

Branching stochastic processes as models of Covid-19 epidemic development

Suriname - 20201214

N. Yanev, V. Stoimenova, D. Atanasov

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Abstract

The results presented here are obtained using the methodology proposed in the paper <https://arxiv.org/abs/2004.14838> for the country Suriname. The data comes from European Centre for Disease Prevention and Control available at <https://opendata.ecdc.europa.eu/covid19/casedistribution/csv>.

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Chapter 1. Observed Infection data

Figure 1.1. Number of the daily reported laboratory-confirmed cases

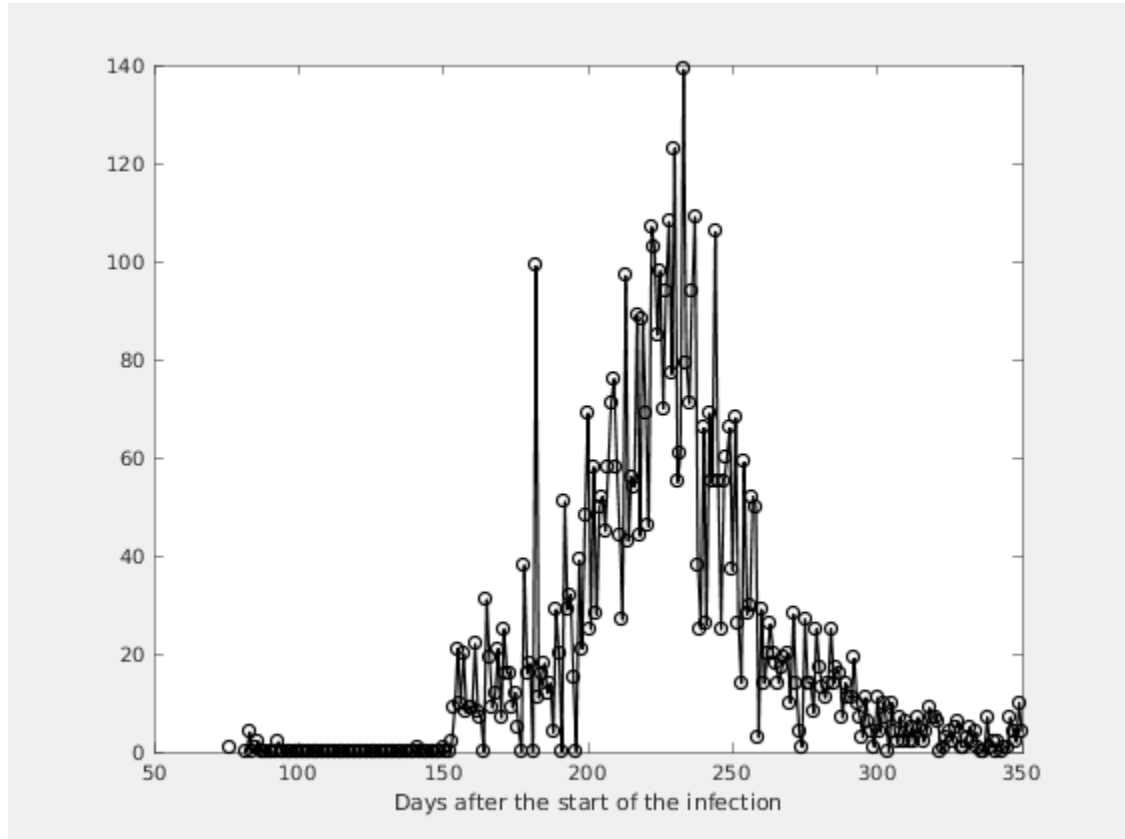
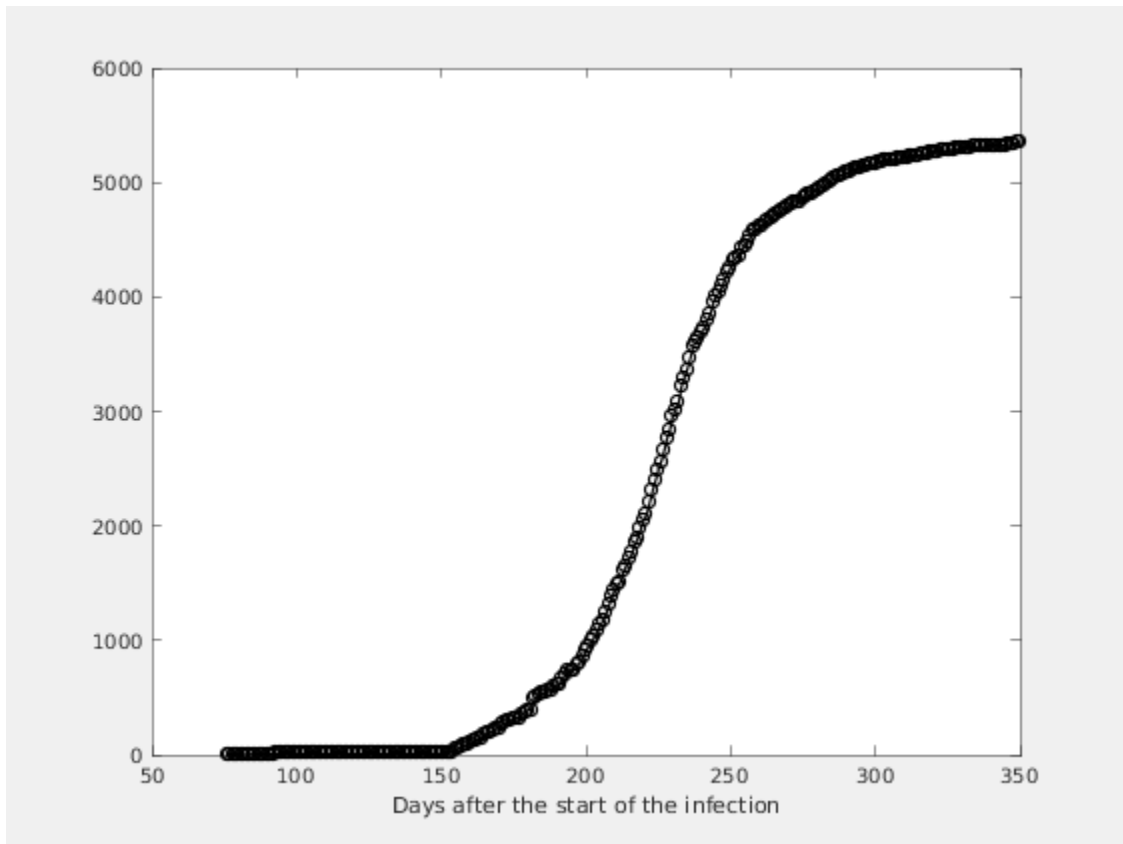


