

Mathematical Modelling For Decision Making of Lockdown during COVID-19

Ahona Ghosh

Brainware University <https://orcid.org/0000-0003-0498-285X>

Sandip Roy (✉ sandipro86@gmail.com)

Brainware University <https://orcid.org/0000-0002-5447-803X>

Suparna Biswas (✉ mailtosuparna@gmail.com)

Maulana Abul Kalam Azad University of Technology <https://orcid.org/0000-0002-6150-9316>

Research Article

Keywords: Lockdown, COVID-19, Corona virus, Ridge regression, 1st world countries, 2nd world countries, 3rd world countries, SIR model, Finite Impulse Response filter, Python.

Posted Date: July 20th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-42770/v1>

License: © ⓘ This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Version of Record: A version of this preprint was published at Applied Intelligence on May 10th, 2021. See the published version at <https://doi.org/10.1007/s10489-021-02463-7>.

Mathematical Modelling For Decision Making of Lockdown during COVID-19

Ahona Ghosh · Sandip Roy · Suparna Biswas

the date of receipt and acceptance should be inserted later

Abstract

Due to the recent worldwide outbreak of COVID-19, there has been a huge change in our lifestyle and it has a severe impact in different fields like finance, education, business, travel and tourism, economy and several others in all the affected countries. In this scenario, people have to be careful and cautious about the symptoms and should act accordingly. Accurate predictions of different factors, like the end date of the pandemic, duration of lockdown and spreading trend can guide us through the pandemic and precautions can be taken accordingly. Multiple attempts have been made to model the virus transmission, but none of them has investigated it at a global level. The novelty of our proposed work lies here. In this paper, at first, we have analysed the nature of spreading of the said disease using data collected from various platforms and then, we have presented a predictive mathematical modelling for fifteen different countries from first, second and third world considered by us to have an idea and indicative data for probable future projections of this pandemic. The prediction can be used by planning commission, health care organizations and the government agencies as well for creating suitable arrangements against this pandemic. Recommendations can be created; advisories created on the basis of the prediction can be implemented region and country wise according to the situation.

Ahona Ghosh
Department of Computational Science, Brainware University, Kolkata, India
E-mail: ahonaghosh95@gmail.com

Sandip Roy
Department of Computational Science, Brainware University, Kolkata, India
E-mail: sandipro86@gmail.com

Suparna Biswas
Department of Computer Science and Engineering, Maulana Abul Kalam Azad University of Technology, West Bengal, India
E-mail: mailtosuparna@gmail.com

Keywords: Lockdown, COVID-19, Corona virus, Ridge regression, 1st world countries, 2nd world countries, 3rd world countries, SIR model, Finite Impulse Response filter, Python.

1 Introduction

COVID-19 (Corona Virus Disease 2019) is the name given by World Health Organization (WHO) to the worldwide spread disease caused by novel corona virus, the most discussed topic nowadays. The virus is totally a new one and previously has not been observed ever, the reason behind calling it ‘novel’, lies here. The present statistics say that in spite of being the most developed country having strong financial background, first world countries like USA, Italy, France, Spain, Germany are suffering more than the other countries in the world due to corona. The origin of this virus was China and the first case was observed in Wuhan of China in December 2019. After that, it began to spread all over the world and affected more than 170 countries till now. The rapid growth in the number of affected and deceased people is very alarming and therefore governments have been forced to take hard decisions like lockdown and sometimes partial lockdown in their respective countries. According to WHO globally 5317625 confirmed cases have been registered, 340214 deaths have been recorded till date [1].

Forecasting methods can help governments to take the right decision and proceed further accordingly, so our approach here is to design a decision-making system for lockdown, which analyses different records of lockdown in different countries and predicts when it will end in the concerned areas. Figure 1 shows that USA is leading in the total number of positive cases of COVID-19 and Spain is after that, where in the second world countries like Kazakhstan, Uzbekistan and Romania and third world countries like Philippines, Mexico and Thailand have not been affected much. Figure 2 shows number of positive cases per 1 million population, here comes the concept of population density, because more the population density, more is the chance of spreading the virus. Spain is facing the greatest number of infections per 1 million population, whereas Italy and France are not much behind. The total number of cases till 26th April, 2020 is shown in Figure 3, we have considered five countries from each of the first world, second world and third world, so that the economy of the affected countries can also relate during the analysis. Based on the economy, their correlation with the trend of recovery (if any) has been attempted to detect. From 15th February to 26th April, the daily new cases have been recorded and shown country wise in Figure 4. The forthcoming situations can be controlled in an efficient manner if systematic forecast is made and guidance from medical persons is provided accordingly.

