Advances in Differential Equations and Control Processes
© 2022 Pushpa Publishing House, Prayagraj, India
http://www.pphmj.com
http://dx.doi.org/10.17654/0974324322027
Volume 28, 2022, Pages 119-134 **P-ISSN: 0974-3243**

ESTIMATION OF PARAMETERS AND STABILITY ANALYSIS OF CORONAVIRUS PANDEMIC

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Received: March 16, 2022; Accepted: May 26, 2022

2020 Mathematics Subject Classification: 92C60, 92D30, 60G25.

Keywords and phrases: Covid-19, Algeria, Repeated MsDTM, equilibrium, stability.

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How to cite this article: Poonam Garg, Ritu Arora, Surbhi Madan and Dhiraj Kumar Singh, Estimation of parameters and stability analysis of Coronavirus pandemic, Advances in Differential Equations and Control Processes 28 (2022), 119-134.

http://dx.doi.org/10.17654/0974324322027

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Abstract

Despite ranking amongst the highest in medical systems in Africa and spending a substantial amount on health sector than other African nations, Algeria suffered a major blow in the first wave of the Covid-19 pandemic. Vaccine hesitancy also affected the country adversely in subsequent waves of the disease. This study estimates the number of Covid-19 cases for Algeria in January 2022 using two numerical methods Multi-step Differential Transform Method (MsDTM) and Repeated MsDTM. Stability analysis of the pandemic for the country has also been discussed in the paper.

1. Introduction

Algeria is the largest African nation in terms of area and tenth largest nation in the world. Till early sixties, Algerian economy was agro-based and shifted gradually to export economy, primarily dealing with petrochemical products [20]. It ranks amongst the highest in terms of health care systems in the African countries, though still lacking behind the wealthier countries [12]. Post the first case of Covid-19 being reported on February 25, 2020 [22]; Algeria implemented all the basic preventive measures like lockdown, use of masks, social distancing and many more, to contain spread of the disease. Even though Algeria's expenditure on health sector is considerably high in comparison to other African countries, still due to lack of preparedness the country suffered a lot of casualties and struggled a lot to control the Covid-19 spread. Strictly implementing all the necessary preventive measures in the initial wave, Algeria managed to lower the peak of daily new cases by the end of May 2020, until a rise in cases again in July 2020 followed by another wave of the disease in November, in the same year.

Algeria initiated vaccination campaign on January 30, 2021, by inoculating a 65-year-old man with Russia's Sputnik-V vaccine [23]. Algeria was amongst the many African country who ordered many vaccines like AstraZeneca, Sputnik V, and Sinovac, but hesitancy for taking the vaccine created a problematic situation in the country. In fact, many researchers worked on studying the safety concerns and ill-effects of these vaccines [8, 14]. The slow pace of vaccination resulted in an increase of Coronavirus cases again in June 2021, reaching the peak in the end of July 2021. Even by the end of January 2022, only about 13 percent of the Algerian population was vaccinated against the disease [18]. A new wave of Covid-19 infection caused by Omicron variant, hit Algeria in December 2021 and the reported number of infected cases almost doubled in comparison to the earlier waves.

With the initial cases of Covid-19 reported from Wuhan, China in late 2019, the disease eventually turned into a pandemic in early 2020 [19], affecting almost the entire world. Managing the spread of the disease required enforcement of restrictions like lockdowns, travel-bans, etc. Despite these measures, owing to the medical systems in various countries being caught unawares, there was a huge loss of lives. Many countries faced tremendous financial crisis. Overall, to save lives and prevent financial crisis, the countries needed to be prepared in advance for future waves of the pandemic. An estimation of the number of cases that might be needed to be handled in future was a necessity. Many researchers worked with this aim, to understand and predict the future course of this disease [4, 6, 7, 15]. This paper is also an attempt in the same direction.

The paper is organized as follows: In Section 2, the model under consideration has been discussed. Further, we discuss Differential Transform Method (DTM) and Multi-step Differential Transform Method (MsDTM). The study of Covid-19 situation in Algeria from January 1 to January 30, 2022 using MsDTM is undertaken in Section 3. Section 4 deals with stability analysis and the states of equilibrium of the model. Section 5 presents the use of Repeated MsDTM, as an improvement over the method used in Section 3, to obtain estimates of Covid-19 cases in Algeria. Section 6 presents conclusion of the results.

2. Mathematical Model

Modelling is an important tool which assists in understanding the spread of diseases. It also helps us to do predictions based on scientific calculations which further facilitate planning and taking informed decisions.

