A Branching Process Model for the Novel Coronavirus (Covid-19) Spread in Greece

Ioanna A. Mitrofani and Vasilis P. Koutras

Abstract—**The novel coronavirus (covid-19) was initially identified at the end of 2019 and caused a global health care crisis. The increased transmissibility of the virus, that led to high mortality, raises the interest of scientists worldwide. Thus, various methods and models have been extensively discussed, so to study and control covid-19 transmission. Mathematical modeling constitutes an important tool to estimate key parameters of the transmission and predict the dynamic of the virus. More precisely, in the relevant literature, epidemiology is considered as a classical application area of branching processes, which are stochastic individual-based processes. In this paper, we develop a classical Galton-Watson branching process approach for the covid-19 spread in Greece at the early stage. This approach is structured in two parts, initial and latter transmission stages, so to provide a comprehensive view of the virus spread through basic and effective reproduction numbers respectively, along with the probability of an outbreak. Additionally, the effectiveness of control measures is discussed, based on a simple exponential smoothing model, which is used to build a non-mitigation scenario. Finally, our primary aim is to model all transmission stages through branching processes in order to analyze the first semiannual spread of the ongoing coronavirus pandemic in the region of Greece.**

Index Terms—**Branching processes, Covid-19, forecasting, mathematical modeling, pandemic.**

I. INTRODUCTION

Coronavirus disease 2019 (covid-19) is an infectious disease caused by severe acute respiratory syndrome (SARS). It was initially detected in December 2019 and has been rapidly spread globally inducing the ongoing pandemic [1]. This novel coronavirus pandemic is deliberated as the biggest worldwide threat and on January 30th, 2020 World Health Organization (WHO) advocated that this new situation is a Public Health Emergency of International Concern, because of the thousands infected cases that were reported and deaths around the globe [1], [2]. In particular, by April 1st, 2020, 872,481 confirmed cases and 43,275 deaths were reported [2]. The first case in Greece was confirmed on February 26th (2020) and by April 21st, 2,401 cases and 121 deaths were reported, even though health and state authorities had applied small-scale control measures, such as the suspension of educational institutions and the closing of cafes, bars, restaurants sports facilities etc. [3]. On March 22nd, the Greek government announced a general lockdown with movement restrictions and after 42 days of quarantine, when the number of daily reported cases decreased to 10, state authorities gradually repealed the restrictions [3]. These control measures, that were among the strictest in Europe, were initially considered as highly effective and whereas the pandemic was internationally ongoing, the case of Greece was treated as a success story [4]. However, at the time of this revision the numbers have been increased to 82,034 total cases and 1,288 deaths. These fluctuations on numbers attract the interest of researchers to model the transmission of the virus to evaluate and quantify the dynamic of the pandemic [1].

Mathematical models of infectious disease transmission effectively describe and simply depict the evolution of diseases by providing quantitative data in epidemiology [2], [5], [6]. Moreover, using mathematical and statistical tools enables to conduct long or short-term forecasts about the spread in population so to support decisions of intervention strategies, outbreak and healthcare management and policy development [2], [5]-[7]. There exist several mathematical models in epidemiology, starting from the simple S-I-R models (Susceptible-Infected-Recovered models), to S-E-I-R models (Susceptible-Exposed-Infected-Recovered models), to more complex proposals [1], [5], [8]. A classical approach of data analytics of virus transmission is described by Galton-Watson branching process and a promising approach that uses advanced mathematical modelling to connect models with machine learning was introduced by Yang *et al.* [5], [9], [10]. However, the majority of analyses focus on human-to-human transmission and this implies two important limitations [5], [9], [11]:

1) Contact tracing data are required and data availability in such emerging cases is limited.
2) The assumption that transmission rates are considered as fixed for mathematical analysis simplicity seems unrealistic.

The main goal of this paper is to develop a simple mathematical model using branching processes in order to analyze the initial and latter stages of the outbreak of covid-19 in Greece and evaluate crucial epidemiological indicators such as the reproduction number and the probability of extinction of the transmission. Finally, through an exponential smoothing model, in a complete absence of control measures a scenario is developed in order to effectively describe the virus transmission in case of Greece and discuss the effectiveness of control measures.

