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Biology Period 3

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Data Collection and Processing

	Mass Change in Gummi Bear (±0.01g)									
	Trial 1		Trial 2		Trial 3		Trial 4		Trial 5	
Molarity (±0.001 M)	Initial	Final	Initial	Final	Initial	Final	Initial	Final	Initial	Final
0.200	2.13	2.68	2.15	2.72	2.12	2.59	2.13	2.78	2.14	2.77
0.400	2.15	2.39	2.17	2.42	2.16	2.30	2.19	2.44	2.12	2.32
0.600	2.11	2.14	2.11	2.16	2.15	2.14	2.11	2.11	2.11	2.09
0.800	2.09	2.01	2.19	2.02	2.13	2.00	2.15	2.01	2.11	2.00
1.000	2.17	1.97	2.09	1.82	2.09	1.85	2.16	2.14	2.14	1.90

In order to process this data, we first found the proportional change in mass. A direct mass change would provide only limited amounts of information, as without the original starting mass to have, it would almost be a meaningless piece of information. However, by finding the proportional difference, the experimenter and the reader would be given a sense of what the numbers mean.

To find this, we would apply the formula

$$\%A = \frac{\Delta A}{A_{initial}}$$

, where $\Delta A = A_{final} - A_{initial}$.

An example of this, using the Trial 1 of M = 0.200 data, would show to be

$$\%A = \frac{2.68 - 2.13}{2.13}$$

$$\%A = 0.26$$

Therefore, the following data table is created.

	Proportional Change in Mass				
Molarity (±0.001 M)	T1	T2	T3	T4	T5
0.200	0.26	0.27	0.22	0.31	0.29
0.400	0.11	0.12	0.06	0.11	0.09
0.600	0.01	0.02	0.00	0.00	-0.01
0.800	-0.04	-0.08	-0.06	-0.07	-0.05
1.000	-0.09	-0.13	-0.11	-0.01	-0.11

To create a graph, the average and the error in the y-direction must be found. A simple averaging method is applied, according to:

$$\bar{x} = \frac{\Sigma x}{n}$$

So that using M = 0.200 data,

$$\bar{x} = \frac{0.26 + 0.27 + 0.22 + 0.31 + 0.29}{5}$$

$$\bar{x} = 0.27$$

The error is then found by:

$$Error = \left| x_{average} - x_{maxDeviation} \right|$$

Using M = 0.200 data again,

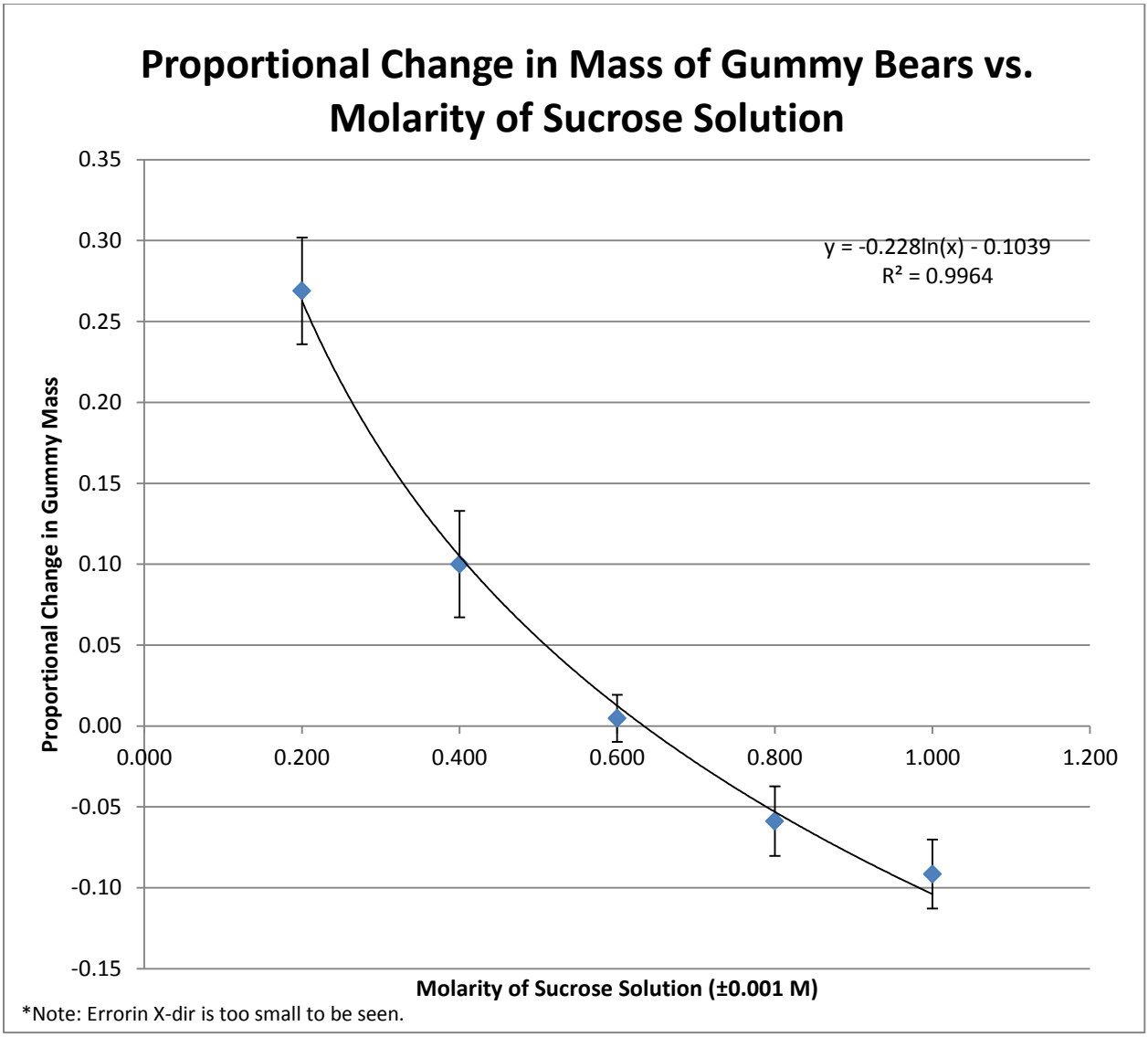
$$Error = |0.31 - 0.27| = 0.03^{Note1}$$