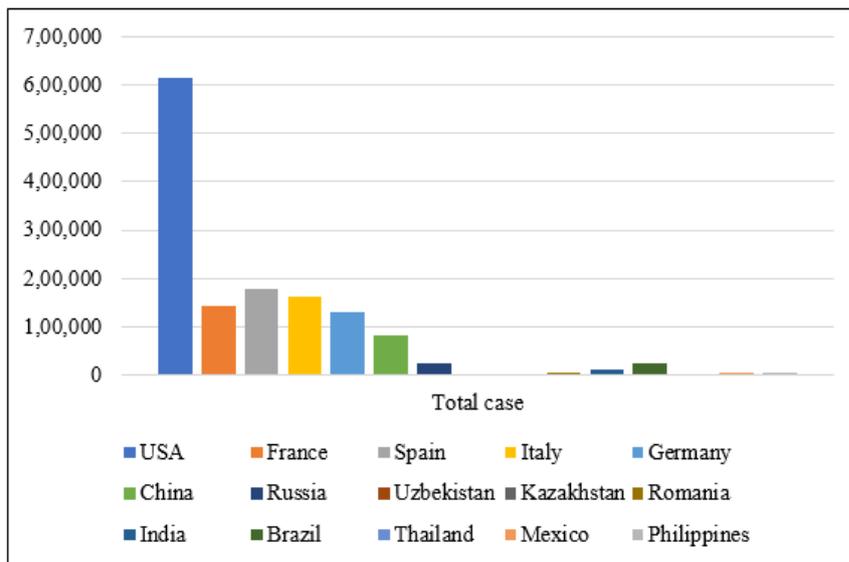


Figure 1. Country wise total cases upto 26.04.2020

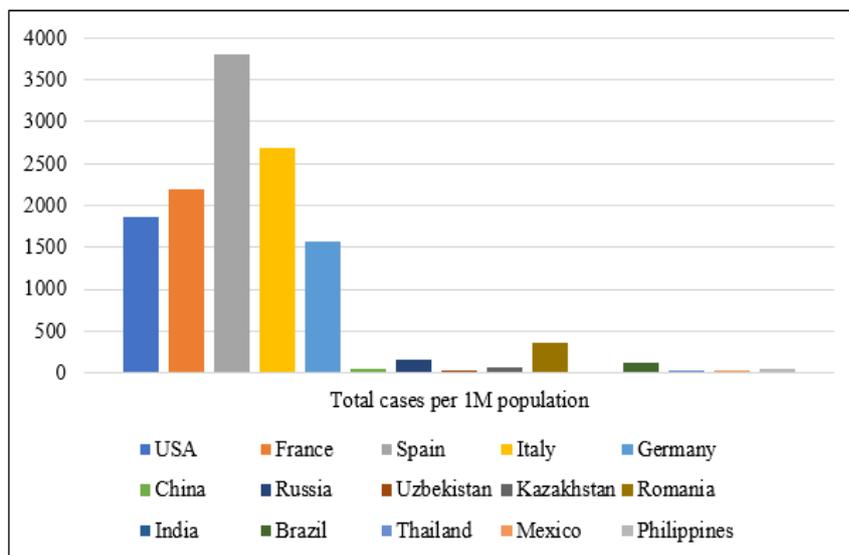


Figure 2. Country wise total cases per 1 milion population

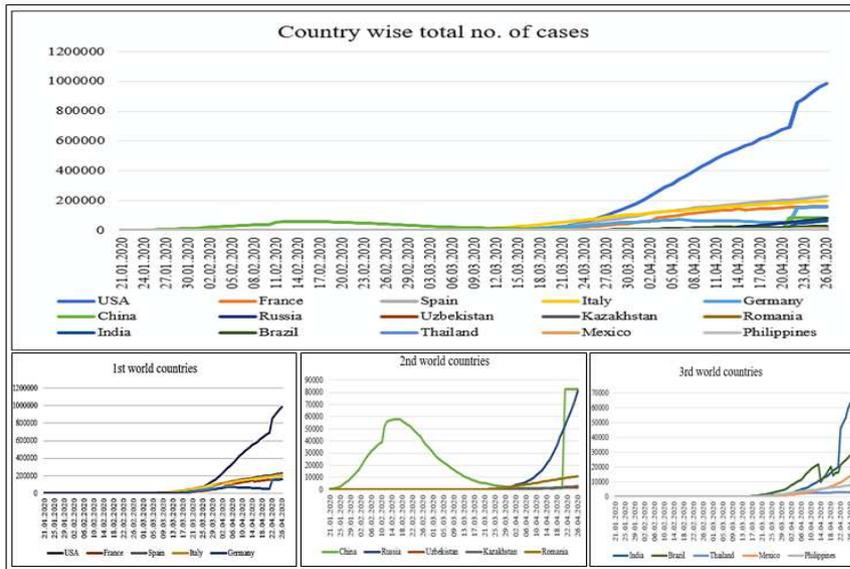


Figure 3. Date and country wise COVID-19 total cases

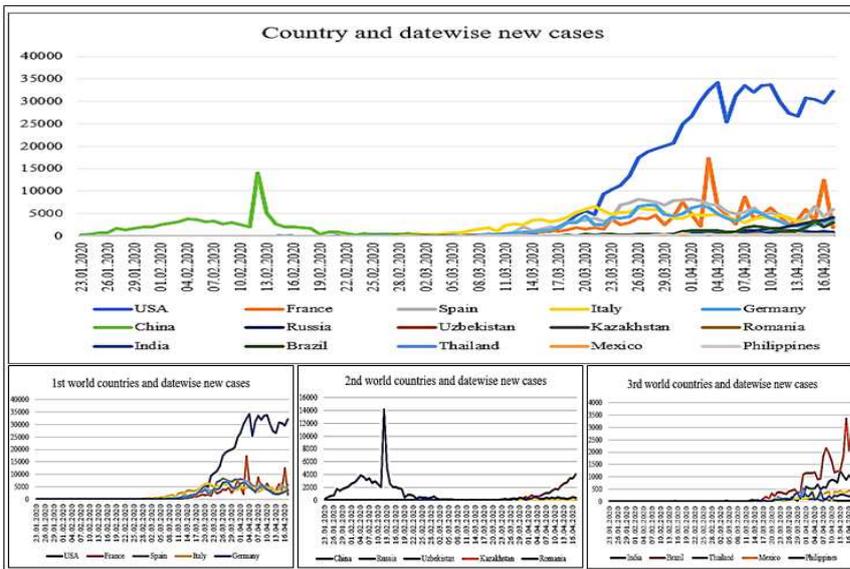


Figure 4. Date and country wise daily new cases

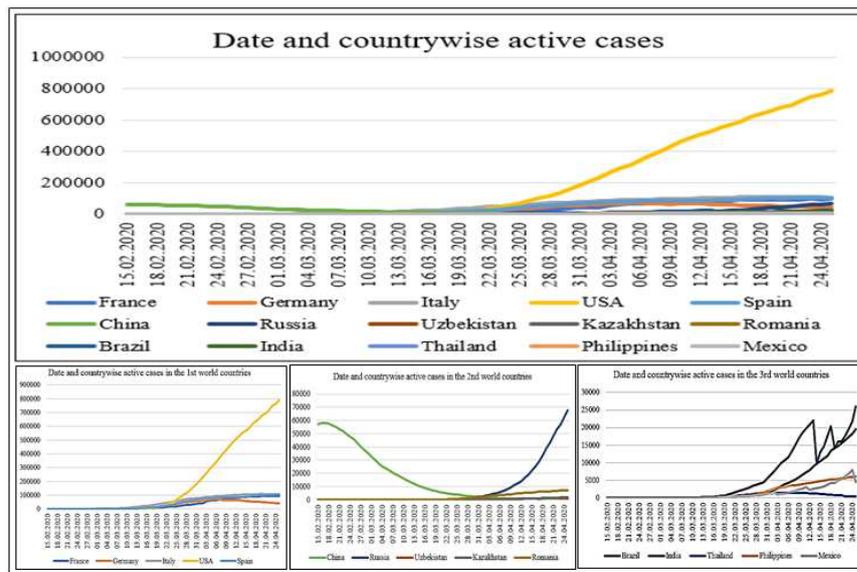


Figure 5. Date and Country wise total active cases

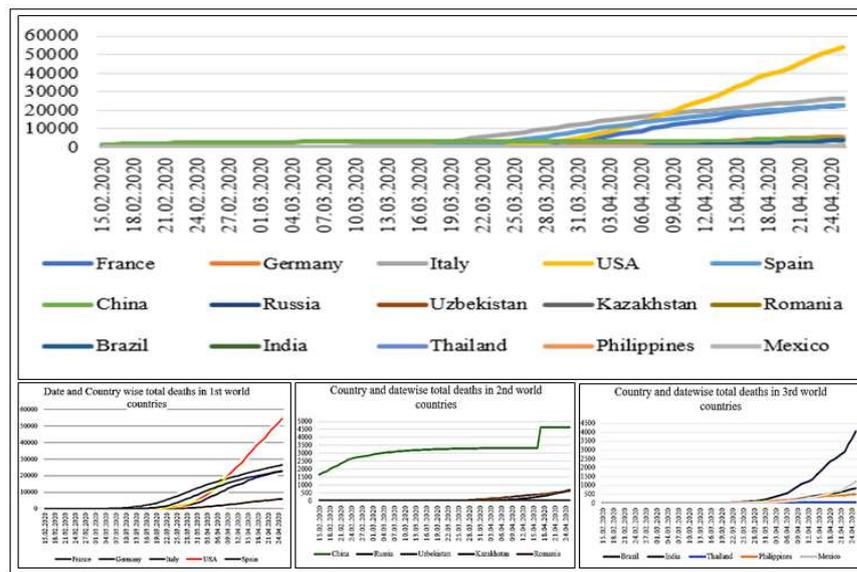


Figure 6. Date and Country wise total deaths

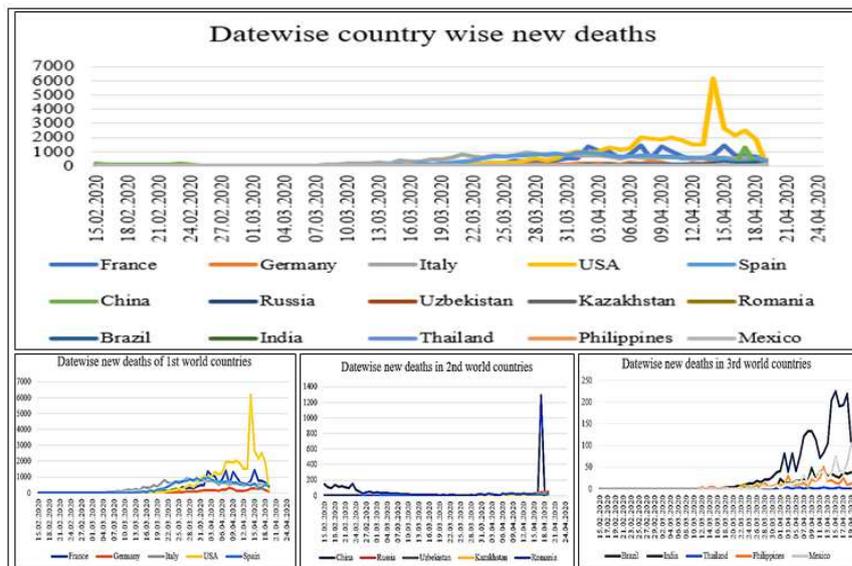


Figure 7. Date and country wise daily new deaths

Now, in the whole world, the death rate due to COVID-19 per day is 15.82%. The recovery rate from COVID-19 per day is 84.18% and the same for first world, second world and third world countries are shown in Table 1, which is very alarming for all. Date and Country wise total active cases, total deaths and daily new deaths have been shown in Figure 5, Figure 6 and Figure 7 respectively. The date wise worldwide cumulative death rate and recovery rates are shown in Figure 8, where it is clear that death and recovery both are undergoing a normal growth proportional to the currently active cases.

Country	Population	Population density (/km ²)	Average recovery rate from COVID 19 per day	Average death rate due to COVID 19 per day
USA	32.82 crores	36	—	—
France	6.7 crores	117	70.56	29.44
Spain	4.69 crores	96		
Italy	6.04 crores	206		
Germany	8.3 crores	227		
China	139.27 crores	379		
Russia	14.45 crores	8.4	95.15	4.85
Uzbekistan	3.3 crores	79		
Kazakhstan	1.83 crores	7		
Romania	1.94 crores	82		
India	135.26 crores	464		
Brazil	20.95 crores	24.66	68.25	17.06
Thailand	6.94 crores	137		
Mexico	12.62 crore	67		
Philippines	10.67 crore	368		

Table 1 Country wise recovery and death rate mapping with population

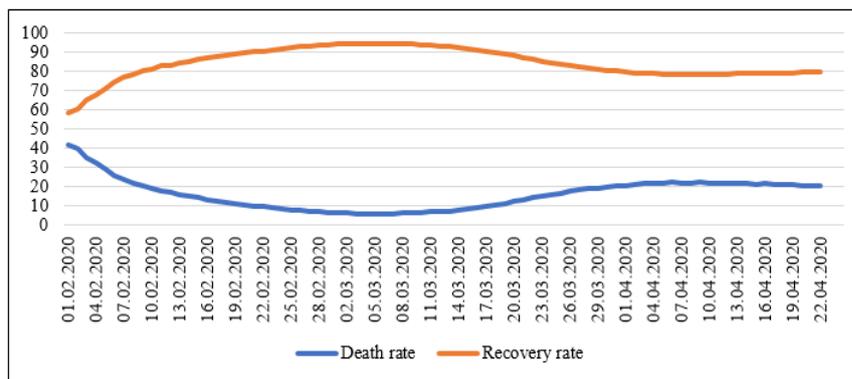


Figure 8. Datewise worldwide cumulative death rate and recovery rate in percentage

In the next section, existing literature in our concerned domain have been reviewed. In section 3, the proposed methodology for predicting the lockdown end dates of lockdown in the fifteen countries from first, second and third world has been discussed. The experimental result with comparison and performance evaluation have been presented in section 4 and finally the concluding statements and future directions of our proposed work have been discussed in Section 5.

2 Literature survey

Several research works are going on with different factors regarding the corona virus outbreak [2] [3] [4]. Somewhere the end dates of COVID-19 in different countries have been predicted [5], the size at the end [6] and somewhere the spread in the concerned countries has been modelled and predicted date wise [7], time series also has played a major role in estimation of transmission rate scaling [8]. Mahalle et al. have [9] discussed some challenges and recommended some strategies to control the outbreak. Different prediction techniques have been adopted using different platforms including mathematical modelling, big data, social media post, data science and machine learning here. Bholal et al. have shown in [10] that the only way to decrease the number of new infective with time is to totally isolate the infective from the susceptible population. Influenza epidemic about a century ago has shown how the situation can gets worse day by day just for the exponential growth due to the large number of susceptible people in India. The same can be repeated if the current situation goes uncontrolled or casually attended. The impact of travel restrictions due to COVID-19 has been discussed in [11] where the modelling results have shown that sustained 90% travel limitations to and from China diffidently affect the epidemic route. The results suggest that isolation, home quarantine and early detection are more effective than the travel restriction, because it has just delayed the progression of the virus within china by 3-5 days, but could not stop

it from propagation.

The current situation of China, mainly six provinces having most of the cases has been analysed in [12] [13] [14] whereas the same for Germany [15], Portugal [16], United States [17], Italy [18], Brazil [19] has been discussed in the recent literature. Although the spread of COVID-19 has been exponentially increased all over the world, still the fatality rate is not so alarming which gives residents of every country to re-establish the confidence to overcome and fight this pandemic together. However, the fatality rate for severe cases has been observed as 10% for which, the governments need to adopt proper series of strategies as early as possible. Numerical analysis of COVID-19 has been conducted in [20] where recovery rate and transmission rate characteristics have been tracked and the future trend has been predicted in addition. Deterministic Susceptible-Infected-Removed(SIR) model can be enhanced to stochastic model in future to achieve a better precision in the experimental result. The novel feature of this specific one is the ability of it to spread in the latent time, thus the time delay has been considered in differential equations formed by Chen et al. for proposal of a dynamic model to describe the pandemic in China [21]. Transmission route of the virus has been analysed in [22] using decision tree and prior algorithms, but due to no implementation in terms of programming or coding, there is a chance of data to be missed and more algorithms need to be added for checking the overall performance of the proposed approach. Spread of COVID-19 in Hubei of China has been modelled and predicted in [23], where the characteristics of populations like effect of age, people having other health problems, steps taken already for controlling the spread have not been studied, whereas decisions like lockdown and social distancing and its effects have been taken into consideration in our model, the novelty of our proposed model lies here.

Yafia has presented a modelling and dynamics with social distancing and isolation effect applied to Moroccan people [24]. Level of abstraction for the available data has been a major concern in [25] where modelling of biological systems has taken place to understand the spreading pattern of covid-19. Li et al. have presented a time series and kinetic analysis model where they have proved that emergency interventions regarding the restriction in people going out by Chinese government have a great impact on the spread of the pandemic [26]. Experimental results find out that bodies of deceased people do not result in additional infection and recovered people get an advantage of the prepared antibodies in their body which prevent reinfections later. Delay in identifying the symptoms and Chinese medicine preparation have been considered as the factors contributing to modified viral shading dynamics patterns of COVID-19 as mentioned by He et al. in [27]. The first 425 cases have been considered by Guan et al. for determination of epidemic characteristics in terms of mean incubation time [28] [29], mean serial interval, confidence interval, basic reproduction number and concluded that transmission took place from the middle of December 2019 in [30]. The transmission record of early stage from January

10 to January 24 has been analysed and observed exponential growth in [31]. The experimental results identify the potential of the virus to cause outbreaks in Mainland China. With the increase in the reporting rate from 8-fold to 0-fold, the mean of basic reproduction number has been calculated in [32] which is a little bit higher than the same measure reported by WHO. The measurement is typically based on the accuracy of determining Susceptible-Infected, which requires sufficient amount of patient samples over a significant follow up time.

In comparison with China, higher death rates and lower recovery rate observed due to Severe Acute Respiratory Syndrome CoronaVirus 2 (SARS-CoV-2) has proved that most of the Italian cases are of severe infection because of delayed lockdown and initially lower restrictions [33][34]. Awareness in general people are mandatory for effective interventions of government, and thus the number of affected people in Iran has been estimated upto 15th April in Zareie et al.'s research work [35]. Twenty countries all over the world have been considered in [36] for providing reliable statistics of the COVID-19 scenario. The transmission model has been characterized using parameters from the existing literature or some reasonable values, which somehow depend on the strength and the speed of drugs to be undertaken. Basic reproduction number, non-affecting period, pre symptom affecting period, probability of severity development, probability of severity diagnosis, probability of mild case diagnosis as well have been the factors contributing to successful pandemic modelling. Being the second epicentre of COVID-19 spread, Italy has been the main focus of the study conducted by Russo et al. in [37] where they have used SEIRD model (S: Susceptible, E: Exposed, I: Infected without symptoms, R: Recovered, D: Deceased) considering two categories of population, Asymptomatic one not having proper symptoms of the disease and another one. i.e. Symptomatic is having significant symptoms. Genetic algorithm has been used to optimize the objective function base on all the combinations of initial predictions of pandemic dynamics.

Control reproduction number and basic reproduction number have been the two factors of analytical calculation in Nadim et al.'s work [38] for observation of the dynamics of this epidemic in five provinces of China. Research outcomes show that for reduction of the burden, management of quarantined people is more effective than the management of isolated people. The effect of border control on the transmission of COVID-19 has been studied by investigating the outbreak trend in mostly visited ten cities of China in [39] where risk assessment has been done. The platform can be used in multiple affected sources to multiple target destinations by keeping the computational complexity constant using different control measurements. Volpert et al. have analysed disease transmission data and found three possible patterns, i.e. growth-decay-growth dynamic, growth-decay dynamics and growth dynamics discussed in [40]. Imposed quarantine should be stricter to be effective, because the current one is not sufficient. The evolution of COVID-19 has been performed and fu-

ture possibilities have been predicted using the extended version of composite Monte-Carlo model integrated with Deep learning and fuzzy rule in [41] where the main focus was decision making where the other existing works have concentrated on disease modelling only. The duration and severity of lockdown should be scheduled against their impact on economy, as whenever these measures will be relaxed a bit, the disease transmission trend will go back to its original exponential growth [42]. Impact of COVID-19 on economy has been evaluated in [43] by solving a stylized production-based asset pricing model with the use of transmission rate estimated by SIR model of China, Japan and Korea. Four mostly infected regions of China and five mostly infected regions of Italy have been the focus of research in [44] where the assumption of COVID-19's omission during summer has been investigated by considering three environmental factors, i.e. highest wind speed, maximum temperature and maximum relative humidity. Research findings show that the first and the third one is negligible, whereas the impact of the second factor to the virus transmission can be ranged between negligible to moderate. However, preliminary data has been used here, it can hold stronger conclusion whenever more data becomes available.

