Rover Publications
United International Journal of Engineering and Sciences (UIJES)
An International Peer-Reviewed Engineering and Science Journal;Impact Factor: 5.735(SJIF)
www.uijes.com Vol-3,Issue-1 ,2022 ISSN:2582-5887

Sensitivity Analysis of Kinetic Growth Model Data: Monod Equation

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Abstract
Simulation modeling of microbial prolieferation had increased in recent years using Monod and advanced kinetic models. Accurate data is limited to advance studies in cell utilization for various applications due to complexity of the process. In this reasearch, behaviour of the Monod parameters at different substrate and biomass levels will be examined using predicted data obtained originally from empirical observations. Method involves deliberate variation of some variables to examine its effects on others starting from the basic Malthus anequation. Results show that, predicted data are mofre conveninent and clearly presents the supposed dynamics of the process compared to ideal experimental results. By implications, improved procedure are necessary to allow for precise estimates of basic cell numbers and substrate concnetration values.

Keywords: Sensitivity analysis, Monod, Growth kinetics, Substrate concnetration, Cell Concnetration

I. INTRODUCTION

The Monod model is the most basic kinetic equation for analysisng the specific growth rate of microorganisms under favourable conditions. Different microorganisms require different environment to grow in size, produce new cells and survive. The surface on which microorganisms carryout these fundamental task is known as a substrate which include hydrogen peroxide and glucose, to mention a few, at neutral or acidic pH and mesophilic, psychrophilic, thermophilic or hydrothermophilic temperatures in susbtrates of high carbon proportion. Microbiologist and bioengineers had therefore tried to study conditions that favour the growth of hundreds of microorganisms to study their kinetic kinetics. This study is however carried out in 3 ways, namely batch, fed-batch and continuous culture in bioreactors and chemostats to generate cell and substrate concnetration data.
In bioengineering or biotechnological research, empirical growth data ususally reported are different and is caused by changing cell adaptation to specific environment, presence of multiple microbial cells in a particular susbtrate, unrealistic cell counting device and difficulty in maintaining conditions of reactor types that harbour them, making them incomparable. However, when this experimental data are used to predict new ones by estimating certain kinetic parameters, these new correlated data happens to be too perfect. It is so, very suitable to work with these predicted data for substrate sensitivity studies especially using the combined Malthus and Monod equations. It is wrong to use Micheles-Menten equation for cell growth analysis as it is used mostly for process involving a single enzymes, while Monod is used for cells, as they are capable of generating more enzymes and substrate. Example is the fungus called yeast which produces maltase that breaks down maltose to glucose.

Objectives of this work is to use an exisitng predicted data of cell centration, X (mg/l) and substrate concentration, S (mg/l) at constant and varying conditions of the initial susbtrate concnetrations, S_0 to examine data flexibility. Nikitina & Chernukha (2020) had used the 1-step Runge-Kutta technique to solve differential erquations in S and X by writing an R programming code in the Jupyter Notebook environment.

2. METHODOLOGY

2.1 Substrate Concnetration

When the growth phase equation (1)[2] and the Malthus equation (2)[3] are combined, the rate constant (k), equivalent to the maximum specific growth rate (μ_{max}) can be predicted using statistical data resulting in the predicted values of X.

$$\frac{dX}{dt} = \mu X \qquad (1)$$

$$\mu = k\left(1 - \frac{X}{X_{max}}\right) \qquad (2)$$

Where, $X_{max} = X_0 + YS_0$ = maximal cell concentration (mg/l), X_0 = initial cell conctration (mg/l) and Y = ratio of mass of cell to mass of substrate consumed $\left(\frac{X-X_0}{S_0-S}\right)$[4]. Predicted S values was determined using Equation (3).

$$S = S_0 - \frac{X-X_0}{Y} \qquad (3)$$

2.2 Monod

Half-saturation, K_s and the maximujm specific growth rate, μ_{max} are the parameters used in optimizing microbial culture. From the Monod equation that relates μ and S, those kinetic constants can be determined by first generating μ values using Equation (4) and (5) successively.

$$\frac{dX}{dt} = kX\left(1 - \frac{X}{X_{max}}\right) \quad (4)$$

$$\mu = \frac{1}{X}\frac{dX}{dt} \quad (5)[2]$$

S_M computed from the given Monod model for Equation (6), can then be used to run appropriate Monod plots from which $\mu_{max}/_2$ corresponding with S is K_s (in mg/l) and the plateau of the hyperbola is μ_{max}.

$$\mu = \frac{\mu_{max} S_M}{K_s + S_M} \quad (6)$$

The values of S, X, μ and S_M are however predicted data obtained using equations and regression analysis. Table 1 shows the predicted values used in this analogy.

