Modeling COVID-19 Pandemic by the λISR Volterra-Fredholm Integral Equation: A Case Study of South Africa

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ABSTRACT

Inspired by the COVID-19 pandemic, this paper investigates the feasibility of obtaining good convergence results for a nonhomogeneous Volterra-Fredholm integral equation model of the second kind. Volterra-Fredholm integral equations are often used to model infection and recovery of diseases in a population and can be used to model a pandemic or an endemic. This model uses a Volterra-Fredholm integral equation of the second kind to predict the number of individuals recovered from the COVID-19 pandemic in South Africa. The integral model was approximated by using the Gaussian Quadrature Method. The λISR model accounts for many variables of the pandemic including the number of initially infected individuals I_0, susceptible individuals S_0, and removed individuals R_0. It also accounts for the initial recovery rate γ, the infectivity of the virus β, removal rate μ, and the total population of South Africa N. In addition to these, we also considered blood type $S(x)$, and the rh factor $\lambda(x)$.

The model was constructed in "person-days," which is the combined variable of time (t, days) and the number of individuals (x). Specific blood types and presence of the rh factor have been shown to have varying susceptibility to infection and severity of infection (requiring intubation), therefore this was an important parameter for this model [1] [2].

Keywords: Volterra-Fredholm, Integral Equation, South Africa, COVID 19, Gaussian Quadrature Method, Person Days

1. INTRODUCTION

Volterra integral equations are often used to model disease behavior, including infection, recovery, and death. Volterra-Fredholm models are known to be used to model the spatio-temporal development of an epidemic, including various other physical and biological models relation to disease in a population [3]. This model uses a Volterra-Fredholm integral equation of the second kind to model recovery from the Omicron variant of COVID-19 in South Africa. The model is measured in person-days, which is the combined variable of both people x and time t. Thus, the model is a double integral with respect to time and people.

As new variants of the disease arise, the susceptibility of a person to get infected and recover changes. The model we designed specifically applies to the Omicron variant that originated in South Africa, where the first case of Omicron was identified on November 11, 2021. This day is used as Day 1 in the model [4]. With only 32.8% of the population fully vaccinated in South Africa, the model does not include a variable for immunity. The portion of the population that is fully vaccinated did not reach the 94% required for herd immunity [5] [6]. Additionally, absence of the rh factor was shown to be protective against infection, and blood types A and AB were shown to have higher infectivity than blood type O [1] [2]. For our analysis, blood type A+ (A with rh factor) was used in the construction of the method.

The model built was founded on the Volterra Integral Equation of the second kind, which usually arise from parabolic boundary value problems and was given by:

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

The Volterra-Fredholm integral equation used in this case has a weakly singular kernel. There are many recent advances on reliable methods of solving these types of integral equations [7] [3]. Also, we considered our model to be a mathematical model based on a 'spatio-temporal model' of an epidemic, thus the integral was a double integral. The study built a model with total infection and recovery data to predict the overall recovery rate over a given time period *T*. Recovery was defined as no longer showing symptoms of the disease, and therefore no longer contagious and able to infect others.

The λISR model

The $\lambda - ISR$ (Infection – Susceptibility – Recovery) model was given by:

$$R(T) = R_0 + I_0 - I_0 e^{-\gamma T} + \frac{\mu\beta}{N} \int_0^N \int_0^T S(x)\lambda(x)I(t)R(t)(1 - e^{-\gamma(T-t)})dtdx \qquad (2)$$

Table 1. Parameters for the λISR model.

Parameter	Variable	Value
Initially Removed	R_0	0.6246*
Initially Infected	I_0	0.0486*
Initially Susceptible	S_0	0.3268*
Infectivity rate	β	3.7[11] [12]
Initial Recovery Rate	γ	0.9093[8]
Removal Rate	μ	1.11804599
Error	ε	Error
Total Population	N	60.6[13]
# of Days Elapsed	T	116**
Infection Curve	I(t)	Eq 5
Recovery Curve	R(t)	Eq 6
Blood Type	S(x)	Eq 7
rh Factor	λ(x)	Eq 8

*Given as percentages of the total population N, I_0 was found from [8] [9] by dividing the total number of infections on Day 1 by the total population. S_0 was found by multiplying the two susceptibility factors, blood type and rh factor, $S_0 = 0.86*0.38$ [10].