2.1 Motivation

In the current situation due to the pandemic, where the worldwide infection and decease rate are really very alarming, the world needs quick recovery and for that, a proper prediction regarding the transmission range, transmission trend and decision making of lockdown measures are needed. From the existing literature, it is clear that there have been many attempts to predict the disease-spreading trend but all of them have considered only either their own country [2] [3] or maximum two or three countries from all over the world. However, as the isolation and social distancing guidelines need to follow the steps taken in the already recovered countries, it is required to analyse the decisions made by all of them [1] and the factors like population density due to which, the decision should vary country wise, also should be taken into account for better understanding and analysis of the situation. In this regard, the objective of our proposed work has come into picture and the approaches like the well known SIR model and regression, which have history of accurate prediction of earlier diseases [15], have been applied in our work to get a better accuracy and efficiency in the prediction.

2.2 Contribution

This paper contributes in the concerned field in terms of prediction for fifteen countries from first, second and third world and in decision making for lockdown there. None of the existing works have considered worldwide disease transmission trend to predict the nature of the virus infection, so the novelty

of our proposed work lies here. The main contributions can be summarized as follows

- The time dependent discrete SIR model has been able to predict and analyse the disease transmission trend.
- Change in the basic reproduction number, which is the indicator of the transmission trend, not the infection rate has shown that after lockdown it has decreased which eventually proves that the decision of lockdown was essential globally to control the massive impact of COVID-19 on the common people, especially to the population of the third world countries where the economic condition to handle the situation is really very poor.
- However, more strictness in the steps taken by the government authorities to maintain the social distancing and lockdown decisions could make the lockdown a success.

The comparative summary of the existing works and the motivation behind taking up our proposed work from their limitations have been presented in Table 2.

Ref. no.	Objective	Data source used	Area considered	Method and Simulation platform	Simulation parameter	Limitation found (if any)
[3]	Virus transmission rate identification	https://www.who.int	States of India	SIR model and Mathematica	Total case, recovered case & death	No consideration of lockdown and social distancing parameters
[6]	Estimation of final affected size	1. https://ourworldindata.org/coronavirus-source-data 2. https://www.worldometers.info/coronavirus	Not defined	MATLAB	Total case, recovered case & death	No consideration of country population density
[7]	Prediction of pandemic end	https://ourworldindata.org/coronavirus-source-data	Singapore and Italy	MATLAB	New cases per day	No consideration of country population density & social distancing
[10]	Prediction of undetectable infected population	http://www.nhc.gov.cn/xcs/yqtb/listgzbds.html	China	MSIER & Python	Total case, recovered case & daily new case	No comparison with the other countries transmission trend
Proposed TDD SIR	Decision making of lockdown	https://www.worldometers.info/coronavirus	Countries all over the world	Time dependent discrete SIR and Seikit learn of Python	Total case, recovered case, daily new case, new death	Stochastic model & more regression methods can be applied to test the result

Table 2 Comparative study of proposed work with existing works

3 Proposed methodology

Hethcote has analysed different mathematical models in [45] and applied them in specific diseases according to the trend of spreading. Contact number, basic reproduction number, replacement number of SIR (S: Susceptible cases, I:

Infected cases, R: Removed cases), MSEIR (M: People having passive immunity, S: Susceptible population, E: People exposed to the disease, but not yet affected, I: Infected and spreading people, R: Recovered people having permanent immunity) [46] and SEIR models [47] have been reviewed and discussed which is used to estimate various disease patterns later. The basic reproduction number denoted as R_0 can be defined as the average number of infected people due to entrance of an infected one into a susceptible population. Age structure, spatial structure and heterogeneity have been considered as the main factors contributing to the trend of disease spread here.

3.1 SIR model for COVID-19

SIR model for detecting any disease as epidemic says that if λ is the density of susceptible birth, then

$$N = S + I + R = 0 \quad (1)$$

Where when $\lambda=0$,

N =total population

S =total susceptible people

I =total infected people

R =total removed people (dead/recovered) and the rate of change in susceptible population w.r.t. time is

$$\frac{ds}{dt} = \lambda - r(t)(1 - \alpha(t))(1 - \mu(t))S(t)I(t) - \alpha(t)S(t) \quad (2)$$

The rate of change in infected population w.r.t. time is

$$\frac{dI}{dt} = r(t)(1 - \alpha(t))(1 - \mu(t))S(t)I(t) - a(t)I(t) - \mu(t)I(t) \quad (3)$$

The rate of change in removed population w.r.t.time is

$$\frac{dR}{dt} = a(t)I(t) + \mu(t)I(t) + \alpha(t)S(t) \quad (4)$$

Where r =rate of getting infected,

a =average rate of recovery death,

α =lockdown rate of susceptible,

μ =isolation rate of infectious.

Therefore, the total change rate

$$\frac{dS}{dt} + \frac{dI}{dt} + \frac{dR}{dt} = 0 \quad (5)$$

The susceptible fraction of the population

$$s(t) = \frac{S(t)}{N} \quad (6)$$

The infected fraction of the population

$$i(t) = \frac{I(t)}{N} \quad (7)$$

The removed fraction of the population

$$r(t) = \frac{R(t)}{N} \quad (8)$$

and

$$s(t) + i(t) + r(t) = 1 \quad (9)$$

It has been assumed that $0 \leq l \leq 1$ and $0 \leq i \leq 1$ where l is the lockdown of susceptible rate and i is the isolation of infectious rate. The fraction of susceptible protected people is $(1-l)S$ and the fraction of un-isolated infectious people is $(1-i)S$. The basic reproduction number denoted by R_0 has been expressed in different forms during the first, second and third phase of outbreak in different countries.

The duration of first, second and third stages of outbreak in all the fifteen countries considered by us have been represented in Table 3 where the 1st phase denotes the appearance stage, the second stage deals with the local transmission and the third stage is concerned about community transmission. The initial stage is where the disease is first introduced and active cases start to emerge for the very beginning, in this stage, almost everyone is protected, because very few people have come across the persons with travel history. The local transmission is the spread of the disease from a person who has a travel history to his local people (family, neighbours and friends) or the spread from a directly contacted infectious person. The community transmission is the most dangerous stage where the source of transmission is very difficult to trace. The newly affected people have no history of being in contact with foreign sourced people or the people belonging to hotspot areas. Phase 4 or the widespread outbreak has been faced by China only until the number of cases and deaths begin to grow exponentially; Italy and USA are apparently in this stage now.

3.2 Time Dependent Discrete SIR (TDDSIR) model

Using time dependent discrete SIR model, equations (2), (3), (4) have been modified

$$S(t+1) - S(t) = \frac{-r(t)S(t)I(t)}{N} \quad (10)$$

$$I(t+1) - I(t) = \frac{r(t)S(t)I(t)}{N} - a(t)I(t) \quad (11)$$

$$R(t+1) - R(t) = a(t)I(t) \quad (12)$$

At the very first stage, the number of confirmed cases is very low and it can be assumed that most of the total population is in susceptible stage ($N \approx S(t)$).

So, by modifying equation (11), we get

$$I(t+1) - i(t) = r(t)I(t) - a(t)I(t) \quad (13)$$

Daily recovery rate and transmission rate can be denoted by

$$a(t) = \frac{R(t+1) - R(t)}{I(t)} \quad (14)$$

and

$$r(t) = \frac{R(t+1) - R(t) + I(t+1) - I(t)}{I(t)} \quad (15)$$

3.2.1 Detection of transmission and recovery rate using Ridge regression

Finite impulse response filter [50] can be used to predict the transmission and recovery rate denoted as follows

$$r'(t) = p_0 + p_1 r(t-1) + p_2 r(t-2) + p_3 r(t-3) + \dots + p_c r(t-c) = p_0 + \sum_{c=1}^C p_c r(t-c) \quad (16)$$

$$a'(t) = q_0 + q_1 a(t-1) + q_2 a(t-2) + q_3 a(t-3) + \dots + q_d a(t-d) = q_0 + \sum_{d=1}^D q_d a(t-d) \quad (17)$$

Where C and D are the orders of the two filters having coefficients p_c ($0 \leq c \leq C$) and q_d ($0 \leq d \leq D$) respectively and $r'(t)$ and $a'(t)$ are the predicted transmission and predicted recovery rate. There are various machine learning methods like partial least square, regularized least square (also called ridge regression) and original least square method to solve the following optimization problem

$$\min_{p_c} \sum_{t=C}^{T-2} (r(t) - r'(t))^2 + \gamma_1 \sum_{c=0}^C p_c^2 \quad (18)$$

and

$$\min_{q_d} \sum_{t=D}^{T-2} (a(t) - a'(t))^2 + \gamma_2 \sum_{d=0}^D q_d^2 \quad (19)$$

Where γ_1 and γ_2 are its regularization parameters respectively.

3.2.2 Detection of number of affected persons and recovered persons

Finite impulse response filter can be used to forecast the amount of affected and recovered population by previously discussed time dependent SIR model. After calculating the transmission rate and recovery rate according to (14) and (15), the ridge regression is used to solve the optimization problems of (18) and (19) keeping the constraints of (16), (17) to learn the pattern of coefficients of finite impulse response filter.

For predicting the affected and recovered population, $r(t)$ and $a(t)$ have been replaced by $r'(t)$ and $a'(t)$ in equation (17) and (18) where the predicted number of affected people and recovered people at time $t = T$ are denoted as $I'(T)$ and $R'(T)$. This leads to

$$I'(T) = (1 + r'(T - 1)) - a'(T - 1)I(T - 1) \quad (20)$$

$$R'(T) = R(T - 1) + a'(T - 1)I(T - 1) \quad (21)$$

When $t > T$ the affected and recovered population can be predicted as follows

$$I(t + 1) = (1 + r'(t) - a'(t))I(t) \quad (22)$$

$$R'(t + 1) = R(t) + a'(t)I(t) \quad (23)$$

The deterministic model for epidemic considered by us is more appropriate to large population. So, when $I(t)$ and $R(t)$ are comparatively trivial, the accuracy may not be as desired, in that case, stochastic model like Markov Chain can be used to approximate and forecast the factors according to requirement in the future and more regression methods can be applied to check if any of them is giving better result. The algorithm of the prediction method is as follows.

ALGORITHM: Predicting time dependent discrete SIR model
Input: $I(t), R(t), 0 \leq t \leq T-1$, regularization parameters γ_1 and γ_2 , two filters C and D , forecasting window F
Output: $r(t), a(t), 0 \leq t \leq T-2$ $r'(t), a'(t), t \geq T-1$ $I'(t), R'(t), t \geq T$
Step 1: Calculate $r(t)$ and $a(t)$ using (15) and (14) respectively when $0 \leq t \leq T-2$
Step 2: Train them with ridge regression using (18) and (19)
Step 3: Calculate $r(T-1)$ and $a'(T-1)$ using (16) and (17)
Step 4: Calculate $I'(T)$ and $R'(T)$ for the next day T using (20) and (21)
Step 5: If $T \leq t \leq T+F$ do Calculate $r'(t)$ and $a'(t)$ using (16) and (17) Estimate $I'(t+1)$ and $R'(t+1)$ using (22) and (23) respectively End if
Step 6: End

3.3 Steady state solutions

According to the steady state solution, the probable duration of susceptibility can be defined by $P(\min(T_L|T_S))$ where T_L is the duration of being alive and T_S is the duration of remaining in susceptible state before being affected. The probable duration can be expressed by

$$P(\min(T_L|T_S)) = \int_0^\infty e^{-(\mu+\lambda)x} dx = \frac{1}{\mu + \lambda} \quad (24)$$

The equilibria of steady state equilibrium states that the basic reproduction number

$$R_0 = \frac{r}{a} \quad (25)$$

where $\frac{dI}{dt} > 0$ when $R_0 > 1$ implies that the number of affected people increases with the increase in reproduction number and decreases with the decrease in the reproduction number.

