



Short Communication

Test for the Presence of Autocorrelation in the Morgan-Mercer-Flodin (MMF) Model used for Modelling the Total Number of COVID-19 Cases for Brazil

A. Aisami¹, Abubakar M. Umar², Motharasan Manogaran³ and M.Y. Shukor^{3*}

¹Department of Biochemistry, Faculty of Science, Gombe State University, Nigeria

²Department of Biological Sciences, Faculty of Science, Gombe State University, P.M.B. 027, Gombe, Nigeria

³Department of Biochemistry, Faculty of Biotechnology and Biomolecular Sciences, Universiti Putra Malaysia, UPM 43400 Serdang, Selangor, Malaysia.

*: *Corresponding author:

Prof. Dr. Mohd. Yunus Abd. Shukor

Department of Biochemistry,

Faculty of Biotechnology and Biomolecular Sciences,

Universiti Putra Malaysia,

UPM 43400 Serdang,

Selangor,

Malaysia.

Email: yunus.upm@gmail.com

HISTORY

Received: 13th April 2021
Received in revised form: 3rd July 2021
Accepted: 23rd July 2021

KEYWORDS

COVID-19
MMF model
Nonlinear regression
Autocorrelation
Durbin-Watson test

ABSTRACT

Mathematical models can be used to conduct COVID-19 pandemic analyses, including theoretical, quantitative, and simulation analyses. COVID-19 pandemic models such as the modified Gompertz, von Bertalanffy, modified logistics including the recent MMF model which was the best model in fitting the total number of COVID-19 cases for Brazil. We were the first to note the high suitability of the MMF model to fit total death and infection cases for COVID-19. The least-squares approach, which is employed in conventional nonlinear regression, including the MMF model, must be subjected to the idea that data points do not rely on one another and that the value of a data point is not impacted by the value of data points that came before or after it. This is known as autocorrelation and the Durbin-Watson test can be utilized to check the conformity of this model to non-autocorrelation. The value of the Durbin-Watson statistics was $d = 0.648$. The statistic is approximately equal to $2(1 - p)$. We then test the hypothesis $H_0: \rho = 0$ versus the alternative hypothesis of $H_1: \rho > 0$. From the Durbin-Watson table [1,2] for $n=50$ and 4 parameters, the lower critical value for dL was 1.206, while the upper critical value dU was 1.537. According to this, the d value was lower than the lower critical value or dL , resulting in the null hypothesis being rejected or indicating that there is evidence of autocorrelation. This demonstrates that the MMF model used in the nonlinear regression model for modelling the total number of COVID-19 cases for Brazil needs remedial action, perhaps identifying potential outliers.

INTRODUCTION

A respiratory disease outbreak that began in Wuhan, China, then spread to numerous other countries affected several countries throughout the world. The virus that caused the outbreak, 2019-nCoV, was discovered [3]. As the global death toll from COVID-19 rises, there is a growing awareness of the inequitable distribution of SARS-COV-2 mortality among vulnerable populations. Elderly persons, people living in densely populated regions, people with low socioeconomic status, refugees, and minorities are all vulnerable groups to consider. Almost every group is in jeopardy. Because these groups have higher infection

rates than the overall population, they are more vulnerable to infection and serious sickness outcomes [4]. For a time, modelling research was concentrated on the dynamics of the epidemic in Wuhan City and Hubei Province [5]. At this early stage, the review of surveillance data from China to provide parameter estimates such as the basic reproduction number (R_0), case fatality rate, and incubation duration has taken a significant amount of time and effort [6]. Parameter estimates for the early attempts at Susceptible-Exposed-Infectious-Recovered (SEIR) style dynamic models were 'stolen' from what was known about other coronaviruses (SARS-CoV and MERS-CoV) and/or gained

by fitting the models to monitoring data gathered during the initial outbreaks [7].

