HIBISCUS PUBLISHER

BULLETIN OF ENVIRONMENTAL SCIENCE & SUSTAINABLE MANAGEMENT

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BESSM VOL 5 NO 1 2021
XENOBIOTICS-DEGRADING BACTERIUM

Runs Test for the Residuals of The Morgan-Mercer-Flodin (MMF) Model Used for Modelling the Total Number of Covid-19 Cases for Brazil

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HISTORY

Received: 25th May 2021
Received in revised form: 14th of May 2021
Accepted: 18th of June, 2021

KEYWORDS

Wald–Wolfowitz runs test
COVID-19
total case
Brazil
MMF model

ABSTRACT

Numerous papers fail to conduct statistical diagnostics of the nonlinear model that was used, and the data may be nonrandom, which is a need for all parametric statistical evaluation procedures that rely on random data. Whenever the diagnostic tests find that the residuals reflect a pattern, there are a range of treatments available, such as nonparametric analysis or transferring to a different model, which should resolve the issue. Organisms' growth including viral infection cases over time usually exhibit a sigmoidal growth profile that exhibits lag time, acceleration to a maximal value and a final phase where the rate decreases and eventually reaches zero or an asymptote (A) is observed. For the analysis of the COVID-19 pandemic, 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 Morgan-Mercer-Flodin (MMF) model found to be the best. We were the first to note on the high suitability of the MMF model to fit total death and infection cases for COVID-19. The least-squares technique used in normal nonlinear regression including in the MMF model must be subjected to the notion that the residual values must be random. In order to satisfy this requirement, we conduct the Wald–Wolfowitz runs test statistical diagnosis tests. The maximum number of runs counting was 5, and the predicted number of runs under the premise of randomness was 25.96. The z-value indicates how many normal errors the number of runs discovered exceeds the anticipated number of runs, and the p-value indicates how severe this z-value is. The significance is the same as with the other data on p-values. The null hypothesis that the residuals are really random can be rejected if the p-value is less than 0.05. Because the p-value was smaller than 0.05, the null hypothesis was dismissed, implying that there is strong evidence of non-randomness of the residues and further remedy is needed.

INTRODUCTION

A respiratory disease outbreak that started in Wuhan, China and expanded to many other nations has affected several countries around the world. The virus responsible for the outbreak, 2019-nCoV, was discovered in late 2019 [1,1–5]. As the global death toll from COVID-19 grows, more people are becoming aware of the unequal distribution of SARS-COV-2 mortality among vulnerable populations. Vulnerable groups to consider include the elderly, people living in densely populated areas, people with low socioeconomic status, refugees, and minorities. Almost every group is in danger. These groups are more prone to infection and adverse illness consequences because they have greater infection rates than the general population [6,7].

In the initial period, mathematical modelling research in Wuhan City and Hubei Province total infectious cases was focused on the dynamics of the pandemic[8]. At this early stage, it has taken a significant amount of time and effort to examine surveillance data from China in order to produce parameter

estimates such as the basic reproduction number (R0), case fatality rate, and incubation duration [9]. Early attempts at Susceptible-Exposed-Infectious-Recovered (SEIR) style dynamic models were 'borrowed' from what was known about other coronaviruses (SARS-CoV and MERS-CoV) and/or gained through fitting the models to monitoring data gathered during the initial outbreaks [10]. COVID-19 pandemic assessments can be carried out with the help of statistical models, including theoretical, quantitative, and simulation models. Mathematical models are then applied for other affected countries to better understand the mode and spread of infection [1,4,11–18].

Organisms growth including viral infection cases over time usually exhibit a sigmoidal growth profile that exhibits lag time (λ), acceleration to a maximal value (μ_m) and a final phase where the rate decreases and eventually reaches zero or an asymptote (A) is observed [19]. The sigmoidal curve can be fitted by different mathematical functions, such as Logistic [19,20], modified Gompertz [19,21], Richards [19,22], Schnute [19,23], Baranyi-Roberts [24], Von Bertalanffy [19,25–27], Buchanan three-phase [28,29], Huang [30–33] and Morgan-Mercer-Flodin (MMF) [34–43,43–47]. For the analysis of the COVID-19 pandemic [8], 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 [41,42,44,46,48–51].