4 Trend of disease progression with lockdown

The resolved factor R depends on S and I, so here we have restricted our implementation to SI. With the progress of disease spreading over a longer time, the new births have been considered. In this scenario, the system can be represented by

$$\frac{ds}{dt} = \lambda - (1 - \alpha)r(1 - \mu)SI - \alpha S \quad (26)$$

$$\frac{dI}{dt} = (1 - \alpha)r(1 - \mu)SI - aI - \mu I \quad (27)$$

To detect the effectiveness of social distancing approach we have divided the infected population into two categories by extending the conventional SIR model. The first one is called Type I who are generally the detectable infected persons and the second one is called Type II who are undetectable infected person. If the probability of an infected people becoming detectable is denoted by p_1 and becoming undetectable is p_2 , then

$$p_1 + p_2 = 1 \quad (28)$$

If the transmission rates among Type I and Type II people are denoted by r_1 and r_2 respectively and the recovery rates for the same are a_1 and a_2 , then

$$R_0 = p_1 \frac{r_1}{a_1} + p_2 \frac{r_2}{a_2} \quad (29)$$

In practical scenario, Type II population has a higher transmission rate than that of a Type I population. The controllable measure of the disease is indicated by spectral radius which in turn shows that if the basic reproduction number $R_0 > 1$, then there is some outbreak, and if it is < 1 , then no outbreak

is there. Allowing all to keep their interpersonal contacts upto a fraction of normal contacts and cancelling mass gatherings, these two approaches of maintaining social distance have been considered here. The lockdown in the whole country announced by government has definitely acted as infection controller and helped India to face the challenge of COVID-19 in the desired form.

5 Experimental Result and Discussion

The following section describes different aspects of our proposed work for analysis of lockdown effect on the disease transmission and discusses the contribution in terms of novelty and performance evaluation as well.

5.1 Dataset preparation and validation

The proposed work for analysis and prediction of worldwide COVID-19 has been carried out using the dataset collected from worldometer[48], which is developed and maintained by an international group of researchers and developers, having an aim of making world statistics available in a time relevant format and has been recognised as the best free reference website by American Library Association. Several researchers considered this for undertaking their research on COVID-19. Number of daily new cases, daily recovered population, datewise total cases and active cases have been used as the parameters for analysis and prediction of the disease transmission trend and impact of lockdown on it.

5.2 Analysis of lockdown effect on disease transmission

There is no confusion that many factors affect the propagation of the virus, establishing a dynamic propagation model from the estimated factors is a tough job, but basic estimation of some parameters like mortality and latency can take place to help people for being cautious about the transmission trend and acting accordingly. The time evolution of the outbreak has been analysed by time dependent SIR model and represented in Figure 9- Figure 11. Result of mathematical modelling in Figure 9 shows date-wise actual recovered population vs predicted recovered population using SIR model from where it is evident that our prediction results are quite near to the reality and proposed model suits its concerned domain.

As it is not feasible to give the whole basic reproduction number calculation and daily new case prediction result in the paper, thus only for one country from each first, second and third world, the same are shown for the duration of ten days, which is from 20.03.2020 to 30.03.2020 in Table 3 and 4 respectively.

Country	21.03	22.03	23.03	24.03	25.03	26.03	27.03	28.03	29.03	30.03
France	0	2.38	0	2.122	4.24	3.32	4.51	0	1.68	5.45
China	0.17	0.08	0.16	0.12	0.12	0.14	0.11	0.15	0.037	0.19
India	0	0	0	0	0.80	0.45	0.65	0.08	0.09	0.34

Table 3 Basic reproduction number calculation from 21.03.2020 to 30.03.2020

Country	21.03	22.03	23.03	24.03	25.03	26.03	27.03	28.03	29.03	30.03
Germany	2516	2509	4183	3935	4332	6615	6933	6822	4740	4450
France	1847	1559	3838	2448	2929	3922	3809	4611	2599	4376
Italy	6557	5560	4789	5249	5210	6203	5909	5974	5217	4050
USA	4848	9400	10311	11366	13451	17388	18743	19452	20065	20732
India	0	1	0	2	3	1	22	17	11	36

justification=centering

Table 4 Daily new case prediction from 21.03.2020 to 30.03.2020

A free machine learning library of Python 3, Scikit-learn has been used for running the ridge regression calculation. Since the transmission rate can never be a negative one, it has been set as 0 when it is 0 and since the data before 15th February, 2020 is very small and sometimes unavailable which can result to a noise in analysing the trend, so only the data onwards 15.02.2020 has been considered here. In an epidemic model, one question always arises that whether the epidemic will end and whether a certain population may be infected from the total population due to the conversion of disease nature from epidemic to pandemic. For answering these questions, the parameter of basic reproduction number is defined as the number of infected people by an already infected person before his/her recovery or death. In the classical SIR model, it is simply the ratio of the number of persons in contact with an infected one and number of days he/she takes to recover which is modified as a function of time in the time dependent SIR model later. When the basic reproduction number is calculated as greater than 1, in that scenario, the disease is said to spread exponentially and a certain fraction of the total population is said to be affected eventually.

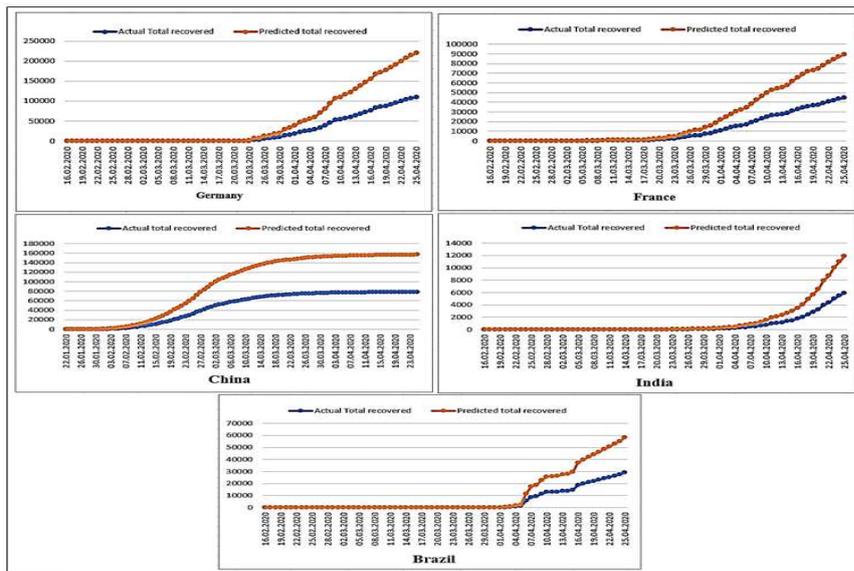


Figure 9. Date-wise actual total recovered population vs predicted total recovered population in five most affected countries

The predicted daily new cases have been compared to the actual daily-infected population in Figure 10 for the most affected twelve countries among the fifteen countries considered by us, where it is clearly seen that SIR model has been able to predict the infection rate and infected population efficiently. Deviation is there but predicted graph is following the pattern of actual one.

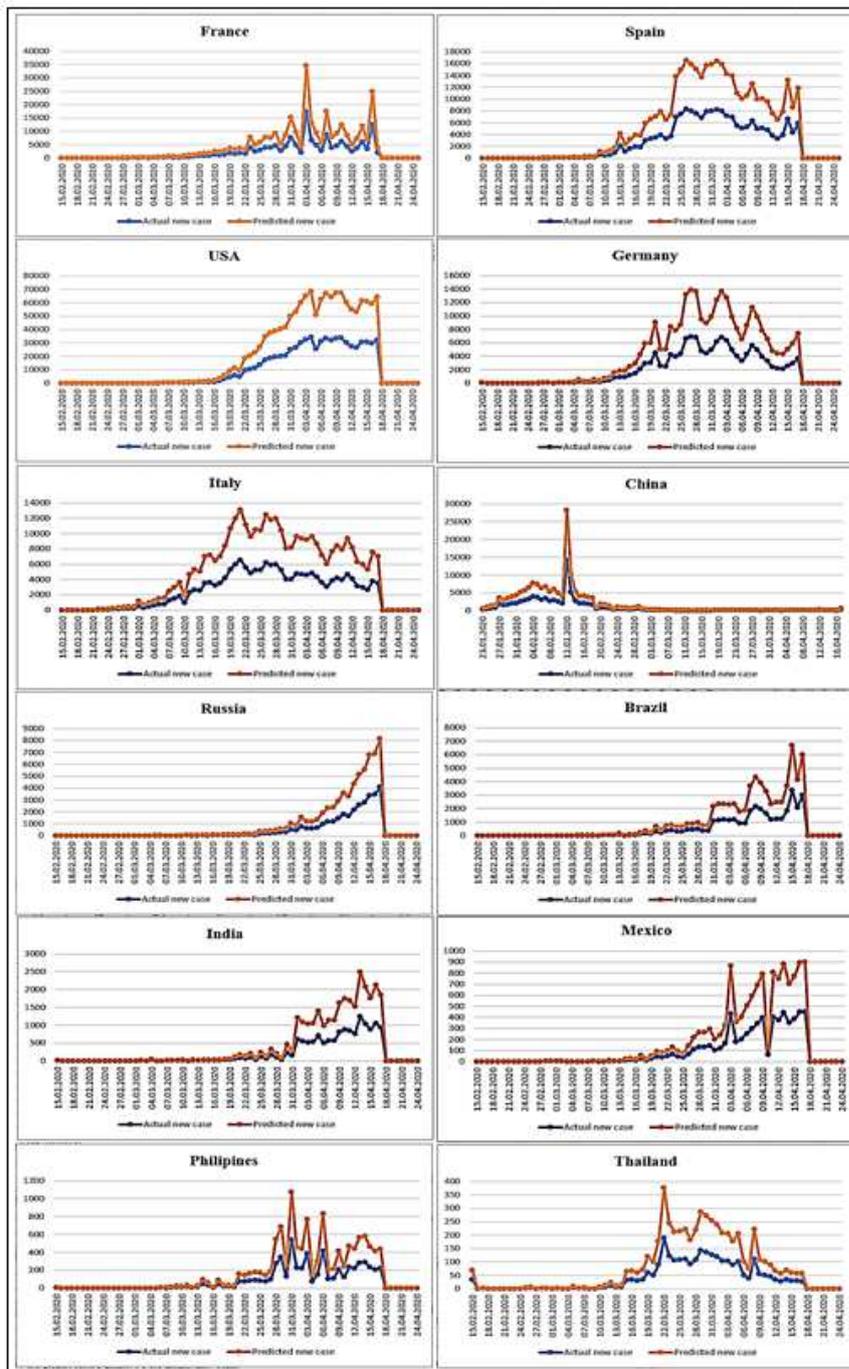


Figure 10. Actual daily new cases vs predicted new cases

The effect of lockdown in the basic reproduction number (R_0) of five most affected countries according to our research, i.e. France, Germany, India, China and Brazil has been shown in Figure 11 where the transmission rate is concerned, not the infected people. After lockdown, the infected population has increased exponentially, it means it has followed its previous trend, but the basic reproduction number, which is basically the ratio of transmission rate and recovery rate, has decreased globally and the change has been marked by the black circles, so we can conclude that lockdown decision is obviously an effective one and if its more strict, then the infected population can also decrease and once the vaccine comes to the market, people will be safe.

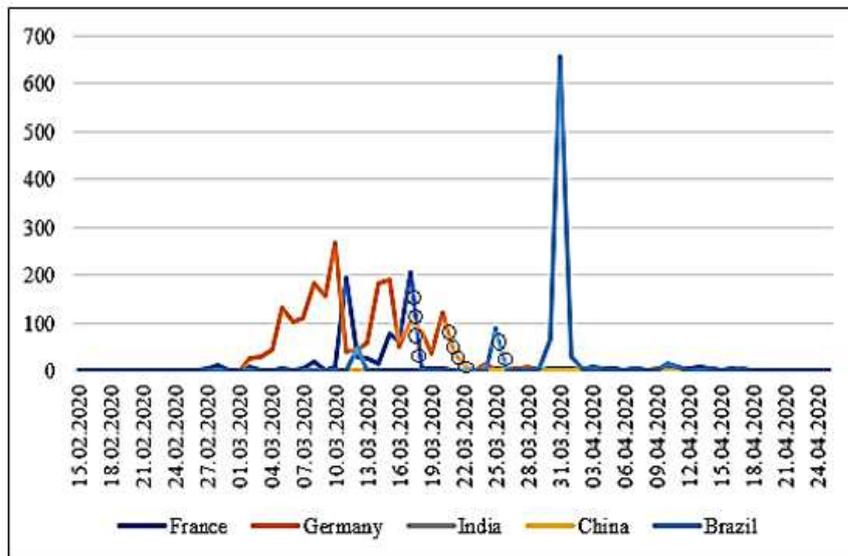


Figure 11. Change in basic reproduction number after lockdown in the five most affected countries

Therefore, the experimental results show that prediction of infected population and recovered population both have some minor error when the predicted result is compared to the actual one. Moreover, we have been able to track the transmission trend and characteristics with respect to time for fifteen countries all over the world. To understand the impact of social distancing during lockdown imposed by the concerned governments, it has been seen that proper social distancing can lead to decrease in propagation rate.