Figure 1.2. Number of the total registered cases



Chapter 2. Estimating of the main parameter and some predictions

Figure 2.1. The Lotka-Nagaev and the Harris type estimator of the growth rate

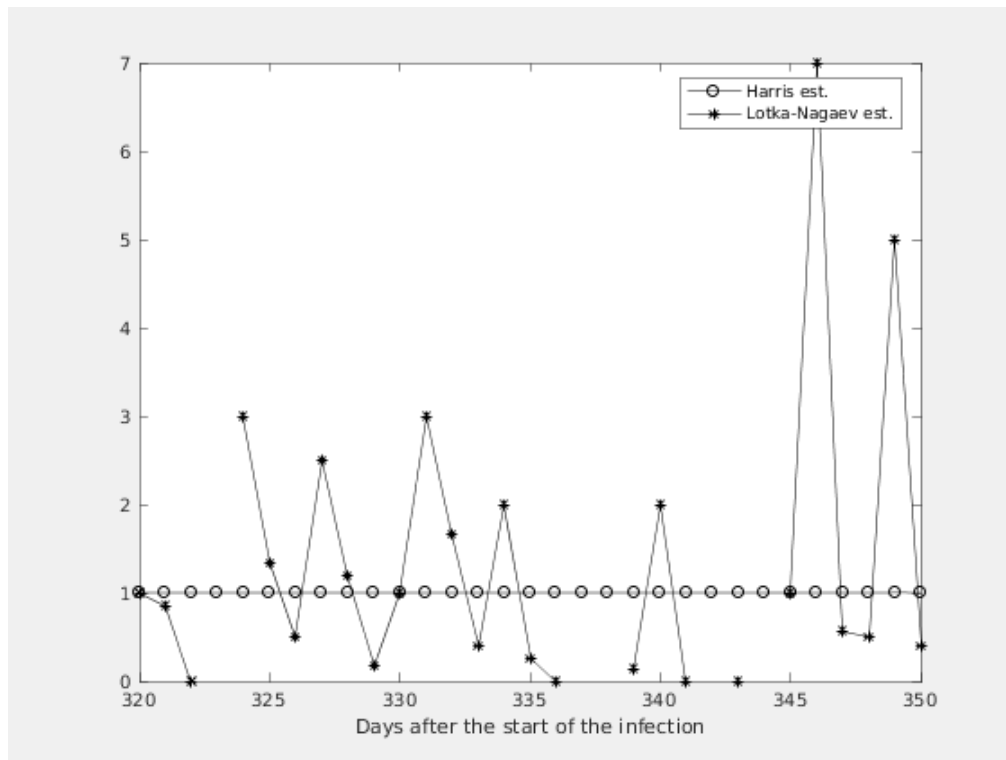


Figure 2.2. Figure

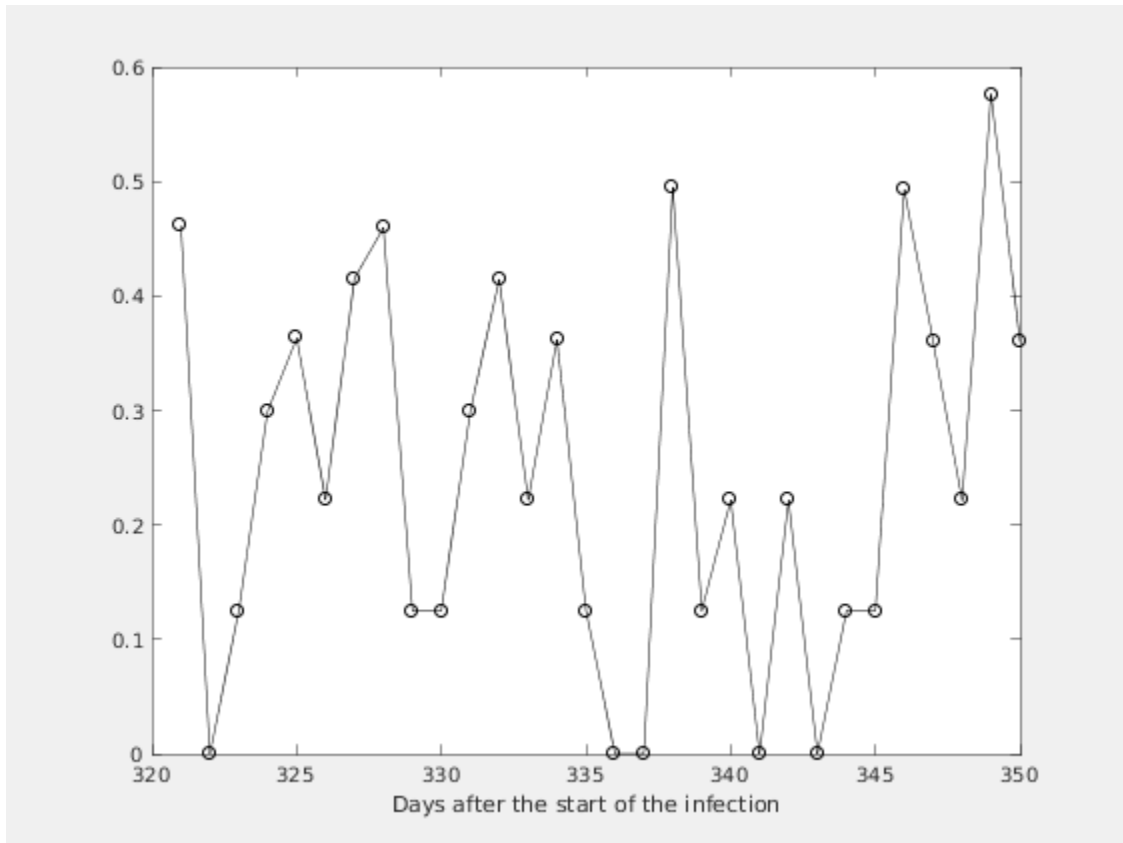


Figure 2.3. Expected number of the nonregistered infected individuals without immigration

