CPE593 Applied Data Structures and Algorithms

Ad Astra Education

Dov Kruger

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Author

Dov Kruger

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Contributors

Jennifer Lloyd Pridhvi Myneni

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1. Prerequisites

This course covers theory of computation in pseudocode but homeworks are in either C++ or Java, and we often delve into practical details of memory performance. Accordingly, you must know C++ or Java well enough to create a data structure involving pointers and dynamic memory in order to be able to handle the material in this class, and write and debug a complex algorithm. If you cannot do this, take C++ or Java first, then take this course.

2. Introduction

The full name of this course is Practical Data Structures and Algorithms, and for the last seven years, I have been curating the best algorithms from many different areas of computer science and giving students a broad overview of the field at the masters level. We do not cover a huge amount of graph theory, but as a result the course gets to touch on many of the fascinating topics in algorithms including number-theoretic, numerical methods, and depending on the semester, sometimes localization (navigation algorithms for robots) and other special topics.

The course has always been in flux, so the notes have always been one file per chapter, not particularly good looking. But this semester, with COVID raging on, it's time to collect this into a better-formatted LaTeX document and try to create a single, coherent set of notes. I won't teach from these notes, we will still type everything in from scratch each period, because looking at already-constructed answers is no way to learn. But now, when students want to check back, there is a document to look at, and with some additional editing, it will be beautiful someday.

3. Analysis of Algorithms

3.1 Assumptions

Data Structures and Algorithms is a theoretical field where we are interested in the asymptotic behavior of algorithms as the scale of the problem grows. Since computers get faster over time, and there are faster and slower machines, we are not interested in a constant factor, but rather are concerned with how the problem grows.

We consider memory to be uniform, without considering faster access for sequential memory, no cache that makes retrieving recent memory faster. These features are good, they can speed up an algorithm but generally only by a constant factor.

All operations are considered to be the same speed. While addition is faster than multiply, again it is only a constant factor and therefore irrelevant.

3.2 Formal notation O(), $\Omega()$, $\Theta()$

$f(n) = O(n)$ means there exists some c for which $cn > f(n)$ $f(n) = \Omega(n)$ means there exists some c for which $cn < f(n)$

Example:

1. $f(n) = 600n + 20000000000, c = 601 O(n)$
2. $O(n^2 + 10000n + .000001n^3 + 10^6) = O(n^3)$

A function that is $f(n) = O(n)$ and $\Omega(n)$ is $\Theta(n)$

Example: How long to find a number in a list of n elements? $O(n)$ $\Omega(1)$

3.3 Asymptotic Growth of Functions

n	1	log_n	$\sqrt{n}$	n	n^2
1	1	0	1	1	1
10	1	3	3	10	10^2
10^2	1	7	10	10^2	10^4
10^3	1	10	33	10^3	10^6
10^6	1	20	1000	10^6	10^12
10^9	1	30	33000	10^9	10^18
10^12	1	40	10^6	10^12	10^24

3.4 Analyzing Code

A key skill in algorithms is to inspect code and determine the complexity. The fundamental building blocks are:

1. A loop that executes n times is $O(n)$
2. Two sequential loops add
3. Nested loops multiply (for each iteration of the outer loop, the inner executes completely)
4. Tail recursion n levels deep is $O(n)$
5. Recursion n levels deep where a function calls itself k times is k^n

Examples of code and complexity.

Code	Complexity	Comment

`for (int i = 0; i < n; i++) {`
 `}`
	$O(n)$	counting n times

`for (int i = 1; i <= n; i++) {`
 `}`
	$O(n)$	

`for (int i = 5; i <= n; i += 3) {`
 `}`
	$O(n)$	constants don't matter

`for (int i = 5; i < 2*n; i += 7) {`
 `}`
	$O(n)$	constants don't matter

`for (int i = 0; i < n; i += n/2) {`
 `}`
	$O(1)$	count by $n/2$ means 2 times

`for (int i = 0; i < p; i += 2) {`
 `}`
	$O(p)$	answer is not always $f(n)$

`for (int i = 1; i < n; i *= 2) {`
 `}`
	$O(logn)$	$log_2(n) = O(logn)$ all logs are s

`for (int i = 1; i < n; i += i) {`
 `}`
	$O(logn)$	$log_2(n) = O(logn)$ all logs are s

	$O(logn)$	$log_3(n) = clog_2(n)$ all logs are s

Code	Complexity	Comment

`for (int i = 0; i < n; i++) {`
`}`
`for (int i = 0; i < n; i++) {`
`}`
	$O(n)$	sequential loops add

`for (int i = 0; i < n; i++) {`
`  for (int j = 0; j < n; j++) {`
`  }`
`}`
	$O(n^2)$	nested loops multiply

`for (int i = 0; i < a; i++) {`
`  for (int j = 0; j < b; j++) {`
`  }`
`}`
	$O(ab)$	nested loops multiply

`for (int i = 0; i < n; i++) {`
`  for (int j = 0; j < i; j++) {`
`  }`
`}`
	$O(n^2)$	$\frac{n(n+1)}{2} = O(n^2)$

`for (int i = 0; i < n; i++) {`
`  for (int j = i; j < n; j++) {`
`  }`
`}`
	$O(n^2)$	$\frac{n(n+1)}{2} = O(n^2)$

`for (int i = 1; i <= n; i *= 2) {`
`  for (int j = 1; j < i; j++) {`
`  }`
`}`
	$O(n)$	$1+2+4+8+...\frac{n}{2}+n = 2n =$

	$O(nlogn)$	

```
input: int N, int D
output: int
begin
  res ← 0
  while N ≥ D
    N ← N − D
    res ← res + 1
  end
  return res
end
```

Algorithm 3.1: Integer division.

```
gcd(a, b)
  if b = 0
    return a
  endif
  return gcd(b, a mod b)
end
```

Algorithm 3.2: Greatest Common Denominator.

```
gcd(a, b)
  if b = 0
    return a
  endif
  return gcd(b, a mod b)
end
```

Algorithm 3.3: Greatest Common Denominator.

Algorithm Fibonacci (iterative) Complexity $O(n)$

```
int fibo(int n) {
  int a = 1, b = 1, c;
  for (int i = 0; i < n; i++) {
    c = a + b;
    a = b;
    b = c;
  }
  return c;
}
```

Algorithm Fibonacci (recursive) Complexity $O(2^n)$

```
int fibo2(int n) {
   if ( n <= 2)
```

```
      return 1;
   return fibo2(n-1) + fibo2(n-2);
}
```

Algorithm Fibonacci (recursive) with dynamic programming Complexity $O(n)$

```
int fibo2(int n) {
   if ( n <= 2)
      return 1;
   static int memo[200] = {0};
   if (memo[n] != 0)
     return memo[n];
   return memo[n] = fibo2(n-1) + fibo2(n-2);
}
```

Algorithm: Primality Test Using trial Division State the complexity

```
bool isPrime_v1(int n) {
  bool prime = true;
  for (int i = 2; i < n; i++) {
    if (n % i == 0)
      prime = false;
  }
  return prime;
}
```

```
bool isPrime_v2(int n) {
  for (int i = 2; i < n; i++) {
    if (n % i == 0)
      return false;
  }
  return true;
}
```

```
bool isPrime_v3(int n) {
  for (int i = 2; i < n/2; i++) {
    if (n % i == 0)
      return false;
  }
  return true;
}
```

```
bool isPrime_v4(int n) {
  if (n % 2 == 0)
    return false;
  for (int i = 3; i < n;  i += 2) {
    if (n % i == 0)
      return false;
  }
  return true;
}
```

```
bool isPrime_v5(int n) {
  for (int i = 2; i <= sqrt(n); i++) {
    if (n % i == 0)
      return false;
  }
  return true;
}
```

Algorithm: Eratosthenes' Sieve

```
void eratosthenes(int n) {
   boolean[] sieve = new boolean[n]; //O(n)
   for (int i = 2; i < n; i++)      //O(n)
     sieve[i] = true;
   for (int i = 2; i < n; i++) {
      if (sieve[i]) {
         print(i);
         for (int j = 2*i; j < n; j += i)
            sieve[j] = false;
      }
  }
```

Algorithm: Improved Eratosthenes

```
ImprovedEratosthenes(n)
for i = 2 to n
     isPrime[i] = true
end
for i = 4 to n step 2
     isPrime[i] = false
end
for i = 3 to n step 2
     if isPrime[i]
```

```
            for j = i*i to n step 2i
                isPrime[j] = false
            end
        end
end
```

4. Number Theoretic Algorithms

4.1 Arbitrary Precision Arithmetic

Many of the algorithms in this chapter are commonly performed on huge numbers, far bigger than the 32 or 64-bit values that can be processed in hardware. The first consideration is the time it will take to do arbitrary precision arithmetic. With a single word, the time is $O(1)$. A slow instruction like division or modulo might take 15 clock cycles, while a fast one like addition might take only 1, but these are still constants. With arbitrary precision arithmetic, the longer the number is, the more time it takes.

To illustrate the complexity of basic operations, we will

		1	1	1	
		9	8	8	9
+		7	9	9	8
	1	7	8	8	7

The above example shows 4 digit arithmetic. We humans can compute one digit at a time, so this takes us 4 units of time and the number can (as in this example) grow by 1 digit to 5. So the complexity of the operation of adding an n-digit number is $O(n)$. On the computer it is no different. However, since the computer can process 64 bits at a time, each additional step adds 18 digits or so. This is much better, but by a constant factor. To grow a number by a factor of 2 will still take twice as long asymptotically.

The next operation to consider is multiplication. By looking at the following example it should be quite clear that not only is multiplication $O(n^2)$ but the number of digits can grow by a factor of 2. This means that a sequence of multiplication can easily create numbers that are gigantic, which in turn take longer to compute.

						9	8	8	9
*						7	9	9	8
					7	9	1	1	2
				8	9	0	0	1	
			8	9	0	0	1		
		6	9	2	2	3			
	7	9	1	0	1	0	1	0	9

Last, consider exponentiation. Since exponentiation is repeated multiplication, the number of digits can double with every multiply. Consider the following huge number exponentiation operations. One is clearly much, much worse than the other:

555555555555^2

$2^{555555555555}$

The first exponentiation, while large and exceeding what can be stored in a 64-bit integer, is only approximately double the number of digits because it is squared. The second expression is gigantic, larger than the number of particles in the universe, with easily more than 3 trillion digits. Why? Because it only takes 30 multiplies for 2 to reach 1 billion, the next 30 doubles that to 18 digits, and there are more than 5.5 trillion doublings.

The complexity of a^b is $O(ab2^b)$

While we will illustrate most of the algorithms in this section with small numbers, if you wish to try them on real problems, the following examples in Java and C++ will show you how you can write multi-precision arithmetic code. In Java, the library is built into the language with the BigInteger class. In C++, gnu provides the gmp (Gnu Multi Precision) library which is not quite as easy to use but includes far more including large floating point numbers as well as integers.

Here is an example Java program that calculates $n!$ in arbitrary precision.

```java
import java.util.Scanner;
import java.math.BigInteger;
public class FactorialMP {
     public static void main(String[] args) {
          BigInteger p = BigInteger.ONE;
          int n;
          Scanner s = new Scanner(System.in);
          n = s.nextInt();
          for (int i = 2; i <= n; i++) {
               p = p.multiply(new BigInteger(i+""));
          }
          System.out.println(p);
     }
}
```

Here is a C/C++ program that does the same using gmp.

```c
#include "gmp.h"
#include <stdio.h>
#include <stdlib.h>
#include <assert.h>

void fact(int n){
  mpz_t p;

  mpz_init_set_ui(p,1); // p = 1
  for (int i = 1; i <= n ; ++i){
    mpz_mul_ui(p,p,i); // p = p * i
  }
  mpz_out_str(stdout,10,p); / print in base 10
  mpz_clear(p);
}

int main(){
  int n;
  cin >> n; // read in the number from keyboard
  fact(n);
  return 0;
}
```

4.2 Greatest Common Denominator and Lowest Common Multiple

The first algorithm in this chapter is GCD, greatest common denominator. It was invented by Euclid more than 2500 year ago, running on the original silicon computer – sand. GCD takes two integer parameters and computes the greatest number that divides both of them. For example:

$gcd(12,18) = 6$

For more information on Euclid or the algorithm, see:
https://en.wikipedia.org/wiki/Euclidean_algorithm

The brute force algorithm, not by Euclid, is what is taught in typical elementary schools. It is easy conceptually, and it works well for small numbers but does not scale well. We simply count from 2 to the smaller of the two numbers and try division. Whenever a number divides both, we record it. This algorithm requires trying every number up to $min(a,b)$ so for large numbers it is very slow.

Algorithm gcdBruteForce

```
gcdbruteForce(a,b)
  biggestDivisor = 1
  for i = 2 to min(a,b)
    if a mod i == 0 and b mod i == 0
       biggestDivisor = i
    end
  end
  return biggestDivisor
end
```

Slightly better, but still $O(n)$ we can start with the biggest number and count down. At least this way, the algorithm can stop as soon as the first divisor is found. Because of the condition it is $\Omega(1)$.

```
gcdbruteForce(a,b)
  for i =  min(a,b) to 2
    if a mod i == 0 and b mod i == 0
       return i
    end
  end
  return 1
end
```

Euclid's algorithm is much more elegant. By taking one number modulo the other, the number gets much smaller, faster. Consider the case where a is big and b is small:

$gcd(1000,11)$

Because the second number is 11, the next stage is $1000 \mod 11$ so must be in $[0,10]$. So the number shrinks drastically. If the two numbers are close, for example:

$gcd(1000,999)$

Then $1000 \mod 999 = 1$, and the next stage will be even smaller. The worst case for gcd is actually the fibonacci series in reverse.

$gcd(55,34) = 21$

$gcd(34,21) = 13$

$gcd(21,13) = 8$

In this worst case, the number is decreasing by a factor of $\phi = \frac{\sqrt{5}+1}{2} \approx 1.618$

The following shows Euclid's algorithm iteratively:

Algorithm gcd (iterative)

```
int gcd(int a, int b) {
  while (b != 0) {
    temp = a \% b;
    a = b;
    b = temp;
  }
  return a;
}
```

The following is the same Euclid's algorithm but using recursion

Algorithm gcd (recursive)

```
int gcd(int a, int b) {
  if (b == 0)
    return a;
  return gcd(b, a \% b);
}
```

The least common multiple algorithm is closely related to GCD. In order to find the lowest number that is a multiple of two numbers, the two numbers must be factored because the smallest number will only use the factors of each once. For example, consider:

$LCM(12,18)$

The prime factors of 12 are 2, 2, 3. The prime factors of 18 are 3, 3, 2. The factors in common are 2, 3, and the extra is 2 from the 12 and 3 from the 18. Together, $2*3*2*3 = 36$ which is the answer. Factoring would be slow, as we will see $O(\sqrt{n}$ so instead we calculate $a*b$ which uses all the factors, and then to eliminate double counting the factors in common, divide by $gcd(a,b)$.

Algorithm LCM

```
int LCM(int a, int b) {
  return a * b / gcd(a,b);
}
```

4.3 Eratosthenes' Sieve

2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25
2	3	~~4~~	5	~~6~~	7	~~8~~	9	~~10~~	11	~~12~~	13	~~14~~	15	~~16~~	17	18	19	20	21	22	23	24	25
2	3		5	~~6~~	7		~~9~~		11	~~12~~	13		~~15~~		17	~~18~~	19	20	~~21~~	22	23	24	25

~~testing~~

Algorithm eratosthenes

```
uint64_t eratosthenes(uint64_t n) {
  uint64_t count = 0;
  bool* isPrime = new bool[n+1]; // allocate giant array of
     boolean (better to do this with bits than bool)
  for (uint64_t i = 2; i <= n; i++)
    isPrime[i] = true;
  for (uint64_t i = 2; i <= n; i ++)
    if (isPrime[i]) {
      count++; // add the new prime and then remove all multiples
          of it starting with $i^2$
      for (uint64_t j = 2*i; j <= n; j += i)
        isPrime[j] = false;
  }
}
```

Eratosthenes' is an algorithm with amazing performance. The complexity is $O(loglogn)$ which is hard to see from the loop. It comes from the fact that the density of prime numbers is very low ($1/logn$). This is not apparent at small numbers, where the primes seem fairly dense (2, 3, 5, 7, 11), but at $n = 10^6$ the density means that only 1 in 20 numbers is prime. at $n = 10^9$ only 1 in 30 is. Furthermore, when the algorithm finds a prime, it must remove all duplicates. As the numbers increase, the increment $j+ = i$ is skipping more and more.

