

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

**Guatemala - week 53**

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### **Abstract**

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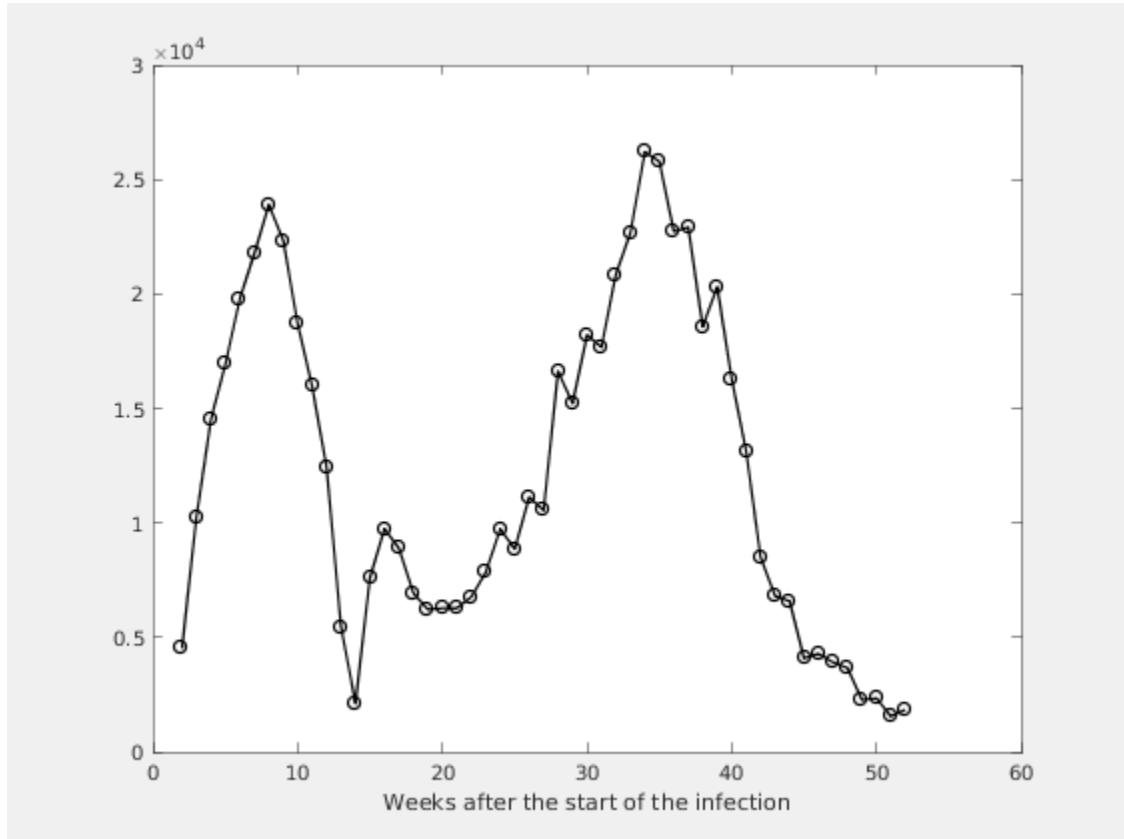
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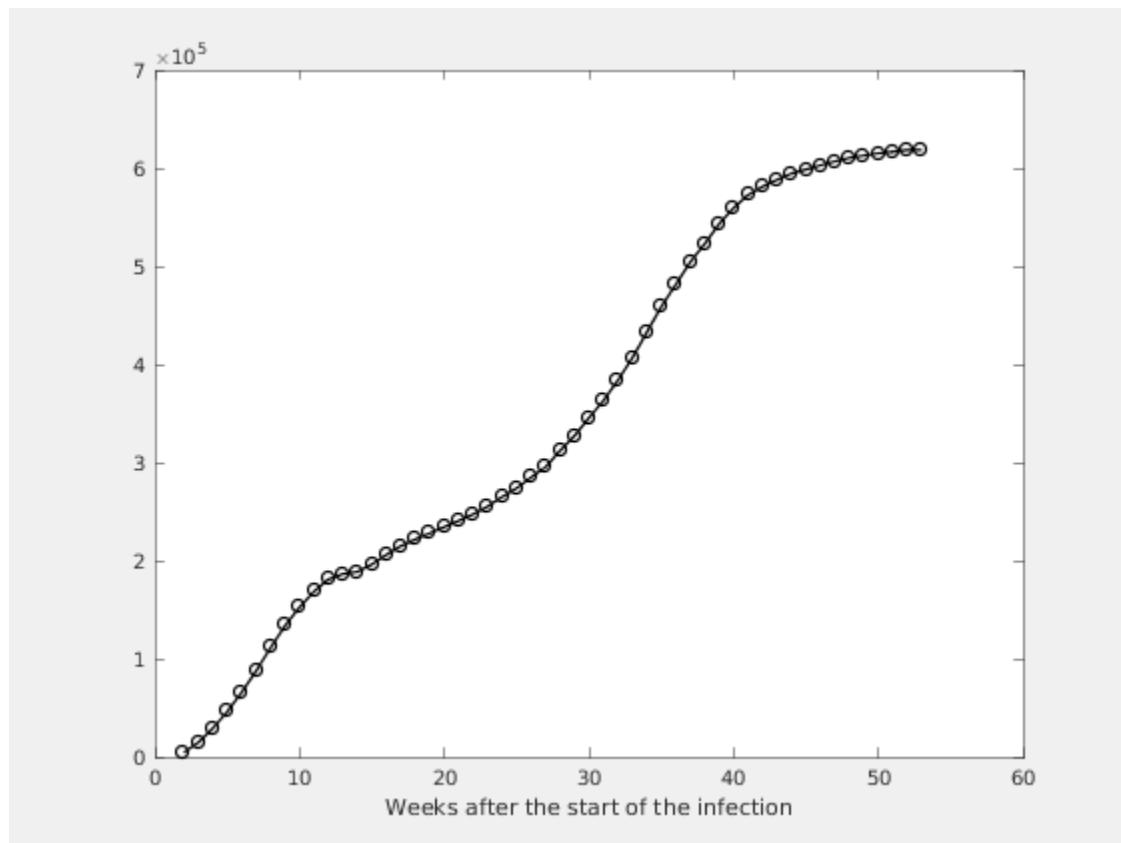
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# Chapter 1. Observed Infection data

