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# Original article

# Time series modelling to forecast the confirmed and recovered cases of COVID-19



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### ABSTRACT

Coronaviruses are enveloped RNA viruses from the Coronaviridae family affecting neurological, gastrointestinal, hepatic and respiratory systems. In late 2019 a new member of this family belonging to the Betacoronavirus genera (referred to as COVID-19) originated and spread quickly across the world calling for strict containment plans and policies. In most countries in the world, the outbreak of the disease has been serious and the number of confirmed COVID-19 cases has increased daily, while, fortunately the recovered COVID-19 cases have also increased. Clearly, forecasting the "confirmed" and "recovered" COVID-19 cases helps planning to control the disease and plan for utilization of health care resources. Time series models based on statistical methodology are useful to model time-indexed data and for forecasting. Autoregressive time series models based on two-piece scale mixture normal distributions, called *TP–SMN–AR* models, is a flexible family of models involving many classical symmetric/asymmetric and light/heavy tailed autoregressive models. In this paper, we use this family of models to analyze the real world time series data of confirmed and recovered COVID-19 cases.

# 1. Introduction

Coronaviridae family includes two main subfamilies Coronavirinae and Torovirinae. The member genera include Alphacoronavirus, Betacoronavirus, Gammacoronavirus, Torovirus, and Bafinivirus. They are a huge family of viruses that affect neurological, gastrointestinal, hepatic and respiratory systems and can be grown among humans, bats, mice, livestock, birds, and others [1–3]. In the Coronaviridae family, a well-known type of virus called SARS coronavirus (SARS-CoV) distributed from animal to animal and humans [4]. Another type of coronavirus, called MERS coronavirus (MERS -CoV), significantly distributed from human to human in 2012 [4]. In 2019 many cases in China with respiratory diseases were reported by the World Health Organization (WHO), with evidence that these cases originated from a seafood market in Wuhan [5]. In 2019 a new type of virus called COVID-19 (novel coronavirus, 2019-nCoV), belonging to the Betacoronavirus genera of Coronaviridae family, spread from Wuhan in China

Evidence that COVID-19 is distributed from human to human has

been verified by the Centers for Disease Control and Prevention (CDC), and also reported that COVID-19 is spreading by touching surfaces, close contact, air, or objects that contain viral particles. The incubation period of COVID-19 is at least 14 days [7], and it can spread to others in the incubation period. Finally note that the incubation period and median age of confirmed cases are respectively 3 days and 47.0 years [8].

Preparation and controlling the outbreak of COVID-19 diseases requires thorough planning and policies. Some researchers have used statistical and mathematical modelling. In China, the number of unreported COVID-19 cases has been mathematically estimated in Refs. [9]. Also based on the information of some Japanese passengers in Wuhan [10], estimated the rate of the infection for COVID-19 in Wuhan. The results indicated a rate of 9.5% for infection and a rate from 0.3% to 0.6%, for death. Based on mathematical modelling in Ref. [11], the transmission risk of COVID-19 is on average about 6.47 persons and predicted the time that the peak of COVID-19 will be reached. Estimation of a sustained human-to-human transmission equal to 0.4 for COVID-19 using the information of 47 patients has been done in Ref.

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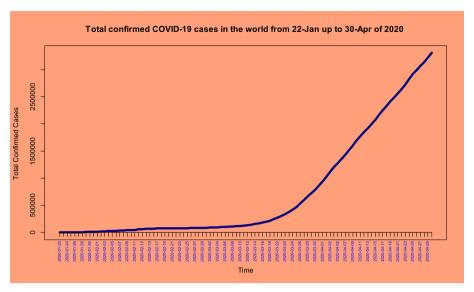


Fig. 1. Time series plot of the total confirmed COVID-19 cases in the world from 22-Jan to 30-Apr of 2020.

[12]. In Ref. [13], based on two scenarios, found that the risk of death is 5.1% and 8.4%.