As good as it is, the original Eratosthenes can be significantly improved. For every prime i, it is removing $2i$, but this has already been done by the loop which removed the multiples of 2, and $3i$ which has already been done by the loop which removed multiples of 3. In fact, the first number that is unique is i^2. In the improved Eratosthenes, we handle 2 as a special case since it is the only even prime. Then all primes discovered are odd. That means that for any prime i found, i^2 is also odd. So when cancelling multiples, it is not necessary to set the number $i^2 + i$ to be false, because $odd + odd = even$. Instead of adding i each time in the inner loop we can add $2i$ which effectively halves the time. This is only a constant factor reduction, the algorithm is still $O(loglogn)$

3	5	7	9	11	13	15	17	19	21	23	25	27	29	31	33	35	37	
3	5	7	~~9~~	11	13	~~15~~	17	19	~~21~~	23	25	~~27~~	29	31	~~33~~	35	37	
3	5	7		11	13		17	19		23	~~25~~		29	31		~~35~~	37	

Algorithm improvedEratosthenes

```
uint64_t improvedEratosthenes(uint64_t n) {
  uint64_t count = 1; // special case for 2 which is even
  bool* isPrime = new bool[n+1]; // allocate giant array of
     boolean (better to do this with bits than bool)
  for (uint64_t i = 3; i <= n; i += 2)
    isPrime[i] = true;
  for (uint64_t i = 3; i <= n; i += 2)
    if (isPrime[i]) {
      count++; // add the new prime and then remove all multiples
          of it starting with $i^2$
      for (uint64_t j = i*i; j <= n; j += 2*i)
```

```
        isPrime[j] = false;
  }
}
```

One final performance tuning, left to the reader, is to implement the array of booleans more efficiently. The code shown here stores each bool as a byte. But a bool requires only one bit. This means that for computing the primes up to 1 billion, instead of needing 1Gbyte, only 125Mb is required. Further optimizations are possible. We can store only the odd numbers since the only even prime is 2, handled as a special case. This brings the storage down to 62.5Mb.

The next efficiency technique is to realize that once a bit vector is used, it is possible to set multiple bits true at the same time. On a PC with a 64-bit CPU, this means that it is possible to set 64 elements of the bit vector true in a single operations, with vastly improved performance. Going further, even 62.5Mb is a fairly large block of memory, so computers will not have enough cache to hold it all. It is therefore more efficient to write not the whole thing, but a range that efficiently fits into cache. Working on a range at a time is called a segmented Eratosthenes' sieve, and is the fastest implementation in this class.

4.4 Prime Number Wheel

Prime number wheels are not in themselves a method of finding primes, but they are a method of skipping tests and making searching for multiple primes faster.

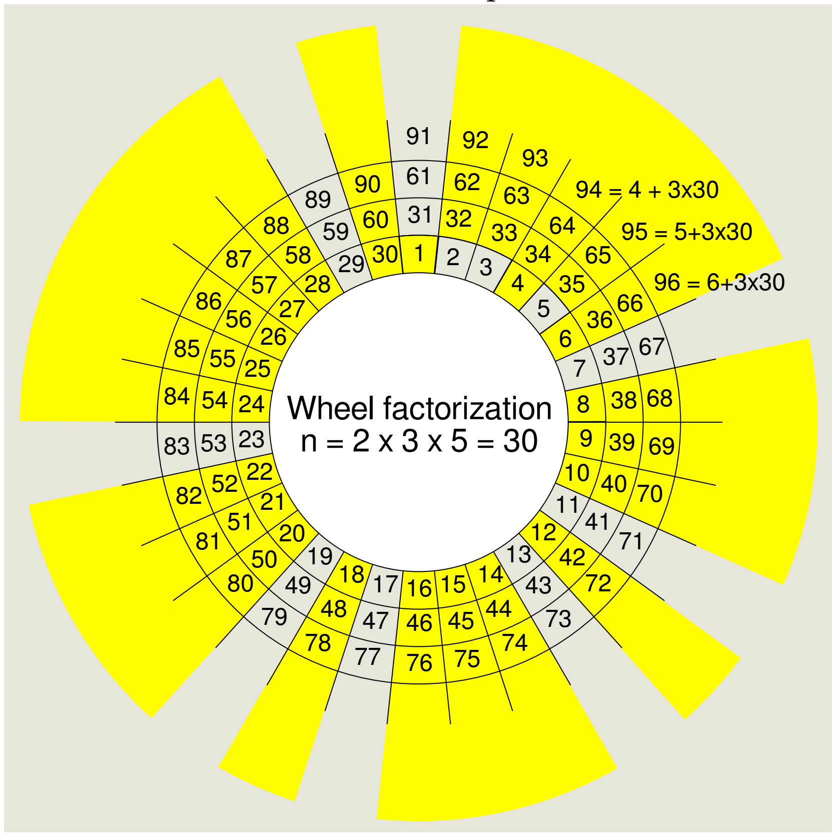
The first level wheel considers numbers modulo the first prime, 2. Since all numbers are either odd or even, obviously there is no point in checking even numbers (aside from 2). Therefore, any prime search can handle 2 as a special case, and the loop can process only odd numbers.

The next level of wheel considers multiples of 2 and 3. Multiplied together, $2 * 3 = 6$ there are 6 possibilities for any number $nmod6$. All entries in the following table are marked Composite if they are definitely not prime. Of the 6 possibilities, 3 are even, and 2 are multiples of 2. There are only 2 numbers which may be prime and must be checked.

0	Composite (2,3)
1	
2	Composite (2)
3	Composite (3)
4	Composite (2)
5	

Note that this does not mean that every number $nmod6 = 1$ is prime. For example, 7, 13, 19 are prime, but the next one 25 is not because is it 5^2. Similarly, $nmod6 = 5$ may be prime, and 5, 11, 17, 23, 29 are prime, but 35 is not.

The following diagram from Wikipedia shows a prime number wheel for $n = 2,3,5 = 30$. Only 8 of every 30 numbers must be checked, which is a little over 1 in 4. Taking this further is difficult because the wheels grow expoentially. Including 7 yields a wheel of size 210. Adding 11 increases the size to 2310, and adding 13 increases to 30030. And the gains come slowly. In order to eliminate 99% of the numbers, it would be necessary to build a wheel of all the numbers up to 256 which would be gigantic.



4.5 Probabilistic Algorithms

Eratosthenes' sieve is the most efficient algorithm for finding large batches of primes. However, while it avoids divisions, it still requires lots of memory and $O(nloglogn)$ computation. It would not be practical to use for a single large number, because it would require finding all primes up to the square root of that number.

For large numbers, it is possible to efficiently tell whether they are prime or not without trial division at all, which is startling. Interestingly, this is not some recent development in computer science, but was discovered by Fermat more than 300 years ago.

Fermat is famous for his "last theorem" in which he famously said he had come up with a marvelous proof but it was too large to write down in the margin. Today, we think that he was mistaken. The only proof mathematicians have come up with since was assisted by a computer and involved 6000 cases and a gigantic proof hundreds of pages long. I wonder whether Fermat was just torturing other mathematicians by claiming to know an answer.

In any case, Fermat's last theorem, that $c^n = a^n + b^n$ is false for any $n > 3$ has no practical application that we know of yet. But his little theorem is incredibly useful.

The little theorem states that if p is prime, then for any witness a where $1 < a < p$ that $a^{p-1} mod p = 1$.

On the surface, this seems useless. For a large number like 124182512581210000000100000007 even the smallest witness $(a = 2)$ would result in the operation $a^{124182512581210000000100000006}$ which is utterly beyond our power to compute. The number of digits is too large to store, requiring more memory than the estimated number of particles in the universe which is a mere 10^{72} or so. But there is a hidden catch. We are not asked to compute this gigantic number. Rather, we are asked to compute it mod n. Modulo is a way to keep numbers small. Consider factorial. If we ask you to compute:

$5! = 5 * 4 * 3 * 2 * 1$

you can readily do it (120). But if we ask for $n = 10^{12}$ then $n!$ is again utterly impossible, huge! Yet what if we ask not for n factorial, but

n! mod 10

Now we only need the last digit, which is easy – it is zero. How do we know? Well, $5! = 120$ the last digit is zero, and any factorial after that must end in zero because zero times anything is zero. In fact, as the numbers in $n!$ keep multiplying, for every 2 and 5, there will be another zero. Consider:

n	$n!$
2	2
3	6
4	24
5	120
...	...
10	3628800
...	...
15	1307674368000

The 10 obviously adds a zero, and the 2 in the 12 and the 5 in the 15 combine to make another 0 at 15. So for $n = 10^12$ not only is the last digit 0, probably at least the last 100 billion digits are zero.

In any case, this shows that computing something mod n is way easier than computing the full number. Using the fact that:

$(a * b) modn = ((amodn) * (bmodn)) modn$ we can keep the number limited and tractable at all times. It only remains to devise an efficient algorithm for computing powers.

Obviously the definition of a^b is to multiply a together b times. This is horrendously inefficient. Instead, consider breaking down the exponent by powers of 2. Suppose we have a^{17}. That can be written:

$a^{17} = a^1 * a^{16}$

$a^{16} = a^{8^2}$

$a^8 = a^{4^2}$

$a^4 = a^{2^2}$

$a^2 = a * a$

So starting from a, repeatedly squaring we can obtain a^2, a^4, a^8, a^{16} in just 4 multiplies. We must multiply two of them together. The power algorithm breaks the exponent down by bits, and for every 1 bit multiplies into prod.

Algorithm power

```
uint64_t power(uint64_t x, uint64_t n,uint64_t  m) {
  uint64_t prod = 1;
  while (n > 0) {
    if (n & 1) { // if n is odd, then 1 bit is set
      prod = prod * x;
    x = x * x;
    n >>= 1; // divide by 2
  }
  return prod;
}
```

For example, consider power(2, 13) which constructs $2^{13} = 2^1 * 2^4 * 2^8$

prod	x	n	comment
2	2	13	17 is odd, multiply (prod=2)
1	4	6	6 is even, no multiply
32	16	3	3 is odd, multiply
8192	256	1	1 is odd, multiply

The powermod algorithm is similar, but at each step the number must be limited by computing it modulo m.

Algorithm powerMod

```
uint64_t powerMod(uint64_t x, uint64_t n,uint64_t  m) {
  uint64_t prod = 1;
  while (n > 0) {
    if (n & 1) { // if n is odd, then 1 bit is set
      prod = prod * x \% m; // compute $prod^x mod n$
    x = x * x \% m;
    n >>= 1; // divide by 2
  }
  return prod;
}
```

Example, compute $powermod(2,16,17)$

prod	x	n	
1	2	16	16 is even, no multiply
1	4	8	8 is even, no multiply
1	16	4	4 is even, no multiply
1	1	2	$256 \mod 17 = 1$
1	1	1	$2^{16} \mod 17 = 1$

Example, compute $powermod(2,40,41)$

prod	x	n	
1	2	40	40 is even, no multiply
1	4	20	20 is even, no multiply
1	16	10	10 is even, no multiply
10	10	5	$16^2 \mod 41 = 10$
10	18	2	$10^2 \mod 41 = 18$
1	37	1	$18^2 \mod 41 = 18$

The final result of 1 is because $(10 * 37) \mod 41 = 1$.

Fermat's algorithm is probabilistic. For a random witness a, $1 < a < p$, it may state that p is prime. But if we try a few, one of them will probably work. And we can easily make the probability that the algorithm fails smaller than the probability that the hardware will fail. At that point, the algorithm is no more "probabilistic" than the computer.

If $powermod(a, p-1, p)$ is not 1, then the number is definitely composite. if the result is 1, then it may be false witness, which is why we must try several. But there is a false positive, rare but it exists.

For a rare class of numbers called Carmichael numbers, Fermat will always return true even though the number is not prime. A Carmichael number is the product of at least 3 primes so it is definitely composite. It is square free, so no Carmichael number has two factors which are the same. The first Carmichael number is 561. See Wikipedia: Carmichael Numbers

There are infinitely many Carmichael numbers, and any of them will return true for all witnesses UNLESS you happen to pick one of the factors of the Carmichael number. For example, for 561, powermod(2, 560, 561) will return 1, thus claiming that it is prime. Any witness to powermod will also return 1 except for the factors of 561 which are 3, 11, 17.

So for a Carmichael number, Fermat requires that we know the factors, in other words that we have to try every possible factor which is what we are trying to avoid in the first place. One approach to solve this problem is to ignore it. There are 3 Carmichael numbers under 2000, a bad failure ratio. But we would never use this algorithm for small numbers. The Wikipedia article states that for numbers under 10^{21} there are approximately 20 million Carmichael numbers. So the chances of picking one are 1 in 50^{12} or so. And as the numbers grow, the probability goes down exponentially. Still, if the small chance means that your web session can be hijacked and your money stolen from the bank, it's a risk we don't wish to take. After Fermat, the next algorithm Miller Rabin solves the problem by splitting off the case of Carmichael numbers and detecting it.

Algorithm Fermat

```
bool fermat(uint64_t p, uint32_t k) {
  for (int i = 0; i < k; i++) {
    uint64_t a = rand(2, p-1);
    if (powerMod(a, p-1, p) != 1)
      return false; // definitely not  prime
  }
 return true; // if all tests passed, probably prime
```

Algorithm MillerRabin

```
MillerRabin(n, k)
  d ← n-1
  s ← number of trailing zeros of d
  d ← leading non-zero digits
WitnessLoop:
  for i ← 1 to k
    a ← random(2, n - 2)
    x ← $a^d$ mod n
    if $x = 1$ or $x = n - 1$ then
      continue WitnessLoop
   repeat $r - 1$ times:
      x ← $x^2$ mod n
      if $x = n - 1$ then
         continue WitnessLoop
      if $x = 1$ then
        return false     // this is the Carmichael case
      end
  end
return true //(probably prime)
```

Algorithm 4.1: MillerRabin

Another competitive algorithm for primality testing is Solovay-Strassen.

Algorithm Solovay- [TBD]

```
SolovayStrassen(n, k)
  for i ← 1 to k
    a ← rand(2, n - 1) // pick a random number from 2 to n-1
    {\displaystyle x\gets \left({\tfrac {a}{n}}\right)}{\
       displaystyle x\gets \left({\tfrac {a}{n}}\right)}
```

```
%     if x = 0 or {\displaystyle a^{(n-1)/2}\not \equiv x{\pmod {n
   }}}a^{(n-1)/2}\not \equiv x{\pmod {n}} then
%       return false //composite
%     end
%   end
%   return  true //probably prime
  end
```

Algorithm 4.2: SolovayStrassen

4.6 RSA Public Key Cryptography

RSA is the Rivest, Shamir, and Adelman cryptosystem used to secure the internet. It relies on the fact that with a computer using a fast primality test like Miller-Rabin or Solovay-Strassen, it is relatively fast to pick two large prime numbers and multiply them together, but very difficult to take the resulting number and factor it back into the primes. In other words, RSA relies on a function that is relatively inexpensive, and its inverse which is extremely slow.

The question today is whether the entire edifice of web-based security built on RSA is secure. And if it is secure, for how much longer? IBM has warned in 2019 that they believed RSA will be insecure within 5 years. Quantum computers with sufficient qubits can break RSA in polynomial time using Schorr's algorithm (see the reference section for the paper).

Also Agrawal, Kayal and Saxena (AKS2002, also in the reference section) proved that it is possible to deterministically prove whether a number is prime or not in polynomial time. The fact that their algorithm is slower than Miller-Rabin and is not used is immaterial. The fact that we can know deterministically whether a number is prime or not without trial division opens the question to whether factoring might also be similarly vulnerable. No one has proved it can not be done.

Boaz Barak, a cryptography professor at Harvard states that there is a much more fundamental problem with the basis for all public key cryptography. It has never been proven that one-way functions exist (see his paper in the references). At the moment, there are a number of problems such as discrete logarithm, elliptic curve cryptography (ECC), and NTRU lattice methods that all provide operations that are fast in one direction and slow in another. The cryptography for each of these methods is based on the fact that a key can be generated quickly but it would take essentially forever to crack it. ECC is specifically supposed to be safe against an attack by quantum computers. However, what professor Barak states in his article is one-way functions may not exist at all. Perhaps we just don't know how to invert these problems efficiently, but we might learn. The stakes are high. Anyone cracking methods that are used for finance could wreak havoc on web transactions, breaking everyone's secrets and stealing money.

RSA Cryptosystem

```
RSAGenerateKey(k)
  p ← random(k) // generate two random keys of k bits
  q ← random(k)
  n ← $p * q$
  select e such that $1 < e < \lambda(n)$
  d \dot e = 1 (mod \psi(n))
end
```

Algorithm 4.3: Algorithm RSAgenerateKey

```
RSAencrypt(m, e, n)
  return ← $m^e mod n$
```

Algorithm 4.4: RSAencrypt

Algorithm RSAencrypt

```
RSAencrypt(m, e, n)
  return true // probably prime
\end{algorithm}

Algorithm RSAdecrypt
\alg{RSAencrypt}{}
RSAdecrypt(c, e, n)
  return \$c^d\$ mod n
```

Algorithm digitalSign

```
digitalSign(m, e, n)
```

Algorithm verifySignature

```
verifySignature(m, e, n)
```

Algorithm DiffieHellman

```
DiffieHellman()
  r = each party picks random number
  encrypt r using other partys public key and send
  sessionKey = r, other key
  encrypt session using symmetric AES256 key, used by both sides
```

4.7 Do one-way Functions Exist?

Algorithm AKS

```
AKS(p, k)
  for k = 1 to n


  end
  return true // probably prime
```

5. Strings

5.1 Searching

Brute force string search is obvious but not very good. It looks for the first letter of the target string. When it finds the desired character, it looks for the remainder of the string. However, because the first character may be found, and then subsequently the match may not happen, there may have to be multiple checks, and this can result in O(kn) time, where n is the length of the string to be searched, and k is the length of the target string.

