

BeCaked: An Explainable Artificial Intelligence Model For COVID-19 Forecasting

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BeCaked: An Explainable Artificial Intelligence Model For COVID-19 Forecasting

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ABSTRACT

From the end of 2019, one of the most serious and largest spread pandemics occurred in Wuhan (China) named *Coronavirus* (COVID-19). As reported by the World Health Organization, there are currently more than 100 million infectious cases with an average mortality rate of about five percent all over the world. To avoid serious consequences on people's lives and the economy, policies and actions need to be suitably made in time. To do that, the authorities need to know the future trend in the development process of this pandemic. This is the reason why forecasting models play an important role in controlling the pandemic situation. However, the behavior of this pandemic is extremely complicated and difficult to be analyzed, so that an effective model is not only considered on accurate forecasting results but also the explainable capability for human experts to take action pro-actively.

With the recent advancement of *Artificial Intelligence* (AI) techniques, the emerging *Deep Learning* (DL) models have been proving highly effective when forecasting this pandemic future from the huge historical data. However, the main weakness of DL models is lacking the explanation capabilities. To overcome this limitation, we introduce a novel combination of the *Susceptible-Infected-Recovered-Deceased* (SIRD) compartmental model and *Variational Autoencoder* (VAE) neural network known as BeCaked. With pandemic data provided by the Johns Hopkins University Center for Systems Science and Engineering, our model achieves 0.98 R^2 and 0.012 $MAPE$ at world level with 31-step forecast and up to 0.99 R^2 and 0.0026 $MAPE$ at country level with 15-step forecast on predicting daily infectious cases. Not only enjoying high accuracy, but BeCaked also offers useful justifications for its results based on the parameters of the SIRD model. Therefore, BeCaked can be used as a reference for authorities or medical experts to make on time right decisions.

Introduction

Deep Learning (DL)¹, a subarea of machine learning, has been applied in many tasks such as speech recognition, object detection, natural language processing, etc. with noticeably high accuracy. Due to its powerful computation capability, DL models are proven highly effective once handling huge datasets whose volumes easily make human beings overwhelming.

Thus, as the pandemic of *Coronavirus* (COVID-19)^{2,3} has been spreading on a worldwide scale and posing a serious threat to daily life of humanity, DL is considered as an effective machine learning approach to analyze the massive dataset of patient records of infected and tested cases, which can be collected in the daily basis and presented as a *sequence* of historical data. Due to its data-driven learning mechanism, DL-based approaches usually introduce highly accurate rates when predicting the increase of infectious epidemics from the past historical data. In particular, a special kind of Deep Learning known as *Recurrent Neural Network* (RNN)⁴ and its advanced version, *Long Short Term Memory* (LSTM)⁵, enjoy visibly better performance once compared to traditional methods such as ARIMA, SEIR, etc.⁶⁻⁸ and deliver significant results for some countries, for instance, Canada⁹ and European countries¹⁰. It is because the operational mechanism of this network kind is effectively suitable to process sequence data.

Nevertheless, the contribution of DL-based methods is limited to the fact that their results are often given in a black-box manner, making them unexplainable in terms of the internal properties of the pandemic. Thus they hardly provide experts with explicit declarative knowledge, based on which a corresponding action plan can be prepared. For instance, let us consider some motivating situations given in Figure 1. Due to a very large number of patient records rapidly collected and processed, a well-trained Deep Learning model can predict a certain increase of infectious cases in the next few days. However, this model generally could not explain for itself the reason behind such a trend. Hence, medical experts suffer difficulty from retrieving the root cause of the situation and proposing proper actions to improve the status. In the other words, the problem which Deep Learning as well as many machine learning models are facing is that predicted output are not accompanied by a

justification or anything that substantiates insight on what the models have learned. To solve this problem, a new generation of machine learning models known as *Explainable Artificial Intelligence* (Explainable AI)¹¹ has emerged and is expected to overcome the weaknesses of the black-box machine learning models. This generation not only makes machine learning models more explainable, while still maintaining a high level of learning performance, but also enables us to trust, understand and productively manage the emerging development of AI systems.

In terms of an epidemic, there have been many studies on modeling and forecasting its future. Technically, we can divide those models into two groups including *mathematical models* and *machine learning models*¹². Most mathematical models are based on a well-known compartmental model introduced by Kermack and McKendrick in 1927¹³. However, the parameters of those models are biasedly determined; thus, they are subjective and unobvious. In this paper, a model called *Susceptible–Infectious–Recovered–Deceased* (SIRD)^{14,15} which is one of the most commonly used mathematical models in the past to calculate epidemic outbreaks, is considered. It is illustrated in Figure 1, when successfully observing the parameters of the SIRD model from the recorded cases, experts can better understand the situation and suggest suitable actions. For example, upon witnessing that the infectious rate is significantly reduced while the deceased rate is relatively high, one can conclude that even though the reported number of infectious cases is still serious, the threat of infection in communities is now under control and suggest to lift the lock-down restriction in some certain regions.

Even though mathematical models can give useful hints for human experts from their internal parameters, to estimate such parameters from vast sources of real historical data is by no means a trivial task, which can be potentially handled by DL models. Hence, the combination of Deep Learning models and the mathematical SIRD model interestingly promises an Explainable AI solution to deal with the terrifying COVID-19 pandemic. In this paper, we propose a semi-supervised model known as *BeCaked* (Be Careful and Keep Distance) to realize this vision. Our work is inspired by the *Variational-LSTM Autoencoder* model¹⁶ where the neural architecture of *Autoencoder* (AE)¹⁷ is combined with the previously discussed LSTM to encode the data produced from LSTM into a higher informative representation for better processing. However, the results from this model are still unexplainable. To address this, we modify the Autoencoder architecture to enforce it to encode the processed sequence data produced by the LSTM layers into SIRD model parameters. Thus, the forecasting results of this end-to-end trainable architecture can be comprehensible for human experts in terms of those SIRD parameters, making our AI approach explainable. Moreover, the model makes use of the advantages of semi-supervised learning algorithms (the Autoencoder network specific), which do not need labeled data accompanied by sophisticated loss functions.

The rest of this paper is organized as follows. In *Section Preliminaries*, we recall background knowledge on the Deep Learning models of LSTM and *Variational Autoencoder* (VAE). The famous SIRD model and its capability of explainability are presented in *Section The SIRD model and its explainability*. Next, the technical details of the BeCaked model are presented in *Section The BeCaked model*. In *Section Performance evaluation*, insightful experiments were conducted with real COVID-19 data. Those experiments also show that our explainable BeCaked not only enjoys high accuracy of prediction, as compared to some *state-of-the-art* (SOTA) models, but can also analyze what is going on with the pandemic, illustrated by real data from some major countries in the world. We discuss our model and its achievements in *Section Discussion*. *Section Related works* highlights some related works and finally *Section Conclusion* concludes the paper. We also attach an appendix about the name "BeCaked" (*Appendix A*) and illustrations of web-based system which we have deployed our BeCaked model on (*Appendix B*) for interested readers.

Preliminaries

LSTM neural network

Modeling time-series data is likely impossible when using the standard *Multilayer Perceptron* (MLP)⁴ because of a lack of correlations between them. Therefore, an *Recurrent Neural Network* (RNN) was developed in the 1986 by Rumelhart⁴ and improved by Werbos (1988)¹⁸ and Elman (1990)¹⁹ for addressing that type of problem. In general, the construction of an RNN is similar to *Feed-forward Neural Network* (FNN)²⁰, with the distinction that a presence of connections between hidden layers, spanning through adjacent time steps. By these connections, an RNN can retain the properties of information because of the share-weighted characteristic, providing an ability to learn temporal correlations with high accuracy even when the locations of featured events are likely far away from each other. Figure 2 presents the basic architecture of an RNN, which has physically one layer. At the time t , this network will produce output $y^{(t)}$ from the input $x^{(t)}$. However, the output of this network at the previous iteration will also be used as part of the input of the next step, or *recurrent input*, together with new actual input. Similar to a typical MLP, RNN uses some layers of perceptron to learn suitable weights in the backpropagation manner when processing input, output and recurrent input, denoted as W_{ax} , W_{ya} and W_{aa} , respectively⁴. Thus, when handling a sequence of data $x^{(t)}$, an RNN can be logically unfolded as a recurrent multilayer network, as depicted in Figure 3.

Even though the RNN is theoretically a simple and powerful model, it is difficult to learn properly due to a limit in learning long-term dependencies, caused by two well-known issues in training a model which are *vanishing* and *exploding gradient*²¹.

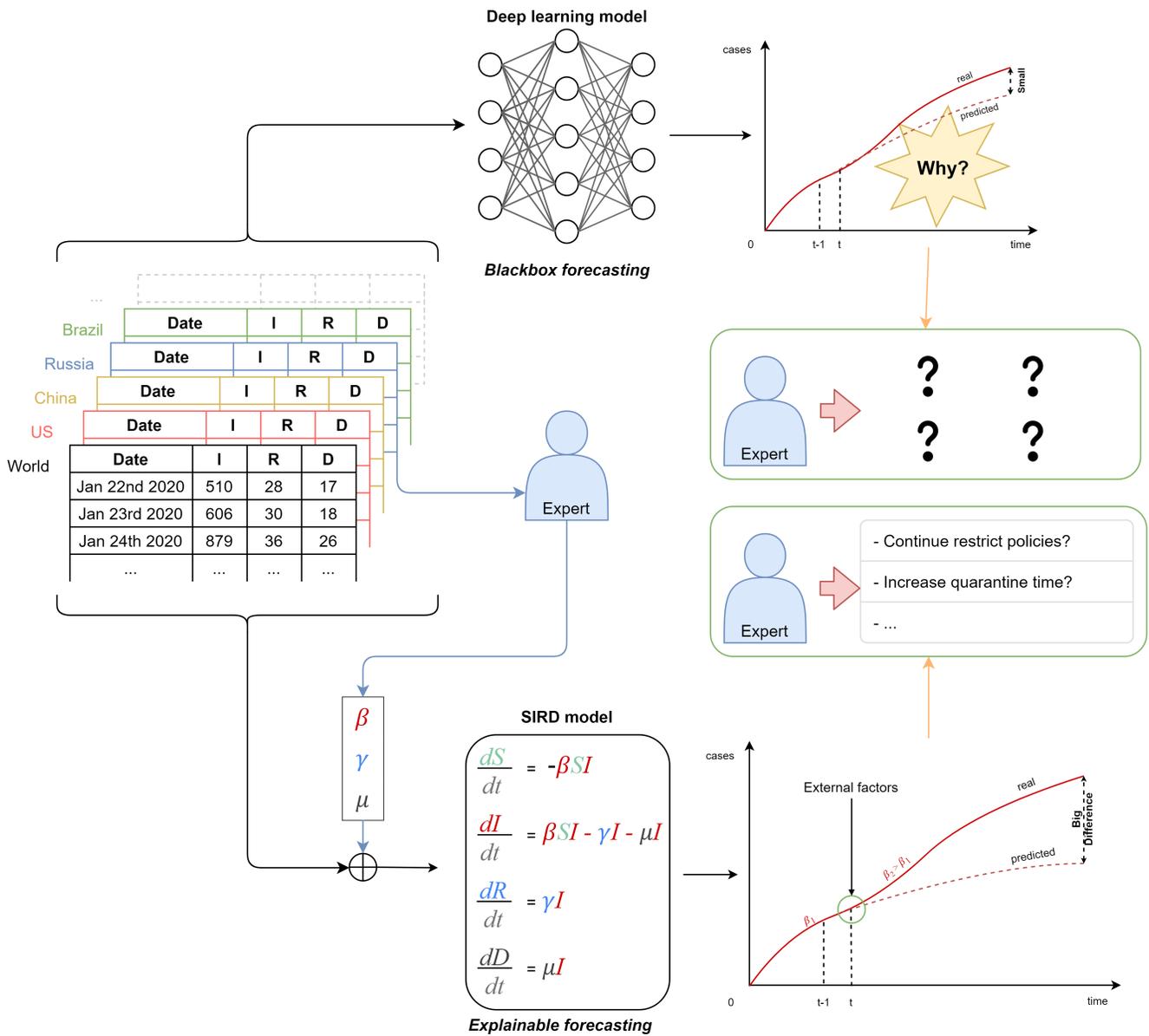


Figure 1. Illustration of the usage of Deep Learning and explainable model for COVID-19 forecast

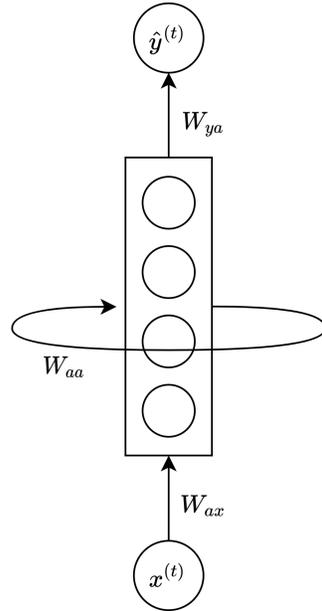


Figure 2. The physical architecture of an RNN

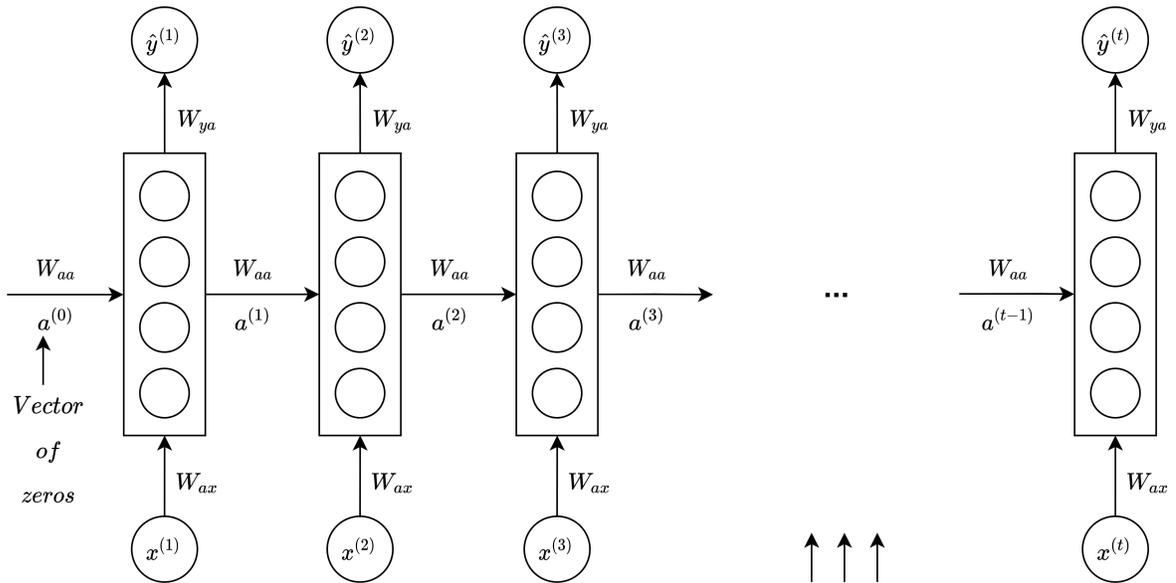


Figure 3. An unfolded RNN

The vanishing gradient will become worse when a *sigmoid*⁴ activation function is used, whereas a *Rectified Linear Unit* (ReLU) can easily lead to an exploding gradient. Fortunately, a formal thorough mathematical explanation of the vanishing and exploding gradient problems was represented by Bengio²², analyzing conditions under which these problems may appear.

