Growth forecast of the covid-19 with the gompertz function, Case study: Italy, spain, Hubei (China) and South Korea

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Abstract— *In this article,carry out an analysis on the growth and expansion models of the new virus outbreak belonging to the Coronavirus family called SARS-CoV-2 and associated with the clinical picture COVID-19. This outbreak of the disease was declared a pandemic by the World Health Organization (WHO) in March 2020, it is now affecting most countries in the world and its accelerated progress is a global concern. A non-linear growth model based on the Gompertz function was designed to characterize the serious pandemic impact in Asian and European countries: Spain, Italy, South Korea, and Hubei (China). The compilation of official data from each area on infected and deceased people until May 11, 2020, to verify the validity of the growth model in the calculated terms. With the obtained values, made a comparison by measuring the forecast errors, using the root indicators of the root mean square error (RMSE), the mean absolute percentage error (MAPE) and the regression coefficient index* R^2*, which yielded highly accurate values of the predicted correlation for infected and dead of 0.99 on the dates considered. Verified the validation of the viral growth model of COVID-19 for these four countries and verified how the different measures taken to alleviate the pandemic have affected the final results of infected and dead countries, obtaining different growth coefficients that could be due to some exogenous factors (such as social, political and health factors, among others) that are difficult to measure and require qualitative methods and resources. The simple and well-structured model can be adapted to different propagation dynamics. Due to its direct and rapid implementation, the model could be useful for health managers and politicians for better decision-making in the control and prevention of this pandemic.*

Keywords— *COVID-19, coronavirus, growth model, Gompertz, pandemic.*

I. INTRODUCTION

In December 2019, in the city of Wuhan (China), severalpneumoniasinduced by a newrespiratory disease were detected ***[1].*** The causative agent was the new coronavirus that was identified and isolated from a single patient in early January, and subsequently verified in other additional patients ***[2]***. This clinical disease was named as COVID-19 and it was discovered that was a novel betacoronavirus, now named SARS-CoV-2. A very rapid scientific response leads to the publication of its genome which reveals shares 88–96% sequence similarity to bat coronaviruses, in keeping with other pathogenic coronaviruses such as SARS-CoV and MERS-CoV***[3-6].***SARS-CoV-2 is a remarkable pathogen which showed a high transmission potential ***[7,8]*** and it is responsible for the international outbreak COVID-19. The fast dispreading of the virus can be explained for different reasons, being the human-to-human transmission way the most proven. ***[9]***. Therefore,close contact between individuals can facilitate transmission ***[10]***by scattering drizzle droplets whencoughing or sneezing.The swift spread of the disease is explained by the virus survival period of several days ***[11,12]***, with active persistence in metal and glass for up to 9 days ***[13].*** Current data seems to suggest that the virus has an incubation period of three to seven days with a mean incubation period of 5.2 days ***[14]***, though other authors suggest periods between 2 and 14 days***[15,16]***. Moreover, asymptomatic, or mildly symptomatic persons can transmit the infection***[17]***, which makes identification very arduous and the number of infected people higher than the official count.

Given the severity of the outbreak and its swift spread, the WHO declared the new disease on January 30 as a public health emergency of international concern ***[18]***. On March 11, the spread reached118,000 cases in 114 countries with 4,291 people dead, the WHO's Director-Generalproclaims COVID-19 as a global pandemic ***[19]***. This declaration forces all countries to take more radical measures to stop the spread of the virus; among those, the confinement of the population and the closure of borders which had already been carried out initially in Hubei on January 23. In Italy, the constrictions began in the northern zone on February 22, going to a total closure on March 9 and the stoppage of all productive activity on March 21. In Spain, the closure of commercial activities begins on 15 March ***[20]***. The measures carried out in South Korea are focused on the initial patients, performing massive tests to all the people ***[21]*** who had been in contact with them, isolating only the affected people and areas***[22]***. With all the measures taken, it is already considered the largest quarantine in history, but the virus continues to spread throughout the world. On May10, the situation is 3,917,366 confirmed infected, 274,361 dead and 181 affected countries ***[23]***.

All this makes the coronavirus is spreading across the globe at an alarming rate and caused more infections and deaths as compared with SARS or MERS***[17]*** which could be due in part to the fact that SARS-CoV-2 is more infectious due its higher R0 values. The speed of transmission has meant that the preventive and control strategies that states have been taking, such as isolation, detection tests and prophylactic measures, although they have somewhat flattened the epidemic curve, have not been able to prevent the spread of the virus throughout the world. Therefore, there is an urgent need to develop models that allow predicting the behaviour of the pandemic in the different affected areas, in order to be able to take the most appropriate prevention and control measures of the outbreak in each circumstance and with sufficient time in advance.Mathematical modeling of the spread of infectious diseases is essential to understand the evolution of epidemics over time.

