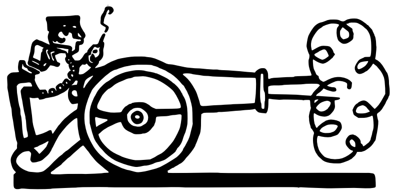
A. Some Challenging Projects

The following pages contain some projects that will challenge you to write programs using the skills you've learned in this book. Give them a try!

Project 1: Cannonball Run

Introduction: The Visitor

Imagine that you're an artilleryman in Napoleon's army. Your job is to fire a cannon, and to drop cannonballs as close as possible to a given target. You take your job seriously, and spend a lot of time thinking about the factors that limit your cannon's accuracy.



Ignoring effects of the wind and rain (which you can't control), you know that if the cannon always fired cannonballs at the same speed and angle, they'd always hit the same spot. But in reality, the speed and angle aren't always the same. Damp gunpowder or badly-formed, ill-fitting cannonballs change the speed, and the cannon doesn't stay in exactly the same position from one shot to the next, tilting a little up or down, or side to side.

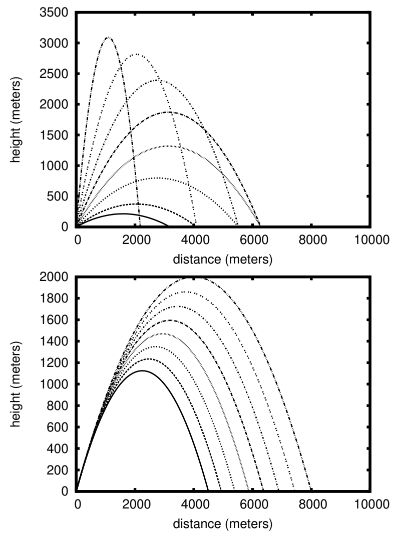


Figure A.1: The figures above illustrate how a cannonball's final position depends on the upward angle at which it's fired (top) and its initial velocity (bottom).

If you could fix even one of these problems you'd deserve a medal! But, sadly, it would take years of experimentation and tons of gunpowder to develop a new cannon design. If only there were some way to accurately simulate a real cannon with something smaller, like the toy cannons that tin soldiers use.

As you're standing beside your cannon, musing about this, a mighty concussion knocks you off your feet! An attack! But no. Rolling onto your stomach and peering through the settling dust you see, not a cannonball's crater, but an oddly-dressed man. He's lying on the ground, waving his hands in the air. "I've done it!", he shouts, "I've done it! I'm the first man to travel back in time!"

Over the course of the next hour you find out that this man has come from the 21st Century, and that the technology of his time is almost magical. The time-traveller has brought with him an object the size of a book which, when unfolded, can display moving images and even play music! The traveller calls it a "computer". This device is the solution to your problem! It can instantly simulate thousands of cannon shots!

Program 1: Simulating the Cannon

This project will require you to write three programs. The first of them will be named "`simulate.cpp`", and it will simulate a cannon. The program will allow the user to specify a speed and vertical angle for the cannonballs, but will add some random "jitter" to these values to simulate the cannon's imperfections. It will also add some random jitter to the side-to-side direction in which the cannon is pointing. The program's output will be a file containing the x, y coordinates at which each simulated cannonball lands[1].

[1] Note that in all of the following we'll ignore the effects of air resistance.

The program should accept all of its parameters on the command line, as described in Section 9.15 of Chapter 9. The usage should be:

```
./simulate nshots vinit theta outfile
```

where:

- `nshots` is the number of cannonballs to fire.
- `vinit` is the ideal initial velocity of the cannonballs (before adding any jitter).
- `theta` is the ideal angle between the cannon and the ground (before adding jitter), expressed in degrees. An angle of zero means the cannon is horizontal, and an angle of 90 means the cannon is pointing straight up into the air. (See Figure A.3.)
- `outfile` is the name of a file into which the program will write the x and y coordinates at which each cannonball lands. Assume that the cannon points along the x axis, but cannonballs may veer by some small random angle, β, to the right or left. (See Figure A.4.)

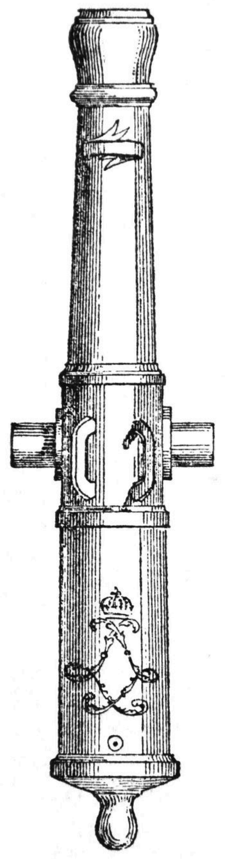


Figure A.2: Canon de 16 Gribeauval.
Source: *Wikimedia Commons*

If the user doesn't supply enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else.

After running the program, the output file should contain two columns of numbers with a space between them. The first column is x and the second column is y.

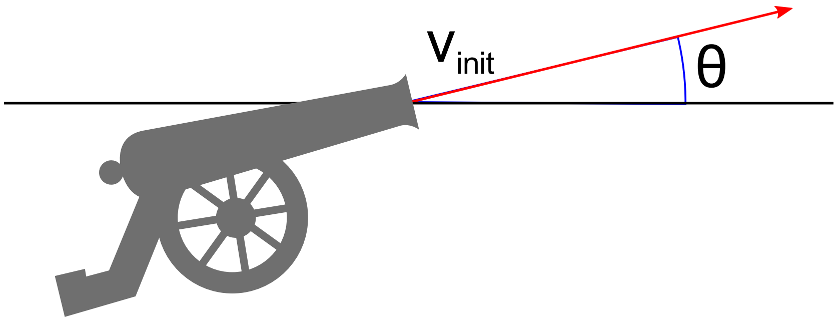


Figure A.3: **Side** view of the cannon's upward angle, θ.

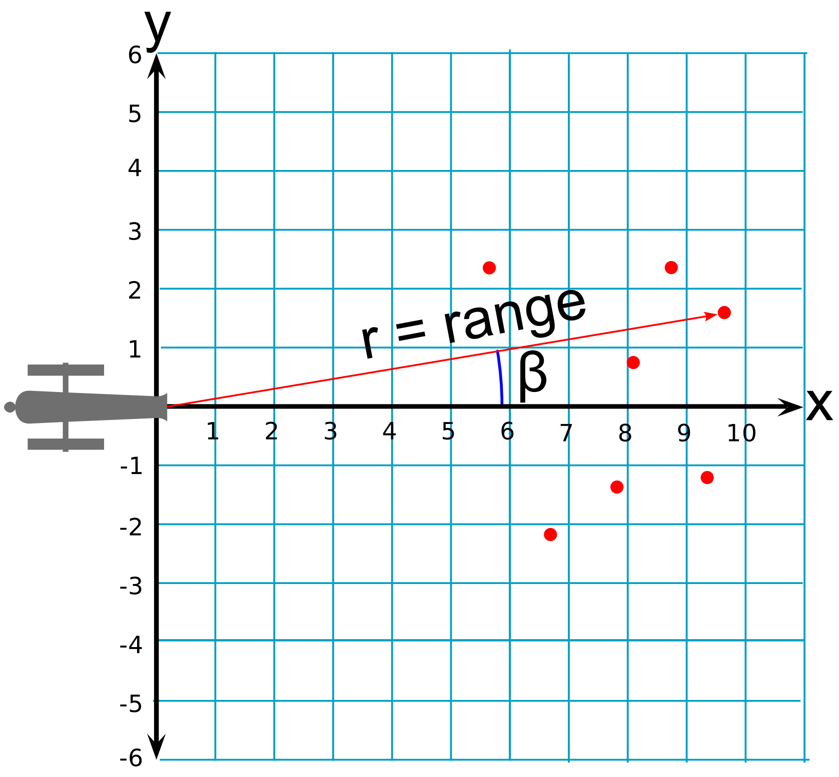


Figure A.4: **Overhead** view of a cannonballs side-to-side angle, β, its range, r, and the landing positions of some cannonballs.

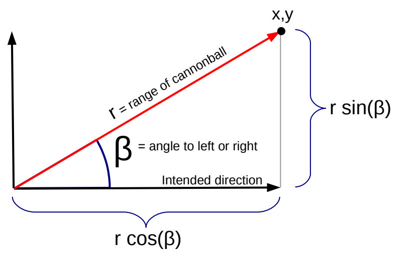


Figure A.5: Finding the x and y coordinates of a cannonball, given its range and the horizontal angle β.

To get you started, the helpful time-traveller has already written much of the program for you (see Program A.1). All you need to do is complete the program by filling in `main` and adding a `help` function that prints out a friendly usage message when the user doesn't supply enough arguments on the command line. As you can see, you'll be using several functions that have appeared in Chapters 9 and 11. These are at the top of Program A.1.

Your program should determine the landing positions of the cannonballs as follows:

1. Convert the upward angle (`theta`) into radians, since C's trigonometry functions use radians instead of degrees. You can use the function `to_radians` to do this. (This function is taken from Chapter 9, Section 9.8.)

2. Open the output file for writing. (See examples like Program 5.3 in Chapter 5.) Note that the name of the file will be in the command-line argument `argv[4]`.

3. Now loop through all of the cannon shots, using a `for` loop.

4. Each time the cannon shoots, set the cannonball's initial velocity and upward angle to the values of `vinit` and `theta`, plus some random "jitter". To do this, use the function named `normal` (taken from Section 11.4 of Chapter 11). The `normal` function generates numbers that tend to be close to zero, but sometimes have other values. (See Figure A.6.)

   - For each shot your program makes, set the cannonball's initial velocity to `vinit + 0.1*vinit*normal()`. This will give a value that tends to be within +/- 10% of the "ideal" velocity, `vinit`.
   - Set each cannonball's upward angle to `theta + 0.01*normal()`. This will give a value that tends to be close the "ideal" angle, `theta`, but has some small random variation.

5. Now that you have the cannonball's velocity and upward angle, use the `range` function (taken from Chapter 9, Section 9.8) to calculate its range. This function takes the cannonball's initial velocity and its upward angle, and returns the cannonball's "range" (the horizontal distance from the launch point to the landing point). (See Figure A.4.)

6. To determine the cannonball's landing position you'll also need to know β, the angle by which its path deviates to the right or left. (See Figure A.4.) Use the `normal` function for this by setting β equal to `0.01*normal()`. This will give you a random, small angle.

7. Now that you have the cannonball's range and the angle β, you calculate the x and y coordinates of its landing spot. See Figure A.5.

8. Finally, write the x and y coordinates into the output file. (See examples like Program 5.3 in Chapter 5 if you don't remember how to do this.)

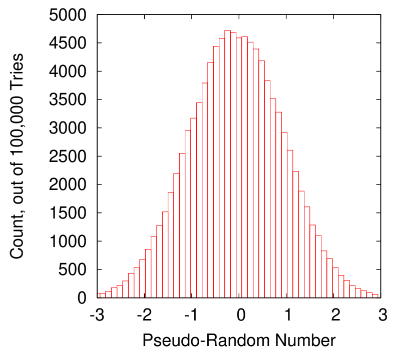


Figure A.6: The `normal` function generates pseudo-random numbers that are most likely to be near zero, with smaller probabilities for other values. This figure shows 100,000 pseudo-random numbers generated by `normal`.

Once you've written and compiled your program, run it like this to produce an output file to use with your next program:

```
./simulate 10000 250 45 simulate.dat
```

Program A.1: simulate.cpp

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>
#include <time.h>

double rand01 () {
  static int needsrand = 1;
  if ( needsrand ) {
    srand(time(NULL));
    needsrand = 0;
  }

  return ( rand()/(double)RAND_MAX );
}

double normal () {
  int nroll = 12;
  double sum = 0;
  int i;

  for ( i=0; i<nroll; i++ ) {
    sum += rand01();
  }

  return ( sum - 6.0 );
}

double g = 9.81; // Acceleration of gravity.

double to_radians ( double degrees ) {
  return ( 2.0 * M_PI * degrees / 360.0 );
}

double time_of_flight ( double v0, double angle ) {
  double t;
  double vy0;
  vy0 = v0 * sin(angle);
  t = 2.0 * vy0 / g;
  return ( t );
}

double range ( double v0, double angle ) {
  double d;
  d = v0 * cos(angle) * time_of_flight( v0, angle );
  return ( d );
}

int main (int argc, char *argv[]) {

        //
        // Insert program here!
        //
}
```

Program 2: Analyzing the Results

Your second program will be named `analyze.cpp`. It will read a data file produced by your first program, and give you a statistical summary of the data it contains.

Like the first program, `analyze` should accept all of its parameters on the command line, and give users a helpful message if they don't give it the right number of arguments. The usage should be:

```
./analyze filename
```

where `filename` is the name of a data file produced by your `simulate.cpp` program.

The output of the `analyze` program should look like this:

```
Average x = 6428.287617
Std. dev. of x = 1286.944844
Min x = 2568.660526
Max x = 13046.427659
Average y = -0.611109
Std. dev. of y = 65.978704
Min y = -284.001774
Max y = 313.589122
```

showing the average values of x and y, the standard deviations of x and y, and the minium and maximum values of x and y.

The helpful time-traveller has come to your aid again, and written some of the program for you (see Program A.2). You'll just need to fill in `main` and write a `help` function.

To analyze the data, the program should proceed as follows:

1. First, open the data file for reading. See Program 7.5 in Chapter 7 for an example of this. Refer to that program to see how to read the data and calculate the average and standard deviation.

2. The time-traveller has kindly provided you with an easy way to find minimum and maximum values, using the two functions `findmin` and `findmax`. Each time you read a new value of x, for example, just say `xmax = findmax(x,xmax,n)`. This will update the value of `xmax` if necessary. When you're done reading all of the data, `xmax` will contain the largest value of x.

Run your program to analyze the `simulate.dat` file you produced earlier. Check to make sure its results look realistic. (Compare them to the sample output above.)

Program A.2: analyze.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
double findmax ( double x, double oldvalue, int n ) {
  if ( n == 0) {
    oldvalue = x;
  } else {
    if ( x > oldvalue ) {
      oldvalue = x;
    }
  }
  return ( oldvalue );
}
double findmin ( double x, double oldvalue, int n ) {
  if ( n == 0 ) {
    oldvalue = x;
  } else {
    if ( x < oldvalue ) {
      oldvalue = x;
    }
  }
  return ( oldvalue );
}
int main ( int argc, char *argv[] ) {

        //
        // Insert program here!
        //

}
```

Program 3: Making Pictures

Your final program will be called `visualize.cpp` and it will let you make pictures like the ones shown in Figure A.8. These figures show the distribution of landing positions of 10,000 simulated cannonballs.

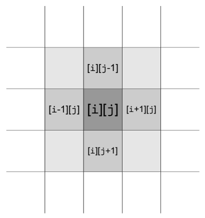


Figure A.7: Each element of `grid` records the number of cannonballs that landed within a particular section of the battlefield.

The figures represent 2-dimensional histograms. We talked about histograms in Chapter 7, but we didn't say much about 2-dimensional ones. Because of that, our friendly time-traveller has written almost all of this program for you. (See Program A.3.)

This program uses a 2-dimensional, `nbins` × `nbins` array named `grid`. Each element of the array represents an area of the battlefield. The number stored in each element is the number of cannonballs that landed in that area.

Like the preceding programs, this one will expect parameters on its command line. Its usage will be:

```
./visualize xmin xmax ymin ymax infile outfile
```

where `xmin`, `xmax`, `ymin`, and `ymax` specify the limits of rectangular area of the battlefield. `infile` is the name of a data file produced by your `simulate` program. `outfile` is the name of a file into which the current program will write its results.