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



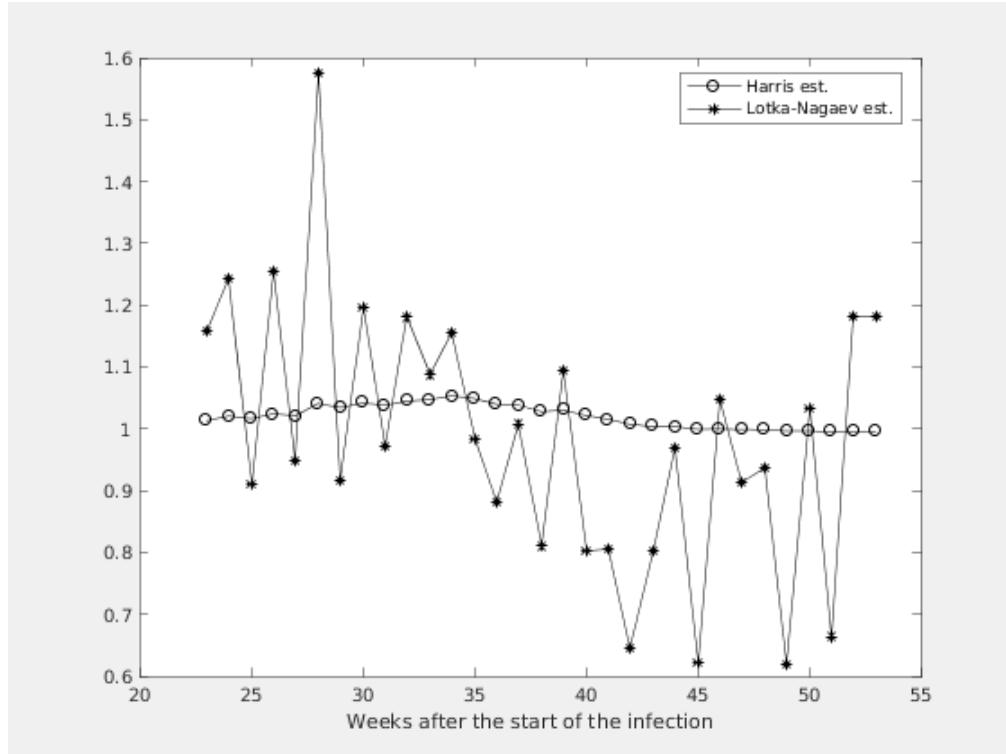
**Figure 1.2. Number of the total registered cases**



