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Time Series Modeling of Coronavirus (COVID-19) Spread in Iran

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Abstract. Various types of Coronaviruses are enveloped RNA viruses from the Coronaviridae family and part of the Coronavirinae subfamily. This family of viruses affects neurological, gastrointestinal, hepatic, and respiratory systems. Recently, a new member of this family, named Covid-19, is moving around the world. The expansion of Covid-19 carries many risks, and its control requires strict planning and special policies. Iran is one of the countries in the world where the outbreak of the disease has been serious and the daily number of confirmed cases is increasing in some places. Prediction of future confirmed cases of the COVID-19 is planning with a certain policy to provide the clinical and medical supplementary. Time series models based on the statistical methodology are useful to model and forecast time-indexed data. In many situations in the real world, the ordinary classical time series models based on the symmetrical and light-tailed distributions cannot lead to a satisfactory result (or predicion). Thus, in our methodology, we consider the analysis of symmetrical/asymmetrical and light/heavy-

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tailed time series data based on the two-piece scale mixture of the normal (TP-SMN) distribution. The proposed model is useful for symmetrical and light-tailed time series data, and it can work well relative to the ordinary Gaussian and symmetry models (especially for COVID-19 datasets). In this study, we fit the proposed model to the historical COVID-19 datasets in Iran. We show that the proposed time series model is the best fitted model to each dataset. Finally, we predict the number of confirmed COVID-19 cases in Iran.

Keywords. Coronaviruses, COVID-19, Prediction, Time Series Modeling, Two Pieces Distributions, Scale Mixture of Normal Distribution.

MSC: 62M10, 62P10.

1 Introduction

Coronaviridae family and part of the Coronavirinae subfamily belong to a huge family of viruses that affect neurological, gastrointestinal, hepatic, and respiratory systems. The Coronaviridae family can grow among humans, bats, mice, livestock, birds, and others, see i.e Chen et al. (2020) and Wang et al. (2006). Prominent examples of the spread of this family of viruses include the spread of SARS coronavirus (SARS- CoV) from animal to animal in 2003 and MERS coronavirus (MERS -CoV) from human to human in 2012 (See Cauchemez et al. (2013) for more details.). In 2019, many cases in China withrespiratory diseases were reported by the "World Health Organization" (WHO), that most of them visited a seafood market in Wuhan, see Organization (2020). In 2019, this new type of virus, which was called COVID-19 (novel coronavirus, 2019-nCoV), has begun to spread in Wuhan of China [Lu et al. (2020)]. Scientists believe that the inhibition of COVID-19 needs further demanding studies.

The idea that the COVID-19 was distributed from human to human has verified by the Centers for Disease Control and Prevention (CDC). They reported that the COVID-19 could be sprout by touching surfaces, close contact, air, or objects that contain viral particles. The incubation period of the COVID-19 is at least 14 days [Cheng and Shan (2020)], and it can be transmittable during this period. Also, note that the median age and incubation period of confirmed cases are ,respectively, 47 years and 3 days [Guan et al. (2020)].

The coronavirus COVID-19 is affecting more than 203 countries and territories around the world and 2 international conveyances. While the spread of the COVID-

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19 has many dangers, the number of daily COVID-19 confirmed cases is increasing in different countries, especially in the United States, Italy, Spanish, Germany, Iran, and other countries. Therefore, preparation and confronting this outbreak requires careful planning and policies. Some researchers have used statistical and mathematical modeling to study COVID-19. In China, the number of unreported COVID-19 cases has been mathematically estimating by Zhao et al. (2020). Based on the information of some Japanese passengers from Wuhan, Nishiura et al. (2020) estimated the rate of the infection for COVID-19 in this city. Results indicate that the infection rate is 9.5% and the death rate ranges from 0.3% to 0.6%. Based on the mathematical modeling of Tang et al. (2020), the transmission risk of COVID-19 is on average about 6.47 persons. They also predicted the peak time of COVID-19. Thompson (2020) estimated a sustained human-to-human transmission equal to 0.4 for COVID-19 using the information of 47 patients. Jung et al. (2020) use two scenarios and found that the risk of death was 5.1% to 8.4%. Modeling and predicting the total confirmed cases is very important for accurate planning of national and health organizations, and it has been studied in several researches such as Firdos et al. (2020), Rahimi et al. (2021.a), Rahimi et al. (2021.b), Kalantari (2021) and Masum et al. (2020).

