

# Brownian Motion and Diffusion Lab

## Group 6

Names of group  
members go here

**Background:**

Statistical probability is an extremely useful tool. While on the surface it may appear a lesser of the more widely known mathematical disciplines it is in fact very useful in understanding data in the real world, and in the laboratory. More specifically for this lab, statistics can help one understand the kinematics and dynamics of biological and chemical systems. Statistics is used to build models to better understand observable data. The majority of the time building such models would be too long and strenuous by hand, so computers are used to generate more accurate models.

Diffusion can be defined as “the random migration of molecules or small particles arising from motion due to thermal energy.” Essentially, it is the motion by which molecules or particles tend to move farther away from one another creating greater entropy. A good visualization is the process by which you can smell someone’s perfume or cologne. The person sprays the smelling liquid onto themselves into a concentrated area. The liquid turns to gas, and the gas particles move and separate from one another through the air as they clash into air molecules. Eventually a cologne/perfume molecule will make its way to your nose, and your olfactory sense will pick up the scent. In a more biological sense, diffusion is important in many aspects. For example, diffusion is the net movement of molecule from one area of high concentration to an area of lower concentration. This random movement required no energy from ATP for example, and ceases when the net movement is 0 and equilibrium is reached. Diffusion is also used in the “breathing” of many species. In mammals’ lungs, oxygen is diffused into blood cells while carbon dioxide is diffused out. Opposite of that, in a plant, oxygen is diffused out and carbon dioxide is diffused during photosynthesis.

An event like diffusion can be modeled using a computer program such as random walk. This program aims to model simple diffusion in a 2-dimensional manner. By listing the number of particles you can then execute a simulation in which the “particles” start in the same place and slowly disperse mimicking diffusion. A particle tends to explore. Meaning, it has no inclination of the past. It wanders and has no tendency to move into regions it has not occupied before. It may enter those regions, but it also will return to the same point multiple times before wandering away. Colloidal motion is the motion of a particle among a sea of other particles, say water for example. The presence of the water molecules causes constant collisions to any given particle. These collisions create a lot of kinetic energy and allow the particle to move in a random manner that can also be better understood using statistics and model. Both of these types of motion are random. This can be further shown by creating a histogram for the data of the positions of a single particle, or several particles. When a histogram is created you’ll see that it creates a Gaussian curve. This asserts firmly that the movement of such objects is random.

**Procedure and Materials:**

For the Brownian motion lab the following materials were used:

A computer equip with logger pro

A microscope

Microscope video capturing kit

The first step was to set up the computer properly by attaching the camera to the microscope and the camera to the computer. Once that was set up accordingly, we tested the video capture on loggerpro to assure its functionality. Next, calibration of the microscope was necessary. To do this we placed several drops of water on each metalized pattern of 10 micron and 100 micron spaced lines and covered it with a cover slip. We calibrated the grid lines of the Levy chamber against the microscope caliper and did this

for all objectives lenses up to 40x. After calibration, we captured clips of polystyrene beads displaying Brownian motion. To do this a few drops of polystyrene solution were placed in the Levy chamber and covered with a cover slip. We measured the size of the bead we planned to film and then captured a thirty second video of the bead in motion. Since the table is touched a lot and easily transfers motion, the microscope apparatus was placed on the floor to reduce vibration and unwanted motion. We repeated this process for both .5 and 1 micron diameter beads in addition to the 2% milk sample in which we captured the fat. After capturing several videos, we plotted the position versus time graph of one of the videos we collected. From this data we were able to calculate the total distance traveled versus time. Next, we also analyzed the data using image J. This procedure tracked the bead of interest as it moved. This enabled us to calculate the distance the bead moved in one frame of video, or the distance it moved one thirtieth of a second.

