container to manage all children of a node, the algorithm is like below.

```
1: function LINK'( $T_1, T_2$ )
2:   if KEY( $T_2$ ) < KEY( $T_1$ ) then
3:     Exchange  $T_1 \leftrightarrow T_2$ 
4:   PARENT( $T_2$ ) ←  $T_1$ 
5:   INSERT-BEFORE(CHILDREN( $T_1$ ),  $T_2$ )
6:   RANK( $T_1$ ) ← RANK( $T_1$ ) + 1
7:   return  $T_1$ 
```

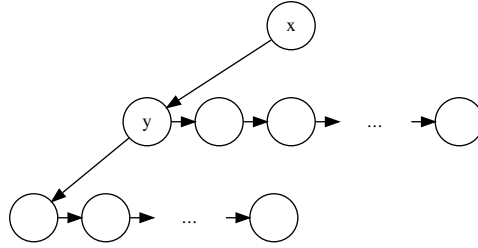


Figure 10.6: Suppose $x < y$, link y to the left side of x and link the original children of x to the right side of y .

It's easy to translate both algorithms to real program. Here we only show the Python program of LINK' for illustration purpose ².

```
def link(t1, t2):
    if t2.key < t1.key:
        (t1, t2) = (t2, t1)
    t2.parent = t1
    t1.children.insert(0, t2)
    t1.rank = t1.rank + 1
    return t1
```

Exercise 10.1

Implement the tree-linking program in your favorite language with left-child, right-sibling method.

We mentioned linking is a constant time algorithm and it is true when using left-child, right-sibling approach. However, if we use container to manage the children, the performance depends on the concrete implementation of the container. If it is plain array, the linking time will be proportion to the number of children. In this chapter, we assume the time is constant. This is true if the container is implemented in linked-list.

Insert a new element to the heap (push)

As the rank of binomial trees in a forest is monotonically increasing, by using the *link* function defined above, it's possible to define an auxiliary function, so that we can insert a new tree, with rank no bigger than the smallest one, to the heap which is a forest actually.

Denote the non-empty heap as $H = \{T_1, T_2, \dots, T_n\}$, we define

$$\text{insert}T(H, T) = \begin{cases} \{T\} & : H = \phi \\ \{T\} \cup H & : \text{Rank}(T) < \text{Rank}(T_1) \\ \text{insert}T(H', \text{link}(T, T_1)) & : \textit{otherwise} \end{cases} \quad (10.2)$$

where

$$H' = \{T_2, T_3, \dots, T_n\}$$

The idea is that for the empty heap, we set the new tree as the only element to create a singleton forest; otherwise, we compare the ranks of the new tree and the first tree in

²The C and C++ programs are also available along with this book

the forest, if they are same, we link them together, and recursively insert the linked result (a tree with rank increased by one) to the rest of the forest; If they are not same, since the pre-condition constraints the rank of the new tree, it must be the smallest, we put this new tree in front of all the other trees in the forest.

From the binomial properties mentioned above, there are at most $O(\lg n)$ binomial trees in the forest, where n is the total number of nodes. Thus function $insertT$ performs at most $O(\lg n)$ times linking, which are all constant time operation. So the performance of $insertT$ is $O(\lg n)$.³

The relative Haskell program is given as below.

```
insertTree [] t = [t]
insertTree ts@(t':ts') t = if rank t < rank t' then t:ts
                          else insertTree ts' (link t t')
```

With this auxiliary function, it's easy to realize the insertion. We can wrap the new element to be inserted as the only leaf of a tree, then insert this tree to the binomial heap.

$$insert(H, x) = insertT(H, node(0, x, \phi)) \quad (10.3)$$

And we can continuously build a heap from a series of elements by folding. For example the following Haskell define a helper function 'fromList'.

```
fromList = foldl insert []
```

Since wrapping an element as a singleton tree takes $O(1)$ time, the real work is done in $insertT$, the performance of binomial heap insertion is bound to $O(\lg n)$.

The insertion algorithm can also be realized with imperative approach.

Algorithm 1 Insert a tree with 'left-child-right-sibling' method.

```
1: function INSERT-TREE( $H, T$ )
2:   while  $H \neq \phi \wedge \text{RANK}(\text{HEAD}(H)) = \text{RANK}(T)$  do
3:      $(T_1, H) \leftarrow \text{EXTRACT-HEAD}(H)$ 
4:      $T \leftarrow \text{LINK}(T, T_1)$ 
5:    $\text{SIBLING}(T) \leftarrow H$ 
6:   return  $T$ 
```

Algorithm 1 continuously linking the first tree in a heap with the new tree to be inserted if they have the same rank. After that, it puts the linked-list of the rest trees as the sibling, and returns the new linked-list.

If using a container to manage the children of a node, the algorithm can be given in Algorithm 2.

Algorithm 2 Insert a tree with children managed by a container.

```
1: function INSERT-TREE'( $H, T$ )
2:   while  $H \neq \phi \wedge \text{RANK}(H[0]) = \text{RANK}(T)$  do
3:      $T_1 \leftarrow \text{POP}(H)$ 
4:      $T \leftarrow \text{LINK}(T, T_1)$ 
5:    $\text{HEAD-INSERT}(H, T)$ 
6:   return  $H$ 
```

³There is interesting observation by comparing this operation with adding two binary numbers. Which will lead to topic of *numeric representation*[3].

In this algorithm, function POP removes the first tree $T_1 = H[0]$ from the forest. And function HEAD-INSERT, insert a new tree before any other trees in the heap, so that it becomes the first element in the forest.

With either INSERT-TREE or INSERT-TREE' defined. Realize the binomial heap insertion is trivial.

Algorithm 3 Imperative insert algorithm

```
1: function INSERT( $H, x$ )
2:   return INSERT-TREE( $H, \text{NODE}(0, x, \phi)$ )
```

The following python program implement the insert algorithm by using a container to manage sub-trees. the 'left-child, right-sibling' program is left as an exercise.

```
def insert_tree(ts, t):
    while ts  $\neq$  [] and t.rank == ts[0].rank:
        t = link(t, ts.pop(0))
    ts.insert(0, t)
    return ts

def insert(h, x):
    return insert_tree(h, BinomialTree(x))
```

Exercise 10.2

Write the insertion program in your favorite imperative programming language by using the 'left-child, right-sibling' approach.

Merge two heaps

When merge two binomial heaps, we actually try to merge two forests of binomial trees. According to the definition, there can't be two trees with the same rank and the ranks are in monotonically increasing order. Our strategy is very similar to merge sort. That in every iteration, we take the first tree from each forest, compare their ranks, and pick the smaller one to the result heap; if the ranks are equal, we then perform linking to get a new tree, and recursively insert this new tree to the result of merging the rest trees.

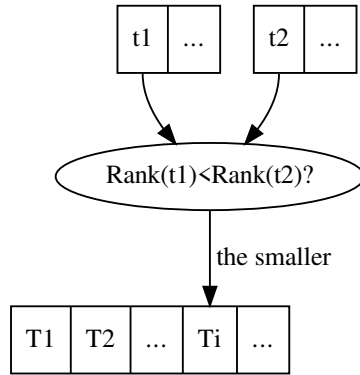
Figure 10.7 illustrates the idea of this algorithm. This method is different from the one given in [4].

We can formalize this idea with a function. For non-empty cases, we denote the two heaps as $H_1 = \{T_1, T_2, \dots\}$ and $H_2 = \{T'_1, T'_2, \dots\}$. Let $H'_1 = \{T_2, T_3, \dots\}$ and $H'_2 = \{T'_2, T'_3, \dots\}$.

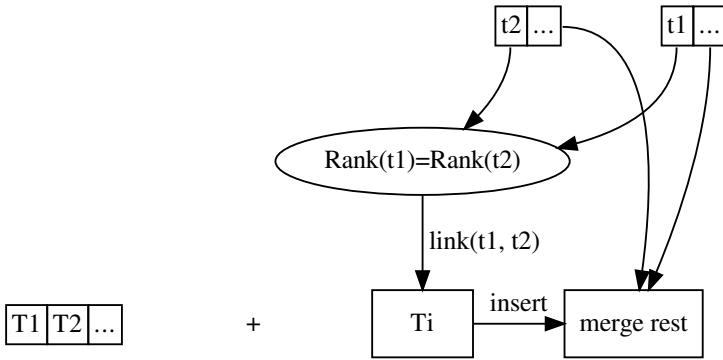
$$\text{merge}(H_1, H_2) = \begin{cases} H_1 & : H_2 = \phi \\ H_2 & : H_1 = \phi \\ \{T_1\} \cup \text{merge}(H'_1, H_2) & : \text{Rank}(T_1) < \text{Rank}(T'_1) \\ \{T'_1\} \cup \text{merge}(H_1, H'_2) & : \text{Rank}(T_1) > \text{Rank}(T'_1) \\ \text{insertT}(\text{merge}(H'_1, H'_2), \text{link}(T_1, T'_1)) & : \text{otherwise} \end{cases} \quad (10.4)$$

To analysis the performance of merge, suppose there are m_1 trees in H_1 , and m_2 trees in H_2 . There are at most $m_1 + m_2$ trees in the merged result. If there are no two trees have the same rank, the merge operation is bound to $O(m_1 + m_2)$. While if there need linking for the trees with same rank, insertT performs at most $O(m_1 + m_2)$ time. Consider the fact that $m_1 = 1 + \lfloor \lg n_1 \rfloor$ and $m_2 = 1 + \lfloor \lg n_2 \rfloor$, where n_1, n_2 are the numbers of nodes in each heap, and $\lfloor \lg n_1 \rfloor + \lfloor \lg n_2 \rfloor \leq 2 \lfloor \lg n \rfloor$, where $n = n_1 + n_2$, is the total number of nodes. the final performance of merging is $O(\lg n)$.

Translating this algorithm to Haskell yields the following program.



(a) Pick the tree with smaller rank to the result.



(b) If two trees have same rank, link them to a new tree, and recursively insert it to the merge result of the rest.

Figure 10.7: Merge two heaps.


```

merge ts1 [] = ts1
merge [] ts2 = ts2
merge ts1@(t1:ts1') ts2@(t2:ts2')
  | rank t1 < rank t2 = t1:(merge ts1' ts2)
  | rank t1 > rank t2 = t2:(merge ts1 ts2')
  | otherwise = insertTree (merge ts1' ts2') (link t1 t2)

```

Merge algorithm can also be described in imperative way as shown in algorithm 4.

Algorithm 4 imperative merge two binomial heaps

```

1: function MERGE( $H_1, H_2$ )
2:   if  $H_1 = \phi$  then
3:     return  $H_2$ 
4:   if  $H_2 = \phi$  then
5:     return  $H_1$ 
6:    $H \leftarrow \phi$ 
7:   while  $H_1 \neq \phi \wedge H_2 \neq \phi$  do
8:      $T \leftarrow \phi$ 
9:     if  $\text{RANK}(H_1) < \text{RANK}(H_2)$  then
10:       $(T, H_1) \leftarrow \text{EXTRACT-HEAD}(H_1)$ 
11:    else if  $\text{RANK}(H_2) < \text{RANK}(H_1)$  then
12:       $(T, H_2) \leftarrow \text{EXTRACT-HEAD}(H_2)$ 
13:    else ▷ Equal rank
14:       $(T_1, H_1) \leftarrow \text{EXTRACT-HEAD}(H_1)$ 
15:       $(T_2, H_2) \leftarrow \text{EXTRACT-HEAD}(H_2)$ 
16:       $T \leftarrow \text{LINK}(T_1, T_2)$ 
17:       $\text{APPEND-TREE}(H, T)$ 
18:    if  $H_1 \neq \phi$  then
19:       $\text{APPEND-TREES}(H, H_1)$ 
20:    if  $H_2 \neq \phi$  then
21:       $\text{APPEND-TREES}(H, H_2)$ 
22:    return  $H$ 

```

Since both heaps contain binomial trees with rank in monotonically increasing order. Each iteration, we pick the tree with smallest rank and append it to the result heap. If both trees have same rank we perform linking first. Consider the APPEND-TREE algorithm, The rank of the new tree to be appended, can't be less than any other trees in the result heap according to our merge strategy, however, it might be equal to the rank of the last tree in the result heap. This can happen if the last tree appended are the result of linking, which will increase the rank by one. In this case, we must link the new tree to be inserted with the last tree. In below algorithm, suppose function $\text{LAST}(H)$ refers to the last tree in a heap, and $\text{APPEND}(H, T)$ just appends a new tree at the end of a forest.

```

1: function APPEND-TREE( $H, T$ )
2:   if  $H \neq \phi \wedge \text{RANK}(T) = \text{RANK}(\text{LAST}(H))$  then
3:      $\text{LAST}(H) \leftarrow \text{LINK}(T, \text{LAST}(H))$ 
4:   else
5:      $\text{APPEND}(H, T)$ 

```

Function APPEND-TREES repeatedly call this function, so that it can append all trees in a heap to the other heap.

```

1: function APPEND-TREES( $H_1, H_2$ )
2:   for each  $T \in H_2$  do

```

3: $H_1 \leftarrow \text{APPEND-TREE}(H_1, T)$

The following Python program translates the merge algorithm.

```

def append_tree(ts, t):
    if ts != [] and ts[-1].rank == t.rank:
        ts[-1] = link(ts[-1], t)
    else:
        ts.append(t)
    return ts

def append_trees(ts1, ts2):
    return reduce(append_tree, ts2, ts1)

def merge(ts1, ts2):
    if ts1 == []:
        return ts2
    if ts2 == []:
        return ts1
    ts = []
    while ts1 != [] and ts2 != []:
        t = None
        if ts1[0].rank < ts2[0].rank:
            t = ts1.pop(0)
        elif ts2[0].rank < ts1[0].rank:
            t = ts2.pop(0)
        else:
            t = link(ts1.pop(0), ts2.pop(0))
        ts = append_tree(ts, t)
    ts = append_trees(ts, ts1)
    ts = append_trees(ts, ts2)
    return ts

```

Exercise 10.3

The program given above uses a container to manage sub-trees. Implement the merge algorithm in your favorite imperative programming language with ‘left-child, right-sibling’ approach.

Pop

Among the forest which forms the binomial heap, each binomial tree conforms to heap property that the root contains the minimum element in that tree. However, the order relationship of these roots can be arbitrary. To find the minimum element in the heap, we can select the smallest root of these trees. Since there are $\lg n$ binomial trees, this approach takes $O(\lg n)$ time.

However, after we locate the minimum element (which is also know as the top element of a heap), we need remove it from the heap and keep the binomial property to accomplish heap-pop operation. Suppose the forest forms the binomial heap consists trees of $B_i, B_j, \dots, B_p, \dots, B_m$, where B_k is a binomial tree of rank k , and the minimum element is the root of B_p . If we delete it, there will be p children left, which are all binomial trees with ranks $p-1, p-2, \dots, 0$.

One tool at hand is that we have defined $O(\lg n)$ merge function. A possible approach is to reverse the p children, so that their ranks change to monotonically increasing order, and forms a binomial heap H_p . The rest of trees is still a binomial heap, we represent it as $H' = H - B_p$. Merging H_p and H' given the final result of pop. Figure 10.8 illustrates this idea.

In order to realize this algorithm, we first need to define an auxiliary function, which

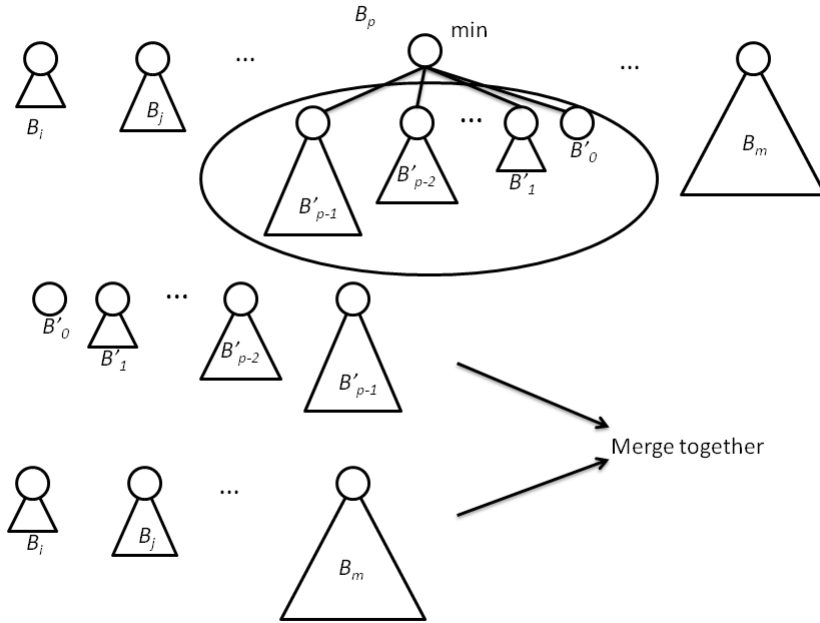


Figure 10.8: Pop the minimum element from a binomial heap.

can extract the tree contains the minimum element at root from the forest.

$$extractMin(H) = \begin{cases} (T, \phi) & : H \text{ is a singleton as } \{T\} \\ (T_1, H') & : Root(T_1) < Root(T') \\ (T', \{T_1\} \cup H'') & : otherwise \end{cases} \quad (10.5)$$

where

$$\begin{aligned} H &= \{T_1, T_2, \dots\} && \text{for the non-empty forest case;} \\ H' &= \{T_2, T_3, \dots\} && \text{is the forest without the first tree;} \\ (T', H'') &= extractMin(H') \end{aligned}$$

The result of this function is a tuple. The first part is the tree which has the minimum element at root, the second part is the rest of the trees after remove the first part from the forest.

This function examine each of the trees in the forest thus is bound to $O(\lg n)$ time.

The relative Haskell program can be give respectively.

```
extractMin [t] = (t, [])
extractMin (t:ts) = if root t < root t' then (t, ts)
                  else (t', t:ts')
  where
    (t', ts') = extractMin ts
```

With this function defined, to return the minimum element is trivial.

```
findMin = root o fst o extractMin
```

Of course, it's possible to just traverse forest and pick the minimum root without remove the tree for this purpose. Below imperative algorithm describes it with 'left child, right sibling' approach.

```

1: function FIND-MINIMUM( $H$ )
2:    $T \leftarrow \text{HEAD}(H)$ 
3:    $min \leftarrow \infty$ 
4:   while  $T \neq \phi$  do
5:     if  $\text{KEY}(T) < min$  then
6:        $min \leftarrow \text{KEY}(T)$ 
7:        $T \leftarrow \text{SIBLING}(T)$ 
8:   return  $min$ 

```

While if we manage the children with collection containers, the link list traversing is abstracted as to find the minimum element among the list. The following Python program shows about this situation.

```

def find_min(ts):
    min_t = min(ts, key=lambda t: t.key)
    return min_t.key

```

Next we define the function to delete the minimum element from the heap by using *extractMin*.

$$\text{delteMin}(H) = \text{merge}(\text{reverse}(\text{Children}(T)), H') \quad (10.6)$$

where

$$(T, H') = \text{extractMin}(H)$$

Translate the formula to Haskell program is trivial and we'll skip it.

To realize the algorithm in procedural way takes extra efforts including list reversing etc. We left these details as exercise to the reader. The following pseudo code illustrate the imperative pop algorithm

```

1: function EXTRACT-MIN( $H$ )
2:    $(T_{min}, H) \leftarrow \text{EXTRACT-MIN-TREE}(H)$ 
3:    $H \leftarrow \text{MERGE}(H, \text{REVERSE}(\text{CHILDREN}(T_{min})))$ 
4:   return  $(\text{KEY}(T_{min}), H)$ 

```

With pop operation defined, we can realize heap sort by creating a binomial heap from a series of numbers, than keep popping the smallest number from the heap till it becomes empty.

$$\text{sort}(xs) = \text{heapSort}(\text{fromList}(xs)) \quad (10.7)$$

And the real work is done in function *heapSort*.

$$\text{heapSort}(H) = \begin{cases} \phi & : H = \phi \\ \{\text{findMin}(H)\} \cup \text{heapSort}(\text{deleteMin}(H)) & : \text{otherwise} \end{cases} \quad (10.8)$$

Translate to Haskell yields the following program.

```

heapSort = hsort o fromList where
    hsort [] = []
    hsort h = (findMin h):(hsort $ deleteMin h)

```

Function fromList can be defined by folding. Heap sort can also be expressed in procedural way respectively. Please refer to previous chapter about binary heap for detail.

Exercise 10.4

- Write the program to return the minimum element from a binomial heap in your favorite imperative programming language with 'left-child, right-sibling' approach.
- Realize the `EXTRACT-MIN-TREE()` Algorithm.
- For 'left-child, right-sibling' approach, reversing all children of a tree is actually reversing a single-direct linked-list. Write a program to reverse such linked-list in your favorite imperative programming language.

More words about binomial heap

As what we have shown that insertion and merge are bound to $O(\lg n)$ time. The results are all ensure for the *worst case*. The amortized performance are $O(1)$. We skip the proof for this fact.

10.3 Fibonacci Heaps

It's interesting that why the name is given as 'Fibonacci heap'. In fact, there is no direct connection from the structure design to Fibonacci series. The inventors of 'Fibonacci heap', Michael L. Fredman and Robert E. Tarjan, utilized the property of Fibonacci series to prove the performance time bound, so they decided to use Fibonacci to name this data structure.[4]

10.3.1 Definition

Fibonacci heap is essentially a lazy evaluated binomial heap. Note that, it doesn't mean implementing binomial heap in lazy evaluation settings, for instance Haskell, brings Fibonacci heap automatically. However, lazy evaluation setting does help in realization. For example in [56], presents a elegant implementation.

Fibonacci heap has excellent performance theoretically. All operations except for pop are bound to amortized $O(1)$ time. In this section, we'll give an algorithm different from some popular textbook[4]. Most of the ideas present here are based on Okasaki's work[57].

Let's review and compare the performance of binomial heap and Fibonacci heap (more precisely, the performance goal of Fibonacci heap).

operation	Binomial heap	Fibonacci heap
insertion	$O(\lg n)$	$O(1)$
merge	$O(\lg n)$	$O(1)$
top	$O(\lg n)$	$O(1)$
pop	$O(\lg n)$	amortized $O(\lg n)$

Consider where is the bottleneck of inserting a new element x to binomial heap. We actually wrap x as a singleton leaf and insert this tree into the heap which is actually a forest.

During this operation, we inserted the tree in monotonically increasing order of rank, and once the rank is equal, recursively linking and inserting will happen, which lead to the $O(\lg n)$ time.

As the lazy strategy, we can postpone the ordered-rank insertion and merging operations. On the contrary, we just put the singleton leaf to the forest. The problem is that when we try to find the minimum element, for example the top operation, the performance will be bad, because we need check all trees in the forest, and there aren't only $O(\lg n)$ trees.

In order to locate the top element in constant time, we must remember where is the tree contains the minimum element as root.

Based on this idea, we can reuse the definition of binomial tree and give the definition of Fibonacci heap as the following Haskell program for example.

```
data BiTree a = Node { rank :: Int
                      , root :: a
                      , children :: [BiTree a]}
```

The Fibonacci heap is either empty or a forest of binomial trees with the minimum element stored in a special one explicitly.

```
data FibHeap a = E | FH { size :: Int
                        , minTree :: BiTree a
                        , trees :: [BiTree a]}
```

For convenient purpose, we also add a size field to record how many elements are there in a heap.

The data layout can also be defined in imperative way as the following ANSI C code.

```
struct node{
  Key key;
  struct node *next, *prev, *parent, *children;
  int degree; /* As known as rank */
  int mark;
};

struct FibHeap{
  struct node *roots;
  struct node *minTr;
  int n; /* number of nodes */
};
```

For generality, Key can be a customized type, we use integer for illustration purpose.

```
typedef int Key;
```

In this chapter, we use the circular doubly linked-list for imperative settings to realize the Fibonacci Heap as described in [4]. It makes many operations easy and fast. Note that, there are two extra fields added. A *degree*, also known as *rank* for a node is the number of children of this node; Flag *mark* is used only in decreasing key operation. It will be explained in detail in later section.

10.3.2 Basic heap operations

As we mentioned that Fibonacci heap is essentially binomial heap implemented in a lazy evaluation strategy, we'll reuse many algorithms defined for binomial heap.

Insert a new element to the heap

Recall the insertion algorithm of binomial tree. It can be treated as a special case of merge operation, that one heap contains only a singleton tree.

$$\mathit{insert}(H, x) = \mathit{merge}(H, \mathit{singleton}(x)) \quad (10.9)$$

where *singleton* is an auxiliary function to wrap an element to a one-leaf-tree.

$$\mathit{singleton}(x) = \mathit{FibHeap}(1, \mathit{node}(1, x, \phi), \phi)$$

Note that function *FibHeap()* accepts three parameters, a size value, which is 1 for this one-leaf-tree, a special tree which contains the minimum element as root, and a list

of other binomial trees in the forest. The meaning of function $node()$ is as same as before, that it creates a binomial tree from a rank, an element, and a list of children.

Insertion can also be realized directly by appending the new node to the forest and updated the record of the tree which contains the minimum element.

```

1: function INSERT( $H, k$ )
2:    $x \leftarrow \text{SINGLETON}(k)$  ▷ Wrap  $x$  to a node
3:   append  $x$  to root list of  $H$ 
4:   if  $T_{min}(H) = \text{NIL} \vee k < \text{KEY}(T_{min}(H))$  then
5:      $T_{min}(H) \leftarrow x$ 
6:    $N(H) \leftarrow N(H)+1$ 

```

Where function $T_{min}()$ returns the tree which contains the minimum element at root. The following C source snippet is a translation for this algorithm.

```

struct FibHeap* insert_node(struct FibHeap* h, struct node* x){
  h = add_tree(h, x);
  if(h->minTr == NULL || x->key < h->minTr->key)
    h->minTr = x;
  h->n++;
  return h;
}

```

Exercise 10.5

Implement the insert algorithm in your favorite imperative programming language completely. This is also an exercise to circular doubly linked list manipulation.

Merge two heaps

Different with the merging algorithm of binomial heap, we post-pone the linking operations later. The idea is to just put all binomial trees from each heap together, and choose one special tree which record the minimum element for the result heap.

$$\text{merge}(H_1, H_2) = \begin{cases} H_1 & : H_2 = \phi \\ H_2 & : H_1 = \phi \\ \text{FibHeap}(s_1 + s_2, T_{1min}, \{T_{2min}\} \cup \mathbb{T}_1 \cup \mathbb{T}_2) & : \text{root}(T_{1min}) < \text{root}(T_{2min}) \\ \text{FibHeap}(s_1 + s_2, T_{2min}, \{T_{1min}\} \cup \mathbb{T}_1 \cup \mathbb{T}_2) & : \text{otherwise} \end{cases} \quad (10.10)$$

where s_1 and s_2 are the size of H_1 and H_2 ; T_{1min} and T_{2min} are the special trees with minimum element as root in H_1 and H_2 respectively; $\mathbb{T}_1 = \{T_{11}, T_{12}, \dots\}$ is a forest contains all other binomial trees in H_1 ; while \mathbb{T}_2 has the same meaning as \mathbb{T}_1 except that it represents the forest in H_2 . Function $root(T)$ return the root element of a binomial tree.

Note that as long as the \cup operation takes constant time, these $merge$ algorithm is bound to $O(1)$. The following Haskell program is the translation of this algorithm.

```

merge h E = h
merge E h = h
merge h1@(FH sz1 minTr1 ts1) h2@(FH sz2 minTr2 ts2)
  | root minTr1 < root minTr2 = FH (sz1+sz2) minTr1 (minTr2:ts2++ts1)
  | otherwise = FH (sz1+sz2) minTr2 (minTr1:ts1++ts2)

```

Merge algorithm can also be realized imperatively by concatenating the root lists of the two heaps.

```

1: function MERGE( $H_1, H_2$ )
2:    $H \leftarrow \Phi$ 

```

```

3:   ROOT( $H$ )  $\leftarrow$  CONCAT(ROOT( $H_1$ ), ROOT( $H_2$ ))
4:   if KEY( $T_{min}(H_1)$ ) < KEY( $T_{min}(H_2)$ ) then
5:      $T_{min}(H) \leftarrow T_{min}(H_1)$ 
6:   else
7:      $T_{min}(H) \leftarrow T_{min}(H_2)$ 
      $N(H) = N(H_1) + N(H_2)$ 
8:   return  $H$ 

```

This function assumes neither H_1 , nor H_2 is empty. And it's easy to add handling to these special cases as the following ANSI C program.

```

struct FibHeap* merge(struct FibHeap* h1, struct FibHeap* h2){
  struct FibHeap* h;
  if(is_empty(h1))
    return h2;
  if(is_empty(h2))
    return h1;
  h = empty();
  h→roots = concat(h1→roots, h2→roots);
  if(h1→minTr→key < h2→minTr→key)
    h→minTr = h1→minTr;
  else
    h→minTr = h2→minTr;
  h→n = h1→n + h2→n;
  free(h1);
  free(h2);
  return h;
}

```

With *merge* function defined, the $O(1)$ insertion algorithm is realized as well. And we can also give the $O(1)$ time top function as below.

$$top(H) = root(T_{min}) \quad (10.11)$$

Exercise 10.6

Implement the circular doubly linked list concatenation function in your favorite imperative programming language.

Extract the minimum element from the heap (pop)

The pop operation is the most complex one in Fibonacci heap. Since we postpone the tree consolidation in merge algorithm. We have to compensate it somewhere. Pop is the only place left as we have defined, insert, merge, top already.

There is an elegant procedural algorithm to do the tree consolidation by using an auxiliary array[4]. We'll show it later in imperative approach section.

In order to realize the purely functional consolidation algorithm, let's first consider a similar number puzzle.

Given a list of numbers, such as $\{2, 1, 1, 4, 8, 1, 1, 2, 4\}$, we want to add any two values if they are same. And repeat this procedure till all numbers are unique. The result of the example list should be $\{8, 16\}$ for instance.

One solution to this problem will as the following.

$$consolidate(L) = fold(meld, \phi, L) \quad (10.12)$$

Where *fold()* function is defined to iterate all elements from a list, applying a specified function to the intermediate result and each element. it is sometimes called as *reducing*. Please refer to Appendix A and the chapter of binary search tree for it.

Table 10.1: Steps of consolidate numbers

number	intermediate result	result
2	2	2
1	1, 2	1, 2
1	(1+1), 2	4
4	(4+4)	8
8	(8+8)	16
1	1, 16	1, 16
1	(1+1), 16	2, 16
2	(2+2), 16	4, 16
4	(4+4), 16	8, 16

$L = \{x_1, x_2, \dots, x_n\}$, denotes a list of numbers; and we'll use $L' = \{x_2, x_3, \dots, x_n\}$ to represent the rest of the list with the first element removed. Function $meld()$ is defined as below.

$$meld(L, x) = \begin{cases} \{x\} & : L = \phi \\ meld(L', x + x_1) & : x = x_1 \\ \{x\} \cup L & : x < x_1 \\ \{x_1\} \cup meld(L', x) & : otherwise \end{cases} \quad (10.13)$$

The *consolidate()* function works as the follows. It maintains an ordered result list L , contains only unique numbers, which is initialized from an empty list ϕ . Each time it process an element x , it firstly check if the first element in L is equal to x , if so, it will add them together (which yields $2x$), and repeatedly check if $2x$ is equal to the next element in L . This process won't stop until either the element to be melt is not equal to the head element in the rest of the list, or the list becomes empty. Table 10.1 illustrates the process of consolidating number sequence $\{2, 1, 1, 4, 8, 1, 1, 2, 4\}$. Column one lists the number 'scanned' one by one; Column two shows the intermediate result, typically the new scanned number is compared with the first number in result list. If they are equal, they are enclosed in a pair of parentheses; The last column is the result of meld, and it will be used as the input to next step processing.

The Haskell program can be give accordingly.

```
consolidate = foldl meld [] where
  meld [] x = [x]
  meld (x':xs) x | x == x' = meld xs (x+x')
                 | x < x'  = x:x':xs
                 | otherwise = x': meld xs x
```

We'll analyze the performance of consolidation as a part of pop operation in later section.

The tree consolidation is very similar to this algorithm except it performs based on rank. The only thing we need to do is to modify $meld()$ function a bit, so that it compare on ranks and do linking instead of adding.

$$meld(L, x) = \begin{cases} \{x\} & : L = \phi \\ meld(L', link(x, x_1)) & : rank(x) = rank(x_1) \\ \{x\} \cup L & : rank(x) < rank(x_1) \\ \{x_1\} \cup meld(L', x) & : otherwise \end{cases} \quad (10.14)$$

The final consolidate Haskell program changes to the below version.

```
consolidate = foldl meld [] where
```

meld [] t = [t]	
meld (t':ts) t	rank t == rank t' = meld ts (link t t')
	rank t < rank t' = t:t':ts
	otherwise = t' : meld ts t

Figure 10.9 and 10.10 show the steps of consolidation when processing a Fibonacci Heap contains different ranks of trees. Comparing with table 10.1 reveals the similarity.

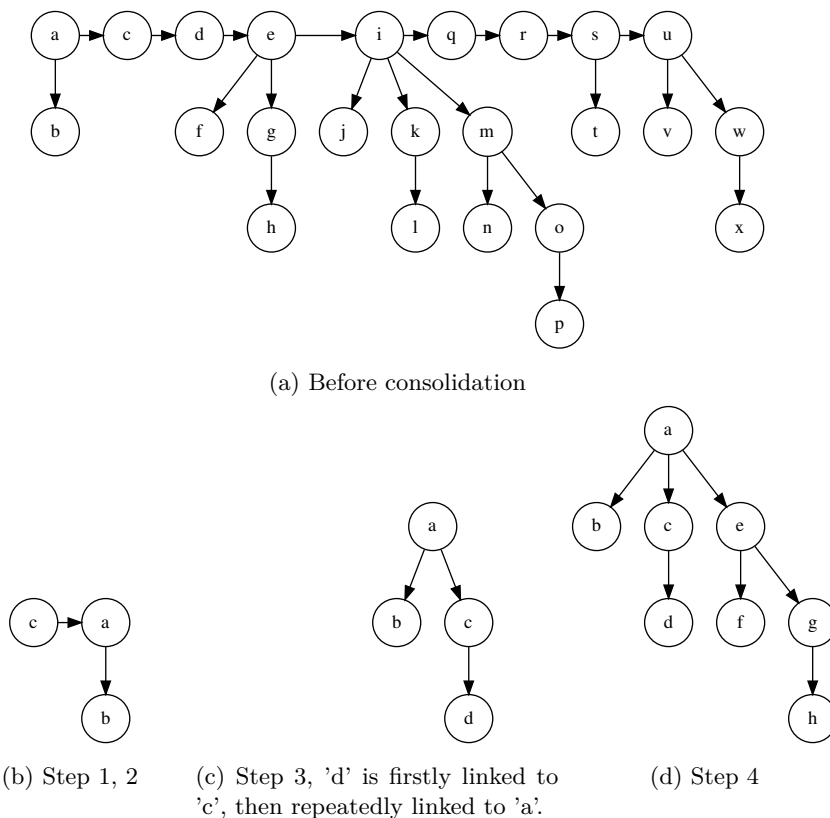


Figure 10.9: Steps of consolidation

After we merge all binomial trees, including the special tree record for the minimum element in root, in a Fibonacci heap, the heap becomes a Binomial heap. And we lost the special tree, which gives us the ability to return the top element in $O(1)$ time.

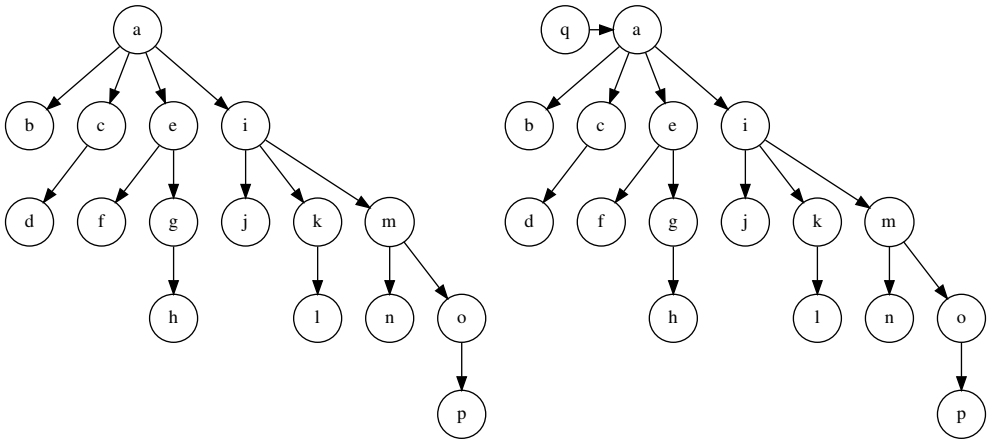
It's necessary to perform a $O(\lg n)$ time search to resume the special tree. We can reuse the function *extractMin()* defined for Binomial heap.

It's time to give the final pop function for Fibonacci heap as all the sub problems have been solved. Let T_{min} denote the special tree in the heap to record the minimum element in root; \mathbb{T} denote the forest contains all the other trees except for the special tree, s represents the size of a heap, and function *children()* returns all sub trees except the root of a binomial tree.

$$deleteMin(H) = \begin{cases} \phi & : \mathbb{T} = \phi \wedge children(T_{min}) = \phi \\ FibHeap(s-1, T'_{min}, \mathbb{T}') & : otherwise \end{cases} \quad (10.15)$$

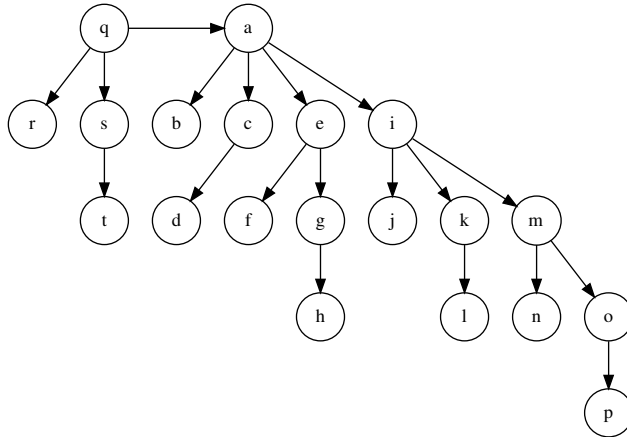
Where

$$(T'_{min}, \mathbb{T}') = extractMin(consolidate(children(T_{min}) \cup \mathbb{T}))$$



(a) Step 5

(b) Step 6



(c) Step 7, 8, 'r' is firstly linked to 'q', then 's' is linked to 'q'.

Figure 10.10: Steps of consolidation

Translate to Haskell yields the below program.

```
deleteMin (FH _ (Node _ x []) []) = E
deleteMin h@(FH sz minTr ts) = FH (sz-1) minTr' ts' where
    (minTr', ts') = extractMin $ consolidate (children minTr ++ ts)
```

The main part of the imperative realization is similar. We cut all children of T_{min} and append them to root list, then perform consolidation to merge all trees with the same rank until all trees are unique in term of rank.

```
1: function DELETE-MIN( $H$ )
2:    $x \leftarrow T_{min}(H)$ 
3:   if  $x \neq NIL$  then
4:     for each  $y \in \text{CHILDREN}(x)$  do
5:       append  $y$  to root list of  $H$ 
6:       PARENT( $y$ )  $\leftarrow NIL$ 
7:     remove  $x$  from root list of  $H$ 
8:      $N(H) \leftarrow N(H) - 1$ 
9:     CONSOLIDATE( $H$ )
10:  return  $x$ 
```

Algorithm CONSOLIDATE utilizes an auxiliary array A to do the merge job. Array $A[i]$ is defined to store the tree with rank (degree) i . During the traverse of root list, if we meet another tree of rank i , we link them together to get a new tree of rank $i + 1$. Next we clean $A[i]$, and check if $A[i + 1]$ is empty and perform further linking if necessary. After we finish traversing all roots, array A stores all result trees and we can re-construct the heap from it.

```
1: function CONSOLIDATE( $H$ )
2:    $D \leftarrow \text{MAX-DEGREE}(N(H))$ 
3:   for  $i \leftarrow 0$  to  $D$  do
4:      $A[i] \leftarrow NIL$ 
5:   for each  $x \in \text{root list of } H$  do
6:     remove  $x$  from root list of  $H$ 
7:      $d \leftarrow \text{DEGREE}(x)$ 
8:     while  $A[d] \neq NIL$  do
9:        $y \leftarrow A[d]$ 
10:       $x \leftarrow \text{LINK}(x, y)$ 
11:       $A[d] \leftarrow NIL$ 
12:       $d \leftarrow d + 1$ 
13:     $A[d] \leftarrow x$ 
14:     $T_{min}(H) \leftarrow NIL$  ▷ root list is NIL at the time
15:    for  $i \leftarrow 0$  to  $D$  do
16:      if  $A[i] \neq NIL$  then
17:        append  $A[i]$  to root list of  $H$ .
18:        if  $T_{min} = NIL \vee \text{KEY}(A[i]) < \text{KEY}(T_{min}(H))$  then
19:           $T_{min}(H) \leftarrow A[i]$ 
```

The only unclear sub algorithm is MAX-DEGREE, which can determine the upper bound of the degree of any node in a Fibonacci Heap. We'll delay the realization of it to the last sub section.

Feed a Fibonacci Heap shown in Figure 10.9 to the above algorithm, Figure 10.11, 10.12 and 10.13 show the result trees stored in auxiliary array A in every steps.

Translate the above algorithm to ANSI C yields the below program.

```
void consolidate(struct FibHeap* h){
```

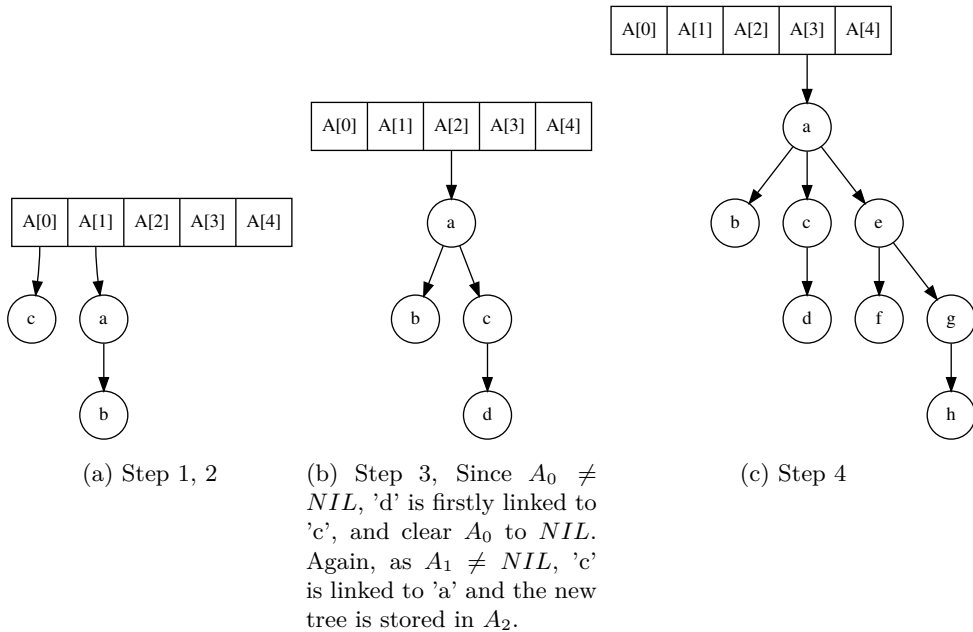


Figure 10.11: Steps of consolidation

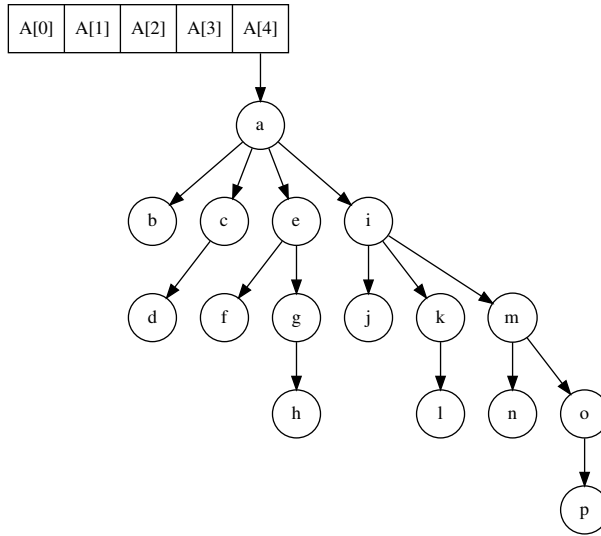
```

if(!h→roots)
    return;
int D = max_degree(h→n)+1;
struct node *x, *y;
struct node** a = (struct node**)malloc(sizeof(struct node*)*(D+1));
int i, d;
for(i=0; i≤D; ++i)
    a[i] = NULL;
while(h→roots){
    x = h→roots;
    h→roots = remove_node(h→roots, x);
    d = x→degree;
    while(a[d]){
        y = a[d]; /* Another node has the same degree as x */
        x = link(x, y);
        a[d++] = NULL;
    }
    a[d] = x;
}
h→minTr = h→roots = NULL;
for(i=0; i≤D; ++i)
    if(a[i]){
        h→roots = append(h→roots, a[i]);
        if(h→minTr == NULL || a[i]→key < h→minTr→key)
            h→minTr = a[i];
    }
free(a);
}

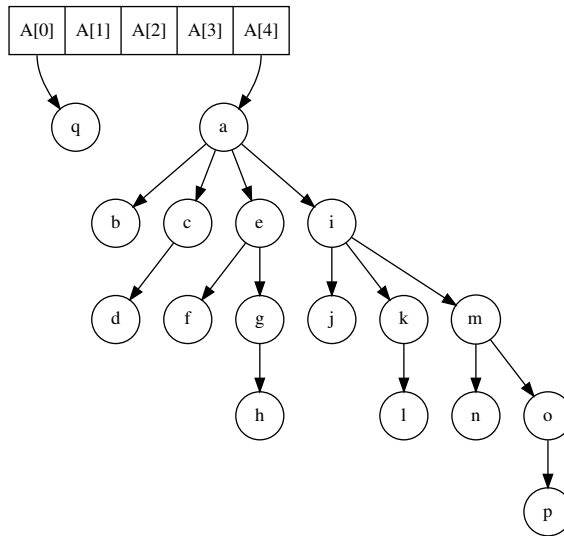
```

Exercise 10.7

Implement the remove function for circular doubly linked list in your favorite imperative programming language.

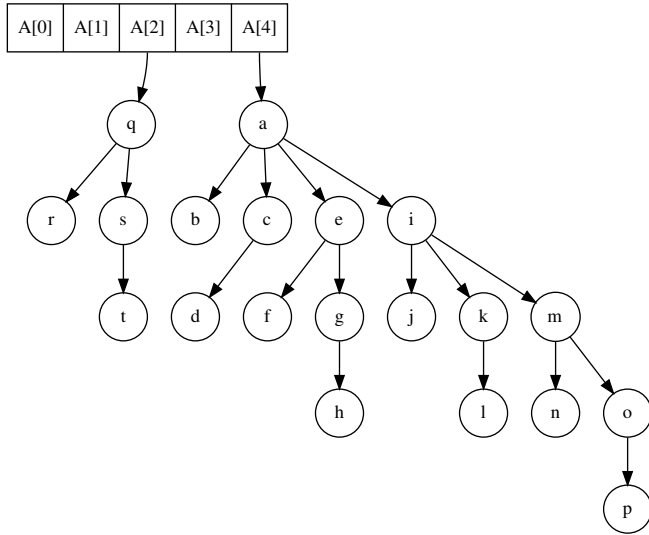


(a) Step 5



(b) Step 6

Figure 10.12: Steps of consolidation



(a) Step 7, 8, Since $A_0 \neq NIL$, 'r' is firstly linked to 'q', and the new tree is stored in A_1 (A_0 is cleared); then 's' is linked to 'q', and stored in A_2 (A_1 is cleared).

Figure 10.13: Steps of consolidation

10.3.3 Running time of pop

In order to analyze the amortize performance of pop, we adopt potential method. Reader can refer to [4] for a formal definition. In this chapter, we only give a intuitive illustration.

Remind the gravity potential energy, which is defined as

$$E = M \cdot g \cdot h$$

Suppose there is a complex process, which moves the object with mass M up and down, and finally the object stop at height h' . And if there exists friction resistance W_f , We say the process works the following power.

$$W = M \cdot g \cdot (h' - h) + W_f$$

Figure 10.14 illustrated this concept.

We treat the Fibonacci heap pop operation in a similar way, in order to evaluate the cost, we firstly define the potential $\Phi(H)$ before extract the minimum element. This potential is accumulated by insertion and merge operations executed so far. And after tree consolidation and we get the result H' , we then calculate the new potential $\Phi(H')$. The difference between $\Phi(H')$ and $\Phi(H)$ plus the contribution of consolidate algorithm indicates the amortized performance of pop.

For pop operation analysis, the potential can be defined as

$$\Phi(H) = t(H) \tag{10.16}$$

Where $t(H)$ is the number of trees in Fibonacci heap forest. We have $t(H) = 1 + length(\mathbb{T})$ for any non-empty heap.

For the n -nodes Fibonacci heap, suppose there is an upper bound of ranks for all trees as $D(n)$. After consolidation, it ensures that the number of trees in the heap forest is at most $D(n) + 1$.

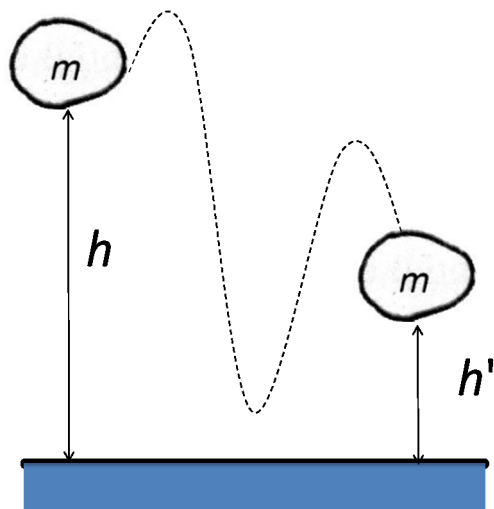


Figure 10.14: Gravity potential energy.

Before consolidation, we actually did another important thing, which also contribute to running time, we removed the root of the minimum tree, and concatenate all children left to the forest. So consolidate operation at most processes $D(n) + t(H) - 1$ trees.

Summarize all the above factors, we deduce the amortized cost as below.

$$\begin{aligned}
 T &= T_{consolidation} + \Phi(H') - \Phi(H) \\
 &= O(D(n) + t(H) - 1) + (D(n) + 1) - t(H) \\
 &= O(D(n))
 \end{aligned} \tag{10.17}$$

If only insertion, merge, and pop function are applied to Fibonacci heap. We ensure that all trees are binomial trees. It is easy to estimate the upper limit $D(n)$ is $O(\lg n)$. (Suppose the extreme case, that all nodes are in only one Binomial tree).

However, we'll show in next sub section that, there is operation can violate the binomial tree assumption.

Exercise 10.8

Why the tree consolidation time is proportion to the number of trees it processed?

10.3.4 Decreasing key

There is a special heap operation left. It only makes sense for imperative settings. It's about decreasing key of a certain node. Decreasing key plays important role in some Graphic algorithms such as Minimum Spanning tree algorithm and Dijkstra's algorithm [4]. In that case we hope the decreasing key takes $O(1)$ amortized time.

However, we can't define a function like $Decrease(H, k, k')$, which first locates a node with key k , then decrease k to k' by replacement, and then resume the heap properties. This is because the time for locating phase is bound to $O(n)$ time, since we don't have a pointer to the target node.

In imperative setting, we can define the algorithm as $DECREASE-KEY(H, x, k)$. Here x is a node in heap H , which we want to decrease its key to k . We needn't perform a search, as we have x at hand. It's possible to give an amortized $O(1)$ solution.

When we decreased the key of a node, if it's not a root, this operation may violate the property Binomial tree that the key of parent is less than all keys of children. So we

need to compare the decreased key with the parent node, and if this case happens, we can cut this node and append it to the root list. (Remind the recursive swapping solution for binary heap which leads to $O(\lg n)$)

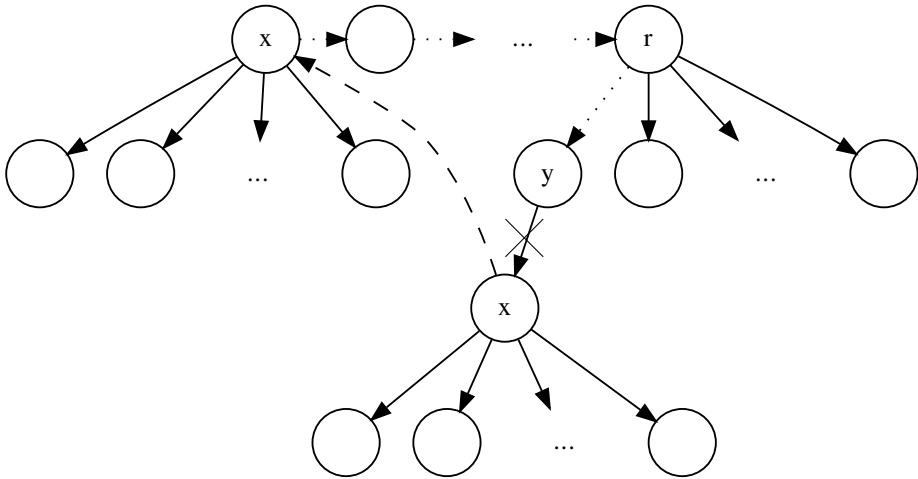


Figure 10.15: $x < y$, cut tree x from its parent, and add x to root list.

Figure 10.15 illustrates this situation. After decreasing key of node x , it is less than y , we cut x off its parent y , and 'past' the whole tree rooted at x to root list.

Although we recover the property of that parent is less than all children, the tree isn't any longer a Binomial tree after it losses some sub tree. If a tree losses too many of its children because of cutting, we can't ensure the performance of merge-able heap operations. Fibonacci Heap adds another constraints to avoid such problem:

If a node losses its second child, it is immediately cut from parent, and added to root list

The final DECREASE-KEY algorithm is given as below.

- 1: **function** DECREASE-KEY(H, x, k)
- 2: KEY(x) $\leftarrow k$
- 3: $p \leftarrow$ PARENT(x)
- 4: **if** $p \neq NIL \wedge k < \text{KEY}(p)$ **then**
- 5: CUT(H, x)
- 6: CASCADING-CUT(H, p)
- 7: **if** $k < \text{KEY}(T_{min}(H))$ **then**
- 8: $T_{min}(H) \leftarrow x$

Where function CASCADING-CUT uses the mark to determine if the node is losing the second child. the node is marked after it losses the first child. And the mark is cleared in CUT function.

- 1: **function** CUT(H, x)
- 2: $p \leftarrow$ PARENT(x)
- 3: remove x from p
- 4: DEGREE(p) \leftarrow DEGREE(p) - 1
- 5: add x to root list of H
- 6: PARENT(x) $\leftarrow NIL$
- 7: MARK(x) $\leftarrow FALSE$

During cascading cut process, if x is marked, which means it has already lost one child. We recursively performs cut and cascading cut on its parent till reach to root.

```

1: function CASCADING-CUT( $H, x$ )
2:    $p \leftarrow$  PARENT( $x$ )
3:   if  $p \neq NIL$  then
4:     if MARK( $x$ ) = FALSE then
5:       MARK( $x$ )  $\leftarrow$  TRUE
6:     else
7:       CUT( $H, x$ )
8:       CASCADING-CUT( $H, p$ )

```

The relevant ANSI C decreasing key program is given as the following.

```

void decrease_key(struct FibHeap* h, struct node* x, Key k){
  struct node* p = x->parent;
  x->key = k;
  if(p && k < p->key){
    cut(h, x);
    cascading_cut(h, p);
  }
  if(k < h->minTr->key)
    h->minTr = x;
}

void cut(struct FibHeap* h, struct node* x){
  struct node* p = x->parent;
  p->children = remove_node(p->children, x);
  p->degree--;
  h->roots = append(h->roots, x);
  x->parent = NULL;
  x->mark = 0;
}

void cascading_cut(struct FibHeap* h, struct node* x){
  struct node* p = x->parent;
  if(p){
    if(!x->mark)
      x->mark = 1;
    else{
      cut(h, x);
      cascading_cut(h, p);
    }
  }
}

```

Exercise 10.9

Prove that DECREASE-KEY algorithm is amortized $O(1)$ time.

10.3.5 The name of Fibonacci Heap

It's time to reveal the reason why the data structure is named as 'Fibonacci Heap'.

There is only one undefined algorithm so far, MAX-DEGREE(n). Which can determine the upper bound of degree for any node in a n nodes Fibonacci Heap. We'll give the proof by using Fibonacci series and finally realize MAX-DEGREE algorithm.

Lemma 10.3.1. *For any node x in a Fibonacci Heap, denote $k = \text{degree}(x)$, and $|x| = \text{size}(x)$, then*

$$|x| \geq F_{k+2} \quad (10.18)$$

Where F_k is Fibonacci series defined as the following.

$$F_k = \begin{cases} 0 & : k = 0 \\ 1 & : k = 1 \\ F_{k-1} + F_{k-2} & : k \geq 2 \end{cases}$$

Proof. Consider all k children of node x , we denote them as y_1, y_2, \dots, y_k in the order of time when they were linked to x . Where y_1 is the oldest, and y_k is the youngest.

Obviously, $|y_i| \geq 0$. When we link y_i to x , children y_1, y_2, \dots, y_{i-1} have already been there. And algorithm LINK only links nodes with the same degree. Which indicates at that time, we have

$$\text{degree}(y_i) = \text{degree}(x) = i - 1$$

After that, node y_i can at most lost 1 child, (due to the decreasing key operation) otherwise, if it will be immediately cut off and append to root list after the second child loss. Thus we conclude

$$\text{degree}(y_i) \geq i - 2$$

For any $i = 2, 3, \dots, k$.

Let s_k be the *minimum possible size* of node x , where $\text{degree}(x) = k$. For trivial cases, $s_0 = 1$, $s_1 = 2$, and we have

$$\begin{aligned} |x| &\geq s_k \\ &= 2 + \sum_{i=2}^k s_{\text{degree}(y_i)} \\ &\geq 2 + \sum_{i=2}^k s_{i-2} \end{aligned}$$

We next show that $s_k > F_{k+2}$. This can be proved by induction. For trivial cases, we have $s_0 = 1 \geq F_2 = 1$, and $s_1 = 2 \geq F_3 = 2$. For induction case $k \geq 2$. We have

$$\begin{aligned} |x| &\geq s_k \\ &\geq 2 + \sum_{i=2}^k s_{i-2} \\ &\geq 2 + \sum_{i=2}^k F_i \\ &= 1 + \sum_{i=0}^k F_i \end{aligned}$$

At this point, we need prove that

$$F_{k+2} = 1 + \sum_{i=0}^k F_i \tag{10.19}$$

This can also be proved by using induction:

- Trivial case, $F_2 = 1 + F_0 = 2$

- Induction case,

$$\begin{aligned}
 F_{k+2} &= F_{k+1} + F_k \\
 &= 1 + \sum_{i=0}^{k-1} F_i + F_k \\
 &= 1 + \sum_{i=0}^k F_i
 \end{aligned}$$

Summarize all above we have the final result.

$$n \geq |x| \geq F_k + 2 \quad (10.20)$$

□

Recall the result of AVL tree, that $F_k \geq \phi^k$, where $\phi = \frac{1+\sqrt{5}}{2}$ is the golden ratio. We also proved that pop operation is amortized $O(\lg n)$ algorithm.

Based on this result. We can define Function *MaxDegree* as the following.

$$\text{MaxDegree}(n) = 1 + \lfloor \log_{\phi} n \rfloor \quad (10.21)$$

The imperative MAX-DEGREE algorithm can also be realized by using Fibonacci sequences.

```

1: function MAX-DEGREE(n)
2:    $F_0 \leftarrow 0$ 
3:    $F_1 \leftarrow 1$ 
4:    $k \leftarrow 2$ 
5:   repeat
6:      $F_k \leftarrow F_{k_1} + F_{k_2}$ 
7:      $k \leftarrow k + 1$ 
8:   until  $F_k < n$ 
9:   return  $k - 2$ 

```

Translate the algorithm to ANSI C given the following program.

```

int max_degree(int n){
  int k, F;
  int F2 = 0;
  int F1 = 1;
  for(F=F1+F2, k=2; F<n; ++k){
    F2 = F1;
    F1 = F;
    F = F1 + F2;
  }
  return k-2;
}

```

10.4 Pairing Heaps

Although Fibonacci Heaps provide excellent performance theoretically, it is complex to realize. People find that the constant behind the big-O is big. Actually, Fibonacci Heap is more significant in theory than in practice.

In this section, we'll introduce another solution, Pairing heap, which is one of the best heaps ever known in terms of performance. Most operations including insertion, finding

minimum element (top), merging are all bounds to $O(1)$ time, while deleting minimum element (pop) is conjectured to amortized $O(\lg n)$ time [58] [3]. Note that this is still a conjecture for 15 years by the time I write this chapter. Nobody has been proven it although there are much experimental data support the $O(\lg n)$ amortized result.

Besides that, pairing heap is simple. There exist both elegant imperative and functional implementations.

10.4.1 Definition

Both Binomial Heaps and Fibonacci Heaps are realized with forest. While a pairing heaps is essentially a K -ary tree. The minimum element is stored at root. All other elements are stored in sub trees.

The following Haskell program defines pairing heap.

```
data PHeap a = E | Node a [PHeap a]
```

This is a recursive definition, that a pairing heap is either empty or a K -ary tree, which is consist of a root node, and a list of sub trees.

Pairing heap can also be defined in procedural languages, for example ANSI C as below. For illustration purpose, all heaps we mentioned later are minimum-heap, and we assume the type of key is integer ⁴. We use same linked-list based left-child, right-sibling approach (aka, binary tree representation[4]).

```
typedef int Key;
struct node{
    Key key;
    struct node *next, *children, *parent;
};
```

Note that the parent field does only make sense for decreasing key operation, which will be explained later on. we can omit it for the time being.

10.4.2 Basic heap operations

In this section, we first give the merging operation for pairing heap, which can be used to realize insertion. Merging, insertion, and finding the minimum element are relative trivial compare to the extracting minimum element operation.

Merge, insert, and find the minimum element (top)

The idea of merging is similar to the linking algorithm we shown previously for Binomial heap. When we merge two pairing heaps, there are two cases.

- Trivial case, one heap is empty, we simply return the other heap as the result;
- Otherwise, we compare the root element of the two heaps, make the heap with bigger root element as a new children of the other.

Let H_1 , and H_2 denote the two heaps, x and y be the root element of H_1 and H_2 respectively. Function *Children()* returns the children of a K -ary tree. Function *Node()*

⁴We can parametrize the key type with C++ template, but this is beyond our scope, please refer to the example programs along with this book

can construct a K-ary tree from a root element and a list of children.

$$\text{merge}(H_1, H_2) = \begin{cases} H_1 & : H_2 = \phi \\ H_2 & : H_1 = \phi \\ \text{Node}(x, \{H_2\} \cup \text{Children}(H_1)) & : x < y \\ \text{Node}(y, \{H_1\} \cup \text{Children}(H_2)) & : \text{otherwise} \end{cases} \quad (10.22)$$

Where

$$\begin{aligned} x &= \text{Root}(H_1) \\ y &= \text{Root}(H_2) \end{aligned}$$

It's obviously that merging algorithm is bound to $O(1)$ time ⁵. The *merge* equation can be translated to the following Haskell program.

```
merge h E = h
merge E h = h
merge h1@(Node x hs1) h2@(Node y hs2) =
  if x < y then Node x (h2:hs1) else Node y (h1:hs2)
```

Merge can also be realized imperatively. With left-child, right sibling approach, we can just link the heap, which is in fact a K-ary tree, with larger key as the first new child of the other. This is constant time operation as described below.

```
1: function MERGE( $H_1, H_2$ )
2:   if  $H_1 = \text{NIL}$  then
3:     return  $H_2$ 
4:   if  $H_2 = \text{NIL}$  then
5:     return  $H_1$ 
6:   if  $\text{KEY}(H_2) < \text{KEY}(H_1)$  then
7:     EXCHANGE( $H_1 \leftrightarrow H_2$ )
8:   Insert  $H_2$  in front of CHILDREN( $H_1$ )
9:   PARENT( $H_2$ )  $\leftarrow H_1$ 
10:  return  $H_1$ 
```

Note that we also update the parent field accordingly. The ANSI C example program is given as the following.

```
struct node* merge(struct node* h1, struct node* h2) {
  if (h1 == NULL)
    return h2;
  if (h2 == NULL)
    return h1;
  if (h2->key < h1->key)
    swap(&h1, &h2);
  h2->next = h1->children;
  h1->children = h2;
  h2->parent = h1;
  h1->next = NULL; /*Break previous link if any*/
  return h1;
}
```

Where function `swap()` is defined in a similar way as Fibonacci Heap.

With merge defined, insertion can be realized as same as Fibonacci Heap in Equation 10.9. Definitely it's $O(1)$ time operation. As the minimum element is always stored in root, finding it is trivial.

$$\text{top}(H) = \text{Root}(H) \quad (10.23)$$

Same as the other two above operations, it's bound to $O(1)$ time.

⁵ Assume \cup is constant time operation, this is true for linked-list settings, including 'cons' like operation in functional programming languages.

Decrease key of a node

There is another operation, to decrease key of a given node, which only makes sense in imperative settings as we explained in Fibonacci Heap section.

The solution is simple, that we can cut the node with the new smaller key from its parent along with all its children. Then merge it again to the heap. The only special case is that if the given node is the root, then we can directly set the new key without doing anything else.

The following algorithm describes this procedure for a given node x , with new key k .

- 1: **function** DECREASE-KEY(H, x, k)
- 2: KEY(x) $\leftarrow k$
- 3: **if** PARENT(x) \neq NIL **then**
- 4: Remove x from CHILDREN(PARENT(x)) PARENT(x) \leftarrow NIL
- 5: **return** MERGE(H, x)
- 6: **return** H

The following ANSI C program translates this algorithm.

```
struct node* decrease_key(struct node* h, struct node* x, Key key) {
  x->key = key; /* Assume key  $\leq$  x->key */
  if(x->parent) {
    x->parent->children = remove_node(x->parent->children, x);
    x->parent = NULL;
    return merge(h, x);
  }
  return h;
}
```

Exercise 10.10

Implement the program of removing a node from the children of its parent in your favorite imperative programming language. Consider how can we ensure the overall performance of decreasing key is $O(1)$ time? Is left-child, right sibling approach enough?

Delete the minimum element from the heap (pop)

Since the minimum element is always stored at root, after delete it during popping, the rest things left are all sub-trees. These trees can be merged to one big tree.

$$\text{pop}(H) = \text{mergePairs}(\text{Children}(H)) \quad (10.24)$$

Pairing Heap uses a special approach that it merges every two sub-trees from left to right in pair. Then merge these paired results from right to left which forms a final result tree. The name of ‘Pairing Heap’ comes from the characteristic of this pair-merging.

Figure 10.16 and 10.17 illustrate the procedure of pair-merging.

The recursive pair-merging solution is quite similar to the bottom up merge sort[3]. Denote the children of a pairing heap as A , which is a list of trees of $\{T_1, T_2, T_3, \dots, T_m\}$ for example. The $\text{mergePairs}()$ function can be given as below.

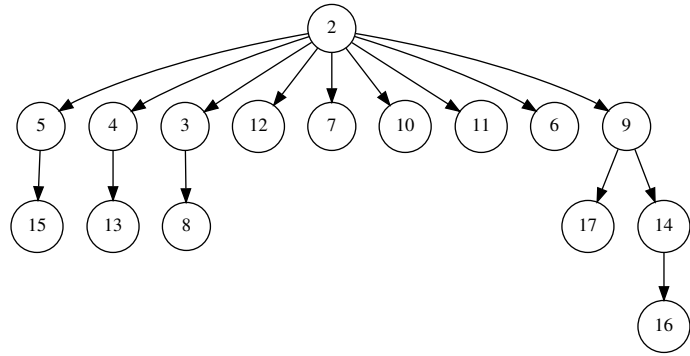
$$\text{mergePairs}(A) = \begin{cases} \Phi & : A = \Phi \\ T_1 & : A = \{T_1\} \\ \text{merge}(\text{merge}(T_1, T_2), \text{mergePairs}(A')) & : \text{otherwise} \end{cases} \quad (10.25)$$

where

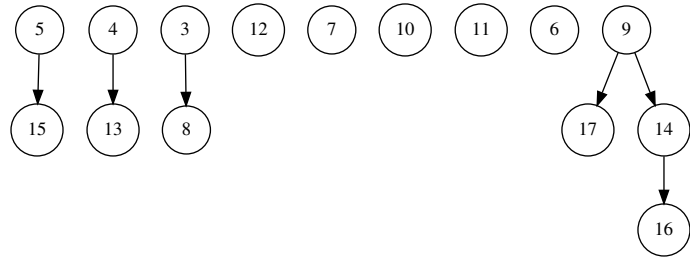
$$A' = \{T_3, T_4, \dots, T_m\}$$

is the rest of the children without the first two trees.

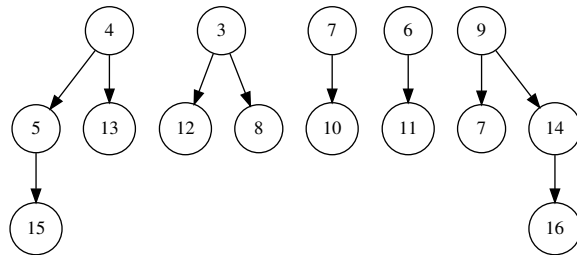
The relative Haskell program of popping is given as the following.



(a) A pairing heap before pop.

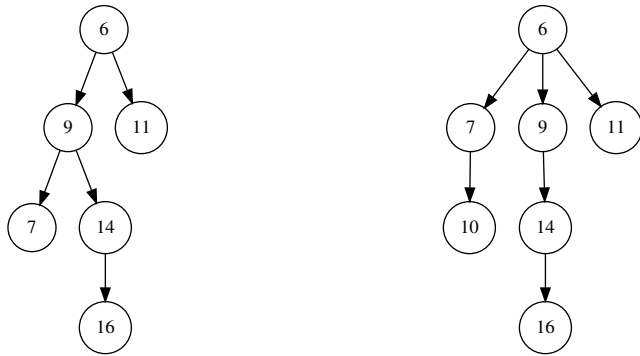


(b) After root element 2 being removed, there are 9 sub-trees left.

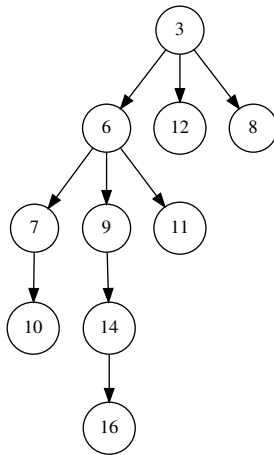


(c) Merge every two trees in pair, note that there are odd number trees, so the last one needn't merge.

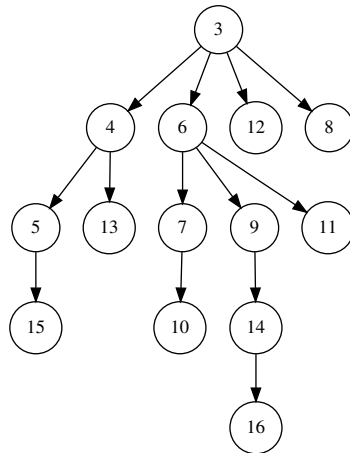
Figure 10.16: Remove the root element, and merge children in pairs.



(a) Merge tree with 9, and tree with root 6. (b) Merge tree with root 7 to the result.



(c) Merge tree with root 3 to the result.



(d) Merge tree with root 4 to the result.

Figure 10.17: Steps of merge from right to left.

```

deleteMin (Node _ hs) = mergePairs hs where
  mergePairs [] = E
  mergePairs [h] = h
  mergePairs (h1:h2:hs) = merge (merge h1 h2) (mergePairs hs)

```

The popping operation can also be explained in the following procedural algorithm.

```

1: function POP( $H$ )
2:    $L \leftarrow NIL$ 
3:   for every 2 trees  $T_x, T_y \in CHILDREN(H)$  from left to right do
4:     Extract  $x$ , and  $y$  from  $CHILDREN(H)$ 
5:      $T \leftarrow MERGE(T_x, T_y)$ 
6:     Insert  $T$  at the beginning of  $L$ 
7:    $H \leftarrow CHILDREN(H)$  ▷  $H$  is either  $NIL$  or one tree.
8:   for  $\forall T \in L$  from left to right do
9:      $H \leftarrow MERGE(H, T)$ 
10:  return  $H$ 

```

Note that L is initialized as an empty linked-list, then the algorithm iterates every two trees in pair in the children of the K -ary tree, from left to right, and performs merging, the result is inserted at the beginning of L . Because we insert to front end, so when we traverse L later on, we actually process from right to left. There may be odd number of sub-trees in H , in that case, it will leave one tree after pair-merging. We handle it by start the right to left merging from this left tree.

Below is the ANSI C program to this algorithm.

```

struct node* pop(struct node* h) {
  struct node *x, *y, *lst = NULL;
  while ((x = h->children) ≠ NULL) {
    if ((h->children = y = x->next) ≠ NULL)
      h->children = h->children->next;
    lst = push_front(lst, merge(x, y));
  }
  x = NULL;
  while((y = lst) ≠ NULL) {
    lst = lst->next;
    x = merge(x, y);
  }
  free(h);
  return x;
}

```

The pairing heap pop operation is conjectured to be amortized $O(\lg n)$ time [58].

Exercise 10.11

Write a program to insert a tree at the beginning of a linked-list in your favorite imperative programming language.

Delete a node

We didn't mention delete in Binomial heap or Fibonacci Heap. Deletion can be realized by first decreasing key to minus infinity ($-\infty$), then performing pop. In this section, we present another solution for delete node.

The algorithm is to define the function $delete(H, x)$, where x is a node in a pairing heap H ⁶.

⁶Here the semantic of x is a reference to a node.

If x is root, we can just perform a pop operation. Otherwise, we can cut x from H , perform a pop on x , and then merge the pop result back to H . This can be described as the following.

$$\text{delete}(H, x) = \begin{cases} \text{pop}(H) & : x \text{ is root of } H \\ \text{merge}(\text{cut}(H, x), \text{pop}(x)) & : \text{otherwise} \end{cases} \quad (10.26)$$

As delete algorithm uses pop, the performance is conjectured to be amortized $O(\lg n)$ time.

Exercise 10.12

- Write procedural pseudo code for delete algorithm.
- Write the delete operation in your favorite imperative programming language
- Consider how to realize delete in purely functional setting.

10.5 Notes and short summary

In this chapter, we extend the heap implementation from binary tree to more generic approach. Binomial heap and Fibonacci heap use Forest of K -ary trees as under ground data structure, while Pairing heap use a K -ary tree to represent heap. It's a good point to post pone some expensive operation, so that the over all amortized performance is ensured. Although Fibonacci Heap gives good performance in theory, the implementation is a bit complex. It was removed in some latest textbooks. We also present pairing heap, which is easy to realize and have good performance in practice.

The elementary tree based data structures are all introduced in this book. There are still many tree based data structures which we can't covers them all and skip here. We encourage the reader to refer to other textbooks about them. From next chapter, we'll introduce generic sequence data structures, array and queue.

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Chapter 11

Queue, not so simple as it was thought

11.1 Introduction

It seems that queues are relative simple. A queue provides FIFO (first-in, first-out) data manipulation support. There are many options to realize queue includes singly linked-list, doubly linked-list, circular buffer etc. However, we'll show that it's not so easy to realize queue in purely functional settings if it must satisfy abstract queue properties.

In this chapter, we'll present several different approaches to implement queue. A queue is a FIFO data structure satisfies the following performance constraints.

- Element can be added to the tail of the queue in $O(1)$ constant time;
- Element can be removed from the head of the queue in $O(1)$ constant time.

These two properties must be satisfied. And it's common to add some extra goals, such as dynamic memory allocation etc.

Of course such abstract queue interface can be implemented with doubly-linked list trivially. But this is a overkill solution. We can even implement imperative queue with singly linked-list or plain array. However, our main question here is about how to realize a purely functional queue as well?

We'll first review the typical queue solution which is realized by singly linked-list and circular buffer in first section; Then we give a simple and straightforward functional solution in the second section. While the performance is ensured in terms of amortized constant time, we need find real-time solution (or worst-case solution) for some special case. Such solution will be described in the third and the fourth section. Finally, we'll show a very simple real-time queue which depends on lazy evaluation.

Most of the functional contents are based on Chris, Okasaki's great work in [3]. There are more than 16 different types of purely functional queue given in that material.

11.2 Queue by linked-list and circular buffer

11.2.1 Singly linked-list solution

Queue can be implemented with singly linked-list. It's easy to add and remove element at the front end of a linked-list in $O(1)$ time. However, in order to keep the FIFO order, if we execute one operation on head, we must perform the inverse operation on tail.

In order to operate on tail, for plain singly linked-list, we must traverse the whole list before adding or removing. Traversing is bound to $O(n)$ time, where n is the length of the list. This doesn't match the abstract queue properties.

The solution is to use an extra record to store the tail of the linked-list. A sentinel is often used to simplify the boundary handling. The following ANSI C ¹ code defines a queue realized by singly linked-list.

```
typedef int Key;

struct Node{
    Key key;
    struct Node* next;
};

struct Queue{
    struct Node *head, *tail;
};
```

Figure 11.1 illustrates an empty list. Both head and tail point to the sentinel NIL node.

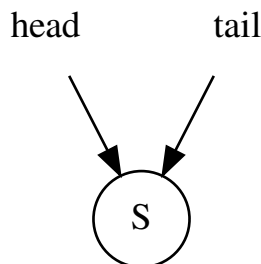


Figure 11.1: The empty queue, both head and tail point to sentinel node.

We summarize the abstract queue interface as the following.

function EMPTY	▷ Create an empty queue
function EMPTY?(Q)	▷ Test if Q is empty
function ENQUEUE(Q, x)	▷ Add a new element x to queue Q
function DEQUEUE(Q)	▷ Remove element from queue Q
function HEAD(Q)	▷ get the next element in queue Q in FIFO order

Note the difference between DEQUEUE and HEAD. HEAD only retrieve next element in FIFO order without removing it, while DEQUEUE performs removing.

In some programming languages, such as Haskell, and most object-oriented languages, the above abstract queue interface can be ensured by some definition. For example, the following Haskell code specifies the abstract queue.

```
class Queue q where
    empty :: q a
    isEmpty :: q a → Bool
    push :: q a → a → q a    — Or named as 'snoc', append, push_back
    pop  :: q a → q a        — Or named as 'tail', pop_front
    front :: q a → a         — Or named as 'head'
```

¹It's possible to parameterize the type of the key with C++ template. ANSI C is used here for illustration purpose.

To ensure the constant time ENQUEUE and DEQUEUE, we add new element to head and remove element from tail.²

```
function ENQUEUE( $Q, x$ )
   $p \leftarrow$  CREATE-NEW-NODE
  KEY( $p$ )  $\leftarrow$   $x$ 
  NEXT( $p$ )  $\leftarrow$  NIL
  NEXT(TAIL( $Q$ ))  $\leftarrow$   $p$ 
  TAIL( $Q$ )  $\leftarrow$   $p$ 
```

Note that, as we use the sentinel node, there are at least one node, the sentinel in the queue. That's why we needn't check the validation of of the tail before we append the new created node p to it.

```
function DEQUEUE( $Q$ )
   $x \leftarrow$  HEAD( $Q$ )
  NEXT(HEAD( $Q$ ))  $\leftarrow$  NEXT( $x$ )
  if  $x =$  TAIL( $Q$ ) then ▷  $Q$  gets empty
    TAIL( $Q$ )  $\leftarrow$  HEAD( $Q$ )
  return KEY( $x$ )
```

As we always put the sentinel node in front of all the other nodes, function HEAD actually returns the next node to the sentinel.

Figure 11.2 illustrates ENQUEUE and DEQUEUE process with sentinel node.

Translating the pseudo code to ANSI C program yields the below code.

```
struct Queue* enqueue(struct Queue* q, Key x) {
  struct Node* p = (struct Node*)malloc(sizeof(struct Node));
  p->key = x;
  p->next = NULL;
  q->tail->next = p;
  q->tail = p;
  return q;
}

Key dequeue(struct Queue* q) {
  struct Node* p = head(q); /*gets the node next to sentinel*/
  Key x = key(p);
  q->head->next = p->next;
  if (q->tail == p)
    q->tail = q->head;
  free(p);
  return x;
}
```

This solution is simple and robust. It's easy to extend this solution even to the concurrent environment (e.g. multicores). We can assign a lock to the head and use another lock to the tail. The sentinel helps us from being dead-locked due to the empty case [59] [60].

Exercise 11.1

- Realize the EMPTY? and HEAD algorithms for linked-list queue.
- Implement the singly linked-list queue in your favorite imperative programming language. Note that you need provide functions to initialize and destroy the queue.

²It's possible to add new element to the tail, while remove element from head, but the operations are more complex than this approach.

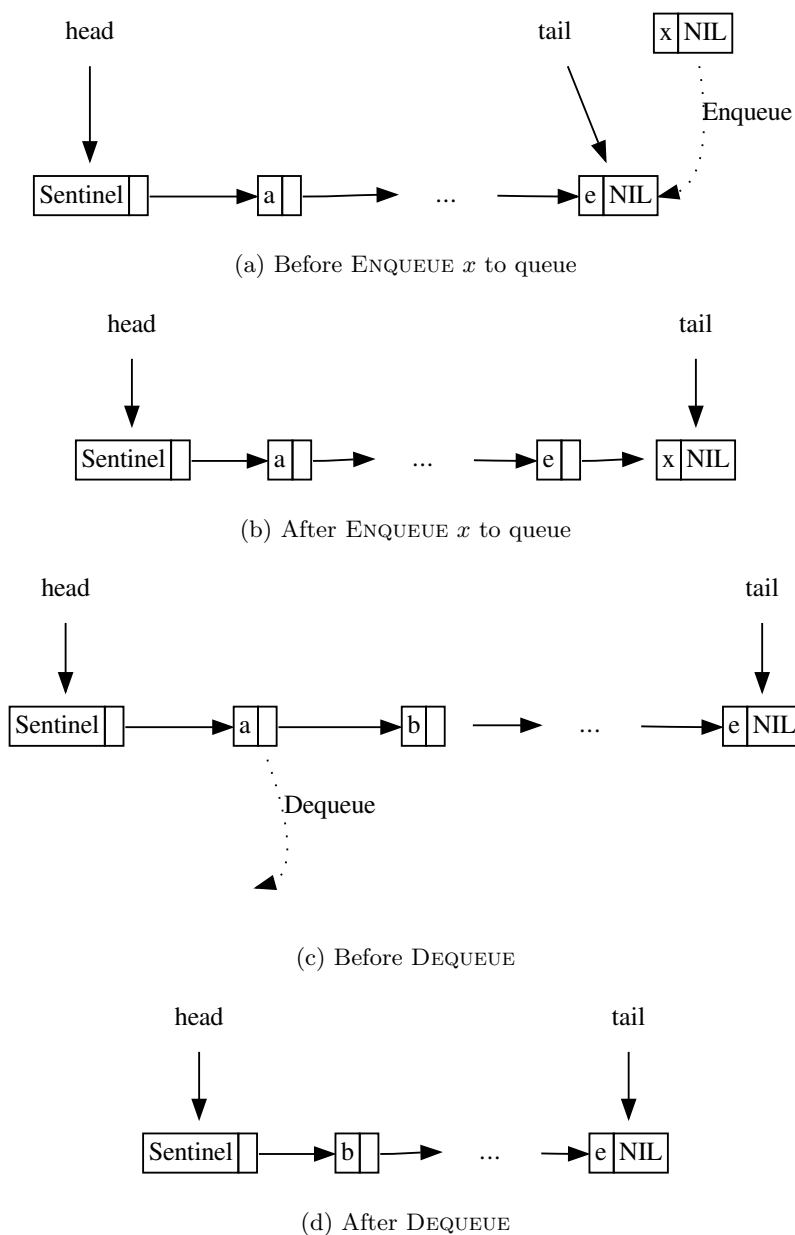


Figure 11.2: ENQUEUE and DEQUEUE to linked-list queue.