II. EPIDEMIOLOGY MODELS AND BRANCHING PROCESSES

In the relevant literature of mathematical modeling of populations considering epidemics, the deterministic models

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constitute powerful tools when the examined population is large enough. On the contrary, stochastic models can provide useful information when the population size is rather small [12]. The theory of branching processes is simple: these processes are often used to model physical systems in which a single-type individual lives for a unit of time and by its death produces n identical copies of itself. More complex extensions of that simple process are for instance the multi-type branching processes [13]. The specific construction of the aforementioned process justifies that these processes are usually applied in biology, physics and epidemiology. So, any individual gives rise to a family size, where family sizes are independent and identically distributed (i.i.d) random variables [14].

Considering populations, two major issues are important: the expected number of population size and the extinction [13], [14]. If d_k is the probability of extinction at the k^{th}-time period, then the smallest positive root of the probability generating function $h(d) = d$ as d_k tends to d, is detected as the probability of ultimate extinction d. In addition, the first derivate of the probability generating function, that is usually formed as $Q(s) = q_k s^k$, is used to calculate the expected number of population size (m) [13], [14]. According to the relevant literature, the expected size of a population (m) could be used as a measure to categorize a branching process into cases and predict the future condition of the system, as follows: If $m > 1$ then $d < 1$: extinction is not guaranteed (supercritical case), if $m < 1$, then $d = 1$: extinction is guaranteed (sub-critical case) and finally if $m = 1$, then $d = 1$: extinction is not guaranteed unless the family size equals 1 (critical case) [14], [13].

S-I-R and S-E-I-R models are two of the basic models for infectious diseases and commonly the branching theory is attached to these models in order to extract useful information about populations such as the probability of transmission extinction or the probability of an outbreak [12]. More specifically, a simple single-type branching process could be applied in a S-I-R model in the infectious stage as a birth-death process [12]. In a S-I-R model, initially the entire closed population (N) is considered as totally susceptible (S), a small number of initially infectious individuals introduced into the large susceptible population and cause an outbreak, thus some individuals become infected and infectious (I), and R means that these individuals are removed from the population either by recovery or death [12], [15]. Some of the limitations of this approximation is the immunity assumption and the uncertainty based on data [12], [16].

A related to S-I-R model is an S-E-I-R model, in which E represents the exposed population and implies the assumption of a delay between the exposure and the infectiousness [16]. An S-E-I-R epidemic could be modeled as a multi-type branching process and through the probability generating functions, the probability of an outbreak can be estimated [12]. According to [17], where a mathematical model for the early dynamics of transmission of covid-19 was presented, a major limitation of that kind of approaches is the uncertainty based on data. However, S-E-I-R models although that are more complex compared to S-I-R models, remain simple and provide reliable information about the potential spread of a pandemic disease such as the Severe Acute Respiratory Syndrome (SARS) [12].

The relevant literature of branching processes-based epidemiology models consists of variable complexity models, however data availability in such emerging situations commonly limits the selection power and leads to simple approaches. The next section provides a branching process epidemiology model.

III. MATHEMATICAL MODELING AND FORMULATION

A branching process approach is considered as classical approximation for epidemics [18]. In addition, whereas the number of infected people is small, it is believed that people behave independently, hence branching processes can sufficiently model early stages of an epidemic [18]. If an infected individual causes $0, 1, 2, \dots$ new infections with probabilities $q_0, q_1, q_2, \dots$, then the progeny generating function is formed as $Q(s) = q_k s^k$ and represents the offspring distribution, where q_k is the probability that an infected individual causes k new infections, in a total susceptible population, before s/he dies or recovers from the infection [18], [19]. It is proven that a two-parameter offspring distribution is more beneficial over one-parameter distribution to model large datasets of infectious diseases, because in such a case the model depicts better the actual transmission of the virus assuming the adaption of the parameters [20]. Thus, generally it is considered that the offspring distribution is a negative binomial distribution with parameters (R_0, k) [21], [22]. To that side, assuming that variable X refers to a sample of counts of infected cases, the pdf of X is formed as shown in (1) and consequently the progeny function is formed as shown in (2) ([21], [22]):

$$P(X = x) = \frac{\Gamma(x+k)}{x!\Gamma(k)}\left(\frac{R_0}{R_0+k}\right)^x \left(\frac{k}{R_0+k}\right)^k \tag{1}$$

$$with\ \Gamma(z) = \int_0^\infty e^{-t} t^{z-1} dt$$

$$Q(z) = (1 + \frac{R_0}{k}(1 - z))^{-k} \tag{2}$$

where, the basic reproduction number, R_0, is the average number of secondary cases infected by one individual in a total susceptible population, and k is the dispersion parameter which measures the transmission heterogeneity of the virus [23]. In fact, the dispersion parameter as a transmission heterogeneity measure, quantifies the variability in the number of secondary cases and could be described as a measure for the impact of the superspreading events (lower values of k signifies higher heterogeneity and higher impact of superspreading events) [23], [24]. However, according to the relevant literature, the offspring distribution is additionally formed as a Poisson or a geometric distribution, which are nested cases of the negative binomial distribution, with $k \to \infty$ and $k \to 1$ respectively [21], [25].

