

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

**Panama - 20201214**

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

### **Abstract**

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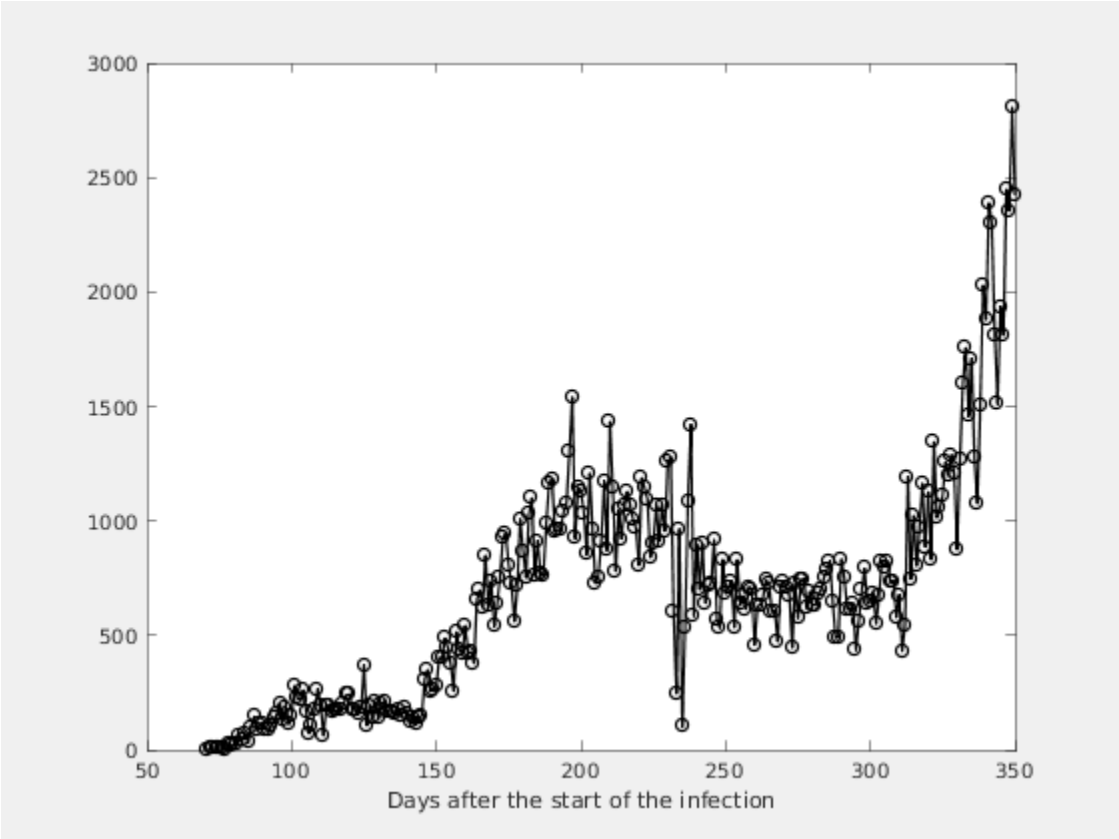
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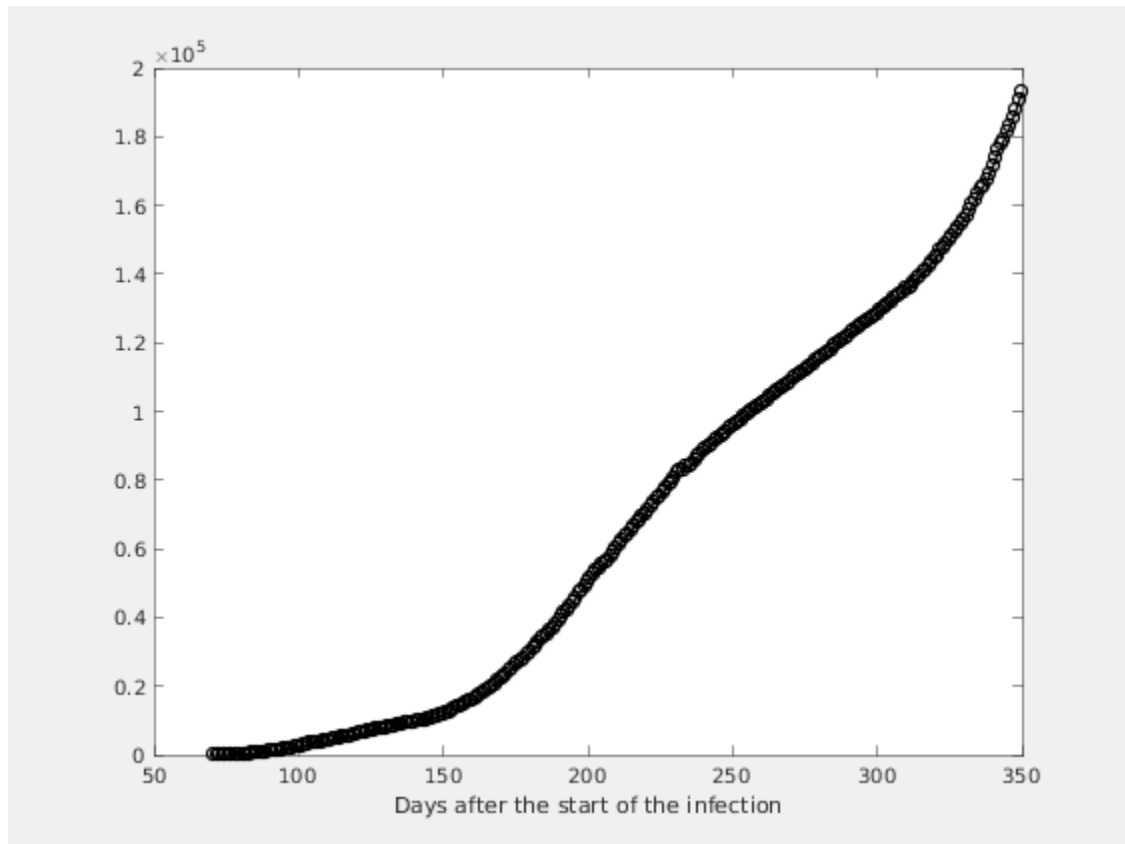
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# Chapter 1. Observed Infection data