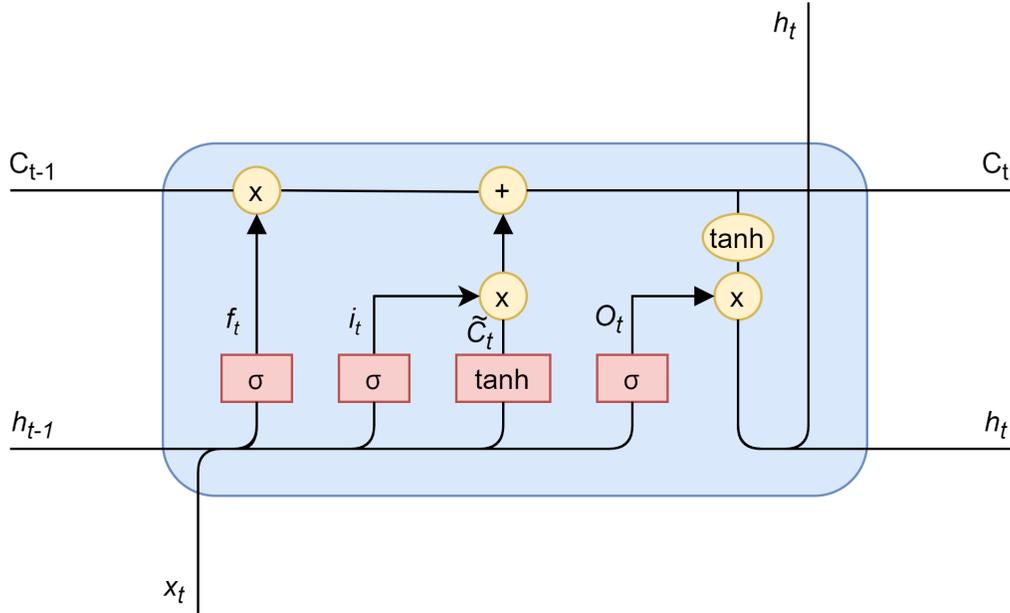


Figure 4. The structure of an LSTM cell

To deal with the long-term dependency problem, a developed version of RNN was introduced by Hochreiter and Schmidhuber in 1997, called *Long Short Term Memory* (LSTM)⁵. LSTM has overcome the limitations of RNN and delivers higher performance by using a hidden layer as a memory cell instead of a recurrent cell (see Figure 4). In the standard LSTM model, processing information is more complicated when modules containing computational blocks are repeated over many timesteps to selectively interact with each other to determine what information will be added or removed. This process is controlled by three gates namely *input gate*, *output gate*, and *forget gate*. Controlling the flow of information inside an LSTM model is calculated using equation (1)-(5).

$$i = \sigma(W_i x_t + W_{hi} h_{t-1} + b_i) \quad (1)$$

$$f = \sigma(W_f x_t + W_{hf} h_{t-1} + b_f) \quad (2)$$

$$o = \sigma(W_o x_t + W_{ho} h_{t-1} + b_o) \quad (3)$$

$$(C)_t = (C)_{t-1} \otimes f + \tanh(W_C x_t + W_{hc} h_{t-1} + b_C) \quad (4)$$

$$h_t = o \otimes \tanh((C)_{t-1}) \quad (5)$$

In equation (1)-(5), i , f , o , (C) , h denote input gate, forget gate, output gate, internal state, and hidden layer, respectively. Here, W_i , W_f , W_o , W_C , and b_i , b_f , b_o , and b_C represent the weights and bias of three gates and a memory cell, in the order given. Concretely, the activation function, *sigmoid*, helps an LSTM model to control the flow of information because the range of this activation function varies from zero to one so that if the value is zero then all of the information is cut off, otherwise the

entire flow of information passes through. Similarly, the output gate allows information to be revealed appropriately due to the *sigmoid* activation function then the weights are updated by the element-wise multiplication of output gate and internal state activated by non-linearity *tanh* function. With the pivotal component is the memory cell accommodating three gates: input, forget, and output gate, LSTM has overcome limitations of RNN, enhancing the ability to remember values over an arbitrary time interval by regulating the flow of information inside the memory cell. Therefore, LSTM possesses a capacity to work tremendously well on learning features from sequential data such as documents, connected handwriting, speech processing, or anomaly detection, etc.²³.

Autoencoder and Variational Autoencoder

Autoencoder (AE)¹⁷ is a type of neural network designed to attempt to copy its input to its output, concurrently producing an *encoding representation* of the input. The network can be described as a construction of two parts, and the internal process can be observed in Figure 5.

- *Encoder*: this part of the neural network will compress the input into a latent-space representation which can be represented as an encoding function $A: f : X \rightarrow H$
- *Decoder*: this part, in contrast to the encoder, try to reconstruct the input from the latent-space representation which can be described as a reconstruction function $B: g : H \rightarrow R$ where the distance between R and X needs to be minimized.

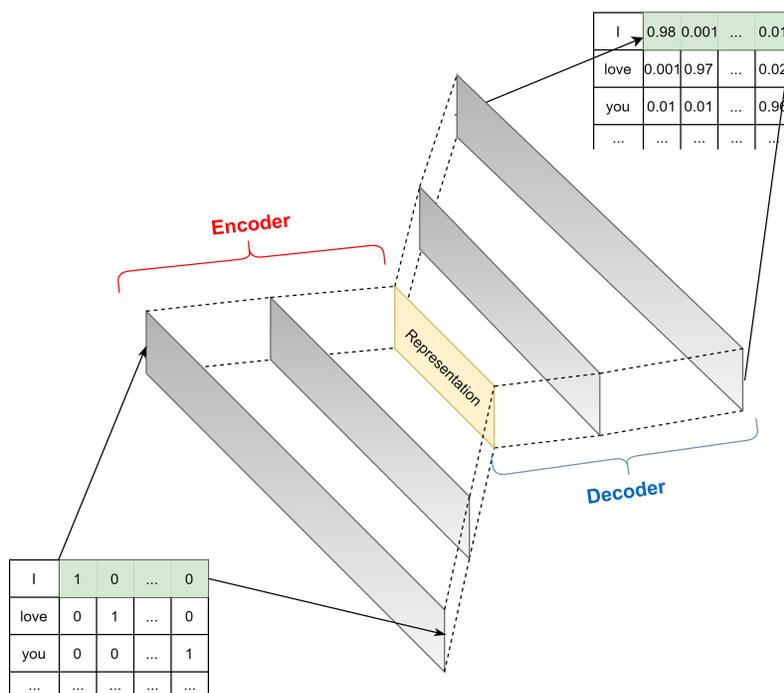


Figure 5. The concept of Autoencoder

Therefore, Autoencoder can be described as an unsupervised learning process that the bottleneck hidden layer will force the network to learn from a latent space representation, resulting from automatically encoding the input data, whereas, the reconstruction loss will make the latent representation contain as much information of the input as possible. This learning method enables machines to have the ability to capture the most meaningful features which accurately represent the input and ignore others that do not really describe the input data.

Perhaps the most popular usage of Autoencoder is *encoding*. As its name suggests, after properly trained, the encoder can be used to encode any input to the corresponding latent-space representation. Autoencoder has been deployed in various fields of AI. In the area of *Natural Language Processing* (NLP), the Autoencoder network is widely used as a basic method for word embedding or machine translation tasks. Also, it has proved its power to solve some problems in *Computer Vision* (CV) such as image compressing²⁴, image denoising²⁵, etc. Recently, the Autoencoder network has been developed with many improvements in order to fit more problem types. With its flexible transformation ability, the Autoencoder can be changed its

training method for other problems (such as *Variational Autoencoder* (VAE)²⁶ for Recommender system²⁷), or its architecture such as adding or removing its hidden layers with more specific ones like *Convolutional Neural Network* (CNN)²⁸, LSTM or itself (such as Autoencoder in Autoencoder for data representation²⁹).

In the standard Autoencoder network, the encoder and the decoder are usually implemented as *Fully-connected* (FC) or CNN. Therefore, the input in Autoencoder is encoded into latent deterministic variables. Whereas, its attention of VAE generates a probabilistic distribution over latent random variables by using Bayes's rule to approximate the probability $p(\text{code}|\text{input})$ with the presence of the mean μ and standard deviation σ . Reversely, the decoder, inversely approximating the probability $p(\text{output}|\text{code})$, will be a scaffolding for the encoder to learn the rich representations of data³⁰. In the original VAE model, the encoder is used to learn the parameters of data distribution from the input space. This architecture can be adapted to learn other kinds of distribution parameters such as the one used in aspect-based opinion summary³¹, which extends the VAE model to learn the parameters of Dirichlet distributions in the problem of topic modeling. In this work, we combine VAE which LSTM to learn the parameters of the SIRD model, to be discussed in the next section.

The SIRD model and its explainability

The *Susceptible-Infected-Recovered-Deceased* (SIRD) model is one of the most commonly used in the past to describe epidemic outbreaks³²⁻³⁴. The model demonstrates four states known as *Susceptible*, *Infectious*, *Recovered* and *Deceased* of people in a population isolated under the spread of an infectious epidemic. In almost infectious epidemic, the simple SIRD model assumes that infected people will be immune from that epidemic if they have recovered³⁵. Figure 6 presents the transitions between states in the SIRD model. In detail, people in *Susceptible* state move to *Infectious* state if they are infected by another one. When a person in *Infectious* state, he can be cured successfully and then moves to *Recovered* state or unluckily moves to *Deceased* state. Due to the assumption about the immune mechanism, people in *Recovered* state cannot be infected again, so that they cannot move back to *Susceptible* state.

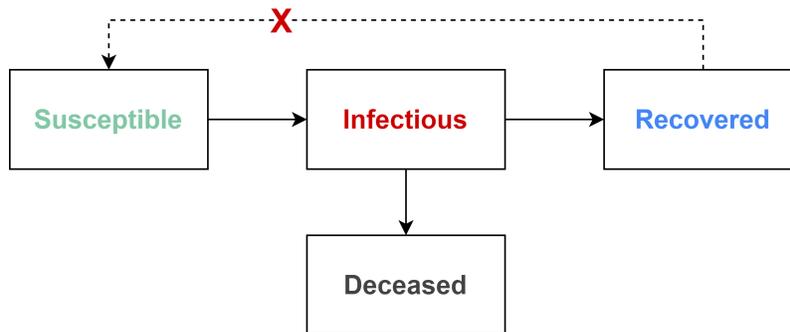


Figure 6. The concept of the SIRD model

More precisely, suppose that t_0 is the initial time that epidemic was recognized, given a specific day t where $t > t_0 > 0$, we denote the functions $S(t)$, $I(t)$, $R(t)$, $D(t)$ as the numbers of susceptible, infectious, recovered and deceased cases at day t , respectively. Moreover, we assume that there are three rate parameters β , γ and μ of the model as follows.

- β : the *rate of transmission*, i.e. the average number of contacts of the persons in the community per day (from the first day to the estimated last day of the pandemic).
- γ : the *rate of recovery*, i.e. the average number of recovered cases in the community per day.
- μ : the *rate of mortality from the epidemic*, i.e. the average number of deceased cases suffering from the infectious cases per day.

Then, given a population of N individuals, the SIRD model consists of four ordinary differential equations describing the relationships between the above functions and factors, given in equation (6a)-(6d).

$$\begin{cases} \frac{dS}{dt} = -\frac{\beta SI}{N} & (6a) \\ \frac{dI}{dt} = \frac{\beta SI}{N} - \gamma I - \mu I & (6b) \\ \frac{dR}{dt} = \gamma I & (6c) \\ \frac{dD}{dt} = \mu I & (6d) \end{cases}$$

The three parameters β , γ and μ , therefore, are very essential to the model. At the early stage, β reflects how the infection would increase if individuals were behaving as usual before being informed of medical conditions or any information related to the infection³². Moreover, β varies depending on how strong the social distancing and hygienic practices that different locations adopt, either because of policy or simply because of voluntary changes in individual behavior³²⁻³⁵. Whereas, γ provides insight into how many people recover from the epidemic in a period of time. Therefore, the average number of days a person is infected is $\frac{1}{\gamma}$ and we can statistically approximate γ based on the average cure time of one person. Finally, μ represents the average mortality rate in a period of time³². Both γ and μ perform the average medical capacity of the region considered.

A unique solution $S(t)$, $I(t)$, $R(t)$, $D(t)$ for the SIRD model, respect to a certain (β, γ, μ) , infectious, recovered and deceased cases at the time t ³²⁻³⁴. According to the meaning of (β, γ, μ) , it is hard to accurately estimate them³⁶. In other words, if we can estimate precisely the value of (β, γ, μ) from the historical data, we can forecast the trend of the pandemic more exactly. Moreover, those parameters can give us more insightful information about the internal status of the pandemic. For instance, if the number of deceased cases $D(t)$ still tends to increase in the next days, alongside the high value of μ while the value of β becomes relatively small, one can conclude that the reason for high mortality rate is due to the unbearably serious health status of the infected people. Meanwhile, the transmission in the community now is well-controlled, which allows the authorities to endorse suitable policy (such as lifting the lock-down restriction on the community, if currently applied). Thus, the SIRD model is regarded as an explainable model, which is very helpful for human experts to deal with real situations.

Nonetheless, having an exact (β, γ, μ) is not trivial since it depends on many factors such as locations, social policies, region economy, medical capacity, etc. Furthermore, according to the epidemiologists, the parameters can only be approximated by the actual circumference at the location that we consider, since they do not remain unchanged in time.

Thus, when historical data become extremely huge like the real COVID-19 data of the world, it is virtually impossible for human experts to evaluate the value of (β, γ, μ) and especially their changes of values when substantial new impacts occurring with the recent data. That urges us to consider using Deep Learning approaches to automatically learn and adjust the values of (β, γ, μ) from real streaming historical data, resulting in an *Explainable AI model* as subsequently discussed.

The BeCaked model

As mentioned before, the SIRD model can bestow a reasonable explanation regarding internal factors of a pandemic. However, it is very hard to determine the suitable values of the crucial parameters (β, γ, μ) of this model from extremely huge sources of historical data. Thus, we enhance the SIRD model by combining it with a Deep Learning architecture to automatically learn the suitable values of those parameters. As a result, we obtain a hybrid model, known as *BeCaked*, as presented in Figure 7. The general ideas of employing Deep Learning techniques in BeCaked are as follows.

- We firstly use LSTM to make predictions of future values by extracting significant features from the input of historical sequential data.
- We combine LSTM with VAE to encode the predicted output as the desired parameters of (β, γ, μ) and use the backpropagation capability of the end-to-end neural network to train the suitable values of those parameters from the input data. We also take advantage of the semi-supervised learning mechanism of VAE to auto-label the training data, as discussed later.

Particularly, in order to deal with the huge volumes of data, our main goal is to also reduce computation costs, simplify the loss function and explain the forecasting results. We carry out this goal in our proposed model architecture shown in Figure 7. The detailed descriptions of BeCaked are discussed as follows.

Input data

Input data of the BeCaked model is a $n \times 4$ matrix, where n indicates the last recent n days to be studied, assumed from 1st to n^{th} day. The i^{th} row of this matrix is a 4-dimension vector of $(S(i), I(i), R(i), D(i))$ of the corresponding i^{th} day, whose meanings had been already explained previously

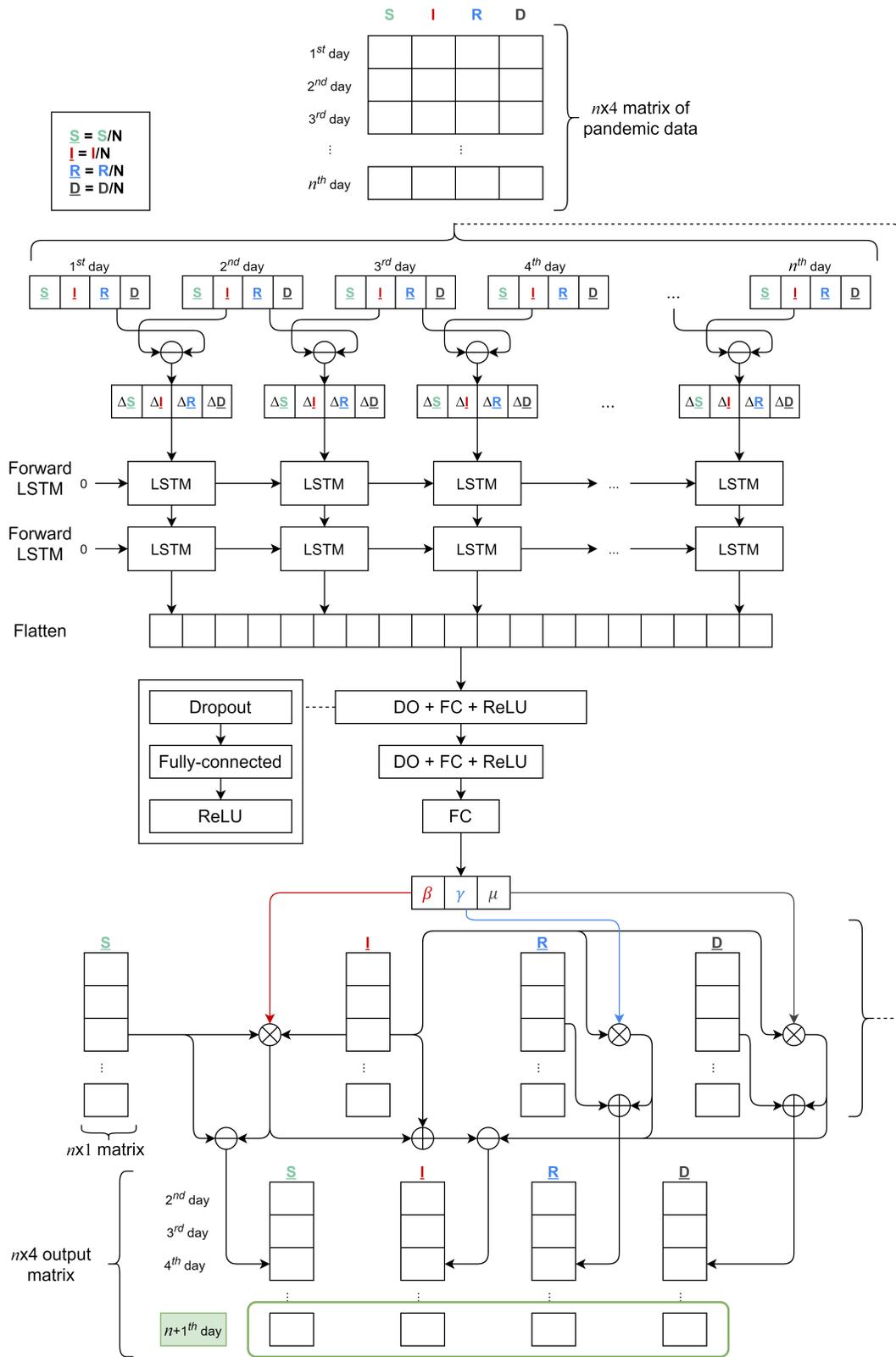


Figure 7. The architecture of BeCaked model

Feature extraction for LSTM layers

From the raw information given from the historical input data and the population N , we then produce feature vectors $V_i = (\Delta S_i, \Delta I_i, \Delta R_i, \Delta D_i)$, where ΔS_i , ΔI_i , ΔR_i , and ΔD_i can be observed in equation (7a)-(7d).

$$\left\{ \begin{array}{l} \Delta S_i = \frac{S(i+1)}{N} - \frac{S(i)}{N} \end{array} \right. \quad (7a)$$

$$\left\{ \begin{array}{l} \Delta I_i = \frac{I(i+1)}{N} - \frac{I(i)}{N} \end{array} \right. \quad (7b)$$

$$\left\{ \begin{array}{l} \Delta R_i = \frac{R(i+1)}{N} - \frac{R(i)}{N} \end{array} \right. \quad (7c)$$

$$\left\{ \begin{array}{l} \Delta D_i = \frac{D(i+1)}{N} - \frac{D(i)}{N} \end{array} \right. \quad (7d)$$

Finally, the sequence of feature vector $\{V_i\}$ will be used as the input for the LSTM layers. In BeCaked, we use two stacked layers of LSTM to increase the abstraction capability from the extracted features.