As it is already mentioned, the expected number of population size and the probability of extinction are considered as crucial information about the evolution of a population. Moreover, taking into account that we focus on the spread of a disease, the expected number of population size stands for R_0 and the probability of extinction refers to the extinction of transmission. Thus, if z is the extinction probability, then (1-z) is the probability of an outbreak. According to branching processes theory, in order to estimate the probability of ultimate extinction z, we need to solve Equation (3):

$$Q(z) = z \tag{3}$$

Since we are interested in the probability of extinction, z is detected as the smallest positive root of (3) and the derivate of the probability generating function is used to calculate the expected population size. However, in order to compute the probability of extinction, we need to estimate the parameters R_0 and k firstly, because these parameters are critical elements of the probability generating function (1), and secondly because R_0 is a typical threshold to detect the transmissibility and determines the epidemic potentiality of virus in the absence of control measures [26]. More precisely, if the basic reproduction number is $R_0 > 1$, in a total susceptible population, then eventually an epidemic occurs; contrariwise, if $R_0 < 1$, the transmission is self-limited and if $R_0 = 1$, the state is characterized as endemic (endemic equilibrium) [27], [28].

Similar to the basic reproduction number R_0, R_{eff} is the effective reproduction number, that represents the average number of secondary infected cases under control measures [26]. Likewise R_0, R_{eff} determines the epidemic potentiality of virus, but under control measures. Consider an epidemic scenario where an outbreak of a virus starts. In the initial stages there is absence of mitigate interventions and as the transmission continues, the government decides to adapt control measures (such as quarantine or massive vaccination etc.) in order to limit the spread of the disease. In fact, the government attempts to reduce an $R_0 > 1$ to an $R_{eff} < 1$ to bring the outbreak under control. So, we can intuitively assume that as long as the basic reproduction number categorizes the spread of a virus as an epidemic or not, the effective reproduction number evaluates measures' effectiveness [26]. Despite the fact that the reproduction number is evaluated differently, the entire process for estimating the probability of ultimate extinction remains identical.

A. Estimating the Parameters: R_0, R_{eff}, k

Considering a population consisting of particles that are able to reproduce independently (offspring) and a typical predecessor i could produce N_i ancestors, then X_g is the size of g^{th} generation, where $g = 0, 1, 2, \dots, G$ for the first G generations and X_g can be computed as the sum of all offspring that each particle produced a generation before $\left(X_g = \sum_{i=0}^{X_{g-1}} N_i\right)$. Then, the described process is a discrete time branching process and N_i are independently and identically distributed (i.i.d) random variables. In addition, the process X_g, $\{X_g : g = 0, 1, 2, \dots, G\}$, has the Markov property, that is the value of X_g depends only on X_{g-1} [29]. One of the major properties that arises form branching process theory is that $R_0 = E[N_i]$. This property along with the Markovian property of the process lead to an efficient estimator for R_0, the Harris estimator [20], [29]:

$$\widehat{R_0} = \frac{\sum_{g=1}^{G} X_g}{\sum_{g=1}^{G} X_{g-1}} \tag{4}$$

However, in the relevant literature there exist several methods to estimate basic reproduction number R_0, such as the Maximum Likelihood Estimator (MLE) [30]. Despite the fact that the notions of R_{eff} and R_0 are close, their evaluation differs. In order to allow the calculation of R_{eff}, the referring population should be divided into chains or clusters of transmission and in some cases contacting data are needed [19]. Nevertheless, a common obstacle for researchers that conduct studies for diseases and spread of viruses such as the corona virus that causes severe respiratory syndrome (SARS), is the lack of data [11]. In this approach, due to limited data availability, we consider one cluster with a limited number of chains. Thus, we assume that the entire cluster has only one R_{eff} (and k, which constitute the cluster's parameters), is evaluated as follows:

$$R_{eff} = k\left(\frac{1}{p} - 1\right) \tag{5}$$

where k is the dispersion parameter and p is the scale parameter of the negative binomial distribution of X_g. The smoothest way to evaluate the parameters of a negative binomial distribution is by using the method of moments (Method of Moments Estimator-MME), where by equating the sample mean $\bar{y}$ to the population mean μ, and the sample variance S^2 to the population variance σ^2, the dispersion and scale parameter are estimated through data by solving (6) and (7) respectively [31]:

$$k = \frac{\bar{y}^2}{S^2 - \bar{y}} \tag{6}$$

$$p = \frac{S^2 - \bar{y}}{S^2} \tag{7}$$

Despite the fact that this approach simply and effectively evaluates dispersion parameter through data, it is proven that several limitations appear, such as [31]:

- If the sample variance is higher than the sample mean, then k is very large.
- If the sample variance is less than the sample mean, then k is negative.
- If the sample variance equals the sample mean, then k is not defined.

IV. THE CASE OF GREECE

The first imported case of COVID-19 in Greece was confirmed on February 26th, when an individual came back from a visit to Northern Italy. Most of the subsequent cases in February and early March were related to people that had been to Italy, Israel and Egypt or their contacts. Until the 22nd of March, when Greek government announced a general lockdown, 624 cases and 2 deaths were reported. The basic reproduction number in March 22nd was estimated to $R_0 = 1.18$ according to (3). Table I and Fig. 1 present all reproduction number from the 27th of February to the 22nd of March.

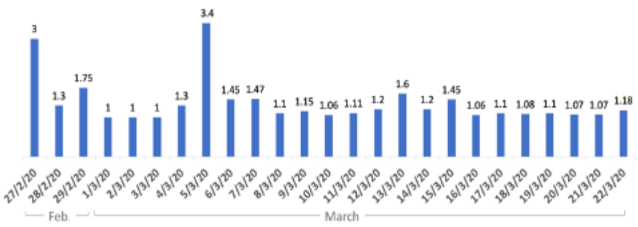

Fig. 1. Reproduction numbers from 27th February to March 22.

TABLE I: REPRODUCTION NUMBERS FROM 27TH FEBRUARY TO MARCH 23

Date	R_0	95% CI	k
27/2/20	3		0.74
28/2/20	1.33	(-1.06 , 3.72)	
29/2/20	1.75	(0.6 , 2.9)	
1/3/20	1	(-0.42 , 2.42)	
2/3/20	1	(0.01 - 2.01)	
3/3/20	1	(0.1 , 1.9)	
4/3/20	1.29	(-0.59 , 1.98)	
5/3/20	3.44	(-0.02 , 6.9)	
6/3/20	1.45	(-0.03 , 2.93)	
7/3/20	1.47	(0.14 , 2.79)	
8/3/20	1.1	(-0.38 , 2.58)	
9/3/20	1.15	(-0.15 , 2.45)	
10/3/20	1.06	(-0.23 , 2.35)	
11/3/20	1.11	(-0.04 , 2.26)	
12/3/20	1.18	(0.15 , 2.21)	
13/3/20	1.6	(0.14 , 3.06)	
14/3/20	1.2	(0.15 , 2.25)	
15/3/20	1.45	(0.33 , 2.57)	
16/3/20	1.06	(-0.21 , 2.33)	
17/3/20	1.1	(-0.02 , 2.22)	
18/3/20	1.08	(-0.03 , 2.19)	
19/3/20	1.11	(0.1 , 2.12)	
20/3/20	1.07	(0.04 , 2.1)	
21/3/20	1.07	(0.08 , 2.06)	
22/3/20	1.18	(0.99 , 1.37)	

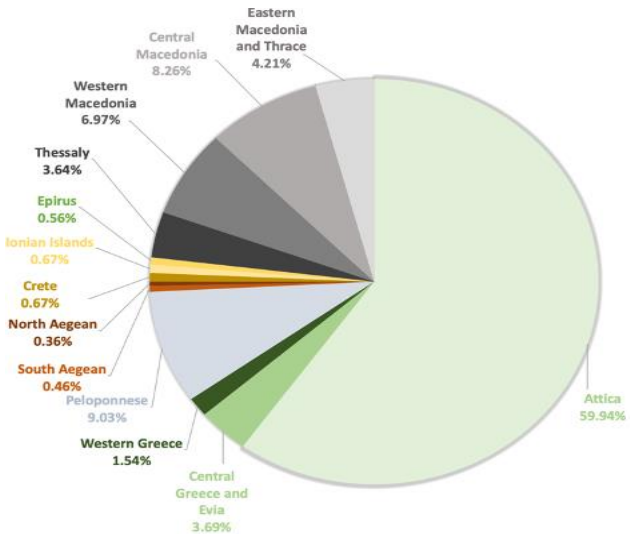

Fig. 2. Geographical distribution of total cases per region during quarantine period.

