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# COVID-19 Pandemic Analysis by the Volterra Integral Equation Models: A Preliminary Study of Brazil, Italy, and South Africa

Yajni Warnapala
*Roger Williams University*, ywarnapala@rwu.edu

Emma Dehetre
*Roger Williams University*

Kate Gilbert
*Roger Williams University*



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# COVID-19 Pandemic Analysis by the Volterra Integral Equation Models: A Preliminary Study of Brazil, Italy, and South Africa

Yajni Warnapala, Emma Dehetre, Kate Gilbert

***Abstract* – The COVID-19 pandemic has affected many people throughout the world. The objective of this research project was to find numerical solutions through the Gaussian Quadrature Method for the Volterra Integral Equation Model. The non-homogenous Volterra Integral Equation of the second kind is used to capture a broader range of disease distributions. Volterra Integral equation models are used in the context of applied mathematics, public health, and evolutionary biology. The mathematical models of this integral equation gave valid convergence results for the COVID-19 data for 3 countries Italy, South Africa and Brazil. The modeling of these countries was done using the Volterra Integral Equation, using the Gaussian Quadrature nodes. Inspired by the COVID-19 pandemic, the IRCD model included the number of initially infected individuals, the rate of infection, contact rate, death rate, fraction of recovered individuals, and the mean time an individual remains infected.**

**This research investigated the feasibility of obtaining accurate convergence results for two models of the Volterra Integral Equation for the geographic locations of Italy, South Africa and Brazil. The IRCD model accounted for the infected rate, number of recovered, contact rate, and the death rate. The first 365 days of the pandemic were analyzed for the IRCD model. The ISR model accounted for the number of initially infected individuals, susceptible individuals, removed individuals, number of contacts per person, the recovery rate, and the total population. The ISR model specifically looked at COVID-19 in Brazil and South Africa for the first 300 days of the pandemic. Both models are mathematically and epidemiologically well posed.**

***Keywords* – Volterra Integral Equation, COVID-19 Pandemic, Italy, Brazil, South Africa**

## I. Introduction

The nonhomogeneous Volterra integral equation of the second kind was used, where K (t, s) is the kernel of the integral equation, and β is the given parameter [3, 4].

$$Y(t) = f(t) + \beta \int_0^t K(t,s)y(s)ds \qquad (1)$$

In the case of the Volterra Integral Equation, the compact operator being employed is a convolution operator,

$$\text{K (s, t)} = \int_0^t K(t-s)\text{y(s)ds} \qquad (2)$$

If the domain is finite, as it is in our case, the Lebesgue integral of K is also finite and is called the Hilbert-Schmidt kernel and the integral operator is compact [1].

Our numerical method works for weakly singular Kernels. A Kernel is singular if it can be written in the form K (t, s) = G (t, s)/$|t-s|^{\alpha}$ where G (t, s) is a continuous function and α £ $\mathbb{R}^n$. This Kernel is weakly singular if $sup \int_0^{365} |G(t,s)|ds < \infty$ [18]. The analysis was conducted for all countries assuming that the regions are closed, bounded and simple connected.

General assumptions were made, which are common to all the models. "The disease is transmitted by direct or indirect contact between an infected individual and a susceptible individual. There is no latent period for the disease, i.e., the disease is transmitted instantaneously when the contact takes place. All susceptible individuals are equally susceptible, and all infected individuals are equally infectious. The population size is large enough to take care of the fluctuations in the spread of the disease, so deterministic models were considered. The population under consideration is closed and has a fixed size."(Chandra, 3) [21] The COVID 19 cases after a period of immunity follows the pattern:

$$\text{S(Susceptible)} \longrightarrow \text{I (Infected)} \longrightarrow \text{R (Recovered)}$$

Where S: Previously unexposed to COVID 19, I: Currently colonized by COVID, R: Successfully cleared from the infection. [21]

## II. IRCD Model

### A. The IRCD Model

The infected rate, number of recovered, contact rate and the death rate (IRCD) were incorporated to build an integral equation of the second kind. The kernel is weakly singular and compact [6, 10].

$$I(t) = I_0 + \frac{R\lambda(t)}{\lambda_0 \tau} \int_0^t p(t-s)b * (t-s)^3 I(s)(1-I(s))ds \quad (3)$$

Lemma 1: A weekly singular integral operator K defined in $\mathbb{R}^n$ with α < n is a compact operator in $L^2$ (0,1) to $L^2$ (0,1) [18].