Some important topics that are required to cope with the consequences of Covid-19 pandemic are modeling and predicting its prevalence along with improving the knowledge of epidemiology. DeFelice et al. (2017) provides forecasting of cases and the transmission risk of West Nile virus (WNV). To observe more modeling and forecasting of the spread of several viruses, such as the hepatitis A virus, Ebola, SARS, influenza A, and MERS we refer to Ture and Kurt (2006) and Nah et al. (2016). Dealing with COVID-19, due to the prevalence and rate of spread of this disease, it is important to design an appropriate plan to accurately predict the number of confirmed cases in the future. An optimization method, named FPASSA-ANFIS, has proposed by Al-qaness et al. (2020) to model the number of confirmed cases of COVID-19 and to predict its future values using recorded datasets in China.

In this paper, we model the total number of confirmed COVID-19 cases in Iran using the time series methodology. It is useful to analyze such a dataset that has been indexed by time. We show that the time series analysis can nicely be helpful in modeling, estimating, and forecasting these serially collected observations [Sharafi and Nematollahi (2016), and Maleki and Nematollahi (2017)]. In our methodology, we utilize a time series model based on asymmetric/heavy-tailed distributions. The reason is that in many real-life time-series data, classical modeling based on the symmetrical/light-tailed distributions does not lead to a satisfactory result. (e.g., Sharafi

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and Nematollahi (2016), and Maleki and Nematollahi (2017)). Specifically, we consider the two-piece scale mixtures of normal (TP-SMN) distributions, introduced by [Sharafi and Nematollahi (2016), and Maleki and Nematollahi (2017), in the direction of time series models [Ghasemi et al. (2020)]. The proposed model includes the symmetric Gaussian and asymmetric heavy-tailed non-Gaussian time series models. We fit all models to the historical COVID-19 datasets in Iran. Then, we choose the data, based on some model selection criteria. The final model is used to predict the number of confirmed COVID-19 cases in Iran from 19-Feb-2020 up to 23-Feb-2021. Therefore, the main contribution points of the current study include an improved time series modeling based on the TP-SMN distributions and a new efficient predictive model to predict and estimate the confirmed COVID-19 cases using past and current reported cases in Iran.

2 Preliminaries

The autoregressive moving-average (ARMA) model is commonly used in the analysis of time series data especially when the main purpose is prediction. The model contains two parts, the autoregression (AR) and the moving average (MA). Whittle (1951) was the first to introduce the model in his thesis entitled "*Hypothesis testing in time series analysis.*" Then, Box et al. (1994) and Brockwell and Davis (2009) studied some of its properties. A stationary time series model $\{X_t\}$ is the ARMA process with p autoregressive and q moving-average terms, denoted by $\{X_t\} \sim ARMA(p, q)$, and contains both AR(p) and MA(q) models. This model is of the form

$$X_t - \varphi_1 X_{t-1} - \cdots - \varphi_p X_{t-p} = \mu + Z_t + \theta_1 Z_{t-1} + \cdots + \theta_q Z_{t-1}, \tag{2.1}$$

where the error terms $\{Z_t\}$ are generally assumed to be uncorrelated and identically distributed random variables (WN) sampled from a distribution with zero mean and constant variance σ^2.

Following the definition of two-piece distributions [Hajrajabi and Maleki (2019)] based on the scale mixture of normal (SMN) family, the pdf of the TP-SMN family for $y \in \mathbb{R}$ is denoted by $Y \sim TP - SMN(\mu, \sigma, \boldsymbol{\nu}, \gamma)$ and is represented as

$$g(y|\mu, \sigma, \gamma, \boldsymbol{\nu}) = \begin{cases} 2(1-\gamma) f_{SMN}(y|\mu, \sigma(1-\gamma), \boldsymbol{\nu}), & y \leqslant \mu, \\ 2\gamma f_{SMN}(y|u, \sigma\gamma, \boldsymbol{\nu}), & y > \mu, \end{cases} \tag{2.2}$$

where $0 < \gamma < 1$ is the slant parameter and $f_{SMN}(.|\mu, \sigma, \nu)$ is the probability density function of the SMN family (for more statistical properties of the P-SMN family see Ghasemi et al. (2020) and Barkhordar et al. (2020)).