Table 1: Predicted Biomass and Substrate Concentrations

Time(hr)	X(mg/l)	S(mgl)	Time(hr)	X(mg/l)	S(mg/l)
0	3.00E+06	900000	504	1.59E+08	510508.3
24	3.72E+06	898210.2	528	1.78E+08	461801.3
48	4.60E+06	895998.8	552	1.98E+08	412908
72	5.69E+06	893269.4	576	2.17E+08	364952.5
96	7.04E+06	889904.9	600	2.35E+08	318974.7
120	8.69E+06	885764.2	624	2.53E+08	275844.2
144	1.07E+07	880678.6	648	2.69E+08	236205.1
168	1.32E+07	874447.4	672	2.83E+08	200454.4
192	1.63E+07	866835.4	696	2.95E+08	168754.5
216	2.00E+07	857570.5	720	3.07E+08	141067.5
240	2.45E+07	846343.6	744	3.16E+08	117202.3
264	2.99E+07	832812.2	768	3.24E+08	96864.25
288	3.64E+07	816608.4	792	3.31E+08	79699.54
312	4.41E+07	797354	816	3.37E+08	65331.35
336	5.31E+07	774684.1	840	3.42E+08	53386.4
360	6.37E+07	748280.2	864	3.46E+08	43512.57
384	7.58E+07	717911.7	888	3.49E+08	35389.25
408	8.96E+07	683485	912	3.52E+08	28732.03
432	1.05E+08	645091.9	936	3.54E+08	23293.68
456	1.22E+08	603049.7	960	3.55E+08	18862.6
480	1.40E+08	557921.8			

3. RESULTS AND DISCUSSION

3.1 Substrate Disappearance and Cell Proliferation

As substrate concentration decreases, microbial population increases as shown in Figure 1.

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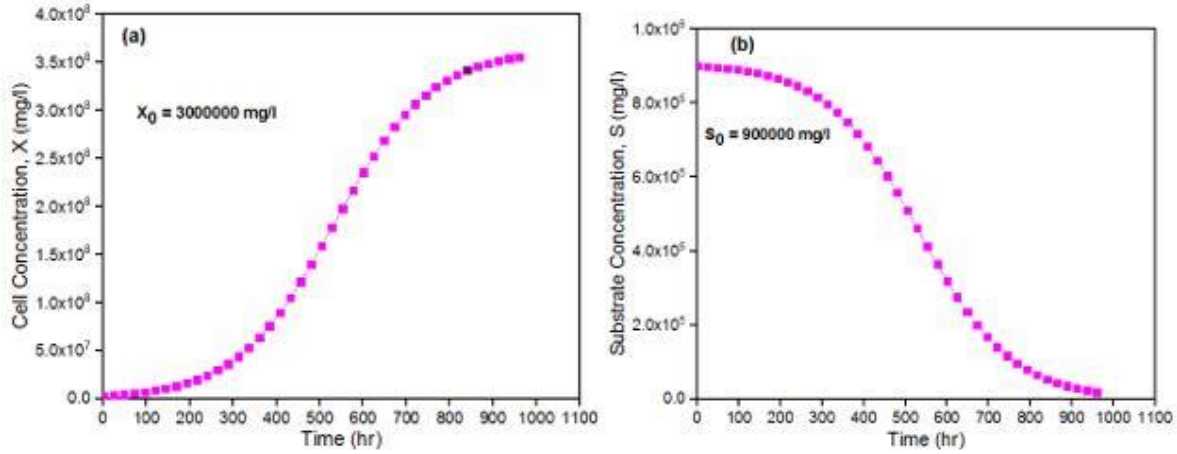

Figure 1: S and X-Time Graph at $\mu_{max} = 0.009\text{hr}^{-1}$ and $K_s = 4 \times 10^8$ mg/l

In a certain reactor with X/S = 3.33 and Y (= 400) which is equal in both estimation using experimental and predicted S and X data, predicted values of S and X at their respective initial amount leads to the growth shown in Figure 1 and is developed following similar procedural steps followed by Liu (2017).

