

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

**Colombia - 20201214**

**N. Yanev, V. Stoimenova, D. Atanasov**

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

### **Abstract**

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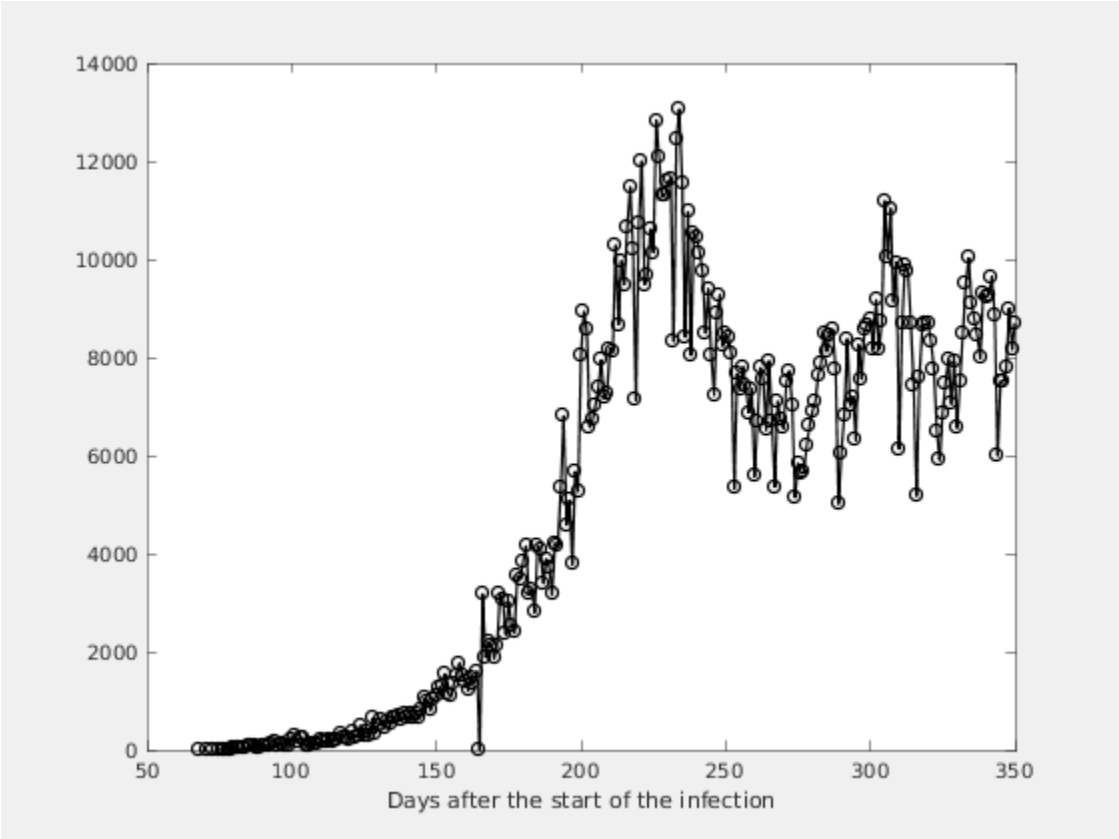
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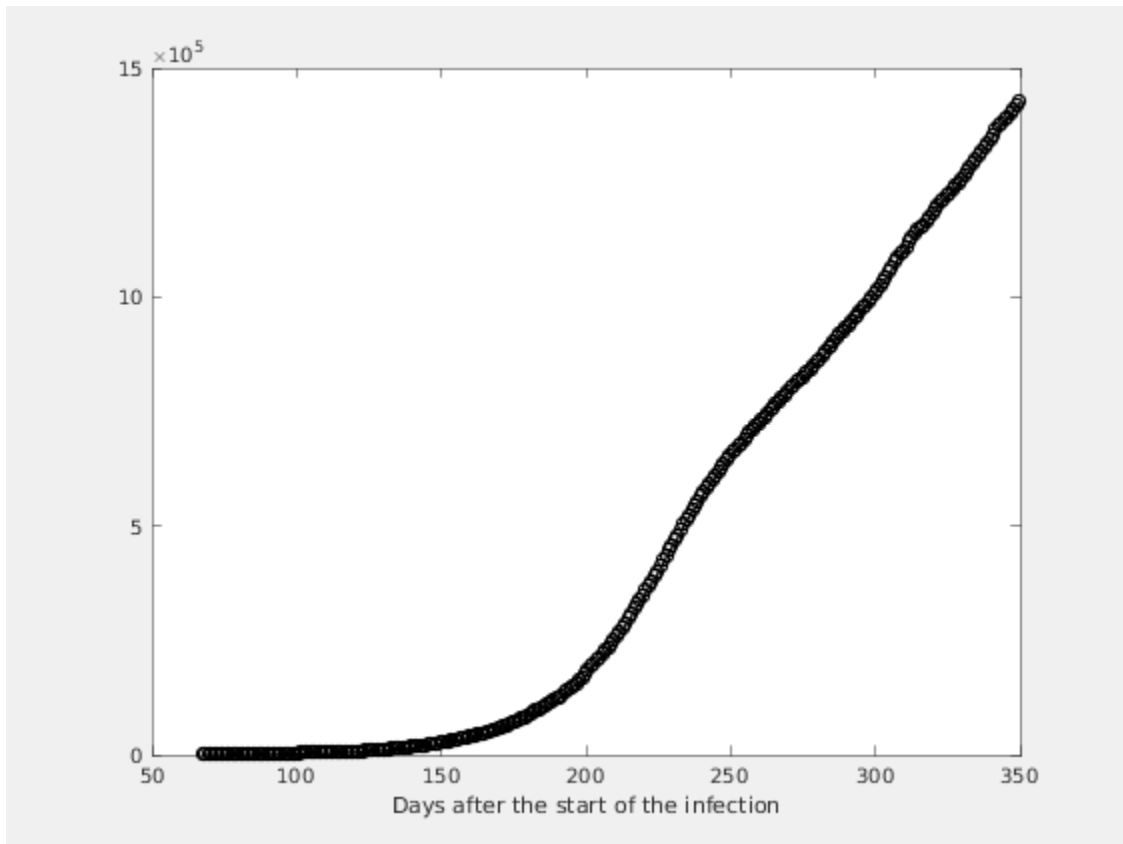
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# Chapter 1. Observed Infection data

