

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

**Mozambique - 20201214**

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

### **Abstract**

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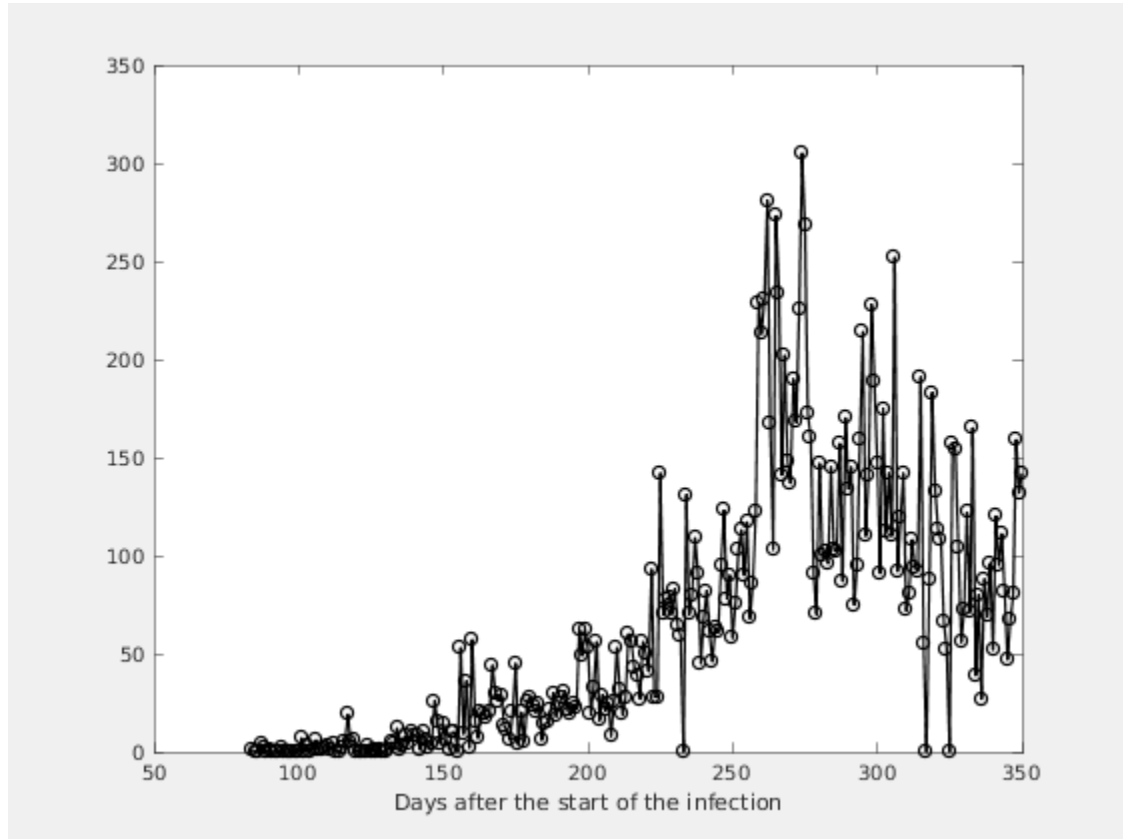
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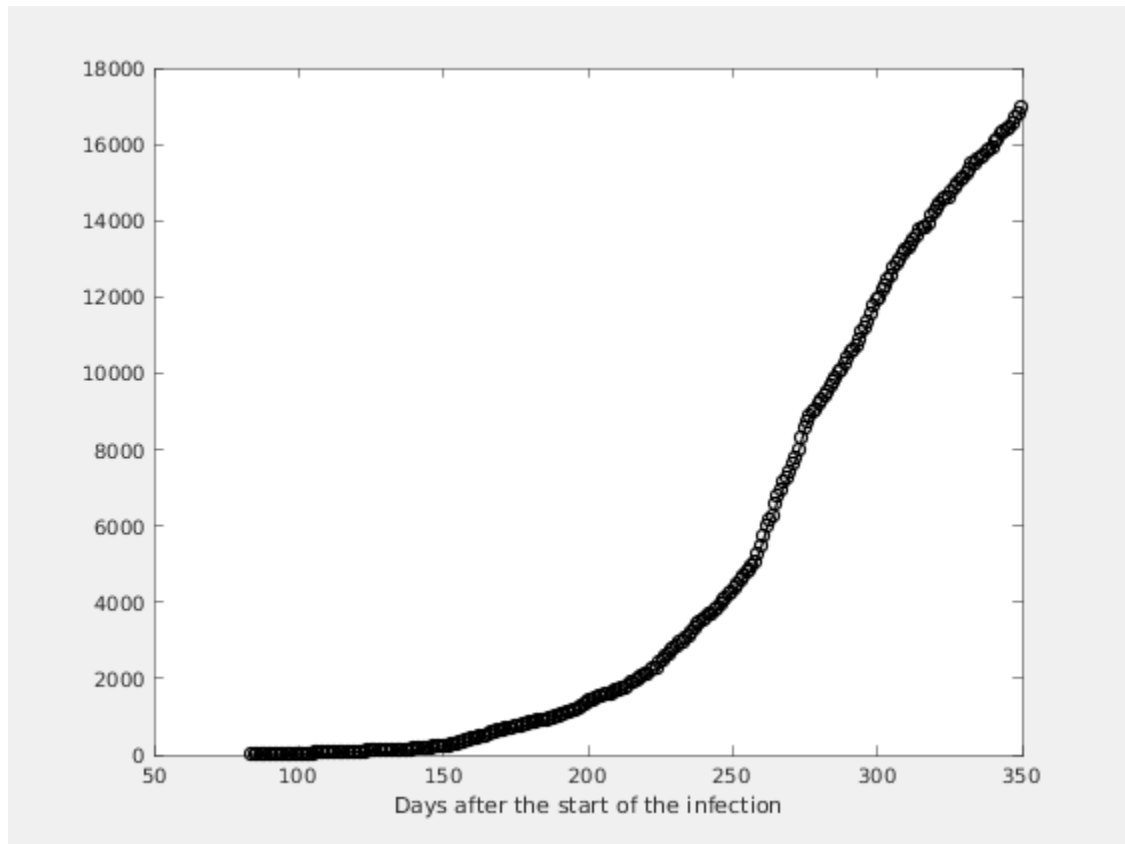
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# Chapter 1. Observed Infection data

