

Time Indexed Covariate Analysis of the Administered Vaccine Doses on Covid-19 Spread

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April 18, 2022

Time indexed covariate analysis of the administered vaccine doses on Covid-19 spread

Mohsen Maleki^a, Mohammad Reza Mahmoudi^{b,*} Hamid Bidram^a, Amir Mosavi^{c, d,*}

^a Department of Statistics, Faculty of Mathematics and Statistics, University of Isfahan, Isfahan, 81746-73441,

Iran

^b Department of Statistics, Faculty of Science, Fasa University, Fasa, Fars, Iran ^c Faculty of Civil Engineering, Technische Universität Dresden, 01069 Dresden, Germany; ^d John von Neumann Faculty of Informatics, Obuda University, 1034 Budapest, Hungary

Abstract

In this study, we focus on the spread of COVID–19 on besides of vaccination of this disease. Total infected cases of COVID–19 have considered and model it by a light/heavy tailed auto–regressive model with innovations belong on the flexible class of the two-piece scale mixtures of normal (*TP–SMN*) family. Also considering the covariate variables which are indexed by time are considered in the model to more accuracy of modeling. An EM type algorithm has considered for finding the maximum likelihood estimations of the model parameters. Modelling and prediction of infected numbers of COVID–19 in the U.S. has considered and vaccinated numbers of COVID–19 is considered as auxiliary (covariate) in the model.

Keywords: Auto-regressive model with covariate; COVID-19 vaccinated cases; ECME-algorithm; Infected numbers of COVID-19; ML estimates; Two-piece scale mixtures of normal family; Vaccinated numbers of COVID-19.

1. Introduction

The rapid spread of the infectious COVID-19 disease has affected whole of the world, and preparation and confronting for the prevalence of COVID-19 diseases requires careful plans and operating. Some mathematically modeling of the spreading of COVID-19, have considered by several mathematician authors, which some of the recent researches are given as follows. The confirmed and recovered cases and also death rate of COVID-19 have

modeled and forecasted via using asymmetry time series by Maleki et al. [1,2]. The cumulative confirmed, recovered and deaths cases of COVID-19 cases for top-16 countries, have forecasted via using statistical machine learning models has done by ArunKumar et al. [3]. ArunKumar et al. [4] have used gated recurrent units and long short-term memory cells and forecast the COVID-19 using the deep layer recurrent neural networks. Lau et al. [5] considered SARIMA model on the infectious diseases. Kalantari [6] forecast the COVID-19 using optimal singular spectrum analysis. Al-qaness et al. [7] forecast the COVID-19 in the Russia and Brazil, using efficient artificial intelligence forecasting models. Amruta et al. [8] have a study on the SARS-CoV-2 mediated neuro-inflammation and the impact of COVID-19 in neurological disorders. Luo et al. [9] considered a novel based on traditional Richards model and its application in COVID-19. The interested reader can refer to [10-15] to see some recent papers published on the COVID-19.

Time series are useful statistical model to forecast and control the datasets which are gathered by time. We can also use some flexible family of distributions with light/heavy tails and symmetry/asymmetry behaviors in the structure of the time series models which can be more expedient for datasets with outliers or/and skewed behavior, (see [16-24]). In this paper we consider a wide class of distributions in the structure of Auto-Regressive model with covariate, which is known as two-piece scale mixtures of normal (*TP–SMN*) family of distributions. The useful *TP–SMN* distributions were introduced by the authors of [25,26] and have used in the several statistical models to show the flexibility and performances of the family (see [27-30]).

Using auxiliary (covariate) on the statistical models we can improve the obtained results, especially in time series models. One of the main application of the time series modelling related to the COVID-19 is to single out the role plaid by the variables of COVID-19 indexed by time, for example by modelling and forecasting of the number of daily confirmed cases. Obviously by increasing the daily number of vaccination it will effect on the daily number of confirmed cases, thus expecting an extensively decay on the confirmed cases in the near future. We will model the infected numbers of COVID-19 by a robust time series models with vaccinated numbers of COVID-19 as a covariate. We have shown in the application section of the work that by using this covariate improves the modelling and predictions.