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

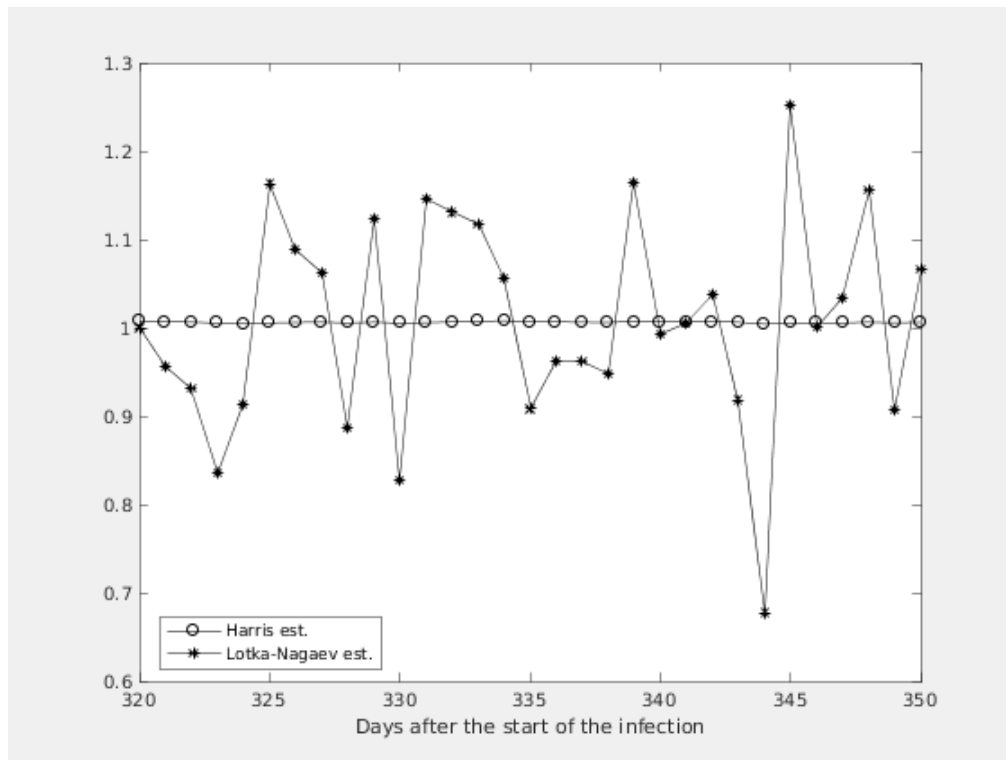