The modelling, estimation and prediction of the prevalence of viruses and the epidemiological characteristics are important issues in providing the equipment needed to cope with their consequences. Forecasting of the cases and transmission risk of West Nile virus (WNV) has been provided by Ref. [14]. For further modelling and forecasting of the spread of several viruses such as the hepatitis A virus, Ebola, SARS, influenza A and MERS, refer to Refs. [15–21]. To have a suitable plan for COVID-19, forecasting the future confirmed cases are critical. An optimization method, named FPASSA-ANFIS, has been proposed by Ref. [22] to model the number of confirmed cases of COVID-19 and to predict its future values using collected data in China. Forecasting various data about COVID-19, by mathematical and statistical models, is very important to a program of cutting the transmission chain of diseases; see, e.g., Ref. [23–26].

According to credible daily reports from the World Health Organization and other world-renowned institutions in the field of public health, the total number of COVID-19 confirmed cases has increased in different countries, especially in U.S.A, Italy, Spain and Iran. Although the spread of COVID-19 has many dangers, fortunately reports show that the total number of COVID-19 recovered cases has also increased. Increasing the number of recovered cases, along with reducing or stabilizing the number of confirmed cases is important to control the spread of the COVID-19 and leads to stability of the rate of infections in the world. So modelling and forecasting the numbers of confirmed and recovered COVID-19 cases has an important role to plan the control of the spread of the COVID-19 in the world. Cumulative numbers of the confirmed and recovered COVID-19 cases, which are reported daily by the proposed organizations, on each day depend on their values on the past days. So using autoregressive time series model can be a useful tool to model, analyze and forecast the confirmed and recovered cases of COVID-19. The SIR epidemic modelling can be done at local (country) level but the autoregressive model can be good to look at overall patterns. The autoregressive time series model is a flexible tool to model dependent data and has been used to estimate and forecast many real practical problems, see Refs. [27-34]. In fact, the autoregressive model, determines the probabilistic behavior of the current values  $X_t$  based on a linear combination of past values  $\{X_{t-1}, X_{t-2}, X_{t-3}, ...\}$ , in the form of:

$$X_t = \phi_1 X_{t-1} + \dots + \phi_p X_{t-p} + Z_t; \quad t = 0, \pm 1, \pm 2, \dots,$$
(1)

where the error terms  $\{Z_t\}$  are generally assumed to be uncorrelated and

identically probabilistically distributed random variables from a distribution, and denoted by  $\{X_t\}\sim AR(p)$ . (see e.g. Ref. [39,40].)

Because in many real world time series data, classical modelling based on the symmetrical/light-tailed distributions are not satisfactory, in our methodology we have used autoregressive time series model (1) based on asymmetric/heavy-tailed TP-SMN distributions. Therefore we assume the error terms  $Z_t$  in (1) are distributed as TP-SMN distributions, denoted by  $Z_t$ -TP-SMN( $\mu$ ,  $\sigma$ ,  $\nu$ ,  $\gamma$ ) and  $\{X_t\}$ -TP-SMN-AR(p). See details of the proposed distributions and model in Ref. [34–38].

In this paper we modeled the total number of confirmed and recovered COVID-19 cases in the world by the proposed autoregressive time series model so-called TP-SMN-AR models which includes the symmetric Gaussian and asymmetric heavy-tailed non-Gaussian autoregressive time series models. The various members of the proposed autoregressive models were fitted initially to the historical numbers of confirmed and recovered COVID-19 cases in the world. Then, the autoregressive time series that has the best fit to each of the dataset is selected. Finally, the selected models are used to predict the number of confirmed and recovered COVID-19 cases in the world from 21-Apr-2020 up to 30-Apr-2020, and we measure the differences between the real and predicted values to show the performance of the models. Therefore, the main contribution points of the current study are as follows: an improved autoregressive time series model based on the TP-SMN distributions, and a new efficient predictive model applied to predict and estimate the confirmed and recovered COVID-19 cases in the world using past and current data. Note that a sample copy of the code is available from the authors upon request.