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

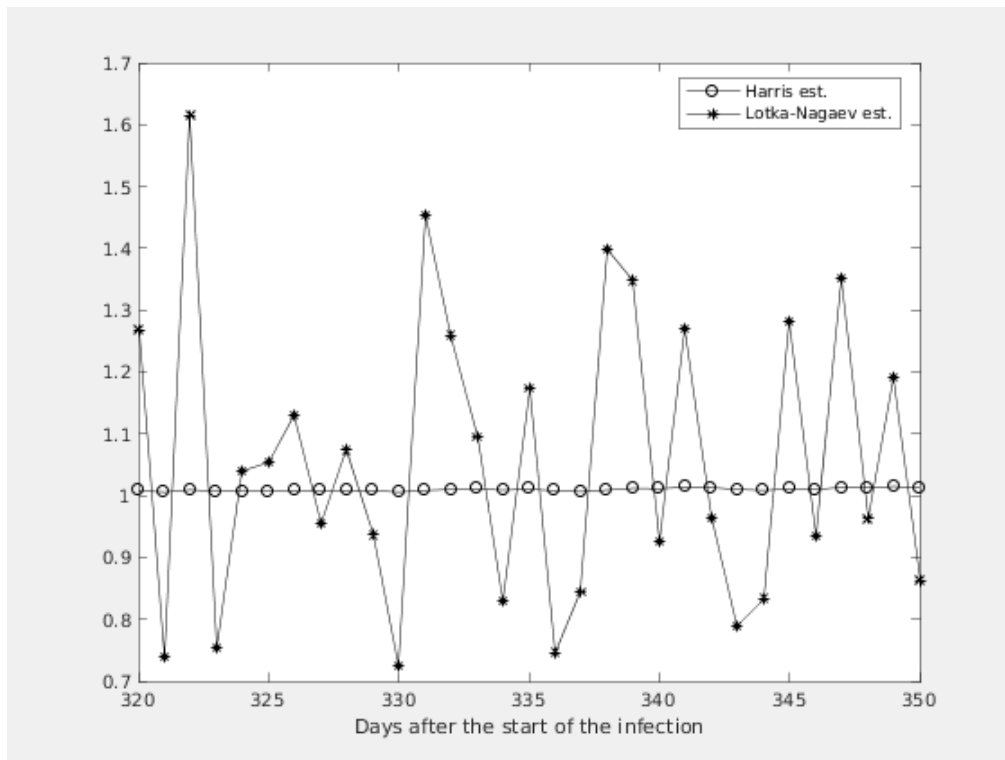