Two key parts of the program have been left for you to fill in. First, near the top of `main`, you need to set all of the elements of `grid` to zero. To do this, you'll need two nested "`for`" loops. Inside the loops, set each element, `grid[xbin][ybin]`, to zero.

Second, near the end of `main`, you need to open the output file for writing and write your results into it. (You'll again need two nested "`for`" loops to do this.)

The file should have three columns, `x`, `y`, and `grid[xbin][ybin]`, where `x` and `y` are the coordinates of the center of the grid element. Use `x=xmin+xbinwidth*(0.5+xbin)`, and `y` similarly, for the center position of each grid element.

There should also be a blank line after every `nbins` rows. See the end of Section 6.12 for an explanation of this blank line, and the last part of Program 6.8 for an example showing how to create it.

After writing and compiling the program, try it out. Use your `analyze` program to find good values for `xmin`, `xmax`, `ymin`, and `ymax`. Use these values and your newest program to process the data in `simulate.dat` and create a new file, `visualize.dat`, that can be plotted with *gnuplot*:

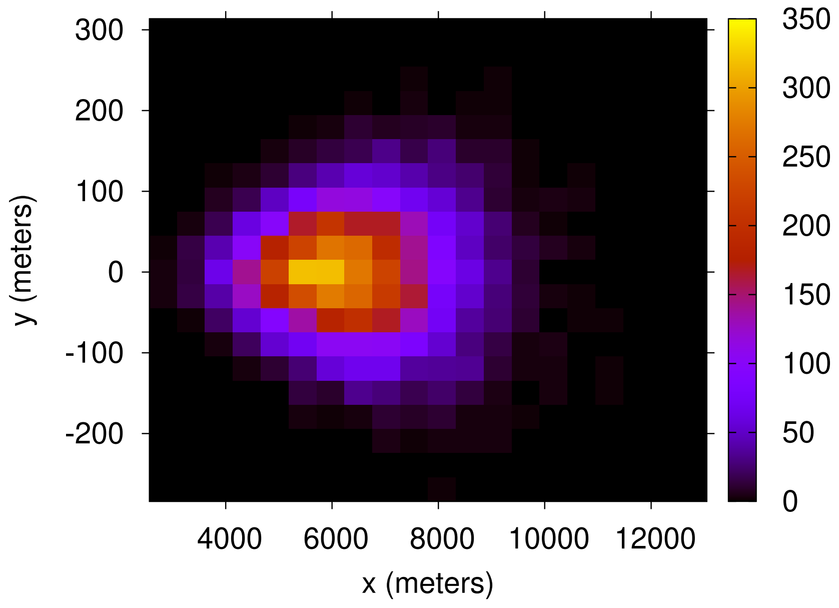
```
./visualize 2569 13046 -284 314 simulate.dat visualize.dat
```

Try plotting your results with *gnuplot*. To produce the top graph in Figure A.8, give *gnuplot* the following command:

```
plot "visualize.dat" with image
```

To produce the bottom graph in Figure A.8, use this *gnuplot* command:

```
splot "visualize.dat" with image, "" with histeps
```



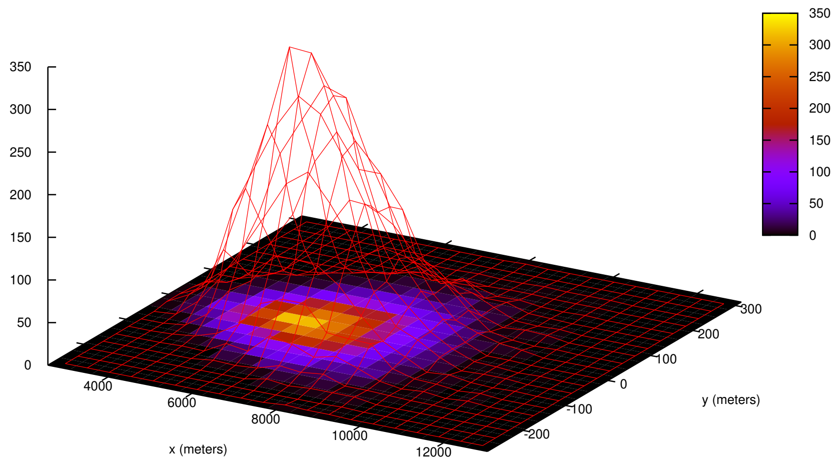


Figure A.8: Two views of the distribution of cannonball landing positions. The color scale shows how many cannonballs (out of 10,000) landed in each grid element.

Program A.3: visualize.cpp

```
#include <stdio.h>
#include <stdlib.h>

void help() {
  printf ("Usage: ./visualize xmin xmax ymin ymax input.dat output.dat\n");
}

int main ( int argc, char *argv[] ) {
  const int nbins = 20;
  int grid[nbins][nbins];
  double x, y;
  double xmin, xmax;
  double ymin, ymax;
  double xbinwidth, ybinwidth;
  FILE *output;
  FILE *input;
  int xbin, ybin;

  if ( argc != 7 ) {
    help();
    exit(1);
  }

  // Insert code here to reset all bins to zero.

  xmin = atof(argv[1]);
  xmax = atof(argv[2]);
  ymin = atof(argv[3]);
  ymax = atof(argv[4]);

  xbinwidth = (xmax - xmin)/(double)nbins;
  ybinwidth = (ymax - ymin)/(double)nbins;

  input = fopen ( argv[5],"r" );

  while ( fscanf(input, "%lf %lf", &x, &y) != EOF ) {
    xbin = (x-xmin)/xbinwidth;
    ybin = (y-ymin)/ybinwidth;
    if ( xbin >= 0 && ybin >= 0 && xbin < nbins && ybin < nbins ) {
      grid[xbin][ybin]++;
    }
  }

  fclose ( input );

  // Insert code here to open the output file and write
  // the contents of "grid" into it.
}
```

Last Words

As your friend from the future fades away in a cloud of sparkles, you stand there savoring your brief glimpse of the future. "If only we had such technology today," you sigh, as you hear your commander shout the order to begin breaking camp.

Figure A.9: Wellington at Waterloo.
Source: *Wikimedia Commons*

While you prepare to march into Russia during the Spring of 1812, far away in England a mathematician named Charles Babbage is looking at mathematical tables, like the ones used by artillerymen for aiming their cannons, and thinking about how these tables could be generated automatically, by machinery instead of humans.

After Napoleon's defeat at Waterloo in 1815, Babbage exchanges ideas with other mathematicians, English and French, and in 1822 he begins work on the series of computing machines that will become the ancestors of all modern computers.

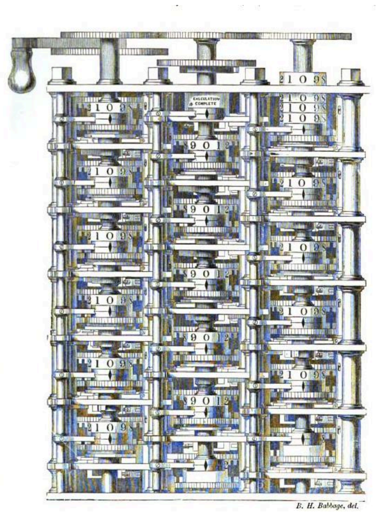


Figure A.10: Part of Babbage's "Difference Engine".
Source: *Wikimedia Commons*

Figure A.11: The Emperor Napoleon (left), and Babbage's brain (right).
Source: *Wikimedia Commons 1, 2*

Project 2: Diffusion Confusion

Introduction: Randomly-Bouncing Molecules

Imagine that you're in a large room full of perfectly still air. At the opposite end of the room is a just-opened bottle of perfume. The volatile molecules from the perfume have started to wander out into the room, bouncing off of molecules in the air. How long would it take these molecules to bounce their way across the room to your nose?

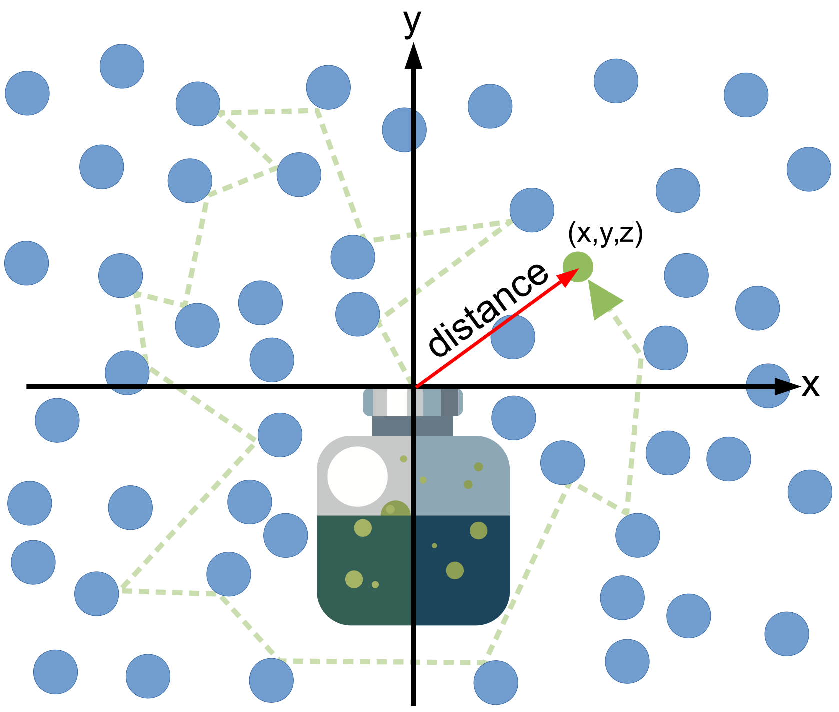


Figure A.12: A molecule leaves the perfume bottle, then bounces around among the air molecules for a while, ending up at a position (x, y, z) some distance from where it started.

A typical speed for a molecule in air is about 1,000 miles per hour, but our perfume molecules don't travel in a straight line. Figure A.12 shows a typical perfume molecule's path. Since it bounces around at random, it tends to linger near the bottle for a long time. The process by which molecules spread out by bouncing around this way is called "diffusion".

In this project you will write three programs: `simulate.cpp`, `analyze.cpp`, and `visualize.cpp`. The first will simulate the paths of perfume molecules through air, the second will analyze the simulated data, and the third will help us visualize one of the results.

Program 1: Simulating the Paths of Molecules

Your first program will be named `simulate.cpp`. It will track the random movement of some number of perfume molecules as they undergo some number of collisions. The program will write the final position of each molecule, and how long it took the molecule to get there, into an output file.

The perfume molecule's path is an example of a random walk, and this program will be very similar to Practice Problem 4 in Chapter 7. One difference is that the new program tracks a random path in three dimensions instead of two, so you'll need to keep track of the molecule's x, y, and z coordinates. Another difference is that we won't assume that each step of the path has the same length, as we did in the earlier program. This time, we'll let the step length vary a little. Each step in the molecule's random path will be the distance from one collision to the next. Finally, the new program won't bother with keeping track of sums or averages.

The program should accept all of its parameters on the command line, as described in Section 9.15 of Chapter 9. The usage should be:

```
./simulate nparticles ncollisions output.dat
```

where:

- `nparticles` is the number of perfume molecules we want to simulate.
- `ncollisions` is the number of collisions each molecule will experience.
- `output.dat` is the name of a file into which the program's results will be written.

If the user doesn't supply enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else. See Section 9.15 of Chapter 9 for an example showing how to do this.

After running the program, its output file should contain four columns of numbers: The x,y, and z coordinates where the molecule ended up, and the time it took to get there. We'll measure time in microseconds (1 microsecond = 10^{-6} seconds) and distances in microns (1 micron = 10^{-6} meters).

Each time a perfume molecule collides with an air molecule, we'll need to generate a new random direction for it, and a new random distance to the next collision. In 3-dimensional space, we can describe a particle's direction with two angles, θ (theta) and φ (phi) (see Figure A.13):

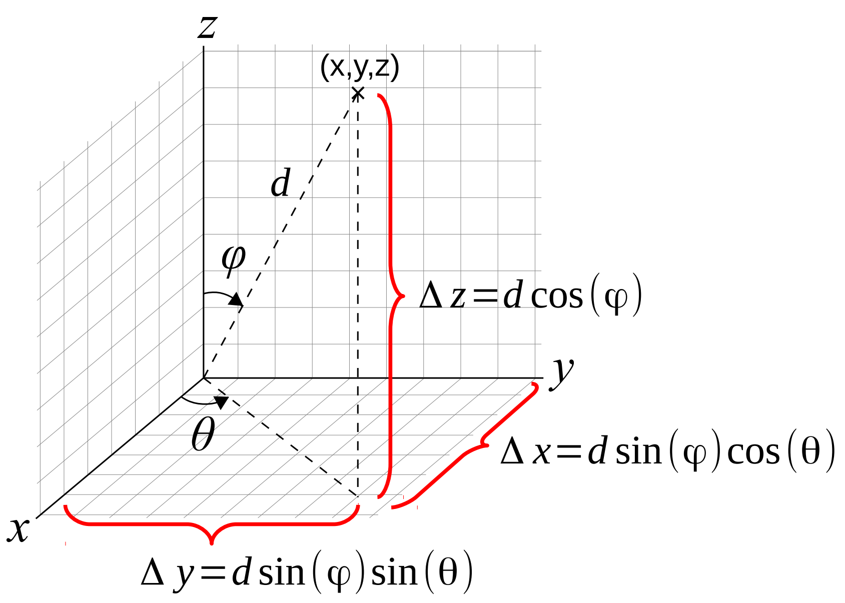


Figure A.13: After a collision, the molecule's new direction is given by two angles, θ and φ. The distance to the next collision is d.

- The angle θ can point in any direction away from the Z axis. It can have any value between zero and 2π radians (360°).
- The angle φ can have any value between straight up (zero) and straight down (π radians, or 180°).

The distance, d, will vary around some average value called the "mean free path", which we'll assume to be 0.14 microns. Each time we generate a value for d we'll do so by adding a little bit of random "jitter" to this distance.

To get you started, I've already written some of the program for you (see Program A.4). All you need to do is complete the program by filling in `main`. As you can see, you'll be using two functions that have appeared in Chapter 11. These are at the top of Program A.4. You'll also see that I've defined the values of the mean free path (`meanpath`) and the speed of the molecules (`speed`), which we assume to be 500 microns/microsecond.

Figure A.14: Trading card for Hoyt's German Cologne, circa 1900.
Source: *Wikimedia Commons*

To track the molecules, your program should do the following:

1. Open the output file for writing[2]. The output file name will be given by `argv[3]`, so you can say something like "`output = fopen(argv[3],"w");`".

2. You'll need a pair of nested `for` loops: An outer loop for each molecule, and an inner one for each collision[3].

3. Keep track of the molecule's position with three variables, `xpos`, `ypos`, and `zpos`. Keep track of the time elapsed with a variable named `t`. Remember to set all of these back to zero whenever you begin tracking a new molecule.

[2] For a reminder about how to write output into files, see examples like Program 5.3 in Chapter 5.

4. Every time the molecule collides, do the following:

   (a) Generate two random angles like this:

   ```
   theta = 2.0*M_PI*rand01();
   phi = M_PI*rand01();
   ```

   (b) Generate a random distance like this:

   ```
   d = meanpath * ( 1.0 + 0.1*normal() );
   ```

   where `normal` is a function shown in Program A.4 below.

   (c) Add Δx, Δy, and Δz (as shown in Figure A.13) to the values of `xpos`, `ypos`, and `zpos`, respectively, to get the molecule's new position[4].

   (d) Update `t` by adding `d/speed` to it. This is the time it will take the molecule to travel the distance `d`.

[3] This is similar to what we did in Program 2.7 in Chapter 2.