The paper is set as follows. Some required aspects of the *TP-SMN* distributions are provided in Section 2. The *TP-SMN* Auto-Regressive (AR) model with time indexed covariate is given in Section 3. In Section 4, the proposed model is fitted on the infected numbers of COVID-19 in the U.S. with vaccinated numbers of COVID-19 covariate. Finally in in Section 5, some conclusions of the work are provided.

2. The TP-SMN distributions

Herein, we briefly review main features of the *TP–SMN* distributions.

Let random variable *X* has renown *SMN* distributions given in [31] denoted by $X \sim SMN(\mu, \sigma, \nu)$. Then *X* possesses the probability density function (PDF) given by,

$$f_{SMN}(x|\mu,\sigma,\boldsymbol{\nu}) = \int_0^\infty \phi(x|\mu,u^{-1}\sigma^2) \, dH(u|\boldsymbol{\nu}), \quad x \in \mathbb{R},$$
(1)

in which $\phi(\cdot | \mu, \sigma^2)$ is the density of $N(\mu, \sigma^2)$ distribution, $H(\cdot | \nu)$ indicates the cumulative distribution function (CDF) related to the scale mixing variable u for each *TP–SMN* members which indexed by the parameters ν .

The applicable *TP–SMN* family is defined via the *SMN* family, which involves asymmetric light-tailed two–piece–normal (*TP–N*), and asymmetric heavy–tailed two–piece–t (*TP–T*), two–piece–slash (*TP–SL*) and two–piece–contaminated–normal (*TP–CN*) distributions and also covers their symmetrically forms. A random variable *Y* distributed with *TP–SMN* distributions denoted by $Y \sim TP-SMN$ (μ, σ, ν, γ) with the PDF

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

where $0 < \gamma < 1$ is the skewness parameter, $f_{SMN}(\cdot | \mu, \sigma, \nu)$ is the *SMN* PDF given in (1).

Mean and variance of $Y \sim TP-SMN(\mu, \sigma, \mathbf{v}, \gamma)$ are $E(Y) = \mu - b\sigma(1-2\gamma)$ and $Var(Y) = \sigma^2[c_2k_2 - b^2c_1^2]$, respectively, where $b = \sqrt{2/\pi} k_1$, $c_r = \gamma^{r+1} + (-1)^r(1-\gamma)^{r+1}$ and k_r is given in Table 1. It is noteworthy that for $\gamma = 0.5$, the well-known *SMN* family (which is symmetric) has extracted from the *TP-SMN* family.

Distributions	$f_{SMN}(\cdot), \ y \in \mathbb{R}$	k _r
TP-N	$\phi(y;\mu,\sigma^2)$	
TP-T	$\frac{\Gamma\left(\frac{\nu+1}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)\sqrt{\pi\nu\sigma}}\left(1+\frac{d}{\nu}\right)^{-\frac{\nu+1}{2}}; \ \boldsymbol{\nu}=\nu$	$\left(\frac{\nu}{2}\right)^{r/2} \frac{\Gamma\left(\frac{\nu-r}{2}\right)}{\Gamma\left(\frac{\nu}{2}\right)}, \nu > r$
TP-SL	$v \int_0^1 u^{v-1} \phi(y; \mu, u^{-1}\sigma^2) \mathrm{d}u; \mathbf{v} = v$	$\frac{2\nu}{2\nu-r}, \nu > \frac{r}{2}$
TP-CN	$\nu \phi(\boldsymbol{y}; \boldsymbol{\mu}, \tau^{-1} \sigma^2) + (1 - \nu) \phi(\boldsymbol{y}; \boldsymbol{\mu}, \sigma^2); \ \boldsymbol{\nu} = (\nu, \tau)^{T}$	$\frac{\nu}{\tau^{r/2}} + 1 - \nu$

Table 1. Some main TP-SMN distributions.

