

Branching stochastic processes as models of Covid-19 epidemic development

Belize - 20201214

N. Yanev, V. Stoimenova, D. Atanasov

Branching stochastic processes as models of Covid-19 epidemic development : Belize - 20201214

Abstract

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

Table of Contents

1. Observed Infection data	1
2. Estimating of the main parameter and some predictions	3

List of Figures

1.1. Number of the daily reported laboratory-confirmed cases	1
1.2. Number of the total registered cases	2
2.1. The Lotka-Nagaev and the Harris type estimator of the growth rate	3
2.2. Figure	4
2.3. Expected number of the nonregistered infected individuals without immigrati- on	5
2.4. Expected number of the nonregistered infected individuals with immigration	6

Chapter 1. Observed Infection data

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

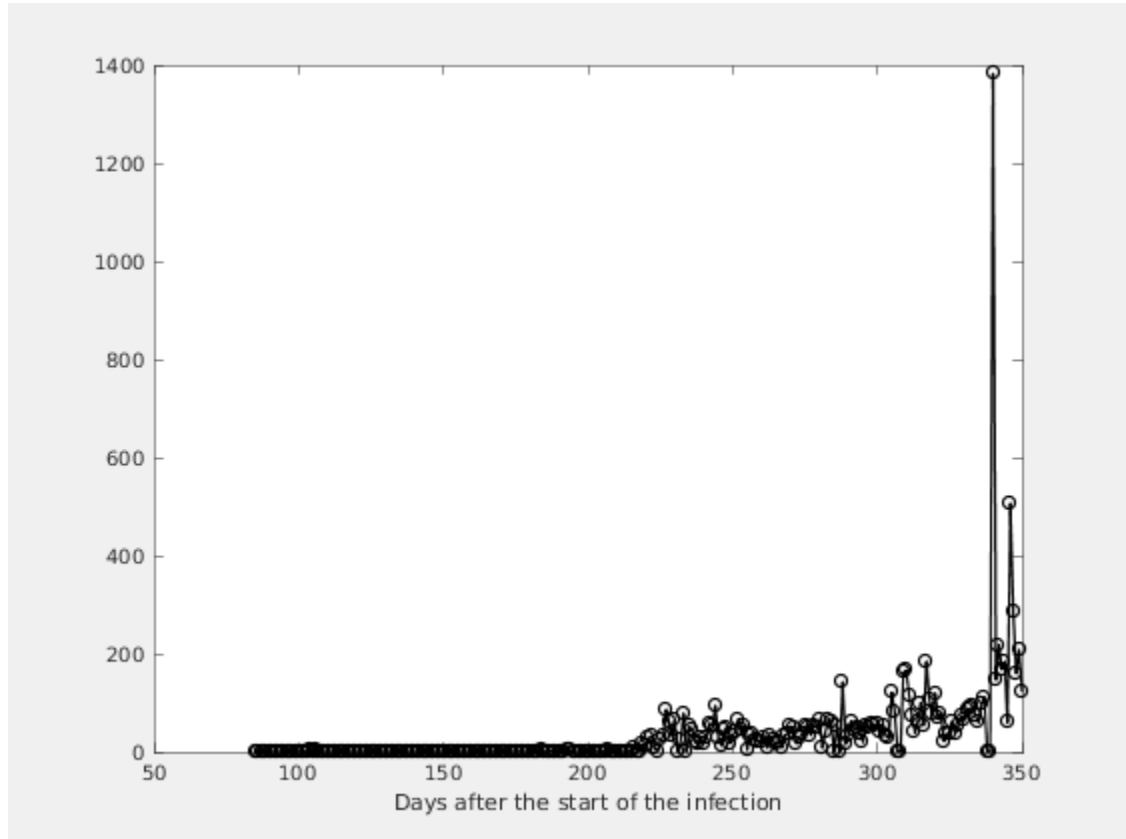
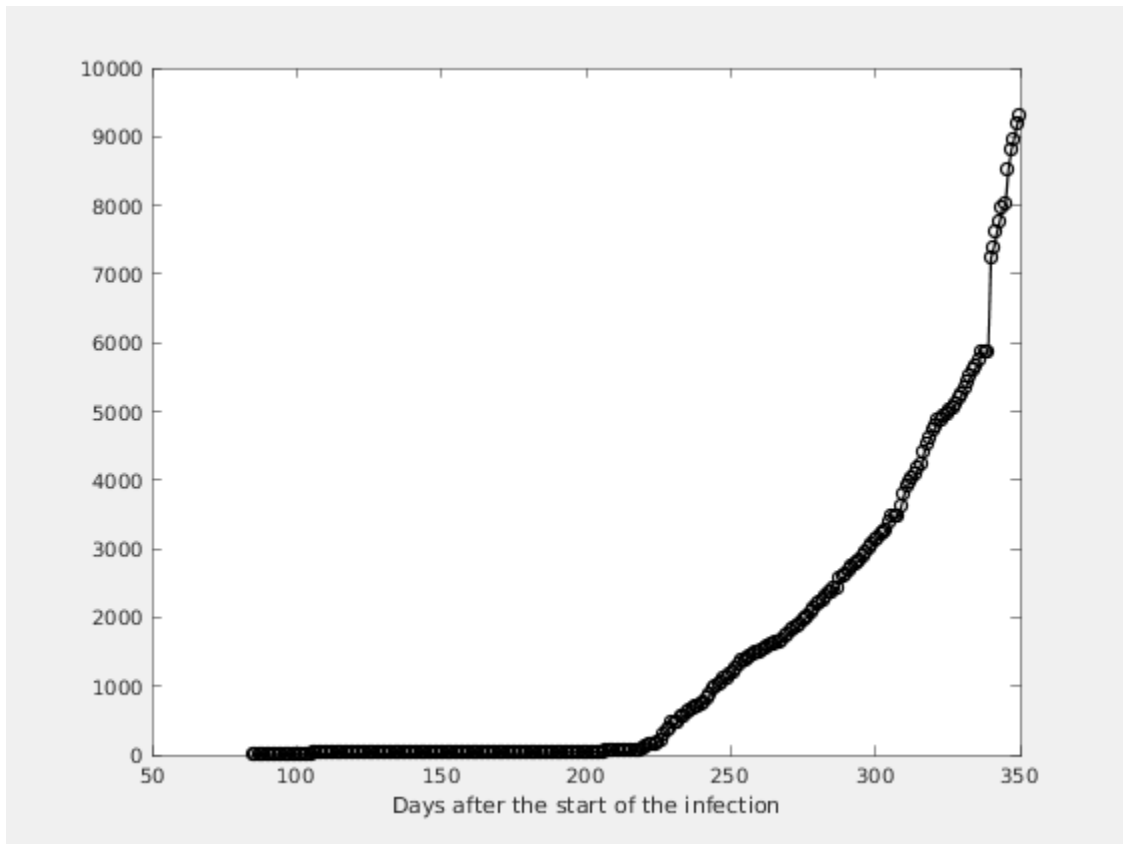