[4] If you're not familiar with the symbols in Figure A.13, remember that θ is `theta` and φ is `phi`. These are the random angles you generated in step (a) above.

5. Use the trick described in Section 4.4 of Chapter 4 to print out progress reports as your program is running. After every 10 molecules, print a message like this on the screen: `Working on molecule 10...` (or 20, or 30, and so on). It's OK if the program prints "`Working on molecule 0`" when it starts.

6. After tracking the molecule through `ncollisions` collisions, write `xpos`, `ypos`, `zpos`, and `t` into the program's output file[5]. These should be written as four numbers separated by single spaces, with a `\n` at the end of the line.

[5] See examples like Program 5.3 in Chapter 5.

Once you've written and compiled your program, run it like this to produce an output file to use with your next program:

```
./simulate 1000 16000 simulate-16000.dat
```

This should produce an output file (`simulate-16000.dat`) containing the final positions and times for 1,000 perfume molecules after each of them bounces 16,000 times.

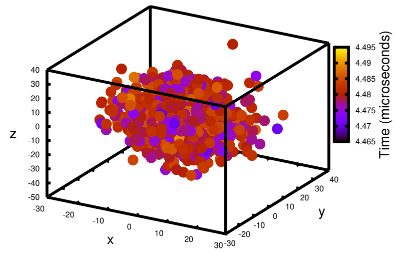


Figure A.15: You can check your first program's results by plotting them with *gnuplot*. This figure shows what you should see if you type:
`splot "simulate-16000.dat" with points palette pointsize 3 pointtype 7`
It shows the final x, y, and z positions of the molecules, color-coded by how long it took them to get there.

Program A.4: simulate.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <time.h>
#include <math.h>

double rand01 () {
  static int needsrand = 1;
  if ( needsrand ) {
    srand(time(NULL));
    needsrand = 0;
  }
  return ( rand()/(1.0+RAND_MAX) );
}

double normal () {
  int nroll = 12;
  double sum = 0;
  int i;

  for ( i=0; i<nroll; i++ ) {
    sum += rand01();
  }
  return ( sum - 6.0 );
}

int main ( int argc, char *argv[] ) {

  double meanpath = 0.14; // Microns per collision
  double speed = 500; // Microns per microsecond

        //
        // Insert program here!
        //
}
```

Program 2: Analyzing the Results

Your second program will be named `analyze.cpp`. It will read a data file produced by your first program, and give you a statistical summary of the data it contains.

Like the first program, `analyze` should accept all of its parameters on the command line, and give users a helpful message if they don't give it the right number of arguments. The usage should be:

```
./analyze input.dat
```

where `input.dat` is the name of a data file produced by your `simulate.cpp` program.

The output of the `analyze` program should look like this:

```
Average distance = 16.292850 microns
Std. dev. of distance = 6.987062 microns
Min distance = 0.684207 microns
Max distance = 45.581858 microns
Average time = 4.480129 microseconds
Std. dev. of time = 0.003552 microseconds
Min time = 4.469744 microseconds
Max time = 4.491567 microseconds
Diffusion Coefficient is 0.29626 cm^2/s
```

where `distance` is the final distance of a molecule from the origin, which is given by

$$distance = \sqrt{x^2 + y^2 + z^2}$$

and `time` is the amount of time the molecule took to get there, which is just the fourth column in your data file.

The "Diffusion Coefficient" is a way of measuring how fast molecules diffuse through the air. It's usually given in units of cm^2/s. If your program calls the average distance `davg` and the average time `tavg`, you can calculate the diffusion coefficient like this:

```
dcm = davg/1.0e4;
tseconds = tavg/1.0e6;
dcoeff = dcm*dcm/2.0/tseconds;
```

where `dcm` is the distance converted to centimeters and `tseconds` is the time converted to seconds. `dcoeff` is the Diffusion Coefficient. It should end up having a value of around 0.3 cm^2/s if your programs are working properly.

Figure A.16: Broken glass perfume amphora from Ephesus, 2nd century CE.

Source: Wikimedia Commons

Again, I've already written some of the program for you (see Program A.5). You'll just need to fill in `main`.

To analyze the data, the program should proceed as follows:

1. First, open the data file for reading. See Program 7.5 in Chapter 7 for an example of this. Refer to that program to see how to read the data and calculate the average and standard deviation.

2. At the top of Program A.5 below I've provided you with an easy way to find minimum and maximum values, using the two functions `findmin` and `findmax`. Each time you read a new value of t, for example, just say `tmax = findmax(t,tmax,n)`, where `n` is the number of molecules you've processed so far. This will update the value of `tmax` if necessary. When you're done reading all of the data, `tmax` will contain the largest value of t. **Note:** It's important that `n` be equal to zero the first time you use these functions.

3. After reading all of the data from the input file, calculate the Diffusion Coefficient (as shown above) and print all of the results.

Figure A.17: "The Perfume Maker", by Rudolf Ernst.

Source: Wikimedia Commons

Program A.5: analyze.cpp

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>
double findmax ( double x, double oldvalue, int n ) {
  if ( n == 0) {
    oldvalue = x;
  } else {
    if ( x > oldvalue ) {
      oldvalue = x;
    }
  }
  return ( oldvalue );
}
double findmin ( double x, double oldvalue, int n ) {
  if ( n == 0 ) {
    oldvalue = x;
  } else {
    if ( x < oldvalue ) {
      oldvalue = x;
    }
  }
  return ( oldvalue );
}
int main ( int argc, char *argv[] ) {

        //
        // Insert program here!
        //

}
```

Program 3: Visualizing the Distance

Your final program will be called `visualize.cpp` and it will let you make pictures like the one shown in Figure A.18. This figure shows the distribution of final distances of 1,000 perfume molecules after 16,000 collisions.

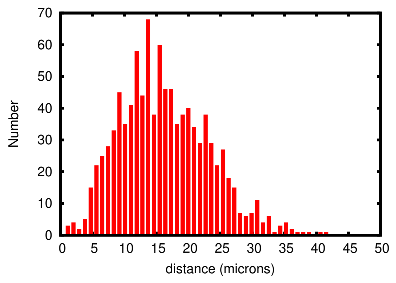


Figure A.18: Distribution of the final positions of 1,000 perfume molecules after each has experienced 16,000 collisions.

This figure is a histogram, like the ones we discussed in Chapter 7. Your third program will be similar to Program 7.1 in that chapter. Again, to get you started, I've written part of the program for you (see Program A.6 below). Notice that I've defined a 50-element array, `bin`, to hold the histogram data.

Like the preceding programs, this one will expect parameters on its command line, and should complain and exit if it doesn't get the proper number of parameters. Its usage will be:

```
./visualize dmin dmax input.dat output.dat
```

where `dmin` and `dmax` are the minimum and maximum distances (as determined by your `analyze` program) `input.dat` is the name of a file produced by your `simulate` program, and `output.dat` is a file into which your new program will write the histogram data.

The output file should contain two columns of numbers, separated by a single space. Unlike Program 7.1, the first column here will contain a distance instead of a bin number (see below for instructions about converting bin number to distance). The second column will be the number of molecules in that bin.

To make the histogram, the program should proceed as follows:

1. First, determine the `binwidth`, like this:

   ```
   binwidth = (dmax-dmin)/nbins;
   ```

2. Next, use a `while` loop to read data from the input file. Each line of the file will contain four values: x, y, z, and t.

3. Every time you read a line, determine the distance from $distance = \sqrt{x^2 + y^2 + z^2}$.

4. Determine which bin this distance belongs in, and increment that bin. Be sure to keep a count of the number of over/underflows, as Program 7.1 does.

5. After processing all of the input data, write the histogram data into

the output file. For each bin of the histogram, write two numbers separated by a single space: the distance represented by that bin, and the number of molecules that fell within it. The distance can be calculated from the bin number, like this:

```
distance = dmin + binwidth*(0.5+i);
```
where `i` is the bin number.

6. Finally, at the bottom of the output file, write a line beginning with a # that tells how many overflows or underflows were seen.

Run your program like this to make a histogram of the data you produced earlier:

```
./visualize  0.684207 45.581858 simulate-16000.dat visualize-16000.dat
```

You can plot the resulting data file with *gnuplot* like this:

```
plot "visualize-16000.dat" with impulses lw 5
```

The result should look like Figure A.18.

Program A.6: visualize.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
int main ( int argc, char *argv[] ) {

  const int nbins=50;
  int bin[nbins];

        //
        // Insert program here!
        //

}
```

Results

What do your results tell you? If you were to run your `simulate` program two more times, like this:

```
./simulate 1000 1000 simulate-1000.dat
./simulate 1000 4000 simulate-4000.dat
```

and then use your `analyze` program to analyze each of these files and your `simulate-1600.dat` file, you might notice a pattern. Every time you increase the number of collisions by a factor of four, the average distance increases by a factor of two. This fact is reflected in the definition of the Diffusion Coefficient, which tells us that the time it takes molecules to travel a given distance by diffusion is:

$$t = \frac{d^2}{2D}$$

where t is the time, d is the distance, and D is the diffusion coefficient.

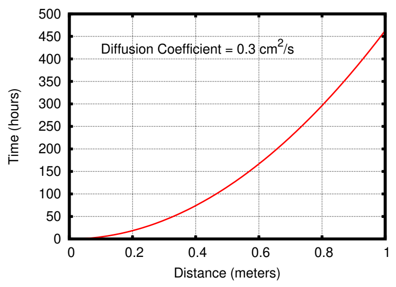
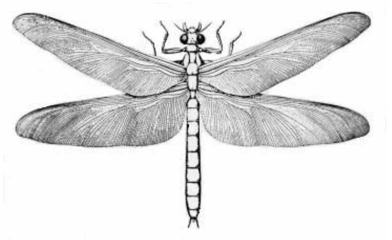


Figure A.19: How long would it take our perfume molecules to diffuse across a room? A long time!

If we plotted time versus distance, we'd get a graph like Figure A.19. As you can see from the graph, it would take hundreds of hours for our perfume molecules to travel even one meter. Diffusion is apparently very slow! Scents usually reach our nose by riding on air currents, rather than through diffusion.

Why is diffusion so slow? From Chemistry class we know that a small amount of air (say, a ballon full) contains on the order of 10^{23} molecules. That's a lot of obstacles to bounce off of. Even though our perfume molecule might be traveling at 1,000 miles per hour, it collides with air molecules billions of times per second, and each collision sends it off in another random direction.

The low speed of diffusion explains why we have lungs, and why there aren't any human-sized insects. Breathing moves oxygen by two mechanisms: *diffusion* and *advection*. When we breath, air is drawn into our lungs by advection (the bulk motion of a fluid) and it brings oxygen molecules along with it. When the air gets down into our lungs, oxygen molecules then diffuse through the thin walls of blood vessels. This is a very short distance, so diffusion can do the job relatively quickly. The blood then carries the oxygen all through our body (advection again).



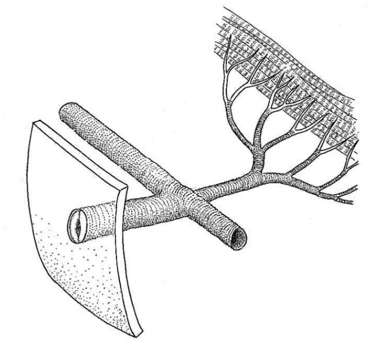


Figure A.20: In the Carboniferous period Earth's oxygen levels were much higher than they are today. This allowed giant inects like the dragonfly *Meganeura* (top) to survive, even without lungs. *Meganeura* had a two-foot wingspan! The bottom illustration shows tracheae inside an insect's body.
Source: Wikimedia Commons and D.G. Mackean

Insects don't have lungs. Their bodies contain hollow tubes called *tracheae* that open to the outside world. Oxygen molecules wander into these tubes by diffusion, and then wander through the tubes until they reach cells inside the insect's body. This is a slow process, but since insects are small, the distances are short. If insects were human-sized, they couldn't get oxygen quickly enough through this mechanism.

Project 3: Proton Power

Introduction: Particle Beam Therapy

We all know that radiation can cause cancer, but radiation can also be used to fight cancer. One example of this is particle beam cancer therapy, in which a beam of charged particles (usually protons or pions) is shot into a tumor with the goal of destroying it.

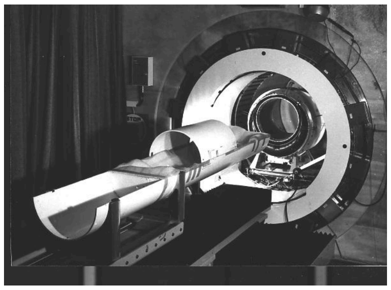


Figure A.21: An apparatus used for pion-beam radiation therapy at the Paul Scherrer Institut. The patient lies in the semicircular cradle, which is inserted into the apparatus behind during treatment.

As particles from such a beam travel through the body, they gradually lose energy and eventually come to rest. As it turns out, much of the particle's energy is lost close to the point at which it stops. This makes such beams well-suited for killing tumors without doing too much damage to the other tissues they pass through on the way to the tumor, or tissues beyond the tumor.

Particles with higher energies will travel farther into the body. By adjusting the energy of the particles, we can cause them to stop at a chosen depth (ideally, inside a tumor).

At moderate energies, a beam of particles traveling through a body loses energy mostly through interactions with electrons. Although it's possible that some of the particles will bump into an atomic nucleus, that doesn't happen very often. Since protons are 2,000 times heavier than electrons, beams of these particles tend to travel in a straight line, knocking puny electrons aside as they go.

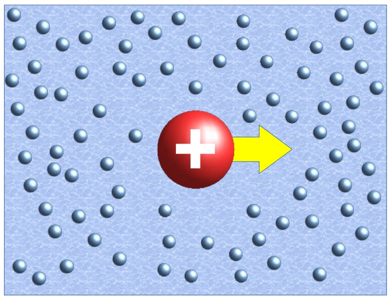


Figure A.22: A proton (shown with a plus sign because of its positive charge) is much larger than the electrons it knocks aside while travelling through the body.

Figure A.23 shows how much energy protons deposit as they travel through the body. The four curves show what happens when you use protons of four different starting energies, ranging from 50 MeV to 125 MeV. The energy deposited damages the body's tissues. The goal is to destroy the tumor without doing too much damage to healthy tissue.

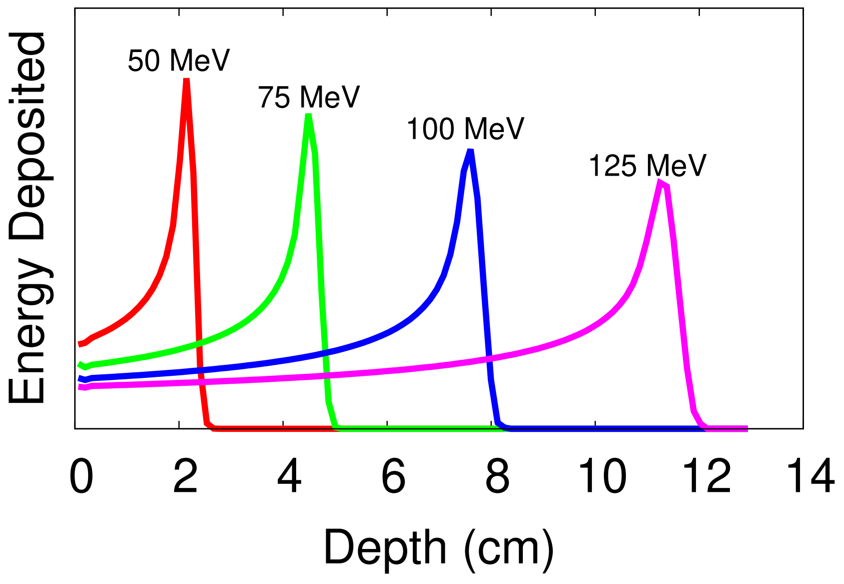


Figure A.23: Energy deposited at various depths by incoming protons having energies of 50, 75, 100, or 125 MeV. As you can see, more energetic protons penetrate to greater depths. Also notice that most of a proton's energy is deposited near its stopping point.

The Assignment

Imagine you're a doctor working at a radiation therapy facility. You have at your command a beam of protons. You can aim the beam precisely, and control its energy.

You're preparing for a visit by a patient with a 2-centimeter-thick tumor buried 8 centimeters deep in her body (see Figure A.24). You need to determine what energy the protons should have in order to deposit most of their energy in the region of the tumor.

A physicist colleague has given you a formula to calculate the energy lost by a particle while going through a thin slice of material. The formula has a form like this[6]:

[6] The actual equation is called the Bethe-Bloch formula.

$$\Delta E = \Delta x \cdot f(E, proton\ properties, material\ properties)$$

where ΔE is the amount of energy the particle loses, Δx is the thickness of the slice, and f is some function that depends on E (the energy at the beginning of the slice) as well as the constant properties of the particle (like charge and mass) and properties of the material (like density).

Unfortunately, your physicist friend tells you that eight centimeters is too big to call a "thin slice". But that's OK, she says. Just treat the eight centimeters as though it was a stack of thinner slices, as shown in Figure A.25. Each time the proton passes through one of the slices, it loses some amount of energy, ΔE. This lost energy damages the tissue in that slice. The proton then enters the next slice with its energy reduced by the amount ΔE.

Your assignment is to write three programs: **`simulate.cpp`**, **`visualize.cpp`**, and **`analyze.cpp`**. The first will simulate the passage of protons through the patient's body, the second will help visualize these results, and the third will help choose the right proton energy.

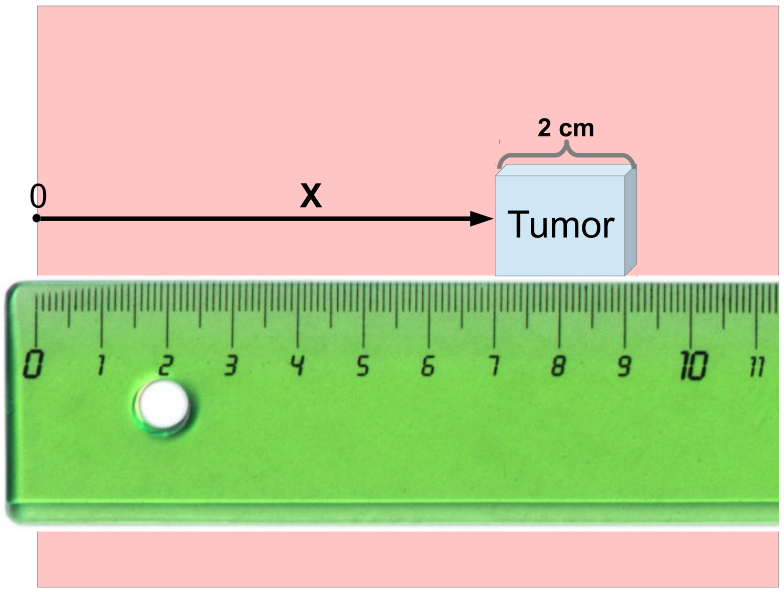


Figure A.24: Our patient's tumor is 2 cm thick, and is centered at a depth of 8 cm. Here "x" represents the depth below the patient's skin.

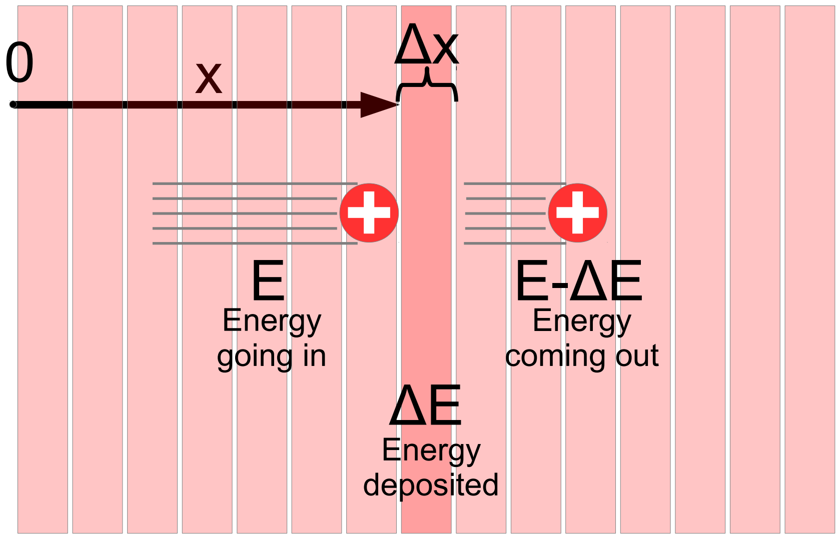


Figure A.25: We can look at the patient's body as a series of thin slices through which the proton must pass. Each time the proton passes through one of the slices, it loses some amount of energy, ΔE. This lost energy damages the tissue in that slice.

Program 1: Simulating Protons

Your first job will be to write a program named **simulate.cpp** that keeps track of the energy that protons lose as they travel through such a stack of thin slices. Each slice will have a thickness of 0.01 cm. Assume each proton travels in a straight line, starting at `x = 0` and progresses along the `x` axis until it runs out of energy. Each time a proton passes through a slice, the program should write the proton's position, energy loss, and remaining energy into an output file.

Figure A.26: The international symbol for ionizing radiation, which was first used at Berkeley Radiation Laboratory in 1946.

Source: Wikimedia Commons

Your physicist friend has kindly provided you with the beginning of a program, but she's too busy to finish it. The part she's written for you is shown in Program A.7. Near the top of the program are some numbers you'll need. The program assumes that humans are just made out of water, since they mostly are.

She's also written some useful functions in a header file named **dedx.h**, which is shown below as Program A.8. The biggest function in it is named `dEdx`, and it does most of the work of calculating how much energy a proton loses while going through one of the slices. Notice that `simulate.cpp` has an `include` statement near the top that fetches `dedx.h`.

Program A.7: simulate.cpp

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>
#include <time.h>
#include "dedx.h"

int main (int argc, char *argv[]) {
  double pmass = 938.27;     // MeV, Proton mass.
  double pcharge = 1.0;      // Proton charge.
  double rho = 1.0;          // Density, g/cm^2, for water.
  double amass = 18.01;      // Atomic mass, AMU, for water.
  double anum = 10.0;        // Atomic number, Z, for water.
  double activation = 75.0; // Activation energy, eV, for water.

  double dx = 0.01;          // Slice thickness, cm.

  int nprotons;
  double estart, energy;
  double x, de;
  FILE *output;

  // Sorry! got to run to a faculty meeting. You'll
  // have to insert the rest of the program here.

}
```