6 Conclusion

The role of lockdown on susceptible people and isolation of infectious people has been discussed in this paper based on the basic reproduction number of SIR model on epidemic spread in general. Three different phases of corona virus

spread in different countries have been considered here for the analysis: Beginning/ first phase of the outbreak (3rd-8th March), Intermediate stage/ second stage of the outbreak (9th-19th march), Third stage of contamination (20th march-till date). In the first stage, the cumulative growth rate was moderate where as in the second stage of the epidemic, the transmission rate gets higher and the infection rate increases drastically. In the third and the final stage, the lockdown and isolation effects have been taken into account; the transmission rate has been smaller when compared to the previous phase. Since the basic reproduction number somewhere depends on the lockdown decision and actions, it has been evident that with the increasing rate of lockdown and isolation, the reproduction number has been less than 1. The challenges of predicting these kinds of parameters include: a) Lack of proper data, b) No proper lockdown imposed by governments, c) No proper tracking of active and new cases.

In future, these shortcomings will be attempted to overcome for getting improved result of the scenario and experimental results show that our proposed approach is well suited in its concerned domain. However, the prediction will change based on some external factors like government decisions and human actions, so we can't train the data as of today to be true for a different situation in future. Our modified SIR model is not only productive than the traditional one, but also more capable of handling and adopting the current situation.

References

1. "World Health Organization," May 2020. [Online]. Available: <https://www.who.int/emergencies/diseases/novel-coronavirus-2019/>
2. Chen, B., Liang, H., Yuan, X., Hu, Y., Xu, M., Zhao, Y., Zhang, B., Tian, F. and Zhu, X., 2020. Roles of meteorological conditions in COVID-19 transmission on a worldwide scale. medRxiv.
3. Sun, P., Lu, X., Xu, C., Sun, W. and Pan, B., 2020. Understanding of COVID-19 based on current evidence. *Journal of medical virology*.
4. Brüssow, H., 2020. The novel coronavirus—a snapshot of current knowledge. *Microbial Biotechnology*, 13(3), pp.607-612.
5. Luo, J., 2020. When Will COVID-19 End? Data-Driven Prediction. Working paper. <https://ddi.sutd.edu.sg>.
6. Batista, M. (2020). Estimation of the final size of the coronavirus epidemic by the SIR model.
7. Arti, M. K., Bhatnagar, K. Modeling and Predictions for COVID 19 Spread in India. ResearchGate, DOI: DOI, 10.
8. Bjørnstad, O. N., Finkenstädt, B. F., Grenfell, B. T. (2002). Dynamics of measles epidemics: estimating scaling of transmission rates using a time series SIR model. *Ecological monographs*, 72(2), 169-184.
9. Mahalle, P., Kalamkar, A. B., Dey, N., Chaki, J., Shinde, G. R. (2020). Forecasting Models for Coronavirus (COVID-19): A Survey of the State-of-the-Art.

10. Bholá, J., Venkateswaran, V.R. and Koul, M., 2020. Corona Epidemic in Indian context: Predictive Mathematical Modelling. medRxiv.
11. Chinazzi, M., Davis, J. T., Ajelli, M., Gioannini, C., Litvinova, M., Merler, S., ...Viboud, C. (2020). The effect of travel restrictions on the spread of the 2019 novel coronavirus (COVID-19) outbreak. *Science*.
12. Liu, T. H. A Time-dependent SIR model for COVID-19 with Undetectable Infected Persons.
13. Lai, S., Bogoch, I. I., Ruktanonchai, N., Watts, A. G., Li, Y., Yu, J., ... Li, Z. (2020). Assessing spread risk of Wuhan novel coronavirus within and beyond China, January-April 2020: a travel network-based modelling study
14. Li, Q., Feng, W., Quan, Y. H. (2020). Trend and forecasting of the COVID-19 outbreak in China. *Journal of Infection*, 80(4), 469-496.
15. Rothe, C., Schunk, M., Sothmann, P., Bretzel, G., Froeschl, G., Wallrauch, C., Zimmer, T., Thiel, V., Janke, C., Guggemos, W. and Seilmaier, M., 2020. Transmission of 2019-nCoV infection from an asymptomatic contact in Germany. *New England Journal of Medicine*, 382(10), pp.970-971.
16. Teles, P. (2020). Predicting the evolution of SARS-Covid-2 in Portugal using an adapted SIR Model previously used in South Korea for the MERS outbreak. arXiv preprint arXiv:2003.10047.
17. Liu, P., Beeler, P., Chakrabarty, R. K. (2020). COVID-19 Progression Timeline and Effectiveness of Response-to-Spread Interventions across the United States. medRxiv.
18. Jia, W., Han, K., Song, Y., Cao, W., Wang, S., Yang, S., ... Liu, M. (2020). Extended SIR prediction of the epidemics trend of COVID-19 in Italy and compared with Hunan, China. medRxiv.
19. Rocha Filho, T. M., dos Santos, F. S. G., Gomes, V. B., Rocha, T. A., Croda, J. H., Ramalho, W. M., Araujo, W. N. (2020). Expected impact of COVID-19 outbreak in a major metropolitan area in Brazil. medRxiv.
20. Bai, Y., Yao, L., Wei, T., Tian, F., Jin, D. Y., Chen, L., Wang, M. (2020). Presumed asymptomatic carrier transmission of COVID-19. *Jama*.
21. Chen, Y., Cheng, J., Jiang, Y. and Liu, K., 2020. A time delay dynamical model for outbreak of 2019-nCoV and the parameter identification. *Journal of Inverse and Ill-posed Problems*, 28(2), pp.243-250.
22. Kim, D., Hong, S., Choi, S. and Yoon, T., 2016. Analysis of transmission route of MERS coronavirus using decision tree and Apriori algorithm. In 2016 18th International Conference on Advanced Communication Technology (ICACT) (pp. 559-565). IEEE.
23. Anstassopoulou, C., Russo, L., Tsakris, A. and Siettos, C., Data-based analysis, modelling and forecasting of the novel coronavirus [2019-nCoV] outbreak. medRxiv. 2020. Preprint. Available from: <https://doi.org/10.1101/2020.02.11>.
24. Lu, J., 2020. A New, Simple Projection Model for COVID-19 Pandemic. medRxiv.
25. Sameni, R., 2020. Mathematical modeling of epidemic diseases; a case study of the COVID-19 coronavirus. arXiv preprint arXiv:2003.11371.
26. Cao, J., Jiang, X. and Zhao, B., 2020. Mathematical modeling and epidemic prediction of COVID-19 and its significance to epidemic prevention and

- control measures. *J BioMed Res Innov*, 1(1), p.103.
27. He, X., Lau, E.H., Wu, P., Deng, X., Wang, J., Hao, X., Lau, Y.C., Wong, J.Y., Guan, Y., Tan, X. and Mo, X., 2020. Temporal dynamics in viral shedding and transmissibility of COVID-19. *Nature medicine*, pp.1-4.
28. Lauer, S.A., Grantz, K.H., Bi, Q., Jones, F.K., Zheng, Q., Meredith, H.R., Azman, A.S., Reich, N.G. and Lessler, J., 2020. The incubation period of coronavirus disease 2019 (COVID-19) from publicly reported confirmed cases: estimation and application. *Annals of internal medicine*, 172(9), pp.577-582.
29. Xia, W., Liao, J., Li, C., Li, Y., Qian, X., Sun, X., Xu, H., Mahai, G., Zhao, X., Shi, L. and Liu, J., 2020. Transmission of corona virus disease 2019 during the incubation period may lead to a quarantine loophole. *MedRxiv*.
31. Li Q, Guan X, Wu P, et al. Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia; 2020. Available from: <https://doi.org/10.1088%2F0951-7715%2F16%2F2%2F308>.
32. Zhao S, Lin Q, Ran J, Musa SS, Yang G, Wang W, et al. Preliminary estimation of the basic reproduction number of novel coronavirus (2019-nCoV) in China, from 2019 to 2020: A data-driven analysis in the early phase of the outbreak. *Int J Infect Dis*. 2020; doi:10.1101/2020.01.23.916395.
33. Wu JT, Leung K, Leung GM. Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *The Lancet*. 2020;doi:10.1016/s0140-6736(20)30260-9.
34. Caccavo, D. (2020). Chinese and Italian COVID-19 outbreaks can be correctly described by a modified SIRD model. *medRxiv*.
35. Zareie, B., Roshani, A., Mansournia, M. A., Rasouli, M. A., Moradi, G. (2020). A model for COVID-19 prediction in Iran based on China parameters. *medRxiv*.
36. Siwiak, M. M., Szczesny, P., Siwiak, M. P. (2020). From a single host to global spread. The global mobilitybased modelling of the COVID-19 pandemic implies higher infection and lower detection rates than current estimates. *medRxiv*.
37. Russo, L., Anastassopoulou, C., Tsakris, A., Bifulco, G. N., Campana, E. F., Toraldo, G., Siettos, C. (2020). Tracing DAY-ZERO and Forecasting the Fade out of the COVID-19 Outbreak in Lombardy, Italy: A Compartmental Modelling and Numerical Optimization Approach. *medRxiv*.
38. Nadim, S. S., Ghosh, I., Chattopadhyay, J. (2020). Short-term predictions and prevention strategies for COVID-2019: A model based study. *arXiv preprint arXiv:2003.08150*.
39. Hossain, M., Junus, A., Zhu, X., Jia, P., Wen, T. H., Pfeiffer, D., Yuan, H. Y. (2020). The effects of border control and quarantine measures on global spread of COVID-19.
40. Volpert, V., Banerjee, M., Petrovskii, S. (2020). On a quarantine model of coronavirus infection and data analysis. *Mathematical Modelling of Natural Phenomena*, 15, 24.
41. Fong, S.J., Li, G., Dey, N., Crespo, R.G. and Herrera-Viedma, E., 2020. Composite Monte Carlo decision making under high uncertainty of novel coro-

- navirus epidemic using hybridized deep learning and fuzzy rule induction. *Applied Soft Computing*, p.106282.
42. Botha, A.E. and Dednam, W., 2020. A simple iterative map forecast of the COVID-19 pandemic. arXiv preprint arXiv:2003.10532.
 43. Toda, A.A., 2020. Susceptible-infected-recovered (sir) dynamics of covid-19 and economic impact. arXiv preprint arXiv:2003.11221.
 44. Bhattacharjee, S., 2020. Statistical investigation of relationship between spread of coronavirus disease (COVID-19) and environmental factors based on study of four mostly affected places of China and five mostly affected places of Italy. arXiv preprint arXiv:2003.11277.
 45. Hethcote, H. W. (2000). The mathematics of infectious diseases. *SIAM review*, 42(4), 599-653.
 46. Almeida, R., da Cruz, A.M.B., Martins, N. and Monteiro, M.T.T., 2019. An epidemiological MSEIR model described by the Caputo fractional derivative. *International Journal of Dynamics and Control*, 7(2), pp.776-784.
 47. Li, M.Y. and Muldowney, J.S., 1995. Global stability for the SEIR model in epidemiology. *Mathematical biosciences*, 125(2), pp.155-164.
 48. "COVID-19 CORONAVIRUS PANDEMIC," May 2020. [Online]. Available: <https://www.worldometers.info/coronavirus>
 49. Z. Hu, Q. Ge, L. Jin, and M. Xiong, "Artificial intelligence forecasting of covid-19 in china," arXiv preprint arXiv:2002.07112, 2020.
 50. Saramaeki, T., Mitra, S.K. and Kaiser, J.F., 1993. Finite impulse response filter design. *Handbook for digital signal processing*, 4, pp.155-277.
 51. Pedregosa, F., Varoquaux, G., Gramfort, A., Michel, V., Thirion, B., Grisel, O., Blondel, M., Prettenhofer, P., Weiss, R., Dubourg, V. and Vanderplas, J., 2011. Scikit-learn: Machine learning in Python. *the Journal of machine Learning research*, 12, pp.2825-2830.