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3 Time Series Modeling of the Confirmed Coronavirus Cases in the Iran

The daily data of the confirmed COVID-19 in Iran and other countries in the world are reported by the World Health Organization (WHO). In this section, we fit time series models to the total confirmed cases in Iran from 19-Feb-2020 up to 23-Feb-2021.

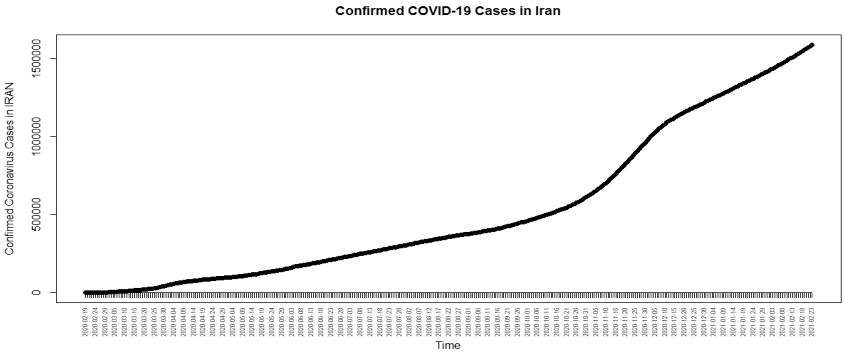

Figure 1: Time series plot of the total confirmed cases of COVID-19 in Iran from 19-Feb of 2020 up to 23-Feb of 2021.

Time series plot of the total cases in Iran confirmed from 19-Feb-2020 up to 23-Feb-2021 is plotted in Figure 1 Considering the period time between 14-Dec-2020 up to 23-Feb-2021, applying three times lag-1 difference operator, i.e., $3(\nabla^3 X_t = X_t - 3X_{t-1} + 3X_{t-2} + X_{t-3})$, will result in a stationary time series, which is displayed in Figure 2. Obviously, the number of total cases in each day depends on the number of them in the previous day(s). Thus, the autoregressive model can be suitable for the COVID-19 data analysis. Partial auto-covariance function (PACF), plotted in Figure 3, demonstrates that AR(6) might be a reasonable model. However, similar to the methodology in Brockwell and Davis (2009), we checked all possible ARMA(p,q) models, and finally found that the following TP-T-AR(6) model is the best model

$$\begin{aligned} Z_t = X_t &+ 0.67040X_{t-1} + 0.70089X_{t-2} + 0.60007X_{t-3} \\ &+ 0.69892X_{t-4} + 0.66159X_{t-5} + 0.45232X_{t-6}, \end{aligned}$$

where

$$\{Z_t\} \sim TP - N(\mu = 19.6787, \sigma = 260.3986, \gamma = 0.4866, = 6/1010).$$

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Histogram of the estimated errors (residuals) with the curve of the estimated TP-T density demonstrate the suitability of the estimated model for the COVID-19 data in Iran (Figure 4). Besides, Figure 5 is the autocorrelation function plot of residuals of the TP-T-AR(6) model, which indicates the appropriateness of the proposed model. But, to assure readers, we eliminated the last 72 data points (14-Dec-2020 up to 23-Feb-2021) and then fitted the TP-SMN-ARMA model together with forecasting the eliminations. Figure 6 and Table 1 show the closeness of forecasted values to observed COVID-19 in Iran. Table 1 contains the predictions with their 98% confidence intervals. (Note that by subtracting the total cased in consecutive days, prediction of the number of daily cased will be obtained).

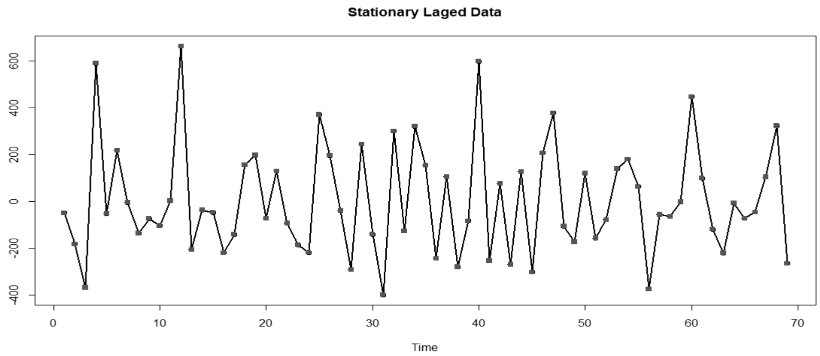

Figure 2: Time series plot of the COVID-19 in Iran after differencing three times with order one of total cases.