Modern mathematical epidemiology can be considered to have started with the studies of Kermack and McKendrick with the classic model of susceptible - infected - recovered (SIR) ***[24]***.Subsequent studies for outbreaks, from SARS ***[25]*** and Cholera ***[26]***, apply more complex models with multiple variants, with the susceptible - infected - recovered - susceptible pattern (SIRS) ***[27]***, where the recovered can be re-infected by not developing immunity; or the susceptible – exposed – infectious-recovered model (SEIR) ***[28]*** where the exposed population is assessed and immunity is evolved. For the description of the growth and development of diseases, the logistic model has been applied; as in the case of bacterial growth ***[29]***, the infectious diseases spreading ***[30]***, or the Gomperzt model that is also used for bacterial sprouting ***[31]***.Currently, the studies that have been carried out on the growth of COVID-19 have focused on specific areas, mainly in China, with the SEIR model by Wu etLeung ***[32]***who predicted the national and international spread of the pandemic, or the study by Yang and Wang***[33]***who introduces a confinement variable. Also, unreported cases have also been studied and estimated in areas of China ***[34]***, and on flights from Japan ***[35]***.Various prediction models have been studied, based on the SEIR model***[36]*** and the logistic model has also been used to successfully predict for 20-day infections***[37]***.The epidemic evolution model has also been studied following the system of differential equations for the susceptible - infected - recovered - dead (SIRD) variables, analysing the temporal dynamics of the disease on the leap from China to Italy and France ***[38]***.

Creating a mathematical model of the spread of infectious diseases is essential to understand the evolution of epidemics over time, the objective of this study is to obtain a model capable of predicting behaviour (number of infections and mortality) to help health systems and politicians in predicting future situations for better decision-making in the control and prevention of this pandemic. Have taken the values of several countries in Europe that are Spain and Italy and two other countries in Asia, which are the Hubei area (China) and South Korea, to apply a growth model based on the Gompertz function and verify its application. . This research is divided into section 2 of the methodology where the workflow followed is explained, in section 3 describe the Gompertz model, in section 4 perform calculations and prognostic models for deaths and infected, ending section 5 with the conclusions of the investigation.

II. METHODOLOGY

The study of the growth prediction of the COVID-19 pandemic using the Gompertz growth model scoped various areas and countries of the world: South Korea, where initially monitoring and control measures were taken that managed to significantly reduce the incidence of the pandemic; Hubei area (China), which was the first area that began with total confinement; and in two European countries, Italy and Spain, where the incidence of infected and dead is very striking. ***Table 1*** shows updated population data for each country ***[39]*** and COVID-19 infections and deaths as of May 11, 2020. Data on confirmed cases and deaths were obtained from WHO ***[23]***, with daily reports presented worldwide from the European Center for Disease Prevention and Control (ECDC) ***[40]***, selecting reports on from Italy, Spain and South Korea. Data for Hubei (China) were obtained from the National Health Commission of the People's Republic of China ***[41]***. It should be noted that on April 16, Hubei's data were updated with values not derived from official statistics, which affected the model and could only be calculated up to that date. In Spain the statistical system was also changed to consider the number of infections, as of April 24, but did not affect considerably the calculations and the results obtained.

Table 1. Summary of country data as of May 11, 2020.

COUNTRY	Population	Life expectancy	Population % aged >65	Infected (2020-05-11)	Dead (2020-05-11)	Fatality rates (CFR)	Infected / 10^6 population	Dead / 10^6 population
Spain	46,400,000	84	20%	227,436	26,744	11.8%	4,902	576
Italy	59,200,000	84	24%	219,814	30,739	14.0%	3,713	519
Hubei (China)	58,160,000	77	12%	68,134	4,512	6.6%	1,171	78
South Korea	51,300,000	83	15%	10,936	258	2.4%	213	5

These initial data show that the most efficient containment system at present is that of South Korea, with an infection rate of 213 people per million inhabitants, and the least effective is that of Spain, with an infection rate of 4,902 per million inhabitants. With regard to deaths, it can be seen that the highest mortality rate is that of Italy, with almost 14% of deaths onthose infected, but the one with the highest mortality rate with respect to the population is again Spain with 576deaths per million inhabitants, and the one with the best data and the lowest mortality rate is again South Korea, with 2,4 % mortality and 5 deaths per million inhabitants.

To carry out the study of propagation and deaths due to COVID-19 using the Gompertz growth model, the following workflow has been followed to obtain the growth forecasts sought, which are shown in ***Figure 1.***

1. The collection of data on the spread and deaths of the countries and areas examineduntil May 11, 2020. The data on the change in the mortality measure in Hubei from April 16, 2020, which changes the curve model obtained.
2. Data preparation and adjusting initial pandemic and death dates by country to make calculations
3. The treatment of assumptions over different rates of spread and maximum number of cases of infection and deaths predicted by country.
4. Estimation of the number of infected and dead in each country using the Gompertz growth function.