**Data used was from November 11, 2021 to March 6,2022.

S(x) denotes the increased susceptibility to severe infection with blood type A, and $\lambda(x)$ denotes the increased protection against severe infection when the rh factor is not present. The model accounts for the relationship between the number of initially removed, infected, and susceptible individuals, given by the equation below [14].

$$N = R_0 + I_0 + S_0 \qquad (3)$$

This study built a model with total infection and recovery data to predict the overall recovery rate over the given time period. The infection curve I(t) and the recovery curve R(t) were functions of time (days), whereas the blood type S(x) and rh factor λ(x) were functions of people. I(t) was found by fitting the number of total infections by day to a logistic4p model. The graphs were constructed using actual values (106), the functions were created by dividing the data by 106. The general form of a log4p equation was given by the following equation.

$$\mathrm{I(t)} = |c| + \frac{d-c}{1+e^{(-a(t-b))}} \tag{4}$$

Where *a* is the growth rate, *b* is the inflection point, *c* is the lower asymptote, and *d* is the upper asymptote. The specific I(t) based on our data was given by the following equation.

$$I(t) = 2.8733378 + \frac{(3.6444572-2.8733378)}{1+e^{(-0.0852777(t-38.158955))}} \tag{5}$$

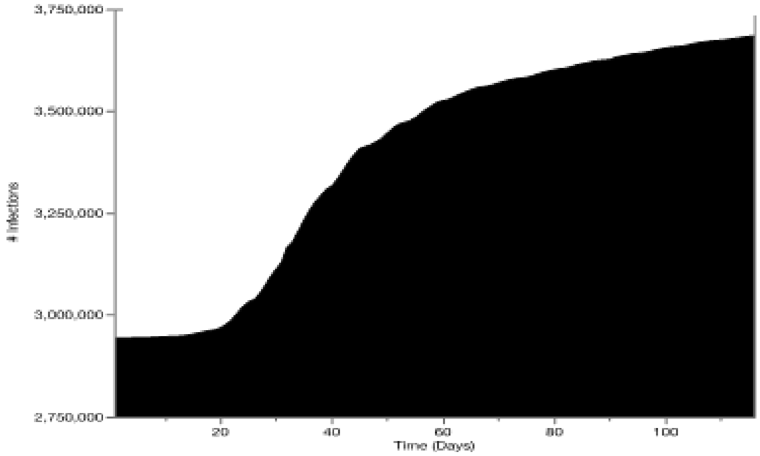


Figure 1. The number of infections I(t) by day in South Africa for the Omicron variant, 1-116 days. South Africa's data were fitted to a log4p model (r^2 equal to 0.99).

Recovery function R(t) was a cubic model given by the following equation.

$$R(t) = 1.418 + 0.0026t - 3.73x10^{-5}t^2 + 2.82x10^{-7}t^3 \tag{6}$$

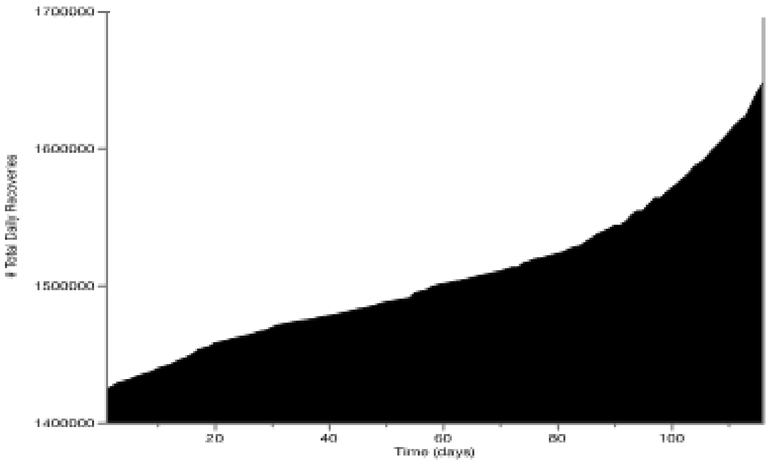


Figure 2. The number of recoveries R(t) by day in South Africa for the Omicron variant, 1-116 days. South Africa's data were fitted to a cubic model (r^2 equal to 0.99). Recovery data is from April 11, 2021 to August 4, 2021- an equivalent number of days for the Omicron variant but not the actual data, as South Africa has yet to report the number of daily recoveries.

S(x) and λ(x) were created by using reported data for the percentages of blood type A and presence of rh factor in the population of South Africa. South Africa was reported to have 86% presence of rh factor and 38% of blood type A [10]. S(x) gave the amount of the population susceptible to infection by blood type A.

$$S(x) = 0.38x + \varepsilon_1 \tag{7}$$

$\lambda(x)$ gave the amount of the population susceptible to infection by the presence of the rh factor.

$$\lambda(x) = 0.86x + \varepsilon_2 \tag{8}$$

The partial derivatives of the model represented the rate of change of recovery in terms of time and in terms of people.

$$\frac{\partial R}{\partial t} = I_0\, \gamma e^{-\gamma t} \tag{9}$$

The rate of recovery in terms of people was directly proportional to the initial number of infections I_0 and the initial recovery rate γ. The rate of recovery in terms of people was given by,

$$\frac{\partial R}{\partial x} = \frac{\mu\beta}{N} S(N)\lambda(N) \int_0^x I(t)R(t)e^{-\gamma(T-t)}dt \tag{10}$$

The rate of recovery in terms of people was directly proportional to removal rate μ, the infectivity β, blood type $S(N)$ and rh factor $\lambda(N)$ and is inversely proportional to the total population N.