A key feature of using the well-known algorithm to estimate the statistical models using the *TP–SMN* distributions is that we can utilize the *TP–SMN* distributions in the form mixture distribution with two–components and distinct supports in (3). So let $Y \sim TP-SMN$ ($\mu, \sigma, \mathbf{v}, \gamma$), then the PDF given in (2) is represented as:

$$g(y|\mu,\sigma_1,\sigma_2,\nu) = 2\pi f_{SMN}(y|\mu,\sigma_1,\nu)I_{(-\infty,\mu]}(y) + 2(1-\pi)f_{SMN}(y|\mu,\sigma_2,\nu)I_{(\mu,+\infty)}(y), \quad (3)$$

where $\pi = \frac{\sigma_1}{\sigma_1 + \sigma_2}$, $\sigma_1 = \sigma(1 - \gamma)$ and $\sigma_2 = \sigma\gamma$, and the parameters σ and γ (respectively scale and slant) in (2) are meliorated as $\sigma = \sigma_1 + \sigma_2$ and $\gamma = \sigma_2/(\sigma_1 + \sigma_2)$.

By employing the latent variables Z_j ; j = 1,2, in terms of the mixture components (3), the proposed *TP–SMN* variable *Y* can be represented in the stochastic form

$$\begin{cases} Y|Z_1 = 1 \sim SMN(\mu, \sigma_1, \boldsymbol{\nu})I_T(y_i), \\ Y|Z_2 = 1 \sim SMN(\mu, \sigma_2, \boldsymbol{\nu})I_{T^c}(y_i), \end{cases}$$
(4)

where $T = (-\infty, \mu)$ and $SMN(\cdot)I_T(\cdot)$ denotes the *SMN*-distributions which are truncated on the interval *T*, and the random vector $\mathbf{Z} = (Z_1, Z_2)^{\mathsf{T}}$ with the probability mass function (PMF) given by:

$$P(\mathbf{Z} = \mathbf{z}) = \pi^{z_1} (1 - \pi)^{z_2}; \quad z_1, z_2 = 0, 1,$$
(5)

and is denoted by $\mathbf{Z} \sim M(1, \pi, 1 - \pi)$. Note that each component-label variable Z_i , i = 1, 2 has also a Bernoulli distribution and $Z_1 + Z_2 = 1$.

3. TP-SMN Auto-Regressive with covariates model

The Auto–Regressive model with covariates and order p based on the *TP–SMN* innovations, indicated using *TP–SMN–ARX*(p) model via intercept is considered and expressed by

$$Y_t = \mu + \sum_{j=1}^p \alpha_j Y_{t-j} + \sum_{k=1}^m \beta_k X_{kt} + \varepsilon_t, \ t = 0, \pm 1, \pm 2, ...,$$
(6)

where $\boldsymbol{\alpha} = (\alpha_1, ..., \alpha_p)^{\mathsf{T}}$ and $\boldsymbol{\beta} = (\beta_1, ..., \beta_m)^{\mathsf{T}}$ are respectively the Auto-Regressive and covariates coefficients vectors, and $\{\varepsilon_t\}$ is a i.i.d. noises distributed sequence as

$$\varepsilon_t \stackrel{iid}{\sim} TP - SMN(0, \sigma, \boldsymbol{\nu}, \gamma), \quad t = 0, \pm 1, \pm 2, \dots.$$
(7)