The following example shows the string ”this is a test” (n=13) being searched for the target string ”test” (k=4) In this case, it seems like the complexity is O(n).

t	h	i	s		i	s		a		t	e	s	t																			
t	t	t	t	t	t	t	t	t	t	t	t	t	t																			

However, if the search string contains many partial matches, the algorithm must keep trying to check whether each one works. In this next case, the string ”xoxoxoxoxoxoxo...” is being search for the pattern ”xoxoy” The first 4 letters match, and it is only when the algorithm encounters the y that it has to start over, and since it is ignorant of the structure, it must do so on the very next letter, doing it all over again

x	o	x	o	x	o	x	o	x	o	x	o	x	o	x	o																	
x	o	x	o	y																												
	x																															
		x	o	x	o	y																										

In the above case, you can see that it will compare the entire target string O(k), fail on the last letter, and do so n/2 times.

```
bfStringSearch(s, target)
  n ← length(s)
  m ← length(target)
  for i = 0 to n − m
    if s[i] = target[i]
      for j = 1 to m − 1
        if s[i+j] ≠ target[j]
          goto nomatch
        end
    end
    return i
nomatch:
  end
  return -1
end
```

Algorithm 5.1: Brute Force String Search

```
BoyerMoore(s, target)
  n ← length(s)
  m ← length(target)
  t ← new int[256] // create a table of offsets
  for i ← 0 to 255
    t[i] ← m
  end
  for i ← 0 to n - 1
    t[target[i]] ← m-i+1 // build the table of offsets
  end

  for i = m to n-1
    advance ← t[s[i]]
    if advance = 0
      for j = m - 1 to 0
        ...
      end
  end
  return -1
end
```

Algorithm 5.2: Boyer-Moore

```
FSM(s, fsm)
  n ← length(s)
  state ← 0        // select initial state
  for i ← 0 to n - 1
    if fsm.found[s[i]]
      return i
    state ← fsm.next[state][s[i]]
  end
end
```

Algorithm 5.3: Finite State Machine

5.2 Longest Common Subsequence and EditDistance

One important problem in string manipulation is discovering how similar two strings are when they do not match.

The Longest Common Subsequence (LCS) defines the cost to compare two strings for the maximum characters they share in common (not sequentially)

```
LCS(a, b)
  if isEmpty(a) or isEmpty(b)
    return 0
  end
  if a[0] == b[0]
    return 1 + LCS(a.substr(1), b.substr(1)) //Note: this cannot
       copy the substring or cost gets very high
  end
  return max(LCS(a,b.substr(1)), LCS(a.substr(1), b))
```

Algorithm 5.4: Longest Common Subsequence

```
LCS(a, b, m, n)
  if m = length(a) or n = length(b)
    return 0
  end
  if memo[m][n] ≠ 0
    return memo[m][n]
  end
  if a[m] == b[n]
    return 1 + LCS(a.substr(1), b.substr(1)) //Note: this cannot
       copy the substring or cost gets very high
  end
  memo[m][n] ← max(LCS(a,b.substr(1)), LCS(a.substr(1), b))
  return memo[m][n]
```

Algorithm 5.5: Longest Common Subsequence with Dynamic Programming

```
LCS(a, b)
  m ← length(a)
  n ← length(b)
  t ← new int[m+1][n+1]
  maxVal ← 0
  for i ← 0; i ≤ m; i++)
    t[i][0] = 0
  for i ← 0; i ≤ n; i++)
    t[0][i] = 0
  for i ← 1; i ≤ m; i++)
    for j ← 1; i ≤ n; j++)
      if (a[i] = b[j]
        t[i][j] ← 1 + t[i−1][j−1]
      else
        t[i][j] ← maxVal ← max(t[i−1][j], t[i][j−1])
      end
```

Algorithm 5.6: Longest Common Subsequence as a single loop

```
EditDistance(a, b, m, n) {
  if (n == s2.length())
    return s1.length() − m;
  if (m == s1.length())
    return s2.length() − n;
  if (s1[m] == s2[n]) return count(s1, s2, m + 1, n + 1);
  if (s1[m] != s2[n]) {
    return 1 + min(EditDistance(s1, s2, m, n+1), EditDistance(s1,
        s2, m+1, n), EditDistance(s1,s2,m+1,n+1));
  }
}
```

Algorithm 5.7: Edit Distance

```
int EditDistance(string s1, string s2) {
  int m = s1.length();
  int n = s2.length();
  for (int i = 0; i ≤ m; i++) {
    v[i][0] = i;
  }
  for (int j = 0; j ≤ n; j++) {
    v[0][j] = j;
  }

  for (int i = 1; i ≤ m; i++) {
    for (int j = 1; j ≤ n; j++) {
      if (s1[i−1] == s2[j−1]) v[i][j] = v[i−1][j−1];
      else v[i][j] = 1 + min(min(v[i][j−1],v[i−1][j]),v[i−1][j
          −1]);
    }
  }
  return v[m][n];
}
```

Algorithm 5.8: Edit Distance with Dynamic Programming

```
Winnowing
(a, b)
```

Algorithm 5.9: Winnowing

5.3 Rope

Rope is a tree structure that replaces simple strings so operations can be performed on large text in O(log n). The concept of rope is a tree of fixed strings, so at the lowest level, the strings are immutable (do not change).

Let's compare operations on a large file, 100 million bytes, using a string and rope.

append

insert multiple times in the middle (typical typing)

concatenation

5.4 Efficient Implementation of Tree Operations for a Text Editor

One potential project is to implement a data structure suitable for use in a text editor, something that wold be able to edit huge files instantly. It must support editing in a particular location because that is what typically happens. A human will type, then delete, then type more in a location. For a large document, the text editor also needs to be able to display what is on the screen efficiently. For a multi-user system like google docs, we can conceive of multiple users across the internet all editing the same document simultaneously.

In order to improve on rope, and add functions to make the above more efficient, we have to develop the following concepts:

Node

A node of the tree can be more complicated than rope. We should consider higher degree such as 4 or 16 so there can be fewer nodes and less overhead. The tradeoff will be complexity, and somewhat more work when inserting and deleting. Operations will still be O(log n).

Line

Rather than having a tree structure down to the individual letter, storing a string for each line will be efficient. At this scale, inserting text would mean replacing one string with another. So leaves in this system are strings, but they can be non-growable strings, every time one is edited just swap it out with a bigger or smaller one.

Cursor

A cursor location is like an iterator into the rope structure. It must represent a location within a document. It is vital that if multiple cursors exist in a document (such as for different users editing the same document simultaneously) that inserting in one does not invalidate the other cursors.

Range

A range within the document is a region defined by a start and end cursor, or a start cursor and length. Again it is vital that multiple people editing a document do not invalidate each others' cursors or ranges.

Window

In order to edit a large buffer we must be able to view a rectangular region. The document is vastly bigger than an individual window in the vertical, but it is also possible that the document is wider than the window.

6. Sorting

6.1 Introduction

Sorting is one of the oldest topics in computer science.

6.2 Bubble Sort

```
BubbleSort(a)
  for i = 0 to a.len - 1
    for j = i+1 to a.len-1;
      if a[j] > a[j+1]
        swap(a[j], a[j+1])
      end
    end
  end
end
```

Algorithm 6.1: BubbleSort

This version of the bubblesort will stop early if a complete pass is made without any swapping. Thus the lower bound on complexity is $\Omega(n)$ Unfortunately, it is also slower in gernal because it takes time to add this test. Insertion set is both faster and similarly has a lower bound of $O(n)$.

```
BubbleSort(a)
  for i = 0 to a.len - 1
    done = true
    for j = i+1 to a.len-1;
      if a[j] > a[j+1]
        swap(a[j], a[j+1])
        done = false
      end
    end
    if done
      return
    end
  end
end
```

Algorithm 6.2: ImprovedBubbleSort

6.3 Selection Sort

```
SelectionSort(a)
  for i = 0 to a.len − 1
    min = a[i]
    minpos = i
    for j = i+1 to a.len−1;
      if a[j] < min
        min = a[j]
        minpos = j
      end
    end
    swap(a[i], a[j])
  end
end
```

Algorithm 6.3: SelectionSort

6.4 Quicksort

Algorithm 6.4: Quicksort

6.5 Heapsort

Heapsort is another $O(nlogn)$ algorithm, but radically different than quicksort. Heapsort does not rely on divide and conquer, and it totally rearranges all the elements even if they are sorted. Nonetheless, in terms of complexity it is competitive with quicksort even though the constant factor is high.

Heapsort relies on first creating a heap, a binary tree in which every parent is bigger than their children. Creation of a heap takes n log n time. Then, by pulling out the root and placing it at the end, which takes log n time, it is possible to create a sorted list with another $O(nlogn)$.

```
makesubheap(a, i, n)
  if $i \geq n$ or $2i \geq n$
```

```
    return
  end
  if $2i+1 \geq n$
    if a[2i] > a[i]
      swap(a[i], a[2i])
      makesubheap(a, 2i, n)
    end
  else
    if a[2i] > a[2i+1]
      if a[2i] > a[2]
        swap(a[i], a[2i])
        makesubheap(a, 2i, n)
      end
    else
      if a[2i+1] > a[i]
        swap(a[i], a[2i+1])
        makesubheap(a, 2i+1, n)
      end
    end
  end
end

MakeHeap(a)
  for i = a.length/2 to 1
    makesubheap(a, i, n)
end
```

Algorithm 6.5: MakeHeap

```
  for i = n-1 to 2
    swap(a[0], a[i])
    makesubheap(a, 0, i-1)
  end
end
```

Algorithm 6.6: rebuildHeap

```
HeapSort(a)
  MakeHeap(a)          // O(n log n)
  rebuildHeap(a, i)  // O(n log n)
end
```

Algorithm 6.7: HeapSort

6.6 Merge sort

Merge sort has a higher constant than quicksort or heapsort, and it requires $O(n)$ extra storage, so it is not generally used for ordinary sorting. However, when the data being sorted is either larger than available memory, therefore on disk or tape, or when the data is in a linkedlist (in other words, for cases where sequential access is far faster than random access) then mergesort is far faster than the alternatives.

Even 50 years ago, with very small RAM capacity and slow magnetic tapes, it was possible to sort hundreds of millions of records by reading in data on two magnetic tapes and writing it out on one. In this way, the speed of each pass of the sort is limited by the sequential access speed of the medium. Today the same is true for hard drives which are far faster when accessing data sequentially.

Mergesort could be called recursively but this is fairly tricky given the need to keep both a primary array and temporary storage. In this case, bottom up is far simpler. It is also far faster because a great deal of time is taken by all the recursive calls. In a mergesort of 1 million elements, the bottom layer merges 500,000 times, each a function call for a recursive version.

Consider a section of an array of size 1. It obviously cannot be in the wrong order. Now consider merging two of them:

1	2
1	2

4	3
3	4

Now consider a list with many such units. First we merge into pairs of elements, each sorted. Then we merge the sorted pairs into groups of 4 elements, all sorted. Finally we merge two groups of 4 into 8. The same principle of divide and conquer is used as in quicksort, but there is no pivot (good) and there is a need for $O(n)$ temporary storage because reading the data must write it back into different memory.

cells of size 1	7	8	6	5	4	3	1	2
cells of size 2	7	8	5	6	3	4	1	2
cells of size 4	5	6	7	8	1	2	3	4
merge 4 into 8	1	2	3	4	5	6	7	8

At any point in time, if two segments are sorted and being merged, if the rightmost element of the left hand group is less than the leftmost element of the righthand group, merging does not need to be done because the two groups are already sorted. For example:

1	4	5	8	12	13	16	19

At the beginning, mergesort is relatively expensive. A way to reduce the cost is to sort the smallest sections using a different method. In the following example, below $n = 8$

insertion sort is used to order each group without requiring temporary storage or the other overhead of mergesort. For an example with a hard drive, the obvious efficient thing to do is read in a number of blocks that fit well into memory, sort them in memory, then write them back and move to the next blocks. In order to avoid the disk seeking back to the start of each group of blocks, it would even be possible to use the temporary storage, read in from one hard drive and write out to another with each group sorted.

The optimal size of the lowest method must be determined by experiment, and is clearly far larger than $n = 8$ shown in the algorithm below. After this initial phase, each group is merged into a group exactly double the size.

```
constexpr int minPartition = 8;
void quicksortSmall(int a[], uint32_t n, uint32_t minPartition) {
  for (uint32_t i = 0; i < n; i += minPartition) {
    for (uint32_t j = i+1; j < i + minPartition; j++) {
      int temp = a[j];
      for (int32_t k = j-1; k > i; k--)
        if (a[k] > temp) // there is a bug here...
         a[k+1] = a[k];
        else {
          a[k+1] = temp;
          break;
        }
     }
  }
}

void bottomUpMergeSort(int* a, uint32_t n) {
  insertionSmall(a, n, minPartition); // first sort each group
  uint32_t partSize = minPartition;
  uint32_t partSize2 = partSize + partSize;
  uint32_t last = n - partSize2;
  int* temp = new int[n]; // allocate temporary storage O(n)

  while (partSize2 < n) {
    // first check whether this pass is necessary
     uint32_t countSortedPartitions = 0;
     for (uint32_t i = 0; i < last; i += partSize2){
       if (a[i+partSize-1] < a[i+partSize]) {
          countSortedPartitions++;
       }
     }
     if (countSortedPartitions == n / partSize2)
       continue; // skip this iteration
     for (uint32_t i = 0; i < last; i += partSize2) {
       uint32_t end1 = i+partSize, end2 = i + partSize2;
       uint32_t j = i + partSize;
       uint32_t dest = i;
      while (i < end1 && j < end2) {
        if (a[i] < a[j])
          temp[dest++] = a[i++];
        else
          temp[dest++] = a[j++];
      }
      while (i <= end1)
        temp[dest++] = a[i++];
      while (j <= end2)
         temp[dest++] = a[j++];
    }
    partSize = partSize2;
    partSize2 = 2*partSize2;
    swap(a, temp); // each iteration, swap pointers so temp is
       the other one
  }
  int log2 = (log(n) - log(minPartition)) / log(2);
  if (log2 \% 2 != 0) { // if data ends in temp, swap back one
     more time
    memcpy(temp, a, n * sizeof(int));
    swap(a, temp);
  }
  delete [] temp; // get rid of temporary storage
}
```

6.7 Radix sorting

6.8 Spreadsort

Spreadsort is a relatively new algorithm due to Steven Ross 2002.

6.9 Shuffling

Shuffling is the reverse of searching. Just as in the physical world, entropy is ever-increasing. It is easier to shuffle an array than to sort it. When we sort an array we are finding one correct ordering amid all the possible $n!$ orders. Sorting is $O(n^2)$ for brute force solutions, and best-case $O(nlogn)$ for any sort involving exchanging elements.

Shuffling is also $O(n^2)$ for a poor solution, which is covered here because it has an interesting feature, and is $O(n)$ for the good solution.

6.9.1 Brute Force Shuffling

The brute force shuffling algorithm takes each element from an array and adds it to a new list. At first, the probability is 100 percent that the algorithm finds an element. But the more elements have been removed, the higher the probability is that the element selected is one that has already been chosen. While this is a very poor algorithm, it is a good illustration of probability in the calculation of complexity.

```
Shuffle(a)
  count = 0
  for i = 0 to a.len − 1
    do
      r ← $random(0, a.len − 1)$
    while a[r] < 0
    b[count] = a[r] // pull the number out and add to the 2nd
       list
    a[r] = −1        // mark no longer there
    count = count + 1
  end
  return b
end
```

Algorithm 6.8: BruteForceShuffle

The complexity of the inner do..while loop is the interesting part of this algorithm. The first time, the loop executes deterministically 1 time. However, as the elements are removed from the original array, the probability of the inner loop finding a random element goes down. The last time, the probability is only $1/n$ that the value is found. How then does this translate into the number of times the loop executes?

