

Branching stochastic processes as models of Covid-19 epidemic development

Cuba - 20201214

N. Yanev, V. Stoimenova, D. Atanasov

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

Abstract

The results presented here are obtained using the methodology proposed in the paper <https://arxiv.org/abs/2004.14838> for the country Cuba. 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 immigra- tion	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

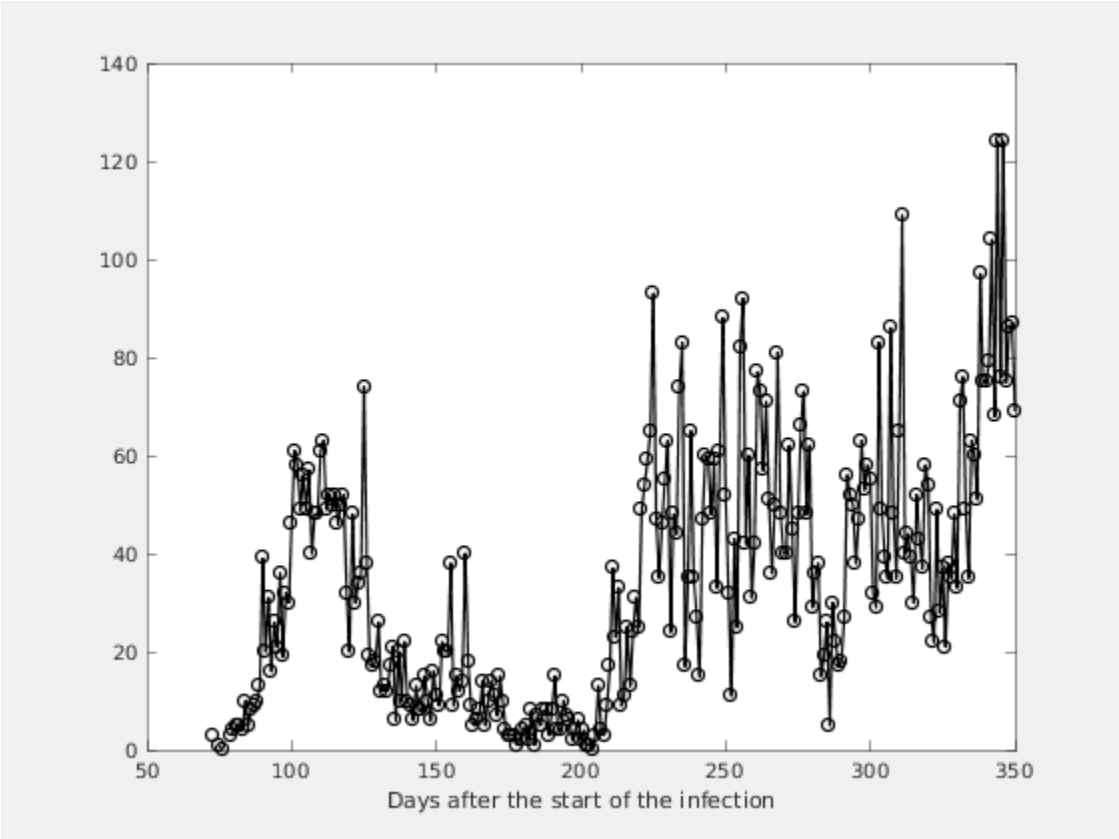
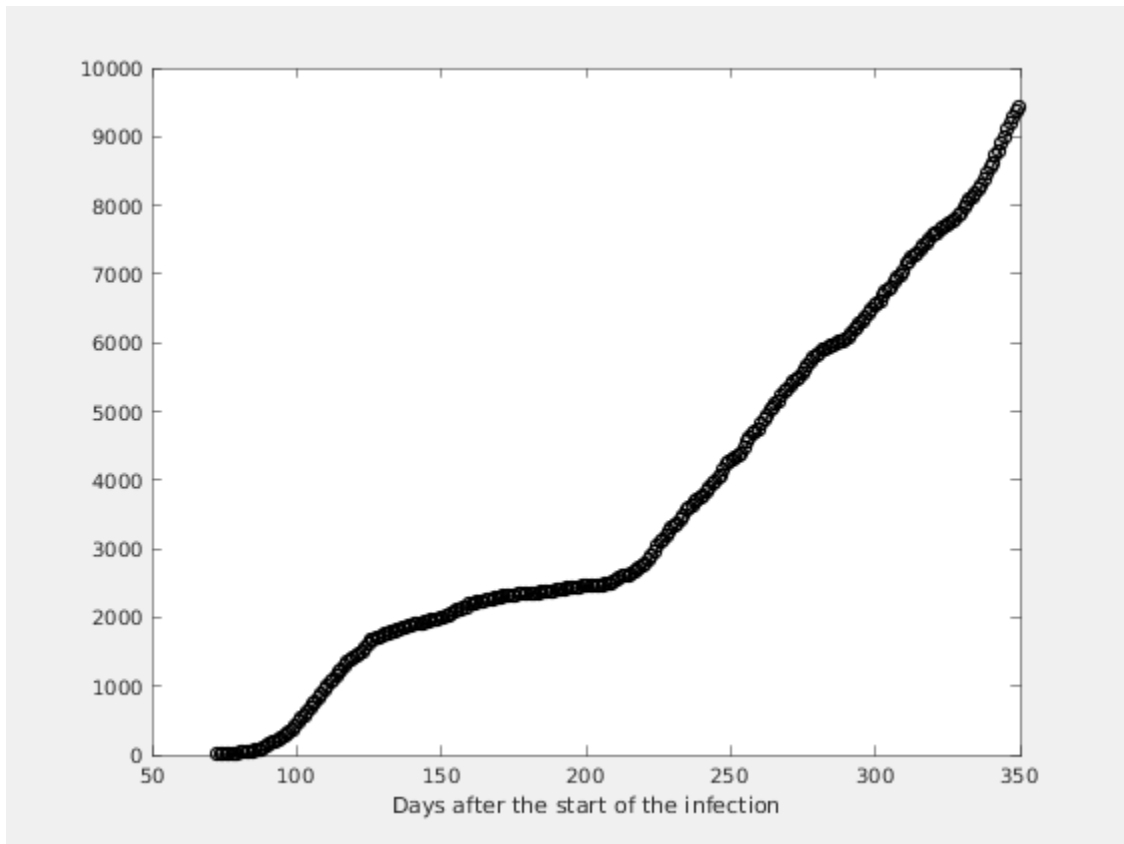