Considering the *ARX* model (6) with parameters $\boldsymbol{\Theta} = (\boldsymbol{\alpha}, \boldsymbol{\beta}, \mu, \sigma_1, \sigma_2, \boldsymbol{\nu})^{\mathsf{T}}$, to have a more appropriate form, the model can be represented by $Y_t = \mu + \boldsymbol{\alpha}^{\mathsf{T}} \boldsymbol{Y}_{t-1} + \boldsymbol{\beta}^{\mathsf{T}} \boldsymbol{X}_t + \varepsilon_t$, for which $\boldsymbol{Y}_{t-1} = (Y_{t-1}, \dots, Y_{t-p})^{\mathsf{T}}$, $\boldsymbol{X}_t = (X_{1t}, \dots, X_{mt})^{\mathsf{T}}$ and $\boldsymbol{Y} = (Y_{-p+1}, \dots, Y_0, Y_1, \dots, Y_n, \boldsymbol{X}_1^{\mathsf{T}}, \dots, \boldsymbol{X}_n^{\mathsf{T}})^{\mathsf{T}}$ as the sample vector.

Considering the non–stochastic part $Y_{-p+1}, ..., Y_0$ of the sample Y, the (conditional) likelihood function related to the *TP–SMN–ARX*(*p*) model is given by

$$\ell(\boldsymbol{\Theta}|\boldsymbol{Y},\boldsymbol{X}) = \sum_{t=1}^{n} \log g_{Y_t|Y_{t-1}=y_{t-1},X_t=x_t}(y_t|\boldsymbol{\alpha}^{\mathsf{T}}\boldsymbol{y}_{t-1} + \boldsymbol{\beta}^{\mathsf{T}}\boldsymbol{x}_t + \mu,\sigma_1,\sigma_2,\boldsymbol{\nu}).$$
(8)

Because of complexities of the *SMN*-densities (1), finding the *ML* estimates related to the *TP-SMN-ARX*(p) model parameters via (8) are difficult process. But considering an appropriate hierarchically representation of the *TP-SMN* distributions on besides of the established *ARX* model, obtaining the *ML* estimates of parameters can be desired by an *EM*-type scheme at the follows.

Consider the complete data $\boldsymbol{D} = (\boldsymbol{Y}^{\mathsf{T}}, \boldsymbol{X}^{\mathsf{T}}, \boldsymbol{U}^{\mathsf{T}})^{\mathsf{T}}$, with observed part of the data $(\boldsymbol{Y}^{\mathsf{T}}, \boldsymbol{X}^{\mathsf{T}})^{\mathsf{T}}$ and missing (latent) part of the data $\boldsymbol{U} = (U_1, \dots, U_n)^{\mathsf{T}}$ and $\boldsymbol{Z}_t = (Z_{t1}, Z_{t2})^{\mathsf{T}}$; $t = 1, 2, \dots, n$. Then, regarding to the mixture representation (4), the PMF in (5) and the well-

known stochastic representation of *SMN* distributions in Andrews and Mallows [31], the *TP-SMN-ARX* model using (6) can be represented in the hierarchically manner

$$Y_{t}|Y_{t-1} = y_{t-1}, X_{t} = x_{t}, U_{t} = u_{t}, Z_{ti} = 1 \stackrel{ind.}{\sim} N(\boldsymbol{\alpha}^{\top} y_{t-1} + \boldsymbol{\beta}^{\top} x_{t} + \mu, u_{t}^{-1} \sigma_{i}^{2}) I_{T_{t}}(y_{t})^{2-i} I_{T_{t}^{c}}(y_{t})^{i-1},$$

$$U_{t}|Z_{ti} = 1 \stackrel{ind.}{\sim} H(u_{t} | \boldsymbol{\nu}),$$

$$Z_{t} \stackrel{iid.}{\sim} M(1, \pi, 1 - \pi),$$
(9)

where $i = 1, 2, T_t = (-\infty, \boldsymbol{\alpha}^\top \boldsymbol{y}_{t-1} + \boldsymbol{\beta}^\top \boldsymbol{x}_t + \mu)$ for t = 1, 2, ..., n and $N(\cdot)I_T(\cdot)$ is the normal distribution truncated on the domain *T*.