The least-squares technique used in normal nonlinear regression including in the MMF model must be subjected to the notion that the residuals of the curve be naturally distributed in a nonlinear regression, as opposed to the typical least square's technique, which requires the residues to be normally distributed in a linear regression. More significantly, the residuals must be random and have identical variance (homoscedastic distribution). The Wald–Wolfowitz runs test is used to determine whether or not randomization has been achieved [52]. The subject of this study is to test for the randomness of the residual for of the MMF model previously used in fitting the total COVID-19 cases in Brazil [43].

MATERIALS AND METHODS

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 [43] was utilized in this study (Fig. 6).

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**);

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

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 [53] was applied to the regression residuals in an effort to detect nonrandomness. In a given model, it is feasible to create an ordered variance of the curve that is either above or below the estimate. The run test contrasts a compound's typically negative and optimistic sequence of residues to determine if it is hazardous. A noteworthy result is often characterized by a shift or mixture of shifts or combinations of shifts between the negative and positive residual values. The greatest possible percentage is frequently used to denote the number of signs runs. The running test evaluates if a big number of sign passes are likely, or an insufficient number of sign passes are likely. A disproportionate number of run signs may suggest a negative serial relationship, but a disproportionate number of runs may indicate that residues are connected with the same sign or that systemic biases exist.

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;

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

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

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

Runs test

From **Table 1**, the maximum number of runs counting was 5, and the predicted number of runs under the premise of randomness was 25.96. The z-value indicates how many normal errors the number of runs discovered exceeds the anticipated number of runs, and the p-value indicates how severe this z-value is. The significance is the same as with the other data on p-values. The null hypothesis that the residuals are really random can be rejected if the p-value is less than 0.05. Because the p-value was smaller than 0.05, the null hypothesis was dismissed, implying that there is strong evidence of non-randomness of the residues and further remedy is needed.

Table. Runs test data from the Morgan-Mercer-Flodin (MMF) Model Used for Modelling the Total Number of Covid-19 Cases for Brazil.

Time (h)	Residuals	Binary	Counting Runs
0	0.0000	1	1
1	-0.0600	0	2
2	-0.1500	0	2
5	-0.2000	0	2
8	-0.4200	0	2
11	-0.0100	0	2
14	-0.1400	0	2
17	0.1500	1	3
20	0.0000	1	3
23	0.1300	1	3
26	0.2400	1	3
29	0.2000	1	3
32	0.1500	1	3
35	0.1000	1	3
38	0.1100	1	3
41	0.050	1	3
44	0.060	1	3
47	-0.01	0	4
50	-0.04	0	4
53	-0.06	0	4
56	-0.11	0	4
59	-0.13	0	4
62	-0.13	0	4
65	-0.12	0	4
68	-0.13	0	4
71	-0.12	0	4
74	-0.1	0	4
77	-0.12	0	4
80	-0.09	0	4
83	-0.09	0	4
86	-0.06	0	4
89	-0.05	0	4
92	-0.04	0	4
95	-0.01	0	4
98	-0.01	0	4
101	0.01	1	5
104	0.01	1	5
107	0.02	1	5
110	0.02	1	5
113	0.03	1	5
116	0.04	1	5
119	0.04	1	5
122	0.06	1	5
125	0.06	1	5
128	0.07	1	5
129	0.07	1	5
130	0.07	1	5
131	0.07	1	5
132	0.07	1	5
133	0.07	1	5

Table 1. Runs test statistical summary for the Morgan-Mercer-Flodin (MMF) Model Used for Modelling the Total Number of Covid-19 Cases for Brazil.

Runs test	Residual data set
R=	5
n0=	24
n1=	26
n=	50
E(R)=	25.96
Var(R)=	12.20
StDev(R)=	3.49
Z=	-6.00
p-value=	0.0000

Using residual measurements, the fitting of a mathematical model may be properly diagnosed scientifically. Residuals are the discrepancies between the predicted and actual quantity values of a mathematical model. The fundamental notion is that a bad model would show a larger gap between projected and actual values.

In time-series regression models, the run approach is commonly used to test for the presence of autocorrelation. Monte Carlo simulation experiments have revealed that the run-time test results in strikingly asymmetrical error rates in the two tails, implying that the use of run-time autocorrelation research may not be stable and that the Durbin-Watson approach will be the preferred method for measuring autocorrelation [54]. 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 Baranyi-Roberts model in fitting an algae growth curve which shows adequacy in the statistics [55], the Buchanan-three-phase model used in the fitting the growth of *Paracoccus* sp. SKG on acetonitrile [56], and *Moraxella* sp. B on monobromoacetic acid (MBA) [57]. The runs tests on the residuals for the Sips and Freundlich models for lead (II) absorption by alginate gel bead were found to be sufficient in biosorption [58]. There are other examples of the use of the runs test of residual in the literature in assessing the health of the nonlinear regression [59–63].