The predictability of epidemiological variables is difficult and therefore the choice on which type of integral equation system that was to be used was a critical component of this analysis. Lowering the complexity and the number of operations was important but the Volterra-Fredholm integral equation method using person-days was preferred.

Gaussian Quadrature Method

For preliminary work, Gaussian Quadrature was used to approximate the integral. The model is a double integral: the integral with respect to time (inner integral) and the integral with respect to people (outer integral). Due to the complexity of the model, the inner integral was not solved analytically, it was approximated numerically. The outer integral was not as complex and was solved analytically, therefore it did not require the use of an approximation method. Gaussian Quadrature Method is well known and widely used for integral approximation and was applied to the inner integral.

To use the Gaussian Quadrature method, the original integral was transformed into an integral from -1 to 1. For the Gaussian Quadrature method, the c_i values were coefficients chosen to minimize the expected error, and P(x) was the Legendre polynomial evaluated at nodes, x_i. The fact that $\int_{-1}^{1} P(x)P_n(x)dx = 0$ whenever P(x) is a polynomial of degree less than *n* was used in converting the integral to the interval [-1,1].

$$\int_a^b f(x)\,dx = \int_{-1}^{1} P(x)\,dx = \sum_{i=1}^{n} c_i P(x_i) \tag{11}$$

Where the coefficients were given by,

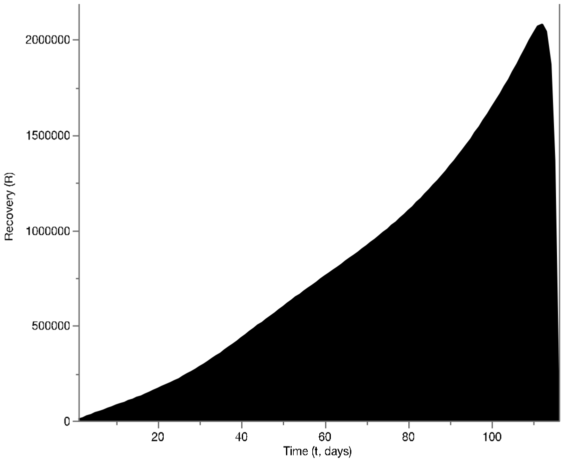
$$c_i = \int_{-1}^{1} \prod_{k=1,k\neq i}^{n} \frac{x-x_i}{x_i-x_k}\,dx \tag{12}$$

Seven nodes were used using values for the weights and abscissae from [15].

2. NUMERICAL ANALYSIS

RESULTS

The reported value for recovery rate in South Africa was 0.973216983 [16]. Evaluation of the model at all given values for the variables gave a recovery rate of 0.9768461153, accuracy to 10^{-2}. The 3-dimensional representation of the model made by graphing both the inner and outer integrals. This representation shows how the model was used to approximate recovery data over a geographical area.



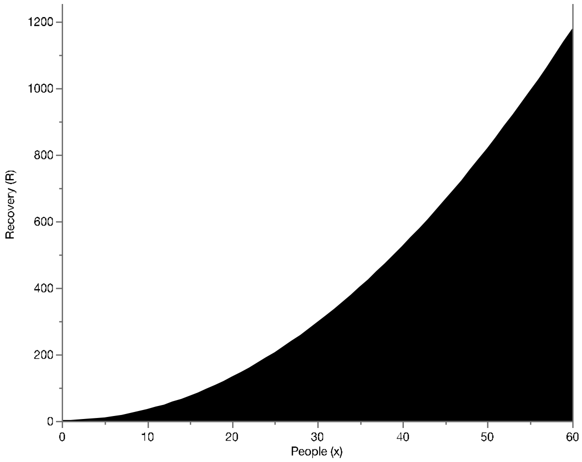


Figure 3. The inner integral, recovery R vs time t.

Figure 4. The outer integral, recovery R vs people x.

The 3D Person Day Model is given by Figure 5. This shape was superimposed onto the geographical area of South Africa to show the approximation of recovery over the given area.