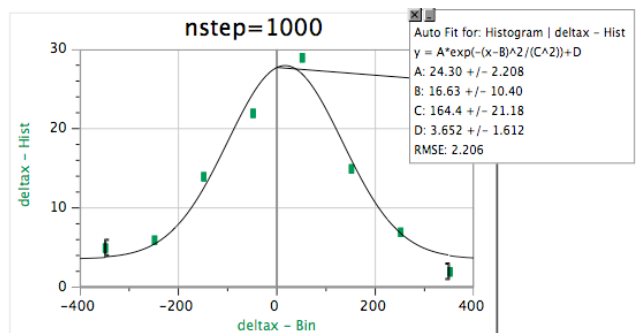
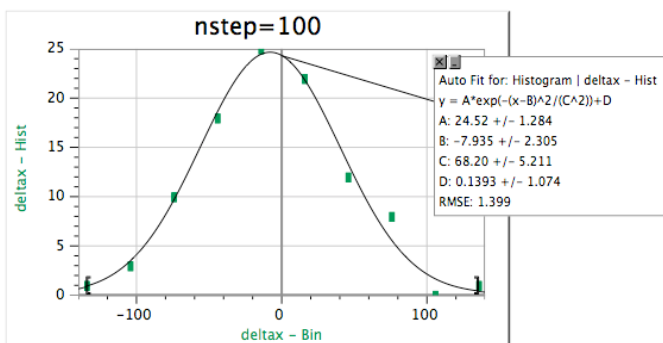
For the diffusion lab the following materials were used:

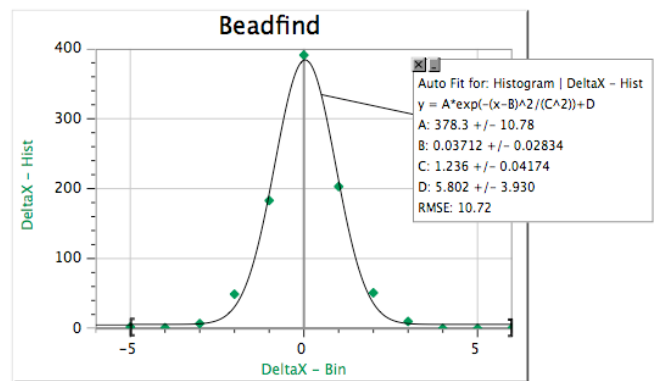
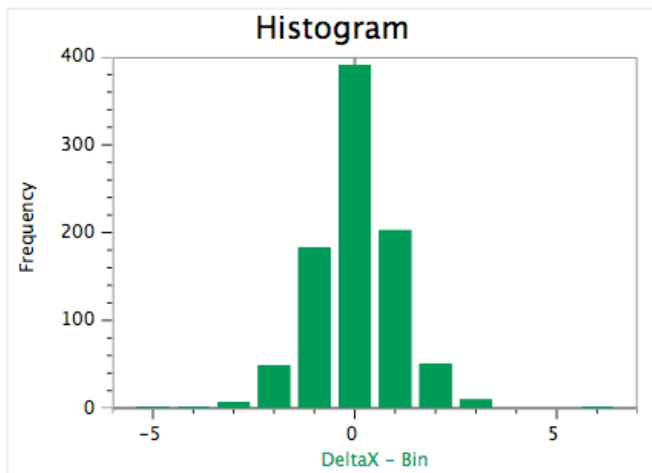
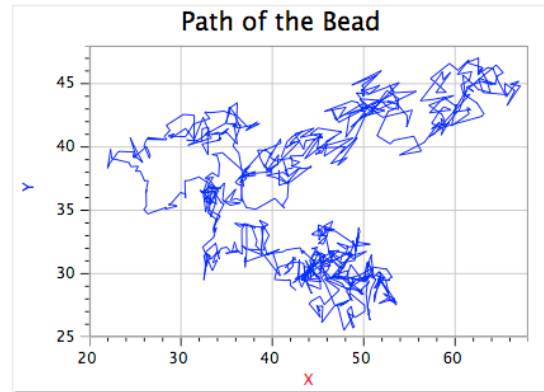
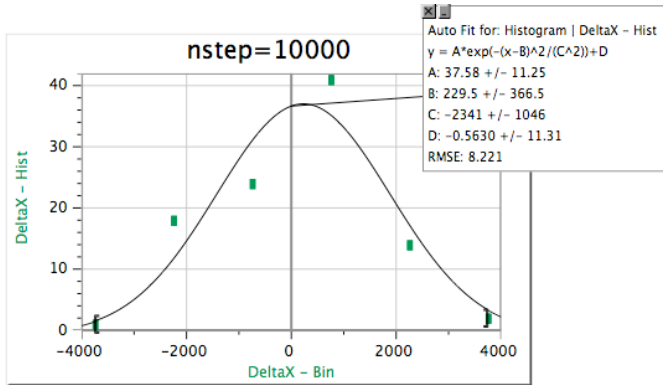
- Petri dish
- Gel
- bromothymol blue
- light table
- cardboard trapezoidal box
- various cameras