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

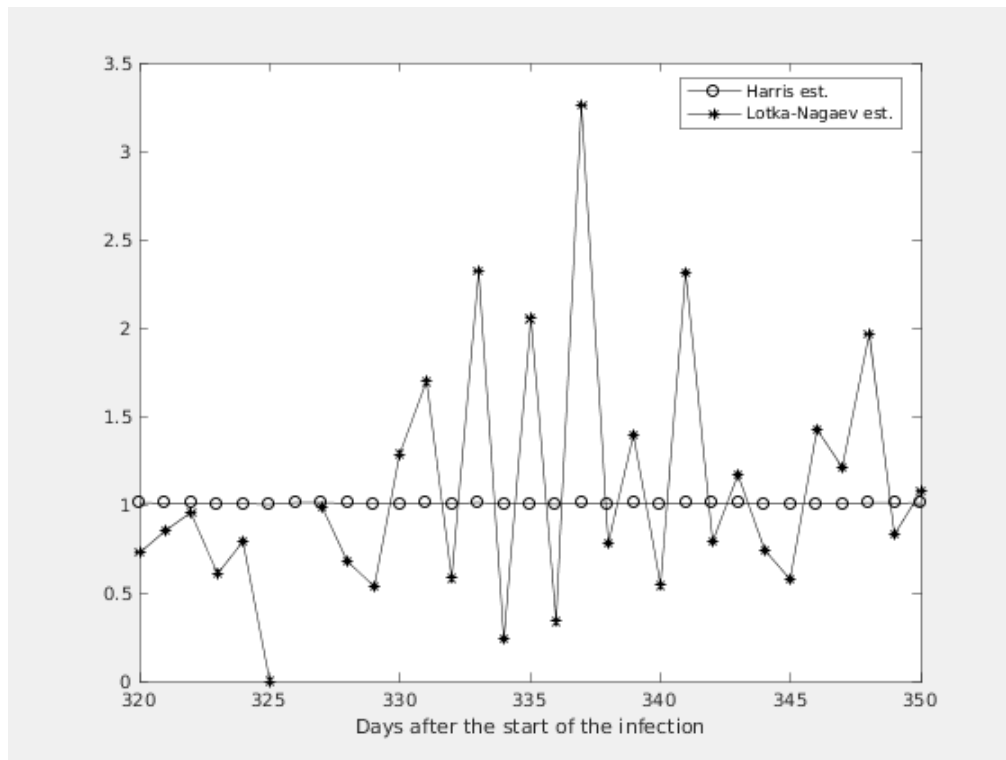
