1. a.

   The formula for Newton’s method is: X_n - $(f(X_n)/f'(X_n)$

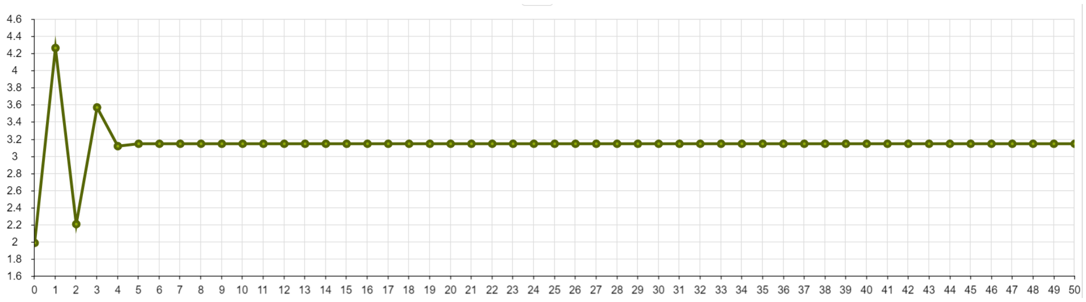
   First step: Stock of X_0 is decided by an input of “Function choice”. For a Function choice of 0, a starting value of 1.985 is given.

   Then, the X_0 is passed into two variables: function($f(X_0)$ and its derivative($f'(X_0)$ for use in the formula. For Function choice 0, $f(x) = Sin(x)$ and $f'(x) = Cos(x)$, and for $x= 1.985$, $f(X_0) = .9154$ and $f'(x) = -.4025$.

   The function and derivative solutions are passed into the change variable, which divides and negates them. For the first iteration of function 0, it solves to 2.274.

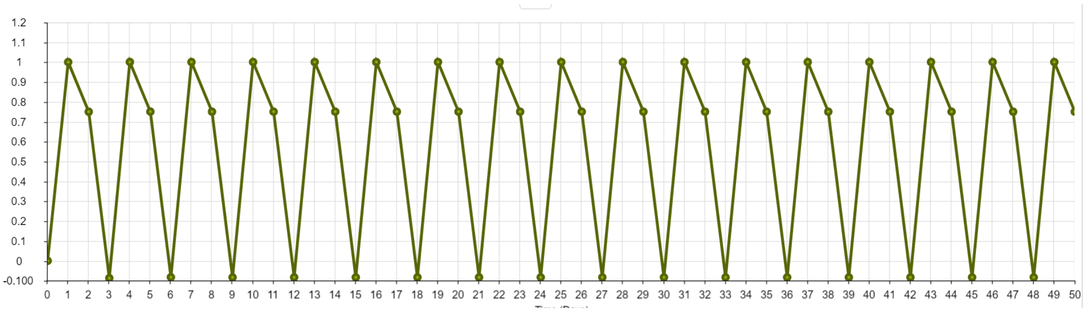
   The value is then passed through the update flow, where it is added to the value of X_0. This value becomes the new X value, now X_1. The process is repeated ad infinitum.

   Function 0: Sin(x), $X_0 = 1.985$

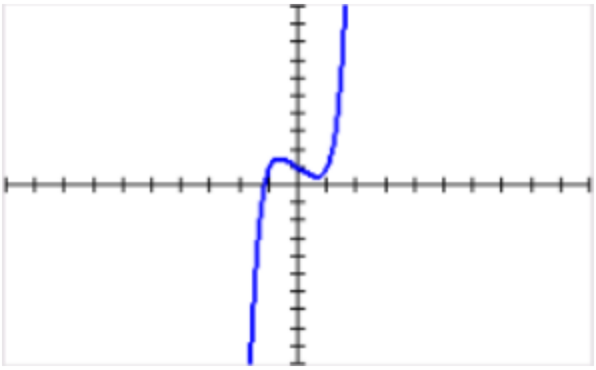


   This functions as intended. The starting value is just to the right of the top of the curve, and the next one is just beyond the root, so it bounces back and eventually gets close(enough) to the root.