To complete the program, you'll need to do the following:

1. First, copy Program A.8 (`dedx.h`) into a file named `dedx.h` and save it. Then create a file named `simulate.cpp` and start by putting the contents of Program A.7 into it. This will be the program that does your proton simulation.
2. Your program should accept three arguments on the command line.[7] When you're done writing your program, you should be able to run it like this:

   ```
   ./simulate nprotons estart output
   ```

   where:

   - `nprotons` is the number of protons you want to simulate.
   - `estart` is the starting energy of the protons.
   - `output` is the name of an output file into which the program will write its results.

   If the user doesn't supply enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else[8].

   Since `nprotons` is an integer, you'll need to use the `atoi` function to convert this command-line argument[9]. For `estart` you'll need to use `atof`, since this number can contain decimal places. The output file name won't need any conversion, since it's already a character string. You can just use that argument directly, like this:

   ```
           output = fopen( argv[3], "w" );
   ```

3. Your program will need a pair of nested loops: An outer "`for`" loop that generates protons, one a at a time, and an inner "`do-while`" loop that tracks each proton through the slices until the proton loses all of its energy.

4. Each time the program starts tracking a new proton it should set the proton's initial position and energy. To be more realistic, the program should add some "wiggle" to these values. In the real world, the particles in a proton beam don't all have exactly the same energy, and they won't necessarily enter the body at exactly the same spot (the patient might move a little, for example). Use the function named "`normal`" (defined in `dedx.h`) for this. Here's how to do it:

   ```
   energy = estart + 0.01*estart*normal();
   ```

[7] We learned how to use command-line arguments in Sections 9.15 and 9.16 of Chapter 9.

[8] See Section 9.16 of Chapter 9 for information about how to do this.

[9] See Problem 5 (`add.cpp`) at the end of Chapter 9.

Figure A.27: A "wind" of charged particles, including many protons, blows outward from the Sun. It interacts with the earth's magnetic field to produce the aurora.
Source: Wikimedia Commons

```
x = 0 + 0.1*normal();
```

This sets the proton's initial energy to `estart` $\pm$ 1% and the starting position to zero cm $\pm$ 1 mm.

5. Each time a proton goes through a slice of tissue, your program should do the following:

   (a) Calculate the amount of energy the proton deposits in the slice (we'll call that "`de`"). Our physicist friend has given us the function named `dEdx` to help us calculate this.

   ```
   de = dx * dEdx(energy, pmass, pcharge, rho, amass, anum, activation);
   ```

   (b) Calculate the proton's new energy:

   ```
   energy = energy - de;
   ```

   (c) Update the proton's position:

   ```
   x = x + dx;
   ```

6. Every time we change the values of `x`, `de`, and `energy`, the program should write those values into the output file specified on the command line[10]. These should be written as three numbers, separated by single spaces, with a `\n` at the end of the line.

7. We can't know in advance how many slices a proton will travel through before its energy is all gone. We just have to look at the energy after each slice, and see if it's still greater than zero[11].

   Near the end of the proton's path, because of the approximations we're making, the `dEdx` function might tell us that the proton loses no energy, even though it has some energy left. That means you also need to check the value of `de` at the end of your "`do-while`" loop:

   ```
   } while ( energy > 0 && de > 0 );
   ```

Once you've written and compiled your program, run it like this to produce an output file to use with your next programs:

```
./simulate 1000 100 100-mev.dat
```

This should produce an output file named `100-mev.dat` containing information about the energy deposited by each proton, in each slice of the patient's body.

[10] See examples like Program 5.3 in Chapter 5.

[11] This is similar to the `baselpi.cpp` program you wrote for Problem 6 in Chapter 4. In that program, we kept calculating smaller and smaller terms, until we got to one that was less than some limit. That program used a "`do-while`" loop, and we can use one of those here, too.

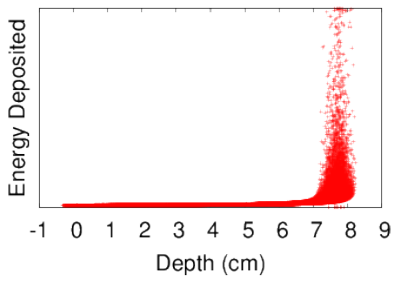


Figure A.28: You can check your first program's results by plotting them with *gnuplot*. This figure shows what you should see if you type:
`plot "100-mev.dat" using 1:2`
It shows the energy deposited in each slice by each proton.

The file `dedx.h`, below, contains a function named `dEdx` for calculating the energy lost (ΔE) in a slice of matter with thickness Δx. This file also contains two random-number functions that we've used before. `rand01` generates random numbers uniformly distributed between zero and one, and `normal` generates random numbers in a Gaussian or "normal" distribution[12].

[12] You can read about both of these in Chapter 11.

Program A.8: dedx.h

```
double rand01 () {
  static int needsrand = 1;
  if ( needsrand ) {
    srand(time(NULL));
    needsrand = 0;
  }
  return ( rand()/(1.0+RAND_MAX) );
}

double normal () {
  int i, nroll = 12;
  double sum = 0;
  for ( i=0; i<nroll; i++ ) {
    sum += rand01();
  }
  return ( sum - 6.0 );
}

// Returns dE/dx, in MeV * cm^2/g (see units of "constant", below.)
double dEdx (double T, double pmass, double pcharge,
             double rho, double a, double z, double activation) {
  const double constant = 0.1535; // MeV cm^2/g
  const double me = 0.5110034; //MeV/c^2, Electron mass.
  double E, p, beta, gamma, wmax, excite;
  double term1, term2, term3, bbdedx;

  E = T + pmass;
  p = sqrt(T*T + 2.0*pmass*T);
  beta = sqrt(p*p/E/E);
  gamma = 1.0/sqrt(1.0-beta*beta);
  wmax = 2.0*me*beta*beta/(1.0-beta*beta); // MeV
  excite = activation/1.0e6 ; // Convert to MeV.

  term1 = constant*rho*z*pcharge*pcharge/a/(beta*beta);
  term2 = log(2.0*me*gamma*gamma*beta*beta*wmax/excite/excite);
  term3 = 2.0*beta*beta;

  bbdedx = term1*(term2-term3);
  if ( bbdedx < 0.0 ) {
        bbdedx = 0.0;
  }

  // Add 10% gaussian noise:
  bbdedx += 0.1*sqrt(bbdedx)*normal();
  return (bbdedx);
}
```

Program A.9: visualize.cpp

```
#include <stdio.h>
#include <stdlib.h>
int main ( int argc, char *argv[] ) {
  const int nbins = 100;
  double hist[nbins];
  FILE *input;
  FILE *output;

  // Gotta go give a lecture. You'll have to
  // write the rest of the program.
}
```

Like the preceding program, this one will expect parameters on its command line, and should complain and exit if it doesn't get the proper number of parameters[13]. Its usage will be:

[13] See Sections 9.15 & 9.16 of Chapter 9.

```
./visualize xmin xmax input output
```

where `xmin` and `xmax` are the minimum and maximum depth we're interested in, in centimeters, `input` is the name of a file produced by your `simulate` program, and `output` is the name of a file into which your program will write the histogram data.

The output file should contain two columns of numbers, separated by a single space. Unlike Program 7.1, the first column here will contain a depth instead of a bin number (see below for instructions about converting bin number to distance). The second column will be the total energy deposited at that depth, in MeV.

To make the histogram, the program should proceed as follows:

1. Make sure the program sets all of the bins to zero at the beginning.
2. Determine the `binwidth`, like this:

   ```
   binwidth = (xmax-xmin)/nbins;
   ```

3. Next, use a `while` loop to read data from the input file. Each line of the file will contain three values: `x`, `de`, and `energy`.
4. Determine which bin this x value belongs in, as Program 7.1 does.
5. Be sure to keep a count of the number of over/underflows, as Program 7.1 does.

Figure A.30: A painting by Gretchen Andrew, from her series "Malignant Epithelial Ovarian Cancer", which aims to "humanize the experience of having cancer".

6. If it's not an over- or underflow, add the value of `de` to this bin. (Note that this is different from Program 7.1, which just adds 1 to the bin.)

7. After processing all of the input data, write the histogram data into the output file. For each bin of the histogram, write two numbers separated by a single space: the depth represented by that bin, and the total amount of energy deposited within it. The depth can be calculated from the bin number, like this:

   ```
   depth = xmin + binwidth*(0.5+i);
   ```
   where `i` is the bin number.

8. Finally, at the bottom of the output file, write a line beginning with a `#` that tells how many overflows or underflows were seen.

Run your program like this to make a histogram of the data you produced earlier:

```
./visualize  0 10 100-mev.dat hist100.dat
```

You can plot the resulting data file with *gnuplot* like this:

```
plot "hist100.dat" with lines
```

The result should look like Figure A.31.

