
This is the **published version** of the bachelor thesis:

Gensana Claus, Carla; Santos Maroño, Mauro, dir. Spatial variation of covid19 spread in Spain analysed by compartmental modelling. 2021. (812 Grau en Biologia)

This version is available at <https://ddd.uab.cat/record/248540>

under the terms of the  license



MAX-PLANCK-GESELLSCHAFT

SPATIAL VARIATION OF COVID19 SPREAD IN SPAIN ANALYSED BY COMPARTMENTAL MODELLING

UAB

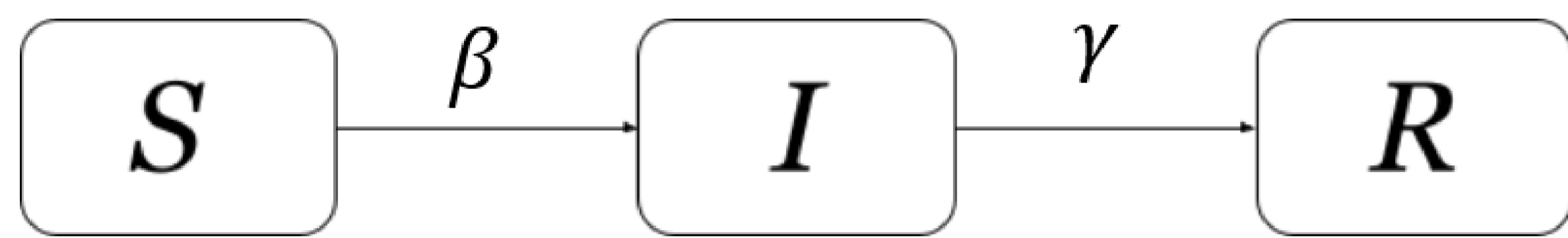
Universitat Autònoma de Barcelona

Carla Gensana Claus

Bachelors degree in Biology

INTRODUCTION

$$\begin{cases} S &= -\beta \cdot \frac{S}{N} \cdot I \\ I &= \beta \cdot \frac{S}{N} \cdot I - \gamma \cdot I \\ R &= \gamma \cdot I \end{cases}$$

