

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

**Guatemala - 20201214**

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

---

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

### **Abstract**

The results presented here are obtained using the methodology 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>.

---

## Table of Contents

1. Observed Infection data .....	1
2. Estimating of the main parameter and some predictions .....	3

---

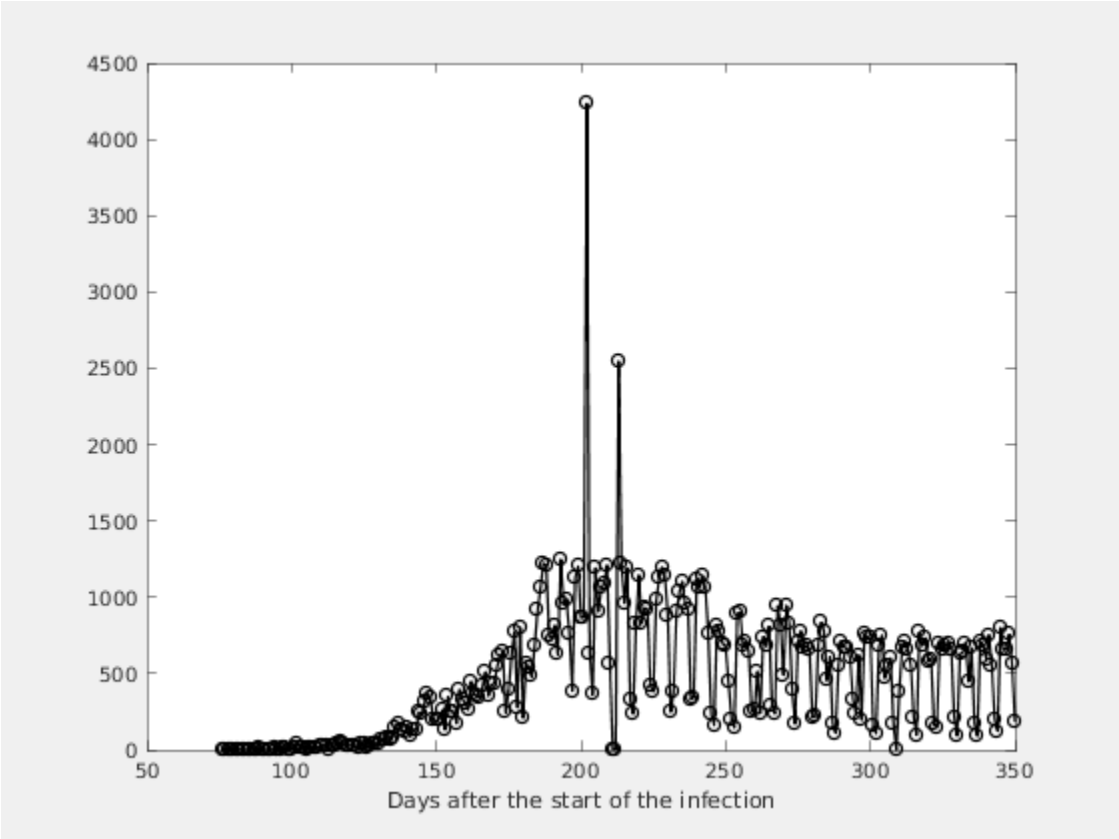