11.2.2 Circular buffer solution

Another typical solution to realize queue is to use plain array as a circular buffer (also known as ring buffer). Oppose to linked-list, array support appending to the tail in constant $O(1)$ time if there are still spaces. Of course we need re-allocate spaces if the array is fully occupied. However, Array performs poor in $O(n)$ time when removing element from head and packing the space. This is because we need shift all rest elements one cell ahead. The idea of circular buffer is to reuse the free cells before the first valid element after we remove elements from head.

The idea of circular buffer can be described in figure 11.3 and 11.4.

If we set a maximum size of the buffer instead of dynamically allocate memories, the queue can be defined with the below ANSI C code.

```
struct QueueBuf{
    Key* buf;
    int head, cnt, size;
};
```

When initialize the queue, we are explicitly asked to provide the maximum size as the parameter.

```
struct QueueBuf* createQ(int max){
    struct QueueBuf* q = (struct QueueBuf*)malloc(sizeof(struct QueueBuf));
    q->buf = (Key*)malloc(sizeof(Key)*max);
    q->size = max;
    q->head = q->cnt = 0;
    return q;
}
```

With the counter variable, we can compare it with zero and the capacity to test if the queue is empty or full.

```
function EMPTY?(Q)
    return COUNT(Q) = 0
```

To realize ENQUEUE and DEQUEUE, an easy way is to calculate the modular of index as the following.

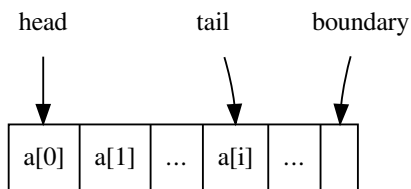
```
function ENQUEUE(Q, x)
    if  $\neg$  FULL?(Q) then
        COUNT(Q)  $\leftarrow$  COUNT(Q) + 1
        tail  $\leftarrow$  (HEAD(Q) + COUNT(Q)) mod SIZE(Q)
        BUFFER(Q)[tail]  $\leftarrow$  x

function HEAD(Q)
    if  $\neg$  EMPTY?(Q) then
        return BUFFER(Q)[HEAD(Q)]

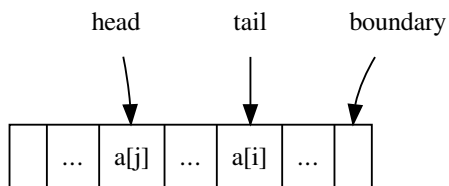
function DEQUEUE(Q)
    if  $\neg$  EMPTY?(Q) then
        HEAD(Q)  $\leftarrow$  (HEAD(Q) + 1) mod SIZE(Q)
        COUNT(Q)  $\leftarrow$  COUNT(Q) - 1
```

However, modular is expensive and slow depends on some settings, so one may replace it by some adjustment. For example as in the below ANSI C program.

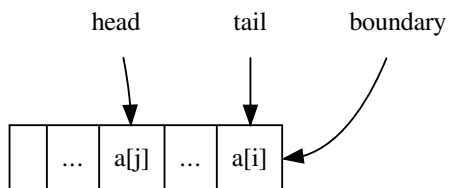
```
void enQ(struct QueueBuf* q, Key x){
    if(!fullQ(q)){
        q->buf[offset(q->head + q->cnt, q->size)] = x;
        q->cnt++;
    }
}
```



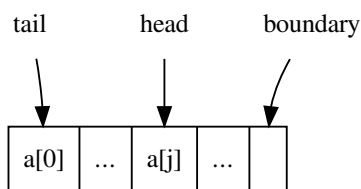
(a) Continuously add some elements.



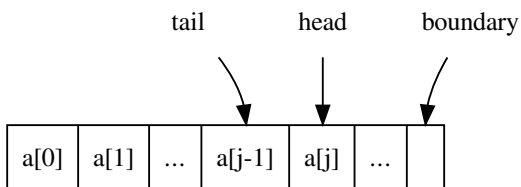
(b) After remove some elements from head, there are free cells.



(c) Go on adding elements till the boundary of the array.



(d) The next element is added to the first free cell on head.



(e) All cells are occupied. The queue is full.

Figure 11.3: A queue is realized with ring buffer.

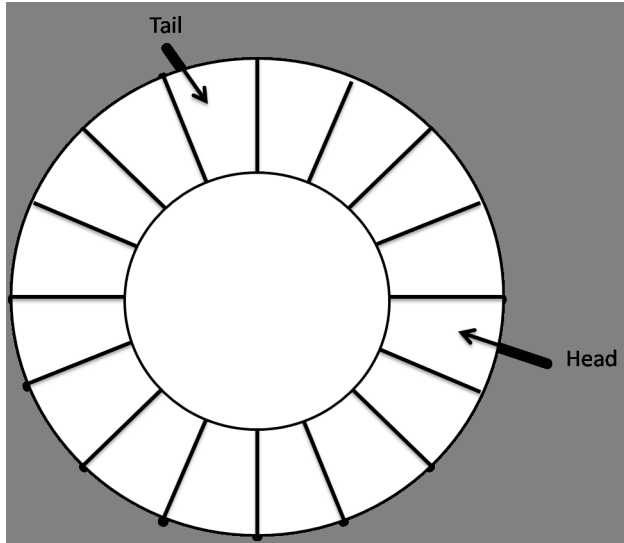


Figure 11.4: The circular buffer.

```

Key headQ(struct Queue* q) {
    return q->buf[q->head]; // %B»İz%
}

Key deQ(struct QueueBuf* q){
    Key x = headQ(q);
    q->head = offset(++q->head, q->size);
    q->cnt--;
    return x;
}

```

Exercise 11.2

The circular buffer is allocated with a maximum size parameter. Can we test the queue is empty or full with only head and tail pointers? Note that the head can be either before or after the tail.

11.3 Purely functional solution

11.3.1 Paired-list queue

We can't just use a list to implement queue, or we can't satisfy abstract queue properties. This is because singly linked-list, which is the back-end data structure in most functional settings, performs well on head in constant $O(1)$ time, while it performs in linear $O(n)$ time on tail, where n is the length of the list. Either dequeue or enqueue will perform proportion to the number of elements stored in the list as shown in figure 11.5.

We neither can add a pointer to record the tail position of the list as what we have done in the imperative settings like in the ANSI C program, because of the nature of purely functional.

Chris Okasaki mentioned a simple and straightforward functional solution in [3]. The idea is to maintain two linked-lists as a queue, and concatenate these two lists in a tail-to-tail manner. The shape of the queue looks like a horseshoe magnet as shown in figure

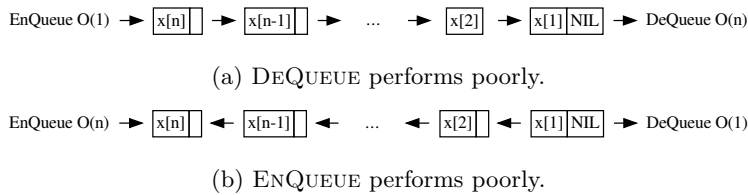
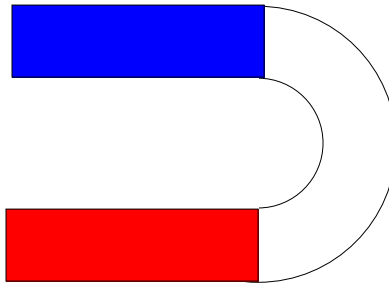


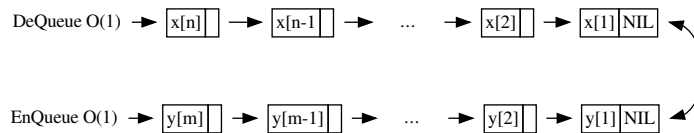
Figure 11.5: DEQUEUE and ENQUEUE can't perform both in constant $O(1)$ time with a list.

11.6.



(a) a horseshoe magnet.

front



rear

(b) concatenate two lists tail-to-tail.

Figure 11.6: A queue with front and rear list shapes like a horseshoe magnet.

With this setup, we push new element to the head of the rear list, which is ensure to be $O(1)$ constant time; on the other hand, we pop element from the head of the front list, which is also $O(1)$ constant time. So that the abstract queue properties can be satisfied.

The definition of such paired-list queue can be expressed in the following Haskell code.

```
type Queue a = ([a], [a])
empty = ([], [])
```

Suppose function $front(Q)$ and $rear(Q)$ return the front and rear list in such setup, and $Queue(F, R)$ create a paired-list queue from two lists F and R . The ENQUEUE (push)

and DEQUEUE (pop) operations can be easily realized based on this setup.

$$\text{push}(Q, x) = \text{Queue}(\text{front}(Q), \{x\} \cup \text{rear}(Q)) \quad (11.1)$$

$$\text{pop}(Q) = \text{Queue}(\text{tail}(\text{front}(Q)), \text{rear}(Q)) \quad (11.2)$$

where if a list $X = \{x_1, x_2, \dots, x_n\}$, function $\text{tail}(X) = \{x_2, x_3, \dots, x_n\}$ returns the rest of the list without the first element.

However, we must next solve the problem that after several pop operations, the front list becomes empty, while there are still elements in rear list. One method is to rebuild the queue by reversing the rear list, and use it to replace front list.

Hence a balance operation will be execute after popping. Let's denote the front and rear list of a queue Q as $F = \text{front}(Q)$, and $R = \text{rear}(Q)$.

$$\text{balance}(F, R) = \begin{cases} \text{Queue}(\text{reverse}(R), \phi) & : F = \phi \\ Q & : \text{otherwise} \end{cases} \quad (11.3)$$

Thus if front list isn't empty, we do nothing, while when the front list becomes empty, we use the reversed rear list as the new front list, and the new rear list is empty.

The new enqueue and dequeue algorithms are updated as below.

$$\text{push}(Q, x) = \text{balance}(F, \{x\} \cup R) \quad (11.4)$$

$$\text{pop}(Q) = \text{balance}(\text{tail}(F), R) \quad (11.5)$$

Sum up the above algorithms and translate them to Haskell yields the following program.

```
balance :: Queue a -> Queue a
balance ([], r) = (reverse r, [])
balance q = q

push :: Queue a -> a -> Queue a
push (f, r) x = balance (f, x:r)

pop :: Queue a -> Queue a
pop ([], _) = error "Empty"
pop (_:f, r) = balance (f, r)
```

Although we only touch the heads of front list and rear list, the overall performance can't be kept always as $O(1)$. Actually, the performance of this algorithm is amortized $O(1)$. This is because the reverse operation takes time proportion to the length of the rear list. it's bound $O(n)$ time, where $N = |R|$. We left the prove of amortized performance as an exercise to the reader.

11.3.2 Paired-array queue - a symmetric implementation

There is an interesting implementation which is symmetric to the paired-list queue. In some old programming languages, such as legacy version of BASIC, There is array supported, but there is no pointers, nor records to represent linked-list. Although we can use another array to store indexes so that we can represent linked-list with implicit array, there is another option to realized amortized $O(1)$ queue.

Compare the performance of array and linked-list. Below table reveals some facts (Suppose both contain n elements).

operation	Array	Linked-list
insert on head	$O(n)$	$O(1)$
insert on tail	$O(1)$	$O(n)$
remove on head	$O(n)$	$O(1)$
remove on tail	$O(1)$	$O(n)$

Note that linked-list performs in constant time on head, but in linear time on tail; while array performs in constant time on tail (suppose there is enough memory spaces, and omit the memory reallocation for simplification), but in linear time on head. This is because we need do shifting when prepare or eliminate an empty cell in array. (see chapter 'the evolution of insertion sort' for detail.)

The above table shows an interesting characteristic, that we can exploit it and provide a solution mimic to the paired-list queue: We concatenate two arrays, head-to-head, to make a horseshoe shape queue like in figure 11.7.

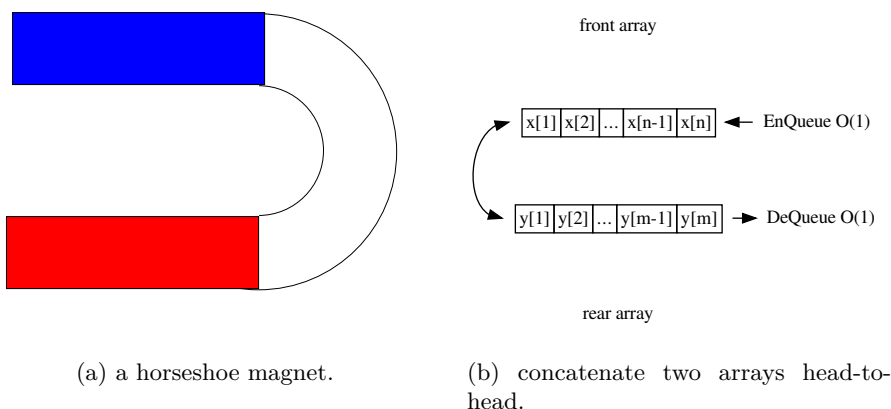


Figure 11.7: A queue with front and rear arrays shapes like a horseshoe magnet.

We can define such paired-array queue like the following Python code ³

```
class Queue:
    def __init__(self):
        self.front = []
        self.rear = []

def is_empty(q):
    return q.front == [] and q.rear == []
```

The relative PUSH() and POP() algorithm only manipulate on the tail of the arrays.

```
function PUSH(Q, x)
    APPEND(REAR(Q), x)
```

Here we assume that the APPEND() algorithm append element x to the end of the array, and handle the necessary memory allocation etc. Actually, there are multiple memory handling approaches. For example, besides the dynamic re-allocation, we can initialize the array with enough space, and just report error if it's full.

```
function POP(Q)
    if FRONT(Q) =  $\phi$  then
        FRONT(Q)  $\leftarrow$  REVERSE(REAR(Q))
        REAR(Q)  $\leftarrow$   $\phi$ 

    n  $\leftarrow$  LENGTH(FRONT(Q))
    x  $\leftarrow$  FRONT(Q)[n]
    LENGTH(FRONT(Q))  $\leftarrow$  n - 1
```

³Legacy Basic code is not presented here. And we actually use list but not array in Python to illustrate the idea. ANSI C and ISO C++ programs are provides along with this chapter, they show more in a purely array manner.

return x

For simplification and pure illustration purpose, the array isn't shrunk explicitly after elements removed. So test if front array is empty (ϕ) can be realized as check if the length of the array is zero. We omit all these details here.

The enqueue and dequeue algorithms can be translated to Python programs straightforwardly.

```
def push(q, x):
    q.rear.append(x)

def pop(q):
    if q.front == []:
        q.rear.reverse()
        (q.front, q.rear) = (q.rear, [])
    return q.front.pop()
```

Similar to the paired-list queue, the performance is amortized $O(1)$ because the reverse procedure takes linear time.

Exercise 11.3

- Prove that the amortized performance of paired-list queue is $O(1)$.
- Prove that the amortized performance of paired-array queue is $O(1)$.

11.4 A small improvement, Balanced Queue

Although paired-list queue is amortized $O(1)$ for popping and pushing, the solution we proposed in previous section performs poor in the worst case. For example, there is one element in the front list, and we push n elements continuously to the queue, here n is a big number. After that executing a pop operation will cause the worst case.

According to the strategy we used so far, all the n elements are added to the rear list. The front list turns to be empty after a pop operation. So the algorithm starts to reverse the rear list. This reversing procedure is bound to $O(n)$ time, which is proportion to the length of the rear list. Sometimes, it can't be acceptable for a very big n .

The reason why this worst case happens is because the front and rear lists are extremely unbalanced. We can improve our paired-list queue design by making them more balanced. One option is to add a balancing constraint.

$$|R| \leq |F| \tag{11.6}$$

Where $R = \text{Rear}(Q)$, $F = \text{Front}(Q)$, and $|L|$ is the length of list L . This constraint ensure the length of the rear list is less than the length of the front list. So that the reverse procedure will be executed once the rear list grows longer than the front list.

Here we need frequently access the length information of a list. However, calculate the length takes linear time for singly linked-list. We can record the length to a variable and update it as adding and removing elements. This approach enables us to get the length information in constant time.

Below example shows the modified paired-list queue definition which is augmented with length fields.

```
data BalanceQueue a = BQ [a] Int [a] Int
```

As we keep the invariant as specified in (11.6), we can easily tell if a queue is empty by testing the length of the front list.

$$F = \phi \Leftrightarrow |F| = 0 \quad (11.7)$$

In the rest part of this section, we suppose the length of a list L , can be retrieved as $|L|$ in constant time.

Push and pop are almost as same as before except that we check the balance invariant by passing length information and performs reversing accordingly.

$$\text{push}(Q, x) = \text{balance}(F, |F|, \{x\} \cup R, |R| + 1) \quad (11.8)$$

$$\text{pop}(Q) = \text{balance}(\text{tail}(F), |F| - 1, R, |R|) \quad (11.9)$$

Where function $\text{balance}()$ is defined as the following.

$$\text{balance}(F, |F|, R, |R|) = \begin{cases} \text{Queue}(F, |F|, R, |R|) & : |R| \leq |F| \\ \text{Queue}(F \cup \text{reverse}(R), |F| + |R|, \phi, 0) & : \text{otherwise} \end{cases} \quad (11.10)$$

Note that the function $\text{Queue}()$ takes four parameters, the front list along with its length (recorded), and the rear list along with its length, and forms a paired-list queue augmented with length fields.

We can easily translate the equations to Haskell program. And we can enforce the abstract queue interface by making the implementation an instance of the Queue type class.

```

instance Queue BalanceQueue where
  empty = BQ [] 0 [] 0

  isEmpty (BQ _ lenf _ _) = lenf == 0

  — Amortized O(1) time push
  push (BQ f lenf r lenr) x = balance f lenf (x:r) (lenr + 1)

  — Amortized O(1) time pop
  pop (BQ (_:f) lenf r lenr) = balance f (lenf - 1) r lenr

  front (BQ (x:_) _ _ _) = x

balance f lenf r lenr
  | lenr ≤ lenf = BQ f lenf r lenr
  | otherwise = BQ (f ++ (reverse r)) (lenf + lenr) [] 0

```

Exercise 11.4

Write the symmetric balance improvement solution for paired-array queue in your favorite imperative programming language.

11.5 One more step improvement, Real-time Queue

Although the extremely worst case can be avoided by improving the balancing as what has been presented in previous section, the performance of reversing rear list is still bound to $O(n)$, where $N = |R|$. So if the rear list is very long, the instant performance is still unacceptable poor even if the amortized time is $O(1)$. It is particularly important in some real-time system to ensure the worst case performance.

As we have analyzed, the bottleneck is the computation of $F \cup \text{reverse}(R)$. This happens when $|R| > |F|$. Considering that $|F|$ and $|R|$ are all integers, so this computation happens when

$$|R| = |F| + 1 \quad (11.11)$$

Both F and the result of $\text{reverse}(R)$ are singly linked-list, It takes $O(|F|)$ time to concatenate them together, and it takes extra $O(|R|)$ time to reverse the rear list, so the total computation is bound to $O(|N|)$, where $N = |F| + |R|$. Which is proportion to the total number of elements in the queue.

In order to realize a real-time queue, we can't computing $F \cup \text{reverse}(R)$ monolithic. Our strategy is to distribute this expensive computation to every pop and push operations. Thus although each pop and push get a bit slow, we may avoid the extremely slow worst pop or push case.

Incremental reverse

Let's examine how functional reverse algorithm is implemented typically.

$$\text{reverse}(X) = \begin{cases} \phi & : X = \phi \\ \text{reverse}(X') \cup \{x_1\} & : \text{otherwise} \end{cases} \quad (11.12)$$

Where $X' = \text{tail}(X) = \{x_2, x_3, \dots\}$.

This is a typical recursive algorithm, that if the list to be reversed is empty, the result is just an empty list. This is the edge case; otherwise, we take the first element x_1 from the list, reverse the rest $\{x_2, x_3, \dots, x_n\}$, to $\{x_n, x_{n-1}, \dots, x_3, x_2\}$ and append x_1 after it.

However, this algorithm performs poor, as appending an element to the end of a list is proportion to the length of the list. So it's $O(N^2)$, but not a linear time reverse algorithm.

There exists another implementation which utilizes an accumulator A , like below.

$$\text{reverse}(X) = \text{reverse}'(X, \phi) \quad (11.13)$$

Where

$$\text{reverse}'(X, A) = \begin{cases} A & : X = \phi \\ \text{reverse}'(X', \{x_1\} \cup A) & : \text{otherwise} \end{cases} \quad (11.14)$$

We call A as *accumulator* because it accumulates intermediate reverse result at any time. Every time we call $\text{reverse}'(X, A)$, list X contains the rest of elements wait to be reversed, and A holds all the reversed elements so far. For instance when we call $\text{reverse}'()$ at i -th time, X and A contains the following elements:

$$X = \{x_i, x_{i+1}, \dots, x_n\} \quad A = \{x_{i-1}, x_{i-2}, \dots, x_1\}$$

In every non-trivial case, we takes the first element from X in $O(1)$ time; then put it in front of the accumulator A , which is again $O(1)$ constant time. We repeat it n times, so this is a linear time ($O(n)$) algorithm.

The latter version of reverse is obviously a *tail-recursion* algorithm, see [5] and [62] for detail. Such characteristic is easy to change from monolithic algorithm to incremental manner.

The solution is state transferring. We can use a state machine contains two types of stat: reversing state S_r to indicate that the reverse is still on-going (not finished), and finish state S_f to indicate the reverse has been done (finished). In Haskell programming language, it can be defined as a type.

```
data State a = | Reverse [a] [a]
               | Done [a]
```

And we can schedule (slow-down) the above $reverse'(X, A)$ function with these two types of state.

$$step(S, X, A) = \begin{cases} (S_f, A) & : S = S_r \wedge X = \phi \\ (S_r, X', \{x_1\} \cup A) & : S = S_r \wedge X \neq \phi \end{cases} \quad (11.15)$$

Each step, we examine the state type first, if the current state is S_r (on-going), and the rest elements to be reversed in X is empty, we can turn the algorithm to finish state S_f ; otherwise, we take the first element from X , put it in front of A just as same as above, but we do NOT perform recursion, instead, we just finish this step. We can store the current state as well as the resulted X and A , the reverse can be continued at any time when we call 'next' $step$ function in the future with the stored state, X and A passed in.

Here is an example of this step-by-step reverse algorithm.

$$\begin{aligned} step(S_r, \text{"hello"}, \phi) &= (S_r, \text{"ello"}, \text{"h"}) \\ step(S_r, \text{"ello"}, \text{"h"}) &= (S_r, \text{"llo"}, \text{"eh"}) \\ \dots & \\ step(S_r, \text{"o"}, \text{"lleh"}) &= (S_r, \phi, \text{"olleh"}) \\ step(S_r, \phi, \text{"olleh"}) &= (S_f, \text{"olleh"}) \end{aligned}$$

And in Haskell code manner, the example is like the following.

```
step $ Reverse "hello" [] = Reverse "ello" "h"
step $ Reverse "ello" "h" = Reverse "llo" "eh"
...
step $ Reverse "o" "lleh" = Reverse [] "olleh"
step $ Reverse [] "olleh" = Done "olleh"
```

Now we can distribute the reverse into steps in every pop and push operations. However, the problem is just half solved. We want to break down $F \cup reverse(R)$, and we have broken $reverse(R)$ into steps, we next need to schedule (slow-down) the list concatenation part $F \cup \dots$, which is bound to $O(|F|)$, into incremental manner so that we can distribute it to pop and push operations.

Incremental concatenate

It's a bit more challenge to implement incremental list concatenation than list reversing. However, it's possible to re-use the result we gained from increment reverse by a small trick: In order to realize $X \cup Y$, we can first reverse X to \overleftarrow{X} , then take elements one by one from \overleftarrow{X} and put them in front of Y just as what we have done in $reverse'$.

$$\begin{aligned} X \cup Y &\equiv reverse(reverse(X)) \cup Y \\ &\equiv reverse'(reverse(X), \phi) \cup Y \\ &\equiv reverse'(reverse(X), Y) \\ &\equiv reverse'(\overleftarrow{X}, Y) \end{aligned} \quad (11.16)$$

This fact indicates us that we can use an extra state to instruct the $step()$ function to continuously concatenating \overleftarrow{F} after R is reversed.

The strategy is to do the total work in two phases:

1. Reverse both F and R in parallel to get $\overleftarrow{F} = reverse(F)$, and $\overleftarrow{R} = reverse(R)$ incrementally;

2. Incrementally take elements from \overleftarrow{F} and put them in front of \overleftarrow{R} .

So we define three types of state: S_r represents reversing; S_c represents concatenating; and S_f represents finish.

In Haskell, these types of state are defined as the following.

```
data State a = Reverse [a] [a] [a] [a]
           | Concat [a] [a]
           | Done [a]
```

Because we reverse F and R simultaneously, so reversing state takes two pairs of lists and accumulators.

The state transferring is defined according to the two phases strategy described previously. Denotes that $F = \{f_1, f_2, \dots\}$, $F' = \text{tail}(F) = \{f_2, f_3, \dots\}$, $R = \{r_1, r_2, \dots\}$, $R' = \text{tail}(R) = \{r_2, r_3, \dots\}$. A state \mathcal{S} , contains it's type S , which has the value among S_r , S_c , and S_f . Note that \mathcal{S} also contains necessary parameters such as F , \overleftarrow{F} , X , A etc as intermediate results. These parameters vary according to the different states.

$$\text{next}(\mathcal{S}) = \begin{cases} (S_r, F', \{f_1\} \cup \overleftarrow{F}, R', \{r_1\} \cup \overleftarrow{R}) & : S = S_r \wedge F \neq \phi \wedge R \neq \phi \\ (S_c, \overleftarrow{F}, \{r_1\} \cup \overleftarrow{R}) & : S = S_r \wedge F = \phi \wedge R = \{r_1\} \\ (S_f, A) & : S = S_c \wedge X = \phi \\ (S_c, X', \{x_1\} \cup A) & : S = S_c \wedge X \neq \phi \end{cases} \quad (11.17)$$

The relative Haskell program is list as below.

```
next (Reverse (x:f) f' (y:r) r') = Reverse f (x:f') r (y:r')
next (Reverse [] f' [y] r') = Concat f' (y:r')
next (Concat _ _ acc) = Done acc
next (Concat (x:f') acc) = Concat f' (x:acc)
```

All left to us is to distribute these incremental steps into every pop and push operations to implement a real-time $O(1)$ purely functional queue.

Sum up

Before we dive into the final real-time queue implementation, let's analyze how many incremental steps are taken to achieve the result of $F \cup \text{reverse}(R)$. According to the balance variant we used previously, $|R| = |F| + 1$, Let's denotes $m = |F|$.

Once the queue gets unbalanced due to some push or pop operation, we start this incremental $F \cup \text{reverse}(R)$. It needs $m + 1$ steps to reverse R , and at the same time, we finish reversing the list F within these steps. After that, we need extra $m + 1$ steps to execute the concatenation. So there are $2m + 2$ steps.

It seems that distribute one step inside one pop or push operation is the natural solution. However, there is a critical question must be answered: Is it possible that before we finish these $2m + 2$ steps, the queue gets unbalanced again due to a series push and pop?

There are two facts about this question, one is good news and the other is bad news.

Let's first show the good news, that luckily, continuously pushing can't make the queue unbalanced again before we finish these $2m + 2$ steps to achieve $F \cup \text{reverse}(R)$. This is because once we start re-balancing, we can get a new front list $F' = F \cup \text{reverse}(R)$ after $2m + 2$ steps. While the next time unbalance is triggered when

$$\begin{aligned} |R'| &= |F'| + 1 \\ &= |F| + |R| + 1 \\ &= 2m + 2 \end{aligned} \quad (11.18)$$

front copy	on-going computation	new rear
$\{f_i, f_{i+1}, \dots, f_M\}$	$(S_r, \overleftarrow{F}, \dots, \overleftarrow{R}, \dots)$	$\{\dots\}$
first $i - 1$ elements popped	intermediate result \overleftarrow{F} and \overleftarrow{R}	new elements pushed

Table 11.1: Intermediate state of a queue before first m steps finish.

That is to say, even we continuously pushing as much elements as possible after the last unbalanced time, when the queue gets unbalanced again, the $2m + 2$ steps exactly get finished at that time point. Which means the new front list F' is calculated OK. We can safely go on to compute $F' \cup reverse(R')$. Thanks to the balance invariant which is designed in previous section.

But, the bad news is that, pop operation can happen at anytime before these $2m + 2$ steps finish. The situation is that once we want to extract element from front list, the new front list $F' = F \cup reverse(R)$ hasn't been ready yet. We don't have a valid front list at hand.

One solution to this problem is to keep a copy of original front list F , during the time we are calculating $reverse(F)$ which is described in phase 1 of our incremental computing strategy. So that we are still safe even if user continuously performs first m pop operations. So the queue looks like in table 11.1 at some time after we start the incremental computation and before phase 1 (reverse F and R simultaneously) ending⁴.

After these M pop operations, the copy of F is exhausted. And we just start incremental concatenation phase at that time. What if user goes on popping?

The fact is that since F is exhausted (becomes ϕ), we needn't do concatenation at all. Since $F \cup \overleftarrow{R} = \phi \cup \overleftarrow{R} = \overleftarrow{R}$.

It indicates us, when doing concatenation, we only need to concatenate those elements haven't been popped, which are still left in F . As user pops elements one by one continuously from the head of front list F , one method is to use a counter, record how many elements there are still in F . The counter is initialized as 0 when we start computing $F \cup reverse(R)$, it's increased by one when we reverse one element in F , which means we need concatenate this element in the future; and it's decreased by one every time when pop is performed, which means we can concatenate one element less; of course we need decrease this counter as well in every steps of concatenation. If and only if this counter becomes zero, we needn't do concatenations any more.

We can give the realization of purely functional real-time queue according to the above analysis.

We first add an idle state S_0 to simplify some state transferring. Below Haskell program is an example of this modified state definition.

```

data State a = Empty
  | Reverse Int [a] [a] [a] [a] — n, f', acc_f' r, acc_r
  | Append Int [a] [a] — n, rev_f', acc
  | Done [a] — result: f ++ reverse r

```

And the data structure is defined with three parts, the front list (augmented with length); the on-going state of computing $F \cup reverse(R)$; and the rear list (augmented with length).

⁴One may wonder that copying a list takes linear time to the length of the list. If so the whole solution would make no sense. Actually, this linear time copying won't happen at all. This is because the purely functional nature, the front list won't be mutated either by popping or by reversing. However, if trying to realize a symmetric solution with paired-array and mutate the array in-place, this issue should be stated, and we can perform a 'lazy' copying, that the real copying work won't execute immediately, instead, it copies one element every step we do incremental reversing. The detailed implementation is left as an exercise.

Here is the Haskell definition of real-time queue.

```
data RealtimeQueue a = RTQ [a] Int (State a) [a] Int
```

The empty queue is composed with empty front and rear list together with idle state S_0 as $Queue(\phi, 0, S_0, \phi, 0)$. And we can test if a queue is empty by checking if $|F| = 0$ according to the balance invariant defined before. Push and pop are changed accordingly.

$$push(Q, x) = balance(F, |F|, \mathcal{S}, \{x\} \cup R, |R| + 1) \quad (11.19)$$

$$pop(Q) = balance(F', |F| - 1, abort(\mathcal{S}), R, |R|) \quad (11.20)$$

The major difference is $abort()$ function. Based on our above analysis, when there is popping, we need decrease the counter, so that we can concatenate one element less. We define this as aborting. The details will be given after $balance()$ function.

The relative Haskell code for push and pop are listed like this.

```
push (RTQ f lenf s r lenr) x = balance f lenf s (x:r) (lenr + 1)
pop (RTQ (_:f) lenf s r lenr) = balance f (lenf - 1) (abort s) r lenr
```

The $balance()$ function first check the balance invariant, if it's violated, we need start re-balance it by starting compute $F \cup reverse(R)$ incrementally; otherwise we just execute one step of the unfinished incremental computation.

$$balance(F, |F|, \mathcal{S}, R, |R|) = \begin{cases} step(F, |F|, \mathcal{S}, R, |R|) & : |R| \leq |F| \\ step(F, |F| + |R|, (S_r, 0, F, \phi, R, \phi)\phi, 0) & : otherwise \end{cases} \quad (11.21)$$

The relative Haskell code is given like below.

```
balance f lenf s r lenr
| lenr ≤ lenf = step f lenf s r lenr
| otherwise = step f (lenf + lenr) (Reverse 0 f [] r []) [] 0
```

The $step()$ function typically transfer the state machine one state ahead, and it will turn the state to idle (S_0) when the incremental computation finishes.

$$step(F, |F|, \mathcal{S}, R, |R|) = \begin{cases} Queue(F', |F|, S_0, R, |R|) & : S' = S_f \\ Queue(F, |F|, S', R, |R|) & : otherwise \end{cases} \quad (11.22)$$

Where $S' = next(\mathcal{S})$ is the next state transferred; $F' = F \cup reverse(R)$, is the final new front list result from the incremental computing. The real state transferring is implemented in $next()$ function as the following. It's different from previous version by adding the counter field n to record how many elements left we need to concatenate.

$$next(\mathcal{S}) = \begin{cases} (S_r, n + 1, F', \{f_1\} \cup \overleftarrow{F}, R', \{r_1\} \cup \overleftarrow{R}) & : S = S_r \wedge F \neq \phi \\ (S_c, n, \overleftarrow{F}, \{r_1\} \cup \overleftarrow{R}) & : S = S_r \wedge F = \phi \\ (S_f, A) & : S = S_c \wedge n = 0 \\ (S_c, n - 1, X', \{x_1\} \cup A) & : S = S_c \wedge n \neq 0 \\ \mathcal{S} & : otherwise \end{cases} \quad (11.23)$$

And the corresponding Haskell code is like this.

```
next (Reverse n (x:f) f' (y:r) r') = Reverse (n+1) f (x:f') r (y:r')
next (Reverse n [] f' [y] r') = Concat n f' (y:r')
next (Concat 0 _ acc) = Done acc
next (Concat n (x:f') acc) = Concat (n-1) f' (x:acc)
next s = s
```

Function *abort()* is used to tell the state machine, we can concatenate one element less since it is popped.

$$abort(\mathcal{S}) = \begin{cases} (S_f, A') & : S = S_c \wedge n = 0 \\ (S_c, n - 1, X'A) & : S = S_c \wedge n \neq 0 \\ (S_r, n - 1, F, \overleftarrow{F}, R, \overleftarrow{R}) & : S = S_r \\ \mathcal{S} & : otherwise \end{cases} \quad (11.24)$$

Note that when $n = 0$ we actually rollback one concatenated element by return A' as the result but not A . (Why? this is left as an exercise.)

The Haskell code for abort function is like the following.

```
abort (Concat 0 _ (_:acc)) = Done acc    — Note! we rollback 1 elem
abort (Concat n f' acc) = Concat (n-1) f' acc
abort (Reverse n f f' r r') = Reverse (n-1) f f' r r'
abort s = s
```

It seems that we've done, however, there is still one tricky issue hidden behind us. If we push an element x to an empty queue, the result queue will be:

$$Queue(\phi, 1, (S_c, 0, \phi, \{x\}), \phi, 0)$$

If we perform pop immediately, we'll get an error! We found that the front list is empty although the previous computation of $F \cup reverse(R)$ has been finished. This is because it takes one more extra step to transfer from the state $(S_c, 0, \phi, A)$ to (S_f, A) . It's necessary to refine the \mathcal{S}' in *step()* function a bit.

$$\mathcal{S}' = \begin{cases} next(next(\mathcal{S})) & : F = \phi \\ next(\mathcal{S}) & : otherwise \end{cases} \quad (11.25)$$

The modification reflects to the below Haskell code:

```
step f lenf s r lenr =
  case s' of
    Done f'  -> RTQ f' lenf Empty r lenr
    s'      -> RTQ f lenf s' r lenr
  where s' = if null f then next $ next s else next s
```

Note that this algorithm differs from the one given by Chris Okasaki in [3]. Okasaki's algorithm executes two steps per pop and push, while the one presents in this chapter executes only one per pop and push, which leads to more distributed performance.

Exercise 11.5

- Why need we rollback one element when $n = 0$ in *abort()* function?
- Realize the real-time queue with symmetric paired-array queue solution in your favorite imperative programming language.
- In the footnote, we mentioned that when we start incremental reversing with in-place paired-array solution, copying the array can't be done monolithic or it will lead to linear time operation. Implement the lazy copying so that we copy one element per step along with the reversing.

11.6 Lazy real-time queue

The key to realize a real-time queue is to break down the expensive $F \cup reverse(R)$ to avoid monolithic computation. Lazy evaluation is particularly helpful in such case. In this section, we'll explore if there is some more elegant solution by exploit laziness.

Suppose that there exists a function $rotate()$, which can compute $F \cup reverse(R)$ incrementally. that's to say, with some accumulator A , the following two functions are equivalent.

$$rotate(X, Y, A) \equiv X \cup reverse(Y) \cup A \quad (11.26)$$

Where we initialized X as the front list F , Y as the rear list R , and the accumulator A is initialized as empty ϕ .

The trigger of rotation is still as same as before when $|F| + 1 = |R|$. Let's keep this constraint as an invariant during the whole rotation process, that $|X| + 1 = |Y|$ always holds.

It's obvious to deduce to the trivial case:

$$rotate(\phi, \{y_1\}, A) = \{y_1\} \cup A \quad (11.27)$$

Denote $X = \{x_1, x_2, \dots\}$, $Y = \{y_1, y_2, \dots\}$, and $X' = \{x_2, x_3, \dots\}$, $Y' = \{y_2, y_3, \dots\}$ are the rest of the lists without the first element for X and Y respectively. The recursion case is ruled out as the following.

$$\begin{aligned} rotate(X, Y, A) &\equiv X \cup reverse(Y) \cup A && \text{Definition of (11.26)} \\ &\equiv \{x_1\} \cup (X' \cup reverse(Y) \cup A) && \text{Associative of } \cup \\ &\equiv \{x_1\} \cup (X' \cup reverse(Y') \cup (\{y_1\} \cup A)) && \text{Nature of reverse and associative of } \cup \\ &\equiv \{x_1\} \cup rotate(X', Y', \{y_1\} \cup A) && \text{Definition of (11.26)} \end{aligned} \quad (11.28)$$

Summarize the above two cases, yields the final incremental rotate algorithm.

$$rotate(X, Y, A) = \begin{cases} \{y_1\} \cup A & : X = \phi \\ \{x_1\} \cup rotate(X', Y', \{y_1\} \cup A) & : otherwise \end{cases} \quad (11.29)$$

If we execute \cup lazily instead of strictly, that is, execute \cup once pop or push operation is performed, the computation of $rotate$ can be distribute to push and pop naturally.

Based on this idea, we modify the paired-list queue definition to change the front list to a lazy list, and augment it with a computation stream. [63]. When the queue triggers re-balance constraint by some pop/push, that $|F| + 1 = |R|$, The algorithm creates a lazy rotation computation, then use this lazy rotation as the new front list F' ; the new rear list becomes ϕ , and a copy of F' is maintained as a stream.

After that, when we performs every push and pop; we consume the stream by forcing a \cup operation. This results us advancing one step along the stream, $\{x\} \cup F''$, where $F'' = tail(F')$. We can discard x , and replace the stream F' with F'' .

Once all of the stream is exhausted, we can start another rotation.

In order to illustrate this idea clearly, we turns to Scheme/Lisp programming language to show example codes, because it gives us explicit control of laziness.

In Scheme/Lisp, we have the following three tools to deal with lazy stream.

```
(define (cons-stream a b) (cons a (delay b)))

(define stream-car car)

(define (stream-cdr s) (cdr (force s)))
```

Function `cons-stream` constructs a 'lazy' list from an element x and an existing list L without really evaluating the value of L ; The evaluation is actually delayed to `stream-cdr`, where the computation is forced. delaying can be realized by lambda calculus as described in[63].

The lazy paired-list queue is defined as the following.

```
(define (make-queue f r s)
  (list f r s))

;; Auxiliary functions
(define (front-lst q) (car q))

(define (rear-lst q) (cadr q))

(define (rots q) (caddr q))
```

A queue is consist of three parts, a front list, a rear list, and a stream which represents the computation of $F \cup reverse(R)$. Create an empty queue is trivial as making all these three parts null.

```
(define empty (make-queue '() '() '()))
```

Note that the front-list is also lazy stream actually, so we need use stream related functions to manipulate it. For example, the following function test if the queue is empty by checking the front lazy list stream.

```
(define (empty? q) (stream-null? (front-lst q)))
```

The push function is almost as same as the one given in previous section. That we put the new element in front of the rear list; and then examine the balance invariant and do necessary balancing works.

$$push(Q, x) = balance(\mathcal{F}, \{x\} \cup R, \mathcal{R}_s) \quad (11.30)$$

Where \mathcal{F} represents the lazy stream of front list; \mathcal{R}_s is the stream of rotation computation. The relative Scheme/Lisp code is give below.

```
(define (push q x)
  (balance (front-lst q) (cons x (rear q)) (rots q)))
```

While pop is a bit different, because the front list is actually lazy stream, we need force an evaluation. All the others are as same as before.

$$pop(Q) = balance(\mathcal{F}', R, \mathcal{R}_s) \quad (11.31)$$

Here \mathcal{F}' , force one evaluation to \mathcal{F} , the Scheme/Lisp code regarding to this equation is as the following.

```
(define (pop q)
  (balance (stream-cdr (front-lst q)) (rear q) (rots q)))
```

For illustration purpose, we skip the error handling (such as pop from an empty queue etc) here.

And one can access the top element in the queue by extract from the front list stream.

```
(define (front q) (stream-car (front-lst q)))
```

The balance function first checks if the computation stream is completely exhausted, and starts new rotation accordingly; otherwise, it just consumes one evaluation by enforcing the lazy stream.

$$balance(Q) = \begin{cases} Queue(\mathcal{F}', \phi, \mathcal{F}') & : \mathcal{R}_s = \phi \\ Queue(\mathcal{F}, R, \mathcal{R}'_s) & : otherwise \end{cases} \quad (11.32)$$

Here \mathcal{F}' is defined to start a new rotation.

$$\mathcal{F}' = \text{rotate}(F, R, \phi) \quad (11.33)$$

The relative Scheme/Lisp program is listed accordingly.

```
(define (balance f r s)
  (if (stream-null? s)
      (let ((newf (rotate f r '())))
        (make-queue newf '() newf))
      (make-queue f r (stream-cdr s))))
```

The implementation of incremental rotate function is just as same as what we analyzed above.

```
(define (rotate xs ys acc)
  (if (stream-null? xs)
      (cons-stream (car ys) acc)
      (cons-stream (stream-car xs)
                    (rotate (stream-cdr xs) (cdr ys)
                            (cons-stream (car ys) acc)))))
```

We used explicit lazy evaluation in Scheme/Lisp. Actually, this program can be very short by using lazy programming languages, for example, Haskell.

```
data LazyRTQueue a = LQ [a] [a] [a] — front, rear, f ++ reverse r

instance Queue LazyRTQueue where
  empty = LQ [] [] []

  isEmpty (LQ f _ _) = null f

  — O(1) time push
  push (LQ f r rot) x = balance f (x:r) rot

  — O(1) time pop
  pop (LQ (_:f) r rot) = balance f r rot

  front (LQ (x:_ _ _) = x

balance f r [] = let f' = rotate f r [] in LQ f' [] f'
balance f r (_:rot) = LQ f r rot

rotate [] [y] acc = y:acc
rotate (x:xs) (y:ys) acc = x : rotate xs ys (y:acc)
```

11.7 Notes and short summary

Just as mentioned in the beginning of this book in the first chapter, queue isn't so simple as it was thought. We've tries to explain algorithms and data structures both in imperative and in function approaches; Sometimes, it gives impression that functional way is simpler and more expressive in most time. However, there are still plenty of areas, that more studies and works are needed to give equivalent functional solution. Queue is such an important topic, that it links to many fundamental purely functional data structures.

That's why Chris Okasaki made intensively study and took a great amount of discussions in [3]. With purely functional queue solved, we can easily implement dequeue with the similar approach revealed in this chapter. As we can handle elements effectively in both head and tail, we can advance one step ahead to realize sequence data structures, which support fast concatenate, and finally we can realize random access data structures to mimic array in imperative settings. The details will be explained in later chapters.

Note that, although we haven't mentioned priority queue, it's quite possible to realized it with heaps. We have covered topic of heaps in several previous chapters.

Exercise 11.6

- Realize dequeue, which support adding and removing elements on both sides in constant $O(1)$ time in purely functional way.
- Realize dequeue in a symmetric solution only with array in your favorite imperative programming language.

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Chapter 12

Sequences, The last brick

12.1 Introduction

In the first chapter of this book, which introduced binary search tree as the ‘hello world’ data structure, we mentioned that neither queue nor array is simple if realized not only in imperative way, but also in functional approach. In previous chapter, we explained functional queue, which achieves the similar performance as its imperative counterpart. In this chapter, we’ll dive into the topic of array-like data structures.

We have introduced several data structures in this book so far, and it seems that functional approaches typically bring more expressive and elegant solution. However, there are some areas, people haven’t found competitive purely functional solutions which can match the imperative ones. For instance, the Ukkonen linear time suffix tree construction algorithm. another examples is Hashing table. Array is also among them.

Array is trivial in imperative settings, it enables randomly accessing any elements with index in constant $O(1)$ time. However, this performance target can’t be achieved directly in purely functional settings as there is only list can be used.

In this chapter, we are going to abstract the concept of array to sequences. Which support the following features

- Element can be inserted to or removed from the head of the sequence quickly in $O(1)$ time;
- Element can be inserted to or removed from the tail of the sequence quickly in $O(1)$ time;
- Support concatenate two sequences quickly (faster than linear time);
- Support randomly access and update any element quickly;
- Support split at any position quickly;

We call these features abstract sequence properties, and it easy to see the fact that even array (here means plain-array) in imperative settings can’t meet them all at the same time.

We’ll provide three solutions in this chapter. Firstly, we’ll introduce a solution based on binary tree forest and numeric representation; Secondly, we’ll show a concatenate-able list solution; Finally, we’ll give the finger tree solution.

Most of the results are based on Chris, Okasaki’s work in [3].

12.2 Binary random access list

12.2.1 Review of plain-array and list

Let's review the performance of plain-array and singly linked-list so that we know how they perform in different cases.

operation	Array	Linked-list
operation on head	$O(n)$	$O(1)$
operation on tail	$O(1)$	$O(n)$
access at random position	$O(1)$	average $O(n)$
remove at given position	average $O(n)$	$O(1)$
concatenate	$O(n_2)$	$O(n_1)$

Because we hold the head of linked list, operations on head such as insert and remove perform in constant time; while we need traverse to the end to perform removing or appending on tail; Given a position i , it need traverse i elements to access it. Once we are at that position, removing element from there is just bound to constant time by modifying some pointers. In order to concatenate two linked-lists, we need traverse to the end of the first one, and link it to the second one, which is bound to the length of the first linked-list;

On the other hand, for array, we must prepare free cell for inserting a new element to the head of it, and we need release the first cell after the first element being removed, all these two operations are achieved by shifting all the rest elements forward or backward, which costs linear time. While the operations on the tail of array are trivial constant time. Array also support accessing random position i by nature; However, removing the element at that position causes shifting all elements after it one position ahead. In order to concatenate two arrays, we need copy all elements from the second one to the end of the first one (ignore the memory re-allocation details), which is proportion to the length of the second array.

In the chapter about binomial heaps, we have explained the idea of using forest, which is a list of trees. It brings us the merit that, for any given number n , by representing it in binary number, we know how many binomial trees need to hold them. That each bit of 1 represents a binomial tree of that rank of bit. We can go one step ahead, if we have a n nodes binomial heap, for any given index $1 < i < n$, we can quickly know which binomial tree in the heap holds the i -th node.

12.2.2 Represent sequence by trees

One solution to realize a random-access sequence is to manage the sequence with a forest of complete binary trees. Figure 12.1 shows how we attach such trees to a sequence of numbers.

Here two trees t_1 and t_2 are used to represent sequence $\{x_1, x_2, x_3, x_4, x_5, x_6\}$. The size of binary tree t_1 is 2. The first two elements $\{x_1, x_2\}$ are leaves of t_1 ; the size of binary tree t_2 is 4. The next four elements $\{x_3, x_4, x_5, x_6\}$ are leaves of t_2 .

For a complete binary tree, we define the depth as 0 if the tree has only a leaf. The tree is denoted as t_i if its depth is $i + 1$. It's obvious that there are 2^i leaves in t_i .

For any sequence contains n elements, it can be turned to a forest of complete binary trees in this manner. First we represent n in binary number like below.

$$n = 2^0 e_0 + 2^1 e_1 + \dots + 2^m e_m \quad (12.1)$$

Where e_i is either 1 or 0, so $n = (e_m e_{m-1} \dots e_1 e_0)_2$. If $e_i \neq 0$, we then need a complete binary tree with size 2^i . For example in figure 12.1, as the length of sequence is 6, which is $(110)_2$ in binary. The lowest bit is 0, so we needn't a tree of size 1; the second bit is 1,

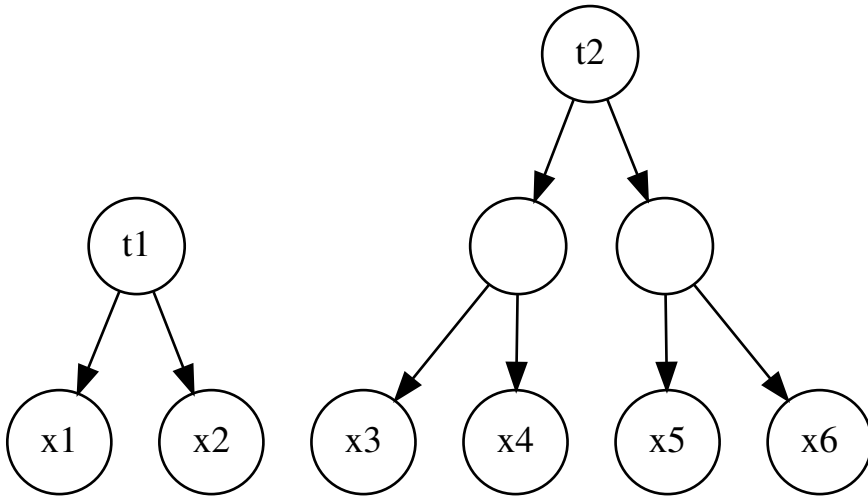


Figure 12.1: A sequence of 6 elements can be represented in a forest.

so we need a tree of size 2, which has depth of 2; the highest bit is also 1, thus we need a tree of size 4, which has depth of 3.

This method represents the sequence $\{x_1, x_2, \dots, x_n\}$ to a list of trees $\{t_0, t_1, \dots, t_m\}$ where t_i is either empty if $e_i = 0$ or a complete binary tree if $e_i = 1$. We call this representation as *Binary Random Access List* [3].

We can reused the definition of binary tree. For example, the following Haskell program defines the tree and the binary random access list.

```

data Tree a = Leaf a
             | Node Int (Tree a) (Tree a) — size, left, right
type BRAList a = [Tree a]
  
```

The only difference from the typical binary tree is that we augment the size information to the tree. This enable us to get the size without calculation at every time. For instance.

```

size (Leaf _) = 1
size (Node sz _ _) = sz
  
```

12.2.3 Insertion to the head of the sequence

The new forest representation of sequence enables many operation effectively. For example, the operation of inserting a new element y in front of sequence can be realized as the following.

1. Create a tree t' , with y as the only one leaf;
2. Examine the first tree in the forest, compare its size with t' , if its size is greater than t' , we just let t' be the new head of the forest, since the forest is a linked-list of tree, insert t' to its head is trivial operation, which is bound to constant $O(1)$ time;
3. Otherwise, if the size of first tree in the forest is equal to t' , let's denote this tree in the forest as t_i , we can construct a new binary tree t'_{i+1} by linking t_i and t' as its left and right children. After that, we recursively try to insert t'_{i+1} to the forest.

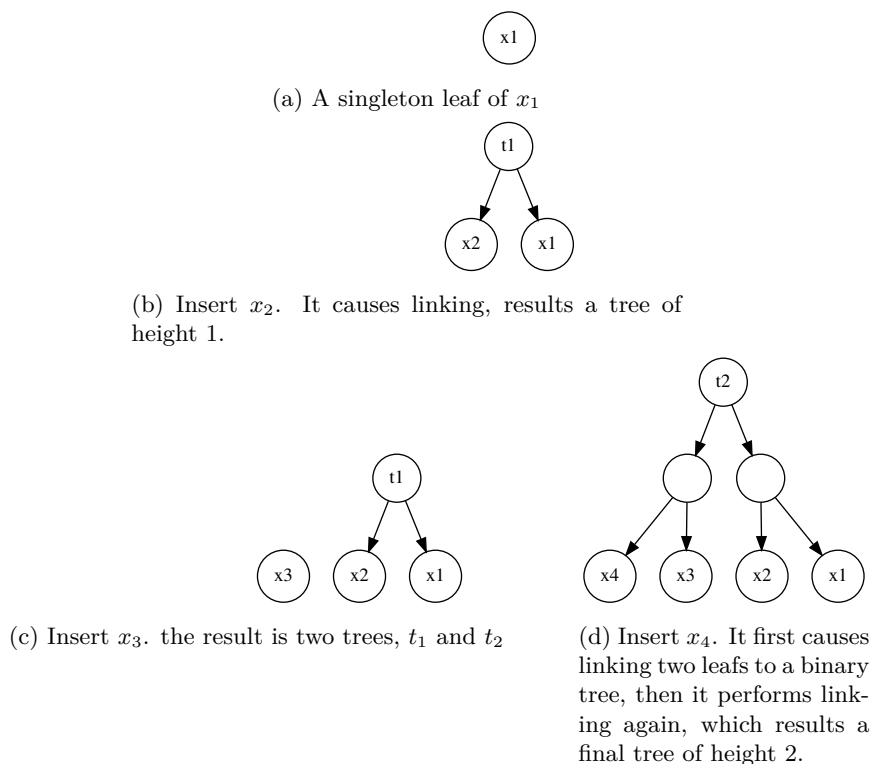


Figure 12.2: Steps of inserting elements to an empty list, 1

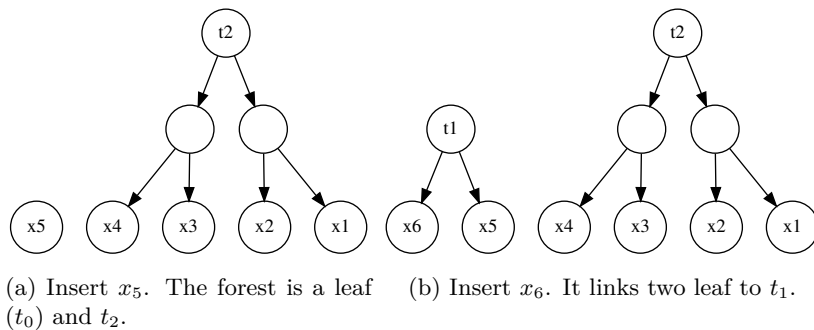


Figure 12.3: Steps of inserting elements to an empty list, 2

Figure 12.2 and 12.3 illustrate the steps of inserting elements x_1, x_2, \dots, x_6 to an empty forest.

As there are at most M trees in the forest, and m is bound to $O(\lg n)$, so the insertion to head algorithm is ensured to perform in $O(\lg n)$ even in worst case. We'll prove the amortized performance is $O(1)$ later.

Let's formalize the algorithm. we define the function of inserting an element in front of a sequence as $insert(S, x)$.

$$insert(S, x) = insertTree(S, leaf(x)) \quad (12.2)$$

This function just wrap element x to a singleton tree with a leaf, and call $insertTree$ to insert this tree to the forest. Suppose the forest $F = \{t_1, t_2, \dots\}$ if it's not empty, and $F' = \{t_2, t_3, \dots\}$ is the rest of trees without the first one.

$$insertTree(F, t) = \begin{cases} \{t\} & : F = \phi \\ \{t\} \cup F & : size(t) < size(t_1) \\ insertTree(F', link(t, t_1)) & : otherwise \end{cases} \quad (12.3)$$

Where function $link(t_1, t_2)$ create a new tree from two small trees with same size. Suppose function $tree(s, t_1, t_2)$ create a tree, set its size as s , makes t_1 as the left child, and t_2 as the right child, linking can be realized as below.

$$link(t_1, t_2) = tree(size(t_1) + size(t_2), t_1, t_2) \quad (12.4)$$

The relative Haskell programs can be given by translating these definitions.

```
cons :: a -> BRAList a -> BRAList a
cons x ts = insertTree ts (Leaf x)

insertTree :: BRAList a -> Tree a -> BRAList a
insertTree [] t = [t]
insertTree (t':ts) t = if size t < size t' then t:t':ts
                      else insertTree ts (link t t')

— Precondition: rank t1 = rank t2
link :: Tree a -> Tree a -> Tree a
link t1 t2 = Node (size t1 + size t2) t1 t2
```

Here we use the Lisp tradition to name the function that insert an element before a list as 'cons'.

Remove the element from the head of the sequence

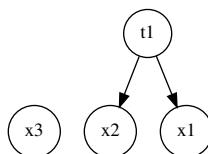
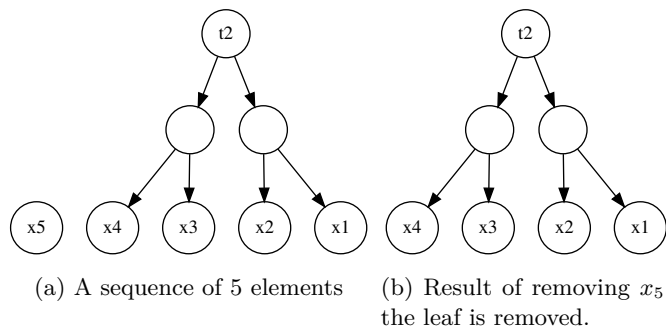
It's not complex to realize the inverse operation of 'cons', which can remove element from the head of the sequence.

- If the first tree in the forest is a singleton leaf, remove this tree from the forest;
- otherwise, we can halve the first tree by unlinking its two children, so the first tree in the forest becomes two trees, we recursively halve the first tree until it turns to be a leaf.

Figure 12.4 illustrates the steps of removing elements from the head of the sequence.

If we assume the sequence isn't empty, so that we can skip the error handling such as trying to remove an element from an empty sequence, this can be expressed with the following definition. We denote the forest $F = \{t_1, t_2, \dots\}$ and the trees without the first one as $F' = \{t_2, t_3, \dots\}$

$$extractTree(F) = \begin{cases} (t_1, F') & : t_1 \text{ is leaf} \\ extractTree(\{t_l, t_r\} \cup F') & : otherwise \end{cases} \quad (12.5)$$



(c) Result of removing x_4 . As there is not leaf tree, the tree is firstly divided into two sub trees of size 2. The first tree is next divided again into two leaves, after that, the first leaf, which contains x_4 is removed. What left in the forest is a leaf tree of x_3 , and a tree of size 2 with elements x_2, x_1 .

Figure 12.4: Steps of removing elements from head

where $\{t_l, t_r\} = \text{unlink}(t_1)$ are the two children of t_1 .

It can be translated to Haskell programs like below.

```
extractTree (t@(Leaf x):ts) = (t, ts)
extractTree (t@(Node _ t1 t2):ts) = extractTree (t1:t2:ts)
```

With this function defined, it's convenient to give *head* and *tail* functions, the former returns the first element in the sequence, the latter return the rest.

$$\text{head}(S) = \text{key}(\text{first}(\text{extractTree}(S))) \quad (12.6)$$

$$\text{tail}(S) = \text{second}(\text{extractTree}(S)) \quad (12.7)$$

Where function *first* returns the first element in a paired-value (as known as tuple); *second* returns the second element respectively. Function *key* is used to access the element inside a leaf. Below are Haskell programs corresponding to these two functions.

```
head' ts = x where (Leaf x, _) = extractTree ts
tail' = snd o extractTree
```

Note that as *head* and *tail* functions have already been defined in Haskell standard library, we given them apostrophes to make them distinct. (another option is to hide the standard ones by importing. We skip the details as they are language specific).

Random access the element in binary random access list

As trees in the forest help managing the elements in blocks, giving an arbitrary index, it's easy to locate which tree this element is stored, after that performing a search in the tree yields the result. As all trees are binary (more accurate, complete binary tree), the search is essentially binary search, which is bound to the logarithm of the tree size. This brings us a faster random access capability than linear search in linked-list setting.

Given an index i , and a sequence S , which is actually a forest of trees, the algorithm is executed as the following ¹.

1. Compare i with the size of the first tree T_1 in the forest, if i is less than or equal to the size, the element exists in T_1 , perform looking up in T_1 ;
2. Otherwise, decrease i by the size of T_1 , and repeat the previous step in the rest of the trees in the forest.

This algorithm can be represented as the below equation.

$$get(S, i) = \begin{cases} lookupTree(T_1, i) & : i \leq |T_1| \\ get(S', i - |T_1|) & : otherwise \end{cases} \quad (12.8)$$

Where $|T| = size(T)$, and $S' = \{T_2, T_3, \dots\}$ is the rest of trees without the first one in the forest. Note that we don't handle out of bound error case, this is left as an exercise to the reader.

Function *lookupTree* is a binary search algorithm. If the index i is 1, we just return the root of the tree, otherwise, we halve the tree by unlinking, if i is less than or equal to the size of the halved tree, we recursively look up the left tree, otherwise, we look up the right tree.

$$lookupTree(T, i) = \begin{cases} root(T) & : i = 1 \\ lookupTree(left(T)) & : i \leq \lfloor \frac{|T|}{2} \rfloor \\ lookupTree(right(T)) & : otherwise \end{cases} \quad (12.9)$$

Where function *left* returns the left tree T_l of T , while *right* returns T_r .

The corresponding Haskell program is given as below.

```
getAt (t:ts) i = if i < size t then lookupTree t i
                else getAt ts (i - size t)

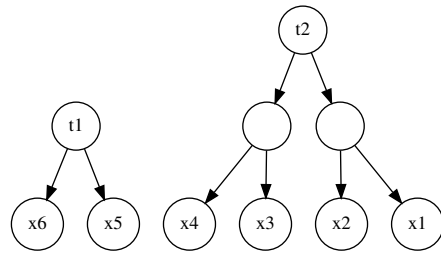
lookupTree (Leaf x) 0 = x
lookupTree (Node sz t1 t2) i = if i < sz `div` 2 then lookupTree t1 i
                               else lookupTree t2 (i - sz `div` 2)
```

Figure 12.5 illustrates the steps of looking up the 4-th element in a sequence of size 6. It first examine the first tree, since the size is 2 which is smaller than 4, so it goes on looking up for the second tree with the updated index $i' = 4 - 2$, which is the 2nd element in the rest of the forest. As the size of the next tree is 4, which is greater than 2, so the element to be searched should be located in this tree. It then examines the left sub tree since the new index 2 is not greater than the half size $4/2=2$; The process next visits the right grand-child, and the final result is returned.

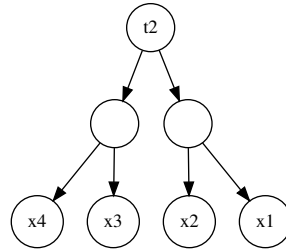
By using the similar idea, we can update element at any arbitrary position i . We first compare the size of the first tree T_1 in the forest with i , if it is less than i , it means the element to be updated doesn't exist in the first tree. We recursively examine the next tree in the forest, comparing it with $i - |T_1|$, where $|T_1|$ represents the size of the first tree. Otherwise if this size is greater than or equal to i , the element is in the tree, we halve the tree recursively until to get a leaf, at this stage, we can replace the element of this leaf with a new one.

$$set(S, i, x) = \begin{cases} \{updateTree(T_1, i, x)\} \cup S' & : i < |T_1| \\ \{T_1\} \cup set(S', i - |T_1|, x) & : otherwise \end{cases} \quad (12.10)$$

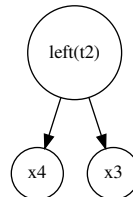
¹We follow the tradition that the index i starts from 1 in algorithm description; while it starts from 0 in most programming languages



(a) $getAt(S, 4)$, $4 > size(t_1) = 2$



(b) $getAt(S', 4 - 2) \Rightarrow lookupTree(t_2, 2)$



(c) $2 \leq \lfloor size(t_2)/2 \rfloor \Rightarrow lookupTree(left(t_2), 2)$



(d) $lookupTree(right(left(t_2)), 1)$, x_3 is returned.

Figure 12.5: Steps of locating the 4-th element in a sequence.

Where $S' = \{T_2, T_3, \dots\}$ is the rest of the trees in the forest without the first one.

Function $setTree(T, i, x)$ performs a tree search and replace the i -th element with the given value x .

$$setTree(T, i, x) = \begin{cases} leaf(x) & : i = 0 \wedge |T| = 1 \\ tree(|T|, setTree(T_l, i, x), T_r) & : i < \lfloor \frac{|T|}{2} \rfloor \\ tree(|T|, T_l, setTree(T_r, i - \lfloor \frac{|T|}{2} \rfloor, x)) & : otherwise \end{cases} \quad (12.11)$$

Where T_l and T_r are left and right sub tree of T respectively. The following Haskell program translates the equation accordingly.

```
setAt :: BRAList a -> Int -> a -> BRAList a
setAt (t:ts) i x = if i < size t then (updateTree t i x):ts
                  else t:setAt ts (i-size t) x

updateTree :: Tree a -> Int -> a -> Tree a
updateTree (Leaf _) 0 x = Leaf x
updateTree (Node sz t1 t2) i x =
  if i < sz `div` 2 then Node sz (updateTree t1 i x) t2
  else Node sz t1 (updateTree t2 (i - sz `div` 2) x)
```

As the nature of complete binary tree, for a sequence with n elements, which is represented by binary random access list, the number of trees in the forest is bound to $O(\lg n)$. Thus it takes $O(\lg n)$ time to locate the tree for arbitrary index i , that contains the element in the worst case. The followed tree search is bound to the heights of the tree, which is $O(\lg n)$ in the worst case as well. So the total performance of random access is $O(\lg n)$.

Exercise 12.1

1. The random access algorithm given in this section doesn't handle the error such as out of bound index at all. Modify the algorithm to handle this case, and implement it in your favorite programming language.
2. It's quite possible to realize the binary random access list in imperative settings, which is benefited with fast operation on the head of the sequence. the random access can be realized in two steps: firstly locate the tree, secondly use the capability of constant random access of array. Write a program to implement it in your favorite imperative programming language.

12.3 Numeric representation for binary random access list

In previous section, we mentioned that for any sequence with n elements, we can represent n in binary format so that $n = 2^0 e_0 + 2^1 e_1 + \dots + 2^m e_m$. Where e_i is the i -th bit, which can be either 0 or 1. If $e_i \neq 0$ it means that there is a complete binary tree with size 2^i .

This fact indicates us that there is an explicit relationship between the binary form of n and the forest. Insertion a new element on the head can be simulated by increasing the binary number by one; while remove an element from the head mimics the decreasing of the corresponding binary number by one. This is as known as *numeric representation* [3].

In order to represent the binary random access list with binary number, we can define two states for a bit. That *Zero* means there is no such a tree with size which is corresponding to the bit, while *One*, means such tree exists in the forest. And we can attach the tree with the state if it is *One*.

The following Haskell program for instance defines such states.

```
data Digit a = Zero
             | One (Tree a)

type RAList a = [Digit a]
```

Here we reuse the definition of complete binary tree and attach it to the state *One*. Note that we cache the size information in the tree as well.

With digit defined, forest can be treated as a list of digits. Let's see how inserting a new element can be realized as binary number increasing. Suppose function $one(t)$ creates a *One* state and attaches tree t to it. And function $getTree(s)$ get the tree which is attached to the *One* state s . The sequence S is a list of digits of states that $S = \{s_1, s_2, \dots\}$, and S' is the rest of digits with the first one removed.

$$insertTree(S, t) = \begin{cases} \{one(t)\} & : S = \phi \\ \{one(t)\} \cup S' & : s_1 = Zero \\ \{Zero\} \cup insertTree(S', link(t, getTree(s_1))) & : otherwise \end{cases} \quad (12.12)$$

When we insert a new tree t to a forest S of binary digits, If the forest is empty, we just create a *One* state, attach the tree to it, and make this state the only digit of the binary number. This is just like $0 + 1 = 1$;

Otherwise if the forest isn't empty, we need examine the first digit of the binary number. If the first digit is *Zero*, we just create a *One* state, attach the tree, and replace the *Zero* state with the new created *One* state. This is just like $(\dots digits \dots 0)_2 + 1 = (\dots digits \dots 1)_2$. For example $6 + 1 = (110)_2 + 1 = (111)_2 = 7$.

The last case is that the first digit is *One*, here we make assumption that the tree t to be inserted has the same size with the tree attached to this *One* state at this stage. This can be ensured by calling this function from inserting a leaf, so that the size of the tree to be inserted grows in a series of $1, 2, 4, \dots, 2^i, \dots$. In such case, we need link these two trees (one is t , the other is the tree attached to the *One* state), and recursively insert the linked result to the rest of the digits. Note that the previous *One* state has to be replaced with a *Zero* state. This is just like $(\dots digits \dots 1)_2 + 1 = (\dots digits' \dots 0)_2$, where $(\dots digits' \dots)_2 = (\dots digits \dots)_2 + 1$. For example $7 + 1 = (111)_2 + 1 = (1000)_2 = 8$

Translating this algorithm to Haskell yields the following program.

```
insertTree :: RAList a -> Tree a -> RAList a
insertTree [] t = [One t]
insertTree (Zero:ts) t = One t : ts
insertTree (One t' :ts) t = Zero : insertTree ts (link t t')
```

All the other functions, including $link()$, $cons()$ etc. are as same as before.

Next let's see how removing an element from a sequence can be represented as binary number deduction. If the sequence is a singleton *One* state attached with a leaf. After removal, it becomes empty. This is just like $1 - 1 = 0$;

Otherwise, we examine the first digit, if it is *One* state, it will be replaced with a *Zero* state to indicate that this tree will be no longer exist in the forest as it being removed. This is just like $(\dots digits \dots 1)_2 - 1 = (\dots digits \dots 0)_2$. For example $7 - 1 = (111)_2 - 1 = (110)_2 = 6$;

If the first digit in the sequence is a *Zero* state, we have to borrow from the further digits for removal. We recursively extract a tree from the rest digits, and halve the extracted tree to its two children. Then the *Zero* state will be replaced with a *One* state

attached with the right children, and the left children is removed. This is something like $(\dots digits \dots 0)_2 - 1 = (\dots digits' \dots 1)_2$, where $(\dots digits' \dots)_2 = (\dots digits)_2 - 1$. For example $4 - 1 = (100)_2 - 1 = (11)_2 = 3$. The following equation illustrated this algorithm.

$$extractTree(S) = \begin{cases} (t, \phi) & : S = \{one(t)\} \\ (t, S') & : s_1 = one(t) \\ (t_l, \{one(t_r)\} \cup S'' & : otherwise \end{cases} \quad (12.13)$$

Where $(t', S'') = extractTree(S')$, t_l and t_r are left and right sub-trees of t' . All other functions, including *head*, *tail* are as same as before.

Numeric representation doesn't change the performance of binary random access list, readers can refer to [64] for detailed discussion. Let's take for example, analyze the average performance (or amortized) of insertion on head algorithm by using aggregation analysis.

Considering the process of inserting $n = 2^m$ elements to an empty binary random access list. The numeric representation of the forest can be listed as the following.

i	forest (MSB ... LSB)
0	0, 0, ..., 0, 0
1	0, 0, ..., 0, 1
2	0, 0, ..., 1, 0
3	0, 0, ..., 1, 1
...	...
$2^m - 1$	1, 1, ..., 1, 1
2^m	1, 0, 0, ..., 0, 0
bits changed	1, 1, 2, ... 2^{m-1} , 2^m

The LSB of the forest changed every time when there is a new element inserted, it costs 2^m units of computation; The next bit changes every two times due to a linking operation, so it costs 2^{m-1} units; the bit next to MSB of the forest changed only one time which links all previous trees to a big tree as the only one in the forest. This happens at the half time of the total insertion process, and after the last element is inserted, the MSB flips to 1.

Sum these costs up yield to the total cost $T = 1 + 1 + 2 + 4 + \dots + 2^{m-1} + 2^m = 2^{m+1}$ So the average cost for one insertion is

$$O(T/N) = O\left(\frac{2^{m+1}}{2^m}\right) = O(1) \quad (12.14)$$

Which proves that the insertion algorithm performs in amortized $O(1)$ constant time. The proof for deletion are left as an exercise to the reader.

12.3.1 Imperative binary random access list

It's trivial to implement the imperative binary random access list by using binary trees, and the recursion can be eliminated by updating the focused tree in loops. This is left as an exercise to the reader. In this section, we'll show some different imperative implementation by using the properties of numeric representation.

Remind the chapter about binary heap. Binary heap can be represented by implicit array. We can use similar approach that use an array of 1 element to represent the leaf; use an array of 2 elements to represent a binary tree of height 1; and use an array of 2^m to represent a complete binary tree of height m .

This brings us the capability of accessing any element with index directly instead of divide and conquer tree search. However, the tree linking operation has to be implemented as array copying as the expense.

The following ANSI C code defines such a forest.

```

#define M sizeof(int) * 8
typedef int Key;

struct List {
    int n;
    Key* tree[M];
};

```

Where n is the number of the elements stored in this forest. Of course we can avoid limiting the max number of trees by using dynamic arrays, for example as the following ISO C++ code.

```

template<typename Key>
struct List {
    int n;
    vector<vector<key> > tree;
};

```

For illustration purpose only, we use ANSI C here².

Let's review the insertion process, if the first tree is empty (a *Zero* digit), we simply set the first tree as a leaf of the new element to be inserted; otherwise, the insertion will cause tree linking anyway, and such linking may be recursive until it reach a position (digit) that the corresponding tree is empty. The numeric representation reveals an important fact that if the first, second, ..., $(i - 1)$ -th trees all exist, and the i -th tree is empty, the result is creating a tree of size 2^i , and all the elements together with the new element to be inserted are stored in this new created tree. What's more, all trees after position i are kept as same as before.

Is there any good methods to locate this i position? As we can use binary number to represent the forest of n element, after a new element is inserted, n increases to $n + 1$. Compare the binary form of n and $n + 1$, we find that all bits before i change from 1 to 0, the i -th bit flip from 0 to 1, and all the bits after i keep unchanged. So we can use bit-wise exclusive or (\oplus) to detect this bit. Here is the algorithm.

function NUMBER-OF-BITS(n)

```

     $i \leftarrow 0$ 
    while  $\lfloor \frac{n}{2} \rfloor \neq 0$  do
         $n \leftarrow \lfloor \frac{n}{2} \rfloor$ 
         $i \leftarrow i + 1$ 
    return  $i$ 

```

$i \leftarrow \text{NUMBER-OF-BITS}(n \oplus (n + 1))$

The NUMBER-OF-BITS process can be easily implemented with bit shifting, for example the below ANSI C code.

```

int nbits(int n) {
    int i=0;
    while(n >= 1)
        ++i;
    return i;
}

```

So the imperative insertion algorithm can be realized by first locating the bit which flip from 0 to 1, then creating a new array of size 2^i to represent a complete binary tree, and moving content of all trees before this bit to this array as well as the new element to be inserted.

function INSERT(L, x)

²The complete ISO C++ example program is available with this book.

```

i ← NUMBER-OF-BITS( $n \oplus (n + 1)$ )
TREE(L)[i + 1] ← CREATE-ARRAY( $2^i$ )
l ← 1
TREE(L)[i + 1][l] ← x
for j ∈ [1, i] do
    for k ∈ [1,  $2^j$ ] do
        l ← l + 1
        TREE(L)[i + 1][l] ← TREE(L)[j][k]
    TREE(L)[j] ← NIL
SIZE(L) ← SIZE(L) + 1
return L

```

The corresponding ANSI C program is given as the following.

```

struct List insert(struct List a, Key x) {
    int i, j, sz;
    Key* xs;
    i = nbits((a.n + 1) ^ a.n);
    xs = a.tree[i] = (Key*)malloc(sizeof(Key)*(1 << i));
    for(j = 0, *xs++ = x, sz = 1; j < i; ++j, sz <<= 1) {
        memcpy((void*)xs, (void*)a.tree[j], sizeof(Key) * (sz));
        xs += sz;
        free(a.tree[j]);
        a.tree[j] = NULL;
    }
    ++a.n;
    return a;
}

```

However, the performance in theory isn't as good as before. This is because the linking operation downgrades from $O(1)$ constant time to linear array copying.

We can again calculate the average (amortized) performance by using aggregation analysis. When insert $n = 2^m$ elements to an empty list which is represented by implicit binary trees in arrays, the numeric presentation of the forest of arrays are as same as before except for the cost of bit flipping.

<i>i</i>	forest (MSB ... LSB)
0	0, 0, ..., 0, 0
1	0, 0, ..., 0, 1
2	0, 0, ..., 1, 0
3	0, 0, ..., 1, 1
...	...
$2^m - 1$	1, 1, ..., 1, 1
2^m	1, 0, 0, ..., 0, 0
bit change cost	$1 \times 2^m, 1 \times 2^{m-1}, 2 \times 2^{m-2}, \dots, 2^{m-2} \times 2, 2^{m-1} \times 1$

The LSB of the forest changed every time when there is a new element inserted, however, it creates leaf tree and performs copying only it changes from 0 to 1, so the cost is half of n unit, which is 2^{m-1} ; The next bit flips as half as the LSB. Each time the bit gets flipped to 1, it copies the first tree as well as the new element to the second tree. the the cost of flipping a bit to 1 in this bit is 2 units, but not 1; For the MSB, it only flips to 1 at the last time, but the cost of flipping this bit, is copying all the previous trees to fill the array of size 2^m .

Summing all to cost and distributing them to the n times of insertion yields the

amortized performance as below.

$$\begin{aligned}
 O(T/N) &= O\left(\frac{1 \times 2^m + 1 \times 2^{m-1} + 2 \times 2^{m-2} + \dots + 2^{m-1} \times 1}{2^m}\right) \\
 &= O\left(1 + \frac{m}{2}\right) \\
 &= O(m)
 \end{aligned}
 \tag{12.15}$$

As $m = O(\lg n)$, so the amortized performance downgrade from constant time to logarithm, although it is still faster than the normal array insertion which is $O(n)$ in average.

The random accessing gets a bit faster because we can use array indexing instead of tree search.

```

function GET( $L, i$ )
  for each  $t \in \text{TREES}(L)$  do
    if  $t \neq \text{NIL}$  then
      if  $i \leq \text{SIZE}(t)$  then
        return  $t[i]$ 
      else
         $i \leftarrow i - \text{SIZE}(t)$ 

```

Here we skip the error handling such as out of bound indexing etc. The ANSI C program of this algorithm is like the following.

```

Key get(struct List a, int i) {
  int j, sz;
  for ( $j = 0, sz = 1; j < M; ++j, sz \ll = 1$ )
    if (a.tree[j]) {
      if ( $i < sz$ )
        break;
       $i -= sz$ ;
    }
  return a.tree[j][i];
}

```

The imperative removal and random mutating algorithms are left as exercises to the reader.

Exercise 12.2

1. Please implement the random access algorithms, including looking up and updating, for binary random access list with numeric representation in your favorite programming language.
2. Prove that the amortized performance of deletion is $O(1)$ constant time by using aggregation analysis.
3. Design and implement the binary random access list by implicit array in your favorite imperative programming language.

12.4 Imperative paired-array list

12.4.1 Definition

In previous chapter about queue, a symmetric solution, naming paired-array is presented. It is capable to operate on both ends of the queue. Because the nature that array supports



Figure 12.6: A paired-array list, which is consist of 2 arrays linking in head-head manner.

fast random access. It can be also used to realize a fast random access sequence in imperative setting.

Figure 12.6 shows the design of paired-array list. Two arrays are linked in head-head manner. To insert a new element on the head of the sequence, the element is appended at the end of front array; To append a new element on the tail of the sequence, the element is appended at the end of rear array;

Here is a ISO C++ code snippet to define the this data structure.

```

template<typename Key>
struct List {
    int n, m;
    vector<Key> front;
    vector<Key> rear;

    List() : n(0), m(0) {}
    int size() { return n + m; }
};

```

Here we use vector provides in standard library to cover the dynamic memory management issues, so that we can concentrate on the algorithm design.

12.4.2 Insertion and appending

Suppose function $\text{FRONT}(L)$ returns the front array, while $\text{REAR}(L)$ returns the rear array. For illustration purpose, we assume the arrays are dynamic allocated. inserting and appending can be realized as the following.

```

function INSERT( $L, x$ )
     $F \leftarrow \text{FRONT}(L)$ 
     $\text{SIZE}(F) \leftarrow \text{SIZE}(F) + 1$ 
     $F[\text{SIZE}(F)] \leftarrow x$ 

```

```

function APPEND( $L, x$ )
     $R \leftarrow \text{REAR}(L)$ 
     $\text{SIZE}(R) \leftarrow \text{SIZE}(R) + 1$ 
     $R[\text{SIZE}(R)] \leftarrow x$ 

```

As all the above operations manipulate the front and rear array on tail, they are all constant $O(1)$ time. And the following are the corresponding ISO C++ programs.

```

template<typename Key>
void insert(List<Key>& xs, Key x) {
    ++xs.n;
    xs.front.push_back(x);
}

template<typename Key>
void append(List<Key>& xs, Key x) {
    ++xs.m;
    xs.rear.push_back(x);
}

```

12.4.3 random access

As the inner data structure is array (dynamic array as vector), which supports random access by nature, it's trivial to implement constant time indexing algorithm.

```

function GET( $L, i$ )
   $F \leftarrow$  FRONT( $L$ )
   $n \leftarrow$  SIZE( $F$ )
  if  $i \leq n$  then
    return  $F[n - i + 1]$ 
  else
    return REAR( $L$ )[ $i - n$ ]

```

Here the index $i \in [1, |L|]$. If it is not greater than the size of front array, the element is stored in front. However, as front and rear arrays are connect head-to-head, so the elements in front array are in reverse order. We need locate the element by subtracting the size of front array by i ; If the index i is greater than the size of front array, the element is stored in rear array. Since elements are stored in normal order in rear, we just need subtract the index i by an offset which is the size of front array.

Here is the ISO C++ program implements this algorithm.

```

template<typename Key>
Key get(List<Key>& xs, int i) {
  if( i < xs.n )
    return xs.front[xs.n-i-1];
  else
    return xs.rear[i-xs.n];
}

```

The random mutating algorithm is left as an exercise to the reader.

12.4.4 removing and balancing

Removing isn't as simple as insertion and appending. This is because we must handle the condition that one array (either front or rear) becomes empty due to removal, while the other still contains elements. In extreme case, the list turns to be quite unbalanced. So we must fix it to resume the balance.

One idea is to trigger this fixing when either front or rear array becomes empty. We just cut the other array in half, and reverse the first half to form the new pair. The algorithm is described as the following.

```

function BALANCE( $L$ )
   $F \leftarrow$  FRONT( $L$ ),  $R \leftarrow$  REAR( $L$ )
   $n \leftarrow$  SIZE( $F$ ),  $m \leftarrow$  SIZE( $R$ )
  if  $F = \phi$  then
     $F \leftarrow$  REVERSE( $R[1 \dots \lfloor \frac{m}{2} \rfloor]$ )
     $R \leftarrow R[\lfloor \frac{m}{2} \rfloor + 1 \dots m]$ 
  else if  $R = \phi$  then
     $R \leftarrow$  REVERSE( $F[1 \dots \lfloor \frac{n}{2} \rfloor]$ )
     $F \leftarrow F[\lfloor \frac{n}{2} \rfloor + 1 \dots n]$ 

```

Actually, the operations are symmetric for the case that front is empty and the case that rear is empty. Another approach is to swap the front and rear for one symmetric case and recursive resumes the balance, then swap the front and rear back. For example below ISO C++ program uses this method.

```

template<typename Key>
void balance(List<Key>& xs) {
  if(xs.n == 0) {

```

```

    back_insert_iterator<vector<Key> > i(xs.front);
    reverse_copy(xs.rear.begin(), xs.rear.begin() + xs.m/2, i);
    xs.rear.erase(xs.rear.begin(), xs.rear.begin() +xs.m/2);
    xs.n = xs.m/2;
    xs.m = xs.n;
} else if(xs.m == 0) {
    swap(xs.front, xs.rear);
    swap(xs.n, xs.m);
    balance(xs);
    swap(xs.front, xs.rear);
    swap(xs.n, xs.m);
}
}
}

```

With BALANCE algorithm defined, it's trivial to implement remove algorithm both on head and on tail.

```

function REMOVE-HEAD( $L$ )
    BALANCE( $L$ )
     $F \leftarrow$  FRONT( $L$ )
    if  $F = \phi$  then
        REMOVE-TAIL( $L$ )
    else
        SIZE( $F$ )  $\leftarrow$  SIZE( $F$ ) - 1

```

```

function REMOVE-TAIL( $L$ )
    BALANCE( $L$ )
     $R \leftarrow$  REAR( $L$ )
    if  $R = \phi$  then
        REMOVE-HEAD( $L$ )
    else
        SIZE( $R$ )  $\leftarrow$  SIZE( $R$ ) - 1

```

There is an edge case for each, that is even after balancing, the array targeted to perform removal is still empty. This happens that there is only one element stored in the paired-array list. The solution is just remove this singleton left element, and the overall list results empty. Below is the ISO C++ program implements this algorithm.

```

template<typename Key>
void remove_head(List<Key>& xs) {
    balance(xs);
    if(xs.front.empty())
        remove_tail(xs); //remove the singleton elem in rear
    else {
        xs.front.pop_back();
        --xs.n;
    }
}

template<typename Key>
void remove_tail(List<Key>& xs) {
    balance(xs);
    if(xs.rear.empty())
        remove_head(xs); //remove the singleton elem in front
    else {
        xs.rear.pop_back();
        --xs.m;
    }
}

```

It's obvious that the worst case performance is $O(n)$ where n is the number of elements

stored in paired-array list. This happens when balancing is triggered, and both reverse and shifting are linear operation. However, the amortized performance of removal is still $O(1)$, the proof is left as exercise to the reader.