Figure 1.2. Number of the total registered cases



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

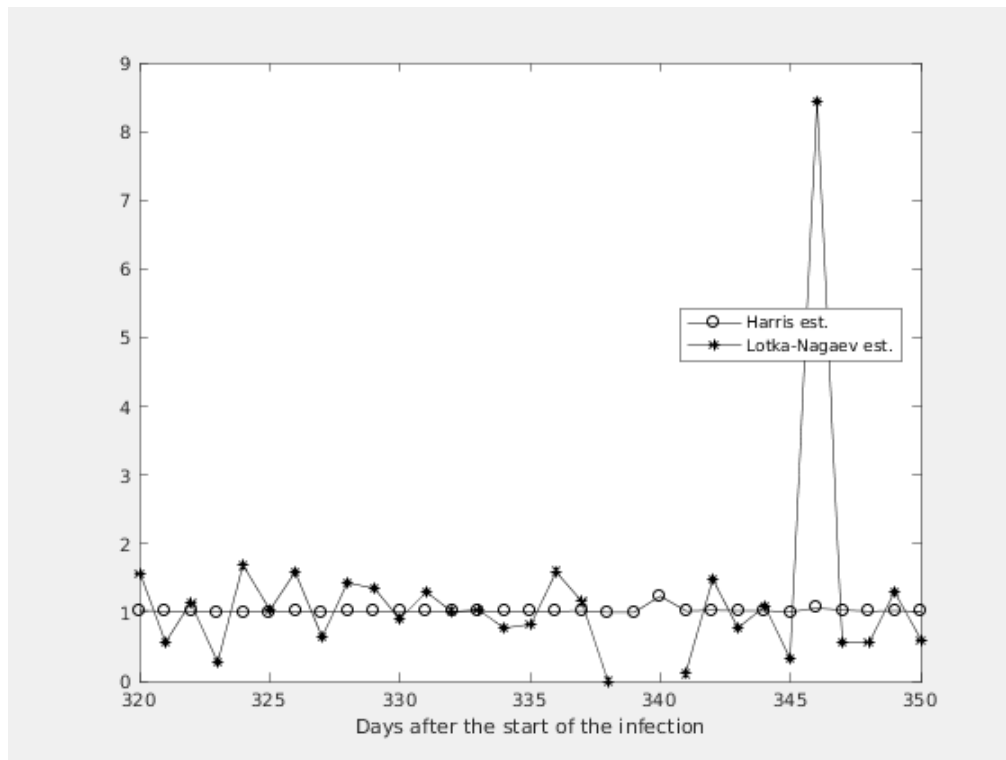


Figure 2.2. Figure

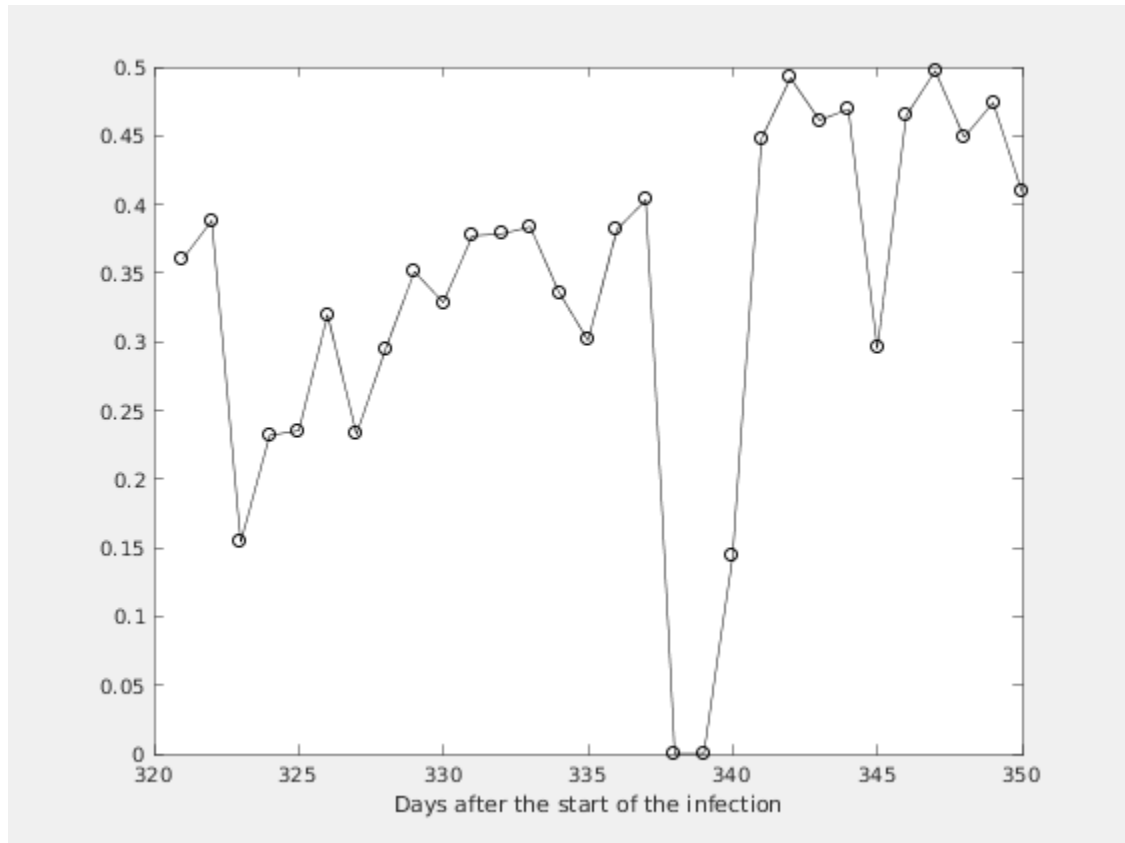


Figure 2.3. Expected number of the nonregistered infected individuals without immigration