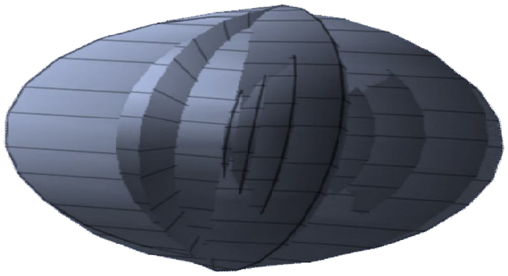


Figure 5. 3D shape depicting both the inner and outer integrals. This shape does not include the portion of the model that is outside of the double integral.

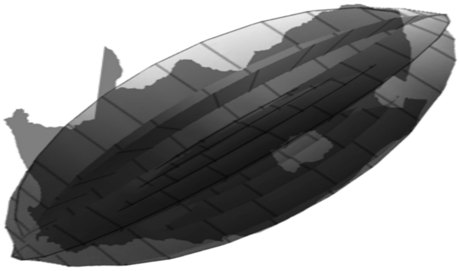


Figure 6. 3D model superimposed onto geographical area of South Africa.

Table 2. Model prediction by province of South Africa. The same values were used for all variables except for population. The results reported are in % Recovery R, which meant the percentage of total recovered individuals over the given time period for each province. All area and population values were sourced from [16].

Province	% Total Area	Population (M)	% Total Population	% Recovery, R
Eastern Cape	0.1351	6.7430	0.1111	0.1085
Free State	0.1038	2.9289	0.0483	0.0472
Gauteng	0.0145	15.4881	0.2556	0.2497
KwaZulu-Natal	0.0755	11.5316	0.1903	0.1859
Limpopo	0.1006	5.8526	0.0966	0.0943
Mpumalanga	0.0612	4.6897	0.0772	0.0754
Northern Cape	0.2982	1.2928	0.0213	0.0208
North West	0.0839	4.1088	0.0678	0.0662
Western Cape	0.1035	7.0057	0.1156	0.1129
Lesotho (ε)*	0.0243	0.9776	0.0161	0.0158
			Total Prediction (Recovery, R)	0.9768
			Reported Value (Recovery, R)	0.9732[17]
			Absolute Error	0.0036

*Lesotho is included as the error term ε to account for the discrepancies in using the best approximation available for population in each province. The population used is not the exact population of Lesotho but rather the difference of N and the sum of the province populations. The area value is the actual area value [18].

ANALYSIS

The model is accurate only to 10^{-2}, there are various drawbacks and assumptions that when addressed, could potentially increase the accuracy of the model. The recovery data used was for an equivalent number of days for the Omicron variant not for the actual data, as South Africa has yet to report recovery data for the Omicron variant. The actual recovery data would increase the accuracy in predicting the recovery rate over the given time period. The model only accounted for blood type A+, as this was the blood type reported to be most susceptible to severe infection. The model can be applied to other blood types when values for $S(x)$ and $\lambda(x)$ are used as the percentages for individuals with other blood types. The epsilons (errors) for $S(x)$ and $\lambda(x)$ were assumed to be zero for the execution of this model.

A previous, somewhat similar, version of this model produced good convergence results with little error when applied to the first two waves of the pandemic [19]. In this research, modifications were made to include susceptibility by blood type and a more accurate infectivity rate β. β was originally the contact rate, reported as the average number of people that one infected individual would infect. For the λISR Volterra-Fredholm model, β was changed to an infectivity variable, no longer reported as an average but a succinct value.

Our model did not account for other variants or factors that affect susceptibility and likelihood of severe infection. These factors include immunity from vaccination or prior infection, and pre-existing health conditions such as obesity. By further modifying β and exploring more variables within the susceptibility functions $S(x)$ and $\lambda(x)$, more accurate predictions might be possible.

Lastly, this model did not include the death rate d. The rate d was assumed to be a part of the removal rate μ, as μ is usually defined as the population moving from an infected population to the recovered or deceased populations.

CONCLUSIONS

The purpose of this original research article was to raise awareness of the many parameters that affected susceptibility to infection and recovery from COVID-19 pandemic in South Africa. By showing the mathematical relationship between these parameters, this model demonstrated the importance of the infectivity variable, and the correlation between blood type, rh factor, and susceptibility to infection. Models such as these will help us better understand the pandemic behavior, and with more knowledge on the indicators of susceptibility to these infections, one can hope to be able to minimize or prevent these pandemics. In the future, if the actual recovery data were available, one can use a higher number of Gaussian Quadrature nodes and obtain a higher degree of convergence for this type of an integral equation. Further research can be also done by adding a new variable of immunity from vaccination and prior infection, and modifying the kernel of the integral.

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AUTHORS' CONTRIBUTIONS

Yajni Warnapala designed the study, performed the theoretical analysis, developed the model, and co-wrote the manuscript. Kate Gilbert managed the data analyses of the study with MAPLE and JMP(SAS), co-wrote the paper and co-managed the literature search. Both authors read and approved the final manuscript.

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