Exercise 12.3

1. Implement the random mutating algorithm in your favorite imperative programming language.
2. We utilized vector provided in standard library to manage memory dynamically, try to realize a version using plain array and manage the memory allocation manually. Compare this version and consider how does this affect the performance?
3. Prove that the amortized performance of removal is $O(1)$ for paired-array list.

12.5 Concatenate-able list

By using binary random access list, we realized sequence data structure which supports $O(\lg n)$ time insertion and removal on head, as well as random accessing element with a given index.

However, it's not so easy to concatenate two lists. As both lists are forests of complete binary trees, we can't merely merge them (Since forests are essentially list of trees, and for any size, there is at most one tree of that size. Even concatenate forests directly is not fast). One solution is to push the element from the first sequence one by one to a stack and then pop those elements and insert them to the head of the second one by using 'cons' function. Of course the stack can be implicitly used in recursion manner, for instance:

$$\text{concat}(s_1, s_2) = \begin{cases} s_2 & : s_1 = \phi \\ \text{cons}(\text{head}(s_1), \text{concat}(\text{tail}(s_1), s_2)) & : \text{otherwise} \end{cases} \quad (12.16)$$

Where function *cons*, *head* and *tail* are defined in previous section.

If the length of the two sequence is n , and m , this method takes $O(N \lg n)$ time repeatedly push all elements from the first sequence to stacks, and then takes $\Omega(n \lg(n + m))$ to insert the elements in front of the second sequence. Note that Ω means the upper limit, There is detailed definition for it in [4].

We have already implemented the real-time queue in previous chapter. It supports $O(1)$ time pop and push. If we can turn the sequence concatenation to a kind of pushing operation to queue, the performance will be improved to $O(1)$ as well. Okasaki gave such realization in [3], which can concatenate lists in constant time.

To represent a concatenate-able list, the data structure designed by Okasaki is essentially a K-ary tree. The root of the tree stores the first element in the list. So that we can access it in constant $O(1)$ time. The sub-trees or children are all small concatenate-able lists, which are managed by real-time queues. Concatenating another list to the end is just adding it as the last child, which is in turn a queue pushing operation. Appending a new element can be realized as that, first wrapping the element to a singleton tree, which is a leaf with no children. Then, concatenate this singleton to finalize appending.

Figure 12.7 illustrates this data structure.

Such recursively designed data structure can be defined in the following Haskell code.

```
data CList a = Empty | CList a (Queue (CList a))
```

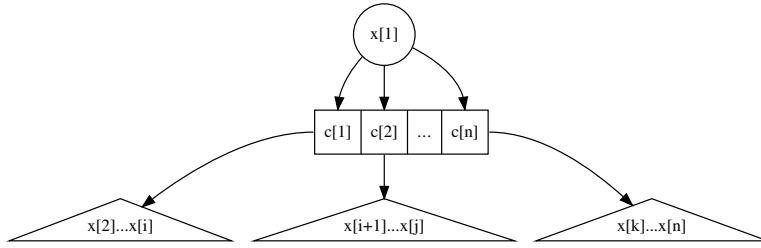
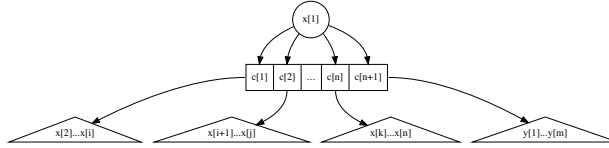

(a) The data structure for list $\{x_1, x_2, \dots, x_n\}$ (b) The result after concatenated with list $\{y_1, y_2, \dots, y_m\}$

Figure 12.7: Data structure for concatenate-able list

It means that a concatenate-able list is either empty or a K-ary tree, which again consists of a queue of concatenate-able sub-lists and a root element. Here we reuse the realization of real-time queue mentioned in previous chapter.

Suppose function $clist(x, Q)$ constructs a concatenate-able list from an element x , and a queue of sub-lists Q . While function $root(s)$ returns the root element of such K-ary tree implemented list. and function $queue(s)$ returns the queue of sub-lists respectively. We can implement the algorithm to concatenate two lists like this.

$$concat(s_1, s_2) = \begin{cases} s_1 & : s_2 = \phi \\ s_2 & : s_1 = \phi \\ clist(x, push(Q, s_2)) & : otherwise \end{cases} \quad (12.17)$$

Where $x = root(s_1)$ and $Q = queue(s_1)$. The idea of concatenation is that if either one of the list to be concatenated is empty, the result is just the other list; otherwise, we push the second list as the last child to the queue of the first list.

Since the push operation is $O(1)$ constant time for a well realized real-time queue, the performance of concatenation is bound to $O(1)$.

The *concat* function can be translated to the below Haskell program.

```
concat x Empty = x
concat Empty y = y
concat (CList x q) y = CList x (push q y)
```

Besides the good performance of concatenation, this design also brings satisfied features for adding element both on head and tail.

$$cons(x, s) = concat(clist(x, \phi), s) \quad (12.18)$$

$$append(s, x) = concat(s, clist(x, \phi)) \quad (12.19)$$

Getting the first element is just returning the root of the K-ary tree.

$$head(s) = root(s) \quad (12.20)$$

It's a bit complex to realize the algorithm that removes the first element from a concatenate-able list. This is because after the root, which is the first element in the

sequence got removed, we have to re-construct the rest things, a queue of sub-lists, to a K-ary tree.

After the root being removed, there left all children of the K-ary tree. Note that all of them are also concatenate-able list, so that one natural solution is to concatenate them all together to a big list.

$$\text{concatAll}(Q) = \begin{cases} \phi & : Q = \phi \\ \text{concat}(\text{front}(Q), \text{concatAll}(\text{pop}(Q))) & : \text{otherwise} \end{cases} \quad (12.21)$$

Where function *front* just returns the first element from a queue without removing it, while *pop* does the removing work.

If the queue is empty, it means that there is no children at all, so the result is also an empty list; Otherwise, we pop the first child, which is a concatenate-able list, from the queue, and recursively concatenate all the rest children to a list; finally, we concatenate this list behind the already popped first children.

With *concatAll* defined, we can then implement the algorithm of removing the first element from a list as below.

$$\text{tail}(s) = \text{linkAll}(\text{queue}(s)) \quad (12.22)$$

The corresponding Haskell program is given like the following.

```

head (CList x _) = x
tail (CList _ q) = linkAll q

linkAll q | isEmptyQ q = Empty
          | otherwise = link (front q) (linkAll (pop q))

```

Function *isEmptyQ* is used to test a queue is empty, it is trivial and we omit its definition. Readers can refer to the source code along with this book.

linkAll algorithm actually traverses the queue data structure, and reduces to a final result. This remind us of *folding* mentioned in the chapter of binary search tree. readers can refer to the appendix of this book for the detailed description of folding. It's quite possible to define a folding algorithm for queue instead of list³ [10].

$$\text{foldQ}(f, e, Q) = \begin{cases} e & : Q = \phi \\ f(\text{front}(Q), \text{foldQ}(f, e, \text{pop}(Q))) & : \text{otherwise} \end{cases} \quad (12.23)$$

Function *foldQ* takes three parameters, a function *f*, which is used for reducing, an initial value *e*, and the queue *Q* to be traversed.

Here are some examples to illustrate folding on queue. Suppose a queue *Q* contains elements {1, 2, 3, 4, 5} from head to tail.

$$\begin{aligned} \text{foldQ}(+, 0, Q) &= 1 + (2 + (3 + (4 + (5 + 0)))) = 15 \\ \text{foldQ}(\times, 1, Q) &= 1 \times (2 \times (3 \times (4 \times (5 \times 1)))) = 120 \\ \text{foldQ}(\times, 0, Q) &= 1 \times (2 \times (3 \times (4 \times (5 \times 0)))) = 0 \end{aligned}$$

Function *linkAll* can be changed by using *foldQ* accordingly.

$$\text{linkAll}(Q) = \text{foldQ}(\text{link}, \phi, Q) \quad (12.24)$$

The Haskell program can be modified as well.

³Some functional programming language, such as Haskell, defined type class, which is a concept of monoid so that it's easy to support folding on a customized data structure.

```
linkAll = foldQ link Empty

foldQ :: (a → b → b) → b → Queue a → b
foldQ f z q | isEmptyQ q = z
            | otherwise = (front q) `f` foldQ f z (pop q)
```

However, the performance of removing can't be ensured in all cases. The worst case is that, user keeps appending n elements to a empty list, and then immediately performs removing. At this time, the K-ary tree has the first element stored in root. There are $n - 1$ children, all are leaves. So *linkAll()* algorithm downgrades to $O(n)$ which is linear time.

Considering the add, append, concatenate and removing operations are randomly performed. The average case is amortized $O(1)$, The proof is left as an exercise to the reader.

Exercise 12.4

1. Can you figure out a solution to append an element to the end of a binary random access list?
2. Prove that the amortized performance of removal operation for concatenate-able list is $O(1)$. Hint: using the banker's method.
3. Implement the concatenate-able list in your favorite imperative language.

12.6 Finger tree

We haven't been able to meet all the performance targets listed at the beginning of this chapter.

Binary random access list enables to insert, remove element on the head of sequence, and random access elements fast. However, it performs poor when concatenates lists. There is no good way to append element at the end of binary random access list.

Concatenate-able list is capable to concatenates multiple lists in a fly, and it performs well for adding new element both on head and tail. However, it doesn't support randomly access element with a given index.

These two examples bring us some ideas:

- In order to support fast manipulation both on head and tail of the sequence, there must be some way to easily access the head and tail position;
- Tree like data structure helps to turn the random access into divide and conquer search, if the tree is well balance, the search can be ensured to be logarithm time.

12.6.1 Definition

Finger tree[66], which was first invented in 1977, can help to realize efficient sequence. And it is also well implemented in purely functional settings[65].

As we mentioned that the balance of the tree is critical to ensure the performance for search. One option is to use balanced tree as the under ground data structure for finger tree. For example the 2-3 tree, which is a special B-tree. (readers can refer to the chapter of B-tree of this book).

A 2-3 tree either contains 2 children or 3. It can be defined as below in Haskell.

```
data Node a = Br2 a a | Br3 a a a
```

In imperative settings, node can be defined with a list of sub nodes, which contains at most 3 children. For instance the following ANSI C code defines node.

```
union Node {
    Key* keys;
    union Node* children;
};
```

Note in this definition, a node can either contain 2 ~ 3 keys, or 2 ~ 3 sub nodes. Where key is the type of elements stored in leaf node.

We mark the left-most none-leaf node as the front finger (or left finger) and the right-most none-leaf node as the rear finger (or right finger). Since both fingers are essentially 2-3 trees with all leafs as children, they can be directly represented as list of 2 or 3 leafs. Of course a finger tree can be empty or contain only one element as leaf.

So the definition of a finger tree is specified like this.

- A finger tree is either empty;
- or a singleton leaf;
- or contains three parts: a left finger which is a list contains at most 3 elements; a sub finger tree; and a right finger which is also a list contains at most 3 elements.

Note that this definition is recursive, so it's quite possible to be translated to functional settings. The following Haskell definition summaries these cases for example.

```
data Tree a = Empty
            | Lf a
            | Tr [a] (Tree (Node a)) [a]
```

In imperative settings, we can define the finger tree in a similar manner. What's more, we can add a parent field, so that it's possible to back-track to root from any tree node. Below ANSI C code defines finger tree accordingly.

```
struct Tree {
    union Node* front;
    union Node* rear;
    Tree* mid;
    Tree* parent;
};
```

We can use NIL pointer to represent an empty tree; and a leaf tree contains only one element in its front finger, both its rear finger and middle part are empty.

Figure 12.8 and 12.9 show some examples of figure tree.

The first example is an empty finger tree; the second one shows the result after inserting one element to empty, it becomes a leaf of one node; the third example shows a finger tree contains 2 elements, one is in front finger, the other is in rear.

If we continuously insert new elements, to the tree, those elements will be put in the front finger one by one, until it exceeds the limit of 2-3 tree. The 4-th example shows such condition, that there are 4 elements in front finger, which isn't balanced any more.

The last example shows that the finger tree gets fixed so that it resumes balancing. There are two elements in the front finger. Note that the middle part is not empty any longer. It's a *leaf* of a 2-3 tree (why it's a leaf is explained later). The content of the leaf is a tree with 3 branches, each contains an element.

We can express these 5 examples as the following Haskell expression.

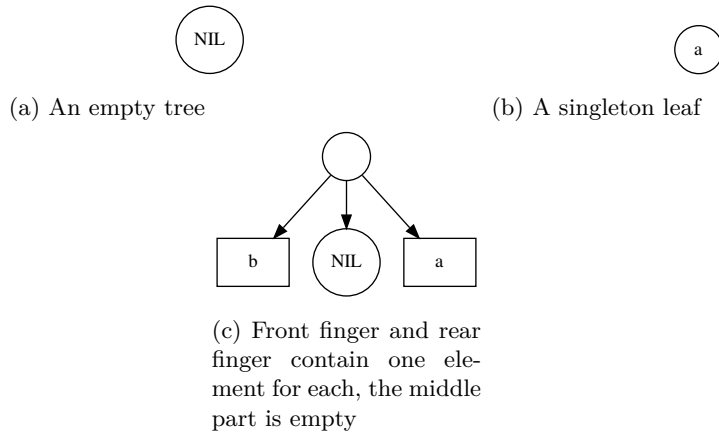


Figure 12.8: Examples of finger tree, 1

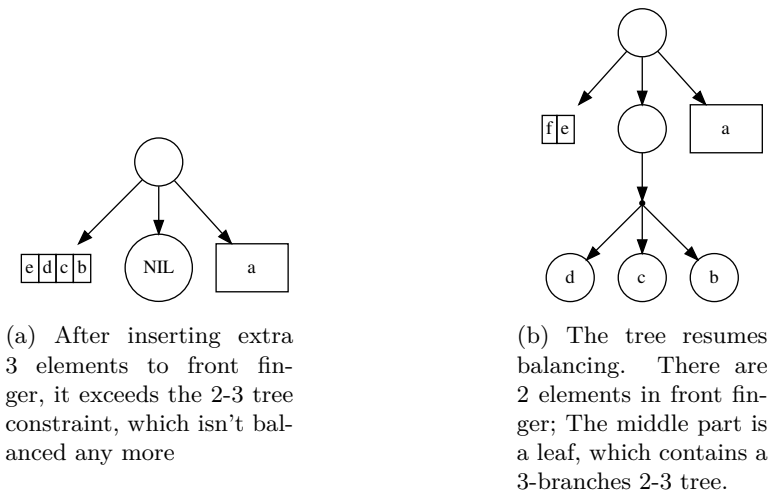


Figure 12.9: Examples of finger tree, 2

```

Empty
Lf a
[b] Empty [a]
[e, d, c, b] Empty [a]
[f, e] Lf (Br3 d c b) [a]

```

In the last example, why the middle part inner tree is a leaf? As we mentioned that the definition of finger tree is recursive. The middle part besides the front and rear finger is a deeper finger tree, which is defined as $Tree(Node(a))$. Every time we go deeper, the $Node$ is embedded one more level. if the element type of the first level tree is a , the element type for the second level tree is $Node(a)$, the third level is $Node(Node(a))$, ..., the n -th level is $Node(Node(Node(...(a)...)) = Node^n(a)$, where n indicates the $Node$ is applied n times.

12.6.2 Insert element to the head of sequence

The examples list above actually reveal the typical process that the elements are inserted one by one to a finger tree. It's possible to summarize these examples to some cases for insertion on head algorithm.

When we insert an element x to a finger tree T ,

- If the tree is empty, the result is a leaf which contains the singleton element x ;
- If the tree is a singleton leaf of element y , the result is a new finger tree. The front finger contains the new element x , the rear finger contains the previous element y ; the middle part is a empty finger tree;
- If the number of elements stored in front finger isn't bigger than the upper limit of 2-3 tree, which is 3, the new element is just inserted to the head of front finger;
- otherwise, it means that the number of elements stored in front finger exceeds the upper limit of 2-3 tree. the last 3 elements in front finger is wrapped in a 2-3 tree and recursively inserted to the middle part. the new element x is inserted in front of the rest elements in front finger.

Suppose that function $leaf(x)$ creates a leaf of element x , function $tree(F, T', R)$ creates a finger tree from three part: F is the front finger, which is a list contains several elements. Similarly, R is the rear finger, which is also a list. T' is the middle part which is a deeper finger tree. Function $tr3(a, b, c)$ creates a 2-3 tree from 3 elements a, b, c ; while $tr2(a, b)$ creates a 2-3 tree from 2 elements a and b .

$$insertT(x, T) = \begin{cases} leaf(x) & : T = \phi \\ tree(\{x\}, \phi, \{y\}) & : T = leaf(y) \\ tree(\{x, x_1\}, insertT(tr3(x_2, x_3, x_4), T'), R) & : T = tree(\{x_1, x_2, x_3, x_4\}, T', R) \\ tree(\{x\} \cup F, T', R) & : otherwise \end{cases} \quad (12.25)$$

The performance of this algorithm is dominated by the recursive case. All the other cases are constant $O(1)$ time. The recursion depth is proportion to the height of the tree, so the algorithm is bound to $O(h)$ time, where h is the height. As we use 2-3 tree to ensure that the tree is well balanced, $h = O(\lg n)$, where n is the number of elements stored in the finger tree.

More analysis reveal that the amortized performance of $insertT$ is $O(1)$ because we can amortize the expensive recursion case to other trivial cases. Please refer to [3] and [65] for the detailed proof.

Translating the algorithm yields the below Haskell program.

```

cons :: a → Tree a → Tree a
cons a Empty = Lf a
cons a (Lf b) = Tr [a] Empty [b]
cons a (Tr [b, c, d, e] m r) = Tr [a, b] (cons (Br3 c d e) m) r
cons a (Tr f m r) = Tr (a:f) m r

```

Here we use the LISP naming convention to illustrate inserting a new element to a list.

The insertion algorithm can also be implemented in imperative approach. Suppose function TREE() creates an empty tree, that all fields, including front and rear finger, the middle part inner tree and parent are empty. Function NODE() creates an empty node.

```

function PREPEND-NODE( $n, T$ )
   $r \leftarrow$  TREE()
   $p \leftarrow r$ 
  CONNECT-MID( $p, T$ )
  while FULL?(FRONT( $T$ )) do
     $F \leftarrow$  FRONT( $T$ )  $\triangleright F = \{n_1, n_2, n_3, \dots\}$ 
    FRONT( $T$ )  $\leftarrow$   $\{n, F[1]\}$   $\triangleright F[1] = n_1$ 
     $n \leftarrow$  NODE()
    CHILDREN( $n$ )  $\leftarrow$   $F[2..]$   $\triangleright F[2..] = \{n_2, n_3, \dots\}$ 
     $p \leftarrow T$ 
     $T \leftarrow$  MID( $T$ )
  if  $T = \text{NIL}$  then
     $T \leftarrow$  TREE()
    FRONT( $T$ )  $\leftarrow$   $\{n\}$ 
  else if |FRONT( $T$ )| = 1  $\wedge$  REAR( $T$ ) =  $\phi$  then
    REAR( $T$ )  $\leftarrow$  FRONT( $T$ )
    FRONT( $T$ )  $\leftarrow$   $\{n\}$ 
  else
    FRONT( $T$ )  $\leftarrow$   $\{n\} \cup$  FRONT( $T$ )
  CONNECT-MID( $p, T$ )  $\leftarrow$   $T$ 
  return FLAT( $r$ )

```

Where the notation $L[i..]$ means a sub list of L with the first $i - 1$ elements removed, that if $L = \{a_1, a_2, \dots, a_n\}$, then $L[i..] = \{a_i, a_{i+1}, \dots, a_n\}$.

Functions FRONT, REAR, MID, and PARENT are used to access the front finger, the rear finger, the middle part inner tree and the parent tree respectively; Function CHILDREN accesses the children of a node.

Function CONNECT-MID(T_1, T_2), connect T_2 as the inner middle part tree of T_1 , and set the parent of T_2 as T_1 if T_2 isn't empty.

In this algorithm, we performs a one pass top-down traverse along the middle part inner tree if the front finger is full that it can't afford to store any more. The criteria for full for a 2-3 tree is that the finger contains 3 elements already. In such case, we extract all the elements except the first one off, wrap them to a new node (one level deeper node), and continuously insert this new node to its middle inner tree. The first element is left in the front finger, and the element to be inserted is put in front of it, so that this element becomes the new first one in the front finger.

After this traversal, the algorithm either reach an empty tree, or the tree still has room to hold more element in its front finger. We create a new leaf for the former case, and perform a trivial list insert to the front finger for the latter.

During the traversal, we use p to record the parent of the current tree we are processing. So any new created tree are connected as the middle part inner tree to p .

Finally, we return the root of the tree r . The last trick of this algorithm is the FLAT function. In order to simplify the logic, we create an empty ‘ground’ tree and set it as the parent of the root. We need eliminate this extra ‘ground’ level before return the root. This flatten algorithm is realized as the following.

```
function FLAT( $T$ )
  while  $T \neq \text{NIL} \wedge T$  is empty do
     $T \leftarrow \text{MID}(T)$ 
  if  $T \neq \text{NIL}$  then
    PARENT( $T$ )  $\leftarrow$  NIL
  return  $T$ 
```

The while loop test if T is trivial empty, that it’s not NIL(= ϕ), while both its front and rear fingers are empty.

Below Python code implements the insertion algorithm for finger tree.

```
def insert( $x$ ,  $t$ ):
  return prepend_node(wrap( $x$ ),  $t$ )

def prepend_node( $n$ ,  $t$ ):
  root = prev = Tree()
  prev.set_mid( $t$ )
  while frontFull( $t$ ):
     $f = t$ .front
     $t$ .front = [ $n$ ] +  $f$ [:1]
     $n = \text{wraps}(f[1:])$ 
    prev =  $t$ 
     $t = t$ .mid
  if  $t$  is None:
     $t = \text{leaf}(n)$ 
  elif len( $t$ .front)==1 and  $t$ .rear == []:
     $t = \text{Tree}([n], \text{None}, t$ .front)
  else:
     $t = \text{Tree}([n]+t$ .front,  $t$ .mid,  $t$ .rear)
  prev.set_mid( $t$ )
  return flat(root)

def flat( $t$ ):
  while  $t$  is not None and  $t$ .empty():
     $t = t$ .mid
  if  $t$  is not None:
     $t$ .parent = None
  return  $t$ 
```

The implementation of function `set_mid`, `frontFull`, `wrap`, `wraps`, `empty`, and tree constructor are trivial enough, that we skip the detail of them here. Readers can take these as exercises.

12.6.3 Remove element from the head of sequence

It’s easy to implement the reverse operation that remove the first element from the list by reversing the `insertT()` algorithm line by line.

Let’s denote $F = \{f_1, f_2, \dots\}$ is the front finger list, M is the middle part inner finger tree. $R = \{r_1, r_2, \dots\}$ is the rear finger list of a finger tree, and $R' = \{r_2, r_3, \dots\}$ is the rest

of element with the first one removed from R .

$$\text{extractT}(T) = \begin{cases} (x, \phi) & : T = \text{leaf}(x) \\ (x, \text{leaf}(y)) & : T = \text{tree}(\{x\}, \phi, \{y\}) \\ (x, \text{tree}(\{r_1\}, \phi, R')) & : T = \text{tree}(\{x\}, \phi, R) \\ (x, \text{tree}(\text{toList}(F'), M', R)) & : T = \text{tree}(\{x\}, M, R), (F', M') = \text{extractT}(M) \\ (f_1, \text{tree}(\{f_2, f_3, \dots\}, M, R)) & : \text{otherwise} \end{cases} \quad (12.26)$$

Where function $\text{toList}(T)$ converts a 2-3 tree to plain list as the following.

$$\text{toList}(T) = \begin{cases} \{x, y\} & : T = \text{tr2}(x, y) \\ \{x, y, z\} & : T = \text{tr3}(x, y, z) \end{cases} \quad (12.27)$$

Here we skip the error handling such as trying to remove element from empty tree etc. If the finger tree is a leaf, the result after removal is an empty tree; If the finger tree contains two elements, one in the front finger, the other in rear, we return the element stored in front finger as the first element, and the resulted tree after removal is a leaf; If there is only one element in front finger, the middle part inner tree is empty, and the rear finger isn't empty, we return the only element in front finger, and borrow one element from the rear finger to front; If there is only one element in front finger, however, the middle part inner tree isn't empty, we can recursively remove a node from the inner tree, and flatten it to a plain list to replace the front finger, and remove the original only element in front finger; The last case says that if the front finger contains more than one element, we can just remove the first element from front finger and keep all the other part unchanged.

Figure 12.10 shows the steps of removing two elements from the head of a sequence. There are 10 elements stored in the finger tree. When the first element is removed, there is still one element left in the front finger. However, when the next element is removed, the front finger is empty. So we ‘borrow’ one tree node from the middle part inner tree. This is a 2-3 tree. it is converted to a list of 3 elements, and the list is used as the new finger. the middle part inner tree change from three parts to a singleton leaf, which contains only one 2-3 tree node. There are three elements stored in this tree node.

Below is the corresponding Haskell program for ‘uncons’.

```
uncons :: Tree a -> (a, Tree a)
uncons (Lf a) = (a, Empty)
uncons (Tr [a] Empty [b]) = (a, Lf b)
uncons (Tr [a] Empty (r:rs)) = (a, Tr [r] Empty rs)
uncons (Tr [a] m r) = (a, Tr (nodeToList f) m' r) where (f, m') = uncons m
uncons (Tr f m r) = (head f, Tr (tail f) m r)
```

And the function `nodeToList` is defined like this.

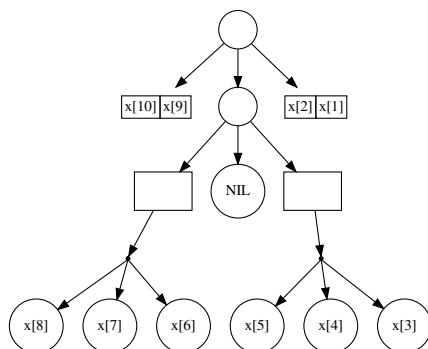
```
nodeToList :: Node a -> [a]
nodeToList (Br2 a b) = [a, b]
nodeToList (Br3 a b c) = [a, b, c]
```

Similar as above, we can define `head` and `tail` function from `uncons`.

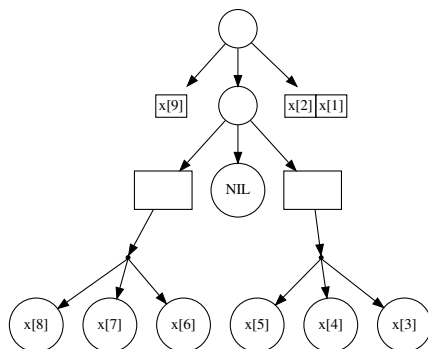
```
head = fst ◦ uncons
tail = snd ◦ uncons
```

12.6.4 Handling the ill-formed finger tree when removing

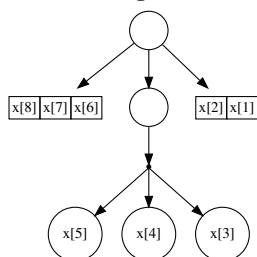
The strategy used so far to remove element from finger tree is a kind of removing and borrowing. If the front finger becomes empty after removing, we borrows more nodes



(a) A sequence of 10 elements represented as a finger tree



(b) The first element is removed. There is one element left in front finger.



(c) Another element is removed from head. We borrowed one node from the middle part inner tree, change the node, which is a 2-3 tree, to a list, and use it as the new front finger. The middle part inner tree becomes a leaf of one 2-3 tree node.

Figure 12.10: Examples of remove 2 elements from the head of a sequence

from the middle part inner tree. However there exists cases that the tree is ill-formed, for example, both the front fingers of the tree and its middle part inner tree are empty. Such ill-formed tree can result from imperatively splitting, which we'll introduce later.

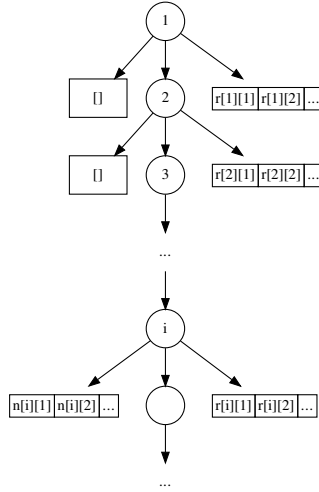


Figure 12.11: Example of an ill-formed tree. The front finger of the i -th level sub tree isn't empty.

Here we developed an imperative algorithm which can remove the first element from finger tree even it is ill-formed. The idea is first perform a top-down traverse to find a sub tree which either has a non-empty front finger or both its front finger and middle part inner tree are empty. For the former case, we can safely extract the first element which is a node from the front finger; For the latter case, since only the rear finger isn't empty, we can swap it with the empty front finger, and change it to the former case.

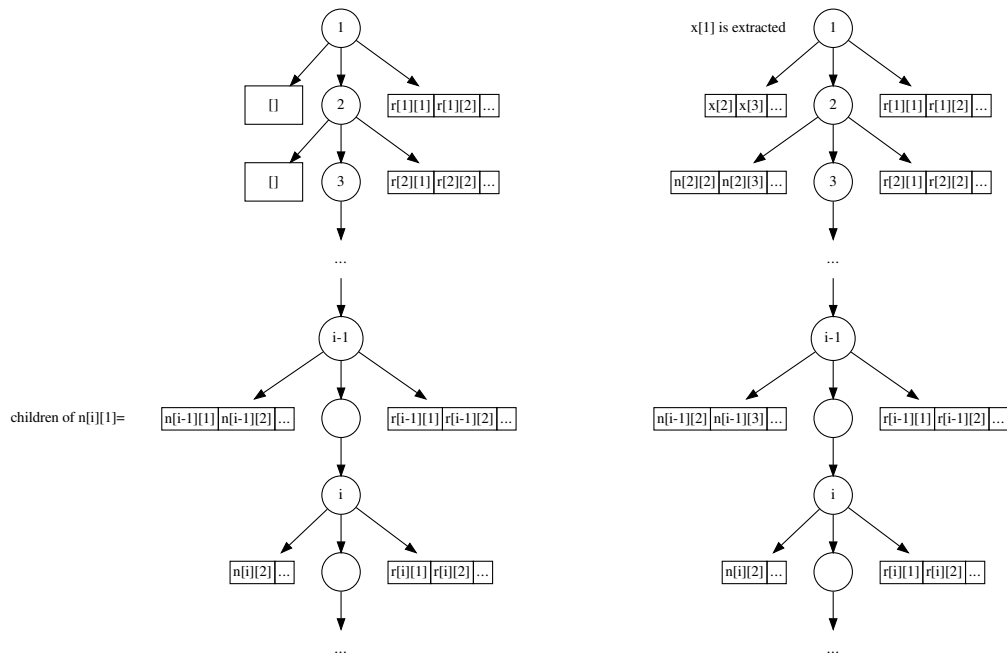
After that, we need examine the node we extracted from the front finger is leaf node (How to do that? this is left as an exercise to the reader). If not, we need go on extracting the first sub node from the children of this node, and left the rest of other children as the new front finger to the parent of the current tree. We need repeatedly go up along with the parent field till the node we extracted is a leaf. At that time point, we arrive at the root of the tree. Figure 12.12 illustrates this process.

Based on this idea, the following algorithm realizes the removal operation on head. The algorithm assumes that the tree passed in isn't empty.

```

function EXTRACT-HEAD( $T$ )
   $r \leftarrow$  TREE()
  CONNECT-MID( $r, T$ )
  while FRONT( $T$ ) =  $\phi \wedge$  MID( $T$ )  $\neq$  NIL do
     $T \leftarrow$  MID( $T$ )
  if FRONT( $T$ ) =  $\phi \wedge$  REAR( $T$ )  $\neq \phi$  then
    EXCHANGE FRONT( $T$ )  $\leftrightarrow$  REAR( $T$ )
   $n \leftarrow$  NODE()
  CHILDREN( $n$ )  $\leftarrow$  FRONT( $T$ )
  repeat
     $L \leftarrow$  CHILDREN( $n$ )                                 $\triangleright L = \{n_1, n_2, n_3, \dots\}$ 
     $n \leftarrow L[1]$                                         $\triangleright n \leftarrow n_1$ 
    FRONT( $T$ )  $\leftarrow L[2..]$                                 $\triangleright L[2..] = \{n_2, n_3, \dots\}$ 
     $T \leftarrow$  PARENT( $T$ )

```



(a) Extract the first element $n[i][1]$ and put its children to the front finger of upper level tree. (b) Repeat this process i times, and finally $x[1]$ is extracted.

Figure 12.12: Traverse bottom-up till a leaf is extracted.

```

if MID( $T$ ) becomes empty then
    MID( $T$ )  $\leftarrow$  NIL
until  $n$  is a leaf
return (ELEM( $n$ ), FLAT( $r$ ))

```

Note that function $\text{ELEM}(n)$ returns the only element stored inside leaf node n . Similar as imperative insertion algorithm, a stub ‘ground’ tree is used as the parent of the root, which can simplify the logic a bit. That’s why we need flatten the tree finally.

Below Python program translates the algorithm.

```

def extract_head(t):
    root = Tree()
    root.set_mid(t)
    while t.front == [] and t.mid is not None:
        t = t.mid
    if t.front == [] and t.rear  $\neq$  []:
        (t.front, t.rear) = (t.rear, t.front)
    n = wraps(t.front)
    while True: # a repeat-until loop
        ns = n.children
        n = ns[0]
        t.front = ns[1:]
        t = t.parent
        if t.mid.empty():
            t.mid.parent = None
            t.mid = None
        if n.leaf:
            break
    return (elem(n), flat(root))

```

Member function `Tree.empty()` returns true if both the front finger and the rear finger are empty. We put a flag `Node.leaf` to mark if a node is a leaf or compound node. The exercise of this section asks the reader to consider some alternatives.

As the ill-formed tree is allowed, the algorithms to access the first and last element of the finger tree must be modified, so that they don't blindly return the first or last child of the finger as the finger can be empty if the tree is ill-formed.

The idea is quite similar to the `EXTRACT-HEAD`, that in case the finger is empty while the middle part inner tree isn't, we need traverse along with the inner tree till a point that either the finger becomes non-empty or all the nodes are stored in the other finger. For instance, the following algorithm can return the first leaf node even the tree is ill-formed.

```
function FIRST-LF(T)
  while FRONT(T) =  $\phi$   $\wedge$  MID(T)  $\neq$  NIL do
    T  $\leftarrow$  MID(T)
  if FRONT(T) =  $\phi$   $\wedge$  REAR(T)  $\neq$   $\phi$  then
    n  $\leftarrow$  REAR(T)[1]
  else
    n  $\leftarrow$  FRONT(T)[1]
  while n is NOT leaf do
    n  $\leftarrow$  CHILDREN(n)[1]
  return n
```

Note the second loop in this algorithm that it keeps traversing on the first sub-node if current node isn't a leaf. So we always get a leaf node and it's trivial to get the element inside it.

```
function FIRST(T)
  return ELEM(FIRST-LF(T))
```

The following Python code translates the algorithm to real program.

```
def first(t):
    return elem(first_leaf(t))

def first_leaf(t):
    while t.front == [] and t.mid is not None:
        t = t.mid
    if t.front == [] and t.rear  $\neq$  []:
        n = t.rear[0]
    else:
        n = t.front[0]
    while not n.leaf:
        n = n.children[0]
    return n
```

To access the last element is quite similar, and we left it as an exercise to the reader.

12.6.5 append element to the tail of the sequence

Because finger tree is symmetric, we can give the realization of appending element on tail by referencing to *insertT* algorithm.

$$appendT(T, x) = \begin{cases} leaf(x) & : T = \phi \\ tree(\{y\}, \phi, \{x\}) & : T = leaf(y) \\ tree(F, appendT(M, tr3(x_1, x_2, x_3)), \{x_4, x\}) & : T = tree(F, M, \{x_1, x_2, x_3, x_4\}) \\ tree(F, M, R \cup \{x\}) & : otherwise \end{cases} \quad (12.28)$$

Generally speaking, if the rear finger is still valid 2-3 tree, that the number of elements is not greater than 4, the new elements is directly appended to rear finger. Otherwise,

we break the rear finger, take the first 3 elements in rear finger to create a new 2-3 tree, and recursively append it to the middle part inner tree. If the finger tree is empty or a singleton leaf, it will be handled in the first two cases.

Translating the equation to Haskell yields the below program.

```
snoc :: Tree a -> a -> Tree a
snoc Empty a = Lf a
snoc (Lf a) b = Tr [a] Empty [b]
snoc (Tr f m [a, b, c, d]) e = Tr f (snoc m (Br3 a b c)) [d, e]
snoc (Tr f m r) a = Tr f m (r++[a])
```

Function name **snoc** is mirror of **cons**, which indicates the symmetric relationship.

Appending new element to the end imperatively is quite similar. The following algorithm realizes appending.

```
function APPEND-NODE( $T, n$ )
   $r \leftarrow \text{TREE}()$ 
   $p \leftarrow r$ 
  CONNECT-MID( $p, T$ )
  while FULL?(REAR( $T$ )) do
     $R \leftarrow \text{REAR}(T)$   $\triangleright R = \{n_1, n_2, \dots, n_{m-1}, n_m\}$ 
    REAR( $T$ )  $\leftarrow \{n, \text{LAST}(R)\}$   $\triangleright$  last element  $n_m$ 
     $n \leftarrow \text{NODE}()$ 
    CHILDREN( $n$ )  $\leftarrow R[1..m-1]$   $\triangleright \{n_1, n_2, \dots, n_{m-1}\}$ 
     $p \leftarrow T$ 
     $T \leftarrow \text{MID}(T)$ 
  if  $T = \text{NIL}$  then
     $T \leftarrow \text{TREE}()$ 
    FRONT( $T$ )  $\leftarrow \{n\}$ 
  else if | REAR( $T$ ) | = 1  $\wedge$  FRONT( $T$ ) =  $\phi$  then
    FRONT( $T$ )  $\leftarrow$  REAR( $T$ )
    REAR( $T$ )  $\leftarrow \{n\}$ 
  else
    REAR( $T$ )  $\leftarrow$  REAR( $T$ )  $\cup \{n\}$ 
  CONNECT-MID( $p, T$ )  $\leftarrow T$ 
  return FLAT( $r$ )
```

And the corresponding Python programs is given as below.

```
def append_node(t, n):
    root = prev = Tree()
    prev.set_mid(t)
    while rearFull(t):
        r = t.rear
        t.rear = r[-1:] + [n]
        n = wraps(r[:-1])
        prev = t
        t = t.mid
    if t is None:
        t = leaf(n)
    elif len(t.rear) == 1 and t.front == []:
        t = Tree(t.rear, None, [n])
    else:
        t = Tree(t.front, t.mid, t.rear + [n])
    prev.set_mid(t)
    return flat(root)
```

12.6.6 remove element from the tail of the sequence

Similar to *appendT*, we can realize the algorithm which remove the last element from finger tree in symmetric manner of *extractT*.

We denote the non-empty, non-leaf finger tree as $tree(F, M, R)$, where F is the front finger, M is the middle part inner tree, and R is the rear finger.

$$removeT(T) = \begin{cases} (\phi, x) & : T = leaf(x) \\ (leaf(y), x) & : T = tree(\{y\}, \phi, \{x\}) \\ (tree(init(F), \phi, last(F)), x) & : T = tree(F, \phi, \{x\}) \wedge F \neq \phi \\ (tree(F, M', toList(R')), x) & : T = tree(F, M, \{x\}), (M', R') = removeT(M) \\ (tree(F, M, init(R)), last(R)) & : otherwise \end{cases} \quad (12.29)$$

Function *toList(T)* is used to flatten a 2-3 tree to plain list, which is defined previously. Function *init(L)* returns all elements except for the last one in list L , that if $L = \{a_1, a_2, \dots, a_{n-1}, a_n\}$, $init(L) = \{a_1, a_2, \dots, a_{n-1}\}$. And Function *last(L)* returns the last element, so that $last(L) = a_n$. Please refer to the appendix of this book for their implementation.

Algorithm *removeT()* can be translated to the following Haskell program, we name it as **unsnoc** to indicate it's the reverse function of **snoc**.

```
unsnoc :: Tree a -> (Tree a, a)
unsnoc (Lf a) = (Empty, a)
unsnoc (Tr [a] Empty [b]) = (Lf a, b)
unsnoc (Tr f@(_:_.) Empty [a]) = (Tr (init f) Empty [last f], a)
unsnoc (Tr f m [a]) = (Tr f m' (nodeToList r), a) where (m', r) = unsnoc m
unsnoc (Tr f m r) = (Tr f m (init r), last r)
```

And we can define a special function **last** and **init** for finger tree which is similar to their counterpart for list.

```
last = snd o unsnoc
init = fst o unsnoc
```

Imperatively removing the element from the end is almost as same as removing on the head. Although there seems to be a special case, that as we always store the only element (or sub node) in the front finger while the rear finger and middle part inner tree are empty (e.g. $Tree(\{n\}, NIL, \phi)$), it might get nothing if always try to fetch the last element from rear finger.

This can be solved by swapping the front and the rear finger if the rear is empty as in the following algorithm.

```
function EXTRACT-TAIL(T)
  r ← TREE()
  CONNECT-MID(r, T)
  while REAR(T) = φ ∧ MID(T) ≠ NIL do
    T ← MID(T)
  if REAR(T) = φ ∧ FRONT(T) ≠ φ then
    EXCHANGE FRONT(T) ↔ REAR(T)
  n ← NODE()
  CHILDREN(n) ← REAR(T)
  repeat
    L ← CHILDREN(n)
    n ← LAST(L)
    REAR(T) ← L[1...m-1]
    T ← PARENT(T)
  ▷ L = {n1, n2, ..., nm-1, nm}
  ▷ n ← nm
  ▷ {n1, n2, ..., nm-1}
```

```

if MID( $T$ ) becomes empty then
    MID( $T$ )  $\leftarrow$  NIL
until  $n$  is a leaf
return (ELEM( $n$ ), FLAT( $r$ ))

```

How to access the last element as well as implement this algorithm to working program are left as exercises.

12.6.7 concatenate

Consider the none-trivial case that concatenate two finger trees $T_1 = \text{tree}(F_1, M_1, R_1)$ and $T_2 = \text{tree}(F_2, M_2, R_2)$. One natural idea is to use F_1 as the new front finger for the concatenated result, and keep R_2 being the new rear finger. The rest of work is to merge M_1, R_1, F_2 and M_2 to a new middle part inner tree.

Note that both R_1 and F_2 are plain lists of node, so the sub-problem is to realize a algorithm like this.

$$\text{merge}(M_1, R_1 \cup F_2, M_2) = ?$$

More observation reveals that both M_1 and M_2 are also finger trees, except that they are one level deeper than T_1 and T_2 in terms of $\text{Node}(a)$, where a is the type of element stored in the tree. We can recursively use the strategy that keep the front finger of M_1 and the rear finger of M_2 , then merge the middle part inner tree of M_1, M_2 , as well as the rear finger of M_1 and front finger of M_2 .

If we denote function $\text{front}(T)$ returns the front finger, $\text{rear}(T)$ returns the rear finger, $\text{mid}(T)$ returns the middle part inner tree. the above merge algorithm can be expressed for non-trivial case as the following.

$$\begin{aligned} \text{merge}(M_1, R_1 \cup F_2, M_2) &= \text{tree}(\text{front}(M_1), S, \text{rear}(M_2)) \\ S &= \text{merge}(\text{mid}(M_1), \text{rear}(M_1) \cup R_1 \cup F_2 \cup \text{front}(M_2), \text{mid}(M_2)) \end{aligned} \quad (12.30)$$

If we look back to the original concatenate solution, it can be expressed as below.

$$\text{concat}(T_1, T_2) = \text{tree}(F_1, \text{merge}(M_1, R_1 \cup F_2, M_2), R_2) \quad (12.31)$$

And compare it with equation 12.30, it's easy to note the fact that concatenating is essentially merging. So we have the final algorithm like this.

$$\text{concat}(T_1, T_2) = \text{merge}(T_1, \phi, T_2) \quad (12.32)$$

By adding edge cases, the $\text{merge}()$ algorithm can be completed as below.

$$\text{merge}(T_1, S, T_2) = \begin{cases} \text{foldR}(\text{insertT}, T_2, S) & : T_1 = \phi \\ \text{foldL}(\text{appendT}, T_1, S) & : T_2 = \phi \\ \text{merge}(\phi, \{x\} \cup S, T_2) & : T_1 = \text{leaf}(x) \\ \text{merge}(T_1, S \cup \{x\}, \phi) & : T_2 = \text{leaf}(x) \\ \text{tree}(F_1, \text{merge}(M_1, \text{nodes}(R_1 \cup S \cup F_2), M_2), R_2) & : \text{otherwise} \end{cases} \quad (12.33)$$

Most of these cases are straightforward. If any one of T_1 or T_2 is empty, the algorithm repeatedly insert/append all elements in S to the other tree; Function foldL and foldR are kinds of for-each process in imperative settings. The difference is that foldL processes the list S from left to right while foldR processes from right to left.

Here are their definition. Suppose list $L = \{a_1, a_2, \dots, a_{n-1}, a_n\}$, $L' = \{a_2, a_3, \dots, a_{n-1}, a_n\}$ is the rest of elements except for the first one.

$$\text{foldL}(f, e, L) = \begin{cases} e & : L = \phi \\ \text{foldL}(f, f(e, a_1), L') & : \text{otherwise} \end{cases} \quad (12.34)$$

$$foldR(f, e, L) = \begin{cases} e & : L = \phi \\ f(a_1, foldR(f, e, L')) & : otherwise \end{cases} \quad (12.35)$$

They are detailed explained in the appendix of this book.

If either one of the tree is a leaf, we can insert or append the element of this leaf to S , so that it becomes the trivial case of concatenating one empty tree with another.

Function *nodes* is used to wrap a list of elements to a list of 2-3 trees. This is because the contents of middle part inner tree, compare to the contents of finger, are one level deeper in terms of *Node*. Consider the time point that transforms from recursive case to edge case. Let's suppose M_1 is empty at that time, we then need repeatedly insert all elements from $R_1 \cup S \cup F_2$ to M_2 . However, we can't directly do the insertion. If the element type is a , we can only insert $Node(a)$ which is 2-3 tree to M_2 . This is just like what we did in the *insertT* algorithm, take out the last 3 elements, wrap them in a 2-3 tree, and recursive perform *insertT*. Here is the definition of *nodes*.

$$nodes(L) = \begin{cases} \{tr2(x_1, x_2)\} & : L = \{x_1, x_2\} \\ \{tr3(x_1, x_2, x_3)\} & : L = \{x_1, x_2, x_3\} \\ \{tr2(x_1, x_2), tr2(x_3, x_4)\} & : L = \{x_1, x_2, x_3, x_4\} \\ \{tr3(x_1, x_2, x_3)\} \cup nodes(\{x_4, x_5, \dots\}) & : otherwise \end{cases} \quad (12.36)$$

Function *nodes* follows the constraint of 2-3 tree, that if there are only 2 or 3 elements in the list, it just wrap them in singleton list contains a 2-3 tree; If there are 4 elements in the lists, it split them into two trees each is consist of 2 branches; Otherwise, if there are more elements than 4, it wraps the first three in to one tree with 3 branches, and recursively call *nodes* to process the rest.

The performance of concatenation is determined by merging. Analyze the recursive case of merging reveals that the depth of recursion is proportion to the smaller height of the two trees. As the tree is ensured to be balanced by using 2-3 tree. it's height is bound to $O(\lg n')$ where n' is the number of elements. The edge case of merging performs as same as insertion, (It calls *insertT* at most 8 times) which is amortized $O(1)$ time, and $O(\lg m)$ at worst case, where m is the difference in height of the two trees. So the overall performance is bound to $O(\lg n)$, where n is the total number of elements contains in two finger trees.

The following Haskell program implements the concatenation algorithm.

```
concat :: Tree a → Tree a → Tree a
concat t1 t2 = merge t1 [] t2
```

Note that there is **concat** function defined in prelude standard library, so we need distinct them either by hiding import or take a different name.

```
merge :: Tree a → [a] → Tree a → Tree a
merge Empty ts t2 = foldr cons t2 ts
merge t1 ts Empty = foldl snoc t1 ts
merge (Lf a) ts t2 = merge Empty (a:ts) t2
merge t1 ts (Lf a) = merge t1 (ts++[a]) Empty
merge (Tr f1 m1 r1) ts (Tr f2 m2 r2) = Tr f1 (merge m1 (nodes (r1 ++ ts ++ f2)) m2) r2
```

And the implementation of *nodes* is as below.

```
nodes :: [a] → [Node a]
nodes [a, b] = [Br2 a b]
nodes [a, b, c] = [Br3 a b c]
nodes [a, b, c, d] = [Br2 a b, Br2 c d]
nodes (a:b:c:xs) = Br3 a b c:nodes xs
```

To concatenate two finger trees T_1 and T_2 in imperative approach, we can traverse the two trees along with the middle part inner tree till either tree turns to be empty. In

every iteration, we create a new tree T , choose the front finger of T_1 as the front finger of T ; and choose the rear finger of T_2 as the rear finger of T . The other two fingers (rear finger of T_1 and front finger of T_2) are put together as a list, and this list is then balanced grouped to several 2-3 tree nodes as N . Note that N grows along with traversing not only in terms of length, the depth of its elements increases by one in each iteration. We attach this new tree as the middle part inner tree of the upper level result tree to end this iteration.

Once either tree becomes empty, we stop traversing, and repeatedly insert the 2-3 tree nodes in N to the other non-empty tree, and set it as the new middle part inner tree of the upper level result.

Below algorithm describes this process in detail.

```

function CONCAT( $T_1, T_2$ )
  return MERGE( $T_1, \phi, T_2$ )

function MERGE( $T_1, N, T_2$ )
   $r \leftarrow$  TREE()
   $p \leftarrow r$ 
  while  $T_1 \neq \text{NIL} \wedge T_2 \neq \text{NIL}$  do
     $T \leftarrow$  TREE()
    FRONT( $T$ )  $\leftarrow$  FRONT( $T_1$ )
    REAR( $T$ )  $\leftarrow$  REAR( $T_2$ )
    CONNECT-MID( $p, T$ )
     $p \leftarrow T$ 
     $N \leftarrow$  NODES(REAR( $T_1$ )  $\cup$  FRONT( $T_2$ ))
     $T_1 \leftarrow$  MID( $T_1$ )
     $T_2 \leftarrow$  MID( $T_2$ )
  if  $T_1 = \text{NIL}$  then
     $T \leftarrow T_2$ 
    for each  $n \in$  REVERSE( $N$ ) do
       $T \leftarrow$  PREPEND-NODE( $n, T$ )
  else if  $T_2 = \text{NIL}$  then
     $T \leftarrow T_1$ 
    for each  $n \in N$  do
       $T \leftarrow$  APPEND-NODE( $T, n$ )
  CONNECT-MID( $p, T$ )
  return FLAT( $r$ )

```

Note that the for-each loops in the algorithm can also be replaced by folding from left and right respectively. Translating this algorithm to Python program yields the below code.

```

def concat(t1, t2):
  return merge(t1, [], t2)

def merge(t1, ns, t2):
  root = prev = Tree() #sentinel dummy tree
  while t1 is not None and t2 is not None:
    t = Tree(t1.size + t2.size + sizeNs(ns), t1.front, None, t2.rear)
    prev.set_mid(t)
    prev = t
    ns = nodes(t1.rear + ns + t2.front)
    t1 = t1.mid
    t2 = t2.mid
  if t1 is None:
    prev.set_mid(foldR(prepend_node, ns, t2))

```

```

elif t2 is None:
    prev.set_mid(reduce(append_node, ns, t1))
return flat(root)

```

Because Python only provides folding function from left as `reduce()`, a folding function from right is given like what we shown in the following code, that it repeatedly applies function in reverse order of the list.

```

def foldR(f, xs, z):
    for x in reversed(xs):
        z = f(x, z)
    return z

```

The only function in question is how to balanced-group nodes to bigger 2-3 trees. As a 2-3 tree can hold at most 3 sub trees, we can firstly take 3 nodes and wrap them to a ternary tree if there are more than 4 nodes in the list and continuously deal with the rest. If there are just 4 nodes, they can be wrapped to two binary trees. For other cases (there are 3 nodes, 2 nodes, 1 node), we simply wrap them all to a tree.

Denote node list $L = \{n_1, n_2, \dots\}$, The following algorithm realizes this process.

```

function NODES(L)
     $N = \phi$ 
    while  $|L| > 4$  do
         $n \leftarrow \text{NODE}()$ 
        CHILDREN( $n$ )  $\leftarrow L[1..3]$   $\triangleright \{n_1, n_2, n_3\}$ 
         $N \leftarrow N \cup \{n\}$ 
         $L \leftarrow L[4..]$   $\triangleright \{n_4, n_5, \dots\}$ 
    if  $|L| = 4$  then
         $x \leftarrow \text{NODE}()$ 
        CHILDREN( $x$ )  $\leftarrow \{L[1], L[2]\}$ 
         $y \leftarrow \text{NODE}()$ 
        CHILDREN( $y$ )  $\leftarrow \{L[3], L[4]\}$ 
         $N \leftarrow N \cup \{x, y\}$ 
    else if  $L \neq \phi$  then
         $n \leftarrow \text{NODE}()$ 
        CHILDREN( $n$ )  $\leftarrow L$ 
         $N \leftarrow N \cup \{n\}$ 
    return  $N$ 

```

It's straight forward to translate the algorithm to below Python program. Where function `wraps()` helps to create an empty node, then set a list as the children of this node.

```

def nodes(xs):
    res = []
    while len(xs) > 4:
        res.append(wraps(xs[:3]))
        xs = xs[3:]
    if len(xs) == 4:
        res.append(wraps(xs[:2]))
        res.append(wraps(xs[2:]))
    elif xs  $\neq$  []:
        res.append(wraps(xs))
    return res

```

Exercise 12.5

1. Implement the complete finger tree insertion program in your favorite imperative programming language. Don't check the example programs along with this chapter before having a try.
2. How to determine a node is a leaf? Does it contain only a raw element inside or a compound node, which contains sub nodes as children? Note that we can't distinguish it by testing the size, as there is case that node contains a singleton leaf, such as $node(1, \{node(1, \{x\})\})$. Try to solve this problem in both dynamic typed language (e.g. Python, lisp etc) and in strong static typed language (e.g. C++).
3. Implement the EXTRACT-TAIL algorithm in your favorite imperative programming language.
4. Realize algorithm to return the last element of a finger tree in both functional and imperative approach. The later one should be able to handle ill-formed tree.
5. Try to implement concatenation algorithm without using folding. You can either use recursive methods, or use imperative for-each method.

12.6.8 Random access of finger tree

size augmentation

The strategy to provide fast random access, is to turn the looking up into tree-search. In order to avoid calculating the size of tree many times, we augment an extra field to tree and node. The definition should be modified accordingly, for example the following Haskell definition adds size field in its constructor.

```
data Tree a = Empty
           | Lf a
           | Tr Int [a] (Tree (Node a)) [a]
```

And the previous ANSI C structure is augmented with size as well.

```
struct Tree {
  union Node* front;
  union Node* rear;
  Tree* mid;
  Tree* parent;
  int size;
};
```

Suppose the function $tree(s, F, M, R)$ creates a finger tree from size s , front finger F , rear finger R , and middle part inner tree M . When the size of the tree is needed, we can call a $size(T)$ function. It will be something like this.

$$size(T) = \begin{cases} 0 & : T = \phi \\ ? & : T = leaf(x) \\ s & : T = tree(s, F, M, R) \end{cases}$$

If the tree is empty, the size is definitely zero; and if it can be expressed as $tree(s, F, M, R)$, the size is s ; however, what if the tree is a singleton leaf? is it 1? No, it can be 1 only if $T = leaf(a)$ and a isn't a tree node, but a raw element stored in finger tree. In most cases, the size is not 1, because a can be again a tree node. That's why we put a '?' in above equation.

The correct way is to call some size function on the tree node as the following.

$$size(T) = \begin{cases} 0 & : T = \phi \\ size'(x) & : T = leaf(x) \\ s & : T = tree(s, F, M, R) \end{cases} \quad (12.37)$$

Note that this isn't a recursive definition since $size \neq size'$, the argument to $size'$ is either a tree node, which is a 2-3 tree, or a plain element stored in the finger tree. To uniform these two cases, we can anyway wrap the single plain element to a tree node of only one element. So that we can express all the situation as a tree node augmented with a size field. The following Haskell program modifies the definition of tree node.

```
data Node a = Br Int [a]
```

The ANSI C node definition is modified accordingly.

```
struct Node {
  Key key;
  struct Node* children;
  int size;
};
```

We change it from union to structure. Although there is a overhead field 'key' if the node isn't a leaf.

Suppose function $tr(s, L)$, creates such a node (either one element being wrapped or a 2-3 tree) from a size information s , and a list L . Here are some example.

$tr(1, \{x\})$ a tree contains only one element
 $tr(2, \{x, y\})$ a 2-3 tree contains two elements
 $tr(3, \{x, y, z\})$ a 2-3 tree contains three elements

So the function $size'$ can be implemented as returning the size information of a tree node. We have $size'(tr(s, L)) = s$.

Wrapping an element x is just calling $tr(1, \{x\})$. We can define auxiliary functions $wrap$ and $unwrap$, for instance.

$$\begin{aligned} wrap(x) &= tr(1, \{x\}) \\ unwrap(n) &= x \quad : \quad n = tr(1, \{x\}) \end{aligned} \quad (12.38)$$

As both front finger and rear finger are lists of tree nodes, in order to calculate the total size of finger, we can provide a $size''(L)$ function, which sums up size of all nodes stored in the list. Denote $L = \{a_1, a_2, \dots\}$ and $L' = \{a_2, a_3, \dots\}$.

$$size''(L) = \begin{cases} 0 & : L = \phi \\ size'(a_1) + size''(L') & : otherwise \end{cases} \quad (12.39)$$

It's quite OK to define $size''(L)$ by using some high order functions. For example.

$$size''(L) = sum(map(size', L)) \quad (12.40)$$

And we can turn a list of tree nodes into one deeper 2-3 tree and vice-versa.

$$\begin{aligned} wraps(L) &= tr(size''(L), L) \\ unwrap(n) &= L \quad : \quad n = tr(s, L) \end{aligned} \quad (12.41)$$

These helper functions are translated to the following Haskell code.

```

size (Br s _) = s
sizeL = sum .(map size)

sizeT Empty = 0
sizeT (Lf a) = size a
sizeT (Tr s _ _ _) = s

```

Here are the wrap and unwrap auxiliary functions.

```

wrap x = Br 1 [x]
unwrap (Br 1 [x]) = x
wraps xs = Br (sizeL xs) xs
unwraps (Br _ xs) = xs

```

We omitted their type definitions for illustration purpose.

In imperative settings, the size information for node and tree can be accessed through the size field. And the size of a list of nodes can be summed up for this field as the below algorithm.

```

function SIZE-NODES( $L$ )
   $s \leftarrow 0$ 
  for  $\forall n \in L$  do
     $s \leftarrow s + \text{SIZE}(n)$ 
  return  $s$ 

```

The following Python code, for example, translates this algorithm by using standard `sum()` and `map()` functions provided in library.

```

def sizeNs(xs):
  return sum(map(lambda x: x.size, xs))

```

As NIL is typically used to represent empty tree in imperative settings, it's convenient to provide a auxiliary size function to uniformed calculate the size of tree no matter it is NIL.

```

function SIZE-TR( $T$ )
  if  $T = \text{NIL}$  then
    return 0
  else
    return SIZE( $T$ )

```

The algorithm is trivial and we skip its implementation example program.

Modification due to the augmented size

The algorithms have been presented so far need to be modified to accomplish with the augmented size. For example the *insertT* function now inserts a tree node instead of a plain element.

$$\text{insertT}(x, T) = \text{insertT}'(\text{wrap}(x), T) \quad (12.42)$$

The corresponding Haskell program is changed as below.

```

cons a t = cons' (wrap a) t

```

After being wrapped, x is augmented with size information of 1. In the implementation of previous insertion algorithm, function *tree(F, M, R)* is used to create a finger tree from

a front finger, a middle part inner tree and a rear finger. This function should also be modified to add size information of these three arguments.

$$tree'(F, M, R) = \begin{cases} fromL(F) & : M = \phi \wedge R = \phi \\ fromL(R) & : M = \phi \wedge F = \phi \\ tree'(unwraps(F'), M', R) & : F = \phi, (F', M') = extractT'(L) \\ tree'(F, M', unwraps(R')) & : R = \phi, (M', R') = removeT'(L) \\ tree(size''(F) + size(M) + size''(R), F, M, R) & : otherwise \end{cases} \quad (12.43)$$

Where $fromL()$ helps to turn a list of nodes to a finger tree by repeatedly inserting all the element one by one to an empty tree.

$$fromL(L) = foldR(insertT', \phi, L)$$

Of course it can be implemented in pure recursive manner without using folding as well.

The last case is the most straightforward one. If none of F , M , and R is empty, it adds the size of these three part and construct the tree along with this size information by calling $tree(s, F, M, R)$ function. If both the middle part inner tree and one of the finger is empty, the algorithm repeatedly insert all elements stored in the other finger to an empty tree, so that the result is constructed from a list of tree nodes. If the middle part inner tree isn't empty, and one of the finger is empty, the algorithm 'borrows' one tree node from the middle part, either by extracting from head if front finger is empty or removing from tail if rear finger is empty. Then the algorithm unwraps the 'borrowed' tree node to a list, and recursively call $tree'()$ function to construct the result.

This algorithm can be translated to the following Haskell code for example.

```
tree f Empty [] = foldr cons' Empty f
tree [] Empty r = foldr cons' Empty r
tree [] m r = let (f, m') = uncons' m in tree (unwraps f) m' r
tree f m [] = let (m', r) = unsnoc' m in tree f m' (unwraps r)
tree f m r = Tr (sizeL f + sizeT m + sizeL r) f m r
```

Function $tree'()$ helps to minimize the modification. $insertT'()$ can be realized by using it like the following.

$$insertT'(x, T) = \begin{cases} leaf(x) & : T = \phi \\ tree'(\{x\}, \phi, \{y\}) & : T = leaf(x) \\ tree'(\{x, x_1\}, insertT'(wraps(\{x_2, x_3, x_4\}), M), R) & : T = tree(s, \{x_1, x_2, x_3, x_4\}) \\ tree'(\{x\} \cup F, M, R) & : otherwise \end{cases} \quad (12.44)$$

And it's corresponding Haskell code is a line by line translation.

```
cons' a Empty = Lf a
cons' a (Lf b) = tree [a] Empty [b]
cons' a (Tr _ [b, c, d, e] m r) = tree [a, b] (cons' (wraps [c, d, e]) m) r
cons' a (Tr _ f m r) = tree (a:f) m r
```

The similar modification for augment size should also be tuned for imperative algorithms, for example, when a new node is prepend to the head of the finger tree, we should update size when traverse the tree.

```
function PREPEND-NODE( $n, T$ )
   $r \leftarrow TREE()$ 
   $p \leftarrow r$ 
  CONNECT-MID( $p, T$ )
  while FULL?(FRONT( $T$ )) do
```

```

    F ← FRONT(T)
    FRONT(T) ← {n, F[1]}
    SIZE(T) ← SIZE(T) + SIZE(n)                                ▷ update size
    n ← NODE()
    CHILDREN(n) ← F[2..]
    p ← T
    T ← MID(T)
if T = NIL then
    T ← TREE()
    FRONT(T) ← {n}
else if | FRONT(T) | = 1 ∧ REAR(T) = φ then
    REAR(T) ← FRONT(T)
    FRONT(T) ← {n}
else
    FRONT(T) ← {n} ∪ FRONT(T)
SIZE(T) ← SIZE(T) + SIZE(n)                                ▷ update size
CONNECT-MID(p, T) ← T
return FLAT(r)

```

The corresponding Python code are modified accordingly as below.

```

def prepend_node(n, t):
    root = prev = Tree()
    prev.set_mid(t)
    while frontFull(t):
        f = t.front
        t.front = [n] + f[1:]
        t.size = t.size + n.size
        n = wraps(f[1:])
        prev = t
        t = t.mid
    if t is None:
        t = leaf(n)
    elif len(t.front)==1 and t.rear == []:
        t = Tree(n.size + t.size, [n], None, t.front)
    else:
        t = Tree(n.size + t.size, [n]+t.front, t.mid, t.rear)
    prev.set_mid(t)
    return flat(root)

```

Note that the tree constructor is also modified to take a size argument as the first parameter. And the `leaf` helper function does not only construct the tree from a node, but also set the size of the tree with the same size of the node inside it.

For simplification purpose, we skip the detailed description of what are modified in `extractT`, `appendT`, `removeT`, and `concat` algorithms. They are left as exercises to the reader.

Split a finger tree at a given position

With size information augmented, it's easy to locate a node at given position by performing a tree search. What's more, as the finger tree is constructed from three part F , M , and R ; and it's nature of recursive, it's also possible to split it into three sub parts with a given position i : the left, the node at i , and the right part.

The idea is straight forward. Since we have the size information for F , M , and R . Denote these three sizes as S_f , S_m , and S_r . if the given position $i \leq S_f$, the node must be stored in F , we can go on seeking the node inside F ; if $S_f < i \leq S_f + S_m$, the node must

be stored in M , we need recursively perform search in M ; otherwise, the node should be in R , we need search inside R .

If we skip the error handling of trying to split an empty tree, there is only one edge case as below.

$$\mathit{splitAt}(i, T) = \begin{cases} (\phi, x, \phi) & : T = \mathit{leaf}(x) \\ \dots & : \mathit{otherwise} \end{cases}$$

Splitting a leaf results both the left and right parts empty, the node stored in leaf is the resulting node.

The recursive case handles the three sub cases by comparing i with the sizes. Suppose function $\mathit{splitAtL}(i, L)$ splits a list of nodes at given position i into three parts: $(A, x, B) = \mathit{splitAtL}(i, L)$, where x is the i -th node in L , A is a sub list contains all nodes before position i , and B is a sub list contains all rest nodes after i .

$$\mathit{splitAt}(i, T) = \begin{cases} (\phi, x, \phi) & : T = \mathit{leaf}(x) \\ (\mathit{fromL}(A), x, \mathit{tree}'(B, M, R)) & : i \leq S_f, (A, x, B) = \mathit{splitAtL}(i, F) \\ (\mathit{tree}'(F, M_l, A), x, \mathit{tree}'(B, M_r, R)) & : S_f < i \leq S_f + S_m \\ (\mathit{tree}'(F, M, A), x, \mathit{fromL}(B)) & : \mathit{otherwise}, (A, x, B) = \mathit{splitAtL}(i - S_f - S_m, L) \end{cases} \quad (12.45)$$

Where M_l, x, M_r, A, B in the third case are calculated as the following.

$$\begin{aligned} (M_l, t, M_r) &= \mathit{splitAt}(i - S_f, M) \\ (A, x, B) &= \mathit{splitAtL}(i - S_f - \mathit{size}(M_l), \mathit{unwraps}(t)) \end{aligned}$$

And the function $\mathit{splitAtL}$ is just a linear traverse, since the length of list is limited not to exceed the constraint of 2-3 tree, the performance is still ensured to be constant $O(1)$ time. Denote $L = \{x_1, x_2, \dots\}$ and $L' = \{x_2, x_3, \dots\}$.

$$\mathit{splitAtL}(i, L) = \begin{cases} (\phi, x_1, \phi) & : i = 0 \wedge L = \{x_1\} \\ (\phi, x_1, L') & : i < \mathit{size}'(x_1) \\ (\{x_1\} \cup A, x, B) & : \mathit{otherwise} \end{cases} \quad (12.46)$$

Where

$$(A, x, B) = \mathit{splitAtL}(i - \mathit{size}'(x_1), L')$$

The solution of splitting is a typical divide and conquer strategy. The performance of this algorithm is determined by the recursive case of searching in middle part inner tree. Other cases are all constant time as we've analyzed. The depth of recursion is proportion to the height of the tree h , so the algorithm is bound to $O(h)$. Because the tree is well balanced (by using 2-3 tree, and all the insertion/removal algorithms keep the tree balanced), so $h = O(\lg n)$ where n is the number of elements stored in finger tree. The overall performance of splitting is $O(\lg n)$.

Let's first give the Haskell program for $\mathit{splitAtL}$ function

```
splitNodesAt 0 [x] = ([], x, [])
splitNodesAt i (x:xs) | i < size x = ([], x, xs)
                    | otherwise = let (xs', y, ys) = splitNodesAt (i-size x) xs
                                   in (x:xs', y, ys)
```

Then the program for $\mathit{splitAt}$, as there is already function defined in standard library with this name, we slightly change the name by adding a apostrophe.

```
splitAt' _ (Lf x) = (Empty, x, Empty)
splitAt' i (Tr _ f m r)
  | i < szf = let (xs, y, ys) = splitNodesAt i f
```

```

        in ((foldr cons' Empty xs), y, tree ys m r)
| i < szf + szm = let (m1, t, m2) = splitAt' (i-szf) m
                  (xs, y, ys) = splitNodesAt (i-szf - sizeT m1) (unwraps t)
        in (tree f m1 xs, y, tree ys m2 r)
| otherwise = let (xs, y, ys) = splitNodesAt (i-szf -szm) r
        in (tree f m xs, y, foldr cons' Empty ys)
where
  szf = sizeL f
  szm = sizeT m

```

Random access

With the help of splitting at any arbitrary position, it's trivial to realize random access in $O(\lg n)$ time. Denote function $mid(x)$ returns the 2-nd element of a tuple, $left(x)$, and $right(x)$ return the first element and the 3-rd element of the tuple respectively.

$$getAt(S, i) = unwrap(mid(splitAt(i, S))) \quad (12.47)$$

It first splits the sequence at position i , then unwraps the node to get the element stored inside it. When mutate the i -th element of sequence S represented by finger tree, we first split it at i , then we replace the middle to what we want to mutate, and re-construct them to one finger tree by using concatenation.

$$setAt(S, i, x) = concat(L, insertT(x, R)) \quad (12.48)$$

where

$$(L, y, R) = splitAt(i, S)$$

What's more, we can also realize a $removeAt(S, i)$ function, which can remove the i -th element from sequence S . The idea is first to split at i , unwrap and return the element of the i -th node; then concatenate the left and right to a new finger tree.

$$removeAt(S, i) = (unwrap(y), concat(L, R)) \quad (12.49)$$

These handy algorithms can be translated to the following Haskell program.

```

getAt t i = unwrap x where (_, x, _) = splitAt' i t
setAt t i x = let (l, _, r) = splitAt' i t in concat' l (cons x r)
removeAt t i = let (l, x, r) = splitAt' i t in (unwrap x, concat' l r)

```

Imperative random access

As we can directly mutate the tree in imperative settings, it's possible to realize $GET-AT(T, i)$ and $SET-AT(T, i, x)$ without using splitting. The idea is firstly implement a algorithm which can apply some operation to a given position. The following algorithm takes three arguments, a finger tree T , a position index at i which ranges from zero to the number of elements stored in the tree, and a function f , which will be applied to the element at i .

```

function APPLY-AT( $T, i, f$ )
  while SIZE( $T$ ) > 1 do
     $S_f \leftarrow$  SIZE-NODES(FRONT( $T$ ))
     $S_m \leftarrow$  SIZE-TR(MID( $T$ ))
    if  $i < S_f$  then
      return LOOKUP-NODES(FRONT( $T$ ),  $i, f$ )
    else if  $i < S_f + S_m$  then
       $T \leftarrow$  MID( $T$ )

```

```

     $i \leftarrow i - S_f$ 
  else
    return LOOKUP-NODES(REAR( $T$ ),  $i - S_f - S_m$ ,  $f$ )
   $n \leftarrow$  FIRST-LF( $T$ )
   $x \leftarrow$  ELEM( $n$ )
  ELEM( $n$ )  $\leftarrow$   $f(x)$ 
  return  $x$ 

```

This algorithm is essentially a divide and conquer tree search. It repeatedly examine the current tree till reach a tree with size of 1 (can it be determined as a leaf? please consider the ill-formed case and refer to the exercise later). Every time, it checks the position to be located with the size information of front finger and middle part inner tree.

If the index i is less than the size of front finger, the location is at some node in it. The algorithm call a sub procedure to look-up among front finger; If the index is between the size of front finger and the total size till middle part inner tree, it means that the location is at some node inside the middle, the algorithm goes on to traverse along the middle part inner tree with an updated index reduced by the size of front finger; Otherwise it means the location is at some node in rear finger, the similar looking up procedure is called accordingly.

After this loop, we've got a node, (can be a compound node) with what we are looking for at the first leaf inside this node. We can extract the element out, and apply the function f on it and store the new value back.

The algorithm returns the previous element before applying f as the final result.

What hasn't been factored is the algorithm LOOKUP-NODES(L , i , f). It takes a list of nodes, a position index, and a function to be applied. This algorithm can be implemented by checking every node in the list. If the node is a leaf, and the index is zero, we are at the right position to be looked up. The function can be applied on the element stored in this leaf, and the previous value is returned; Otherwise, we need compare the size of this node and the index to determine if the position is inside this node and search inside the children of the node if necessary.

```

function LOOKUP-NODES( $L$ ,  $i$ ,  $f$ )
  loop
    for  $\forall n \in L$  do
      if  $n$  is leaf  $\wedge i = 0$  then
         $x \leftarrow$  ELEM( $n$ )
        ELEM( $n$ )  $\leftarrow$   $f(x)$ 
        return  $x$ 
      if  $i <$  SIZE( $n$ ) then
         $L \leftarrow$  CHILDREN( $n$ )
        break
     $i \leftarrow i -$  SIZE( $n$ )

```

The following are the corresponding Python code implements the algorithms.

```

def applyAt(t, i, f):
    while t.size > 1:
        szf = sizeNs(t.front)
        szm = sizeT(t.mid)
        if i < szf:
            return lookupNs(t.front, i, f)
        elif i < szf + szm:
            t = t.mid
            i = i - szf
        else:
            return lookupNs(t.rear, i - szf - szm, f)
    n = first_leaf(t)

```

```

    x = elem(n)
    n.children[0] = f(x)
    return x

def lookupNs(ns, i, f):
    while True:
        for n in ns:
            if n.leaf and i == 0:
                x = elem(n)
                n.children[0] = f(x)
                return x
            if i < n.size:
                ns = n.children
                break
        i = i - n.size

```

With auxiliary algorithm that can apply function at a given position, it's trivial to implement the GET-AT and SET-AT by passing special functions for applying.

```

function GET-AT( $T, i$ )
    return APPLY-AT( $T, i, \lambda_x.x$ )

```

```

function SET-AT( $T, i, x$ )
    return APPLY-AT( $T, i, \lambda_y.x$ )

```

That is we pass *id* function to implement getting element at a position, which doesn't change anything at all; and pass constant function to implement setting, which set the element to new value by ignoring its previous value.

Imperative splitting

It's not enough to just realizing APPLY-AT algorithm in imperative settings, this is because removing element at arbitrary position is also a typical case.

Almost all the imperative finger tree algorithms so far are kind of one-pass top-down manner. Although we sometimes need to book keeping the root. It means that we can even realize all of them without using the parent field.

Splitting operation, however, can be easily implemented by using parent field. We can first perform a top-down traverse along with the middle part inner tree as long as the splitting position doesn't located in front or rear finger. After that, we need a bottom-up traverse along with the parent field of the two split trees to fill out the necessary fields.

```

function SPLIT-AT( $T, i$ )
     $T_1 \leftarrow \text{TREE}()$ 
     $T_2 \leftarrow \text{TREE}()$ 
    while  $S_f \leq i < S_f + S_m$  do
         $T'_1 \leftarrow \text{TREE}()$ 
         $T'_2 \leftarrow \text{TREE}()$ 
        FRONT( $T'_1$ )  $\leftarrow$  FRONT( $T$ )
        REAR( $T'_2$ )  $\leftarrow$  REAR( $T$ )
        CONNECT-MID( $T_1, T'_1$ )
        CONNECT-MID( $T_2, T'_2$ )
         $T_1 \leftarrow T'_1$ 
         $T_2 \leftarrow T'_2$ 
         $i \leftarrow i - S_f$ 
         $T \leftarrow \text{MID}(T)$ 
    if  $i < S_f$  then
        ( $X, n, Y$ )  $\leftarrow$  SPLIT-NODES(FRONT( $T$ ),  $i$ )

```

▷ Top-down pass

```

    T'_1 ← FROM-NODES(X)
    T'_2 ← T
    SIZE(T'_2) ← SIZE(T) - SIZE-NODES(X) - SIZE(n)
    FRONT(T'_2) ← Y
else if S_f + S_m ≤ i then
    (X, n, Y) ← SPLIT-NODES(REAR(T), i - S_f - S_m)
    T'_2 ← FROM-NODES(Y)
    T'_1 ← T
    SIZE(T'_1) ← SIZE(T) - SIZE-NODES(Y) - SIZE(n)
    REAR(T'_1) ← X
CONNECT-MID(T_1, T'_1)
CONNECT-MID(T_2, T'_2)
i ← i - SIZE-TR(T'_1)
while n is NOT leaf do ▷ Bottom-up pass
    (X, n, Y) ← SPLIT-NODES(CHILDREN(n), i)
    i ← i - SIZE-NODES(X)
    REAR(T_1) ← X
    FRONT(T_2) ← Y
    SIZE(T_1) ← SUM-SIZES(T_1)
    SIZE(T_2) ← SUM-SIZES(T_2)
    T_1 ← PARENT(T_1)
    T_2 ← PARENT(T_2)
return (FLAT(T_1), ELEM(n), FLAT(T_2))

```

The algorithm first creates two trees T_1 and T_2 to hold the split results. Note that they are created as 'ground' trees which are parents of the roots. The first pass is a top-down pass. Suppose S_f , and S_m retrieve the size of the front finger and the size of middle part inner tree respectively. If the position at which the tree to be split is located at middle part inner tree, we reuse the front finger of T for new created T'_1 , and reuse rear finger of T for T'_2 . At this time point, we can't fill the other fields for T'_1 and T'_2 , they are left empty, and we'll finish filling them in the future. After that, we connect T_1 and T'_1 so the latter becomes the middle part inner tree of the former. The similar connection is done for T_2 and T'_2 as well. Finally, we update the position by deducing it by the size of front finger, and go on traversing along with the middle part inner tree.

When the first pass finishes, we are at a position that either the splitting should be performed in front finger, or in rear finger. Splitting the nodes in finger results a tuple, that the first part and the third part are lists before and after the splitting point, while the second part is a node contains the element at the original position to be split. As both fingers hold at most 3 nodes because they are actually 2-3 trees, the nodes splitting algorithm can be performed by a linear search.

```

function SPLIT-NODES(L, i)
  for j ∈ [1, LENGTH(L)] do
    if i < SIZE(L[j]) then
      return (L[1...j - 1], L[j], L[j + 1... LENGTH(L)])
  i ← i - SIZE(L[j])

```

We next create two new result trees T'_1 and T'_2 from this tuple, and connected them as the final middle part inner tree of T_1 and T_2 .

Next we need perform a bottom-up traverse along with the result trees to fill out all the empty information we skipped in the first pass.

We loop on the second part of the tuple, the node, till it becomes a leaf. In each iteration, we repeatedly splitting the children of the node with an updated position i .

The first list of nodes returned from splitting is used to fill the rear finger of T_1 ; and the other list of nodes is used to fill the front finger of T_2 . After that, since all the three parts of a finger tree – the front and rear finger, and the middle part inner tree – are filled, we can then calculate the size of the tree by summing these three parts up.

```
function SUM-SIZES( $T$ )
    return SIZE-NODES(FRONT( $T$ )) + SIZE-TR(MID( $T$ )) + SIZE-NODES(REAR( $T$ ))
```

Next, the iteration goes on along with the parent fields of T_1 and T_2 . The last 'black-box' algorithm is FROM-NODES(L), which can create a finger tree from a list of nodes. It can be easily realized by repeatedly perform insertion on an empty tree. The implementation is left as an exercise to the reader.

The example Python code for splitting is given as below.

```
def splitAt( $t$ ,  $i$ ):
    ( $t1$ ,  $t2$ ) = (Tree(), Tree())
    while szf( $t$ ) ≤  $i$  and  $i$  < szf( $t$ ) + szm( $t$ ):
        fst = Tree(0,  $t$ .front, None, [])
        snd = Tree(0, [], None,  $t$ .rear)
         $t1$ .set_mid(fst)
         $t2$ .set_mid(snd)
        ( $t1$ ,  $t2$ ) = (fst, snd)
         $i$  =  $i$  - szf( $t$ )
         $t$  =  $t$ .mid

    if  $i$  < szf( $t$ ):
        ( $xs$ ,  $n$ ,  $ys$ ) = splitNs( $t$ .front,  $i$ )
         $sz$  =  $t$ .size - sizeNs( $xs$ ) -  $n$ .size
        ( $fst$ ,  $snd$ ) = (fromNodes( $xs$ ), Tree( $sz$ ,  $ys$ ,  $t$ .mid,  $t$ .rear))
    elif szf( $t$ ) + szm( $t$ ) ≤  $i$ :
        ( $xs$ ,  $n$ ,  $ys$ ) = splitNs( $t$ .rear,  $i$  - szf( $t$ ) - szm( $t$ ))
         $sz$  =  $t$ .size - sizeNs( $ys$ ) -  $n$ .size
        ( $fst$ ,  $snd$ ) = (Tree( $sz$ ,  $t$ .front,  $t$ .mid,  $xs$ ), fromNodes( $ys$ ))
     $t1$ .set_mid(fst)
     $t2$ .set_mid(snd)

     $i$  =  $i$  - sizeT( $fst$ )
    while not  $n$ .leaf:
        ( $xs$ ,  $n$ ,  $ys$ ) = splitNs( $n$ .children,  $i$ )
         $i$  =  $i$  - sizeNs( $xs$ )
        ( $t1$ .rear,  $t2$ .front) = ( $xs$ ,  $ys$ )
         $t1$ .size = sizeNs( $t1$ .front) + sizeT( $t1$ .mid) + sizeNs( $t1$ .rear)
         $t2$ .size = sizeNs( $t2$ .front) + sizeT( $t2$ .mid) + sizeNs( $t2$ .rear)
        ( $t1$ ,  $t2$ ) = ( $t1$ .parent,  $t2$ .parent)

    return (flat( $t1$ ), elem( $n$ ), flat( $t2$ ))
```

The program to split a list of nodes at a given position is listed like this.

```
def splitNs( $ns$ ,  $i$ ):
    for  $j$  in range(len( $ns$ )):
        if  $i$  <  $ns$ [ $j$ ].size:
            return ( $ns$ [: $j$ ],  $ns$ [ $j$ ],  $ns$ [ $j$ +1:])
     $i$  =  $i$  -  $ns$ [ $j$ ].size
```

With splitting defined, removing an element at arbitrary position can be realized trivially by first performing a splitting, then concatenating the two result tree to one big tree and return the element at that position.

```
function REMOVE-AT( $T$ ,  $i$ )
    ( $T_1$ ,  $x$ ,  $T_2$ ) ← SPLIT-AT( $T$ ,  $i$ )
    return ( $x$ , CONCAT( $T_1$ ,  $T_2$ ))
```

Exercise 12.6

1. Another way to realize *insertT'* is to force increasing the size field by one, so that we needn't write function *tree'*. Try to realize the algorithm by using this idea.
2. Try to handle the augment size information as well as in *insertT'* algorithm for the following algorithms (both functional and imperative): *extractT'*, *appendT'*, *removeT'*, and *concat'*. The *head*, *tail*, *init* and *last* functions should be kept unchanged. Don't refer to the download-able programs along with this book before you take a try.
3. In the imperative APPLY-AT algorithm, it tests if the size of the current tree is greater than one. Why don't we test if the current tree is a leaf? Tell the difference between these two approaches.
4. Implement the FROM-NODES(*L*) in your favorite imperative programming language. You can either use looping or create a folding-from-right sub algorithm.