The first step for this lab was to create a gel that was composed of 75% water and 25% glycerin. The gel filled the petri dish. Next, we placed a drop of bromothymol blue into the center of the gel and petri dish. An initial picture of the dish and the bromothymol blue was taken by placing the dish on the light table so that the blue color could clearly be seen. The cardboard trapezoid was placed over the petri dish and the light table to block outside light and to give a focused view of the petri dish. Pictures of the gel and bromothymol blue were taken in intervals throughout the week by repeating the above procedure. Next, we were to analyze the photos. To analyze the photos we also used image J. To do this we upload a picture into the program and set the scale. Next select the portion of the picture we wish to analyze and set the color scale. This color scale determines the concentration of the bromothymol blue (darker is more concentrated and lighter is less concentrated). The image that appears is upside down so inversion was necessary. The image shown is now a Gaussian curve. The curve shows how diffusion led the particles further and further away from each other, slowly lessening the concentration.

### Modeling:

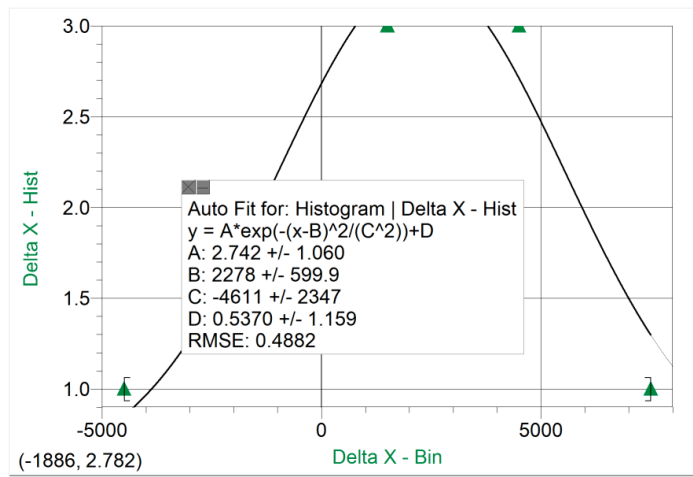
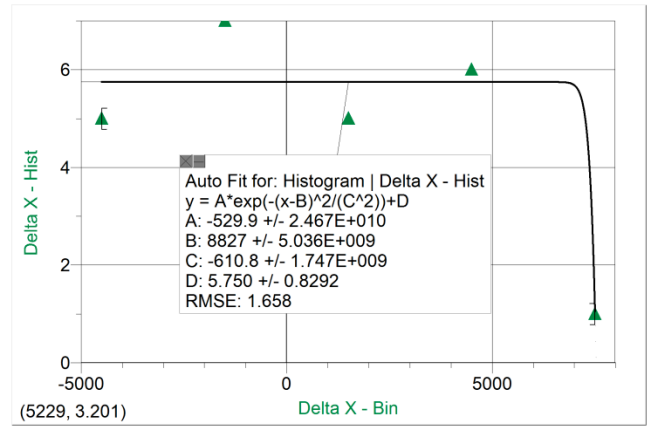
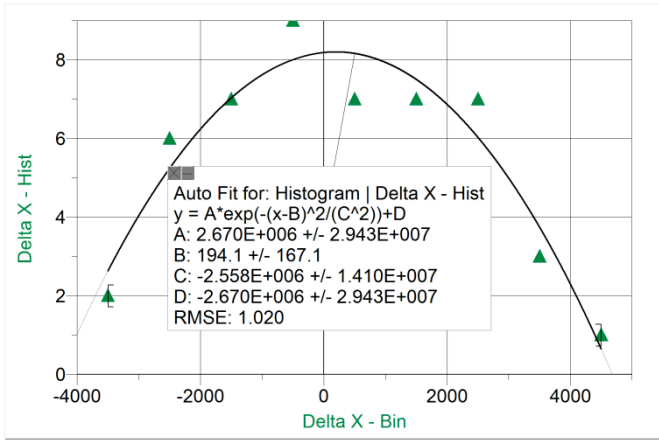
#### Brownian Motion and SimpleWalker