### B. Analysis of the IRCD Model – Italy

The first cases of Italian residents were detected in a hospital near Milan and in a small town in the region of Veneto. It took two weeks to reach 3,916 detected cases, among which 2,612 were in Lombardy, 870 in Emilia Romagna, and 488 in Veneto [14]. After two months there were 147,577 cases and 18,849 people lost their

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Yajni Warnapala is a Professor of the Mathematics Department at Roger Williams University of Bristol, RI, USA. Email: ywarnapala@rwu.edu

Emma Dehetre is a student at Roger Williams University of Bristol, RI, USA. Email: edehetre246@g.rwu.edu

Kate Gilbert is a student at Roger Williams University of Bristol, RI, USA. Email: kgilbert721@g.rwu.edu

lives [5]. The IRCD model was developed for Italy to model the number of cases from the pandemic.

TABLE I
IRCD MODEL VARIABLES

| Symbol | Symbol Meaning | Value |
|---|---|---|
| I(t) | Fraction of Infected | *Determined from IRCD model* |
| $t$ | Number of days since Feb 13, 2020 | *Included in the IRCD model* |
| $I_0$ | Fraction Initially Infected | $I_0 = 4.9618 * 10^{-8}$ |
| $R$ | Average Rate of Infection | $R = 4.686 * 10^{-4}$ |
| $\lambda(t)$ | Contact Rate | $\lambda(t) = 2.58t^3$ |
| $\lambda_0$ | Initial Contact Rate | $\lambda_0 = 2.58t$ |
| $b$ | Average Death Rate | $b = 4.324 * 10^{-8}$ |
| p(s) | Fraction of Recovered | $p(s) = 0.0013 - (1.59 * 10^{-4})s + (5.17 * 10^{-6})s^2 - (4.89 * 10^{-8})s^3 + (1.78 * 10^{-10})s^4 - (2.15 * 10^{-13})s^5$ |
| $\tau$ | Mean Time an Individual Remains Infected | $\tau = \int_0^t p(s)b * (s)^3 ds$ |
| $I(s)$ | Fraction of Infected from 0 to 365 Days | $I(s) = 0.0013 - (1.63 * 10^{-4})s + (5.44 * 10^{-6})s^2 - (5.13 * 10^{-8})s^3 + (1.867 * 10^{-10})s^4 - (2.231 * 10^{-13})s^5$ |

The median age in Italy is 47.3 years old [15], the median income is 16,844 euros [15], average household size is 2.58 people [13], and every citizen of Italy has health coverage under Italy's National Health Service [16].

Rate of change of infection in Italy: [7]

$$\frac{dI(t)}{dt} = \frac{Rt}{\tau}\left(2 - \frac{bt^4P(t)}{\tau}\right)\int_0^t p(t-s)b * (t-s)^3 I(s)\big(1 - I(s)\big)ds \quad (4)$$

Here I(t) denote the fraction of the population that is infected at time t, where t is the number of days since Feb 13, 2020, $I_0$ is the fraction of the population that was initially infected at time zero, R denotes the average rate of infection, b is the average rate of deaths, p(s) is the fraction that have recovered, and $\tau$ is the mean time an individual remains infected. The two variables $\lambda(t)$ and $\lambda_o$, which are the contact rate at any time t and the initial contact rate, both depend on the average household size in Italy which is 2.58 [13].

For Italy, the variables were computed from three models: total cases, total deaths, and number recovered. A quintic fit was used for the three models, given by the following equation:

$$F(t) = a + bt + ct^2 + dt^3 + ft^4 + gt^5 \quad (5)$$

where a = Intercept and b = Slope. Each of the models had an R-Squared value of 0.99 or better and chi-squared values all less than 0.0001, meaning all the variables are statistically significant.