12.7 Notes and short summary

Although we haven't been able to give a purely functional realization to match the $O(1)$ constant time random access as arrays in imperative settings. The result finger tree data structure achieves an overall well performed sequence. It manipulates fast in amortized $O(1)$ time both on head and on tail, it can also concatenate two sequence in logarithmic time as well as break one sequence into two sub sequences at any position. While neither arrays in imperative settings nor linked-list in functional settings satisfies all these goals. Some functional programming languages adopt this sequence realization in its standard library [67].

Just as the title of this chapter, we've presented the last corner stone of elementary data structures in both functional and imperative settings. We needn't concern about being lack of elementary data structures when solve problems with some typical algorithms.

For example, when writing a MTF (move-to-front) encoding algorithm[68], with the help of the sequence data structure explained in this chapter. We can implement it quite straightforward.

$$mtf(S, i) = \{x\} \cup S'$$

where $(x, S') = removeAt(S, i)$.

In the next following chapters, we'll first explain some typical divide and conquer sorting methods, including quick sort, merge sort and their variants; then some elementary searching algorithms, and string matching algorithms will be covered.

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Chapter 13

Divide and conquer, Quick sort vs. Merge sort

13.1 Introduction

It's proved that the best approximate performance of comparison based sorting is $O(n \lg n)$ [51]. In this chapter, two divide and conquer sorting algorithms are introduced. Both of them perform in $O(n \lg n)$ time. One is quick sort. It is the most popular sorting algorithm. Quick sort has been well studied, many programming libraries provide sorting tools based on quick sort.

In this chapter, we'll first introduce the idea of quick sort, which demonstrates the power of divide and conquer strategy well. Several variants will be explained, and we'll see when quick sort performs poor in some special cases. That the algorithm is not able to partition the sequence in balance.

In order to solve the unbalanced partition problem, we'll next introduce about merge sort, which ensure the sequence to be well partitioned in all the cases. Some variants of merge sort, including nature merge sort, bottom-up merge sort are shown as well.

Same as other chapters, all the algorithm will be realized in both imperative and functional approaches.

13.2 Quick sort

Consider a teacher arranges a group of kids in kindergarten to stand in a line for some game. The kids need stand in order of their heights, that the shortest one stands on the left most, while the tallest stands on the right most. How can the teacher instruct these kids, so that they can stand in a line by themselves?

There are many strategies, and the quick sort approach can be applied here:

1. The first kid raises his/her hand. The kids who are shorter than him/her stands to the left to this child; the kids who are taller than him/her stands to the right of this child;
2. All the kids move to the left, if there are, repeat the above step; all the kids move to the right repeat the same step as well.

Suppose a group of kids with their heights as $\{102, 100, 98, 95, 96, 99, 101, 97\}$ with [cm] as the unit. The following table illustrate how they stand in order of height by following this method.



Figure 13.1: Instruct kids to stand in a line

102	100	98	95	96	99	101	97	
100	98	95	96	99	101	97	<i>102</i>	
98	95	96	99	97	<i>100</i>	101	<i>102</i>	
95	96	97	98	99	<i>100</i>	<i>101</i>	<i>102</i>	
<i>95</i>	96	97	98	99	<i>100</i>	<i>101</i>	<i>102</i>	
<i>95</i>	<i>96</i>	97	98	99	<i>100</i>	<i>101</i>	<i>102</i>	
<i>95</i>	<i>96</i>	<i>97</i>	98	99	<i>100</i>	<i>101</i>	<i>102</i>	

At the beginning, the first child with height 102 cm raises his/her hand. We call this kid the pivot and mark this height in bold. It happens that this is the tallest kid. So all others stands to the left side, which is represented in the second row in the above table. Note that the child with height 102 cm is in the final ordered position, thus we mark it italic. Next the kid with height 100 cm raise hand, so the children of heights 98, 95, 96 and 99 cm stand to his/her left, and there is only 1 child of height 101 cm who is taller than this pivot kid. So he stands to the right hand. The 3rd row in the table shows this stage accordingly. After that, the child of 98 cm high is selected as pivot on left hand; while the child of 101 cm high on the right is selected as pivot. Since there are no other kids in the unsorted group with 101 cm as pivot, this small group is ordered already and the kid of height 101 cm is in the final proper position. The same method is applied to the group of kids which haven't been in correct order until all of them are stands in the final position.

13.2.1 Basic version

Summarize the above instruction leads to the recursive description of quick sort. In order to sort a sequence of elements L .

- If L is empty, the result is obviously empty; This is the trivial edge case;
- Otherwise, select an arbitrary element in L as a pivot, recursively sort all elements not greater than the pivot, put the result on the left hand of the pivot, *and* recursively sort all elements which are greater than the pivot, put the result on the right hand of the pivot.

Note that the emphasized word *and*, we don't use 'then' here, which indicates it's quite OK that the recursive sort on the left and right can be done in parallel. We'll return this parallelism topic soon.

Quick sort was first developed by C. A. R. Hoare in 1960 [51], [78]. What we describe here is a basic version. Note that it doesn't state how to select the pivot. We'll see soon that the pivot selection affects the performance of quick sort dramatically.

The most simple method to select the pivot is always choose the first one so that quick sort can be formalized as the following.

$$\text{sort}(L) = \begin{cases} \phi & : L = \phi \\ \text{sort}(\{x|x \in L', x \leq l_1\}) \cup \{l_1\} \cup \text{sort}(\{x|x \in L', l_1 < x\}) & : \textit{otherwise} \end{cases} \quad (13.1)$$

Where l_1 is the first element of the non-empty list L , and L' contains the rest elements $\{l_2, l_3, \dots\}$. Note that we use Zermelo Frankel expression (ZF expression for short)¹, which is also known as list comprehension. A ZF expression $\{a|a \in S, p_1(a), p_2(a), \dots\}$ means taking all element in set S , if it satisfies all the predication p_1, p_2, \dots . ZF expression is originally used for representing *set*, we extend it to express list for the sake of brevity. There can be duplicated elements, and different permutations represent for different list. Please refer to the appendix about list in this book for detail.

It's quite straightforward to translate this equation to real code if list comprehension is supported. The following Haskell code is given for example:

```
sort [] = []
sort (x:xs) = sort [y | y<-xs, y ≤ x] ++ [x] ++ sort [y | y<-xs, x < y]
```

This might be the shortest quick sort program in the world at the time when this book is written. Even a verbose version is still very expressive:

```
sort [] = []
sort (x:xs) = as ++ [x] ++ bs where
  as = sort [ a | a ← xs, a ≤ x]
  bs = sort [ b | b ← xs, x < b]
```

There are some variants of this basic quick sort program, such as using explicit filtering instead of list comprehension. The following Python program demonstrates this for example:

```
def sort(xs):
    if xs == []:
        return []
    pivot = xs[0]
    as = sort(filter(lambda x : x ≤ pivot, xs[1:]))
    bs = sort(filter(lambda x : pivot < x, xs[1:]))
    return as + [pivot] + bs
```

13.2.2 Strict weak ordering

We assume the elements are sorted in monotonic none decreasing order so far. It's quite possible to customize the algorithm, so that it can sort the elements in other ordering criteria. This is necessary in practice because users may sort numbers, strings, or other complex objects (even list of lists for example).

The typical generic solution is to abstract the comparison as a parameter as we mentioned in chapters about insertion sort and selection sort. Although it needn't the total ordering, the comparison must satisfy *strict weak ordering* at least [79] [52].

For the sake of brevity, we only considering sort the elements by using less than or equal (equivalent to not greater than) in the rest of the chapter.

13.2.3 Partition

Observing that the basic version actually takes two passes to find all elements which are greater than the pivot as well as to find the others which are not respectively. Such

¹Name for the two mathematics who found the modern set theory.

partition can be accomplished by only one pass. We explicitly define the partition as below.

$$\text{partition}(p, L) = \begin{cases} (\phi, \phi) & : L = \phi \\ (\{l_1\} \cup A, B) & : p(l_1), (A, B) = \text{partition}(p, L') \\ (A, \{l_1\} \cup B) & : \neg p(l_1) \end{cases} \quad (13.2)$$

Note that the operation $\{x\} \cup L$ is just a ‘cons’ operation, which only takes constant time. The quick sort can be modified accordingly.

$$\text{sort}(L) = \begin{cases} \phi & : L = \phi \\ \text{sort}(A) \cup \{l_1\} \cup \text{sort}(B) & : \text{otherwise}, (A, B) = \text{partition}(\lambda_x x \leq l_1, L') \end{cases} \quad (13.3)$$

Translating this new algorithm into Haskell yields the below code.

```

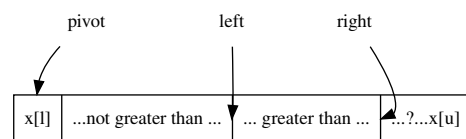
sort [] = []
sort (x:xs) = sort as ++ [x] ++ sort bs where
    (as, bs) = partition (<= x) xs

partition _ [] = ([], [])
partition p (x:xs) = let (as, bs) = partition p xs in
    if p x then (x:as, bs) else (as, x:bs)

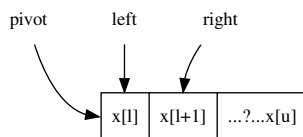
```

The concept of partition is very critical to quick sort. Partition is also very important to many other sort algorithms. We’ll explain how it generally affects the sorting methodology by the end of this chapter. Before further discussion about fine tuning of quick sort specific partition, let’s see how to realize it in-place imperatively.

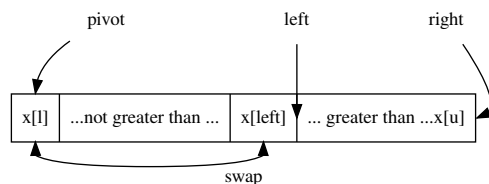
There are many partition methods. The one given by Nico Lomuto [4] [4] will be used here as it’s easy to understand. We’ll show other partition algorithms soon and see how partitioning affects the performance.



(a) Partition invariant



(b) Start



(c) Finish

Figure 13.2: Partition a range of array by using the left most element as pivot.

Figure 13.2 shows the idea of this one-pass partition method. The array is processed from left to right. At any time, the array consists of the following parts as shown in figure 13.2 (a):

- The left most cell contains the pivot; By the end of the partition process, the pivot will be moved to the final proper position;
- A segment contains all elements which are not greater than the pivot. The right boundary of this segment is marked as ‘left’;
- A segment contains all elements which are greater than the pivot. The right boundary of this segment is marked as ‘right’; It means that elements between ‘left’ and ‘right’ marks are greater than the pivot;
- The rest of elements after ‘right’ mark haven’t been processed yet. They may be greater than the pivot or not.

At the beginning of partition, the ‘left’ mark points to the pivot and the ‘right’ mark points to the the second element next to the pivot in the array as in Figure 13.2 (b); Then the algorithm repeatedly advances the right mark one element after the other till passes the end of the array.

In every iteration, the element pointed by the ‘right’ mark is compared with the pivot. If it is greater than the pivot, it should be among the segment between the ‘left’ and ‘right’ marks, so that the algorithm goes on to advance the ‘right’ mark and examine the next element; Otherwise, since the element pointed by ‘right’ mark is less than or equal to the pivot (not greater than), it should be put before the ‘left’ mark. In order to achieve this, the ‘left’ mark needs be advanced by one, then exchange the elements pointed by the ‘left’ and ‘right’ marks.

Once the ‘right’ mark passes the last element, it means that all the elements have been processed. The elements which are greater than the pivot have been moved to the right hand of ‘left’ mark while the others are to the left hand of this mark. Note that the pivot should move between the two segments. An extra exchanging between the pivot and the element pointed by ‘left’ mark makes this final one to the correct location. This is shown by the swap bi-directional arrow in figure 13.2 (c).

The ‘left’ mark (which points the pivot finally) partitions the whole array into two parts, it is returned as the result. We typically increase the ‘left’ mark by one, so that it points to the first element greater than the pivot for convenient. Note that the array is modified in-place.

The partition algorithm can be described as the following. It takes three arguments, the array A , the lower and the upper bound to be partitioned ².

```

1: function PARTITION( $A$ ,  $l$ ,  $u$ )
2:    $p \leftarrow A[l]$                                      ▷ the pivot
3:    $L \leftarrow l$                                        ▷ the left mark
4:   for  $R \in [l + 1, u]$  do                             ▷ iterate on the right mark
5:     if  $\neg(p < A[R])$  then                             ▷ negate of  $<$  is enough for strict weak order
6:        $L \leftarrow L + 1$ 
7:       EXCHANGE  $A[L] \leftrightarrow A[R]$ 
8:   EXCHANGE  $A[L] \leftrightarrow p$ 
9:   return  $L + 1$                                        ▷ The partition position

```

²The partition algorithm used here is slightly different from the one in [4]. The latter uses the last element in the slice as the pivot.

Below table shows the steps of partitioning the array $\{3, 2, 5, 4, 0, 1, 6, 7\}$.

(l) 3	(r) 2	5	4	0	1	6	7	initialize, $pivot = 3, l = 1, r = 2$
3	(l)(r) 2	5	4	0	1	6	7	$2 < 3$, advance l , ($r = l$)
3	(l) 2	(r) 5	4	0	1	6	7	$5 > 3$, move on
3	(l) 2	5	(r) 4	0	1	6	7	$4 > 3$, move on
3	(l) 2	5	4	(r) 0	1	6	7	$0 < 3$
3	2	(l) 0	4	(r) 5	1	6	7	Advance l , then swap with r
3	2	(l) 0	4	5	(r) 1	6	7	$1 < 3$
3	2	0	(l) 1	5	(r) 4	6	7	Advance l , then swap with r
3	2	0	(l) 1	5	4	(r) 6	7	$6 > 3$, move on
3	2	0	(l) 1	5	4	6	(r) 7	$7 > 3$, move on
1	2	0	3	(l+1) 5	4	6	7	r passes the end, swap pivot and

This version of partition algorithm can be implemented in ANSI C as the following.

```
int partition(Key* xs, int l, int u) {
    int pivot, r;
    for (pivot = l, r = l + 1; r < u; ++r)
        if (!(xs[pivot] < xs[r])) {
            ++l;
            swap(xs[l], xs[r]);
        }
    swap(xs[pivot], xs[l]);
    return l + 1;
}
```

Where `swap(a, b)` can either be defined as function or a macro. In ISO C++, `swap(a, b)` is provided as a function template. the type of the elements can be defined somewhere or abstracted as a template parameter in ISO C++. We omit these language specific details here.

With this partition method realized, the imperative in-place quick sort can be accomplished as the following.

```
1: procedure QUICK-SORT( $A, l, u$ )
2:   if  $l < u$  then
3:      $m \leftarrow$  PARTITION( $A, l, u$ )
4:     QUICK-SORT( $A, l, m - 1$ )
5:     QUICK-SORT( $A, m, u$ )
```

When sort an array, this procedure is called by passing the whole range as the lower and upper bounds. `QUICK-SORT($A, 1, |A|$)`. Note that when $l \geq u$ it means the array slice is either empty, or just contains only one element, both can be treated as ordered, so the algorithm does nothing in such cases.

Below ANSI C example program completes the basic in-place quick sort.

```
void quicksort(Key* xs, int l, int u) {
    int m;
    if (l < u) {
        m = partition(xs, l, u);
        quicksort(xs, l, m - 1);
        quicksort(xs, m, u);
    }
}
```

13.2.4 Minor improvement in functional partition

Before exploring how to improve the partition for basic version quick sort, it's obviously that the one presented so far can be defined by using folding. Please refer to the appendix

A of this book for definition of folding.

$$\text{partition}(p, L) = \text{fold}(f(p), (\phi, \phi), L) \quad (13.4)$$

Where function f compares the element to the pivot with predicate p (which is passed to f as a parameter, so that f is in curried form, see appendix A for detail. Alternatively, f can be a lexical closure which is in the scope of partition , so that it can access the predicate in this scope.), and update the result pair accordingly.

$$f(p, x, (A, B)) = \begin{cases} (\{x\} \cup A, B) & : p(x) \\ (A, \{x\} \cup B) & : \text{otherwise}(\neg p(x)) \end{cases} \quad (13.5)$$

Note we actually use pattern-matching style definition. In environment without pattern-matching support, the pair (A, B) should be represented by a variable, for example P , and use access functions to extract its first and second parts.

The example Haskell program needs to be modified accordingly.

```

sort [] = []
sort (x:xs) = sort small ++ [x] ++ sort big where
  (small, big) = foldr f ([], []) xs
  f a (as, bs) = if a ≤ x then (a:as, bs) else (as, a:bs)

```

Accumulated partition

The partition algorithm by using folding actually accumulates to the result pair of lists (A, B) . That if the element is not greater than the pivot, it's accumulated to A , otherwise to B . We can explicitly express it which save spaces and is friendly for tail-recursive call optimization (refer to the appendix A of this book for detail).

$$\text{partition}(p, L, A, B) = \begin{cases} (A, B) & : L = \phi \\ \text{partition}(p, L', \{l_1\} \cup A, B) & : p(l_1) \\ \text{partition}(p, L', A, \{l_1\} \cup B) & : \text{otherwise} \end{cases} \quad (13.6)$$

Where l_1 is the first element in L if L isn't empty, and L' contains the rest elements except for l_1 , that $L' = \{l_2, l_3, \dots\}$ for example. The quick sort algorithm then uses this accumulated partition function by passing the $\lambda_x x \leq \text{pivot}$ as the partition predicate.

$$\text{sort}(L) = \begin{cases} \phi & : L = \phi \\ \text{sort}(A) \cup \{l_1\} \cup \text{sort}(B) & : \text{otherwise} \end{cases} \quad (13.7)$$

Where A, B are computed by the accumulated partition function defined above.

$$(A, B) = \text{partition}(\lambda_x x \leq l_1, L', \phi, \phi)$$

Accumulated quick sort

Observe the recursive case in the last quick sort definition. the list concatenation operations $\text{sort}(A) \cup \{l_1\} \cup \text{sort}(B)$ actually are proportion to the length of the list to be concatenated. Of course we can use some general solutions introduced in the appendix A of this book to improve it. Another way is to change the sort algorithm to accumulated manner. Something like below:

$$\text{sort}'(L, S) = \begin{cases} S & : L = \phi \\ \dots & : \text{otherwise} \end{cases}$$

Where S is the accumulator, and we call this version by passing empty list as the accumulator to start sorting: $\text{sort}(L) = \text{sort}'(L, \phi)$. The key intuitive is that after the

partition finishes, the two sub lists need to be recursively sorted. We can first recursively sort the list contains the elements which are greater than the pivot, then link the pivot in front of it and use it as an *accumulator* for next step sorting.

Based on this idea, the '...' part in above definition can be realized as the following.

$$\text{sort}'(L, S) = \begin{cases} S & : L = \phi \\ \text{sort}(A, \{l_1\} \cup \text{sort}(B, ?)) & : \text{otherwise} \end{cases}$$

The problem is what's the accumulator when sorting B . There is an important invariant actually, that at every time, the accumulator S holds the elements have been sorted so far. So that we should sort B by accumulating to S .

$$\text{sort}'(L, S) = \begin{cases} S & : L = \phi \\ \text{sort}(A, \{l_1\} \cup \text{sort}(B, S)) & : \text{otherwise} \end{cases} \quad (13.8)$$

The following Haskell example program implements the accumulated quick sort algorithm.

```

asort xs = asort' xs []

asort' [] acc = acc
asort' (x:xs) acc = asort' as (x:asort' bs acc) where
  (as, bs) = part xs [] []
  part [] as bs = (as, bs)
  part (y:ys) as bs | y ≤ x = part ys (y:as) bs
                    | otherwise = part ys as (y:bs)

```

Exercise 13.1

- Implement the recursive basic quick sort algorithm in your favorite imperative programming language.
- Same as the imperative algorithm, one minor improvement is that besides the empty case, we needn't sort the singleton list, implement this idea in the functional algorithm as well.
- The accumulated quick sort algorithm developed in this section uses intermediate variable A, B . They can be eliminated by defining the partition function to mutually recursive call the sort function. Implement this idea in your favorite functional programming language. Please don't refer to the downloadable example program along with this book before you try it.

13.3 Performance analysis for quick sort

Quick sort performs well in practice, however, it's not easy to give theoretical analysis. It needs the tool of probability to prove the average case performance.

Nevertheless, it's intuitive to calculate the best case and worst case performance. It's obviously that the best case happens when every partition divides the sequence into two slices with equal size. Thus it takes $O(\lg n)$ recursive calls as shown in figure 13.3.

There are total $O(\lg n)$ levels of recursion. In the first level, it executes one partition, which processes n elements; In the second level, it executes partition two times, each processes $n/2$ elements, so the total time in the second level bounds to $2O(n/2) = O(n)$ as well. In the third level, it executes partition four times, each processes $n/4$ elements.

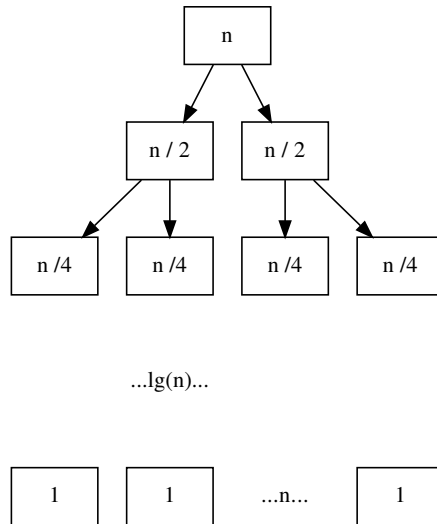


Figure 13.3: In the best case, quick sort divides the sequence into two slices with same length.

The total time in the third level is also bound to $O(n)$; ... In the last level, there are n small slices each contains a single element, the time is bound to $O(n)$. Summing all the time in each level gives the total performance of quick sort in best case as $O(n \lg n)$.

However, in the worst case, the partition process unluckily divides the sequence to two slices with unbalanced lengths in most time. That one slices with length $O(1)$, the other is $O(n)$. Thus the recursive time degrades to $O(n)$. If we draw a similar figure, unlike in the best case, which forms a balanced binary tree, the worst case degrades into a very unbalanced tree that every node has only one child, while the other is empty. The binary tree turns to be a linked list with $O(n)$ length. And in every level, all the elements are processed, so the total performance in worst case is $O(n^2)$, which is as same poor as insertion sort and selection sort.

Let's consider when the worst case will happen. One special case is that all the elements (or most of the elements) are same. Nico Lomuto's partition method deals with such sequence poor. We'll see how to solve this problem by introducing other partition algorithm in the next section.

The other two obvious cases which lead to worst case happen when the sequence has already in ascending or descending order. Partition the ascending sequence makes an empty sub list before the pivot, while the list after the pivot contains all the rest elements. Partition the descending sequence gives an opponent result.

There are other cases which lead quick sort performs poor. There is no completely satisfied solution which can avoid the worst case. We'll see some engineering practice in next section which can make it very seldom to meet the worst case.

13.3.1 Average case analysis ★

In average case, quick sort performs well. There is a vivid example that even the partition divides the list every time to two lists with length 1 to 9. The performance is still bound to $O(n \lg n)$ as shown in [4].

This subsection need some mathematic background, reader can safely skip to next part.

There are two methods to proof the average case performance, one uses an important

fact that the performance is proportion to the total comparing operations during quick sort [4]. Different with the selections sort that every two elements have been compared. Quick sort avoid many unnecessary comparisons. For example suppose a partition operation on list $\{a_1, a_2, a_3, \dots, a_n\}$. Select a_1 as the pivot, the partition builds two sub lists $A = \{x_1, x_2, \dots, x_k\}$ and $B = \{y_1, y_2, \dots, y_{n-k-1}\}$. In the rest time of quick sort, The element in A will never be compared with any elements in B .

Denote the final sorted result as $\{a_1, a_2, \dots, a_n\}$, this indicates that if element $a_i < a_j$, they will not be compared any longer if and only if some element a_k where $a_i < a_k < a_j$ has ever been selected as pivot before a_i or a_j being selected as the pivot.

That is to say, the only chance that a_i and a_j being compared is either a_i is chosen as pivot or a_j is chosen as pivot before any other elements in ordered range $a_{i+1} < a_{i+2} < \dots < a_{j-1}$ are selected.

Let $P(i, j)$ represent the probability that a_i and a_j being compared. We have:

$$P(i, j) = \frac{2}{j - i + 1} \quad (13.9)$$

Since the total number of compare operation can be given as:

$$C(n) = \sum_{i=1}^{n-1} \sum_{j=i+1}^n P(i, j) \quad (13.10)$$

Note the fact that if we compared a_i and a_j , we won't compare a_j and a_i again in the quick sort algorithm, and we never compare a_i onto itself. That's why we set the upper bound of i to $n - 1$; and lower bound of j to $i + 1$.

Substitute the probability, it yields:

$$\begin{aligned} C(n) &= \sum_{i=1}^{n-1} \sum_{j=i+1}^n \frac{2}{j - i + 1} \\ &= \sum_{i=1}^{n-1} \sum_{k=1}^{n-i} \frac{2}{k + 1} \end{aligned} \quad (13.11)$$

Using the harmonic series [80]

$$H_n = 1 + \frac{1}{2} + \frac{1}{3} + \dots = \ln n + \gamma + \epsilon_n$$

$$C(n) = \sum_{i=1}^{n-1} O(\lg n) = O(n \lg n) \quad (13.12)$$

The other method to prove the average performance is to use the recursive fact that when sorting list of length n , the partition splits the list into two sub lists with length i and $n - i - 1$. The partition process itself takes cn time because it examine every element with the pivot. So we have the following equation.

$$T(n) = T(i) + T(n - i - 1) + cn \quad (13.13)$$

Where $T(n)$ is the total time when perform quick sort on list of length n . Since i is

equally like to be any of $0, 1, \dots, n - 1$, taking math expectation to the equation gives:

$$\begin{aligned}
 T(n) &= E(T(i)) + E(T(n - i - 1)) + cn \\
 &= \frac{1}{n} \sum_{i=0}^{n-1} T(i) + \frac{1}{n} \sum_{i=0}^{n-1} T(n - i - 1) + cn \\
 &= \frac{1}{n} \sum_{i=0}^{n-1} T(i) + \frac{1}{n} \sum_{j=0}^{n-1} T(j) + cn \\
 &= \frac{2}{n} \sum_{i=0}^{n-1} T(i) + cn
 \end{aligned} \tag{13.14}$$

Multiply by n to both sides, the equation changes to:

$$nT(n) = 2 \sum_{i=0}^{n-1} T(i) + cn^2 \tag{13.15}$$

Substitute n to $n - 1$ gives another equation:

$$(n - 1)T(n - 1) = 2 \sum_{i=0}^{n-2} T(i) + c(n - 1)^2 \tag{13.16}$$

Subtract equation (13.15) and (13.16) can eliminate all the $T(i)$ for $0 \leq i < n - 1$.

$$nT(n) = (n + 1)T(n - 1) + 2cn - c \tag{13.17}$$

As we can drop the constant time c in computing performance. The equation can be one more step changed like below.

$$\frac{T(n)}{n + 1} = \frac{T(n - 1)}{n} + \frac{2c}{n + 1} \tag{13.18}$$

Next we assign n to $n - 1, n - 2, \dots$, which gives us $n - 1$ equations.

$$\begin{aligned}
 \frac{T(n - 1)}{n} &= \frac{T(n - 2)}{n - 1} + \frac{2c}{n} \\
 \frac{T(n - 2)}{n - 1} &= \frac{T(n - 3)}{n - 2} + \frac{2c}{n - 1} \\
 &\dots \\
 \frac{T(2)}{3} &= \frac{T(1)}{2} + \frac{2c}{3}
 \end{aligned}$$

Sum all them up, and eliminate the same components in both sides, we can deduce to a function of n .

$$\frac{T(n)}{n + 1} = \frac{T(1)}{2} + 2c \sum_{k=3}^{n+1} \frac{1}{k} \tag{13.19}$$

Using the harmonic series mentioned above, the final result is:

$$O\left(\frac{T(n)}{n + 1}\right) = O\left(\frac{T(1)}{2} + 2c \ln n + \gamma + \epsilon_n\right) = O(\lg n) \tag{13.20}$$

Thus

$$O(T(n)) = O(n \lg n) \tag{13.21}$$

Exercise 13.2

- Why Lomuto's methods performs poor when there are many duplicated elements?

13.4 Engineering Improvement

Quick sort performs well in most cases as mentioned in previous section. However, there does exist the worst cases which downgrade the performance to quadratic. If the data is randomly prepared, such case is rare, however, there are some particular sequences which lead to the worst case and these kinds of sequences are very common in practice.

In this section, some engineering practices are introduced which either help to avoid poor performance in handling some special input data with improved partition algorithm, or try to uniform the possibilities among cases.

13.4.1 Engineering solution to duplicated elements

As presented in the exercise of above section, N. Lomuto's partition method isn't good at handling sequence with many duplicated elements. Consider a sequence with n equal elements like: $\{x, x, \dots, x\}$. There are actually two methods to sort it.

1. The normal basic quick sort: That we select an arbitrary element, which is x as the pivot, partition it to two sub sequences, one is $\{x, x, \dots, x\}$, which contains $n - 1$ elements, the other is empty. then recursively sort the first one; this is obviously quadratic $O(n^2)$ solution.
2. The other way is to only pick those elements strictly smaller than x , and strictly greater than x . Such partition results two empty sub sequences, and n elements equal to the pivot. Next we recursively sort the sub sequences contains the smaller and the bigger elements, since both of them are empty, the recursive call returns immediately; The only thing left is to concatenate the sort results in front of and after the list of elements which are equal to the pivot.

The latter one performs in $O(n)$ time if all elements are equal. This indicates an important improvement for partition. That instead of binary partition (split to two sub lists and a pivot), ternary partition (split to three sub lists) handles duplicated elements better.

We can define the ternary quick sort as the following.

$$\text{sort}(L) = \begin{cases} \phi & : L = \phi \\ \text{sort}(S) \cup \text{sort}(E) \cup \text{sort}(G) & : \textit{otherwise} \end{cases} \quad (13.22)$$

Where S, E, G are sub lists contains all elements which are less than, equal to, and greater than the pivot respectively.

$$\begin{aligned} S &= \{x | x \in L, x < l_1\} \\ E &= \{x | x \in L, x = l_1\} \\ G &= \{x | x \in L, l_1 < x\} \end{aligned}$$

The basic ternary quick sort can be implemented in Haskell as the following example code.

```
sort [] = []
sort (x:xs) = sort [a | a<-xs, a<x] ++
               x:[b | b<-xs, b==x] ++ sort [c | c<-xs, c>x]
```

Note that the comparison between elements must support abstract 'less-than' and 'equal-to' operations. The basic version of ternary sort takes linear $O(n)$ time to concatenate the three sub lists. It can be improved by using the standard techniques of accumulator.

Suppose function $sort'(L, A)$ is the accumulated ternary quick sort definition, that L is the sequence to be sorted, and the accumulator A contains the intermediate sorted result so far. We initialize the sorting with an empty accumulator: $sort(L) = sort'(L, \phi)$.

It's easy to give the trivial edge cases like below.

$$sort'(L, A) = \begin{cases} A & : L = \phi \\ \dots & : otherwise \end{cases}$$

For the recursive case, as the ternary partition splits to three sub lists S, E, G , only S and G need recursive sort, E contains all elements equal to the pivot, which is in correct order thus needn't to be sorted any more. The idea is to sort G with accumulator A , then concatenate it behind E , then use this result as the new accumulator, and start to sort S :

$$sort'(L, A) = \begin{cases} A & : L = \phi \\ sort(S, E \cup sort(G, A)) & : otherwise \end{cases} \quad (13.23)$$

The partition can also be realized with accumulators. It is similar to what has been developed for the basic version of quick sort. Note that we can't just pass only one predication for pivot comparison. It actually needs two, one for less-than, the other for equality testing. For the sake of brevity, we pass the pivot element instead.

$$partition(p, L, S, E, G) = \begin{cases} (S, E, G) & : L = \phi \\ partition(p, L', \{l_1\} \cup S, E, G) & : l_1 < p \\ partition(p, L', S, \{l_1\} \cup E, G) & : l_1 = p \\ partition(p, L', S, E, \{l_1\} \cup G) & : p < l_1 \end{cases} \quad (13.24)$$

Where l_1 is the first element in L if L isn't empty, and L' contains all rest elements except for l_1 . Below Haskell program implements this algorithm. It starts the recursive sorting immediately in the edge case of partition.

```

sort xs = sort' xs []

sort' [] r = r
sort' (x:xs) r = part xs [] [x] [] r where
  part [] as bs cs r = sort' as (bs ++ sort' cs r)
  part (x':xs') as bs cs r | x' < x = part xs' (x':as) bs cs r
                           | x' == x = part xs' as (x':bs) cs r
                           | x' > x = part xs' as bs (x':cs) r

```

Richard Bird developed another version in [1], that instead of concatenating the recursively sorted results, it uses a list of sorted sub lists, and performs concatenation finally.

```

sort xs = concat $ pass xs []

pass [] xss = xss
pass (x:xs) xss = step xs [] [x] [] xss where
  step [] as bs cs xss = pass as (bs:pass cs xss)
  step (x':xs') as bs cs xss | x' < x = step xs' (x':as) bs cs xss
                             | x' == x = step xs' as (x':bs) cs xss
                             | x' > x = step xs' as bs (x':cs) xss

```

2-way partition

The cases with many duplicated elements can also be handled imperatively. Robert Sedgewick presented a partition method [69], [4] which holds two pointers. One moves

from left to right, the other moves from right to left. The two pointers are initialized as the left and right boundaries of the array.

When start partition, the left most element is selected as the pivot. Then the left pointer i keeps advancing to right until it meets any element which is not less than the pivot; On the other hand³, The right pointer j repeatedly scans to left until it meets any element which is not greater than the pivot.

At this time, all elements before the left pointer i are strictly less than the pivot, while all elements after the right pointer j are greater than the pivot. i points to an element which is either greater than or equal to the pivot; while j points to an element which is either less than or equal to the pivot, the situation at this stage is illustrated in figure 13.4 (a).

In order to partition all elements less than or equal to the pivot to the left, and the others to the right, we can exchange the two elements pointed by i , and j . After that the scan can be resumed. We repeat this process until either i meets j , or they overlap.

At any time point during partition. There is invariant that all elements before i (including the one pointed by i) are not greater than the pivot; while all elements after j (including the one pointed by j) are not less than the pivot. The elements between i and j haven't been examined yet. This invariant is shown in figure 13.4 (b).

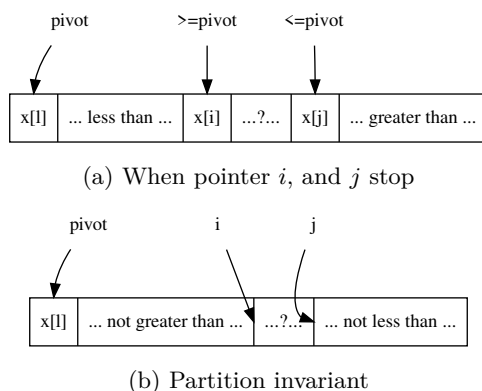


Figure 13.4: Partition a range of array by using the left most element as the pivot.

After the left pointer i meets the right pointer j , or they overlap each other, we need one extra exchanging to move the pivot located at the first position to the correct place which is pointed by j . Next, the elements between the lower bound and j as well as the sub slice between i and the upper bound of the array are recursively sorted.

This algorithm can be described as the following.

```

1: procedure SORT( $A, l, u$ )                                ▷ sort range  $[l, u]$ 
2:   if  $u - l > 1$  then                                    ▷ More than 1 element for non-trivial case
3:      $i \leftarrow l, j \leftarrow u$ 
4:      $pivot \leftarrow A[l]$ 
5:     loop
6:       repeat
7:          $i \leftarrow i + 1$ 
8:       until  $A[i] \geq pivot$                                 ▷ Need handle error case that  $i \geq u$  in fact.
9:       repeat
10:         $j \leftarrow j - 1$ 
11:      until  $A[j] \leq pivot$                                 ▷ Need handle error case that  $j < l$  in fact.
```

³We don't use 'then' because it's quite OK to perform the two scans in parallel.


```

12:         if  $j < i$  then
13:             break
14:             EXCHANGE  $A[i] \leftrightarrow A[j]$ 
15:     EXCHANGE  $A[l] \leftrightarrow A[j]$  ▷ Move the pivot
16:     SORT( $A, l, j$ )
17:     SORT( $A, i, u$ )

```

Consider the extreme case that all elements are equal, this in-place quick sort will partition the list to two equal length sub lists although it takes $\frac{n}{2}$ unnecessary swaps. As the partition is balanced, the overall performance is $O(n \lg n)$, which avoid downgrading to quadratic. The following ANSI C example program implements this algorithm.

```

void qsort(Key* xs, int l, int u) {
    int i, j, pivot;
    if (l < u - 1) {
        pivot = i = l; j = u;
        while (1) {
            while (i < u && xs[++i] < xs[pivot]);
            while (j ≥ l && xs[pivot] < xs[--j]);
            if (j < i) break;
            swap(xs[i], xs[j]);
        }
        swap(xs[pivot], xs[j]);
        qsort(xs, l, j);
        qsort(xs, i, u);
    }
}

```

Comparing this algorithm with the basic version based on N. Lumoto's partition method, we can find that it swaps fewer elements, because it skips those have already in proper sides of the pivot.

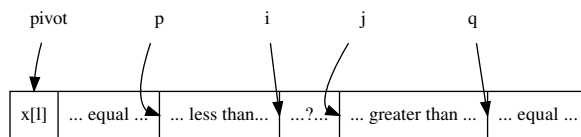
3-way partition

It's obviously that, we should avoid those unnecessary swapping for the duplicated elements. What's more, the algorithm can be developed with the idea of ternary sort (as known as 3-way partition in some materials), that all the elements which are strictly less than the pivot are put to the left sub slice, while those are greater than the pivot are put to the right. The middle part holds all the elements which are equal to the pivot. With such ternary partition, we need only recursively sort the ones which differ from the pivot. Thus in the above extreme case, there aren't any elements need further sorting. So the overall performance is linear $O(n)$.

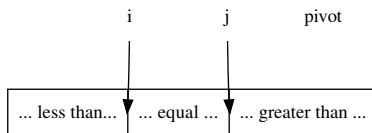
The difficulty is how to do the 3-way partition. Jon Bentley and Douglas McIlroy developed a solution which keeps those elements equal to the pivot at the left most and right most sides as shown in figure 13.5 (a) [70] [71].

The majority part of scan process is as same as the one developed by Robert Sedgewick, that i and j keep advancing toward each other until they meet any element which is greater then or equal to the pivot for i , or less than or equal to the pivot for j respectively. At this time, if i and j don't meet each other or overlap, they are not only exchanged, but also examined if the elements pointed by them are identical to the pivot. Then necessary exchanging happens between i and p , as well as j and q .

By the end of the partition process, the elements equal to the pivot need to be swapped to the middle part from the left and right ends. The number of such extra exchanging operations are proportion to the number of duplicated elements. It's zero operation if elements are unique which there is no overhead in the case. The final partition result is shown in figure 13.5 (b). After that we only need recursively sort the 'less-than' and 'greater-than' sub slices.



(a) Invariant of 3-way partition



(b) Swapping the equal parts to the middle

Figure 13.5: 3-way partition.

This algorithm can be given by modifying the 2-way partition as below.

```

1: procedure SORT( $A, l, u$ )
2:   if  $u - l > 1$  then
3:      $i \leftarrow l, j \leftarrow u$ 
4:      $p \leftarrow l, q \leftarrow u$  ▷ points to the boundaries for equal elements
5:      $pivot \leftarrow A[l]$ 
6:     loop
7:       repeat
8:          $i \leftarrow i + 1$ 
9:         until  $A[i] \geq pivot$  ▷ Skip the error handling for  $i \geq u$ 
10:      repeat
11:         $j \leftarrow j - 1$ 
12:        until  $A[j] \leq pivot$  ▷ Skip the error handling for  $j < l$ 
13:      if  $j \leq i$  then
14:        break ▷ Note the difference form the above algorithm
15:      EXCHANGE  $A[i] \leftrightarrow A[j]$ 
16:      if  $A[i] = pivot$  then ▷ Handle the equal elements
17:         $p \leftarrow p + 1$ 
18:        EXCHANGE  $A[p] \leftrightarrow A[i]$ 
19:      if  $A[j] = pivot$  then
20:         $q \leftarrow q - 1$ 
21:        EXCHANGE  $A[q] \leftrightarrow A[j]$ 
22:      if  $i = j \wedge A[i] = pivot$  then ▷ A special case
23:         $j \leftarrow j - 1, i \leftarrow i + 1$ 
24:      for  $k$  from  $l$  to  $p$  do ▷ Swap the equal elements to the middle part
25:        EXCHANGE  $A[k] \leftrightarrow A[j]$ 
26:         $j \leftarrow j - 1$ 
27:      for  $k$  from  $u - 1$  down-to  $q$  do
28:        EXCHANGE  $A[k] \leftrightarrow A[i]$ 
29:         $i \leftarrow i + 1$ 
30:      SORT( $A, l, j + 1$ )
31:      SORT( $A, i, u$ )

```

This algorithm can be translated to the following ANSI C example program.

```

void qsort2(Key* xs, int l, int u) {
    int i, j, k, p, q, pivot;
    if (l < u - 1) {
        i = p = l; j = q = u; pivot = xs[l];
        while (1) {
            while (i < u && xs[++i] < pivot);
            while (j >= l && pivot < xs[--j]);
            if (j <= i) break;
            swap(xs[i], xs[j]);
            if (xs[i] == pivot) { ++p; swap(xs[p], xs[i]); }
            if (xs[j] == pivot) { --q; swap(xs[q], xs[j]); }
        }
        if (i == j && xs[i] == pivot) { --j, ++i; }
        for (k = l; k <= p; ++k, --j) swap(xs[k], xs[j]);
        for (k = u-1; k >= q; --k, ++i) swap(xs[k], xs[i]);
        qsort2(xs, l, j + 1);
        qsort2(xs, i, u);
    }
}

```

It can be seen that the the algorithm turns to be a bit complex when it evolves to 3-way partition. There are some tricky edge cases should be handled with caution. Actually, we just need a ternary partition algorithm. This remind us the N. Lumoto's method, which is straightforward enough to be a start point.

The idea is to change the invariant a bit. We still select the first element as the pivot, as shown in figure 13.6, at any time, the left most section contains elements which are strictly less than the pivot; the next section contains the elements equal to the pivot; the right most section holds all the elements which are strictly greater than the pivot. The boundaries of three sections are marked as i , k , and j respectively. The rest part, which is between k and j are elements haven't been scanned yet.

At the beginning of this algorithm, the 'less-than' section is empty; the 'equal-to' section contains only one element, which is the pivot; so that i is initialized to the lower bound of the array, and k points to the element next to i . The 'greater-than' section is also initialized as empty, thus j is set to the upper bound.

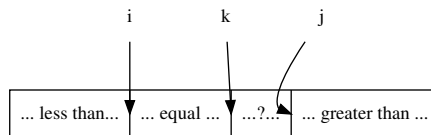


Figure 13.6: 3-way partition based on N. Lumoto's method.

When the partition process starts, the element pointed by k is examined. If it's equal to the pivot, k just advances to the next one; If it's greater than the pivot, we swap it with the last element in the unknown area, so that the length of 'greater-than' section increases by one. It's boundary j moves to the left. Since we don't know if the elements swapped to k is still greater than the pivot, it should be examined again repeatedly. Otherwise, if the element is less than the pivot, we can exchange it with the first one in the 'equal-to' section to resume the invariant. The partition algorithm stops when k meets j .

- 1: **procedure** SORT(A, l, u)
- 2: **if** $u - l > 1$ **then**
- 3: $i \leftarrow l, j \leftarrow u, k \leftarrow l + 1$
- 4: $pivot \leftarrow A[i]$
- 5: **while** $k < j$ **do**
- 6: **while** $pivot < A[k]$ **do**

```

7:         j ← j - 1
8:         EXCHANGE A[k] ↔ A[j]
9:         if A[k] < pivot then
10:            EXCHANGE A[k] ↔ A[i]
11:            i ← i + 1
12:            k ← k + 1
13:     SORT(A, l, i)
14:     SORT(A, j, u)

```

Compare this one with the previous 3-way partition quick sort algorithm, it's more simple at the cost of more swapping operations. Below ANSI C program implements this algorithm.

```

void qsort(Key* xs, int l, int u) {
    int i, j, k; Key pivot;
    if (l < u - 1) {
        i = l; j = u; pivot = xs[l];
        for (k = l + 1; k < j; ++k) {
            while (pivot < xs[k]) { --j; swap(xs[j], xs[k]); }
            if (xs[k] < pivot) { swap(xs[i], xs[k]); ++i; }
        }
        qsort(xs, l, i);
        qsort(xs, j, u);
    }
}

```

Exercise 13.3

- All the quick sort imperative algorithms given in this section use the first element as the pivot, another method is to choose the last one as the pivot. Realize the quick sort algorithms, including the basic version, Sedgewick version, and ternary (3-way partition) version by using this approach.

13.5 Engineering solution to the worst case

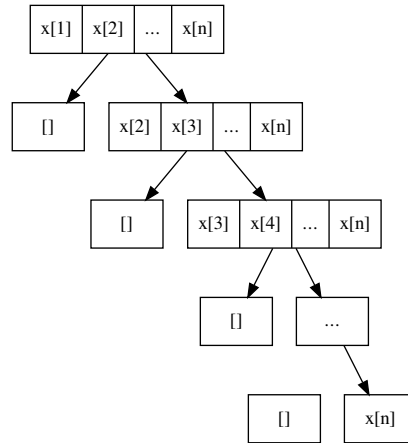
Although the ternary quick sort (3-way partition) solves the issue for duplicated elements, it can't handle some typical worst cases. For example if many of the elements in the sequence are ordered, no matter it's in ascending or descending order, the partition result will be two unbalanced sub sequences, one with few elements, the other contains all the rest.

Consider the two extreme cases, $\{x_1 < x_2 < \dots < x_n\}$ and $\{y_1 > y_2 > \dots > y_n\}$. The partition results are shown in figure 13.7.

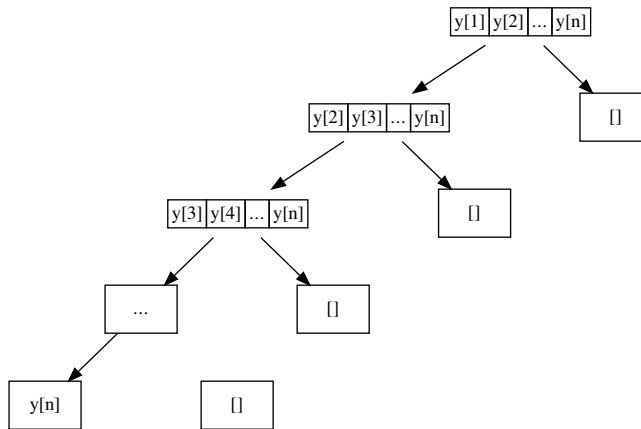
It's easy to give some more worst cases, for example, $\{x_m, x_{m-1}, \dots, x_2, x_1, x_{m+1}, x_{m+2}, \dots, x_n\}$ where $\{x_1 < x_2 < \dots < x_n\}$; Another one is $\{x_n, x_1, x_{n-1}, x_2, \dots\}$. Their partition result trees are shown in figure 13.8.

Observing that the bad partition happens easily when blindly choose the first element as the pivot, there is a popular work around suggested by Robert Sedgewick in [69]. Instead of selecting the fixed position in the sequence, a small sampling helps to find a pivot which has lower possibility to cause a bad partition. One option is to examine the first element, the middle, and the last one, then choose the median of these three element. In the worst case, it can ensure that there is at least one element in the shorter partitioned sub list.

Note that there is one tricky in real-world implementation. Since the index is typically represented in limited length words, it may cause overflow when calculating the middle

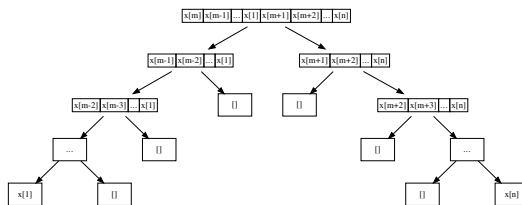


(a) The partition tree for $\{x_1 < x_2 < \dots < x_n\}$, There aren't any elements less than or equal to the pivot (the first element) in every partition.

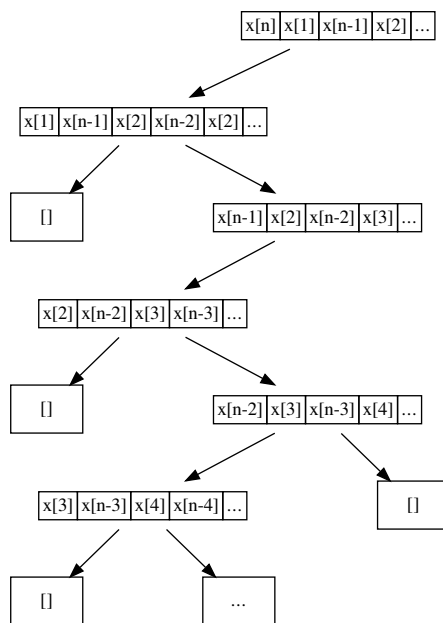


(b) The partition tree for $\{y_1 > y_2 > \dots > y_n\}$, There aren't any elements greater than or equal to the pivot (the first element) in every partition.

Figure 13.7: The two worst cases.



(a) Except for the first partition, all the others are unbalanced.



(b) A zig-zag partition tree.

Figure 13.8: Another two worst cases.

index by the naive expression $(l + u) / 2$. In order to avoid this issue, it can be accessed as $l + (u - l) / 2$. There are two methods to find the median, one needs at most three comparisons [70]; the other is to move the minimum value to the first location, the maximum value to the last location, and the median value to the middle location by swapping. After that we can select the middle as the pivot. Below algorithm illustrated the second idea before calling the partition procedure.

```

1: procedure SORT( $A, l, u$ )
2:   if  $u - l > 1$  then
3:      $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$  ▷ Need handle overflow error in practice
4:     if  $A[m] < A[l]$  then ▷ Ensure  $A[l] \leq A[m]$ 
5:       EXCHANGE  $A[l] \leftrightarrow A[m]$ 
6:     if  $A[u - 1] < A[l]$  then ▷ Ensure  $A[l] \leq A[u - 1]$ 
7:       EXCHANGE  $A[l] \leftrightarrow A[u - 1]$ 
8:     if  $A[u - 1] < A[m]$  then ▷ Ensure  $A[m] \leq A[u - 1]$ 
9:       EXCHANGE  $A[m] \leftrightarrow A[u - 1]$ 
10:    EXCHANGE  $A[l] \leftrightarrow A[m]$ 
11:     $(i, j) \leftarrow$  PARTITION( $A, l, u$ )
12:    SORT( $A, l, i$ )
13:    SORT( $A, j, u$ )

```

It's obviously that this algorithm performs well in the 4 special worst cases given above. The imperative implementation of median-of-three is left as exercise to the reader.

However, in purely functional settings, it's expensive to randomly access the middle and the last element. We can't directly translate the imperative median selection algorithm. The idea of taking a small sampling and then finding the median element as pivot can be realized alternatively by taking the first 3. For example, in the following Haskell program.

```

qsort [] = []
qsort [x] = [x]
qsort [x, y] = [min x y, max x y]
qsort (x:y:z:rest) = qsort (filter (< m) (s:rest)) ++ [m] ++ qsort (filter (≥ m) (l:rest))
  where
    xs = [x, y, z]
    [s, m, l] = [minimum xs, median xs, maximum xs]

```

Unfortunately, none of the above 4 worst cases can be well handled by this program, this is because the sampling is not good. We need telescope, but not microscope to profile the whole list to be partitioned. We'll see the functional way to solve the partition problem later.

Except for the median-of-three, there is another popular engineering practice to get good partition result. instead of always taking the first element or the last one as the pivot. One alternative is to randomly select one. For example as the following modification.

```

1: procedure SORT( $A, l, u$ )
2:   if  $u - l > 1$  then
3:     EXCHANGE  $A[l] \leftrightarrow A[ \text{RANDOM}(l, u) ]$ 
4:      $(i, j) \leftarrow$  PARTITION( $A, l, u$ )
5:     SORT( $A, l, i$ )
6:     SORT( $A, j, u$ )

```

The function $\text{RANDOM}(l, u)$ returns a random integer i between l and u , that $l \leq i < u$. The element at this position is exchanged with the first one, so that it is selected as the pivot for the further partition. This algorithm is called *random quick sort* [4].

Theoretically, neither median-of-three nor random quick sort can avoid the worst case completely. If the sequence to be sorted is randomly distributed, no matter choosing the

first one as the pivot, or the any other arbitrary one are equally in effect. Considering the underlying data structure of the sequence is singly linked-list in functional setting, it's expensive to strictly apply the idea of random quick sort in purely functional approach.

Even with this bad news, the engineering improvement still makes sense in real world programming.

13.6 Other engineering practice

There is some other engineering practice which doesn't focus on solving the bad partition issue. Robert Sedgewick observed that when the list to be sorted is short, the overhead introduced by quick sort is relative expense, on the other hand, the insertion sort performs better in such case [4], [70]. Sedgewick, Bentley and McIlroy tried different threshold, as known as 'Cut-Off', that when there are less than 'Cut-Off' elements, the sort algorithm falls back to insertion sort.

```

1: procedure SORT( $A, l, u$ )
2:   if  $u - l > \text{CUT-OFF}$  then
3:     QUICK-SORT( $A, l, u$ )
4:   else
5:     INSERTION-SORT( $A, l, u$ )

```

The implementation of this improvement is left as exercise to the reader.

Exercise 13.4

- Can you figure out more quick sort worst cases besides the four given in this section?
- Implement median-of-three method in your favorite imperative programming language.
- Implement random quick sort in your favorite imperative programming language.
- Implement the algorithm which falls back to insertion sort when the length of list is small in both imperative and functional approach.

13.7 Side words

It's sometimes called 'true quick sort' if the implementation equipped with most of the engineering practice we introduced, including insertion sort fall-back with cut-off, in-place exchanging, choose the pivot by median-of-three method, 3-way-partition.

The purely functional one, which express the idea of quick sort perfect can't take all of them. Thus someone think the functional quick sort is essentially tree sort.

Actually, quick sort does have close relationship with tree sort. Richard Bird shows how to derive quick sort from binary tree sort by deforestation [72].

Consider a binary search tree creation algorithm called *unfold*. Which turns a list of elements into a binary search tree.

$$\text{unfold}(L) = \begin{cases} \phi & : L = \phi \\ \text{tree}(T_l, l_1, T_r) & : \text{otherwise} \end{cases} \quad (13.25)$$

Where

$$\begin{aligned} T_l &= \text{unfold}(\{a \mid a \in L', a \leq l_1\}) \\ T_r &= \text{unfold}(\{a \mid a \in L', l_1 < a\}) \end{aligned} \quad (13.26)$$

The interesting point is that, this algorithm creates tree in a different way as we introduced in the chapter of binary search tree. If the list to be unfold is empty, the result is obviously an empty tree. This is the trivial edge case; Otherwise, the algorithm set the first element l_1 in the list as the key of the node, and recursively creates its left and right children. Where the elements used to form the left child are those which are less than or equal to the key in L' , while the rest elements which are greater than the key are used to form the right child.

Remind the algorithm which turns a binary search tree to a list by in-order traversing:

$$toList(T) = \begin{cases} \phi & : T = \phi \\ toList(left(T)) \cup \{key(T)\} \cup toList(right(T)) & : otherwise \end{cases} \quad (13.27)$$

We can define quick sort algorithm by composing these two functions.

$$quickSort = toList \cdot unfold \quad (13.28)$$

The binary search tree built in the first step of applying *unfold* is the intermediate result. This result is consumed by *toList* and dropped after the second step. It's quite possible to eliminate this intermediate result, which leads to the basic version of quick sort.

The elimination of the intermediate binary search tree is called *deforestation*. This concept is based on Burstle-Darlington's work [9].

13.8 Merge sort

Although quick sort performs perfectly in average cases, it can't avoid the worst case no matter what engineering practice is applied. Merge sort, on the other kind, ensure the performance is bound to $O(n \lg n)$ in all the cases. It's particularly useful in theoretical algorithm design and analysis. Another feature is that merge sort is friendly for linked-space settings, which is suitable for sorting nonconsecutive stored sequences. Some functional programming and dynamic programming environments adopt merge sort as the standard library sorting solution, such as Haskell, Python and Java (later than Java 7).

In this section, we'll first brief the intuitive idea of merge sort, provide a basic version. After that, some variants of merge sort will be given including nature merge sort, and bottom-up merge sort.

13.8.1 Basic version

Same as quick sort, the essential idea behind merge sort is also divide and conquer. Different from quick sort, merge sort enforces the divide to be strictly balanced, that it always splits the sequence to be sorted at the middle point. After that, it recursively sort the sub sequences and merge the sorted two sequences to the final result. The algorithm can be described as the following.

In order to sort a sequence L ,

- Trivial edge case: If the sequence to be sorted is empty, the result is obvious empty;
- Otherwise, split the sequence at the middle position, recursively sort the two sub sequences and merge the result.

The basic merge sort algorithm can be formalized with the following equation.

$$sort(L) = \begin{cases} \phi & : L = \phi \\ merge(sort(L_1), sort(L_2)) & : otherwise, (L_1, L_2) = splitAt(\lfloor \frac{|L|}{2} \rfloor, L) \end{cases} \quad (13.29)$$

Merge

There are two ‘black-boxes’ in the above merge sort definition, one is the *splitAt* function, which splits a list at a given position; the other is the *merge* function, which can merge two sorted lists into one.

As presented in the appendix of this book, it’s trivial to realize *splitAt* in imperative settings by using random access. However, in functional settings, it’s typically realized as a linear algorithm:

$$\textit{splitAt}(n, L) = \begin{cases} (\phi, L) & : n = 0 \\ (\{l_1\} \cup A, B) & : \textit{otherwise}, (A, B) = \textit{splitAt}(n - 1, L') \end{cases} \quad (13.30)$$

Where l_1 is the first element of L , and L' represents the rest elements except of l_1 if L isn’t empty.

The idea of merge can be illustrated as in figure 13.9. Consider two lines of kids. The kids have already stood in order of their heights. that the shortest one stands at the first, then a taller one, the tallest one stands at the end of the line.

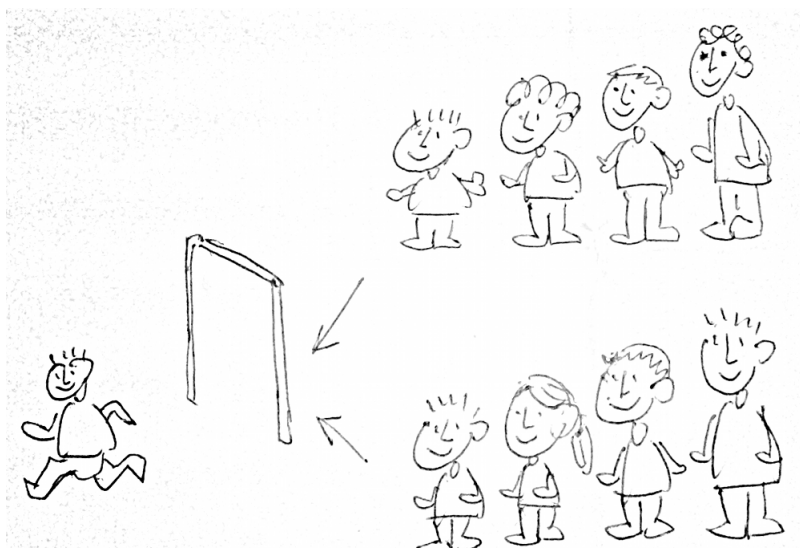


Figure 13.9: Two lines of kids pass a door.

Now let’s ask the kids to pass a door one by one, every time there can be at most one kid pass the door. The kids must pass this door in the order of their height. The one can’t pass the door before all the kids who are shorter than him/her.

Since the two lines of kids have already been ‘sorted’, the solution is to ask the first two kids, one from each line, compare their height, and let the shorter kid pass the door; Then they repeat this step until one line is empty, after that, all the rest kids can pass the door one by one.

This idea can be formalized in the following equation.

$$\textit{merge}(A, B) = \begin{cases} A & : B = \phi \\ B & : A = \phi \\ \{a_1\} \cup \textit{merge}(A', B) & : a_1 \leq b_1 \\ \{b_1\} \cup \textit{merge}(A, B') & : \textit{otherwise} \end{cases} \quad (13.31)$$

Where a_1 and b_1 are the first elements in list A and B ; A' and B' are the rest elements except for the first ones respectively. The first two cases are trivial edge cases. That merge

one sorted list with an empty list results the same sorted list; Otherwise, if both lists are non-empty, we take the first elements from the two lists, compare them, and use the minimum as the first one of the result, then recursively merge the rest.

With *merge* defined, the basic version of merge sort can be implemented like the following Haskell example code.

```
msort [] = []
msort [x] = [x]
msort xs = merge (msort as) (msort bs) where
  (as, bs) = splitAt (length xs `div` 2) xs

merge xs [] = xs
merge [] ys = ys
merge (x:xs) (y:ys) | x <= y = x : merge xs (y:ys)
                    | x > y = y : merge (x:xs) ys
```

Note that, the implementation differs from the algorithm definition that it treats the singleton list as trivial edge case as well.

Merge sort can also be realized imperatively. The basic version can be developed as the below algorithm.

```
1: procedure SORT(A)
2:   if |A| > 1 then
3:      $m \leftarrow \lfloor \frac{|A|}{2} \rfloor$ 
4:     X ← COPY-ARRAY(A[1...m])
5:     Y ← COPY-ARRAY(A[m + 1...|A|])
6:     SORT(X)
7:     SORT(Y)
8:     MERGE(A, X, Y)
```

When the array to be sorted contains at least two elements, the non-trivial sorting process starts. It first copy the first half to a new created array *X*, and the second half to a second new array *Y*. Recursively sort them; and finally merge the sorted result back to *A*.

This version uses the same amount of extra spaces of *A*. This is because the MERGE algorithm isn't in-place at the moment. We'll introduce the imperative in-place merge sort in later section.

The merge process almost does the same thing as the functional definition. There is a verbose version and a simplified version by using sentinel.

The verbose merge algorithm continuously checks the element from the two input arrays, picks the smaller one and puts it back to the result array *A*, it then advances along the arrays respectively until either one input array is exhausted. After that, the algorithm appends the rest of the elements in the other input array to *A*.

```
1: procedure MERGE(A, X, Y)
2:    $i \leftarrow 1, j \leftarrow 1, k \leftarrow 1$ 
3:    $m \leftarrow |X|, n \leftarrow |Y|$ 
4:   while  $i \leq m \wedge j \leq n$  do
5:     if  $X[i] < Y[j]$  then
6:        $A[k] \leftarrow X[i]$ 
7:        $i \leftarrow i + 1$ 
8:     else
9:        $A[k] \leftarrow Y[j]$ 
10:       $j \leftarrow j + 1$ 
11:     $k \leftarrow k + 1$ 
12:   while  $i \leq m$  do
13:      $A[k] \leftarrow X[i]$ 
```

```

14:     k ← k + 1
15:     i ← i + 1
16:     while j ≤ n do
17:         A[k] ← Y[j]
18:         k ← k + 1
19:         j ← j + 1

```

Although this algorithm is a bit verbose, it can be short in some programming environment with enough tools to manipulate array. The following Python program is an example.

```

def msort(xs):
    n = len(xs)
    if n > 1:
        ys = [x for x in xs[:n/2]]
        zs = [x for x in xs[n/2:]]
        ys = msort(ys)
        zs = msort(zs)
        xs = merge(xs, ys, zs)
    return xs

def merge(xs, ys, zs):
    i = 0
    while ys ≠ [] and zs ≠ []:
        xs[i] = ys.pop(0) if ys[0] < zs[0] else zs.pop(0)
        i = i + 1
    xs[i:] = ys if ys ≠ [] else zs
    return xs

```

Performance

Before dive into the improvement of this basic version, let's analyze the performance of merge sort. The algorithm contains two steps, divide step, and merge step. In divide step, the sequence to be sorted is always divided into two sub sequences with the same length. If we draw a similar partition tree as what we did for quick sort, it can be found this tree is a perfectly balanced binary tree as shown in figure 13.3. Thus the height of this tree is $O(\lg n)$. It means the recursion depth of merge sort is bound to $O(\lg n)$. Merge happens in every level. It's intuitive to analyze the merge algorithm, that it compare elements from two input sequences in pairs, after one sequence is fully examined the rest one is copied one by one to the result, thus it's a linear algorithm proportion to the length of the sequence. Based on this facts, denote $T(n)$ the time for sorting the sequence with length n , we can write the recursive time cost as below.

$$\begin{aligned}
 T(n) &= T\left(\frac{n}{2}\right) + T\left(\frac{n}{2}\right) + cn \\
 &= 2T\left(\frac{n}{2}\right) + cn
 \end{aligned}
 \tag{13.32}$$

It states that the cost consists of three parts: merge sort the first half takes $T\left(\frac{n}{2}\right)$, merge sort the second half takes also $T\left(\frac{n}{2}\right)$, merge the two results takes cn , where c is some constant. Solve this equation gives the result as $O(n \lg n)$.

Note that, this performance doesn't vary in all cases, as merge sort always uniformly divides the input.

Another significant performance indicator is space occupation. However, it varies a lot in different merge sort implementation. The detail space bounds analysis will be explained in every detailed variants later.

For the basic imperative merge sort, observe that it demands same amount of spaces as the input array in every recursion, copies the original elements to them for recursive sort, and these spaces can be released after this level of recursion. So the peak space requirement happens when the recursion enters to the deepest level, which is $O(n \lg n)$.

The functional merge sort consume much less than this amount, because the underlying data structure of the sequence is linked-list. Thus it needn't extra spaces for merge⁴. The only spaces requirement is for book-keeping the stack for recursive calls. This can be seen in the later explanation of even-odd split algorithm.

Minor improvement

We'll next improve the basic merge sort bit by bit for both the functional and imperative realizations. The first observation is that the imperative merge algorithm is a bit verbose. [4] presents an elegant simplification by using positive ∞ as the sentinel. That we append ∞ as the last element to the both ordered arrays for merging⁵. Thus we needn't test which array is not exhausted. Figure 13.10 illustrates this idea.

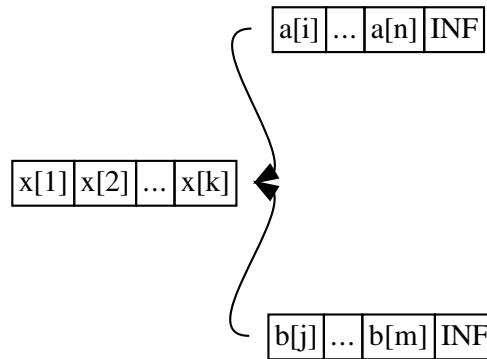


Figure 13.10: Merge with ∞ as sentinels.

```

1: procedure MERGE(A, X, Y)
2:   APPEND(X,  $\infty$ )
3:   APPEND(Y,  $\infty$ )
4:   i  $\leftarrow$  1, j  $\leftarrow$  1
5:   for k  $\leftarrow$  from 1 to |A| do
6:     if X[i] < Y[j] then
7:       A[k]  $\leftarrow$  X[i]
8:       i  $\leftarrow$  i + 1
9:     else
10:      A[k]  $\leftarrow$  Y[j]
11:      j  $\leftarrow$  j + 1

```

The following ANSI C program implements this idea. It embeds the merge inside. `INF` is defined as a big constant number with the same type of `Key`. Where the type can either be defined elsewhere or we can abstract the type information by passing the comparator as parameter. We skip these implementation and language details here.

```

void msort(Key* xs, int l, int u) {
    int i, j, m;

```

⁴The complex effects caused by lazy evaluation is ignored here, please refer to [72] for detail

⁵For sorting in monotonic non-increasing order, $-\infty$ can be used instead

```

Key *as, *bs;
if (u - l > 1) {
    m = l + (u - l) / 2; /* avoid int overflow */
    msort(xs, l, m);
    msort(xs, m, u);
    as = (Key*) malloc(sizeof(Key) * (m - l + 1));
    bs = (Key*) malloc(sizeof(Key) * (u - m + 1));
    memcpy((void*)as, (void*)(xs + l), sizeof(Key) * (m - l));
    memcpy((void*)bs, (void*)(xs + m), sizeof(Key) * (u - m));
    as[m - l] = bs[u - m] = INF;
    for (i = j = 0; l < u; ++l)
        xs[l] = as[i] < bs[j] ? as[i++] : bs[j++];
    free(as);
    free(bs);
}
}

```

Running this program takes much more time than the quick sort. Besides the major reason we'll explain later, one problem is that this version frequently allocates and releases memories for merging. While memory allocation is one of the well known bottle-neck in real world as mentioned by Bentley in [4]. One solution to address this issue is to allocate another array with the same size to the original one as the working area. The recursive sort for the first and second halves needn't allocate any more extra spaces, but use the working area when merging. Finally, the algorithm copies the merged result back.

This idea can be expressed as the following modified algorithm.

```

1: procedure SORT(A)
2:    $B \leftarrow \text{CREATE-ARRAY}(|A|)$ 
3:   SORT'(A, B, 1, |A|)

4: procedure SORT'(A, B, l, u)
5:   if  $u - l > 0$  then
6:      $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$ 
7:     SORT'(A, B, l, m)
8:     SORT'(A, B, m + 1, u)
9:     MERGE'(A, B, l, m, u)

```

This algorithm duplicates another array, and pass it along with the original array to be sorted to SORT' algorithm. In real implementation, this working area should be released either manually, or by some automatic tool such as GC (Garbage collection). The modified algorithm MERGE' also accepts a working area as parameter.

```

1: procedure MERGE'(A, B, l, m, u)
2:    $i \leftarrow l, j \leftarrow m + 1, k \leftarrow l$ 
3:   while  $i \leq m \wedge j \leq u$  do
4:     if  $A[i] < A[j]$  then
5:        $B[k] \leftarrow A[i]$ 
6:        $i \leftarrow i + 1$ 
7:     else
8:        $B[k] \leftarrow A[j]$ 
9:        $j \leftarrow j + 1$ 
10:     $k \leftarrow k + 1$ 
11:   while  $i \leq m$  do
12:      $B[k] \leftarrow A[i]$ 
13:      $k \leftarrow k + 1$ 
14:      $i \leftarrow i + 1$ 
15:   while  $j \leq u$  do

```

```

16:      B[k] ← A[j]
17:      k ← k + 1
18:      j ← j + 1
19:      for i ← from l to u do
20:      A[i] ← B[i]

```

▷ Copy back

By using this minor improvement, the space requirement reduced to $O(n)$ from $O(n \lg n)$. The following ANSI C program implements this minor improvement. For illustration purpose, we manually copy the merged result back to the original array in a loop. This can also be realized by using standard library provided tool, such as `memcpy`.

```

void merge(Key* xs, Key* ys, int l, int m, int u) {
    int i, j, k;
    i = k = l; j = m;
    while (i < m && j < u)
        ys[k++] = xs[i] < xs[j] ? xs[i++] : xs[j++];
    while (i < m)
        ys[k++] = xs[i++];
    while (j < u)
        ys[k++] = xs[j++];
    for(; l < u; ++l)
        xs[l] = ys[l];
}

void msort(Key* xs, Key* ys, int l, int u) {
    int m;
    if (u - l > 1) {
        m = l + (u - l) / 2;
        msort(xs, ys, l, m);
        msort(xs, ys, m, u);
        merge(xs, ys, l, m, u);
    }
}

void sort(Key* xs, int l, int u) {
    Key* ys = (Key*) malloc(sizeof(Key) * (u - l));
    kmsort(xs, ys, l, u);
    free(ys);
}

```

This new version runs faster than the previous one. In my test machine, it speeds up about 20% to 25% when sorting 100,000 randomly generated numbers.

The basic functional merge sort can also be fine tuned. Observe that, it splits the list at the middle point. However, as the underlying data structure to represent list is singly linked-list, random access at a given position is a linear operation (refer to appendix A for detail). Alternatively, one can split the list in an even-odd manner. That all the elements in even position are collected in one sub list, while all the odd elements are collected in another. As for any list, there are either same amount of elements in even and odd positions, or they differ by one. So this divide strategy always leads to well splitting, thus the performance can be ensured to be $O(n \lg n)$ in all cases.

The even-odd splitting algorithm can be defined as below.

$$\text{split}(L) = \begin{cases} (\phi, \phi) & : L = \phi \\ (\{l_1\}, \phi) & : |L| = 1 \\ (\{l_1\} \cup A, \{l_2\} \cup B) & : \text{otherwise, } (A, B) = \text{split}(L'') \end{cases} \quad (13.33)$$

When the list is empty, the split result are two empty lists; If there is only one element in the list, we put this single element, which is at position 1, to the odd sub list, the even sub list is empty; Otherwise, it means there are at least two elements in the list, We pick

the first one to the odd sub list, the second one to the even sub list, and recursively split the rest elements.

All the other functions are kept same, the modified Haskell program is given as the following.

```
split [] = ([], [])
split [x] = ([x], [])
split (x:y:xs) = (x:xs', y:ys') where (xs', ys') = split xs
```

13.9 In-place merge sort

One drawback for the imperative merge sort is that it requires extra spaces for merging, the basic version without any optimization needs $O(n \lg n)$ in peak time, and the one by allocating a working area needs $O(n)$.

It's nature for people to seek the in-place version merge sort, which can reuse the original array without allocating any extra spaces. In this section, we'll introduce some solutions to realize imperative in-place merge sort.

13.9.1 Naive in-place merge

The first idea is straightforward. As illustrated in figure 13.11, sub list A , and B are sorted, when performs in-place merge, the invariant ensures that all elements before i are merged, so that they are in non-decreasing order; every time we compare the i -th and the j -th elements. If the i -th is less than the j -th, the marker i just advances one step to the next. This is the easy case. Otherwise, it means that the j -th element is the next merge result, which should be put in front of i . In order to achieve this, all elements between i and j , including the i -th should be shift to the end by one cell. We repeat this process till all the elements in A and B are put to the correct positions.

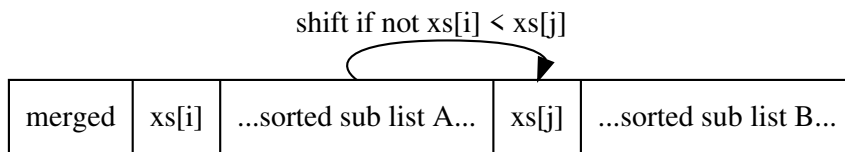


Figure 13.11: Naive in-place merge

```
1: procedure MERGE( $A, l, m, u$ )
2:   while  $l \leq m \wedge m \leq u$  do
3:     if  $A[l] < A[m]$  then
4:        $l \leftarrow l + 1$ 
5:     else
6:        $x \leftarrow A[m]$ 
7:       for  $i \leftarrow m$  down-to  $l + 1$  do ▷ Shift
8:          $A[i] \leftarrow A[i - 1]$ 
9:        $A[l] \leftarrow x$ 
```

However, this naive solution downgrades merge sort overall performance to quadratic $O(n^2)$! This is because that array shifting is a linear operation. It is proportion to the length of elements in the first sorted sub array which haven't been compared so far.

The following ANSI C program based on this algorithm runs very slow, that it takes about 12 times slower than the previous version when sorting 10,000 random numbers.


```

void naive_merge(Key* xs, int l, int m, int u) {
    int i; Key y;
    for(; l < m && m < u; ++l)
        if (!(xs[l] < xs[m])) {
            y = xs[m++];
            for (i = m - 1; i > l; --i) /* shift */
                xs[i] = xs[i-1];
            xs[l] = y;
        }
}

void msort3(Key* xs, int l, int u) {
    int m;
    if (u - l > 1) {
        m = l + (u - l) / 2;
        msort3(xs, l, m);
        msort3(xs, m, u);
        naive_merge(xs, l, m, u);
    }
}

```

13.9.2 in-place working area

In order to implement the in-place merge sort in $O(n \lg n)$ time, when sorting a sub array, the rest part of the array must be reused as working area for merging. As the elements stored in the working area, will be sorted later, they can't be overwritten. We can modify the previous algorithm, which duplicates extra spaces for merging, a bit to achieve this. The idea is that, every time when we compare the first elements in the two sorted sub arrays, if we want to put the less element to the target position in the working area, we in-turn exchange what stored in the working area with this element. Thus after merging, the two sub arrays store what the working area previously contains. This idea can be illustrated in figure 13.12.

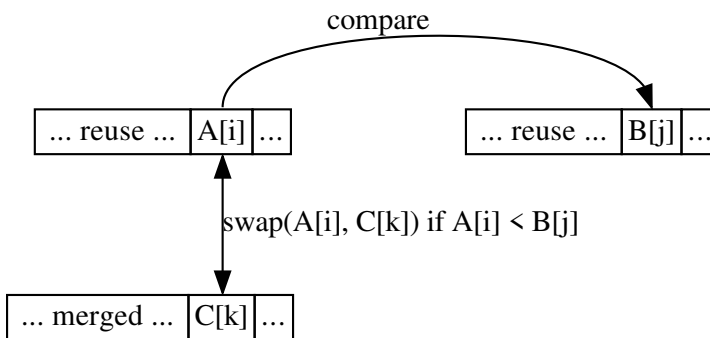


Figure 13.12: Merge without overwriting working area.

In our algorithm, both the two sorted sub arrays, and the working area for merging are parts of the original array to be sorted. we need supply the following arguments when merging: the start points and end points of the sorted sub arrays, which can be represented as ranges; and the start point of the working area. The following algorithm for example, uses $[a, b)$ to indicate the range include a , exclude b . It merges sorted range $[i, m)$ and range $[j, n)$ to the working area starts from k .

1: **procedure** MERGE($A, [i, m), [j, n), k$)

```

2:  while  $i < m \wedge j < n$  do
3:      if  $A[i] < A[j]$  then
4:          EXCHANGE  $A[k] \leftrightarrow A[i]$ 
5:           $i \leftarrow i + 1$ 
6:      else
7:          EXCHANGE  $A[k] \leftrightarrow A[j]$ 
8:           $j \leftarrow j + 1$ 
9:       $k \leftarrow k + 1$ 
10:  while  $i < m$  do
11:      EXCHANGE  $A[k] \leftrightarrow A[i]$ 
12:       $i \leftarrow i + 1$ 
13:       $k \leftarrow k + 1$ 
14:  while  $j < m$  do
15:      EXCHANGE  $A[k] \leftrightarrow A[j]$ 
16:       $j \leftarrow j + 1$ 
17:       $k \leftarrow k + 1$ 

```

Note that, the following two constraints must be satisfied when merging:

1. The working area should be within the bounds of the array. In other words, it should be big enough to hold elements exchanged in without causing any out-of-bound error;
2. The working area can be overlapped with either of the two sorted arrays, however, it should be ensured that there are not any unmerged elements being overwritten;

This algorithm can be implemented in ANSI C as the following example.

```

void wmerge(Key* xs, int i, int m, int j, int n, int w) {
    while (i < m && j < n)
        swap(xs, w++, xs[i] < xs[j] ? i++ : j++);
    while (i < m)
        swap(xs, w++, i++);
    while (j < n)
        swap(xs, w++, j++);
}

```

With this merging algorithm defined, it's easy to imagine a solution, which can sort half of the array; The next question is, how to deal with the rest of the unsorted part stored in the working area as shown in figure 13.13?

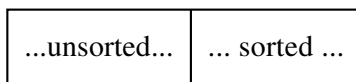


Figure 13.13: Half of the array is sorted.

One intuitive idea is to recursively sort another half of the working area, thus there are only $\frac{1}{4}$ elements haven't been sorted yet. Which is shown in figure 13.14. The key point at this stage is that we must merge the sorted $\frac{1}{4}$ elements B with the sorted $\frac{1}{2}$ elements A sooner or later.

Is the working area left, which only holds $\frac{1}{4}$ elements, big enough for merging A and B ? Unfortunately, it isn't in the settings shown in figure 13.14.

However, the second constraint mentioned before gives us a hint, that we can exploit it by arranging the working area to overlap with either sub array if we can ensure the unmerged elements won't be overwritten under some well designed merging schema.

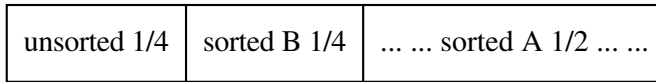
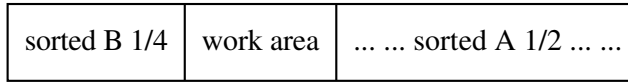
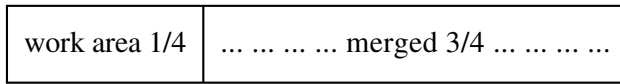


Figure 13.14: A and B must be merged at sometime.

Actually, instead of making the second half of the working area be sorted, we can make the first half be sorted, and put the working area between the two sorted arrays as shown in figure 13.15 (a). This setup effects arranging the working area to overlap with the sub array A . This idea is proposed in [74].



(a)



(b)

Figure 13.15: Merge A and B with the working area.

Let's consider two extreme cases:

1. All the elements in B are less than any element in A . In this case, the merge algorithm finally moves the whole contents of B to the working area; the cells of B holds what previously stored in the working area; As the size of area is as same as B , it's OK to exchange their contents;
2. All the elements in A are less than any element in B . In this case, the merge algorithm continuously exchanges elements between A and the working area. After all the previous $\frac{1}{4}$ cells in the working area are filled with elements from A , the algorithm starts to overwrite the first half of A . Fortunately, the contents being overwritten are not those unmerged elements. The working area is in effect advances toward the end of the array, and finally moves to the right side; From this time point, the merge algorithm starts exchanging contents in B with the working area. The result is that the working area moves to the left most side which is shown in figure 13.15 (b).

We can repeat this step, that always sort the second half of the unsorted part, and exchange the sorted sub array to the first half as working area. Thus we keep reducing the working area from $\frac{1}{2}$ of the array, $\frac{1}{4}$ of the array, $\frac{1}{8}$ of the array, ... The scale of the merge problem keeps reducing. When there is only one element left in the working area, we needn't sort it any more since the singleton array is sorted by nature. Merging a singleton array to the other is equivalent to insert the element. In practice, the algorithm can finalize the last few elements by switching to insertion sort.

The whole algorithm can be described as the following.

- 1: **procedure** SORT(A, l, u)
- 2: **if** $u - l > 0$ **then**
- 3: $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$
- 4: $w \leftarrow l + u - m$
- 5: SORT'(A, l, m, w) ▷ The second half contains sorted elements

```

6:   while  $w - l > 1$  do
7:      $u' \leftarrow w$ 
8:      $w \leftarrow \lceil \frac{l+u'}{2} \rceil$            ▷ Ensure the working area is big enough
9:     SORT'(A, w, u', l)           ▷ The first half holds the sorted elements
10:    MERGE(A, [l, l + u' - w], [u', u], w)
11:    for  $i \leftarrow w$  down-to  $l$  do           ▷ Switch to insertion sort
12:       $j \leftarrow i$ 
13:      while  $j \leq u \wedge A[j] < A[j - 1]$  do
14:        EXCHANGE  $A[j] \leftrightarrow A[j - 1]$ 
15:         $j \leftarrow j - 1$ 

```

Note that in order to satisfy the first constraint, we must ensure the working area is big enough to hold all exchanged in elements, that's way we round it by ceiling when sort the second half of the working area. Note that we actually pass the ranges including the end points to the algorithm MERGE.