# 2. Modelling the confirmed and recovered cases of the COVID-19 in the world

The coronavirus (COVID-19) is affecting about 212 countries and territories around the world and two international conveyances. The daily data for COVID-19 in the world are reported by the China National Health Commission (NHC) and World Health Organization (WHO). In this part we fit the *TP–SMN–AR* time series model to the total confirmed COVID-19 cases from 22-Jan-2020 to 30-Apr-2020 and also to the total recovered COVID-19 cases from 02-Feb-2020 to 30-Apr-2020, in the world.

Time series plots of the total confirmed and recovered cases are plotted in Fig. 1 and Fig. 2 respectively. The proposed time series plots are not stationary because they are increasing and show signs of a trend. After some suitable transformations described in Ref. [40], we

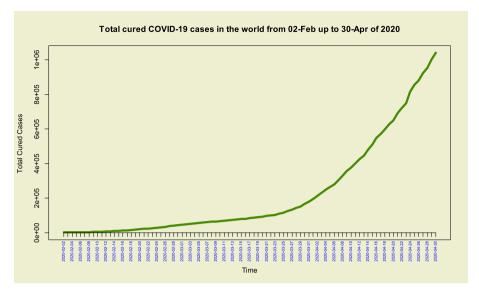


Fig. 2. Time series plot of the total recovered COVID-19 cases in the world from 02-Feb to 30-Apr of 2020.

obtain stationary data. Also using model selection criteria [34,39,40] the best TP–SMN–AR models (the autoregressive models based on the two-piece t distributions) were fitted to the stationary series of the confirmed and recovered cases and are given by.

• The confirmed COVID-19 cases; TP-SMN-AR(7) model:

$$X_{t} = -0.9399X_{t-1} - 1.0438X_{t-2} - 1.1067X_{t-3} - 0.9825X_{t-4} - 0.9364X_{t-5} - 0.8105X_{t-6} - 0.3623X_{t-7} + Z_{t},$$

where

$$Z_t \sim TP - T(\mu = -103.3424, \ \sigma = 4084.3481, \ \gamma = 0.4559, \ \nu = 2.1000).$$

• The recovered COVID-19 cases; TP-SMN-AR(2) model:

$$X_t = -0.5865X_{t-1} - 0.2020X_{t-2} + Z_t,$$

where

$$Z_t \sim TP - T (\mu = -0.0048, \ \sigma = 0.0250, \ \gamma = 0.4756, \ \nu = 3.1146).$$

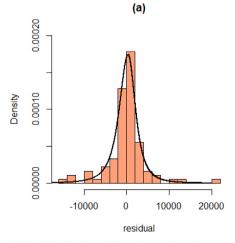
The histograms of the estimated errors (residuals) based on the estimated heavy-tailed *TP–SMN* densities are superimposed in Fig. 3 and show the suitable performance of the estimated models to the stationary series of total confirmed and recovered COVID-19 cases

datasets. Also the auto-correlation function (*ACF*) plots of the residuals presented in Fig. 4 show the suitability of the fitted models.

To further demonstrate the goodness of fit of the model, we eliminated the last 10 days of the confirmed and recovered cases (2020-Apr-21 to 2020-Apr-30), and then fitted the *TP-SMN-AR* models and provided forecasts. Table 1 contains the predictions and 98% confidence intervals for this analysis. Also Fig. 5, Fig. 6 and Fig. 7, show the forecasted values which are superimposed on the plots of the real values of the confirmed and recovered COVID-19 cases in the world.

To evaluate the accuracy of the predictions, we use the mean relative percentage error (*MAPE*), which for the confirmed COVID-19 cases is 0.22% and for the recovered COVID-19 cases is 1.6% which are reasonably low values demonstrating the suitability of the proposed models for prediction.

Finally note that the proposed *TP–SMN–AR* models include as special or limiting cases the more standard autoregressive time series models used in the literature. In particular, some model selection criteria such as Akaike information criteria (AIC), Bayesian information criteria (BIC), and Box–Pierce and Ljung–Box tests on the residuals, demonstrate that the proposed fitted *TP–SMN–AR* models are more reasonable than other well-known counterparts.