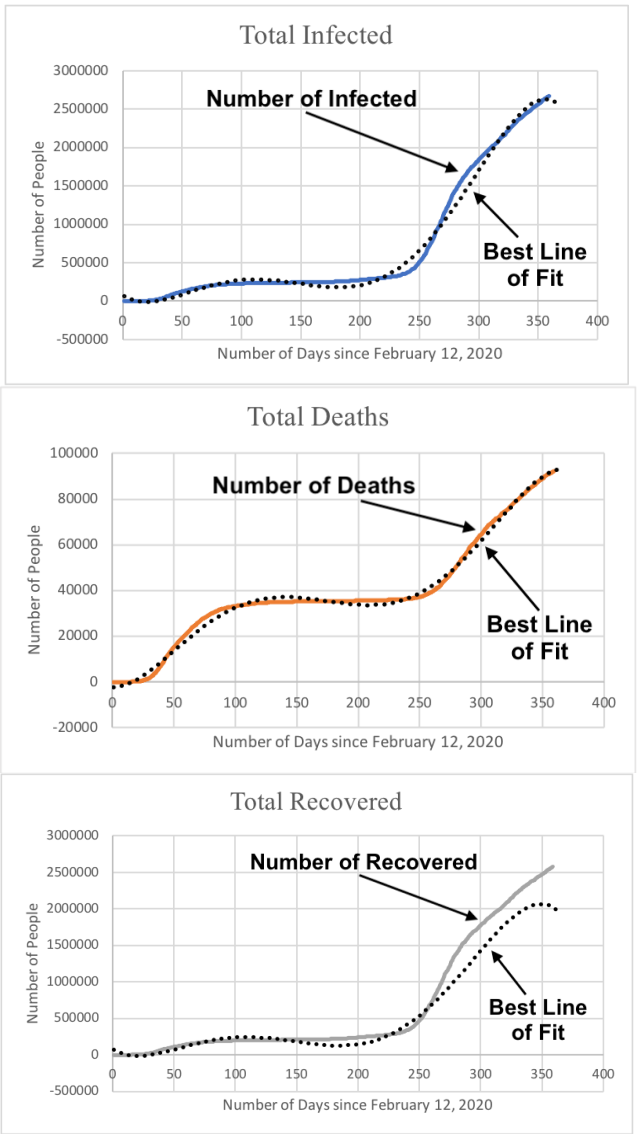


Fig. 1: The total number of infected people (top), number of deaths (middle), and number of people that have recovered (bottom) with the respective quantic best line of fit (dotted black line) over 365 days since February 13, 2020. The inflection point was at 285 days [19].

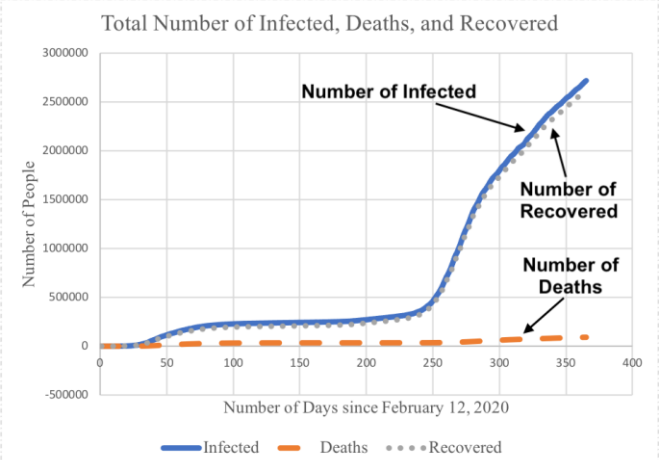


Fig. 2: The total number of people infected (solid), number of deaths (dashed), and number of people that have recovered (dotted) over 365 days since February 13, 2020 [17].

## III. ISR Model

### A. The ISR Model

The first case of COVID-19 in South Africa arose when a group of people returned from Milan, Italy to Durban South Africa on March 1, 2020 [2]. The COVID-19 virus was first detected in Brazil on February 26, 2020 in the city of Sao Paulo after a man returned there from Turin, Italy [20].

Similar to the IRCD model, the Kernel of the ISR Model is weakly singular. However, a weakly singular integral is Hölder continuous, which is satisfactory for the continuity necessary in the Galerkin Method. The ISR Model for both countries were developed as two distinct models for each of the two waves of the pandemic. The model includes the unknown function $\lambda(t)$, that is hypothesized to be a variable of combining age, preexisting health conditions, income, access to healthcare, etcetera. Studies have shown that there are behavioral responses that differ among groups in these socioeconomic areas, changing the risk of infection and one's ability to recover [8].