3.2 Varying Initial Substrate Concentration

Research had been carried out to determine microbial concentration in certain organic materials as well as the concentration of the substrate such as carbohydrate in wastewater, animal residue and some lignocellulosic materials. Sensitivity of S when X is constant and vice versa will enable researchers to venture into materials with certain desired concentrations; example is in the production of biofertilizers and biogas, where amount of X and S is highly important.

For a system with constant X_0=3× 〖10〗 ^6 mg/l at μ_max= 0.009 hr-1 and K_s=4× 〖10〗 ^8 mg/l, at different initial substrate concentrations, S_0, which is 1× 〖10〗 ^5, 3× 〖10〗 ^5, 7× 〖10〗 ^5, 9× 〖10〗 ^5, 1.1× 〖10〗 ^6, 1.3× 〖10〗 ^6 and 1.5× 〖10〗 ^6 mg/l, Figure 2 shows that there is a proportional relationship with X.

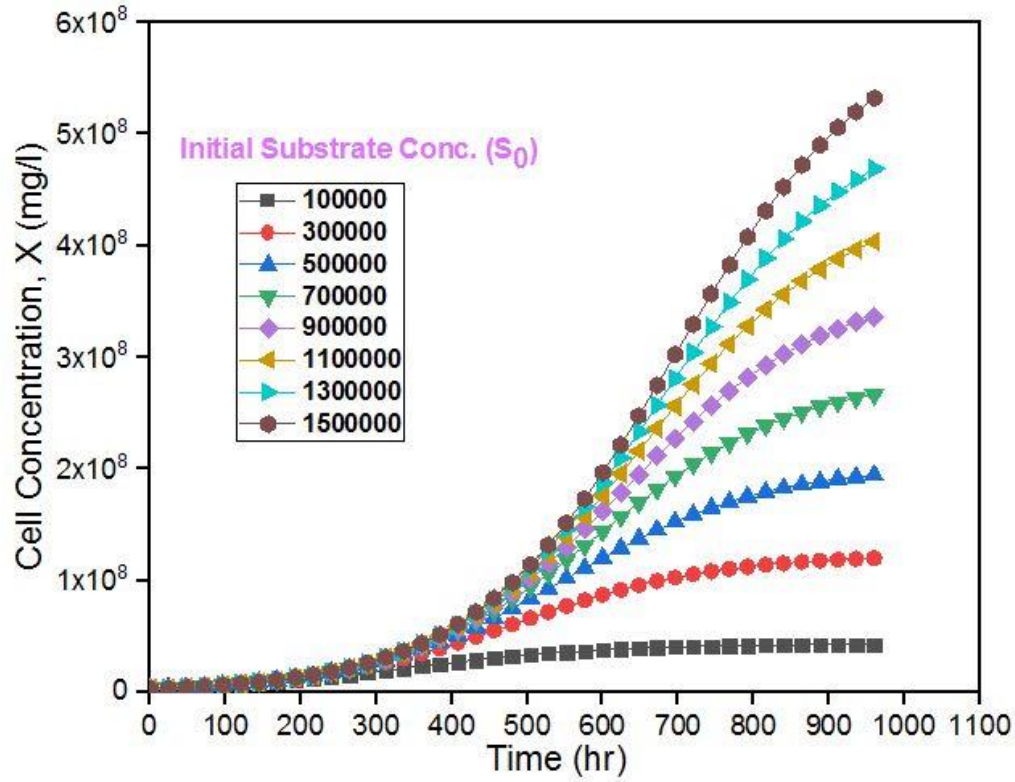

Figure 2: Cell Concentration at Different Initial Substrate Concentration

That is, the medium with the highest amount of initial S_0, will produce the most cells as sufficient nutrient is present for the metabolism of the organisms. S_0=1500000mg/l produces maximal cell density equivalent to 5.82× 〖10〗^8 mg/l while tge medium with the lowest initial value, S_0= 100000 mg/l produces maximum X = 4.29× 〖10〗^7 mg/l at the end of the process. Same with Figure 1, increase in X corresponds to a respective decrease in S from their initial values as shown in Figure 3.