An *ECME* algorithm generated by Liu and Rubin [32] and the hierarchical form of the *TP-SMN-ARX* model in (9) is utilized in to extract the *ML* estimates of the parameters.

Regarding the hierarchical form (9), conclude the conditional completed log–likelihood function attributed to the *TP-SMN-ARX(p)* model given by

$$\ell(\mathbf{\Theta}) = -n\log(\sigma_1 + \sigma_2) - \frac{1}{2}\sum_{t=1}^n \sum_{i=1}^2 W_{ti} \left(\frac{Y_t - \alpha^\top Y_{t-1} - \beta^\top X_t - \mu}{\sigma_i}\right)^2 + \sum_{t=1}^n \sum_{i=1}^2 Z_{ti} \log h(U_t|\mathbf{\nu}),$$

where $\mathbf{\Theta} = (\boldsymbol{\alpha}^{\mathsf{T}}, \boldsymbol{\beta}^{\mathsf{T}}, \mu, \sigma_1, \sigma_2, \boldsymbol{\nu})^{\mathsf{T}}$ and $W_{ti} = U_t Z_{ti}$ for t = 1, 2, ..., n and i = 1, 2. Defining the quantities $\hat{z}_{ti} = E[Z_{ti}|\widehat{\mathbf{\Theta}}, \mathbf{Y}, \mathbf{X}]$ and $\hat{w}_{ti} = E[U_t Z_{ti}|\widehat{\mathbf{\Theta}}, \mathbf{Y}, \mathbf{X}]$, and according to the properties of the conditional expectation, $\hat{w}_{ti} = \hat{\kappa}_{ti}\hat{z}_{ti}$ is obtained where $\hat{z}_{t1} = I_{(-\infty, \hat{\alpha}^{\mathsf{T}}y_{t-1}+\hat{\beta}^{\mathsf{T}}x_t+\hat{\mu}]}(y_t)$ for $\hat{z}_{t2} = 1 - \hat{z}_{t1}$ and $\hat{\kappa}_{ti} = E[U_t|\widehat{\mathbf{\Theta}}, y_t, x_t, Z_{ti} = 1]$ for the *TP-SMN-ARX* members, are considered by

• *TP-N-ARX* model: $\hat{\kappa}_{ti} = 1$,

•
$$TP-T-ARX \text{ model:}$$
 $\hat{\kappa}_{ti} = \frac{\hat{\nu}+1}{\hat{\nu}+d_{ti}},$

•
$$TP-SL-ARX \text{ model:} \quad \hat{\kappa}_{ti} = \frac{2\hat{\nu}+1}{d_{ti}} \frac{P_1(\hat{\nu}+3/2, d_{ti}/2)}{P_1(\hat{\nu}+1/2, d_{ti}/2)}$$

• *TP-CN-ARX* model: $\hat{\kappa}_{ti} = \frac{\hat{\tau}^2 \hat{v} e^{-\hat{\tau} d} ti^{/2} + (1-\hat{v}) e^{-d} ti^{/2}}{\hat{\tau} \hat{v} e^{-\hat{\tau} d} ti^{/2} + (1-\hat{v}) e^{-d} ti^{/2}},$

where $d_{ti} = \left(\frac{y_t - \hat{\alpha}^T y_{t-1} - \hat{\beta}^T x_t - \hat{\mu}}{\hat{\sigma}_i}\right)^2$ and $P_x(a, b)$ denotes the evaluated cumulative distribution function (CDF) of the Gamma(a, b) distribution at point x.