COVID-19 pandemic analyses can be performed using statistical models, including theoretical, quantitative and simulation. Organisms growth including viral infection cases over time usually exhibit a sigmoidal growth profile that exhibits lag time (\square), acceleration to a maximal value (\square_m) and a final phase where the rate decreases and eventually reaches zero or an asymptote (A) is observed [8]. The sigmoidal curve can be fitted by different mathematical functions, such as Logistic [8,9], modified Gompertz [8,10], Richards [8,11], Schnute [8,12], Baranyi-Roberts [13], Von Bertalanffy [8,14–16], Buchanan three-phase [17,18], Huang [19–22] and and Morgan-Mercer-Flodin (MMF) [23–32,32–36]. For the analysis of the COVID-19 pandemic [5], strong predictive ability was employed models, such as updated Gompertz and Bertalanffy and logistics. The total infection case of SARS-CoV-2 in Brazil as of 15th of July 2020 to the 20th of December 2020 was modelled using several primary growth models with the MMF models found to be the best [32]. We were the first to note the high suitability of the MMF model to fit total death and infection cases for COVID-19 [30,31,33,35,37–40].

The least-squares technique used in normal nonlinear regression including in the MMF model must be subjected to the notion that data points do not rely on one another and that the value of a data point is not affected by the value of data points that came before or after it. This is called autocorrelation. In the most extreme case of autocorrelation, temperature drift occurs throughout the duration of time measurements, and this drift influences the results of the measurements as they occur in a series of visible patterns. Another example is a spectrophotometer with a tungsten light that has been overused. The presence of autocorrelation cannot be avoided in certain circumstances, such as when the number of creatures that appear each year in a specific area is highly associated with and dependent on the number of creatures that appeared the prior year [41]. That of bacteria is very similar, in that any event that affects the current or previous quantities of cells will be seen in a more pronounced manner at a later period than it is at the moment of the event itself. The Durbin-Watson statistic is one of the most often used methods to determine whether or not there is autocorrelation. Draper and Smith's technique of calculating the level of significance is used to determine the level of significance in this method [1,42,43]. To test for the adequacy of the MMF model previously used in fitting the total COVID-19 cases in Brazil [32], as far as autocorrelation is concerned, the Durbin-Watson test was utilized in this study.

MATERIALS AND METHODS

Acquisition of Data

Data on the mathematical modelling of the total number of COVID-19 cases for Brazil using the MMF model (**Equation 1**) from our previous works [32] was utilized in this study (Fig. 6).

$$y = y_{max} - \frac{(y_{max} - \beta)}{1 + (\mu_m t)^\delta} \quad (\text{Equation 1})$$

Durbin-Watson test

In the Durbin-Watson test, a statistical calculation is carried out to test for the level of significance [42].

$$d = \frac{\sum_{t=2}^T (\hat{e}_t - \hat{e}_{t-1})^2}{\sum_{t=1}^T \hat{e}_t^2} \quad (1)$$

In this test, the usual hypothesis where $H_0: \rho = 0$ versus the alternative $H_1: \rho > 0$ is performed. The statistic is approximately equal to $2(1 - \rho)$. When the value is zero, the Durbin-Watson test statistic is 2, and when the value is one, the Durbin-Watson test statistic is 0. Non-autocorrelation was indicated by a d value near 2, while positive autocorrelation was indicated by a d value around 0. Negative autocorrelation is shown by d values approaching 4 (**Eqn. 1**).

When the Durbin-Watson test statistics are low, the null hypothesis should be rejected because it indicates the presence of autocorrelation. Unlike Because there is no distribution of the - value in the Durbin-Watson test statistics associated with d, such as the t- or z-statistics, tables must be used in hypothesis testing.

The decision rule for the Durbin-Watson bounds test is

- if $d >$ upper bound, fail to reject the null hypothesis of no serial correlation,
- if $d <$ lower bound, reject the null hypothesis and conclude that positive autocorrelation is present,
- if lower bound $< d <$ upper bound, the test is inconclusive.