### B. Analysis of the ISR Model – Brazil and South Africa

The ISR Model (infected, Susceptible and Recovered Model) developed for Brazil and South Africa was given by:

$$R(t) = (R_0 + I_0 - I_0 e^{-\gamma t}) + \frac{\tan^{-1}\beta}{N*\lambda(t)} \int_0^t I(x)S(x)R(x)(1 - e^{-\gamma(t-x)})\,dx \quad (6)$$

$I_0 e^{-\gamma t}$ is the fraction of the population that was initially infectious and is still alive and infectious at time t. $\lambda(t)$ is an unknown function dependent on number of days since infection and is inversely proportional to the recovery rate. For example, it is a variable that might be a combination of age, preexisting health conditions, income, access to healthcare, type of housing, etcetera.

For Brazil for 0-200 days the unknown function is given below, similar functions were found also for above 200 days for both countries.

$$\lambda(t) = 0.241 - 0.002t + 1.67 * 10^{-5}t^2 \quad (7)$$

For Brazil 201-300 days, $R_0$ was squared in the beginning of the R(t) model:

$$R(t) = (R_0^2 + I_0 - I_0 e^{-\gamma t}) + \frac{tan^{-1}\beta}{N*\lambda(t)} \int_0^t I_1(x)S(x)R(x)(1 - e^{-\gamma(t-x)})dx \quad (8)$$

For South Africa for 0-200 days the unknown function was given by:

$$\lambda(t) = 9.64 - 0.37t + 0.0035 - 13.91 * 10^{-5}t^3 + 1.33 * 10^{-7}t^4 - 1.73 * 10^{-10}t^5 \quad (9)$$

For South Africa for 201-300 days, $R_0$ was raised to the fourth power in the beginning of the R(t) model:

$$R(t) = (R_0^4 + I_0 - I_0 e^{-\gamma t}) + \frac{tan^{-1}\beta}{N*\lambda(t)} \int_0^t I_1(x)S(x)R(x)(1 - e^{-\gamma(t-x)})dx \quad (10)$$

TABLE II
VARIABLES FOR BRAZIL

| Variable | | 0-200 days | 201-300 days |
|---|---|---|---|
| $R_0$ | Fraction Initially removed | 0.63599984 | 0.61361521 |
| $I_0$ | Fraction Initially infected | $1.622911695 \times 10^{-7}$ | 0.02238479 |
| β | Contact rate | 2.5 | 2.5 |
| γ | Recovery rate | 0.868 | 0.8111 |
| I(x) | Infection model | $I(x) = \lvert -123490.2 \rvert + \frac{(5339709.9 + 123490.2)}{1 + e^{(-0.0331(x-142.98))}}$ | $I_1(x)$ |
| S(x) | Susceptible Individuals | 0.364 | 0.364 |
| R(x) | Average Recovery Rate | 0.8799 | 0.5705 |

Where $I_0>0$, $R_0>0$, the total population N=209500000, and $I_1(x)=3559964.5+\frac{11781579-3559964.5}{1+e^{-0.0388931(x-347.34397)^{0.3331939}}}$.

TABLE III
VARIABLES FOR SOUTH AFRICA

| Variable | | 0-200 days | 201-300 days |
|---|---|---|---|
| $R_0$ | Fraction Initially removed | 0.76999978 | 0.758433 |
| $I_0$ | Fraction Initially infected | $2.24991346 \times 10^{-7}$ | 0.011567 |
| β | Contact rate | 2.5 | 2.5 |
| γ | Recovery rate | 0.902 | 0.7973 |
| I(x) | Infection model | $I(x) = 2221.5572 + \frac{(657092.72 - 2221.5572)}{1 + e^{(-0.075(x-131.21))^{0.0872}}}$ | $I_2(x)$ |
| S(x) | Susceptible Individuals | 0.23 | 0.23 |
| R(x) | Average Recovery Rate | 0.8871 | 0.5367 |

Where $I_0>0$, $R_0>0$, the total population N=57780000, and $I_2(x)=683750.09+\frac{1494912.3-3683750.09}{1+e^{-0.1410159(x-314.09441)^{0.2927988}}}$.

$$R'(t) = \gamma I_0 e^{-\gamma t} - \frac{\tan^{-1}\beta\lambda(t)'}{N*\lambda(t)^2} \int_0^t R(x)I(x)S(x)(1 - e^{-\gamma(t-x)}) \quad (11)$$

This is the rate of change of recovery [6]. The infection rate curve was modeled by, $c + \frac{(d-c)}{1+e^{(-a(x-b))^f}}$ where a = growth rate or steepness of the curve, b = inflection point, c = minimum asymptote, d = maximum asymptote, f = power or asymmetry factor (if included). In the above ISR model, $R_0$ is the number of removed individuals, $I_0$ is the number of initially infected individuals, I(x) is the number of infections by day, $\gamma$ is the initial recovery rate, $S_0$ is the number of susceptible individuals at the beginning of the pandemic, and t is the time in days since the start of the pandemic. The assumption is that $R_0 = N - I_0 - S_0$ where N is the total population.