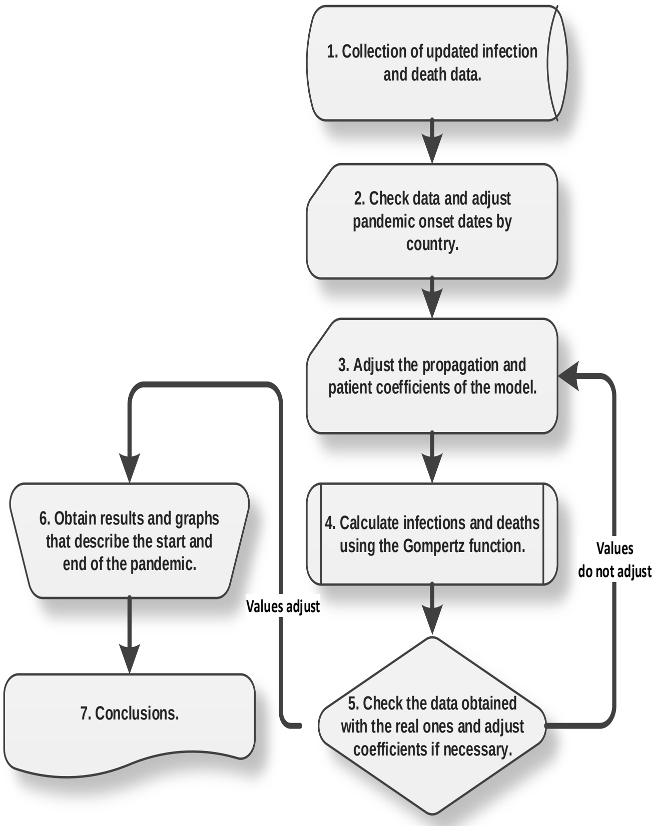

Fig.1: Research flowchart

5. To contrast and verify the results obtained versus actual facts, adjusting the coefficients of growth and prognosis of cases to obtain the values that best fit the current situation, checking their validity by

calculating the values of R^2, RMSE and MAPE for each estimate and country.

6. With the predicted values that best fit the reality of each country, obtain the sigmoid graph that describes the growth and estimated end of the pandemic for each country, for infected and dead.
7. Conclusions and description of more accurate methods to contain future pandemics.

Table 2. Summary of characteristic and predicted values of COVID-19 infections

Forecast infected characteristic values - GOMPERTZ METHOD						
Country	***Constant growth***	***Infection forecast***	***RMSE***	***MAPE***	***R^2***	***Forecast infected / 10^6 population***
Spain	0.071	253,000	6,903	16.31%	0.9972	5,453
Italy	0.061	243,000	4,279	9.28%	0.9994	4,105

2.1 GOMPERTZ MODEL

The mathematical model of growth used to predict the pandemic is the Gompertz model, which belongs to the family of sigmoid curve modelling ***[42],*** initially appliedto model human mortality. There are different types of Gompertz curves depending on the parameters involved, but they all have a double exponential as a common characteristic element. With the function defined for human mortality, Charles P. Winsor ***[43]*** began to study the growth of biological phenomena, demonstrating its usefulness in biological and bacterial growth curves. Later studies by Laird ***[44]***, in some tumours concluded that the exponential model was not totally adequate for the description of growth and that an exponential Gompertz model could explain the observed growth. The Gompertz model was used by many authors in growth studies of all kinds, such as population growth ***[45]***, growth of animal fetuses***[46]***, chickens growing ***[47]*** and weight growth in fish in Canada ***[48]***. Among multiple options to express the Gompertz's model, since this family of functions comprises a wide variety of curves with double exponential as common feature, this study of growth and development of the COVID-19 addresses the following model.

$$\boldsymbol{f(t) = k^{\left\{\left(ln^{\left(\frac{X_0}{k}\right)}\right)\left(e^{-\alpha(t-t_0)}\right)\right\}}},$$

$$\boldsymbol{t \geq t_0} \;, \quad \boldsymbol{\alpha} > 0, \quad k > \boldsymbol{X_0} > 0$$

Considering ***"k"*** the maximum predicted number of patients infected or dead in the development of the pandemic, ***"X_0"*** is the number of initial patients, infected or dead, when the pandemic starts at instant ***"t_0"***, andconsider ***"t"*** the prediction time, and ***"α"*** is the growth rate characteristic of the pandemic. For biological growth calculations estrict the values of t ≥ t0 ≥ 0 and the value of initial patients X0 = f (t0)> 0.