RESULTS AND DISCUSSION

The value of the Durbin-Watson statistics was $d = 0.648$. The statistic is approximately equal to $2(1 - \rho)$. We then test the hypothesis $H_0: \rho = 0$ versus the alternative hypothesis of $H_1: \rho > 0$. From the Durbin-Watson table [1,2] for $n = 50$ and 4 parameters, the lower critical value for d_L was 1.206, while the upper critical value d_U was 1.537. According to this, the d value was lower than the lower critical value or d_L , resulting in the null hypothesis being rejected or indicating that there is evidence of autocorrelation. This demonstrates that the MMF model used in the nonlinear regression model for modelling the total number of COVID-19 cases for Brazil needs remedial action, perhaps identifying potential outliers.

Autocorrelation is a measure of the degree of correlation (similarity) between two or more adjacent observations, and it is defined as Space autocorrelation is a measure of a variable's association with itself over time and space, and it can be either negative or positive depending on the variables involved. Negative spatial autocorrelation is noticed when unique values are found adjacent to one another; on the other hand, positive spatial autocorrelation is exhibited when undifferentiated values are found close to one another. However, even though it is a fundamental theory in spatial statistics, its characteristics and calculations are commonly misunderstood and misrepresented. It has both advantages and disadvantages. It has advantages in that it allows for spatial interpolation, but it has disadvantages in that statistical testing becomes more complex. Temporal autocorrelation is an extension of this notion; however, it is a little more complicated to understand and apply.

The time that simply goes in one direction is taken into consideration in temporal autocorrelation, but things with complicated shapes and more than two dimensions are taken into consideration in spatial autocorrelation, where determining what is close by might be challenging. A variable's organised spatial variation in a dataset is measured using this method. In places that are close to one another and have values of variables that are

indistinguishable from one another, positive spatial autocorrelation is seen. Whenever there is a negative spatial autocorrelation, the values that are adjacent to each other are not the same as each other [44–50].

Auto-related data causes the degree of freedom from statistics on inferential tests and leads to faux correlations between variables [51]. In a fundamental modelling exercise such as modified Gompertz and other models, the usage of the Durbin Watson test to test for autocorrelation data in time series are widespread [52–56]. The Breusch-Godfrey Lagrange multiplier test is another method of detection of autocorrelation. When autocorrelation is identified, the researcher can fix the condition using numerous methods of transformation, such as Cochrane-Orcutt [57], Hildreth-Lu, or Prais-Winsten that can alleviate the presence of autocorrelation [58].

The Durbin-Watson test statistic evaluates the null hypothesis that residuals in regular less-field regression are not auto-related to the alternative that residuals in an AR1 process in which the current value is based on the immediately previous value, which is an autoregressive process. The statistical range of Durbin-Watson is between 0 and 4. Non-self-correlation is a value almost 2; positive autocorrelation is an indication for value towards 0; negative autocorrelation is an indication for value towards 4. In all feasible circumstances, the exact critical values of Durbin-Watson statistics are not tabled because of the reliance of any computed Durbin Watson value on the corresponding data matrix [52,53].

The crucial values were instead set by Durbin and Watson at the top and lower limits. The hypothesis of zero autocorrelation against the alternative positive self-relation of the first-order is typically utilised in tabular boundaries since positive autocorrelation is considerably more common in practice than negative autocorrelation. To use the table, the sample size must be cross-referenced to the number of regressors, eliminating the constant from the regressors count. When you do not have a permanent regression term, traditional Durbin Watson tables are not applicable. Instead, a proper set of Durbin-Watson tables must be referenced. Also, when the lagged variable is shown on a regressor, the traditional Durbin-Watson tables do not apply. For this example, Durbin suggested different testing methodologies.

Several factors might have contributed to the introduction of autocorrelation into the data [59], including the following:
1. Carryover of effect is a significant cause of autocorrelation, at least in part, due to the frequency with which it occurs. For example, statistics on monthly household expenditures are influenced by the same category of expenditure from the preceding month's data. A measure of autocorrelation may be found in both cross-sectional and time-series data sets. When looking at cross-sectional data, the feature under consideration is common in that it allows for the discovery of equal units. When working with time-series data, the element that causes self-correlation is the element of time. It is possible to have autocorrelation in data when certain sample units are ordered in the data. Another factor that contributes to autocorrelation is the effect of removing specific variables from an equation. It is not possible to include all of the variables in a regression model when using regression modelling techniques such as regression modelling. There are a variety of reasons for this, not the least of which is that certain variables are qualitative, that direct observations on the variable are not always accessible, and so on. The autocorrelation in the resulting data is caused by the cumulative impact of the variables that were eliminated [60–65].