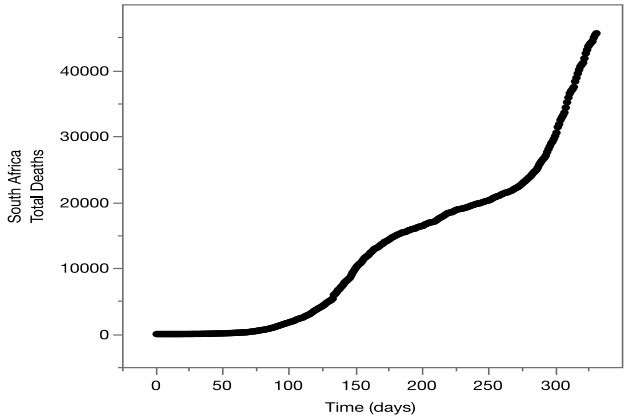


Fig. 3: Total deaths by day (1-331) in South Africa. Day 1 is considered to be the day COVID-19 was declared a pandemic, March 11, 2020.

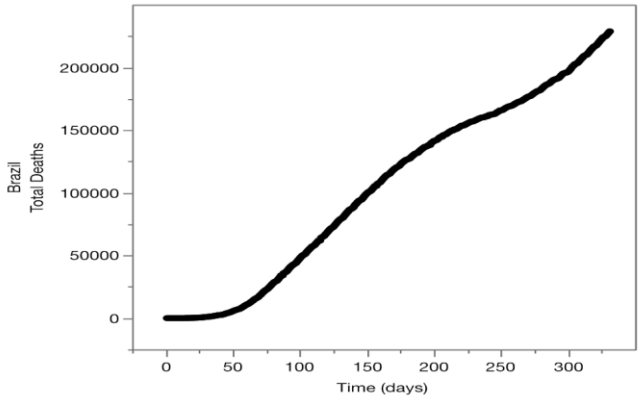


Fig. 4: Total deaths by day (1-331) in Brazil. Day 1 is considered to be the day COVID-19 was declared a pandemic, March 11, 2020.

## IV. Numerical Results

By standard Theorems [11] there is a unique solution of (3) and (6) and initial conditions which exists on a maximal interval and depends on both the parameters given and the initial data. The solutions will remain bounded, and I and R are nonnegative and positively invariant with respect to the system I, S and R where S +I +R =1. We approximated the integrals with 7 Gaussian Quadrature nodes, the results are given below. Heterogeneous mixing is the preferred method for mixing with a particular activity and age structured population significant in the COVID-19 spread. The incubation period was also significant and was assumed that the latent period of disease is very small being only 5 days and that there is no incubation time for the disease to show. In the future we might need to consider time delay models. Variable infectivity might also play a role as COVID-19 infected individuals are highly infective in the initial stages of getting the infection. [21]

### A. The Numerical Results of the IRCD Model

The Volterra Integral Equation is difficult to solve analytically. Therefore, a numerical approximation is necessary. The Adomian Decomposition was used to prove convergence of the equation. The Gaussian Quadrature Method was used based on an inner product of the Legendre Polynomials. The method was computed in the spherical coordinate system. The variable of integration is transformed to create a new integral equation on the unit sphere, which leads to the use of Spherical Harmonics based on Legendre Polynomials. This set of polynomials have the property in which any two of its polynomials are orthogonal.

TABLE IV
IRCD Model (Gaussian Quadrature nodes N=7)

| Number of Days Since Feb. 13, 2020 | Number of Infected Individuals (%) | IRCD Model Prediction (%) | Absolute Error |
|---|---|---|---|
| 50 | 0.0019 | 0.0008 | 0.0011 |
| 100 | 0.0038 | 0.0014 | 0.0023 |
| 150 | 0.0040 | 0.0073 | 0.0032 |
| 200 | 0.0044 | 0.0289 | 0.0244 |
| 250 | 0.0074 | 0.0342 | 0.0264 |
| 300 | 0.0295 | 0.0348 | 0.0050 |

The IRCD model predicts the fraction of infected up to an accuracy of $10^{-2}$. The best convergence results were found for 50 days.