Note 1: The reason this value does not seem to correspond is because both 0.31 and 0.27 are rounded values, and in calculating the error the absolute values were used.

Therefore, the following data table is created:

Molarity (±0.001 M)	Ave. % Change	Error
0.200	0.27	0.03
0.400	0.10	0.03
0.600	0.00	0.01
0.800	-0.06	0.02
1.000	-0.09	0.02

Which produces the following graph:



Conclusion:

Through this experiment, we have tried to calculate the molarity of sucrose solution by finding where the gummy bear was isotonic as compared to a known sucrose solution. Our reasoning was that if the two items were indeed isotonic, the gummy bear would neither gain nor lose mass. Through our graphical analysis, we determined that a best fit line would be modeled by the natural logarithm function, as shown evident by the high r^2 value as well as how the line passes

through all of the uncertainty regions. The x-intercept as calculated by this model would be 0.63, meaning that the molarity of the gummy bear is around 0.63M.

The reason that we used a natural logarithmic fit, and not a linear fit, is because of the problems with a linear fit. With a linear fit, as the molarity of the sucrose solution increases, the gummy bear would eventually lose more than 100% of its mass, when the sucrose solution is greater than 3 M. Clearly, this does not make any sense. Also, the natural log regression fits the data much better.

Because of the extremely close fit with this regression, as well as the M=0.600 case, where the percent change was already approximately 0, we have a high confidence in how the molarity of sucrose within the gummy bear is around 0.63M. Because the reporter did not do the experiment, it is difficult to determine weaknesses of this experiment. However, one problem is that not all gummy bears are created equal. As evident from the initial data, where all the gummy bears had a varying mass, it is also possible that the gummy bears have a slightly varying concentration of sucrose solution, resulting in a random error.

Another possible error is that at the end of the 24 hour period, the gummy bears have not yet reached perfect equilibrium with the surrounding solution. This would result in data that is just a little off in either direction, meaning the systematic error may actually balance itself out through averages, but the error may lean towards one direction as well.

One improvement that could be made to the experiment would be to leave the gummy bears in the solution for greater than 24 hours. Although the 24 hour period is likely to be enough in order for the soaked gummy bear to be isotonic in relation to the solution, leaving the bear in the solution for a longer period would better this probability. In addition, having more conditions

where M=0.300, 0.500 etc. may be able to increase the certainty that a logarithmic fit is the best fit for the data. Of course, having more trials would also allow us to have more certainty that the average is an accurate average. However, the high correlation and good fit means that this lab is already an exceptionally prepared lab.