Figures

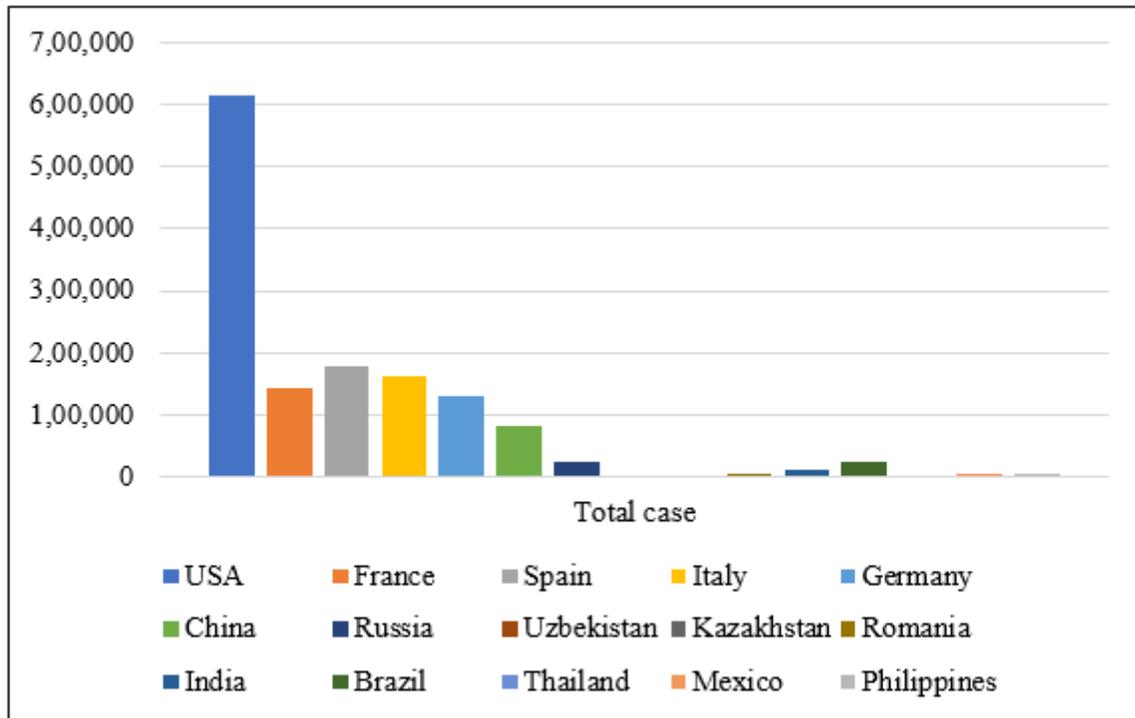


Figure 1

Country wise total cases upto 26.04.2020

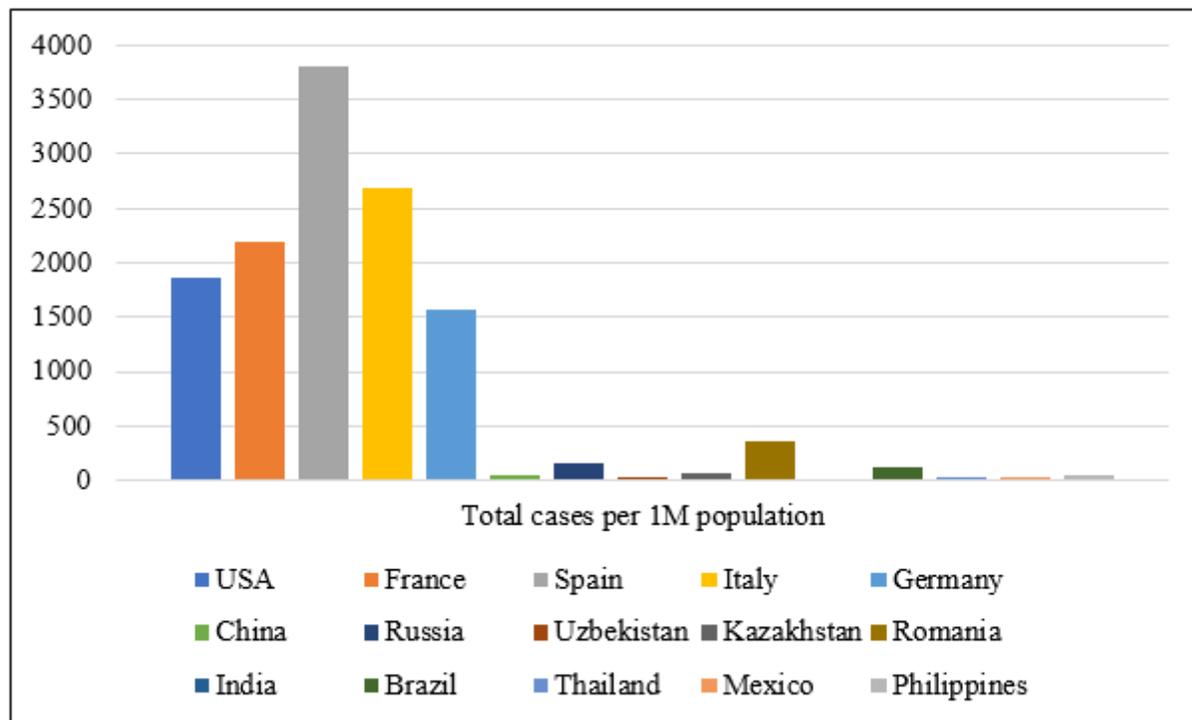


Figure 2

Country wise total cases per 1 million population

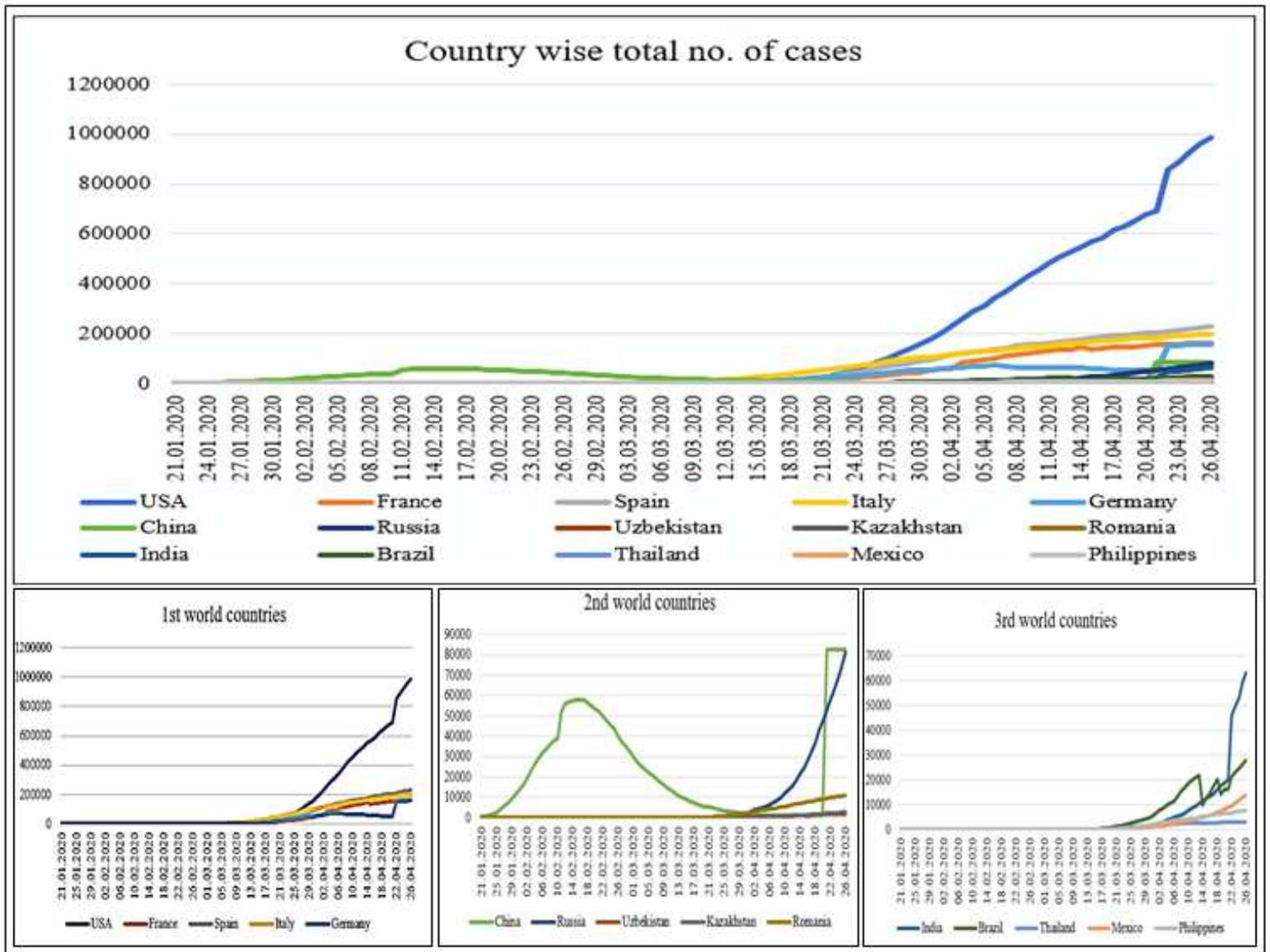


Figure 3

Date and country wise COVID-19 total cases

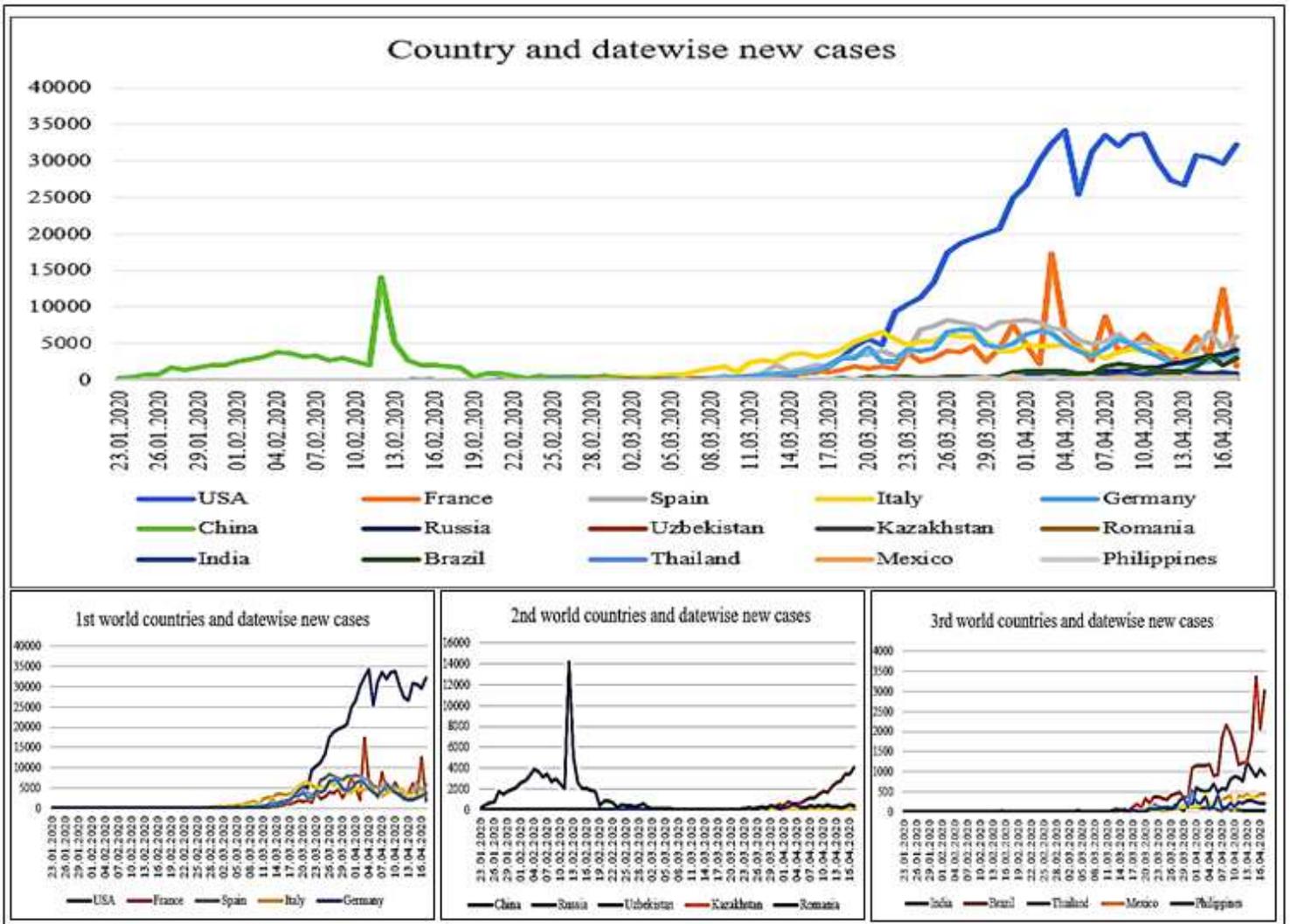


Figure 4

Date and country wise daily new cases

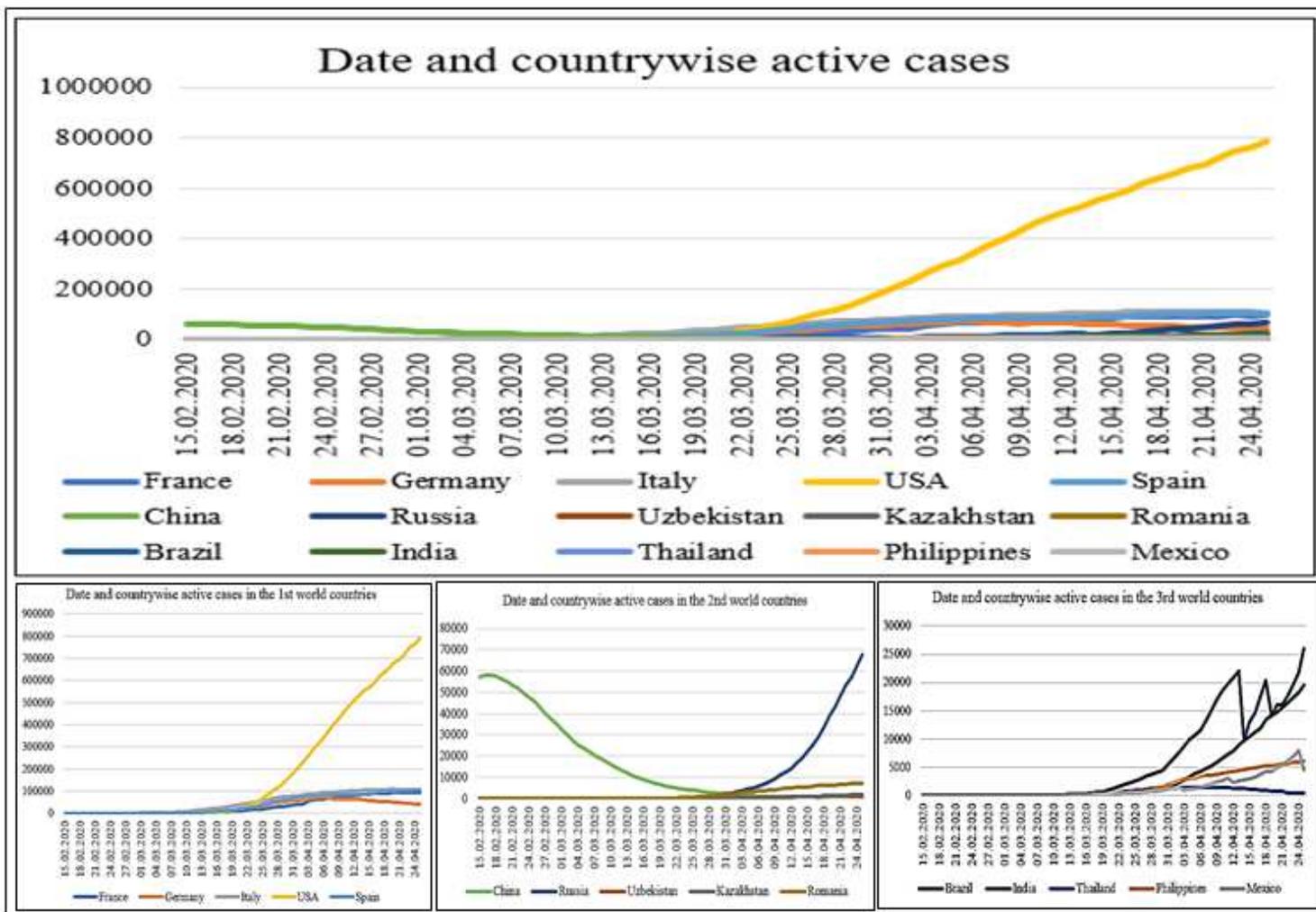