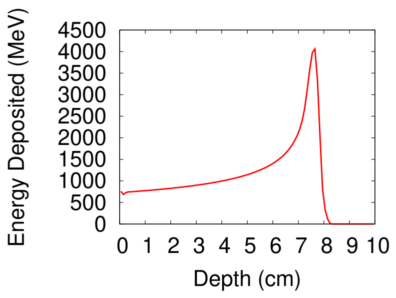


Figure A.31: The total energy deposited at each depth by a 1,000 100-MeV protons.

Program 3: Analyzing the Data

Your last program will be called **`analyze.cpp`**. It will read data produced by your first program and determine how much total energy was deposited in the patient's body, and how much energy was deposited in the tumor.

Like the preceding programs, this one should accept all of its parameters on the command line, and give users a helpful message if they don't give it the right number of arguments. The usage should be:

```
./analyze input tcenter tsize
```

Where "`input`" is the name of a data file produced by your `simulate` program, "`tcenter`" is the depth of the center of the tumor, in cm, and "`tsize`" is the size of the tumor, in cm.

Program A.10: analyze.cpp

```
#include <stdio.h>
#include <stdlib.h>
int main ( int argc, char *argv[] ) {

        // Ack! My lab is on fire (again)!
        // You're on your own here!

}
```

Once again, your physicist friend has written the first part of the program for you, as shown in Program A.10. She didn't have time for much, but you shouldn't have any trouble completing it. Here's how to do it:

1. First, make sure you define two `double` variables to keep track of the total amount of energy and the amount of energy deposited in the tumor. Make sure both of these are set to zero initially.
2. Next, you'll need to find the depth at which the tumor begins, and the depth at which it ends. These can be found from `tcenter` and `tsize`, like this:

   ```
   xmin = tcenter - tsize/2.0;
   xmax = tcenter + tsize/2.0;
   ```
3. Use a `while` loop to read data from the input file. Each line of the file will contain three values: `x`, `de`, and `energy`.
4. Each time you read a `de` value, add it to the total energy.
5. If `x` is between `xmin` and `xmax`, also add `de` to the amount of energy deposited in the tumor.
6. After reading all of the data, print your results in a nice way that tells the user the total energy and the energy in the tumor. Also tell the user what *fraction* of the total energy was deposited in the tumor, expressed as a percentage. Note that you can tell `printf` to print a percent sign by writing %%.

After you've written your program, run it like this:

```
./analyze 100-mev.dat 8 2
```

This tells the program to read the data for 100 Mev protons that you produced with your `simulate` program, and look at the amount of energy that would end up in a two-centimeter-thick tumor located at a depth of eight centimeters. The program's output should look something like this:

Figure A.32: A Russian "Proton" rocket.
Source: Wikimedia Commons

Figure A.33: The BBC Micro"Proton" computer.
Source: Wikimedia Commons

Figure A.34: A 2016 "Proton Persona" automobile.
Source: Wikimedia Commons

```
Total energy deposited: 102252.422287 MeV
Energy deposited in tumor: 28645.976102 MeV
Fraction deposited in tumor: 28.014961%
```

Results

Using the tools you've written you could find the proton energy that best suits your patient's needs. For example, you could simulate protons of several energies using your `simulate` program:

```
./simulate 1000  50  50-mev.dat
./simulate 1000  75  75-mev.dat
./simulate 1000 100 100-mev.dat
./simulate 1000 125 125-mev.dat
```

then take a look at the energy distribution created by each energy:

```
./visualize 0 10  50-mev.dat hist50.dat
./visualize 0 10  75-mev.dat hist75.dat
./visualize 0 10 100-mev.dat hist100.dat
./visualize 0 10 125-mev.dat hist125.dat
```

You'd see distributions like those shown in Figure A.23 in the introduction. Each distribution has a distinct peak, called the "Bragg peak", near the end of the proton's path. If you saw that one of these peaks lies in the region of the tumor, you might use your `analyze` program to see what fraction of the energy would go into the tumor, like this:

```
./analyze 100-mev.dat 8 2
```

Congratulations, Doctor! You've helped a patient along the road to recovery.

If you're interested in learning more about proton beam therapy, you can find information here:

- Proton Therapy, from Wikipedia.
- The evolution of proton beam therapy: Current and future status, from the NIH's National Center for Biotechnology Information.
- The physics of proton therapy, by Wayne D Newhauser and Rui Zhang.

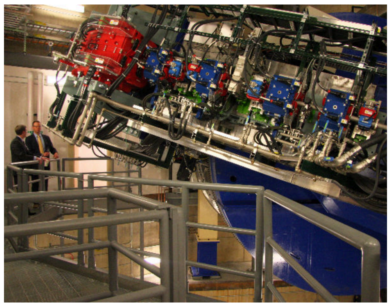


Figure A.35: Proton therapy is a valuable treatment for some types of cancer. It's becoming more widely used, with over 100 treatment centers online now or in planning. Shown above are a facility in Orsay, France (top) and the Mayo Clinic in the US (bottom). The cost, while still significant, is coming down. The ability to minimize radiation damage to surrounding tissues makes it particularly appealing in pediatric cases, where collateral radiation damage can have long-term effects on development.

Project 4: Population Explosion

Introduction

Imagine that a derelict boat washes up on the shore of an uninhabited island. Aboard the boat is a crew of ten rats, all grateful to be on dry land again. Finding plenty of food and water on the island, the happy rats settle down and begin raising families[14].

Boat (1922-1928), Adriano de Sousa Lopes.
Source: Wikimedia Commons

[14] This is reminiscent of the famous radio drama Three Skeleton Key, first broadcast in 1949. If you want to hear a scary story, you can listen to it here: mp3 at archive.org

We might wonder how rapidly our rat population grows in their new island home. Common brown Norway rats are known to have a very high reproductive rate of 0.015 offspring per day. In a perfect environment, we might expect their population to grow over time like this:

$$N(t) = N_0 e^{0.015t}$$

where $N(t)$ is the population after t days, given an initial population of N_0. If we graphed the population over a few years, we'd see something like Figure A.36.

This predicts a rat population of 6 trillion trillion after 10 years! Clearly that's unrealistic. Although there are a lot of rats in the world, their total population is probably only a few billion[15].

The problem is that our estimate assumes that birth and death rates will stay the same as the population grows. Observations of the natural world show that this isn't really the case. For example, populations typically share a limited amount of food and other resources. As the population grows, food is harder to find and some individuals die of starvation. Malnutrition also throttles population growth by reducing birth rates. Typically death rates increase and birth rates decline as populations grow. Taking these effects into account, a more realistic graph of our rat population might look like Figure A.37.

This graph shows the population initially increasing, but then levelling

Floating from place to place like this (a phenomenon called "rafting") is one way organisms colonize new territories. About 50 million years ago the first lemurs floated on wind-swept debris across the Mozambique Channel from the African mainland to the island of Madagascar. In 1995, a dozen iguanas floating on trees uprooted by a hurricane colonized the previously iguana-fee Caribbean island of Anguilla.
Sources: Wikimedia Commons and Wikimedia Commons.

[15] *See https://www.worldatlas.com/articles/how-many-rats-are-there-in-the-world.html*

off at some constant value. This value (called the *carrying capacity* of the environment) is the population at which the birth rate is equal to the death rate. When these rates are equal, the population no longer increases. The S-shaped curve of this graph is called a *logistic curve* and is typical of the growth of a population colonizing a new, initially resource-rich, environment.

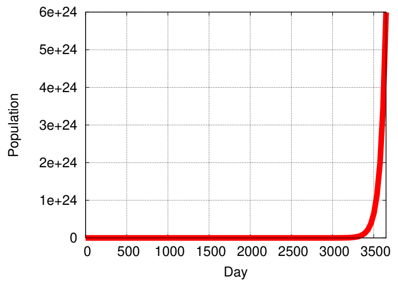


Figure A.36: Rat population given by the equation $N(t) = N_0 e^{0.015t}$.

The Assignment

Now consider a post-apocalyptic scenario where a group of 100 humans is stranded on an island. The island is a pleasant place where the plants and animals could easily provide food and shelter for a population of 1,000 humans. Resigned to their fate, the humans settle down and begin making the best of a bad situation. Ultimately, they have children who grow up knowing no home but the island. These children have grandchildren, and so on down the generations.

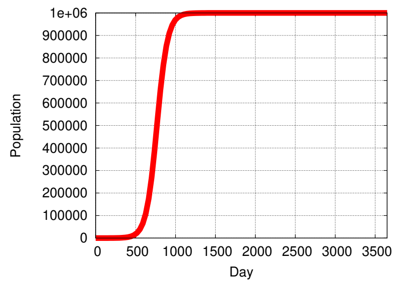


Figure A.37: Rat population with limited resources.

Your task in this project is to write three programs that simulate, visualize, and analyze the growth of such a population.

In order to write a program to model the population's growth, we'll need to know how birth and death rates change as the population increases. The shape of the functions governing birth and death rates will vary from one species to another, and will generally depend on many environmental factors. For the purpose of our simulation, though, let's assume that these rates depend solely on the amount of food available per individual. When food is plentiful, the birth rate is high and the death rate is low. In times of famine, the birth rate is low, and the death rate is high.

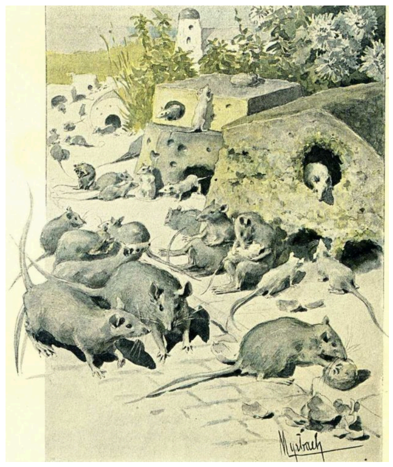


Illustration from Jules Verne's story La Famille Raton, written in 1886.

Source: *Wikimedia Commons*

We'll assume that we're told the total food-producing capacity of the environment, in terms of the number of individuals that can be fully fed. To find each person's share of this bounty (his or her *ration*), we can just divide the total amount of food by the number of people. Birth and death rates will be functions that depend on this ration.

Figure A.38 shows the shapes of the two functions we'll use. These functions give the annual probability of dying or having offspring when the ration has various values. When the ration is 1, everybody is well fed: the annual probability of having offspring is at its maximum, and the probability of dying is at some minimum value due purely to accident, disease, or old age. As the ration approaches zero, the probability of dying approaches 1 (100%) and the probability of giving birth trails off to some tiny value. We'll assume that if the ration is greater than 1, the birth and death rates stay constant at the same values they had when the ration was 1. (We'll ignore any possible ill-effects of overeating!)

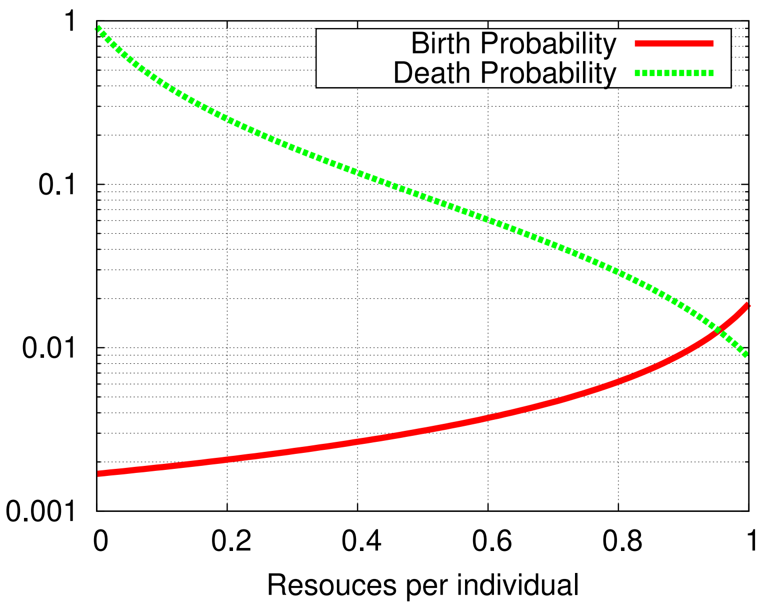


Figure A.38: Annual probability of birth or death as a function of ration.

The birth probability function we've graphed looks like this:

$$b(r) = \begin{cases} \dfrac{b_{max}}{10(1-r)+1} & \text{if } r \leq 1 \\ b_{max} & \text{if } r > 1 \end{cases} \tag{A.1}$$

and the death probability function looks like this:

$$d(r) = \begin{cases} d_{min} + \dfrac{1}{10r+1} - 0.09 & \text{if } r \leq 1 \\ d_{min} & \text{if } r > 1 \end{cases} \tag{A.2}$$

where r is the ration, b_{max} is the maximum probability per year of having offspring, and d_{min} is the minimum probability per year of dying.

Now let's get programming! You'll be writing three programs: **`simulate.cpp`**, **`visualize.cpp`**, and **`analyze.cpp`**. The first will simulate the population's growth, the second will help visualize the results, and the third will do some statistical analysis on them.

Program 1: Simulating Population Growth

Your first job will be to write a program named **`simulate.cpp`** that simulates the growth of the population over some number of years and writes its results into a file.

Théodore Géricault's *The Raft of the Medusa* (1818-1819).

Source: Wikimedia Commons

Our simulation program's strategy will be this: We'll give the program an initial population, the total amount of food, the values of b_{max} and d_{min}, and tell it how many years to simulate. The program will then loop through the years, one at a time. For each year it will loop through all of the individuals in the population. For each person, the program will check to see whether the person has offspring during that year and whether the person dies during that year, using the $b(r)$ and $d(r)$ functions in Equations A.1 and A.2 above. If the person dies, the population will be reduced by one. If the person has offspring, the population will increase by one[16].

[16] for simplicity, we're assuming one child per person per year, at most.

The program should accept all of its parameters on the command line, as described in Section 9.15 of Chapter 9. The usage should be:

```
./simulate population food bmax dmin nyears outfile
```

where:

- `population` is the initial population.
- `food` is the total amount of food the island can produce, in terms of the number of people who can be well-fed.
- `bmax` is b_{max} from Equation A.1 above.
- `dmin` is d_{min} from Equation A.2 above.
- `nyears` is the number of years to simulate.
- `outfile` is the name of a data file into which the program will write its results.

To get you started, I've already written some of the program for you (see Program A.11). All you need to do is complete the program by filling in `main` and the two functions `birthprob` and `deathprob`. Notice that I've added a handy function named `rand01` near the top of the program[17]. It can be used to generate a random number between zero and one.

[17] This function is described in Section 11.4 in Chapter 11.

Program A.11: simulate.cpp

```
#include <math.h>
#include <stdlib.h>
#include <time.h>
#include <stdio.h>

double rand01 () {
  static int needsrand = 1;
  if ( needsrand ) {
    srand(time(NULL));
    needsrand = 0;
  }
  return ( rand()/(1.0+RAND_MAX) );
}

double birthprob ( double bmax, double ration ) {
        // Insert function here.
}

double deathprob ( double dmin, double ration ) {
        // Insert function here.
}

int main ( int argc, char *argv[] ) {
  double population;
  double popgrowth;
  int nyears;
  int year;
  int individual;
  double food;
  double ration;
  double bmax, dmin;
  double bprob, dprob;
  FILE *output;

  // Insert program here.
}
```

To complete the program, you'll need to add code to do the following:

1. Check to make sure the user has supplied enough command-line arguments. If there aren't enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else[18].

[18] See Section 9.16 of Chapter 9 for an example of how to do this.

2. Convert the command-line arguments into the variables `population`, `food`, `bmax`, `dmin`, and `nyears` by using the **`atoi`** and **`atof`** functions. The last command-line argument (the output file name) doesn't need to be converted. You can just use it directly, like this:

```
output = fopen( argv[6], "w" );
```

3. Your program will need a pair of nested "`for`" loops: An outer loop that goes through all the years, and an inner loop that goes through all of the individuals in the population and, for each one, checks to see whether that person died or had offspring during the current year.