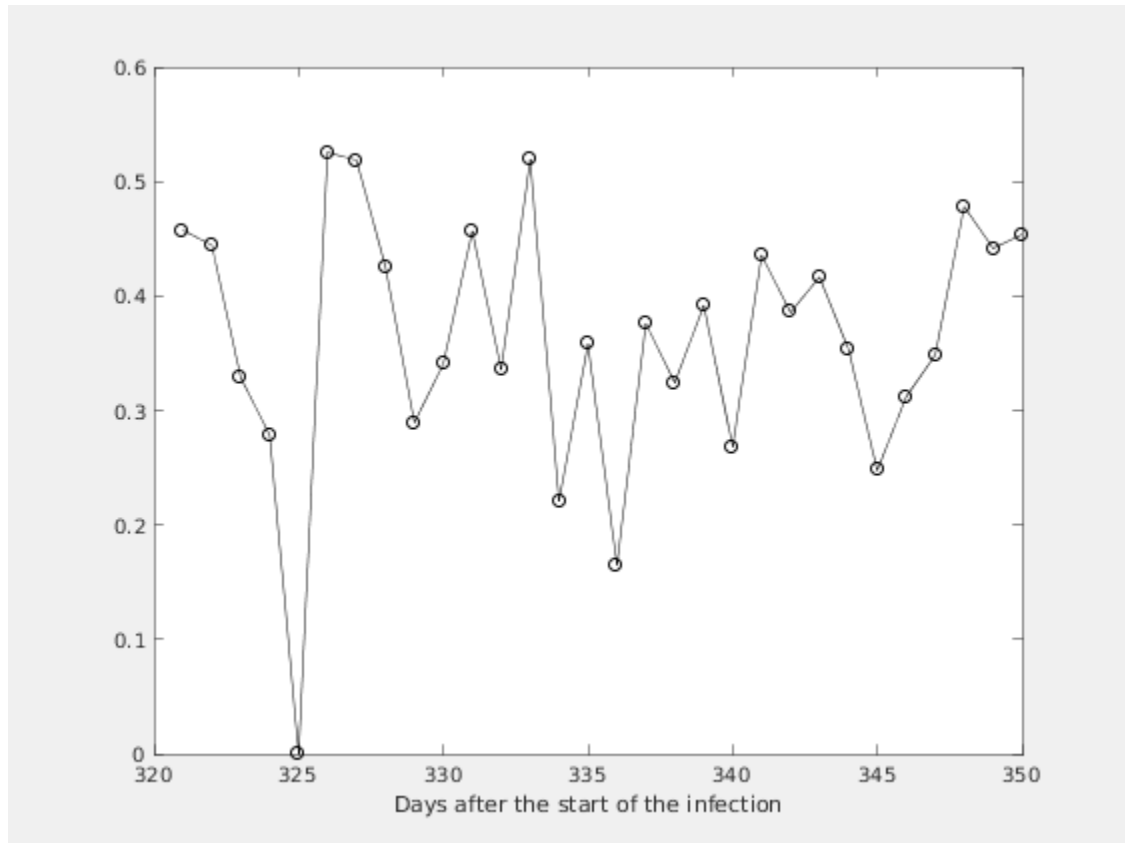
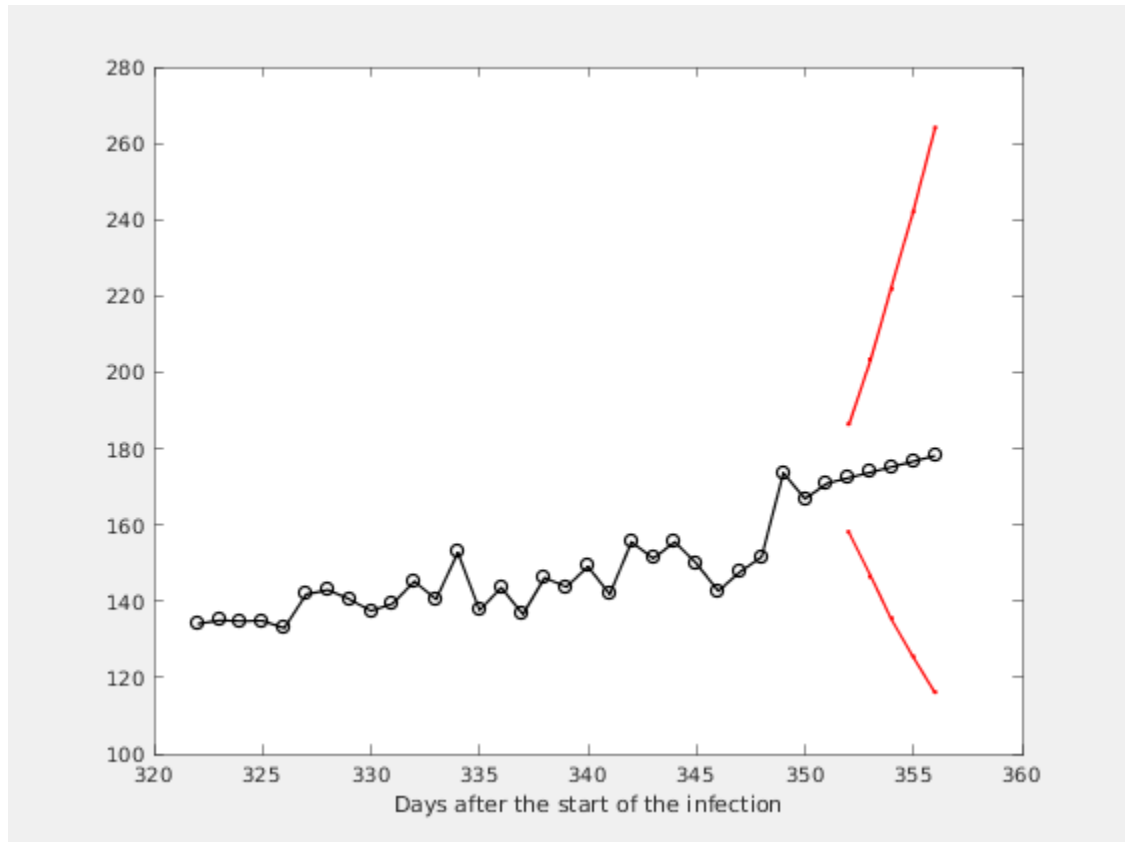