Determination of *Q*-function as of $Q(\Theta|\widehat{\Theta}^{(k)}) = E_{\theta}[\ell(\Theta)|\widehat{\Theta}^{(k)}, Y, X]$ is the E-Step of the *ECME*-algorithm on the (k + 1)th algorithm's iteration as

$$Q(\boldsymbol{\Theta}|\widehat{\boldsymbol{\Theta}}^{(k)}) = -n\log(\sigma_1 + \sigma_2) - \frac{1}{2}\sum_{t=1}^n \sum_{i=1}^2 \widehat{w}_{ti}^{(k)} \left(\frac{Y_t - \boldsymbol{\alpha}^\top \boldsymbol{Y}_{t-1} - \boldsymbol{\beta}^\top \boldsymbol{X}_t - \mu}{\sigma_i}\right)^2 \\ + \sum_{i=1}^n \sum_{j=1}^2 E[Z_{ti}\log h(\boldsymbol{U}_t|\boldsymbol{\nu})|\widehat{\boldsymbol{\Theta}}^{(k)}, \boldsymbol{Y}, \boldsymbol{X}],$$

where $\widehat{w}_{ti}^{(k)} = E[U_t Z_{ti} | \widehat{\Theta}^{(k)}, \boldsymbol{Y}, \boldsymbol{X}] = \widehat{\kappa}_{ti}^{(k)} \widehat{z}_{ti}^{(k)}$ and hereafter consider $\widehat{\omega}_t^{(k)} = \sum_{i=1}^2 \widehat{w}_{ti}^{(k)} / \sigma_i^{2(k)}$.

Conditional maximizations of the ECME–algorithm on the (k + 1)th algorithm's iteration as follows:

CM-step of the algorithm for coefficients:

$$\widehat{\boldsymbol{\alpha}}^{(k+1)} = \left(\sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)} \boldsymbol{Y}_{t-1} \boldsymbol{Y}_{t-1}^{\mathsf{T}}\right)^{-1} \sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)} \left(\boldsymbol{Y}_{t} - \widehat{\boldsymbol{\beta}}^{\mathsf{T}(k)} \boldsymbol{X}_{t} - \widehat{\boldsymbol{\mu}}^{(k)}\right) \boldsymbol{Y}_{t-1}$$
$$\widehat{\boldsymbol{\beta}}^{(k+1)} = \left(\sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)} \boldsymbol{X}_{t} \boldsymbol{X}_{t}^{\mathsf{T}}\right)^{-1} \sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)} \left(\boldsymbol{Y}_{t} - \widehat{\boldsymbol{\alpha}}^{\mathsf{T}(k+1)} \boldsymbol{Y}_{t-1} - \widehat{\boldsymbol{\mu}}^{(k)}\right) \boldsymbol{X}_{t},$$

CM-step of the algorithm for intercept (location parameter):

$$\hat{\mu}^{(k+1)} = \frac{\sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)} \big(Y_{t} - \widehat{\boldsymbol{\alpha}}^{\top (k+1)} \boldsymbol{Y}_{t-1} - \widehat{\boldsymbol{\beta}}^{\top (k+1)} \boldsymbol{X}_{t} \big)}{\sum_{t=1}^{n} \widehat{\omega}_{t}^{(k)}}.$$

CM-step of the algorithm for scale parameters:

Solving the stressed cubic equations $\sigma_i^3 + p\sigma_i + q = 0$, conclude the update $\hat{\sigma}_i^{(k+1)}$ for i = 1, 2, where $p = -\frac{1}{n} \sum_{t=1}^n \widehat{w}_{ti}^{(k)} (X_t - \widehat{\alpha}^{\top (k+1)} Y_{t-1} - \widehat{\beta}^{\top (k+1)} X_t - \widehat{\mu}^{(k+1)})^2$, for which $q = p\sigma_2 I_{(i=1)} + p\sigma_1 I_{(i=2)}$. It is noteworthy that p < 0 implies q < 0, therefor the proposed cubic equation possesses a positive unique just root.