As it can be obtained in Table I, the basic reproduction number is firmly greater than 1 for the entire period before quarantine. More precisely, the day of the announcement of the quarantine, R_0 was estimated to 1.18 (95% CI: (0.99, 1.37)) according to (4), the dispersion parameter k was 0.74 according to (6) and based on these, the probability of spread extinction was estimated to 0 according to (3). To this side, the probability of an outbreak was 1, a fact that according to the relevant branching processes literature, advocates the adoption of mitigation measures such as a general lockdown and quarantine. Greek government, through these measures, attempted to reduce the basic reproduction number to $R_{eff} < 1$, so to bring the outbreak under control.

In order to use branching processes for the estimation of R_{eff}, the population was divided into clusters/chains of transmission. We assume that Greece is considered as one cluster and each region as one transmission chain. In fact, due to limited data availability, we presume that the entire Greece composes one cluster consisting of 13 transmission chains, one for each region. Fig. 2 depicts the percentage geographical distribution of total cases per region through quarantine period.

By the end of quarantine, the 4th of May that the new cases per day were under 10, the effective reproduction number R_{eff} was estimated to 0.0003 (95% CI: (-6.7 , 6.7)) according to (5) which indicates that the number of secondary infections caused by one infected individual is noticeably reduced and the dispersion parameter (k) was 0.23. According to the new estimation of the parameters, the probability of the spread extinction was 1, an approximation that forces the probability of an outbreak to be 0. These findings prove that the general lockdown was a highly effective measure so to control a general spread of the virus.

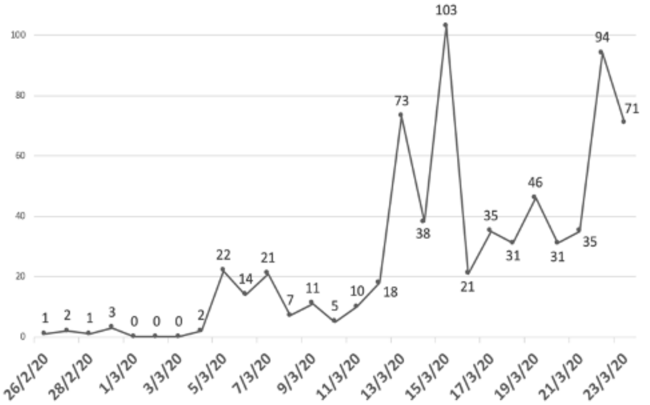

Fig. 3. Real data of reported new cases of corona virus transmission without mitigation actions.

However, the available data, from National Public Health Organization (NPHO) of Greece for the summer period, revealed a different evolution of the virus transmission despite the fact that Greek government has done smaller mitigation interventions such as the closing of bars and restaurants at 12p.m. and the extensive usage of masks. More precisely, by the end of the summer period almost 300 new cases per day were reported. Repealing the general lockdown along with the opening of country's borders and allowing the normal operation of stores relieved Greek economy but led to an uncontrolled rise of the transmission, brought new imported cases and transmission chains roughly detected. Within this widespread of corona virus in Greece during summer period, data was noisy and deprived models' accuracy. This scenario could have been seen in the complete absence of initial control measures.

Thus, in order to scheme an assumptive state of the virus transmission in which no mitigation actions were adopted, we conduct an additional analysis.

A. The Scenario without Mitigation

A simple Exponential Smoothing (ETS) model is used to forecast the transmission of corona virus in Greece in total absence of control measures. This model is actually used in order highlight the necessity and the effectiveness of quarantine measures.