### B. The Numerical Results of the ISR Model

For the ISR model 7 Gaussian nodes were used. We approximated the integrals by a sum by using the Gaussian Quadrature Method, as the integrals cannot be solved analytically. In order to use the method, we first converted the original integral to an integral bounded from -1 to 1. Since the integrals in our models do not have a closed form, we used the Gaussian Quadrature method to approximate the integrals. The method uses a sum with Galerkin coefficients to approximate the given integrals and minimize the expected error, and $p(x_i)$ are the Legendre polynomials evaluated at its nodes, with $c_i$ the corresponding weights.

$$\int_a^b K(x)dx = \int_{-1}^{1} R(x)\,dx = \sum_{i=1}^{n} c_i p(x_i) \qquad (12)$$

TABLE V
ISR Model – Brazil (Gaussian Quadrature nodes N=7)

| Number of Days since beginning of the pandemic | Number of Infected individuals (%) | ISR Model Prediction (%) | Absolute Error |
|---|---|---|---|
| 50 | 0.8944 | 0.8884 | 0.006 |
| 100 | 0.8990 | 0.8933 | 0.0057 |
| 150 | 0.8888 | 0.8877 | 0.0011 |
| 200 | 0.8111 | 0.8101 | 0.0009 |
| 250 | 0.5533 | 0.5538 | 0.0005 |
| 300 | 0.4057 | 0.4057 | 0.00001 |

The ISR model predicts the recovery rate to the accuracy of $10^{-3}$ for 0-200 days and $10^{-4}$ for 201-300 days. The best convergence results were found for 300 days.

TABLE VI
ISR Model – South Africa (Gaussian Quadrature nodes N=7)

| Number of Days since beginning of the pandemic | Number of Infected individuals (%) | ISR Model Prediction (%) | Absolute Error |
|---|---|---|---|
| 50 | 0.7807 | 0.7803 | 0.0004 |
| 100 | 0.9250 | 0.9261 | 0.0011 |
| 150 | 0.9015 | 0.9015 | 0.00002 |
| 200 | 0.7973 | 0.7975 | 0.002 |
| 250 | 0.5066 | 0.5042 | 0.024 |
| 300 | 0.4038 | 0.4002 | 0.036 |

In South Africa, IR Model predicts the recovery rate up to accuracy of $10^{-3}$ for 0-200 days and $10^{-2}$ for 201-300 days. The best convergence results were found for 150 days.

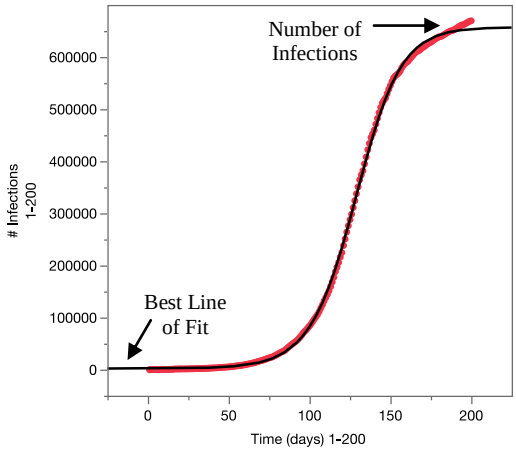


Fig. 5: Infections in Brazil from days 0 to 200 (red). The curve was fit to a log4p model for in JMP (black).

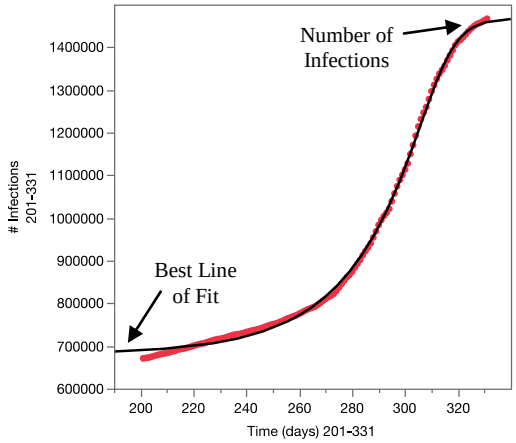


Fig. 6: Infections in Brazil from days 200-331(red). The curve was fit to a log5p model for 201-350 days in JMP (black).

