Infectious Disease Model- COVID 19-Volterra Integral Equation

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Introduction

Inspired by the COVID-19 pandemic, this research investigates the feasibility of obtaining good convergence results for a model of the Volterra integral equation over the surface (geographic location). The Gallerkin Method was used to numerically solve the exterior boundary value problem. This model accounts for the number of initially infected individuals, suscept individuals, removed individuals, number of contacts per person, the recovery rate, and the total population. This model specifically looks at COVID-19 in South Africa for the first 200 days of the pandemic. The model accounts for the geography of the countries and uses Green's Theorem. The numerical results of this research are expected to find good convergence for this model as well as limitations of the model such as the assumption for the number of contacts.

Volterra Integral Equation (RI) Model

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

$$R(t) = (R_0 + I_0 - I_0 e^{-\gamma t}) + \int_0^t I(x)\,(1 - e^{-\gamma(t-x)})\, dx \quad (1)^*$$

$$I(x) = c + \frac{(d - c)}{1 + e^{(-a(x-b))f}} \quad (2)$$

Where R_0 is the number of removed individuals, I_0 is the number of infected individuals, S_0 is the number of suscept individuals at the beginning of the pandemic, β is the number of contacts per infected individual, I(x) is the number of infections by day, γ is the recovery rate, t is the time in days since the start of the pandemic, and N is the total population. The RI model (Equation 1*) and relationships were adapted from [1]. The proposed RI model for the first 200 days of the pandemic is shown as equation 3. The parameter values are as outlined in Table 1.

$$R(200) = (44490587 + 13 - 13e^{-0.902*200}) + (9.951549325x10^{-9}) * \left[\int_0^{200} 2161.389\, dx + \int_0^{200} \frac{(1 - e^{-0.902(200-x)})}{(1 + e^{-0.0725942(x-136.61883)})} dx\right] \quad (3)$$

Parametric Values for RI Model

Variable	Value
R_0	44490587
I_0	13
γ	0.902
N	57780000
S_0	13289400
t	200

Table 1. Values of the specific parameters of the RI model (based on data as of Oct, 1 2020.) This is the table for equation 1, the recovery-infected model.

Variable	Value
*a	0.0725942
*b	136.61883
**c	2161.389
*d	2659821.37
*f	0.9052645

Table 2. Values of the specific parameters of the I(x) equation (based on data as of Oct, 1 2020. This is the table for equation 2, the infection model.

