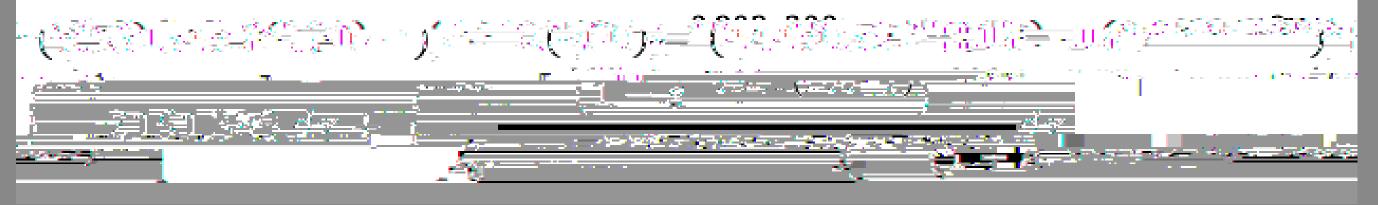




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 $\underline{P(+)} = (\underline{P} + \underline{I})$ <u>[(~) (1</u> (d-c)

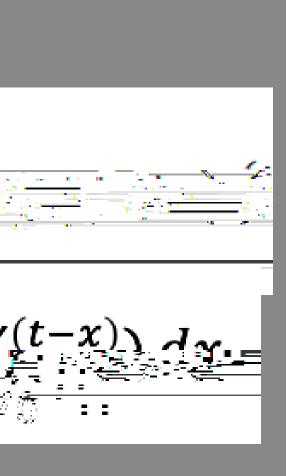
·(- ·) · Where \mathbb{R}_0 is the number of removed individuals, \mathbb{I}_0 is the number of infected individuals, S_0 is the number of suscept individuals at the beginning of the pandemic, is the number of contacts per infected individual, I(x) is the number of infections by day, is the recovery 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.