Parameter encoding

The output of LSTM layers are then flattened as a 1-dimension vector, from which we encode into (β, γ, μ) parameters. The encoding process is carried out by the typical MLP technique, including two FC layers enhanced with drop-out techniques and ReLU activation functions employed.

Thus, the BeCaked model can be regarded as a variation of the VAE model whose encoder consists of LSTM layers and FC layers previously described. The output of this encoder is then the parameters of (β, γ, μ) , trainable by the model decoder as subsequently discussed.

Decoding process

From the encoded parameters of (β, γ, μ) , the decoder will attempt to produce the desired output, which is also a $n \times 4$ matrix similar to the input matrix. However, the output matrix captures the information from 2^{nd} to $(n+1)^{th}$ day from the historical data. Thus, the labeling process for our encoder-decoder mechanism can be done automatically, like all other VAE systems.

In order to decode the output matrix from the three parameters (β, γ, μ) learned with the n -day input data, the decoder approximates the SIRD model with the *Euler* method³⁷ because it is the easiest but most efficient way for approximating differential equations. We present the equations for approximating the SIRD model using the Euler method with step $h = 1$ in equation (8a)-(8d). The reason why we choose Euler instead of *Runge-Kutta*³⁸ or other methods is that it is the most suitable solving method for the data we have and step $h = 1$ is corresponding to a day in the data.

$$\left\{ \begin{array}{l} \frac{S(i+1)}{N} = \frac{S(i)}{N} - \beta \frac{S(i)}{N} \frac{I(i)}{N} \end{array} \right. \quad (8a)$$

$$\left\{ \begin{array}{l} \frac{I(i+1)}{N} = \frac{I(i)}{N} + \beta \frac{S(i)}{N} \frac{I(i)}{N} - \gamma \frac{I(i)}{N} - \mu \frac{I(i)}{N} \end{array} \right. \quad (8b)$$

$$\left\{ \begin{array}{l} \frac{R(i+1)}{N} = \frac{R(i)}{N} + \gamma \frac{I(i)}{N} \end{array} \right. \quad (8c)$$

$$\left\{ \begin{array}{l} \frac{D(i+1)}{N} = \frac{D(i)}{N} + \mu \frac{I(i)}{N} \end{array} \right. \quad (8d)$$

In equation(8a)-(8d), $S(i+1)$, $I(i+1)$, $R(i+1)$, $D(i+1)$ represent the number of susceptible, infectious, recovered, and deceased cases at the $(i+1)^{th}$ day which is right after the i^{th} day corresponding.

In order to simplify the model, we normalize all data by dividing them for the population N . Consider we have normalized functions as in equation (9a)-(9d).

$$\left\{ \begin{array}{l} \underline{S}(i) = \frac{S(i)}{N} \end{array} \right. \quad (9a)$$

$$\left\{ \begin{array}{l} \underline{I}(i) = \frac{I(i)}{N} \end{array} \right. \quad (9b)$$

$$\left\{ \begin{array}{l} \underline{R}(i) = \frac{R(i)}{N} \end{array} \right. \quad (9c)$$

$$\left\{ \begin{array}{l} \underline{D}(i) = \frac{D(i)}{N} \end{array} \right. \quad (9d)$$

Then the equation (8a)-(8d) can be written as equation (10a)-(10d).

$$\begin{cases} \underline{S}(i+1) = \underline{S}(i) - \beta \underline{S}(i) \underline{I}(i) & (10a) \\ \underline{I}(i+1) = \underline{I}(i) + \beta \underline{S}(i) \underline{I}(i) - \gamma \underline{I}(i) - \mu \underline{I}(i) & (10b) \\ \underline{R}(i+1) = \underline{R}(i) + \gamma \underline{I}(i) & (10c) \\ \underline{D}(i+1) = \underline{D}(i) + \mu \underline{I}(i) & (10d) \end{cases}$$

Training process

In the training process, after the input data goes through all layers of our model, we calculate the *Mean Squared Error* (MSE)³⁹ loss function (equation (11)) between the output of BeCaked and the real data. The reason that we choose MSE is the fact that it is simple and reflects the true error rate between the real data and the forecasting results so that it is better for optimization purpose, compared to *Root Mean Squared Error* (RMSE) or other loss functions. Then we use *Adam optimizer*³⁰ to update our model weights because it is the most suitable for noisy data. Let Y_i and \hat{Y}_i be the i^{th} vectors from actual data and the predicted values of BeCaked, w.r.t the $n \times 4$ output matrix discussed in the decoding process, the MSE of an epoch in the training process is evaluated as (11).

$$MSE = \frac{1}{n} \sum_{i=1}^n (Y_i - \hat{Y}_i)^2 \quad (11)$$

Since BeCaked is an end-to-end VAE neural network as previous described, the loss function given in equation (11) can be used to update the weights of the whole system by the typical backpropagation manner (note that the decoder does not use any trainable weights and will not be updated during the training process). When the loss values become stable, the training process is converged and BeCaked now is able to predict (β, γ, μ) from any given sources of real input data.

Explainability of BeCaked

As previously described, the basic operational mechanism of BeCaked is taking (β, γ, μ) and data in the previous days to calculate the number of susceptible, infectious, recovered, and deceased cases in the next days. The most important thing that helps this model be successful is choosing the correct features of the input data so that the model can learn how to estimate (β, γ, μ) in the best way. In other words, BeCaked can serve not only as a regression system with the predicted values for the future, but also as a VAE generating the parameters of (β, γ, μ) with an explanation of the regressed value at the same time.

Also, the key idea which makes our model explainable is the way we infer the value of (β, γ, μ) . On the one hand, our decoder ensures that the inferred values of (β, γ, μ) are mathematically correct to give accurate predictions on the training data. On the other hand, BeCaked manipulates the encoding process by taking into account the relationship between the difference in the number of considered cases in the previous days and the (β, γ, μ) of the following days. This is a varied flow correlation³³⁻³⁵, so that if the more quickly the difference in the number of cases in the previous day increases, the higher the parameter correspondingly is. For example, if we have recovered cases in three consecutive days as respectively (5,10,20) the recovery rate will be considered increasing. Meanwhile, if the recovered cases are (5,10,12), the recovery case can be regarded as decreasing even though the number of recovered people still keeps increasing daily.

Code Availability

Our implementation of proposed model is available at <https://github.com/nguyenquangduc2000/BeCaked>.

Performance evaluation

Data preparation and pre-processing

In this evaluation process, we used the dataset provided by the *Johns Hopkins University Center for System Science and Engineering* (JHU CSSE)^{40,41}. This dataset is collected from January 2020 until now from various sources such as the *World Health Organization* (WHO), *European Centre for Disease Prevention and Control* (ECDC), *United States Centre for Disease Prevention and Control* (US CDC), etc.^{40,41}. In detail, this dataset contains the daily number of total infectious (including recovered and deceased cases), recovered, and deceased cases in all countries around the world.

In our experiment, we used the data from January 2020 to the end of June 2020 as training data and the July 2020 data for the testing period. As presented in *Section The BeCaked model*, we need the input containing four values in each day: susceptible, infectious, recovered, and deceased, but with the above dataset, we only have total infectious, recovered, and deceased cases. Therefore, we need to have a total population of the world and recalculate all the required input. The data about

world population is provided by Worldometers⁴². The equations (12a)-(12d) show how to calculate the input for BeCaked model from the dataset.

$$\begin{cases} \text{Input}_{\text{Susceptible}} = \text{Total_Population} - \text{Total_Infectious} & (12a) \\ \text{Input}_{\text{Infectious}} = \text{Total_Infectious} - \text{Recovered} - \text{Deceased} & (12b) \\ \text{Input}_{\text{Recovered}} = \text{Recovered} & (12c) \\ \text{Input}_{\text{Deceased}} = \text{Deceased} & (12d) \end{cases}$$

The input of our model are then normalized into percentages by dividing all data for the total population to match with the input of our proposed method described in *Section The BeCaked model*.

Global evaluation

In the evaluation process, to choose the most optimal day lag number n , we conduct the experiments on global using different day lag numbers. According to the result of McAloon’s study (2020)⁴³, the day lag number varies from 5 to 14 days, so that, we test our model with 7, 10 and 14 day lag to find the most suitable one.

To determine the suitable value n of the lag days, we used the *recursive strategy*⁴⁴ to perform k -step forecasting. In details, a k -step forecasting process is described as follows. Firstly, we only use n -day data (June $(30 - n + 1)^{th}$ - June 30^{th}) as the initial input for forecasting the next $n + 1^{th}$ day (the number n is corresponding to n -day lag), which n is set as 7, 10, 14, respectively. Then, we repeat that process k times. At each step, we predict the number of cases (susceptible, infectious, recovered, deceased) for the next day and use it (our predicted cases) as the input for the next iteration. In this process, because the testing data is July 2020 data, the number step k varies from 1 to 31, we then eventually choose k as the possible maximal value of 31.

In Table 1, we have shown our forecast results using 7, 10 and 14 day lag in *R Squared* (R^2) (equation (13)) and *Mean Absolute Percentage Error* (*MAPE*) (equation (14)) metric.

$$R^2 = 1 - \frac{RSS}{TSS} \quad (13)$$

The *RSS*, *TSS* in equation (13) denote for the *Residual Sum of Squares* and the *Total Sum of Squares*. The R^2 metric given in equation (13) provides an insight into the similarity between real and predicted data. The closer to 1 the R^2 is, the more explainable the model is. The *MAPE* given in equation (14) tells us about the mean of the total percentage errors for k -step forecasting. If the value of this *MAPE* metric is closer to 0, it indicates the better results.

$$MAPE = \frac{1}{k} \sum_{i=1}^k \frac{|Y_i - \hat{Y}_i|}{Y_i} \quad (14)$$

In equation (14), k , Y_i , \hat{Y}_i denote for the number of steps, the actual cases and our predicted cases corresponding.

	7-day	10-day	14-day
<i>Total infectious cases</i>			
R^2	0.77284	0.99790	0.95795
<i>MAPE</i>	0.05592	0.00509	0.02552
<i>Daily infectious cases</i>			
R^2	0.89739	0.98050	0.87828
<i>MAPE</i>	0.12455	0.01268	0.05842
<i>Recovered cases</i>			
R^2	0.45429	0.98784	0.67187
<i>MAPE</i>	0.10912	0.01869	0.08676
<i>Deceased cases</i>			
R^2	-22.25663	0.98904	-12.13873
<i>MAPE</i>	0.32878	0.00676	0.24510

Table 1. Comparison of BeCaked performance with 7, 10 and 14 day lag

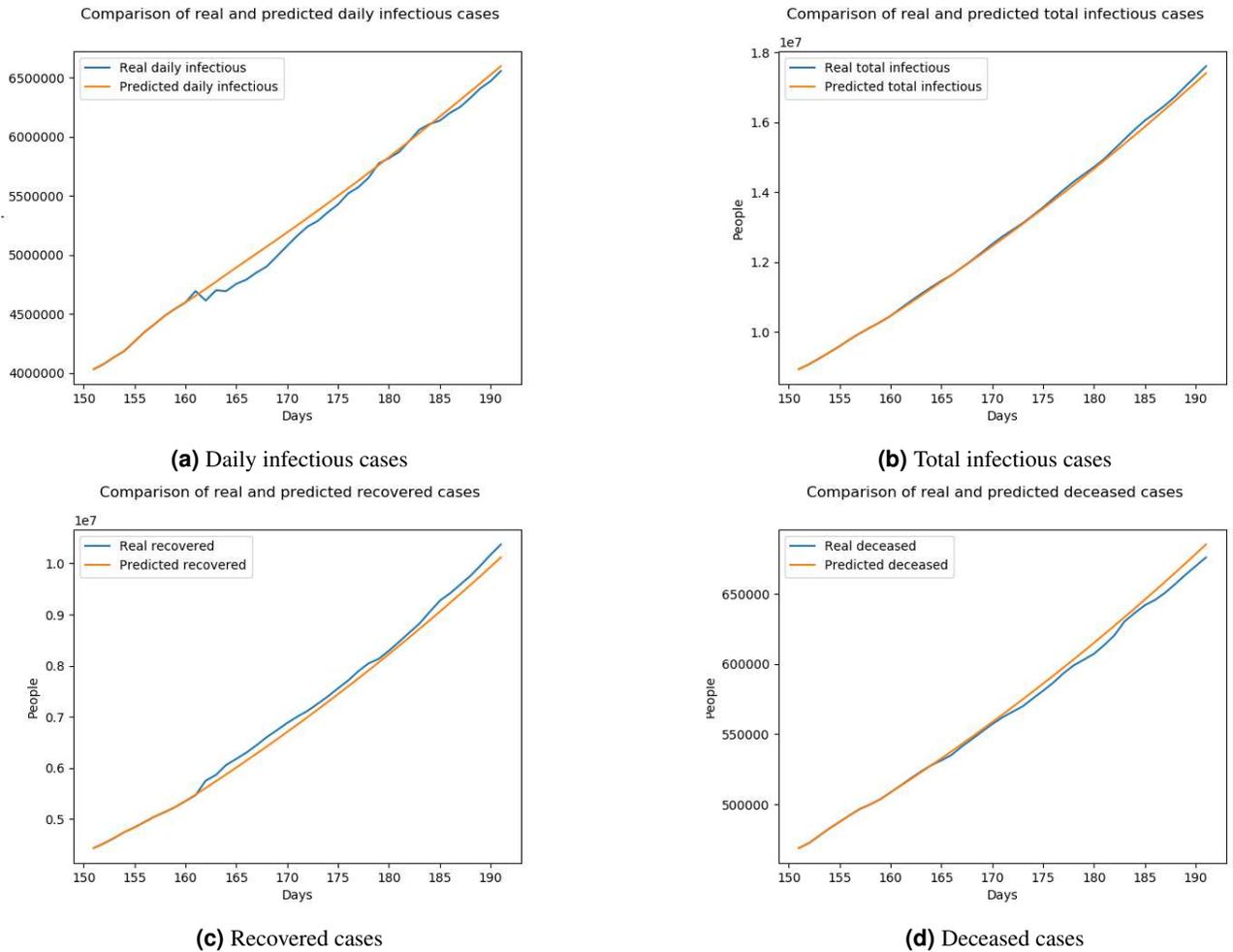


Figure 8. Comparison of the number of cases between real data and BeCaked forecasting results from 161st-191st day (Jul. 1st 2020 - Jul. 31st 2020) of the world

According to the results shown in Table 1, the highest performance of our model was achieved with 10-day lag, so that we chose the number of day lag as 10 for further evaluations. We also visualized our results for a better overview using 10-day lag. Figure 8a shows the comparison of daily infectious cases between real data and BeCaked forecasting results while Figure 8b shows that of the total infectious cases. Also, the comparison of recovered and deceased cases are presented in Figure 8c and Figure 8d respectively. Moreover, we visualized the (β, γ, μ) corresponding to the results of forecasting in Figure 9. In this period (July 01st - July 31st), this pandemic in many countries started to be controlled, so that the overall transmission rate decreased. Due to the slower speed of transmission, the recovery rate increased. The hidden truth here is that the health system in those countries was load-reduced and doctors could pay more attention to currently infected patients. Because of the above reasons, the mortality rate decreased too.

In Table 3, we compared our model with some top-tier forecasting-specialized others from statistical models to machine learning models including *Autoregressive Integrated Moving Average (ARIMA)*¹², *Ridge*⁴⁵, *Least Absolute Selection Shrinkage Operator (LASSO)*⁴⁶, *Support Vector Machine for Regression (SVR)*⁴⁷, *Decision Tree Regression (DTR)*⁴⁸, *Random Forest Regression (RFR)*⁴⁹ and *Gradient Boost Regression (GBR)*⁵⁰. Except for ARIMA, the other models use the same number of day lag n as our BeCaked does (which is 10) to forecast the future. The specific configurations of each model are listed in Table 2. Even though these models are widely used in predicting the future for time-series data and achieving comparative results⁴⁴, in the case of the COVID-19 long time forecasting problem, with the exception of our model, only Ridge and LASSO have acceptable results. Our model is proved to attain overall comparative performance with those mentioned methods by these results given below.