In this paper, we have considered a nonlinear deterministic mathematical model to study the dynamics of spread of Covid-19 in Algeria. The model under consideration is a compartment based SIR model which was first introduced by Kermack and McKendrick [9]. In this model, the whole population $n(t)$ is divided into three disjoint compartments - susceptible $s(t)$, infectives $i(t)$ and recovered $r(t)$. While constructing the model, following assumptions were considered:

- New individuals are added to the susceptible compartment through natural births at the rate μ.
- Persons in the infectives compartment can infect the susceptible population at the rate β.
- The recovered compartment has those individuals who have either recovered or died and hence removed from the previous compartment i.e., i compartment with the rate γ.
- Those who have recovered cannot get infected again.
- Rate of birth and rate of death μ are considered as same so that total population $n(t)$ or n is constant, for a short duration of time.

The changes that take place during the spread of the disease over a period of time t is depicted in Figure 1. Here, the rate of infection is denoted by β, the rate of recovery is denoted by γ and μ represents the rate of birth/death.

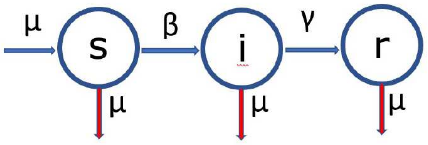

Figure 1. SIR model with natural birth and death.

Based on the dynamics of the spread of the Covid-19, the SIR Mathematical model is governed by the following system of nonlinear differential equations [3]:

$$\frac{ds}{dt} = \mu n - \beta si - \mu s, \quad \frac{di}{dt} = \beta si - \mu i - \gamma i, \quad \frac{dr}{dt} = \gamma i - \mu r. \tag{1}$$

For the sake of convenience, we denote $s(t)$, $i(t)$ and $r(t)$ by s, i, r, respectively. We solved the above system of equations by Multi-step Differential Transform Method (MsDTM) and Repeated Multi-step Differential Transform Method (RMsDTM) to obtain estimates of s, i, and r for Algeria from January 1 to January 30, 2022. Both these methods are based on Differential Transform Method (DTM), introduced in 1984 by Zhou [17].

DTM is used to solve boundary value differential equations [1, 11]. In this method, the kth coefficient of Taylor series of an analytical function is called its kth *differential transform*. The function is then defined in terms of this transform and is called the *inverse differential transform*. So, for an analytical function ϕ defined on $[a, b]$ whose Taylor series about $c \in [a, b]$ is

$$\sum_{k=0}^{\infty} \frac{\phi^{(k)}(0)}{k!}(x-c)^k,$$

the kth differential transform, denoted by Φ is given by $\Phi(k) = \frac{\phi^{(k)}(0)}{k!}$. The inverse transform of Φ is $\sum_{k=0}^{\infty} \Phi(k)(x-c)^k$. The function ϕ approximated as a Kth degree polynomial, obtained from the inverse transform, is given by

$$\phi(x) = \sum_{k=0}^{K} \Phi(k)(x-c)^k. \tag{2}$$

Using the properties of the differential transform function [11], the system of differential equations in (1) gets transformed to:

$$\begin{cases} S(k+1) = \dfrac{1}{k+1}\left(\mu n - \beta \sum\nolimits_{m=0}^{\infty} (S(m)I(k-m)) - \mu S(k)\right), \\ I(k+1) = \dfrac{1}{k+1}\left(\beta \sum\nolimits_{m=0}^{k} (S(m)I(k-m) - \mu I(k) - \gamma I(k))\right), \\ R(k+1) = \dfrac{1}{k+1}(\gamma I(k) - \mu R(k)), \end{cases} \tag{3}$$

S, I and R thus obtained are used to find the susceptible, infectives and recovered (the inverse differential transform, as given in (2)) at time t.

Multi-step differential transform method (MsDTM) [16] is an improvement of the DTM. In MsDTM the time period under consideration, say $[0, T]$ is divided into p equal sub-intervals, say $[t_{i-1}, t_i]$, $i = 1, \dots, p$ of length $\frac{T}{p}$ each; where $t_0 = 0$ and $t_p = T$. Initially DTM is applied to the function ϕ on the first sub-interval $[0, t_1]$ with given initial condition $\phi(0)$ on the function ϕ. The values of ϕ are obtained on this interval (denoted by ϕ_1) and the last value, $\phi(t_1)$ (or $\phi_1(t_1)$) is used as the initial condition for the second interval to obtain the function (denoted by ϕ_2) on second interval. The method is repeated for all subsequent intervals to determine the complete function ϕ on $[0, T]$ as follows:

$$\phi(x) = \begin{cases} \phi_1(x) \\ \phi_2(x) \\ \vdots \\ \phi_p(x) \end{cases} \qquad \text{where } \phi_i(x) = \sum_{k=0}^{K} \Phi(k)(x - t_{i-1})^k, \quad x \in [t_{i-1}, t_i]$$

for $i = 1, \ldots, p$. In this manner, updated values of the function are used as initial conditions at various levels, giving a better approximation of the function.

