

# **Branching stochastic processes as models of Covid-19 epidemic development**

**Dominica - 20201214**

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## **Branching stochastic processes as models of Covid-19 epidemic development : Dominica - 20201214**

### **Abstract**

The results presented here are obtained using the methodology proposed in the paper <https://arxiv.org/abs/2004.14838> for the country Dominica. 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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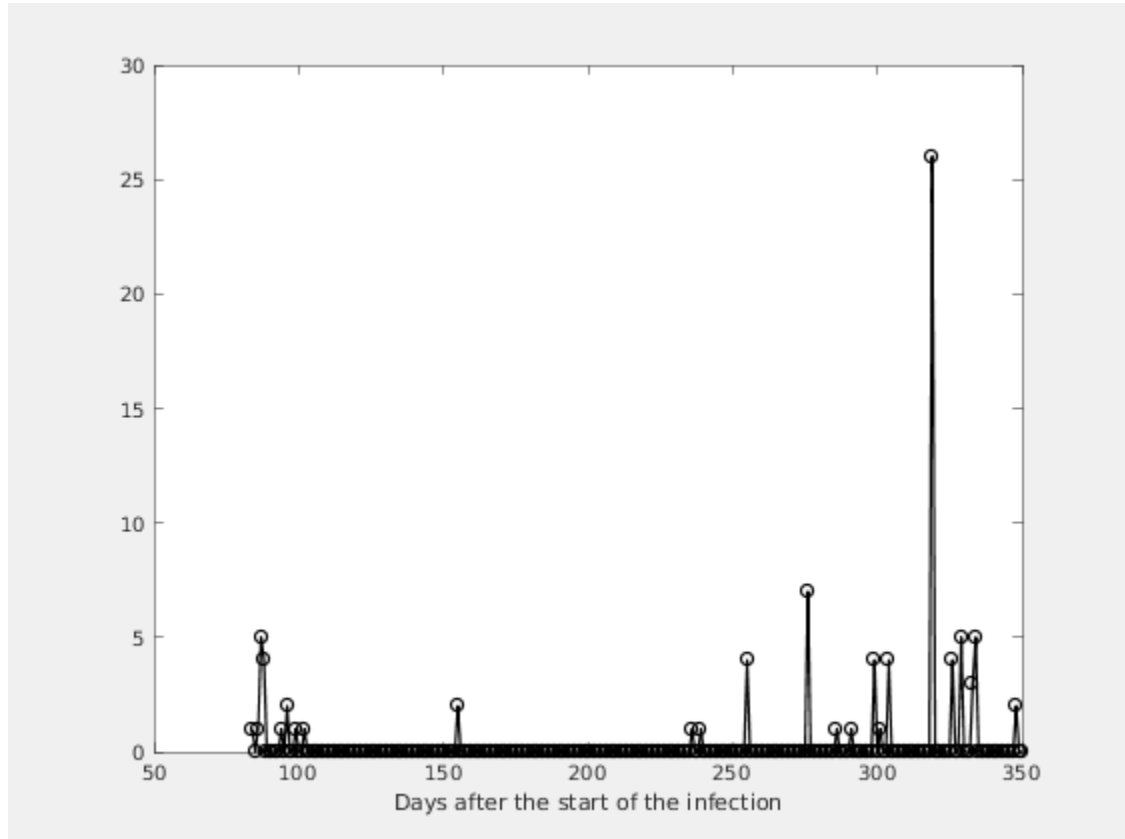
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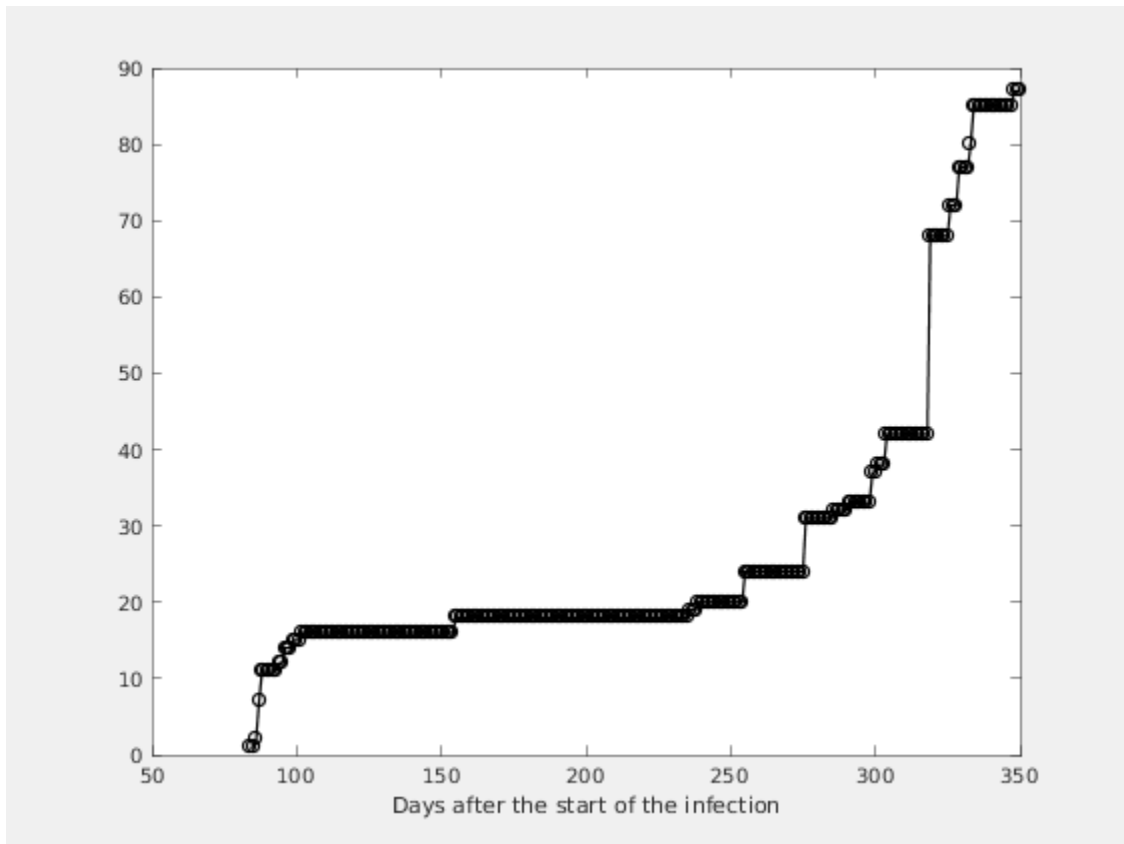
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# Chapter 1. Observed Infection data