Next, we develop a Sort' algorithm, which mutually recursive call Sort and exchange the result to the working area.

```

1: procedure SORT'(A, l, u, w)
2:   if  $u - l > 0$  then
3:      $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$ 
4:     SORT(A, l, m)
5:     SORT(A, m + 1, u)
6:     MERGE(A, [l, m], [m + 1, u], w)
7:   else           ▷ Exchange all elements to the working area
8:     while  $l \leq u$  do
9:       EXCHANGE  $A[l] \leftrightarrow A[w]$ 
10:       $l \leftarrow l + 1$ 
11:       $w \leftarrow w + 1$ 

```

Different from the naive in-place sort, this algorithm doesn't shift the array during merging. The main algorithm reduces the unsorted part in sequence of $\frac{n}{2}, \frac{n}{4}, \frac{n}{8}, \dots$, it takes $O(\lg n)$ steps to complete sorting. In every step, It recursively sorts half of the rest elements, and performs linear time merging.

Denote the time cost of sorting n elements as $T(n)$, we have the following equation.

$$T(n) = T\left(\frac{n}{2}\right) + c\frac{n}{2} + T\left(\frac{n}{4}\right) + c\frac{3n}{4} + T\left(\frac{n}{8}\right) + c\frac{7n}{8} + \dots \quad (13.34)$$

substitute n with its half, we get another one:

$$T\left(\frac{n}{2}\right) = T\left(\frac{n}{4}\right) + c\frac{n}{4} + T\left(\frac{n}{8}\right) + c\frac{3n}{8} + T\left(\frac{n}{16}\right) + c\frac{7n}{16} + \dots \quad (13.35)$$

Substract (13.34) and (13.35) we have:

$$T(n) - T\left(\frac{n}{2}\right) = T\left(\frac{n}{2}\right) + cn\left(\frac{1}{2} + \frac{1}{2} + \dots\right)$$

There are total $\lg n$ times $\frac{1}{2}$ added together, therefore, the recursive time can be expressed as:

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

Solving this equation by using telescope method, gets the result $O(n \lg^2 n)$.

The following ANSI C code completes the implementation by using the example `wmerge` program given above.

```

void imsort(Key* xs, int l, int u);

void wsort(Key* xs, int l, int u, int w) {
    int m;
    if (u - l > 1) {
        m = l + (u - l) / 2;
        imsort(xs, l, m);
        imsort(xs, m, u);
        wmerge(xs, l, m, m, u, w);
    }
    else
        while (l < u)
            swap(xs, l++, w++);
}

void imsort(Key* xs, int l, int u) {
    int m, n, w;
    if (u - l > 1) {
        m = l + (u - l) / 2;
        w = l + u - m;
        wsort(xs, l, m, w); /* the last half contains sorted elements */
        while (w - l > 2) {
            n = w;
            w = l + (n - l + 1) / 2; /* ceiling */
            wsort(xs, w, n, l); /* the first half contains sorted elements */
            wmerge(xs, l, l + n - w, n, u, w);
        }
        for (n = w; n > l; --n) /*switch to insertion sort*/
            for (m = n; m < u && xs[m] < xs[m-1]; ++m)
                swap(xs, m, m - 1);
    }
}

```

However, this program doesn't run faster than the version we developed in previous section, which doubles the array in advance as working area. In my machine, it is about 60% slower when sorting 100,000 random numbers due to many swap operations.

13.9.3 In-place merge sort vs. linked-list merge sort

The in-place merge sort is still a live area for research. In order to save the extra spaces for merging, some overhead has been introduced, which increases the complexity of the merge sort algorithm. However, if the underlying data structure isn't array, but linked-list, merge can be achieved without any extra spaces as shown in the even-odd functional merge sort algorithm presented in previous section.

In order to make it clearer, we can develop a purely imperative linked-list merge sort solution. The linked-list can be defined as a record type as shown in appendix A like below.

```

struct Node {
    Key key;
    struct Node* next;
};

```

We can define an auxiliary function for node linking. Assume the list to be linked isn't empty, it can be implemented as the following.

```

struct Node* link(struct Node* x, struct Node* ys) {
    x->next = ys;
    return x;
}

```

One method to realize the imperative even-odd splitting, is to initialize two empty sub lists. Then iterate the list to be split. Every time, we link the current node in front of the first sub list, then exchange the two sub lists. So that, the second sub list will be linked at the next time iteration. This idea can be illustrated as below.

```

1: function SPLIT( $L$ )
2:    $(A, B) \leftarrow (\phi, \phi)$ 
3:   while  $L \neq \phi$  do
4:      $p \leftarrow L$ 
5:      $L \leftarrow \text{NEXT}(L)$ 
6:      $A \leftarrow \text{LINK}(p, A)$ 
7:     EXCHANGE  $A \leftrightarrow B$ 
8:   return  $(A, B)$ 

```

The following example ANSI C program implements this splitting algorithm embedded.

```

struct Node* msort(struct Node* xs) {
    struct Node *p, *as, *bs;
    if (!xs || !xs->next) return xs;

    as = bs = NULL;
    while(xs) {
        p = xs;
        xs = xs->next;
        as = link(p, as);
        swap(as, bs);
    }
    as = msort(as);
    bs = msort(bs);
    return merge(as, bs);
}

```

The only thing left is to develop the imperative merging algorithm for linked-list. The idea is quite similar to the array merging version. As long as neither of the sub lists is exhausted, we pick the less one, and append it to the result list. After that, it just need link the non-empty one to the tail the result, but not a looping for copying. It needs some carefulness to initialize the result list, as its head node is the less one among the two sub lists. One simple method is to use a dummy sentinel head, and drop it before returning. This implementation detail can be given as the following.

```

struct Node* merge(struct Node* as, struct Node* bs) {
    struct Node s, *p;
    p = &s;
    while (as && bs) {
        if (as->key < bs->key) {
            link(p, as);
            as = as->next;
        }
        else {
            link(p, bs);
            bs = bs->next;
        }
        p = p->next;
    }
    if (as)
        link(p, as);
    if (bs)
        link(p, bs);
    return s.next;
}

```

Exercise 13.5

- Proof the performance of in-place merge sort is bound to $O(n \lg n)$.

13.10 Nature merge sort

Knuth gives another way to interpret the idea of divide and conquer merge sort. It just likes burn a candle in both ends [51]. This leads to the nature merge sort algorithm.

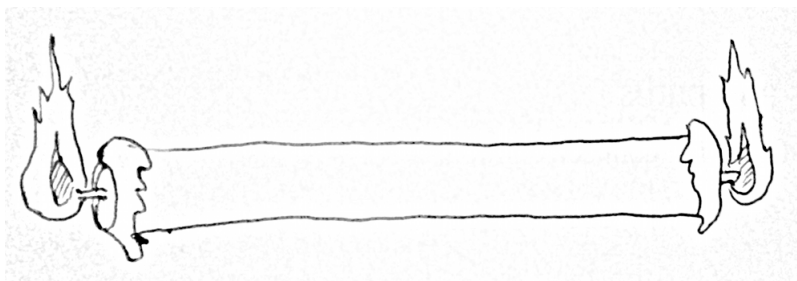


Figure 13.16: Burn a candle from both ends

For any given sequence, we can always find a non-decreasing sub sequence starts at any position. One particular case is that we can find such a sub sequence from the left-most position. The following table list some examples, the non-decreasing sub sequences are in bold font.

15 , 0, 4, 3, 5, 2, 7, 1, 12, 14, 13, 8, 9, 6, 10, 11
8, 12, 14 , 0, 1, 4, 11, 2, 3, 5, 9, 13, 10, 6, 15, 7
0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15

The first row in the table illustrates the worst case, that the second element is less than the first one, so the non-decreasing sub sequence is a singleton list, which only contains the first element; The last row shows the best case, the the sequence is ordered, and the non-decreasing list is the whole; The second row shows the average case.

Symmetrically, we can always find a non-decreasing sub sequence from the end of the sequence to the left. This indicates us that we can merge the two non-decreasing sub sequences, one from the beginning, the other form the ending to a longer sorted sequence. The advantage of this idea is that, we utilize the nature ordered sub sequences, so that we needn't recursive sorting at all.

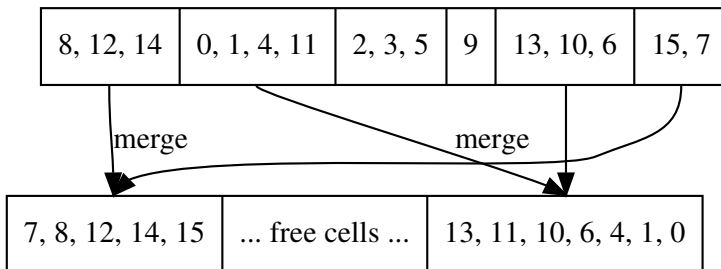


Figure 13.17: Nature merge sort

Figure 13.17 illustrates this idea. We starts the algorithm by scanning from both ends, finding the longest non-decreasing sub sequences respectively. After that, these two sub

sequences are merged to the working area. The merged result starts from beginning. Next we repeat this step, which goes on scanning toward the center of the original sequence. This time we merge the two ordered sub sequences to the right hand of the working area toward the left. Such setup is easy for the next round of scanning. When all the elements in the original sequence have been scanned and merged to the target, we switch to use the elements stored in the working area for sorting, and use the previous sequence as new working area. Such switching happens repeatedly in each round. Finally, we copy all elements from the working area to the original array if necessary.

The only question left is when this algorithm stops. The answer is that when we start a new round of scanning, and find that the longest non-decreasing sub list spans to the end, which means the whole list is ordered, the sorting is done.

Because this kind of merge sort proceeds the target sequence in two ways, and uses the nature ordering of sub sequences, it's named *nature two-way merge sort*. In order to realize it, some carefulness must be paid. Figure 13.18 shows the invariant during the nature merge sort. At anytime, all elements before marker a and after marker d have been already scanned and merged. We are trying to span the non-decreasing sub sequence $[a, b]$ as long as possible, at the same time, we span the sub sequence from right to left to span $[c, d]$ as long as possible as well. The invariant for the working area is shown in the second row. All elements before f and after r have already been processed (Note that they may contain several ordered sub sequences). For the odd times (1, 3, 5, ...), we merge $[a, b]$ and $[c, d]$ from f toward right; while for the even times (2, 4, 6, ...), we merge the two sorted sub sequences after r toward left.

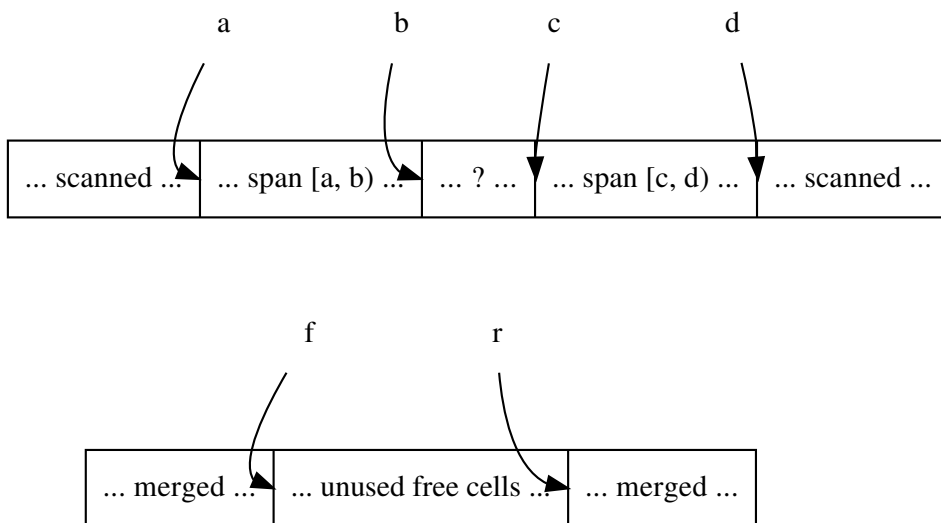


Figure 13.18: Invariant during nature merge sort

For imperative realization, the sequence is represented by array. Before sorting starts, we duplicate the array to create a working area. The pointers a, b are initialized to point the left most position, while c, d point to the right most position. Pointer f starts by pointing to the front of the working area, and r points to the rear position.

```

1: function SORT( $A$ )
2:   if  $|A| > 1$  then
3:      $n \leftarrow |A|$ 
4:      $B \leftarrow$  CREATE-ARRAY( $n$ )            $\triangleright$  Create the working area
5:     loop

```



```

6:      [a, b] ← [1, 1)
7:      [c, d] ← [n + 1, n + 1)
8:      f ← 1, r ← n           ▷ front and rear pointers to the working area
9:      t ← False              ▷ merge to front or rear
10:     while b < c do         ▷ There are still elements for scan
11:         repeat              ▷ Span [a, b)
12:             b ← b + 1
13:         until b ≥ c ∨ A[b] < A[b - 1]
14:         repeat              ▷ Span [c, d)
15:             c ← c - 1
16:         until c ≤ b ∨ A[c - 1] < A[c]
17:         if c < b then      ▷ Avoid overlap
18:             c ← b
19:         if b - a ≥ n then  ▷ Done if [a, b) spans to the whole array
20:             return A
21:         if t then          ▷ merge to front
22:             f ← MERGE(A, [a, b), [c, d), B, f, 1)
23:         else                ▷ merge to rear
24:             r ← MERGE(A, [a, b), [c, d), B, r, -1)
25:             a ← b, d ← c
26:             t ← ¬t         ▷ Switch the merge direction
27:     EXCHANGE A ↔ B        ▷ Switch working area
28:     return A

```

The merge algorithm is almost as same as before except that we need pass a parameter to indicate the direction for merging.

```

1: function MERGE(A, [a, b), [c, d), B, w, Δ)
2:   while a < b ∧ c < d do
3:     if A[a] < A[d - 1] then
4:       B[w] ← A[a]
5:       a ← a + 1
6:     else
7:       B[w] ← A[d - 1]
8:       d ← d - 1
9:     w ← w + Δ
10:  while a < b do
11:    B[w] ← A[a]
12:    a ← a + 1
13:    w ← w + Δ
14:  while c < d do
15:    B[w] ← A[d - 1]
16:    d ← d - 1
17:    w ← w + Δ
18:  return w

```

The following ANSI C program implements this two-way nature merge sort algorithm. Note that it doesn't release the allocated working area explicitly.

```

int merge(Key* xs, int a, int b, int c, int d, Key* ys, int k, int delta) {
    for(; a < b && c < d; k += delta )
        ys[k] = xs[a] < xs[d-1] ? xs[a++] : xs[--d];
    for(; a < b; k += delta)
        ys[k] = xs[a++];
    for(; c < d; k += delta)

```

```

        ys[k] = xs[--d];
    return k;
}

Key* sort(Key* xs, Key* ys, int n) {
    int a, b, c, d, f, r, t;
    if(n < 2)
        return xs;
    for(;;) {
        a = b = 0;
        c = d = n;
        f = 0;
        r = n-1;
        t = 1;
        while(b < c) {
            do { /* span [a, b) as much as possible */
                ++b;
            } while( b < c && xs[b-1] ≤ xs[b] );
            do{ /* span [c, d) as much as possible */
                --c;
            } while( b < c && xs[c] ≤ xs[c-1] );
            if( c < b )
                c = b; /* eliminate overlap if any */
            if( b - a ≥ n)
                return xs; /* sorted */
            if( t )
                f = merge(xs, a, b, c, d, ys, f, 1);
            else
                r = merge(xs, a, b, c, d, ys, r, -1);
            a = b;
            d = c;
            t = !t;
        }
        swap(&xs, &ys);
    }
    return xs; /*can't be here*/
}

```

The performance of nature merge sort depends on the actual ordering of the sub arrays. However, it in fact performs well even in the worst case. Suppose that we are unlucky when scanning the array, that the length of the non-decreasing sub arrays are always 1 during the first round scan. This leads to the result working area with merged ordered sub arrays of length 2. Suppose that we are unlucky again in the second round of scan, however, the previous results ensure that the non-decreasing sub arrays in this round are no shorter than 2, this time, the working area will be filled with merged ordered sub arrays of length 4, ... Repeat this we get the length of the non-decreasing sub arrays doubled in every round, so there are at most $O(\lg n)$ rounds, and in every round we scanned all the elements. The overall performance for this worst case is bound to $O(n \lg n)$. We'll go back to this interesting phenomena in the next section about bottom-up merge sort.

In purely functional settings however, it's not sensible to scan list from both ends since the underlying data structure is singly linked-list. The nature merge sort can be realized in another approach.

Observe that the list to be sorted is consist of several non-decreasing sub lists, that we can pick every two of such sub lists and merge them to a bigger one. We repeatedly pick and merge, so that the number of the non-decreasing sub lists halves continuously and finally there is only one such list, which is the sorted result. This idea can be formalized in the following equation.

$$\text{sort}(L) = \text{sort}'(\text{group}(L)) \quad (13.36)$$

Where function $\text{group}(L)$ groups the elements in the list into non-decreasing sub lists.

This function can be described like below, the first two are trivial edge cases.

- If the list is empty, the result is a list contains an empty list;
- If there is only one element in the list, the result is a list contains a singleton list;
- Otherwise, The first two elements are compared, if the first one is less than or equal to the second, it is linked in front of the first sub list of the recursive grouping result; or a singleton list contains the first element is set as the first sub list before the recursive result.

$$group(L) = \begin{cases} \{L\} & : |L| \leq 1 \\ \{\{l_1\} \cup L_1, L_2, \dots\} & : l_1 \leq l_2, \{L_1, L_2, \dots\} = group(L') \\ \{\{l_1\}, L_1, L_2, \dots\} & : otherwise \end{cases} \quad (13.37)$$

It's quite possible to abstract the grouping criteria as a parameter to develop a generic grouping function, for instance, as the following Haskell code ⁶.

```
groupBy' :: (a -> a -> Bool) -> [a] -> [[a]]
groupBy' _ [] = [[]]
groupBy' _ [x] = [[x]]
groupBy' f (x:xs@(x':_)) | f x x' = (x:ys):yss
                        | otherwise = [x]:r
where
  r@(ys:yss) = groupBy' f xs
```

Different from the *sort* function, which sorts a list of elements, function *sort'* accepts a list of sub lists which is the result of grouping.

$$sort'(\mathbb{L}) = \begin{cases} \phi & : \mathbb{L} = \phi \\ L_1 & : \mathbb{L} = \{L_1\} \\ sort'(mergePairs(\mathbb{L})) & : otherwise \end{cases} \quad (13.38)$$

The first two are the trivial edge cases. If the list to be sorted is empty, the result is obviously empty; If it contains only one sub list, then we are done. We need just extract this single sub list as result; For the recursive case, we call a function *mergePairs* to merge every two sub lists, then recursively call *sort'*.

The next undefined function is *mergePairs*, as the name indicates, it repeatedly merges pairs of non-decreasing sub lists into bigger ones.

$$mergePairs(L) = \begin{cases} L & : |L| \leq 1 \\ \{merge(L_1, L_2)\} \cup mergePairs(L'') & : otherwise \end{cases} \quad (13.39)$$

When there are less than two sub lists in the list, we are done; otherwise, we merge the first two sub lists L_1 and L_2 , and recursively merge the rest of pairs in L'' . The type of the result of *mergePairs* is list of lists, however, it will be flattened by *sort'* function finally.

The *merge* function is as same as before. The complete example Haskell program is given as below.

```
mergesort = sort' o groupBy' (<=)

sort' [] = []
sort' [xs] = xs
sort' xss = sort' (mergePairs xss) where
  mergePairs (xs:ys:xss) = merge xs ys : mergePairs xss
  mergePairs xss = xss
```

⁶There is a 'groupBy' function provided in the Haskell standard library 'Data.List'. However, it doesn't fit here, because it accepts an equality testing function as parameter, which must satisfy the properties of reflexive, transitive, and symmetric. but what we use here, the less-than or equal to operation doesn't conform to symmetric. Refer to appendix A of this book for detail.

Alternatively, observing that we can first pick two sub lists, merge them to an intermediate result, then repeatedly pick next sub list, and merge to this ordered result we've gotten so far until all the rest sub lists are merged. This is a typical folding algorithm as introduced in appendix A.

$$\text{sort}(L) = \text{fold}(\text{merge}, \phi, \text{group}(L)) \quad (13.40)$$

Translate this version to Haskell yields the folding version.

```
mergesort' = foldl merge [] o groupBy' (<=)
```

Exercise 13.6

- Is the nature merge sort algorithm realized by folding is equivalent with the one by using *mergePairs* in terms of performance? If yes, prove it; If not, which one is faster?

13.11 Bottom-up merge sort

The worst case analysis for nature merge sort raises an interesting topic, instead of realizing merge sort in top-down manner, we can develop a bottom-up version. The great advantage is that, we needn't do book keeping any more, so the algorithm is quite friendly for purely iterative implementation.

The idea of bottom-up merge sort is to turn the sequence to be sorted into n small sub sequences each contains only one element. Then we merge every two of such small sub sequences, so that we get $\frac{n}{2}$ ordered sub sequences each with length 2; If n is odd number, we left the last singleton sequence untouched. We repeatedly merge these pairs, and finally we get the sorted result. Knuth names this variant as 'straight two-way merge sort' [51]. The bottom-up merge sort is illustrated in figure 13.19

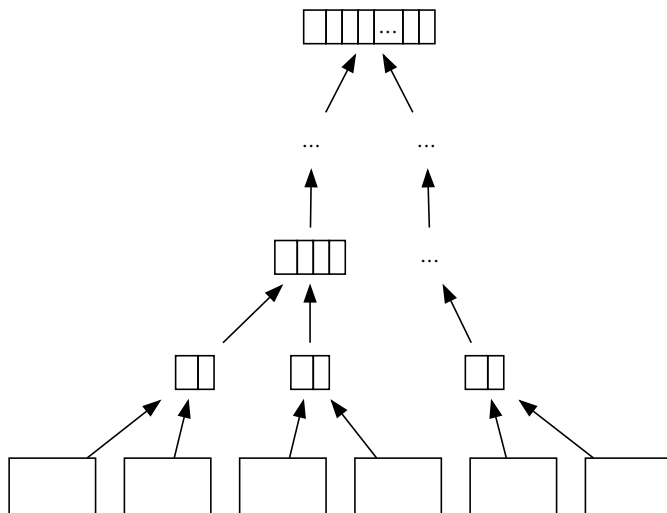


Figure 13.19: Bottom-up merge sort

Different with the basic version and even-odd version, we needn't explicitly split the list to be sorted in every recursion. The whole list is split into n singletons at the very beginning, and we merge these sub lists in the rest of the algorithm.

$$\text{sort}(L) = \text{sort}'(\text{wraps}(L)) \quad (13.41)$$

$$\text{wraps}(L) = \begin{cases} \phi & : L = \phi \\ \{\{l_1\}\} \cup \text{wraps}(L') & : \text{otherwise} \end{cases} \quad (13.42)$$

Of course *wraps* can be implemented by using mapping as introduced in appendix A.

$$\text{sort}(L) = \text{sort}'(\text{map}(\lambda_x \cdot \{x\}, L)) \quad (13.43)$$

We reuse the function *sort'* and *mergePairs* which are defined in section of nature merge sort. They repeatedly merge pairs of sub lists until there is only one.

Implement this version in Haskell gives the following example code.

```
sort = sort' ◦ map (λx→[x])
```

This version is based on what Okasaki presented in [3]. It is quite similar to the nature merge sort only differs in the way of grouping. Actually, it can be deduced as a special case (the worst case) of nature merge sort by the following equation.

$$\text{sort}(L) = \text{sort}'(\text{groupBy}(\lambda_{x,y} \cdot \text{False}, L)) \quad (13.44)$$

That instead of spanning the non-decreasing sub list as long as possible, the predicate always evaluates to false, so the sub list spans only one element.

Similar with nature merge sort, bottom-up merge sort can also be defined by folding. The detailed implementation is left as exercise to the reader.

Observing the bottom-up sort, we can find it's in tail-recursion call manner, thus it's quite easy to translate into purely iterative algorithm without any recursion.

```
1: function SORT(A)
2:   B ←  $\phi$ 
3:   for  $\forall a \in A$  do
4:     B ← APPEND( $\{a\}$ )
5:   N ← |B|
6:   while N > 1 do
7:     for i ← from 1 to  $\lfloor \frac{N}{2} \rfloor$  do
8:       B[i] ← MERGE(B[2i - 1], B[2i])
9:     if ODD(N) then
10:      B[ $\lceil \frac{N}{2} \rceil$ ] ← B[N]
11:    N ←  $\lceil \frac{N}{2} \rceil$ 
12:   if B =  $\phi$  then
13:     return  $\phi$ 
14:   return B[1]
```

The following example Python program implements the purely iterative bottom-up merge sort.

```
def mergesort(xs):
    ys = [[x] for x in xs]
    while len(ys) > 1:
        ys.append(merge(ys.pop(0), ys.pop(0)))
    return [] if ys == [] else ys.pop()

def merge(xs, ys):
```

```

zs = []
while xs ≠ [] and ys ≠ []:
    zs.append(xs.pop(0) if xs[0] < ys[0] else ys.pop(0))
return zs + (xs if xs ≠ [] else ys)

```

The Python implementation combines multiple rounds of merging by consuming the pair of lists on the head, and appending the merged result to the tail. This greatly simplifies the logic of handling odd sub lists case as shown in the above pseudo code.

Exercise 13.7

- Implement the functional bottom-up merge sort by using folding.
- Implement the iterative bottom-up merge sort only with array indexing. Don't use any library supported tools, such as list, vector etc.

13.12 Parallelism

We mentioned in the basic version of quick sort, that the two sub sequences can be sorted in parallel after the divide phase finished. This strategy is also applicable for merge sort. Actually, the parallel version quick sort and merge sort, do not only distribute the recursive sub sequences sorting into two parallel processes, but divide the sequences into p sub sequences, where p is the number of processors. Ideally, if we can achieve sorting in T' time with parallelism, which satisfies $O(n \lg n) = pT'$. We say it is linear speed up, and the algorithm is parallel optimal.

However, a straightforward parallel extension to the sequential quick sort algorithm which samples several pivots, divides p sub sequences, and independently sorts them in parallel, isn't optimal. The bottleneck exists in the divide phase, which we can only achieve $O(n)$ time in average case.

The straightforward parallel extension to merge sort, on the other hand, block at the merge phase. Both parallel merge sort and quick sort in practice need good designs in order to achieve the optimal speed up. Actually, the divide and conquer nature makes merge sort and quick sort relative easy for parallelism. Richard Cole found the $O(\lg n)$ parallel merge sort algorithm with n processors in 1986 in [76].

Parallelism is a big and complex topic which is out of the scope of this elementary book. Readers can refer to [76] and [77] for details.

13.13 Short summary

In this chapter, two popular divide and conquer sorting methods, quick sort and merge sort are introduced. Both of them meet the upper performance limit of the comparison based sorting algorithms $O(n \lg n)$. Sedgewick said that quick sort is the greatest algorithm invented in the 20th century. Almost all programming environments adopt quick sort as the default sorting tool. As time goes on, some environments, especially those manipulate abstract sequence which is dynamic and not based on pure array switch to merge sort as the general purpose sorting tool⁷.

The reason for this interesting phenomena can be partly explained by the treatment in this chapter. That quick sort performs perfectly in most cases, it needs fewer swapping than most other algorithms. However, the quick sort algorithm is based on swapping, in

⁷Actually, most of them are kind of hybrid sort, balanced with insertion sort to achieve good performance when the sequence is short

purely functional settings, swapping isn't the most efficient way due to the underlying data structure is singly linked-list, but not vectorized array. Merge sort, on the other hand, is friendly in such environment, as it costs constant spaces, and the performance can be ensured even in the worst case of quick sort, while the latter downgrade to quadratic time. However, merge sort doesn't performs as well as quick sort in purely imperative settings with arrays. It either needs extra spaces for merging, which is sometimes unreasonable, for example in embedded system with limited memory, or causes many overhead swaps by in-place workaround. In-place merging is till an active research area.

Although the title of this chapter is 'quick sort vs. merge sort', it's not the case that one algorithm has nothing to do with the other. Quick sort can be viewed as the optimized version of tree sort as explained in this chapter. Similarly, merge sort can also be deduced from tree sort as shown in [75].

There are many ways to categorize sorting algorithms, such as in [51]. One way is to from the point of view of easy/hard partition, and easy/hard merge [72].

Quick sort, for example, is quite easy for merging, because all the elements in the sub sequence before the pivot are no greater than any one after the pivot. The merging for quick sort is actually trivial sequence concatenation.

Merge sort, on the other hand, is more complex in merging than quick sort. However, it's quite easy to divide no matter what concrete divide method is taken: simple divide at the middle point, even-odd splitting, nature splitting, or bottom-up straight splitting. Compare to merge sort, it's more difficult for quick sort to achieve a perfect dividing. We show that in theory, the worst case can't be completely avoided, no matter what engineering practice is taken, median-of-three, random quick sort, 3-way partition etc.

We've shown some elementary sorting algorithms in this book till this chapter, including insertion sort, tree sort, selection sort, heap sort, quick sort and merge sort. Sorting is still a hot research area in computer science. At the time when this chapter is written, people are challenged by the buzz word 'big data', that the traditional convenient method can't handle more and more huge data within reasonable time and resources. Sorting a sequence of hundreds of Gigabytes becomes a routine in some fields.

Exercise 13.8

- Design an algorithm to create binary search tree by using merge sort strategy.

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Chapter 14

Searching

14.1 Introduction

Searching is quite a big and important area. Computer makes many hard searching problems realistic. They are almost impossible for human beings. A modern industry robot can even search and pick the correct gadget from the pipeline for assembly; A GPS car navigator can search among the map, for the best route to a specific place. The modern mobile phone is not only equipped with such map navigator, but it can also search for the best price for Internet shopping.

This chapter just scratches the surface of elementary searching. One good thing that computer offers is the brute-force scanning for a certain result in a large sequence. The divide and conquer search strategy will be briefed with two problems, one is to find the k -th big one among a list of unsorted elements; the other is the popular binary search among a list of sorted elements. We'll also introduce the extension of binary search for multiple-dimension data.

Text matching is also very important in our daily life, two well-known searching algorithms, Knuth-Morris-Pratt (KMP) and Boyer-Moore algorithms will be introduced. They set good examples for another searching strategy: information reusing.

Besides sequence search, some elementary methods for searching solution for some interesting problems will be introduced. They were mostly well studied in the early phase of AI (artificial intelligence), including the basic DFS (Depth first search), and BFS (Breadth first search).

Finally, Dynamic programming will be briefed for searching optimal solutions, and we'll also introduce about greedy algorithm which is applicable for some special cases.

All algorithms will be realized in both imperative and functional approaches.

14.2 Sequence search

Although modern computer offers fast speed for brute-force searching, and even if the Moore's law could be strictly followed, the grows of huge data is too fast to be handled well in this way. We've seen a vivid example in the introduction chapter of this book. It's why people study the computer search algorithms.

14.2.1 Divide and conquer search

One solution is to use divide and conquer approach. That if we can repeatedly scale down the search domain, the data being dropped needn't be examined at all. This will

definitely speed up the search.

***k*-selection problem**

Consider a problem of finding the k -th smallest one among n elements. The most straightforward idea is to find the minimum first, then drop it and find the second minimum element among the rest. Repeat this minimum finding and dropping k steps will give the k -th smallest one. Finding the minimum among n elements costs linear $O(n)$ time. Thus this method performs $O(kn)$ time, if k is much smaller than n .

Another method is to use the ‘heap’ data structure we’ve introduced. No matter what concrete heap is used, e.g. binary heap with implicit array, Fibonacci heap or others, Accessing the top element followed by popping is typically bound $O(\lg n)$ time. Thus this method, as formalized in equation (14.1) and (14.2) performs in $O(k \lg n)$ time, if k is much smaller than n .

$$\text{top}(k, L) = \text{find}(k, \text{heapify}(L)) \quad (14.1)$$

$$\text{find}(k, H) = \begin{cases} \text{top}(H) & : k = 0 \\ \text{find}(k - 1, \text{pop}(H)) & : \textit{otherwise} \end{cases} \quad (14.2)$$

However, heap adds some complexity to the solution. Is there any simple, fast method to find the k -th element?

The divide and conquer strategy can help us. If we can divide all the elements into two sub lists A and B , and ensure all the elements in A is not greater than any elements in B , we can scale down the problem by following this method¹:

1. Compare the length of sub list A and k ;
2. If $k < |A|$, the k -th smallest one must be contained in A , we can drop B and *further search* in A ;
3. If $|A| < k$, the k -th smallest one must be contained in B , we can drop A and *further search* the $(k - |A|)$ -th smallest one in B .

Note that the *italic font* emphasizes the fact of recursion. The ideal case always divides the list into two equally big sub lists A and B , so that we can halve the problem each time. Such ideal case leads to a performance of $O(n)$ linear time.

Thus the key problem is how to realize dividing, which collects the first m smallest elements in one sub list, and put the rest in another.

This reminds us the partition algorithm in quick sort, which moves all the elements smaller than the pivot in front of it, and moves those greater than the pivot behind it. Based on this idea, we can develop a divide and conquer k -selection algorithm, which is called quick selection algorithm.

1. Randomly select an element (the first for instance) as the pivot;
2. Moves all elements which aren’t greater than the pivot in a sub list A ; and moves the rest to sub list B ;
3. Compare the length of A with k , if $|A| = k - 1$, then the pivot is the k -th smallest one;
4. If $|A| > k - 1$, recursively find the k -th smallest one among A ;

¹This actually demands a more accurate definition of the k -th smallest in L : It’s equal to the k -th element of L' , where L' is a permutation of L , and L' is in monotonic non-decreasing order.

5. Otherwise, recursively find the $(k - 1 - |A|)$ -th smallest one among B ;

This algorithm can be formalized in below equation. Suppose $0 < k \leq |L|$, where L is a non-empty list of elements. Denote l_1 as the first element in L . It is chosen as the pivot; L' contains the rest elements except for l_1 . $(A, B) = \text{partition}(\lambda_x \cdot x \leq l_1, L')$. It partitions L' by using the same algorithm defined in the chapter of quick sort.

$$\text{top}(k, L) = \begin{cases} l_1 & : |A| = k - 1 \\ \text{top}(k - 1 - |A|, B) & : |A| < k - 1 \\ \text{top}(k, A) & : \textit{otherwise} \end{cases} \quad (14.3)$$

$$\text{partition}(p, L) = \begin{cases} (\phi, \phi) & : L = \phi \\ (\{l_1\} \cup A, B) & : p(l_1), (A, B) = \text{partition}(p, L') \\ (A, \{l_1\} \cup B) & : \neg p(l_1) \end{cases} \quad (14.4)$$

The following Haskell example program implements this algorithm.

```

top n (x:xs) | len == n - 1 = x
             | len < n - 1 = top (n - len - 1) bs
             | otherwise = top n as
  where
    (as, bs) = partition (<= x) xs
    len = length as

```

The partition function is provided in Haskell standard library, the detailed implementation can be referred to previous chapter about quick sort.

The lucky case is that, the k -th smallest element is selected as the pivot at the very beginning. The partition function examines the whole list, and finds that there are $k - 1$ elements not greater than the pivot, we are done in just $O(n)$ time. The worst case is that either the maximum or the minimum element is selected as the pivot every time. The partition always produces an empty sub list, that either A or B is empty. If we always pick the minimum as the pivot, the performance is bound to $O(kn)$. If we always pick the maximum as the pivot, the performance is $O((n - k)n)$.

The best case (not the lucky case), is that the pivot always partition the list perfectly. The length of A is nearly as same as the length of B . The list is halved every time. It needs about $O(\lg n)$ partitions, each partition takes linear time proportion to the length of the halved list. This can be expressed as $O(n + \frac{n}{2} + \frac{n}{4} + \dots + \frac{n}{2^m})$, where m is the smallest number satisfies $\frac{n}{2^m} < k$. Summing the series leads to the result of $O(n)$.

The average case analysis needs tool of mathematical expectation. It's quite similar to the proof given in previous chapter of quick sort. It's left as an exercise to the reader.

Similar as quick sort, this divide and conquer selection algorithm performs well most time in practice. We can take the same engineering practice such as media-of-three, or randomly select the pivot as we did for quick sort. Below is the imperative realization for example.

```

1: function TOP( $k, A, l, u$ )
2:   EXCHANGE  $A[l] \leftrightarrow A[\text{RANDOM}(l, u)]$            ▷ Randomly select in  $[l, u]$ 
3:    $p \leftarrow \text{PARTITION}(A, l, u)$ 
4:   if  $p - l + 1 = k$  then
5:     return  $A[p]$ 
6:   if  $k < p - l + 1$  then
7:     return TOP( $k, A, l, p - 1$ )
8:   return TOP( $k - p + l - 1, A, p + 1, u$ )

```

This algorithm searches the k -th smallest element in range of $[l, u]$ for array A . The boundaries are included. It first randomly selects a position, and swaps it with the first

one. Then this element is chosen as the pivot for partitioning. The partition algorithm in-place moves elements and returns the position where the pivot being moved. If the pivot is just located at position k , then we are done; if there are more than $k - 1$ elements not greater than the pivot, the algorithm recursively searches the k -th smallest one in range $[l, p - 1]$; otherwise, k is deduced by the number of elements before the pivot, and recursively searches the range after the pivot $[p + 1, u]$.

There are many methods to realize the partition algorithm, below one is based on N. Lumoto's method. Other realizations are left as exercises to the reader.

```

1: function PARTITION(A, l, u)
2:    $p \leftarrow A[l]$ 
3:    $L \leftarrow l$ 
4:   for  $R \leftarrow l + 1$  to  $u$  do
5:     if  $\neg(p < A[R])$  then
6:        $L \leftarrow L + 1$ 
7:       EXCHANGE  $A[L] \leftrightarrow A[R]$ 
8:   EXCHANGE  $A[L] \leftrightarrow p$ 
9:   return  $L$ 

```

Below ANSI C example program implements this algorithm. Note that it handles the special case that either the array is empty, or k is out of the boundaries of the array. It returns -1 to indicate the search failure.

```

int partition(Key* xs, int l, int u) {
    int r, p = l;
    for (r = l + 1; r < u; ++r)
        if (!(xs[p] < xs[r]))
            swap(xs, ++l, r);
    swap(xs, p, l);
    return l;
}

/* The result is stored in xs[k], returns k if u-l ≥ k, otherwise -1 */
int top(int k, Key* xs, int l, int u) {
    int p;
    if (l < u) {
        swap(xs, l, rand() % (u - l) + l);
        p = partition(xs, l, u);
        if (p - l + 1 == k)
            return p;
        return (k < p - l + 1) ? top(k, xs, l, p) :
            top(k - p + l - 1, xs, p + 1, u);
    }
    return -1;
}

```

There is a method proposed by Blum, Floyd, Pratt, Rivest and Tarjan in 1973, which ensures the worst case performance being bound to $O(n)$ [4], [81]. It divides the list into small groups. Each group contains no more than 5 elements. The median of each group among these 5 elements are identified quickly. Then there are $\frac{n}{5}$ median elements selected. We repeat this step, and divide them again into groups of 5, and recursively select the *median of median*. It's obviously that the final 'true' median can be found in $O(\lg n)$ time. This is the best pivot for partitioning the list. Next, we halve the list by this pivot and recursively search for the k -th smallest one. The performance can be calculated as the following.

$$T(n) = c_1 \lg n + c_2 n + T\left(\frac{n}{2}\right) \quad (14.5)$$

Where c_1 and c_2 are constant factors for the median of median and partition computation respectively. Solving this equation with telescope method or the master theory in

[4] gives the linear $O(n)$ performance.

In case we just want to pick the top k smallest elements, but don't care about the order of them, the algorithm can be adjusted a little bit to fit.

$$\text{tops}(k, L) = \begin{cases} \phi & : k = 0 \vee L = \phi \\ A & : |A| = k \\ A \cup \{l_1\} \cup \text{tops}(k - |A| - 1, B) & : |A| < k \\ \text{tops}(k, A) & : \textit{otherwise} \end{cases} \quad (14.6)$$

Where A, B have the same meaning as before that, $(A, B) = \textit{partition}(\lambda x \cdot x \leq l_1, L')$ if L isn't empty. The relative example program in Haskell is given as below.

```

tops _ [] = []
tops 0 _ = []
tops n (x:xs) | len == n = as
              | len < n = as ++ [x] ++ tops (n-len-1) bs
              | otherwise = tops n as
  where
    (as, bs) = partition (<= x) xs
    len = length as

```

binary search

Another popular divide and conquer algorithm is binary search. We've shown it in the chapter about insertion sort. When I was in school, the teacher who taught math played a magic to me, He asked me to consider a natural number less than 1000. Then he asked me some questions, I only replied 'yes' or 'no', and finally he guessed my number. He typically asked questions like the following:

- Is it an even number?
- Is it a prime number?
- Are all digits same?
- Can it be divided by 3?
- ...

Most of the time he guessed the number within 10 questions. My classmates and I all thought it's unbelievable.

This game will not be so interesting if it downgrades to a popular TV program, that the price of a product is hidden, and you must figure out the exact price in 30 seconds. The host of the program tells you if your guess is higher or lower to the fact. If you win, the product is yours. The best strategy is to use similar divide and conquer approach to perform a binary search. So it's common to find such conversation between the player and the host:

- P: 1000;
- H: High;
- P: 500;
- H: Low;
- P: 750;

- H: Low;
- P: 890;
- H: Low;
- P: 990;
- H: Bingo.

My math teacher told us that, because the number we considered is within 1000, if he can halve the numbers every time by designing good questions, the number will be found in 10 questions. This is because $2^{10} = 1024 > 1000$. However, it would be boring to just ask it is higher than 500, is lower than 250, ... Actually, the question ‘is it even’ is very good, because it always halve the numbers².

Come back to the binary search algorithm. It is only applicable to a sequence of ordered number. I’ve seen programmers tried to apply it to unsorted array, and took several hours to figure out why it doesn’t work. The idea is quite straightforward, in order to find a number x in an ordered sequence A , we firstly check middle point number, compare it with x , if they are same, then we are done; If x is smaller, as A is ordered, we need only recursively search it among the first half; otherwise we search it among the second half. Once A gets empty and we haven’t found x yet, it means x doesn’t exist.

Before formalizing this algorithm, there is a surprising fact need to be noted. Donald Knuth stated that ‘Although the basic idea of binary search is comparatively straightforward, the details can be surprisingly tricky’. Jon Bentley pointed out that most binary search implementation contains errors, and even the one given by him in the first version of ‘Programming pearls’ contains an error undetected over twenty years [4].

There are two kinds of realization, one is recursive, the other is iterative. The recursive solution is as same as what we described. Suppose the lower and upper boundaries of the array are l and u inclusive.

```

1: function BINARY-SEARCH( $x, A, l, u$ )
2:   if  $u < l$  then
3:     Not found error
4:   else
5:      $m \leftarrow l + \lfloor \frac{u-l}{2} \rfloor$  ▷ avoid overflow of  $\lfloor \frac{l+u}{2} \rfloor$ 
6:     if  $A[m] = x$  then
7:       return  $m$ 
8:     if  $x < A[m]$  then
9:       return BINARY-SEARCH( $x, A, l, m - 1$ )
10:    else
11:     return BINARY-SEARCH( $x, A, m + 1, u$ )

```

As the comment highlights, if the integer is represented with limited words, we can’t merely use $\lfloor \frac{l+u}{2} \rfloor$ because it may cause overflow if l and u are big.

Binary search can also be realized in iterative manner, that we keep updating the boundaries according to the middle point comparison result.

```

1: function BINARY-SEARCH( $x, A, l, u$ )
2:   while  $l < u$  do
3:      $m \leftarrow l + \lfloor \frac{u-l}{2} \rfloor$ 
4:     if  $A[m] = x$  then
5:       return  $m$ 

```

²When the author revise this chapter, Microsoft released a game in social networks. User can consider a person’s name, the AI robot asks 16 questions next. The user only answers with yes or no. The robot will tell you who is that person. Can you figure out how the robot works?


```

6:      if  $x < A[m]$  then
7:           $u \leftarrow m - 1$ 
8:      else
9:           $l \leftarrow m + 1$ 
      return NIL

```

The implementation is very good exercise, we left it to the reader. Please try all kinds of methods to verify your program.

Since the array is halved every time, the performance of binary search is bound to $O(\lg n)$ time.

In purely functional settings, the list is represented with singly linked-list. It's linear time to randomly access the element for a given position. Binary search doesn't make sense in such case. However, it good to analyze what the performance will downgrade to. Consider the following equation.

$$bsearch(x, L) = \begin{cases} Err & : L = \phi \\ b_1 & : x = b_1, (A, B) = splitAt(\lfloor \frac{|L|}{2} \rfloor, L) \\ bsearch(x, A) & : B = \phi \vee x < b_1 \\ bsearch(x, B') & : otherwise \end{cases}$$

Where b_1 is the first element if B isn't empty, and B' holds the rest except for b_1 . The *splitAt* function takes $O(n)$ time to divide the list into two subs A and B (see the appendix A, and the chapter about merge sort for detail). If B isn't empty and x is equal to b_1 , the search returns; Otherwise if it is less than b_1 , as the list is sorted, we need recursively search in A , otherwise, we search in B . If the list is empty, we raise error to indicate search failure.

As we always split the list in the middle point, the number of elements halves in each recursion. In every recursive call, we takes linear time for splitting. The splitting function only traverses the first half of the linked-list, Thus the total time can be expressed as.

$$T(n) = c\frac{n}{2} + c\frac{n}{4} + c\frac{n}{8} + \dots$$

This results $O(n)$ time, which is as same as the brute force search from head to tail:

$$search(x, L) = \begin{cases} Err & : L = \phi \\ l_1 & : x = l_1 \\ search(x, L') & : otherwise \end{cases}$$

As we mentioned in the chapter about insertion sort, the functional approach of binary search is through binary search tree. That the ordered sequence is represented in a tree (self balanced tree if necessary), which offers logarithm time searching ³.

Although it doesn't make sense to apply divide and conquer binary search on linked-list, binary search can still be very useful in purely functional settings. Consider solving an equation $a^x = y$, for given natural numbers a and y , where $a \leq y$. We want to find the integer solution for x if there is. Of course brute-force naive searching can solve it. We can examine all numbers one by one from 0 for a^0, a^1, a^2, \dots , stops if $a^i = y$ or report that there is no solution if $a^i < y < a^{i+1}$ for some i . We initialize the solution domain as $X = \{0, 1, 2, \dots\}$, and call the below exhausted searching function *solve*(a, y, X).

$$solve(a, y, X) = \begin{cases} x_1 & : a^{x_1} = y \\ solve(a, y, X') & : a^{x_1} < y \\ Err & : otherwise \end{cases}$$

³Some readers may argue that array should be used instead of linked-list, for example in Haskell. This book only deals with purely functional sequences in finger-tree. Different from the Haskell array, it can't support constant time random accessing

This function examines the solution domain in monotonic increasing order. It takes the first candidate element x_1 from X , compare a^{x_1} and y , if they are equal, then x_1 is the solution and we are done; if it is less than y , then x_1 is dropped, and we search among the rest elements represented as X' ; Otherwise, since $f(x) = a^x$ is non-decreasing function when a is natural number, so the rest elements will only make $f(x)$ bigger and bigger. There is no integer solution for this equation. The function returns error to indicate no solution.

The computation of a^x is expensive for big a and x if precession must be kept⁴. Can it be improved so that we can compute as less as possible? The divide and conquer binary search can help. Actually, we can estimate the upper limit of the solution domain. As $a^y \leq y$, We can search in range $\{0, 1, \dots, y\}$. As the function $f(x) = a^x$ is non-decreasing against its argument x , we can firstly check the middle point candidate $x_m = \lfloor \frac{0+y}{2} \rfloor$, if $a^{x_m} = y$, the solution is found; if it is less than y , we can drop all candidate solutions before x_m ; otherwise we drop all candidate solutions after it; Both halve the solution domain. We repeat this approach until either the solution is found or the solution domain becomes empty, which indicates there is no integer solution.

The binary search method can be formalized as the following equation. The non-decreasing function is abstracted as a parameter. To solve our problem, we can just call it as $bsearch(f, y, 0, y)$, where $f(x) = a^x$.

$$bsearch(f, y, l, u) = \begin{cases} Err & : u < l \\ m & : f(m) = y, m = \lfloor \frac{l+u}{2} \rfloor \\ bsearch(f, y, l, m-1) & : f(m) > y \\ bsearch(f, y, m+1, u) & : f(m) < y \end{cases} \quad (14.7)$$

As we halve the solution domain in every recursion, this method computes $f(x)$ in $O(\log y)$ times. It is much faster than the brute-force searching.

2 dimensions search

It's quite natural to think that the idea of binary search can be extended to 2 dimensions or even more general – multiple-dimensions domain. However, it is not so easy.

Consider the example of a $m \times n$ matrix M . The elements in each row and each column are in strict increasing order. Figure 14.1 illustrates such a matrix for example.

$$\begin{bmatrix} 1 & 2 & 3 & 4 & \dots \\ 2 & 4 & 5 & 6 & \dots \\ 3 & 5 & 7 & 8 & \dots \\ 4 & 6 & 8 & 9 & \dots \\ \dots & & & & \end{bmatrix}$$

Figure 14.1: A matrix in strict increasing order for each row and column.

Given a value x , how to locate all elements equal to x in the matrix quickly? We need develop an algorithm, which returns a list of locations (i, j) so that $M_{i,j} = x$.

Richard Bird in [1] mentioned that he used this problem to interview candidates for entry to Oxford. The interesting story was that, those who had some computer background at school tended to use binary search. But it's easy to get stuck.

The usual way follows binary search idea is to examine element at $M_{\frac{m}{2}, \frac{n}{2}}$. If it is less than x , we can only drop the elements in the top-left area; If it is greater than x , only

⁴One alternative is to reuse the result of a^n when compute $a^{n+1} = aa^n$. Here we consider for general form monotonic function $f(n)$

the bottom-right area can be dropped. Both cases are illustrated in figure 14.2, the gray areas indicate elements can be dropped.

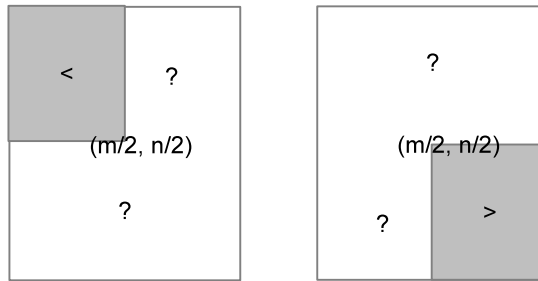


Figure 14.2: Left: the middle point element is smaller than x . All elements in the gray area are less than x ; Right: the middle point element is greater than x . All elements in the gray area are greater than x .

The problem is that the solution domain changes from a rectangle to a 'L' shape in both cases. We can't just recursively apply search on it. In order to solve this problem systematically, we define the problem more generally, using brute-force search as a start point, and keep improving it bit by bit.

Consider a function $f(x, y)$, which is strict increasing for its arguments, for instance $f(x, y) = a^x + b^y$, where a and b are natural numbers. Given a value z , which is a natural number too, we want to solve the equation $f(x, y) = z$ by finding all none negative integral candidate pairs (x, y) .

With this definition, the matrix search problem can be specialized by below function.

$$f(x, y) = \begin{cases} M_{x,y} & : 1 \leq x \leq m, 1 \leq y \leq n \\ -1 & : otherwise \end{cases}$$

Brute-force 2D search

As all solutions should be found for $f(x, y)$. One can immediately give the brute force solution by embedded looping.

```

1: function SOLVE( $f, z$ )
2:    $A \leftarrow \phi$ 
3:   for  $x \in \{0, 1, 2, \dots, z\}$  do
4:     for  $y \in \{0, 1, 2, \dots, z\}$  do
5:       if  $f(x, y) = z$  then
6:          $A \leftarrow A \cup \{(x, y)\}$ 
7:   return  $A$ 

```

This definitely calculates f for $(z + 1)^2$ times. It can be formalized as in (14.8).

$$solve(f, z) = \{(x, y) | x \in \{0, 1, \dots, z\}, y \in \{0, 1, \dots, z\}, f(x, y) = z\} \quad (14.8)$$

Saddleback search

We haven't utilize the fact that $f(x, y)$ is strict increasing yet. Dijkstra pointed out in [82], instead of searching from bottom-left corner, starting from the top-left leads to one

effective solution. As illustrated in figure 14.3, the search starts from $(0, z)$, for every point (p, q) , we compare $f(p, q)$ with z :

- If $f(p, q) < z$, since f is strict increasing, for all $0 \leq y < q$, we have $f(p, y) < z$. We can drop all points in the vertical line section (in red color);
- If $f(p, q) > z$, then $f(x, q) > z$ for all $p < x \leq z$. We can drop all points in the horizontal line section (in blue color);
- Otherwise if $f(p, q) = z$, we mark (p, q) as one solution, then both line sections can be dropped.

This is a systematical way to scale down the solution domain rectangle. We keep dropping a row, or a column, or both.

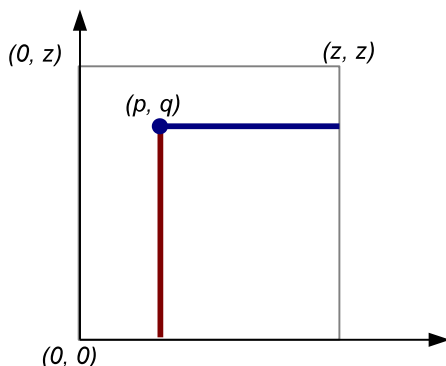


Figure 14.3: Search from top-left.

This method can be formalized as a function $search(f, z, p, q)$, which searches solutions for equation $f(x, y) = z$ in rectangle with top-left corner (p, q) , and bottom-right corner $(z, 0)$. We start the searching by initializing $(p, q) = (0, z)$ as $solve(f, z) = search(f, z, 0, z)$

$$search(f, z, p, q) = \begin{cases} \phi & : p > z \vee q < 0 \\ search(f, z, p + 1, q) & : f(p, q) < z \\ search(f, z, p, q - 1) & : f(p, q) > z \\ \{(p, q)\} \cup search(f, z, p + 1, q - 1) & : otherwise \end{cases} \quad (14.9)$$

The first clause is the edge case, there is no solution if (p, q) isn't top-left to $(z, 0)$. The following example Haskell program implements this algorithm.

```

solve f z = search 0 z where
  search p q | p > z || q < 0 = []
              | z' < z = search (p + 1) q
              | z' > z = search p (q - 1)
              | otherwise = (p, q) : search (p + 1) (q - 1)
  where z' = f p q

```

Considering the calculation of f may be expensive, this program stores the result of $f(p, q)$ to variable z' . This algorithm can also be implemented in iterative manner, that the boundaries of solution domain keeps being updated in a loop.

- 1: **function** SOLVE(f, z)
- 2: $p \leftarrow 0, q \leftarrow z$

```

3:    $S \leftarrow \phi$ 
4:   while  $p \leq z \wedge q \geq 0$  do
5:      $z' \leftarrow f(p, q)$ 
6:     if  $z' < z$  then
7:        $p \leftarrow p + 1$ 
8:     else if  $z' > z$  then
9:        $q \leftarrow q - 1$ 
10:    else
11:       $S \leftarrow S \cup \{(p, q)\}$ 
12:       $p \leftarrow p + 1, q \leftarrow q - 1$ 
13:  return  $S$ 

```

It's intuitive to translate this imperative algorithm to real program, as the following example Python code.

```

def solve(f, z):
    (p, q) = (0, z)
    res = []
    while p ≤ z and q ≥ 0:
        z1 = f(p, q)
        if z1 < z:
            p = p + 1
        elif z1 > z:
            q = q - 1
        else:
            res.append((p, q))
            (p, q) = (p + 1, q - 1)
    return res

```

It is clear that in every iteration, At least one of p and q advances to the bottom-right corner by one. Thus it takes at most $2(z + 1)$ steps to complete searching. This is the worst case. There are three best cases. The first one happens that in every iteration, both p and q advance by one, so that it needs only $z + 1$ steps; The second case keeps advancing horizontally to right and ends when p exceeds z ; The last case is similar, that it keeps moving down vertically to the bottom until q becomes negative.

Figure 14.4 illustrates the best cases and the worst cases respectively. Figure 14.4 (a) is the case that every point $(x, z - x)$ in diagonal satisfies $f(x, z - x) = z$, it uses $z + 1$ steps to arrive at $(z, 0)$; (b) is the case that every point (x, z) along the top horizontal line gives the result $f(x, z) < z$, the algorithm takes $z + 1$ steps to finish; (c) is the case that every point $(0, x)$ along the left vertical line gives the result $f(0, x) > z$, thus the algorithm takes $z + 1$ steps to finish; (d) is the worst case. If we project all the horizontal sections along the search path to x axis, and all the vertical sections to y axis, it gives the total steps of $2(z + 1)$.

Compare to the quadratic brute-force method ($O(z^2)$), we improve to a linear algorithm bound to $O(z)$.

Bird imagined that the name ‘saddleback’ is because the 3D plot of f with the smallest bottom-left and the largest top-right and two wings looks like a saddle as shown in figure 14.5

Improved saddleback search

We haven't utilized the binary search tool so far, even the problem extends to 2-dimension domain. The basic saddleback search starts from the top-left corner $(0, z)$ to the bottom-right corner $(z, 0)$. This is actually over-general domain. we can constraint it a bit more accurate.

Since f is strict increasing, we can find the biggest number m , that $0 \leq m \leq z$, along the y axis which satisfies $f(0, m) \leq z$; Similarly, we can find the biggest n , that

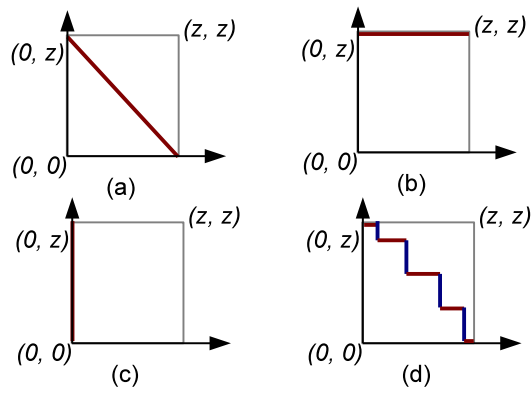


Figure 14.4: The best cases and the worst cases.

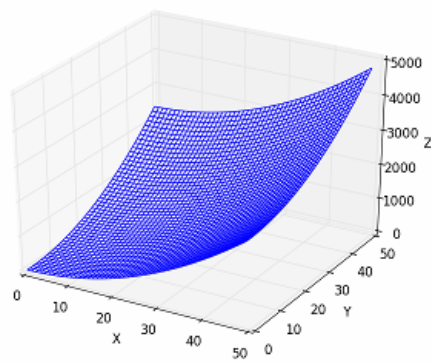


Figure 14.5: Plot of $f(x, y) = x^2 + y^2$.

$0 \leq n \leq z$, along the x axis, which satisfies $f(n, 0) \leq z$; And the solution domain shrinks from $(0, z) - (z, 0)$ to $(0, m) - (n, 0)$ as shown in figure 14.6.

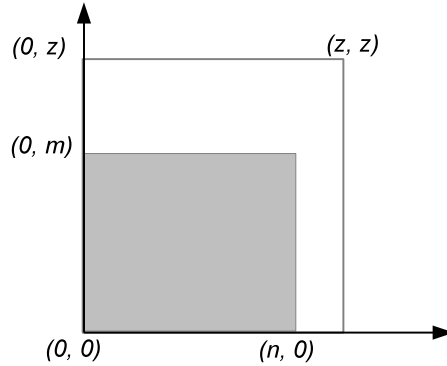


Figure 14.6: A more accurate search domain shown in gray color.

Of course m and n can be found by brute-force like below.

$$\begin{aligned} m &= \max(\{y \mid 0 \leq y \leq z, f(0, y) \leq z\}) \\ n &= \max(\{x \mid 0 \leq x \leq z, f(x, 0) \leq z\}) \end{aligned} \quad (14.10)$$

When searching m , the x variable of f is bound to 0. It turns to be one dimension search problem for a strict increasing function (or in functional term, a Curried function $f(0, y)$). Binary search works in such case. However, we need a bit modification for equation (14.7). Different from searching a solution $l \leq x \leq u$, so that $f(x) = y$ for a given y ; we need search for a solution $l \leq x \leq u$ so that $f(x) \leq y < f(x + 1)$.

$$bsearch(f, y, l, u) = \begin{cases} l & : u \leq l \\ m & : f(m) \leq y < f(m + 1), m = \lfloor \frac{l+u}{2} \rfloor \\ bsearch(f, y, m + 1, u) & : f(m) \leq y \\ bsearch(f, y, l, m - 1) & : otherwise \end{cases} \quad (14.11)$$

The first clause handles the edge case of empty range. The lower boundary is returned in such case; If the middle point produces a value less than or equal to the target, while the next one evaluates to a bigger value, then the middle point is what we are looking for; Otherwise if the point next to the middle also evaluates to a value not greater than the target, the lower bound is set as the middle point plus one, and we perform recursively binary search; In the last case, the middle point evaluates to a value greater than the target, upper bound is updated as the point proceeds to the middle for further recursive searching. The following Haskell example code implements this modified binary search.

```
bsearch f y (l, u) | u <= l = l
                  | f m <= y = if f (m + 1) <= y
                              then bsearch f y (m + 1, u) else m
                  | otherwise = bsearch f y (l, m-1)
where m = (l + u) `div` 2
```

Then m and n can be found with this binary search function.

$$\begin{aligned} m &= bsearch(\lambda_y \cdot f(0, y), z, 0, z) \\ n &= bsearch(\lambda_x \cdot f(x, 0), z, 0, z) \end{aligned} \quad (14.12)$$

And the improved saddleback search shrinks to this new search domain $solve(f, z) = search(f, z, 0, m)$:

$$search(f, z, p, q) = \begin{cases} \phi & : p > n \vee q < 0 \\ search(f, z, p + 1, q) & : f(p, q) < z \\ search(f, z, p, q - 1) & : f(p, q) > z \\ \{(p, q)\} \cup search(f, z, p + 1, q - 1) & : otherwise \end{cases} \quad (14.13)$$

It's almost as same as the basic saddleback version, except that it stops if p exceeds n , but not z . In real implementation, the result of $f(p, q)$ can be calculated once, and stored in a variable as shown in the following Haskell example.

```
solve' f z = search 0 m where
  search p q | p > n || q < 0 = []
             | z' < z = search (p + 1) q
             | z' > z = search p (q - 1)
             | otherwise = (p, q) : search (p + 1) (q - 1)
  where z' = f p q
  m = bsearch (f 0) z (0, z)
  n = bsearch (\x -> f x 0) z (0, z)
```

This improved saddleback search firstly performs binary search two rounds to find the proper m , and n . Each round is bound to $O(\lg z)$ times of calculation for f ; After that, it takes $O(m + n)$ time in the worst case; and $O(\min(m, n))$ time in the best case. The overall performance is given in the following table.

	times of evaluation f
worst case	$2 \log z + m + n$
best case	$2 \log z + \min(m, n)$

For some function $f(x, y) = a^x + b^y$, for positive integers a and b , m and n will be relative small, that the performance is close to $O(\lg z)$.

This algorithm can also be realized in imperative approach. Firstly, the binary search should be modified.

```
1: function BINARY-SEARCH( $f, y, (l, u)$ )
2:   while  $l < u$  do
3:      $m \leftarrow \lfloor \frac{l+u}{2} \rfloor$ 
4:     if  $f(m) \leq y$  then
5:       if  $y < f(m + 1)$  then
6:         return  $m$ 
7:        $l \leftarrow m + 1$ 
8:     else
9:        $u \leftarrow m$ 
10:  return  $l$ 
```

Utilize this algorithm, the boundaries m and n can be found before performing the saddleback search.

```
1: function SOLVE( $f, z$ )
2:    $m \leftarrow$  BINARY-SEARCH( $\lambda_y \cdot f(0, y), z, (0, z)$ )
3:    $n \leftarrow$  BINARY-SEARCH( $\lambda_x \cdot f(x, 0), z, (0, z)$ )
4:    $p \leftarrow 0, q \leftarrow m$ 
5:    $S \leftarrow \phi$ 
6:   while  $p \leq n \wedge q \geq 0$  do
7:      $z' \leftarrow f(p, q)$ 
8:     if  $z' < z$  then
9:        $p \leftarrow p + 1$ 
10:    else if  $z' > z$  then
```



```

11:          $q \leftarrow q - 1$ 
12:     else
13:          $S \leftarrow S \cup \{(p, q)\}$ 
14:          $p \leftarrow p + 1, q \leftarrow q - 1$ 
15:     return  $S$ 

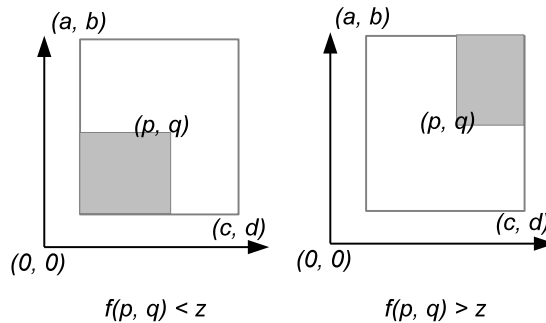
```

The implementation is left as exercise to the reader.

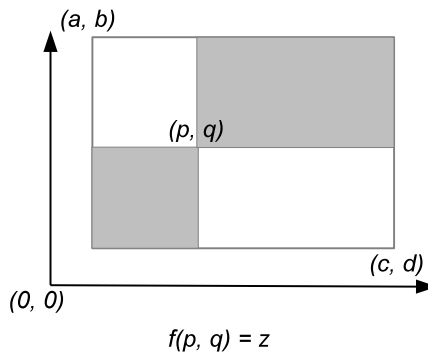
More improvement to saddleback search

In figure 14.2, two cases are shown for comparing the value of the middle point in a matrix with the given value. One case is the center value is smaller than the given value, the other is bigger. In both cases, we can only throw away $\frac{1}{4}$ candidates, and left a 'L' shape for further searching.

Actually, one important case is missing. We can extend the observation to any point inside the rectangle searching area. As shown in the figure 14.7.



(a) If $f(p, q) \neq z$, only lower-left or upper-right sub area (in gray color) can be thrown. Both left a 'L' shape.



(b) If $f(p, q) = z$, both sub areas can be thrown, the scale of the problem is halved.

Figure 14.7: The efficiency of scaling down the search domain.

Suppose we are searching in a rectangle from the upper-left corner (a, b) to the lower-right corner (c, d) . If the (p, q) isn't the middle point, and $f(p, q) \neq z$. We can't ensure the area to be dropped is always $1/4$. However, if $f(p, q) = z$, as f is strict increasing, we

are not only sure both the lower-left and the upper-right sub areas can be thrown, but also all the other points in the column p and row q . The problem can be scaled down fast, because only $1/2$ area is left.

This indicates us, instead of jumping to the middle point to start searching. A more efficient way is to find a point which evaluates to the target value. One straightforward way to find such a point, is to perform binary search along the center horizontal line or the center vertical line of the rectangle.

The performance of binary search along a line is logarithmic to the length of that line. A good idea is to always pick the shorter center line as shown in figure 14.8. That if the height of the rectangle is longer than the width, we perform binary search along the horizontal center line; otherwise we choose the vertical center line.

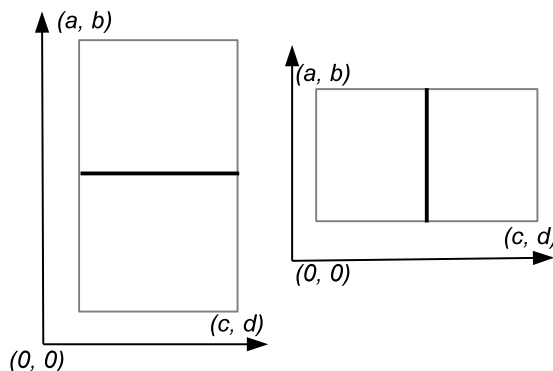


Figure 14.8: Binary search along the shorter center line.

However, what if we can't find a point (p, q) in the center line, that satisfies $f(p, q) = z$? Let's take the center horizontal line for example. even in such case, we can still find a point that $f(p, q) < z < f(p + 1, q)$. The only difference is that we can't drop the points in column p and row q completely.

Combine this conditions, the binary search along the horizontally line is to find a p , satisfies $f(p, q) \leq z < f(p + 1, q)$; While the vertical line search condition is $f(p, q) \leq z < f(p, q + 1)$.

The modified binary search ensures that, if all points in the line segment give $f(p, q) < z$, the upper bound will be found; and the lower bound will be found if they all greater than z . We can drop the whole area on one side of the center line in such case.

Sum up all the ideas, we can develop the efficient improved saddleback search as the following.

1. Perform binary search along the y axis and x axis to find the tight boundaries from $(0, m)$ to $(n, 0)$;
2. Denote the candidate rectangle as $(a, b) - (c, d)$, if the candidate rectangle is empty, the solution is empty;
3. If the height of the rectangle is longer than the width, perform binary search along the center horizontal line; otherwise, perform binary search along the center vertical line; denote the search result as (p, q) ;
4. If $f(p, q) = z$, record (p, q) as a solution, and recursively search two sub rectangles $(a, b) - (p - 1, q + 1)$ and $(p + 1, q - 1) - (c, d)$;

5. Otherwise, $f(p, q) \neq z$, recursively search the same two sub rectangles plus a line section. The line section is either $(p, q + 1) - (p, b)$ as shown in figure 14.9 (a); or $(p + 1, q) - (c, q)$ as shown in figure 14.9 (b).

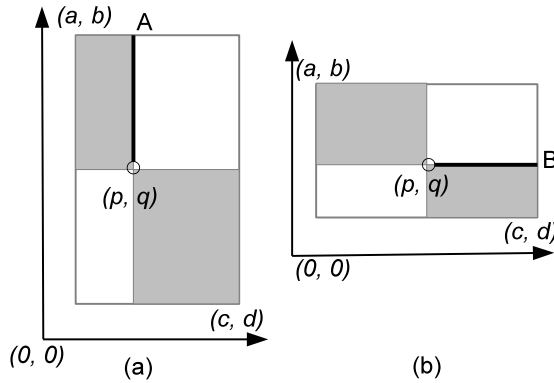


Figure 14.9: Recursively search the gray areas, the bold line should be included if $f(p, q) \neq z$.

This algorithm can be formalized as the following. The equation (14.11), and (14.12) are as same as before. A new *search* function should be defined.

Define $Search_{(a,b),(c,d)}$ as a function for searching rectangle with top-left corner (a, b) , and bottom-right corner (c, d) .

$$search_{(a,b),(c,d)} = \begin{cases} \phi & : c < a \vee d < b \\ csearch & : c - a < b - d \\ rsearch & : otherwise \end{cases} \quad (14.14)$$

Function *csearch* performs binary search in the center horizontal line to find a point (p, q) that $f(p, q) \leq z < f(p + 1, q)$. This is shown in figure 14.9 (a). There is a special edge case, that all points in the lines evaluate to values greater than z . The general binary search will return the lower bound as result, so that $(p, q) = (a, \lfloor \frac{b+d}{2} \rfloor)$. The whole upper side includes the center line can be dropped as shown in figure 14.10 (a).

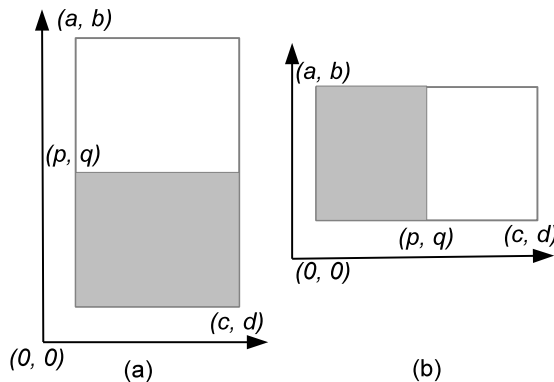


Figure 14.10: Edge cases when performing binary search in the center line.

$$csearch = \begin{cases} search_{(p,q-1),(c,d)} & : z < f(p,q) \\ search_{(a,b),(p-1,q+1)} \cup \{(p,q)\} \cup search_{(p+1,q-1),(c,d)} & : f(p,q) = z \\ search_{(a,b),(p,q+1)} \cup search_{(p+1,q-1),(c,d)} & : otherwise \end{cases} \quad (14.15)$$

Where

$$q = \lfloor \frac{b+d}{2} \rfloor \\ p = bsearch(\lambda x \cdot f(x, q), z, (a, c))$$

Function *rsearch* is quite similar except that it searches in the center horizontal line.

$$rsearch = \begin{cases} search_{(a,b),(p-1,q)} & : z < f(p,q) \\ search_{(a,b),(p-1,q+1)} \cup \{(p,q)\} \cup search_{(p+1,q-1),(c,d)} & : f(p,q) = z \\ search_{(a,b),(p-1,q+1)} \cup search_{(p+1,q),(c,d)} & : otherwise \end{cases} \quad (14.16)$$

Where

$$p = \lfloor \frac{a+c}{2} \rfloor \\ q = bsearch(\lambda y \cdot f(p, y), z, (d, b))$$

The following Haskell program implements this algorithm.

```
search f z (a, b) (c, d) | c < a || b < d = []
                        | c - a < b - d = let q = (b + d) `div` 2 in
                                      csearch (bsearch (\x -> f x q) z (a, c), q)
                        | otherwise = let p = (a + c) `div` 2 in
                                      rsearch (p, bsearch (f p) z (d, b))

where
  csearch (p, q) | z < f p q = search f z (p, q - 1) (c, d)
                | f p q == z = search f z (a, b) (p - 1, q + 1) ++
                              (p, q) : search f z (p + 1, q - 1) (c, d)
                | otherwise = search f z (a, b) (p, q + 1) ++
                              search f z (p + 1, q - 1) (c, d)
  rsearch (p, q) | z < f p q = search f z (a, b) (p - 1, q)
                | f p q == z = search f z (a, b) (p - 1, q + 1) ++
                              (p, q) : search f z (p + 1, q - 1) (c, d)
                | otherwise = search f z (a, b) (p - 1, q + 1) ++
                              search f z (p + 1, q) (c, d)
```

And the main program calls this function after performing binary search in *X* and *Y* axes.

```
solve f z = search f z (0, m) (n, 0) where
  m = bsearch (f 0) z (0, z)
  n = bsearch (\x -> f x 0) z (0, z)
```

Since we drop half areas in every recursion, it takes $O(\log(mn))$ rounds of search. However, in order to locate the point (p, q) , which halves the problem, we must perform binary search along the center line. which will call f about $O(\log(\min(m, n)))$ times. Denote the time of searching a $m \times n$ rectangle as $T(m, n)$, the recursion relationship can be represented as the following.

$$T(m, n) = \log(\min(m, n)) + 2T\left(\frac{m}{2}, \frac{n}{2}\right) \quad (14.17)$$

Suppose $m > n$, using telescope method, for $m = 2^i$, and $n = 2^j$. We have:

$$\begin{aligned} T(2^i, 2^j) &= j + 2T(2^{i-1}, 2^{j-1}) \\ &= \sum_{k=0}^{i-1} 2^k (j - k) \\ &= O(2^i (j - i)) \\ &= O(m \log(n/m)) \end{aligned} \quad (14.18)$$

Richard Bird proved that this is asymptotically optimal by a lower bound of searching a given value in $m \times n$ rectangle [1].

The imperative algorithm is almost as same as the functional version. We skip it for the sake of brevity.

Exercise 14.1

- Prove that the average case for the divide and conquer solution to k -selection problem is $O(n)$. Please refer to previous chapter about quick sort.
- Implement the imperative k -selection problem with 2-way partition, and median-of-three pivot selection.
- Implement the imperative k -selection problem to handle duplicated elements effectively.
- Realize the median-of-median k -selection algorithm and implement it in your favorite programming language.
- The $\text{tops}(k, L)$ algorithm uses list concatenation likes $A \cup \{l_1\} \cup \text{tops}(k - |A| - 1, B)$. It is linear operation which is proportion to the length of the list to be concatenated. Modify the algorithm so that the sub lists are concatenated by one pass.
- The author considered another divide and conquer solution for the k -selection problem. It finds the maximum of the first k elements and the minimum of the rest. Denote them as x , and y . If x is smaller than y , it means that all the first k elements are smaller than the rest, so that they are exactly the top k smallest; Otherwise, There are some elements in the first k should be swapped.

```

1: procedure TOPS( $k, A$ )
2:    $l \leftarrow 1$ 
3:    $u \leftarrow |A|$ 
4:   loop
5:      $i \leftarrow \text{MAX-AT}(A[l..k])$ 
6:      $j \leftarrow \text{MIN-AT}(A[k + 1..u])$ 
7:     if  $A[i] < A[j]$  then
8:       break
9:     EXCHANGE  $A[l] \leftrightarrow A[j]$ 
10:    EXCHANGE  $A[k + 1] \leftrightarrow A[i]$ 
11:     $l \leftarrow \text{PARTITION}(A, l, k)$ 
12:     $u \leftarrow \text{PARTITION}(A, k + 1, u)$ 

```

Explain why this algorithm works? What's the performance of it?

- Implement the binary search algorithm in both recursive and iterative manner, and try to verify your version automatically. You can either generate randomized data, test your program with the binary search invariant, or compare with the built-in binary search tool in your standard library.
- Find the solution to calculate the median of two sorted arrays A and B . The time should be bound to $O(\lg(|A| + |B|))$.
- Implement the improved saddleback search by firstly performing binary search to find a more accurate solution domain in your favorite imperative programming language.

- Realize the improved 2D search, by performing binary search along the shorter center line, in your favorite imperative programming language.
- Someone considers that the 2D search can be designed as the following. When search a rectangle, as the minimum value is at bottom-left, and the maximum at top-right. If the target value is less than the minimum or greater than the maximum, then there is no solution; otherwise, the rectangle is divided into 4 sub rectangles at the center point, then perform recursively searching.
 - 1: **procedure** SEARCH(f, z, a, b, c, d) ▷ (a, b): bottom-left (c, d): top-right
 - 2: **if** $z \leq f(a, b) \vee f(c, d) \geq z$ **then**
 - 3: **if** $z = f(a, b)$ **then**
 - 4: record (a, b) as a solution
 - 5: **if** $z = f(c, d)$ **then**
 - 6: record (c, d) as a solution
 - 7: **return**
 - 8: $p \leftarrow \lfloor \frac{a+c}{2} \rfloor$
 - 9: $q \leftarrow \lfloor \frac{b+d}{2} \rfloor$
 - 10: SEARCH(f, z, a, q, p, d)
 - 11: SEARCH(f, z, p, q, c, d)
 - 12: SEARCH(f, z, a, b, p, q)
 - 13: SEARCH(f, z, p, b, c, q)

What's the performance of this algorithm?

14.2.2 Information reuse

One interesting behavior is that people learning while searching. We do not only remember lessons which cause search fails, but also learn patterns which lead to success. This is a kind of information reusing, no matter the information is positive or negative. However, It's not easy to determine what information should be kept. Too little information isn't enough to help effective searching, while keeping too much is expensive in term of spaces.

In this section, we'll first introduce two interesting problems, Boyer-Moore majority number problem and the maximum sum of sub vector problem. Both reuse information as little as possible. After that, two popular string matching algorithms, Knuth-Morris-Pratt algorithm and Boyer-Moore algorithm will be introduced.

Boyer-Moore majority number

Voting is quite critical to people. We use voting to choose the leader, make decision or reject a proposal. In the months when I was writing this chapter, there are three countries in the world voted their presidents. All of the three voting activities utilized computer to calculate the result.

Suppose there is a country in a small island wants a new president. According to the constitution, only if the candidate wins more than half of the votes can be selected as the president. Given a series of votes, such as A, B, A, C, B, B, D, ..., can we develop a program tells who is the new president if there is, or indicate nobody wins more than half of the votes?

Of course this problem can be solved with brute-force by using a map. As what we did in the chapter of binary search tree⁵.

⁵There is a probabilistic sub-linear space counting algorithm published in 2004, named as 'Count-min sketch'[84].

```

template<typename T>
T majority(const T* xs, int n, T fail) {
    map<T, int> m;
    int i, max = 0;
    T r;
    for (i = 0; i < n; ++i)
        ++m[xs[i]];
    for (typename map<T, int>::iterator it = m.begin(); it ≠ m.end(); ++it)
        if (it→second > max) {
            max = it→second;
            r = it→first;
        }
    return max * 2 > n ? r : fail;
}

```

This program first scan the votes, and accumulates the number of votes for each individual with a map. After that, it traverse the map to find the one with the most of votes. If the number is bigger than the half, the winner is found otherwise, it returns a special value to indicate fail.

The following pseudo code describes this algorithm.

```

1: function MAJORITY(A)
2:   M ← empty map
3:   for  $\forall a \in A$  do
4:     PUT(M, a, 1+ GET(M, a))
5:   max ← 0, m ← NIL
6:   for  $\forall (k, v) \in M$  do
7:     if max < v then
8:       max ← v, m ← k
9:   if max > |A|50% then
10:    return m
11:  else
12:    fail

```

For m individuals and n votes, this program firstly takes about $O(n \log m)$ time to build the map if the map is implemented in self balanced tree (red-black tree for instance); or about $O(n)$ time if the map is hash table based. However, the hash table needs more space. Next the program takes $O(m)$ time to traverse the map, and find the majority vote. The following table lists the time and space performance for different maps.

map	time	space
self-balanced tree	$O(n \log m)$	$O(m)$
hashing	$O(n)$	$O(m)$ at least

Boyer and Moore invented a clever algorithm in 1980, which can pick the majority element with only one scan if there is. Their algorithm only needs $O(1)$ space [83].

The idea is to record the first candidate as the winner so far, and mark him with 1 vote. During the scan process, if the winner being selected gets another vote, we just increase the vote counter; otherwise, it means somebody vote against this candidate, so the vote counter should be decreased by one. If the vote counter becomes zero, it means this candidate is voted out; We select the next candidate as the new winner and repeat the above scanning process.

Suppose there is a series of votes: A, B, C, B, B, C, A, B, A, B, B, D, B. Below table illustrates the steps of this processing.

winner	count	scan position
A	1	A , B, C, B, B, C, A, B, A, B, B, D, B
A	0	A, B , C, B, B, C, A, B, A, B, B, D, B
C	1	A, B, C , B, B, C, A, B, A, B, B, D, B
C	0	A, B, C, B , B, C, A, B, A, B, B, D, B
B	1	A, B, C, B, B , C, A, B, A, B, B, D, B
B	0	A, B, C, B, B, C , A, B, A, B, B, D, B
A	1	A, B, C, B, B, C, A , B, A, B, B, D, B
A	0	A, B, C, B, B, C, A, B , A, B, B, D, B
A	1	A, B, C, B, B, C, A, B, A , B, B, D, B
A	0	A, B, C, B, B, C, A, B, A, B , B, D, B
B	1	A, B, C, B, B, C, A, B, A, B, B , D, B
B	0	A, B, C, B, B, C, A, B, A, B, B, D , B
B	1	A, B, C, B, B, C, A, B, A, B, B, D, B

The key point is that, if there exists the majority greater than 50%, it can't be voted out by all the others. However, if there are not any candidates win more than half of the votes, the recorded 'winner' is invalid. Thus it is necessary to perform a second round scan for verification.

The following pseudo code illustrates this algorithm.

```

1: function MAJORITY( $A$ )
2:    $c \leftarrow 0$ 
3:   for  $i \leftarrow 1$  to  $|A|$  do
4:     if  $c = 0$  then
5:        $x \leftarrow A[i]$ 
6:     if  $A[i] = x$  then
7:        $c \leftarrow c + 1$ 
8:     else
9:        $c \leftarrow c - 1$ 
10:  return  $x$ 

```

If there is the majority element, this algorithm takes one pass to scan the votes. In every iteration, it either increases or decreases the counter according to the vote is support or against the current selection. If the counter becomes zero, it means the current selection is voted out. So the new one is selected as the updated candidate for further scan.

The process is linear $O(n)$ time, and the spaces needed are just two variables. One for recording the selected candidate so far, the other is for vote counting.