In certain situations, further better approximation may be obtained by considering different values of the parameters at equal time intervals and applying MsDTM on these intervals thereafter. This is desirable in case the parameters show variation in that time period. Use of different parameters at equal intervals is followed in Repeated MsDTM [2, 10], making it more accurate than MsDTM.

3. Numerical Simulation: MsDTM

Multi-step Differential Transform Method is used to obtain solution of system of equations given in (3). The computational part is executed using programming in Mathematica software [13]. The initial conditions used are the susceptible, active infected and recovered in Algeria on December 31, 2021 [21, 24]. Initial values of the parameters β and γ are found using these initial values of s, i and r. The initial conditions are stated in Table 1.

Table 1. Initial conditions

$s(0)$	44940254
$i(0)$	62072
$r(0)$	156360
β	3.497191×10^{-10}
γ	7.933459×10^{-3}
μ	1.29671×10^{-5}

With these initial conditions, using MsDTM the number of susceptible, active infectives and recovered are obtained for the chosen period. The estimates are plotted with the actual numbers in Figure 2 and Figure 3.

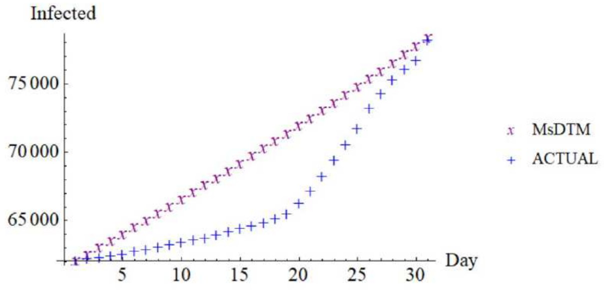

Figure 2. MsDTM estimation for infectives vs actual infectives.

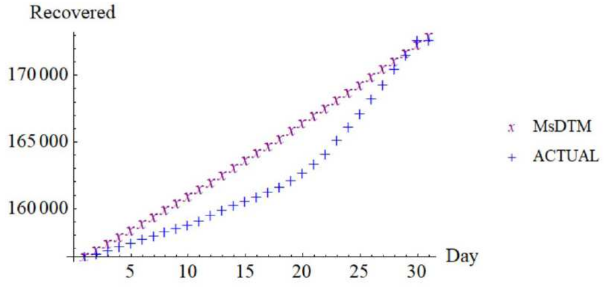

Figure 3. MsDTM estimation for recovered vs actual recovered.

We observe that for β and γ calculated over a period of 30 days, the graph coincides with actual data in the beginning and towards the end of the considered period. In between, the values are differing from the actual ones.

4. Stability Analysis

To find the disease-free equilibrium points and endemic equilibrium points for Covid-19, stability analysis is done for the non-linear differential equations (1).

Since we are trying to find the equilibrium points, so $\frac{ds}{dt} = 0,$ $\frac{di}{dt} = 0,$ $\frac{dr}{dt} = 0.$ Thus, for equilibrium we get the following conditions from (1):

$$\mu n - \beta si - \mu s = 0, \tag{4}$$

$$\beta si - \mu i - \gamma i = 0, \tag{5}$$

$$\gamma i - \mu r = 0. \tag{6}$$

We linearize the above system of equations (1) and find the Jacobian Matrix based on the equations as

$$J = \begin{bmatrix} -\beta i - \mu & -\beta s & 0 \\ \beta i & \beta s - \mu - \gamma & 0 \\ 0 & \gamma & -\mu \end{bmatrix}.$$