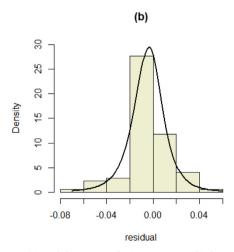


Fig. 3. Histograms of the residuals of the fitted models on the confirmed COVID-19 cases (a), and the recovered COVID-19 cases (b) datasets in the world, with their superimposed estimated densities.

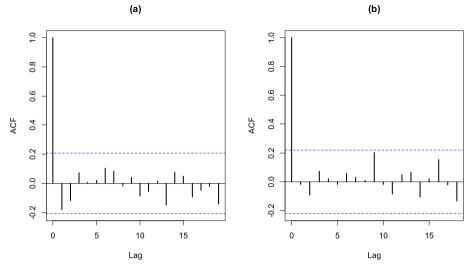


Fig. 4. ACF of the residuals of the fitted models on the confirmed COVID-19 cases (a), and the recovered COVID-19 cases (b).

**Table 1**The real values of the total confirmed and recovered COVID-19 cases in the world data from 2020-Apr-21 to 2020-Apr-30 with predictions and 98% confidence interval.

COVID-19 Data	Date	Real value	Prediction	Lower C·I.	Upper
Confirmed Cases	2020-Apr-21 2020-Apr-22 2020-Apr-23 2020-Apr-24 2020-Apr-25 2020-Apr-26 2020-Apr-27	2556720 2637439 2722857 2828682 2919404 2993292 3059944 3136505	2556806 2637409 2721410 2808860 2937529 3004212 3064943 3129841	2545942 2626722 2710914 2798439 2925690 2992353 3052694 3117773	2568200 2648536 2732294 2819720 2948566 3015772 3077488 3143146
Recovered Cases	2020-Apr-29 2020-Apr-30 2020-Apr-21 2020-Apr-22 2020-Apr-24 2020-Apr-25 2020-Apr-26 2020-Apr-27 2020-Apr-28 2020-Apr-29 2020-Apr-30	3218183 3304220 691650 718761 746924 815145 854466 877411 921320 953309 1000033 1039028	3218199 3302211 670555 722622 753685 775550 864671 904511 914058 954201 985264 1038689	3204951 3289979 638016 689342 716873 737065 818679 854466 865114 903560 932903 984279	3231956 3315769 707815 761654 795415 858978 914842 957290 968022 1010487 1043419 1099247

# 3. Conclusion

Coronaviruses are a huge family of viruses that affect neurological, gastrointestinal, hepatic, and respiratory systems. The number of confirmed cases has increased daily in different countries, especially in U.S.A, Italy, Spain, Iran, China and others. The spread of COVID-19 has many dangers and needs strict special plans and policies. Therefore, to consider plans and policies, predicting and forecasting the future confirmed and recoveries cases are critical. The autoregressive time series models are a useful tool to model data over time. However, some of the standard time series models are based on the assumption that the error term or residuals are symmetric (Gaussian). There exist many situations in the real world that the assumption of symmetric distribution of the error terms is not satisfactory. In our methodology, we considered autoregressive time series models based on the two-piece scale mixture normal (TP-SMN) distributions. The results indicated that the proposed method performed well in forecasting confirmed and recovered COVID-19 cases in the world. Using model selection criteria, the proposed models were also more reasonable than the standard Gaussian autoregressive time series model which is the simplest member of our proposed models. For future works, we suggest that the researchers apply cyclostationary, almost cyclostationary and simple processes [41-47] based on the TP-SMN distributions, instead of stationary

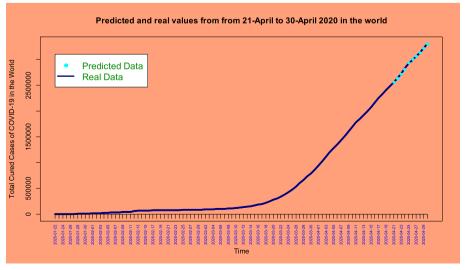


Fig. 5. Time series plot of the confirmed COVID-19 cases data and predicted data from 2020-Apr-21 to 30-Apr of 2020.