This sigmoid curve has the characteristic of being monotonous in its growth, being limited in time and presenting a point of inflection where the curve goes from concave to convex reaching approximately 37% of the growth that comes to depend on "X_0" and can be defined for "k >X_{0e}" at the point:

Inflection point dimension: $\boldsymbol{\left(\frac{ln\frac{k}{X_0}}{b} + t_0, \frac{k}{e}\right)}$and approximate percentage of growth at that point: $\boldsymbol{37} \times \boldsymbol{\left(1 - \frac{X_0}{k-X_0}\right)}$ %

III. RESULTS

With the data obtained from infected and dead, carried out the forecast calculations for the Gompertz model using the mathematical modeling software IBM SPSS Statistics ***[49]***, to check and calculate multiple mobilizations for the ***"α"*** growth rate of deaths and infections, and with multiple values also of the ***"k"*** value with the maximum predicted number of deaths and infected per country. With the different values obtained, compared the predicted values with the current actual values, performing a quantitative examination of the fit using error measurement indices commonly used to evaluate prediction models ***[50]***. Using Karl Pearson's R^2 regression index ***[51]*** to justify its greater or lesser correlation ***[52]***, also comparing the model accuracy of the different regressions by calculating the RMSE***[53]*** and MAPE***[54]***, which is a forecast indicator that measures the size of the absolute error in percentage terms, giving us a relative measure of the error. The functions used for accuracy calculations are as follows:

$$\boldsymbol{RMSE = \left[\frac{1}{t}\sum_{i=1}^{t}(u_p - u_o)^2\right]^{1/2} \quad MAPE = \frac{100}{t}\sum_{i=1}^{t}\left|\frac{k_r - k_f}{k_r}\right|}$$

Where **"t"** is the number of observations, **"u"** is the residue of the estimates, the subscript **"p"** is the predicted residue and **"o"** the observed residue, "k_r" is the actual number of infected or dead and "k_f" is the estimated number of infected or dead according to the analysed prediction model.

3.1 PREDICTION OF INFECTED

Making the calculations for the number of infected, it is seen as the data from Spain and Italy has a lower growth but the final value is much higher than that obtained in Hubei and South Korea, as it has not yet reached the tipping point of stabilization of cases, but are already reducing the daily cases, while Hubei and South Korea data are stabilized and near the end of the pandemic. The characteristic values obtained in the modeling of the pandemic for the final predicted number of infected people can be seen in ***Table 2***, where it can be seen how the values of infected people per million inhabitants are very high in Spain and Italy, with 5,453 and 4,105 infected people per million inhabitants respectively, and in Hubei and South Korea they remain at values very similar to the current 1,172 and 214 infected people per million inhabitants respectively, as these areas are in the upper part of the stability curve and the end of the pandemic.

The dates taken to make the calculations of infected differ from country to country, as they have different dates of the beginning of the virus infections in the countries. Perform the infected forecast calculations by comparing them with the actual values for the dates chosen for each country and check their suitability. The daily infected values have been calculated until the date that the pandemic disappears and the number of infected goes to 0, calculating the end date of the pandemic according to this Gompertz model with the corresponding coefficients of each country used. In Hubei, the end of the infections is forecast for May, in South Korea in June, in Spain in September and the last to emerge from the pandemic would be Italy in October, all of them in 2020.The following ***Table 3*** shows the dates that have been taken to make the forecasts of infected people by country, as well as the expected end date of the pandemic in each case.

Table.3: Dates used for end of pandemic estimates and forecasts by country

COUNTRY	***INFECTED***	
	Start date	***Forecast end date***
Spain	2020-02-24	September 2020
Italy	2020-02-20	October 2020
Hubei (China)	2020-01-22	*May 2020*
South Korea	2020-01-31	*June 2020*

The following ***Figure 2*** shows the real and predicted values calculated for the accumulated number of infected by country, verifying how Hubei and South Korea are at the end of the pandemic with very little increase in those infected over time. ***Figure 3*** shows the real and calculated values for new infected per day by country, where you can see the approximate time period calculated for the reduction of infected, which is verified with the change in trend of the daily infected curve. As can be seen from the correlation factors R^2 for all countries, there is a very high correlation between the predicted and actual calculated values. Can also see how the spread values are lower in Spain and Italy, but with more cases of contagion, mainly due to the time elapsed for these countries to take measures to stop the pandemic, being the case of the fastest contagion in South Korea. and China but with fewer infected, by taking radical measures of confinement and monitoring of infected to stop the pandemic, with different methods in these countries, which have managed to paralyze the pandemic as soon as possible in these areas. The model that best fit is Hubei's since it is at the end of the pandemic and its fit to the Gompertz model is very good. The models of the rest of the countries have a considerable adjustment, being the one that least adjusts that of South Korea, since they have several sources of infection that were identified late.