The introduction of autocorrelation into the data might be caused by incorrectly defining the kind of connection. It is aimed to develop a linear relationship between the research and the explanatory factors in the link between the research and the explanatory variables. Because of a log or exponential factor in the model, the data exhibits autocorrelation. This is due to the model's linearity being questioned. It is referred to as a measurement error or error-in-variable for a variable when the difference between observed and actual values is more than one standard deviation.

Furthermore, the presence of measurement errors in the dependent variable may result in autocorrelation in the data set, which is undesirable. It is also known as serial correlation or autocorrelation. It is defined as the correlation of one signal with a delayed replica of itself as a function of time delay. Informally, it is the degree to which two observations are comparable as a function of the time-lapse between the observations. When it comes to locating recurring patterns, the study of autocorrelation is a mathematical method that can be used to determine the presence of a periodic signal that has been disguised by noise or to identify the missing fundamental frequency in a signal hinted by its harmonic frequencies. It is frequently used in signal processing to analyse functions or series of values, such as time-domain signals, and is particularly useful in signal processing.

CONCLUSION

The results of the autocorrelation exercise reveal that there is a presence of autocorrelation in the MMF model utilized in fitting the total number of COVID-19 infectious cases in Brazil. Based on the d value, which was lower than the lower critical value or dL , resulting in the null hypothesis being rejected or indicating that there is evidence of autocorrelation. This demonstrates that the MMF model used in the nonlinear regression model for modelling the total number of COVID-19 cases for Brazil needs remedial action, perhaps identifying potential outliers.

REFERENCES

The citation style we use is Vancouver (Bracket). Available for example from the free Zotero and many other reference management software. References should be Times New Roman, 8 font size.

1. Durbin J, Watson GS. Testing for serial correlation in least squares regression.III. *Biometrika*. 1971;58(1):1–19.
2. Park S-B. On the small-sample power of Durbin's h test. *J Am Stat Assoc*. 1975 Mar 1;70(349):60–3.
3. Guo Y-R, Cao Q-D, Hong Z-S, Tan Y-Y, Chen S-D, Jin H-J, et al. The origin, transmission and clinical therapies on coronavirus disease 2019 (COVID-19) outbreak – an update on the status. *Mil Med Res*. 2020 Mar 13;7(1):11.
4. Shadmi E, Chen Y, Dourado I, Faran-Perach I, Furler J, Hangoma P, et al. Health equity and COVID-19: global perspectives. *Int J Equity Health*. 2020 Jun 26;19(1):104.
5. Jia L, Li K, Jiang Y, Guo X, Zhao T. Prediction and analysis of Coronavirus Disease 2019. *ArXiv200305447 Q-Bio* [Internet]. 2020 Mar 16 [cited 2020 Jul 20]; Available from: <http://arxiv.org/abs/2003.05447>
6. Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. *Nat Med* [Internet]. 2020 Apr [cited 2020 Jul 23];26(4):450–2. Available from: <http://www.nature.com/articles/s41591-020-0820-9>
7. Tuite AR, Fisman DN, Greer AL. Mathematical modelling of COVID-19 transmission and mitigation strategies in the population of Ontario, Canada. *Can Med Assoc J* [Internet]. 2020 May 11 [cited 2020 Jul 23];192(19):E497–505. Available from: <http://www.cmaj.ca/lookup/doi/10.1503/cmaj.200476>