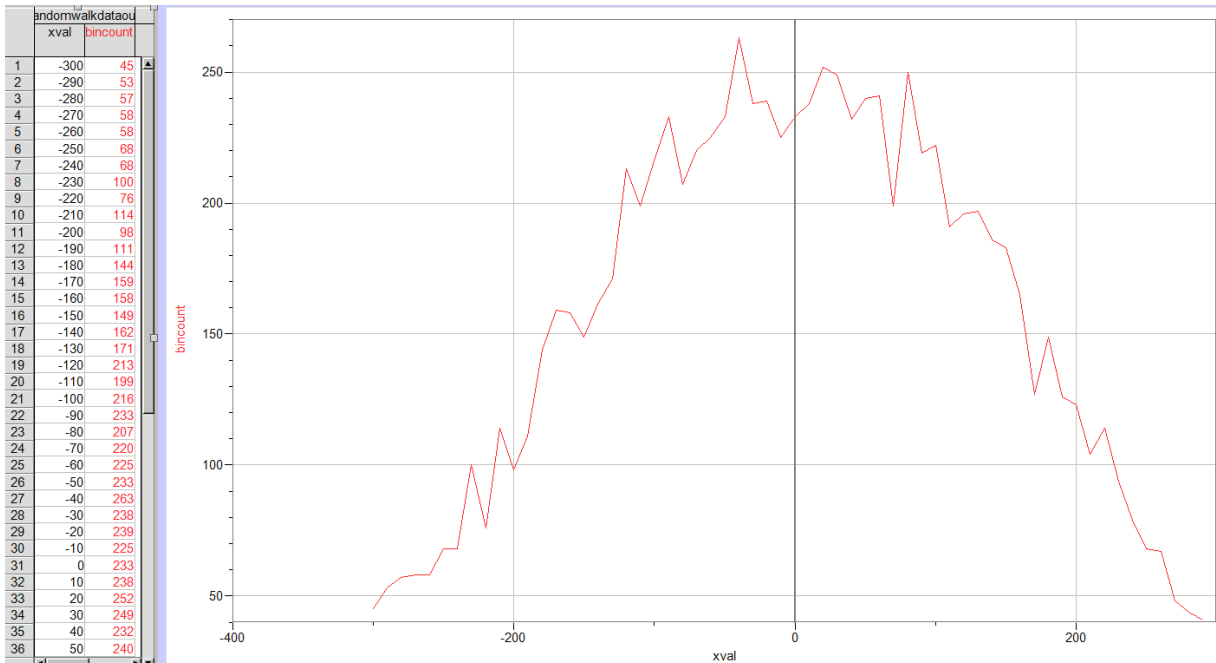


During the bead find section of the lab, we used the 1-micron bead as our primary subject of analysis. After recording the positions of each frame that the bead took, we made a histogram of x-positions and found that values closest to zero were the most common. This means that the bead's position was generally around the area in which it started, only straying further a few times, as is reflected in the histogram. By running a simulation that mimics Brownian motion, called Simple Walker, we saw that our bead followed the normal path that any particle would under the influence of Brownian motion. In this program we sampled 100 movements per frame, 1000, and 10000. These runs are represented in the graphs above, which all follow Gaussian curves, just like the bead. It should be noted that the higher the value for nstep, the less Gaussian-like the curve became.