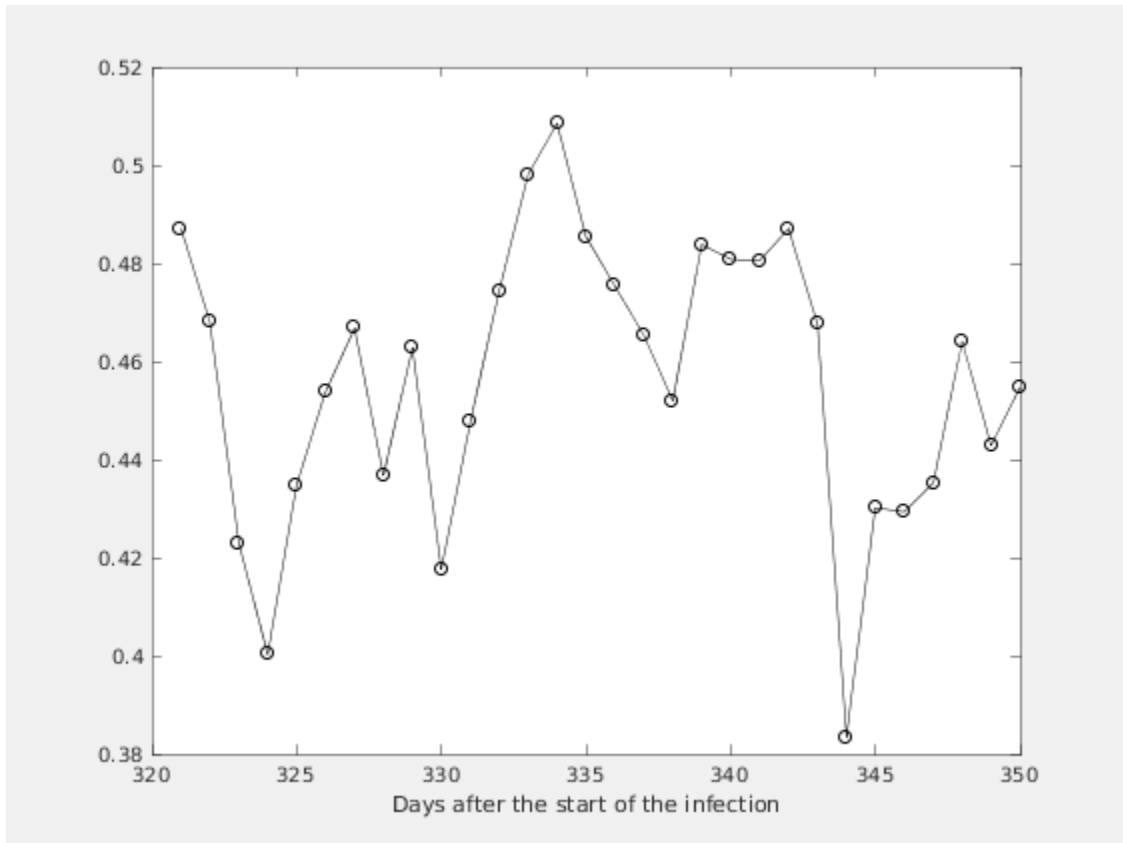
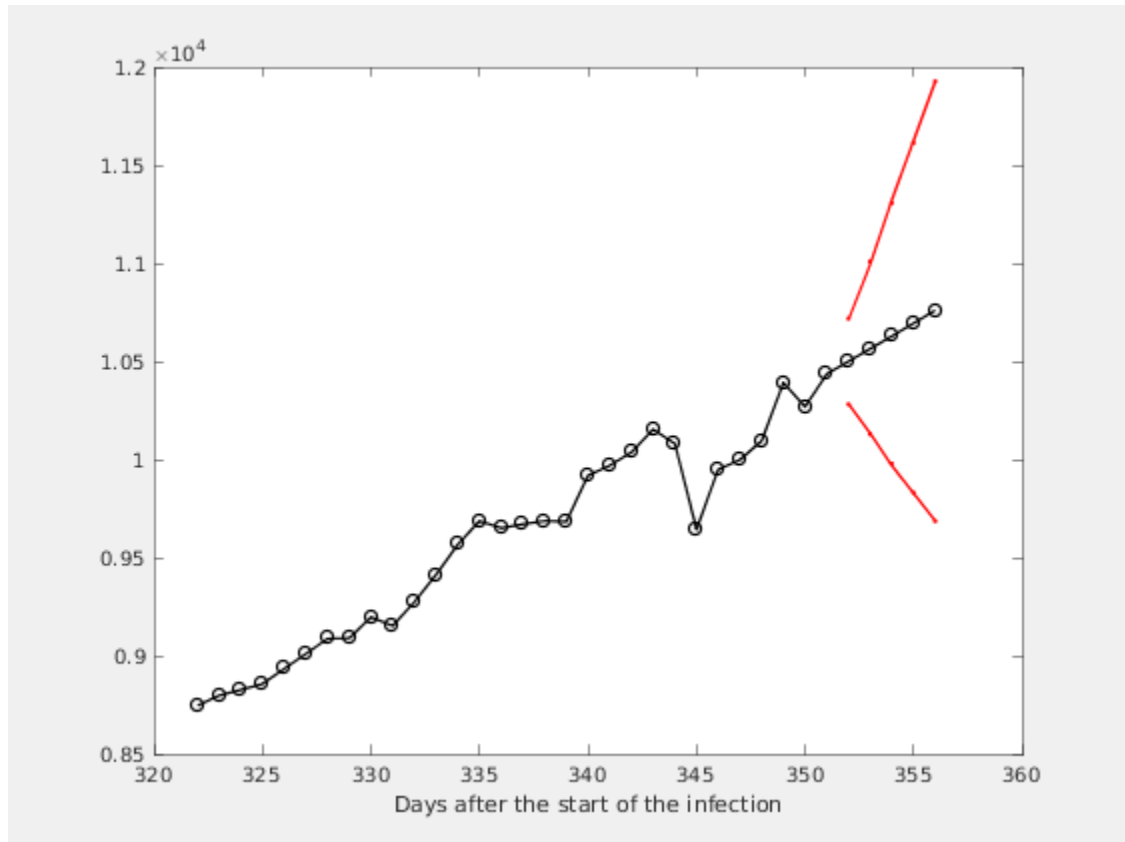