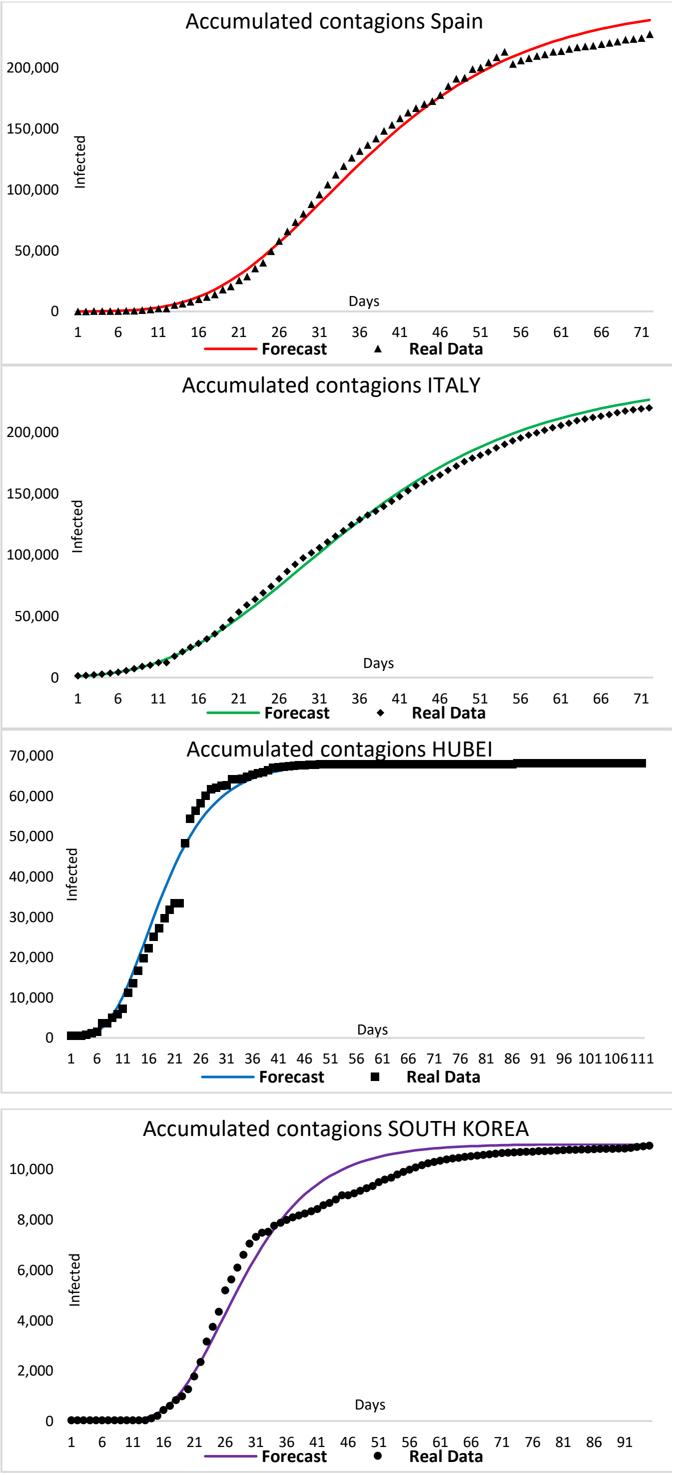

Fig.2: Accumulated contagion forecast until of May 11.