Although this algorithm can find the majority element if there is. it still picks an element even there isn't. The following modified algorithm verifies the final result with another round of scan.

```

1: function MAJORITY( $A$ )
2:    $c \leftarrow 0$ 
3:   for  $i \leftarrow 1$  to  $|A|$  do
4:     if  $c = 0$  then
5:        $x \leftarrow A[i]$ 
6:     if  $A[i] = x$  then
7:        $c \leftarrow c + 1$ 
8:     else
9:        $c \leftarrow c - 1$ 
10:   $c \leftarrow 0$ 
11:  for  $i \leftarrow 1$  to  $|A|$  do
12:    if  $A[i] = x$  then
13:       $c \leftarrow c + 1$ 

```



```

14:   if  $c > \%50|A|$  then
15:     return  $x$ 
16:   else
17:     fail

```

Even with this verification process, the algorithm is still bound to $O(n)$ time, and the space needed is constant. The following ISO C++ program implements this algorithm ⁶.

```

template<typename T>
T majority(const T* xs, int n, T fail) {
    T m;
    int i, c;
    for (i = 0, c = 0; i < n; ++i) {
        if (!c)
            m = xs[i];
        c += xs[i] == m ? 1 : -1;
    }
    for (i = 0, c = 0; i < n; ++i, c += xs[i] == m);
    return c * 2 > n ? m : fail;
}

```

Boyer-Moore majority algorithm can also be realized in purely functional approach. Different from the imperative settings, which use variables to record and update information, accumulators are used to define the core algorithm. Define function $maj(c, n, L)$, which takes a list of votes L , a selected candidate c so far, and a counter n . For non empty list L , we initialize c as the first vote l_1 , and set the counter as 1 to start the algorithm: $maj(l_1, 1, L')$, where L' is the rest votes except for l_1 . Below are the definition of this function.

$$maj(c, n, L) = \begin{cases} c & : L = \phi \\ maj(c, n+1, L') & : l_1 = c \\ maj(l_1, 1, L') & : n = 0 \wedge l_1 \neq c \\ maj(c, n-1, L') & : otherwise \end{cases} \quad (14.19)$$

We also need to define a function, which can verify the result. The idea is that, if the list of votes is empty, the final result is a failure; otherwise, we start the Boyer-Moore algorithm to find a candidate c , then we scan the list again to count the total votes c wins, and verify if this number is not less than the half.

$$majority(L) = \begin{cases} fail & : L = \phi \\ c & : c = maj(l_1, 1, L'), |\{x | x \in L, x = c\}| > \%50|L| \\ fail & : otherwise \end{cases} \quad (14.20)$$

Below Haskell example code implements this algorithm.

```

majority :: (Eq a) => [a] -> Maybe a
majority [] = Nothing
majority (x:xs) = let m = maj x 1 xs in verify m (x:xs)

maj c n [] = c
maj c n (x:xs) | c == x = maj c (n+1) xs
               | n == 0 = maj x 1 xs
               | otherwise = maj c (n-1) xs

verify m xs = if 2 * (length $ filter (==m) xs) > length xs
              then Just m else Nothing

```

⁶We actually uses the ANSI C style. The C++ template is only used to generalize the type of the element

Maximum sum of sub vector

Jon Bentley presents another interesting puzzle which can be solved by using quite similar idea in [4]. The problem is to find the maximum sum of sub vector. For example in the following array, The sub vector {19, -12, 1, 9, 18} yields the biggest sum 35.

3	-13	19	-12	1	9	18	-16	15	-15
---	-----	----	-----	---	---	----	-----	----	-----

Note that it is only required to output the value of the maximum sum. If all the numbers are positive, the answer is definitely the sum of all. Another special case is that all numbers are negative. We define the maximum sum is 0 for an empty sub vector.

Of course we can find the answer with brute-force, by calculating all sums of sub vectors and picking the maximum. Such naive method is typical quadratic.

```

1: function MAX-SUM(A)
2:   m ← 0
3:   for i ← 1 to |A| do
4:     s ← 0
5:     for j ← i to |A| do
6:       s ← s + A[j]
7:       m ← MAX(m, s)
8:   return m
    
```

The brute force algorithm does not reuse any information in previous search. Similar with Boyer-Moore majority vote algorithm, we can record the maximum sum end to the position where we are scanning. Of course we also need record the biggest sum found so far. The following figure illustrates this idea and the invariant during scan.

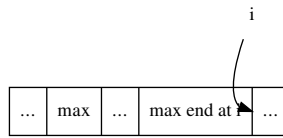


Figure 14.11: Invariant during scan.

At any time when we scan to the *i*-th position, the max sum found so far is recorded as *A*. At the same time, we also record the biggest sum end at *i* as *B*. Note that *A* and *B* may not be the same, in fact, we always maintain $B \leq A$. and when *B* becomes greater than *A* by adding with the next element, we update *A* with this new value. When *B* becomes negative, this happens when the next element is a negative number, we reset it to 0. The following tables illustrated the steps when we scan the example vector {3, -13, 19, -12, 1, 9, 18, -16, 15, -15}.

max sum	max end at <i>i</i>	list to be scan
0	0	{3, -13, 19, -12, 1, 9, 18, -16, 15, -15}
3	3	{-13, 19, -12, 1, 9, 18, -16, 15, -15}
3	0	{19, -12, 1, 9, 18, -16, 15, -15}
19	19	{-12, 1, 9, 18, -16, 15, -15}
19	7	{1, 9, 18, -16, 15, -15}
19	8	{9, 18, -16, 15, -15}
19	17	{18, -16, 15, -15}
35	35	{-16, 15, -15}
35	19	{15, -15}
35	34	{-15}
35	19	{}

This algorithm can be described as below.

```

1: function MAX-SUM( $V$ )
2:    $A \leftarrow 0, B \leftarrow 0$ 
3:   for  $i \leftarrow 1$  to  $|V|$  do
4:      $B \leftarrow \text{MAX}(B + V[i], 0)$ 
5:      $A \leftarrow \text{MAX}(A, B)$ 

```

It is trivial to implement this linear time algorithm, that we skip the details here.

This algorithm can also be defined in functional approach. Instead of mutating variables, we use accumulator to record A and B . In order to search the maximum sum of list L , we call the below function with $\text{max}_{sum}(0, 0, L)$.

$$\text{max}_{sum}(A, B, L) = \begin{cases} A & : L = \phi \\ \text{max}_{sum}(A', B', L') & : \textit{otherwise} \end{cases} \quad (14.21)$$

Where

$$\begin{aligned} B' &= \text{max}(l_1 + B, 0) \\ A' &= \text{max}(A, B') \end{aligned}$$

Below Haskell example code implements this algorithm.

```

maxsum = msum 0 0 where
  msum a _ [] = a
  msum a b (x:xs) = let b' = max (x+b) 0
                       a' = max a b'
                    in msum a' b' xs

```

KMP

String matching is another important type of searching. Almost all the software editors are equipped with tools to find string in the text. In chapters about Trie, Patricia, and suffix tree, we have introduced some powerful data structures which can help to search string. In this section, we introduce another two string matching algorithms all based on information reusing.

Some programming environments provide built-in string search tools, however, most of them are brute-force solution including ‘strstr’ function in ANSI C standard library, ‘find’ in C++ standard template library, ‘indexOf’ in Java Development Kit etc. Figure 14.12 illustrate how such character-by-character comparison process works.

Suppose we search a pattern P in text T , as shown in figure 14.12 (a), at offset $s = 4$, the process examines every character in P and T to check if they are same. It successfully matches the first 4 characters ‘anan’. However, the 5th character in the pattern string is ‘y’. It doesn’t match the corresponding character in the text, which is ‘t’.

At this stage, the brute-force solution terminates the attempt, increases s by one to 5, and restart the comparison between ‘anaym’ and ‘nantho...’. Actually, we can increase s not only by one. This is because we have already known that the first four characters ‘anan’ have been matched, and the failure happens at the 5th position. Observe the two letters prefix ‘an’ of the pattern string is also a suffix of ‘anan’ that we have matched so far. A more effective way is to shift s by two but not one, which is shown in figure 14.12 (b). By this means, we reused the information that 4 characters have been matched. This helps us to skip invalid positions as many as possible.

Knuth, Morris and Pratt presented this idea in [85] and developed a novel string matching algorithm. This algorithm is later called as ‘KMP’, which is consist of the three authors’ initials.

For the sake of brevity, we denote the first k characters of text T as T_k . Which means T_k is the k -character prefix of T .

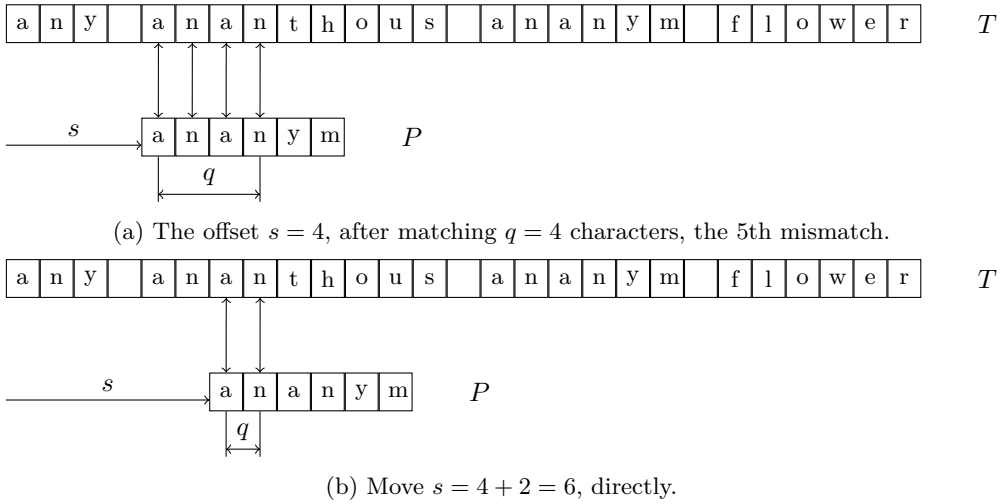


Figure 14.12: Match ‘anany’ in ‘any ananthous anany flower’.

The key point to shift s effectively is to find a function of q , where q is the number of characters matched successfully. For instance, q is 4 in figure 14.12 (a), as the 5th character doesn’t match.

Consider what situation we can shift s more than 1. As shown in figure 14.13, if we can shift the pattern P ahead, there must exist k , so that the first k characters are as same as the last k characters of P_q . In other words, the prefix P_k is suffix of P_q .

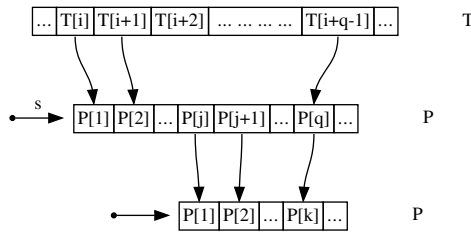


Figure 14.13: P_k is both prefix of P_q and suffix of P_q .

It’s possible that there is no such a prefix that is the suffix at the same time. If we treat empty string as both the prefix and the suffix of any others, there must be at least one solution that $k = 0$. It’s also quite possible that there are multiple k satisfy. To avoid missing any possible matching positions, we have to find the biggest k . We can define a *prefix function* $\pi(q)$ which tells us where we can fallback if the $(q + 1)$ -th character does not match [4].

$$\pi(q) = \max\{k | k < q \wedge P_k \sqsupseteq P_q\} \tag{14.22}$$

Where \sqsupseteq is read as ‘is suffix of’. For instance, $A \sqsupseteq B$ means A is suffix of B . This function is used as the following. When we match pattern P against text T from offset s , If it fails after matching q characters, we next look up $\pi(q)$ to get a fallback q' , and retry to compare $P[q']$ with the previous unmatched character. Based on this idea, the core algorithm of KMP can be described as the following.

1: **function** KMP(T, P)

```

2:    $n \leftarrow |T|, m \leftarrow |P|$ 
3:   build prefix function  $\pi$  from  $P$ 
4:    $q \leftarrow 0$  ▷ How many characters have been matched so far.
5:   for  $i \leftarrow 1$  to  $n$  do
6:     while  $q > 0 \wedge P[q + 1] \neq T[i]$  do
7:        $q \leftarrow \pi(q)$ 
8:     if  $P[q + 1] = T[i]$  then
9:        $q \leftarrow q + 1$ 
10:    if  $q = m$  then
11:      found one solution at  $i - m$ 
12:       $q \leftarrow \pi(q)$  ▷ look for next solution

```

Although the definition of prefix function $\pi(q)$ is given in equation (14.22), realizing it blindly by finding the longest suffix isn't effective. Actually we can use the idea of information reusing again to build the prefix function.

The trivial edge case is that, the first character doesn't match. In this case the longest prefix, which is also the suffix is definitely empty, so $\pi(1) = k = 0$. We record the longest prefix as P_k . In this edge case $P_k = P_0$ is the empty string.

After that, when we scan at the q -th character in the pattern string P , we hold the invariant that the prefix function values $\pi(i)$ for i in $\{1, 2, \dots, q - 1\}$ have already been recorded, and P_k is the longest prefix which is also the suffix of P_{q-1} . As shown in figure 14.14, if $P[q] = P[k + 1]$, A bigger k than before is found, we can increase the maximum of k by one; otherwise, if they are not same, we can use $\pi(k)$ to fallback to a shorter prefix $P_{k'}$ where $k' = \pi(k)$, and check if the next character after this new prefix is same as the q -th character. We need repeat this step until either k becomes zero (which means only empty string satisfies), or the q -th character matches.

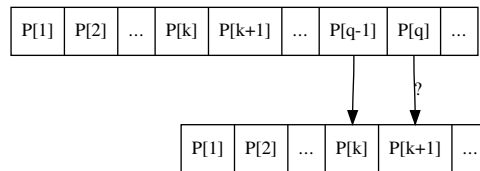


Figure 14.14: P_k is suffix of P_{q-1} , $P[q]$ and $P[k + 1]$ are compared.

Realizing this idea gives the KMP prefix building algorithm.

```

1: function BUILD-PREFIX-FUNCTION( $P$ )
2:    $m \leftarrow |P|, k \leftarrow 0$ 
3:    $\pi(1) \leftarrow 0$ 
4:   for  $q \leftarrow 2$  to  $m$  do
5:     while  $k > 0 \wedge P[q] \neq P[k + 1]$  do
6:        $k \leftarrow \pi(k)$ 
7:     if  $P[q] = P[k + 1]$  then
8:        $k \leftarrow k + 1$ 
9:      $\pi(q) \leftarrow k$ 
10:  return  $\pi$ 

```

The following table lists the steps of building prefix function for pattern string 'ananyam'. Note that the k in the table actually means the maximum k satisfies equation (14.22).

q	P_q	k	P_k
1	a	0	""
2	an	0	""
3	ana	1	a
4	anan	2	an
5	anany	0	""
6	anany m	0	""

Translating the KMP algorithm to Python gives the below example code.

```

def kmp_match(w, p):
    n = len(w)
    m = len(p)
    fallback = fprefix(p)
    k = 0 # how many elements have been matched so far.
    res = []
    for i in range(n):
        while k > 0 and p[k] != w[i]:
            k = fallback[k] #fall back
        if p[k] == w[i]:
            k = k + 1
        if k == m:
            res.append(i+1-m)
            k = fallback[k-1] # look for next
    return res

def fprefix(p):
    m = len(p)
    t = [0]*m # fallback table
    k = 0
    for i in range(2, m):
        while k > 0 and p[i-1] != p[k]:
            k = t[k-1] #fallback
        if p[i-1] == p[k]:
            k = k + 1
        t[i] = k
    return t

```

The KMP algorithm builds the prefix function for the pattern string as a kind of pre-processing before the search. Because of this, it can reuse as much information of the previous matching as possible.

The amortized performance of building the prefix function is $O(m)$. This can be proved by using potential method as in [4]. Using the similar method, it can be proved that the matching algorithm itself is also linear. Thus the total performance is $O(m + n)$ at the expense of the $O(m)$ space to record the prefix function table.

It seems that varies pattern string would affect the performance of KMP. Considering the case that we are finding pattern string 'aaa...a' of length m in a string 'aaa...a' of length n . All the characters are same, when the last character in the pattern is examined, we can only fallback by 1, and this 1 character fallback repeats until it falls back to zero. Even in this extreme case, KMP algorithm still holds its linear performance (why?). Please try to consider more cases such as $P = aaaa...b$, $T = aaaa...a$ and so on.

Purely functional KMP algorithm

It is not easy to realize KMP matching algorithm in purely functional manner. The imperative algorithm represented so far intensely uses array to record prefix function values. Although it is possible to utilize sequence like structure in purely functional settings, it is typically implemented with finger tree. Unlike native arrays, finger tree

needs logarithm time for random accessing⁷.

Richard Bird presents a formal program deduction to KMP algorithm by using fold fusion law in chapter 17 of [1]. In this section, we show how to develop purely functional KMP algorithm step by step from a brute-force prefix function creation method.

Both text string and pattern are represented as singly linked-list in purely functional settings. During the scan process, these two lists are further partitioned, every one is broken into two parts. As shown in figure 14.15, The first j characters in the pattern string have been matched. $T[i + 1]$ and $P[j + 1]$ will be compared next. If they are same, we need append the character to the matched part. However, since strings are essentially singly linked list, such appending is proportion to j .

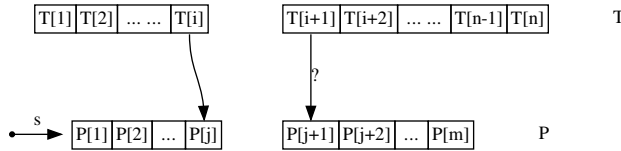


Figure 14.15: The first j characters in P are matched, next compare $P[j + 1]$ with $T[i + 1]$.

Denote the first i characters as T_p , which means the prefix of T , the rest characters as T_s for suffix; Similarly, the first j characters as P_p , and the rest as P_s ; Denote the first character of T_s as t , the first character of P_s as p . We have the following ‘cons’ relationship.

$$\begin{aligned} T_s &= \text{cons}(t, T'_s) \\ P_s &= \text{cons}(p, P'_s) \end{aligned}$$

If $t = p$, note the following updating process is bound to linear time.

$$\begin{aligned} T'_p &= T_p \cup \{t\} \\ P'_p &= P_p \cup \{p\} \end{aligned}$$

We’ve introduced a method in the chapter about purely functional queue, which can solve this problem. By using a pair of front and rear list, we can turn the linear time appending to constant time linking. The key point is to represent the prefix part in reverse order.

$$\begin{aligned} T &= T_p \cup T_s = \text{reverse}(\text{reverse}(T_p)) \cup T_s = \text{reverse}(\overleftarrow{T_p}) \cup T_s \\ P &= P_p \cup P_s = \text{reverse}(\text{reverse}(P_p)) \cup P_s = \text{reverse}(\overleftarrow{P_p}) \cup P_s \end{aligned} \tag{14.23}$$

The idea is to using pair $(\overleftarrow{T_p}, T_s)$ and $(\overleftarrow{P_p}, P_s)$ instead. With this change, the if $t = p$, we can update the prefix part fast in constant time.

$$\begin{aligned} \overleftarrow{T'_p} &= \text{cons}(t, \overleftarrow{T_p}) \\ \overleftarrow{P'_p} &= \text{cons}(p, \overleftarrow{P_p}) \end{aligned} \tag{14.24}$$

The KMP matching algorithm starts by initializing the success prefix parts to empty strings as the following.

$$\text{search}(P, T) = \text{kmp}(\pi, (\phi, P)(\phi, T)) \tag{14.25}$$

⁷Again, we don’t use native array, even it is supported in some functional programming environments like Haskell.

Where π is the prefix function we explained before. The core part of KMP algorithm, except for the prefix function building, can be defined as below.

$$kmp(\pi, (\overleftarrow{P}_p, P_s), (\overleftarrow{T}_p, T_s)) = \begin{cases} \{\overleftarrow{T}_p\} & : P_s = \phi \wedge T_s = \phi \\ \phi & : P_s \neq \phi \wedge T_s = \phi \\ \{\overleftarrow{T}_p\} \cup kmp(\pi, \pi(\overleftarrow{P}_p, P_s), (\overleftarrow{T}_p, T_s)) & : P_s = \phi \wedge T_s \neq \phi \\ kmp(\pi, (\overleftarrow{P}'_p, P'_s), (\overleftarrow{T}'_p, T'_s)) & : t = p \\ kmp(\pi, \pi(\overleftarrow{P}_p, P_s), (\overleftarrow{T}'_p, T'_s)) & : t \neq p \wedge \overleftarrow{P}_p = \phi \\ kmp(\pi, \pi(\overleftarrow{P}_p, P_s), (\overleftarrow{T}_p, T_s)) & : t \neq p \wedge \overleftarrow{P}_p \neq \phi \end{cases} \quad (14.26)$$

The first clause states that, if the scan successfully ends to both the pattern and text strings, we get a solution, and the algorithm terminates. Note that we use the right position in the text string as the matching point. It's easy to use the left position by subtracting with the length of the pattern string. For sake of brevity, we switch to right position in functional solutions.

The second clause states that if the scan arrives at the end of text string, while there are still rest of characters in the pattern string haven't been matched, there is no solution. And the algorithm terminates.

The third clause states that, if all the characters in the pattern string have been successfully matched, while there are still characters in the text haven't been examined, we get a solution, and we fallback by calling prefix function π to go on searching other solutions.

The fourth clause deals with the case, that the next character in pattern string and text are same. In such case, the algorithm advances one character ahead, and recursively performs searching.

If the the next characters are not same and this is the first character in the pattern string, we just need advance to next character in the text, and try again. Otherwise if this isn't the first character in the pattern, we call prefix function π to fallback, and try again.

The brute-force way to build the prefix function is just to follow the definition equation (14.22).

$$\pi(\overleftarrow{P}_p, P_s) = (\overleftarrow{P}'_p, P'_s) \quad (14.27)$$

where

$$\begin{aligned} P'_p &= longest(\{s | s \in prefixes(P_p), s \sqsupset P_p\}) \\ P'_s &= P - P'_p \end{aligned}$$

Every time when calculate the fallback position, the algorithm naively enumerates all prefixes of P_p , checks if it is also the suffix of P_p , and then pick the longest one as result. Note that we reuse the subtraction symbol here for list differ operation.

There is a tricky case which should be avoided. Because any string itself is both its prefix and suffix. Say $P_p \sqsubset P_p$ and $P_p \sqsupset P_p$. We shouldn't enumerate P_p as a candidate prefix. One solution of such prefix enumeration can be realized as the following.

$$prefixes(L) = \begin{cases} \{\phi\} & : L = \phi \vee |L| = 1 \\ cons(\phi, map(\lambda s. cons(l_1, s), prefixes(L'))) & : otherwise \end{cases} \quad (14.28)$$

Below Haskell example program implements this version of string matching algorithm.

```
kmpSearch1 ptn text = kmpSearch' next ([], ptn) ([], text)
```



```

kmpSearch' _ (sp, []) (sw, []) = [length sw]
kmpSearch' _ _ (_, []) = []
kmpSearch' f (sp, []) (sw, ws) = length sw : kmpSearch' f (f sp []) (sw, ws)
kmpSearch' f (sp, (p:ps)) (sw, (w:ws))
  | p == w = kmpSearch' f ((p:sp), ps) ((w:sw), ws)
  | otherwise = if sp == [] then kmpSearch' f (sp, (p:ps)) ((w:sw), ws)
                else kmpSearch' f (f sp (p:ps)) (sw, (w:ws))

next sp ps = (sp', ps') where
  prev = reverse sp
  prefix = longest [xs | xs ← inits prev, xs `isSuffixOf` prev]
  sp' = reverse prefix
  ps' = (prev ++ ps) \\ prefix
  longest = maximumBy (compare `on` length)

inits [] = [[]]
inits [_] = [[]]
inits (x:xs) = [] : (map (x:) $ inits xs)

```

This version does not only perform poorly, but it is also complex. We can simplify it a bit. Observing the KMP matching is a scan process from left to the right of the text, it can be represented with folding (refer to Appendix A for detail). Firstly, we can augment each character with an index for folding like below.

$$zip(T, \{1, 2, \dots\}) \quad (14.29)$$

Zippping the text string with infinity natural numbers gives list of pairs. For example, text string ‘The quick brown fox jumps over the lazy dog’ turns into (T, 1), (h, 2), (e, 3), ... (o, 42), (g, 43).

The initial state for folding contains two parts, one is the pair of pattern (P_p, P_s) , with prefix starts from empty, and the suffix is the whole pattern string (ϕ, P) . For illustration purpose only, we revert back to normal pairs but not $(\overleftarrow{P}_p, P_s)$ notation. It can be easily replaced with reversed form in the finalized version. This is left as exercise to the reader. The other part is a list of positions, where the successful matching are found. It starts from empty list. After the folding finishes, this list contains all solutions. What we need is to extract this list from the final state. The core KMP search algorithm is simplified like this.

$$kmp(P, T) = snd(fold(search, ((\phi, P), \phi), zip(T, \{1, 2, \dots\}))) \quad (14.30)$$

The only ‘black box’ is the *search* function, which takes a state, and a pair of character and index, and it returns a new state as result. Denote the first character in P_s as p and the rest characters as P'_s ($P_s = cons(p, P'_s)$), we have the following definition.

$$search(((P_p, P_s), L), (c, i)) = \begin{cases} ((P_p \cup p, P'_s), L \cup \{i\}) & : p = c \wedge P'_s = \phi \\ ((P_p \cup p, P'_s), L) & : p = c \wedge P'_s \neq \phi \\ ((P_p, P_s), L) & : P_p = \phi \\ search((\pi(P_p, P_s), L), (c, i)) & : otherwise \end{cases} \quad (14.31)$$

If the first character in P_s matches the current character c during scan, we need further check if all the characters in the pattern have been examined, if so, we successfully find a solution, This position i in list L is recorded; Otherwise, we advance one character ahead and go on. If p does not match c , we need fallback for further retry. However, there is an edge case that we can’t fallback any more. P_p is empty in this case, and we need do nothing but keep the current state.

The prefix-function π developed so far can also be improved a bit. Since we want to find the longest prefix of P_p , which is also suffix of it, we can scan from right to left

instead. For any non empty list L , denote the first element as l_1 , and all the rest except for the first one as L' , define a function $init(L)$, which returns all the elements except for the last one as below.

$$init(L) = \begin{cases} \phi & : |L| = 1 \\ cons(l_1, init(L')) & : otherwise \end{cases} \quad (14.32)$$

Note that this function can not handle empty list. The idea of scan from right to left for P_p is first check if $init(P_p) \sqsupset P_p$, if yes, then we are done; otherwise, we examine if $init(init(P_p))$ is OK, and repeat this till the left most. Based on this idea, the prefix-function can be modified as the following.

$$\pi(P_p, P_s) = \begin{cases} (P_p, P_s) & : P_p = \phi \\ fallback(init(P_p), cons(last(P_p), P_s)) & : otherwise \end{cases} \quad (14.33)$$

Where

$$fallback(A, B) = \begin{cases} (A, B) & : A \sqsupset P_p \\ (init(A), cons(last(A), B)) & : otherwise \end{cases} \quad (14.34)$$

Note that fallback always terminates because empty string is suffix of any string. The $last(L)$ function returns the last element of a list, it is also a linear time operation (refer to Appendix A for detail). However, it's constant operation if we use \overleftarrow{P}_p approach. This improved prefix-function is bound to linear time. It is still quite slower than the imperative algorithm which can look up prefix-function in constant $O(1)$ time. The following Haskell example program implements this minor improvement.

```
failure ([], ys) = ([], ys)
failure (xs, ys) = fallback (init xs) (last xs:ys) where
  fallback as bs | as `isSuffixOf` xs = (as, bs)
                 | otherwise = fallback (init as) (last as:bs)

kmpSearch ws txt = snd $ foldl f (([], ws), []) (zip txt [1..]) where
  f (p@(xs, (y:ys)), ns) (x, n) | x == y = if ys==[] then ((xs++[y], ys), ns++[n])
                                 else ((xs++[y], ys), ns)
                                 | xs == [] = (p, ns)
                                 | otherwise = f (failure p, ns) (x, n)
  f (p, ns) e = f (failure p, ns) e
```

The bottleneck is that we can not use native array to record prefix functions in purely functional settings. In fact the prefix function can be understood as a state transform function. It transfer from one state to the other according to the matching is success or fail. We can abstract such state changing as a tree. In environment supporting algebraic data type, Haskell for example, such state tree can be defined like below.

```
data State a = E | S a (State a) (State a)
```

A state is either empty, or contains three parts: the current state, the new state if match fails, and the new state if match succeeds. Such definition is quite similar to the binary tree. We can call it 'left-fail, right-success' tree. The state we are using here is (P_p, P_s) .

Similar as imperative KMP algorithm, which builds the prefix function from the pattern string, the state transforming tree can also be built from the pattern. The idea is to build the tree from the very beginning state (ϕ, P) , with both its children empty. We replace the left child with a new state by calling π function defined above, and replace the right child by advancing one character ahead. There is an edge case, that when the

state transfers to (P, ϕ) , we can not advance any more in success case, such node only contains child for failure case. The build function is defined as the following.

$$build((P_p, P_s), \phi, \phi) = \begin{cases} build(\pi(P_p, P_s), \phi, \phi) & : P_s = \phi \\ build((P_p, P_s), L, R) & : otherwise \end{cases} \quad (14.35)$$

Where

$$\begin{aligned} L &= build(\pi(P_p, P_s), \phi, \phi) \\ R &= build((P_s \cup \{p\}, P'_s), \phi, \phi) \end{aligned}$$

The meaning of p and P'_s are as same as before, that p is the first character in P_s , and P'_s is the rest characters. The most interesting point is that the build function will never stop. It endless build a infinite tree. In strict programming environment, calling this function will freeze. However, in environments support lazy evaluation, only the nodes have to be used will be created. For example, both Haskell and Scheme/Lisp are capable to construct such infinite state tree. In imperative settings, it is typically realized by using pointers which links to ancestor of a node.

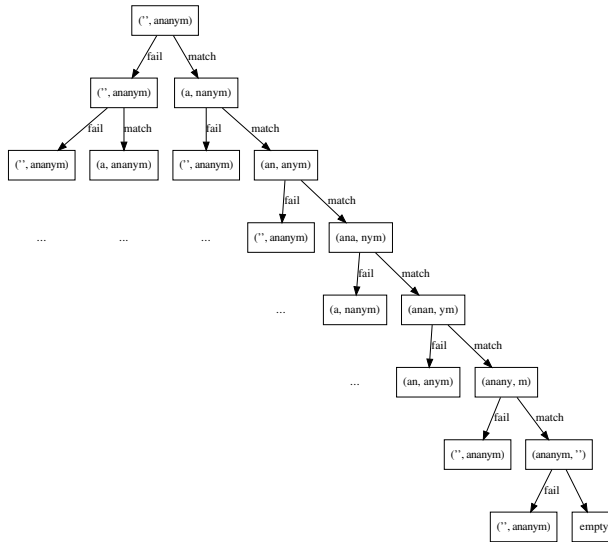


Figure 14.16: The infinite state tree for pattern ‘anonym’.

Figure 14.16 illustrates such an infinite state tree for pattern string ‘anonym’. Note that the right most edge represents the case that the matching continuously succeed for all characters. After that, since we can’t match any more, so the right sub-tree is empty. Base on this fact, we can define a auxiliary function to test if a state indicates the whole pattern is successfully matched.

$$match((P_p, P_s), L, R) = \begin{cases} True & : P_s = \phi \\ False & : otherwise \end{cases} \quad (14.36)$$

With the help of state transform tree, we can realize KMP algorithm in an automaton manner.

$$kmp(P, T) = snd(fold(search, (Tr, []), zip(T, \{1, 2, \dots\}))) \quad (14.37)$$

Where the tree $Tr = build((\phi, P), \phi, \phi)$ is the infinite state transform tree. Function $search$ utilizes this tree to transform the state according to match or fail. Denote the

first character in P_s as p , the rest characters as P'_s , and the matched positions found so far as A .

$$\text{search}(\(((P_p, P_s), L, R), A), (c, i)) = \begin{cases} (R, A \cup \{i\}) & : p = c \wedge \text{match}(R) \\ (R, A) & : p = c \wedge \neg \text{match}(R) \\ (\(((P_p, P_s), L, R), A) & : P_p = \phi \\ \text{search}((L, A), (c, i)) & : \text{otherwise} \end{cases} \quad (14.38)$$

The following Haskell example program implements this algorithm.

```
data State a = E | S a (State a) (State a) — state, ok-state, fail-state
deriving (Eq, Show)

build :: (Eq a) => State ([a], [a]) -> State ([a], [a])
build (S s@(xs, []) E E) = S s (build (S (failure s) E E)) E
build (S s@(xs, (y:ys)) E E) = S s l r where
  l = build (S (failure s) E E) — fail state
  r = build (S (xs++[y], ys) E E)

matched (S (_, []) _ _) = True
matched _ = False

kmpSearch3 :: (Eq a) => [a] -> [a] -> [Int]
kmpSearch3 ws txt = snd $ foldl f (auto, []) (zip txt [1..]) where
  auto = build (S ([], ws) E E)
  f (s@(S (xs, ys) l r), ns) (x, n)
    | [x] `isPrefixOf` ys = if matched r then (r, ns++[n])
    else (r, ns)
    | xs == [] = (s, ns)
    | otherwise = f (l, ns) (x, n)
```

The bottle-neck is that the state tree building function calls π to fallback. While current definition of π isn't effective enough, because it enumerates all candidates from right to the left every time.

Since the state tree is infinite, we can adopt some common treatment for infinite structures. One good example is the Fibonacci series. The first two Fibonacci numbers are defined as 0 and 1; the rest Fibonacci numbers can be obtained by adding the previous two numbers.

$$\begin{aligned} F_0 &= 0 \\ F_1 &= 1 \\ F_n &= F_{n-1} + F_{n-2} \end{aligned} \quad (14.39)$$

Thus the Fibonacci numbers can be list one by one as the following

$$\begin{aligned} F_0 &= 0 \\ F_1 &= 1 \\ F_2 &= F_1 + F_0 \\ F_3 &= F_2 + F_1 \\ &\dots \end{aligned} \quad (14.40)$$

We can collect all numbers in both sides, and define $F = \{0, 1, F_1, F_2, \dots\}$, Thus we have the following equation.

$$\begin{aligned} F &= \{0, 1, F_1 + F_0, F_2 + F_1, \dots\} \\ &= \{0, 1\} \cup \{x + y | x \in \{F_0, F_1, F_2, \dots\}, y \in \{F_1, F_2, F_3, \dots\}\} \\ &= \{0, 1\} \cup \{x + y | x \in F, y \in F'\} \end{aligned} \quad (14.41)$$

Where $F' = \text{tail}(F)$ is all the Fibonacci numbers except for the first one. In environments support lazy evaluation, like Haskell for instance, this definition can be expressed like below.

```
fibs = 0 : 1 : zipWith (+) fibs (tail fibs)
```

The recursive definition for infinite Fibonacci series indicates an idea which can be used to get rid of the fallback function π . Denote the state transfer tree as T , we can define the transfer function when matching a character on this tree as the following.

$$\text{trans}(T, c) = \begin{cases} \text{root} & : T = \phi \\ R & : T = ((P_p, P_s), L, R), c = p \\ \text{trans}(L, c) & : \text{otherwise} \end{cases} \quad (14.42)$$

If we match a character against empty node, we transfer to the root of the tree. We'll define the root later soon. Otherwise, we compare if the character c is as same as the first character p in P_s . If they match, then we transfer to the right sub tree for this success case; otherwise, we transfer to the left sub tree for fail case.

With transfer function defined, we can modify the previous tree building function accordingly. This is quite similar to the previous Fibonacci series definition.

$$\text{build}(T, (P_p, P_s)) = ((P_p, P_s), T, \text{build}(\text{trans}(T, p), (P_p \cup \{p\}, P'_s)))$$

The right hand of this equation contains three parts. The first one is the state that we are matching (P_p, P_s) ; If the match fails, Since T itself can handle any fail case, we use it directly as the left sub tree; otherwise we recursive build the right sub tree for success case by advancing one character ahead, and calling transfer function we defined above.

However, there is an edge case which has to be handled specially, that if P_s is empty, which indicates a successful match. As defined above, there isn't right sub tree any more. Combining these cases gives the final building function.

$$\text{build}(T, (P_p, P_s)) = \begin{cases} ((P_p, P_s), T, \phi) & : P_s = \phi \\ ((P_p, P_s), T, \text{build}(\text{trans}(T, p), (P_p \cup \{p\}, P'_s))) & : \text{otherwise} \end{cases} \quad (14.43)$$

The last brick is to define the root of the infinite state transfer tree, which initializes the building.

$$\text{root} = \text{build}(\phi, (\phi, P)) \quad (14.44)$$

And the new KMP matching algorithm is modified with this root.

$$\text{kmp}(P, T) = \text{snd}(\text{fold}(\text{trans}, (\text{root}, []), \text{zip}(T, \{1, 2, \dots\}))) \quad (14.45)$$

The following Haskell example program implements this final version.

```
kmpSearch ws txt = snd $ foldl tr (root, []) (zip txt [1..]) where
  root = build' E ([], ws)
  build' fails (xs, []) = S (xs, []) fails E
  build' fails s@(xs, (y:ys)) = S s fails succs where
    succs = build' (fst (tr (fails, []) (y, 0))) (xs++[y], ys)
  tr (E, ns) _ = (root, ns)
  tr ((S (xs, ys) fails succs), ns) (x, n)
    | [x] `isPrefixOf` ys = if matched succs then (succs, ns++[n]) else (succs, ns)
    | otherwise = tr (fails, ns) (x, n)
```

Figure 14.17 shows the first 4 steps when search 'anaym' in text 'anal'. Since the first 3 steps all succeed, so the left sub trees of these 3 states are not actually constructed. They are marked as '?'. In the fourth step, the match fails, thus the right sub tree needn't be built. On the other hand, we must construct the left sub tree, which is on top of the result of $\text{trans}(\text{right}(\text{right}(\text{right}(T))), n)$, where function $\text{right}(T)$ returns the right sub

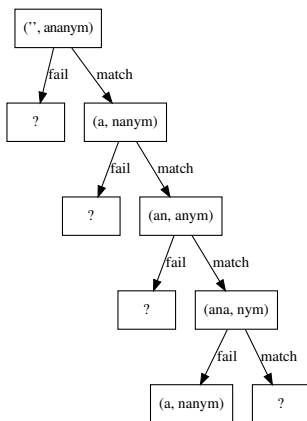


Figure 14.17: On demand construct the state transform tree when searching ‘anym’ in text ‘anal’.

tree of T . This can be further expanded according to the definition of building and state transforming functions till we get the concrete state $((a, nananym), L, R)$. The detailed deduce process is left as exercise to the reader.

This algorithm depends on the lazy evaluation critically. All the states to be transferred are built on demand. So that the building process is amortized $O(m)$, and the total performance is amortized $O(n + m)$. Readers can refer to [1] for detailed proof of it.

It’s worth of comparing the final purely functional and the imperative algorithms. In many cases, we have expressive functional realization, however, for KMP matching algorithm, the imperative approach is much simpler and more intuitive. This is because we have to mimic the raw array by a infinite state transfer tree.

Boyer-Moore

Boyer-Moore string matching algorithm is another effective solution invented in 1977 [86]. The idea of Boyer-Moore algorithm comes from the following observation.

The bad character heuristics

When attempt to match the pattern, even if there are several characters from the left are same, it fails if the last one does not match, as shown in figure 14.18. What’s more, we wouldn’t find a match even if we slide the pattern down by 1, or 2. Actually, the length of the pattern ‘anany’ is 6, the last character is ‘m’, however, the corresponding character in the text is ‘h’. It does not appear in the pattern at all. We can directly slide the pattern down by 6.

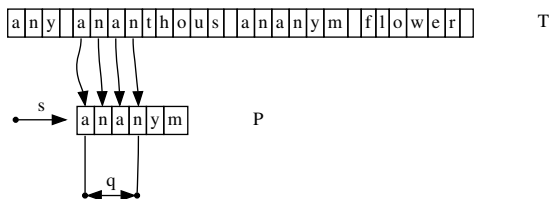
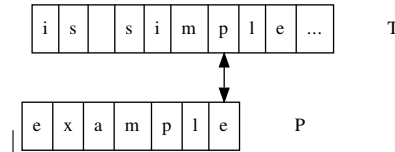
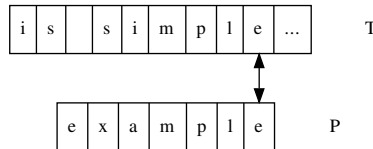


Figure 14.18: Since character ‘h’ doesn’t appear in the pattern, we wouldn’t find a match if we slide the pattern down less than the length of the pattern.

This leads to *the bad-character rule*. We can do a pre-processing for the pattern. If the character set of the text is already known, we can find all characters which don't appear in the pattern string. During the later scan process, as long as we find such a bad character, we can immediately slide the pattern down by its length. The question is what if the unmatched character does appear in the pattern? While, in order not to miss any potential matches, we have to slide down the pattern to check again. This is shown as in the figure 14.19



(a)
The
last
char-
ac-
ter
in
the
pat-
tern
'e'
doesn't
match
'p'.
How-
ever,
'p'
ap-
pears
in
the
pat-
tern.



(b) We have to slide the pattern down by 2 to check again.

Figure 14.19: Slide the pattern if the unmatched character appears in the pattern.

It's quite possible that the unmatched character appears in the pattern more than one position. Denote the length of the pattern as $|P|$, the character appears in positions p_1, p_2, \dots, p_i . In such case, we take the right most one to avoid missing any matches.

$$s = |P| - p_i \quad (14.46)$$

Note that the shifting length is 0 for the last position in the pattern according to the above equation. Thus we can skip it in realization. Another important point is that since

the shifting length is calculated against the position aligned with the last character in the pattern string, (we deduce it from $|P|$), no matter where the mismatching happens when we scan from right to the left, we slide down the pattern string by looking up the bad character table with the one in the text aligned with the last character of the pattern. This is shown in figure 14.20.

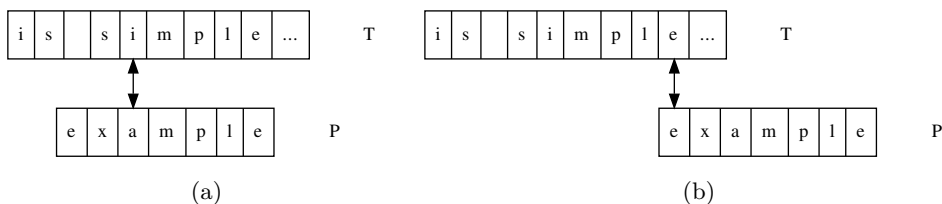


Figure 14.20: Even the mismatching happens in the middle, between char ‘i’ and ‘a’, we look up the shifting value with character ‘e’, which is 6 (calculated from the first ‘e’, the second ‘e’ is skipped to avoid zero shifting).

There is a good result in practice, that only using the bad-character rule leads to a simple and fast string matching algorithm, called Boyer-Moore-Horspool algorithm [87].

```

1: procedure BOYER-MOORE-HORSPOOL( $T, P$ )
2:   for  $\forall c \in \Sigma$  do
3:      $\pi[c] \leftarrow |P|$ 
4:   for  $i \leftarrow 1$  to  $|P| - 1$  do ▷ Skip the last position
5:      $\pi[P[i]] \leftarrow |P| - i$ 
6:    $s \leftarrow 0$ 
7:   while  $s + |P| \leq |T|$  do
8:      $i \leftarrow |P|$ 
9:     while  $i \geq 1 \wedge P[i] = T[s + i]$  do ▷ scan from right
10:       $i \leftarrow i - 1$ 
11:     if  $i < 1$  then
12:       found one solution at  $s$ 
13:        $s \leftarrow s + 1$  ▷ go on finding the next
14:     else
15:        $s \leftarrow s + \pi[T[s + |P|]]$ 

```

The character set is denoted as Σ , we first initialize all the values of sliding table π as the length of the pattern string $|P|$. After that we process the pattern from left to right, update the sliding value. If a character appears multiple times in the pattern, the latter value, which is on the right hand, will overwrite the previous value. We start the matching scan process by aligning the pattern and the text string from the very left. However, for every alignment s , we scan from the right to the left until either there is unmatched character or all the characters in the pattern have been examined. The latter case indicates that we’ve found a match; while for the former case, we look up π to slide the pattern down to the right.

The following example Python code implements this algorithm accordingly.

```

def bmh_match(w, p):
    n = len(w)
    m = len(p)
    tab = [m for _ in range(256)] # table to hold the bad character rule.
    for i in range(m-1):
        tab[ord(p[i])] = m - 1 - i
    res = []
    offset = 0

```



```

while offset + m ≤ n:
    i = m - 1
    while i ≥ 0 and p[i] == w[offset+i]:
        i = i - 1
    if i < 0:
        res.append(offset)
        offset = offset + 1
    else:
        offset = offset + tab[ord(w[offset + m - 1])]
return res

```

The algorithm firstly takes about $O(|\Sigma| + |P|)$ time to build the sliding table. If the character set size is small, the performance is dominated by the pattern and the text. There is definitely the worst case that all the characters in the pattern and text are same, e.g. searching 'aa...a' (m of 'a', denoted as a^m) in text 'aa.....a' (n of 'a', denoted as a^n). The performance in the worst case is $O(mn)$. This algorithm performs well if the pattern is long, and there are constant number of matching. The result is bound to linear time. This is as same as the best case of full Boyer-Moore algorithm which will be explained next.

The good suffix heuristics

Consider searching pattern 'abbabab' in text 'bbbababbabab...' like figure 14.21. By using the bad-character rule, the pattern will be slid by two.

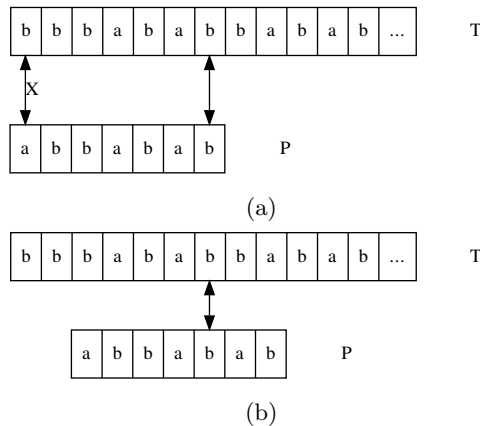


Figure 14.21: According to the bad-character rule, the pattern is slid by 2, so that the next 'b' is aligned.

Actually, we can do better than this. Observing that before the unmatched point, we have already successfully matched 6 characters 'bbabab' from right to the left. Since 'ab', which is the prefix of the pattern is also the suffix of what we matched so far, we can directly slide the pattern to align this suffix as shown in figure 14.22.

This is quite similar to the pre-processing of KMP algorithm, However, we can't always skip so many characters. Consider the following example as shown in figure 14.23. We have matched characters 'bab' when the unmatched happens. Although the prefix 'ab' of the pattern is also the suffix of 'bab', we can't slide the pattern so far. This is because 'bab' appears somewhere else, which starts from the 3rd character of the pattern. In order not to miss any potential matching, we can only slide the pattern by two.

The above situation forms the two cases of *the good-suffix rule*, as shown in figure 14.24.

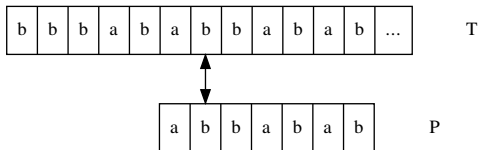


Figure 14.22: As the prefix ‘ab’ is also the suffix of what we’ve matched, we can slide down the pattern to a position so that ‘ab’ are aligned.

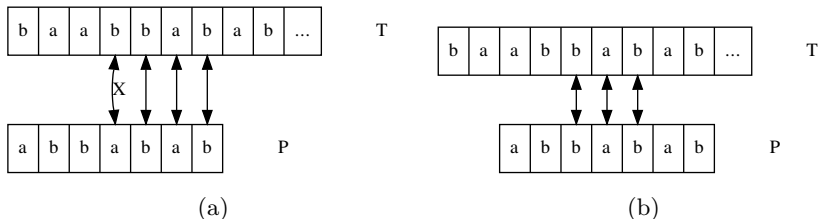


Figure 14.23: We’ve matched ‘bab’, which appears somewhere else in the pattern (from the 3rd to the 5th character). We can only slide down the pattern by 2 to avoid missing any potential matching.

Both cases in good suffix rule handle the situation that there are multiple characters have been matched from right. We can slide the pattern to the right if any of the the following happens.

- Case 1 states that if a part of the matching suffix occurs as a prefix of the pattern, and the matching suffix doesn’t appear in any other places in the pattern, we can slide the pattern to the right to make this prefix aligned;
- Case 2 states that if the matching suffix occurs some where else in the pattern, we can slide the pattern to make the right most occurrence aligned.

Note that in the scan process, we should apply case 2 first whenever it is possible, and then examine case 1 if the whole matched suffix does not appears in the pattern. Observe that both cases of the good-suffix rule only depend on the pattern string, a table can be built by pre-process the pattern for further looking up.

For the sake of brevity, we denote the suffix string from the i -th character of P as \overline{P}_i . That \overline{P}_i is the sub-string $P[i]P[i + 1] \dots P[m]$.

For case 1, we can check every suffix of P , which includes $\overline{P}_m, \overline{P}_{m-1}, \overline{P}_{m-2}, \dots, \overline{P}_2$ to examine if it is the prefix of P . This can be achieved by a round of scan from right to the left.

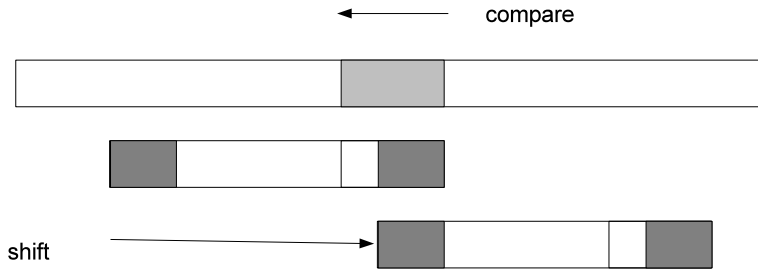
For case 2, we can check every prefix of P includes P_1, P_2, \dots, P_{m-1} to examine if the longest suffix is also a suffix of P . This can be achieved by another round of scan from left to the right.

```

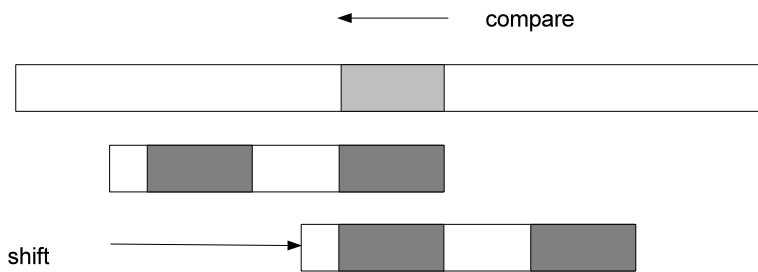
1: function GOOD-SUFFIX( $P$ )
2:    $m \leftarrow |P|$ 
3:    $\pi_s \leftarrow \{0, 0, \dots, 0\}$ 
4:    $l \leftarrow 0$ 
5:   for  $i \leftarrow m - 1$  down-to 1 do
6:     if  $\overline{P}_i \sqsubset P$  then
7:        $l \leftarrow i$ 
8:      $\pi_s[i] \leftarrow l$ 

```

\triangleright Initialize the table of length m
 \triangleright The last suffix which is also prefix of P
 \triangleright First loop for case 1
 $\triangleright \sqsubset$ means ‘is prefix of’



(a) Case 1, Only a part of the matching suffix occurs as a prefix of the pattern.



(b) Case 2, The matching suffix occurs somewhere else in the pattern.

Figure 14.24: The light gray section in the text represents the characters have been matched; The dark gray parts indicate the same content in the pattern.

```

9:   for  $i \leftarrow 1$  to  $m$  do                                     ▷ Second loop for case 2
10:      $s \leftarrow$  SUFFIX-LENGTH( $P_i$ )
11:     if  $s \neq 0 \wedge P[i - s] \neq P[m - s]$  then
12:        $\pi_s[m - s] \leftarrow m - i$ 
13:   return  $\pi_s$ 

```

This algorithm builds the good-suffix heuristics table π_s . It first checks every suffix of P from the shortest to the longest. If the suffix $\overline{P_i}$ is also the prefix of P , we record this suffix, and use it for all the entries until we find another suffix $\overline{P_j}$, $j < i$, and it is also the prefix of P .

After that, the algorithm checks every prefix of P from the shortest to the longest. It calls the function SUFFIX-LENGTH(P_i), to calculate the length of the longest suffix of P_i , which is also suffix of P . If this length s isn't zero, which means there exists a sub-string, that appears as the suffix of the pattern. It indicates that case 2 happens. The algorithm overwrites the s -th entry from the right of the table π_s . Note that to avoid finding the same occurrence of the matched suffix, we test if $P[i - s]$ and $P[m - s]$ are same.

Function SUFFIX-LENGTH is designed as the following.

```

1: function SUFFIX-LENGTH( $P_i$ )
2:    $m \leftarrow |P|$ 
3:    $j \leftarrow 0$ 
4:   while  $P[m - j] = P[i - j] \wedge j < i$  do
5:      $j \leftarrow j + 1$ 
6:   return  $j$ 

```

The following Python example program implements the good-suffix rule.

```

def good_suffix(p):
    m = len(p)
    tab = [0 for _ in range(m)]
    last = 0
    # first loop for case 1
    for i in range(m-1, 0, -1): # m-1, m-2, ..., 1
        if is_prefix(p, i):
            last = i
            tab[i - 1] = last
    # second loop for case 2
    for i in range(m):
        slen = suffix_len(p, i)
        if slen  $\neq$  0 and p[i - slen]  $\neq$  p[m - 1 - slen]:
            tab[m - 1 - slen] = m - 1 - i
    return tab

# test if p[i..m-1] 'is prefix of' p
def is_prefix(p, i):
    for j in range(len(p) - i):
        if p[j]  $\neq$  p[i+j]:
            return False
    return True

# length of the longest suffix of p[..i], which is also a suffix of p
def suffix_len(p, i):
    m = len(p)
    j = 0
    while p[m - 1 - j] == p[i - j] and j < i:
        j = j + 1
    return j

```

It's quite possible that both the bad-character rule and the good-suffix rule can be applied when the unmatched happens. The Boyer-Moore algorithm compares and picks the

bigger shift so that it can find the solution as quick as possible. The bad-character rule table can be explicitly built as below

```

1: function BAD-CHARACTER( $P$ )
2:   for  $\forall c \in \Sigma$  do
3:      $\pi_b[c] \leftarrow |P|$ 
4:   for  $i \leftarrow 1$  to  $|P| - 1$  do
5:      $\pi_b[P[i]] \leftarrow |P| - i$ 
6:   return  $\pi_b$ 

```

The following Python program implements the bad-character rule accordingly.

```

def bad_char(p):
    m = len(p)
    tab = [m for _ in range(256)]
    for i in range(m-1):
        tab[ord(p[i])] = m - 1 - i
    return tab

```

The final Boyer-Moore algorithm firstly builds the two rules from the pattern, then aligns the pattern to the beginning of the text and scans from right to the left for every alignment. If any unmatched happens, it tries both rules, and slides the pattern with the bigger shift.

```

1: function BOYER-MOORE( $T, P$ )
2:    $n \leftarrow |T|, m \leftarrow |P|$ 
3:    $\pi_b \leftarrow$  BAD-CHARACTER( $P$ )
4:    $\pi_s \leftarrow$  GOOD-SUFFIX( $P$ )
5:    $s \leftarrow 0$ 
6:   while  $s + m \leq n$  do
7:      $i \leftarrow m$ 
8:     while  $i \geq 1 \wedge P[i] = T[s + i]$  do
9:        $i \leftarrow i - 1$ 
10:    if  $i < 1$  then
11:      found one solution at  $s$ 
12:       $s \leftarrow s + 1$  ▷ go on finding the next
13:    else
14:       $s \leftarrow s + \max(\pi_b[T[s + m]], \pi_s[i])$ 

```

Here is the example implementation of Boyer-Moore algorithm in Python.

```

def bm_match(w, p):
    n = len(w)
    m = len(p)
    tab1 = bad_char(p)
    tab2 = good_suffix(p)
    res = []
    offset = 0
    while offset + m ≤ n:
        i = m - 1
        while i ≥ 0 and p[i] == w[offset + i]:
            i = i - 1
        if i < 0:
            res.append(offset)
            offset = offset + 1
        else:
            offset = offset + max(tab1[ord(w[offset + m - 1])], tab2[i])
    return res

```

The Boyer-Moore algorithm published in original paper is bound to $O(n+m)$ in worst case only if the pattern doesn't appear in the text [86]. Knuth, Morris, and Pratt proved

this fact in 1977 [88]. However, when the pattern appears in the text, as we shown above, Boyer-Moore performs $O(nm)$ in the worst case.

Richard Birds shows a purely functional realization of Boyer-Moore algorithm in chapter 16 in [1]. We skipped it in this book.

Exercise 14.2

- Proof that Boyer-Moore majority vote algorithm is correct.
- Given a list, find the element occurs most. Are there any divide and conquer solutions? Are there any divide and conquer data structures, such as map can be used?
- How to find the elements occur more than $1/3$ in a list? How to find the elements occur more than $1/m$ in the list?
- If we reject the empty array as valid sub-array, how to realize the maximum sum of sub-arrays puzzle?
- Bentley presents a divide and conquer algorithm to find the maximum sum in $O(n \log n)$ time in [4]. The idea is to split the list at the middle point. We can recursively find the maximum sum in the first half and second half; However, we also need to find maximum sum cross the middle point. The method is to scan from the middle point to both ends as the following.

```

1: function MAX-SUM( $A$ )
2:   if  $A = \phi$  then
3:     return 0
4:   else if  $|A| = 1$  then
5:     return MAX(0,  $A[1]$ )
6:   else
7:      $m \leftarrow \lfloor \frac{|A|}{2} \rfloor$ 
8:      $a \leftarrow$  MAX-FROM(REVERSE( $A[1\dots m]$ ))
9:      $b \leftarrow$  MAX-FROM( $A[m + 1\dots |A|]$ )
10:     $c \leftarrow$  MAX-SUM( $A[1\dots m]$ )
11:     $d \leftarrow$  MAX-SUM( $A[m + 1\dots |A|]$ )
12:    return MAX( $a + b, c, d$ )

```

```

13: function MAX-FROM( $A$ )
14:    $sum \leftarrow 0, m \leftarrow 0$ 
15:   for  $i \leftarrow 1$  to  $|A|$  do
16:      $sum \leftarrow sum + A[i]$ 
17:      $m \leftarrow$  MAX( $m, sum$ )
18:   return  $m$ 

```

It's easy to deduce the time performance is $T(n) = 2T(n/2) + O(n)$. Implement this algorithm in your favorite programming language.

- Given a $m \times n$ matrix contains positive and negative numbers, find the sub metrics with maximum sum of its elements.
- Given n non-negative integers representing an elevation map where the width of each bar is 1, compute how much water it is able to trap after raining. Figure 14.25 shows an example. For example, Given $\{0, 1, 0, 2, 1, 0, 1, 3, 2, 1, 2, 1\}$, the result is 6.
- Explain why KMP algorithm perform in linear time even in the seemed 'worst' case.

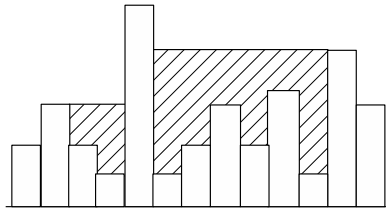


Figure 14.25: Shaded areas are waters.

- Implement the purely functional KMP algorithm by using reversed P_p to avoid the linear time appending operation.
- Deduce the state of the tree $left(right(right(right(T))))$ when searching ‘anonym’ in text ‘anal’.

14.3 Solution searching

One interesting thing that computer programming can offer is solving puzzles. In the early phase of classic artificial intelligent, people developed many methods to search for solutions. Different from the sequence searching and string matching, the solution doesn’t obviously exist among a candidates set. It typically need construct the solution while trying varies of attempts. Some problems are solvable, while others are not. Among the solvable problems, not all of them just have one unique solution. For example, a maze may have multiple ways out. People sometimes need search for the best one.

14.3.1 DFS and BFS

DFS and BFS stand for deep-first search and breadth-first search. They are typically introduced as graph algorithms in textbooks. Graph is a comprehensive topic which is hard to be covered in this elementary book. In this section, we’ll show how to use DFS and BFS to solve some real puzzles without formal introduction about the graph concept.

Maze

Maze is a classic and popular puzzle. Maze is amazing to both kids and adults. Figure 14.26 shows an example maze. There are also real maze gardens can be found in parks for fun. In the late 1990s, maze-solving games were quite often hold in robot mouse competition all over the world.

There are multiple methods to solve maze puzzle. We’ll introduce an effective, yet not the best one in this section. There are some well known sayings about how to find the way out in maze, while not all of them are true.

For example, one method states that, wherever you have multiple ways, always turn right. This doesn’t work as shown in figure 14.27. The obvious solution is first to go along the top horizontal line, then turn right, and keep going ahead at the ‘T’ section. However, if we always turn right, we’ll endless loop around the inner big block.

This example tells us that the decision when there are multiple choices matters the solution. Like the fairy tale we read in our childhood, we can take some bread crumbs in a maze. When there are multiple ways, we can simply select one, left a piece of bread

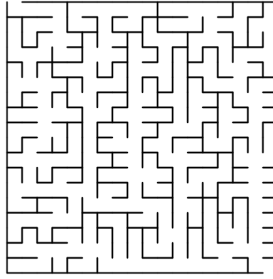


Figure 14.26: A maze

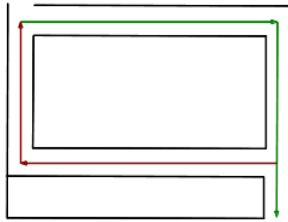


Figure 14.27: It leads to loop way if always turns right.

crumbs to mark this attempt. If we enter a dead end, we go back to the last place where we've made a decision by back-tracking the bread crumbs. Then we can alter to another way.

At any time, if we find there have been already bread crumbs left, it means we have entered a loop, we must go back and try different ways. Repeat these try-and-check steps, we can either find the way out, or give the 'no solution' fact. In the later case, we back-track to the start point.

One easy way to describe a maze, is by a $m \times n$ matrix, each element is either 0 or 1, which indicates if there is a way at this cell. The maze illustrated in figure 14.27 can be defined as the following matrix.

0	0	0	0	0	0
0	1	1	1	1	0
0	1	1	1	1	0
0	1	1	1	1	0
0	1	1	1	1	0
0	0	0	0	0	0
1	1	1	1	1	0

Given a start point $s = (i, j)$, and a goal $e = (p, q)$, we need find all solutions, that are the paths from s to e .

There is an obviously recursive exhaustive search method. That in order to find all paths from s to e , we can check all connected points to s , for every such point k , we recursively find all paths from k to e . This method can be illustrated as the following.

- Trivial case, if the start point s is as same as the target point e , we are done;
- Otherwise, for every connected point k to s , recursively find the paths from k to e ; If e can be reached via k , put section $s-k$ in front of each path between k and e .

However, we have to leave 'bread crumbs' to avoid repeatedly trying the same attempts. This is because otherwise in the recursive case, we start from s , find a connected point k , then we further try to find paths from k to e . Since s is connected to k as well, so in the next recursion, we'll try to find paths from s to e again. It turns to be the very same origin problem, and we are trapped in infinite recursions.

Our solution is to initialize an empty list, use it to record all the points we've visited so far. For every connected point, we look up the list to examine if it has already been visited. We skip all the visited candidates and only try those new ones. The corresponding algorithm can be defined like this.

$$\text{solveMaze}(m, s, e) = \text{solve}(s, \{\phi\}) \quad (14.47)$$

Where m is the matrix which defines a maze, s is the start point, and e is the end point. Function solve is defined in the context of solveMaze , so that the maze and the end point can be accessed. It can be realized recursively like what we described above⁸.

$$\text{solve}(s, P) = \begin{cases} \{\{s\} \cup p \mid p \in P\} & : s = e \\ \text{concat}(\{ \text{solve}(s', \{\{s\} \cup p \mid p \in P\}) \mid & : \text{otherwise} \\ s' \in \text{adj}(s), \neg \text{visited}(s') \}) & \end{cases} \quad (14.48)$$

Note that P also serves as an accumulator. Every connected point is recorded in all the possible paths to the current position. But they are stored in reversed order, that is the newly visited point is put to the head of all the lists, and the starting point is the last one. This is because the appending operation is linear ($O(n)$, where n is the number of elements stored in a list), while linking to the head is just constant time. We can output the result in correct order by reversing all possible solutions in equation (14.47)⁹:

$$\text{solveMaze}(m, s, e) = \text{map}(\text{reverse}, \text{solve}(s, \{\phi\})) \quad (14.49)$$

We need define functions $\text{adj}(p)$ and $\text{visited}(p)$, which finds all the connected points to p , and tests if point p has been visited respectively. Two points are connected if and only if they are next cells horizontally or vertically in the maze matrix, and both have zero value.

$$\text{adj}((x, y)) = \{(x', y') \mid (x', y') \in \{(x-1, y), (x+1, y), (x, y-1), (x, y+1)\}, \\ 1 \leq x' \leq M, 1 \leq y' \leq N, m_{x'y'} = 0\} \quad (14.50)$$

Where M and N are the widths and heights of the maze.

Function $\text{visited}(p)$ examines if point p has been recorded in any lists in P .

$$\text{visited}(p) = \exists \text{path} \in P, p \in \text{path} \quad (14.51)$$

The following Haskell example code implements this algorithm.

```

solveMaze m from to = map reverse $ solve from [[]] where
  solve p paths | p == to = map (p:) paths
                | otherwise = concat [solve p' (map (p:) paths) |
                                      p' <- adjacent p,
                                      not $ visited p' paths]

adjacent (x, y) = [(x', y') |
                  (x', y') <- [(x-1, y), (x+1, y), (x, y-1), (x, y+1)],
                  inRange (bounds m) (x', y'),
                  m ! (x', y') == 0]

visited p paths = any (p `elem`) paths

```

⁸Function concat can flatten a list of lists. For example. $\text{concat}(\{\{a, b, c\}, \{x, y, z\}\}) = \{a, b, c, x, y, z\}$. Refer to appendix A for detail.

⁹the detailed definition of reverse can be found in the appendix A.

For a maze defined as matrix like below example, all the solutions can be given by this program.

```

mz = [[0, 0, 1, 0, 1, 1],
      [1, 0, 1, 0, 1, 1],
      [1, 0, 0, 0, 0, 0],
      [1, 1, 0, 1, 1, 1],
      [0, 0, 0, 0, 0, 0],
      [0, 0, 0, 1, 1, 0]]

maze = listArray ((1,1), (6, 6)) o concat

solveMaze (maze mz) (1,1) (6, 6)

```

As we mentioned, this is a style of 'exhaustive search'. It recursively searches all the connected points as candidates. In a real maze solving game, a robot mouse competition for instance, it's enough to just find a route. We can adapt to a method close to what described at the beginning of this section. The robot mouse always tries the first connected point, and skip the others until it gets stuck. We need some data structure to store the 'bread crumbs', which help to remember the decisions being made. As we always attempt to find the way on top of the latest decision, it is the last-in, first-out manner. A stack can be used to realize it.

At the very beginning, only the starting point s is stored in the stack. we pop it out, find, for example, points a , and b , are connected to s . We push the two possible paths: $\{a, s\}$ and $\{b, s\}$ to the stack. Next we pop $\{a, s\}$ out, and examine connected points to a . Then all the paths with 3 steps will be pushed back. We repeat this process. At anytime, each element stored in the stack is a path, from the starting point to the farthest place can arrive in the reversed order. This can be illustrated in figure 14.28.

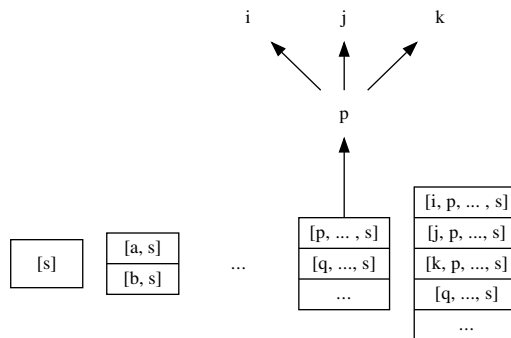


Figure 14.28: The stack is initialized with a singleton list of the starting point s . s is connected with point a and b . Paths $\{a, s\}$ and $\{b, s\}$ are pushed back. In some step, the path ended with point p is popped. p is connected with points i , j , and k . These 3 points are expanded as different options and pushed back to the stack. The candidate path ended with q won't be examined unless all the options above fail.

The stack can be realized with a list. The latest option is picked from the head, and the new candidates are also added to the head. The maze puzzle can be solved by using such a list of paths:

$$\text{solveMaze}'(m, s, e) = \text{reverse}(\text{solve}'(\{\{s\}\})) \quad (14.52)$$

As we are searching the first, but not all the solutions, *map* isn't used here. When the stack is empty, it means that we've tried all the options and failed to find a way out.

There is no solution; otherwise, the top option is popped, expanded with all the adjacent points which haven't been visited before, and pushed back to the stack. Denote the stack as S , if it isn't empty, the top element is s_1 , and the new stack after the top being popped as S' . s_1 is a list of points represents path P . Denote the first point in this path as p_1 , and the rest as P' . The solution can be formalized as the following.

$$\text{solve}'(S) = \begin{cases} \phi & : S = \phi \\ s_1 & : s_1 = e \\ \text{solve}'(S') & : C = \{c | c \in \text{adj}(p_1), c \notin P'\} = \phi \\ \text{solve}'(\{\{p\} \cup P | p \in C\} \cup S) & : \text{otherwise}, C \neq \phi \end{cases} \quad (14.53)$$

Where the *adj* function is defined above. This updated maze solution can be implemented with the below example Haskell program ¹⁰.

```
dfsSolve m from to = reverse $ solve [[from]] where
  solve [] = []
  solve (c@(p:path):cs)
    | p == to = c — stop at the first solution
    | otherwise = let os = filter (`notElem` path) (adjacent p) in
                  if os == []
                  then solve cs
                  else solve ((map (:c) os) ++ cs)
```

It's quite easy to modify this algorithm to find all solutions. When we find a path in the second clause, instead of returning it immediately, we record it and go on checking the rest memorized options in the stack till until the stack becomes empty. We left it as an exercise to the reader.

The same idea can also be realized imperatively. We maintain a stack to store all possible paths from the starting point. In each iteration, the top option path is popped, if the farthest position is the end point, a solution is found; otherwise, all the adjacent, not visited yet points are appended as new paths and pushed back to the stack. This is repeated till all the candidate paths in the stacks are checked.

We use the same notation to represent the stack S . But the paths will be stored as arrays instead of list in imperative settings as the former is more effective. Because of this the starting point is the first element in the path array, while the farthest reached place is the right most element. We use p_n to represent $\text{LAST}(P)$ for path P . The imperative algorithm can be given as below.

```
1: function SOLVE-MAZE( $m, s, e$ )
2:    $S \leftarrow \phi$ 
3:   PUSH( $S, \{s\}$ )
4:    $L \leftarrow \phi$  ▷ the result list
5:   while  $S \neq \phi$  do
6:      $P \leftarrow \text{POP}(S)$ 
7:     if  $e = p_n$  then
8:       ADD( $L, P$ )
9:     else
10:      for  $\forall p \in \text{ADJACENT}(m, p_n)$  do
11:        if  $p \notin P$  then
12:          PUSH( $S, P \cup \{p\}$ )
13:   return  $L$ 
```

The following example Python program implements this maze solving algorithm.

```
def solve(m, src, dst):
```

¹⁰The same code of *adjacent* function is skipped

```

stack = [[src]]
s = []
while stack != []:
    path = stack.pop()
    if path[-1] == dst:
        s.append(path)
    else:
        for p in adjacent(m, path[-1]):
            if not p in path:
                stack.append(path + [p])
return s

def adjacent(m, p):
    (x, y) = p
    ds = [(0, 1), (0, -1), (1, 0), (-1, 0)]
    ps = []
    for (dx, dy) in ds:
        x1 = x + dx
        y1 = y + dy
        if 0 <= x1 and x1 < len(m[0]) and
           0 <= y1 and y1 < len(m) and m[y][x] == 0:
            ps.append((x1, y1))
    return ps

```

And the same maze example given above can be solved by this program like the following.

```

mz = [[0, 0, 1, 0, 1, 1],
       [1, 0, 1, 0, 1, 1],
       [1, 0, 0, 0, 0, 0],
       [1, 1, 0, 1, 1, 1],
       [0, 0, 0, 0, 0, 0],
       [0, 0, 0, 1, 1, 0]]

solve(mz, (0, 0), (5,5))

```

It seems that in the worst case, there are 4 options (up, down, left, and right) at each step, each option is pushed to the stack and eventually examined during backtracking. Thus the complexity is bound to $O(4^n)$. The actual time won't be so large because we filtered out the places which have been visited before. In the worst case, all the reachable points are visited exactly once. So the time is bound to $O(n)$, where n is the number of points connected in total. As a stack is used to store candidate solutions, the space complexity is $O(n^2)$.

Eight queens puzzle

The eight queens puzzle is also a famous problem. Although chess has very long history, this puzzle was first published in 1848 by Max Bezzel[89]. Queen in the chess game is quite powerful. It can attack any other pieces in the same row, column and diagonal at any distance. The puzzle is to find a solution to put 8 queens in the board, so that none of them attack each other. Figure 14.29 (a) illustrates the places can be attacked by a queen and 14.29 (b) shows a solution of 8 queens puzzle.

It's obviously that the puzzle can be solved by brute-force, which takes P_{64}^8 times. This number is about 4×10^{10} . It can be easily improved by observing that, no two queens can be in the same row, and each queen must be put on one column between 1 to 8. Thus we can represent the arrangement as a permutation of $\{1, 2, 3, 4, 5, 6, 7, 8\}$. For instance, the arrangement $\{6, 2, 7, 1, 3, 5, 8, 4\}$ means, we put the first queen at row 1, column 6, the second queen at row 2 column 2, ..., and the last queen at row 8, column 4. By this means, we need only examine $8! = 40320$ possibilities.

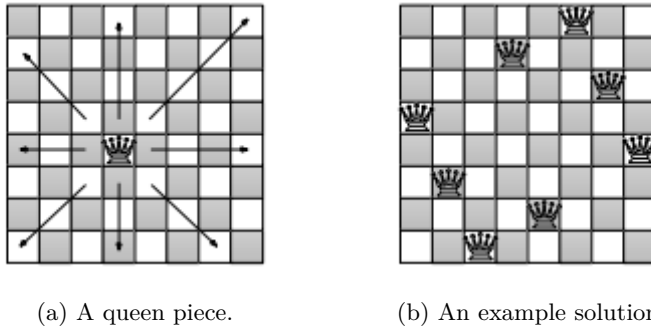


Figure 14.29: The eight queens puzzle.

We can find better solutions than this. Similar to the maze puzzle, we put queens one by one from the first row. For the first queen, there are 8 options, that we can put it at one of the eight columns. Then for the next queen, we again examine the 8 candidate columns. Some of them are not valid because those positions will be attacked by the first queen. We repeat this process, for the i -th queen, we examine the 8 columns in row i , find which columns are safe. If none column is valid, it means all the columns in this row will be attacked by some queen we've previously arranged, we have to backtrack as what we did in the maze puzzle. When all the 8 queens are successfully put to the board, we find a solution. In order to find all the possible solutions, we need record it and go on to examine other candidate columns and perform back tracking if necessary. This process terminates when all the columns in the first row have been examined. The below equation starts the search.

$$\text{solve}(\{\phi\}, \phi) \quad (14.54)$$

In order to manage the candidate attempts, a stack S is used as same as in the maze puzzle. The stack is initialized with one empty element. And a list L is used to record all possible solutions. Denote the top element in the stack as s_1 . It's actually an intermediate state of assignment, which is a partial permutation of 1 to 8. after pops s_1 , the stack becomes S' . The solve function can be defined as the following.

$$\text{solve}(S, L) = \begin{cases} L : S = \phi \\ \text{solve}(S', \{s_1\} \cup L) : |s_1| = 8 \\ \text{solve}\left(\left\{ \begin{array}{l} \{i\} \cup s_1 \mid i \in [1, 8], \\ i \notin s_1, \\ \text{safe}(i, s_1) \end{array} \right\} \cup S', L\right) : \text{otherwise} \end{cases} \quad (14.55)$$

If the stack is empty, all the possible candidates have been examined, it's not possible to backtrack any more. L has been accumulated all found solutions and returned as the result; Otherwise, if the length of the top element in the stack is 8, a valid solution is found. We add it to L , and go on finding other solutions; If the length is less than 8, we need try to put the next queen. Among all the columns from 1 to 8, we pick those not already occupied by previous queens (through the $i \notin s_1$ clause), and must not be attacked in diagonal direction (through the safe predication). The valid assignments will be pushed to the stack for the further searching.

Function $\text{safe}(x, C)$ detects if the assignment of a queen in position x will be attacked by other queens in C in diagonal direction. There are 2 possible cases, 45° and 135° directions. Since the row of this new queen is $y = 1 + |C|$, where $|C|$ is the length of C , the safe function can be defined as the following.

$$\text{safe}(x, C) = \forall (c, r) \in \text{zip}(\text{reverse}(C), \{1, 2, \dots\}), |x - c| \neq |y - r| \quad (14.56)$$

Where *zip* takes two lists, and pairs every elements in them to a new list. Thus If $C = \{c_{i-1}, c_{i-2}, \dots, c_2, c_1\}$ represents the column of the first $i-1$ queens has been assigned, the above function will check list of pairs $\{(c_1, 1), (c_2, 2), \dots, (c_{i-1}, i-1)\}$ with position (x, y) forms any diagonal lines.

Translating this algorithm into Haskell gives the below example program.

```
solve = dfsSolve [[]] [] where
  dfsSolve [] s = s
  dfsSolve (c:cs) s
    | length c == 8 = dfsSolve cs (c:s)
    | otherwise = dfsSolve ([ (x:c) | x <- [1..8] \\ c,
                             not $ attack x c] ++ cs) s
  attack x cs = let y = 1 + length cs in
                 any (\(c, r) -> abs(x - c) == abs(y - r)) $
                 zip (reverse cs) [1..]
```

Observing that the algorithm is tail recursive, it's easy to transform it into imperative realization. Instead of using list, we use array to represent queens assignment. Denote the stack as S , and the possible solutions as A . The imperative algorithm can be described as the following.

```
1: function SOLVE-QUEENS
2:    $S \leftarrow \{\phi\}$ 
3:    $L \leftarrow \phi$  ▷ The result list
4:   while  $S \neq \phi$  do
5:      $A \leftarrow \text{POP}(S)$  ▷  $A$  is an intermediate assignment
6:     if  $|A| = 8$  then
7:       ADD( $L, A$ )
8:     else
9:       for  $i \leftarrow 1$  to 8 do
10:        if VALID( $i, A$ ) then
11:          PUSH( $S, A \cup \{i\}$ )
12:   return  $L$ 
```

The stack is initialized with the empty assignment. The main process repeatedly pops the top candidate from the stack. If there are still queens left, the algorithm examines possible columns in the next row from 1 to 8. If a column is safe, that it won't be attacked by any previous queens, this column will be appended to the assignment, and pushed back to the stack. Different from the functional approach, since array, but not list, is used, we needn't reverse the solution assignment any more.

Function VALID checks if column x is safe with previous queens put in A . It filters out the columns have already been occupied, and calculates if any diagonal lines are formed with existing queens.

```
1: function VALID( $x, A$ )
2:    $y \leftarrow 1 + |A|$ 
3:   for  $i \leftarrow 1$  to  $|A|$  do
4:     if  $x = A[i] \vee |y - i| = |x - A[i]|$  then
5:       return False
6:   return True
```

The following Python example program implements this imperative algorithm.

```
def solve():
  stack = [[]]
  s = []
  while stack != []:
    a = stack.pop()
    if len(a) == 8:
      s.append(a)
```

```

    else:
        for i in range(1, 9):
            if valid(i, a):
                stack.append(a+[i])
    return s

def valid(x, a):
    y = len(a) + 1
    for i in range(1, y):
        if x == a[i-1] or abs(y - i) == abs(x - a[i-1]):
            return False
    return True

```

Although there are 8 optional columns for each queen, not all of them are valid and thus further expanded. Only those columns haven't been occupied by previous queens are tried. The algorithm only examines 15720, which is far less than $8^8 = 16777216$, possibilities [89].

It's quite easy to extend the algorithm, so that it can solve n queens puzzle, where $n \geq 4$. However, the time cost increases fast. The backtrack algorithm is just slightly better than the one permuting the sequence of 1 to 8 (which is bound to $o(n!)$). Another extension to the algorithm is based on the fact that the chess board is square, which is symmetric both vertically and horizontally. Thus a solution can generate other solutions by rotating and flipping. These aspects are left as exercises to the reader.

Peg puzzle

I once received a puzzle of the leap frogs. It said to be homework for 2nd grade student in China. As illustrated in figure 14.30, there are 6 frogs in 7 stones. Each frog can either hop to the next stone if it is not occupied, or leap over one frog to another empty stone. The frogs on the left side can only move to the right, while the ones on the right side can only move to the left. These rules are described in figure 14.31

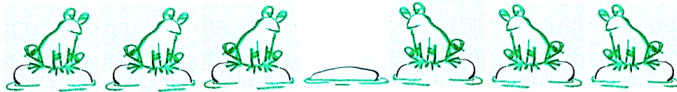


Figure 14.30: The leap frogs puzzle.

The goal of this puzzle is to arrange the frogs to jump according to the rules, so that the positions of the 3 frogs on the left are finally exchange with the ones on the right. If we denote the frog on the left as 'A', on the right as 'B', and the empty stone as 'O'. The puzzle is to find a solution to transform from 'AAAOBBB' to 'BBBOAAA'.

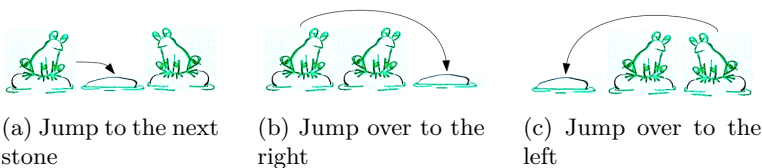


Figure 14.31: Moving rules.

This puzzle is just a special form of the peg puzzles. The number of pegs is not limited to 6. it can be 8 or other bigger even numbers. Figure 14.32 shows some variants.

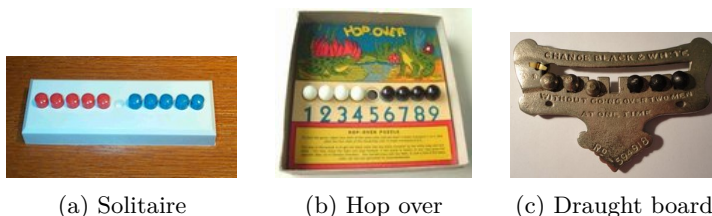


Figure 14.32: Variants of the peg puzzles from <http://home.comcast.net/stegman-n/jumping.htm>

We can solve this puzzle by programming. The idea is similar to the 8 queens puzzle. Denote the positions from the left most stone as 1, 2, ..., 7. In ideal cases, there are 4 options to arrange the move. For example when start, the frog on 3rd stone can hop right to the empty stone; symmetrically, the frog on the 5th stone can hop left; Alternatively, the frog on the 2nd stone can leap right, while the frog on the 6th stone can leap left.

We can record the state and try one of these 4 options at every step. Of course not all of them are possible at any time. If get stuck, we can backtrack and try other options.

As we restrict the left side frogs only moving to the right, and the right frogs only moving to the left, the moves are not reversible. There won't be any repetition cases as what we have to deal with in the maze puzzle. However, we still need record the steps in order to print them out finally.

In order to enforce these restriction, let A, O, B in representation 'AAAOBBB' be -1, 0, and 1 respectively. A state L is a list of elements, each element is one of these 3 values. It starts from $\{-1, -1, -1, 0, 1, 1, 1\}$. $L[i]$ access the i -th element, its value indicates if the i -th stone is empty, occupied by a frog from left side, or occupied by a frog from right side. Denote the position of the vacant stone as p . The 4 moving options can be stated as below.

- Leap left: $p < 6$ and $L[p + 2] > 0$, swap $L[p] \leftrightarrow L[p + 2]$;
- Hop left: $p < 7$ and $L[p + 1] > 0$, swap $L[p] \leftrightarrow L[p + 1]$;
- Leap right: $p > 2$ and $L[p - 2] < 0$, swap $L[p - 2] \leftrightarrow L[p]$;
- Hop right: $p > 1$ and $L[p - 1] < 0$, swap $L[p - 1] \leftrightarrow L[p]$.

Four functions $leap_l(L)$, $hop_l(L)$, $leap_r(L)$ and $hop_r(L)$ are defined accordingly. If the state L does not satisfy the move restriction, these function return L unchanged, otherwise, the changed state L' is returned accordingly.