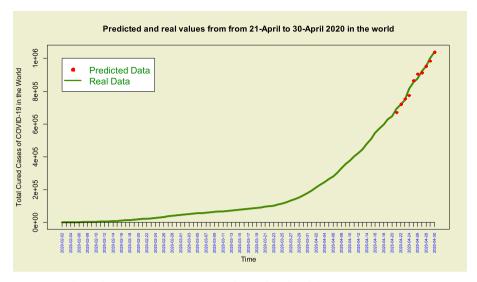


Fig. 6. Time series plot of the recovered COVID-19 cases data and predicted data from 2020-Apr-21 to 30-Apr of 2020.

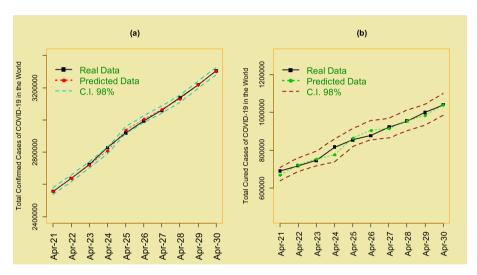


Fig. 7. Time series plots of the real values and predicted confirmed COVID-19 cases (a) and recovered COVID-19 cases (b) datasets from 2020-Apr-21 up to 2020-Apr-30 with 98% confidence intervals.

processes.

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# CRediT authorship contribution statement

Mohsen Maleki: Data curation, Validation, Writing - original draft.

Mohammad Reza Mahmoudi: Conceptualization, Methodology,
Software, Supervision. Darren Wraith: Visualization, Investigation,
Writing - review & editing. Kim-Hung Pho: Visualization,
Investigation, Writing - review & editing.

# Declaration of competing interest

The authors declare no conflict of interest.

# References

- Chen Y, Liu Q, Guo D. Emerging coronaviruses: genome structure, replication, and pathogenesis. J Med Virol 2020. https://doi.org/10.1002/jmv.25681.
- [2] Ge XY, Li JL, Yang XL, Chmura AA, Zhu G, Epstein JH, Mazet JK, Hu B, Zhang W,

- Peng C, et al. Isolation and characterization of a bat SARS-like coronavirus that uses the ACE2 receptor. Nature 2013;503:535–8.
- [3] Wang LF, Shi Z, Zhang S, Field H, Daszak P, Eaton BT. Review of bats and SARS. Emerg Infect Dis 2006;12:1834.
- [4] Cauchemez S, Van Kerkhove M, Riley S, Donnelly C, Fraser C, Ferguson N. Transmission scenarios for Middle East Respiratory Syndrome Coronavirus (MERS-CoV) and how to tell them apart. Euro Surveill. Bull. Eur. Sur Les Mal. Transm. Eur. Commun. Dis. Bull. 2013;18:20503.
- [5] Organization WH. Novel coronavirus (2019-nCoV) 2020. 2020 Available online:https://www.who.int/, (accessed on 27 January 2020).
- [6] Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, Wang W, Song H, Huang B, Zhu N, et al. Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. Lancet 2020;395:565–74.
- [7] Cheng ZJ, Shan J. Novel coronavirus: where we are and what we know. Infection 2019;2020. https://doi.org/10.1007/s15010-020-01401-y.
- 8] Guan WJ, Ni ZY, Hu Y, Liang WH, Ou CQ, He JX, Liu L, Shan H, Lei CL, Hui DS, et al. Clinical characteristics of 2019 novel coronavirus infection in China. medRxiv 2020. https://doi.org/10.1101/2020.02.06.20020974 Available online: https://www.medrxiv.org/content/early/2020/02/09/2020.02.06.20020974.full.pdf (accessed on 9 February 2020).
- [9] Zhao S, Musa SS, Lin Q, Ran J, Yang G, Wang W, Lou Y, Yang L, Gao D, He D, et al. Estimating the unreported number of novel coronavirus (2019-nCoV) cases in China in the first half of january 2020: a data-driven modelling analysis of the early outbreak. J Clin Med 2020;9:388.
- [10] Nishiura H, Kobayashi T, Yang Y, Hayashi K, Miyama T, Kinoshita R, Linton NM, Jung Sm, Yuan B, Suzuki A, et al. The rate of underascertainment of novel coronavirus (2019-nCoV) infection: estimation using Japanese passengers data on evacuation flights. J Clin Med 2020;9:419.
- [11] Tang B, Wang X, Li Q, Bragazzi NL, Tang S, Xiao Y, Wu J. Estimation of the

