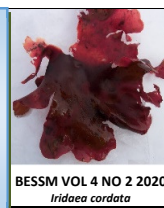


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Short communication

Test of the Randomness of Residuals for the von Bertalanffy model Fitting *P. aeruginosa* Growth Inhibition by Phytochemicals from *Adantum philippensis* Extract

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ABSTRACT

Numerous publications ignore statistical diagnosing of the nonlinear model utilized, and the data might be nonrandom- an essential necessity for all of the parametric statistical evaluation approaches. In cases where the diagnostic tests demonstrate that the residuals reveal a pattern, then a variety of remedies for example nonparametric analysis or shifting to another model should cure the problem. In order for randomness to be met we perform the Wald-Wolfowitz runs test statistical diagnosis tests. In this study, a test for the randomness of the residual for the von Bertalanffy model used in fitting the growth of *Pseudomonas aeruginosa* biofilm in the presence of the phytochemicals from the plant *Adantum philippensis* was carried out using the Wald-Wolfowitz runs test. The number of runs was 13, the expected number of runs under the assumption of randomness was 7.514, indicating the series of residuals had adequate runs and as the p-value was greater than 0.05, the null hypothesis is not discarded, suggesting no compelling proof of non-randomity of the residues.

INTRODUCTION

Phytochemicals are compounds produced mainly by plants that have a biochemical or medicinal impact. Plants are the prime basis for the manufacturing of various active ingredients in the pharmaceutical industry. Plant chemicals show pharmacological results that are useful for the management of bacterial and fungal infections, as well as cancer and diabetes [1]. Present multi-resistance bacterial as well as biofilm present a problem with resistance not just to conventional but also to new therapies. Screening and production of novel active products for newer improved alternate biofilm management approaches have encouraged the development of novel drugs and antimicrobials [2].

Biofilms are a three-dimensional, surface-attached, lightweight, structured, and embedded microbial population in a matrix of proteins, polysaccharides and other self-produced extra-cell materials [3]. Foodborne pathogens are typically

competent to bind to multiple (inert or living) surface forms and to form organic films. The bacteria inside them, after the biofilm is produced, are less vulnerable than their counterpart to antibiotics and other chemical agents and planktonic cells [4]. Phenol, terpenoid, flavonoid and starch containing phytochemicals hinder the development of biofilms. In the absence and presence of targeted phytochemicals, a nonlinear regression of appropriate bacterial growth models is required to mathematically assess the growth rate of a bacterial biofilm. Models such as von Bertalanffy, Baranyi-Roberts, modified Schnute, modified Richards, modified Gompertz, Modified Logistics and Huang are among popular growth models.

However, it is critical that the residuals of the curve using the usual the least square approach require that the residues to be naturally distributed in a nonlinear regression. of equal variance (homoscedastic), and more importantly the residuals must be random. In order for randomness to be met we perform the Wald-Wolfowitz runs test [5] statistical diagnosis tests. The subject of

this study is test for the randomness of the residual for the von Bertalanffy model used in fitting the growth of *P. aeruginosa* biofilm in the presence of the phytochemicals from the plant *Adantum philippensis*.

METHODOLOGY

A predictive mathematical modeling of the biofilm inhibiting potentials of phytochemicals from *A. philippense* extract and adhesion with *P. aeruginosa* showed that the von Bertalanffy was found to be the best model (published elsewhere).

Residuals

Residuals are very important in assessing the health of a curve from a particular used model. Mathematically, residual for the i^{th} observation in a given data set can be defined as follows (Eqn. 1);

$$e_i = y_i - f(x_i; \hat{\beta}) \quad (\text{Eqn. 1})$$

where y_i denotes the i^{th} response from a given data set while x_i is the vector of explanatory variables to each set at the i^{th} observation corresponding values in the data set.

Runs test

The runs test [6] was performed to the residuals of the regression in an effort to identify nonrandomness. In a specific model, an ordered variance of the curve could be calculated above or below estimate [5]. The run test contrasts the usually negative and optimistic sequence of residues. An outstanding result is typically demonstrated by a shift or combination between the negative and positive residual values. The number of sign runs is normally shown with the highest possible proportion. The running test measures the chance of a many or an insufficient amount of sign passes. Too many run signs may show that there is a negative serial association, and that too little runs can reveal that residues are correlated with the very same sign or that systemic biases occur.