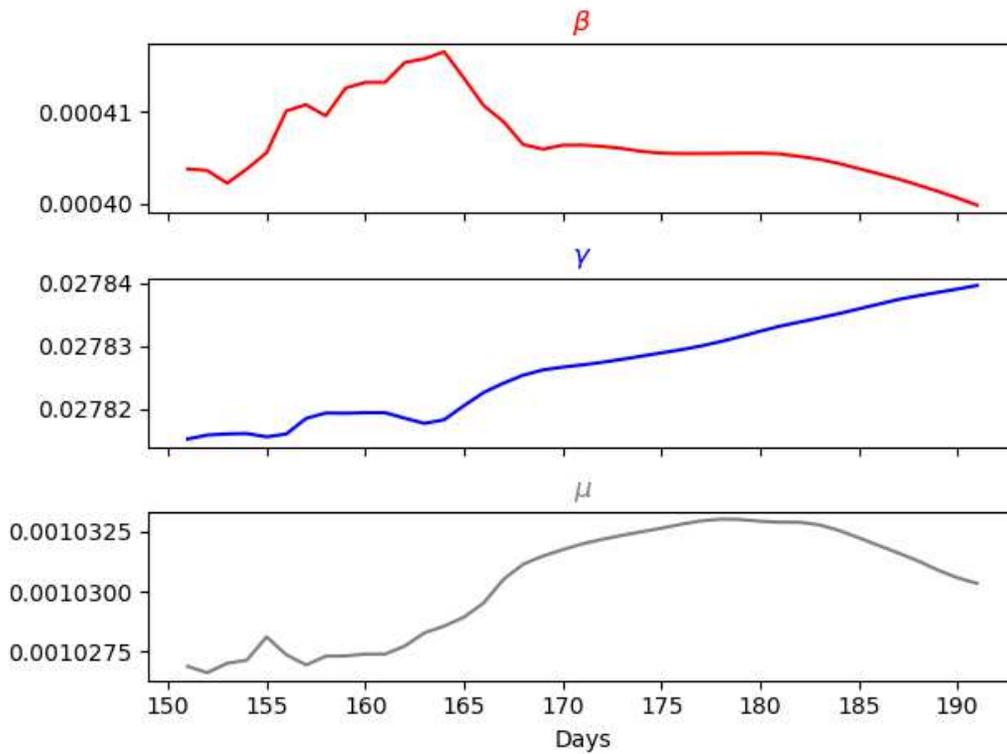


Figure 9. Predicted transition rates from 161st-191st day (Jul. 1st 2020 - Jul. 31st 2020) of the world

Model	Configurations
ARIMA	$p = 1; d = 0; q = 0;$
Ridge	$\alpha = 1; solver = svd; tolerance = 10^{-3};$
LASSO	$\alpha = 1; max_iter = 1000; selection = cyclic; tolerance = 10^{-4};$
SVR	$kernel = rbf; \gamma = scale; C = 1; \epsilon = 0.1; tolerance = 10^{-3};$
DTR	$criterion = mse; splitter = best; min_samples_split = 2; min_samples_leaf = 1;$
RFR	$n_estimators = 100; criterion = mse; min_samples_split = 2; min_samples_leaf = 1;$
GBR	$loss = least_squared; n_estimators = 100; criterion = friedman_mse;$ $min_samples_split = 2; min_samples_leaf = 1; max_depth = 3; tolerance = 10^{-4};$

Table 2. Configurations of top-tier forecasting-specialized methods

	BeCaked	ARIMA	Ridge	LASSO	SVR	DTR	RFR	GBR
<i>Total infectious cases</i>								
R^2	0.99790	-2.84161	0.98777	0.99907	-18.11617	-2.84160	-2.99678	-2.84598
MAPE	0.00509	0.23243	0.01346	0.00112	0.62084	0.23243	0.23929	0.23262
<i>Daily infectious cases</i>								
R^2	0.98050	-2.31481	0.39289	0.92269	-29.01740	-2.31481	-2.44266	-2.32188
MAPE	0.01268	0.38969	0.03052	0.00350	0.78887	0.38969	0.39887	0.38998
<i>Recovered cases</i>								
R^2	0.98784	-3.07765	0.76234	0.96656	-13.46395	-3.07765	-3.24544	-3.08040
MAPE	0.01869	0.29221	0.07195	0.01153	0.64754	0.29221	0.30097	0.29236
<i>Deceased cases</i>								
R^2	0.98904	-2.81195	0.88473	0.53645	-46.32486	-2.81195	-2.95304	-2.82239
MAPE	0.00676	0.13248	0.01988	0.04018	0.55858	0.13248	0.13594	0.13274

Table 3. Comparison of BeCaked and top-tier forecasting-specialized methods with 31-step forecast

Country evaluation

At the country level, we also conducted the same evaluation process as we did in global scale. We chose six countries with different locations, social policies, and anti-epidemic strategies, etc. for testing our model in various conditions.

Firstly, we fit our model for each country until the end of June 2020. Then, we used the July 2020 cases for the testing phase. In this comparison, we used the same methods with configurations as we did at the whole world level. These below evaluations were done in 1-step (Table 4), 7-step (Table 5) and 15-step (Table 6) forecasting using the daily infectious cases. The reason why we did more comparisons will be discussed in *Section Discussion*.

In July 2020, many countries began to have better control of the development of this COVID-19 pandemic by restricting outside agents from spreading viruses. However, some countries have reopened after lockdown, such as the United State, Australia, Italy, etc. This became a favorable condition for external factors to directly influence the increase in the number of cases in those countries. Therefore, to effectively forecast the long-time situation of those countries, a forecasting model must have the ability to adapt to emerging changes in the pandemic exponential growth rate. Due to that, the below comparing results reflected the strong adaptive capacity of our BeCaked model along with others.

	BeCaked	ARIMA	Ridge	LASSO	SVR	DTR	RFR	GBR
<i>Australia</i>								
R^2	0.99112	0.98329	0.99337	0.99531	-0.48798	0.98342	0.96787	0.98299
MAPE	0.04703	0.10236	0.01093	0.04078	0.85609	0.10204	0.14942	0.10344
<i>Italy</i>								
R^2	0.96381	0.94660	0.92646	0.88220	-22.56497	0.94889	0.90082	0.94876
MAPE	0.00496	0.01655	0.00024	0.05999	0.93214	0.01684	0.02570	0.02165
<i>Russia</i>								
R^2	0.92922	0.91663	0.98479	0.92367	-108.89720	0.91643	0.87353	0.91854
MAPE	0.00004	0.02856	0.00007	0.00938	0.77448	0.02851	0.04442	0.02938
<i>Spain</i>								
R^2	0.98765	0.97214	0.98591	0.98362	-10.84390	0.97212	0.94968	0.97053
MAPE	0.00174	0.01418	0.00325	0.01881	0.74045	0.01406	0.02173	0.01522
<i>United Kingdom</i>								
R^2	0.99833	0.98713	0.99764	0.96375	-449.89408	0.98748	0.96991	0.98463
MAPE	0.00030	0.00255	0.00014	0.00437	0.52586	0.00249	0.00397	0.00282
<i>United States</i>								
R^2	0.99688	0.98676	0.99648	0.99461	-9.99942	0.98676	0.96834	0.98633
MAPE	0.00552	0.02644	0.00004	0.00069	0.62264	0.02642	0.04185	0.02687

Table 4. Comparison of BeCaked and top-tier forecasting-specialized methods at country level with 1-step forecast

For a more challenging evaluation, we kept the training set to the end of June 2020 while stimulating the progress of long-term forecasting. In detail, firstly, we used 10 final days of June 2020 cases as the initial input and predict the pandemic in

	BeCaked	ARIMA	Ridge	LASSO	SVR	DTR	RFR	GBR
<i>Australia</i>								
R^2	0.88112	0.74039	0.99115	0.98878	-0.94255	0.73989	0.68456	0.73797
MAPE	0.18610	0.32529	0.06932	0.11617	0.88976	0.32524	0.36291	0.32645
<i>Italy</i>								
R^2	0.89690	0.66110	-0.20361	0.63946	-20.00836	0.69335	0.53913	0.69311
MAPE	0.02365	0.06104	0.00444	0.12168	0.93036	0.06223	0.06936	0.06644
<i>Russia</i>								
R^2	0.85845	0.70449	0.92995	0.84984	-106.05299	0.70217	0.59478	0.71031
MAPE	0.00222	0.10383	0.00087	0.02079	0.77662	0.10370	0.11736	0.10442
<i>Spain</i>								
R^2	0.98013	0.68411	0.98210	0.93588	-12.06027	0.68644	0.61741	0.68019
MAPE	0.00836	0.05367	0.01601	0.04576	0.74972	0.05306	0.05929	0.05420
<i>United Kingdom</i>								
R^2	0.99413	0.77401	0.98469	0.84731	-456.43229	0.77985	0.72832	0.76877
MAPE	0.00119	0.01027	0.00164	0.00918	0.52910	0.01004	0.01131	0.01037
<i>United States</i>								
R^2	0.98679	0.79943	0.98702	0.97658	-11.07041	0.79943	0.74460	0.79768
MAPE	0.01900	0.09879	0.00080	0.00067	0.64423	0.09871	0.11258	0.09912

Table 5. Comparison of BeCaked and top-tier forecasting-specialized methods at country level with 7-step forecast

	BeCaked	ARIMA	Ridge	LASSO	SVR	DTR	RFR	GBR
<i>Australia</i>								
R^2	0.09703	-0.10753	0.92366	0.86414	-1.69800	-0.12140	-0.20682	-0.12229
MAPE	0.40278	0.50951	0.18428	0.26379	0.92842	0.51087	0.53734	0.51162
<i>Italy</i>								
R^2	0.61706	-0.07923	-10.41220	-2.08983	-16.35794	0.07287	-0.17657	0.07720
MAPE	0.05745	0.10709	0.01292	0.23014	0.92750	0.10942	0.11508	0.11293
<i>Russia</i>								
R^2	0.27693	-0.09658	-0.28502	-0.71668	-102.60031	-0.09129	-0.19068	-0.07648
MAPE	0.01246	0.18125	0.00158	0.05668	0.77912	0.18115	0.19226	0.18170
<i>Spain</i>								
R^2	0.90753	-0.19684	0.65409	0.38282	-13.40342	-0.22237	-0.28920	-0.23309
MAPE	0.01356	0.09955	0.06038	0.11265	0.75909	0.09886	0.10272	0.09994
<i>United Kingdom</i>								
R^2	0.99278	-0.06679	0.90663	-0.10126	-465.84698	-0.02151	-0.12357	-0.04241
MAPE	0.00268	0.02080	0.00436	0.02445	0.53362	0.02024	0.02146	0.02054
<i>United States</i>								
R^2	0.94760	-0.04783	0.96380	0.93578	-12.74072	-0.04770	-0.15771	-0.05102
MAPE	0.04370	0.18476	0.00917	0.00477	0.67073	0.18467	0.19654	0.18503

Table 6. Comparison of BeCaked and top-tier forecasting-specialized methods at country level with 15-step forecast

July and August 2020. On the next day in stimulating, we used the data of nine last days of June and July 1st as the input and re-produce the forecasting until the end of August. This process is the same as the natural behavior of almost real-life forecast systems as we need to re-run the forecasting each day to get the most accurate result. With this testing, our model shows not only its performance but also its capacity of catching the changes of the pandemic. Figure 10-13 show the predicting results of daily infectious cases at the beginning and middle of July and August 2020 corresponding. According to these figures, we can observe that, like other prediction models, BeCaked only works well when given sufficient input of historical data. As a result, in Figure 13, BeCaked enjoys good accuracy in all countries when forecasting.

Moreover, unlike other blackbox-like prediction models, BeCaked can also provide an explanation for its results, in terms of the parameters (β , γ , μ). For example, in Figure 13, let us consider the cases of Spain and the United Kingdom. Even though the predicted curves of those two countries run in similar shapes, their parameters tell us different stories. The common things between those two countries are that they failed to control the transmission rate (maybe their lock-down policy did not make sufficient impacts). However, in Spain, they had been suffering from a high mortality rate for a long time, showing that their health system had difficulty in dealing with a large number of infectious cases, even though the recovery rate had also been increasing (i.e. more patients were cured daily). In contrast, in the United Kingdom, the rates of recovery cases and mortality cases gradually reduced at the early stage, indicating that the government somehow well controlled the situation in this period, which was also implied by the reduction of the transmission rate. However, when the transmission rate began to increase (corresponding to the time the lock-down policy had been relaxed in this country), the situation had been worse quickly in terms of mortality. At the end of this experiment, even though the regression models of two countries generate two similar shapes, like previously discussed, the parameters (β , γ , μ) indicate that Spain already controlled the situation and things would be improved. Meanwhile, the United Kingdom still had a hard time awaiting ahead. Real data taken afterward confirmed our predictions.

In other countries, BeCaked can also be able to tell us what happened “behind the scenes” of the generated results. In Australia, the major turn occurred when the government succeeded in controlling the transmission rate by their lock-down policy. From that point, the recovery rate increased and the mortality rate decreased in this country, leading to the stable situation they are enjoying now.

Meanwhile, in Russia, things are up and down many times, reflecting the rapid policy changing of this country during this period. However, this country generally attempts to maintain less direct contact in the community to reduce the transmission rate, which makes our model promise a better situation for them.

In the United States, their social distancing policy had somehow proved effective when both transmission rate and mortality rate had been gradually reduced. However, the absolute number of infectious cases has still stably increased, which can be explained by the reduced number of recovery cases. This shows that the country was struggling to handle the infected patients in the previous days of the outbreak.

In a broader view, we can consider that Spain and the United Kingdom had an almost unchanged policy which leads to a familiar situation, so that our model can predict their pandemic future accurately in the very early time. The evidence for this is that the shape of β , γ , μ line of these two nations at Figure 10 to Figure 13 are almost the same. Australia and the United States, in the past, faced the same situation but they did not provide any actions or policies to prevent external factors from spreading the virus. This is the reason why their infectious case increased dramatically. But, because in the past, they have faced this situation, our model can give good forecast results after “realizing” this situation (after about 30 days). Considering the parameter lines of the two above nations, we can see that in the stimulating progression, they are not stable. But in general, their directions are the same as the first forecast. Towards Italy and Russia, our model takes a little bit more time to change the direction of the forecast line, due to the strange situation. We can get this by comparing the parameter lines in Figure 10 to Figure 13 of Australia and Russia. The direction of these lines has changed as the policies of these two nations become loose. To be simple, it is because there is no pattern of this situation in the training data (pandemic data until the end of June 2020).

With the above result, we can consider that our proposed solution can catch up with the change in the pandemic situation. With the unchanged training set, our model can give very good forecast results if the situation is more stable. In case a strange situation occurs, our model needs time to give a more accurate forecast.

In the real-life application, the forecasting models are updated regularly using reinforcement learning methods in order to make them more “update” to new situations. Therefore, to get better results of our model in real-life, we need to fine-tune it with new data every one or two weeks.

Discussion

Forecasting a pandemic has never been easy, especially for this COVID-19 situation. The effectiveness of a forecasting model not only comes from the exact results but also the explanation or the root cause of those predicted numbers. Until now, almost no pure mathematical or machine learning model can achieve that double standard. Therefore, we tried to combine both models to create an Explainable AI one to solve that problem. The combination of Variational Autoencoder and SIRD we have

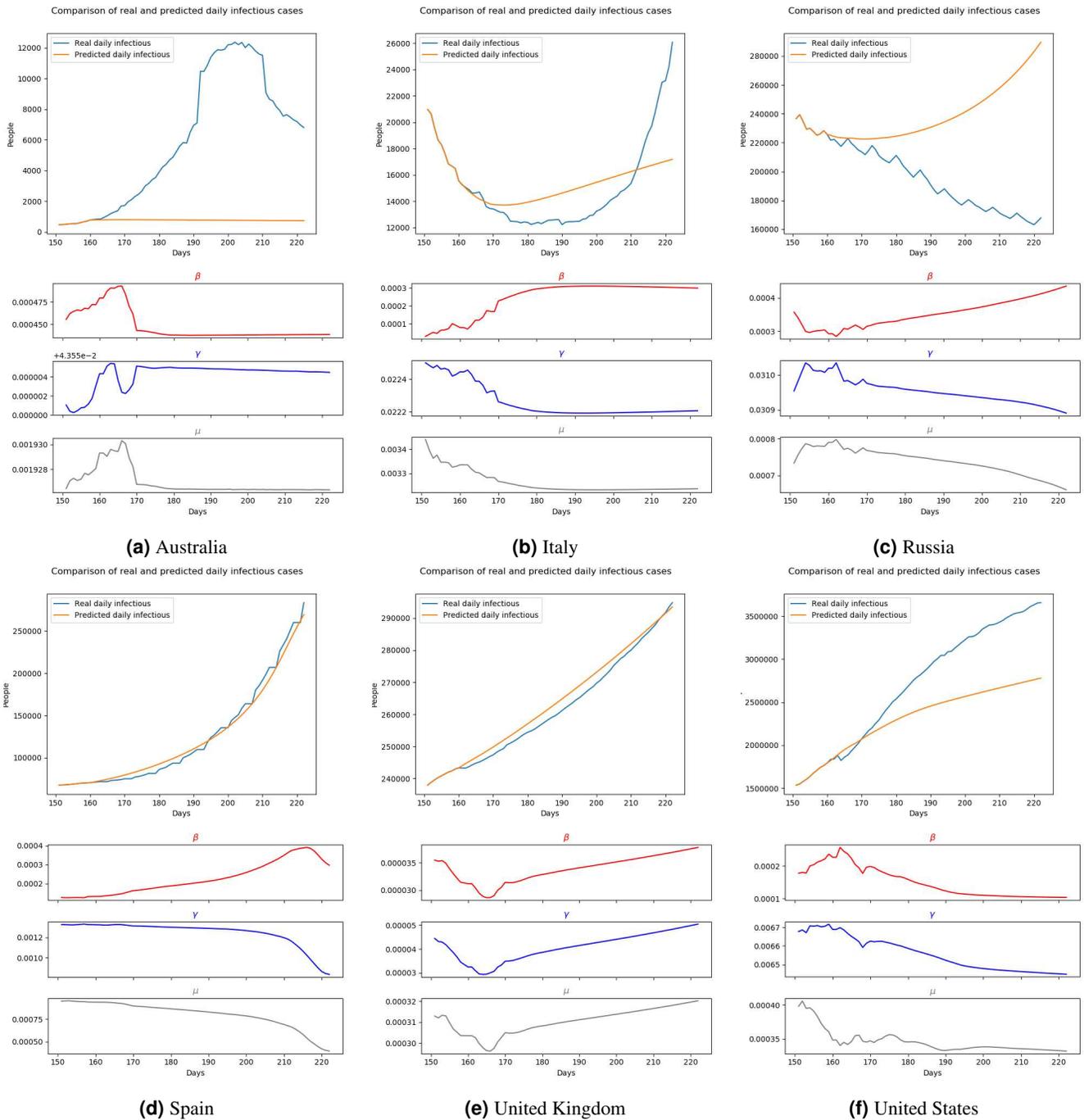


Figure 10. Forecasting results with transition rates of 161th-222nd day (Jul. 1st 2020 - Aug. 31st 2020) using data of 151st-160th day (Jun. 21st 2020 - Jun. 30th 2020)