*p value is <0.0001 ** p value is 0.001

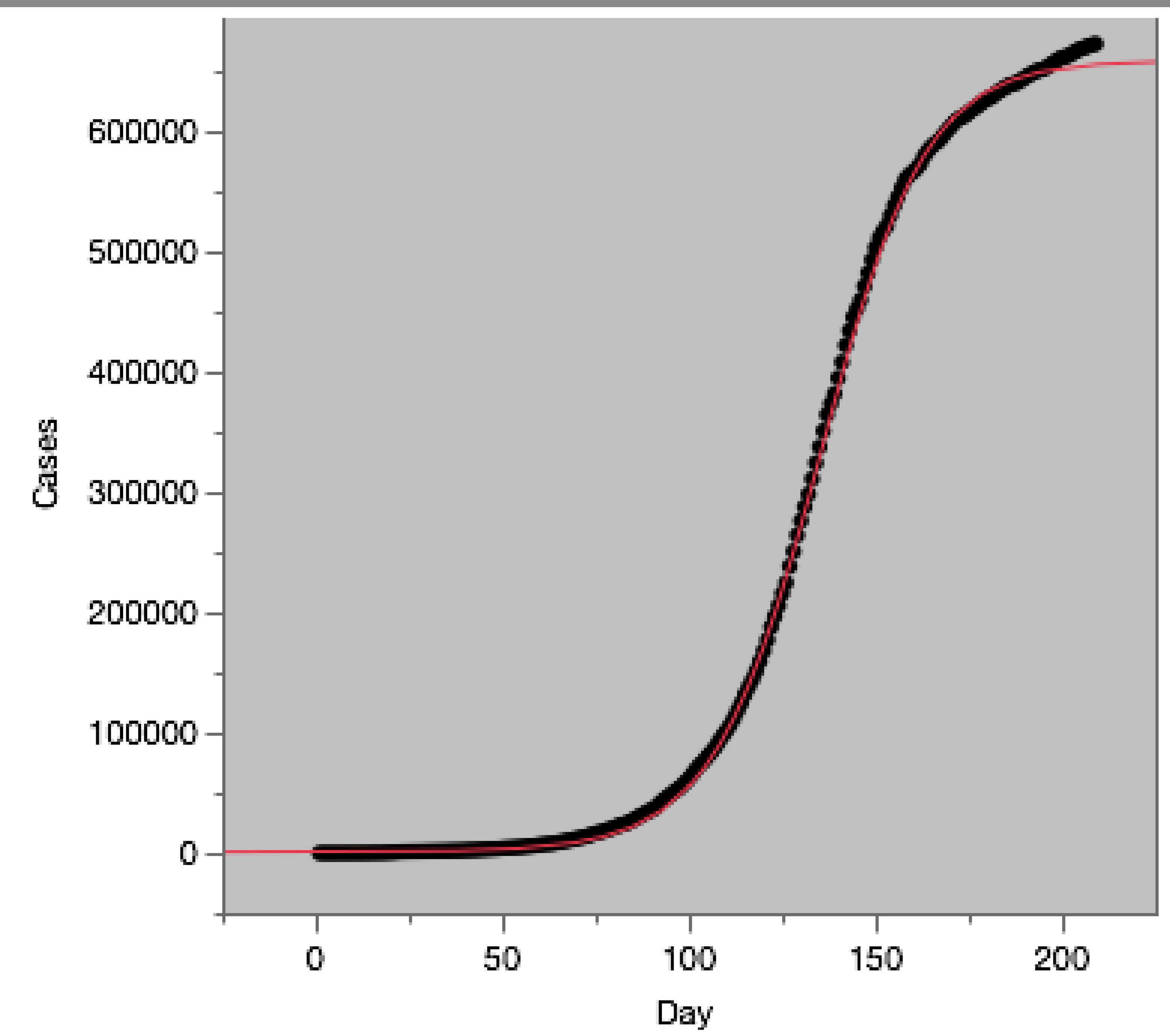

Figure 1. From equation 2, the number of infections for South Africa (March-October, t=200). Inflection point is at 137, R-square for the curve is 0.9996314.

Gaussian Quadrature- Gallerkin Method

The Gallerkin method is going to be used to numerically approximate the inner integral. For preliminary work, Gaussian quadrature (n=5) was used to approximate the integral. The values for R0, I0, S, β, N, and γ were found from [2][3]. The values for I(x) were obtained from JMP (SAS) by fitting the infection curve to the data for number of infections per day from South Africa (logistic 5p). In order to use the Gaussian Quadrature method, the original integral was transformed into an integral from -1 to 1.

$$\int_a^b f(x)\, dx = \int_{-1}^{1} P(x)\, dx = \sum_{i=1}^{n} c_i P(x_i) \quad (4)$$

$$c_i = \int_{-1}^{1} \prod_{j=1, j\neq i}^{n} \frac{x - x_i}{x_i - x_j} dx \quad (5)$$

This is the Guassian Quadrature method where the c_i values are coefficients, chosen to minimize the expected error, and P(x) is the Legendre polynomial evaluated at the nodes, x_i.

Numerical Results

With the results from the approximated integral, R(t) was found to be equal to 0.6628765684 with 5 nodes and 0.6639487881 with 4 nodes. This would indicate that about 66% of the number of infections over the course of the first 200 days had recovered during that time.

Coefficient	4 Nodes	5 nodes	Root	4 Nodes	5 Nodes
c_1	0.3478548451	0.2369268850	x_1	0.8611363116	0.9061798459
c_2	0.6521451549	0.4786286705	x_2	0.3399810436	0.5384693101
c_3	0.6521451549	0.5688888889	x_3	-0.3399810436	0
c_4	0.3478548451	0.4786286705	x_4	-0.8611363116	-0.5384693101
c_5		0.2369268850	x_5		-0.9061798459

Table 3. Specific values of c_i and x_i for the Gaussian Quadrature with 4 nodes and 5 nodes.

Conclusion

For the model to be accurate, the assumption about R_0 would be have to be changed. The accuracy of the RI model also depends on the number of Gaussian Quadrature nodes used to approximate the inner integral. With 5 Gaussian Quadrature nodes, there is only accuracy to 10^{-2}. In South Africa, with the inflection point at 137 days, the number of infections per day started to decrease. Fitting the curve of infections with Log 5p gives high significance values for each parameter of the model.

Future Work

Future work for this model will be extended to Brazil and the United States. FOTRAN 77 programming will be used to approximate the inner integral with higher Gaussian quadrature nodes. The modified model does not have β, the number of contacts per infected individual. Future work include a form of β in the RI model. The assumption for the number of removed individuals at the beginning of the pandemic (R_0) was defined as $R_0 = N - I_0 - S_0$.

References

[1] Greenhalgh, S.; Rozins, C. Generalized differential equation compartmental models of infectious disease transmission. *bioRxiv*. **2020**.

[2] South Africa: COVID-19 daily graph. *Saifaddin*. **2020**. Date accessed: October 1, 2020.

[3] South Africa COVID-19 Corona Tracker. *Weising*. **2020**. Date accessed: October 1, 2020.

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