By solving differential equations (4), (5) and (6); we obtain the disease free equilibrium point and endemic equilibrium point. Disease free equilibrium point is $E_0 = (s_0, i_0, r_0) \to (n, 0, 0)$. When we attain disease free equilibrium, the disease will not spread further as in this case $i = 0$ and $r = 0$. The endemic equilibrium point (s^*, i^*, r^*) for Covid-19 is obtained as

$$s^* = \frac{(\gamma + \mu)n}{\beta},$$

$$i^* = \left(\frac{\beta - \gamma - \mu}{\beta(\gamma + \mu)}\right)\mu n,$$

$$r^* = -\frac{\gamma(-\beta + \gamma + \mu)n}{\beta(\gamma + \mu)}.$$

For $n = 45158686$, $\beta = 3.497191 \times 10^{-10}$, $\gamma = 7.933459 \times 10^{-03}$ and $\mu = 1.29671 \times 10^{-5}$, the endemic point thus obtained is

$$(2.2722311 \times 10^7, 3.6612021 \times 10^4, 2.2399763 \times 10^7).$$

The characteristic equation of the matrix J at the endemic point (s^*, i^*, r^*) is given by

$$-1.3193431 \times 10^{-12} - (1.0207960 \times 10^{-7})\lambda - 0.0000387\,\lambda^2 - \lambda^3 = 0. \tag{7}$$

Now, from equation (7), we obtain

$$\lambda_1 = -0.0000129, \quad \lambda_2 = -0.0000129 - 0.0003187i,$$

$$\lambda_3 = 0.0000129 + 0.0003187i.$$

We observe that the characteristic equation (7) has one real root which is negative and two complex roots with negative real parts, implying that the endemic equilibrium point is asymptotically stable. This shows that the disease will eventually be eradicated [5].

5. Numerical Simulation: RMsDTM

The estimates for Covid-19 cases using MsDTM were calculated in Section 3. In this method, the initial values of s, i and r (or the function being calculated) are updated at each iteration. However the rate of transmission, rate of recovery and birth/fatality rates (or the parameters used in an equation) are taken to be same throughout. Sometimes this results in an approximation which is not very correct, especially in situations where these parameters are changing rapidly or showing much variation. Repeated MsDTM takes this into consideration and uses the variation of parameters with change in circumstances. In the case of Algeria, the rate of transmission for Covid-19 was showing much variation during January 2022. So, we divide the period of 30 days into 5 intervals of 6 days each and consider the values of parameters in accordance with the time, as given in Table 2. The value of μ, the birth/fatality rate is same as given in Table 1.

Table 2. Parameters and inverse differential polynomials for s, i, r

Days	β	γ	Inverse differential polynomials
1-6	1.432411×10^{-10}	0.004172650	$s(x) = 292.343x^2 - 396.743x + 44940254$ $i(x) = 0.156x^2 + 139.766x + 62072$ $r(x) = 0.290x^2 + 256.977x + 156360$
7-12	1.755153×10^{-10}	0.005047816	$s(x) = 292.093x^2 - 493.459x + 4.49414\times 10^7$ $i(x) = 0.249x^2 + 177.872x + 62916.3$ $r(x) = 0.447x^2 + 315.542x + 157912$
13-18	2.165543×10^{-10}	0.005733323	$s(x) = 291.556x^2 - 619.988x + 4.49419\times 10^7$ $i(x) = 0.504x^2 + 255.079x + 63992.6$ $r(x) = 0.729x^2 + 364.818x + 159822$
19-24	6.180224×10^{-10}	0.012400290	$s(x) = 278.855x^2 - 1817.6x + 4.49416\times 10^7$ $i(x) = 7.696x^2 + 1006.83x + 65541.4$ $r(x) = 6.237x^2 + 810.632x + 162037$
25-30	5.952624×10^{-10}	0.012313220	$s(x) = 278.981x^2 - 1919.35x + 4.49337\times 10^7$ $i(x) = 7.432x^2 + 1036.41x + 71867.4$ $r(x) = 6.375x^2 + 882.751x + 167132$

For RMsDTM, using the parameters given in Table 2 for five periods of 6 days each, MsDTM is applied to each period. The approximations of the Covid-19 cases are thus obtained. These numbers are depicted in Figure 4 and Figure 5.

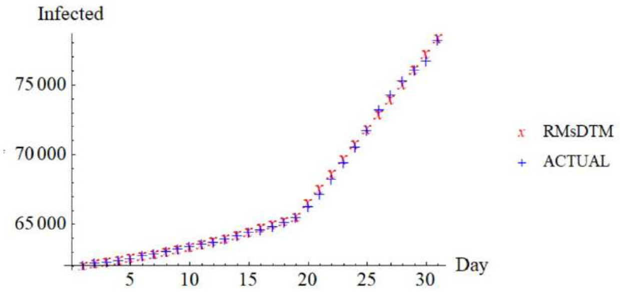

Figure 4. RMsDTM estimation for infectives vs actual infectives.