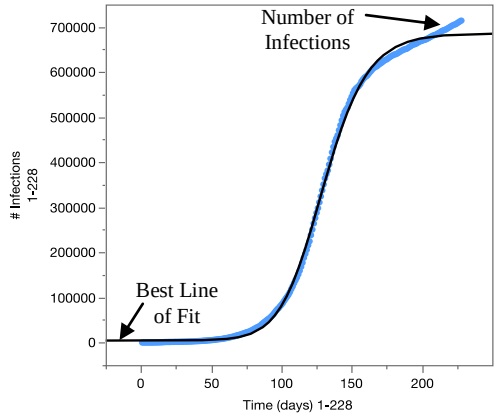


Fig. 7: Infections in South Africa from days 1-228 (blue). The curve was fit to a log5p model in JMP (black).

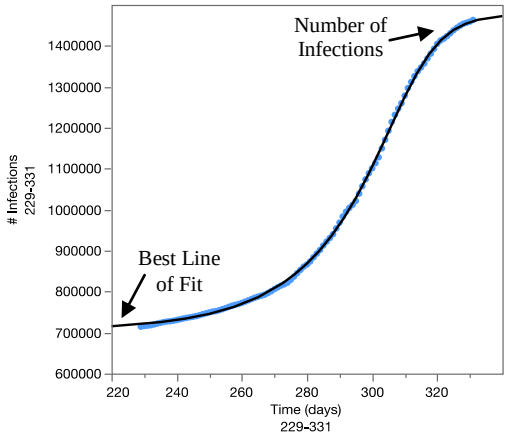


Fig. 8: Infections in South Africa from days 229-331 (blue). The curve was fit to a log5p model in JMP (black).

"The above models are very general in nature. It may be noted that these models follow a Black Box approach and do not consider the mechanism of transmission of the disease. In fact, the structure of a disease plays an important role in the modeling. It may be noted that a disease can be transmitted directly or indirectly. The direct mode of transmission could be by viral agents of COVID-19. The indirect mode of transmission could be due to vectors or carriers. Thus, modeling of the COVID-19 pandemic requires further considerations." (Chandra, 18) [21]

## V. Conclusions

The IRCD Model approximated the integral using the Gaussian Quadrature method with 7 nodes and had an accuracy of up to $10^{-3}$ for 50 to 300 days after February 13, 2020. This model has the potential to accurately model and predict the future of COVID-19 cases in Italy and countries with similar COVID-19 pandemic patterns. The function modeling the death rate and contact rates were modified from a linear function to a cubic function after increasing the Gaussian Quadrature nodes for a more realistic picture of the model. The assumption was made that the contact rate between people during this pandemic began as the average family size and has increased as the virus has slowed down.

The accuracy of the ISR model also depended on the number of Gaussian Quadrature nodes used to approximate the integral. With 10 Gaussian Quadrature nodes, there was accuracy of up to $10^{-4}$. In Brazil, with the inflection points at 142 days and 347 days, the number of infections per day started to decrease. Fitting the curve of infections with Log 5p gave high significance (p value <0.0001) values for each parameter in the ISR model as well as the overall model. In South Africa, the inflection point was at 131 days and 314 days. Both models gave accurate convergence results with only few nodes.

Future work for these models will be extended to other countries in Europe, Latin America, and Africa. FORTRAN 77 programming will be used to approximate the integrals with a higher number of Gaussian quadrature nodes. Further spatial non-uniformity needs to be considered. Thus, the spatial spread of covid becomes important in such cases. Also, Vertical Transmission has occurred in some cases where the offspring of infected members were born infective. So, the birth in the infective class needs to be considered as well. Models with Compartments might also need to be considered- as in many cases the population can be placed in different compartments, where inter-compartmental interaction takes place [9, 12]. Stochastic Models were not considered in this research. So far, we have considered only deterministic models, and the random effects have not been considered. This is fine if the population size is large, however, for smaller population sizes the stochastic models will be required. Further we plan to test the IRCD model for South Africa and Brazil and the ISR model will be tested for Italy with minor adjustments to the death rate functions. [21]

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