When we parsed the data (taking every other, every fourth, and every ninth data point), the standard deviation increased with time. The results are shown below.



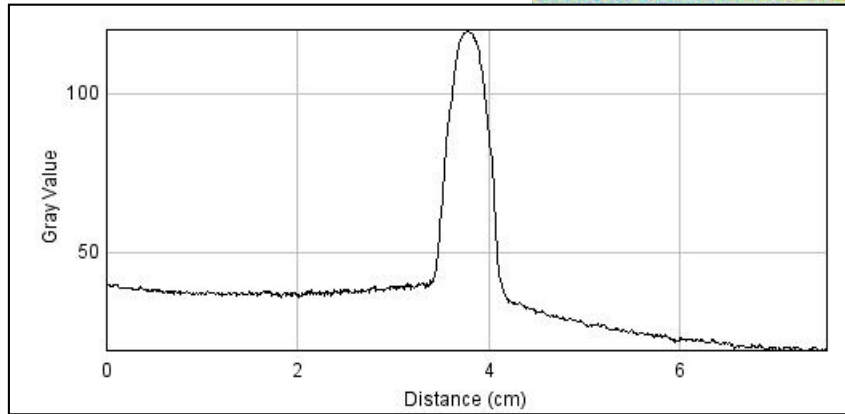
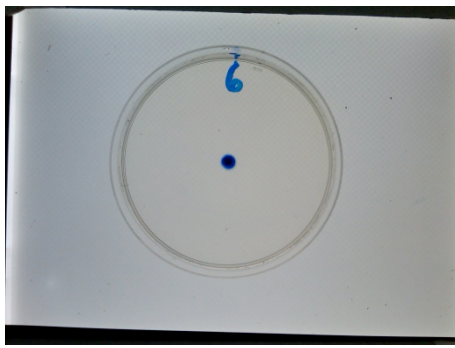
### Diffusion and RandomWalk



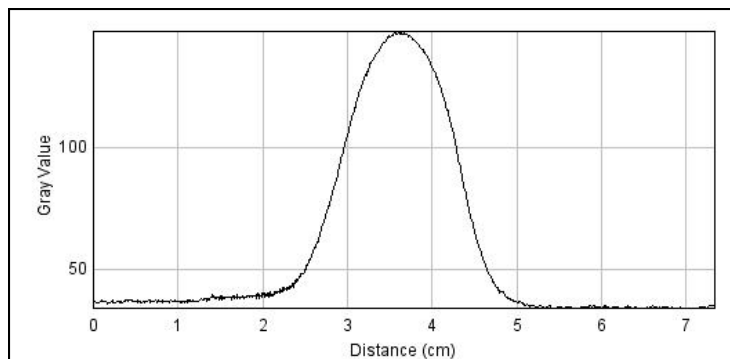
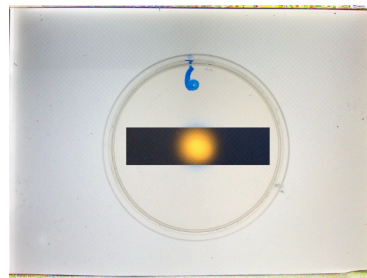
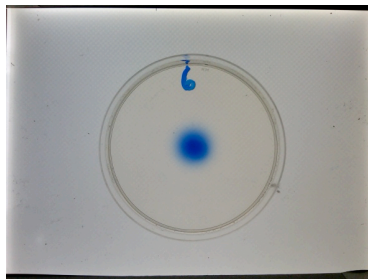
**Results and Analysis:**