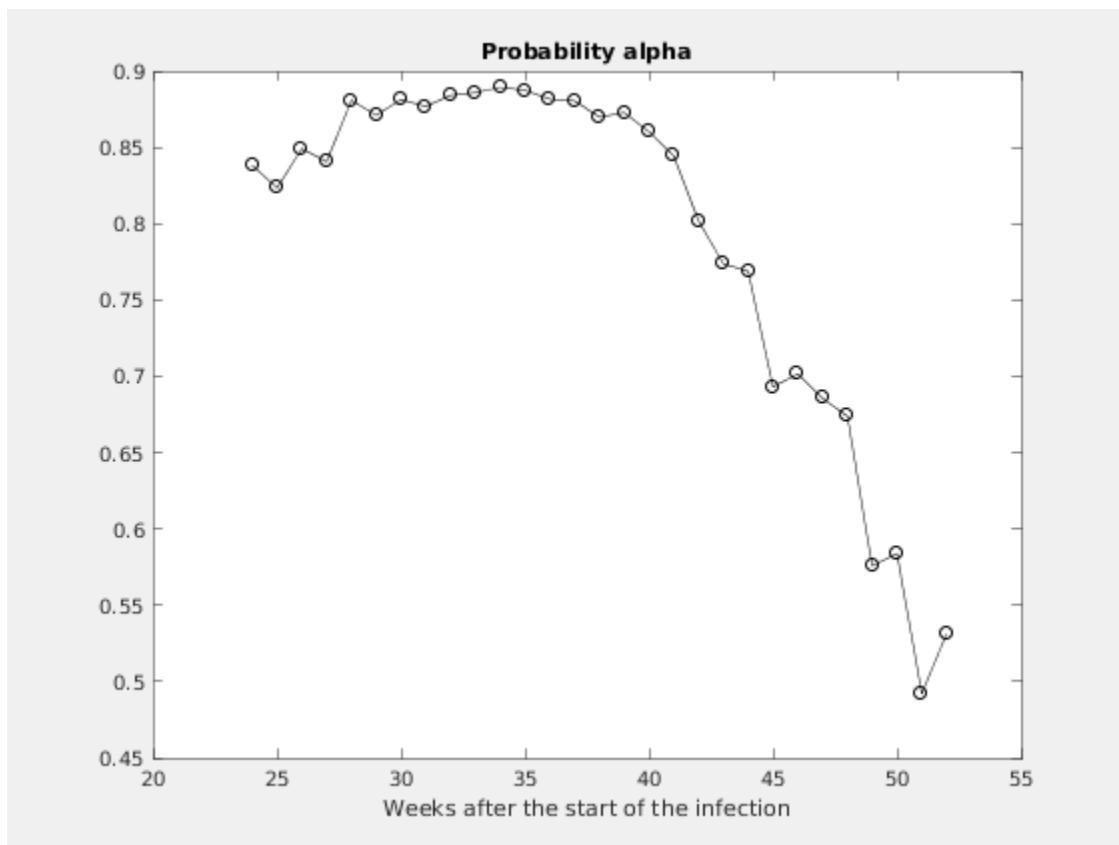
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# Chapter 2. Estimating of the main parameter and some predictions

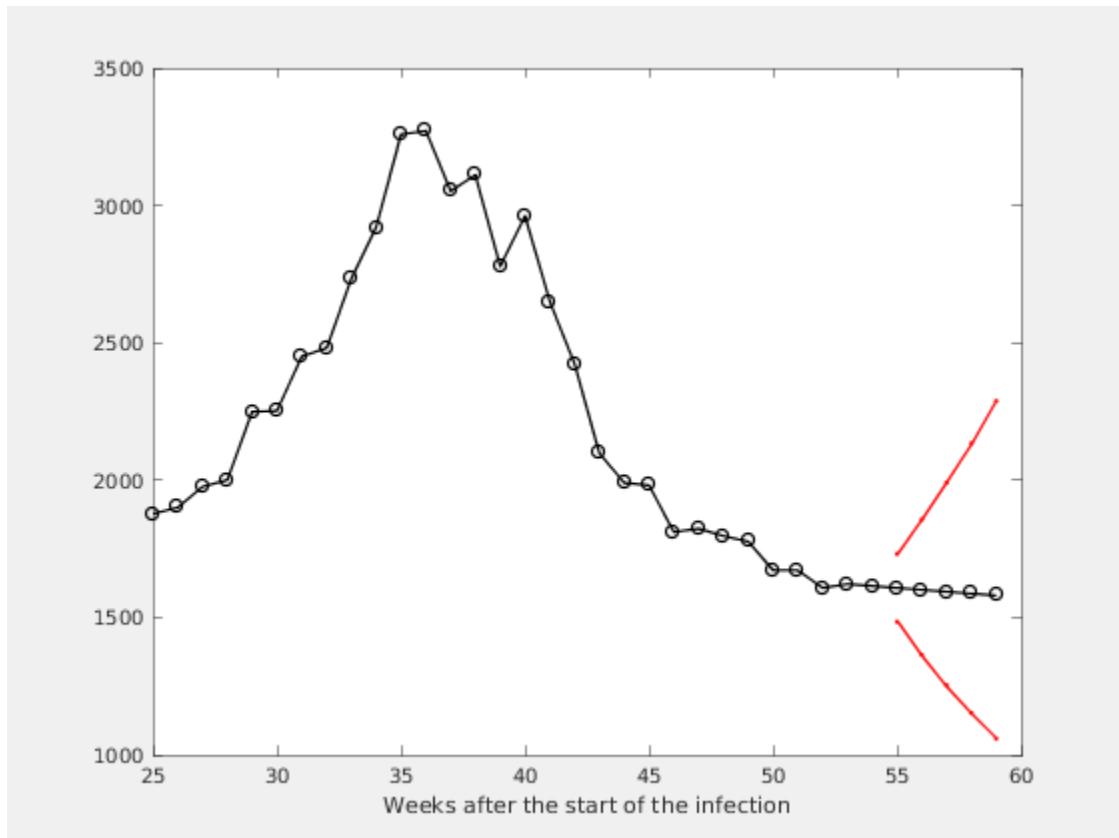
Figure 2.1. The Lotka-Nagaev and the Harris type estimator of the growth rate