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



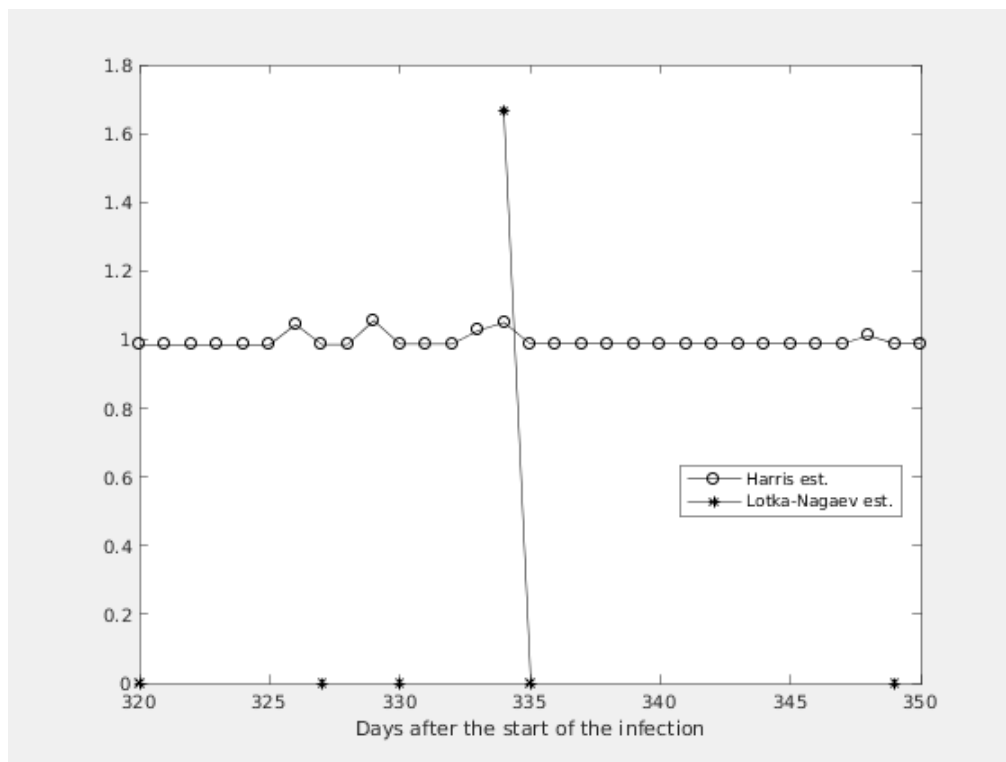
**Figure 1.2. Number of the total registered cases**



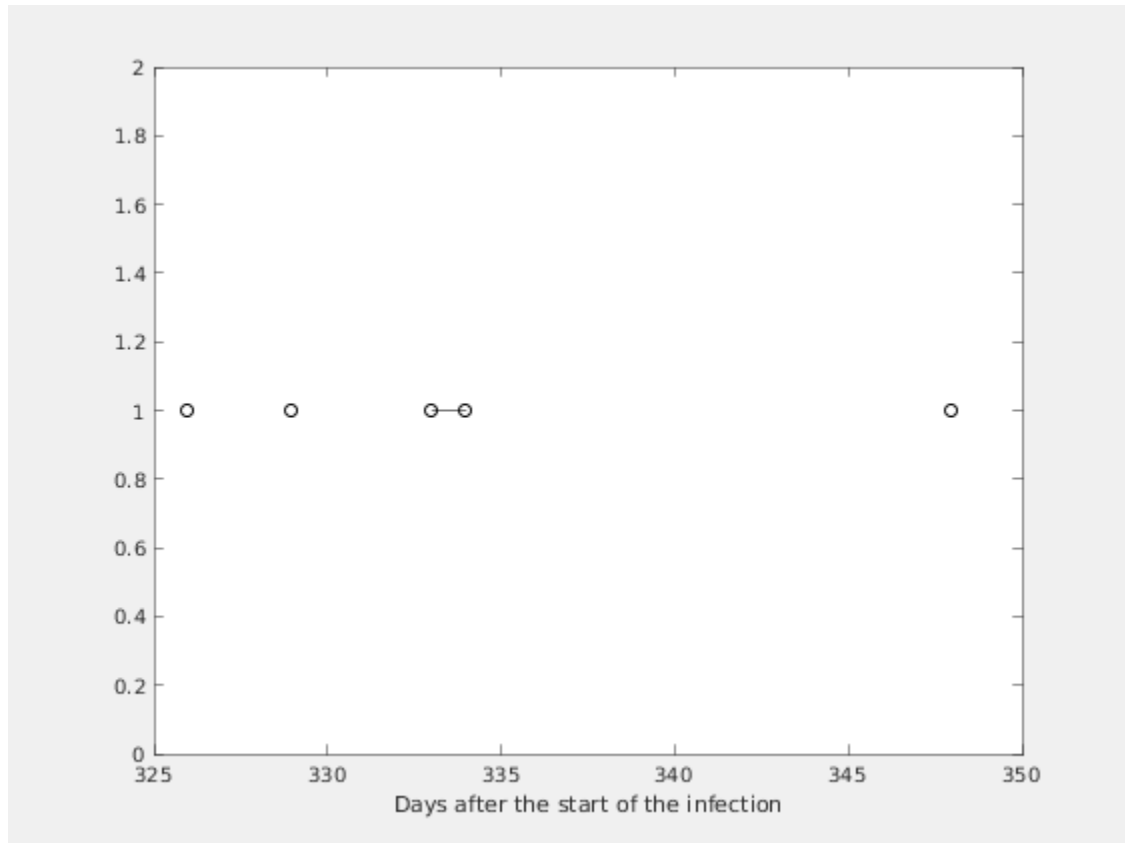
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# Chapter 2. Estimating of the main parameter and some predictions