**Image J Analysis of the Pictures**

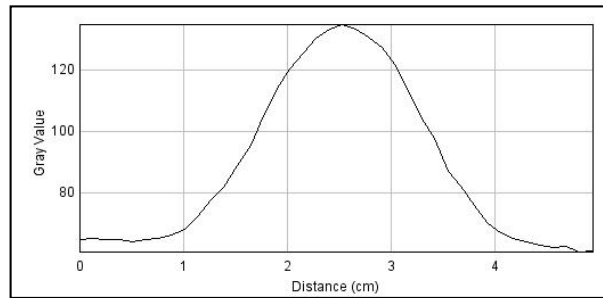
March 30 3:42 PM



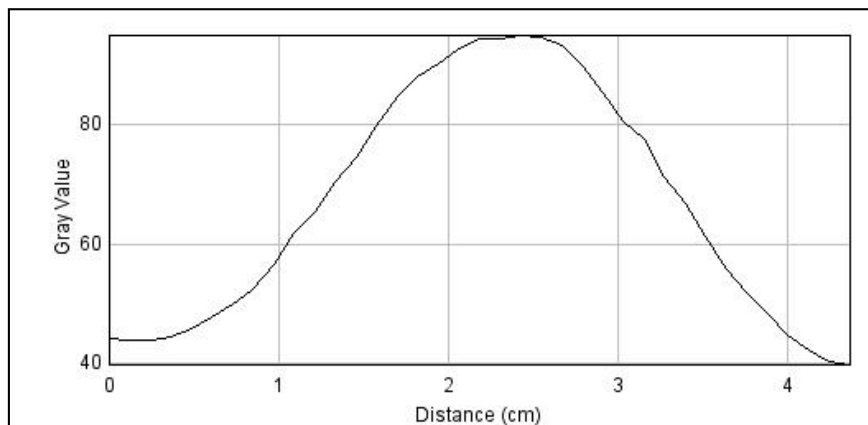
March 31 7:43 AM



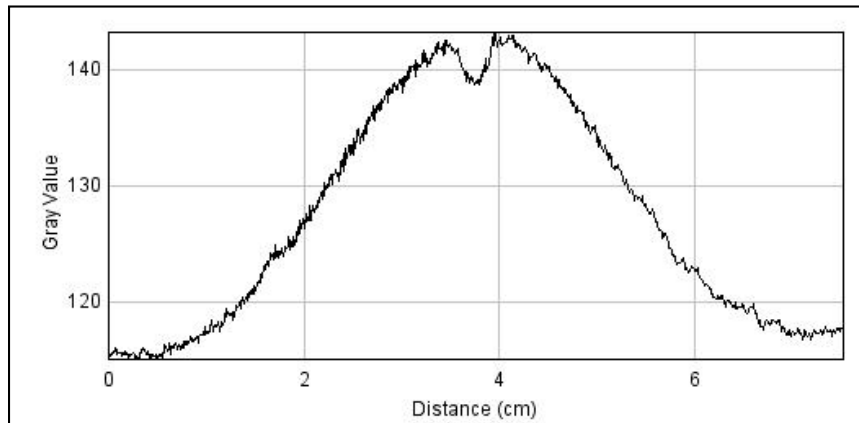
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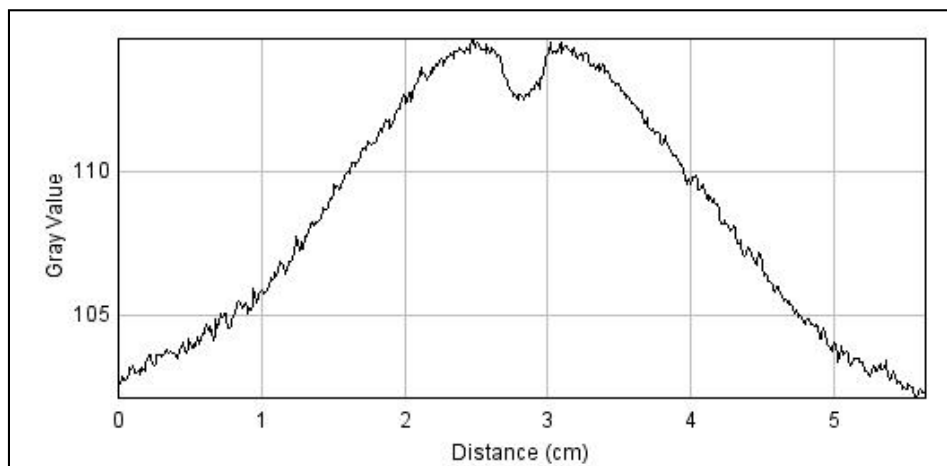
April 1 2:58 PM