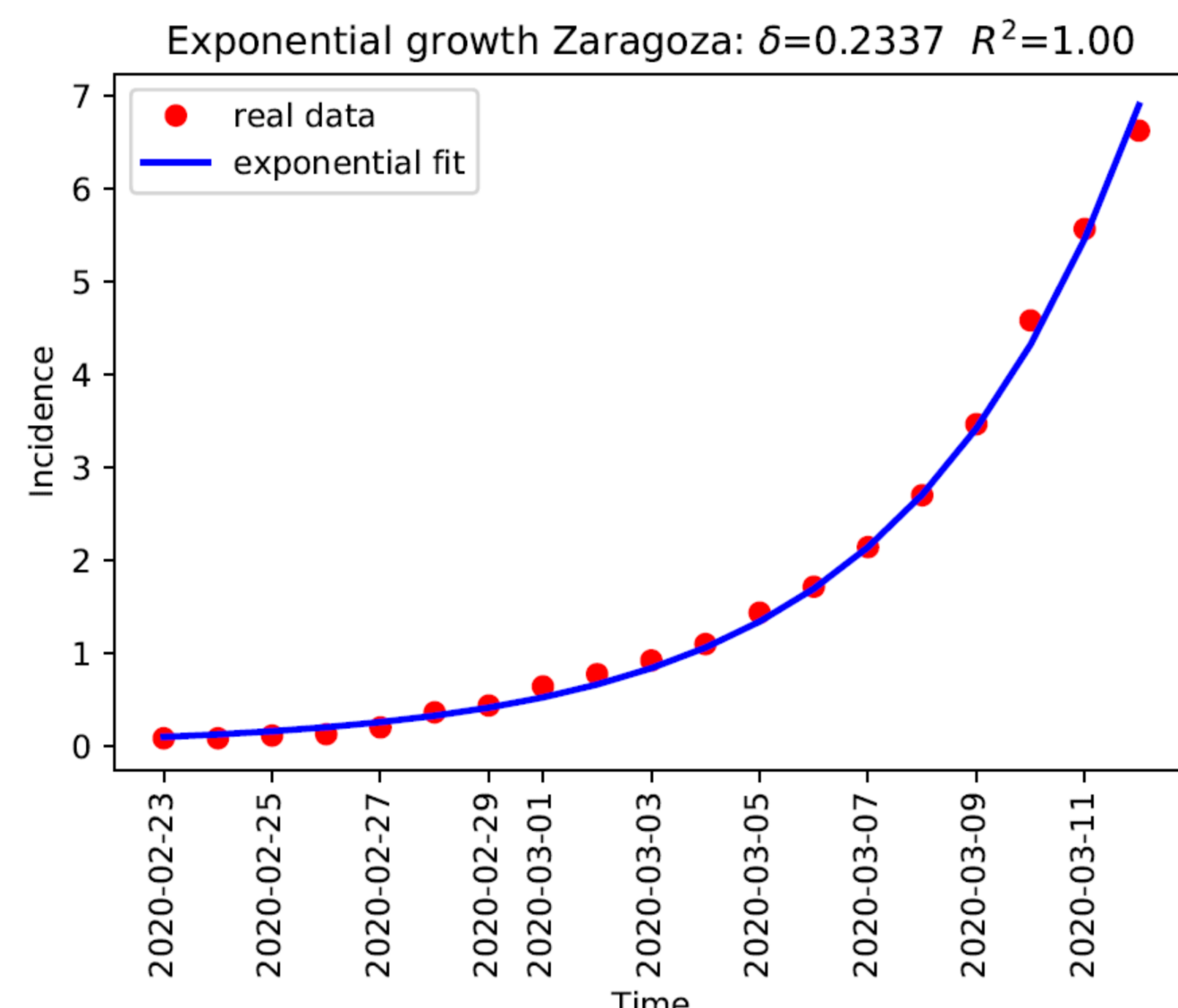
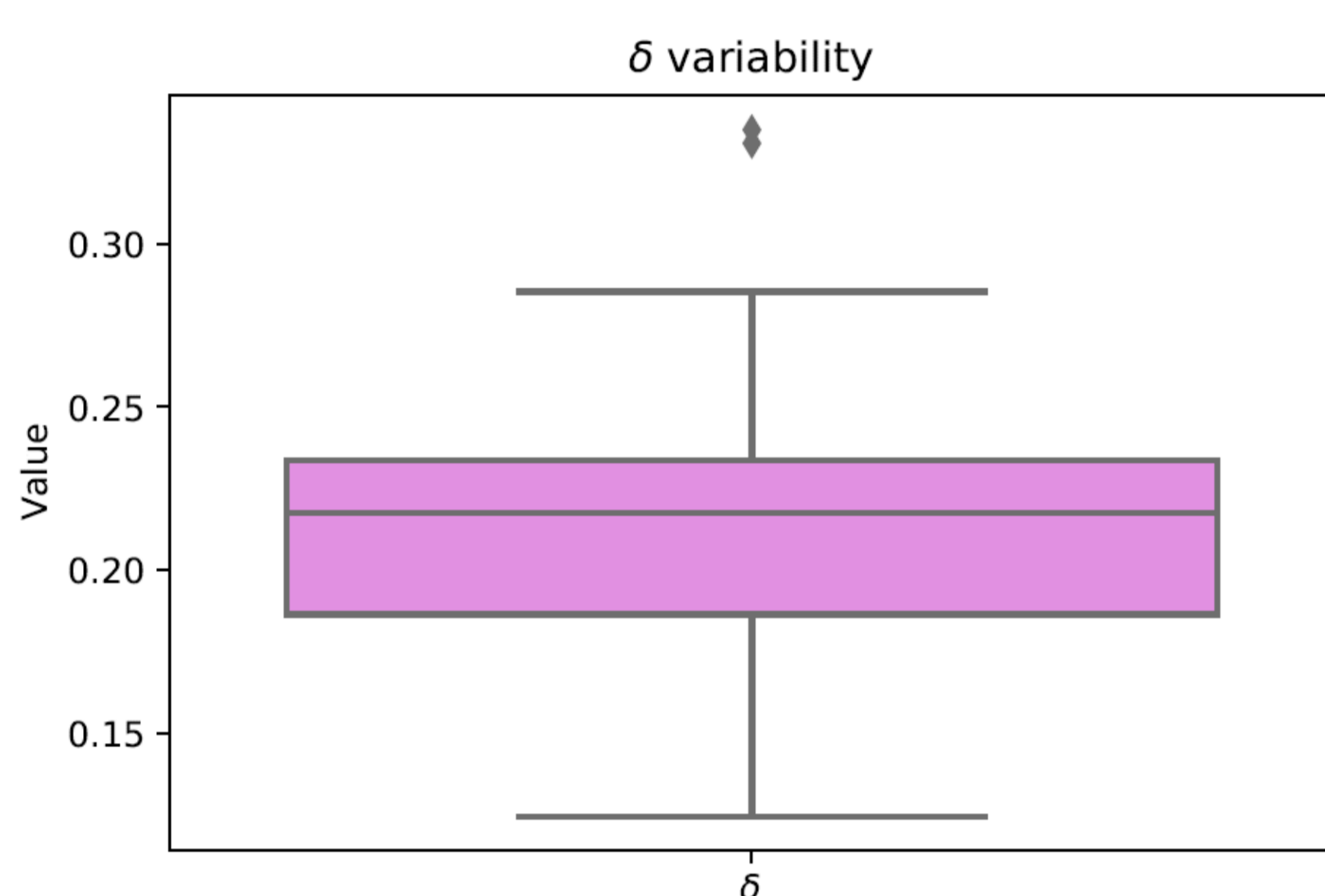