Figure 2.2. Figure

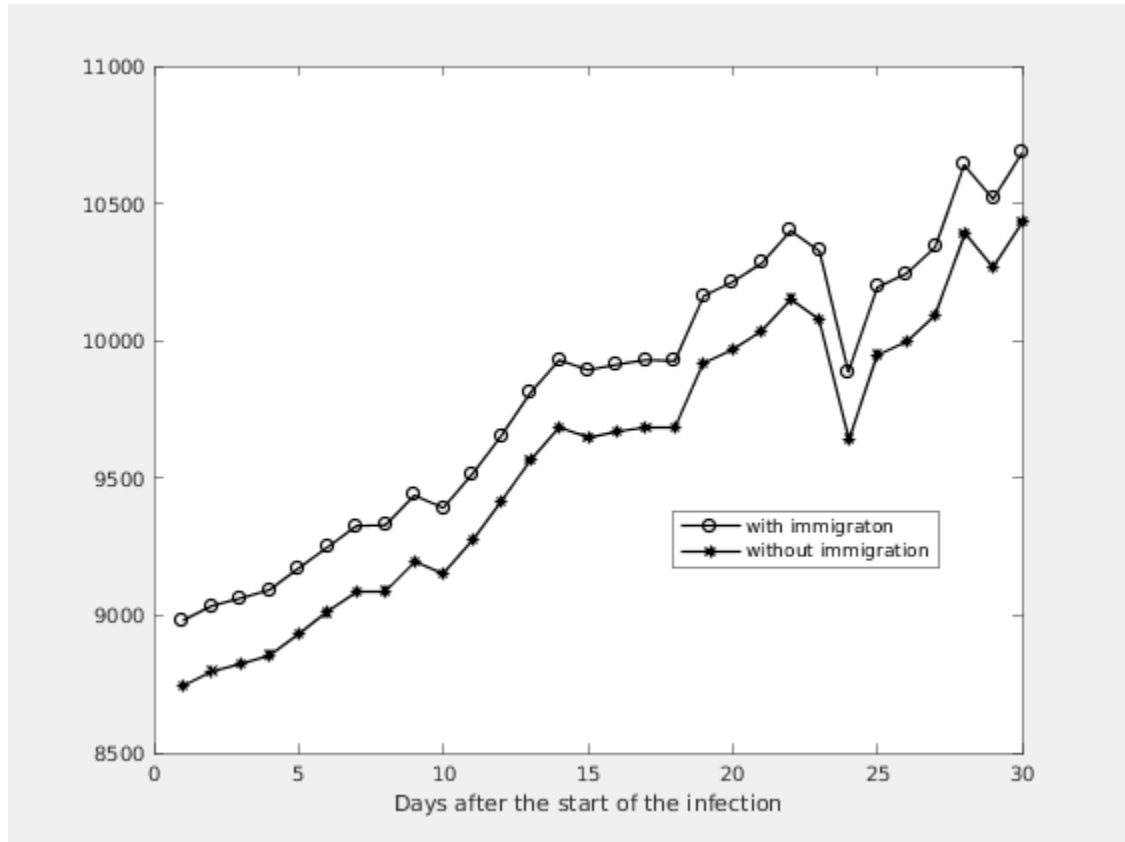




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	M1	A1
4	1.0054	0.9841 - 1.0268	0.3834	9644	9887
3	1.0056	0.9842 - 1.0270	0.4301	9950	10195
2	1.0064	0.9852 - 1.0277	0.4294	9999	10244
1	1.0058	0.9846 - 1.0270	0.4352	10095	10341
0	1.0061	0.9850 - 1.0273	0.4641	10391	10639