Figure 1.2. Number of the total registered cases



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

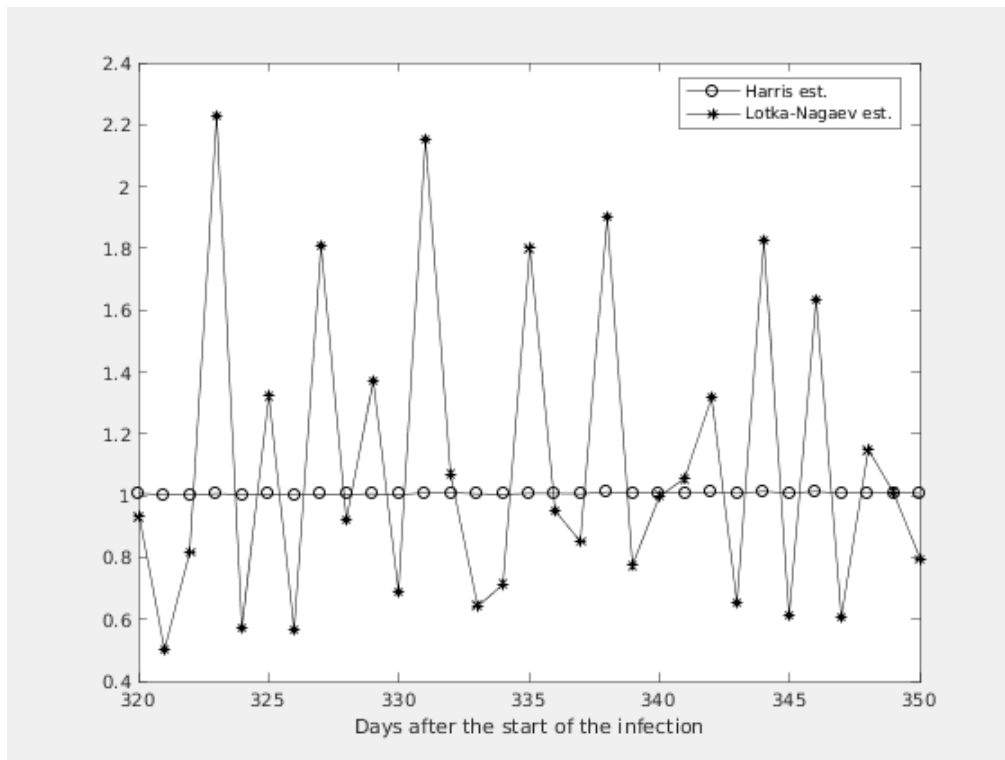


Figure 2.2. Figure

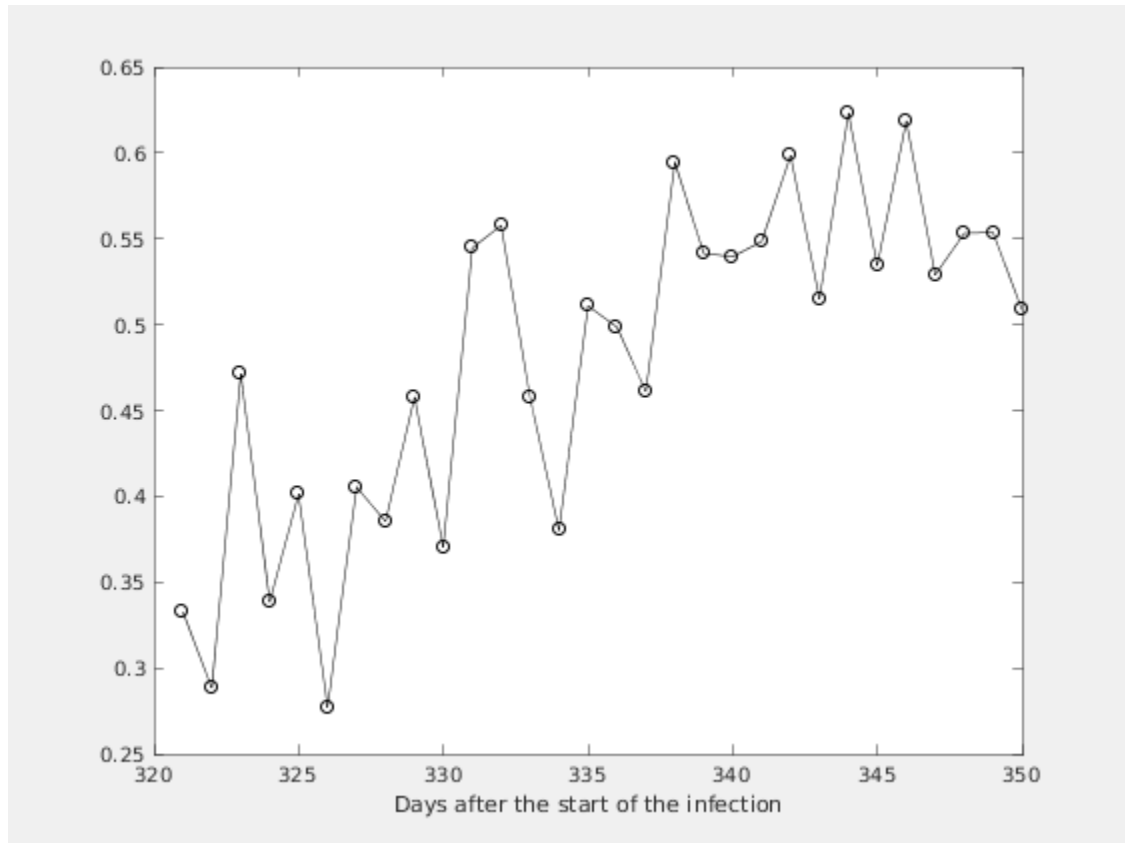


Figure 2.3. Expected number of the nonregistered infected individuals without immigration