CONCLUSION

The Wald–Wolfowitz runs test was used in this work to assess the randomness of the residual for data from the Morgan-Mercer-Flodin (MMF) Model Used for Modelling the Total Number of Covid-19 Cases for Brazil. In this experiment, the highest number of runs counting was 5, and the anticipated number of runs on the assumption of randomness was 25.96. It is indicated by the z-value how many normal mistakes have been detected when the number of runs discovered exceeds the anticipated number of runs, and it is indicated by the p-value how severe this z-value is. The importance of the data on p-values is the same as it is for the other data. If the p-value is less than 0.05, the null hypothesis, which states that the residuals are truly random, can be ruled out. Because the p-value was less than 0.05, the null hypothesis was rejected, meaning that there is substantial evidence of non-randomness of the residues and that further remediation is required to eliminate this data such as the discovery of possible outliers, is necessary.

CONFLICT OF INTEREST

"The authors declare that there is no conflict of interests regarding the publication of this article."

REFERENCES

1. Areepong Y, Sunthornwat R. Predictive models for cumulative confirmed COVID-19 cases by day in Southeast Asia. CMES - Comput Model Eng Sci. 2020;125(3):927–42.
2. Andreopoulos P, Kalogeropoulos K, Tragaki A, Stathopoulos N. Could historical mortality data predict mortality due to unexpected events? ISPRS Int J Geo-Inf. 2021;10(5).
3. Chalkiadakis I, Yan H, Peters GW, Shevchenko PV. Infection rate models for COVID-19: Model risk and public health news sentiment exposure adjustments. PLoS ONE. 2021;16(6 June).
4. Gupta R, Pandey G, Pal SK. Comparative analysis of epidemiological models for COVID-19 pandemic predictions. Biostat Epidemiol. 2021;
5. Salehi M, Arashi M, Bekker A, Ferreira J, Chen D-G, Esmaeili F, et al. A Synergetic R-Shiny Portal for Modeling and Tracking of COVID-19 Data. Front Public Health. 2021;8.
6. 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 [Internet]. 2020 Jun 26 [cited 2020 Jul 23];19(1):104. Available from: https://doi.org/10.1186/s12939-020-01218-z
7. Dorn A van, Cooney RE, Sabin ML. COVID-19 exacerbating inequalities in the US. The Lancet [Internet]. 2020 Apr [cited 2020

