

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

**SanMarino - week 53**

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## **Branching stochastic processes as models of Covid-19 epidemic development : SanMarino - week 53**

### **Abstract**

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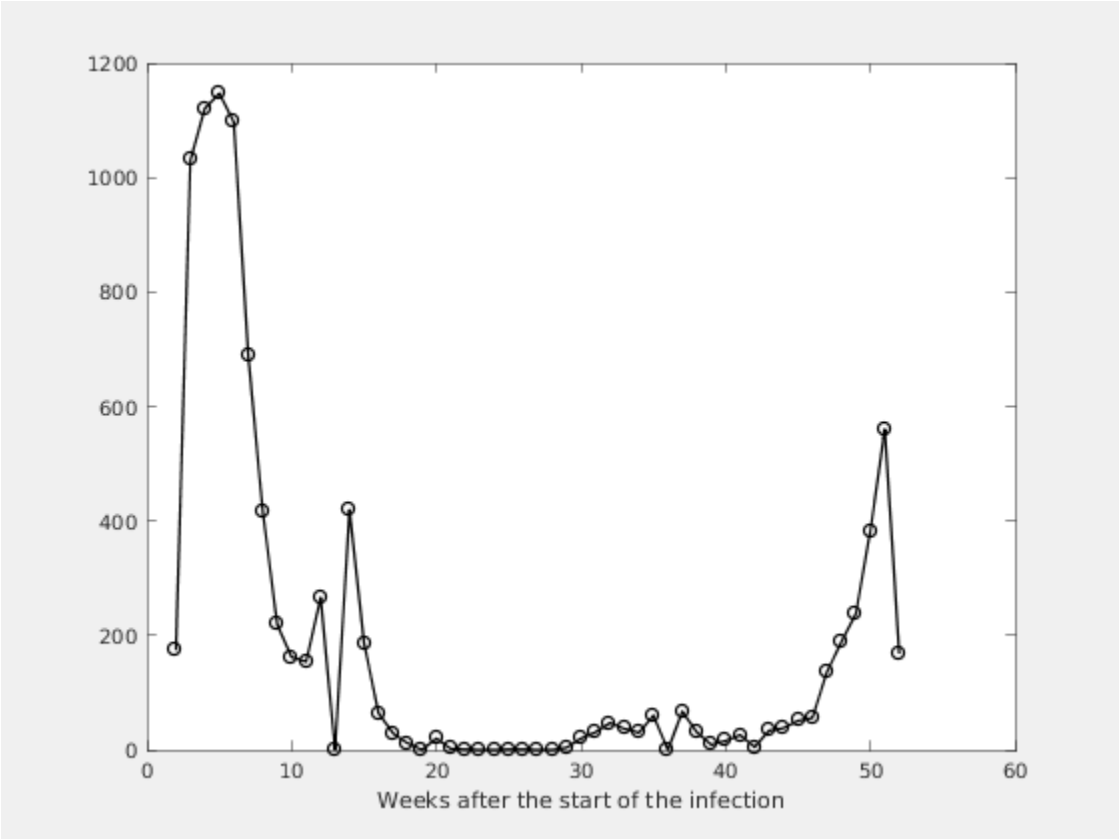
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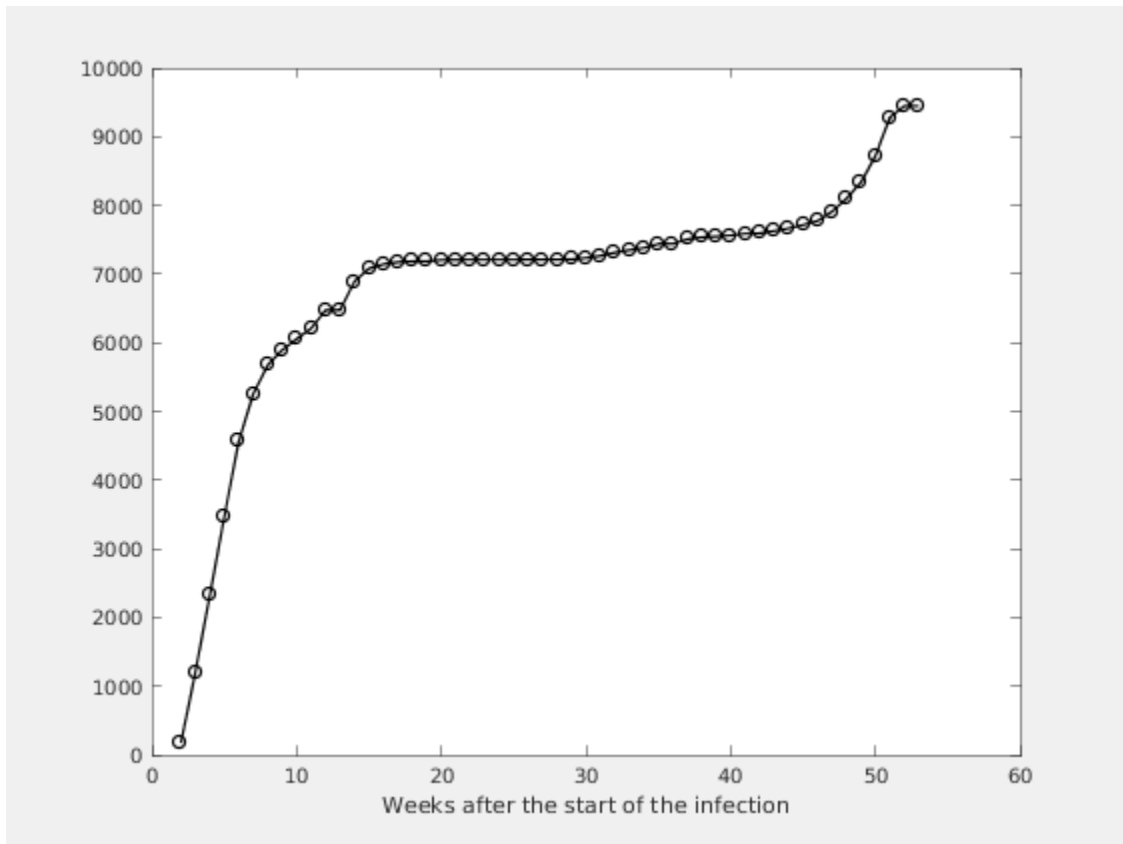
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# Chapter 1. Observed Infection data