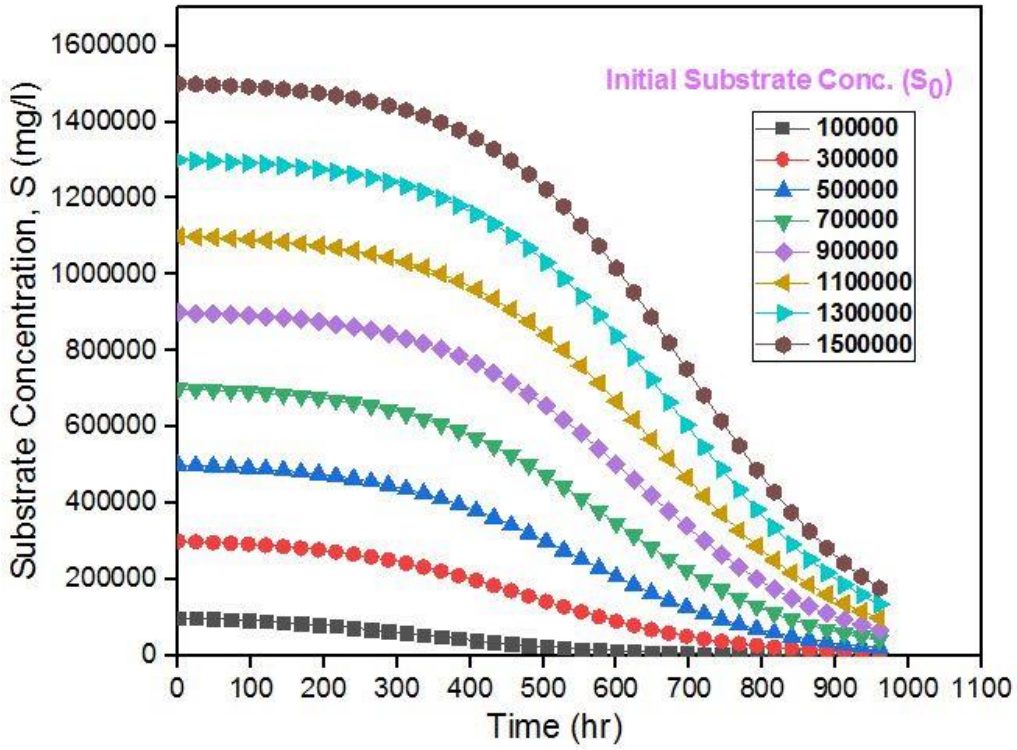

Figure 3: Substrate Concentration from Different Initial Values

Though, microbial growth rate will be inhibited by the substrate when S is high, increase in S imply a corresponding increase in the reaction rate, because more substrate molecules agitate and collide with enzyme molecules generated by the cells to form more product. Enzymes do not work faster even when the substrate is plentiful, so if rate of reaction requires increase, enzyme concentration should be increased not S. when amount of available S goes beyond the volume of enzyme, then breaking down of substrate automatically stops.

3.3 Change In Kinetic Parameters

The kinetic parameters, μ_max and K_s are not peculiar to Monod model alone – they are also part of several other models likes the Yano & Koga inhibition model, Moser, Powell, Han and Levenspiel, Dabes, Wagman and Tseng, Luong, Andrew substrate inhibition and decay rate models, Blackman, Haldane, Heijnen and Romein and Double exponential growth kinetic models among others, which can be estimated by fitting to empirical or correlated results as explained earlier. Where Y = 400, S_0 = 100000 mg/l and X_0=3× 〖10〗^6 mg/l, different combinations of μ_max and K_s as shown in Figure 4 will give different μ versus S line.