CML-step of the algorithm for scale mixing parameters:

$$\boldsymbol{\nu}^{(k+1)} = \operatorname{argmax}_{\boldsymbol{\nu}} \ell\left(\widehat{\boldsymbol{\alpha}}^{\top(k+1)}, \widehat{\boldsymbol{\beta}}^{\top(k+1)}, \widehat{\boldsymbol{\mu}}^{(k+1)}, \widehat{\sigma}_{1}^{(k+1)}, \widehat{\sigma}_{2}^{(k+1)}, \boldsymbol{\nu} \middle| \boldsymbol{Y}, \boldsymbol{X}\right),$$

where the log-likelihood function $\ell(\cdot|\mathbf{Y}, \mathbf{X})$ is in (8).

A sufficient convergence rule for the algorithm iterates is satisfied when $|\ell(\widehat{\Theta}^{(k+1)}|Y,X)/\ell(\widehat{\Theta}^{(k)}|Y,X) - 1| \leq \varepsilon$, for the known values of the tolerance ε . In the work we employed $\varepsilon = 10^{-2}$, while choosing the tolerance values may vary in other statistical models.

4. Application

This section investigates the infected numbers of COVID–19 since 19–Jan–2021 to 27– Mar–2021 related to the U.S. (see Fig 1) and vaccinated numbers of COVID–19 in there and in the corresponding time (see Fig 2), and fit the *TP–SMN–ARX* to the proposed datasets.

After some suitable transformations in Brockwell and Davis [33], the stationary data which are ready to modeling are obtained and plotted in Fig 3. Using some model selection criteria and considering the PACF (partial auto-correlation function) diagram, shown in Fig 4 conclude that the best TP–T–ARX(5) model was fitted to the stationary series of the infected numbers of COVID–19 in the form of

TP-SMN-ARX model:

$$\begin{aligned} Y_t &= -9139.5940 - 0.6390 \, Y_{t-1} - 0.4393 \, Y_{t-2} - 0.4123 \, Y_{t-3} - 0.4340 \, Y_{t-4} - 0.3338 \, Y_{t-5} \\ &\quad + 0.0029 \, X_t + \varepsilon_t, \end{aligned}$$
where $\varepsilon_t \sim TP - T(0, \sigma = 23211.9000, \gamma = 0.5582, \nu = 3.0939). \end{aligned}$

Gaussian-ARX model:

$$Y_{t} = -1995.2399 - 0.6627 Y_{t-1} - 0.3799 Y_{t-2} - 0.3730 Y_{t-3} - 0.3878 Y_{t-4} - 0.2617 Y_{t-5} + 0.0036 X_{t} + \varepsilon_{t},$$
where $\varepsilon_{t} \sim N(0, \sigma = 17888.5400)$.

According to log-likelihood and Akaike information criterion (AIC) criteria, which are recorded in Table 2, the TP–T–ARX model is more reasonable than ordinary Gaussian–ARX model. The ACF (auto–correlation function) diagram of estimated innovations (residuals) is shown in Fig. 5 (Left), and also the histogram of estimated innovations for which the

estimated heavy-tailed TP-T density is superimposed on it, is given in Fig. 5 (Right). Fig. 5 shows some reasonability of the proposed estimated model to the stationary series of infected numbers of COVID-19 related to the U.S.



Infected numbers of COVID-19 in the U.S.

Fig 1. Infected numbers of COVID-19 plot related to U.S. since 19-Jan to 27-Mar in 2021.







Fig 3. Differenced transform the infected numbers of COVID-19 plot.

PACF of differenced data

Fig 4. PACF of the differenced data (stationary).

To investigate the suitability and goodness of fit tests for the proposed fitted TP–SMN– ARX model, P–values of the Box–Pierce and Ljung–Box tests on the estimated innovations are recorded in Table2. Note that the large P–values (near to one) of the proposed tests on the estimated innovations of TP–T–ARX model, demonstrate the reasonability proposed fitted TP–SMN–ARX model. Also comparing the corresponding P–values of the proposed tests on the ordinary Gaussian–ARX model, show the better performances of the TP–SMN– ARX model (see Table 2).