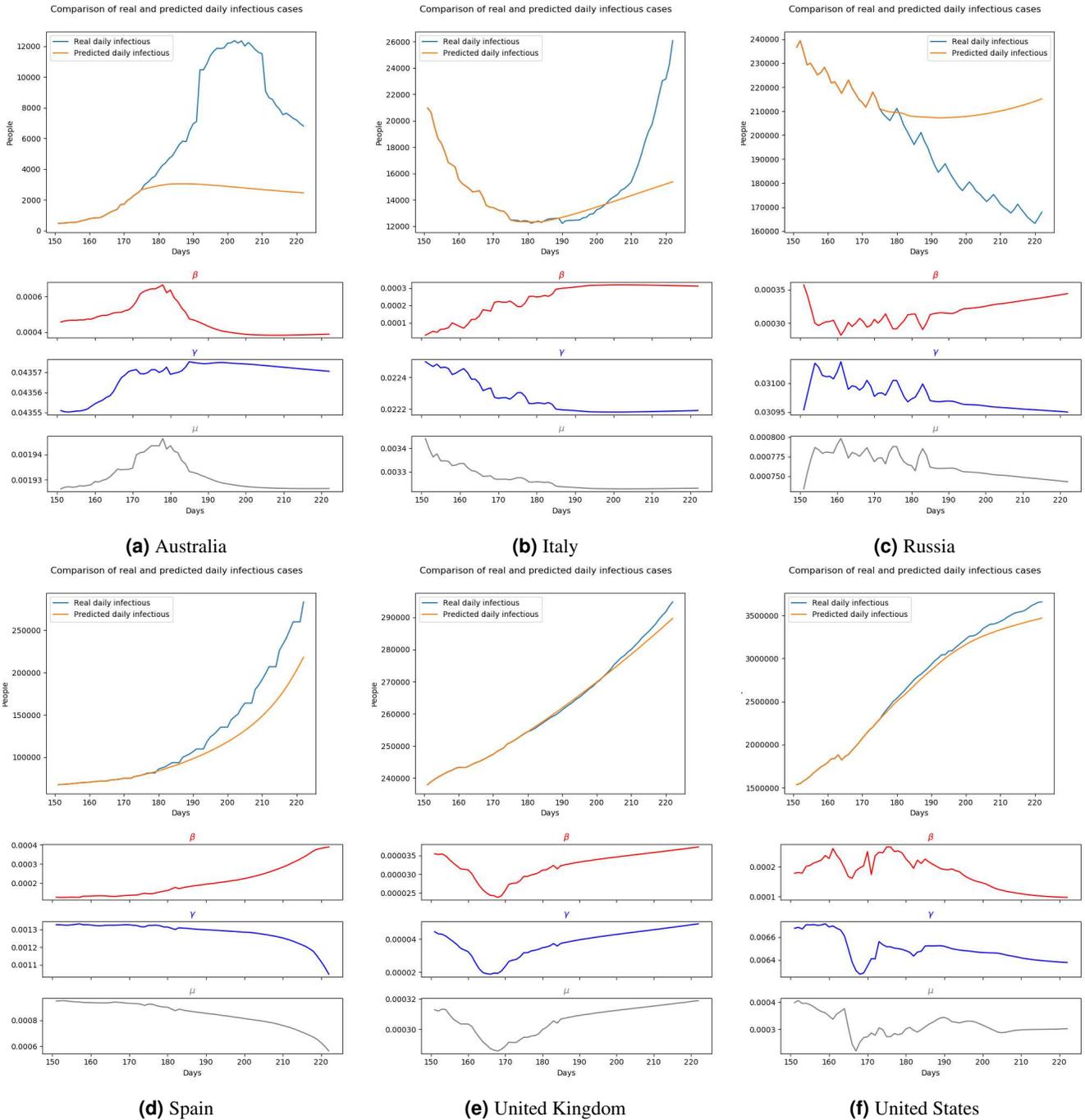


Figure 11. Forecasting results with transition rates of 176th-222nd day (Jul. 16th 2020 - Aug. 31st 2020) using data of 166th-175th day (Jul. 6th 2020 - Jul. 15th 2020)

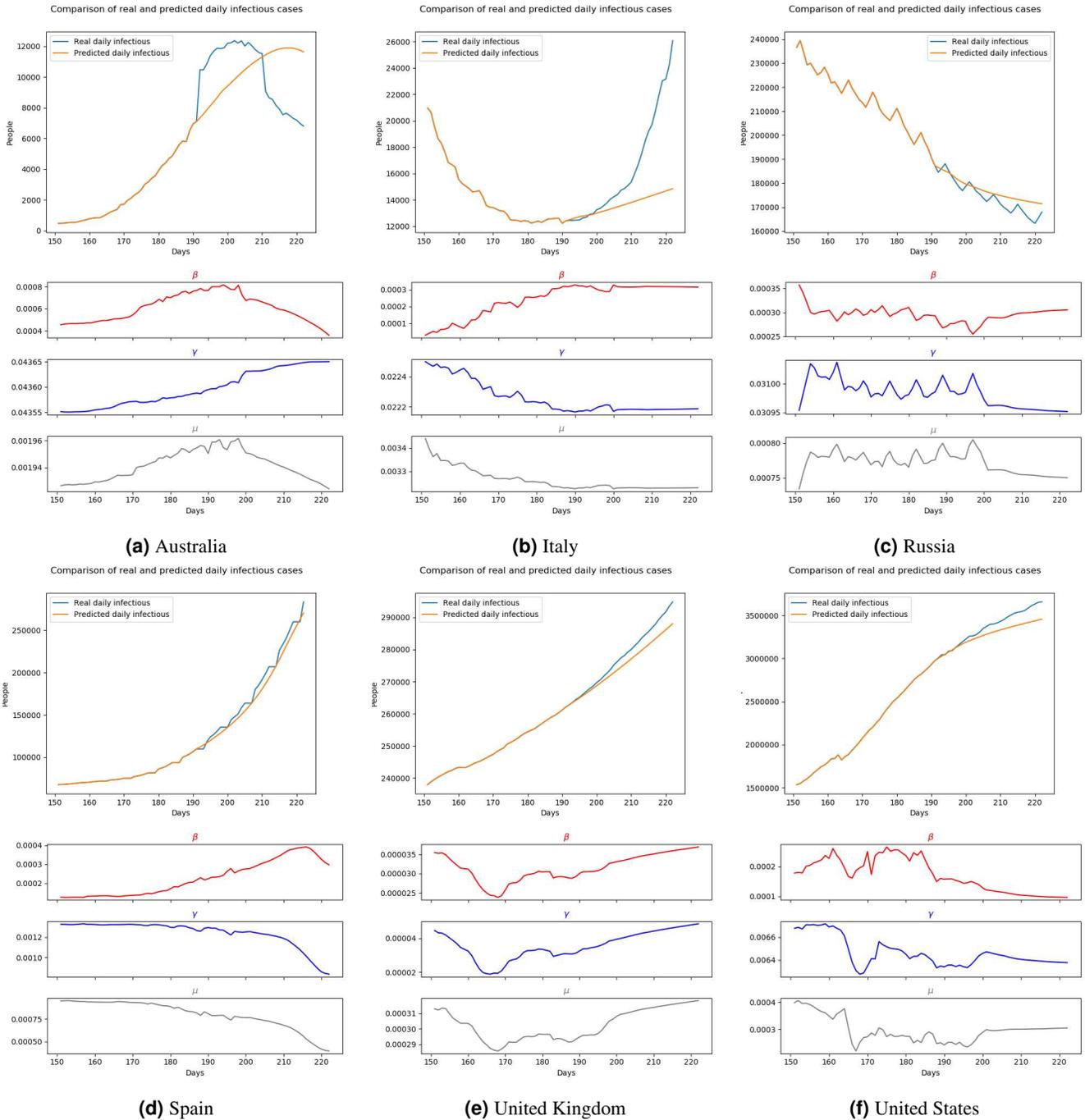


Figure 12. Forecasting results with transition rates of 192th-222nd day (Aug. 1st 2020 - Aug. 31st 2020) using data of 182nd-191th day (Jul. 22nd 2020 - Jul. 31st 2020)

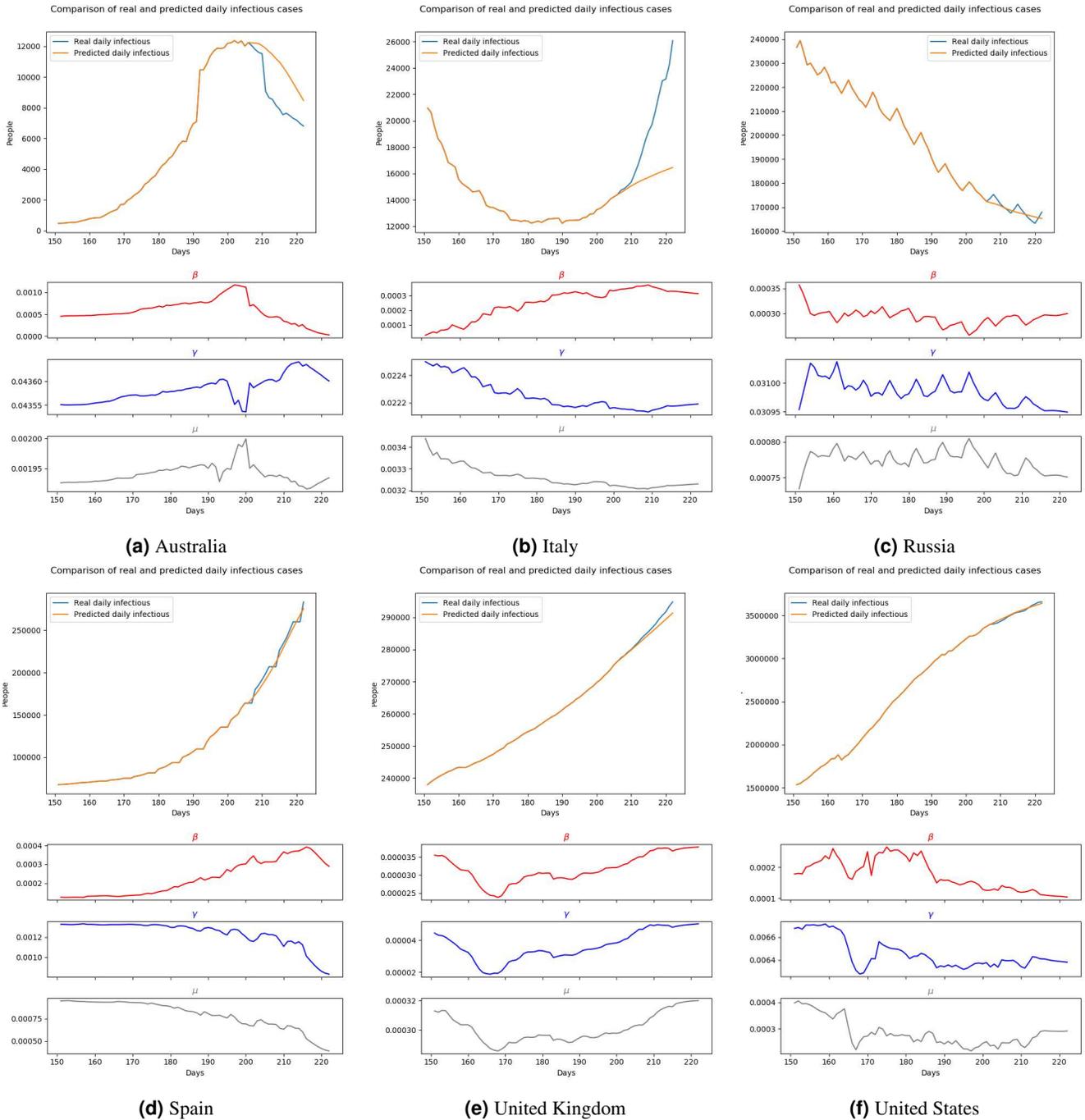


Figure 13. Forecasting results with transition rates of 207th-222nd day (Aug. 16th 2020 - Aug. 31st 2020) using data of 197th-206th day (Aug. 6th 2020 - Jul. 15th 2020)

constructed can overcome the limitations of each other and take advantage of semi-supervised learning to be more efficient in the training process.

With the support of Deep Learning, based on the number of infectious, recovered and deceased cases, our BeCaked model can determine the (β , γ , μ) parameters of the SIRD model. Using these parameters, the differential equations can be solved properly to predict the development trend of the COVID-19 pandemic. The significance of BeCaked model is to make the predictions among these parameters of the differential equations based on the number of infectious, recovered, and deceased cases in the past, instead of accurately predicting the number of those cases. Therefore, it can predict the trend of an increase, decrease, or a peak in the number of susceptible, infectious, recovered and deceased cases. These predictions can help the authorities to give appropriate strategies in order to deal with the spread of this pandemic.

In the evaluation process, we compared the performance between our BeCaked model and current top-tier forecasting-specialized models to prove the reliability of ours. In the whole world evaluation, our model scored almost the highest performance, while at the country level, its effectiveness drops significantly in some countries at 15-step forecast. The mystery behind this unusual is the difference between an open system and a closed system. The whole world system can be considered as a closed system because there is no outside factor affecting the COVID-19 pandemic situation. Contrasting to the country level, each country is an open system due to many unforeseen factors such as illegal entry, inaccurate testing, etc. Therefore, when applying any forecasting model to any open system, the most important and effective decision of the model is "how quickly the model is able to catch up with the trend of the pandemic". Due to that, when comparing at the country level, we only compare up to 15-step forecasting, because the previous study⁴³ shows that 14 days is the period for the situation of this pandemic changes.

The COVID-19 pandemic, in general, is an infectious disease with a large scale, so that its development rule follows the transition process of the SIRD model and reflects on (β , γ , μ) parameters. This is the factorial that gives our model the power to maintain its performance in long-time forecasting. Although our model can adapt to new pandemic situation, it takes a time to realize the trend depending on local policies of the area being considered (for examples, in case of Spain, it takes effect immediately while in case of Russia, it takes about 30 days). This is the foreseen problem because the factors that affect the infection of this pandemic are diverse. Some important factorials such as age, underlying medical conditions, restriction policies, quarantines, etc. are said to be very region-specific and we lack information about those factors. In conclusion, despite achieving noticeable performance, our model should be carefully used as a reference for epidemiologists in order to ensure no wrong decision or policies will be made due to unusual situations or forecasting lag.

Related works

Since the COVID-19 pandemic began to spread, there has been a lot of researches to solve the problem of sequencing the virus gene, finding a cure, a vaccine, predicting the effect and extent of transmission spread of the pandemic, etc. To be honest, we cannot deny the benefits of pandemic forecasting models. Thanks to them, countries can detect infected people early and slow down the spread of this pandemic. Since then, medical researchers have more time to research and find vaccines and medicines. In this section, we analyze the advantages and disadvantages of the latest mathematical and Deep Learning models to predict this pandemic and compare them with the model we have proposed.

Mathematical models

Most of the mathematical models currently used for epidemic prediction are developed based on the *Susceptible-Infectious-Recovered* (SIR) model of Kermack and McKendrick¹³. The common point of these mathematical prediction models is the reliability and the predictable results. By converting factors that influence epidemic into differential equations and integrating them with existing equations, researchers have created more variations with more realistic predictability than the original one and suitable for many types of epidemic. Some highlighted recent research can be listed as follows: SEIRD⁷, SIRD¹⁵, SEIPEHRF⁵¹, etc. The main weakness of these mathematical models is that they require transition rates between states and those numbers are not easy to estimate accurately. Because the experts estimate those rates are still human, so that their predictions still contain "humanity" and sometimes do not have enough "sensitivity". Therefore, the performance of those models is often not high as they were expected.

Some other methods that can be used to forecast this pandemic are regression-based methods. These models depend on both their hyperparameters and the historical data. As a consequence, their performances are almost the same as the SIR-based model. Some methods can be listed such as *Geographically Weighted Regression* (GWR)²⁷, ARIMA¹⁰ and its extensions.