TABLE II: FORECASTING OF NEW CASES/DAY USING ETS MODEL

Date	New cases/day (fcst)	Date	New cases/day (fcst)
24/3/20	67	28/4/20	159
25/3/20	69	29/4/20	162
26/3/20	72	30/4/20	164
27/3/20	75	1/5/20	167
28/3/20	77	2/5/20	170
29/3/20	80	3/5/20	172
30/3/20	82	4/5/20	175
31/3/20	85	5/5/20	178
1/4/20	88	6/5/20	180
2/4/20	90	7/5/20	183
3/4/20	93	8/5/20	186
4/4/20	96	9/5/20	188
5/4/20	98	10/5/20	191
6/4/20	101	11/5/20	194
7/4/20	104	12/5/20	196
8/4/20	106	13/5/20	199
9/4/20	109	14/5/20	201
10/4/20	112	15/5/20	204
11/4/20	114	16/5/20	207
12/4/20	117	17/5/20	209
13/4/20	119	18/5/20	212
14/4/20	122	19/5/20	215
15/4/20	125	20/5/20	217
16/4/20	127	21/5/20	220
17/4/20	130	22/5/20	223
18/4/20	133	23/5/20	225
19/4/20	135	24/5/20	228
20/4/20	138	25/5/20	231
21/4/20	141	26/5/20	233
22/4/20	143	27/5/20	236
23/4/20	146	28/5/20	238
24/4/20	149	29/5/20	241
25/4/20	151	30/5/20	244
26/4/20	154	31/5/20	246
27/4/20	157	**Total cases:**	10,800

Real data, from the initial phase of the transmission (Fig. 3) in Greece until the 23th of March, was the pillars of the model and the output is presented in Table II as new cases per day for the period: 24th of March to 31st of May. According to this approach, by the end of May there would be 246 new cases per day and the total cases are estimated to be close to 10,000. The outputs underline that in the total absence of control measures, the virus transmission would tend to be uncontrollable since the number of new cases per day increases importantly.

Fig. 5 provides a comprehensive view of the scenario in which no mitigation action was adopted and complies with the aforementioned assumption about the roughly controllable spread of the virus. In this graph, the red line depicts the forecasted new cases in a complete absence control measures according to the aforementioned model and the dashed lines refer to the upper/lower confidence bounds of the forecasted data, while the gray line shows the actual data of new cases for the same period. The positive slope of the red line, proves that quarantine was an efficient control measure because in the absence of control measures the number of new cases per day would be increased, contrarily to the mitigation scenario in which this number actually decreases. In addition, in order to achieve a smooth and clear view of the results, the data for 69 days is formed into 10-day time periods. To that side, Table III. presents the alternatively formatted outputs and Fig. 4 visualizes the results.

TABLE III: FORECASTING OF NEW CASES/TIME PERIOD

New cases per time period		
March	Period 3	678
April	Period 1	1,111
	Period 2	1,288
	Period 3	1,385
May	Period 1	1,790
	Period 2	2,054
	Period 3	2,565
	Total Cases:	10,800

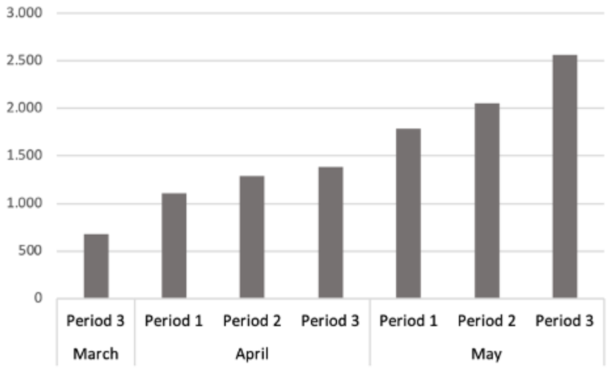

Fig. 4. Forecasting of new cases/time period.

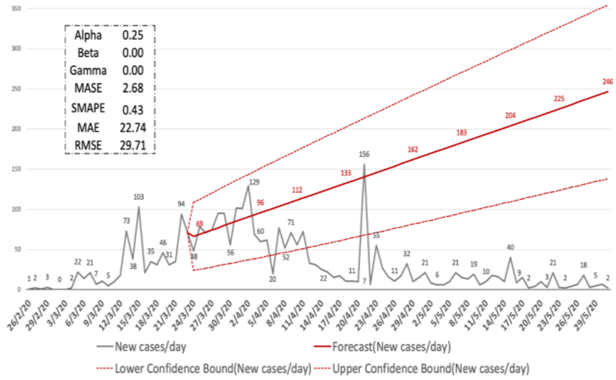

Fig. 5. Graph of real data of new cases/day before and at the quarantine period till the end of May and forecasted new cases/day in a complete absence of control measures.