Figure 5

Date and Country wise total active cases

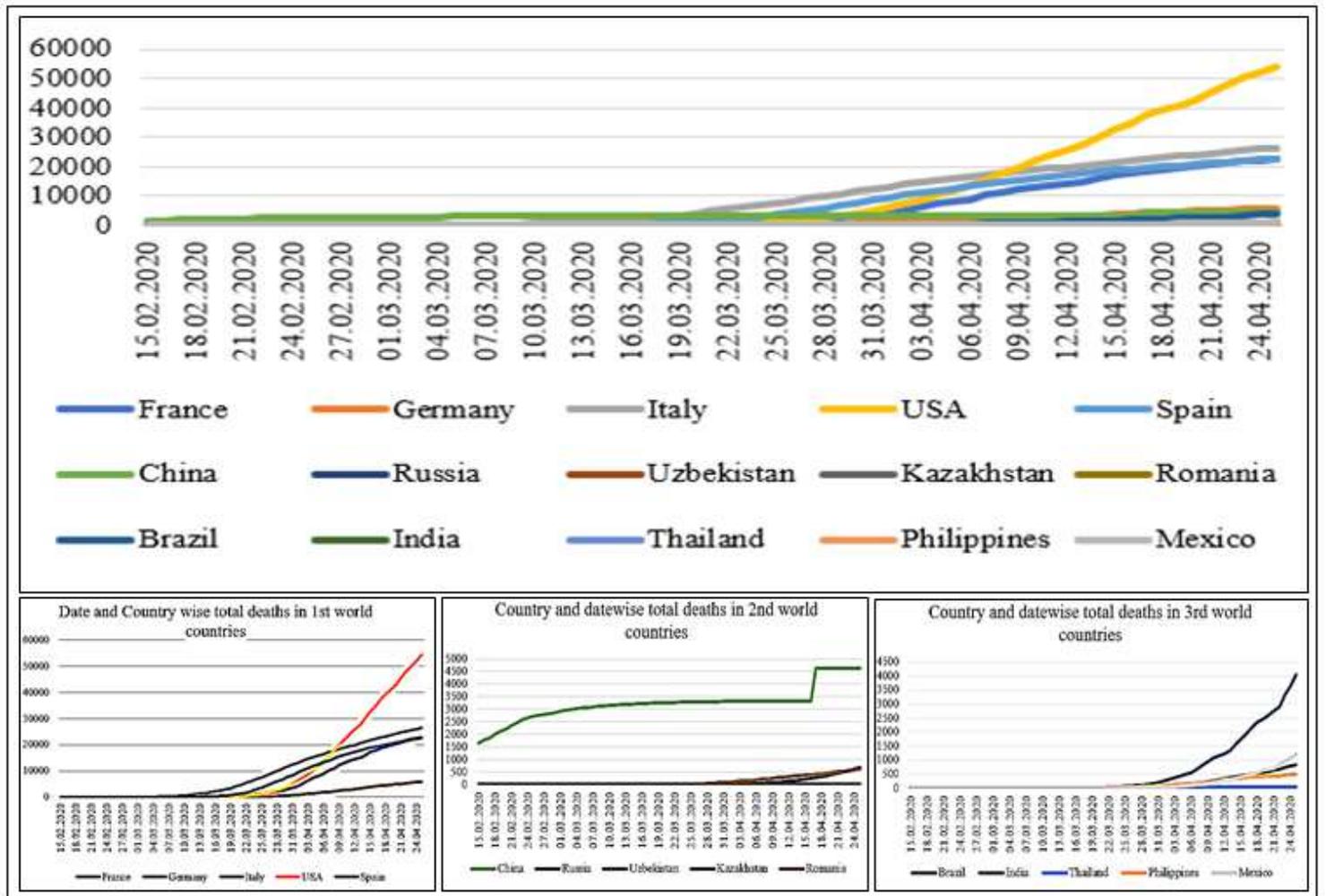


Figure 6

Date and Country wise total deaths

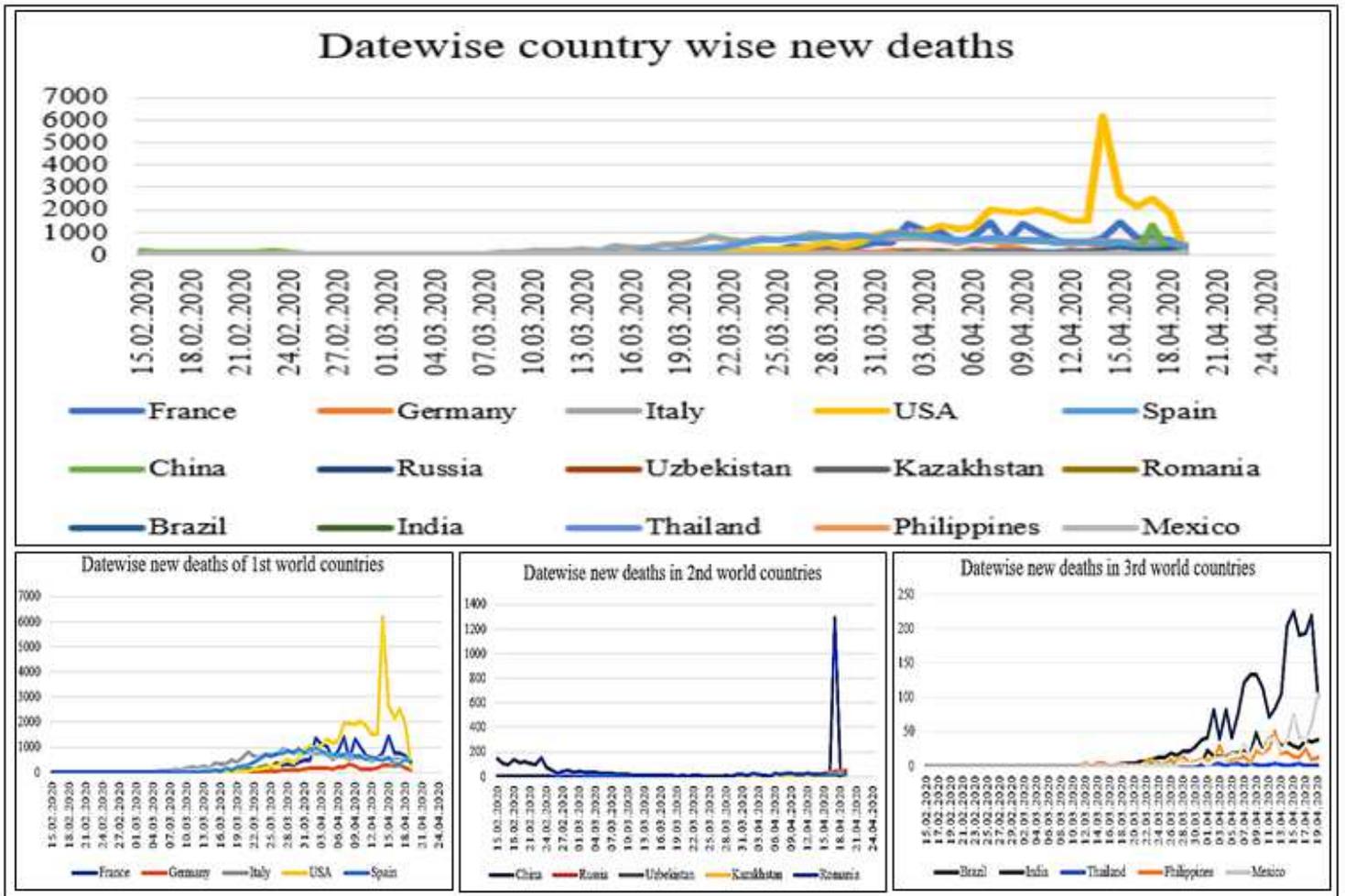


Figure 7

Date and country wise daily new deaths

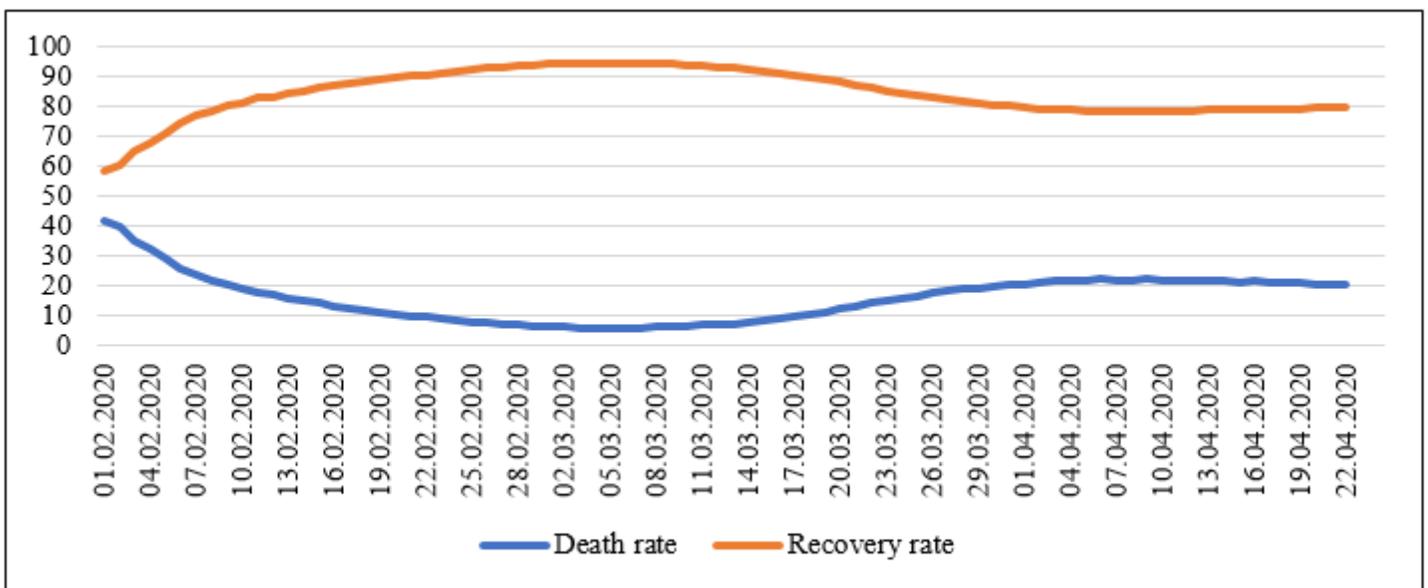


Figure 8

Date-wise worldwide cumulative death rate and recovery rate in percentage

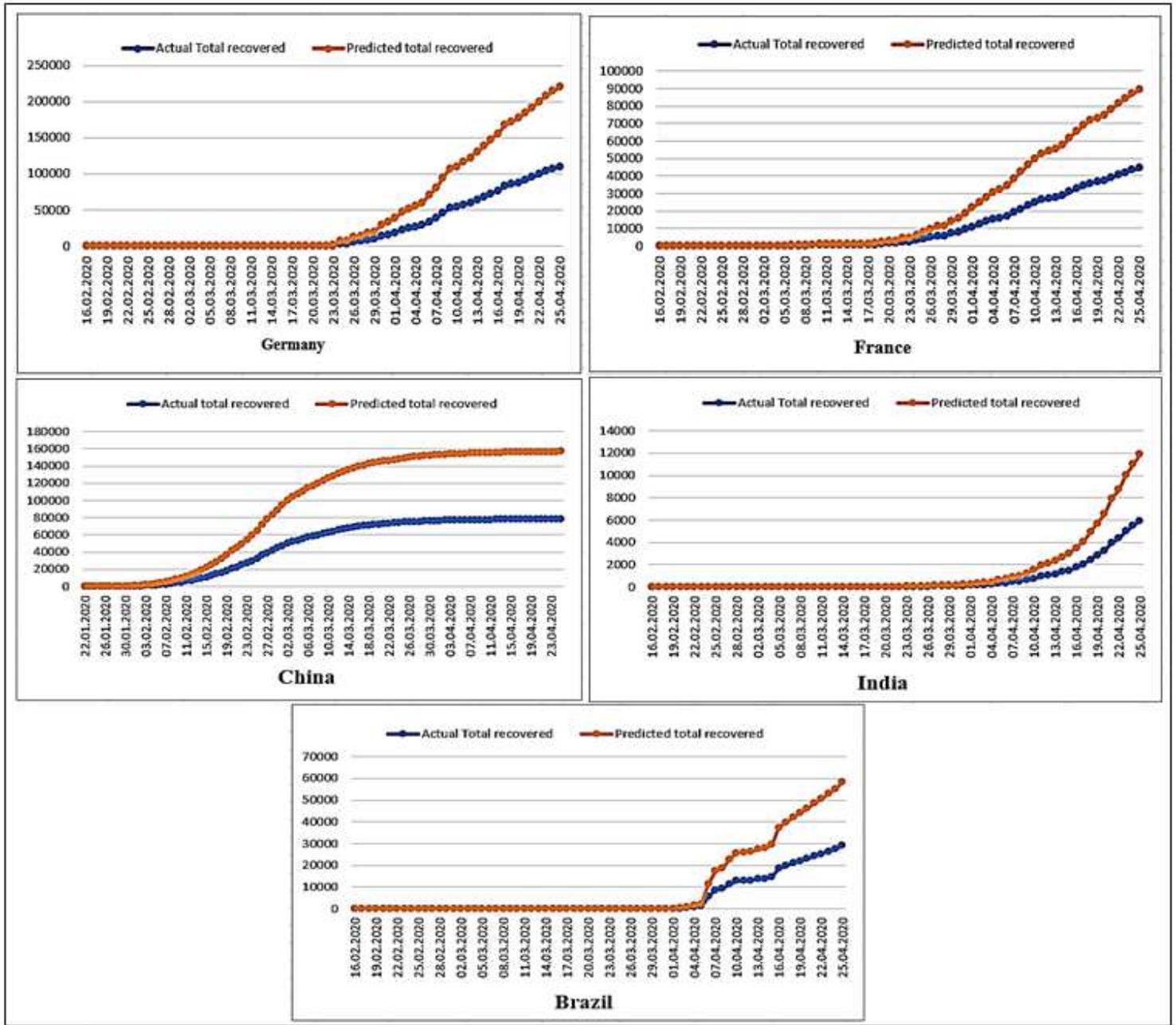


Figure 9

