HIBISCUS PUBLISHER

BIOREMEDIATION SCIENCE AND TECHNOLOGY RESEARCH

Website: http://journal.hibiscuspublisher.com/index.php/BSTR


**Short Communication**

# Bartlett and the Levene's Tests of Homoscedasticity of the Modified Gompertz Model Used in Fitting of *Burkholderia* sp. strain Neni-11 Growth on Acrylamide

Mohd. Yunus Shukor[1]*

[1]Department of Biochemistry, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, UPM 43400 Serdang, Selangor, Malaysia.

*Corresponding author:
Associate Prof. Dr. Mohd Yunus Shukor
Department of Biochemistry,
Faculty of Biotechnology and Biomolecular Sciences,
Universiti Putra Malaysia,
UPM 43400 Serdang, Selangor, Malaysia
Tel: +60389478292
Email: mohdyunus@upm.edu.my / yunus.upm@gmail.com

**HISTORY**

Received: 7th April 2016
Received in revised form: 10th May 2016
Accepted: 15th of May 2016

**KEYWORDS**

modified Gompertz
bacterial growth
homoscedasticity
Bartlett's test
Levene's test

**ABSTRACT**

Most often than not, microorganism's growth curve is sigmoidal in characteristics. The modified Gompertz model via nonlinear regression using the least square method is one of the most popular methods to describe the growth curve. One of the assumptions of a good model is that the variance of the data must be homogenous (homoscedasticity). In this work, two statistical diagnostics; the Bartlett and the Levene's tests was performed to a modified Gompertz model utilized to model the growth of the bacterium *Burkholderia* sp. strain Neni-11 on acrylamide in order to satisfy the requirement above and found that data conformed to the requirement indicating the modified Gompertz model is a robust model for modelling the bacterial growth process.

## INTRODUCTION

The nonlinear regression utilizes the ordinary least squares method for mathematically fitting the nonlinear curve of the Luong model. However, the use of statistical tests to choose the best model relies heavily on the residuals of the curve to be normally distributed, of equal variance (homoscedastic) and random. Nevertheless, the usage of statistical tests to select the ideal model depends heavily on the residuals of the curve to generally be normally distributed, of equal variance (homoscedastic) and random.

The nonlinear regression utilizes the ordinary least squares method for mathematically fitting the nonlinear curve of the Luong model. However, the use of statistical tests to choose the best model relies heavily on the residuals of the curve to be normally distributed, of equal variance (homoscedastic) and random. Nevertheless, the usage of statistical tests to select the ideal model depends heavily on the residuals of the curve to generally be normally distributed, of equal variance (homoscedastic) and random. One of many assumptions of parametric-based nonlinear regression is that the within-group variances of the groups are all the same (exhibit homoscedasticity). If the variances are different from each other (exhibit heteroscedasticity), then the model is not statistically adequate to explain the data [1]. Several tests are available to check the equality of variances on residual data from three or more samples and include those of Cochran, Bartlett, Brown–Forsythe and Levene; the F-test is used to check for homogeneity of two variances.

The equality of variance or homoscedasticity can be presented and assessed visually roughly in the form of a residual graph where evidence of possible heteroscedasticity can be ascertained from the points dispersion around the central line that tends to increase as the concentrations were increased. Under this condition, the variances are not homogeneous. The function of the Bartlett's and the Levene's tests is to further confirm this observation [2–4]. In this work, Bartlett's test would be used to test for homogeneity of variance (homoscedasticity) or equality of variance of the residuals [4–7].

## MATERIALS AND METHODS

### Acquisition of Data

Data on the growth of the bacterium *Burkholderia* sp. strain Neni-11 on acrylamide from Figure 6 as modelled using the modified Gompertz model from our previous works [8] was utilized in this study (**Fig. 1**).

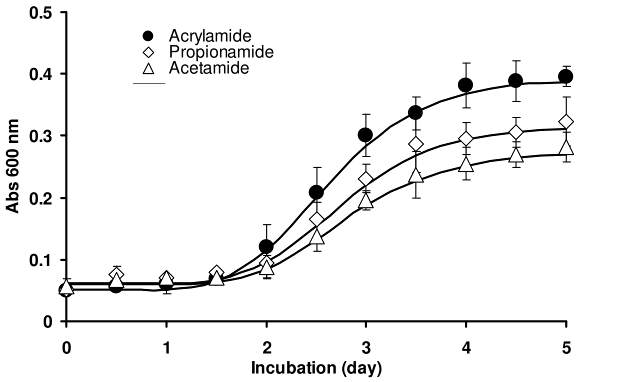


**Fig 1**. The growth of *Burkholderia* sp. strain Neni-11 on acrylamide, propionamide and acetamide as modelled using the modified Gompertz model (solid lines) (Fig. 6 from [5] reproduced with permission from Hibiscus Publisher).