   The outer loop might start like this:

   ```
   for ( year=0; year<nyears; year++ ) {
   ```

   and the inner loop might start like this:

   ```
   for ( individual=0; individual<population; individual++ ) {
   ```

Crowded Boardwalk, Atlantic City, New Jersey (1910).
Source: Wikimedia Commons

4. At the beginning of each year the program will need to do a few things:

   - Find the `ration` by dividing `food` by `population`
   - Find the probability of having offspring, which we'll call `bprob`, by using the `birthprob` function defined at the top of the program (we'll describe this and the `deathprob` function below).
   - Find the probability of dying, which we'll call `dprob`, by using the `deathprob` function defined at the top of the program.
   - Set `popgrowth` to zero. We'll use this variable to keep track of how much the population grows during the current year. (If there are more deaths than births, this number might be negative, but that's OK.)

5. Inside the inner loop we'll do some things for each individual who's currently in the population:

   - Check to see if that person had offspring during the year. We do this by using the `rand01` function to give us a random number between zero and one, and then checking to see if that number is less than `bprob`. If it is, then we add 1 to `popgrowth`, indicating that a person has been added to the population this year.
   - Similarly, we check to see if the person died this year. We do this by looking to see if `rand01` gives us a number less than `dprob`. If it does, then we subtract 1 from `popgrowth`, indicating that a person has been removed from the population. (Remember that it's OK for `popgrowth` to be negative.)

6. At the end of each year, we add `popgrowth` to `population` to get

the new value for `population`, and we write data about this year into our output file. The values of `year`, `population`, `popgrowth`, `bprob`, `dprob`, and `ration` should be written to the file, in that order, separated by spaces[19].

[19] See Chapter 5 for information about writing data into a file.

7. The last step in completing the program is to write the two functions `birthprob` and `deathprob`. The `birthprob` function takes the value of `bmax` and `ration` and uses the relationship shown in Equation A.1 to calculate the birth probability. Similarly, `deathprob` uses `dmin` and `ration` to calculate the death probability, as given by Equation A.2. Note that you'll need an `if/else` statement in each of these functions, to deal with the cases when `ration` is less than one or greater than one.[20]

Edoardo Matania, *Die geschlossene Bank* (1870s).
Source: Wikimedia Commons

After you've completed your program, compile it and run it three times, with these arguments:

```
./simulate 2000 1000 0.0182 0.0077 1000 hipop.dat
./simulate  500 1000 0.0182 0.0077 1000 medpop.dat
./simulate  100 1000 0.0182 0.0077 1000 lopop.dat
```

[20] See Chapter 3 for information about writing `if/else` statements, and Chapter 9 for information about writing functions.

The three simulations are the same except for the starting population. In the first one, the initial population is higher than the amount of food available in the environment (2,000 people, but only food enough for 1,000). The second simulation has an initial population of 500, with the same amount of food, and the third simulation shows what happens when the initial population is only 100. The values used for `bmax` and `dmin` are actual current worldwide average values for birth and death rates in human populations[21]. Each of the simulations tracks the population growth over a period of 1,000 years.

[21] CIA World Factbook, estimated values for 2018.

You can plot your results by giving *gnuplot* the command:

```
plot [0:300] "hipop.dat" with lines, "medpop.dat" with lines, "lopop.dat" with lines
```

which shows just the first 300 years. The result should look something like Figure A.39. Notice that, in all cases, the population eventually settles down to a stable level that's slightly greater than 1,000 individuals.

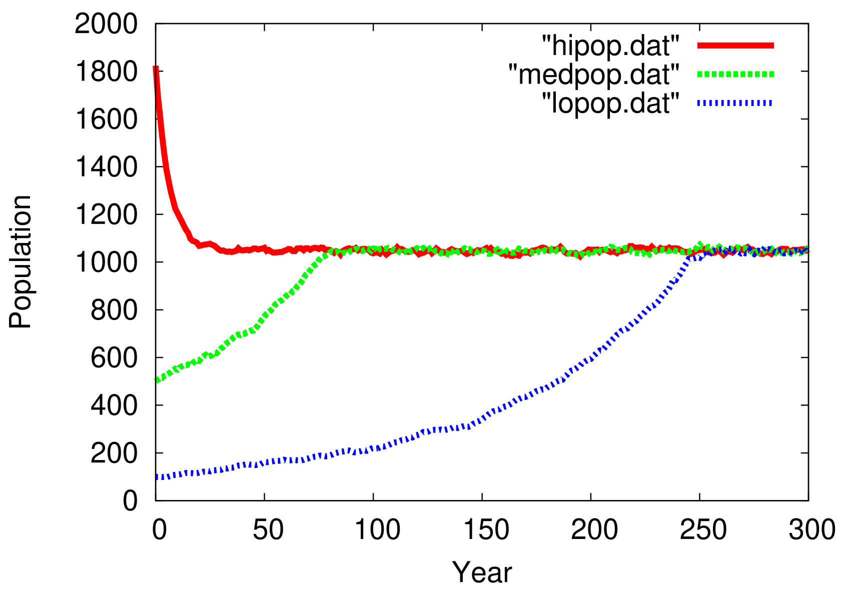


Figure A.39: Population growth when there is sufficient food for 1,000 people, starting with populations of 100, 500, and 2,000 people.

Program 2: Visualizing the Stable Population

So now we know that the island's population always tends toward a particular value, but what is that value exactly? Let's start to investigate this by writing a program to visualize the data from our simulations in a different way. The program will be called **visualize.cpp** and it will let you make graphs like the one shown in Figure A.40. This graph shows population on the horizontal axis, divided into 50 bins. The vertical axis shows how many years had a population within each bin.

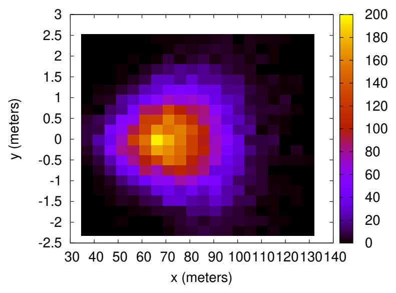


Figure A.40: Histogram of population values from `lopop.dat`.

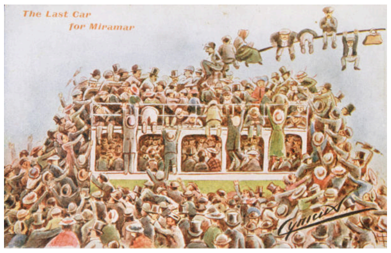
This figure is a histogram, like the ones we discussed in Chapter 7. Your program will be similar to Program 7.1 in that chapter. Again, to get you started, I've written part of the program for you (see Program A.12 below). Notice that I've defined a 50-element array, `bin`, to hold the histogram data.

Program A.12: visualize.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
int main ( int argc, char *argv[] ) {
  const int nbins=50;
  int bin[nbins];
  double binwidth;
  int binno;
  int overunderflow=0;
  int i;
  FILE *input;
  FILE *output;

  // Insert program here.

}
```



"Cynicus", *The last car for Miramar* (c. 1910).
Source: Wikimedia Commons

Like the preceding program, this one will expect parameters on its command line, and should complain and exit if it doesn't get the proper number of parameters. Its usage will be:

```
./visualize popmin popmax inputfile outputfile
```

where `popmin` and `popmax` are the minimum and maximum population you want to include in your histogram, `inputfile` is the name of a file produced by your `simulate.cpp` program, and `outputfile` is a file into which your new program will write the histogram data.

The input and output files can be opened like this[22]:

```
input  = fopen(argv[3],"r");
output = fopen(argv[4],"w");
```

[22] Notice that we open one file for reading (with `"r"`) and the other for writing (with `"w"`).

The output file should contain two columns of numbers, separated by a single space. Unlike Program 7.1, the first column here will contain a population value instead of a bin number (see below for instructions about converting bin number to population). The second column will be the number of years in that bin.

To make the histogram, the program should proceed as follows:

1. First, determine the `binwidth`, like this:

   ```
   binwidth = (popmax-popmin)/nbins;
   ```

2. Next, use a `while` loop to read data from the input file[23]. Each line of the file will contain six values: `year`, `population`, `popgrowth`, `bprob`, `dprob`, and `ration`. The first value is an integer, and the other five are `double`s.

[23] See Chapter 5 for information about reading data from files.

3. Determine which bin this population value belongs in, and increment that bin. Be sure to keep a count of the number of over/underflows, as Program 7.1 does. Since the range of our histogram is `popmin` to `popmax`, the bin number will be:

   ```
   binno = (population-popmin)/binwidth;
   ```

4. After processing all of the input data, write the histogram data into the output file. For each bin of the histogram, write two numbers separated by a single space: the population value represented by that bin, and the value of `bin[i]`. The population value can be calculated from the bin number, like this:

   ```
   population = popmin + binwidth*(0.5+i);
   ```

where `i` is the bin number.

5. Finally, at the bottom of the output file, write a line beginning with a # that tells how many overflows or underflows were seen.

Run your program like this to make a histogram of the data you produced earlier. Start out by looking at population values between 0 and 1,100:

```
./visualize 0 1100 lopop.dat visualize.dat
```

You can plot the resulting data file with *gnuplot* like this:

```
plot "visualize.dat" with impulses lw 5
```

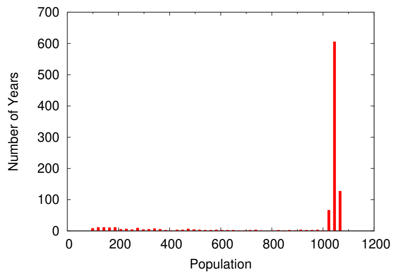


Figure A.41: A histogram of population values from `lopop.dat` in the range 0 to 1,100.

The graph should look like Figure A.41. Now let's zoom in on the region around a population of 1,000 by running your visualize program again, this time setting `popmin` to 1,000 and `popmax` to 1,100:

```
./visualize 1000 1100 lopop.dat visualize.dat
```

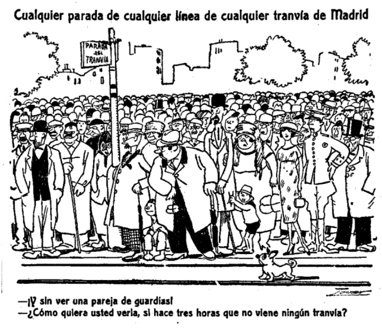
You can plot the resulting data file with *gnuplot* like this:

```
plot "visualize.dat" with impulses lw 5
```

The result should look like Figure A.40 at the beginning of this section.

As you can see, the population values cluster around 1,040 or so, slightly above the 1,000 individuals that can be fully fed. Think for a minute about what this means: We're finding that the population tends to settle in at a level where there's not quite enough food to go around. This raises the death rate and lowers the birth rate until the two rates are equal. In your final program you'll find an exact value for this equilibrium population.

Program 3: Finding the Mean and Standard Deviation


Cualquier parada de cualquier línea de cualquier tranvía de Madrid
PARADA DEL TRANVÍA
—¡Y sin ver una pareja de guardias!
—¿Cómo quiera usted verla, si hace tres horas que no viene ningún tranvía?

Manuel Tovar Siles, *"Any stop of any line of any tramway of Madrid"* (1920).
Source: *Wikimedia Commons*

Your third program will be named **`analyze.cpp`**. It will read a data file produced by your first program, and give you a statistical summary of the data it contains.

Like the first two programs, `analyze` should accept all of its parameters on the command line, and give users a helpful message if they don't give it the right number of arguments. The usage should be:

```
./analyze popmin popmax inputfile
```

where `popmin` and `popmax` delimit the range of population values you're interested in, as they do in your preceding program, and `inputfile` is the name of a data file produced by your `simulate.cpp` program.

The output of the `analyze` program should look like this:

```
Mean population = 1046.245636
Std. dev. = 9.590271
```

Again, I've written some of the program for you (see Program A.13). You'll just need to fill in `main`.

Program A.13: analyze.cpp

```
#include <stdio.h>
#include <math.h>
#include <stdlib.h>
int main ( int argc, char *argv[] ) {
  int year;
  double population, popgrowth;
  int popmin, popmax;
  double dprob, bprob, ration;
  double sum=0;
  double sum2=0;
  double mean, stddev;
  int nvalues=0;
  FILE *input;

  // Insert program here.

}
```

To analyze the data, the program should proceed as follows:

1. First, open the data file for reading. See Program 7.5 in Chapter 7 for an example of this. Refer to that program to see how to read the data and calculate the average and standard deviation.
2. Like your `visualize.cpp` program, this new program should use a `while` loop to read data from the input file. Each line of the file will contain six values: `year`, `population`, `popgrowth`, `bprob`, `dprob`, and `ration`.
3. Unlike Program 7.5, our new program will need to check to see whether a population value is between `popmin` and `popmax` before adding it to `sum` and `sum2`.

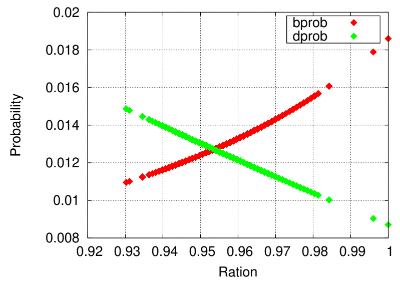


Figure A.42: `bprob` and `dprob` versus `ration`, from our `lopop.dat` simulation.

If you run your program like this:

```
./analyze 1000 1100 lopop.dat
```

you should see that the mean population value is about[24] 1,046, which corresponds to a ration of $1,000/1,046$ or about 95.6%. If we plot our simulation's birth and death probabilities versus ration, using *gnuplot* commands like this:

[24] The value you see will vary, because the simulation uses random numbers