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

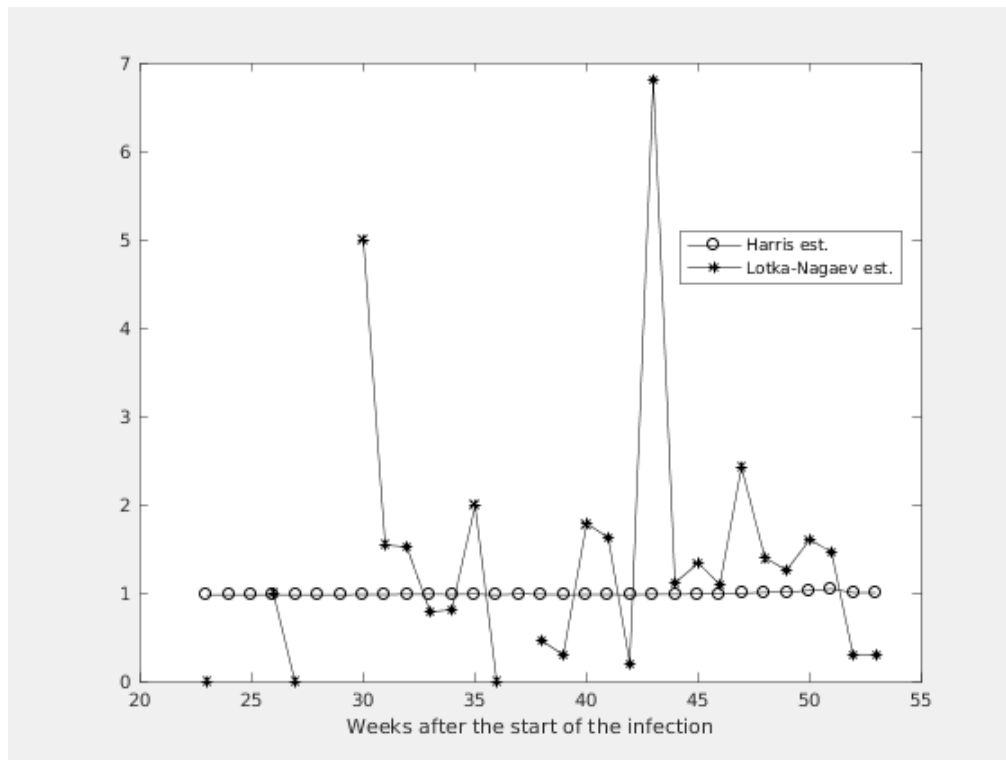