## List of Figures

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

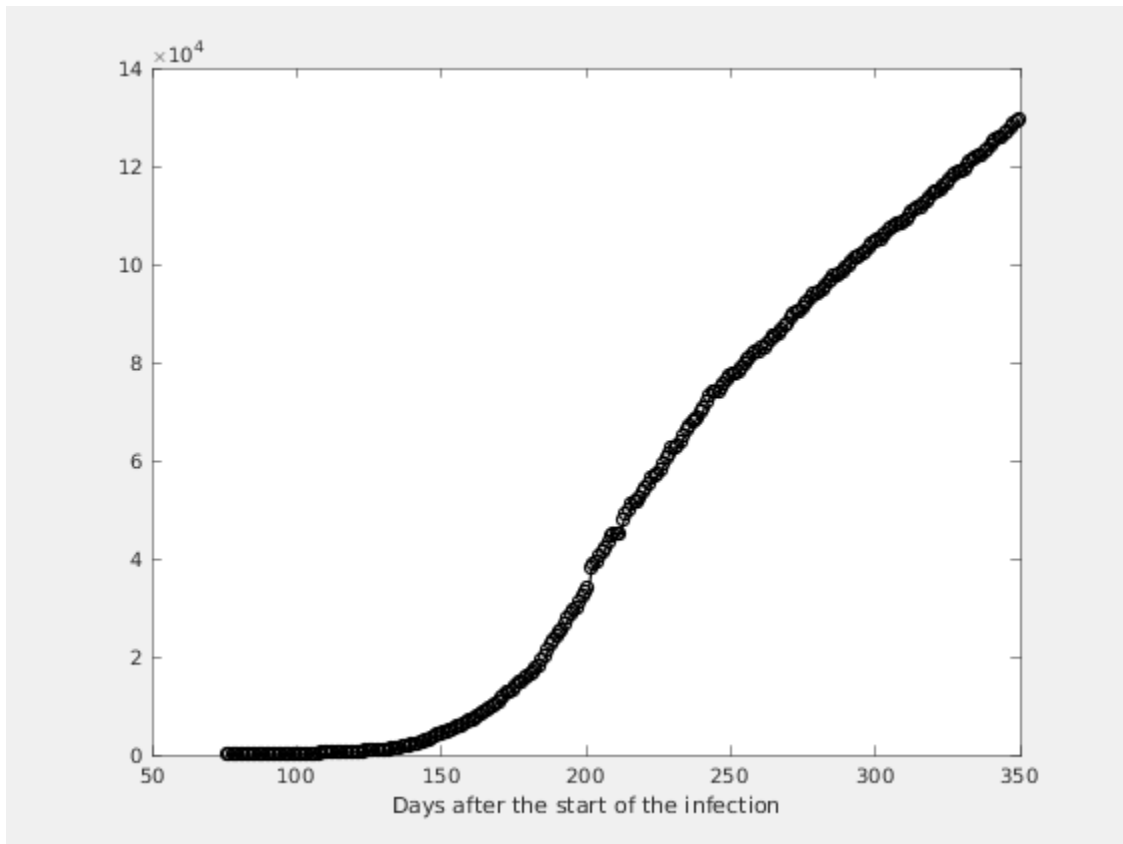
---

# 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

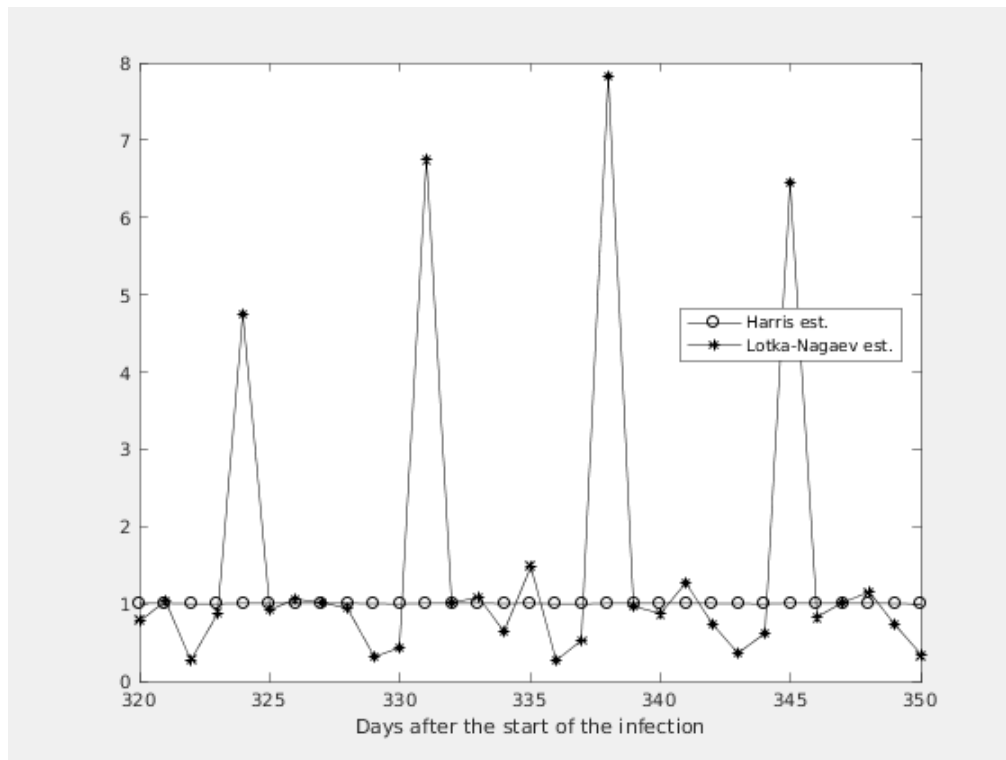
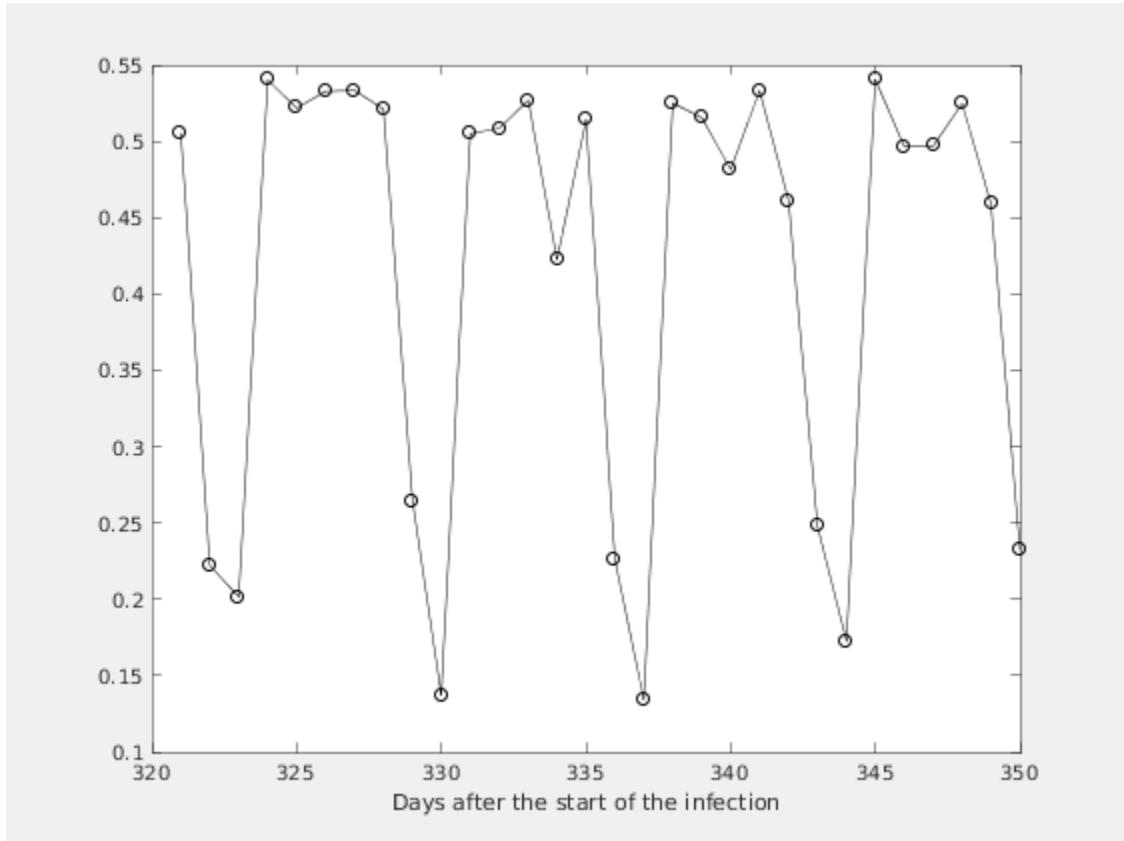
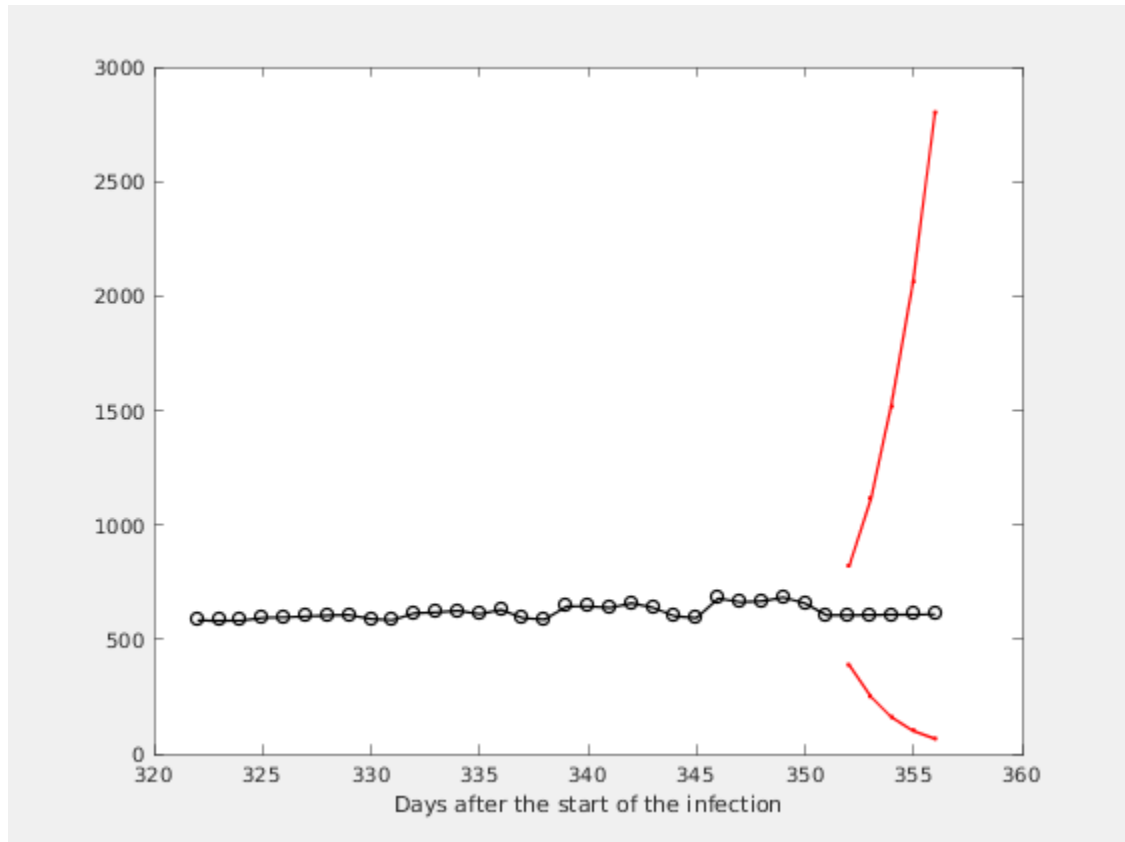