With a probability of $1/n$ it is not guaranteed that the last number will be found in n tries. However, while the probability is not $n\frac{1}{n} = 1$, it is on the order of n. It might take $2n$ or $3n$, but the expected value is on the order of n. Since the outer loop is also $O(n)$ the complexity of the algorithm is therefore $O(n^2)$

6.9.2 Unfair Shuffling

A shuffle is first and foremost supposed to be fair. That is, every value is supposed to be equally likely to wind up in any location. This second algorithm, while efficient, turns out to be unfair for a very subtle reason.

```
UnfairShuffle(a)
  for i = 0 to a.len − 1
    swap(a[i], a[random(0,a.len −1)]
  end
end
```

Algorithm 6.9: UnfairShuffle

Because each random number is selected from the entire list, a number can be moved to a position, and then can be moved again. Numbers that are near the beginning when sorted (0, 1) are more likely to be moved twice, and this has a noticable effect on the distribution of probabilities of where they will end up. Consider an array of 10 elements with 0 to 9, for example. The number zero is the first element and will be placed first. If it is placed at element 9, it has multiple chances of being moved again if the random selection happens to pick 9 again, and will definitely be moved again when i becomes 9. So the odds that the number 0 ends up in the last slot is noticeably lower. See the table below for a frequency distribution given $n = 10^7$ trials.

	0	1	2	3	4	5	6	7	8	9
0:	0.1	0.13	0.12	0.11	0.1	0.098	0.092	0.087	0.082	0.077
1:	0.1	0.094	0.12	0.12	0.11	0.1	0.096	0.091	0.086	0.082
2:	0.1	0.095	0.09	0.12	0.11	0.11	0.1	0.096	0.091	0.086
3:	0.1	0.095	0.091	0.087	0.12	0.11	0.11	0.1	0.096	0.092
4:	0.1	0.096	0.092	0.089	0.086	0.12	0.11	0.11	0.1	0.098
5:	0.1	0.097	0.093	0.091	0.088	0.086	0.12	0.11	0.11	0.1
6:	0.1	0.097	0.095	0.093	0.091	0.089	0.087	0.12	0.12	0.11
7:	0.1	0.098	0.096	0.095	0.093	0.092	0.091	0.09	0.12	0.12
8:	0.1	0.099	0.098	0.097	0.097	0.096	0.095	0.095	0.094	0.13
9:	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1	0.1

6.9.3 Fischer-Yates Shuffling

Only a slight modification is needed to make the unfair shuffle fair. Each time we pick a random number, we are selecting one value for the final list. Once selected, we must never pick again. Assuming a fair random number generator, this will work.

The following algorithm counts down rather than up, and each time, it picks a random element and puts it last. Then it never looks that that element again. The critical difference is that the random number is selected from 0 to i, not the length of the array.

```
FischerYates(a)
  for i = a.len - 1 to 1
    swap(a[i], a[random(0,i)]
end
```

Algorithm 6.10: FischerYates

6.10 References

https://en.wikipedia.org/wiki/Insertion_sort
https://en.wikipedia.org/wiki/Quicksort
https://en.wikipedia.org/wiki/Heapsort
https://en.wikipedia.org/wiki/Merge_sort

https://en.wikipedia.org/wiki/Radix_sort
https://en.wikipedia.org/wiki/Spreadsort
see the ref directory for the original papers on spreadsort

7. Searching

7.1 Introduction

Sorting is one of the oldest topics in computer science.

7.2 Linear Search

```
LinearSearch(a)
end
```

Algorithm 7.1: LinearSearch

7.3 Binary Search

```
BinarySearch(a, target)
  L ← 0
  R ← $a.len - 1$
  while R > L
    guess = (L + R) / 2
    if a[guess] > target
      R = guess − 1
    else if a[guess] < target
      L = guess + 1
    else
      return guess
    end
  end
  return −1  // not found
end
```

Algorithm 7.2: BinarySearch

The following algorithm is recursive instead of iterative.

```
BinarySearch(a)
end
```

Algorithm 7.3: BinarySearch

One very useful test in binary search is to check whether the value is completely out of range. If many searches are for values out of the range of the array, then this can reduce complexity for those cases from $O(logn)$ to $O(1)$

```
BinarySearch(a, target)
  if target < a[0] || target > a[a.len-1]
    return -1
  end
  L ← 0
  R ← $a.len - 1$
  while R > L
    guess = (L + R) / 2
    if a[guess] > target
      R = guess - 1
    else if a[guess] < target
      L = guess + 1
    else
      return guess
    end
  end
  return -1  // not found
end
```

Algorithm 7.4: BinarySearch

For a similar solution in continuous floating point, see the bisection algorithm for finding roots.

7.4 Golden Mean Search

```
GoldenMeanSearch(a)
end
```

Algorithm 7.5: GoldenMeanSearch

8. Dynamic Arrays

8.1 Introduction

8.2 Bad Dynamic Arrays

A list that is supposed to grow must allocate new memory whenever it runs out of space. The obvious implementation is an object that contains a pointer to memory and a size. Each time we add to the list, the size must grow. Each add operation is $O(n)$ and doing this n times yields a total of $O(n^2)$. For a list of 1 million elements, that would be $10^1 2$ operations, and on a computer capable of on the order of 1 billion operations per second, that is 1000 seconds, or about 20 minutes minimum. In practice it is much more because allocating all that memory requires a huge amount of time. In any case, even 10 million elements becomes completely intractable.

In the next section, we show that adding a size and a capacity is the crucial feature that allows the list to grow for a time until it reaches full, and most important, it must double in size every time. In this way, the grow only happens $logn$ times and the result is $O(2n)$

8.3 Operations

When building lists we must support a variety of operations including:

- Add an element to the end
- Add an element to the start
- Insert an element at position i
- Remove an element from the end
- Remove an element from the start
- Remote an element at position i
- Get the current size of the list

- Get ith element
- Set ith element

There are many higher level operations that can be built on top of these functions. Operations such as find, replace, are all

8.4 Dynamic Arrays

As we have seen, a dynamic array that only has a current size is $O(n)$ for all add operations, which means that adding n elements is a prohibitive $O(n^2)$. In order to do better, the dynamic array must not grow every time. By defining a dynamic array that has a capacity (how large the array is) and a size (how many elements are currently used) it is possible to reduce the number of times that the grow method is called. If grow is by 2, then the grow function will be called every other time, and the complexity is still $O(n)$. If it is called every 5th time, the same is true asymptotically. The standard solution used by vector in C++ and ArrayList in Java is to double in size each time. Consider growing a list to 1 million elements; the list starts with 1 element, doubles to 2 (calling grow) doubles again to 4, then 8, and so on up to n. There are $logn$ times that the list will grow.

The complexity is: $1 + 2 + 4 + ... + (n/2) + n = n(\frac{1}{n} + \frac{2}{n} + \frac{4}{n} + ... + 1) = n(2) = O(n)$

In other words, using the doubling strategy, growing a list only takes twice as long as pre-allocating the right size, it is still $O(n)$. Having said this, if the list size is known in advance, pre-allocating the right size is an easy way to double the speed of that part of the code.

8.5 Iterators

9. LinkedLists

9.1 Introduction

Linked Lists are data structures that start with a pointer and contain a sequence of objects (nodes) each containing some data and pointers to the next and possibly the previous node. Because each element is not contiguous in memory, LinkedLists are efficient for data that is inserted in any order. It is no more expensive to insert at the beginning or the middle of a list than at the end. It is, however, inefficient to reach a particular element or location because it requires starting from the beginning (or for some variants, from the end) and scanning forward or backward.

LinkedLists then are not better or worse than dynamic arrays. Each is better at one specific purpose. Dynamic arrays are more efficient for building a list sequentially adding at the end and for random access of any item in the list. LinkedLists are better for insertion from the beginning or in the middle. LinkedLists provide excellen practice for data structures with pointers, so this chapter prepares you to work with trees which are similar but more complex.

9.2 The Four Varieties of LinkedList

There are four kinds of LinkedList. The object can contain a pointer to head, or a pointer to head and tail. And each node can contain a pointer to the next node (a singly linked list), or a pointer to next and previous (a doubly linked List). The following diagram shows the four different kinds of LinkedList.

`Lists/LinkedLists.pdf`

9.3 Iterators

10. Stacks and Queues

11. Trees, Balanced Trees, and Tries

12. Hashing

12.1 What is hashing?

Hashing is a technique of rapid search that turns the target data into the location where it may be found in O(1) time. No faster search is possible, but there are difficulties. The critical part of any hash algorithm is the function which turns the bits of the input into where to locate them. A poorly chosen hash function may result in many values located in the same place (collisions) which will then require a seconday means to find the right one. In this chapter, we cover how to organize a hashmap to efficiently find the data, how to write a good hash functions

12.2 Hash Functions: Key to Hashing

12.2.1 Hash function for integers

The goal of a hash function is to uniformly spread the values.

12.2.2 Hash function for strings

Hashing strings must not collide for anagrams because many words contain the same letters (tea, eat, ate, eta).

Hashing strings must uniformly use the entire hashmap, it's not great if short words all bunch up low in the hash map.

Ideally, if we could hash 4 or 8 bytes at a time, we could do fewer operations, but in some circumstances, bytes are not aligned (meaning we have to read twice to read a single 4 or 8byte chunk). Worse yet, if we don't know the length of the string it is hard to do this. Theoretically of course, it does not matter if we do strings 1 byte at a time or 8, but in practice that is a huge constant factor.

The following hash is representative but not great or tested. Note the tricks. Because each pair of shifts is ored, the compiler recognizes that is a rotate operation so it is optimized into a single instruction, and we don't throw out any bits. We use xor to combine the bits because that is bit-neutral. If we used or, there would be more and more ones. If we used and, there would be zeros unless two coincided. A function like this must be heavily tested, but something of this type should work well. Given two different rotates mixes bits across different parts of the hash, the bits of any byte have been xored in 17 bits away and 7 bits away and since those numbers are prime, the next time those will be shifted 17+17 and 17+7 ... so in just two cycles we will have mixed up a lot of bits.

The more complicated this kind of function gets, the better it probably hashes the bits, but also the slower it gets. That's the tradeoff.

```
hash(key)
  sum = 0 // or set an arbitrary constant with 1s and 0s
  for i = 0 to len(key)-1
    sum = ((sum << 17) | (sum >> 15)) ^ ((sum << 7) | (sum >> 25)
       ) ^ key[i]
  end
  return sum
```

Algorithm 12.1: hash

12.2.3 Hash function for objects and pointers

Objects in most programming languages like C++ and Java are guaranteed to be at a unique location. For mapping objects therefore, we can use that location and hash it. That means a hash algorithm capable of hashing pointers.

The vital fact is that pointers are typically wordaligned. This means that the hash function must use all bins even though the numbers will all be multiples of 4 for a 32bit computer or 8 for a 64bit computer.

Imagine if the hash function leaves the low 2 or 3 bits intact. This means, for a hash map of 10k buckets, that only every 4th one is used. That would be disastrous and could result in way more collisions than planned.

The following table shows what it would look like if values hashed only to even multiples of 4 elements:

A				B				C				D			

The above table, which we think has 16 elements, effectively has only 4, and with 4 elements would have likely had a collision.

12.3 Linear Probing

```
LinearProbing.insert(key, value)
  h ← hash(key)
  do
     h ← (h + 1) mod size
```

```
    p ← table[h mod size]
  while table[h] ≠ null
    h ← $h+1$
    if $h \geq size$
      h ← 0
    end
  end
  table[j] ← (key,value)
end
```

Algorithm 12.2: LinearProbing.insert

12.4 Handling Collisions

Collisions in hashing are inevitable. And in the case of the linear probing algorithm, if a collision happens in one bucket it spills over to the next. Because of this property, busy buckets can ”ruin the neighborhood” for other bucket near them. The solution is to have an excess of buckets so that the probability is that there is always an empty bucket next to each one that is used. This means that linear probing does best with 100 percent extra space, or to put it another way, 50 percent open space.

s = “abc” a=1, b= 2, c=3 a=97 b=98 c=99

```
hash(s)
  sum ← 0
  for i ← 0 to length(s)
      sum ← sum + s[i]
  return sum
end
```

Algorithm 12.3: SimpleHashString

The above algorithm is very poor because for any words with the same letters the hash value is the same. For example, eat, ate, tea all would hash to the same value.

A much more effective approach is to weight each letter by different amounts so that ab does not have the same hash value as ba.

```
hash(s) {
  sum ← 0
  for i ← 0 to length(s)
      sum ← sum * 26 + s[i]
  return sum
}
```

Algorithm 12.4: Base26tashString

This algorithm too has a problem, in that long string will see the initial parts multiplied by large values and not affect the bottom bits as much. In order to make sure that every letter affects as much as possible, between adding in the new letters we can shift/rotate so that bits from early affect high bits and low bits. The exact winning design of a hash function requires vast amounts of testing, but the following is schematic.

```
hash(s) {
  sum← length(s)
  for i ← 0 to length(s)
     sum ← ((sum << 17) | (sum >> 15)) ^ ((sum << 7) | (sum >>
        25)) + s[i]
  return sum
}
```

Algorithm 12.5: Hash with bit mixing

The above code uses some very specific tricks. First, the numbers of the bit shifts are not divisible by a power of 2 so successive shifts will cover more of the word, overlapping in complex ways. Second, because $17 + 15 = 32$, and $7 + 25 = 32$ both of the ored terms are converted by C++ into a single rotate rather than two shifts and an or. This menas the above code only has 4 operations: 2 rotates, an XOR to combine them, and an addition to add in the new letter (which could also be an XOR).

12.5 The Birthday Paradox

What is the probability that two people in a class of 20 have the same birthday?

Given hash function f(x) = x^2 and data 5, 9, 16, 31

show the table after each insert

					5		
	9				5		
16	9				5	31	

12.6 Quadratic Probing

In linear probing, a collision results in moving to the next bucket over. If that is full, then the algorithm must keep scanning forward until it finds an empty bucket. Quadratic probing tries to get away from the neighborhood with the collision faster, by first adding 1, the next time $2^2 = 4$, the next time $3^2 = 9$, and so on. We cover it in the course for completeness, but Quadratic Probing isn't very useful. Far more important is a good hash function that uniformly spreads the values across the entire table.

To visualize the problem, consider a pathological hash function f(x) = 1 which always puts each object in the same bucket, resulting in 100 percent collision rate. The following tables show what it would look like to put in 5 values into the table both with linear probing and quadratic probing. Both have exactly the same collision resolution, except quadratic probing is more complicated and expensive.

		1					
		1	2				
		1	2	3			

		1					
		1	2				
		1	2				3

```
QuadraticProbing.insert(key, value)
  h ← hash(key)
  i ← 1
  do
     h ← (h + i*i) mod size
    i ← i + 1
    p ← table[h mod size]
  while table[h] ≠ null
    h = h + 1
    if h >= size
      h = 0
    end
  end
  table[j] ← (key,value)
end
```

Algorithm 12.6: QuadraticProbing.insert

12.7 Linear Chaining

Linear chaining is a different scheme where every bucket in the hash table is a linked list. The head pointer is null if the bucket is empty. Linear chaining creates far fewer collisions because one back bucket does not poison its neighborhood. It is still vulnerable to a bad hash function because if a function puts too many elements in one bucket, the collisions result in a large linked list, and traversal is $O(n)$ rather than $O(1)$.

When inserting items into the bucket, insert first (ie build the linked list in reverse). This is a good strategy because in general, the most recent item is the most likely to be accessed again (the principle of locality).

Linear chaining is better than linear probing for collisions because each bucket does not affect its neighbors, and it also uses less memory for empty buckets which only need a single pointer to null. However, when buckets are filled the nodes must contain not only the data but a pointer to the next node, so there is more memory for these. Another advantage of linear chaining is that an empty bucket is represented by null. With linear probing, there must be a value designating an empty bucket, and that value can therefore not be represented in the hashmap.

12.8 Perfect Hashing

For data that is known in advance, it is possible to create a special hash table that may be faster by completely eliminating collisions. This would normally be completely impossible because of the birthday paradox. Consider an example with 1000 elements stored in a table with 1 million buckets. On the surface, it would seem fairly easy to achieve no collisions: after all, only one bin in 1000 is occupied. But if the hash function for whatever reason gives the same number for two values, it does not matter how many bins there are, and with so many values, that becomes quite probable.

Perfect hashing defeats this problem by breaking a large number of elements using a hash function, so that no bin has more than a few elements. Because collisions don't matter, the hash function can be simple and fast. Then, each bucket uses a second simple but different hash function to resolve any collisions. Because each bucket has very few elements, the birthday paradox works in reverse and even a relatively simple hash function can separate those elements, as long as it is different from the main one.

The following example illustrates perfect hashing using the hash function $f(x) = x \mod n$. The secondary hash function is also $f(x) = x \mod m$ but m is the size of the secondary table which is chosen to be different (and always relatively prime) to the larger table. It is possible to write code that will automatically find a hashmap using this scheme that has no collisions for the data chosen, and once found, this can be somewhat faster than hashmaps with more complicated hash functions, even though it requires two hash evaluations per lookup.