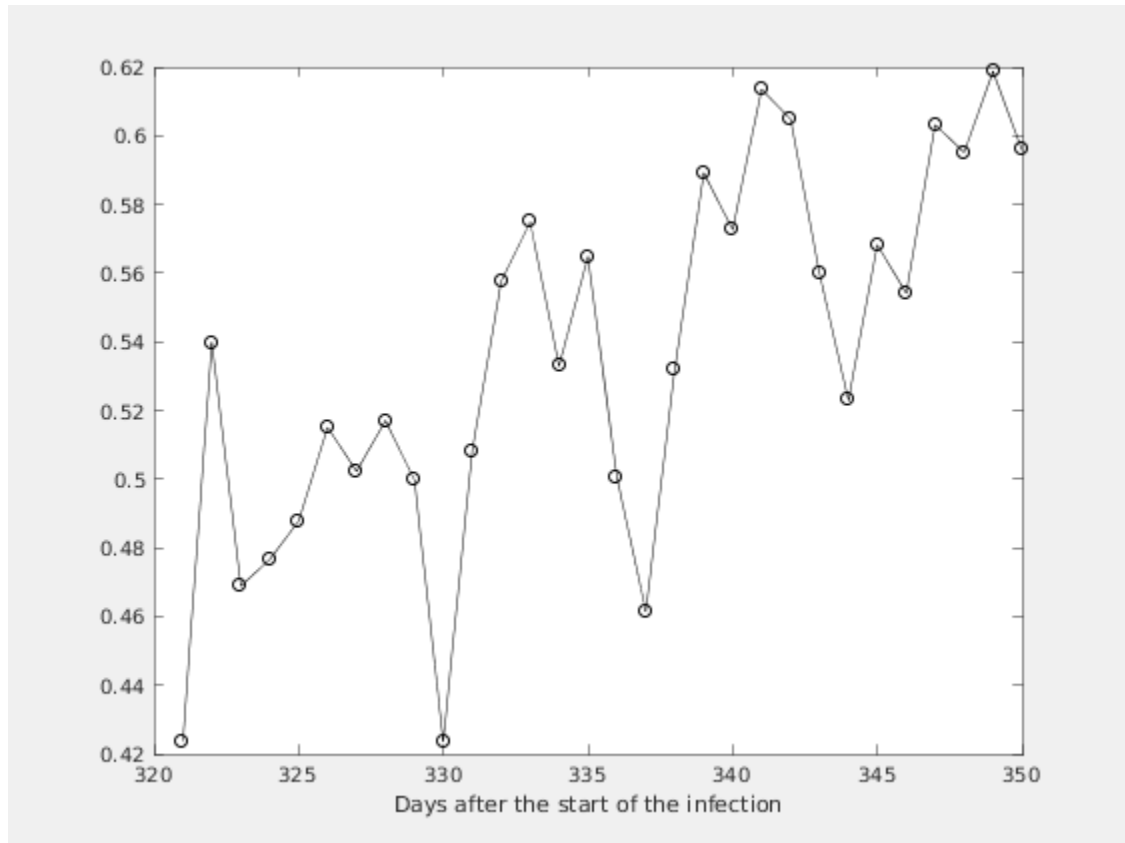
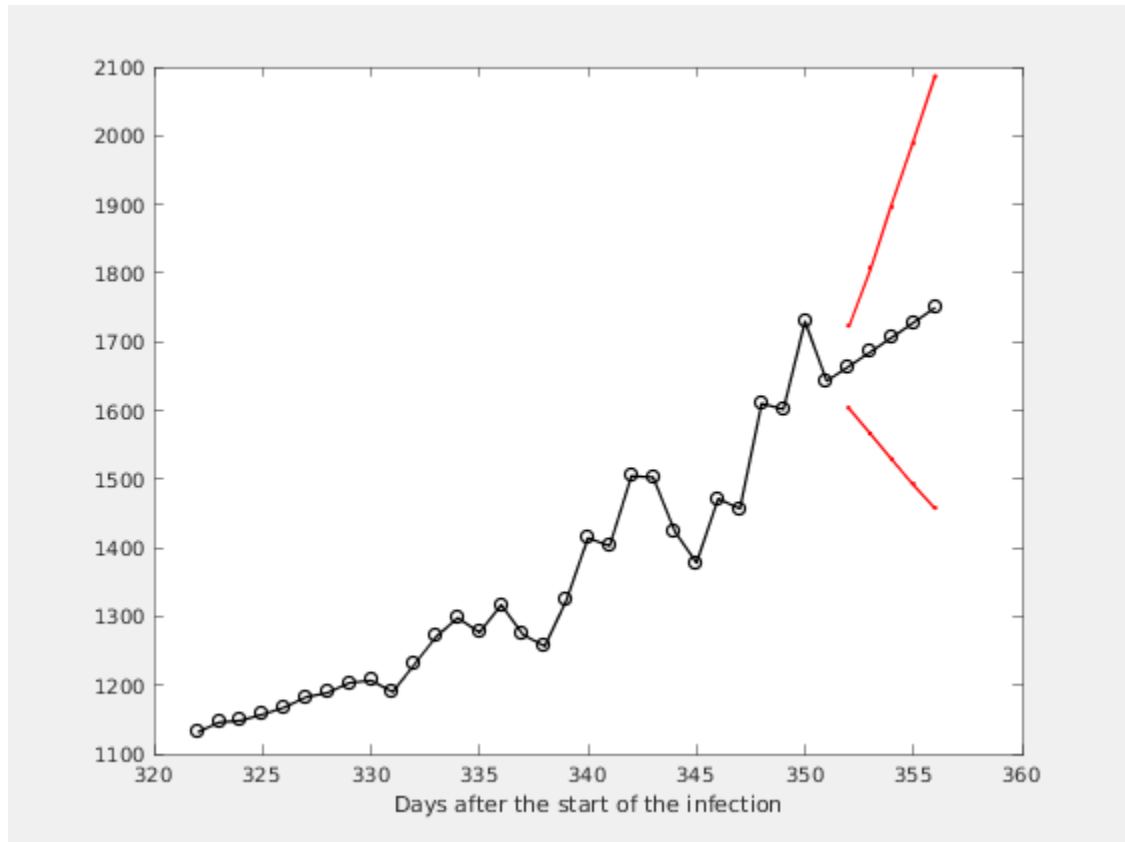