Figure 2.2. Figure

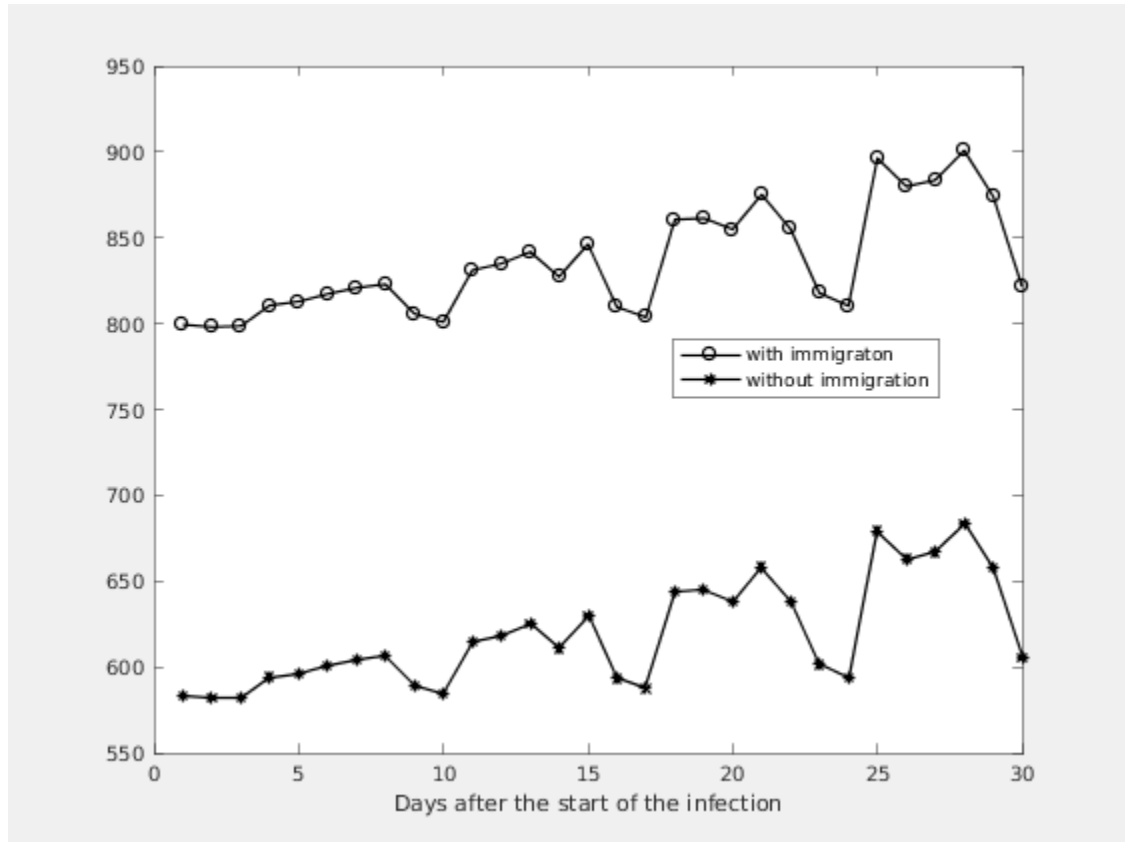




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	M1	A1
4	1.0052	0.6393 - 1.3710	0.1728	594	810
3	1.0052	0.6396 - 1.3708	0.5404	679	896
2	1.0059	0.6422 - 1.3696	0.4965	663	880
1	1.0043	0.6422 - 1.3665	0.4971	667	884
0	1.0014	0.6409 - 1.3619	0.5247	684	901