April 4 3:06 PM

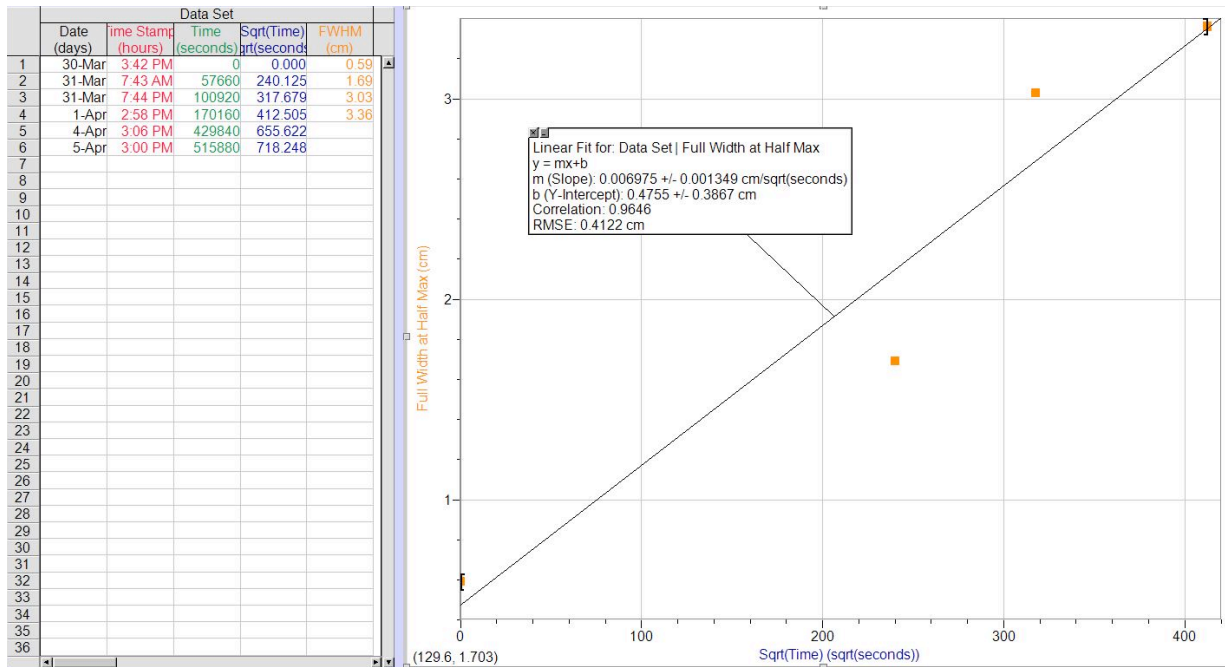


April 5 3:00 PM





These are all the pictures taken of our gel with date and time. The first picture on the left after the time stamp is the original. The second one is the picture after Image J analysis. The third is the profile we got from the analysis. After getting all the profiles from Image J, we measured the Full Width at Half Max (FWHM) and plotted  $\sqrt{\text{Time}}$  vs. FWHM.



You'll notice on the data table that there are no values for FWHM for the April 4 and 5 photos. This is because on those profiles half max was below the bottom of the bell curve and not shown on the profile, so FWHM could not be measured. However this is the graph for  $\sqrt{\text{Time}}$  vs. FWHM for the first four photos. The standard deviation increases with time. For a true Gaussian distribution, FWHM should increase linearly with the  $\sqrt{\text{Time}}$ . However, our data is skewed because we did not take photos at regular time intervals. But in the closer time intervals, the fit is linear.