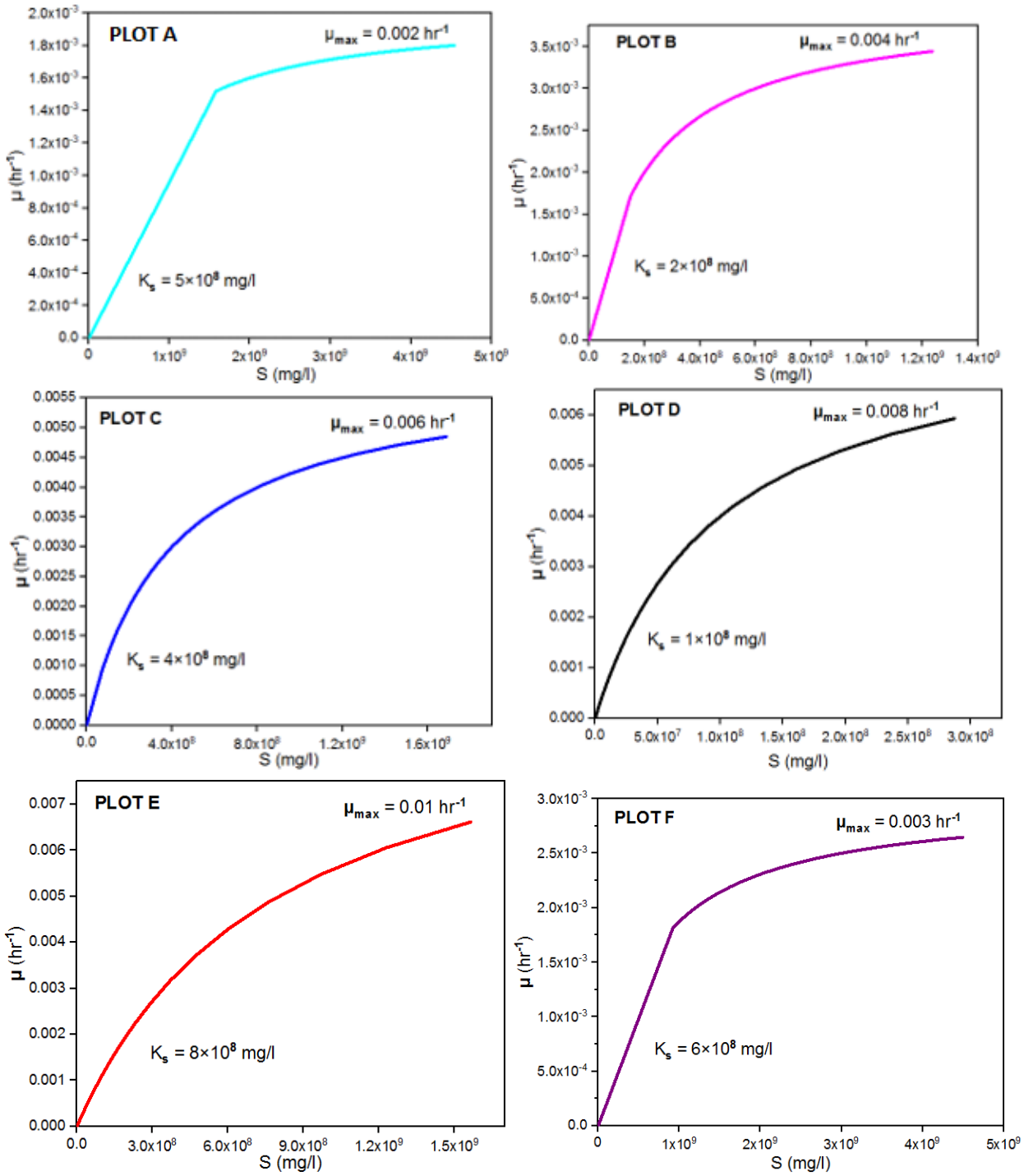

Figure 4: Parameters from Specific Growth Rate-Time Graphs

In the figure, an increase in μ_max from 0.002hr-1 in PLOT A, to 0.003hr-1 in PLOT F shows a corresponding increase in K_s for the same substrate concentration. The same trend is observed moving from PLOT F-A, C-E, D-E and B-C. Exceptions are PLOT A-B, A-D, F-D and F-B indicating a decrease in the end plot values of K_s. But findings of Agarry et al. (2010) shows that as μ_max decreases, K_s increase when there is jump in S_0.

3.4 Yield Coefficient

It was found that, when X_0= 3000000 mg/l and S_0= 100000 mg/l, μ_max increases slowly at every 100 interval of Y. An increase in S_0 to 200000 mg/l at constant X_0 value stated, reduces Y, whereas at constant S_0= 100000 mg/l, decrease in X_0 result in increase in Y. Figure 5 shows that Y above 700 tends to give a constant but high μ_max.