Machine learning models

Towards machine learning methods for forecasting, the very first thing that need to be mentioned is that they achieve high performance when being applied in this COVID-19 pandemic. There are so many models, vary from simple to complex in their architecture. Recent studies notice that they can assemble some external factors of the pandemic to make the prediction

more accurate. We can consider some outstanding ones such as LSTM-based methods^{7,10}, Variational-LSTM Autoencoder¹⁶, NARNN¹⁰, etc. However, as a trade-off, they are extremely complex and need more detailed input data (such as the contact information, the number of testing or quarantines, etc.) that will result in an unsuitable situation when using those SOTA models in developing countries where modern technology is not reachable⁵². Also, besides their good performance, the only things we get from those models are the number of cases. They can not give us insights into how they predict those values. Therefore, although their forecasting performances are usually high, they could not convince epidemiologists about its reliability. Because the pandemic situation changes every hour, every day, those models can predict well at this moment, but no guarantee that they will do the same for further moments. Moreover, experts need more information than the only number of cases to control the pandemic, so that we can easily consider that almost machine learning models could not satisfy them.

Our proposed BeCaked model also takes advantage of the LSTM layer when using it to extract “sequence” features of historical time-series data. As a result, our model can find the relationship between the difference in the number of considered cases in the previous days and the parameters (β , γ , μ) of the SIRD model. This is the same as for the above LSTM-based methods that successfully find the relationship between the number of cases in the past and the future. While those methods can not elucidate clearly their forecasting results, our BeCaked one represents the forecasting by explanations based on the connection of (β , γ , μ) and cases. Therefore, not only has our model high precision, but also denotes the reason why its predictions are like that.

Conclusion

Summary

With the model we have proposed, the pandemic has been modeled and forecasted relatively accurately. We expect this model to be widely applied in each country and region as a reference source in pandemic prevention. In the future, we will continue to experiment with more extensive variations of the SIRD model on more detailed pandemic data sets. Also, we will try to combine many other SOTA techniques for continuously-like data with mathematical models to solve other related problems as mentioned in *Section Related works*. At the same time, we will also continue to maintain the website, update disease data daily and conduct reinforcement learning methods on the proposed model to have future forecasts as accurate as possible.

This model is a non-profit community project, which is of great significance for development in all aspects if properly applied. The forecast of the situation of the COVID-19 pandemic enabled the government and citizens together to comply with necessary regulations such as quarantine to prevent the spread of the COVID-19 pandemic. Policies and regulations are essential and are most effective when implemented before it is too late. For example, if we predict the resurgence of the COVID-19 pandemic after a peaceful period, we will be more proactive in preventing as well as reducing the number of people infected and fatal.

The COVID-19 pandemic has had a great impact on people’s lives, seriously affecting the economy and society. Therefore, if everyone works together to prevent the epidemic of COVID-19, then socio-economic life can return to stability and continue to develop. This is the core purpose that this study wants to achieve.

Future development

The combining of VAE, an AI technique, and the SIRD model is one of the most interesting and promising medical and computer science projects if it is further developed in the future. The application of computer science, especially Artificial Intelligence in medicine, is a step towards the future. In one day not far, computers can replace humans to do complex things, the things that require constant calculation and repetition. Like forecasting using the SIRD model, computer science in general and artificial intelligence in particular play a very important role to approximate the variables β , γ and μ . It is the AI that helps us complete the differential equation to be able to predict the situation of the COVID-19 pandemic. But computer science does not stop at predicting the situation of the COVID-19 pandemic. With this model, we can apply to find the suitable coefficients for problems using the differential equation or other complex stools in issues such as gene sequencing, diet generating, prediction of other diseases, etc. Moreover, with the development of Artificial Intelligence, we can apply it to medicine such as diagnosing, screening disease, revealing risk factors, etc. in each patient. The world is evolving and the intersection of the fields is of utmost importance. This has contributed to making people’s lives become better, especially since human health issues are being cared for more and more.

Our explainable AI model of BeCaked still has much rooms for further improvements. Firstly, the basic SIRD model can be replaced by other upgraded models such as SEIR⁷ or SEIPEHRF⁵¹. Moreover, we can further encode additional information such as travel history or contact information to make the model predictions closer to practical situations. In terms of Deep Learning techniques, the latest encoding models such as BERT⁵³ or GPT-3⁵⁴ can also be considered as well to make the encoded information more meaningful.

Data Availability

The COVID-19 data analysed during the current study are available from Johns Hopkins University Center for Systems Science and Engineering in the COVID-19 repository, <https://github.com/CSSEGISandData/COVID-19>.

The world and countries population data analysed during the current study are available from Worldometer on their website, <https://www.worldometers.info/world-population/population-by-country>.

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Appendix

Appendix A. The novel name "BeCaked"

In view of the fact that a new variant of coronavirus and COVID-19, the illness they cause, are disastrously spreading among communities in many countries. Therefore, a set of effective non-pharmaceutical interventions, known as social distancing, helps to reduce the spread of this pandemic without pharmaceutical treatments by keeping an acceptable distance from each other (the distance specifically differs from country to country), avoiding gatherings into crowded places. The name "BeCaked" resulting from that strong motivation, standing for Be Careful and Keep Distance, is named in the spirit of encouraging people to strictly comply with the coronavirus legislation in order to protect themselves and their society. Up till now, our website system which can be visited at <http://cse.hcmut.edu.vn/BeCaked> has fully implemented for visualizing and observing purposes.

Appendix B. BeCaked web-based system illustrations

In order to simplify the use of the BeCaked model and respond to a wide variety of users, we implemented a website to statistic and visualize the forecasting results of BeCaked model. Our website includes two main parts: overview and future forecast.

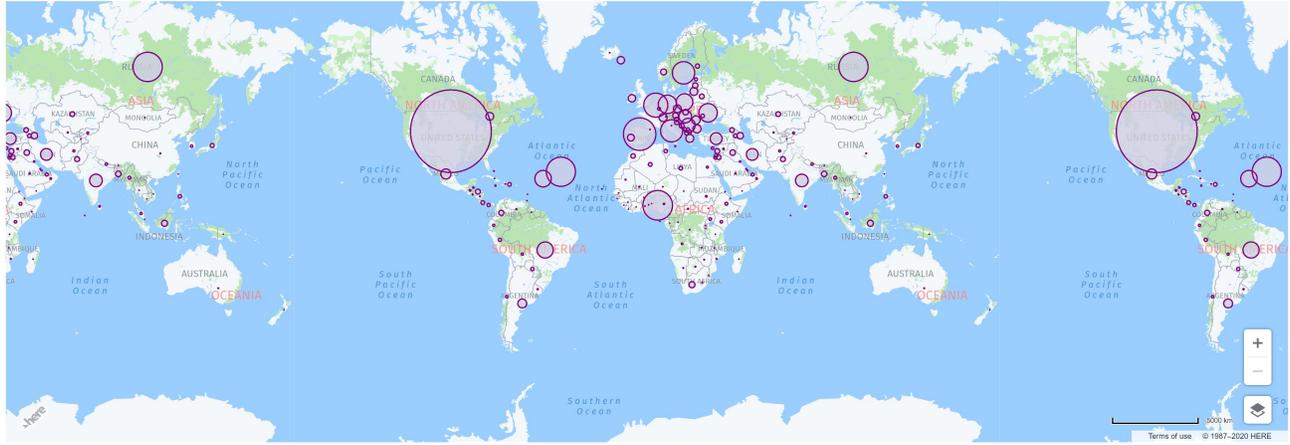
The overview page shown in Figure 14 includes a map which shows the spread-level of the epidemic in nations, statistics of the latest infectious, recovered and deceased cases, 30 days of epidemic history and a future 30-day forecasting results. Users can change the type of cases shown in the world map by clicking on the total cases of that type located under the map. Also, users can search the cases of a specific country by entering the country name in the search box above the information table.

The forecast for the future shows a long-term forecast for the COVID-19 pandemic. Users can get a reliable prediction for a specific period of time by entering the start and end date. Our system will then return the forecasting results of infectious, recovered and deceased cases of each day, and a line chart represents those metrics to give the user a more overview of the spread of this pandemic during that time. An example of using this page is presented in Figure 15. In this example, we get the forecasting results from January 22nd 2020 to June 28th 2023. Moreover, users can search for specific day cases by typing the day in the search box.

Author contributions statement

Conceptualization: Thinh T. Nguyen and Khuong A. Nguyen. Methodology: Duc Q. Nguyen and Nghia Q. Vo. Software: Duc Q. Nguyen. Analysis: Duc Q. Nguyen, Nghia Q. Vo, Thinh T. Nguyen, Dang N. Tran, Khuong A. Nguyen. and Tho T. Quan. Validation: Duc Q. Nguyen, Nghia Q. Vo, Dang N. Tran, Khuong A. Nguyen and Tho T. Quan. Paper preparation: Duc Q. Nguyen, Quang H. Nguyen and Tho T. Quan. All authors reviewed the manuscript.

COVID-19 Current Infectious Map



Total Infectious
71,704,885.0

Current Infectious
23,242,934.0

Recovered
46,856,934.0

Deceased
1,605,017.0

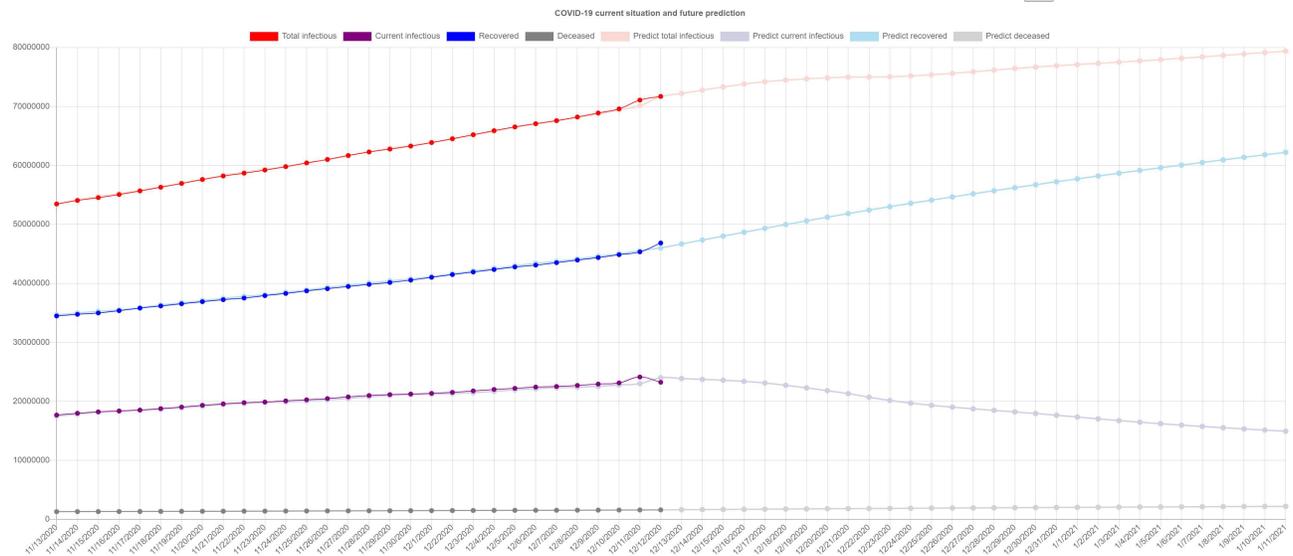
Show 10 entries

Search:

No.	Country	Total population	Total infectious	Current infectious	Recovered	Deceased
1	Mauritania	-	10,780	2,536	8,022	222
2	Slovakia	-	130,794	34,230	95,416	1,148
3	North Macedonia	-	73,025	22,203	48,726	2,096
4	Cameroon	-	25,143	849	23,851	443
5	Lesotho	-	2,250	887	1,319	44
6	Bahamas	-	7,648	1,442	6,043	163
7	Cuba	-	9,354	846	8,371	137
8	Greece	-	123,842	97,228	23,074	3,540
9	Costa Rica	-	150,947	36,430	112,622	1,895
10	Jordan	-	257,275	40,596	213,344	3,335

Showing 1 to 10 of 191 entries

Previous 1 2 3 4 5 ... 20 Next



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Figure 14. Homepage of web user interface

From to

Show 10 entries

Search:

No.	Day	Total infectious	Current infectious	Recovered	Deceased
1	22 / 01 / 2020	555.0	510.0	28.0	17.0
2	23 / 01 / 2020	654.0	605.0	30.0	18.0
3	24 / 01 / 2020	941.0	879.0	36.0	26.0
4	25 / 01 / 2020	1,434.0	1,353.0	39.0	42.0
5	26 / 01 / 2020	2,118.0	2,010.0	52.0	56.0
6	27 / 01 / 2020	2,927.0	2,784.0	61.0	82.0
7	28 / 01 / 2020	5,578.0	5,340.0	107.0	131.0
8	29 / 01 / 2020	6,167.0	5,908.0	126.0	133.0
9	30 / 01 / 2020	8,235.0	7,921.0	143.0	171.0
10	31 / 01 / 2020	9,927.0	9,492.0	222.0	213.0