   Function 1: x^5-x+1, $X_0 = 0$



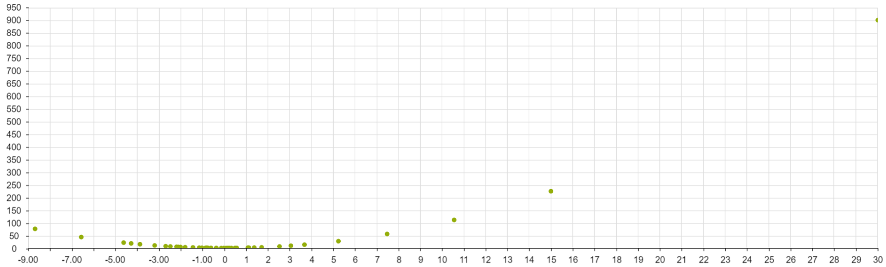
   Graph of the function:



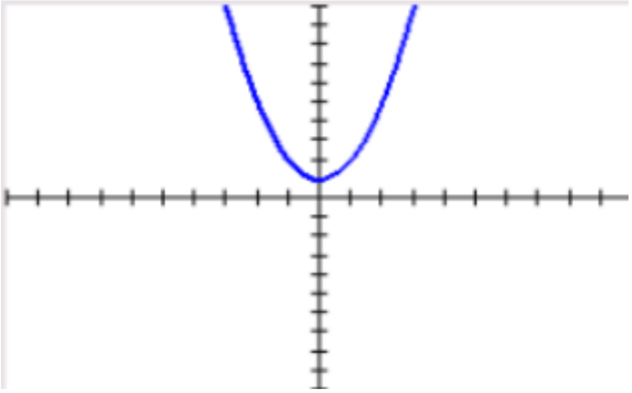
A starting value of 0 isn't a great place here, because the local minimum at a little less than 1 is closer than the root at a little lower than -1, so it's drawn to the local minimum, and then it never finds the root.

Function 2: $x^2 + 1$, $X_0 = 30$

Phase Shift(a still picture at the end doesn't tell much of a story though):

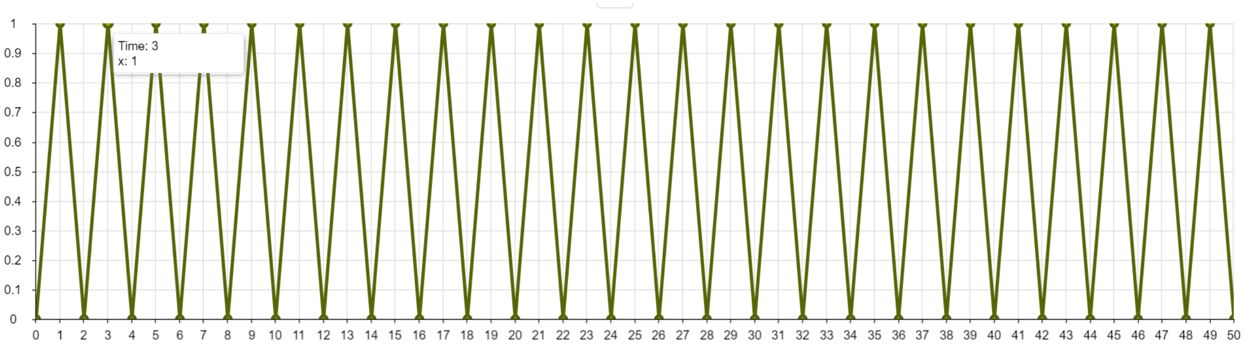


The function doesn't have a root:

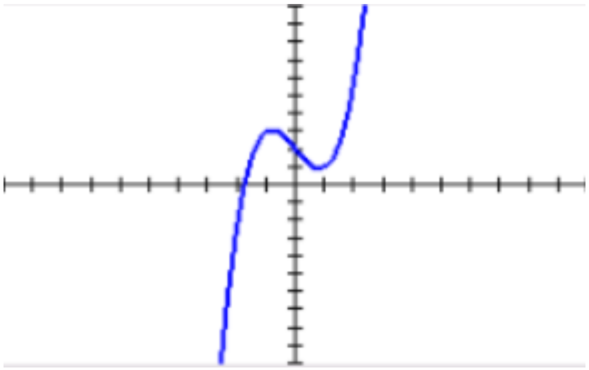


So the function goes back and forth, trying to find the axis, but it never will :(