We can also explicitly maintain a stack S to the attempts as well as the historic movements. The stack is initialized with a singleton list of starting state. The solution is accumulated to a list M , which is empty at the beginning:

$$solve(\{\{-1, -1, -1, 0, 1, 1, 1\}\}, \phi) \quad (14.57)$$

As far as the stack isn't empty, we pop one intermediate attempt. If the latest state is equal to $\{1, 1, 1, 0, -1, -1, -1\}$, a solution is found. We append the series of moves till this state to the result list M ; otherwise, We expand to next possible state by trying all four possible moves, and push them back to the stack for further search. Denote the top

element in the stack S as s_1 , and the latest state in s_1 as L . The algorithm can be defined as the following.

$$\text{solve}(S, M) = \begin{cases} M & : S = \phi \\ \text{solve}(S', \{\text{reverse}(s_1)\} \cup M) & : L = \{1, 1, 1, 0, -1, -1, -1\} \\ \text{solve}(P \cup S', M) & : \text{otherwise} \end{cases} \quad (14.58)$$

Where P are possible moves from the latest state L :

$$P = \{L' | L' \in \{\text{leap}_l(L), \text{hop}_l(L), \text{leap}_r(L), \text{hop}_r(L)\}, L \neq L'\}$$

Note that the starting state is stored as the last element, while the final state is the first. That is the reason why we reverse it when adding to solution list.

Translating this algorithm to Haskell gives the following example program.

```
solve = dfsSolve [[[-1, -1, -1, 0, 1, 1, 1]]] [] where
  dfsSolve [] s = s
  dfsSolve (c:cs) s
    | head c == [1, 1, 1, 0, -1, -1, -1] = dfsSolve cs (reverse c:s)
    | otherwise = dfsSolve ((map (:c) $ moves $ head c) ++ cs) s

moves s = filter (/=s) [leapLeft s, hopLeft s, leapRight s, hopRight s] where
  leapLeft [] = []
  leapLeft (0:y:1:ys) = 1:y:0:ys
  leapLeft (y:ys) = y:leapLeft ys
  hopLeft [] = []
  hopLeft (0:1:ys) = 1:0:ys
  hopLeft (y:ys) = y:hopLeft ys
  leapRight [] = []
  leapRight (-1:y:0:ys) = 0:y:(-1):ys
  leapRight (y:ys) = y:leapRight ys
  hopRight [] = []
  hopRight (-1:0:ys) = 0:(-1):ys
  hopRight (y:ys) = y:hopRight ys
```

Running this program finds 2 symmetric solutions, each takes 15 steps. One solution is list in the below table.

step	-1	-1	-1	0	1	1	1
1	-1	-1	0	-1	1	1	1
2	-1	-1	1	-1	0	1	1
3	-1	-1	1	-1	1	0	1
4	-1	-1	1	0	1	-1	1
5	-1	0	1	-1	1	-1	1
6	0	-1	1	-1	1	-1	1
7	1	-1	0	-1	1	-1	1
8	1	-1	1	-1	0	-1	1
9	1	-1	1	-1	1	-1	0
10	1	-1	1	-1	1	0	-1
11	1	-1	1	0	1	-1	-1
12	1	0	1	-1	1	-1	-1
13	1	1	0	-1	1	-1	-1
14	1	1	1	-1	0	-1	-1
15	1	1	1	0	-1	-1	-1

Observe that the algorithm is in tail recursive manner, it can also be realized imperatively. The algorithm can be more generalized, so that it solve the puzzles of n frogs on each side. We represent the start state $\{-1, -1, \dots, -1, 0, 1, 1, \dots, 1\}$ as s , and the mirrored end state as e .

1: **function** SOLVE(s, e)

```

2:  S ← {{s}}
3:  M ← φ
4:  while S ≠ φ do
5:    s1 ← POP(S)
6:    if s1[1] = e then
7:      ADD(M, REVERSE(s1))
8:    else
9:      for ∀m ∈ MOVES(s1[1]) do
10:        PUSH(S, {m} ∪ s1)
11:  return M

```

The possible moves can be also generalized with procedure MOVES to handle arbitrary number of frogs. The following Python program implements this solution.

```

def solve(start, end):
    stack = [[start]]
    s = []
    while stack ≠ []:
        c = stack.pop()
        if c[0] == end:
            s.append(reversed(c))
        else:
            for m in moves(c[0]):
                stack.append([m]+c)
    return s

def moves(s):
    ms = []
    n = len(s)
    p = s.index(0)
    if p < n - 2 and s[p+2] > 0:
        ms.append(swap(s, p, p+2))
    if p < n - 1 and s[p+1] > 0:
        ms.append(swap(s, p, p+1))
    if p > 1 and s[p-2] < 0:
        ms.append(swap(s, p, p-2))
    if p > 0 and s[p-1] < 0:
        ms.append(swap(s, p, p-1))
    return ms

def swap(s, i, j):
    a = s[:]
    (a[i], a[j]) = (a[j], a[i])
    return a

```

For 3 frogs in each side, we know that it takes 15 steps to exchange them. It's interesting to examine the table that how many steps are needed along with the number of frogs in each side. Our program gives the following result.

number of frogs	1	2	3	4	5	...
number of steps	3	8	15	24	35	...

It seems that the number of steps are all square numbers minus one. It's natural to guess that the number of steps for n frogs in one side is $(n + 1)^2 - 1$. Actually we can prove it is true.

Compare to the final state and the start state, each frog moves ahead $n + 1$ stones in its opposite direction. Thus total $2n$ frogs move $2n(n + 1)$ stones. Another important fact is that each frog on the left has to meet every one on the right one time. And leap will happen when meets. Since the frog moves two stones ahead by leap, and there are total n^2 meets happen, so that all these meets cause moving $2n^2$ stones ahead. The rest moves are not leap, but hop. The number of hops are $2n(n + 1) - 2n^2 = 2n$. Sum up all n^2 leaps and $2n$ hops, the total number of steps are $n^2 + 2n = (n + 1)^2 - 1$.

Summary of DFS

Observe the above three puzzles, although they vary in many aspects, their solutions show quite similar common structures. They all have some starting state. The maze starts from the entrance point; The 8 queens puzzle starts from the empty board; The leap frogs start from the state of 'AAAOBBB'. The solution is a kind of searching, at each attempt, there are several possible ways. For the maze puzzle, there are four different directions to try; For the 8 queens puzzle, there are eight columns to choose; For the leap frogs puzzle, there are four movements of leap or hop. We don't know how far we can go when make a decision, although the final state is clear. For the maze, it's the exit point; For the 8 queens puzzle, we are done when all the 8 queens being assigned on the board; For the leap frogs puzzle, the final state is that all frogs exchanged.

We use a common approach to solve them. We repeatedly select one possible candidate to try, record where we've achieved; If we get stuck, we backtrack and try other options. We are sure by using this strategy, we can either find a solution, or tell that the problem is unsolvable.

Of course there can be some variation, that we can stop when find one answer, or go on searching all the solutions.

If we draw a tree rooted at the starting state, expand it so that every branch stands for a different attempt, our searching process is in a manner, that it searches deeper and deeper. We won't consider any other options in the same depth unless the searching fails so that we've to backtrack to upper level of the tree. Figure 14.33 illustrates the order we search a state tree. The arrow indicates how we go down and backtrack up. The number of the nodes shows the order we visit them.

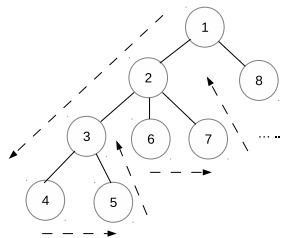


Figure 14.33: Example of DFS search order.

This kind of search strategy is called 'DFS' (Deep-first-search). We widely use it unintentionally. Some programming environments, Prolog for instance, adopt DFS as the default evaluation model. A maze is given by a set of rule base, such as:

```

c(a, b). c(a, e).
c(b, c). c(b, f).
c(e, d), c(e, f).
c(f, c).
c(g, d). c(g, h).
c(h, f).

```

Where predicate $c(X, Y)$ means place X is connected with Y . Note that this is a directed predicate, we can make Y to be connected with X as well by either adding a symmetric rule, or create a undirected predicate. Figure 14.34 shows such a directed graph. Given two places X and Y , Prolog can tell if they are connected by the following program.

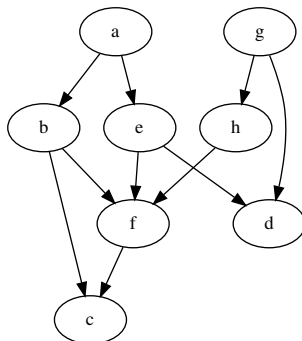


Figure 14.34: A directed graph.

```

go(X, X).
go(X, Y) :- c(X, Z), go(Z, Y)

```

This program says that, a place is connected with itself. Given two different places X and Y , if X is connected with Z , and Z is connected with Y , then X is connected with Y . Note that, there might be multiple choices for Z . Prolog selects a candidate, and go on further searching. It only tries other candidates if the recursive searching fails. In that case, Prolog backtracks and tries other alternatives. This is exactly what DFS does.

DFS is quite straightforward when we only need a solution, but don't care if the solution takes the fewest steps. For example, the solution it gives, may not be the shortest path for the maze. We'll see some more puzzles next. They demands to find the solution with the minimum attempts.

The wolf, goat, and cabbage puzzle

This puzzle says that a farmer wants to cross a river with a wolf, a goat, and a bucket of cabbage. There is a boat. Only the farmer can drive it. But the boat is small. it can only hold one of the wolf, the goat, and the bucket of cabbage with the farmer at a time. The farmer has to pick them one by one to the other side of the river. However, the wolf would eat the goat, and the goat would eat the cabbage if the farmer is absent. The puzzle asks to find the fast solution so that they can all safely go cross the river.

The key point to this puzzle is that the wolf does not eat the cabbage. The farmer can safely pick the goat to the other side. But next time, no matter if he pick the wolf or the cabbage to cross the river, he has to take one back to avoid the conflict. In order to find the fast the solution, at any time, if the farmer has multiple options, we can examine all of them in parallel, so that these different decisions compete. If we count the number of the times the farmer cross the river without considering the direction, that crossing the river back and forth means 2 times, we are actually checking the complete possibilities after 1 time, 2 times, 3 times, ... When we find a situation, that they all arrive at the other bank, we are done. And this solution wins the competition, which is the fast solution.

The problem is that we can't examine all the possible solutions in parallel ideally. Even with a super computer equipped with many CPU cores, the setup is too expensive to solve such a simple puzzle.

Let's consider a lucky draw game. People blindly pick from a box with colored balls. There is only one black ball, all the others are white. The one who pick the black ball wins the game; Otherwise, he must return the ball to the box and wait for the next chance. In order to be fair enough, we can setup a rule that no one can try the second time before all others have tried. We can line people to a queue. Every time the first guy pick a ball,



Figure 14.35: The wolf, goat, cabbage puzzle

if he does not win, he then stands at the tail of the queue to wait for the second try. This queue helps to ensure our rule.

We can use the quite same idea to solve our puzzle. The two banks of the river can be represented as two sets A and B . A contains the wolf, the goat, the cabbage and the farmer; while B is empty. We take an element along with the farmer from one set to the other each time. The two sets can't hold conflict things if the farmer is absent. The goal is to exchange the contents of A and B with fewest steps.

We initialize a queue with state $A = \{w, g, c, p\}$, $B = \phi$ as the only element. As far as the queue isn't empty, we pick the first element from the head, expand it with all possible options, and put these new expanded candidates to the tail of the queue. If the first element on the head is the final goal, that $A = \phi$, $B = \{w, g, c, p\}$, we are done. Figure 14.37 illustrates the idea of this search order. Note that as all possibilities in the same level are examined, there is no need for back-tracking.

There is a simple way to treat the set. A four bits binary number can be used, each bit stands for a thing, for example, the wolf $w = 1$, the goat $g = 2$, the cabbage $c = 4$, and the farmer $p = 8$. That 0 stands for the empty set, 15 stands for a full set. Value 3, solely means there are a wolf and a goat on the river bank. In this case, the wolf will eat the goat. Similarly, value 6 stands for another conflicting case. Every time, we move the highest bit (which is 8), or together with one of the other bits (4 or 2, or 1) from one number to the other. The possible moves can be defined as below.

$$mv(A, B) = \begin{cases} \{(A - 8 - i, B + 8 + i) | i \in \{0, 1, 2, 4\}, i = 0 \vee A\bar{\wedge}i \neq 0\} & : B < 8 \\ \{(A + 8 + i, B - 8 - i) | i \in \{0, 1, 2, 4\}, i = 0 \vee B\bar{\wedge}i \neq 0\} & : \textit{Otherwise} \end{cases} \quad (14.59)$$

Where $\bar{\wedge}$ is the bitwise-and operation.

the solution can be given by reusing the queue defined in previous chapter. Denote the queue as Q , which is initialed with a singleton list $\{(15, 0)\}$. If Q is not empty, function $DeQ(Q)$ extracts the head element M , the updated queue becomes Q' . M is a list of pairs, stands for a series of movements between the river banks. The first element in $m_1 = (A', B')$ is the latest state. Function $EnQ'(Q, L)$ is a slightly different enqueue operation. It pushes all the possible moving sequences in L to the tail of the queue one by one and returns the updated queue. With these notations, the solution function is

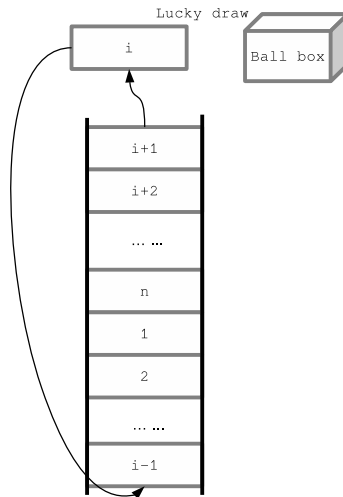


Figure 14.36: A lucky-draw game, the i -th person goes from the queue, pick a ball, then join the queue at tail if he fails to pick the black ball.

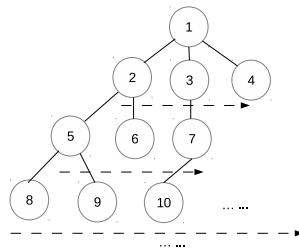


Figure 14.37: Start from state 1, check all possible options 2, 3, and 4 for next step; then all nodes in level 3, ...

defined like below.

$$\text{solve}(Q) = \begin{cases} \phi & : Q = \phi \\ \text{reverse}(M) & : A' = 0 \\ \text{solve}(\text{En}Q'(Q', \left\{ \{m\} \cup M \mid \begin{array}{l} m \in \text{mv}(m_1), \\ \text{valid}(m, M) \end{array} \right\})) & : \text{otherwise} \end{cases} \quad (14.60)$$

Where function $\text{valid}(m, M)$ checks if the new moving candidate $m = (A'', B'')$ is valid. That neither A'' nor B'' is 3 or 6, and m hasn't been tried before in M to avoid any repeatedly attempts.

$$\text{valid}(m, M) = A'' \neq 3, A'' \neq 6, B'' \neq 3, B'' \neq 6, m \notin M \quad (14.61)$$

The following example Haskell program implements this solution. Note that it uses a plain list to represent the queue for illustration purpose.

```
import Data.Bits

solve = bfsSolve [[(15, 0)]] where
  bfsSolve :: [[(Int, Int)]] -> [(Int, Int)]
  bfsSolve [] = [] -- no solution
  bfsSolve (c:cs) | (fst $ head c) == 0 = reverse c
                  | otherwise = bfsSolve (cs ++ map (:c)
                                          (filter (\valid` c) $ moves $ head c))
  valid (a, b) r = not $ or [ a `elem` [3, 6], b `elem` [3, 6],
                              (a, b) `elem` r ]

moves (a, b) = if b < 8 then trans a b else map swap (trans b a) where
  trans x y = [(x - 8 - i, y + 8 + i)
               | i <- [0, 1, 2, 4], i == 0 || (x .&. i) /= 0]
  swap (x, y) = (y, x)
```

This algorithm can be easily modified to find all the possible solutions, but not just stop after finding the first one. This is left as the exercise to the reader. The following shows the two best solutions to this puzzle.

Solution 1:

Left	river	Right
wolf, goat, cabbage, farmer		
wolf, cabbage		goat, farmer
wolf, cabbage, farmer		goat
cabbage		wolf, goat, farmer
goat, cabbage, farmer		wolf
goat		wolf, cabbage, farmer
goat, farmer		wolf, cabbage
		wolf, goat, cabbage, farmer

Solution 2:

Left	river	Right
wolf, goat, cabbage, farmer		
wolf, cabbage		goat, farmer
wolf, cabbage, farmer		goat
wolf		goat, cabbage, farmer
wolf, goat, farmer		cabbage
goat		wolf, cabbage, farmer
goat, farmer		wolf, cabbage
		wolf, goat, cabbage, farmer

This algorithm can also be realized imperatively. Observing that our solution is in tail recursive manner, we can translate it directly to a loop. We use a list S to hold all the

solutions can be found. The singleton list $\{(15, 0)\}$ is pushed to queue when initializing. As long as the queue isn't empty, we extract the head C from the queue by calling DEQ procedure. Examine if it reaches the final goal, if not, we expand all the possible moves and push to the tail of the queue for further searching.

```

1: function SOLVE
2:    $S \leftarrow \phi$ 
3:    $Q \leftarrow \phi$ 
4:   ENQ( $Q, \{(15, 0)\}$ )
5:   while  $Q \neq \phi$  do
6:      $C \leftarrow$  DEQ( $Q$ )
7:     if  $c_1 = (0, 15)$  then
8:       ADD( $S, \text{REVERSE}(C)$ )
9:     else
10:      for  $\forall m \in \text{MOVES}(C)$  do
11:        if VALID( $m, C$ ) then
12:          ENQ( $Q, \{m\} \cup C$ )
13:   return  $S$ 

```

Where MOVES, and VALID procedures are as same as before. The following Python example program implements this imperative algorithm.

```

def solve():
    s = []
    queue = [(0xf, 0)]
    while queue  $\neq$  []:
        cur = queue.pop(0)
        if cur[0] == (0, 0xf):
            s.append(reverse(cur))
        else:
            for m in moves(cur):
                queue.append([m]+cur)
    return s

def moves(s):
    (a, b) = s[0]
    return valid(s, trans(a, b) if b < 8 else swaps(trans(b, a)))

def valid(s, mv):
    return [(a, b) for (a, b) in mv
             if a not in [3, 6] and b not in [3, 6] and (a, b) not in s]

def trans(a, b):
    masks = [ 8 | (1<<i) for i in range(4)]
    return [(a ^ mask, b | mask) for mask in masks if a & mask == mask]

def swaps(s):
    return [(b, a) for (a, b) in s]

```

There is a minor difference between the program and the pseudo code, that the function to generate candidate moving options filters the invalid cases inside it.

Every time, no matter the farmer drives the boat back and forth, there are m options for him to choose, where m is the number of objects on the river bank the farmer drives from. m is always less than 4, that the algorithm won't take more than n^4 times at step n . This estimation is far more than the actual time, because we avoid trying all invalid cases. Our solution examines all the possible moving in the worst case. Because we check recorded steps to avoid repeated attempt, the algorithm takes about $O(n^2)$ time to search for n possible steps.

Water jugs puzzle

This is a popular puzzle in classic AI. The history of it should be very long. It says that there are two jugs, one is 9 quarts, the other is 4 quarts. How to use them to bring up from the river exactly 6 quarts of water?

There are various versions of this puzzle, although the volume of the jugs, and the target volume of water differ. The solver is said to be young Blaise Pascal when he was a child, the French mathematician, scientist in one story, and Siméon Denis Poisson in another story. Later in the popular Hollywood movie ‘Die-Hard 3’, actor Bruce Willis and Samuel L. Jackson were also confronted with this puzzle.

Pólya gave a nice way to solve this problem backwards in [90].

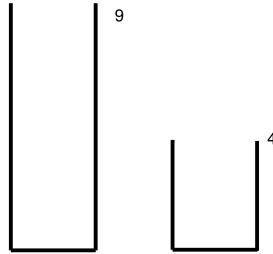


Figure 14.38: Two jugs with volume of 9 and 4.

Instead of thinking from the starting state as shown in figure 14.38. Pólya pointed out that there will be 6 quarts of water in the bigger jug at the final stage, which indicates the second last step, we can fill the 9 quarts jug, then pour out 3 quarts from it. In order to achieve this, there should be 1 quart of water left in the smaller jug as shown in figure 14.39.

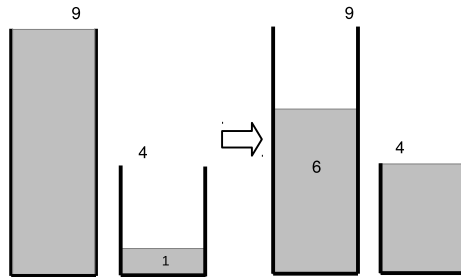


Figure 14.39: The last two steps.

It’s easy to see that fill the 9 quarts jug, then pour to the 4 quarts jug twice can bring 1 quarts of water. As shown in figure 14.40. At this stage, we’ve found the solution. By reversing our findings, we can give the correct steps to bring exactly 6 quarts of water.

Pólya’s methodology is general. It’s still hard to solve it without concrete algorithm. For instance, how to bring up 2 gallons of water from 899 and 1147 gallon jugs?

There are 6 ways to deal with 2 jugs in total. Denote the smaller jug as A , the bigger jug as B .

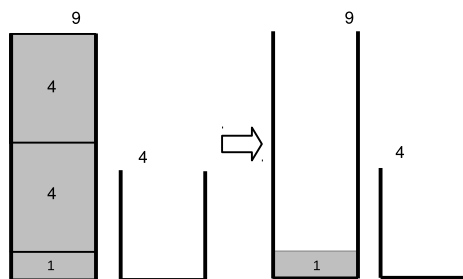


Figure 14.40: Fill the bigger jugs, and pour to the smaller one twice.

- Fill jug A from the river;
- Fill jug B from the river;
- Empty jug A ;
- Empty jug B ;
- Pour water from jug A to B ;
- Pour water from jug B to A .

The following sequence shows an example. Note that in this example, we assume that $a < b < 2a$.

A	B	operation
0	0	start
a	0	fill A
0	a	pour A into B
a	a	fill A
$2a - b$	b	pour A into B
$2a - b$	0	empty B
0	$2a - b$	pour A into B
a	$2a - b$	fill A
$3a - 2b$	b	pour A into B
...

No matter what the above operations are taken, the amount of water in each jug can be expressed as $xa + yb$, where a and b are volumes of jugs, for some integers x and y . All the amounts of water we can get are linear combination of a and b . We can immediately tell given two jugs, if a goal g is solvable or not.

For instance, we can't bring 5 gallons of water with two jugs of volume 4 and 6 gallon. The number theory ensures that, the 2 water jugs puzzle can be solved if and only if g can be divided by the greatest common divisor of a and b . Written as:

$$\gcd(a, b) | g \quad (14.62)$$

Where $m|n$ means n can be divided by m . What's more, if a and b are relatively prime, which means $\gcd(a, b) = 1$, it's possible to bring up any quantity g of water.

Although $\gcd(a, b)$ enables us to determine if the puzzle is solvable, it doesn't give us the detailed pour sequence. If we can find some integer x and y , so that $g = xa + yb$. We can arrange a sequence of operations (even it may not be the best solution) to solve it.

The idea is that, without loss of generality, suppose $x > 0, y < 0$, we need fill jug A by x times, and empty jug B by y times in total.

Let's take $a = 3, b = 5$, and $g = 4$ for example, since $4 = 3 \times 3 - 5$, we can arrange a sequence like the following.

A	B	operation
0	0	start
3	0	fill A
0	3	pour A into B
3	3	fill A
1	5	pour A into B
1	0	empty B
0	1	pour A into B
3	1	fill A
0	4	pour A into B

In this sequence, we fill A by 3 times, and empty B by 1 time. The procedure can be described as the following:

Repeat x times:

1. Fill jug A ;
2. Pour jug A into jug B , whenever B is full, empty it.

So the only problem left is to find the x and y . There is a powerful tool in number theory called, *Extended Euclid algorithm*, which can achieve this. Compare to the classic Euclid GCD algorithm, which can only give the greatest common divisor, The extended Euclid algorithm can give a pair of x, y as well, so that:

$$(d, x, y) = gcd_{ext}(a, b) \quad (14.63)$$

where $d = gcd(a, b)$ and $ax + by = d$. Without loss of generality, suppose $a < b$, there exists quotient q and remainder r that:

$$b = aq + r \quad (14.64)$$

Since d is the common divisor, it can divide both a and b , thus d can divide r as well. Because r is less than a , we can scale down the problem by finding GCD of a and r :

$$(d, x', y') = gcd_{ext}(r, a) \quad (14.65)$$

Where $d = x'r + y'a$ according to the definition of the extended Euclid algorithm. Transform $b = aq + r$ to $r = b - aq$, substitute r in above equation yields:

$$\begin{aligned} d &= x'(b - aq) + y'a \\ &= (y' - x'q)a + x'b \end{aligned} \quad (14.66)$$

This is the linear combination of a and b , so that we have:

$$\begin{cases} x = y' - x'q \\ y = x' \end{cases} \quad (14.67)$$

Note that this is a typical recursive relationship. The edge case happens when $a = 0$.

$$gcd(0, b) = b = 0a + 1b \quad (14.68)$$

Summarize the above result, the extended Euclid algorithm can be defined as the following:

$$gcd_{ext}(a, b) = \begin{cases} (b, 0, 1) & : a = 0 \\ (d, y' - x' \frac{b}{a}, x') & : otherwise \end{cases} \quad (14.69)$$

Where d, x', y' are defined in equation (14.65).

The 2 water jugs puzzle is almost solved, but there are still two detailed problems need to be tackled. First, extended Euclid algorithm gives the linear combination for the greatest common divisor d . While the target volume of water g isn't necessarily equal to d . This can be easily solved by multiplying x and y by m times, where $m = g/gcd(a, b)$; Second, we assume $x > 0$, to form a procedure to fill jug A with x times. However, the extended Euclid algorithm doesn't ensure x to be positive. For instance $gcd_{ext}(4, 9) = (1, -2, 1)$. Whenever we get a negative x , since $d = xa + yb$, we can continuously add b to x , and decrease y by a till x is greater than zero.

At this stage, we are able to give the complete solution to the 2 water jugs puzzle. Below is an example Haskell program.

```

extGcd 0 b = (b, 0, 1)
extGcd a b = let (d, x', y') = extGcd (b `mod` a) a in
              (d, y' - x' * (b `div` a), x')

solve a b g | g `mod` d /= 0 = [] — no solution
            | otherwise = solve' (x * g `div` d)

  where
    (d, x, y) = extGcd a b
    solve' x | x < 0 = solve' (x + b)
             | otherwise = pour x [(0, 0)]
    pour 0 ps = reverse ((0, g):ps)
    pour x ps@((a', b'):_ ) | a' == 0 = pour (x - 1) ((a, b'):ps) — fill a
                           | b' == b = pour x ((a', 0):ps) — empty b
                           | otherwise = pour x ((max 0 (a' + b' - b),
                                                  min (a' + b') b):ps)

```

Although we can solve the 2 water jugs puzzle with extended Euclid algorithm, the solution may not be the best. For instance, when we are going to bring 4 gallons of water from 3 and 5 gallons jugs. The extended Euclid algorithm produces the following sequence:

```

[(0, 0), (3, 0), (0, 3), (3, 3), (1, 5), (1, 0), (0, 1), (3, 1),
(0, 4), (3, 4), (2, 5), (2, 0), (0, 2), (3, 2), (0, 5), (3, 5),
(3, 0), (0, 3), (3, 3), (1, 5), (1, 0), (0, 1), (3, 1), (0, 4)]

```

It takes 23 steps to achieve the goal, while the best solution only need 6 steps:

```

[(0, 0), (0, 5), (3, 2), (0, 2), (2, 0), (2, 5), (3, 4)]

```

Observe the 23 steps, and we can find that jug B has already contained 4 gallons of water at the 8-th step. But the algorithm ignores this fact and goes on executing the left 15 steps. The reason is that the linear combination x and y we find with the extended Euclid algorithm are not the only numbers satisfying $g = xa + by$. For all these numbers, the smaller $|x| + |y|$, the less steps are needed. There is an exercise to addressing this problem in this section.

The interesting problem is how to find the best solution? We have two approaches, one is to find x and y to minimize $|x| + |y|$; the other is to adopt the quite similar idea as the wolf-goat-cabbage puzzle. We focus on the latter in this section. Since there are at

most 6 possible options: fill A , fill B , pour A into B , pour B into A , empty A and empty B , we can try them in parallel, and check which decision can lead to the best solution. We need record all the states we've achieved to avoid any potential repetition. In order to realize this parallel approach with reasonable resources, a queue can be used to arrange our attempts. The elements stored in this queue are series of pairs (p, q) , where p and q represent the volume of waters contained in each jug. These pairs record the sequence of our operations from the beginning to the latest. We initialize the queue with the singleton list contains the starting state $\{(0, 0)\}$.

$$\text{solve}(a, b, g) = \text{solve}'\{\{(0, 0)\}\} \quad (14.70)$$

Every time, when the queue isn't empty, we pick a sequence from the head of the queue. If this sequence ends with a pair contains the target volume g , we find a solution, we can print this sequence by reversing it; Otherwise, we expand the latest pair by trying all the possible 6 options, remove any duplicated states, and add them to the tail of the queue. Denote the queue as Q , the first sequence stored on the head of the queue as S , the latest pair in S as (p, q) , and the rest of pairs as S' . After popping the head element, the queue becomes Q' . This algorithm can be defined like below:

$$\text{solve}'(Q) = \begin{cases} \phi & : Q = \phi \\ \text{reverse}(S) & : p = g \vee q = g \\ \text{solve}'(\text{En}Q'(Q', \{\{s'\} \cup S' | s' \in \text{try}(S)\})) & : \text{otherwise} \end{cases} \quad (14.71)$$

Where function $\text{En}Q'$ pushes a list of sequence to the queue one by one. Function $\text{try}(S)$ will try all possible 6 options to generate new pairs of water volumes:

$$\text{try}(S) = \{s' | s' \in \left\{ \begin{array}{l} \text{fill}A(p, q), \text{fill}B(p, q), \\ \text{pour}A(p, q), \text{pour}B(p, q), \\ \text{empty}A(p, q), \text{empty}B(p, q) \end{array} \right\}, s' \notin S'\} \quad (14.72)$$

It's intuitive to define the 6 options. For fill operations, the result is that the volume of the filled jug is full; for empty operation, the result volume is empty; for pour operation, we need test if the jug is big enough to hold all the water.

$$\begin{aligned} \text{fill}A(p, q) &= (a, q) & \text{fill}B(p, q) &= (p, b) \\ \text{empty}A(p, q) &= (0, q) & \text{empty}B(p, q) &= (p, 0) \\ \text{pour}A(p, q) &= (\text{max}(0, p + q - b), \text{min}(x + y, b)) \\ \text{pour}B(p, q) &= (\text{min}(x + y, a), \text{max}(0, x + y - a)) \end{aligned} \quad (14.73)$$

The following example Haskell program implements this method:

```

solve' a b g = bfs [[(0, 0)]] where
  bfs [] = []
  bfs (c:cs) | fst (head c) == g || snd (head c) == g = reverse c
             | otherwise = bfs (cs ++ map (:c) (expand c))
  expand ((x, y):ps) = filter (`notElem` ps) $ map (\f -> f x y)
                    [fillA, fillB, pourA, pourB, emptyA, emptyB]
  fillA _ y = (a, y)
  fillB x _ = (x, b)
  emptyA _ y = (0, y)
  emptyB x _ = (x, 0)
  pourA x y = (max 0 (x + y - b), min (x + y) b)
  pourB x y = (min (x + y) a, max 0 (x + y - a))

```

This method always returns the fast solution. It can also be realized in imperative approach. Instead of storing the complete sequence of operations in every element in the queue, we can store the unique state in a global history list, and use links to track the operation sequence, this can save spaces.

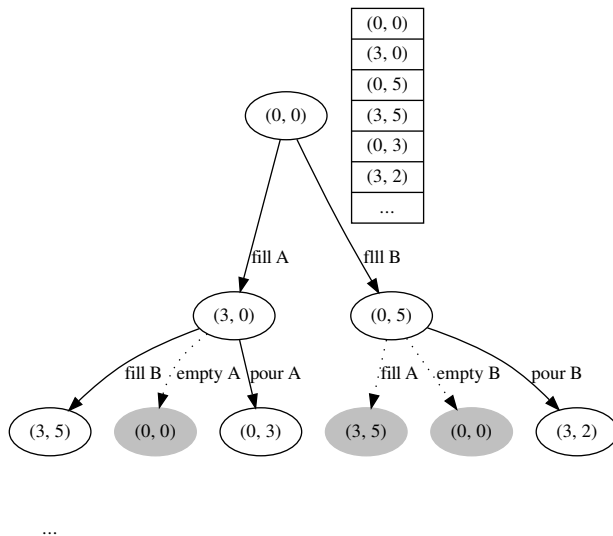


Figure 14.41: All attempted states are stored in a global list.

The idea is illustrated in figure 14.41. The initial state is $(0, 0)$. Only ‘fill A’ and ‘fill B’ are possible. They are tried and added to the record list; Next we can try and record ‘fill B’ on top of $(3, 0)$, which yields new state $(3, 5)$. However, when try ‘empty A’ from state $(3, 0)$, we would return to the start state $(0, 0)$. As this previous state has been recorded, it is ignored. All the repeated states are in gray color in this figure.

With such settings, we needn’t remember the operation sequence in each element in the queue explicitly. We can add a ‘parent’ link to each node in figure 14.41, and use it to back-traverse to the starting point from any state. The following example ANSI C code shows such a definition.

```

struct Step {
    int p, q;
    struct Step* parent;
};

struct Step* make_step(int p, int q, struct Step* parent) {
    struct Step* s = (struct Step*) malloc(sizeof(struct Step));
    s->p = p;
    s->q = q;
    s->parent = parent;
    return s;
}

```

Where p, q are volumes of water in the 2 jugs. For any state s , define functions $p(s)$ and $q(s)$ return these 2 values, the imperative algorithm can be realized based on this idea as below.

- 1: **function** SOLVE(a, b, g)
- 2: $Q \leftarrow \phi$
- 3: PUSH-AND-RECORD($Q, (0, 0)$)
- 4: **while** $Q \neq \phi$ **do**
- 5: $s \leftarrow \text{POP}(Q)$
- 6: **if** $p(s) = g \vee q(s) = g$ **then**
- 7: **return** s
- 8: **else**

```

9:      C ← EXPAND(s)
10:     for  $\forall c \in C$  do
11:         if  $c \neq s \wedge \neg \text{VISITED}(c)$  then
12:             PUSH-AND-RECORD(Q, c)
13:     return NIL

```

Where PUSH-AND-RECORD does not only push an element to the queue, but also record this element as visited, so that we can check if an element has been visited before in the future. This can be implemented with a list. All push operations append the new elements to the tail. For pop operation, instead of removing the element pointed by head, the head pointer only advances to the next one. This list contains historic data which has to be reset explicitly. The following ANSI C code illustrates this idea.

```

struct Step *steps[1000], **head, **tail = steps;

void push(struct Step* s) { *tail++ = s; }

struct Step* pop() { return *head++; }

int empty() { return head == tail; }

void reset() {
    struct Step **p;
    for (p = steps; p  $\neq$  tail; ++p)
        free(*p);
    head = tail = steps;
}

```

In order to test a state has been visited, we can traverse the list to compare p and q .

```

int eq(struct Step* a, struct Step* b) {
    return a→p == b→p && a→q == b→q;
}

int visited(struct Step* s) {
    struct Step **p;
    for (p = steps; p  $\neq$  tail; ++p)
        if (eq(*p, s)) return 1;
    return 0;
}

```

The main program can be implemented as below:

```

struct Step* solve(int a, int b, int g) {
    int i;
    struct Step *cur, *cs[6];
    reset();
    push(make_step(0, 0, NULL));
    while (!empty()) {
        cur = pop();
        if (cur→p == g || cur→q == g)
            return cur;
        else {
            expand(cur, a, b, cs);
            for (i = 0; i < 6; ++i)
                if (!eq(cur, cs[i]) && !visited(cs[i]))
                    push(cs[i]);
        }
    }
    return NULL;
}

```

Where function `expand` tries all the 6 possible options:

```

void expand(struct Step* s, int a, int b, struct Step** cs) {
    int p = s→p, q = s→q;
    cs[0] = make_step(a, q, s); /*fill A*/
    cs[1] = make_step(p, b, s); /*fill B*/
    cs[2] = make_step(0, q, s); /*empty A*/
    cs[3] = make_step(p, 0, s); /*empty B*/
    cs[4] = make_step(max(0, p + q - b), min(p + q, b), s); /*pour A*/
    cs[5] = make_step(min(p + q, a), max(0, p + q - a), s); /*pour B*/
}

```

And the result steps is back tracked in reversed order, it can be output with a recursive function:

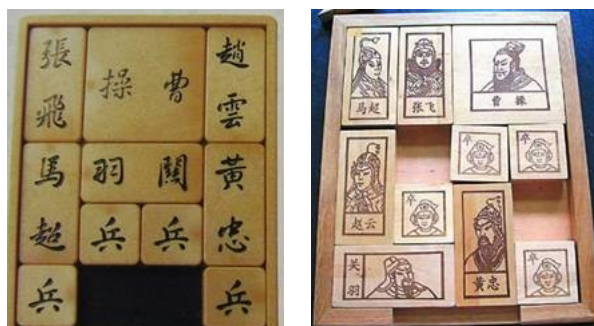
```

void print(struct Step* s) {
    if (s) {
        print(s→parent);
        printf("%d, %d\n", s→p, s→q);
    }
}

```

Kloski

Kloski is a block sliding puzzle. It appears in many countries. There are different sizes and layouts. Figure 14.42 illustrates a traditional Kloski game in China.



(a) Initial layout of blocks (b) Block layout after several movements

Figure 14.42: ‘Huarong Dao’, the traditional Kloski game in China.

In this puzzle, there are 10 blocks, each is labeled with text or icon. The smallest block has size of 1 unit square, the biggest one is 2×2 units size. Note there is a slot of 2 units wide at the middle-bottom of the board. The biggest block represents a king in ancient time, while the others are enemies. The goal is to move the biggest block to the slot, so that the king can escape. This game is named as ‘Huarong Dao’, or ‘Huarong Escape’ in China. Figure 14.43 shows the similar Kloski puzzle in Japan. The biggest block means daughter, while the others are her family members. This game is named as ‘Daughter in the box’ in Japan (Japanese name: *hakoiri musume*).

In this section, we want to find a solution, which can slide blocks from the initial state to the final state with the minimum movements.

The intuitive idea to model this puzzle is to use a 5×4 matrix representing the board. All pieces are labeled with a number. The following matrix M , for example, shows the initial state of the puzzle.



Figure 14.43: ‘Daughter in the box’, the Kloski game in Japan.

$$M = \begin{bmatrix} 1 & 10 & 10 & 2 \\ 1 & 10 & 10 & 2 \\ 3 & 4 & 4 & 5 \\ 3 & 7 & 8 & 5 \\ 6 & 0 & 0 & 9 \end{bmatrix}$$

In this matrix, the cells of value i mean the i -th piece covers this cell. The special value 0 represents a free cell. By using sequence 1, 2, ... to identify pieces, a special layout can be further simplified as an array L . Each element is a list of cells covered by the piece indexed with this element. For example, $L[4] = \{(3, 2), (3, 3)\}$ means the 4-th piece covers cells at position $(3, 2)$ and $(3, 3)$, where (i, j) means the cell at row i and column j .

The starting layout can be written as the following Array.

$$\{\{(1, 1), (2, 1)\}, \{(1, 4), (2, 4)\}, \{(3, 1), (4, 1)\}, \{(3, 2), (3, 3)\}, \{(3, 4), (4, 4)\}, \{(5, 1)\}, \{(4, 2)\}, \{(4, 3)\}, \{(5, 4)\}, \{(1, 2), (1, 3), (2, 2), (2, 3)\}\}$$

When moving the Kloski blocks, we need examine all the 10 blocks, checking each block if it can move up, down, left and right. it seems that this approach would lead to a very huge amount of possibilities, because each step might have 10×4 options, there will be about 40^n cases in the n -th step.

Actually, there won't be so much options. For example, in the first step, there are only 4 valid moving: the 6-th piece moves right; the 7-th and 8-th move down; and the 9-th moves left.

All others are invalid moving. Figure 14.44 shows how to test if the moving is possible.

The left example illustrates sliding block labeled with 1 down. There are two cells covered by this block. The upper 1 moves to the cell previously occupied by this same block, which is also labeled with 1; The lower 1 moves to a free cell, which is labeled with 0;

The right example, on the other hand, illustrates invalid sliding. In this case, the upper cells could move to the cell occupied by the same block. However, the lower cell labeled with 1 can't move to the cell occupied by other block, which is labeled with 2.

In order to test the valid moving, we need examine all the cells a block will cover. If they are labeled with 0 or a number as same as this block, the moving is valid. Otherwise it conflicts with some other block. For a layout L , the corresponding matrix is M , suppose we want to move the k -th block with $(\Delta x, \Delta y)$, where $|\Delta x| \leq 1, |\Delta y| \leq 1$. The following equation tells if the moving is valid:

$$\begin{aligned} \text{valid}(L, k, \Delta x, \Delta y) : \\ \forall (i, j) \in L[k] \Rightarrow \quad & i' = i + \Delta y, j' = j + \Delta x, \\ & (1, 1) \leq (i', j') \leq (5, 4), M_{i'j'} \in \{k, 0\} \end{aligned} \quad (14.74)$$

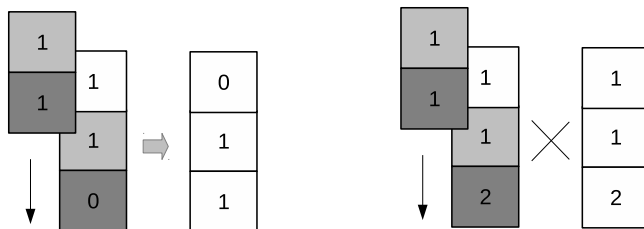


Figure 14.44: Left: both the upper and the lower 1 are OK; Right: the upper 1 is OK, the lower 1 conflicts with 2.

Another important point to solve Kloski puzzle, is about how to avoid repeated attempts. The obvious case is that after a series of sliding, we end up a matrix which have been transformed from. However, it is not enough to only avoid the same matrix. Consider the following two metrics. Although $M_1 \neq M_2$, we need drop options to M_2 , because they are essentially the same.

$$M_1 = \begin{bmatrix} 1 & 10 & 10 & 2 \\ 1 & 10 & 10 & 2 \\ 3 & 4 & 4 & 5 \\ 3 & 7 & 8 & 5 \\ 6 & 0 & 0 & 9 \end{bmatrix} \quad M_2 = \begin{bmatrix} 2 & 10 & 10 & 1 \\ 2 & 10 & 10 & 1 \\ 3 & 4 & 4 & 5 \\ 3 & 7 & 6 & 5 \\ 8 & 0 & 0 & 9 \end{bmatrix}$$

This fact tells us, that we should compare the layout, but not merely matrix to avoid repetition. Denote the corresponding layouts as L_1 and L_2 respectively, it's easy to verify that $\|L_1\| = \|L_2\|$, where $\|L\|$ is the normalized layout, which is defined as below:

$$\|L\| = \text{sort}(\{\text{sort}(l_i) \mid \forall l_i \in L\}) \tag{14.75}$$

In other words, a normalized layout is ordered for all its elements, and every element is also ordered. The ordering can be defined as that $(a, b) \leq (c, d) \Leftrightarrow an + b \leq cn + d$, where n is the width of the matrix.

Observing that the Kloski board is symmetric, thus a layout can be mirrored from another one. Mirrored layout is also a kind of repeating, which should be avoided. The following M_1 and M_2 show such an example.

$$M_1 = \begin{bmatrix} 10 & 10 & 1 & 2 \\ 10 & 10 & 1 & 2 \\ 3 & 5 & 4 & 4 \\ 3 & 5 & 8 & 9 \\ 6 & 7 & 0 & 0 \end{bmatrix} \quad M_2 = \begin{bmatrix} 3 & 1 & 10 & 10 \\ 3 & 1 & 10 & 10 \\ 4 & 4 & 2 & 5 \\ 7 & 6 & 2 & 5 \\ 0 & 0 & 9 & 8 \end{bmatrix}$$

Note that, the normalized layouts are symmetric to each other. It's easy to get a mirrored layout like this:

$$\text{mirror}(L) = \{\{(i, n - j + 1) \mid \forall (i, j) \in l\} \mid \forall l \in L\} \tag{14.76}$$

We find that the matrix representation is useful in validating the moving, while the layout is handy to model the moving and avoid repeated attempt. We can use the similar approach to solve the Kloski puzzle. We need a queue, every element in the queue contains two parts: a series of moving and the latest layout led by the moving. Each moving is in form of $(k, (\Delta y, \Delta x))$, which means moving the k -th block, with Δy in row, and Δx in column in the board.

The queue contains the starting layout when initialized. Whenever this queue isn't empty, we pick the first one from the head, checking if the biggest block is on target, that $L[10] = \{(4, 2), (4, 3), (5, 2), (5, 3)\}$. If yes, then we are done; otherwise, we try to move every block with 4 options: left, right, up, and down, and store all the possible, unique new layout to the tail of the queue. During this searching, we need record all the normalized layouts we've ever found to avoid any duplication.

Denote the queue as Q , the historic layouts as H , the first layout on the head of the queue as L , its corresponding matrix as M . and the moving sequence to this layout as S . The algorithm can be defined as the following.

$$\text{solve}(Q, H) = \begin{cases} \phi & : Q = \phi \\ \text{reverse}(S) & : L[10] = \{(4, 2), (4, 3), (5, 2), (5, 3)\} \\ \text{solve}(Q', H') & : \text{otherwise} \end{cases} \quad (14.77)$$

The first clause says that if the queue is empty, we've tried all the possibilities and can't find a solution; The second clause finds a solution, it returns the moving sequence in reversed order; These are two edge cases. Otherwise, the algorithm expands the current layout, puts all the valid new layouts to the tail of the queue to yield Q' , and updates the normalized layouts to H' . Then it performs recursive searching.

In order to expand a layout to valid unique new layouts, we can define a function as below:

$$\text{expand}(L, H) = \{(k, (\Delta y, \Delta x)) \mid \forall k \in \{1, 2, \dots, 10\}, \\ \forall (\Delta y, \Delta x) \in \{(0, -1), (0, 1), (-1, 0), (1, 0)\}, \\ \text{valid}(L, k, \Delta x, \Delta y), \text{unique}(L', H)\} \quad (14.78)$$

Where L' is the the new layout by moving the k -th block with $(\Delta y, \Delta x)$ from L , M' is the corresponding matrix, and M'' is the matrix to the mirrored layout of L' . Function unique is defined like this:

$$\text{unique}(L', H) = M' \notin H \wedge M'' \notin H \quad (14.79)$$

We'll next show some example Haskell Kloski programs. As array isn't mutable in the purely functional settings, tree based map is used to represent layout ¹¹. Some type synonyms are defined as below:

```
import qualified Data.Map as M
import Data.Ix
import Data.List (sort)

type Point = (Integer, Integer)
type Layout = M.Map Integer [Point]
type Move = (Integer, Point)

data Ops = Op Layout [Move]
```

The main program is almost as same as the $\text{solve}(Q, H)$ function defined above.

¹¹Alternatively, finger tree based sequence shown in previous chapter can be used

```

solve :: [Ops] → [[[Point]]] → [Move]
solve [] _ = [] — no solution
solve (Op x seq : cs) visit
  | M.lookup 10 x == Just [(4, 2), (4, 3), (5, 2), (5, 3)] = reverse seq
  | otherwise = solve q visit'
  where
    ops = expand x visit
    visit' = map (layout ∘ move x) ops ++ visit
    q = cs ++ [Op (move x op) (op:seq) | op ← ops ]

```

Where function `layout` gives the normalized form by sorting. `move` returns the updated map by sliding the i -th block with $(\Delta y, \Delta x)$.

```

layout = sort ∘ map sort ∘ M.elems

move x (i, d) = M.update (Just ∘ map (flip shift d)) i x

shift (y, x) (dy, dx) = (y + dy, x + dx)

```

Function `expand` gives all the possible new options. It can be directly translated from `expand(L, H)`.

```

expand :: Layout → [[[Point]]] → [Move]
expand x visit = [(i, d) | i ← [1..10],
                          d ← [(0, -1), (0, 1), (-1, 0), (1, 0)],
                          valid i d, unique i d] where
  valid i d = all (λp → let p' = shift p d in
                      inRange (bounds board) p' &&
                      (M.keys $ M.filter (elem p') x) `elem` [[i], []])
  unique i d = let mv = move x (i, d) in
               all (`notElem` visit) (map layout [mv, mirror mv])

```

Note that we also filter out the mirrored layouts. The `mirror` function is given as the following.

```

mirror = M.map (map (λ (y, x) → (y, 5 - x)))

```

This program takes several minutes to produce the best solution, which takes 116 steps. The final 3 steps are shown as below:

...

```

['5', '3', '2', '1']
['5', '3', '2', '1']
['7', '9', '4', '4']
['A', 'A', '6', '0']
['A', 'A', '0', '8']

```

```

['5', '3', '2', '1']
['5', '3', '2', '1']
['7', '9', '4', '4']
['A', 'A', '0', '6']
['A', 'A', '0', '8']

```

```

['5', '3', '2', '1']
['5', '3', '2', '1']
['7', '9', '4', '4']
['0', 'A', 'A', '6']

```

```
['0', 'A', 'A', '8']
```

total 116 steps

The Kloski solution can also be realized imperatively. Note that the $solve(Q, H)$ is tail-recursive, it's easy to transform the algorithm with looping. We can also link one layout to its parent, so that the moving sequence can be recorded globally. This can save some spaces, as the queue needn't store the moving information in every element. When output the result, we only need back-tracking to the starting layout from the last one.

Suppose function $LINK(L', L)$ links a new layout L' to its parent layout L . The following algorithm takes a starting layout, and searches for best moving sequence.

```

1: function SOLVE( $L_0$ )
2:    $H \leftarrow ||L_0||$ 
3:    $Q \leftarrow \phi$ 
4:   PUSH( $Q$ , LINK( $L_0$ , NIL))
5:   while  $Q \neq \phi$  do
6:      $L \leftarrow POP(Q)$ 
7:     if  $L[10] = \{(4, 2), (4, 3), (5, 2), (5, 3)\}$  then
8:       return  $L$ 
9:     else
10:      for each  $L' \in EXPAND(L, H)$  do
11:        PUSH( $Q$ , LINK( $L', L$ ))
12:        APPEND( $H$ ,  $||L'||$ )
13:  return NIL ▷ No solution

```

The following example Python program implements this algorithm:

```

class Node:
    def __init__(self, l, p = None):
        self.layout = l
        self.parent = p

def solve(start):
    visit = set([normalize(start)])
    queue = deque([Node(start)])
    while queue:
        cur = queue.popleft()
        layout = cur.layout
        if layout[-1] == [(4, 2), (4, 3), (5, 2), (5, 3)]:
            return cur
        else:
            for brd in expand(layout, visit):
                queue.append(Node(brd, cur))
                visit.add(normalize(brd))
    return None # no solution

```

Where `normalize` and `expand` are implemented as below:

```

def normalize(layout):
    return tuple(sorted([tuple(sorted(r)) for r in layout]))

def expand(layout, visit):
    def bound(y, x):
        return 1 ≤ y and y ≤ 5 and 1 ≤ x and x ≤ 4
    def valid(m, i, y, x):
        return m[y - 1][x - 1] in [0, i]
    def unique(brd):
        (m, n) = (normalize(brd), normalize(mirror(brd)))
        return m not in visit and n not in visit
    s = []

```

```

d = [(0, -1), (0, 1), (-1, 0), (1, 0)]
m = matrix(layout)
for i in range(1, 11):
    for (dy, dx) in d:
        if all(bound(y + dy, x + dx) and valid(m, i, y + dy, x + dx)
              for (y, x) in layout[i - 1]):
            brd = move(layout, (i, (dy, dx)))
            if unique(brd):
                s.append(brd)
return s

```

Like most programming languages, arrays are indexed from 0 but not 1 in Python. This has to be handled properly. The rest functions including `mirror`, `matrix`, and `move` are implemented as the following.

```

def mirror(layout):
    return [[(y, 5 - x) for (y, x) in r] for r in layout]

def matrix(layout):
    m = [[0]*4 for _ in range(5)]
    for (i, ps) in zip(range(1, 11), layout):
        for (y, x) in ps:
            m[y - 1][x - 1] = i
    return m

def move(layout, delta):
    (i, (dy, dx)) = delta
    m = dup(layout)
    m[i - 1] = [(y + dy, x + dx) for (y, x) in m[i - 1]]
    return m

def dup(layout):
    return [r[:] for r in layout]

```

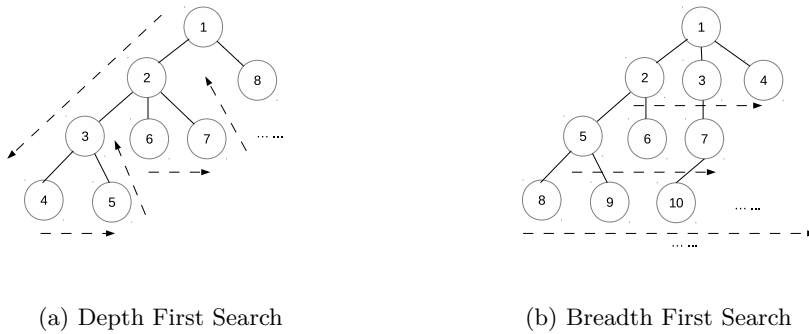
It's possible to modify this Kloski algorithm, so that it does not only stop at the first solution, but also search all the solutions. In such case, the computation time is bound to the size of a space V , where V holds all the layouts can be transformed from the starting layout. If all these layouts are stored globally, with a parent field point to the predecessor, the space requirement of this algorithm is also bound to $O(V)$.

Summary of BFS

The above three puzzles, the wolf-goat-cabbage puzzle, the water jugs puzzle, and the Kloski puzzle show some common solution structure. Similar to the DFS problems, they all have the starting state and the end state. The wolf-goat-cabbage puzzle starts with the wolf, the goat, the cabbage and the farmer all in one side, while the other side is empty. It ends up in a state that they all moved to the other side. The water jugs puzzle starts with two empty jugs, and ends with either jug contains a certain volume of water. The Kloski puzzle starts from a layout and ends to another layout that the biggest block begging slid to a given position.

All problems specify a set of rules which can transfer from one state to another. Different from the DFS approach, we try all the possible options 'in parallel'. We won't search further until all the other alternatives in the same step have been examined. This method ensures that the solution with the minimum steps can be found before those with more steps. Review and compare the two figures we've drawn before shows the difference between these two approaches. For the later one, because we expand the searching horizontally, it is called as Breadth-first search (BFS for short).

As we can't perform search really in parallel, BFS realization typically utilizes a queue to store the search options. The candidate with less steps pops from the head, while the



(a) Depth First Search

(b) Breadth First Search

Figure 14.45: Search orders for DFS and BFS.

new candidate with more steps is pushed to the tail of the queue. Note that the queue should meet constant time enqueue and dequeue requirement, which we've explained in previous chapter of queue. Strictly speaking, the example functional programs shown above don't meet this criteria. They use list to mimic queue, which can only provide linear time pushing. Readers can replace them with the functional queue we explained before.

BFS provides a simple method to search for optimal solutions in terms of the number of steps. However, it can't search for more general optimal solution. Consider another directed graph as shown in figure 14.46, the length of each section varies. We can't use BFS to find the shortest route from one city to another.

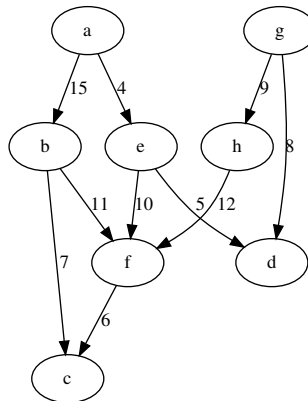


Figure 14.46: A weighted directed graph.

Note that the shortest route from city a to city c isn't the one with the fewest steps $a \rightarrow b \rightarrow c$. The total length of this route is 22; But the route with more steps $a \rightarrow e \rightarrow f \rightarrow c$ is the best. The length of it is 20. The coming sections introduce other algorithms to search for optimal solution.

14.3.2 Search the optimal solution

Searching for the optimal solution is quite important in many aspects. People need the 'best' solution to save time, space, cost, or energy. However, it's not easy to find the best solution with limited resources. There have been many optimal problems can only

be solved by brute-force. Nevertheless, we've found that, for some of them, There exists special simplified ways to search the optimal solution.

Grady algorithm

Huffman coding

Huffman coding is a solution to encode information with the shortest length of code. Consider the popular ASCII code, which uses 7 bits to encode characters, digits, and symbols. ASCII code can represent $2^7 = 128$ different symbols. With 0, 1 bits, we need at least $\log_2 n$ bits to distinguish n different symbols. For text with only case insensitive English letters, we can define a code table like below.

char	code	char	code
A	00000	N	01101
B	00001	O	01110
C	00010	P	01111
D	00011	Q	10000
E	00100	R	10001
F	00101	S	10010
G	00110	T	10011
H	00111	U	10100
I	01000	V	10101
J	01001	W	10110
K	01010	X	10111
L	01011	Y	11000
M	01100	Z	11001

With this code table, text 'INTERNATIONAL' is encoded to 65 bits.

00010101101100100100100011011000000110010001001110101100000011010

Observe the above code table, which actually maps the letter 'A' to 'Z' from 0 to 25. There are 5 bits to represent every code. Code zero is forced as '00000' but not '0' for example. Such kind of coding method, is called fixed-length coding.

Another coding method is variable-length coding. That we can use just one bit '0' for 'A', two bits '10' for C, and 5 bits '11001' for 'Z'. Although this approach can shorten the total length of the code for 'INTERNATIONAL' from 65 bits dramatically, it causes problem when decoding. When processing a sequence of bits like '1101', we don't know if it means '1' followed by '101', which stands for 'BF'; or '110' followed by '1', which is 'GB', or '1101' which is 'N'.

The famous Morse code is variable-length coding system. That the most used letter 'E' is encoded as a dot, while 'Z' is encoded as two dashes and two dots. Morse code uses a special pause separator to indicate the termination of a code, so that the above problem won't happen. There is another solution to avoid ambiguity. Consider the following code table.

char	code	char	code
A	110	E	1110
I	101	L	1111
N	01	O	000
R	001	T	100

Text 'INTERNATIONAL' is encoded to 38 bits only:

10101100111000101110100101000011101111

If decode the bits against the above code table, we won't meet any ambiguity symbols. This is because there is no code for any symbol is the prefix of another one. Such code is called *prefix-code*. (You may wonder why it isn't called as non-prefix code.) By using prefix-code, we needn't separators at all. So that the length of the code can be shorten.

This is a very interesting problem. Can we find a prefix-code table, which produce the shortest code for a given text? The very same problem was given to David A. Huffman in 1951, who was still a student in MIT[91]. His professor Robert M. Fano told the class that those who could solve this problem needn't take the final exam. Huffman almost gave up and started preparing the final exam when he found the most efficient answer.

The idea is to create the coding table according to the frequency of the symbol appeared in the text. The more used symbol is assigned with the shorter code.

It's not hard to process some text, and calculate the occurrence for each symbol. So that we have a symbol set, each one is augmented with a weight. The weight can be the number which indicates the frequency this symbol occurs. We can use the number of occurrence, or the probabilities for example.

Huffman discovered that a binary tree can be used to generate prefix-code. All symbols are stored in the leaf nodes. The codes are generated by traversing the tree from root. When go left, we add a zero; and when go right we add a one.

Figure 14.47 illustrates a binary tree. Taking symbol 'N' for example, starting from the root, we first go left, then right and arrive at 'N'. Thus the code for 'N' is '01'; While for symbol 'A', we can go right, right, then left. So 'A' is encode to '110'. Note that this approach ensures none code is the prefix of the other.

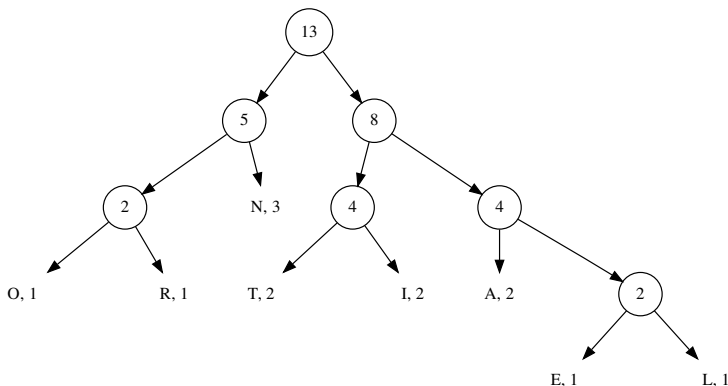


Figure 14.47: An encoding tree.

Note that this tree can also be used directly for decoding. When scan a series of bits, if the bit is zero, we go left; if the bit is one, we go right. When arrive at a leaf, we decode a symbol from that leaf. And we restart from the root of the tree for the coming bits.

Given a list of symbols with weights, we need build such a binary tree, so that the symbol with greater weight has shorter path from the root. Huffman developed a bottom-up solution. When start, all symbols are put into a leaf node. Every time, we pick two nodes, which has the smallest weight, and merge them into a branch node. The weight of this branch is the sum of its two children. We repeatedly pick the two smallest weighted nodes and merge till there is only one tree left. Figure 14.48 illustrates such a building process.

We can reuse the binary tree definition to formalize Huffman coding. We augment the weight information, and the symbols are only stored in leaf nodes. The following C like definition, shows an example.

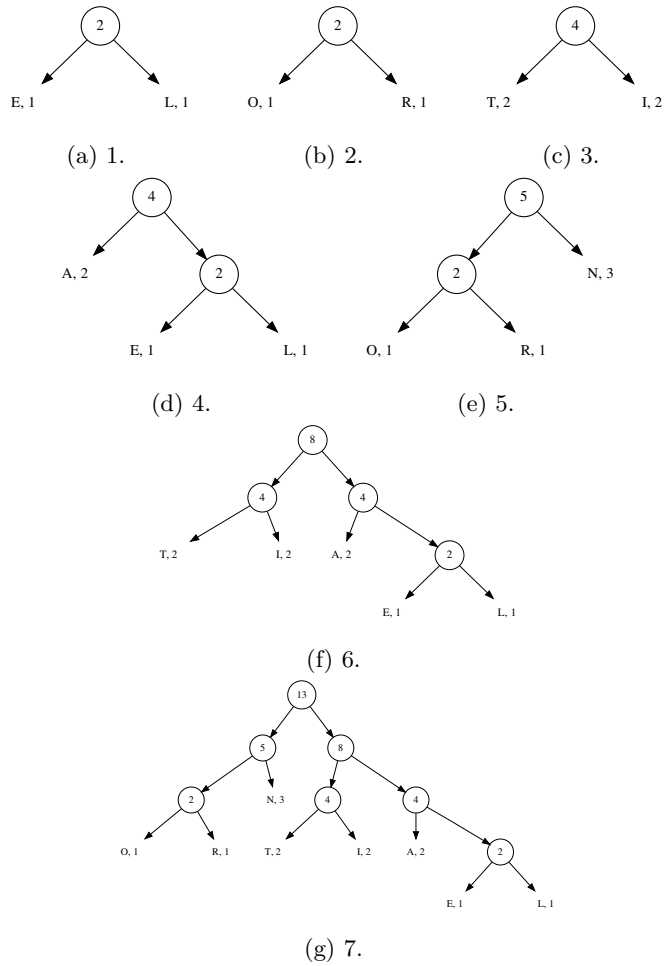


Figure 14.48: Steps to build a Huffman tree.

```

struct Node {
    int w;
    char c;
    struct Node *left, *right;
};

```

Some limitation can be added to the definition, as empty tree isn't allowed. A Huffman tree is either a leaf, which contains a symbol and its weight; or a branch, which only holds total weight of all leaves. The following Haskell code, for instance, explicitly specifies these two cases.

```

data HTr w a = Leaf w a | Branch w (HTr w a) (HTr w a)

```

When merge two Huffman trees T_1 and T_2 to a bigger one, These two trees are set as its children. We can select either one as the left, and the other as the right. the weight of the result tree T is the sum of its two children. so that $w = w_1 + w_2$. Define $T_1 < T_2$ if $w_1 < w_2$, One possible Huffman tree building algorithm can be realized as the following.

$$build(A) = \begin{cases} T_1 & : A = \{T_1\} \\ build(\{merge(T_a, T_b)\} \cup A') & : otherwise \end{cases} \quad (14.80)$$

A is a list of trees. It is initialized as leaves for all symbols and their weights. If there is only one tree in this list, we are done, the tree is the final Huffman tree. Otherwise, The two smallest tree T_a and T_b are extracted, and the rest trees are hold in list A' . T_a and T_b are merged to one bigger tree, and put back to the tree list for further recursive building.

$$(T_a, T_b, A') = extract(A) \quad (14.81)$$

We can scan the tree list to extract the 2 nodes with the smallest weight. Below equation shows that when the scan begins, the first 2 elements are compared and initialized as the two minimum ones. An empty accumulator is passed as the last argument.

$$extract(A) = extract'(min(T_1, T_2), max(T_1, T_2), \{T_3, T_4, \dots\}, \phi) \quad (14.82)$$

For every tree, if its weight is less than the smallest two we've ever found, we update the result to contain this tree. For any given tree list A , denote the first tree in it as T_1 , and the rest trees except T_1 as A' . The scan process can be defined as the following.

$$extract'(T_a, T_b, A, B) = \begin{cases} (T_a, T_b, B) & : A = \phi \\ extract'(T'_a, T'_b, A', \{T_b\} \cup A) & : T_1 < T_b \\ extract'(T_a, T_b, A', \{T_1\} \cup A) & : otherwise \end{cases} \quad (14.83)$$

Where $T'_a = min(T_1, T_a)$, $T'_b = max(T_1, T_a)$ are the updated two trees with the smallest weights.

The following Haskell example program implements this Huffman tree building algorithm.

```

build [x] = x
build xs = build ((merge x y) : xs') where
    (x, y, xs') = extract xs

extract (x:y:xs) = min2 (min x y) (max x y) xs [] where
    min2 x y [] xs = (x, y, xs)
    min2 x y (z:zs) xs | z < y = min2 (min z x) (max z x) zs (y:xs)
                       | otherwise = min2 x y zs (z:xs)

```

This building solution can also be realized imperatively. Given an array of Huffman nodes, we can use the last two cells to hold the nodes with the smallest weights. Then we scan the rest of the array from right to left. Whenever there is a node with the smaller weight, this node will be exchanged with the bigger one of the last two. After all nodes have been examined, we merge the trees in the last two cells, and drop the last cell. This shrinks the array by one. We repeat this process till there is only one tree left.

```

1: function HUFFMAN(A)
2:   while |A| > 1 do
3:     n ← |A|
4:     for i ← n - 2 down to 1 do
5:       if A[i] < MAX(A[n], A[n - 1]) then
6:         EXCHANGE A[i] ↔ MAX(A[n], A[n - 1])
7:       A[n - 1] ← MERGE(A[n], A[n - 1])
8:       DROP(A[n])
9:   return A[1]

```

The following C++ example program implements this algorithm. Note that this algorithm needn't the last two elements being ordered.

```

typedef vector<Node*> Nodes;

bool lessp(Node* a, Node* b) { return a->w < b->w; }

Node* max(Node* a, Node* b) { return lessp(a, b) ? b : a; }

void swap(Nodes& ts, int i, int j, int k) {
    swap(ts[i], ts[ts[j] < ts[k] ? k : j]);
}

Node* huffman(Nodes ts) {
    int n;
    while((n = ts.size()) > 1) {
        for (int i = n - 3; i ≥ 0; --i)
            if (lessp(ts[i], max(ts[n-1], ts[n-2])))
                swap(ts, i, n-1, n-2);
        ts[n-2] = merge(ts[n-1], ts[n-2]);
        ts.pop_back();
    }
    return ts.front();
}

```

The algorithm merges all the leaves, and it need scan the list in each iteration. Thus the performance is quadratic. This algorithm can be improved. Observe that each time, only the two trees with the smallest weights are merged. This reminds us the heap data structure. Heap ensures to access the smallest element fast. We can put all the leaves in a heap. For binary heap, this is typically a linear operation. Then we extract the minimum element twice, merge them, then put the bigger tree back to the heap. This is $O(\lg n)$ operation if binary heap is used. So the total performance is $O(n \lg n)$, which is better than the above algorithm. The next algorithm extracts the node from the heap, and starts Huffman tree building.

$$\text{build}(H) = \text{reduce}(\text{top}(H), \text{pop}(H)) \quad (14.84)$$

This algorithm stops when the heap is empty; Otherwise, it extracts another nodes from the heap for merging.

$$\text{reduce}(T, H) = \begin{cases} T & : H = \phi \\ \text{build}(\text{insert}(\text{merge}(T, \text{top}(H)), \text{pop}(H))) & : \text{otherwise} \end{cases} \quad (14.85)$$

Function *build* and *reduce* are mutually recursive. The following Haskell example program implements this algorithm by using heap defined in previous chapter.

```

huffman' :: (Num a, Ord a) => [(b, a)] -> HTr a b
huffman' = build' o Heap.fromList o map (\(c, w) -> Leaf w c) where
  build' h = reduce (Heap.findMin h) (Heap.deleteMin h)
  reduce x Heap.E = x
  reduce x h = build' $ Heap.insert (Heap.deleteMin h) (merge x (Heap.findMin h))

```

The heap solution can also be realized imperatively. The leaves are firstly transformed to a heap, so that the one with the minimum weight is put on the top. As far as there are more than 1 elements in the heap, we extract the two smallest, merge them to a bigger one, and put back to the heap. The final tree left in the heap is the result Huffman tree.

```

1: function HUFFMAN'(A)
2:   BUILD-HEAP(A)
3:   while |A| > 1 do
4:     Ta ← HEAP-POP(A)
5:     Tb ← HEAP-POP(A)
6:     HEAP-PUSH(A, MERGE(Ta, Tb))
7:   return HEAP-POP(A)

```

The following example C++ code implements this heap solution. The heap used here is provided in the standard library. Because the max-heap, but not min-heap would be made by default, a greater predication is explicitly passed as argument.

```

bool greaterp(Node* a, Node* b) { return b->w < a->w; }

Node* pop(Nodes& h) {
  Node* m = h.front();
  pop_heap(h.begin(), h.end(), greaterp);
  h.pop_back();
  return m;
}

void push(Node* t, Nodes& h) {
  h.push_back(t);
  push_heap(h.begin(), h.end(), greaterp);
}

Node* huffman1(Nodes ts) {
  make_heap(ts.begin(), ts.end(), greaterp);
  while (ts.size() > 1) {
    Node* t1 = pop(ts);
    Node* t2 = pop(ts);
    push(merge(t1, t2), ts);
  }
  return ts.front();
}

```

When the symbol-weight list has been already sorted, there exists a linear time method to build the Huffman tree. Observe that during the Huffman tree building, it produces a series of merged trees with weight in ascending order. We can use a queue to manage the merged trees. Every time, we pick the two trees with the smallest weight from both the queue and the list, merge them and push the result to the queue. All the trees in the list will be processed, and there will be only one tree left in the queue. This tree is the result Huffman tree. This process starts by passing an empty queue as below.

$$build'(A) = reduce'(extract''(\phi, A)) \quad (14.86)$$

Suppose A is in ascending order by weight, At any time, the tree with the smallest weight is either the header of the queue, or the first element of the list. Denote the header

of the queue is T_a , after pops it, the queue is Q' ; The first element in A is T_b , the rest elements are hold in A' . Function $extract''$ can be defined like the following.

$$extract''(Q, A) = \begin{cases} (T_b, (Q, A')) & : Q = \phi \\ (T_a, (Q', A)) & : A = \phi \vee T_a < T_b \\ (T_b, (Q, A')) & : otherwise \end{cases} \quad (14.87)$$

Actually, the pair of queue and tree list can be viewed as a special heap. The tree with the minimum weight is continuously extracted and merged.

$$reduce'(T, (Q, A)) = \begin{cases} T & : Q = \phi \wedge A = \phi \\ reduce'(extract''(push(Q'', merge(T, T')), A'')) & : otherwise \end{cases} \quad (14.88)$$

Where $(T', (Q'', A'')) = extract''(Q, A)$, which means extracting another tree. The following Haskell example program shows the implementation of this method. Note that this program explicitly sort the leaves, which isn't necessary if the leaves are ordered. Again, the list, but not a real queue is used here for illustration purpose. List isn't good at pushing new element, please refer to the chapter of queue for details about it.

```

huffman'' :: (Num a, Ord a) => [(b, a)] -> HTr a b
huffman'' = reduce o wrap o sort o map (\(c, w) -> Leaf w c) where
  wrap xs = delMin ([], xs)
  reduce (x, ([], [])) = x
  reduce (x, h) = let (y, (q, xs)) = delMin h in
                  reduce $ delMin (q ++ [merge x y], xs)
  delMin ([], (x:xs)) = (x, ([], xs))
  delMin ((q:qs), []) = (q, (qs, []))
  delMin ((q:qs), (x:xs)) | q < x = (q, (qs, (x:xs)))
                          | otherwise = (x, ((q:qs), xs))

```

This algorithm can also be realized imperatively.

```

1: function HUFFMAN''(A) ▷ A is ordered by weight
2:   Q ← ϕ
3:   T ← EXTRACT(Q, A)
4:   while Q ≠ ϕ ∨ A ≠ ϕ do
5:     PUSH(Q, MERGE(T, EXTRACT(Q, A)))
6:     T ← EXTRACT(Q, A)
7:   return T

```

Where function EXTRACT(Q, A) extracts the tree with the smallest weight from the queue and the array of trees. It mutates the queue and array if necessary. Denote the head of the queue is T_a , and the first element of the array as T_b .

```

1: function EXTRACT(Q, A)
2:   if Q ≠ ϕ ∧ (A = ϕ ∨ Ta < Tb) then
3:     return POP(Q)
4:   else
5:     return DETACH(A)

```

Where procedure DETACH(A), removes the first element from A , and returns this element as result. In most imperative settings, as detaching the first element is slow linear operation for array, we can store the trees in descending order by weight, and remove the last element. This is a fast constant time operation. The below C++ example code shows this idea.

```

Node* extract(queue<Node*>& q, Nodes& ts) {
  Node* t;
  if (!q.empty() && (ts.empty() || lessp(q.front(), ts.back()))) {

```

```

    t = q.front();
    q.pop();
} else {
    t = ts.back();
    ts.pop_back();
}
return t;
}

Node* huffman2(Nodes ts) {
    queue<Node*> q;
    sort(ts.begin(), ts.end(), greaterp);
    Node* t = extract(q, ts);
    while (!q.empty() || !ts.empty()) {
        q.push(merge(t, extract(q, ts)));
        t = extract(q, ts);
    }
    return t;
}

```

Note that the sorting isn't necessary if the trees have already been ordered. It can be a linear time reversing in case the trees are in ascending order by weight.

There are three different Huffman tree building methods explained. Although they follow the same approach developed by Huffman, the result trees varies. Figure 14.49 shows the three different Huffman trees built with these methods.

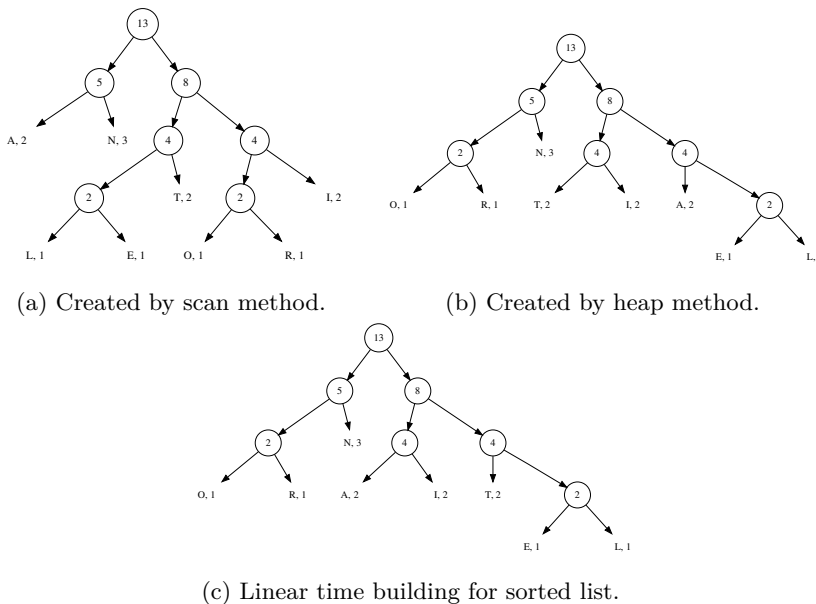


Figure 14.49: Variation of Huffman trees for the same symbol list.

Although these three trees are not identical. They are all able to generate the most efficient code. The formal proof is skipped here. The detailed information can be referred to [91] and Section 16.3 of [4].

The Huffman tree building is the core idea of Huffman coding. Many things can be easily achieved with the Huffman tree. For example, the code table can be generated by traversing the tree. We start from the root with the empty prefix p . For any branches, we append a zero to the prefix if turn left, and append a one if turn right. When a leaf node is arrived, the symbol represented by this node and the prefix are put to the code table.

Denote the symbol of a leaf node as c , the children for tree T as T_l and T_r respectively. The code table association list can be built with $code(T, \phi)$, which is defined as below.

$$code(T, p) = \begin{cases} \{(c, p)\} & : \text{leaf}(T) \\ code(T_l, p \cup \{0\}) \cup code(T_r, p \cup \{1\}) & : \text{otherwise} \end{cases} \quad (14.89)$$

Where function $leaf(T)$ tests if tree T is a leaf or a branch node. The following Haskell example program generates a map as the code table according to this algorithm.

```
code tr = Map.fromList $ traverse [] tr where
  traverse bits (Leaf _ c) = [(c, bits)]
  traverse bits (Branch _ l r) = (traverse (bits ++ [0]) l) ++
                                (traverse (bits ++ [1]) r)
```

The imperative code table generating algorithm is left as exercise. The encoding process can scan the text, and look up the code table to output the bit sequence. The realization is skipped here.

The decoding process is realized by looking up the Huffman tree according to the bit sequence. We start from the root, whenever a zero is received, we turn left, otherwise if a one is received, we turn right. If a leaf node is arrived, the symbol represented by this leaf is output, and we start another looking up from the root. The decoding process ends when all the bits are consumed. Denote the bit sequence as $B = \{b_1, b_2, \dots\}$, all bits except the first one are hold in B' , below definition realizes the decoding algorithm.

$$decode(T, B) = \begin{cases} \{c\} & : B = \phi \wedge leaf(T) \\ \{c\} \cup decode(root(T), B) & : leaf(T) \\ decode(T_l, B') & : b_1 = 0 \\ decode(T_r, B') & : otherwise \end{cases} \quad (14.90)$$

Where $root(T)$ returns the root of the Huffman tree. The following Haskell example code implements this algorithm.

```
decode tr cs = find tr cs where
  find (Leaf _ c) [] = [c]
  find (Leaf _ c) bs = c : find tr bs
  find (Branch _ l r) (b:bs) = find (if b == 0 then l else r) bs
```

Note that this is an on-line decoding algorithm with linear time performance. It consumes one bit per time. This can be clearly noted from the below imperative realization, where the index keeps increasing by one.

```
1: function DECODE( $T, B$ )
2:    $W \leftarrow \phi$ 
3:    $n \leftarrow |B|, i \leftarrow 1$ 
4:   while  $i < n$  do
5:      $R \leftarrow T$ 
6:     while  $\neg \text{LEAF}(R)$  do
7:       if  $B[i] = 0$  then
8:          $R \leftarrow \text{LEFT}(R)$ 
9:       else
10:         $R \leftarrow \text{RIGHT}(R)$ 
11:       $i \leftarrow i + 1$ 
12:     $W \leftarrow W \cup \text{SYMBOL}(R)$ 
13:  return  $W$ 
```

This imperative algorithm can be implemented as the following example C++ program.


```

string decode(Node* root, const char* bits) {
    string w;
    while (*bits) {
        Node* t = root;
        while (!isleaf(t))
            t = '0' == *bits++ ? t->left : t->right;
        w += t->c;
    }
    return w;
}

```

Huffman coding, especially the Huffman tree building shows an interesting strategy. Each time, there are multiple options for merging. Among the trees in the list, Huffman method always selects two trees with the smallest weight. This is the best choice at that merge stage. However, these series of *local* best options generate a global optimal prefix code.

It's not always the case that the local optimal choice also leads to the global optimal solution. In most cases, it doesn't. Huffman coding is a special one. We call the strategy that always choosing the local best option as *greedy* strategy.

Greedy method works for many problems. However, it's not easy to tell if the greedy method can be applied to get the global optimal solution. The generic formal proof is still an active research area. Section 16.4 in [4] provides a good treatment for Matroid tool, which covers many problems that greedy algorithm can be applied.

Change-making problem

We often change money when visiting other countries. People tend to use credit card more often nowadays than before, because it's quite convenient to buy things without considering much about changes. If we changed some money in the bank, there are often some foreign money left by the end of the trip. Some people like to change them to coins for collection. Can we find a solution, which can change the given amount of money with the least number of coins?

Let's use USA coin system for example. There are 5 different coins: 1 cent, 5 cent, 25 cent, 50 cent, and 1 dollar. A dollar is equal to 100 cents. Using the greedy method introduced above, we can always pick the largest coin which is not greater than the remaining amount of money to be changed. Denote list $C = \{1, 5, 25, 50, 100\}$, which stands for the value of coins. For any given money X , the change coins can be generated as below.

$$\text{change}(X, C) = \begin{cases} \phi & : X = 0 \\ \{c_m\} \cup \text{change}(X - c_m, C) & : \textit{otherwise}, \\ & c_m = \max(\{c \in C, c \leq X\}) \end{cases} \quad (14.91)$$

If C is in descending order, c_m can be found as the first one not greater than X . If we want to change 1.42 dollar, This function produces a coin list of $\{100, 25, 5, 5, 5, 1, 1\}$. The output coins list can be easily transformed to contain pairs $\{(100, 1), (25, 1), (5, 3), (1, 2)\}$. That we need one dollar, a quarter, three coins of 5 cent, and 2 coins of 1 cent to make the change. The following Haskell example program outputs result as such.

```

solve x = assoc o change x where
    change 0 _ = []
    change x cs = let c = head $ filter (<= x) cs in c : change (x - c) cs

assoc = (map (\cs -> (head cs, length cs))) o group

```

As mentioned above, this program assumes the coins are in descending order, for instance like below.

```
solve 142 [100, 50, 25, 5, 1]
```

This algorithm is tail recursive, it can be transformed to a imperative looping.

```
1: function CHANGE( $X, C$ )
2:    $R \leftarrow \phi$ 
3:   while  $X \neq 0$  do
4:      $c_m = \max(\{c \in C, c \leq X\})$ 
5:      $R \leftarrow \{c_m\} \cup R$ 
6:      $X \leftarrow X - c_m$ 
7:   return  $R$ 
```

The following example Python program implements this imperative version and manages the result with a dictionary.

```
def change(x, coins):
    cs = {}
    while x  $\neq$  0:
        m = max([c for c in coins if c  $\leq$  x])
        cs[m] = 1 + cs.setdefault(m, 0)
        x = x - m
    return cs
```

For a coin system like USA, the greedy approach can find the optimal solution. The amount of coins is the minimum. Fortunately, our greedy method works in most countries. But it is not always true. For example, suppose a country have coins of value 1, 3, and 4 units. The best change for value 6, is to use two coins of 3 units, however, the greedy method gives a result of three coins: one coin of 4, two coins of 1. Which isn't the optimal result.

Summary of greedy method

As shown in the change making problem, greedy method doesn't always give the best result. In order to find the optimal solution, we need dynamic programming which will be introduced in the next section.

However, the result is often good enough in practice. Let's take the word-wrap problem for example. In modern software editors and browsers, text spans to multiple lines if the length of the content is too long to be hold. With word-wrap supported, user needn't hard line breaking. Although dynamic programming can wrap with the minimum number of lines, it's overkill. On the contrary, greedy algorithm can wrap with lines approximate to the optimal result with quite effective realization as below. Here it wraps text T , not to exceeds line width W , with space s between each word.

```
1:  $L \leftarrow W$ 
2: for  $w \in T$  do
3:   if  $|w| + s > L$  then
4:     Insert line break
5:      $L \leftarrow W - |w|$ 
6:   else
7:      $L \leftarrow L - |w| - s$ 
```

For each word w in the text, it uses a greedy strategy to put as many words in a line as possible unless it exceeds the line width. Many word processors use a similar algorithm to do word-wrapping.