- transmission risk of the 2019-nCoV and its implication for public health interventions. J Clin Med 2020;9:462.
- [12] Thompson RN. Novel coronavirus outbreak in wuhan, China, 2020: intense surveillance is vital for preventing sustained transmission in new locations. J Clin Med 2020:9:498
- [13] Jung SM, Akhmetzhanov AR, Hayashi K, Linton NM, Yang Y, Yuan B, Kobayashi T, Kinoshita R, Nishiura H. Real time estimation of the risk of death from novel coronavirus (2019-nCoV) infection: inference using exported cases. J Clin Med 2020:9:523.
- [14] DeFelice NB, Little E, Campbell SR, Shaman J. Ensemble forecast of human West Nile virus cases and mosquito infection rates. Nat Commun 2017;8:1–6.
- [15] Ture M, Kurt I. Comparison of four different time series methods to forecast hepatitis A virus infection. Expert Syst Appl 2006;31:41–6.
- [16] Shaman J, Karspeck A. Forecasting seasonal outbreaks of influenza. Proc Natl Acad Sci USA 2012;109:20425–30. J. Clin. Med. 2020, 9, 674 14 of 15.
- [17] Shaman J, Karspeck A, Yang W, Tamerius J, Lipsitch M. Real-time influenza forecasts during the 2012–2013 season. Nat Commun 2013;4:1–10.
- [18] Shaman J, Yang W, Kandula S. Inference and forecast of the current west african Ebola outbreak in Guinea, Sierra Leone and Liberia. PLoS Curr 2014;6. https://doi. org/10.1371/currents.outbreaks.3408774290b1a0f2dd7cae877c8b8ff6.
- [19] Massad E, Burattini MN, Lopez LF, Coutinho FA. Forecasting versus projection models in epidemiology: the case of the SARS epidemics. Med Hypotheses 2005;65:17–22.
- [20] Ong JBS, Mark I, Chen C, Cook AR, Lee HC, Lee VJ, Lin RTP, Tambyah PA, Goh LG. Real-time epidemic monitoring and forecasting of H1N1-2009 using influenza-like illness from general practice and family doctor clinics in Singapore. PloS One 2010;5. https://doi.org/10.1371/journal.pone.0010036.
- [21] Nah K, Otsuki S, Chowell G, Nishiura H. Predicting the international spread of Middle East respiratory syndrome (MERS). BMC Infect Dis 2016;16:356.
- [22] Al-qaness MAA, Ewees AA, Fan H, Abd El Aziz M. Optimization method for fore-casting confirmed cases of COVID-19 in China. J Clin Med 2020;9:674.
- [23] Woolhouse M. How to make predictions about future infectious disease risks. Philos Trans R Soc Lond B Biol Sci 2011;366(1573):2045-2054. https://doi.org/10.1098/ rstb.2010.0387.
- [24] Funk S, Camacho A, Kucharski AJ, Eggo RM, Edmunds WJ. Real-time forecasting of infectious disease dynamics with a stochastic semi-mechanistic model. Epidemics 2018;22:56-61. https://doi.org/10.1016/j.epidem.2016.11.003.
- [25] Jia L, Li K, Jiang Y, Guo X, Zhao T. Prediction and analysis of coronavirus disease vol. 2020. 2019https://arxiv.org/ftp/arxiv/papers/2003/2003.05447.pdf.
- [26] Mahmoudi MR, Maleki M. A new method to detect periodically correlated structure. Comput. Stat. 2017;32(4):1569–81.
- [27] Maleki M, Arellano-Valle RB. Maximum a-posteriori estimation of autoregressive processes based on finite mixtures of scale-mixtures of skew-normal distributions. J Stat Comput Simulat 2017;87:1061–83.
- [28] Maleki M, Nematollahi AR. Autoregressive models with mixture of scale mixtures of Gaussian innovations. Iran J Sci Technol A (Sciences) 2017;41:1099–107.
- [29] Zarrin P, Maleki M, Khodadadi Z, Arellano-Valle RB. Time series process based on

- the unrestricted skew normal process. J Stat Comput Simulat 2018;89(1):38–51.