### Discussion:

#### Calculating Avogadro's Number

The formula to calculate Avogadro's number from Brownian motion is

$$N = \frac{RTt}{3\pi\eta r s^2}$$

where N = Avogadro's number

R = gas constant = 8.315  $\text{J/molK}$

T = temperature in Kelvin

t = time

$\eta$  = viscosity

r = radius

s = standard deviation

To find viscosity, we looked up online how to calculate it in a mixture of glycerin and water. The equation was: (viscosity of water)(.75)+(viscosity of glycerin)(.25) which was (.001 Pa\*s)\*(0.75) + (1.5 Pa\*s)\*(0.25) = .376 Pa\*s. Everything else we just plugged in the numbers from our Brownian motion analysis:

$$N = \frac{RTt}{3\pi\eta rs^2} = \frac{(8.315 \text{ kg/m}^2\text{s}^2\text{molK})(293\text{K})(30\text{s})}{3\pi(0.37575 \text{ kg/ms})(5 \cdot 10^{-7}\text{m})(1.236 \cdot 10^{-6}\text{m})^2} = 1.35 \cdot 10^{22} \text{ mol}^{-1}$$

Calculating the Diffusion Constant

Here you want to use the data from the Brownian motion part of the experiment, as outlined in readings for the lab, but you did not use the viscosity of water

The slope of the graph of  $t^{1/2}$  vs the standard deviation was 0.006975, which can also be represented by the equation,  $2.35 \cdot (2D)^{1/2}$ , where D is the Diffusion Constant. Since the slope is measured in centimeters, it must be converted to meters, giving us .00006975. Solving for D, we get  $4.4 \cdot 10^{-10}$  as our diffusion constant.

Calculating the Number of Collisions in One Frame

$$\frac{V_{rms}}{\text{mean free path}} = \text{collisions per second}$$

In the following equation  $v_{rms}$  comes from the FWHM of the Beadfind graph on page 4. Since we don't have the number of water molecules or the volume, I substituted pressure divided by Boltzmann's constant and temperature from the universal gas law. The water with the bead in it was at standard atmospheric pressure 1 atm = 101,300 Pa and the temperature in the room was 20°C = 293K.

$$\frac{v_{rms}}{\frac{1}{4\sqrt{2}\pi(N/V)r^2}} = v_{rms} 4\sqrt{2}\pi(N/V)r^2 = v_{rms} 4\sqrt{2}\pi\left(\frac{P}{k_b T}\right)r^2 = (1.236 \text{ m/s}) 4\sqrt{2} \left(\frac{101300 \text{ Pa}}{(1.38 \cdot 10^{-23} \text{ J/K})(293\text{K})}\right) (5 \cdot 10^{-7})^2 = 4.38 \cdot 10^{12} \text{ collisions/second}$$

This number is the collisions per second. One frame of the video is 1/30<sup>th</sup> of a second, so to find the collisions per frame, we simply divide by 30.

$$\frac{4.38 \cdot 10^{12}}{30} = 1.46 \cdot 10^{12} \text{ collisions/frame}$$

N/V comes from the density of water! But PV=nRt only works for a dilute gas, not for liquid water!

Conclusion:

In this lab we compared diffusion and Brownian motion to random walk programs and saw that the results were very similar. In the bead find part of the lab, both the random walk and the bead find programs gave results that showed Gaussian curves. Since the data from the bead find program matches the simple walk curve, which means that its motion was truly random. Also, with the diffusion part of the lab, the results with random walk matched up because both showed concentrations in the middle, and spread out over time, as was shown by the increasing full-width-at-half-maximum value.

Overall, you did a nice job fitting the data and extracting quantitative values from the images. You were maybe fighting the deadline for turning the lab in, so weren't able to think as deeply as you would have liked about the analysis as you would have liked. There are some pretty easy places where plugging in the correct numbers (like the density of water) would have made a big difference in the results.

You don't have any references listed, that is a major omission. Surely the quotes you have in the introduction came from somewhere!