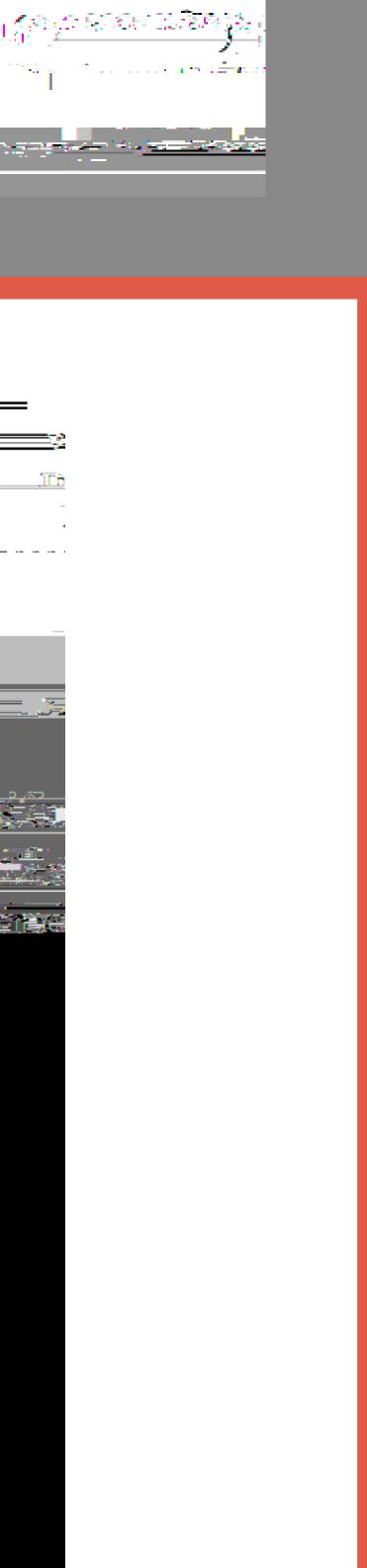


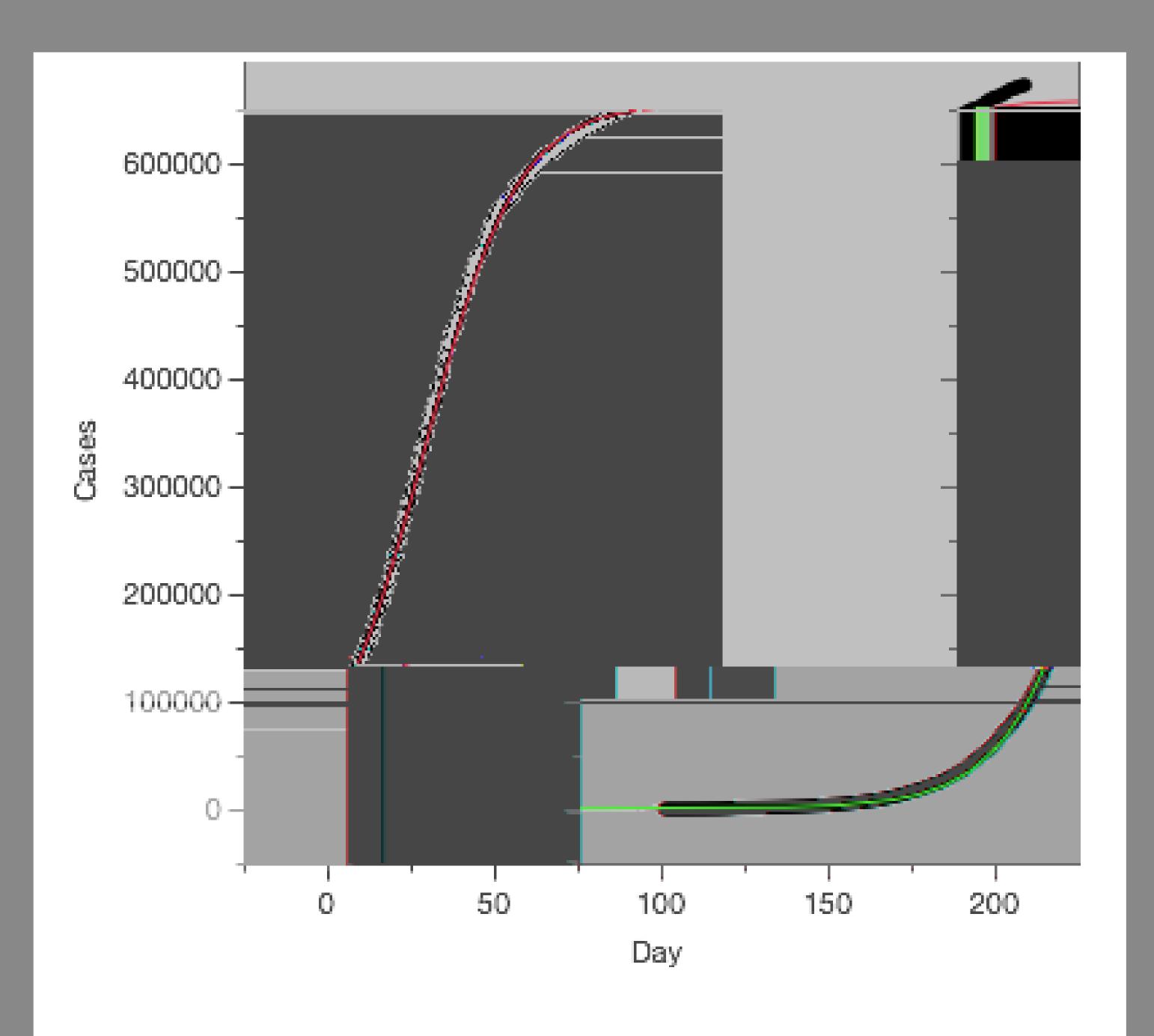
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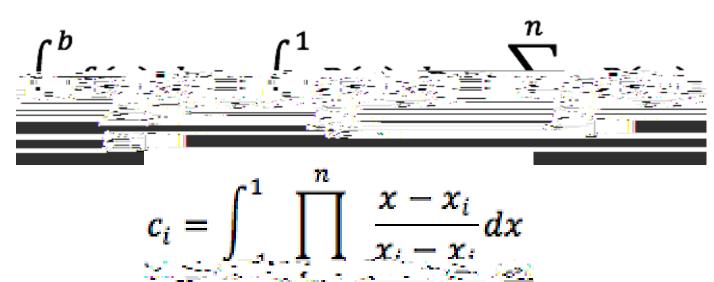
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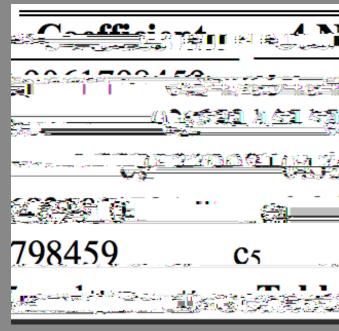


This is the Guassian Quadrature method where the Ci values are coefficients, chosen to minimize the expected error, and P(x) is the Legendre polynomial evaluated at the nodes, \mathbf{x}_{i} .

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a

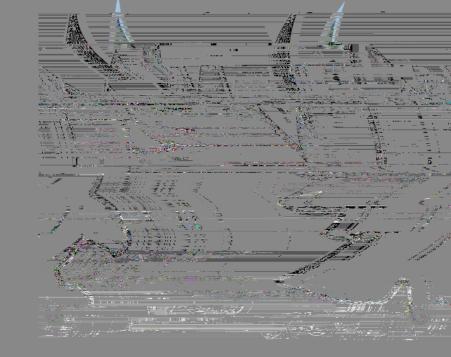
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For the model to be accurate, the assumption about ${f R}_0$ would be have to be changed. The accuracy of the RI model also depends on the number of Gaussian Quadrature nodes used to approximate the inner integral. With 5 Gaussian Quadrature nodes, 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.

 $\mathbf{R}_{\mathbf{0}}$





0.2369268850 x5 -0.9061 <u>e de se de se se se de s</u>