To evaluate the accuracy of obtained data predictions, the mean absolute error (MAE), mean relative percentage error (MAPE) and Root Mean Squared Error (RMSE) indexes are used. These indexes are calculated respectively as:

$$MAE = \frac{1}{n}\sum_{t=1}^{n}|X_t - \widehat{X_t}|, \quad MAPE = \frac{1}{n}\sum_{t=1}^{n}\left|\frac{\widehat{X_t}}{X_t} - 1\right|, \quad RMSE = \sqrt{\frac{1}{n}\sum_{t=1}^{n}\left(X_t - \widehat{X_t}\right)^2},$$

It can evaluate the accuracy of suggested data predictions of COVID-19 in Iran. For our proposed predictions, the value of these indexes are MAE= 106.7, MAPE=0.000068 and RMSE= 15820.3, showing the suitability of the proposed model for the prediction purposes.

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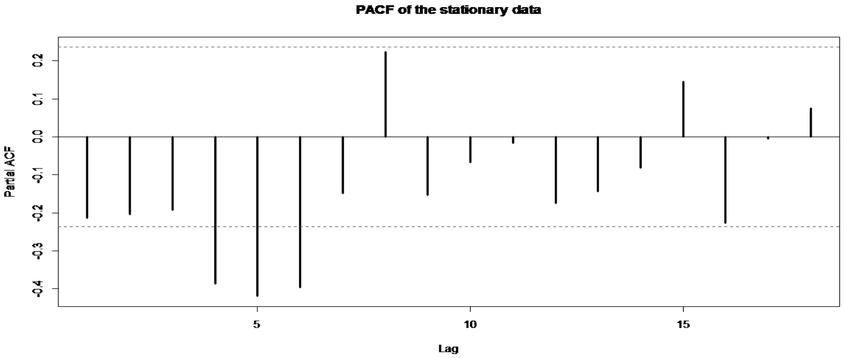

Figure 3: PACF of the transformed total COVID-19 data in Iran.

Finally the p-value= 0.9645 from the Box-Pierce and p-value=0.9595 from the Ljung-Box tests indicate that the residuals are independent. Also, the auto-correlation function (ACF) plot of residuals, presented in Figure 7, shows the suitability of the TP-T-AR(6) model to the total number of confirmed cased of the COVID-19 dataset in Iran

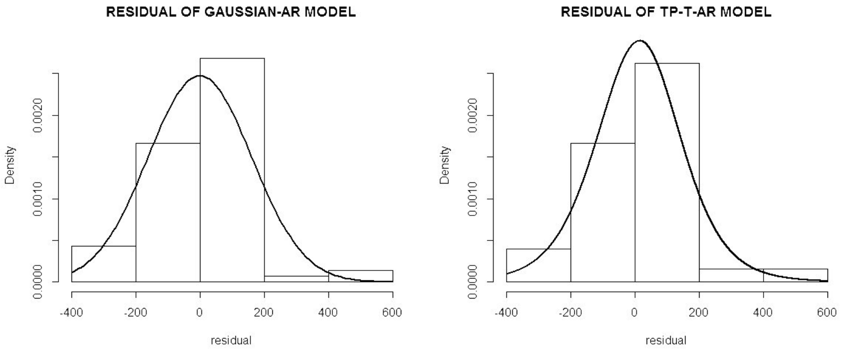

Figure 4: Histogram of residuals for the Gaussian (Left) and TP-N (Right) fitted time series models on COVID-19 data in Iran with the corresponding estimated densities.