Model	TP-T	'-ARX	Gaussian–ARX		
Log-likelihood	-664.5078		-729.1800		
AIC	1350	.0790	1474.3600		
Test	Box-Pierce	Ljung-Box	Box-Pierce	Ljung-Box	
P-values	0.9882	0.9625	0.9613	0.8821	

 Table 2. P-values of the Box-Pierce and Ljung-Box tests on the residuals of the TP-SMN-ARX and ordinary Gaussian-ARX models.



Fig 5. Sample ACF diagram of the estimated innovations of the fitted model (Left) Histogram of the estimated innovations of the fitted model via superimposed estimated TP-T density (Right).

To shoe further reasonability of the fitted model, we predicted the 10 data of the infected cases (2021-Mar-15 up to 2021-Mar-24), then fitted the TP–SMN–ARX models on them and forecast these data. Table 3 contains the predictions with and without covariate and 95% confidence intervals for them. Also Fig. 6, show the forecasted values based on the modelling with and without covariate which superimposed the diagram of the real values of infected numbers of COVID-19 related to U.S. Percent Relative Prediction Error (PRPE) of the predicted values via the model with covariate is 0.0762 % while is 0.1469 % for the model without covariate. So the results and Fig. 6 shows the importance of the covariate (considering the vaccination) on the modelling and predictions of the infected cases.

Table 3. Real values of the infected numbers of COVID-19 related to the U.S. since 2021-Mar-15 to 2021-Mar-24 with and							
without vaccinated numbers covariate and predictions with 95% confidence interval.							
COVID 10 in			Dradiction	Dradiction			

COVID-19 in the U.S.	Date	Real value	Prediction without covariate	Prediction with covariate	Lower C.I.	Upper C.I.
	2021-03-15	30181273	30154131	30175035	30148628	30214710
infected	2021-03-16	30234911	30219435	30222759	30184850	30263368
cases	2021-03-17	30298419	30256412	30285499	30248798	30324452
	2021-03-18	30361971	30338946	30355790	30318956	30394125

2021-03-19	30487505	30415297	30414364	30341297	30492385
2021-03-20	30534590	30648341	30593349	30537136	30672910
2021-03-21	30581123	30541449	30596553	30547796	30659999
2021-03-22	30641164	30581496	30621390	30582911	30663694
2021-03-23	30708302	30672908	30686643	30649897	30727696
2021-03-24	30776056	30756192	30769650	30703639	30810684

5. Conclusion

Coronaviruses are a wide category that affects gastrointestinal, hepatic, neurological and respiratory systems. Extended vaccination might reduce the prevalence of COVID-19 diseases. In our methodology, by considering a robust class of time series models with covariate, to model the infected numbers of COVID-19 in the U.S. with the vaccinated COVID-19 cases as the covariate. Performances of the proposed fitted model show that it would be better considering the vaccinated numbers of COVID-19 as the covariate, to predict infected numbers of COVID-19. Also there exist other desirable results that can be obtained by the model described in this paper, for example mobility data (indexed by time, for example in the daily form) can be a covariate to better modelling and prediction of the death rate of COVID-19. The free source *R* software [34] version 4.0.5 with a core i7 760 processor 2.8 GHz is used to implements the algorithms.

Predicted and real values



Fig 6. The experimental values and predicted infected numbers of COVID-19 related to the U.S. time series plots since 2021-Mar-15 up to 2021-Mar-24 with and without vaccinated numbers covariate.

Availability of data and materials: The data used in this research are available by the corresponding author upon reasonable request.

Compliance with Ethical Standards

Ethics approval: The author confirms that this article is original research and has not been published or presented previously in any journal or conference in any language (in whole or in part).

Competing Interests: The author has no conflict of interest.

Funding statement No funds, grants, or other support was received.

Consent to Participate and Consent to Publish: Not applicable.

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