Most epidemiological modelling is done at a national level, assuming that the whole country is homogeneous. This may be problematic for large territories where the interaction networks can differ greatly between regions. For this reason, I decided to study this spatial variability by applying a simple model, the SIR, at a scale smaller than the whole country - the Spanish provinces - and comparing the spread dynamics in different locations.

In the SIR model, healthy individuals are classified in the susceptible (S) state. When a susceptible individual is in contact with an infected one, which happens with rate β known as the **effective contact rate**, it becomes infected (I).

After that they can either die or recover with lifelong immunity, which is represented by the removed (R) compartment. The rate at which people leave the I compartment to enter the R is called **removal rate** and it is denoted as γ ^{[1][2]}.

Q1. WHAT HAPPENED AT THE BEGINNING?

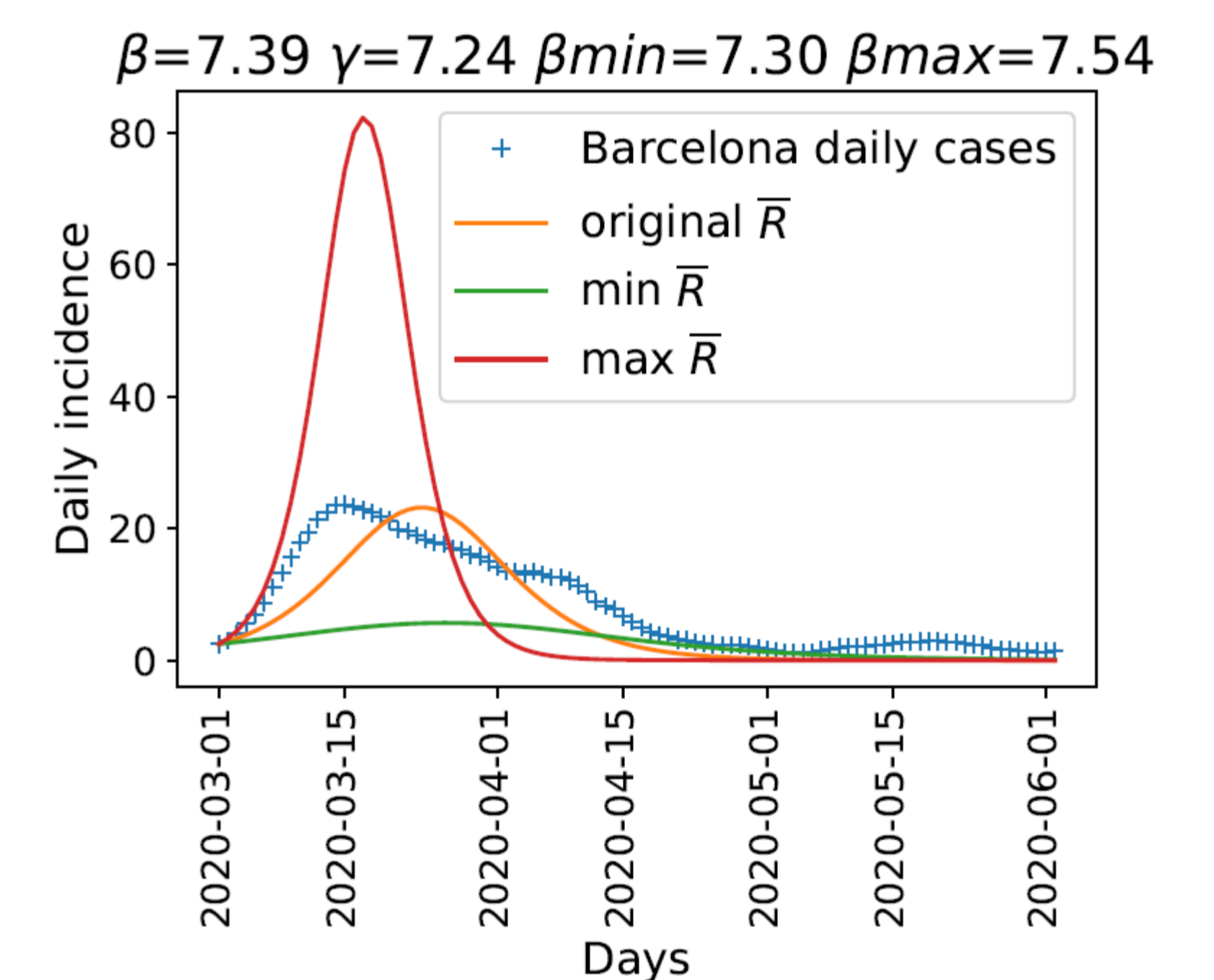
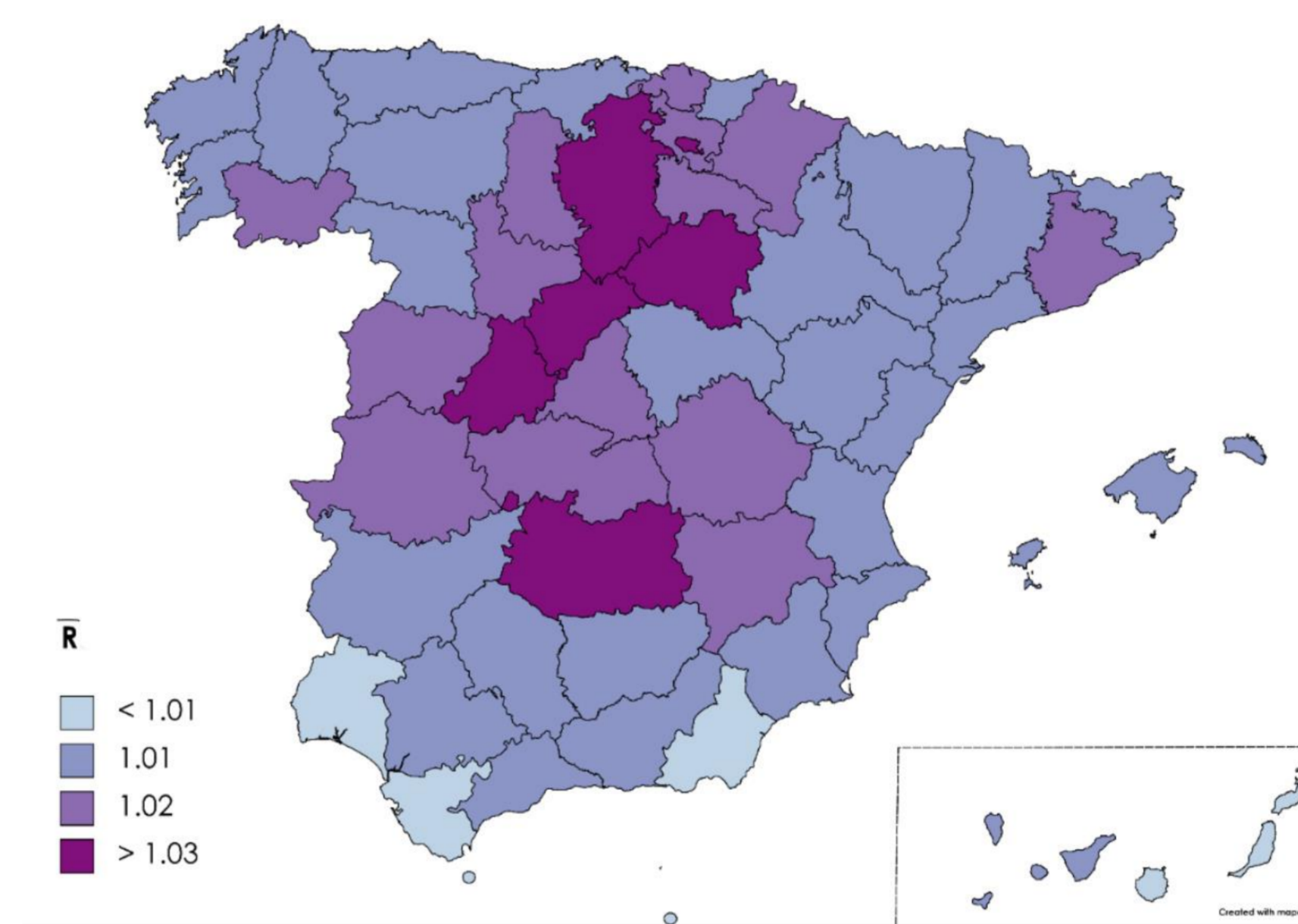