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

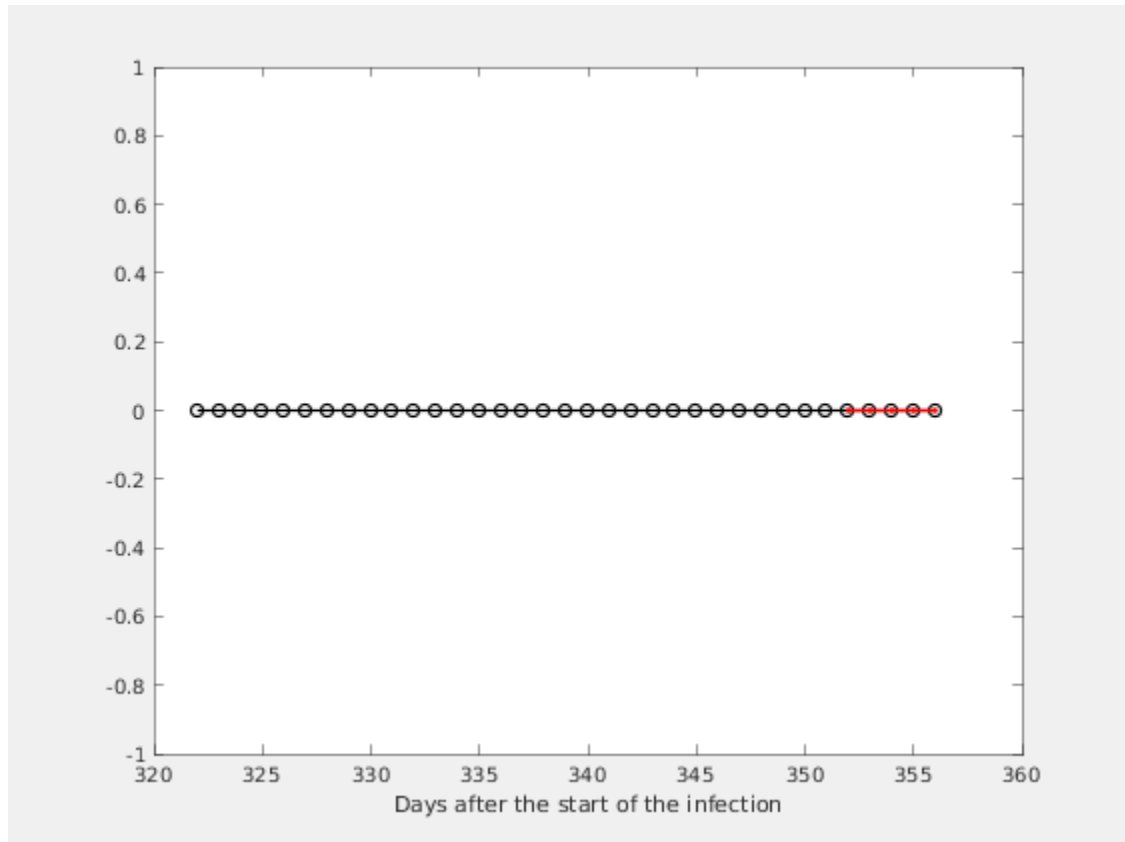


**Figure 2.2. Figure**

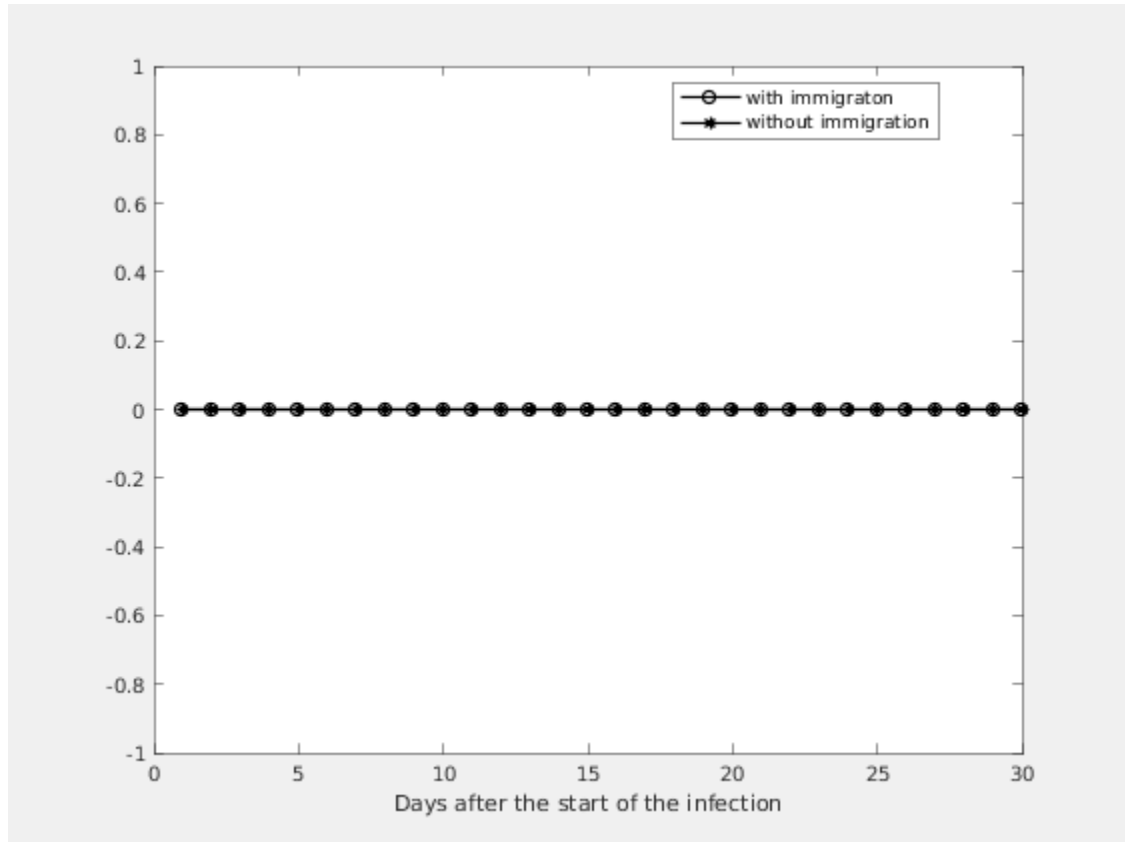




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	M1	A1
4	0.9882	0.3469 - 1.6295	NaN	0	0
3	0.9882	0.3469 - 1.6295	NaN	0	0
2	1.0118	0.3708 - 1.6528	NaN	0	0
1	0.9885	0.3472 - 1.6298	NaN	0	0
0	0.9885	0.3586 - 1.6184	1.0000	0	0