However, real data of new cases per day for the summer period revealed a different evolution of the virus transmission despite quarantine or smaller mitigation interventions. Fig. 6 shows that some days after repealing quarantine (4th of May) the transmission was still under control, but if quarantine was extended until the end of May, based on the forecast model (red line), the transmission would have stopped. Repealing the general lockdown along with the opening of country's borders and allowing the normal operation of stores led to an uncontrolled rise of the transmission, brought new imported cases and transmission chains roughly detected.

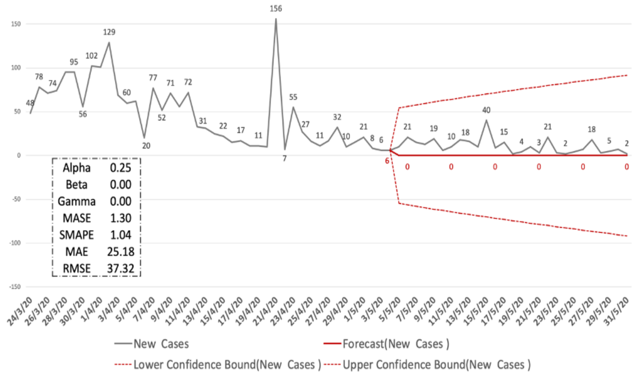

Fig. 6. Graph of real data of new cases/day from quarantine period till the end of May and forecasted new cases/day for the prolongation of quarantine period scenario.

More precisely, in Fig. 7 the red line refers to new cases per day in extended-lockdown scenario and arises as forecast based on the simple ETS model. The gray line depicts real data of new cases per day for the summer period. As it can be obtained, the positive slope of real data (gray line) along with the negative slope of the red line prove that the prolongation of quarantine would be an efficient choice because the number of new cases/day tends fast to zero, so the transmission of the virus would have been stopped. In addition, we can assume that the aforementioned smaller mitigation actions were not efficient enough so to set under control the transmission of corona virus, especially comparing to a general lockdown which was proven efficient.

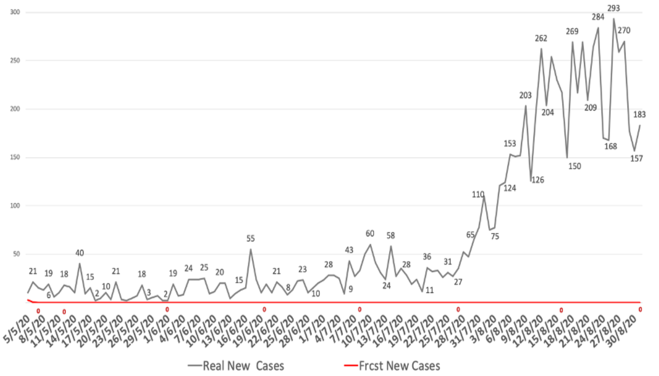

Fig. 7. Graph of real data of new cases/day and forecasted new cases/day for the prolongation of quarantine period scenario (May-August).

V. CONCLUSIONS

This paper considers the development of a simple mathematical model using branching processes to analyze the initial and latter transmission stages of the covid-19 pandemic outbreak in Greece. The results depict a reasonably increased R_0 that implies an aggressive spread of the virus. However, the adopted control measures issued by health authorities and adopted by Greek government were proven efficient because the R_0=1.18 was reduced to an R_{eff} = 0.0003. To that side, the additional approach of non-mitigation scenario based on a simple Exponential Smoothing (ETS) approach complies with the aforementioned admission. Repealing the movement restrictions and restarting business activity along with opening of Greek borders to tourists, so to support Greek economy, significantly raised the number of reported cases and led to new transmission chains roughly detected.

The lack of available data induced to consider the entire Greece as one cluster which is a slightly unrealistic assumption and the major limitation of the proposed model. However, despite the limitations and the fact this approximation is simple, we conclude that the proposed approach is proven beneficial and meets the initial aims.

CONFLICT OF INTEREST

The authors declare no conflict of interest.

AUTHOR CONTRIBUTIONS

I.A.M. and V.P. K. developed the models, processed data and executed the analysis; I.A.M. wrote the manuscript; both I.A.M. and V.P. K had approved the final version.

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