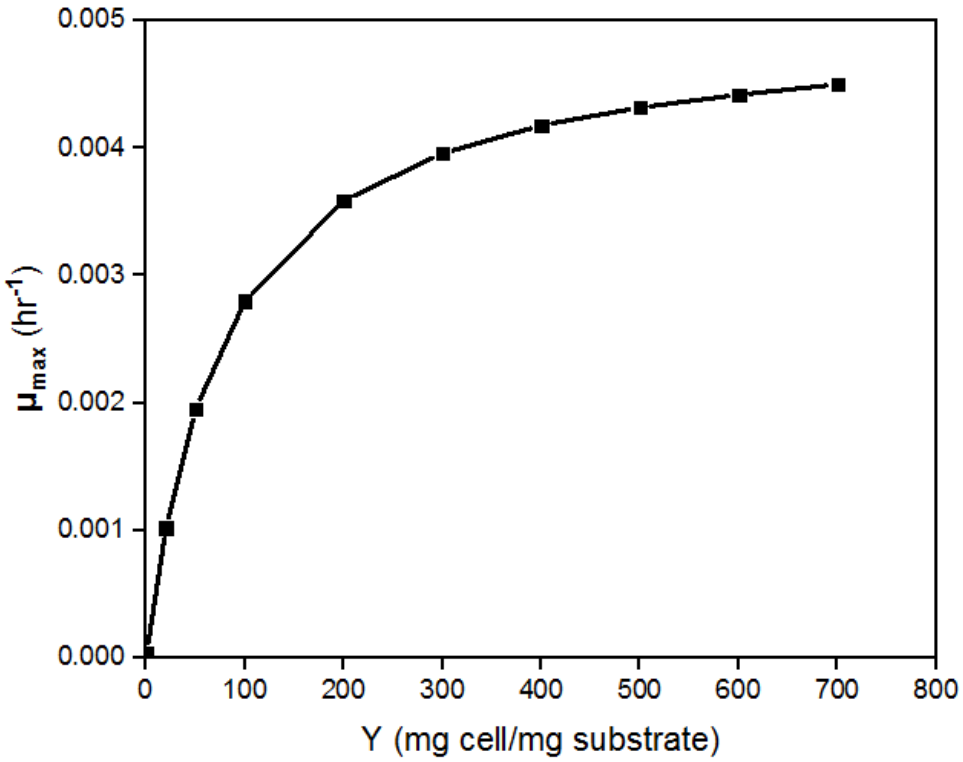

Figure 5: Maximum Specific Growth Rate with Yield Coefficient

From Y = 50, Figure 5 can be described as a nonlinear relationship of μ_{max} and Y as well as in Monod plots of μ against S. But below 50, a linear plot is obvious – same with the Monod line. Therefore high Y is synonymous with high μ_{max} value and high S and vice versa.

4. CONCLUSION

In conclusion, kinetic parameter values are hardly available for many microorganisms in nature together with substrate type. Predicted data presented in this work covers only the range of values of X and S, from the initial to the final at time = 960 hours. Many microorganisms are capable of multiplying beyond this period. Methods of determining cell density should be carefully studied to suggest ways to improve the accuracy of data obtainable.

REFERENCE

[1]M. A. Nikitina and I. M. Chernukha, "Studying growth kinetics of microbial populations using information technology. Solving the Cauchy problem," in *BIO Web of Conferences*, 2020, vol. 23, pp. 1–6, doi: https://doi.org/10.1051/bioconf/20202302004.

[2]F. Rezvani, F. Ardestani, and G. Najafpour, "Growth kinetic models of five species of Lactobacilli and lactose consumption in batch submerged," *Brazilian J. Microbiol.*, vol. 48, no. 2, pp. 251–258, 2017, doi: 10.1016/j.bjm.2016.12.007.

[3]P. Sakthiselvan, S. S. Meenambiga, and R. Madhumathi, *Kinetic studies of on cell growth*. IntechOPen, 2019.

[4]G. C. Okpokwasili and C. O. Nweke, "Microbial growth and substrate utilization kinetics," *African J. Biotechnol.*, vol. 5, no. 4, pp. 305–317, 2005, [Online]. Available: http://www.academicjournals.org/AJB%0D.

[5]S. Liu, "How cells grow," in *Bioprocess Engineering: Kinetics, Sustainability, and Reactor Design*, 2nd ed., Elsevier B. V, 2017, pp. 629–697.

[6]S. E. Agarry, B. O. Solomon, and T. O. K. Audu, "Substrate utilization and inhibition kinetics: Batch degradation of phenol by indigenous monoculture of Pseudomonas aeruginosa," *Int. J. Biotechnol. Mol. Biol. Res.*, vol. 1, no. 2, pp. 22–30, 2010, [Online]. Available: http://www.academicjournals.org/IJBMBR ISSN.