8. Zwietering MH, Jongenburger I, Rombouts FM, Van't Riet K. Modeling of the bacterial growth curve. *Appl Environ Microbiol.* 1990;56(6):1875–81.
9. Ricker FJ. Growth rates and models. In: Hoar WS, Brett JR, Randall DJ, editors. *Fish Physiology*. New York: Academic Press; 1979. p. 677–743. (Bioenergetics and Growth; vol. Volume 8).
10. Gompertz B. On the nature of the function expressive of the law of human mortality, and on a new mode of determining the value of life contingencies. *Philos Trans R Soc.* 1825;115:513–85.
11. Richards, F.J. A flexible growth function for empirical use. *J Exp Bot.* 1959;10:290–300.
12. Schnute J. A versatile growth model with statistically stable parameters. *Can J Fish Aquat Sci.* 1981;38:1128–40.
13. Baranyi J, Roberts TA. A dynamic approach to predicting bacterial growth in food. *Int J Food Microbiol.* 1994;23(3–4):277–94.
14. von Bertalanffy L. *heoretische Biologie, Zweiter Band: Stoffwechsel, Wachstum.* A Francke AG Verlag, Bern, Switzerland; 1951. 418 p.
15. Anderson MJ, Millar RB, Blom WM, Diebel CE. Nonlinear multivariate models of successional change in community structure using the von Bertalanffy curve. *Oecologia.* 2005;146(2):279–86.
16. Schofield MR, Barker RJ, Taylor P. Modeling individual specific fish length from capture-recapture data using the von bertalanffy growth curve. *Biometrics.* 2013;69(4):1012–21.
17. Buchanan RL. Predictive food microbiology. *Trends Food Sci Technol.* 1993;4(1):6–11.
18. Peleg M, Corradini MG, Normand MD. The logistic (Verhulst) model for sigmoid microbial growth curves revisited. *Food Res Int.* 2007;40(7):808–18.
19. Huang L, Hwang C-A, Phillips J. Evaluating the effect of temperature on microbial growth rate-the Ratkowsky and a Bělehrádek-Type models. *J Food Sci.* 2011;76(8):M547–57.
20. Fang T, Gurtler JB, Huang L. Growth Kinetics and Model Comparison of *Cronobacter sakazakii* in Reconstituted Powdered Infant Formula. *J Food Sci.* 2012;77(9):E247–55.
21. Halmi MIE, Shukor MS, Johari WLW, Shukor MY. Evaluation of several mathematical models for fitting the growth of the algae *Dunaliella tertiolecta*. *Asian J Plant Biol.* 2014;2(1):1–6.
22. Huang L. Direct construction of predictive models for describing growth of *Salmonella Enteritidis* in liquid eggs - A one-step approach. *Food Control.* 2015;57:76–81.
23. Morgan PH, Mercer LP, Flodin NW. General model for nutritional responses of higher organisms. *Proc Natl Acad Sci.* 1975 Nov 1;72(11):4327–31.
24. Khamis A, Ismail Z, Haron K, Mohammed AT. Nonlinear Growth Models for Modeling Oil Palm Yield Growth. *J Math Stat.* 2005 Sep 30;1(3):225–33.
25. Topal M, Bolukbasi ŞC. Comparison of nonlinear growth curve models in broiler chickens. *J Appl Anim Res.* 2008 Dec 1;34(2):149–52.
26. Tariq M, Iqbal F, Eyduran E, Bajwa M, Huma Z, Waheed A. Comparison of non-linear functions to describe the growth in Mengali sheep breed of Balochistan. *Pak J Zool.* 2013 Jun 1;45:661–5.
27. Wijeratne AW, Karunaratne JA. Morgan-Mercer-Flodin model for long term trend analysis of currency exchange rates of some selected countries. *Int J Bus Excell.* 2013 Dec 2;7(1):76–87.
28. Augustine A, Imelda J, Paulraj R, David NS. Growth kinetic profiles of *Aspergillus niger* S14 a mangrove isolate and *Aspergillus oryzae* NCIM 1212 in solid state fermentation. *Indian J Fish.* 2015;62(3):100–6.
29. Kemper CM. Growth and development of the brush-tailed rabbit-rat (*Conilurus penicillatus*), a threatened tree-rat from northern Australia. *Aust Mammal.* 2020 Jun 5;
30. Aisami A, Shukor MYA. Predictive Mathematical Modelling of the Total Number of COVID-19 Cases for the Kingdom of Saudi Arabia. *J Environ Microbiol Toxicol.* 2020 Jul 31;8(1):11–5.
31. Shukor MYA, Sabo IA, Yahuza S, Dan-Iya BI, Wada SA. Prediction of Cumulative Death Cases in The United States Due to COVID-19 Using Mathematical Models. *J Environ Microbiol Toxicol.* 2020 Jul 31;8(1):37–41.
32. Uba G, Yakasai HM, Abubakar A, Shukor MYA. Predictive Mathematical Modelling of the Total Number of COVID-19 Cases for Brazil. *J Environ Microbiol Toxicol.* 2020 Jul 31;8(1):16–20.