### Test for equality of variance

### Bartlett's test

Bartlett's test is used to test the null hypothesis, $H_o$ that all $k$ population variances are equal against the alternative that at least the two are different. If there a $k$ samples with size $N_i$, sample variance of the $i$th group $S_i^2$ and $S_p^2$ is the pooled variance and the Bartlett's test statistic is;

$$\chi^2 = \frac{(N-k)\ln\left(S_p^2\right) - \sum_{i=1}^{k}(N_i - 1)\ln\left(S_i^2\right)}{1 + \frac{1}{3(k-1)}\left(\sum_{i=1}^{k}\left(\frac{1}{N_i - 1}\right) - \frac{1}{N-k}\right)} \qquad \textbf{(Eqn. 1)}$$

Where $N=\sum_{i=1}^{k}(n_i)$ and $S_p^2=\frac{1}{N-k}\sum_i (n_i-1)S_i^2$ are the variance pooled estimate. The test statistics have an approximately a $\chi^2_{k-1}$ distribution. The null hypothesis is rejected if $\chi^2 > \chi^2_{k-1,\alpha}$ where for a $\chi^2_{k-1}$ distribution, $\chi^2_{k-1,\alpha}$ is the upper tail critical value.

### Levene's test

The test statistic, W, is defined as follows:

$$W = \frac{(N-k)}{(k-1)} \frac{\sum_{i=1}^{k} N_i (Z_{i\cdot} - Z_{\cdot\cdot})^2}{\sum_{i=1}^{k} N_i (Z_{ij} - Z_{i\cdot})^2} \qquad \textbf{(Eqn. 2)}$$

Where,

$k$ is the number of different groups to which the sampled cases belong,
$N_i$ is the number of cases in the $i$-th group,
$N$ is the total number of cases in all groups,
$Y_{ij}$ is the value of the measured variable for the $j$-th case from the $i$-th group,

$$Z_{ij} = \begin{cases} |Y_{ij} - \bar{Y}_{i.}|, & \bar{Y}_{i.} \text{ is a mean of the } i\text{-th group,} \\ |Y_{ij} - \tilde{Y}_{i.}|, & \tilde{Y}_{i.} \text{ is a median of the } i\text{-th group.} \end{cases}$$

The test statistic for the Levene's test or $W$ is roughly F-distributed and has $N$-$k$ and $k$-$1$ degrees of freedom, and hence is the significance of the outcome $w$ of $W$ tested against the quantile of the F-distribution, which is $F$ with $k$-$1$ and $N$-$k$ degrees of freedom. The selected level of significance or alpha is usually 0.05 or 0.01.

## RESULTS AND DISCUSSION

The Bartlett tests is adequate to test for homogeneity of variance (homoscedasticity) or equality of variance of the residuals [9]. The results of the Bartlett's test show that the value of $\chi 2$ was at 15.904 and the critical value was 18.31. Using the CHIDIST function from Excel, a probability of 0.188 was obtained (not significant) indicating that there were no real differences between the variances of the residuals.

The Levenes's test gave a p-value of 0.435, also indicating that there were no real differences between the variances of the residuals. Levene's test for homogeneity of variances [2] is sturdy and it is generally utilized to check out the probable presence of homoscedasticity especially for data coming from 3 or more samples. It is actually much less affected to nonnormality compared to Bartlett's test [4], which needs to be utilized as long as there is certainly persuading proof that the trial outcomes originate from a normal distribution. It is strongly suggested the utilization of the Levene test to evaluate for homogeneity of variances for groups of analytical data.

In conclusion, the test for the homogeneity of variance for the Luong model in fitting of the reduction curve in this bacterium is adequate. The tests statistics carried out in this work is important since if the results obtained violated the homogeneity of variance then a remedy can be made which include transformation of the data by various transformation methods such as the square-root transformation for count data or the log transformation for size data and the Arcsine transformation for proportion data to name a few.

## REFERENCES


1. Shukor MS, Shukor MY. Statistical diagnostic tests of the Luong model in fitting molybdenum reduction from the bacterium *Bacillus* sp. strain A.rzi. J Environ Microbiol Toxicol. 2014;2(2):53–7.
2. Brown MB, Forsythe AB. Robust tests for the equality of variances. J Am Stat Assoc. 1974;69(346):364–7.
3. Bartlett MS. Properties of sufficiency and statistical tests. Proc R Soc Lond Ser Math Phys Sci. 1937;268–82.
4. Snedecor GW, Cochran WG. Statistical methods. 7th ed. Ames Iowa: Iowa State University Press; 1980.
5. Motulsky HJ, Ransnas LA. Fitting curves to data using nonlinear regression: a practical and nonmathematical review. FASEB J Off Publ Fed Am Soc Exp Biol. 1987;1(5):365–74.
6. López S, Prieto M, Dijkstra J, Dhanoa MS, France J. Statistical evaluation of mathematical models for microbial growth. Int J Food Microbiol. 2004;96(3):289–300.
7. Mcdonald JH, Dunn KW. Statistical tests for measures of colocalization in biological microscopy. J Microsc. 2013;252(3):295–302.
8. Mansur R, Gusmanizar N, Dahalan FA, Masdor NA, Ahmad SA, Shukor MS, et al. Isolation and characterization of a molybdenum-reducing and amide-degrading *Burkholderia cepacia* strain neni-11 in soils from west Sumatera, Indonesia. IIOAB. 2016;7(1):28–40.
9. Jarque CM, Bera AK. Efficient tests for normality, homoscedasticity and serial independence of regression residuals: Monte Carlo evidence. Econ Lett. 1981;7(4):313–8.