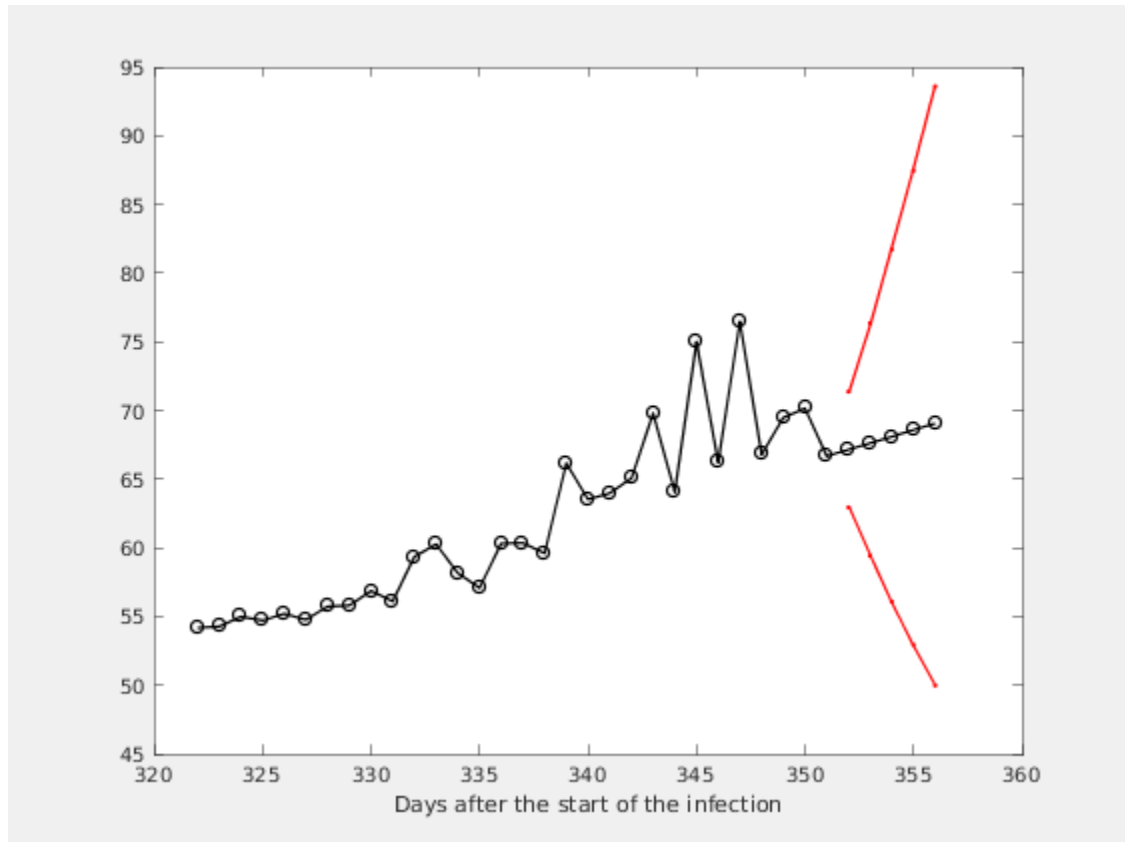
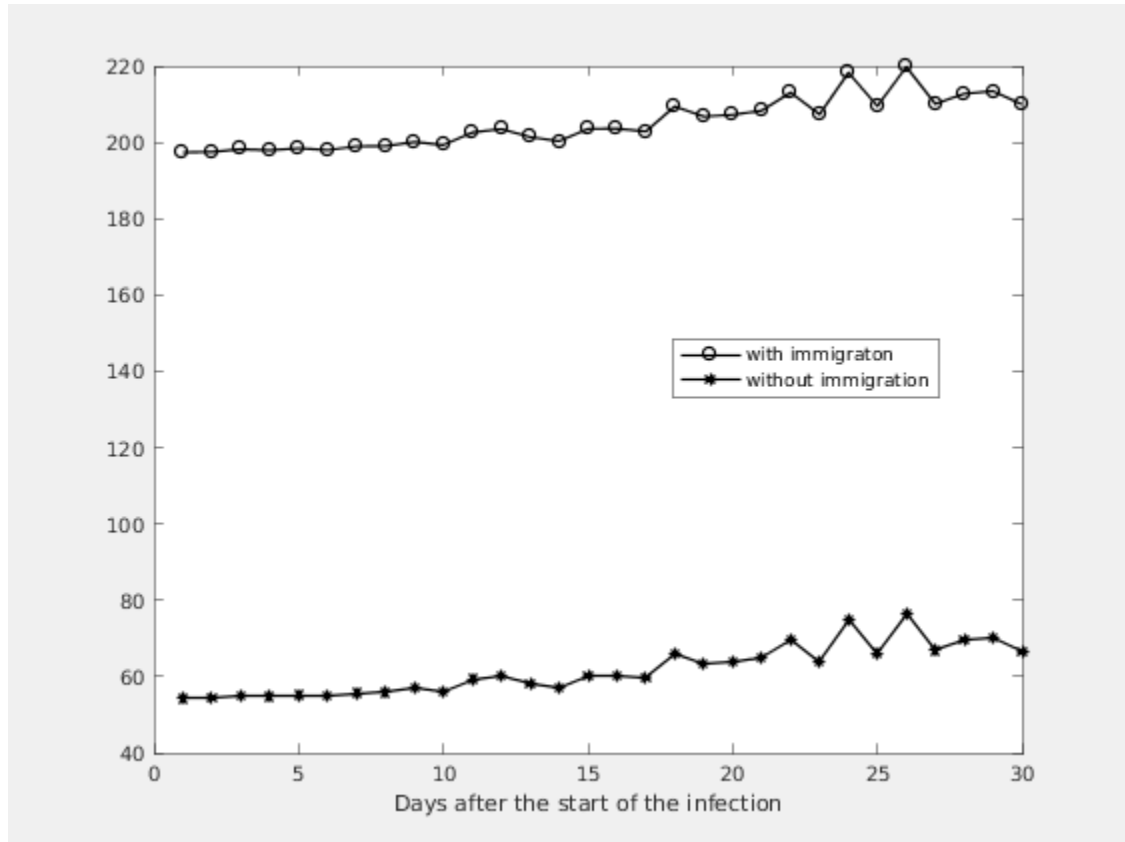


Figure 2.4. Expected number of the nonregistered infected individuals with immigration



Estimation of the model parameters.

k	m	ci	alpha	M1	A1
4	1.0135	0.9486 - 1.0784	0.6231	75	218
3	1.0079	0.9433 - 1.0725	0.5344	66	209
2	1.0090	0.9445 - 1.0736	0.6185	76	220
1	1.0091	0.9448 - 1.0733	0.5289	67	210
0	1.0071	0.9432 - 1.0709	0.5531	69	213