33. Uba G, Yakasai HM, Abubakar A, Shukor MYY. Prediction of Cumulative Death Cases in Brazil Due to Covid-19 Using Mathematical Models. *Bull Environ Sci Sustain Manag.* 2020 Jul 31;4(1):13–9.
34. Yahuza S, Sabo IA, Dan-Iya BI, Shukor MYY. Prediction of Cumulative Death Cases in Nigeria Due to COVID-19 Using Mathematical Models. *Bull Environ Sci Sustain Manag.* 2020 Jul 31;4(1):20–4.
35. Yakasai HM, Shukor MYA. Predictive Mathematical Modelling of the Total Number of COVID-19 Cases for The United States. *Bioremediation Sci Technol Res.* 2020 Jul 31;8(1):11–6.
36. Umar AM, Shukor MYA. Predictive Mathematical Modelling of the Total Number of COVID-19 Cases for Indonesia. *J Environ Microbiol Toxicol.* 2020 Aug 1;8(1):27–31.
37. Nyoni T. Prediction of daily new Covid -19 cases in Indonesia using artificial neural networks. *Int J Adv Res Innov Ideas Educ.* 2020 Dec 15;6(6):2174–87.
38. Supriatna AK, Husniah H. Modeling Covid-19 cumulative data in Indonesia using Morgan-Mercer-Flodin growth equation. In: *Proceedings of the International Conference on Industrial Engineering and Operations Management*. Harare, Zimbabwe; 2020.
39. Uba G, Yakasai HM, Abubakar A, Shukor MYY. Prediction of Cumulative Death Cases in Brazil Due to Covid-19 Using Mathematical Models. *Bull Environ Sci Sustain Manag.* 2020 Jul 31;4(1):13–9.
40. Yahuza S, Sabo IA, Dan-Iya BI, Shukor MYY. Prediction of Cumulative Death Cases in Nigeria Due to COVID-19 Using Mathematical Models. *Bull Environ Sci Sustain Manag.* 2020 Jul 31;4(1):20–4.
41. Mcdonald JH, Dunn KW. Statistical tests for measures of colocalization in biological microscopy. *J Microsc.* 2013;252(3):295–302.
42. Draper NR, Smith H. *Applied Regression Analysis*. Wiley, New York; 1981.
43. Fahidy TZ. An application of Durbin–Watson statistics to electrochemical science. *Electrochimica Acta.* 2006;51(17):3516–20.
44. Huo L, Kim T-H, Kim Y, Lee DJ. A residual-based test for autocorrelation in quantile regression models. *J Stat Comput Simul.* 2017;87(7):1305–22.
45. Gaspard G, Kim D, Chun Y. Residual spatial autocorrelation in macroecological and biogeographical modeling: A review. *J Ecol Environ.* 2019;43(1).
46. Gilcher M, Ruf T, Emmerling C, Udelhoven T. Remote sensing based binary classification of maize. Dealing with residual autocorrelation in sparse sample situations. *Remote Sens.* 2019;11(18).
47. Miceli PA, Blair WD. Note on Autocorrelation of the Residuals of the NCV Kalman Filter Tracking a Maneuvering Target. In: *IEEE National Radar Conference - Proceedings*. 2020.
48. Chevalier M, Mod H, Broennimann O, Di Cola V, Schmid S, Niculita-Hirzel H, et al. Low spatial autocorrelation in mountain biodiversity data and model residuals. *Ecosphere.* 2021;12(3).
49. Kim D. Predicting the magnitude of residual spatial autocorrelation in geographical ecology. *Ecography.* 2021;44(7):1121–30.
50. Silva WDSE, Fernandes FA, Muniz FR, Muniz JA, Fernandes TJ. *Eucalyptus grandis* x *eucalyptus urophylla* growth curve in different site classifications, considering residual autocorrelation. *Rev Bras Biom.* 2021;39(1):122–38.
51. Legendre P, Troussellier M. Aquatic heterotrophic bacteria: Modeling in the presence of spatial autocorrelation. *Limnol Oceanogr.* 1988 Sep 1;33(5):1055–67.
52. Cayré ME, Vignolo G, Garro O. Modeling lactic acid bacteria growth in vacuum-packaged cooked meat emulsions stored at three temperatures. *Food Microbiol.* 2003 Oct 1;20(5):561–6.
53. Koirala SR, Gentry RW, Perfect E, Schwartz JS, Sayler GS. Temporal variation and persistence of bacteria in streams. *J Environ Qual.* 2008 Jul 1;37(4):1559–66.
54. Shukor MS, Shukor MY. Test for the presence of autocorrelation in the Buchanan model used in the fitting of the growth of the catechol-degrading *Candida parapsilopsis*. *J Environ Microbiol Toxicol.* 2014;2(2):45–6.
55. Halmi MIE, Shukor MS, Masdor NA, Shamaan NA, Shukor MY. Test of randomness of residuals for the modified Gompertz model