Example: insert 1, 9, 18, 17, 26 into a hashmap size $n = 8$ using perfect hashing. The function is simple and fast, and in any case there are 5 elements in only 8 buckets. Bucket 1 contains 1, 9, and 17. Bucket 2 contains 18 and 26. We then pick a secondary hash table size for each bucket. For bucket 1, because there are 3 elements we should choose at least 3 or we are guaranteed a collision. We can start with 3. Never choose 4, because it evenly divides the original hash table with size 8. When we insert the numbers into the second hash table, we get $1 \mod 3 = 1$, $9 \mod 3 = 0$, $17 \mod 3 = 2$. So each value which was in the same bin happens to be in different bins in the secondary table, and all collisions are resolved. For bin 2 we select size 3 (because the original size 8 is evenly divisible by 2). $18 \mod 3 = 0$ and $26 \mod 3 = 2$ so again, collisions are resolved.

The following example shows what would happen when values do collide. The algorithm simply picks the next size for the secondary hash table and tries again. Example: insert 1, 25, 33, 20, 84, 92 into a perfect hash table size $n = 8$. Bin 1 gets elements 1, 25, 33 and bin 4 gets 20, 82, and 92. To resolve the collisions, the algorithm selects the first relatively prime size (3) for the secondary table and tries to insert the three numbers but this time $1 \mod 3 = 1$ and $25 \mod 3 = 1$ so there is a collision. The algorithm then tries size 5 (skipping 4 because it evenly divides the main table size). The result is $1 \mod 5 = 1, 25 \mod 5 = 0, 36 \mod 5 = 1$. Still no good, and the algorithm selects size 7. $1 \mod 7 = 1, 25 \mod 7 = 4, 36 \mod 7 = 1$. Again a collision, the algorithm selects 9. $1 \mod 9 = 1, 25 \mod 9 = 7, 36 \mod 9 = 0$. The collision is resolved.

12.9 Cryptographic Hashing and Digital Signatures

A cryptographic hash is one that not only evenly mixes the bits, but one that is deliberately designed to be difficult to construct an equivalent hash value with a different set of bytes. Imagine a document composed of letters. If we add the letters together to get a checksum, which is a primitive hash value, it would be easy to create a new document that is equivalent to the old one, that still has the same hash value. Suppose embedded in the document is the text:

"I hereby bequeath to my children all of my possessions."

A criminal wishes to change the will. In order to change the statement to:

"I hereby bequeath to Fred Wilson all of my possessions."

All the criminal has to do is calculate the change in the checksum and add or subtract letters to achieve the same one. The goal with cryptographic hashing is to make that difficult or impossible.

By definition, if a hash is 256 bits, far smaller than the document that it hashes, then there must be multiple documents for which the value is the same. However, the hope is that all the other documents are nonsensical and will be obviously wrong.

In order to sign a document, we make use of RSA (see Number Theoretic chapter). In assymetric encryption, there are two operators. Anyone can encrypt E() a message using the public key, and only the possessor of the private key can decrypt D() the message. And because they are inverses, $E(D(m)) = D(E(m)) = m$.

To digitally sign a document, the author computes a secure cryptographic hash, then decrypts it, even though it was never encrypted. The hash is appended to the document.

$doc, D(hash(doc))$

The receiver gets the document and computes the hash, then encrypts the hash that is appended with it:

$hash(doc), E(D(hash(doc))$

Since $E()$ and $D()$ are inverses, the two should match. If they do, the document is supposed to be as originally written. To prevent tampering by a third party along the way, who could at least try to generate a bogus (meaningless) document which hashes to the same value, it is recommended that the entire message be encrypted so that only the recipient can read it.

12.10 Avoiding Overuse of Hashing

There is a natural tendency having learned hashing to use it too much, since it is very powerful. The following situations are special cases where hashing can be simplified into an array. Remember that any time the keys have a pattern, inverting it is potentially the best possible hash function.

- The values are sequential integers $n, n+1, n+2$, ... (use an array $x[i-n]$)
- The values are an arithmetic series $n, n+k, n+2k$, ... (use an array $x[(i-n)/k]$)
- The values are floating point $n, n+0.1, n+0.2$, ... For this one, you have to be careful because of roundoff error. If you can come up with any expression that rounds this off and turns the result into an integer, do it.
- The values are integers in a range $[a,b]$ with many holes. If the range is not too big, just use an array. If memory requirements are too large and there are many holes, then use hashing.
- The values are in a geometric series n, nk, nk^2, ... (use an array, $x[c_1 log(i-n)]$

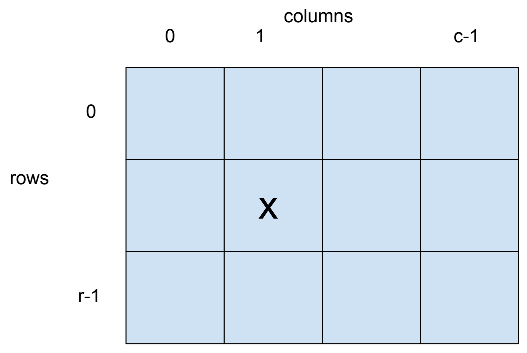
12.11 References

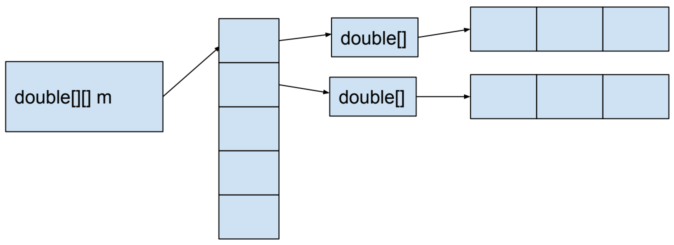
- Bob Jenkin's Hash: `http://burtleburtle.net/bob/index.html`
- Paul Hsieh SuperFastHash: `http://www.azillionmonkeys.com/qed/hash.html`
- Stanford Bit Hacks: `https://graphics.stanford.edu/~seander/bithacks.html`

13. Matrices

13.1 Matrix Representations

A matrix is a two-dimensional table of numbers. The dimension of a matrix is rows and columns. A matrix can be viewed as representing a set of equations, one per row, or as a space of column vectors. An ordinary matrix is represented in one of two ways. Either as an array of rows, each containing an array of columns (Fig. 1), or as a single block of memory (Fig. 2).





The identity matrix is a square matrix n x n in which all elements are zero except the main diagonal which is 1. The following example is a 3x3 identity matrix:

$$\begin{bmatrix} 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{bmatrix}$$

There are a number of matrix types where many of the elements are zero, and in such cases, it is possible to represent it in other ways that are more compact and often much faster for various algorithms.

An upper triangular matrix has all zero elements below the main diagonal (Fig. 3). A lower triangular matrix has zero elements above the main diagonal (Fig. 4). Both of these are not better in complexity than an ordinary matrix because they essentially have $n^2/2 = O(n^2)$ elements.

A diagonal matrix, however, has a big advantage, because only the elements on the main diagonal are non-zero (Fig. 5). Diagonal matrices will be able to do some operations like multiplication in $O(n)$ instead of $O(n^3)$ which is a major win. Last, a tridiagonal matrix has non-zero elements on the main diagonal, and on diagonal on either side. Tridiagonal matrices have approximately 3 times as many non-zero elements as a diagonal, but this is $3n$ so complexity is still $O(n)$.

An orthogonal matrix is one in which each column is perpendicular (normal) to the others. For example: $\begin{bmatrix} 2 & 2 \\ -2 & 2 \end{bmatrix}$

A normal vector is a vector with unit length. A normal matrix has normal vectors in all columns. $\begin{bmatrix} \frac{1}{\sqrt{3}} & \frac{\sqrt{2}}{\sqrt{3}} \\ \frac{1}{\sqrt{3}} & \frac{1}{\sqrt{3}} \\ \frac{1}{\sqrt{3}} & 0 \end{bmatrix}$

An orthonormal matrix has columns that are all normal to each other (orthogonal) and unit length (normal). $\begin{bmatrix} \frac{\sqrt(2)}{2} & \frac{\sqrt(2)}{2} \\ \frac{\sqrt(-2)}{2} - 2 & \frac{\sqrt(2)}{2} \end{bmatrix}$

The inverse of a matrix is a matrix such t $AA^{-1} = A^{-1}A = I$

A sparse matrix is one where most of the elements are zero.

13.2 Operations

In this chapter we will learn algorithms to implement matrix algorithms including

identity	Generate an identity matrix
Gauss-Jordan	solve a system $A\vec{x} = B$
GramSchmidt	Turn a matrix into an orthonormal one
partial pivoting	Find the largest row to do row-reduction for numerical stability
full pivoting	Use the largest element in the matrix to do row-reduction for greater numerical sta
inverse	Compute the inverse of A
dot product	$v_1 \cdot v_2 = v_{1x}v_{2x} + v_{1y}v_{2y} + v_{1z}v_{2z}$
LU Factorization	Solving same matrix against multiple constants faster
Least squares	Generalized least squares fit of any degree

13.3 Representations

A regular rectangular matrix can be stored as an array of pointers to rows, or as a single block of continuous memory. The single block is somewhat faster because in order to jump between rows, the indexed must go to the pointer for each row and find where it is, but the overhead is not serious for the actual operations because jumping between rows is also suboptimal for sequential block memory. Computers are optimized for sequential access. So when we access row 0, col 0, row 0, col1, etc memory can keep up with the CPU. When we access row 0 col 0, then row 1, col 0, we are skipping however many elements are in a row, and this can significantly slow down the algorithm. So much so that for doing matrix multiplication, it is worth computing the transpose of the matrix, then using the transpose as a copy where each column is sequential. This is used in real libraries such as the Intel matrix library for a factor of 2-3 in speed.

An upper triangular matrix has a first row with n elements, a second row with $n-1$, and so on. The rest are zero and therefore may be ignored although this will require an if statement in the index computation.

The total number of non-zero elements is $n(n+1)/2$ including the main diagonal. Given row r and column c, The code to access a given element is:

```
get(r, c)
  if c > r
```

```
    return 0
  return m[r * (r+1)/2 + c -r]  %todo: one of these is wrong!
end
```

Algorithm 13.1: get

A lower triangular matrix has a first row with 1 elements, a second row with 2, and so on. The rest are zero and therefore may be ignored although this will require an if statement in the index computation.

```
get(r, c)
  if $c < r$
    return 0
  return m[r * (r+1)/2 + c -r]
end
```

Algorithm 13.2: get

Upper and lower triangular matrices are not that useful from a complexity point of view because they are still n/2 elements and therefore all the interested algorithms are still $O(n^3)$ although it may be lower by a factor of 8.

Diagonal and Tridiagonal Matrices are fundamentally better, and they are used in many algorithms where the problem is constrained. A diagonal matrix has non-zero elements only on the main diagonal and therefore uses storage $O(n)$.

The algorithm to access the elements of a diagonal matrix is

```
get(r, c)
  if $c \neq r$
    return 0
  return m[r]
end
```

Algorithm 13.3: get

A tridiagonal matrix has elements on the main diagonal, and one up and down as well. It looks like this:

The logic for computing the index of a tridiagonal seems confusing since the first and last rows have 2 elements instead of 3. The easy way to think of it is to assume that all rows have 3 elements. In that case, assuming we ask for one of the elmeents that exists, the index is: $3r + c - r$ which can be simplified to $2r + c$. If we then subtract 1 we can eliminate the bogus first element. $2r + c - 1$. The algorithm to access the elements of a tridiagonal matrix is

```
get(r, c)
  if $abs(r - c) > 1$
    return 0
  return m[2*r + c]
```

```
end
```

Algorithm 13.4: get

The total number of non-zero elements is $n(n+1)/2$ including the main diagonal. Given row r and column c, The code to access a given element is:

```
get(r, c)
  return r * (r+1)/2 + c -r
end
```

Algorithm 13.5: get

13.4 Addition

Matrix addition is a simple $O(n^2)$ operation.

$C = A + B$

adds every corresponding element of A and B and stores the result in C. The row and column sizes of A, B, and C must be the same for this to make any sense.

$$\begin{bmatrix} 0 & 1 \\ 3 & 3 \end{bmatrix} = \begin{bmatrix} 1 & 3 \\ 2 & 4 \end{bmatrix} + \begin{bmatrix} -1 & -2 \\ 1 & -1 \end{bmatrix}$$

13.5 Multiplication

Multiplication for a matrix of size (m,n) by a matrix of size (n,p) is $O(mnp)$. When the matrices are square with all dimensions of size n, the complexity is $O(n^3)$. The complexity of n^3 obviously gets bad fast – a mere $n = 1000$ results in 10^9 operations. Also, when dealing with matrices, the non-ideal nature of computer memory becomes apparent. RAM is designed for sequential access. It is far faster given a request for memory location i to get location $i+1$. But part of the multiplication algorithm goes down the columns of B. In a practical library, this problem can be solved by transposing the rows and columns of B, and then performing a modified matrix multiply.

```
Mult(a, b)
  assert cols(a) = rows(b)

  for k = 0 to rows(a)-1
    for j = 0 to cols(b)-1
      ans(k,j) = 0
      for i = 0 to cols(a)-1
        ans(k, j) += a(i,j) * b(j,k)
      end
    end
  end
end
```

Algorithm 13.6: Multiplication

Faster Multiplication by storing temporary result in a scalar

```
Mult(a, b)
  assert cols(a) = rows(b)

  for k = 0 to rows(a)-1
    for j = 0 to cols(b)-1
      dot = 0
      for i = 0 to cols(a)-1
        dot += a(i,j) * b(j,k)
      end
      a(k,j) = dot
    end
  end
end
```

Algorithm 13.7: Multiplication

13.6 Gauss-Jordan Elimination

Solving a system of n equations in n unknowns can be represented as:

$A\vec{x} = B$

Row reduction is commonly taught in high school algebra, but the algorithm used will not work except in very small, very well-conditioned systems. The coefficients from a set of n equations is converted to a matrix. The element (1,1) is used to zero out the elements below it, which must also modify the entire row and the constant vector B as well.

$x + 2y - 3z = -5$
3x - y + z = 8
2x + 3y + 2z = 13

$$A = \begin{bmatrix} 1 & 2 & -3 \\ 3 & -1 & 1 \\ 2 & 3 & 2 \end{bmatrix}, B = \begin{bmatrix} -5 \\ 8 \\ 13 \end{bmatrix}$$

Row reduction uses the first row to wipe out the second. First we calculate the ratio needed to multiply the 1 to zero out the 3 below it.

$s = -3/1 = -3$

Then the entire augmented first row (including B) is multiplied by this scalar and added to the second row:

$$\begin{array}{c|c|c} 1 & 2 & -3 \\ 0 & -7 & 10 \\ 2 & 3 & 2 \end{array} \begin{array}{c} x \\ y \\ z \end{array} = \begin{array}{c} -5 \\ 23 \\ 13 \end{array}$$

The complexity of reducing a single row is $O(n)$ The complexity of reducing all rows from the first one is $n(n-1) = O(n^2)$. This example is only a 3 x 3 matrix, but in general for n x n, the next row requires $(n-1)(n-2) = O(n^2)$ also, and the sum of all the n^2 is $O(n^3$. In fact, all interesting fundamental matrix algorithms are $O(n^3)$ unless highly optimized.

```
GaussJordan(A, x, B)
  for k = 0 to rows(a)-1
    partialPivot(A, B, k); // this can be partial or full
       pivoting. See algorithms
    for j = k+1 to cols(b)-1
      s = -A(j,k) / A(k,k)
      ans(j,k) = 0            // zero out the elements below the
         pivot
      for i = j+1 to cols(a)-1
        ans(j, i) += s * A(k,i)  // do a row reduction with the
           ratio computed
      end
      B(j) += s * B(k)           // do the same thing to the
         augmented matrix including the solution
    end
  end
  backSubstitute(A, x, B)
end
```

Algorithm 13.8: Gauss-Jordan

```
partialPivot(A, B, k)
  pivotloc = k
  pivot = A(k,k)
  for i = k+1 to n-1
    if A(i,k) > pivot
      pivot = A(i,k)
      pivotloc = i
    end
  end
 if pivotLoc ≠ k
   for i = 0 to n-1
     swap(A(k,i), A(pivotLoc,i))
   end
 end
end
```

Algorithm 13.9: PartialPivot

Full pivoting not only switches rows, it selects the biggest element in a column. This means the algorithm effectively does variable substitution so for full pivoting we must store which column corresponds to which original variable

```
FullPivot(A, B, n)
[TBD]
end
```

Algorithm 13.10: FullPivot

```
backSubstitute(A, B, n)
  for k= n-1 downto 0
    B(k) /= A(k,k)
    A(k,k) = 1
    var = B(k)              // hold the current variable in a scalar
    for j = k-1 downto 0
      B(j) -= var * A(j,k) // subtract off the variable just solved for
    end
  end
end
```

Algorithm 13.11: BackSubstitute

13.7

13.8 Gram-Schmidt Orthogonalization

```
Gram-Schmidt(m)
  for i = 0 to n-1
    invmag ← mag(m[i][])
    for j = 0 to n-1              // normalize the matrix
      m(i,j) = m(i,j) * invmag
    end
    // next, subtract the previous basis vectors
    for k = 0 to i-1
      subtract(m, i, j)
    end

  end
end
```

Algorithm 13.12: Gram-Schmidt

13.9 Least Squares

A least squares linear fit is the best line through data. It has two parameters, the vertical position and the slope. However, using a matrix of n equations against m unknowns, if n is bigger than m it is possible to solve for any general fit. The following algorithms show the specific solution for a linear least squares fit, and the general matrix form for any polynomial.

```
LeastSquares(m)
```

Algorithm 13.13: LeastSquares

$A^T A x = A^T B$

14. Backtracking

15. Graph Theory

16. Data Compression

16.1 Information Theory

Data compression is built on a theory of information originated by Shannon in the 1950s.