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Table 1: Real values of the COVID-19 in Iran from 14-Feb-2021 up to 23-Feb-2021 with predictions and 98% confidence intervals

Date	Real value	Prediction	Lower	Upper
14-Feb-2021	1518263	1518040	1517618	1518467
15-Feb-2021	1526023	1525927	1525515	1526344
16-Feb-2021	1534034	1534033	1533622	1534452
17-Feb-2021	1542076	1542117	1541707	1542536
18-Feb-2021	1550142	1550033	1549625	1550449
19-Feb-2021	1558159	1558107	1557700	1558524
20-Feb-2021	1566081	1566154	1565750	1566572
21-Feb-2021	1574012	1574202	1573798	1574618
22-Feb-2021	1582275	1582164	1581758	1582575
23-Feb-2021	1590605	1590776	1590374	1591187

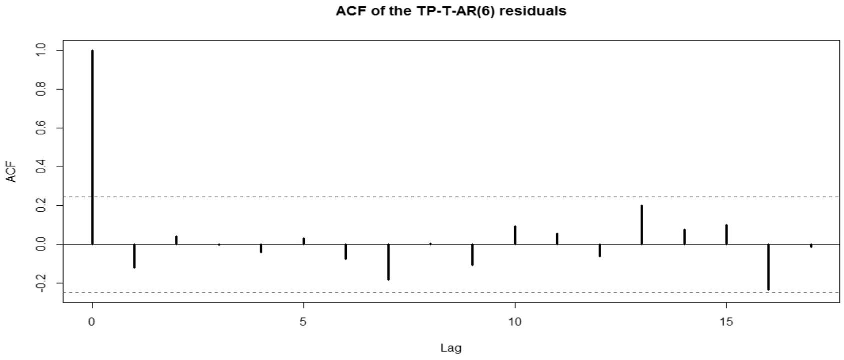

Figure 5: Time series plot of COVID-19 data and predicted data from 18-Mar-2020 up to 31-Mar-2020 in Iran.

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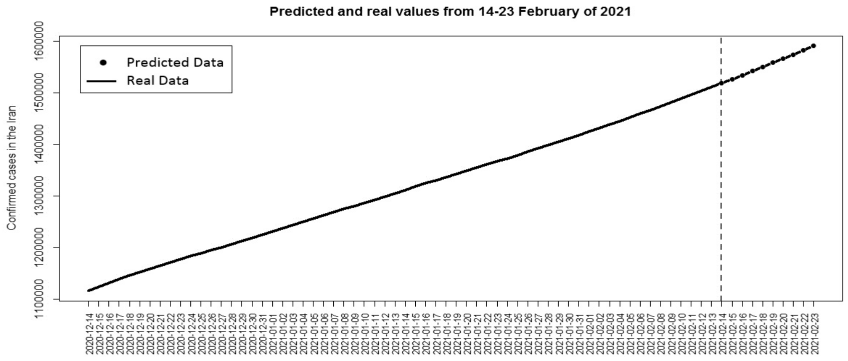

Figure 6: ACF of the residuals of the fitted time series model to total number of COVID-19 in Iran.

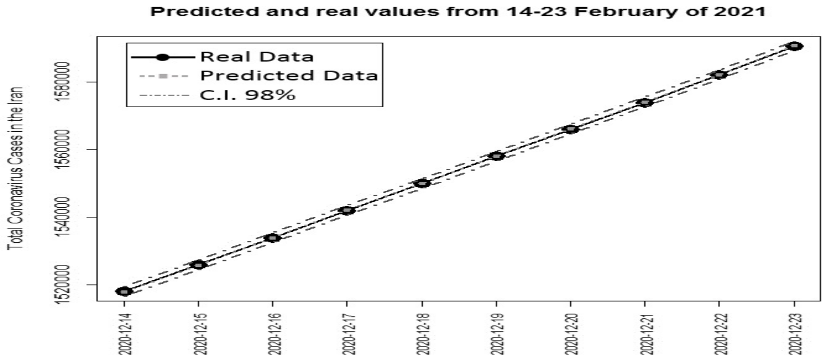

Figure 7: prediction of COVID-19 data from 14-Feb-2020 up to 23-Feb-2020 in Iran with 98% confidence interval.

4 Conclusion

Various types of Coronaviruses from a huge family of viruses that affect neurological, gastrointestinal, hepatic, and respiratory systems. Increasing the number of confirmed COVID-19 cases in the world is the main issue that needs strict special plans and policies. Time series models are useful statistical tools for modeling, estimating, and

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forecasting the future number. The symmetrical/asymmetrical and light/heavy-tailed TP-SMN-AR time series models were fitted to the total number of daily confirmed COVID-19 cases in Iran. The proposed time series models were fitted initially to the historical COVID-19 dataset in Iran, and the selected models were used to predict the number of confirmed COVID-19 cases. Results indicate that the proposed method performs well in forecasting the future confirmed COVID-19 cases in Iran. The R code is available upon request.

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