- used in the fitting the growth of sludge microbes on PEG 600. *J Environ Microbiol Toxicol*. 2015 Oct 30;3(1):9–11.
56. Halmi MIE, Shukor MS, Masdor NA, Shamaan NA, Shukor MY. Test for the presence of autocorrelation in the modified Gompertz model used in the fitting the growth of sludge microbes on PEG 600. *J Environ Microbiol Toxicol*. 2015 Oct 30;3(1):6–8.
 57. Cochran D, Orcutt GH. Application of Least Squares Regression to Relationships Containing Auto-Correlated Error Terms. *J Am Stat Assoc*. 1949 Mar 1;44(245):32–61.
 58. Dagenais MG. Parameter estimation in regression models with errors in the variables and autocorrelated disturbances. *J Econom*. 1994 Sep 1;64(1):145–63.
 59. Shalabh. Prediction of values of variables in linear measurement error model. *J Appl Stat*. 2000 May 1;27(4):475–82.
 60. Fassò A. Residual autocorrelation distribution in the validation data set. *J Time Ser Anal*. 2000;21(2):143–53.
 61. Hepple LW. Exact testing for spatial autocorrelation among regression residuals. *Environ Plan A*. 1998;30(1):85–108.
 62. Monti AC. A proposal for a residual autocorrelation test in linear models. *Biometrika*. 1994;81(4):776–80.
 63. Leung Y, Mei C-L, Zhang W-X. Testing for spatial autocorrelation among the residuals of the geographically weighted regression. *Environ Plan A*. 2000;32(5):871–90.
 64. Elam E. Reduction in hedging risk from adjusting for autocorrelation in the residuals of a price level regression. *J Futur Mark*. 1991;11(3):371–84.
 65. Melo ALP, Torres RA, e Silva FF, Ribeiro Júnior JI, Rodrigues MT, Menezes GRO. Effect of residual autocorrelation in the genetic evaluation of goats for milk yield and the shape of the lactation curve [Efeito da autocorrelação residual na avaliação genética de cabras para a produção de leite e para o formato da curva de lactação]. *Arq Bras Med Vet E Zootec*. 2011;63(3):609–15.