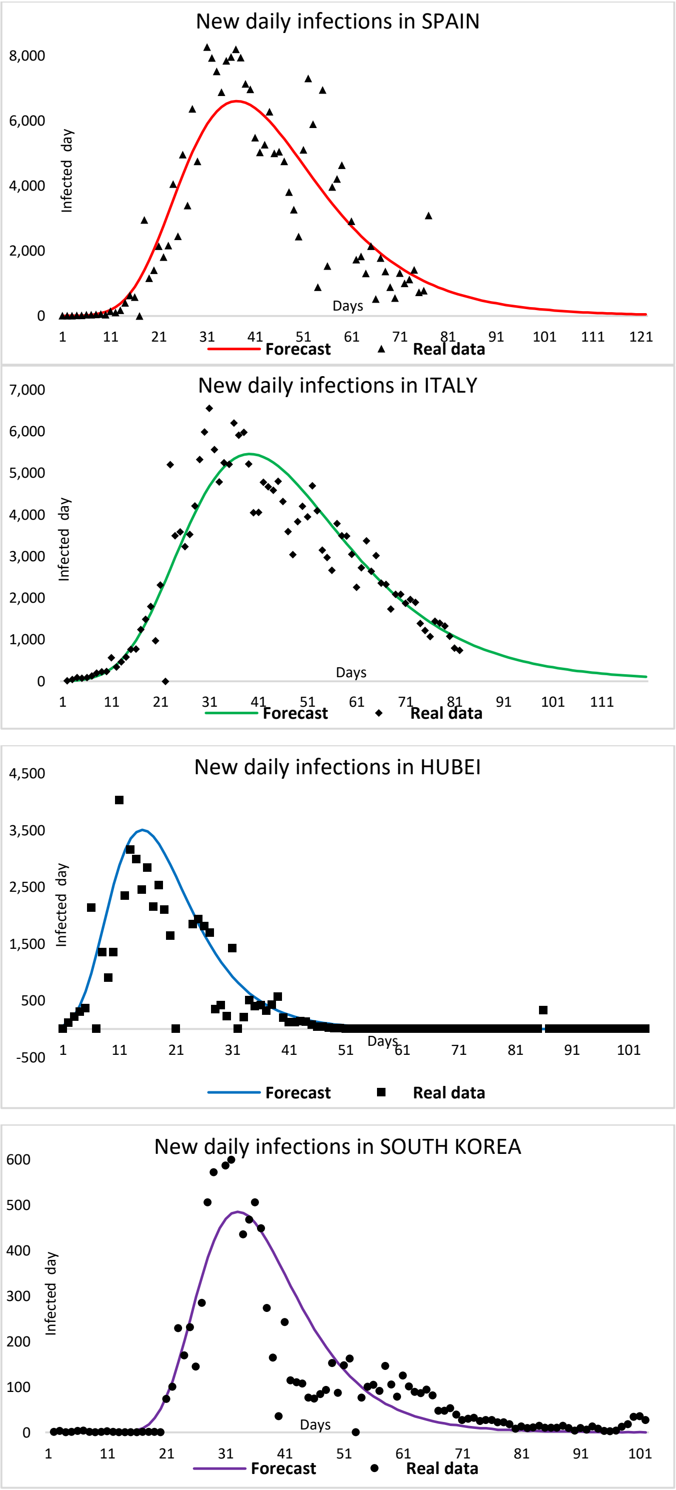

Fig.3: Forecast of new daily infections by country.

3.2 MORTALITY FORECAST

With the same model as Gompertz, began to calculate the growth of the number of deaths from the pandemic. In this case, can see how the growth data is very similar in all the countries studied, with South Korea being the lowest again, which also has the fewest expected deaths. The values obtained with the Gompertz model also have a very high correlation adjustment coefficient R^2, with an almost perfect adaptation to the real values. The characteristic values obtained in the pandemic model for the number of deaths can be seen in ***Table 4***, where it must be taken into account that the Hubei data are taken up to the date of April 16, 2020, which were subsequently adjusted data on deaths and the growth curve is no longer applicable as there are no real values throughout the series, therefore the values up to that date and those obtained on May 11, 2020 are used.

Table 4. Summary of characteristic values of deaths from COVID-19

Deaths characteristic values - GOMPERTZ METHOD								
Country	*Constant growth*	*Death forecast*	*RMSE*	*MAPE*	*R^2*	**Fatality rates (CFR)**	*Forecast death / 10^6 population*	*End date of pandemic deaths*
Spain	0.073	29,000	542	16.26%	0.9987	11.5%	625	**August 2020**
Italy	0.06	34,000	375	12.21%	0.9996	14.0%	574	**September 2020**
Hubei (China) (Until 04-16-20)	0.09	3,225	56	3.43%	0.9990	4.7%	55	**May 2020**
Hubei (China) (Until 05-11-20)		4,520				6.6%	78	**May 2020**
South Korea	0.058	280	6	9.86%	0.9988	2.5%	5	**June 2020**

The highest mortality values are obtained in Italy and Spain with 14% and 11.5% of the infected population respectively, and the lowest, again, in South Korea and Hubei with 2.5% and 4.7% (until 04-14-20) and 6.6% (until 05-11-20) of the infected population respectively, also achieving the lowest number of deaths per million inhabitants, being only 5 and 55 (until 04-14-20) and 78 (until 05-11-20) deaths per million inhabitants respectively, while the highest values are obtained in Spain and Italy with 625 and 574 deaths per million inhabitants respectively. With the forecasts obtained, the forecast of the end date of daily deaths from this pandemic has also been calculated, which in Hubei predicts the end of deaths for May, in South Korea for June, in Spain for August and in Italy for September 2020. The dates chosen for the forecasts are from the beginning of the deaths confirmed by countries, except in Hubei which is from January 22, 2020.

In the following ***Figure 4*** shows the actual and predicted values calculated for cumulative deaths by country, and in ***Figure 5*** showing the actual and predicted values of daily deaths by country. In the daily deaths curve, it can be seen how the shape of the curve decreases with time and an approximate date of the end of the deaths from the pandemic can be predicted. Again, the correlation factors R2 for all countries are very high, from the calculated and predicted values with respect to the real values. It must be taken into account, what how the data from the Hubei curve can be observed the jump that occurs on April 17 due to the update of data on that date, where 1290 more deaths were added. For Hubei, the curve for the values until April 16 has been estimated. South Korea again having the lowest value of deaths and in the curves can see how South Korea and Hubei are already in the stabilization zone and Spain and Italy are already in the zone of decrease in the number of cases. In the South Korean curve for daily deaths, due to the stochastic noise of such small numbers, it is impossible to adapt the curve of the values obtained to the real one.