Date-wise actual total recovered population vs predicted total recovered population in five most affected countries

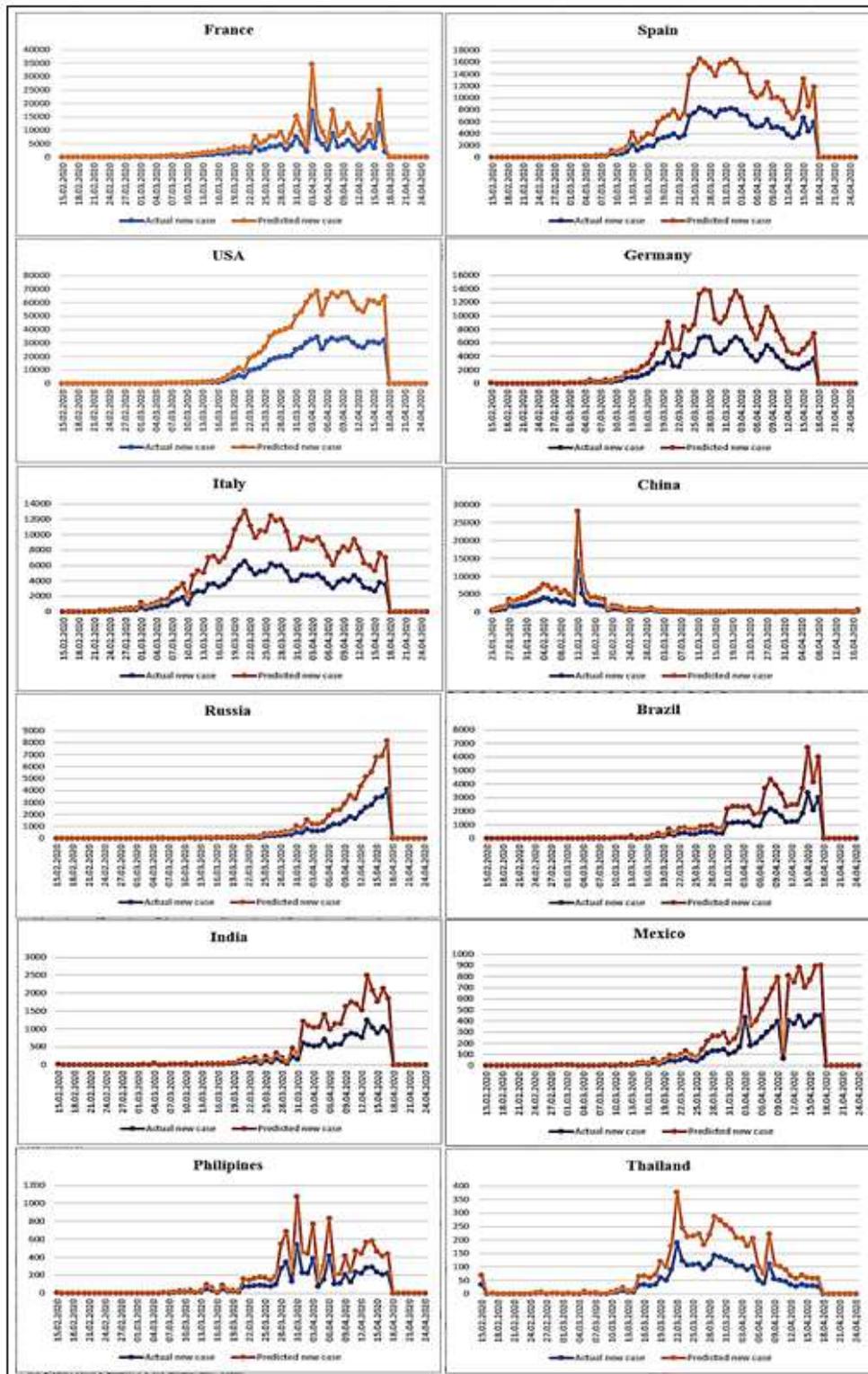


Figure 10

Actual daily new cases vs predicted new cases

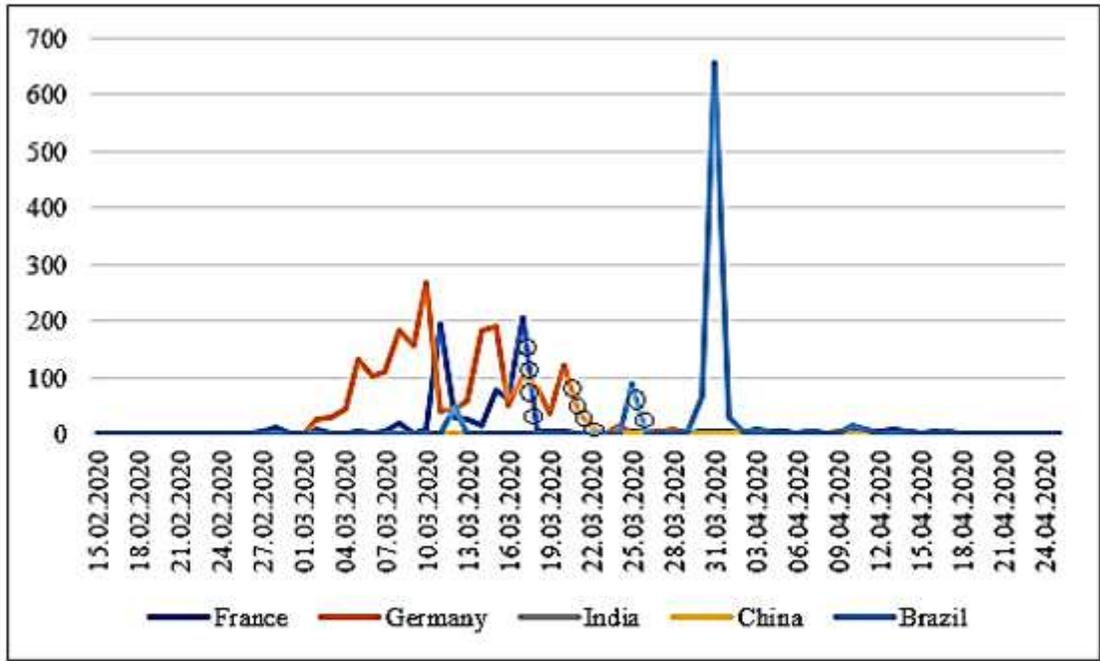


Figure 11

Change in basic reproduction number after lockdown in the five most affected countries

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [Task1.xlsx](#)