There are many cases, the strict optimal result, but not the approximate one is necessary. Dynamic programming can help to solve such problems.

Dynamic programming

In the change-making problem, we mentioned the greedy method can't always give the optimal solution. For any coin system, are there any way to find the best changes?

Suppose we have find the best solution which makes X value of money. The coins needed are contained in C_m . We can partition these coins into two collections, C_1 and C_2 . They make money of X_1 , and X_2 respectively. We'll prove that C_1 is the optimal solution for X_1 , and C_2 is the optimal solution for X_2 .

Proof. For X_1 , Suppose there exists another solution C'_1 , which uses less coins than C_1 . Then changing solution $C'_1 \cup C_2$ uses less coins to make X than C_m . This is conflict with the fact that C_m is the optimal solution to X . Similarity, we can prove C_2 is the optimal solution to X_2 . \square

Note that it is not true in the reverse situation. If we arbitrary select a value $Y < X$, divide the original problem to find the optimal solutions for sub problems Y and $X - Y$. Combine the two optimal solutions doesn't necessarily yield optimal solution for X . Consider this example. There are coins with value 1, 2, and 4. The optimal solution for making value 6, is to use 2 coins of value 2, and 4; However, if we divide $6 = 3 + 3$, since each 3 can be made with optimal solution $3 = 1 + 2$, the combined solution contains 4 coins ($1 + 1 + 2 + 2$).

If an optimal problem can be divided into several sub optimal problems, we call it has optimal substructure. We see that the change-making problem has optimal substructure. But the dividing has to be done based on the coins, but not with an arbitrary value.

The optimal substructure can be expressed recursively as the following.

$$\text{change}(X) = \begin{cases} \phi & : X = 0 \\ \text{least}(\{c \cup \text{change}(X - c) \mid c \in C, c \leq X\}) & : \text{otherwise} \end{cases} \quad (14.92)$$

For any coin system C , the changing result for zero is empty; otherwise, we check every candidate coin c , which is not greater then value X , and recursively find the best solution for $X - c$; We pick the coin collection which contains the least coins as the result.

Below Haskell example program implements this top-down recursive solution.

```
change _ 0 = []
change cs x = minimumBy (compare `on` length)
                  [c:change cs (x - c) | c <- cs, c <= x]
```

Although this program outputs correct answer `[2, 4]` when evaluates `change [1, 2, 4] 6`, it performs very bad when changing 1.42 dollar with USA coins system. It failed to find the answer within 15 minutes in a computer with 2.7GHz CPU and 8G memory.

The reason why it's slow is because there are a lot of duplicated computing in the top-down recursive solution. When it computes `change(142)`, it needs to examine `change(141)`, `change(137)` and `change(42)`. While `change(141)` next computes to smaller values by deducing with 1, 2, 25, 50 and 100 cents. it will eventually meets value 137, 117, 92, and 42 again. The search space explodes with power of 5.

This is quite similar to compute Fibonacci numbers in a top-down recursive way.

$$F_n = \begin{cases} 1 & : n = 1 \vee n = 2 \\ F_{n-1} + F_{n-2} & : \text{otherwise} \end{cases} \quad (14.93)$$

When we calculate F_8 for example, we recursively calculate F_7 and F_6 . While when we calculate F_7 , we need calculate F_6 again, and F_5 , ... As shown in the below expand forms, the calculation is doubled every time, and the same value is calculate again and again.

$$\begin{aligned}
F_8 &= F_7 + F_6 \\
&= F_6 + F_5 + F_5 + F_4 \\
&= F_5 + F_4 + F_4 + F_3 + F_4 + F_3 + F_3 + F_2 \\
&= \dots
\end{aligned}$$

In order to avoid duplicated computation, a table F can be maintained when calculating the Fibonacci numbers. The first two elements are filled as 1, all others are left blank. During the top-down recursive calculation, if need F_k , we first look up this table for the k -th cell, if it isn't blank, we use that value directly. Otherwise we need further calculation. Whenever a value is calculated, we store it in the corresponding cell for looking up in the future.

```

1:  $F \leftarrow \{1, 1, NIL, NIL, \dots\}$ 
2: function FIBONACCI( $n$ )
3:   if  $n > 2 \wedge F[n] = NIL$  then
4:      $F[n] \leftarrow$  FIBONACCI( $n - 1$ ) + FIBONACCI( $n - 2$ )
5:   return  $F[n]$ 

```

By using the similar idea, we can develop a new top-down change-making solution. We use a table T to maintain the best changes, it is initialized to all empty coin list. During the top-down recursive computation, we look up this table for smaller changing values. Whenever a intermediate value is calculated, it is stored in the table.

```

1:  $T \leftarrow \{\phi, \phi, \dots\}$ 
2: function CHANGE( $X$ )
3:   if  $X > 0 \wedge T[X] = \phi$  then
4:     for  $c \in C$  do
5:       if  $c \leq X$  then
6:          $C_m \leftarrow \{c\} \cup$  CHANGE( $X - c$ )
7:         if  $T[X] = \phi \vee |C_m| < |T[X]|$  then
8:            $T[X] \leftarrow C_m$ 
9:   return  $T[X]$ 

```

The solution to change 0 money is definitely empty ϕ , otherwise, we look up $T[X]$ to retrieve the solution to change X money. If it is empty, we need recursively calculate it. We examine all coins in the coin system C which is not greater than X . This is the sub problem of making changes for money $X - c$. The minimum amount of coins plus one coin of c is stored in $T[X]$ finally as the result.

The following example Python program implements this algorithm just takes 8000 ms to give the answer of changing 1.42 dollar in US coin system.

```

tab = [[] for _ in range(1000)]

def change(x, cs):
    if x > 0 and tab[x] == []:
        for s in [[c] + change(x - c, cs) for c in cs if c <= x]:
            if tab[x] == [] or len(s) < len(tab[x]):
                tab[x] = s
    return tab[x]

```

Another solution to calculate Fibonacci number, is to compute them in order of $F_1, F_2, F_3, \dots, F_n$. This is quite natural when people write down Fibonacci series.

```

1: function FIBO( $n$ )
2:    $F = \{1, 1, NIL, NIL, \dots\}$ 
3:   for  $i \leftarrow 3$  to  $n$  do
4:      $F[i] \leftarrow F[i - 1] + F[i - 2]$ 
5:   return  $F[n]$ 

```

We can use the quite similar idea to solve the change making problem. Starts from zero money, which can be changed by an empty list of coins, we next try to figure out how to change money of value 1. In US coin system for example, A cent can be used; The next values of 2, 3, and 4, can be changed by two coins of 1 cent, three coins of 1 cent, and 4 coins of 1 cent. At this stage, the solution table looks like below

0	1	2	3	4
ϕ	{1}	{1, 1}	{1, 1, 1}	{1, 1, 1, 1}

The interesting case happens for changing value 5. There are two options, use another coin of 1 cent, which need 5 coins in total; The other way is to use 1 coin of 5 cent, which uses less coins than the former. So the solution table can be extended to this.

0	1	2	3	4	5
ϕ	{1}	{1, 1}	{1, 1, 1}	{1, 1, 1, 1}	{5}

For the next change value 6, since there are two types of coin, 1 cent and 5 cent, are less than this value, we need examine both of them.

- If we choose the 1 cent coin, we need next make changes for 5; Since we've already known that the best solution to change 5 is {5}, which only needs a coin of 5 cents, by looking up the solution table, we have one candidate solution to change 6 as {5, 1};
- The other option is to choose the 5 cent coin, we need next make changes for 1; By looking up the solution table we've filled so far, the sub optimal solution to change 1 is {1}. Thus we get another candidate solution to change 6 as {1, 5};

It happens that, both options yield a solution of two coins, we can select either of them as the best solution. Generally speaking, the candidate with fewest number of coins is selected as the solution, and filled into the table.

At any iteration, when we are trying to change the $i < X$ value of money, we examine all the types of coin. For any coin c not greater than i , we look up the solution table to fetch the sub solution $T[i - c]$. The number of coins in this sub solution plus the one coin of c are the total coins needed in this candidate solution. The fewest candidate is then selected and updated to the solution table.

The following algorithm realizes this bottom-up idea.

```

1: function CHANGE( $X$ )
2:    $T \leftarrow \{\phi, \phi, \dots\}$ 
3:   for  $i \leftarrow 1$  to  $X$  do
4:     for  $c \in C, c \leq i$  do
5:       if  $T[i] = \phi \vee 1 + |T[i - c]| < |T[i]|$  then
6:          $T[i] \leftarrow \{c\} \cup T[i - c]$ 
7:   return  $T[X]$ 

```

This algorithm can be directly translated to imperative programs, like Python for example.

```

def changemk(x, cs):
    s = [[] for _ in range(x+1)]
    for i in range(1, x+1):
        for c in cs:
            if c <= i and (s[i] == [] or 1 + len(s[i-c]) < len(s[i])):
                s[i] = [c] + s[i-c]
    return s[x]

```

Observe the solution table, it's easy to find that, there are many duplicated contents being stored.

6	7	8	9	10	...
{1, 5}	{1, 1, 5}	{1, 1, 1, 5}	{1, 1, 1, 1, 5}	{5, 5}	...

This is because the optimal sub solutions are completely copied and saved in parent solution. In order to use less space, we can only record the ‘delta’ part from the sub optimal solution. In change-making problem, it means that we only need to record the coin being selected for value i .

```

1: function CHANGE'(X)
2:    $T \leftarrow \{0, \infty, \infty, \dots\}$ 
3:    $S \leftarrow \{NIL, NIL, \dots\}$ 
4:   for  $i \leftarrow 1$  to  $X$  do
5:     for  $c \in C, c \leq i$  do
6:       if  $1 + T[i - c] < T[i]$  then
7:          $T[i] \leftarrow 1 + T[i - c]$ 
8:          $S[i] \leftarrow c$ 
9:   while  $X > 0$  do
10:    PRINT( $S[X]$ )
11:     $X \leftarrow X - S[X]$ 

```

Instead of recording the complete solution list of coins, this new algorithm uses two tables T and S . T holds the minimum number of coins needed for changing value 0, 1, 2, ...; while S holds the first coin being selected for the optimal solution. For the complete coin list to change money X , the first coin is thus $S[X]$, the sub optimal solution is to change money $X' = X - S[X]$. We can look up table $S[X']$ for the next coin. The coins for sub optimal solutions are repeatedly looked up like this till the beginning of the table. Below Python example program implements this algorithm.

```

def chgm(x, cs):
    cnt = [0] + [x+1] * x
    s = [0]
    for i in range(1, x+1):
        coin = 0
        for c in cs:
            if c  $\leq$  i and  $1 + \text{cnt}[i-c] < \text{cnt}[i]$ :
                cnt[i] = 1 + cnt[i-c]
                coin = c
        s.append(coin)
    r = []
    while x > 0:
        r.append(s[x])
        x = x - s[x]
    return r

```

This change-making solution loops n times for given money n . It examines at most the full coin system in each iteration. The time is bound to $\Theta(nk)$ where k is the number of coins for a certain coin system. The last algorithm adds $O(n)$ spaces to record sub optimal solutions with table T and S .

In purely functional settings, There is no means to mutate the solution table and look up in constant time. One alternative is to use finger tree as we mentioned in previous chapter ¹². We can store the minimum number of coins, and the coin leads to the sub optimal solution in pairs.

The solution table, which is a finger tree, is initialized as $T = \{(0,0)\}$. It means change 0 money need no coin. We can fold on list $\{1, 2, \dots, X\}$, start from this table, with a binary function $change(T, i)$. The folding will build the solution table, and we can construct the coin list from this table by function $make(X, T)$.

$$makeChange(X) = make(X, fold(change, \{(0,0)\}, \{1, 2, \dots, X\})) \quad (14.94)$$

¹²Some purely functional programming environments, Haskell for instance, provide built-in array; while other almost pure ones, such as ML, provide mutable array

In function $change(T, i)$, all the coins not greater than i are examined to select the one lead to the best result. The fewest number of coins, and the coin being selected are formed to a pair. This pair is inserted to the finger tree, so that a new solution table is returned.

$$change(T, i) = insert(T, fold(sel, (\infty, 0), \{c | c \in C, c \leq i\})) \quad (14.95)$$

Again, folding is used to select the candidate with the minimum number of coins. This folding starts with initial value $(\infty, 0)$, on all valid coins. function $sel((n, c), c')$ accepts two arguments, one is a pair of length and coin, which is the best solution so far; the other is a candidate coin, it examines if this candidate can make better solution.

$$sel((n, c), c') = \begin{cases} (1 + n', c') & : 1 + n' < n, (n', c') = T[i - c'] \\ (n, c) & : otherwise \end{cases} \quad (14.96)$$

After the solution table is built, the coins needed can be generated from it.

$$make(X, T) = \begin{cases} \phi & : X = 0 \\ \{c\} \cup make(X - c, T) & : otherwise, (n, c) = T[X] \end{cases} \quad (14.97)$$

The following example Haskell program uses `Data.Sequence`, which is the library of finger tree, to implement change making solution.

```
import Data.Sequence (Seq, singleton, index, (>))

changemk x cs = makeChange x $ foldl change (singleton (0, 0)) [1..x] where
  change tab i = let sel c = min (1 + fst (index tab (i - c)), c)
                in tab |> (foldr sel ((x + 1), 0) $ filter (<= i) cs)
  makeChange 0 _ = []
  makeChange x tab = let c = snd $ index tab x in c : makeChange (x - c) tab
```

It's necessary to memorize the optimal solution to sub problems no matter using the top-down or the bottom-up approach. This is because a sub problem is used many times when computing the overall optimal solution. Such properties are called overlapping sub problems.

Properties of dynamic programming

Dynamic programming was originally named by Richard Bellman in 1940s. It is a powerful tool to search for optimal solution for problems with two properties.

- Optimal sub structure. The problem can be broken down into smaller problems, and the optimal solution can be constructed efficiently from solutions of these sub problems;
- Overlapping sub problems. The problem can be broken down into sub problems which are reused several times in finding the overall solution.

The change-making problem, as we've explained, has both optimal sub structures, and overlapping sub problems.

Longest common subsequence problem

The longest common subsequence problem, is different with the longest common substring problem. We've show how to solve the later in the chapter of suffix tree. The longest common subsequence needn't be consecutive part of the original sequence.

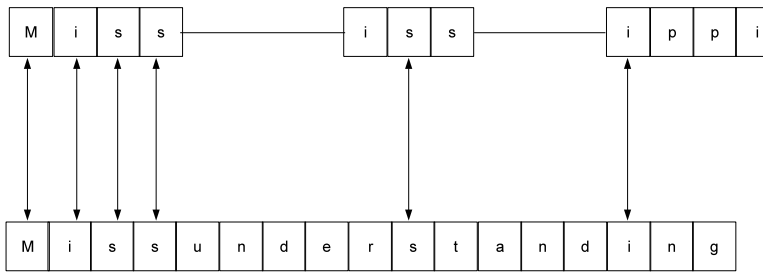


Figure 14.50: The longest common subsequence

For example, The longest common substring for text “Mississippi”, and “Missunderstanding” is “Miss”, while the longest common subsequence for them are “Misssi”. This is shown in figure 14.50.

If we rotate the figure vertically, and consider the two texts as two pieces of source code, it turns to be a ‘diff’ result between them. Most modern version control tools need calculate the difference content among the versions. The longest common subsequence problem plays a very important role.

If either one of the two strings X and Y is empty, the longest common subsequence $LCS(X, Y)$ is definitely empty; Otherwise, denote $X = \{x_1, x_2, \dots, x_n\}$, $Y = \{y_1, y_2, \dots, y_m\}$, if the first elements x_1 and y_1 are same, we can recursively find the longest subsequence of $X' = \{x_2, x_3, \dots, x_n\}$ and $Y' = \{y_2, y_3, \dots, y_m\}$. And the final result $LCS(X, Y)$ can be constructed by concatenating x_1 with $LCS(X', Y')$; Otherwise if $x_1 \neq y_1$, we need recursively find the longest common subsequences of $LCS(X, Y')$ and $LCS(X', Y)$, and pick the longer one as the final result. Summarize these cases gives the below definition.

$$LCS(X, Y) = \begin{cases} \phi & : X = \phi \vee Y = \phi \\ \{x_1\} \cup LCS(X', Y') & : x_1 = y_1 \\ \text{longer}(LCS(X, Y'), LCS(X', Y)) & : \text{otherwise} \end{cases} \quad (14.98)$$

Note that this algorithm shows clearly the optimal substructure, that the longest common subsequence problem can be broken to smaller problems. The sub problem is ensured to be at least one element shorter than the original one.

It’s also clear that, there are overlapping sub-problems. The longest common subsequences to the sub strings are used multiple times in finding the overall optimal solution.

The existence of these two properties, the optimal substructure and the overlapping sub-problem, indicates the dynamic programming can be used to solve this problem.

A 2-dimension table can be used to record the solutions to the sub-problems. The rows and columns represent the substrings of X and Y respectively.

		a	n	t	e	n	n	a
		1	2	3	4	5	6	7
b	1							
a	2							
n	3							
a	4							
n	5							
a	6							

This table shows an example of finding the longest common subsequence for strings “antenna” and “banana”. Their lengths are 7, and 6. The right bottom corner of this table is looked up first, Since it’s empty we need compare the 7th element in “antenna” and the 6th in “banana”, they are both ‘a’, Thus we need next recursively look up the cell at row 5, column 6; It’s still empty, and we repeated this till either get a trivial case that one substring becomes empty, or some cell we are looking up has been filled before. Similar to the change-making problem, whenever the optimal solution for a sub-problem is found, it is recorded in the cell for further reusing. Note that this process is in the reversed order comparing to the recursive equation given above, that we start from the right most element of each string.

Considering that the longest common subsequence for any empty string is still empty, we can extended the solution table so that the first row and column hold the empty strings.

		a	n	t	e	n	n	a
		ϕ	ϕ	ϕ	ϕ	ϕ	ϕ	ϕ
b	ϕ							
a	ϕ							
n	ϕ							
a	ϕ							
n	ϕ							
a	ϕ							

Below algorithm realizes the top-down recursive dynamic programming solution with such a table.

```

1:  $T \leftarrow \text{NIL}$ 
2: function LCS( $X, Y$ )
3:    $m \leftarrow |X|, n \leftarrow |Y|$ 
4:    $m' \leftarrow m + 1, n' \leftarrow n + 1$ 
5:   if  $T = \text{NIL}$  then
6:      $T \leftarrow \{\{\phi, \phi, \dots, \phi\}, \{\phi, \text{NIL}, \text{NIL}, \dots\}, \dots\}$   $\triangleright m' \times n'$ 
7:   if  $X \neq \phi \wedge Y \neq \phi \wedge T[m'][n'] = \text{NIL}$  then
8:     if  $X[m] = Y[n]$  then
9:        $T[m'][n'] \leftarrow \text{APPEND}(\text{LCS}(X[1..m - 1], Y[1..n - 1]), X[m])$ 
10:    else
11:       $T[m'][n'] \leftarrow \text{LONGER}(\text{LCS}(X, Y[1..n - 1]), \text{LCS}(X[1..m - 1], Y))$ 
12:    return  $T[m'][n']$ 

```

The table is firstly initialized with the first row and column filled with empty strings; the rest are all NIL values. Unless either string is empty, or the cell content isn’t NIL, the last two elements of the strings are compared, and recursively computes the longest common subsequence with substrings. The following Python example program implements this algorithm.

```

def lcs(xs, ys):
    m = len(xs)
    n = len(ys)

```

```

global tab
if tab is None:
    tab = [[]]*(n+1) + [[]] + [None]*n for _ in xrange(m)
if m  $\neq$  0 and n  $\neq$  0 and tab[m][n] is None:
    if xs[-1] == ys[-1]:
        tab[m][n] = lcs(xs[:-1], ys[:-1]) + xs[-1]
    else:
        (a, b) = (lcs(xs, ys[:-1]), lcs(xs[:-1], ys))
        tab[m][n] = a if len(b) < len(a) else b
return tab[m][n]

```

The longest common subsequence can also be found in a bottom-up manner as what we've done with the change-making problem. Besides that, instead of recording the whole sequences in the table, we can just store the lengths of the longest subsequences, and later construct the subsubsequence with this table and the two strings. This time, the table is initialized with all values set as 0.

```

1: function LCS( $X, Y$ )
2:    $m \leftarrow |X|, n \leftarrow |Y|$ 
3:    $T \leftarrow \{\{0, 0, \dots\}, \{0, 0, \dots\}, \dots\}$   $\triangleright (m+1) \times (n+1)$ 
4:   for  $i \leftarrow 1$  to  $m$  do
5:     for  $j \leftarrow 1$  to  $n$  do
6:       if  $X[i] = Y[j]$  then
7:          $T[i+1][j+1] \leftarrow T[i][j] + 1$ 
8:       else
9:          $T[i+1][j+1] \leftarrow \text{MAX}(T[i][j+1], T[i+1][j])$ 
10:  return GET( $T, X, Y, m, n$ )

11: function GET( $T, X, Y, i, j$ )
12:  if  $i = 0 \vee j = 0$  then
13:    return  $\phi$ 
14:  else if  $X[i] = Y[j]$  then
15:    return APPEND(GET( $T, X, Y, i-1, j-1$ ),  $X[i]$ )
16:  else if  $T[i-1][j] > T[i][j-1]$  then
17:    return GET( $T, X, Y, i-1, j$ )
18:  else
19:    return GET( $T, X, Y, i, j-1$ )

```

In the bottom-up approach, we start from the cell at the second row and the second column. The cell is corresponding to the first element in both X , and Y . If they are same, the length of the longest common subsequence so far is 1. This can be yielded by increasing the length of empty sequence, which is stored in the top-left cell, by one; Otherwise, we pick the maximum value from the upper cell and left cell. The table is repeatedly filled in this manner.

After that, a back-track is performed to construct the longest common subsequence. This time we start from the bottom-right corner of the table. If the last elements in X and Y are same, we put this element as the last one of the result, and go on looking up the cell along the diagonal line; Otherwise, we compare the values in the left cell and the above cell, and go on looking up the cell with the bigger value.

The following example Python program implements this algorithm.

```

def lcs(xs, ys):
    m = len(xs)
    n = len(ys)
    c = [[0]*(n+1) for _ in xrange(m+1)]
    for i in xrange(1, m+1):
        for j in xrange(1, n+1):

```

```

        if xs[i-1] == ys[j-1]:
            c[i][j] = c[i-1][j-1] + 1
        else:
            c[i][j] = max(c[i-1][j], c[i][j-1])

    return get(c, xs, ys, m, n)

def get(c, xs, ys, i, j):
    if i==0 or j==0:
        return []
    elif xs[i-1] == ys[j-1]:
        return get(c, xs, ys, i-1, j-1) + [xs[i-1]]
    elif c[i-1][j] > c[i][j-1]:
        return get(c, xs, ys, i-1, j)
    else:
        return get(c, xs, ys, i, j-1)

```

The bottom-up dynamic programming solution can also be defined in purely functional way. The finger tree can be used as a table. The first row is filled with $n + 1$ zero values. This table can be built by folding on sequence X . Then the longest common subsequence is constructed from the table.

$$LCS(X, Y) = \text{construct}(\text{fold}(f, \{\{0, 0, \dots, 0\}\}, \text{zip}(\{1, 2, \dots\}, X))) \quad (14.99)$$

Note that, since the table need be looked up by index, X is zipped with natural numbers. Function f creates a new row of this table by folding on sequence Y , and records the lengths of the longest common sequence for all possible cases so far.

$$f(T, (i, x)) = \text{insert}(T, \text{fold}(\text{longest}, \{0\}, \text{zip}(\{1, 2, \dots\}, Y))) \quad (14.100)$$

Function *longest* takes the intermediate filled row result, and a pair of index and element in Y , it compares if this element is the same as the one in X . Then fills the new cell with the length of the longest one.

$$\text{longest}(R, (j, y)) = \begin{cases} \text{insert}(R, 1 + T[i-1][j-1]) & : x = y \\ \text{insert}(R, \max(T[i-1][j], T[i][j-1])) & : \text{otherwise} \end{cases} \quad (14.101)$$

After the table is built. The longest common sub sequence can be constructed recursively by looking up this table. We can pass the reversed sequences \overleftarrow{X} , and \overleftarrow{Y} together with their lengths m and n for efficient building.

$$\text{construct}(T) = \text{get}((\overleftarrow{X}, m), (\overleftarrow{Y}, n)) \quad (14.102)$$

If the sequences are not empty, denote the first elements as x and y . The rest elements are hold in \overleftarrow{X}' and \overleftarrow{Y}' respectively. The function *get* can be defined as the following.

$$\text{get}((\overleftarrow{X}, i), (\overleftarrow{Y}, j)) = \begin{cases} \phi & : \overleftarrow{X} = \phi \wedge \overleftarrow{Y} = \phi \\ \text{get}((\overleftarrow{X}', i-1), (\overleftarrow{Y}', j-1)) \cup \{x\} & : x = y \\ \text{get}((\overleftarrow{X}', i-1), (\overleftarrow{Y}, j)) & : T[i-1][j] > T[i][j-1] \\ \text{get}((\overleftarrow{X}, i), (\overleftarrow{Y}', j-1)) & : \text{otherwise} \end{cases} \quad (14.103)$$

Below Haskell example program implements this solution.

```

lcs' xs ys = construct $ foldl f (singleton $ fromList $ replicate (n+1) 0)
              (zip [1..] xs) where
  (m, n) = (length xs, length ys)
  f tab (i, x) = tab |> (foldl longer (singleton 0) (zip [1..] ys)) where
    longer r (j, y) = r |> if x == y

```

```

                then 1 + (tab `index` (i-1) `index` (j-1))
                else max (tab `index` (i-1) `index` j) (r `index` (j-1))
construct tab = get (reverse xs, m) (reverse ys, n) where
  get ([], 0) ([], 0) = []
  get ((x:xs), i) ((y:ys), j)
    | x == y = get (xs, i-1) (ys, j-1) ++ [x]
    | (tab `index` (i-1) `index` j) > (tab `index` i `index` (j-1)) =
      get (xs, i-1) ((y:ys), j)
    | otherwise = get ((x:xs), i) (ys, j-1)

```

Subset sum problem

Dynamic programming does not limit to solve the optimization problem, but can also solve some more general searching problems. Subset sum problem is such an example. Given a set of integers, is there a non-empty subset sums to zero? for example, there are two subsets of $\{11, 64, -82, -68, 86, 55, -88, -21, 51\}$ both sum to zero. One is $\{64, -82, 55, -88, 51\}$, the other is $\{64, -82, -68, 86\}$.

Of course summing to zero is a special case, because sometimes, people want to find a subset, whose sum is a given value s . Here we are going to develop a method to find all the candidate subsets.

There is obvious a brute-force exhausting search solution. For every element, we can either pick it or not. So there are total 2^n options for set with n elements. Because for every selection, we need check if it sums to s . This is a linear operation. The overall complexity is bound to $O(n2^n)$. This is the exponential algorithm, which takes very huge time if the set is big.

There is a recursive solution to subset sum problem. If the set is empty, there is no solution definitely; Otherwise, let the set is $X = \{x_1, x_2, \dots\}$. If $x_1 = s$, then subset $\{x_1\}$ is a solution, we need next search for subsets $X' = \{x_2, x_3, \dots\}$ for those sum to s ; Otherwise if $x_1 \neq s$, there are two different kinds of possibilities. We need search X' for both sum s , and sum $s - x_1$. For any subset sum to $s - x_1$, we can add x_1 to it to form a new set as a solution. The following equation defines this algorithm.

$$\text{solve}(X, s) = \begin{cases} \phi & : X = \phi \\ \{\{x_1\}\} \cup \text{solve}(X', s) & : x_1 = s \\ \text{solve}(X', s) \cup \{\{x_1\}\} \cup \{S \mid S \in \text{solve}(X', s - x_1)\} & : \text{otherwise} \end{cases} \quad (14.104)$$

There are clear substructures in this definition, although they are not in a sense of optimal. And there are also overlapping sub-problems. This indicates the problem can be solved with dynamic programming with a table to memorize the solutions to sub-problems.

Instead of developing a solution to output all the subsets directly, let's consider how to give the existence answer firstly. That output 'yes' if there exists some subset sum to s , and 'no' otherwise.

One fact is that, the upper and lower limit for all possible answer can be calculated in one scan. If the given sum s doesn't belong to this range, there is no solution obviously.

$$\begin{cases} s_l = \sum\{x \in X, x < 0\} \\ s_u = \sum\{x \in X, x > 0\} \end{cases} \quad (14.105)$$

Otherwise, if $s_l \leq s \leq s_u$, since the values are all integers, we can use a table, with $s_u - s_l + 1$ columns, each column represents a possible value in this range, from s_l to s_u . The value of the cell is either true or false to represents if there exists subset sum to this value. All cells are initialized as false. Starts from the first element x_1 in X , definitely, set $\{x_1\}$ can sum to x_1 , so that the cell represents this value in the first row can be filled as true.

	s_l	$s_l + 1$...	x_1	...	s_u
x_1	F	F	...	T	...	F

With the next element x_2 , There are three possible sums. Similar as the first row, $\{x_2\}$ sums to x_2 ; For all possible sums in previous row, they can also been achieved without x_2 . So the cell below to x_1 should also be filled as true; By adding x_2 to all possible sums so far, we can also get some new values. That the cell represents $x_1 + x_2$ should be true.

	s_l	$s_l + 1$...	x_1	...	x_2	...	$x_1 + x_2$...	s_u
x_1	F	F	...	T	...	F	...	F	...	F
x_2	F	F	...	T	...	T	...	T	...	F

Generally speaking, when fill the i -th row, all the possible sums constructed with $\{x_1, x_2, \dots, x_{i-1}\}$ so far can also be achieved with x_i . So the cells previously are true should also be true in this new row. The cell represents value x_i should also be true since the singleton set $\{x_i\}$ sums to it. And we can also adds x_i to all previously constructed sums to get the new results. Cells represent these new sums should also be filled as true.

When all the elements are processed like this, a table with $|X|$ rows is built. Looking up the cell represents s in the last row tells if there exists subset can sum to this value. As mentioned above, there is no solution if $s < s_l$ or $s_u < s$. We skip handling this case for the sake of brevity.

```

1: function SUBSET-SUM( $X, s$ )
2:    $s_l \leftarrow \sum\{x \in X, x < 0\}$ 
3:    $s_u \leftarrow \sum\{x \in X, x > 0\}$ 
4:    $n \leftarrow |X|$ 
5:    $T \leftarrow \{\{False, False, \dots\}, \{False, False, \dots\}, \dots\}$   $\triangleright n \times (s_u - s_l + 1)$ 
6:   for  $i \leftarrow 1$  to  $n$  do
7:     for  $j \leftarrow s_l$  to  $s_u$  do
8:       if  $X[i] = j$  then
9:          $T[i][j] \leftarrow True$ 
10:      if  $i > 1$  then
11:         $T[i][j] \leftarrow T[i][j] \vee T[i-1][j]$ 
12:         $j' \leftarrow j - X[i]$ 
13:        if  $s_l \leq j' \leq s_u$  then
14:           $T[i][j] \leftarrow T[i][j] \vee T[i-1][j']$ 
15:   return  $T[n][s]$ 

```

Note that the index to the columns of the table, doesn't range from 1 to $s_u - s_l + 1$, but maps directly from s_l to s_u . Because most programming environments don't support negative index, this can be dealt with $T[i][j - s_l]$. The following example Python program utilizes the property of negative indexing.

```

def solve(xs, s):
    low = sum([x for x in xs if x < 0])
    up = sum([x for x in xs if x > 0])
    tab = [[False]*(up-low+1) for _ in xs]
    for i in xrange(0, len(xs)):
        for j in xrange(low, up+1):
            tab[i][j] = (xs[i] == j)
            j1 = j - xs[i];
            tab[i][j] = tab[i][j] or tab[i-1][j] or
                (low <= j1 and j1 <= up and tab[i-1][j1])
    return tab[-1][s]

```

Note that this program doesn't use different branches for $i = 0$ and $i = 1, 2, \dots, n - 1$. This is because when $i = 0$, the row index to $i - 1 = -1$ refers to the last row in the table, which are all false. This simplifies the logic one more step.

With this table built, it's easy to construct all subsets sum to s . The method is to

look up the last row for cell represents s . If the last element $x_n = s$, then $\{x_n\}$ definitely is a candidate. We next look up the previous row for s , and recursively construct all the possible subsets sum to s with $\{x_1, x_2, x_3, \dots, x_{n-1}\}$. Finally, we look up the second last row for cell represents $s - x_n$. And for every subset sums to this value, we add element x_n to construct a new subset, which sums to s .

```

1: function GET( $X, s, T, n$ )
2:    $S \leftarrow \phi$ 
3:   if  $X[n] = s$  then
4:      $S \leftarrow S \cup \{X[n]\}$ 
5:   if  $n > 1$  then
6:     if  $T[n-1][s]$  then
7:        $S \leftarrow S \cup \text{GET}(X, s, T, n-1)$ 
8:     if  $T[n-1][s - X[n]]$  then
9:        $S \leftarrow S \cup \{\{X[n]\} \cup S' \mid S' \in \text{GET}(X, s - X[n], T, n-1)\}$ 
10:  return  $S$ 

```

The following Python example program translates this algorithm.

```

def get(xs, s, tab, n):
    r = []
    if xs[n] == s:
        r.append([xs[n]])
    if n > 0:
        if tab[n-1][s]:
            r = r + get(xs, s, tab, n-1)
        if tab[n-1][s - xs[n]]:
            r = r + [[xs[n]] + ys for ys in get(xs, s - xs[n], tab, n-1)]
    return r

```

This dynamic programming solution to subset sum problem loops $O(n(s_u - s_l + 1))$ times to build the table, and recursively uses $O(n)$ time to construct the final solution from this table. The space it used is also bound to $O(n(s_u - s_l + 1))$.

Instead of using table with n rows, a vector can be used alternatively. For every cell represents a possible sum, the list of subsets are stored. This vector is initialized to contain all empty sets. For every element in X , we update the vector, so that it records all the possible sums which can be built so far. When all the elements are considered, the cell corresponding to s contains the final result.

```

1: function SUBSET-SUM( $X, s$ )
2:    $s_l \leftarrow \sum\{x \in X, x < 0\}$ 
3:    $s_u \leftarrow \sum\{x \in X, x > 0\}$ 
4:    $T \leftarrow \{\phi, \phi, \dots\}$   $\triangleright s_u - s_l + 1$ 
5:   for  $x \in X$  do
6:      $T' \leftarrow \text{DUPLICATE}(T)$ 
7:     for  $j \leftarrow s_l$  to  $s_u$  do
8:        $j' \leftarrow j - x$ 
9:       if  $x = j$  then
10:         $T'[j] \leftarrow T'[j] \cup \{x\}$ 
11:       if  $s_l \leq j' \leq s_u \wedge T[j'] \neq \phi$  then
12:         $T'[j] \leftarrow T'[j] \cup \{\{x\} \cup S \mid S \in T[j']\}$ 
13:      $T \leftarrow T'$ 
14:  return  $T[s]$ 

```

The corresponding Python example program is given as below.

```

def subsetsum(xs, s):
    low = sum([x for x in xs if x < 0])

```

```

up = sum([x for x in xs if x > 0])
tab = [[] for _ in xrange(low, up+1)]
for x in xs:
    tab1 = tab[:]
    for j in xrange(low, up+1):
        if x == j:
            tab1[j].append([x])
        j1 = j - x
        if low ≤ j1 and j1 ≤ up and tab[j1] ≠ []:
            tab1[j] = tab1[j] + [[x] + ys for ys in tab[j1]]
    tab = tab1
return tab[s]

```

This imperative algorithm shows a clear structure, that the solution table is built by looping every element. This can be realized in purely functional way by folding. A finger tree can be used to represent the vector spans from s_l to s_u . It is initialized with all empty values as in the following equation.

$$\text{subsetsum}(X, s) = \text{fold}(\text{build}, \{\phi, \phi, \dots\}, X)[s] \quad (14.106)$$

After folding, the solution table is built, the answer is looked up at cell s ¹³.

For every element $x \in X$, function *build* folds the list $\{s_l, s_l + 1, \dots, s_u\}$, with every value j , it checks if it equals to x and appends the singleton set $\{x\}$ to the j -th cell. Not that here the cell is indexed from s_l , but not 0. If the cell corresponding to $j - x$ is not empty, the candidate solutions stored in that place are also duplicated and add element x is added to every solution.

$$\text{build}(T, x) = \text{fold}(f, T, \{s_l, s_l + 1, \dots, s_u\}) \quad (14.107)$$

$$f(T, j) = \begin{cases} T'[j] \cup \{\{x\} \cup Y \mid Y \in T[j']\} & : s_l \leq j' \leq s_u \wedge T[j'] \neq \phi, j' = j - x \\ T' & : \text{otherwise} \end{cases} \quad (14.108)$$

Here the adjustment is applied on T' , which is another adjustment to T as shown as below.

$$T' = \begin{cases} \{x\} \cup T[j] & : x = j \\ T & : \text{otherwise} \end{cases} \quad (14.109)$$

Note that the first clause in both equation (14.108) and (14.109) return a new table with certain cell being updated with the given value.

The following Haskell example program implements this algorithm.

```

subsetsum xs s = foldl build (fromList [[] | _ <- [l..u]]) xs `idx` s where
  l = sum $ filter (< 0) xs
  u = sum $ filter (> 0) xs
  idx t i = index t (i - l)
  build tab x = foldl (\t j → let j' = j - x in
    adjustIf (l ≤ j' && j' ≤ u && tab `idx` j' /= [])
      (++) [(x:ys) | ys <- tab `idx` j'] j
      (adjustIf (x == j) ([x]:) j t)) tab [l..u]
  adjustIf pred f i seq = if pred then adjust f (i - l) seq else seq

```

Some materials like [16] provide common structures to abstract dynamic programming. So that problems can be solved with a generic solution by customizing the precondition, the comparison of candidate solutions for better choice, and the merge method for sub solutions. However, the variety of problems makes things complex in practice. It's important to study the properties of the problem carefully.

¹³Again, here we skip the error handling to the case that $s < s_l$ or $s > s_u$. There is no solution if s is out of range.

Exercise 14.3

- Realize a maze solver by using the stack approach, which can find all the possible paths.
- There are 92 distinct solutions for the 8 queens puzzle. For any one solution, rotating it 90° , 180° , 270° gives solutions too. Also flipping it vertically and horizontally also generate solutions. Some solutions are symmetric, so that rotation or flip gives the same one. There are 12 unique solutions in this sense. Modify the program to find the 12 unique solutions. Improve the program, so that the 92 distinct solutions can be found with fewer search.
- Make the 8 queens puzzle solution generic so that it can solve n queens puzzle.
- Make the functional solution to the leap frogs puzzle generic, so that it can solve n frogs case.
- Modify the wolf, goat, and cabbage puzzle algorithm, so that it can find all possible solutions.
- Give the complete algorithm definition to solve the 2 water jugs puzzle with extended Euclid algorithm.
- We needn't the exact linear combination information x and y in fact. After we know the puzzle is solvable by testing with GCD, we can blindly execute the process that: fill A , pour A into B , whenever B is full, empty it till there is expected volume in one jug. Realize this solution. Can this one find faster solution than the original version?
- Compare to the extended Euclid method, the BFS approach is a kind of brute-force searching. Improve the extended Euclid approach by finding the best linear combination which minimize $|x| + |y|$.
- John Horton Conway introduced the sliding tile puzzle. Figure 14.51 shows a simplified version. There are 8 cells, 7 of them are occupied by pieces labeled from 1 to 7. Each piece can slide to the free cell if they are connected. The line between cells means there is a connectoin. The goal is to reverse the pieces from 1, 2, 3, 4, 5, 6, 7 to 7, 6, 5, 4, 3, 2, 1 by sliding. Develop a program to solve this puzzle.

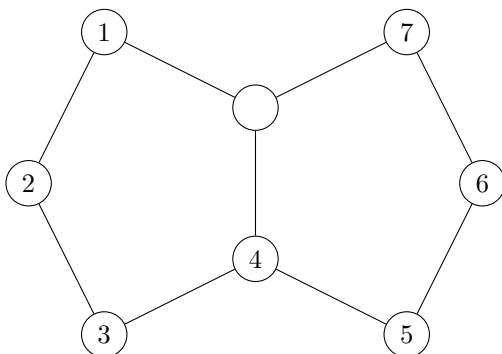


Figure 14.51: Conway sliding puzzle

- Realize the imperative Huffman code table generating algorithm.

- One option to realize the bottom-up solution for the longest common subsequence problem is to record the direction in the table. Thus, instead of storing the length information, three values like 'N', for north, 'W' for west, and 'NW' for northwest are used to indicate how to construct the final result. We start from the bottom-right corner of the table, if the cell value is 'NW', we go along the diagonal by moving to the cell in the upper-left; if it's 'N', we move vertically to the upper row; and move horizontally if it's 'W'. Implement this approach in your favorite programming language.
- Given a list of non-negative integers, find the maximum sum composed by numbers that none of them are adjacent.
- Levenshtein edit distance is defined as the cost of converting from one string s to another string t . It is widely used in spell-checking, OCR correction etc. There are three operations allowed in Levenshtein edit distance. Insert a character; delete a character; and substitute a character. Each operation mutate one character a time. The following exaple shows how to convert string “kitten” to “sitting”. The Levenshtein edit distance is 3 in this case.
 1. kitten → sitten (substitution of 's' for 'k');
 2. sitten → sittin (substitution of 'i' for 'e');
 3. sitten → sitting (insertion of 'g' at the end).

Develop a program to calculate Levenshtein edit distance for two strings with Dynamic Programming.

14.4 Short summary

This chapter introduces the elementary methods about searching. Some of them instruct the computer to scan for interesting information among the data. They often have some structure, that can be updated during the scan. This can be considered as a special case for the information reusing approach. The other commonly used strategy is divide and conquer, that the scale of the search domain is kept decreasing till some obvious result. This chapter also explains methods to search for solutions among domains. The solutions typically are not the elements being searched. They can be a series of decisions or some operation arrangement. If there are multiple solutions, sometimes, people want to find the optimized one. For some spacial cases, there exist simplified approach such as the greedy methods. And dynamic programming can be used for more wide range of problems when they shows optimal substructures.

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Appendix A

Imperative delete for red-black tree

We need handle more cases for imperative *delete* than *insert*. To resume balance after cutting off a node from the red-black tree, we perform rotations and re-coloring. When delete a black node, rule 5 will be violated because the number of black nodes along the path through that node reduces by one. We introduce ‘doubly-black’ to maintain the number of black nodes unchanged. Below example program adds ‘doubly black’ to the color definition:

```
data Color {RED, BLACK, DOUBLY_BLACK}
```

When delete a node, we re-use the binary search tree *delete* in the first step, then further fix the balance if the node is black.

```
1: function DELETE( $T, x$ )
2:    $p \leftarrow$  PARENT( $x$ )
3:    $q \leftarrow$  NIL
4:   if LEFT( $x$ ) = NIL then
5:      $q \leftarrow$  RIGHT( $x$ )
6:     REPLACE( $x$ , RIGHT( $x$ ))           ▷ replace  $x$  with its right sub-tree
7:   else if RIGHT( $x$ ) = NIL then
8:      $q \leftarrow$  LEFT( $x$ )
9:     REPLACE( $x$ , LEFT( $x$ ))           ▷ replace  $x$  with its left sub-tree
10:  else
11:     $y \leftarrow$  MIN(RIGHT( $x$ ))
12:     $p \leftarrow$  PARENT( $y$ )
13:     $q \leftarrow$  RIGHT( $y$ )
14:    KEY( $x$ )  $\leftarrow$  KEY( $y$ )
15:    copy data from  $y$  to  $x$ 
16:    REPLACE( $y$ , RIGHT( $y$ ))           ▷ replace  $y$  with its right sub-tree
17:     $x \leftarrow y$ 
18:  if COLOR( $x$ ) = BLACK then
19:     $T \leftarrow$  DELETE-FIX( $T$ , MAKE-BLACK( $p, q$ ),  $q =$  NIL?)
20:  release  $x$ 
21:  return  $T$ 
```

DELETE takes the root T and the node x to be deleted as the parameters. x can be located through *lookup*. If x has an empty sub-tree, we cut off x , then replace it with the other sub-tree q . Otherwise, we locate the minimum node y in the right sub-tree of

x , then replace x with y . We cut off y after that. If x is black, we call $\text{MAKE-BLACK}(p, q)$ to maintain the blackness before further fixing.

```

1: function MAKE-BLACK( $p, q$ )
2:   if  $p = \text{NIL}$  and  $q = \text{NIL}$  then
3:     return NIL ▷ The tree was singleton
4:   else if  $q = \text{NIL}$  then
5:      $n \leftarrow \text{Doubly Black NIL}$ 
6:      $\text{PARENT}(n) \leftarrow p$ 
7:     return  $n$ 
8:   else
9:     return BLACKEN( $q$ )

```

If both p and q are empty, we are deleting the only leaf from a singleton tree. The result is empty. If the parent p is not empty, but q is, we are deleting a black leaf. We use NIL to replace that black leaf. As NIL is already black, we change it to 'doubly black' NIL to maintain the blackness. Otherwise, if neither p nor q is empty, we call $\text{BLACKEN}(q)$. If q is red, it changes to black; if q is already black, it changes to doubly black. As the next step, we need eliminate the doubly blackness through tree rotations and re-coloring. There are three different cases ([4], pp292). The doubly black node can be NIL or not in all the cases.

Case 1. *The sibling of the doubly black node is black, and it has a red sub-tree.* We can rotate the tree to fix the doubly black. There are 4 sub-cases, all can be transformed to a uniformed structure as shown in figure A.1.

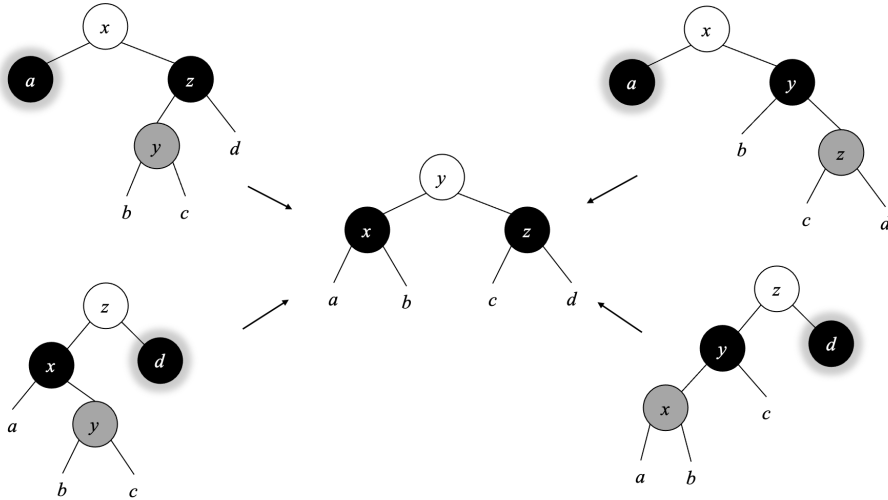


Figure A.1: The doubly black node has a black sibling, and a red nephew. It can be fixed with a rotation.

```

1: function DELETE-FIX( $T, x, f$ )
2:    $n \leftarrow \text{NIL}$ 
3:   if  $f = \text{True}$  then ▷  $x$  is doubly black NIL
4:      $n \leftarrow x$ 
5:   if  $x = \text{NIL}$  then ▷ Delete the singleton leaf
6:     return NIL
7:   while  $x \neq T$  and  $\text{COLOR}(x) = \mathcal{B}^2$  do ▷  $x$  is doubly black, but not the root
8:     if  $\text{SIBLING}(x) \neq \text{NIL}$  then ▷ The sibling is not empty
9:        $s \leftarrow \text{SIBLING}(x)$ 

```

```

10:      ...
11:      if  $s$  is black and  $\text{LEFT}(s)$  is red then
12:          if  $x = \text{LEFT}(\text{PARENT}(x))$  then ▷  $x$  is the left
13:              set  $x$ ,  $\text{PARENT}(x)$ , and  $\text{LEFT}(s)$  all black
14:               $T \leftarrow \text{ROTATE-RIGHT}(T, s)$ 
15:               $T \leftarrow \text{ROTATE-LEFT}(T, \text{PARENT}(x))$ 
16:          else ▷  $x$  is the right
17:              set  $x$ ,  $\text{PARENT}(x)$ ,  $s$ , and  $\text{LEFT}(s)$  all black
18:               $T \leftarrow \text{ROTATE-RIGHT}(T, \text{PARENT}(x))$ 
19:      else if  $s$  is black and  $\text{RIGHT}(s)$  is red then
20:          if  $x = \text{LEFT}(\text{PARENT}(x))$  then ▷  $x$  is the left
21:              set  $x$ ,  $\text{PARENT}(x)$ ,  $s$ , and  $\text{RIGHT}(s)$  all black
22:               $T \leftarrow \text{ROTATE-LEFT}(T, \text{PARENT}(x))$ 
23:          else ▷  $x$  is the right
24:              set  $x$ ,  $\text{PARENT}(x)$ , and  $\text{RIGHT}(s)$  all black
25:               $T \leftarrow \text{ROTATE-LEFT}(T, s)$ 
26:               $T \leftarrow \text{ROTATE-RIGHT}(T, \text{PARENT}(x))$ 
27:      ...

```

Case 2. *The sibling of the doubly black is red.* We can rotate the tree to change the doubly black node to black. As shown in figure A.2, change a or c to black. We can add this fixing to the previous implementation.

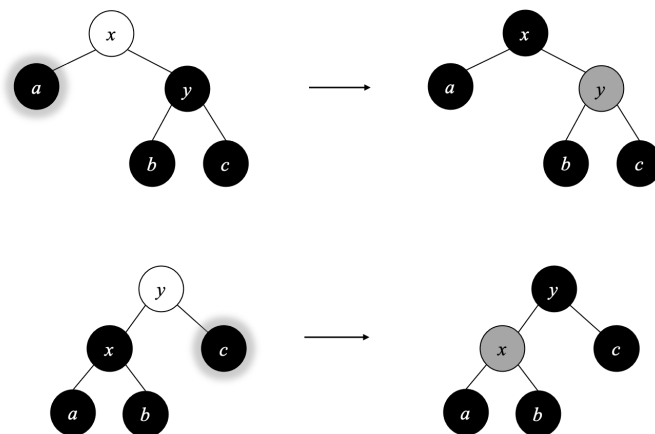


Figure A.2: The sibling of the doubly black is red

```

1: function DELETE-FIX( $T, x, f$ )
2:      $n \leftarrow \text{NIL}$ 
3:     if  $f = \text{True}$  then ▷  $x$  is doubly black NIL
4:          $n \leftarrow x$ 
5:     if  $x = \text{NIL}$  then ▷ Delete the singleton leaf
6:         return NIL
7:     while  $x \neq T$  and  $\text{COLOR}(x) = \mathcal{B}^2$  do
8:         if  $\text{SIBLING}(x) \neq \text{NIL}$  then
9:              $s \leftarrow \text{SIBLING}(x)$ 
10:            if  $s$  is red then ▷ The sibling is red
11:                set  $\text{PARENT}(x)$  red
12:                set  $s$  black
13:            if  $x = \text{LEFT}(\text{PARENT}(x))$  then ▷  $x$  is the left

```

```

14:          $T \leftarrow \text{ROTATE-LEFT}T, \text{PARENT}(x)$ 
15:     else ▷  $x$  is the right
16:          $T \leftarrow \text{ROTATE-RIGHT}T, \text{PARENT}(x)$ 
17:     else if  $s$  is black and  $\text{LEFT}(s)$  is red then
18:         ...

```

Case 3. *The sibling of the doubly black node, and its two sub-trees are all black.* In this case, we re-color the sibling to red, change the doubly black node back to black, then move the doubly blackness up to the parent. As shown in figure A.3, there are two symmetric sub-cases.

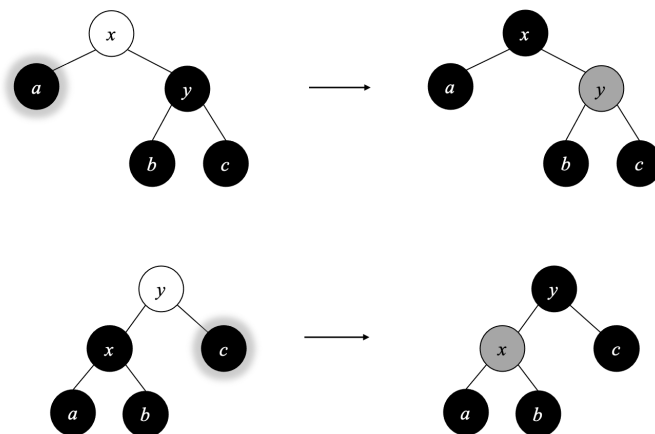


Figure A.3: move the blackness up

The sibling of the doubly black isn't empty in all above 3 cases. Otherwise, we change the doubly black node back to black, and move the blackness up. When reach the root, we force the root to be black to complete fixing. It also terminates if the doubly black node is eliminated after re-color in the midway. At last, if the doubly black node passed in is empty, we turn it back to normal NIL.

```

1: function DELETE-FIX( $T, x, f$ )
2:      $n \leftarrow \text{NIL}$ 
3:     if  $f = \text{True}$  then ▷  $x$  is a doubly black NIL
4:          $n \leftarrow x$ 
5:     if  $x = \text{NIL}$  then ▷ Delete the singleton leaf
6:         return NIL
7:     while  $x \neq T$  and  $\text{COLOR}(x) = \mathcal{B}^2$  do
8:         if  $\text{SIBLING}(x) \neq \text{NIL}$  then ▷ The sibling is not empty
9:              $s \leftarrow \text{SIBLING}(x)$ 
10:            if  $s$  is red then ▷ The sibling is red
11:                set  $\text{PARENT}(x)$  red
12:                set  $s$  black
13:                if  $x = \text{LEFT}(\text{PARENT}(x))$  then ▷  $x$  is the left
14:                     $T \leftarrow \text{ROTATE-LEFT}T, \text{PARENT}(x)$ 
15:                else ▷  $x$  is the right
16:                     $T \leftarrow \text{ROTATE-RIGHT}T, \text{PARENT}(x)$ 
17:            else if  $s$  is black and  $\text{LEFT}(s)$  is red then
18:                if  $x = \text{LEFT}(\text{PARENT}(x))$  then ▷  $x$  is the left
19:                    set  $x, \text{PARENT}(x),$  and  $\text{LEFT}(s)$  all black
20:                     $T \leftarrow \text{ROTATE-RIGHT}(T, s)$ 

```



```

21:         T ← ROTATE-LEFT(T, PARENT(x))
22:     else                                     ▷ x is the right
23:         set x, PARENT(x), s, and LEFT(s) all black
24:         T ← ROTATE-RIGHT(T, PARENT(x))
25:     else if s is black and RIGHT(s) is red then
26:         if x = LEFT(PARENT(x)) then         ▷ x is the left
27:             set x, PARENT(x), s, and RIGHT(s) all black
28:             T ← ROTATE-LEFT(T, PARENT(x))
29:         else                                   ▷ x is the right
30:             set x, PARENT(x), and RIGHT(s) all black
31:             T ← ROTATE-LEFT(T, s)
32:             T ← ROTATE-RIGHT(T, PARENT(x))
33:     else if s, LEFT(s), and RIGHT(s) are all black then
34:         set x black
35:         set s red
36:         BLACKEN(PARENT(x))
37:         x ← PARENT(x)
38:     else                                     ▷ move the blackness up
39:         set x black
40:         BLACKEN(PARENT(x))
41:         x ← PARENT(x)
42:     set T black
43:     if n ≠ NIL then
44:         replace n with NIL
45:     return T

```

When fixing, we pass in the root T , the node x (can be doubly black), and a flag f . The flag is true if x is doubly black NIL. We record it with n , and replace n with the normal NIL after fixing.

Below is the example program implements delete:

```

Node del(Node t, Node x) {
    if x == null then return t
    var parent = x.parent;
    Node db = null; //doubly black

    if x.left == null {
        db = x.right
        x.replaceWith(db)
    } else if x.right == null {
        db = x.left
        x.replaceWith(db)
    } else {
        var y = min(x.right)
        parent = y.parent
        db = y.right
        x.key = y.key
        y.replaceWith(db)
        x = y
    }
    if x.color == Color.BLACK {
        t = deleteFix(t, makeBlack(parent, db), db == null);
    }
    remove(x)
    return t
}

```

Where `makeBlack` checks if the node changes to doubly black, and handles the special case of doubly black NIL.

```
Node makeBlack(Node parent, Node x) {
    if parent == null and x == null then return null
    return if x == null
        then replace(parent, x, Node(0, Color.DOUBLY_BLACK))
        else blacken(x)
}
```

The function `replace(parent, x, y)` replaces the child of the `parent`, which is `x`, with `y`.

```
Node replace(Node parent, Node x, Node y) {
    if parent == null {
        if y != null then y.parent = null
    } else if parent.left == x {
        parent.setLeft(y)
    } else {
        parent.setRight(y)
    }
    if x != null then x.parent = null
    return y
}
```

The function `blacken(node)` changes the red node to black, and the black node to doubly black:

```
Node blacken(Node x) {
    x.color = if isRed(x) then Color.BLACK else Color.DOUBLY_BLACK
    return x
}
```

Below example program implements the fixing:

```
Node deleteFix(Node t, Node db, Bool isDBEmpty) {
    var dbEmpty = if isDBEmpty then db else null
    if db == null then return null // delete the root
    while (db != t and db.color == Color.DOUBLY_BLACK) {
        var s = db.sibling()
        var p = db.parent
        if (s != null) {
            if isRed(s) {
                // the sibling is red
                p.color = Color.RED
                s.color = Color.BLACK
                t = if db == p.left then leftRotate(t, p)
                    else rightRotate(t, p)
            } else if isBlack(s) and isRed(s.left) {
                // the sibling is black, and one sub-tree is red
                if db == p.left {
                    db.color = Color.BLACK
                    p.color = Color.BLACK
                    s.left.color = p.color
                    t = rightRotate(t, s)
                    t = leftRotate(t, p)
                } else {
                    db.color = Color.BLACK
                    p.color = Color.BLACK
                    s.color = p.color
                    s.left.color = Color.BLACK
                    t = rightRotate(t, p)
                }
            }
        } else if isBlack(s) and isRed(s.right) {
            if (db == p.left) {
```

```

        db.color = Color.BLACK
        p.color = Color.BLACK
        s.color = p.color
        s.right.color = Color.BLACK
        t = leftRotate(t, p)
    } else {
        db.color = Color.BLACK
        p.color = Color.BLACK
        s.right.color = p.color
        t = leftRotate(t, s)
        t = rightRotate(t, p)
    }
} else if isBlack(s) and isBlack(s.left) and
isBlack(s.right) {
    // the sibling and both sub-trees are black.
    // move blackness up
    db.color = Color.BLACK
    s.color = Color.RED
    blacken(p)
    db = p
}
} else { // no sibling, move blackness up
    db.color = Color.BLACK
    blacken(p)
    db = p
}
}
t.color = Color.BLACK
if (dbEmpty ≠ null) { // change the doubly black nil to nil
    dbEmpty.replaceWith(null)
    delete dbEmpty
}
return t
}

```

Where `isBlack(x)` tests if a node is black, the NIL node is also black.

```

Bool isBlack(Node x) = (x == null or x.color == Color.BLACK)
Bool isRed(Node x) = (x ≠ null and x.color == Color.RED)

```

Before returning the final result, we check the doubly black NIL, and call the `replaceWith` function defined in `Node`.

```

data Node<T> {
    //...
    void replaceWith(Node y) = replace(parent, this, y)
}

```

The program terminates when reach the root or the doubly blackness is eliminated. As we maintain the red-black tree balanced, the delete algorithm is bound to $O(\lg n)$ time for the tree of n nodes.

Exercise A.1

1. Write a program to test if a tree satisfies the 5 red-black tree rules. Use this program to verify the red-black tree delete implementation.

Appendix B

AVL tree - proofs and the delete algorithm

B.1 Height increment

When insert an element, the increment of the height can be deduced into 4 cases:

$$\begin{aligned}
 \Delta H &= |T'| - |T| \\
 &= 1 + \max(|r'|, |l'|) - (1 + \max(|r|, |l|)) \\
 &= \max(|r'|, |l'|) - \max(|r|, |l|) \\
 &= \begin{cases} \delta \geq 0, \delta' \geq 0: & \Delta r \\ \delta \leq 0, \delta' \geq 0: & \delta + \Delta r \\ \delta \geq 0, \delta' \leq 0: & \Delta l - \delta \\ otherwise: & \Delta l \end{cases} \tag{B.1}
 \end{aligned}$$

Proof. When insert, the height can not increase both on left and right. We can explain the 4 cases from the balance factor definition, which is the difference of the right and left sub-trees:

1. If $\delta \geq 0$ and $\delta' \geq 0$, it means the height of the right sub-tree is not less than the left sub-tree before and after insertion. In this case, the height increment is only 'contributed' from the right, which is Δr .
2. If $\delta \leq 0$, it means the height of left sub-tree is not less than the right before. Since $\delta' \geq 0$ after insert, we know the height of right sub-tree increases, and the left side keeps same ($|l'| = |l|$). The height increment is:

$$\begin{aligned}
 \Delta H &= \max(|r'|, |l'|) - \max(|r|, |l|) \quad \{\delta \leq 0 \text{ and } \delta' \geq 0\} \\
 &= |r'| - |l| \quad \{|l| = |l'|\} \\
 &= |r| + \Delta r - |l| \\
 &= \delta + \Delta r
 \end{aligned}$$

3. If $\delta \geq 0$ and $\delta' \leq 0$, similar to the above case, we have the following:

$$\begin{aligned}
 \Delta H &= \max(|r'|, |l'|) - \max(|r|, |l|) \quad \{\delta \geq 0 \text{ and } \delta' \leq 0\} \\
 &= |l'| - |r| \\
 &= |l| + \Delta l - |r| \\
 &= \Delta l - \delta
 \end{aligned}$$

4. Otherwise, δ and δ' are not bigger than zero. It means the height of the left sub-tree is not less than the right. The height increment is only ‘contributed’ from the left, which is Δl .

□

B.2 Balance adjustment after insert

The balance factors are ± 2 in the 4 cases shown in figure B.1. After fixing, $\delta(y)$ resumes to 0. The height of left and right sub-trees are equal.

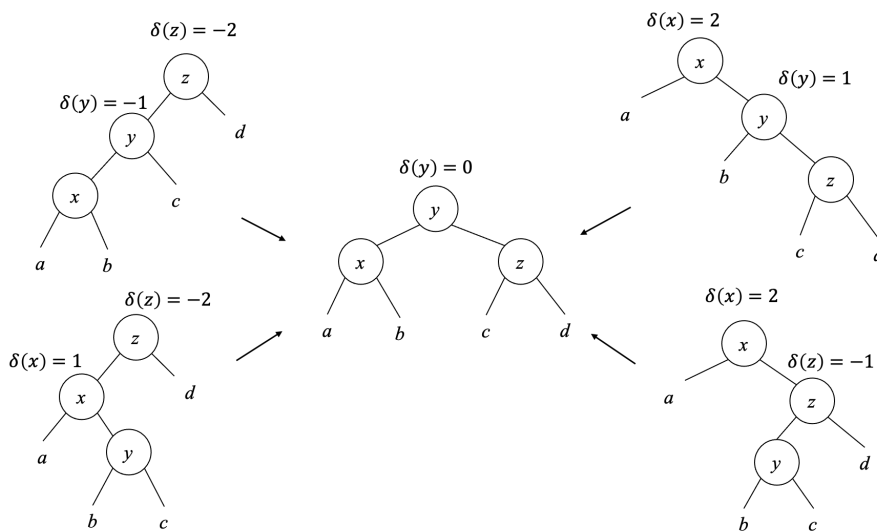


Figure B.1: Fix 4 cases to the same structure

The four cases are left-left, right-right, right-left, and left-right. Let the balance factors before fixing be $\delta(x)$, $\delta(y)$, and $\delta(z)$, after fixing, they change to $\delta'(x)$, $\delta'(y)$, and $\delta'(z)$ respectively. We next prove that, $\delta'(y) = 0$ for all 4 cases after fixing, and give the result of $\delta'(x)$ and $\delta'(z)$.

Proof. We break into 4 cases:

Left-left

The sub-tree x keeps unchanged, hence $\delta'(x) = \delta(x)$. As $\delta(y) = -1$ and $\delta(z) = -2$, we have:

$$\begin{aligned} \delta(y) = |c| - |x| = -1 &\Rightarrow |c| = |x| - 1 \\ \delta(z) = |d| - |y| = -2 &\Rightarrow |d| = |y| - 2 \end{aligned} \quad (\text{B.2})$$

After fixing:

$$\begin{aligned} \delta'(z) &= |d| - |c| && \{from(B.2)\} \\ &= |y| - 2 - (|x| - 1) \\ &= |y| - |x| - 1 && \{x \text{ is sub-tree of } y \Rightarrow |y| - |x| = 1\} \\ &= 0 \end{aligned} \quad (\text{B.3})$$

For $\delta'(y)$, we have the following:

$$\begin{aligned}
 \delta'(y) &= |z| - |x| \\
 &= 1 + \max(|c|, |d|) - |x| \quad \{\text{by (B.3), } |c| = |d|\} \\
 &= 1 + |c| - |x| \quad \{\text{by (B.2)}\} \\
 &= 1 + |x| - 1 - |x| \\
 &= 0
 \end{aligned} \tag{B.4}$$

Summarize the above, the balance factors change to the following in left-left case:

$$\begin{aligned}
 \delta'(x) &= \delta(x) \\
 \delta'(y) &= 0 \\
 \delta'(z) &= 0
 \end{aligned} \tag{B.5}$$

Right-right

The right-right case is symmetric to left-left:

$$\begin{aligned}
 \delta'(x) &= 0 \\
 \delta'(y) &= 0 \\
 \delta'(z) &= \delta(z)
 \end{aligned} \tag{B.6}$$

Right-left

Consider $\delta'(x)$, after fixing, it is:

$$\delta'(x) = |b| - |a| \tag{B.7}$$

Before fixing, the height of z can be obtained as:

$$\begin{aligned}
 |z| &= 1 + \max(|y|, |d|) \quad \{\delta(z) = -1 \Rightarrow |y| > |d|\} \\
 &= 1 + |y| \\
 &= 2 + \max(|b|, |c|)
 \end{aligned} \tag{B.8}$$

Since $\delta(x) = 2$, we have:

$$\begin{aligned}
 \delta(x) = 2 &\Rightarrow |z| - |a| = 2 \quad \{\text{by (B.8)}\} \\
 &\Rightarrow 2 + \max(|b|, |c|) - |a| = 2 \\
 &\Rightarrow \max(|b|, |c|) - |a| = 0
 \end{aligned} \tag{B.9}$$

If $\delta(y) = |c| - |b| = 1$, then:

$$\max(|b|, |c|) = |c| = |b| + 1 \tag{B.10}$$

Take this into (B.9) gives:

$$\begin{aligned}
 |b| + 1 - |a| = 0 &\Rightarrow |b| - |a| = -1 \quad \{\text{by (B.7)}\} \\
 &\Rightarrow \delta'(x) = -1
 \end{aligned} \tag{B.11}$$

If $\delta(y) \neq 1$, then $\max(|b|, |c|) = |b|$. Take this into (B.9) gives:

$$\begin{aligned}
 |b| - |a| = 0 &\quad \{\text{by (B.7)}\} \\
 &\Rightarrow \delta'(x) = 0
 \end{aligned} \tag{B.12}$$

Summarize the 2 cases, we obtain the result of $\delta'(x)$ in $\delta(y)$ as the following:

$$\delta'(x) = \begin{cases} \delta(y) = 1 : & -1 \\ \text{otherwise} : & 0 \end{cases} \tag{B.13}$$

For $\delta'(z)$, from the definition, it equals to:

$$\begin{aligned}\delta'(z) &= |d| - |c| && \{\delta(z) = -1 = |d| - |y|\} \\ &= |y| - |c| - 1 && \{|y| = 1 + \max(|b|, |c|)\} \\ &= \max(|b|, |c|) - |c|\end{aligned}\quad (\text{B.14})$$

If $\delta(y) = |c| - |b| = -1$, then $\max(|b|, |c|) = |b| = |c| + 1$. Take this into (B.14), we have $\delta'(z) = 1$. If $\delta(y) \neq -1$, then $\max(|b|, |c|) = |c|$. We have $\delta'(z) = 0$. Combined these two cases, we obtain the result of $\delta'(z)$ in $\delta(y)$ as below:

$$\delta'(z) = \begin{cases} \delta(y) = -1 : & 1 \\ \text{otherwise} : & 0 \end{cases}\quad (\text{B.15})$$

Finally, for $\delta'(y)$, we deduce it like below:

$$\begin{aligned}\delta'(y) &= |z| - |x| \\ &= \max(|c|, |d|) - \max(|a|, |b|)\end{aligned}\quad (\text{B.16})$$

There are three cases:

1. If $\delta(y) = 0$, then $|b| = |c|$. According to (B.13) and (B.15), we have $\delta'(x) = 0 \Rightarrow |a| = |b|$, and $\delta'(z) = 0 \Rightarrow |c| = |d|$. These lead to $\delta'(y) = 0$.
2. If $\delta(y) = 1$, from (B.15), we have $\delta'(z) = 0 \Rightarrow |c| = |d|$.

$$\begin{aligned}\delta'(y) &= \max(|c|, |d|) - \max(|a|, |b|) && \{|c| = |d|\} \\ &= |c| - \max(|a|, |b|) && \{\text{from (B.13): } \delta'(x) = -1 \Rightarrow |b| - |a| = -1\} \\ &= |c| - (|b| + 1) && \{\delta(y) = 1 \Rightarrow |c| - |b| = 1\} \\ &= 0\end{aligned}$$

3. If $\delta(y) = -1$, from (B.13), we have $\delta'(x) = 0 \Rightarrow |a| = |b|$.

$$\begin{aligned}\delta'(y) &= \max(|c|, |d|) - \max(|a|, |b|) && \{|a| = |b|\} \\ &= \max(|c|, |d|) - |b| && \{\text{from (B.15): } |d| - |c| = 1\} \\ &= |c| + 1 - |b| && \{\delta(y) = -1 \Rightarrow |c| - |b| = -1\} \\ &= 0\end{aligned}$$

All three cases lead to the same result $\delta'(y) = 0$. Summarize all above, we get the updated balance factors after fixing as below:

$$\begin{aligned}\delta'(x) &= \begin{cases} \delta(y) = 1 : & -1 \\ \text{otherwise} : & 0 \end{cases} \\ \delta'(y) &= 0 \\ \delta'(z) &= \begin{cases} \delta(y) = -1 : & 1 \\ \text{otherwise} : & 0 \end{cases}\end{aligned}\quad (\text{B.17})$$

Left-right

Left-right is symmetric to the right-left case. With similar method, we can obtain the new balance factors that is identical to (B.17). □

B.3 Delete algorithm

Deletion may reduce the height of the sub-tree. If the balance factor exceeds the range of $[-1, 1]$, then we need fixing.

B.3.1 Functional delete

When delete, we re-use the binary search tree *delete* in the first step, then check the balance factors and perform fixing. The result is a pair $(T', \Delta H)$, where T' is the new tree and ΔH is the height decrement. We define *delete* as below:

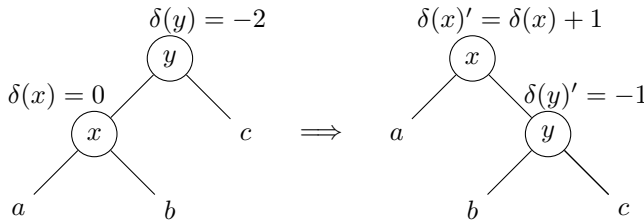
$$delete = fst \circ del \tag{B.18}$$

where $del(T, k)$ does the actual work to delete element k from T :

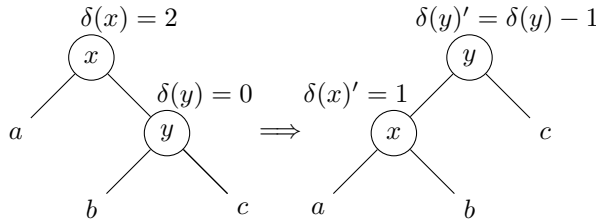
$$del \ \emptyset \ k = (\emptyset, 0)$$

$$del(l, k', r, \delta) = \begin{cases} k < k' : & tree \ (del \ l \ k) \ k' \ (r, 0) \ \delta \\ k > k' : & tree \ (l, 0) \ k' \ (del \ r \ k) \ \delta \\ k = k' : & \begin{cases} l = \emptyset : & (r, -1) \\ r = \emptyset : & (l, -1) \\ else : & tree \ (l, 0) \ k'' \ (del \ r \ k'') \ \delta \\ & \text{where } k'' = \min(r) \end{cases} \end{cases} \tag{B.19}$$

If the tree is empty, the result is $(\emptyset, 0)$; otherwise, let the tree be $T = (l, k', r, \delta)$. We compare the k and k' , lookup and delete recursively. When $k = k'$, we locate the node to be deleted. If it has either empty sub-tree, we cut the node off, and replace it with the other sub-tree; otherwise, we use the minimum k'' in the right sub-tree to replace k' , and cut k'' off. We re-use the *tree* function and ΔH result. Additional to the *insert* cases, there are two cases violate AVL rule, and need fixing. As shown in figure B.2, both cases can be fixed by a tree rotation. We define them as pattern matching:



(a) Fix case A



(b) Fix case B

Figure B.2: delete fix

$$\begin{aligned} \dots \\ balance((a, x, b, \delta(x)), y, c, -2) \ \Delta H &= (a, x, (b, y, c, -1), \delta(x) + 1, \Delta H) \\ balance(a, x, (b, y, c, \delta(y)), 2) \ \Delta H &= ((a, x, b, 1), y, c, \delta(y) - 1, \Delta H) \\ \dots \end{aligned} \tag{B.20}$$

Below is the example program:

```

delete t x = fst $ del t x where
  del Empty _ = (Empty, 0)
  del (Br l k r d) x
    | x < k = node (del l x) k (r, 0) d
    | x > k = node (l, 0) k (del r x) d
    | isEmpty l = (r, -1)
    | isEmpty r = (l, -1)
    | otherwise = node (l, 0) k' (del r k') d where k' = min r

```

Where `min` and `isEmpty` are defined as below:

```

min (Br Empty x _ _) = x
min (Br l _ _ _) = min l

isEmpty Empty = True
isEmpty _ = False

```

With the additional two, there are total 7 cases in `balance` implementation:

```

balance (Br (Br (Br a x b dx) y c (-1)) z d (-2), dH) =
  (Br (Br a x b dx) y (Br c z d 0) 0, dH-1)
balance (Br a x (Br b y (Br c z d dz) 1) 2, dH) =
  (Br (Br a x b 0) y (Br c z d dz) 0, dH-1)
balance (Br (Br a x (Br b y c dy) 1) z d (-2), dH) =
  (Br (Br a x b dx') y (Br c z d dz') 0, dH-1) where
    dx' = if dy == 1 then -1 else 0
    dz' = if dy == -1 then 1 else 0
balance (Br a x (Br (Br b y c dy) z d (-1)) 2, dH) =
  (Br (Br a x b dx') y (Br c z d dz') 0, dH-1) where
    dx' = if dy == 1 then -1 else 0
    dz' = if dy == -1 then 1 else 0
— Delete specific
balance (Br (Br a x b dx) y c (-2), dH) =
  (Br a x (Br b y c (-1)) (dx+1), dH)
balance (Br a x (Br b y c dy) 2, dH) =
  (Br (Br a x b 1) y c (dy-1), dH)
balance (t, d) = (t, d)

```

B.3.2 Imperative delete

The imperative *delete* uses tree rotations for fixing. In the first step, we re-use the binary search tree algorithm to delete the node x from tree T ; then in the second step, check the balance factor and perform rotation.

```

1: function DELETE( $T, x$ )
2:   if  $x = \text{NIL}$  then
3:     return  $T$ 
4:    $p \leftarrow \text{PARENT}(x)$ 
5:   if LEFT( $x$ ) = NIL then
6:      $y \leftarrow \text{RIGHT}(x)$ 
7:     replace  $x$  with  $y$ 
8:   else if RIGHT( $x$ ) = NIL then
9:      $y \leftarrow \text{LEFT}(x)$ 
10:    replace  $x$  with  $y$ 
11:   else
12:      $z \leftarrow \text{MIN}(\text{RIGHT}(x))$ 
13:     copy data from  $z$  to  $x$ 
14:      $p \leftarrow \text{PARENT}(z)$ 
15:      $y \leftarrow \text{RIGHT}(z)$ 

```

```

16:     replace  $z$  with  $y$ 
17:     return AVL-DELETE-FIX( $T, p, y$ )

```

When delete node x , we record its parent in p . If either sub-tree is empty, we cut off x , and replace it with the other sub-tree. Otherwise if neither sub-tree is empty, we locate the minimum element z of the right sub-tree, copy data from z to x , then cut z off. Finally, we call AVL-DELETE-FIX with the root T , the parent p , and the replacement node y . Let the balance factor of p be $\delta(p)$, and it changes to $\delta(p)'$ after delete. There are three cases:

1. $|\delta(p)| = 0, |\delta(p)'| = 1$. After delete, although a sub-tree height decreases, the parent still satisfies the AVL rule. The algorithm terminates as the tree is still balanced;
2. $|\delta(p)| = 1, |\delta(p)'| = 0$. Before the delete, the height difference between the two sub-trees is 1; while after delete, the higher sub-tree shrinks by 1. Both sub-trees have the same height now. As the result, the height of the parent also decrease by 1. We need continue the bottom-up update along the parent reference to the root;
3. $|\delta(p)| = 1, |\delta(p)'| = 2$. After delete, the tree violates the AVL height rule, we need rotate the tree to fix it.

For case 3, the implementation is similar to the insert fixing. We need add two additional sub-cases as shown in figure B.2.

```

1: function AVL-DELETE-FIX( $T, p, x$ )
2:   while  $p \neq \text{NIL}$  do
3:      $l \leftarrow \text{LEFT}(p), r \leftarrow \text{RIGHT}(p)$ 
4:      $\delta \leftarrow \delta(p), \delta' \leftarrow \delta$ 
5:     if  $x = l$  then
6:        $\delta' \leftarrow \delta' + 1$ 
7:     else
8:        $\delta' \leftarrow \delta' - 1$ 
9:     if  $p$  is leaf then ▷  $l = r = \text{NIL}$ 
10:       $\delta' \leftarrow 0$ 
11:    if  $|\delta| = 1 \wedge |\delta'| = 0$  then
12:       $x \leftarrow p$ 
13:       $p \leftarrow \text{PARENT}(x)$ 
14:    else if  $|\delta| = 0 \wedge |\delta'| = 1$  then
15:      return  $T$ 
16:    else if  $|\delta| = 1 \wedge |\delta'| = 2$  then
17:      if  $\delta' = 2$  then
18:        if  $\delta(r) = 1$  then ▷ Right-right
19:           $\delta(p) \leftarrow 0$ 
20:           $\delta(r) \leftarrow 0$ 
21:           $p \leftarrow r$ 
22:           $T \leftarrow \text{LEFT-ROTATE}(T, p)$ 
23:        else if  $\delta(r) = -1$  then ▷ Right-left
24:           $\delta_y \leftarrow \delta(\text{LEFT}(r))$ 
25:          if  $\delta_y = 1$  then
26:             $\delta(p) \leftarrow -1$ 
27:          else
28:             $\delta(p) \leftarrow 0$ 
29:             $\delta(\text{LEFT}(r)) \leftarrow 0$ 
30:          if  $\delta_y = -1$  then

```

```

31:          $\delta(r) \leftarrow 1$ 
32:     else
33:          $\delta(r) \leftarrow 0$ 
34:     else ▷ Delete specific right-right
35:          $\delta(p) \leftarrow 1$ 
36:          $\delta(r) \leftarrow \delta(r) - 1$ 
37:          $T \leftarrow \text{LEFT-ROTATE}(T, p)$ 
38:         break ▷ No further height change
39:     else if  $\delta' = -2$  then
40:         if  $\delta(l) = -1$  then ▷ Left-left
41:              $\delta(p) \leftarrow 0$ 
42:              $\delta(l) \leftarrow 0$ 
43:              $p \leftarrow l$ 
44:              $T \leftarrow \text{RIGHT-ROTATE}(T, p)$ 
45:         else if  $\delta(l) = 1$  then ▷ Left-right
46:              $\delta_y \leftarrow \delta(\text{RIGHT}(l))$ 
47:             if  $\delta_y = -1$  then
48:                  $\delta(p) \leftarrow 1$ 
49:             else
50:                  $\delta(p) \leftarrow 0$ 
51:                  $\delta(\text{RIGHT}(l)) \leftarrow 0$ 
52:             if  $\delta_y = 1$  then
53:                  $\delta(l) \leftarrow -1$ 
54:             else
55:                  $\delta(l) \leftarrow 0$ 
56:         else ▷ Delete specific left-left
57:              $\delta(p) \leftarrow -1$ 
58:              $\delta(l) \leftarrow \delta(l) + 1$ 
59:              $T \leftarrow \text{RIGHT-ROTATE}(T, p)$ 
60:             break ▷ No further height change
▷ Height decreases, go on bottom-up updating
61:      $x \leftarrow p$ 
62:      $p \leftarrow \text{PARENT}(x)$ 
63:     if  $p = \text{NIL}$  then ▷ Delete the root
64:         return  $x$ 
65:     return  $T$ 

```

Exercise B.1

1. Compare the imperative tree fixing for *insert* and *delete*, there are similarities. Develop a common fix function for both *insert* and *delete*.

B.4 Example program

The main *delete* program:

```

Node del(Node t, Node x) {
    if  $x == \text{null}$  then return  $t$ 
    Node y
    var parent =  $x.\text{parent}$ 
    if  $x.\text{left} == \text{null}$  {
         $y = x.\text{replaceWith}(x.\text{right})$ 

```

```

} else if x.right == null {
    y = x.replaceWith(x.left)
} else {
    y = min(x.right)
    x.key = y.key
    parent = y.parent
    x = y
    y = y.replaceWith(y.right)
}
t = deleteFix(t, parent, y)
release(x)
return t
}

```

Where `replaceWith` is defined in the chapter of red-black tree. `release(x)` releases the memory of a node. Function `deleteFix` is implemented as below:

```

Node deleteFix(Node t, Node parent, Node x) {
    int d1, d2, dy
    Node p, l, r
    while parent != null {
        d2 = d1 = parent.delta
        d2 = d2 + if x == parent.left then 1 else -1
        if isLeaf(parent) then d2 = 0
        parent.delta = d2
        p = parent
        l = parent.left
        r = parent.right
        if abs(d1) == 1 and abs(d2) == 0 {
            x = parent
            parent = x.parent
        } else if abs(d1) == 0 and abs(d2) == 1 {
            return t
        } else if abs(d1) == 1 and abs(d2) == 2 {
            if d2 == 2 {
                if r.delta == 1 { // right-right
                    p.delta = 0
                    r.delta = 0
                    parent = r
                    t = leftRotate(t, p)
                } else if r.delta == -1 { // right-left
                    dy = r.left.delta
                    p.delta = if dy == 1 then -1 else 0
                    r.left.delta = 0
                    r.delta = if dy == -1 then 1 else 0
                    parent = r.left
                    t = rightRotate(t, r)
                    t = leftRotate(t, p)
                } else { // delete specific right-right
                    p.delta = 1
                    r.delta = r.delta - 1
                    t = leftRotate(t, p)
                    break // no further height change
                }
            }
            } else if d2 == -2 {
                if (l.delta == -1) { // left-left
                    p.delta = 0
                    l.delta = 0
                    parent = l
                    t = rightRotate(t, p)
                } else if l.delta == 1 { // left-right
                    dy = l.right.delta
                    l.delta = if dy == 1 then -1 else 0
                    l.right.delta = 0
                    p.delta = if dy == -1 then 1 else 0
                    parent = l.right;
                }
            }
        }
    }
}

```

```
        t = leftRotate(t, l)
        t = rightRotate(t, p)
    } else { // delete specific left-left
        p.delta = -1
        l.delta = l.delta + 1
        t = rightRotate(t, p)
        break // no further height change
    }
}
// height decreases, go on bottom-up update
x = parent
parent = x.parent
}
}
if parent == null then return x // delete the root
return t
}
```

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