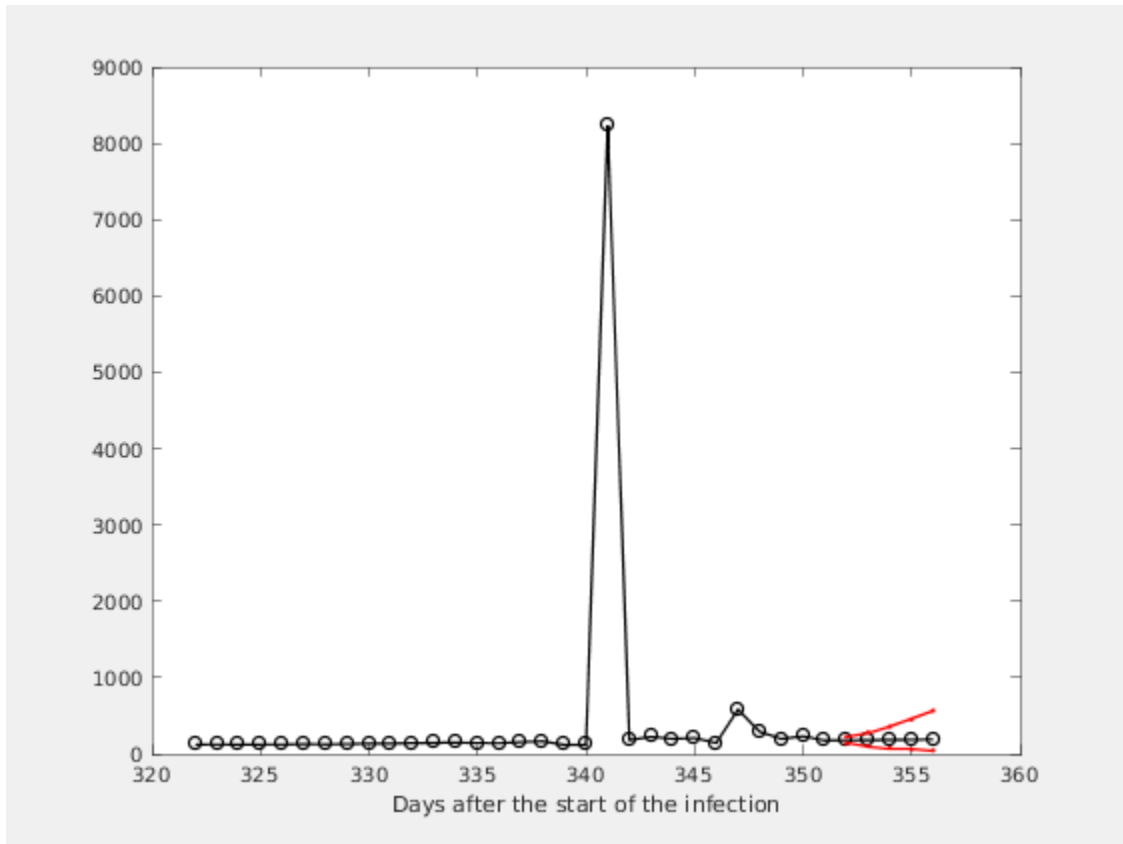
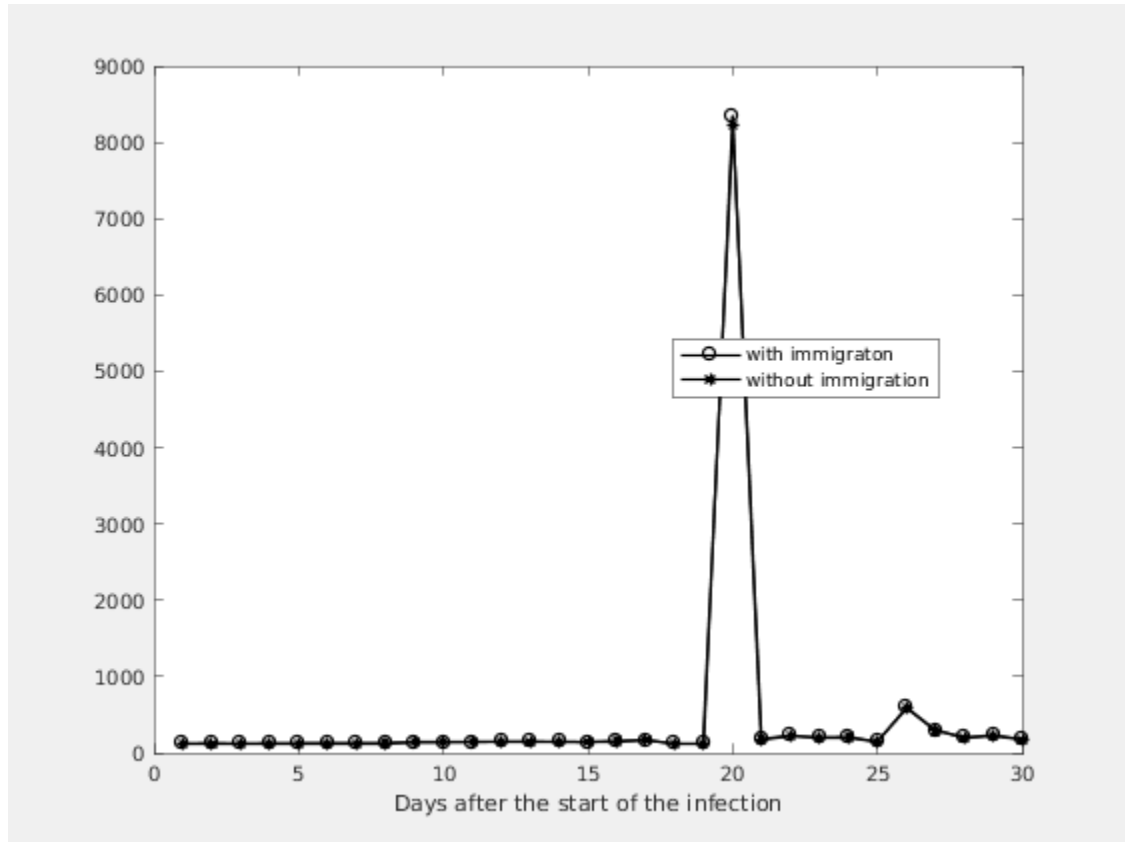


Figure 2.4. Expected number of the nonregistered infected individuals with immigration



Estimation of the model parameters.

k	m	ci	alpha	M1	A1
4	1.0630	0.8086 - 1.3175	0.4693	208	211
3	1.0335	0.7823 - 1.2846	0.2953	143	145
2	1.0181	0.7483 - 1.2878	0.4647	583	591
1	1.0231	0.7617 - 1.2845	0.4971	289	293
0	1.0132	0.7566 - 1.2698	0.4489	196	199