Showing 1 to 10 of 1,326 entries

Previous ... Next

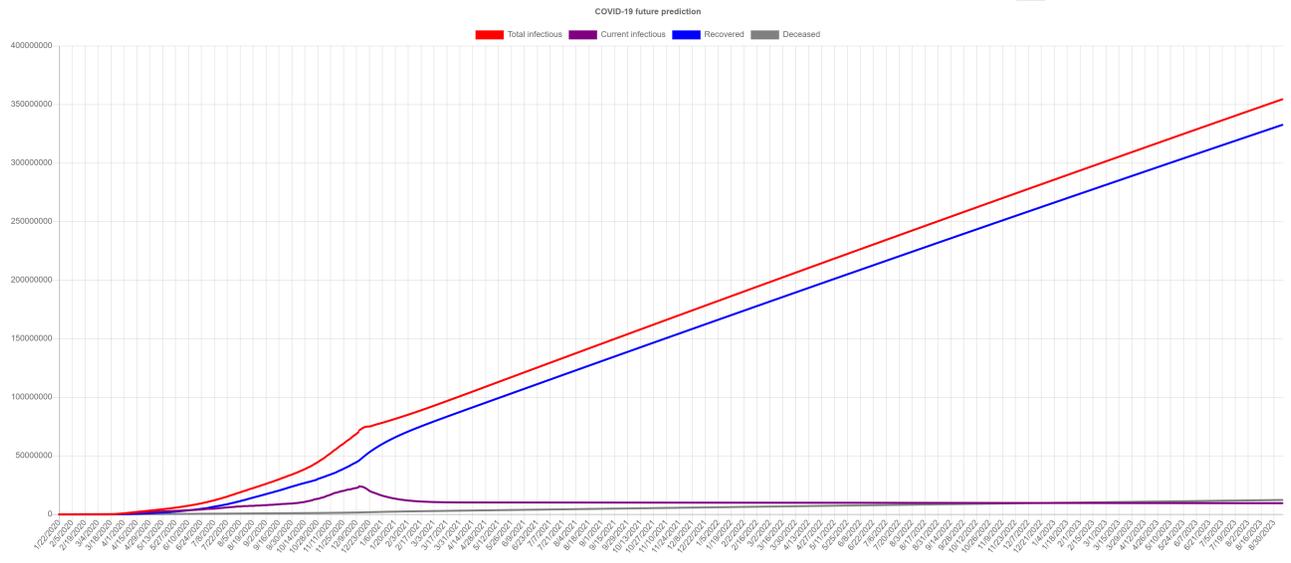


Figure 15. Long-time forecasting page

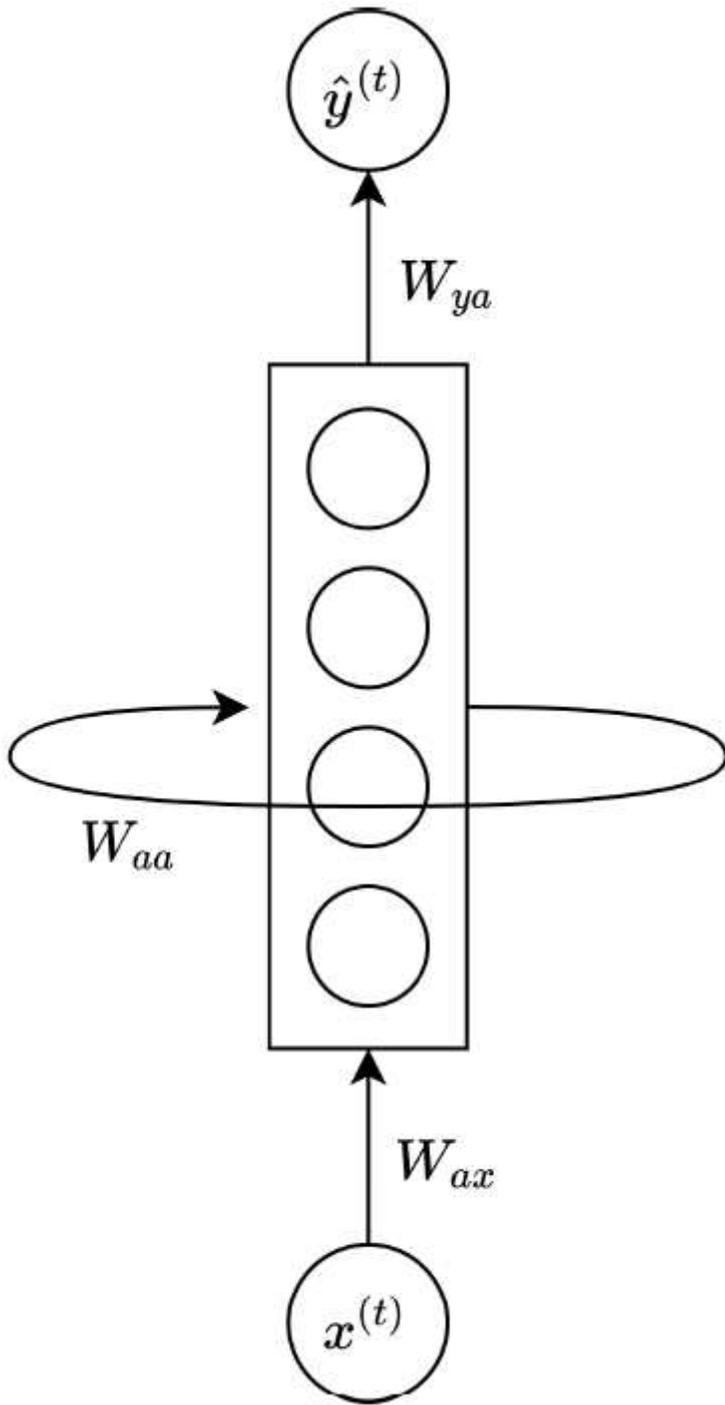


Figure 2

The physical architecture of an RNN

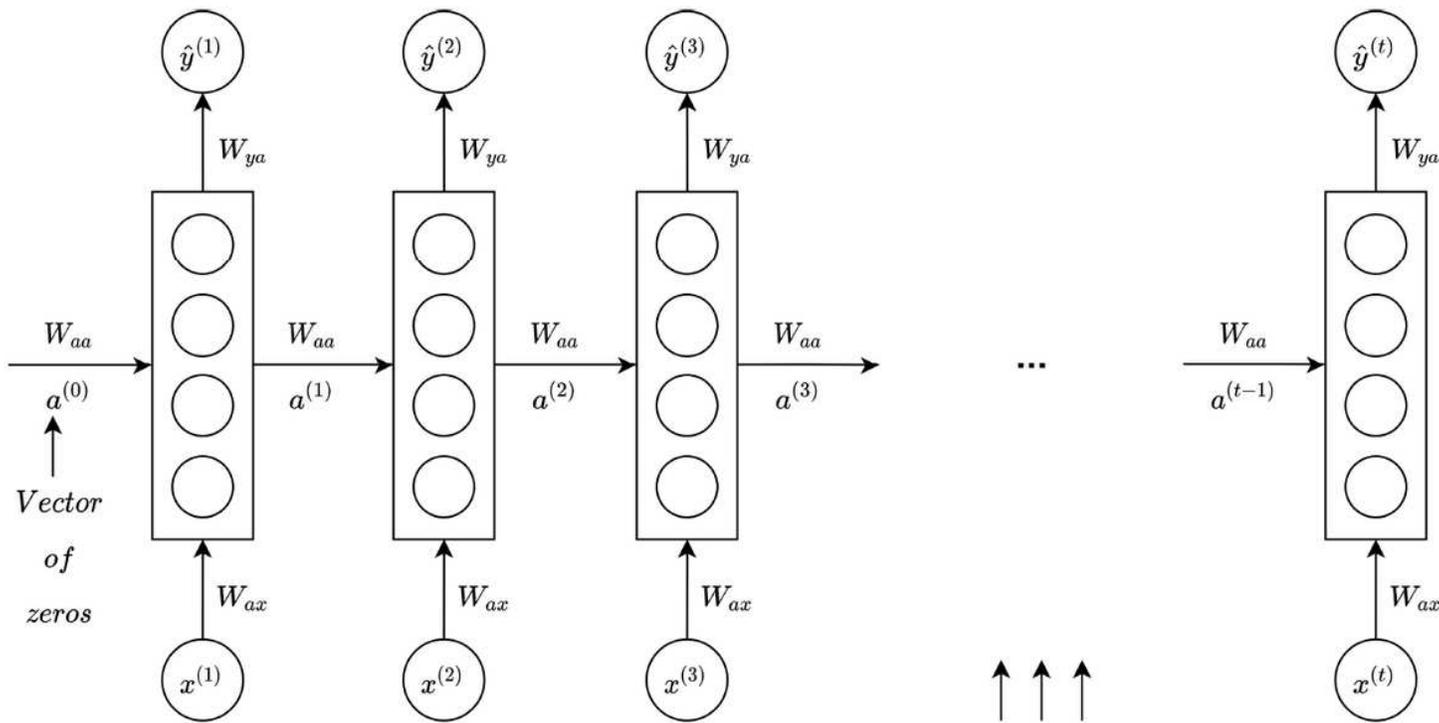


Figure 3

An unfolded RNN

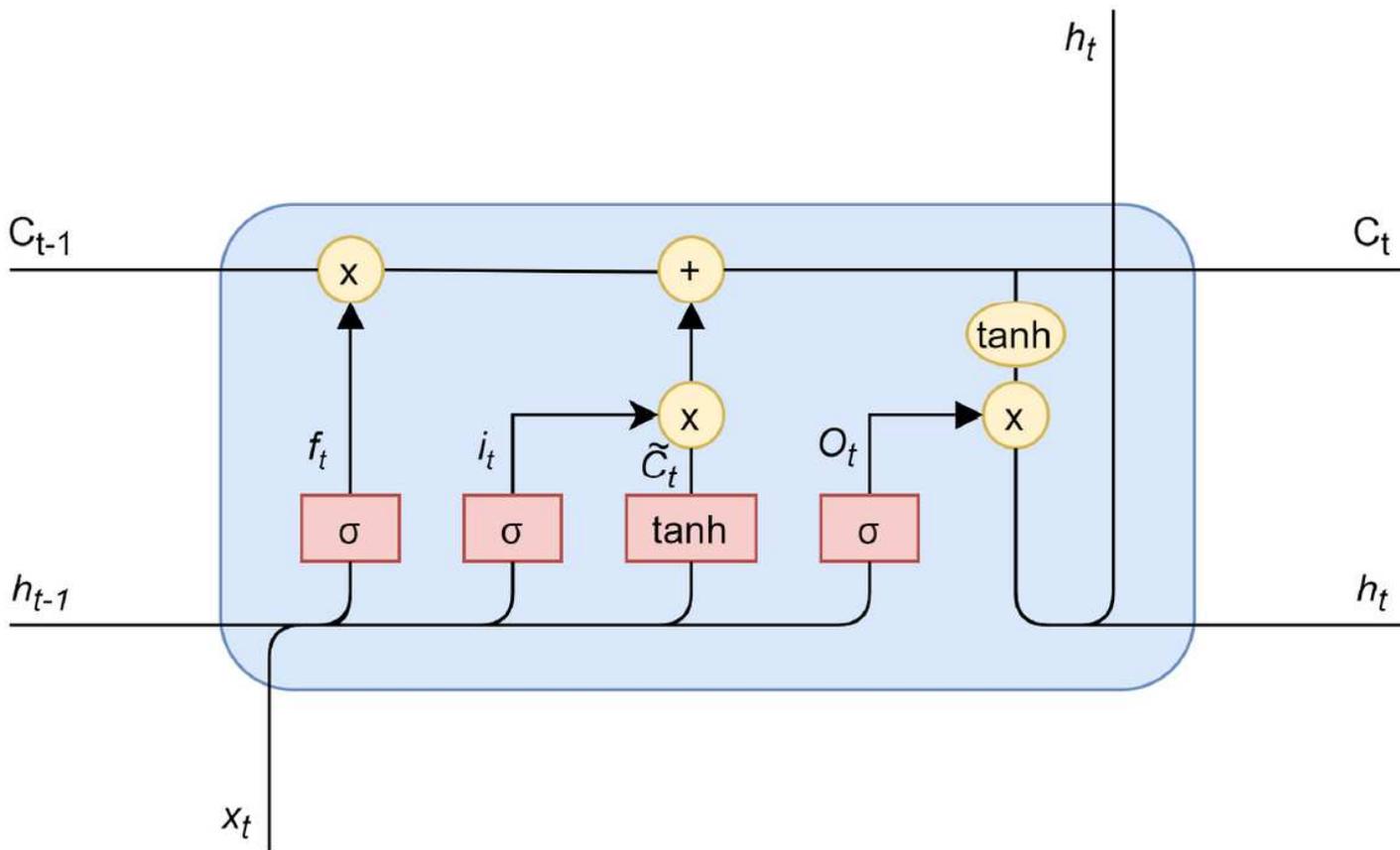


Figure 4

The structure of an LSTM cell

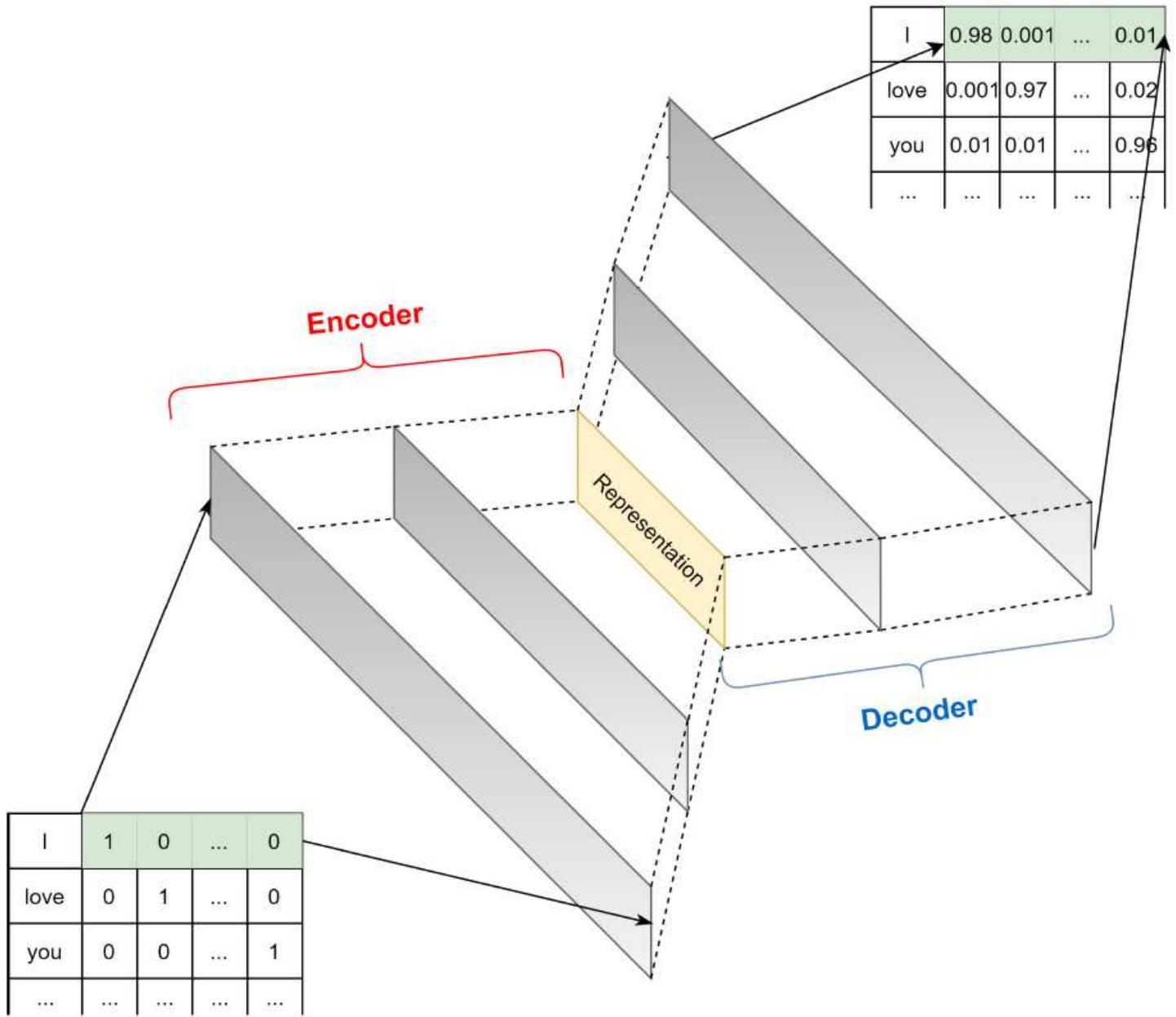


Figure 5

The concept of Autoencoder

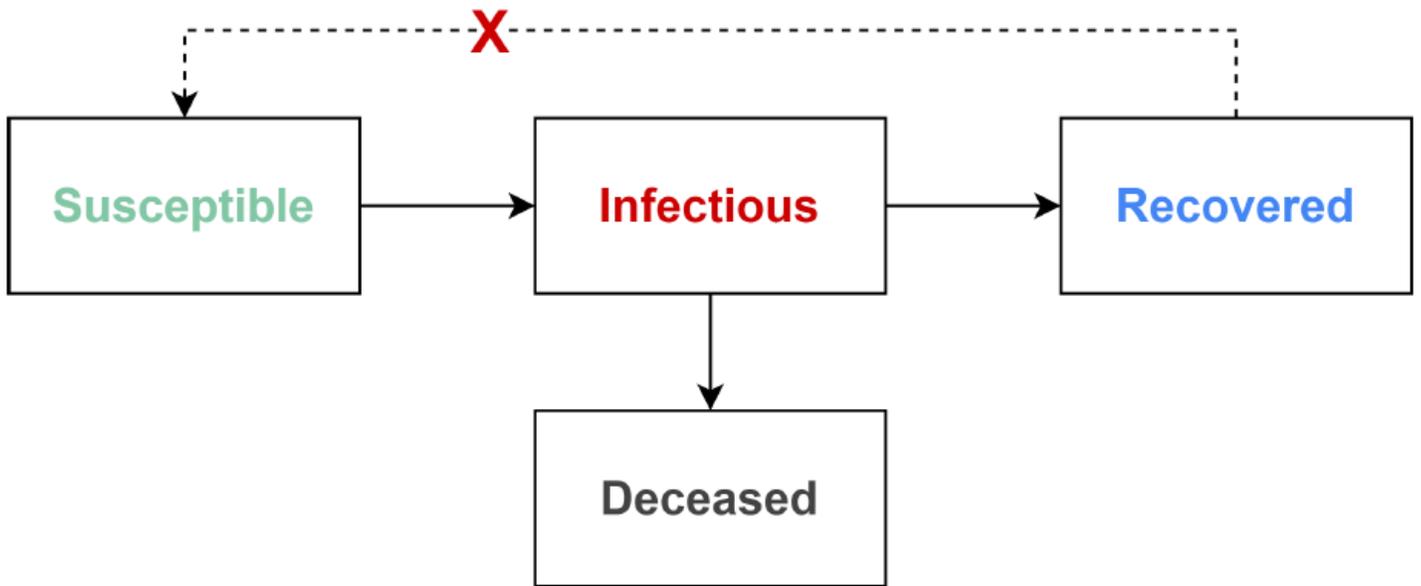


Figure 6

The concept of the SIRD model

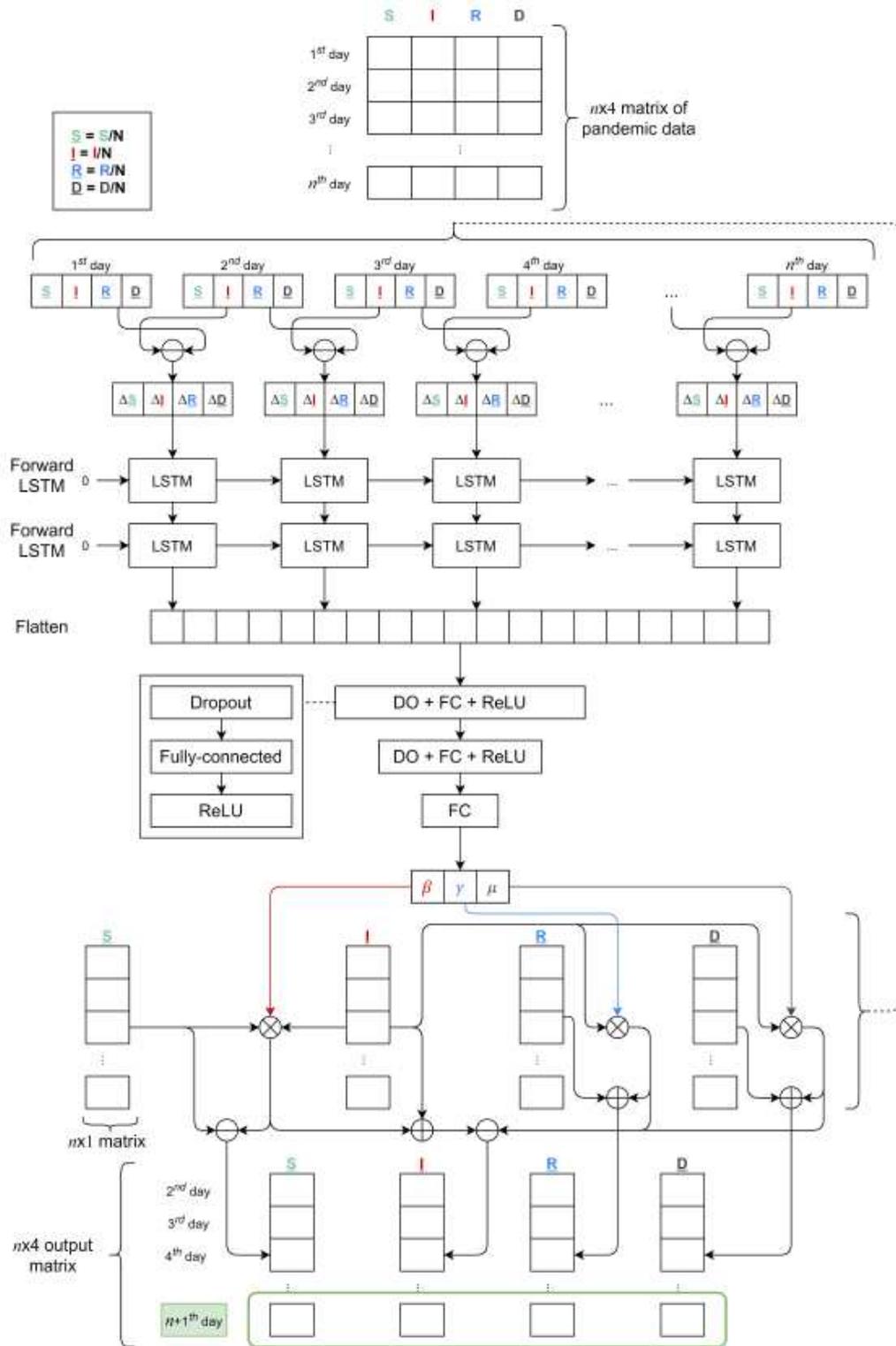
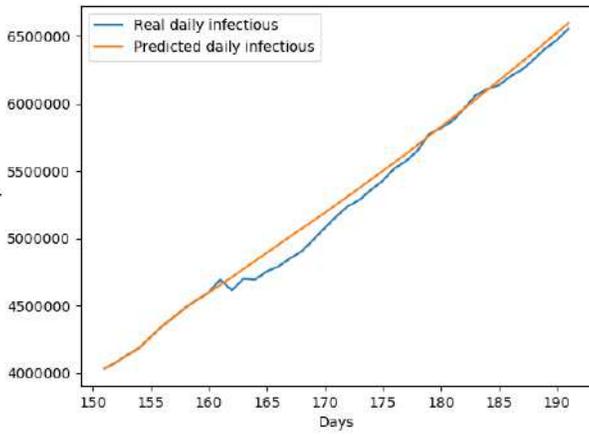