Data compression is the act of writing data in a more compact form that uses fewer bits in such a way that the original data may be retrieved.

By definition, n bits have 2^n possible combinations. If all n-bit groups appear at random equally likely, there is no opportunity to compress. However, if some patters are non-uniform and show

Bit entropy is the predictability of bits. If bits are truly random, there is no way of compressing them. However, there are many seemingly random sequences of bits that in fact, have an underlyign structure. For example, analyzed statistically, the digits of pi are random, and the only way of encoding them is to store all the digits. However, there are programs that can not only compute the digits of pi, but can do so random access (ie, calculate the digits between 10000 and 10032). Given this ability, the most compact way of storing the digits of pi is to store a program capable of computing it.

Similarly, the Mandelbrot set is a complicated mathematical shape, and storing a high resolution image of a region can take Megabytes. Yet a small program can generate that image. The notion of using a program to construct the data, and computing the lower bound of size as the program is called Kolmogorov Complexity after the mathematician who defined it.

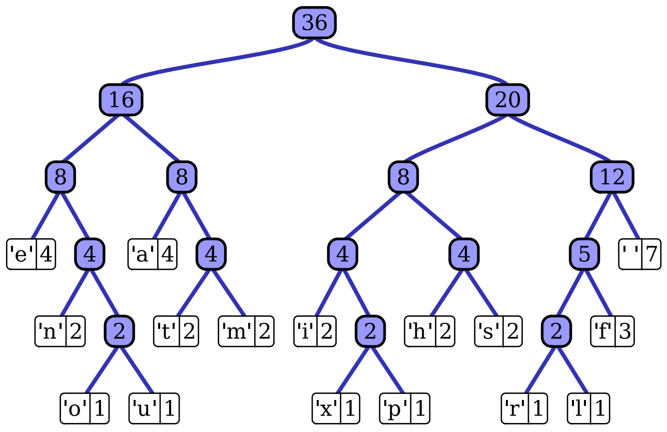
16.2 Run-Length Encoding (RLE)

Run-length encoding stores the number of each symbol along with the symbol. This can be very effective when there are many repeated values. For example, the string: aaaaaaabbbbbbbaaaaa could be encoded a7b7a5. The size of the lengths must be decided of course. The longer the allowable number of repeats, the more bits must be allocated to the counts (the log of the maximum number). For example, suppose the length is encoded as a single byte 1-256 since there is no point in encoding 0. Then for a sequence with 500 a, we would need: a256a244 for a total of 4 bytes.

16.3 Huffman Coding

Huffman coding allocates variablesized bit sequences to different symbols. The most common symbols get the shortest bit length. This reduces the average bit length for the input, unless the input is random. Unfortunately, assigning an integer number of bits does not perfectly match the distribution found, so Huffman is not optimal. For example, if 40 percent of the characters found are the letter 'e' then we can assign the bit 0 to e. Any other letter will require a 1 followed by a code to identify. By doing so, The letter e is as short as possible, but the remaining 60 percent of the input will be lengthened by 1 bit.

The following diagram shows the tree that the algorith must generate in order to encode as Huffman:



The algorithm for Huffman encoding is as follows:

Algorithm HuffmanEncode

```
HuffmanEncode(C)
  n = C.size
  Q = priorityQueue()
  for i = 1 to n
    n = node(C[i])
    Q.push(n)
  end
  while Q.size() is not equal to 1
    Z = new node()
    Z.left = x = Q.pop
    Z.right = y = Q.pop
    Z.frequency = x.frequency + y.frequency
    Q.push(Z)
  end
  return Q
end
```

Algorithm 16.1: HuffmanEncode

Algorithm HuffmanDecode

```
HuffmanDecode(root, S):      // root represents the root of Huffman Tree
 n ← S.length                // S refers to bit−stream to be decompressed
 for i ← 1 to n
 current ← root
   while current.left ≠ null and current.right ≠ null
     if S[i] = 0
       current ← current.left
     else
       current ← current.right
     end
     i ← i + 1
   end
   print current.symbol
 end
end
```

Algorithm 16.2: HuffmanDecode

16.4 Lempel-Ziv-Welch

Lempel–Ziv–Welch (LZW) is a universal lossless data compression algorithm created by Abraham Lempel, Jacob Ziv, and Terry Welch. It builds a dictionary of words as the source file is read. Any word that appears again can be encoded as the index of the word. In this way patterns, even very long ones that appear frequently can be reduced in size to the number of bits necessary to encode them in the dictionary. The more words there are, the more bits are needed to store them, and this can limit the savings. For example, in English the words ”and”, ”or”, ”but” appear very frequently, but given 1000 words in a dictionary, each with a code would be 10 bits, so the ratio of compression from two bytes (”or”) to 10 bits is not that large. On the other hand, in a repetitive text using formulaic language, like a math text, if the text ”without loss of generality” keeps occurring, it can be encoded as a single ”word” in the dictionary. Note that the match is exact, so if sometimes the phrase is at the start of a sentence ”Without loss of generality” then that would be an entirely different word in the dictionary, and there would therefore be two codes reserved for it. Also, note that the dictionary starts empty for each file. The first time a dictionary word is found the dictionary is augmented, so LZW works best when there are long sequences that repeat many times. For a sequence that only repeats twice, compression should be less than a factor of 2.

```
 s = ""; // initialize with empty string
 while (there is still data to be read)
   ch ← character input
   if (dictionary contains s+ch)
```

```
      s = s+ch;
    else
      encode s to output file;
       add s+ch to dictionary;
       s ← ch
    end
  end
  encode s to output file;
```

Algorithm 16.3: LZWEncode

```
prevcode = read in a code;
decode/output prevcode;
while (there is still data to read)
  currcode ← read in a code;
  entry ← dictionary[currcode]
  output entry;
  ch ← first char of entry;
  add ((translation of prevcode)+ch) to dictionary;
  prevcode ← currcode
end
```

Algorithm 16.4: LZWDecode

16.5 Burroughs-Wheeler

BurroughsWheeler is the underlying algorithm used by the Unix utility bzip2. It is a block compression algorithm that yield substantially higher compression than Huffman or LZW. It increases compression over LZW with three distinct phases.

- The algorithm attempts to transform the input into something more compressible by rotating bytes so that series of the same byte occur together, making them more amenable to compression.
- Movetofront encoding. Given sequences of the letters close to each other, they encode them as integer deltas and if the numbers are small, these are highly repetitive (many 0,1,2)
- Finally Huffman code the resulting data, and since short sequences are assigned to common values, the average length goes down substantially.

16.5.1 Burrows-Wheeler transform

The following excellent explanation is borrowed from an assignment in a Princeton CS class:

The goal of the Burrows-Wheeler transform is not to compress a message, but rather to transform it into a form that is more amenable to compression. The transform rearranges the characters in the input so that that there are lots of clusters with repeated characters, but in such a way that it is still possible to recover the original input. It relies on the following intuition: if you see the letters hen in English text, then most of the time the letter preceding it is t or w. If you could somehow group all such preceding letters together (mostly t's and some w's), then you would have an easy opportunity for data compression.

First treat the input string as a cyclic string and sort the N suffixes of length N. The following example shows how it works for the text message "abracadabra". The 11 original suffixes are abracadabra, bracadabraa, ..., aabracadabra, and appear in rows 0 through 10 of the table below. Sorting these 11 strings yields the sorted suffixes. Ignore the next array for now - it is only needed for decoding.

i	Original Suffixes	Sorted Suffixes	t	next
0	a b r a c a d a b r a	a a b r a c a d a b	r	2
1	b r a c a d a b r a a	a b r a a b r a c a	d	5
*2	r a c a d a b r a a b	a b r a c a d a b r	a	6
3	a c a d a b r a a b r	a c a d a b r a a b	r	7
4	c a d a b r a a b r a	a d a b r a a b r a	c	8
5	a d a b r a a b r a c	b r a a b r a c a d	a	9
6	d a b r a a b r a c a	b r a c a d a b r a	a	10
7	a b r a a b r a c a d	c a d a b r a a b r	a	4
8	b r a a b r a c a d a	d a b r a a b r a c	a	1
9	r a a b r a c a d a b	r a a b r a c a d a	b	0
10	a a b r a c a d a b r	r a c a d a b r a a	b	3

16.5.2 Move to front encoding

The concept behind move-to-front encoding is to maintain an ordered list of legal symbols, and repeatedly read in symbols from the input message, print out the position in which that symbol appears, and move that symbol to the front of the list. As a simple example, if the initial ordering over a 6 symbol alphabet is a b c d e f, and we want to encode the input caaabcccaccf, then we would update the movetofront lists as follows

movetofront	in	out
a b c d e f	c	2
c a b d e f	a	1
a c b d e f	a	0
a c b d e f	a	0
a c b d e f	b	2
b a c d e f	c	2
c b a d e f	c	0
c b a d e f	c	0
c b a d e f	a	2
a c b d e f	c	1
c a b d e f	f	5
f c a b d e		

After the first two passes, the result is Huffman encoded, and since there are many small numbers, the resulting average compression ratio is highly efficient.

16.5.3 Decompression of Burrows-Wheeler

16.6 Arithmetic Encoding

For encodings like Huffman or dictionaries like LZW, the problem is that there are not always an even power of 2 of symbols. For example, with 64 symbols in a dictionary we need 6 bits to represent all of them. With 65 symbols, every symbol grows to 7 bits even though most of the last half of the dictionary is empty. Arithmetic encoding uses multiplication and division which is slower but allows tighter packing of values that do not fit evenly into k bits. For example, suppose we have the following sequence of numbers:

4	0	3	1	4	3	3	0	2	2	3

Each number requires 3 bits, but since no value above 4 exists, really there are just 5 values not 7 (0 to 4). In order to encode in a 32 bit number, we can hold just 10 values if they are each 3 bits with 2 bits left over. Instead, we multiply by 5 each time and store using base 5:

$((((((((((4*5+0)*5+3)*5+1)*5+4)*5+3)*5+3)*5+0)*5+2)*5+2)*5+3 =$ 40386313

To unpack take the number mod 5 and remove the last number, then divide by 5 and repeat. Division of course is the slowest operation so this is less efficient than working with bits, but with the data shown we can fit 13 numbers using base 5, and still have a maximum of value of 1 billion. There is not enough to fit a 14th number but at more computational cost, that capacity could be used as well. There are effectively 2 bits remaining in the number.

16.7 Prediction by Partial Match (PPM)

16.8 ZPaq and the Hutter Prize

In the early 2000, Matthew Mahoney, a professor at Florida Institute of Technology, wrote a paper on data compression using a neural network. Essentially, the neural network determines the kind of data, and once it recognizes it, it selects the most appropriate engine from a set of standard ones, and begins to predict what each bit will be. With an accurate prediction of bits, the only encoding needed is when the prediction is wrong. Prediction methods are extremely powerful because in theory, as the predictors become more and more intelligent, the limiting factor is very fundamental – how much knowledge is really encoded in the data?

The current generation of predictors based on Dr Mahoney's concept are very, very slow. It takes 8 hours to compress 1Gbyte of data, but these engines can compress more than any other algorithm. The Hutter prize was founded to encourage research in this area and to explore the ultimate limits of how compactly information can be encoded. It consists of a one gigabyte section of Wikipedia. A bounty is paid any time a new program can successfully compress the data further. The size of the data includes the program. If it did not, we could write a "program" that included the entire gigabyte, write out 1 byte, and bring back the data from the code. The challenge of course is to not only encode it, but to do so with the simplest possible program and model. The Hutter prize is clearly related to Kolmogorov complexity. They are in effect writing a program, although most of it are neural network models, to squeeze out redundant bits and reconstitute information.

Huffman Coding	`https://en.wikipedia.org/wiki/Huffman_coding`
LZW Compression	`https://en.wikipedia.org/wiki/Lempel%E2%80%93Ziv%E2%80%93Welch`
Prediction by Partial Match	`https://en.wikipedia.org/wiki/Prediction_by_partial_matching`
Hutter Prize	`https://analyticsindiamag.com/hutter-prize-data-compression`
Matthew Mahoney Data Compression	`http://mattmahoney.net/dc/`

17. Numerical Algorithms

17.1 Properties of Floating Point

Floating point numbers are approximations to the reals. A floating point number has a sign bit, an exponent controlling the position of the "binary" point (not the decimal point.

17.1.1 IEEE754

The following table shows the IEEE754 standard for single, double and quad precision.

C++ type	bits	exponent	mantissa	digits	minval	maxval
float	32	8	24	7	$1.23e-38$	$1.23e+38$
double	64	11	53	15	$1.23e-308$	$1.23e+308$
???	128	15	113	34	$6.4751751e-4966$	$1.23e+4966$

17.1.2 Roundoff Error

Floating point is not exact. In decimal, fractions that are not divisible by 10 are not exactly representable, like $1/3 = 0.3333333$. Because the fractions in floating point are expressed in binary, fractions such as $1/10 = 0.1$ are not exactly representable. Example:

```
int main() {
  for (float x = 0.0f; x < 10; x += 0.1f)
    cout << x;
  }
  return 0;
}
```

17.1.3 Associativity breaks down

Because there is a finite accuracy , and numbers can be both very large ($1.234567e + 10$) and small, operations such as add do not result in the full accuracy from both numbers. Therefore the order of operations will change the answer. The associative property does not hold in floating point: $a + b + c \neq a + (b + c)$

Here is an example of a hypothetical 3-digit computer adding from large to small

	1.23
$+$	.899
$=$	2.12
$+$	.478
$=$	2.59

The same numbers in a different order

	.899
$+$	.478
$=$	1.377
$+$	1.23
$=$	2.60

The second result is more accurate because adding the small numbers keeps more information from the lower digits, and results in a higher sum. From this you can see that the result is off by one in the second digit just after a single operation.

17.1.4 resolution is not uniform

Floating point has a constant number of digits. Single precision. for example, has 7 digits accuracy. The distance between 1.0 and 1.0000001 is not the same as $1.0e + 10$ and $1.0000001e + 10$.

17.1.5 Subtractive Cancellation

When two numbers are known to a high accuracy and are nearly equal, subtracting them can, in a single step, cancel almost all the accuracy.

For example: $t1 = 74.00001, t2 = 74.00000$ $t1 - t0 = 1e - 5$

The answer has only a single digit accuracy.

17.2 Root Finding

For some equations there is an analytical equation for finding the root, but not for all. For some equations, writing a program to find the root to a desired precision is the only approach that works. There are three methods discussed here. First, bisection which is simple and guaranteed given an initial condition, but also slow. Then there is NewtonRaphson that is fast and dangerous, and finally the method recommended in numerical recipes which uses an exponential approximation and is quite robust and fast.

For an example, take an easy function such as:

$f(x) = x^2 - 3$

The function is by inspection, obviously zero at $x = \pm\sqrt{3}$

17.2.1 Bisection

If a function is continuous, and on an interval $[a, b], f(a) < 0 and f(b) > 0$ then somewhere in that interval the function must cross zero. This is the principle of bisection, which works by divide and conquer, to keep dividing the interval in half each time. Given the initial brackets are in the neighborhood of the root, every iteration gives one more bit accuracy, so for double precision, 53 iterations should yield maximum accuracy.

17.2.2 NewtonRaphson

Newton's method requires that you have the analytical derivative. If you do, this method certainly converges quickly. It is confusingly called quadratic, meaning that each iteration doubles the number of digits accuracy.

Newton requires an initial guess. If this guess is outside the zone of convergence, then the solution will diverge instead of converging. But within the zone, the number of correct bits in the answer will double each time.

Starting with an initial guess x_0 compute each guess as $x_{n+1} = x_n - \frac{f(x_n)|}{f'(x_n)}$

Example:

$$\text{f(x) = x}^2 - 2$$
$$f'(x) = 2x$$
$$x_0 = 3$$
$$x_1 = x_0 - \frac{3^2-2}{2*3} = \frac{7}{6} = 3 - 1.16666 = 1.833333$$
$$x_2 = x_1 - \frac{x_1^2-2}{2*x_1} = 1.440476$$
$$x_3 = x_2 - \frac{x_2^2-2}{2*x_2} = 1.1414529$$

The third approximation is already accurate to 4 significant digits.

17.3 Ridder's Method

Ridder's method fits an exponential curve to the function to approximate where the root will be. It is quadratic (doubles the number of digits) under many but not all circumstances. It should be a lot more reliable than Newton's method, which can go crazy if the derivative goes to zero (a one-way ride to infinity) or if outside the radius of convergence, Newton's method will work in reverse, getting further from the root each time.