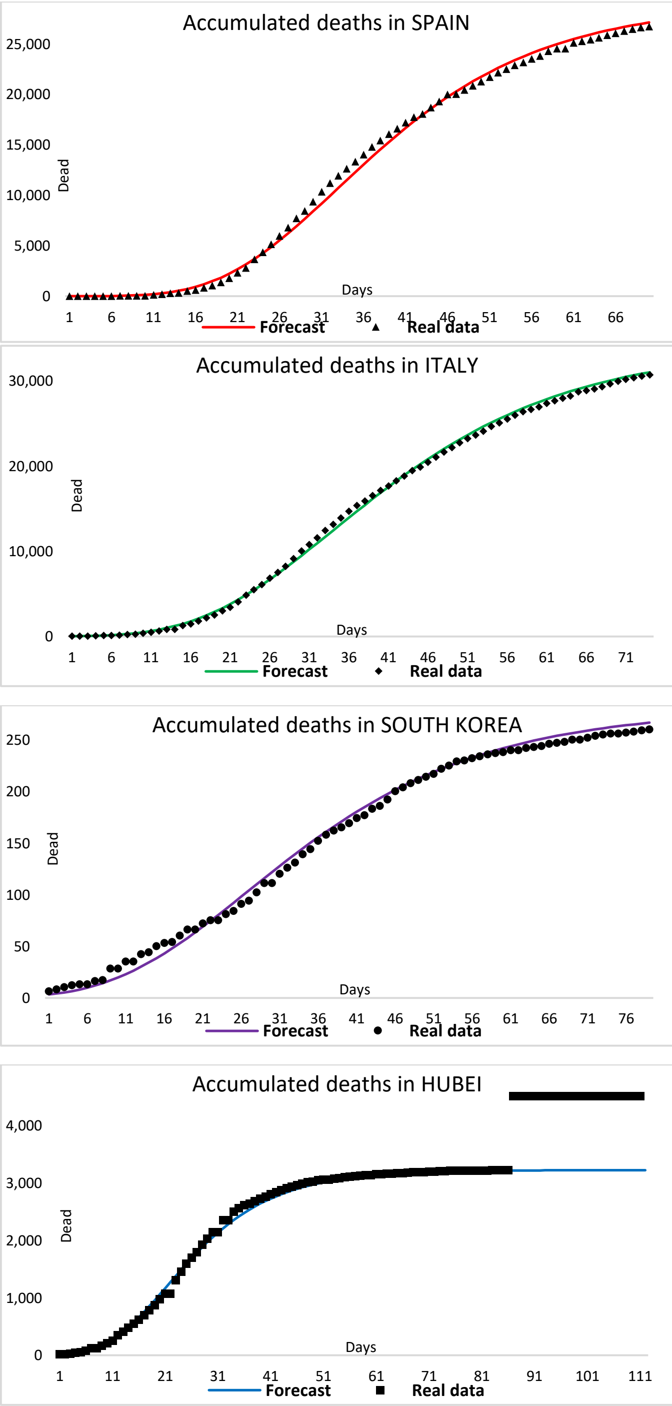

Fig.4: Accumulated death forecast until of May 11.