Figure 2.2. Figure

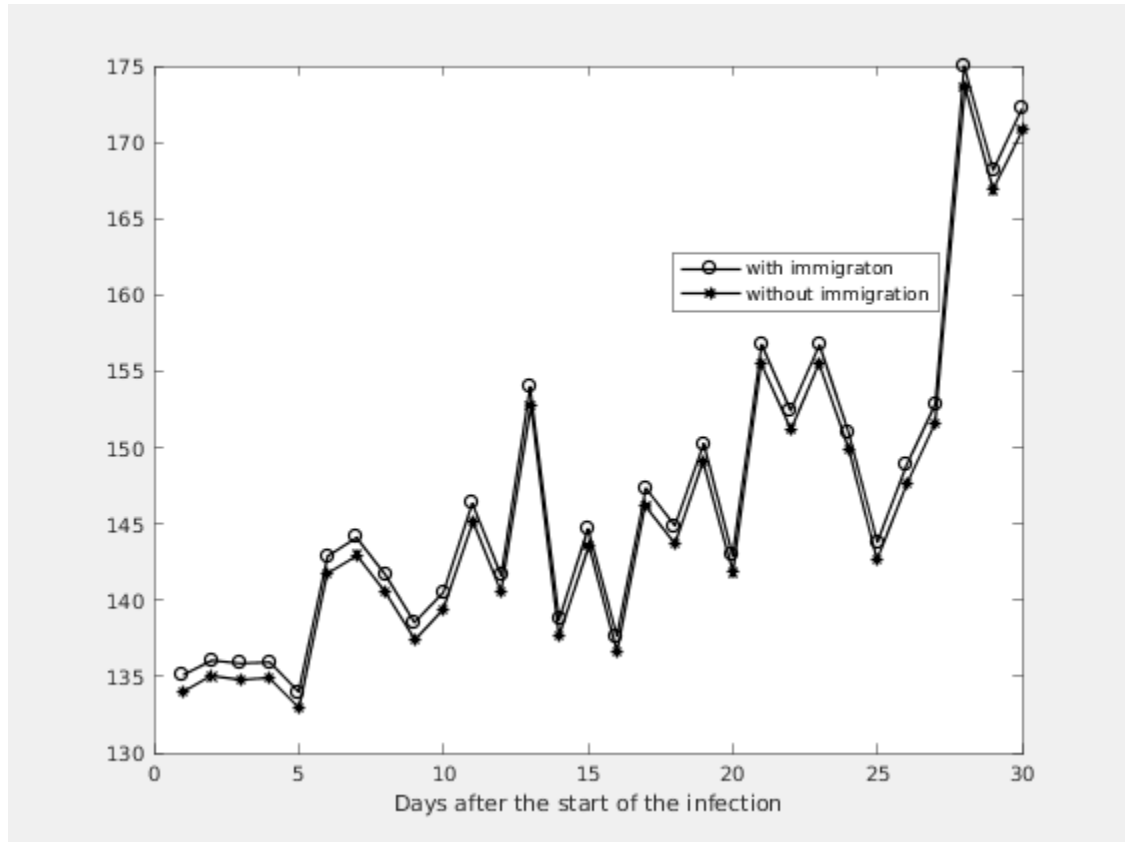




**Figure 2.3. Expected number of the nonregistered infected individuals without immigration**



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



**Estimation of the model parameters.**

k	m	ci	alpha	M1	A1
4	1.0040	0.9195 - 1.0886	0.3537	150	151
3	1.0049	0.9206 - 1.0891	0.2478	143	144
2	1.0096	0.9256 - 1.0935	0.3121	148	149
1	1.0079	0.9242 - 1.0915	0.3482	152	153
0	1.0084	0.9247 - 1.0921	0.4780	174	175