The test statistic is

H_0 = the sequence was produced randomly
 H_a = the sequence was not produced randomly

$$Z = \frac{R - \bar{R}}{sR} \quad (\text{Eqn. 2})$$

Where Z is the test statistic, $\bar{R}$ is the expected number of runs, R is the observed number of runs and sR is the standard deviation of the runs. The computation of the values of $\bar{R}$ and sR (n_1 is positive while n_2 is negative signs) is as follows;

$$\bar{R} = \frac{2n_1n_2}{n_1+n_2} + 1 \quad (\text{Eqn. 3})$$

$$s^2R = \frac{2n_1n_2(2n_1n_2 - n_1 - n_2)}{(n_1+n_2)^2(n_1+n_2-1)} \quad (\text{Eqn. 4})$$

As an example

Test statistic: $Z = 3.0$

Significance level: $\alpha = 0.05$

Critical value (upper tail): $Z_{1-\alpha/2} = 1.96$

Critical region: Reject H_0 if $|Z| > 1.96$

If the test statistical value (Z) is greater than the critical value, then the dismissal of the null hypothesis at the significance

stage of 0.05 implies that the sequence was generated in a non-random manner.

RESULTS AND DISCUSSION

The fitting of a mathematical model may be scientifically diagnosed exactly by utilizing residual measures. Residuals are the difference between the predicted and actual quantity values of a given mathematical model. The general concept would be that a weak model would display a larger discrepancy between the expected and the actual values.

Runs test

From **Table 1**, the number of runs was 13, the expected number of runs under the assumption of randomness was 7.514, indicating the series of residuals had adequate runs. The z-value shows how many normal errors the number of runs found is beyond the predicted number of runs, and the accompanying p-value indicates how extreme this z-value is. The meaning is the same as the other data on p-values. If the p-value is less than 0.05, the null hypothesis that the residuals are indeed random can be dismissed. As the p-value was greater than 0.05, however, the null hypothesis is not discarded, suggesting no compelling proof of non-randomity of the residues and does reflect noise.

Table 1. Runs test for randomness.

Runs test	Residual data set
R=	5
n0=	8
n1=	5
n=	13
E(R)=	7.514
Var(R)=	2.643
StDev(R)=	1.626
Z=	-1.325
p-value=	0.093

The run test is a significant method to diagnose non-randomness in non-linear regression dependent on the residues [6]. The run test could identify systemic variation of the curve, such as above or under segment estimation, by using a particular model. The run test tests the set of residues that are normally favorable and negative. Strong run is typically characterized by rotating or matching the amount of positive and negative residual values. The number of sign runs is typically calculated as a percentage of the maximum total number [5].

In time-series regression models, the run procedure is often used as a test tool for the existence of autocorrelation. Precisely, simulation experiments using Monte Carlo have shown that the run-time test causes strikingly asymmetrical error rates in the two tails, indicating that the usage of run-time autocorrelation research might not be stable and that the Durbin-Watson approach will be the preferred method for measuring autocorrelation [7].

Previous similar studies based on looking at the randomness of the residuals justify the method use in this study. For instance the use of the the Buchanan-three-phase model used in the fitting the growth of *Paracoccus* sp. SKG on acetonitrile [8], the Baranyi-Roberts model in fitting an algae growth curve which shows adequacy in the statistics [9], and *Moraxella* sp. B on monobromoacetic acid (MBA) [10]. In biosorption, the runs test carried out on the residuals for the Sips and Freundlich models for lead (II) uptake by alginate gel bead were found to be adequate [11].

CONCLUSION

In this study, a test for the randomness of the residual for the von Bertalanffy model used in fitting the growth of *P. aeruginosa* biofilm in the presence of the phytochemicals from the plant *Adiantum philippensis* was carried out using the Wald–Wolfowitz runs test. The number of runs was 13, the expected number of runs under the assumption of randomness was 7.514, indicating the series of residuals had adequate runs and as the p-value was greater than 0.05, the null hypothesis is not discarded, suggesting no compelling proof of non-randomity of the residues.

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