Figure 2.2. Figure

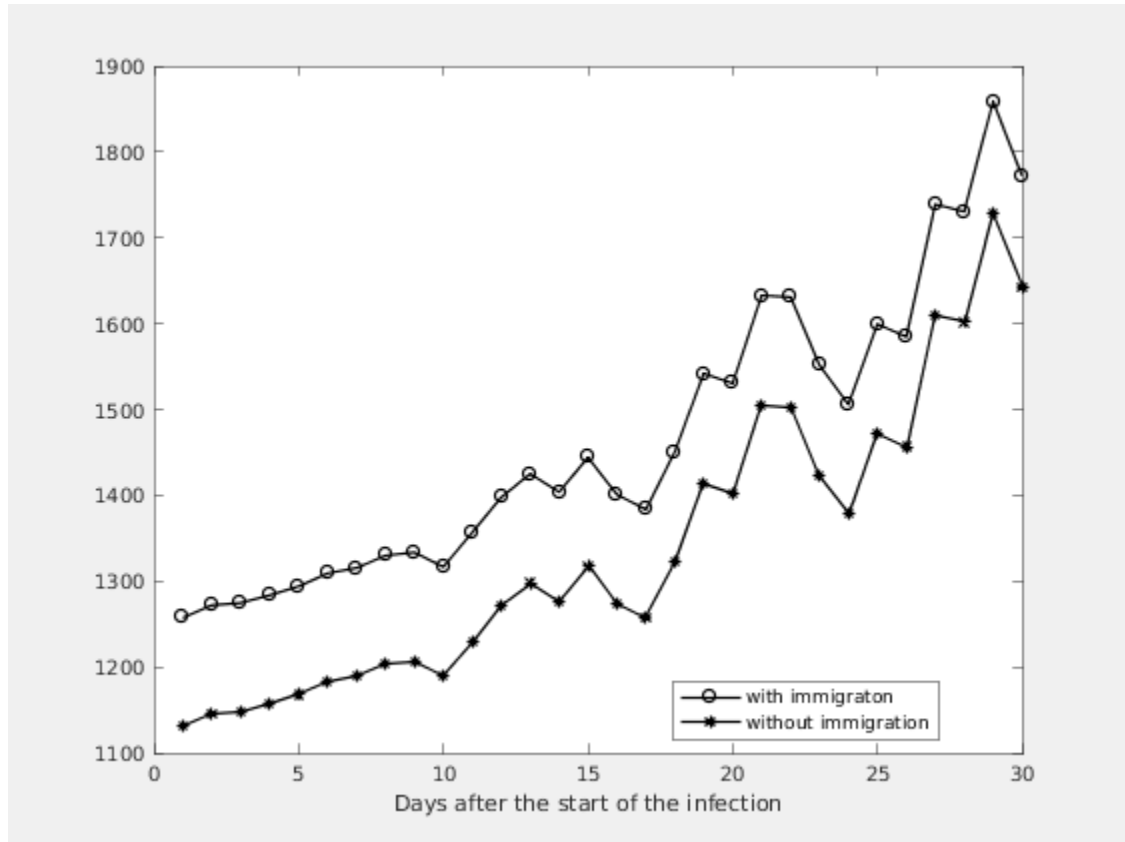




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	M1	A1
4	1.0100	0.9725 - 1.0475	0.5230	1378	1506
3	1.0134	0.9760 - 1.0507	0.5682	1471	1599
2	1.0127	0.9756 - 1.0498	0.5542	1457	1585
1	1.0149	0.9779 - 1.0520	0.6031	1610	1739
0	1.0127	0.9759 - 1.0495	0.5952	1602	1730