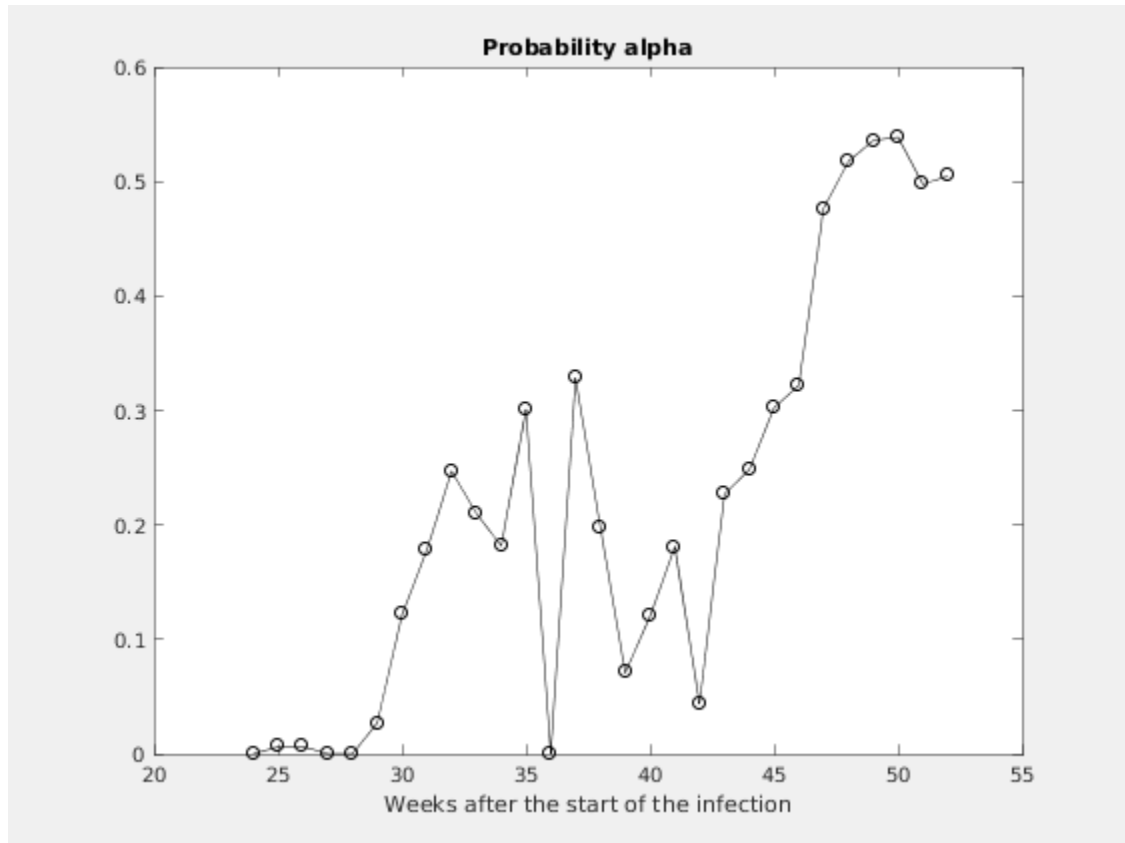
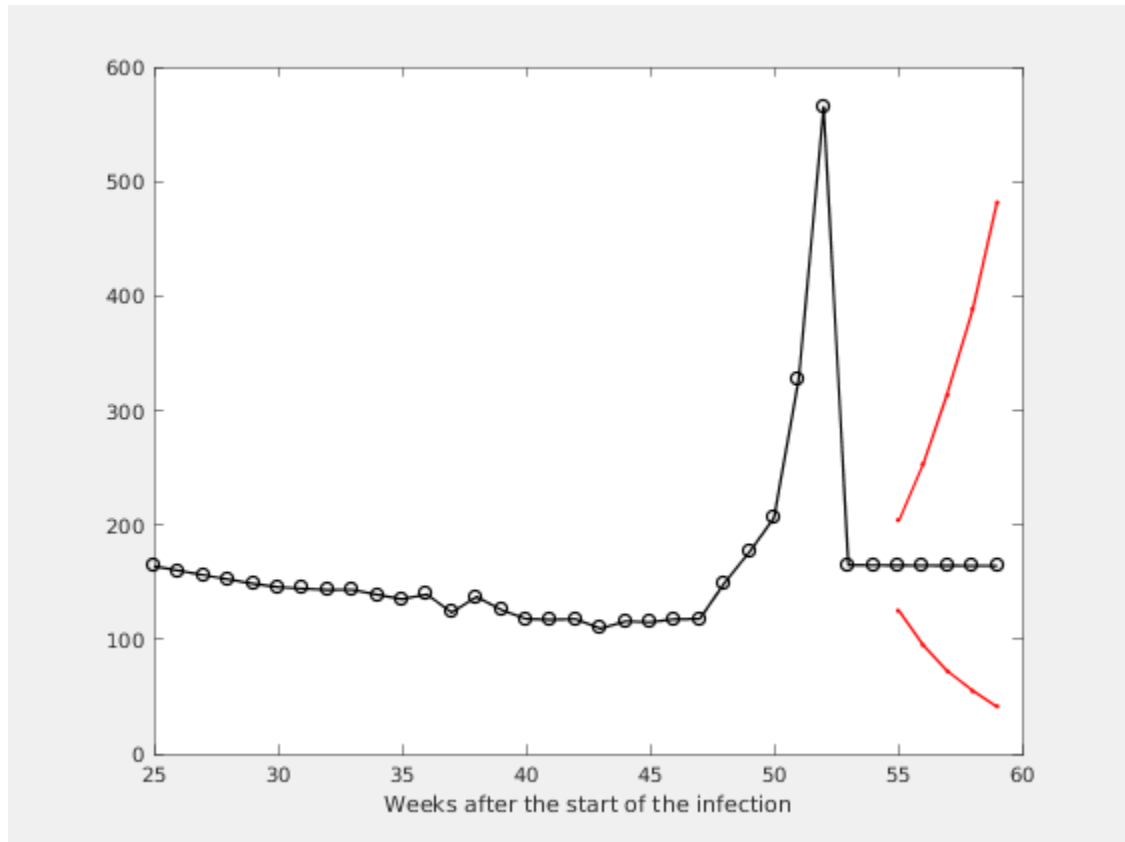