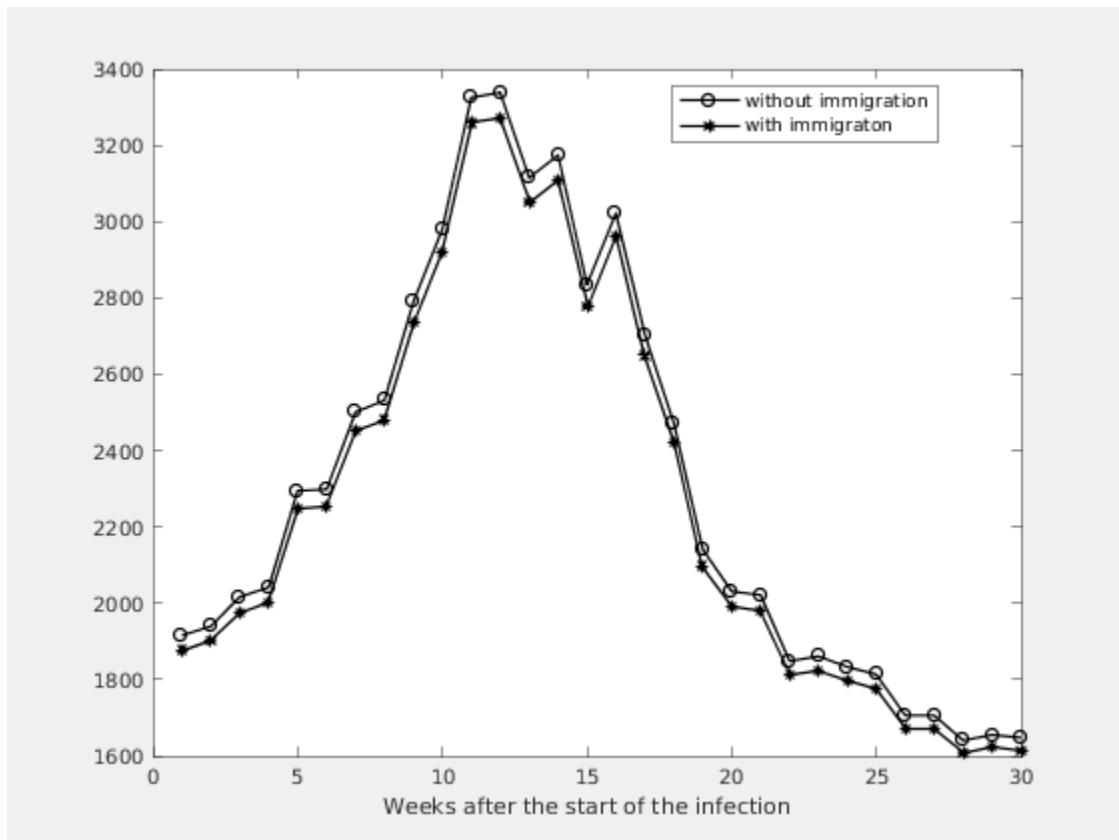
**Figure 2.2. Figure**



**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	A1	M1
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4	0.9963	0.9155 - 1.0772	0.6855	1796	1833
3	0.9965	0.9167 - 1.0762	0.6738	1777	1813
2	0.9952	0.9161 - 1.0743	0.5759	1672	1706
1	0.9957	0.9176 - 1.0738	0.5839	1672	1706
0	0.9957	0.9183 - 1.0730	0.4922	1608	1641