17.4 Numerical Integration

Numerical integration is a rich field, needed because some integrals are not analytically solvable. We cover trapezoidal for understanding the concepts in a simple method. Gaussian integration is better than trapezoidal for many reasons. We can see that higher order can be better, but is not always better. Then it turns out that using a clever cancellation scheme called Romberg is even more efficient than the Gaussian schemes.

Last, because integration over a range could have a problem because some areas have higher error than others, adaptive quadrature can help focus on the areas that need finer approximation.

17.4.1 Trapezoidal Method

Given a function on an interval, and choosing two points to represent the height of the function, what would be the best way to sample it? Since we don't know the function, you would have to expect the answer to be symmetric. We wish to pick two points which in this case will be the two endpoints of the region. Then we pick two weights w_0 and w_1 and solve for them so they match a known function. We pick polynomials as the function, because polynomials can approximate many functions well (though not all).

All approximations will be on $x = [0,1]$ which can be transformed to any region $[a,b]$ without loss of generality.

We start by approximating the zeroth order polynomial $f(x) = 1$. Given that the two points to sample the function are $x_0 = 0$ and $x_1 = 1$, and the fact that we need the overall weight to be 1 (if not, the function will be multiplied by a constant factor. For the function we know the area $A = 1$. With these facts, we can solve for the weights:

$h = 1$

$w_0 = w_1$

$A = 1 = h(w_0 f(0) + w_1 f(1)) \implies w_0 + w_1 = 1$

Solving, we get $w_0 = w_1 = 0.5$

In order not to require intuition stating that the two weights are equal, we could also go to the next polynomial of degree 1

$f(x) = x$

The area on $[0,1] = 0.5$

$0.5 = w_0 f(0) + w_1 f(1) = w_1$

Therefore $w_1 = 0.5$ and since the two sum to 1, w_0 is also 0.5.

Having used both polynomials, we now have a polynomial fit that works for zeroth and first order. Any polynomial of these degrees will be an exact fit. Any higher degree, or a function that does not look like a polynomial will have error.

For example, the polynomial $f(x) = 3x + 2$ when integrated on $[0,1]$ is $3/2x^2 + 2x = 3.5$

Trapezoidal would yield $h(0.5 * f(0) + 0.5 * f(1)) = 0.5(0 + 3.5) = 1.75$

For a higher order polynomial or arbitrary function, the trapezoidal method is an approximation. The error will grow depending on how closely the function approximates the polynomials trapezoidal maps. SInce it maps constant and linear terms, the first error term is $O(h^2)$. In order to get an accurate answer we will keep reducing the width of the sections (h). Every time h is divided by 2, the error term will decrease by $h^2 = 4$.

Example

$f(x) = 4x^2$

First, we know the answer, useful in checking the method. Integrating: $4/3x^3$ and evaluating on $[0,1]$ we get $A = 4/3$.

Starting with trapezoidal:

$I_0 = 0.5 * (0.5 * 0 + 0.5 * 4) = 1$

We know the real answer, so the error is $1/3$. Next, divide the region into two slices $[0,0.5]$ and $[0.5,1]$.

The following diagram shows the two points on the ends are used once each, so their weight of 0.5 is global. But all the internal points are used twice, one for the left

The most efficient way to increase the number of slices in trapezoidal is to exactly double them. Then, the midpoint of each slice then becomes an edge. Given the weights are 0.5 on the edge and 1 on the interior, if the first sum with 2 slices is called S_1 then the second $S_2 = S_1 + P_2$. The new points are added with weight 1.

The value of the first integral approximation

$I_1 = S_1 * h_1$

The value of the second approximation

$I_2 = S_2 * h_2$.

In general, the value of the integral is not known which is why it is being computed. Therefore the way to use any integration method is to compute successive values I_1, I_2, I_4, ... and stop when:

$abs(I_n - I_{n-1}) < eps$

```
double trap(Func f, double a, double b, double eps) {
  double S1 = 0.5*(f(a) + f(b));
  double S2 = S1 + f((a+b)*0.5);
  double h = (b-a) * 0.5;
  while (abs(S2-S1) > eps) {
    S1 = S2;
    double h2 = h * 0.5;
    double internalSum = 0; // sum all internal points
    for (double x = a+h2; x < b; x += h)
      internalSum += f(x);
    S2 = S1 + internalSum;
  }
  return S2 * h;
}
```

17.4.2 Midpoint Method

Trapezoidal is simple, has $O(h^2)$ error and if doubled each time, can robustly approach the answer. But it has certain disadvantages. Trapezoidal requires values on the endpoints, and sometimes the endpoints can be poles and therefore cannot be evaluated.

Midpoint as it turns out is exactly the same as trapezoidal $O(h^2)$ error but has only a single point to evaluate, dead center of the interval.

17.4.3 Gaussian Quadrature

Gaussian Quadrature is an interesting generalization of midpoint and trapezoidal method. It asks the question, where should the points be on a region to optimal sample the function? For example, with the two points of the trapezoidal method we can solve up to a 2nd order polynomial, that is the constant and linear term, but not the quadratic term because there are two weights, two unknowns which uniquely determine a linear function. However, with the same two points if we allow the x position to vary, there are 4 unknowns, and the first error term is $O(h^4)$.

It turns out that the optimal points for sampling the value of the function is at the roots of the Legendre polynomials. A graph of these polynomials is shown here.

numeric/LegendrePolynomials.pdf

The Wikipedia article in the references has a table of values and weights for different order solutions. Here we will reproduce just order 2 and 3.

order	points	weights
1	0	1
2	$\pm\sqrt{\frac{1}{3}}$	1
3	0	$\frac{8}{9}$
	$\pm\sqrt{\frac{1}{3}}$	1

Wikipedia: Gauss Quadrature

17.4.4 Romberg

Romberg is a devilishly clever optimization of either trapezoidal or midpoint. The EulerMaclauren theorem states that the error terms for these second order methods will only be even powers of two. Thus the approximation:

$I_n = I + O(h^2) + O(h^4) + O(h^6) + ...$

has a leading h^2 term, and the next one is not h^3.

We can take advantage of this relationship in the following way: First compute 3 successive Integration answers, for example I_1, I_2, I_4. Since each successive approximation has h which is half the previous one, and since the leading error term is $O(h^2)$, for each answer, the error term is related to h but divided by 4.

Therefore, we can compute: $R1 = \frac{4I_2 - I_1}{3}$. Since the error term for I_2 is $1/4$ the term for I_1 is exactly 4 times bigger than $I4$, and the leading error term cancels, leaving only $O(h^4)$. If two Romberg sums are computed, the same thing can be done with these to cancel out the h^4 term:

$R_1 = \frac{4I_2 - I_1}{3}$ $R_2 = \frac{4I_3 - I_2}{3}$

$Q_1 = \frac{16R_2 - R_1}{15}$

The resulting answer thus has a leading error term of $O(h^6)$ with almost no additional computational effort. This amazing trick can be done twice, perhaps with one more layer, but that is the limit because small amounts of roundoff error mean that the errors are not actually identical in practice.

Nonetheless, because Romberg takes almost no computation, it presumably dominates over Gauss Quadrature in terms of computational efficiency.

17.4.5 Adaptive Quadrature

In an integral in which there is a pole, or sections where the values are large as well as sections where they are small, it may take a large number of slices to get the answer to the desired accuracy.

In such cases, what is needed is a recursive scheme to break up the integral into smaller pieces and solve each piece to the desired accuracy (ie a divide and conquer strategy).

17.5 Solving Ordinary Differential Equations

17.6 Introduction

A differential equation starts at a location and using local (derivative) rules, computes the next position. The algorithm takes a small step forward, computes the new derivative and determines the next step. There is an error due to the finite step size. The smaller the step size, like integration, the smaller the error. But since roundoff error will kick in after enough small steps, The simplest algorithm is Euler (1st order approximation), effectively just an integration. Given a function $f'(x,t)$, presumably a function of x and time:

$y = x_0 + f'(x,t)dt$

17.6.1 Runge-Kutta Methods

Runge-Kutta methods work by choosing intermediate values of dt, computing some trial points, and then using the information, jumping forward by a larger dt. Think of this as testing to see what the function is doing. The most famous is RK45, which cleverly computes two separate Runge-Kutta steps using some of the same values for efficiency. Given two separate estimates, a 4th order and a 5th order, by comparing the answers we can get an estimate of the error efficiently.

```
RKF45(r, c)
  $k_1 = hf(t_k, y_k)$
  $k_2 = hf(t_k + \frac{1}{4}h, y_k + \frac{1}{4}k_1)$
  $k_3 = hf(t_k + \frac{3}{8}h, y_k + \frac{3}{32}k_1 + \frac{9}{32}k_2)$
  $k_4 = hf(t_k + \frac{12}{13}h, y_k + \frac{1932}{2197}k_1 + \frac{7200}{2197}k_2 + \frac{7296}{2197}k_3)$
  $k_5 = hf(t_k + h, y_k + \frac{439}{216}k_1 - 8k_2 + \frac{3680}{513}k_3 - \frac{845}{4104}k_4)$
  $k_6 = hf(t_k + \frac{1}{2}h, y_k - \frac{8}{27}k_1 + 2k_2 - \frac{3533}{2565}k_3 + \frac{1859}{4104}k_4 - \frac{11}{40}k_5)$

  $y_{k+1} = y_k + \frac{25}{216}k_1 + \frac{1408}{2565}k_3 + \frac{2197}{4101}k_4 - \frac{1}{5}k_5$
//or, use a 5th order step
  $y_{k+1} = y_k + \frac{16}{135}k_1 + \frac{6656}{12825}k_3 + \frac{28561}{56430}k_4 - \frac{9}{50}k_5 + \frac{2}{55}k_6$
```

```
end
```

Algorithm 17.1: Runge-Kutta-Fehlberg or RKF45

The optimal step size sh can be determined by multiplying the scalar s times the current step size h

$s = (\frac{tolh}{2z_{k+1} - y_{k+1}})^{1/4}$

17.6.2 Predictor-Corrector Methods

Runge Kutta methods are more efficient than low order methods because they permit a larger ΔT for the same accuracy. However, they do require many invocations of the function, and if the function is slow (for example, a gravity simulation in which the accelerations of every body on every body must be computed for each timestep) then the method still has very high computational cost.

One way to reduce the cost is with a predictor-corrector method. The predictor is an equation which uses the last n points of the differential equation to compute an estimate for the next value, and having computed the estimate, the corrector back-computes and attempts to fix any error. The difficulty with predictor-corrector schemes is that they require storage, and if an error is discovered, it may be necessary to backup multiple steps and recompute. Thus very often, predictor-corrector methods must use something like RK45 to get them started and to recover if the error climbs too high.

The Adams-Bashforth Predictor corrector is

Predictor: $y_{n+1} = y_n + \frac{h}{24}(55y'_n - 59y'_{n-1} + 37y'_{n-2} - 9y'_{n-3}$

Corrector: $y_{n+1} = y_n + \frac{h}{24}(9y'_{n+1} + 19y'_n - 5y'_{n-1} - y'_{n-2}$

17.7 Fast Fourier Transform (FFT)

A Fourier transform is an analytical transformation to turn a function amplitude as a function of time and decompose it into frequency. The Discrete Fourier Transform (DFT) takes a set of complex numbers $x_0, x_1, ..., x_{N-1}$

$X_k = \Sigma_1^{N-1} x_n e^{-i2/N}, k = 0, 1, 2, ... N - 1$

A DFT with $n = 4096$ points is $O(n^2)$ including N^2 complex multiplications and $N(N-1)$ additions. An efficient implementation would be about 30 million operations. By comparison, a Cooley-Tukey transform which is $O(nlogn)$ takes approximately $30,000$. Fast Fourier transforms can be done on any size n, but is most efficient for powers of 2.

The accuracy of numerical Fourier transform is limited by the resolution of the data coming in. For example with n points, the maximum resolution is $1/n$.

```
[$x_0$, ..., $N-1$] ← FFT(x, N, s)
  if N = 1 then
    $X_0 \leftarrow x_0$
  else
    $[X_0,...,X_{N/2-1}] \leftarrow FFT(x,N/2,2s)$
    $[X_{N/2},...,N-1] \leftarrow FFT(x+s,N/2,2s)$
    for k = 0 to $N/2-1$ do
      t ← $X_k$
      $X_k \leftarrow t + e^{-2\pi ik/N}X_k + N/2$
      $X_k + N/2 \leftarrow t - e^{-2\pi ik/N}X_k + N/2$
    end
  end
```

Algorithm 17.2: FFT

The following is a slightly modified version of the FFT found in Numerical Recipes. It is fairly efficient, and can be used both as the forward FFT, and the inverse operation. It uses an array of double, and each pair is a complex, so the variable n is the number of complex numbers, and nn is the number of individual values.

In order to compute $cos(2\pi m/n)$ and $sin(2\pi m/n)$ recursively as m doubles, they use a recursion relation for speed. First, $wr = 1$ and $wi = 0$ which are the first cos and sin values. Then, at the end of each loop a recursion relationship computes the values of the next cos and sin using a double angle formula for speed (although with a modern computer it is less certain how fast this is).

```
/*
   *******************************************************************************

Replace data[1..2*nn] by its discrete Fourier transform, if isign
   =1
or replaces data[1..2*nn] by
nn times its inverse discrete Fourier transform, if isign=-1

data is a complex array of length nn or, equivalently,
a real array of length 2*nn.
nn MUST be an integer power of 2 (this is not checked).
*******************************************************************************
   */
void Fourier(double data[], uint32_t nn, int isign) {
  uint32_t m;
  uint32_t n = nn << 1;
  uint32_t j=1;

  // Reverse the bits of the positions
  for (uint32_t i = 1; i < n; i += 2) {
     if (j > i) {
      swap(data[j], data[i]); /* Exchange the two complex numbers
          . */
      swap(data[j+1],data[i+1]);
    }
    m = nn;
    while (m >= 2 && j > m) {
      j -= m;
      m >>= 1;
    }
    j += m;
  }

  uint32_t mmax = 2;
  uint32_t istep;
  while (n > mmax) { /* Outer loop executed log2 nn times. */
    istep=mmax << 1;
    double theta=isign*(6.28318530717959/mmax); // Initialize the
        trigonometric recurrence
    double wtemp = sin(0.5*theta);
    double wpr = -2.0*wtemp*wtemp;
    double wpi = sin(theta);
    double wr = 1.0; //cos(2pi*m/n)
    double wi = 0.0; //-sin(2pi*m/n)
    for (m = 1; m < mmax; m += 2) {
      for (int i = m; i <= n; i += istep) {
        j = i + mmax; // Danielson-Lanczos formula.
        double tempr = wr*data[j] - wi*data[j+1];
        double tempi = wr*data[j+1] + wi*data[j];
        data[j] = data[i] - tempr;
        data[j+1] = data[i+1] - tempi;
        data[i] += tempr;
        data[i+1] += tempi;
      }
      wr=(wtemp=wr)*wpr-wi*wpi+wr; // Trigonometric recurrence.
      wi=wi*wpr+wtemp*wpi+wi;
    }
    mmax=istep;
  }
}
```

To see what the code does, I printed out the code of the inner loop with the values of i and j for $n = 8$. Here is the result. The swaps seem wrong to me, but the code is straight out of their book, so the error is probably mine, this algorithm is still new to me. Note all the inefficiencies because of reading from memory, multiplying by 1 and zero (or worse, nearly zero giving roundoff errors). One big improvement is to write a function that does all the manipulation up to $n = 8$ and continue FFT from that point. By hand-coding the bottom 8 passes, the special cases with 1 and 0 can remove many multiplications, and with a vectorized implementation using AVX2 instructions for example, all the calculations can be done in registers, probably a staggering improvement in performance.