Function 3: x^3-2x+2, $X_0 = 0$

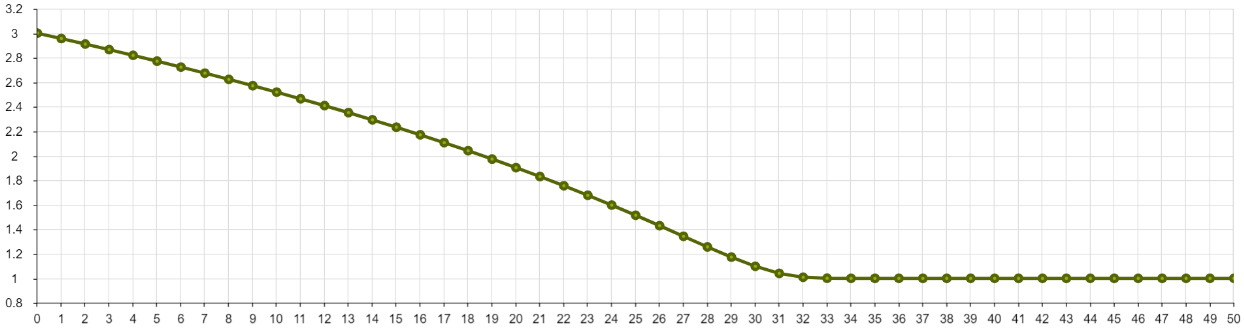


Graph of the Function:



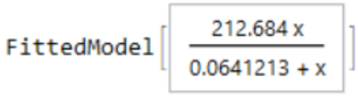
We have the same problem as we had in function 1: the initial guess wasn't good enough, and so the method runs out of places to go, because it's going to immediately go right.

C.

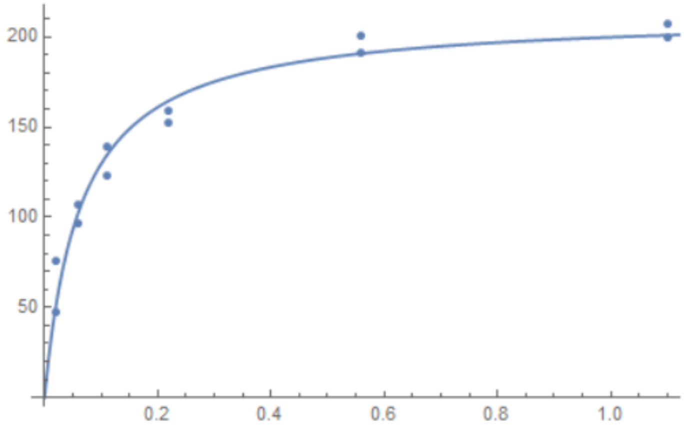


[Link to the InsightMaker]

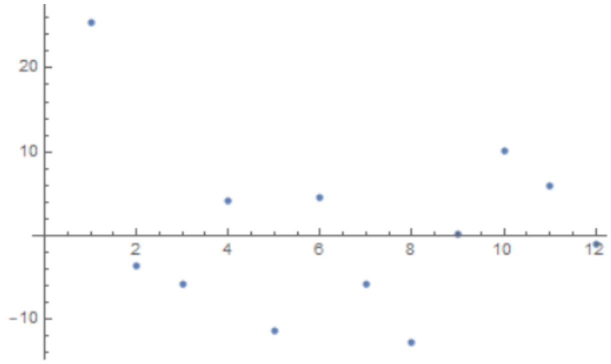
2. I used mathematica’s NonLinearModelFit function. Following the rigor mortis example, I placed the data into two lists, then combined them into a table where x = concentration and y = velocity. I used this table and the function ((a * x) / (b + x)) to fit the data to the function and make a graph:



$$\text{FittedModel}\left[\frac{212.684\,x}{0.0641213+x}\right]$$



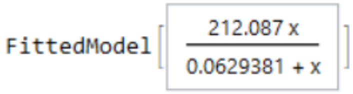
Plot of Residuals:



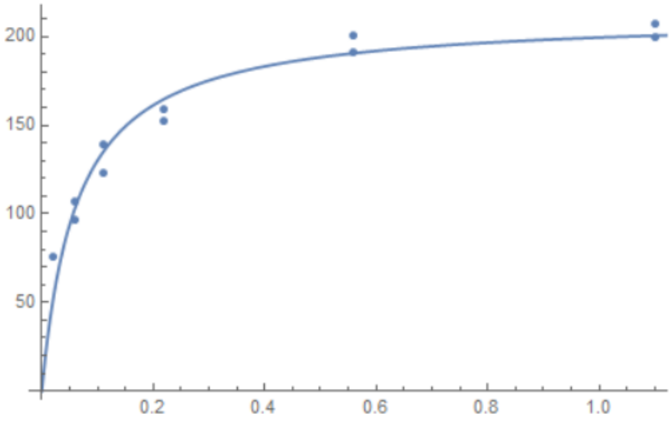
I wanted this to be in here so you can see my thoughts even though they turned out to be wrong, and it’s not relevant. The next relevant section is Parameters Summary.

Looking at the residuals, I don't like that very first one, it looks like an outlier, so I wanted to investigate(turns out that's not exactly right--there IS an outlier, but it doesn't have anything to do with the residuals, and it's not even that point). I started by finding the median and the IQR to get a range of what's considered an outlier. The lower bound was 52, so I removed the point, as it had a velocity of 47. But then I questioned if this is an appropriate method for determining outliers(all I have is this hammer!), so I repeated this process on the residuals data(median, IQR, etc), and that also determined it to be an outlier

I repeated the process with the residuals data, and it's still an outlier, so I took it out, and re-modeled:



FittedModel[$\frac{212.087\,x}{0.0629381 + x}$]



It gives nearly the exact same model, and exactly the same parameters. So I put it back in: If it's not going to make a big difference, there's no reason to miss a potentially important piece of information, and with only 12 data points, we need as many as we can get.

Parameter Summary:

	Estimate	Standard Error	t-Statistic	P-Value
a	212.684	6.94716	30.6145	3.24116*10^-11
b	0.0641213	0.00828095	7.74323	0.0000156513

The r^2 given by mathematica's r^2 function is .999, which is pretty significant. However, knowing that r^2 isn't a great measure for non-linear functions, I adjusted it using the formula that we used in the rigor mortis example. That gave me .953, which is a bit more reasonable while still being significant--instead of 99% of the data being explained by the model(which, from the graph, we can tell is a bit of a stretch), 95% of the data is explained by the model.

Confidence Intervals:
a: (197.205, 228.163)
b: (0.0456702, 0.0825724)
So, we're 95% confident that the true value of a is somewhere between 197.205 and 228.163, and the true value of b is somewhere between 0.0456702 and 0.0825724, which is supported by our (significant) estimates in the summary.

From the Bestiary of Functions, we can see that a is where the function asymptotes at. That is, the higher the concentration of the substrate(Puromycin), the higher the velocity of the reaction. However, at a certain point, it can only react so fast due to surface area, and likely other factors(I'm not much of a chemist). So we would expect the fastest possible reaction times to be between 197.205 and 228.163.

Also I came across this cool website while trying to figure out what was happening and thought you might like it. It ended up not helping me much but did confirm that I wasn't insane while trying to make sense of what's going on:
http://biomodel.uah.es/en/metab/enzimas/MM-regresion.htm

This might be weird, but I really enjoyed this exam. Despite being incredibly frustrated because I don't know Mathematica, I feel like I learned a lot about it. Should I have known how to use mathematica coming into this? Maybe. But I know now!

Here’s my helper(she wasn’t much help…)!