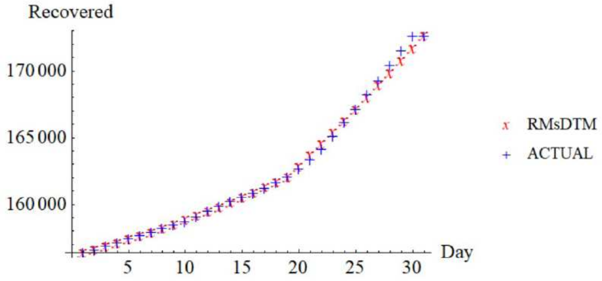

Figure 5. RMsDTM estimation for recovered vs actual recovered.

It is evident from these figures that the method gives a very close estimation. In both the graphs of infectives and recovered, the estimated values are almost overlapping the actual values.

The errors in estimated number of infectives and estimated number of recovered calculated using MsDTM and RMsDTM are tabulated in Table 3 and Table 4.

From Table 3 and Table 4, it can be seen that the errors in the estimations using RMsDTM is very less in comparison to the errors in estimations using MsDTM. The error in estimated number of infectives found using RMsDTM is sometimes as less as 1.47 (Day 7) and error in estimated number of recovered goes as low as 0.36 (Day 24), whereas in MsDTM there is at least an error of 196.18 (Day 30) in estimated number of infectives and an error of 205.09 (Day 28) in estimated number of recovered. This shows that RMsDTM is an improvement over MsDTM.

Table 3. Comparison of error in estimated number of infectives using MsDTM and RMsDTM

Day	**MsDTM**	**RMsDTM**	**Day**	**MsDTM**	**RMsDTM**
1	330.17	14.08	16	5432.11	166.03
2	731.06	39.15	17	5701.45	146.72
3	1130.67	87.71	18	5890.98	44.43
4	1476.02	78.58	19	5672.70	283.96
5	1772.09	16.77	20	5347.60	427.87
6	2130.48	13.28	21	4842.36	402.94
7	2447.75	1.40	22	4202.47	254.86
8	2790.89	12.02	23	3676.92	233.44
9	3138.90	24.15	24	3041.74	114.36
10	3510.79	56.78	25	2166.90	299.79
11	3878.17	80.93	26	1667.11	329.08
12	4171.57	27.59	27	1294.84	219.82
13	4480.00	60.17	28	1083.10	60.73
14	4748.47	49.76	29	1042.87	524.28
15	5109.95	129.39	30	196.18	192.57

Table 4. Comparison of error in estimated number of recovered using MsDTM and RMsDTM

Day	**MsDTM**	**RMsDTM**	**Day**	**MsDTM**	**RMsDTM**
1	260.33	25.27	16	3512.50	90.74
2	502.48	29.11	17	3657.12	49.18
3	721.44	6.54	18	3772.02	24.90
4	954.23	5.44	19	3754.22	207.96
5	1202.84	4.84	20	3658.72	371.31
6	1449.71	9.66	21	3450.00	429.70
7	1664.56	5.33	22	3028.76	283.96
8	1926.37	64.21	23	2578.97	118.67
9	2202.16	134.00	24	2166.65	0.36
10	2394.92	117.68	25	1696.79	174.23
11	2526.11	36.27	26	1220.91	346.36
12	2686.44	19.24	27	658.68	596.18
13	2872.89	7.69	28	205.09	728.88
14	3096.47	38.32	29	282.87	886.89
15	3310.18	71.79	30	322.82	57.60

6. Conclusion

In Section 3, we estimated the number of Covid-19 cases for the chosen period using MsDTM. In this method, the parameters β and γ were calculated over a period of 30 days. We note that the estimated values so obtained matched with the actual data in the beginning and towards the end of this period. However, in between the numbers differed from the actual number of cases. In Section 5, the number of Covid-19 cases for the same period was calculated using RMsDTM. We observed that the errors in the estimations using RMsDTM in comparison to the errors in estimations using MsDTM was significantly low. This is due to the fact that in RMsDTM the parameters β and γ were updated 5 times at an interval of 6 days, in coherence with the prevailing trend of the infection at that point of time. This resulted in more accurate estimation. Stability analysis of the Covid-19 pandemic in Algeria has been attempted in Section 4. The disease-free equilibrium points and the endemic equilibrium points for Covid-19 in the country have been obtained.

From the analysis, we may conclude that the disease will eventually be wiped out (post the endemic equilibrium point) as the endemic equilibrium point is asymptotically stable.

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