One very nice group project would be to try to take advantage of AVX2 and use the 32 registers to do this and more, to try to keep the calculation in registers up to n= 16 or 32, whatever can be managed, while calculating the fourier in single precision floating point doing multiple operations at one time using the vectorized instructions.

```
swap 9, 3
swap 10, 4
swap 13, 7
swap 14, 8
double tempr = 1*data[3] - 0*data[4];
double tempi = 1*data[4] + 0*data[3];
data[3] = data[1] - tempr;
data[4] = data[2] - tempi;
data[1] += tempr;
data[2] += tempi;
double tempr = 1*data[7] - 0*data[8];
double tempi = 1*data[8] + 0*data[7];
data[7] = data[5] - tempr;
data[8] = data[6] - tempi;
data[5] += tempr;
data[6] += tempi;
double tempr = 1*data[11] - 0*data[12];
double tempi = 1*data[12] + 0*data[11];
data[11] = data[9] - tempr;
data[12] = data[10] - tempi;
data[9] += tempr;
data[10] += tempi;
double tempr = 1*data[15] - 0*data[16];
double tempi = 1*data[16] + 0*data[15];
data[15] = data[13] - tempr;
data[16] = data[14] - tempi;
data[13] += tempr;
data[14] += tempi;
double tempr = 1*data[5] - 0*data[6];
double tempi = 1*data[6] + 0*data[5];
data[5] = data[1] - tempr;
data[6] = data[2] - tempi;
data[1] += tempr;
data[2] += tempi;
double tempr = 1*data[13] - 0*data[14];
double tempi = 1*data[14] + 0*data[13];
data[13] = data[9] - tempr;
```

```
data[14] = data[10] - tempi;
data[9] += tempr;
data[10] += tempi;
double tempr = -6.66134e-16*data[7] - 1*data[8]; // roundoff!
   this should be 0*data[7]!
double tempi = -6.66134e-16*data[8] + 1*data[7]; // roundoff!
   this should be 0*data[8]!
data[7] = data[3] - tempr;
data[8] = data[4] - tempi;
data[3] += tempr;
data[4] += tempi;
double tempr = -6.66134e-16*data[15] - 1*data[16]; //roundoff
double tempi = -6.66134e-16*data[16] + 1*data[15]; //roundoff
data[15] = data[11] - tempr;
data[16] = data[12] - tempi;
data[11] += tempr;
data[12] += tempi;
double tempr = 1*data[9] - 0*data[10];
double tempi = 1*data[10] + 0*data[9];
data[9] = data[1] - tempr;
data[10] = data[2] - tempi;
data[1] += tempr;
data[2] += tempi;
double tempr = 0.707107*data[11] - 0.707107*data[12]; // could be
    wr*(data[11]-data[12])
double tempi = 0.707107*data[12] + 0.707107*data[11];
data[11] = data[3] - tempr;
data[12] = data[4] - tempi;
data[3] += tempr;
data[4] += tempi;
double tempr = -7.77156e-16*data[13] - 1*data[14]; // more
   roundoff
double tempi = -7.77156e-16*data[14] + 1*data[13]; // more
   roundoff
data[13] = data[5] - tempr;
data[14] = data[6] - tempi;
data[5] += tempr;
data[6] += tempi;
double tempr = -0.707107*data[15] - 0.707107*data[16];
double tempi = -0.707107*data[16] + 0.707107*data[15];
data[15] = data[7] - tempr;
data[16] = data[8] - tempi;
data[7] += tempr;
data[8] += tempi;
```

In all, it should be possible to make the implementation at least 30% more efficient by implementing non-recursively and computing special cases below n=8. It might even be higher than that given that modern computers are typically limited by memory latency. Those first passes can be implemented as 16 sequential reads followed by everything in register, followed by 8 sequential writes. Not only is this faster for memory access, but since there is so much less memory accessed, 4 cores could easily be used, each one taking a group of 16 numbers, working in parallel. For parallel access, since memory is the limiting factor, designing the algorithm to minimize memory accesses is critical to performance.

17.8 References

Numerical Recipes

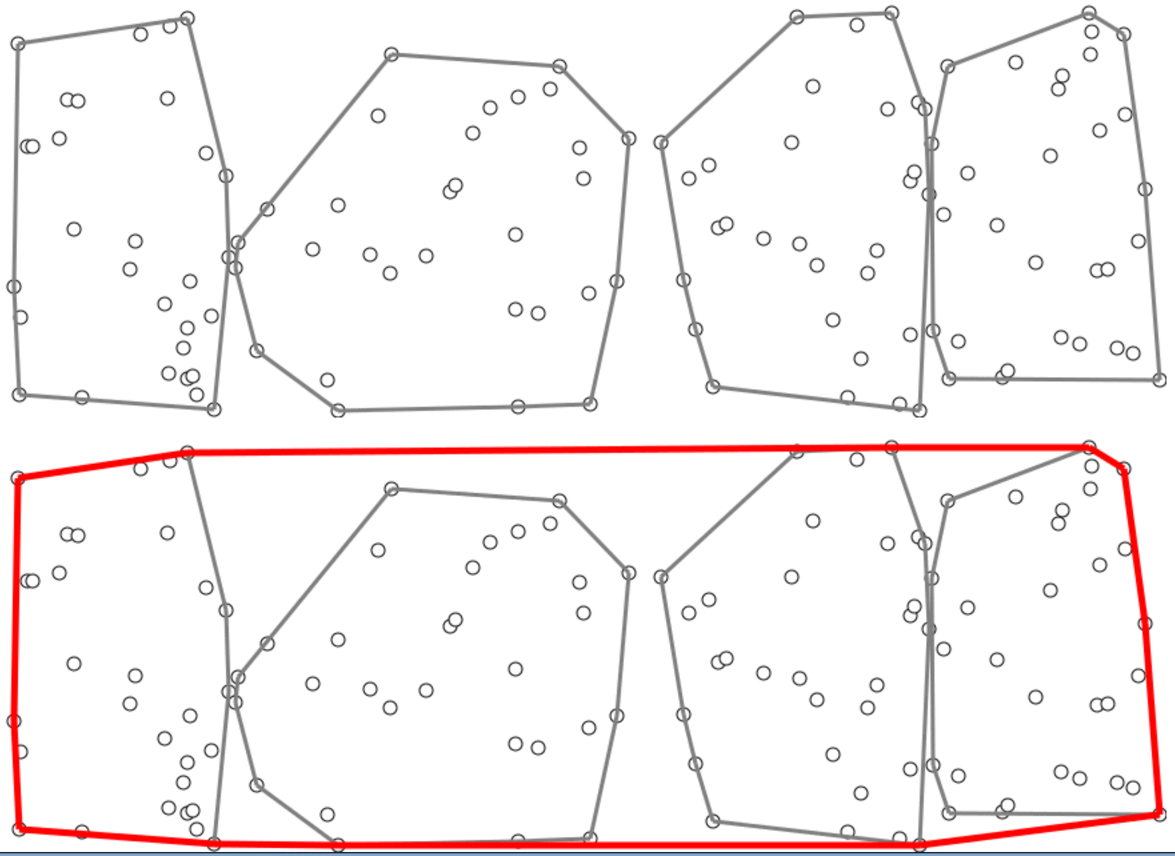
18. Graphical Algorithms

18.1 Convex Hull

The convex hull problem is simply stated. Given a set of points find the smallest convex polygon and encloses them all. In three dimensions, the analogous problem would be to find a polyhedron.

There are many algorithms as usual, but the best currently is due to Chan which is $O(nlogh)$ where n is the number of points, and h is the size of the output polygon, which is usually much smaller than n.

The following diagram shows how the Chan algorithm splits the points into groups, solves the hull of each groups, then combines them into a single hull.



Chan algorithm goes here 1

Algorithm 18.1: Chan Algorithm

18.2 Delaunay Triangulation

18.3 Grid Assignment

18.4 Box Packing

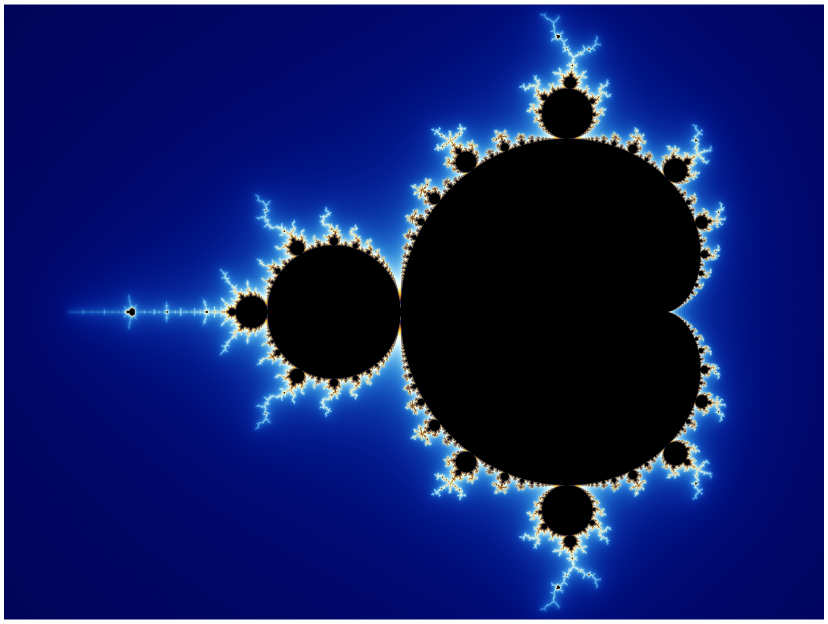
18.5 Mandelbrot Set

This algorithm does not quite fit into this chapter, but it is graphical, and doesn't fit anywhere else. The Mandelbrot set was invented or discovered by Bernard Mandelbrot. For any point C in the complex plane, repeatedly compute:

$Z = C$

$Z = Z^2 + C$

The magnitude of some points will increase fast, others will stay small forever. After any point has a magnitude of 2, it will quickly go to infinity. By counting how many times it takes to get to a magnitude of 2.0, and then colorizing a picture according to the counts, we can create the extraordinary images of the Mandelbrot set. One of the properties of the set is that it is self-similar at all levels. If you blow up a region you can see that it contains features looking exactly like the main one. In this picture, black is set to those points that never escape to infinity.


This image courtesy of Dr. Wolfgang Beyer from Wikimedia.

The Mandelbrot set can be computed brute force by a triple-nested loop. The complexity is the resolution in the x and y, (m, n) and the number of iterations k computed in order to calculate the colors. At first k can be just 64, but as the algorithm zooms into an area, it may grow to millions and be the dominating cost.

```
  for i = 1 to m
    for j = 1 to n
      z = $c_{ij}$
      count = 0
      while $abs(z) < c_{ij}$
        count ← count + 1
      end
      pixel(i,j) = colorlookup[count]
    end
  end
end
```

Algorithm 18.2: Mandelbrot

Mandelbrot is an ideal algorithm for parallelization. After all, every pixel involves a separate computation that is completely independent, and memory only needs to be written once for each pixel. It should be possible to compute in parallel on a modern multi-core CPU, but also to use vectorized instructions like AVX2. With vectorization though, there is a problem that if one pixel ends earlier than others, they must all go in lockstep until the last one is done. Still, it may be possible to achieve a great deal of speedup with vectorization. GPU programming is also potentially huge, as the GPU has thousands of execution units and is ideal for computation of this type.

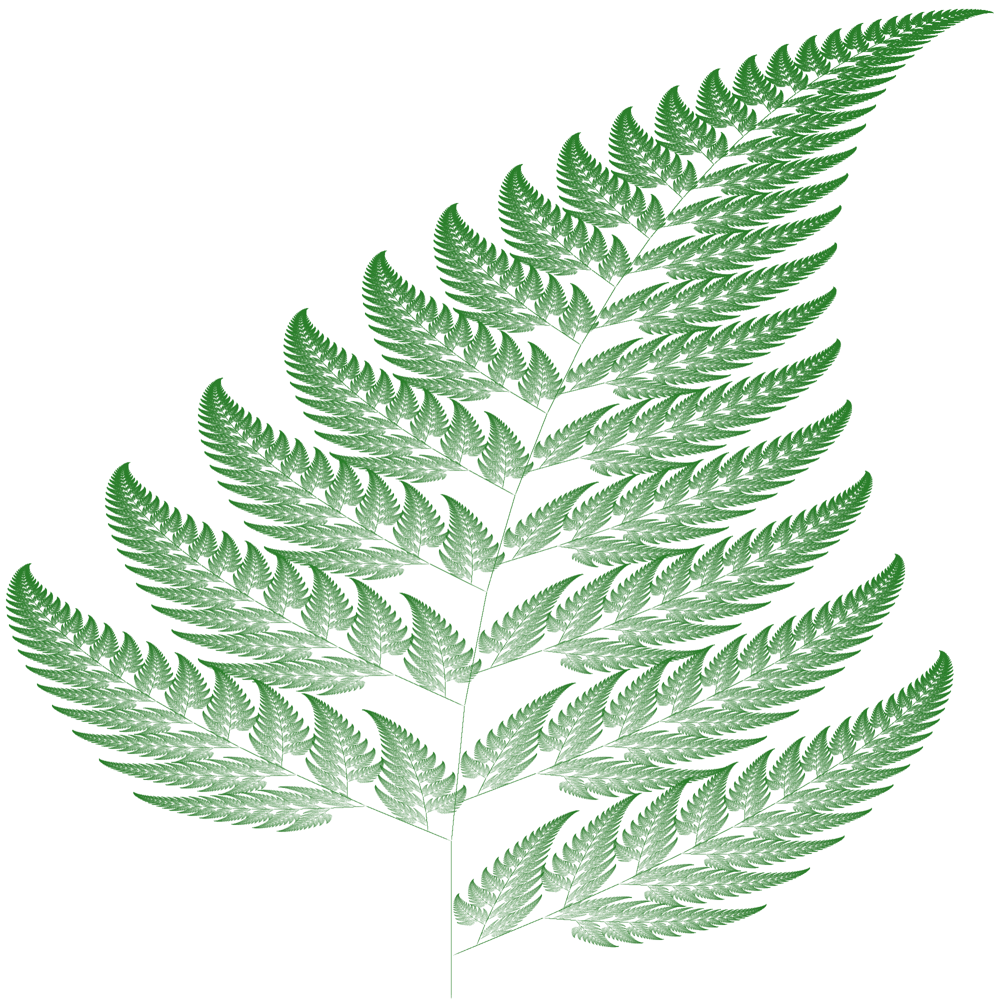
Potentially a huge win are algorithmic improvements. For example, at any resolution, if a rectangle can be computed, and every element on the edge of the rectangle is black (maximum iterations) then it should be provable that every interior element must be black as well, and there is no reason to compute the interior. Figuring out an optimal strategy to calculate edges to eliminate the maximum amount of interior is an interesting problem for an arbitrary region of the Mandelbrot set.

https://en.wikipedia.org/wiki/Mandelbrot_set

18.6 Barnsley Ferns

Another fascinating graphical algorithm that doesn't fit anywhere else in this course is Barnsley ferns. Using only a simple iterative system with a small matrix, it is possible to generate a set of points that look like ferns, and with slight tweaks, many different kinds of plants. One might think based on the pictures that these plants are recursively constructed by big leaves which branch to smaller leaves. But the amazing thing is that the iterative system doesn't work that way. If you watch the pixels added, they jump around in seemingly random order, yet as more dots are added, the plant emerges. The question of course is whether any plant has DNA programming somehow encodes a mechanism like this (which seems utterly impossible), or whether a plant has equally simple instructions that branch off at random intervals, getting smaller for each branch.

The following image shows a Barnsley fern.



The algorithm is to start at coordinate (0,0) and repeatedly apply an affine transformation which can translate rotate and scale the fern. Each affine transformation is a 2x2 matrix:

$$f_1(x,y) = \begin{bmatrix} 0.0 & 0.0 \\ 0.0 & 0.16 \end{bmatrix}$$
$$f_2(x,y) = \begin{bmatrix} 0.85 & 0.04 \\ -0.04 & 0.85 \end{bmatrix}$$
$$f_3(x,y) = \begin{bmatrix} 0.2 & -0.26 \\ 0.23 & 0.22 \end{bmatrix}$$
$$f_4(x,y) = \begin{bmatrix} 0.15 & 0.28 \\ 0.26 & 0.24 \end{bmatrix}$$

The odd thing is that each of these transforms is computed with a probability, and the result draws the fern. The dots are not drawn sequentially from biggest leaf to smallest. They fill in at random, since the transformations are being chosen randomly, yet the result will look like a fern every time. And by picking different numbers for the matrices and different probabilities, different plants can be generated.

Drawing a fern like this takes tens of thousands of points. It is not fast, but it allows realistic drawing of plants which can be used in movies, for example.

The following example draws a Barnsley fern in processing:

```
/*
  Barnsley Fern
*/

// creating canvas
void setup() {
  size(800, 800);
  background(255);
  stroke(35, 140, 35);
  strokeWeight(1);
}

void draw() {
  float x = 0, y = 0;
  float temp;
  for (int j = 0; j < 100; j++) // because draw is slow, do 100
     of these each time
    for (int i = 0; i < 100; i++) { // iterate each point 100
       times
      float px = map(x, -2.1820, 2.6558, 0, width); // pick
         initial point
      float py = map(y, 0, 9.9983, height, 0);
      point(px, py);
      float r = random(1);// pick a random transform

      //now compute the next x,y value using transform
      if (r < 0.01) {
        x = 0;
        y = 0.16 * y;
      } else if (r < 0.86) {
        temp =  0.85 * x + 0.04 * y;
        y = -0.04 * x + 0.85 * y + 1.6;
        x = temp;
      } else if (r < 0.93) {
        temp =  0.20 * x - 0.26 * y;
        y =  0.23 * x + 0.22 * y + 1.6;
        x = temp;
      } else {
        temp = -0.15 * x + 0.28 * y;
        y =  0.26 * x + 0.24 * y + 0.44;
        x = temp;
      }
    }
}}
```

For more details, see: https://en.wikipedia.org/wiki/Barnsley_fern