Figure 2.2. Figure

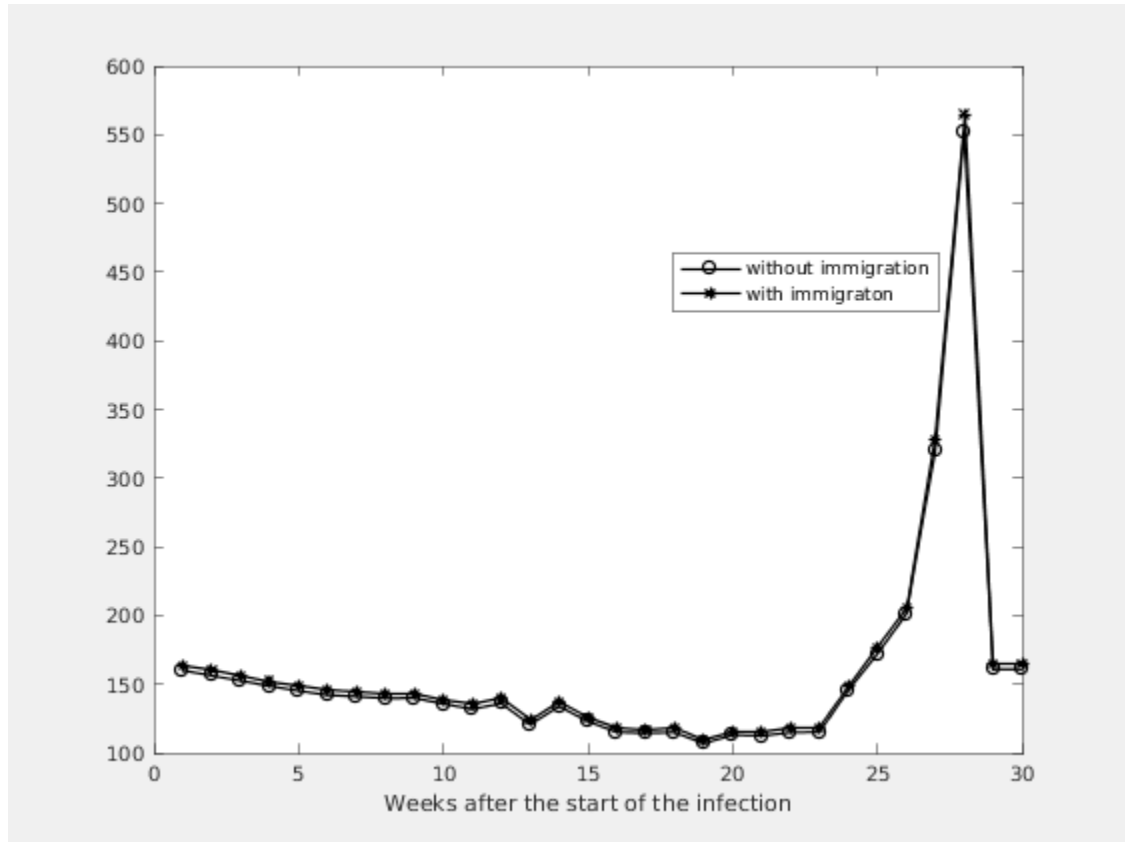




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	A1	M1
4	1.0079	0.7404 - 1.2754	0.4766	149	146
3	1.0251	0.7627 - 1.2874	0.5176	176	172
2	1.0443	0.7878 - 1.3007	0.5359	206	201
1	0.9994	0.7479 - 1.2508	0.5388	328	320
0	0.9994	0.7547 - 1.2440	0.4978	565	551