I plotted the data in function of time for most of the provinces between dates 20th of February and 1st of March.

At the beginning of the pandemic, there were no non-pharmaceutical interventions that could try to stop the spread of the disease. At that moment, almost all the population is susceptible, thus, the differential equation for the I compartment can be simplified to an exponential.

Nonetheless, exponential growth does not give enough information about what happens next. In order to know that, the SIR model should be applied.

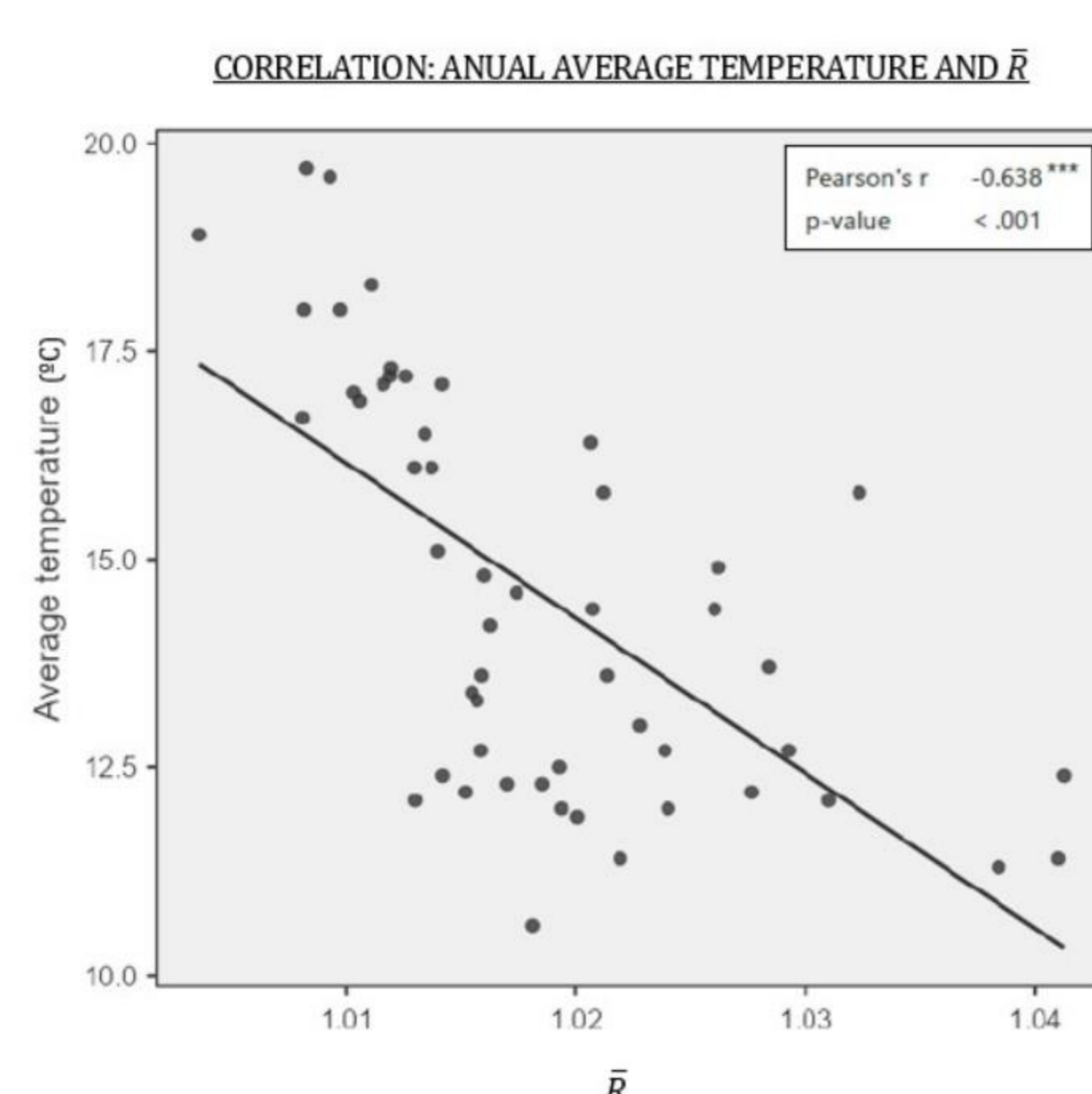
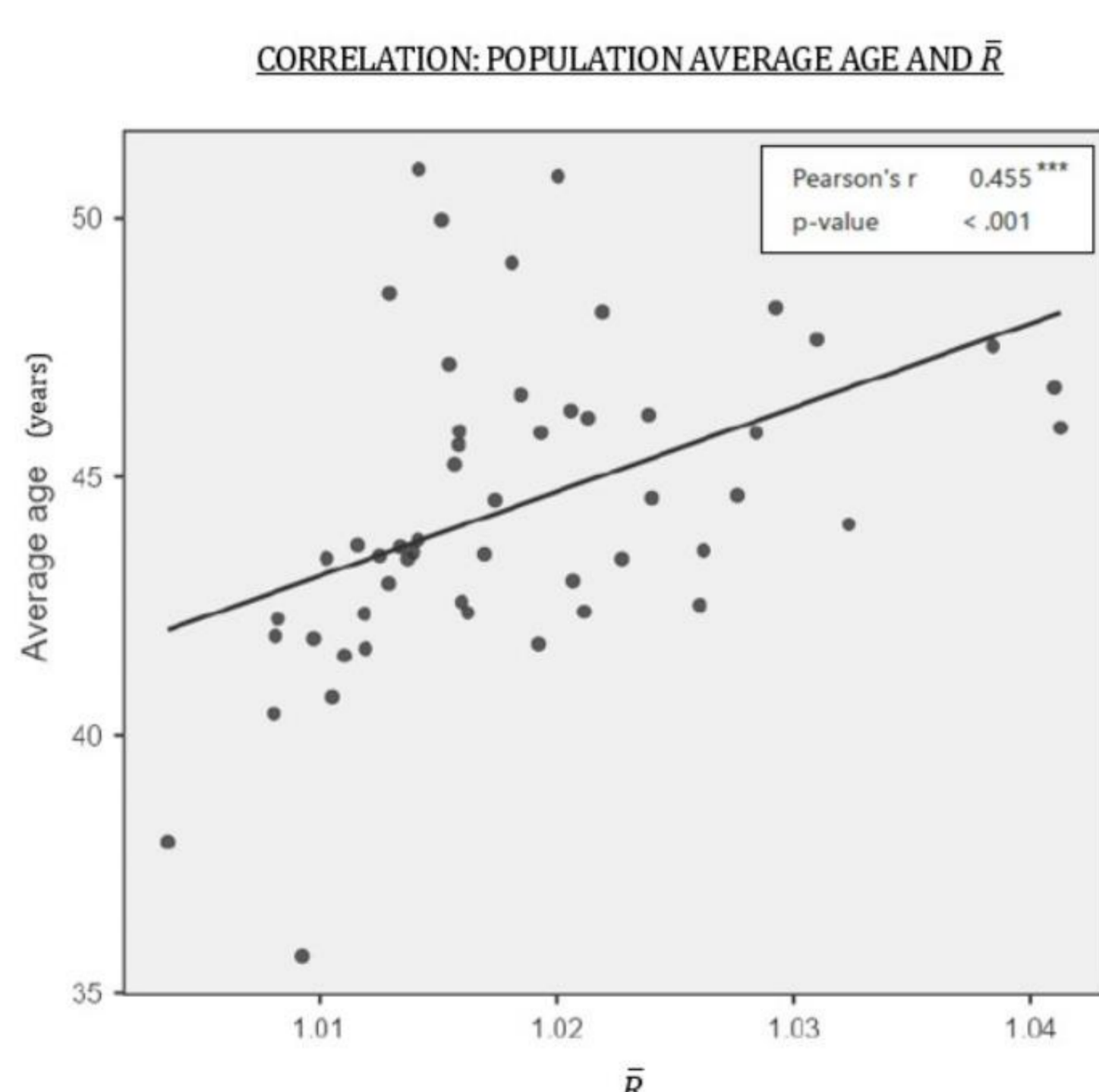
Q2. WHAT WOULD HAVE HAPPENED IF ALL PROVINCES HAD THE SAME SPREAD DYNAMICS?