Jul 23];395(10232):1243–4. Available from: https://linkinghub.elsevier.com/retrieve/pii/S014067362030893X
8. 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
9. 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
10. 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
11. Català M, Alonso S, Alvarez-Lacalle E, López D, Cardona P-J, Prats C. Empirical model for short-time prediction of COVID-19 spreading. PLoS Comput Biol. 2020;16(12).
12. Mahanty C, Kumar R, Mishra BK, Hemanth DJ, Gupta D, Khanna A. Prediction of COVID-19 active cases using exponential and non-linear growth models. Expert Syst. 2020;
13. Shukor MY, Alam MS. Mathematical Modelling of the Growth of SARS-CoV-2 (COVID-19) and SARS-CoV (SARS) Viruses in Vero E6 Cells. Journalf Environ Microbiol Toxicol. 2020;8(1):1–4.
14. Spanakis M, Zoumpoulakis M, Patelarou AE, Patelarou E, Tzanakis N. Covid-19 epidemic: Comparison of three european countries with different outcome using gompertz function method. Pneumon. 2020;33(2):1–6.
15. Valencia M, Becerra JE, Reyes JC, Castro KG. Assessment of early mitigation measures against COVID-19 in Puerto Rico: March 15-May 15, 2020. PLoS ONE. 2020;15(10 October).
16. Ahmadi A, Fadaei Y, Shirani M, Rahmani F. Modeling and Forecasting Trend of COVID-19 Epidemic in Iran. medRxiv. 2020 Mar 27;2020.03.17.20037671.
17. Liang K. Mathematical model of infection kinetics and its analysis for COVID-19, SARS and MERS. Infect Genet Evol. 2020 Aug 1;82:104306.
18. Sunthornwat R, Areepong Y. Predictive models for the number of cumulative cases for spreading coronavirus disease 2019 in the world. Eng Appl Sci Res. 2021;48(4):432–45.
19. Zwietering MH, Jongenburger I, Rombouts FM, Van't Riet K. Modeling of the bacterial growth curve. Appl Environ Microbiol. 1990;56(6):1875–81.
20. 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).
21. 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.
22. Richards, F.J. A flexible growth function for empirical use. J Exp Bot. 1959;10:290–300.
23. Schnute J. A versatile growth model with statistically stable parameters. Can J Fish Aquat Sci. 1981;38:1128–40.
24. Baranyi J, Roberts TA. A dynamic approach to predicting bacterial growth in food. Int J Food Microbiol. 1994;23(3–4):277–94.
25. von Bertalanffy L. heoretische Biologie, Zweiter Band: Stoffwechsel,Wachstum. A FranckeAG Verlag, Bern, Switzerland; 1951. 418 p.
26. 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.
27. 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.
28. Buchanan RL. Predictive food microbiology. Trends Food Sci Technol. 1993;4(1):6–11.
29. Peleg M, Corradini MG, Normand MD. The logistic (Verhulst) model for sigmoid microbial growth curves revisited. Food Res Int. 2007;40(7):808–18.
30. 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.
31. 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.
32. 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.
33. 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.
34. 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.
35. 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.
36. Topal M, Bolukbasi ŞC. Comparison of nonlinear growth curve models in broiler chickens. J Appl Anim Res. 2008 Dec 1;34(2):149–52.
37. 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.
38. 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.
39. 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.
40. 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;
41. 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.
42. 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.
43. 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.
44. 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.
45. 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.
46. 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.
47. 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.
48. 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.
49. Supriatna AK, Husniah H. Modeling Covid-19 cummulative data in Indonesia using Morgan-Mercer-Flodin growth equation. In: Proceedings of the International Conference on Industrial Engineering and Operations Management. Harare, Zimbabwe; 2020.
50. 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.
51. 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.
52. 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.
53. Draper NR, Smith H. Applied Regression Analysis. Wiley, New York; 1981.

54. Huitema BE, McKean JW, Zhao J. The runs test for autocorrelated errors: unacceptable properties. J Educ Behav Stat. 1996;21(4):390–404.
55. 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.
56. Gunasekaran B, Shukor MS, Masdor NA, Shamaan NA, Shukor MY. Test of randomness of residuals for the Buchanan-three-phase model used in the fitting the growth of *Paracoccus* sp. SKG on acetonitrile. J Environ Bioremediation Toxicol. 2015;3(1):12–4.
57. Sabullah MK, Shukor MS, Masdor NA, Shamaan NA, Shukor MY. Test of randomness of residuals for the Buchanan-three-phase model used in the fitting the growth of *Moraxella* sp. B on monobromoacetic acid (MBA). Bull Environ Sci Manag. 2015;3(1):13–5.
58. Cataldo S, Gianguzza A, Merli M, Muratore N, Piazzese D, Turco Liveri ML. Experimental and robust modeling approach for lead(II) uptake by alginate gel beads: Influence of the ionic strength and medium composition. J Colloid Interface Sci. 2014 Nov 15;434:77–88.
59. Cooper S-M, Baker JS, Eaton ZE, Matthews N. A simple multistage field test for the prediction of anaerobic capacity in female games players. Br J Sports Med. 2004;38(6):784–9.
60. Worthington AC, Higgs H. Efficiency in the Australian stock market, 1875-2006: A note on extreme long-run random walk behaviour. Appl Econ Lett. 2009;16(3):301–6.
61. Abu GA, Abachi PT, Oloja-Ojabo ED. Long-run relationship between agricultural crop prices and supply response in Benue State, Nigeria: 1990-2010. Eur J Soc Sci. 2011;24(4):565–75.
62. Burns RD, Hannon JC, Brusseau TA, Eisenman PA, Shultz BB, Saint-Maurice PF, et al. Development of an aerobic capacity prediction model from one-mile run/walk performance in adolescents aged 13-16 years. J Sports Sci. 2016;34(1):18–26.
63. Gardiner SK, Mansberger SL. Effect of restricting perimetry testing algorithms to reliable sensitivities on test-retest variability. Invest Ophthalmol Vis Sci. 2016;57(13):5631–6.