```
set xrange [0.92:1]
set yrange [0.008:0.02]
plot "lopop.dat" using 6:4, "" using 6:5
```

(column 6 of our output file is `ration`, column 4 is `bprob` and column 5 is `dprob`) we would see something like Figure A.42. This confirms that birth probability and death probability are equal when the ration is around 95.6%, the ration where our analysis shows that our population is stable.

Thomas Malthus (left) and Charles Darwin.

Conclusion

In 1798, English scholar Thomas Robert Malthus wrote *An Essay on the Principle of Population*, in which he observed that English populations were growing more rapidly than the increase in agricultural production. Malthus anticipated the phenomenon we've explored in this project: Populations tend to grow to the point where resources are no longer sufficient for everyone, causing death rates to increase and birth rates to decline until the population stabilizes. Malthus's ideas about competition for scarce resources were an inspiration for Charles Darwin's theory of evolution by natural selection.

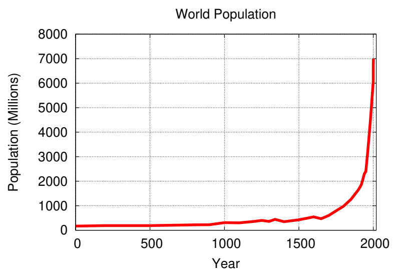


Figure A.43: World population growth.
Source: Wikimedia Commons

Such plateaus in population have occurred many times in human history, but have typically been temporary and limited to a geographic region. In Malthus's time, for example, England was heading for a shortage of food, while Russia had an overabundance of agricultural capacity. Malthus expected these shortages to last only until new agricultural land had been developed, or until improvements in agriculture increased the yield of existing land.

Arnold Böcklin, *The Isle of the Dead*, third version (1883) and *The Isle of the Living* (1888).
Source: Wikimedia Commons and Wikimedia Commons

Globally, the human race has shown no slowing of its exponential growth rate (see Figure A.43). So far, development of new land and improvements in agricultural science have, on average, kept ahead of population growth, but humans also depend on fresh water, shelter, and other limited resources. Some people estimate[25] that the global

[25] See https://en.wikipedia.org/wiki/Planetary_boundaries.

population already exceeds the Earth's carrying capacity[26].

What will happen to our islanders? Will they find a clever way to avoid a "Malthusian crisis?" Let's wish them luck, and the same for the inhabitants of this island Earth.

[26] Apparently we're not running short of physical space. John Brunner's novel Stand on Zanzibar notes that 7 billion people (the current population of Earth) could fit on the island of Zanzibar – if they stood shoulder to shoulder!

Project 5: Yard Sale!

Introduction

Every August a 630-mile-long yard sale stretches from Michigan to Alabama along US Highway 127. It's called the "World's Longest Yard Sale". Thousands of people visit it. In the early 21st century Economists began to realize that yard sales like this provide a good model for the whole world's economy. By simulating the interactions between buyers and sellers at such a sale, we can make predictions about wealth distribution that match data observed in the real world. The trick is to assume that the economy is made up of many, many one-to-one interactions where a buyer and a seller exchange some wealth.

Source: Wikimedia Commons

Economists gauge a person's wealth by looking not just at how much money you have, but also the value of the goods you own. Imagine that I'm a vendor at the yard sale and you're a shopper. If you pay me five dollars for a toaster, an economist would traditionally have said that there was no net change in either person's wealth: I have your five dollars, but you now have a toaster worth five dollars.

Source: Wikimedia Commons

But is it really? What if, when you get home, you find that the toaster doesn't work. Then you really have a toaster worth less than five dollars, but I still have your money. We could say that you've lost some wealth by giving me five dollars and getting something worth less than that, and I've gained some wealth by getting five dollars in exchange for a worthless toaster. In that case, wealth has flowed from you to me, making you poorer and me richer.

This happened because you mis-judged the value of the toaster. Traditionally, economists have assumed that shoppers are good at judging the value of things, and economic models have used this assumption to make predictions about the economy. But recently economists have become interested in models that take into account the fact that buyers and sellers often make mistakes about the value of things. A seller might sell a "worthless" painting for five dollars, only to find later that it's a valuable Picasso, or a buyer might pay a lot of money for a "Rolex" watch only to find that it's a cheap knock-off.

Anirban Chakraborti, who first proposed the "yard sale" model of economics in 2002.

The mistakes we make are usually small, but we probably always make some small error when we assign a value to something we buy or sell. The effect of this is that wealth flows around the economy, with some people becoming more wealthy than others. If everyone had an equal chance of gaining or losing an equal amount because of these mistakes, we might assume that, on average, they don't matter, and that any inequalities of wealth would even out over time. But the yard sale models that Economists have developed, and which match real-world economic data, make an additional assumption: They assume that the biggest possible mistake in each transaction is the total wealth of the *poorest* person involved in the transaction. (A person with only one dollar can't buy the five-dollar toaster, no matter whether the toaster is broken or not.) By doing this we're ignoring people who win the lottery or accidentally sell a Picasso for five dollars, but it turns out that those situations are rare and don't have much effect on the economy as a whole[27].

[27] These models also assume that wealth of any kind can be exchanged. I can pay you five dollars for that toaster, or I can trade you a record player for it. My wealth includes both the money I have and the value of the items I own.

In this project we're going to write three programs that investigate such a yard-sale model of the economy. The first program (**`simulate.cpp`**) will simulate lots of interactions between buyers and sellers. The second (**`visualize.cpp`**) will visualize the distribution of wealth after some time has passed. The third (**`analyze.cpp`**) will analyze the data and boil it down to a single number that measures how evenly wealth is distributed. Let's get started!

Program 1: Buyers and Sellers

Our first program will be named **`simulate.cpp`**, and it should start out like Program A.14 below. The program will simulate many random transactions between pairs of people, and track the wealth flowing from person to person. We'll assume everybody starts out with the same amount of wealth.

How the Program Works

The program should accept three parameters on the command line: The initial wealth of each person, the number of transactions we want

Program A.14: simulate.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <time.h>
int main ( int argc, char* argv[] ) {
  const int N = 10000;  // Number of people.
  double wealth[N];     // Wealth of each person.
  double wstart;        // Starting wealth of each person.
  double mistake;       // Size of a mistake.
  double flip;          // A random number, used for deciding who made the mistake.
  double ntransactions; // Number of transactions.
  int alice, bob;       // The two people involved in a transaction.
  int poor;             // which of the two people is poorer.
  int i;
  FILE *output;

  srand( time(NULL) );  // Set the seed of the random number generator.

  // Put the rest of the program here!

}
```

to simulate, and the name of a file we want to write our results into. For example:

```
./simulate 100 2e+5 output.dat
```

The first number is the initial wealth of each person, the second is how many transactions we want to simulate[28], and the final argument is the name of the output file we want to create.

[28] This number is in C-style scientific notation. In this example, we've used `2e+5` which is 2×10^5, or 200,000. See Section 4.3 of Chapter 4.

The program should assume that this is a very big yard sale, with 10,000 people swapping money and goods. That's the population of a small town or a rural county. To keep track of how much wealth each person has, it should use an array with 10,000 elements. The wealth of person number `i` will be `wealth[i]`. A person's wealth will generally be a number with decimal places, so `wealth` will need to be an array of `double`s.

We'll start each person out with the same amount of wealth. Let's call it `wstart`. After setting the initial wealths, the program should enter a loop that simulates some number of random transactions. For each transaction, we'll pick two people at random. Let's call them `alice` and `bob`, and their wealths will be `wealth[alice]` and `wealth[bob]`.

After we've picked two people, we need to see which one is poorer by comparing their wealths. Let's have another variable, `poor`, and say that if Alice is poorer, `poor=alice` and if Bob is poorer, `poor=bob`.

Now assume that somebody makes a mistake in the transaction. Remember that we're limiting the size of the mistake to the wealth of the poorer person, so at most the mistake will be `wealth[poor]`. Let's say that the size of the mistake is a random number between zero and one, multiplied by `wealth[poor]`.

Aaah, wealth! (Portuguese actor António Silva portraying a wealthy man)
Source: Wikimedia Commons

Then we "flip a coin" to decide which person, Alice or Bob, benefits from this mistake. We do this by generating a random number between zero and one. If this number is greater than 0.5 Alice wins, otherwise Bob wins. If Alice wins, the amount of the mistake is added to her wealth and subtracted from Bob's wealth. If Bob wins, the mistake is added to his wealth and subtracted from Alice's.

After the program has done the requested number of transactions, it should write the final wealth of each person into the file specified on the command line. The output file should have two columns separated by a space: person number and the wealth of that person.

How to Write the Program

To get you started, Program A.14 shows part of `simulate.cpp`. It includes all of the variables you'll need. You just need to write the middle part, where all the work gets done. To complete the program, you'll need to add code to do the following:

1. Check to make sure the user has supplied enough command-line arguments. If there aren't enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else[29].

[29] See Section 9.16 of Chapter 9 for an example of how to do this.

2. Convert the command-line arguments into the variables `wstart` and `ntransactions` by using the **`atof`** function[30].The last command-line argument (the output file name) doesn't need to be converted. You can just use it directly, like this:

   ```
   output = fopen( argv[3], "w" );
   ```

[30] Notice that we've chosen to make `ntransactions` a `double`, even though it will always have some integer value. That's because we'll be using large numbers of transactions, and it's convenient to write things like `1e+7` instead of `10000000`, so we don't have to carefully count zeros. C only lets you use scientific notation with `double`s.

3. Next you'll need a "`for`" loop to set the initial wealth of each person to `wstart`.

4. Then you'll need a second "`for`" loop that goes through `ntransactions`

transactions. During each transaction the program will need to do several things:

(a) Pick two random people to be Alice and Bob for this transaction. You might do something like this:

```
alice = rand()/(1.0+RAND_MAX) * N;
bob   = rand()/(1.0+RAND_MAX) * N;
```

Notice that this generates a random number between zero and (almost) one, and then multiplies it by `N`, the total number of people [31].

[31] On rare occasions, at random, it will turn out that "Alice" and "Bob" are the same person, but we won't worry about that. It happens rarely, and it won't affect the results.

(b) Then we need to use an "`if`" statement to check which person has the smaller wealth. Set the variable `poor` to equal either `alice` or `bob`, as appropriate.

(c) Next the program needs to determine a random size for the mistake that's made in this transaction. Remember that it should be an amount between zero and `wealth[poor]`. One way to do this is:

```
mistake = wealth[poor]*rand()/(1.0+RAND_MAX);
```

(d) As the last thing in the loop the program should "flip a coin" to see whether Alice or Bob gets the benefit of the mistake. To do this, generate a random number between zero and one, and then use an "`if`" statement to see if it's greater than 0.5. If it is, then Alice wins. Transfer `mistake` amount of wealth from the loser to the winner.

5. After the loop is done, the program should write its results into a file[32]. This should be done with a third "`for`" loop. For each person, there should be one line in the file with two numbers separated by a space. For person "`i`" the numbers should be `i` and `wealth[i]`.

[32] See examples like Program 5.3 in Chapter 5.

Running the Program

After you've created the program, run it several times to make some output files that you'll use with the next two programs. Try these commands:

```
./simulate 100 0 simulate-0.dat
./simulate 100 1e+4 simulate-10K.dat
./simulate 100 1e+6 simulate-1M.dat
./simulate 100 1e+9 simulate-1G.dat
```

Those commands will create four output files representing a starting wealth of $100 for each person, and simulating 0 transactions, 10 thousand transactions, then 1 million and 1 billion transactions. If you look inside any of these files with *nano* you should see two columns of numbers. The first column will be the person number (an integer) and the second column will be that person's wealth (a number with decimal places) after the specified number of transactions. You can graph the results with *gnuplot* if you like, using *gnuplot* commands like:

```
plot "simulate-1M.dat" with impulses
```

You should see graphs like the ones in Figure A.44.

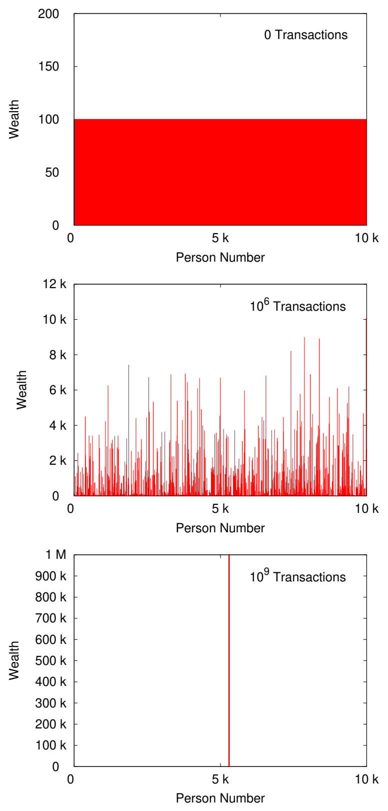


Figure A.44: The top graph shows the distribution of wealth after 0 transactions. Everybody has the same amount of money ($100). The middle graph shows the situation after 1 million transactions. Now some people have a lot more wealth than others. The bottom graph show the situation after 1 billion transactions. Now one random, lucky person has *all* of the money, and everyone else has nothing!

Look at what happens as the number of transactions increases. At zero transactions everybody has the same amount of money. After a million transactions wealth has spread around, and some people have thousands of dollars. This isn't too surprising. But after a billion transactions we find that one lucky person has *all* of the money, and nobody else has any! If you run this billion-transaction simulation several times, you'll find that one person always ends up with all the money, but it will be a different person each time.

That's something that economists have found to be an inescapable property of the yard sale model: If you let it run long enough one person inevitably ends up with all the wealth.

Program 2: Visualizing at the results

Let's take a closer look at how our simulation distributes wealth. To investigate this, we might make a graph that shows wealth across the bottom, divided into equal-sized ranges like $0-$25, $25-$50, $50-$75, and so on. On the vertical axis we could show how many people have a wealth in each range. We learned in Chapter 7 that a graph like this is called a histogram.

The next program you'll write is named **`visualize.cpp`** and it will make histograms of the simulated wealth data created by your first program. The new program will be similar to Program 7.1 in Chapter 7. It should start out like Program A.15 below.

Program A.15: visualize.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
int main ( int argc, char *argv[] ) {
  const int nbins=100;
  int bin[nbins];      // How many people are in each wealth range.
  double binsize;      // Width of wealth ranges.
  int n;               // "Person number".
  double wealth;       // Wealth of that person.
  double maxwealth;    // Maximum wealth we want to graph.
  int binno;           // Bin number for a person, based on person's wealth.
  int overunderflow=0; // How many people were outside the range of the graph?
  int i;
  FILE *input;
  FILE *output;

  // Insert program here.

}
```

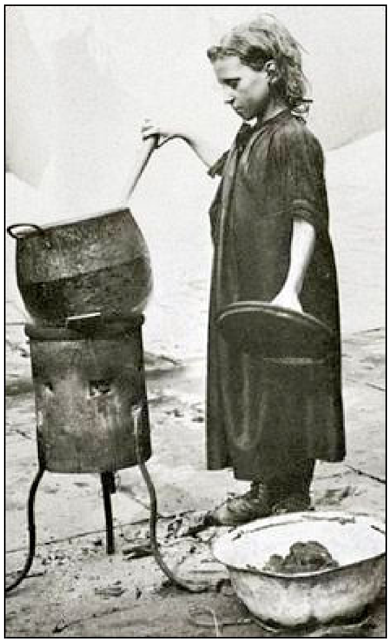
How the Program Works

Like the preceding program, this one will expect parameters on its command line, and should complain and exit if it doesn't get the proper number of parameters. Its usage will be:

```
./visualize maxwealth input.dat output.dat
```

where `maxwealth` is the maximum wealth you want to include in your histogram, `input.dat` is the name of a file produced by your `simulate.cpp` program, and `output.dat` is a file into which your new program will write the histogram data.

The output file should contain two columns of numbers, separated by a single space. Unlike Program 7.1, the first column here will contain a wealth value instead of a bin number (see below for instructions about converting bin number to wealth). The second column will be the number of people who have that amount of wealth.


Postcard: "Youth poverty at the beginning of the 20th century in Europe."
Source: Wikimedia Commons

How to Write the Program

To make the histogram, the program should proceed as follows:

1. Check to make sure the user has supplied enough command-line arguments. If there aren't enough command-line arguments, the

program should print out a friendly usage message and then stop without trying to do anything else.

2. Convert the first command-line argument into the variable `maxwealth` by using the **`atof`** function. The other two command-line arguments (the input and output file names) don't need to be converted. The input and output files can be opened like this[33]:

```
input  = fopen(argv[2],"r");
output = fopen(argv[3],"w");
```

[33] Notice that we open one file for reading (with `"r"`) and the other for writing (with `"w"`).

3. Next, determine the `binwidth`, like this:

```
binwidth = maxwealth/nbins;
```

4. Use a "`for`" loop to set all the elements of `bin` to zero.

5. Now use a `while` loop to read data from the input file[34]. Each line of the file will contain two values: A person number and that person's wealth. The first value is an integer, and second is a `double`.

[34] See Chapter 5 for information about reading data from files. In particular, look at Program 5.4.

6. Determine which bin each person's wealth value belongs in, and increment that bin. Be sure to keep a count of the number of over/underflows, as Program 7.1 does. Since the size of each bin is `binwidth`, the bin number will be:

```
binno = wealth/binwidth;
```

7. After processing all of the input data, write the histogram data into the output file. For each bin of the histogram, write two numbers separated by a single space: the first number is the wealth value represented by that bin, and the second is the value of `bin[i]`. The wealth value can be calculated from the bin number, like this:

```
wealth = binwidth*(0.5+i);
```

where `i` is the bin number. This will give you the wealth at the midpoint of that bin's wealth range.

8. Finally, at the bottom of the output file, write a line beginning with a `#` that tells how many overflows or underflows were seen.

After you've written the program, run it a few times like this to create histograms from the files you created previously, limiting the graph to a maximum wealth of $2,500:

```
./visualize 2500 simulate-0.dat visualize-0.dat
./visualize 2500 simulate-10K.dat visualize-10K.dat
./visualize 2500 simulate-1M.dat visualize-1M.dat
./visualize 2500 simulate-1G.dat visualize-1G.dat
```

You can use *gnuplot* to view the histograms by giving it commands like:

```
set log y
set yrange [0.1:]
plot "visualize-10K.dat" with impulses
```

This will draw a vertical line for each wealth range, with the height of the line indicating the number of people who have a wealth in that range. The first command makes the Y-axis logarithmic. If we didn't do this, we wouldn't be able to the bins that only have a few people in them. Your graphs should look something like the ones shown in Figure A.46.

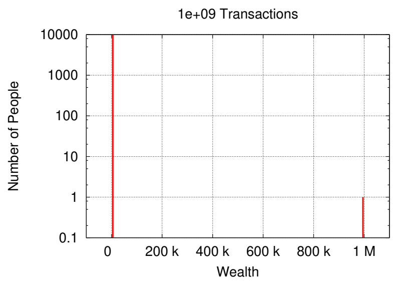


Figure A.45: Wealth distribution after 1 billion transactions, showing wealth up to $1 million.

You can see that the data in the last graphs is starting to run off the right-hand edge of the graph. The total amount of money in our population is $1 million ($100 per person × 10,000 people). Let's graph the data from our longest simulation using this as `maxwealth`. To do that, run your `visualize` program again, like this:

```
./visualize 1000000 simulate-1G.dat visualize-long-1G.dat
```

This extends the wealth scale out to $1,000,000. If you graph the new file with *gnuplot* (again using a logarithmic Y-axis) you should see something like Figure A.45.

This is another way of seeing that only one person ends up with all of the money. The short spike on the right-hand side represents the one person who now has 1 million dollars. The tall spike on the left-hand side is everyone else, with zero dollars[35].

[35] Sometimes after a billion transactions you'll find that there are still two people who have some money. After more transactions, though, one of them always ends up with all of the money.

Program 3: Quantifying Wealth Inequality

Our simulated economy produces severe wealth inequality, but how does it compare to real-life economies? How can we measure the amount of wealth inequality? One way of quantifying it is called the "Gini Coefficient[36]".

[36] See https://en.wikipedia.org/wiki/Gini_coefficient.

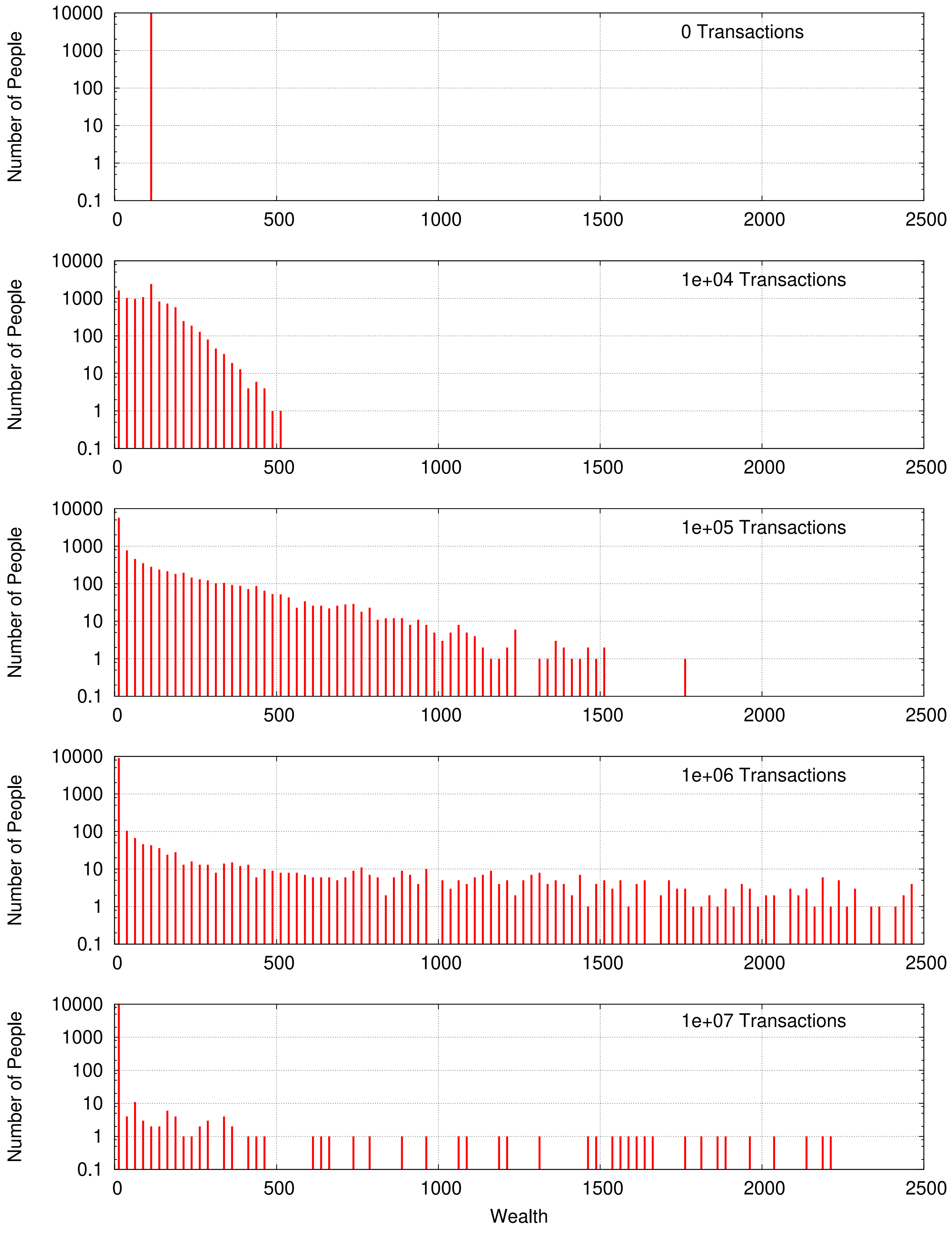


Figure A.46: Histograms of wealth after different numbers of transactions.

The Gini Coefficient starts by measuring the average difference in wealth between any two individuals in the population. (It ignores the sign of this difference by taking the absolute value.) Then it divides the result by the total amount of wealth in the population. A Gini Coefficient of zero corresponds to an economy where everybody has the same amount of wealth. A value of one corresponds to an economy where a single person has all the wealth, and everyone else has nothing. Real-life economies fall somewhere between these two extremes.

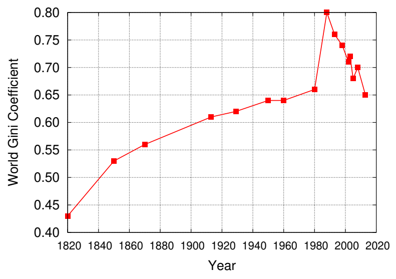


Figure A.47: Estimated world-wide Gini Coefficient, by year. See Milanovic and World Bank in the "Further Reading" section below.

Researchers at the World Bank have estimated values for the world-wide Gini Coefficient for various years, beginning with 1820 (see Figure A.47). The value seems to have risen to a peak of about 0.8 in the 1980s and then begun a downward trend. The current value is about 0.65[37]. Your third program, **`analyze.cpp`**, will read the data produced by your simulation and calculate the Gini Coefficient for your simulated economy.

[37] Note that some writers refer to the "Gini Index", which is just 100 times the Gini Coefficient. That means the current world-wide Gini Index is about 65.

How the Program Works

Like the first two programs, this one should accept arguments on the command line. In this case, there will be just one argument: the name of a data file produced by your `simulate.cpp` program. For example, you should be able to run your latest program like this:

```
./analyze simulate-10K.dat
```

Your program should start by reading the data from the data file and putting it back into a 10,000-element array called `wealth`, just like the array you used in your first program.

Next your program will need to add up the total wealth of all of the people. You'll need this later for calculating the Gini Coefficient.

"Children sleeping in Mulberry Street" (detail), by Jacob Riis (1890).
Source: Wikimedia Commons

After that, you'll need to go through each pair of people in the population, find the difference in their income, and add its absolute value to a sum. You should do this with two nested "`for`" loops. Once the wealth differences have all been added up, you can use that sum and the total wealth to calculate the Gini Coefficient. Mathematically, the Gini Coefficient is defined as:

$$\texttt{gini} = \frac{\sum_{\texttt{i}}\sum_{\texttt{j}} |\,\texttt{wealth[i]} - \texttt{wealth[j]}\,|}{2\texttt{N}\sum_{\texttt{i}} \texttt{wealth[i]}}$$

Program A.16 below shows how your program should start. It contains all the variables you'll need. You just need to fill in the rest of the program.

Program A.16: analyze.cpp

```
#include <stdio.h>
#include <stdlib.h>
#include <math.h>
int main ( int argc, char* argv[] ) {
  const int N = 10000;  // Number of people.
  double wealth[N];     // Wealth of each person.
  double sum = 0;       // Sum of all the wealth.
  double sumdiff = 0;   // Sum of wealth differences between pairs of people.
  double gini;          // Gini coeffficient.
  int n;                // ``Person number''
  int i,j;
  FILE *input;

  // Add the rest of the program here.
}
```

How to Write the Program

1. Check to make sure the user has supplied enough command-line arguments. If there aren't enough command-line arguments, the program should print out a friendly usage message and then stop without trying to do anything else.
2. The only command-line argument (the input file name) doesn't need to be converted. You can just use it directly, like this:

   ```
   input = fopen( argv[1], "r" );
   ```
3. Next you'll need a "`for`" loop that repeats 10,000 times (the value of `N` in the program) and reads one line out of the input file each time. The input file has two columns of data: the person number and that person's wealth. That means you should have a statement like this for reading a line from the input file:

   ```
   fscanf( input, "%d %lf", &n, &wealth[i] );
   ```
   As you read each `wealth` value, add it to the value of `sum`. This will give you the sum of all the wealth in the population, which you'll need later for calculating the Gini Coefficient.
4. Now the program needs to find the difference in wealth between each pair of people in the population. To do this you'll need a pair of nested "`for`" loops. Use the `fabs` function to get the absolute value of the wealth difference, and then add it to `sumdiff` like this:

   ```
   sumdiff += fabs( wealth[i] - wealth[j] );
   ```

Note that this will actually count each pair of people twice. For example, if `i` is 20 and `j` is 30, the sum will include both `wealth[20] - wealth[30]` and `wealth[30] - wealth[20]`. We'll take care of this later by dividing `sumdiff` by 2 when doing the Gini Coefficient calculation.

5. Finally, the program just needs to calculate the Gini Coefficient and print it out. The Gini Coefficient will be equal to `sumdiff/( 2.0*N*sum )`.

The Gini Coefficient calculated by your program will be a value between zero and one. If you run it with your simulation data for 10,000 transactions, like this:

```
./analyze simulate-10K.dat
```

you should see a Gini Coefficient of about 0.37. If you run it with the simulation data for 1 billion transactions, the value should be much higher, almost 1.0. Figure A.48 shows how the Gini Coefficient varies with the number of transactions. As you can see, it approaches a value of one for large numbers of transactions, meaning that only a few people end up with all of the wealth.

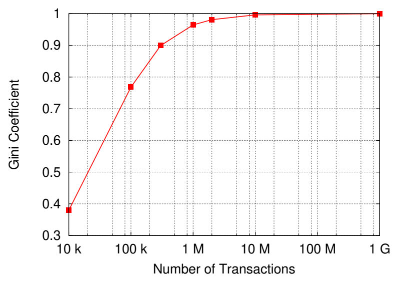


Figure A.48: Gini Coefficient calculated for various numbers of transactions using our yard sale simulation.

Conclusion

So what does this model of economics tell us about the real world? Although there is great inequality of wealth (for example, five billionaires now have more wealth than the poorest half of humanity combined), it seems unrealistic that one person would end up with all of it.

The yard sale model seems pretty simple. It just makes two assumptions: pairs of people exchange wealth, and poor people can't spend more money than they have. Why does it make a prediction that's so different from what we see in the world around us? Clearly there's some factor that we're leaving out of our model.

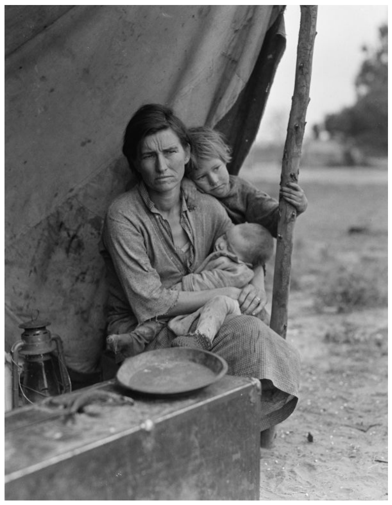
It might seem that everybody at the yard sale has an equal opportunity to gain wealth, and at first they do. Initially wealth is distributed evenly among all of them, with perfect symmetry. But this initial symmetry is spontaneously broken as soon as some people become a little poorer than others. Poorer people in the model are always at an economic disadvantage because poverty limits the size of the economic risks they can take. This creates a tendency for the rich to get richer and the poor to get poorer, causing the yard sale model to inevitably collapse into oligarchy.

Why doesn't this happen in the real world? Mathematician Bruce Boghosian at Tufts University and his economist colleagues have shown that by transferring a small fraction of wealth from rich people to poor people after each transaction, the yard sale model's wealth distribution can be stabilized. In the real world, this corresponds to the wealth redistribution that's done by taxes and social programs.

Lou Hoover, First Lady of the United States, with her sons.

With this one small change, Boghosian has found the modified yard sale model can match recent European and U.S. wealth distribution patterns to within 2%. By making two more tweaks, allowing people to go into debt and accounting for advantages that wealthier people have in business transactions, the model can match U.S. data over a span of several decades with an accuracy of a fraction of a percent.

Boghosian also points to economies where social programs have broken down, like Armenia after the fall of the Soviet Union. In those cases, the economy really does devolve into oligarchy, with all of the wealth being held by a few people after an initial struggle for resources, just as our unmodified yard sale model would predict.


Migrant Mother, Photo by Dorothea Lange.
Source: Wikimedia Commons

In a 2019 *Scientific American* article Boghosian said

> "We find it noteworthy that the best-fitting model for empirical wealth distribution discovered so far is one that would be completely unstable without redistribution rather than one based on a supposed equilibrium of market forces. In fact, these mathematical models demonstrate that far from wealth trickling down to the poor, the natural inclination of wealth is to flow upward, so that the 'natural' wealth distribution in a free-market economy is one of complete oligarchy. It is only redistribution that sets limits on inequality."

Further Reading

- *"The Mathematics of Inequality"*, https://now.tufts.edu/articles/mathematics-inequality.
- Bruce M. Boghosian, *"Is Inequality Inevitable?"* (originally published under the title *"The Inescapable Casino"*), Scientific American 321, 5, 70-77 (November 2019).
- Anirban Chakraborti, *"Distributions of money in model markets of economy"*, https://arxiv.org/abs/cond-mat/0205221.
- Branko Milanovic, *"Global Inequality and the Global Inequality Extraction Ratio"*, http://documents1.worldbank.org/curated/en/389721468330911675/pdf/WPS5044.pdf.
- World Bank, *"Poverty and Prosperity 2016 / Taking on Inequality"*, https://openknowledge.worldbank.org/bitstream/handle/10986/25078/9781464809583.pdf.