The relationship between β and γ is called R_0 , as we consider constant parameters, we call it \bar{R} . To illustrate the amplitude of different disease propagation dynamics across Spain I show the number of cases if the whole country would have followed a dynamic described by the largest and lowest of the \bar{R} fitted from different provinces.

As an example, if Barcelona had the maximum \bar{R} (Segovia's) at the moment the confinement took place; its incidence would be around 80 people for 100.000 inhabitants which means that, at the peak, it would have had approximately 4500 new infections in a single day. Compared to the real data this is an increase of more than 3200 daily cases.

Q3. WHAT FACTORS COULD HAVE AN INFLUENCE ON \bar{R} ?



Potential factors that could explain the parameter distributions across the map of Spain were: population density, average age, temperature and annual rains.

Correlations were found only with average age and temperature. The former showed a strong positive correlation which could be an indicator that the disease affected more older people.

A negative correlation was found with both maxima and average temperature. In winter the nasal mucosa structure changes which could make it more susceptible to viral infections.

CONCLUSIONS AND PERSPECTIVES

The analysis of Spain COVID data reveals that there is some spatial variability between the different provinces of Spain in the way the epidemic propagated locally. Even though the \bar{R} differences between provinces are not big, its impact can be very important.

Nonetheless, the conclusions drawn from this analysis should be considered with caution. Indeed, the basic SIR model with constant parameters is too simple to represent an accurate description of this pandemic. In particular, this model does not consider confinement or other non-pharmaceutical interventions that changed the situation dramatically.

This measures are the responsible for the observed decrease of cases, which is fundamentally different from what is usually described with a simple SIR model as, in this case, the decrease results from reaching herd immunity.

REFERENCES

- [1] "Modelling COVID-19-SIR model," 2021. [Online]. Available: <https://sites.google.com/umich.edu/manymodelscovid19/home/the-models-of-covid-19/sir-model>
- [2] F. Brauer, *Compartmental Models in Epidemiology. Lecture notes in Mathematics*, 2008.