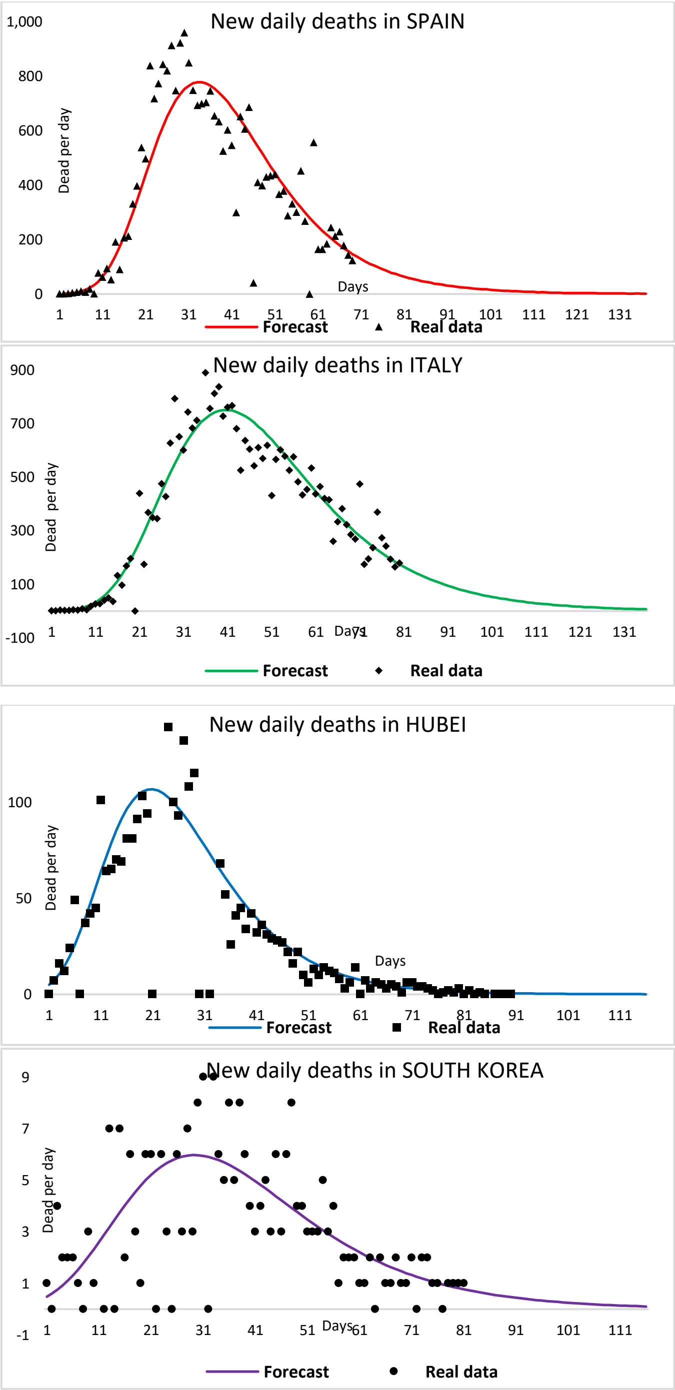

Fig.5: Forecast of new daily deaths by country.

IV. DISCUSSION

This work verifies the use of the mortality growth model to analyze the growth and development of unexpected pandemics, for mortality and new infections of COVID-19. Specifically, show the utility of mathematical modeling of the COVID-19 pandemic when using the Gompertz sigmoid curve growth model. The simulation model presents good results and excellent prognoses, with the correlation index being greater than 0.999 in all cases, both for mortality and for those infected, giving very low MAPE values for both mortality and those infected. It is verified as in Spain due to the change in the system of confirmation of contagions carried out on April 23***[55]***, the measurement values of infected the MAPE rises to 16% and is the highest of the four calculated cases, giving strange values as of this date .

Have also verified that the short-term estimates are correct for all cases, this study being valid to estimate the mortality and infections of the pandemic with respect to infected individuals, who were detected with symptoms. As such, this study does not apply to asymptomatic patients since they cannot have real data on them. The limitations shown in the study are mainly due to changes in counting the deceased or the infected, which generates problems and erratic data in the statistics of the studied areas. In order to estimate the growth indicators and the peak of infections or deaths, it is necessary to have enough evolution data to be able to make an estimate as accurate as possible, which is why the use of this growth model is limited if you do not have sufficient data on the evolution of the sick or deceased. Another significant limitation of the study are external pandemic containment factors, which are applied by each state. Such factors can cause growth patterns to decrease or increase significantly if the correct measures are taken to contain cases and stop the spread of the virus. Meanwhile, it is worth noting the importance of obtaining reliable data from government health entities to make the correct mathematical predictions.

V. CONCLUSIONS

This study demonstrates the validity of the proposed model, based on Gompertz techniques widely applied to biology, to describe the pandemic growth of COVID-19, both in the number of infections and deaths, emulate dynamic progression and predict the peak of the trend change. Verify how the model is adaptable to different countries with different socio-political circumstances, adjusting the growth coefficients for each case. The result is a theoretical curve that is very close to the real evolution of the pandemic, achieving forecasts with high correlation coefficients with respect to real cases, greater than 0.99 in all cases and countries, both of infections and deaths. Therefore, the Gompertz model could be an appropriate procedure to analyse the growth and development of unexpected pandemics with sudden and general outbreaks, describing epidemiological stability indices based on those obtained in the different countries that have already reached the peak. of no growth.

Taking into account that the countries studied have treated the pandemic in a different way and with different actions, the proposed model can reveal how South Korea's strategy has been more efficient to control this pandemic than those carried out by European countries. , where the number of deaths and infections are extremely high. Have shown that the Asian viral pandemic treatment strategy is much more efficient in these cases than the European one. Our results show that the South Korean procedure based on the systematic control of all those infected, their monitoring, control and isolation is the way to go. Their strategy to combat this exponential invasion of the virus consists of the isolation of groups that have been in contact with the virus, the use of preventive protections for the main contagion through masks, and control through massive population tests. In contrast, the European system with partial confinement and spot testing has been very ineffective in avoiding or mitigating pandemic damage.

The model presented in this document may be extended to other affected countries. The model design will be periodically updated during the global outbreak. The research results could be the basis for future studies related to the evaluation of the impacts of the pandemic on the economy, the ecosystem, and renewable energies, among others. The authors hope that this project will be of some help to health and political authorities during the difficult times of this global outbreak.

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