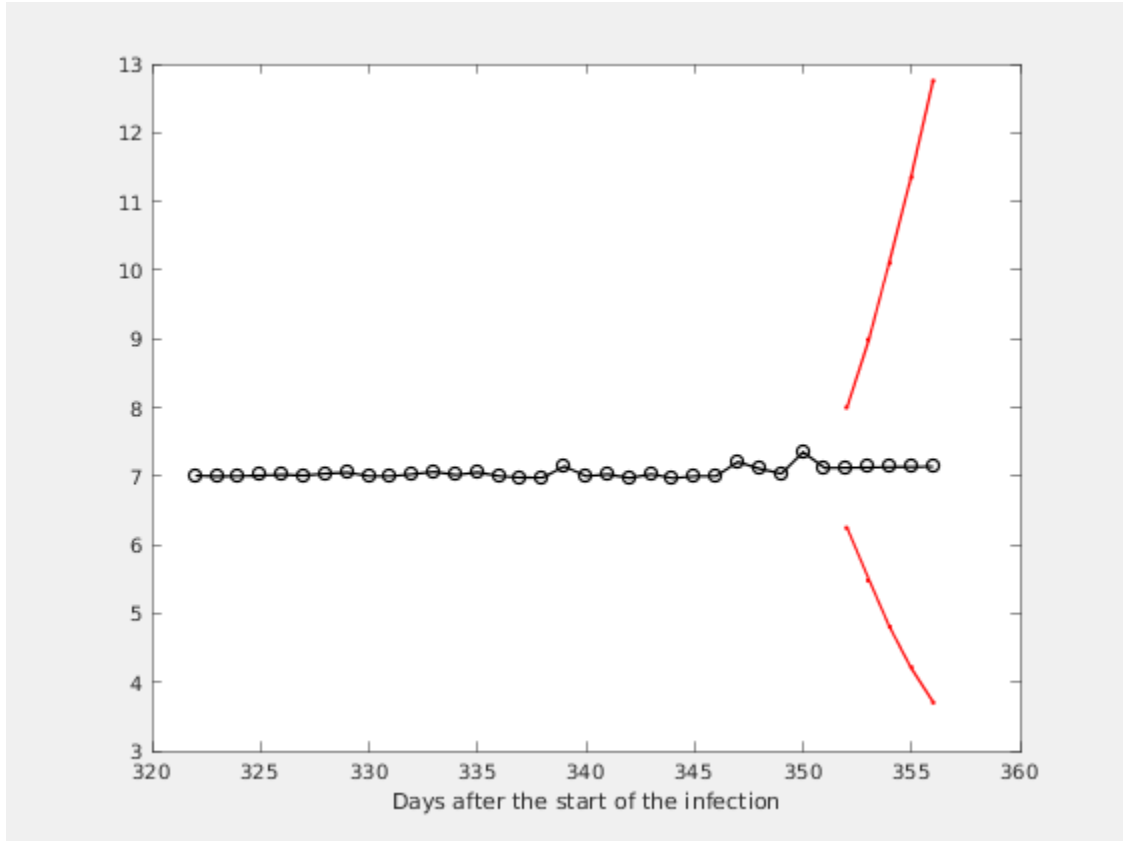
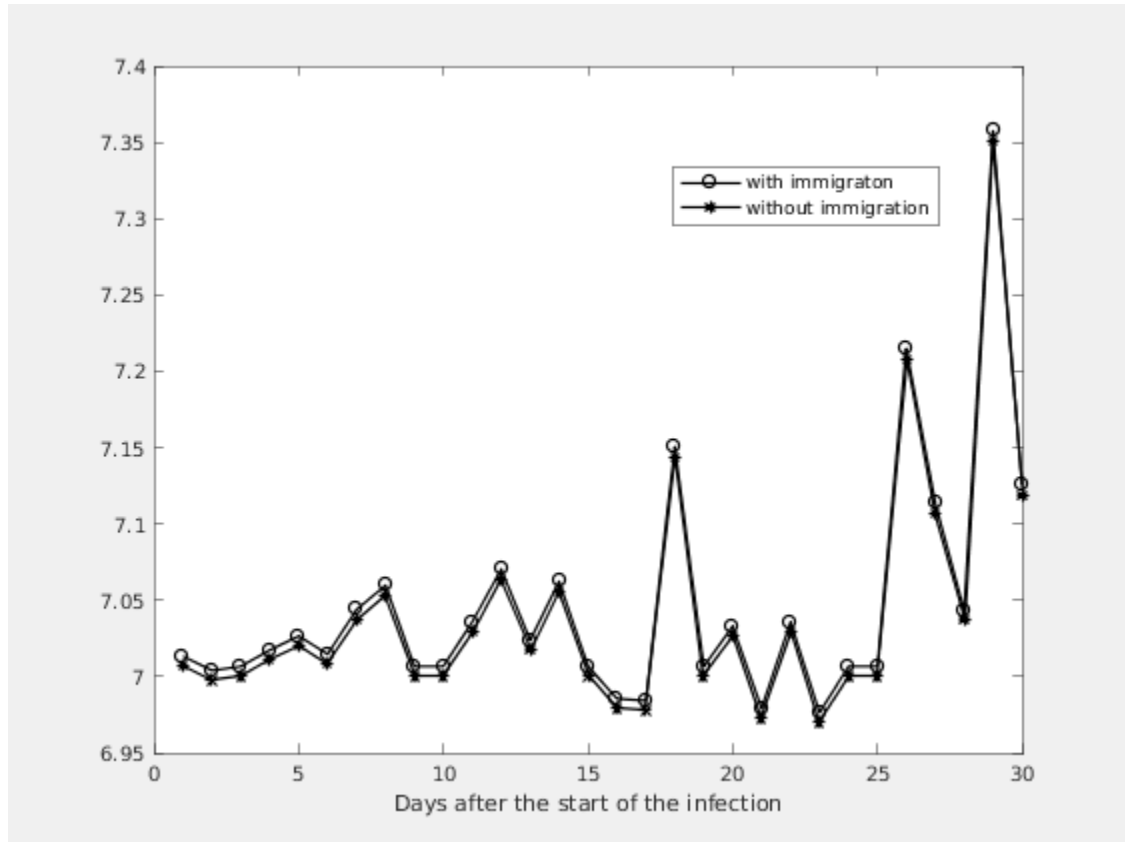


Figure 2.4. Expected number of the nonregistered infected individuals with immigration



Estimation of the model parameters.

k	m	ci	alpha	M1	A1
4	1.0011	0.8769 - 1.1254	0.1250	7	7
3	1.0006	0.8766 - 1.1245	0.1250	7	7
2	1.0002	0.8760 - 1.1243	0.4927	7	7
1	1.0017	0.8779 - 1.1254	0.3601	7	7
0	1.0006	0.8772 - 1.1240	0.2213	7	7