  [30] Maleki M, Arellano-Valle RB, Dey DK, Mahmoudi MR, Jalali SM. A Bayesian approach to robust skewed Autoregressive process. Calcutta Statistical Association
- Bulltaine 2018;69:165–82.
  31] Hajrajabi A, Maleki M. Nonlinear semiparametric autoregressive model with finite
- [31] Hajrajabi A, Maleki M. Nonlinear semiparametric autoregressive model with finit mixtures of scale mixtures of skew normal innovations. J Appl Stat 2019;46(11):2010–29.
- [32] Maleki M, Wraith D, Mahmoudi MR, Contreras-Reyes JE. Asymmetric heavy-tailed vector auto-regressive processes with application to financial data. J Stat Comput Simulat 2020;90(2):324–40.
- [33] Ghasami S, Khodadadi Z, Maleki M. Autoregressive processes with generalized hyperbolic innovations. Commun Stat Simulat Comput 2018. https://doi.org/10. 1080/03610918.2018.1535066.
- [34] Ghasami S, Maleki M, Khodadadi Z. Leptokurtic and platykurtic class of robust symmetrical and asymmetrical time series models. J Comput Appl Math 2020. https://doi.org/10.1016/j.cam.2020.112806.
- [35] Moravveji M, Khodadadi Z, Maleki M. A bayesian analysis of two-piece distributions based on the scale mixtures of normal family. Iran J Sci Technol A (Sciences) 2019;43(3):991–1001.
- [36] Maleki M, Mahmoudi MR, Contreras-Reyes JE. Robust mixture modelling based on two-piece scale mixtures of normal family. Axioms 2019;8(2):38.
- [37] Maleki M, Barkhordar Z, Khodadadi Z, Wraith D. A robust class of homoscedastic nonlinear regression models. J Stat Comput Simulat 2019;89(14):2765–81.
- [38] Hoseinzaseh A, Maleki M, Khodadadi Z, Contreras-Reyes JE. The Skew-Reflected-Gompertz distribution for analyzing symmetric and asymmetric data. J Comput Appl Math 2019;349:132–41.
- [39] Box George, Jenkins Gwilym M, Reinsel Gregory C. Time series analysis: forecasting and control. third ed. Prentice-Hall0130607746; 1994.
- [40] Brockwell PJ, Davis RA. Time series: theory and methods. second ed. New York: Springer; 2009.
- [41] Mahmoudi MR, Maleki M, Pak A. Testing the difference between two independent time series models. Iran J Sci Technol A (Sciences) 2017;41:665–9.
- [42] Mahmoudi MR, Heydari MH, Avazzadeh Z. On the asymptotic distribution for the periodograms of almost periodically correlated (cyclostationary) processes. Digit Signal Process 2018;81:186–97.
- [43] Mahmoudi MR, Nematollahi AR, Soltani AR. On the detection and estimation of the simple harmonizable processes. Iran J Sci Technol A (Sciences) 2015;39(2):239–42.
- [44] Nematollahi AR, Soltani AR, Mahmoudi MR. Periodically correlated modeling by means of the periodograms asymptotic distributions. Stat Pap 2017;58(4):1267–78.
- [45] Mahmoudi MR, Heydari MH, Avazzadeh Z, Pho KH. Goodness of fit test for almost cyclostationary processes. Digit Signal Process 2020;96:102597.
- [46] Mahmoudi MR, Heydari MH, Roohi R. A new method to compare the spectral densities of two independent periodically correlated time series. Math Comput Simulat 2019;160:103-10.
- [47] Mahmoudi MR, Heydari MH, Avazzadeh Z. Testing the difference between spectral densities of two independent periodically correlated (cyclostationary) time series models. Commun Stat Theor Methods 2019;48(9):2320–8.