Figure 7

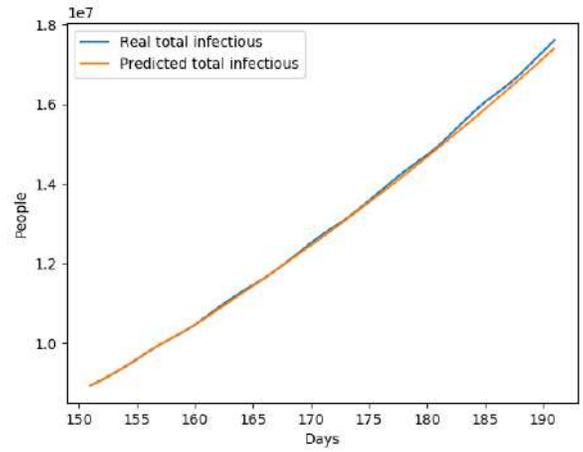
The architecture of BeCaked model

Comparison of real and predicted daily infectious cases



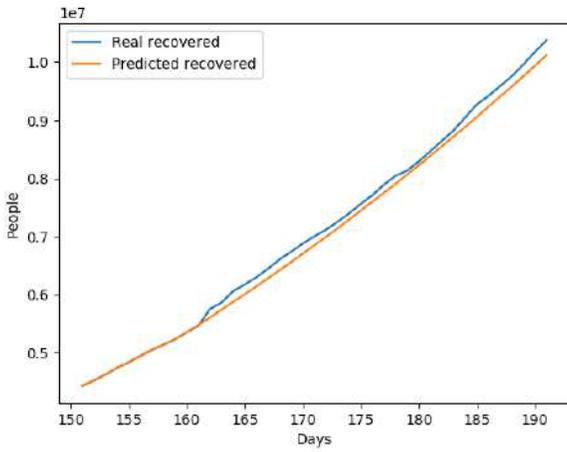
(a) Daily infectious cases

Comparison of real and predicted total infectious cases



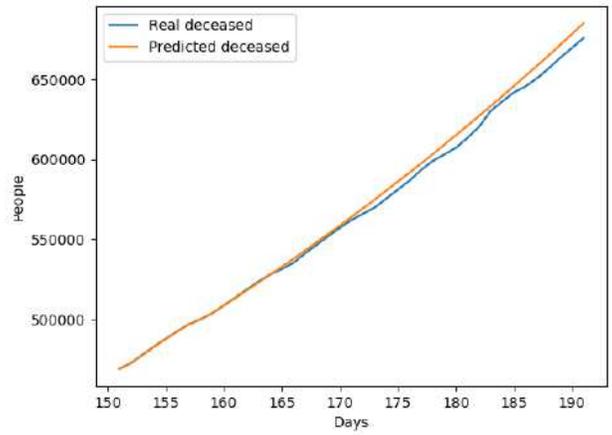
(b) Total infectious cases

Comparison of real and predicted recovered cases



(c) Recovered cases

Comparison of real and predicted deceased cases



(d) Deceased cases

Figure 8

Comparison of the number of cases between real data and BeCaked forecasting results from 161st-191st day (Jul. 1st 2020 - Jul. 31st 2020) of the world

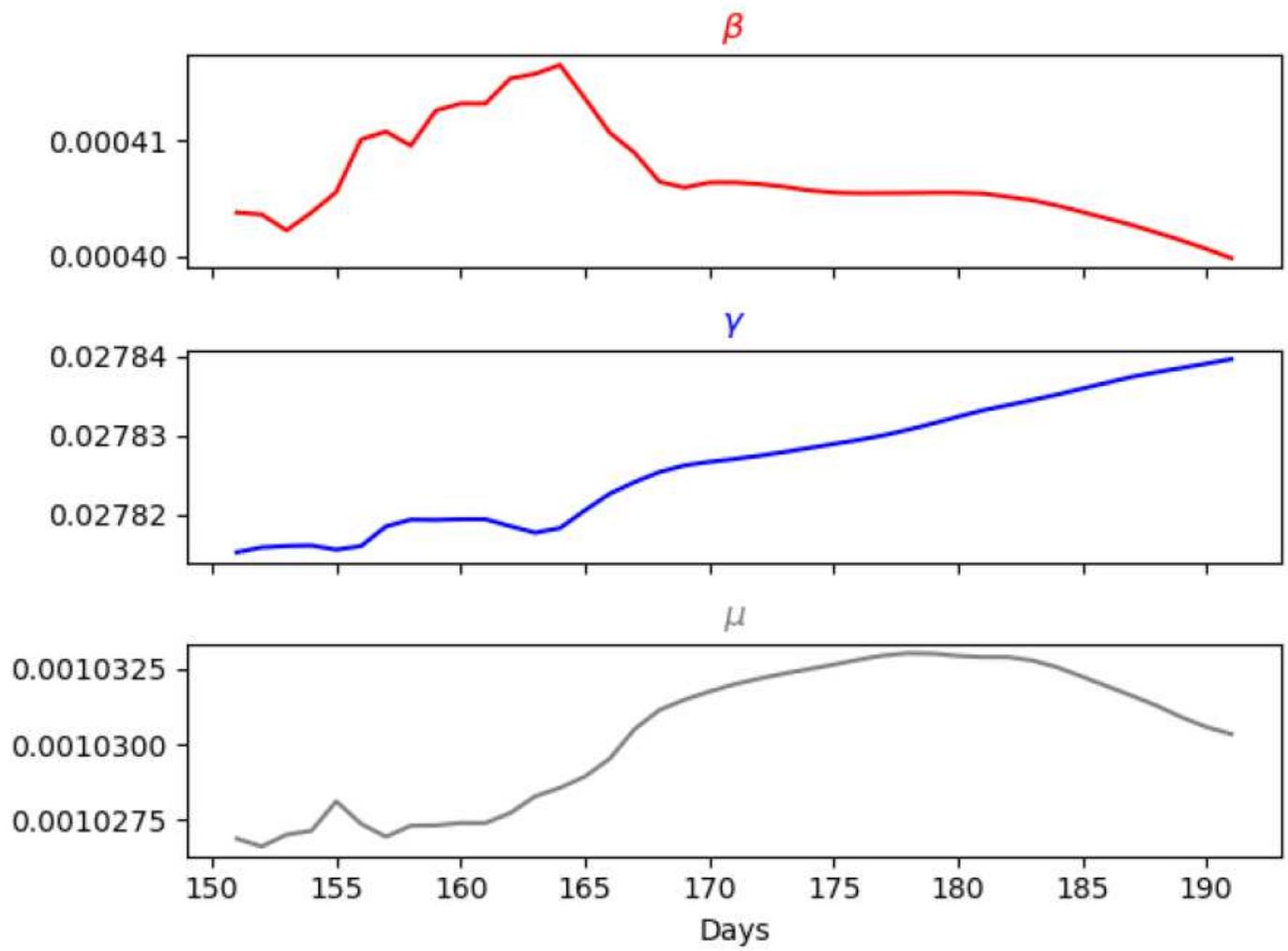


Figure 9

Predicted transition rates from 161st-191st day (Jul. 1st 2020 - Jul. 31st 2020) of the world

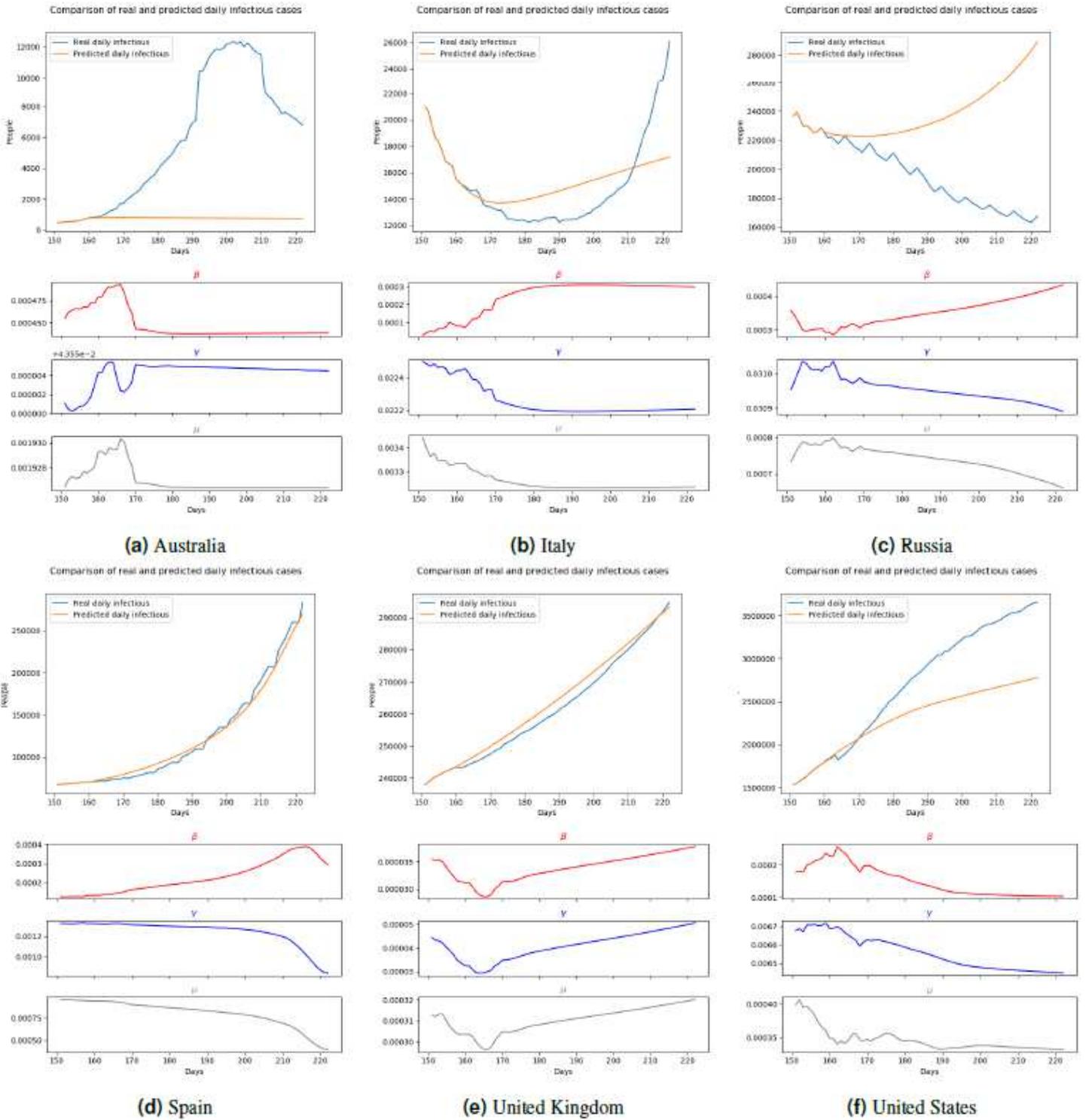


Figure 10

Forecasting results with transition rates of 161th-222nd day (Jul. 1st 2020 - Aug. 31st 2020) using data of 151st-160th day (Jun. 21st 2020 - Jun. 30th 2020)

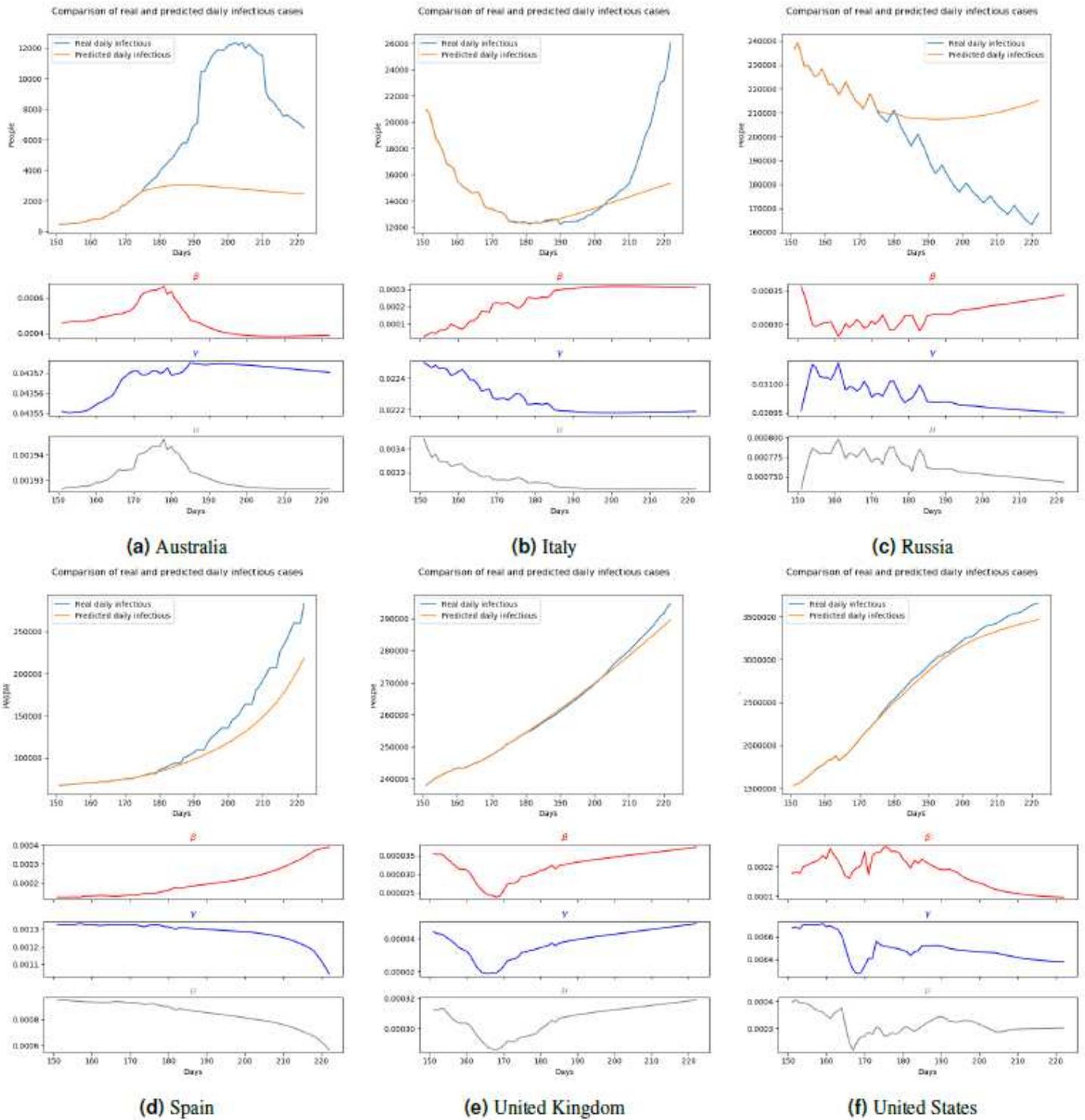


Figure 11

Forecasting results with transition rates of 176th-222nd day (Jul. 16th 2020 - Aug. 31st 2020) using data of 166th-175th day (Jul. 6th 2020 - Jul. 15th 2020)

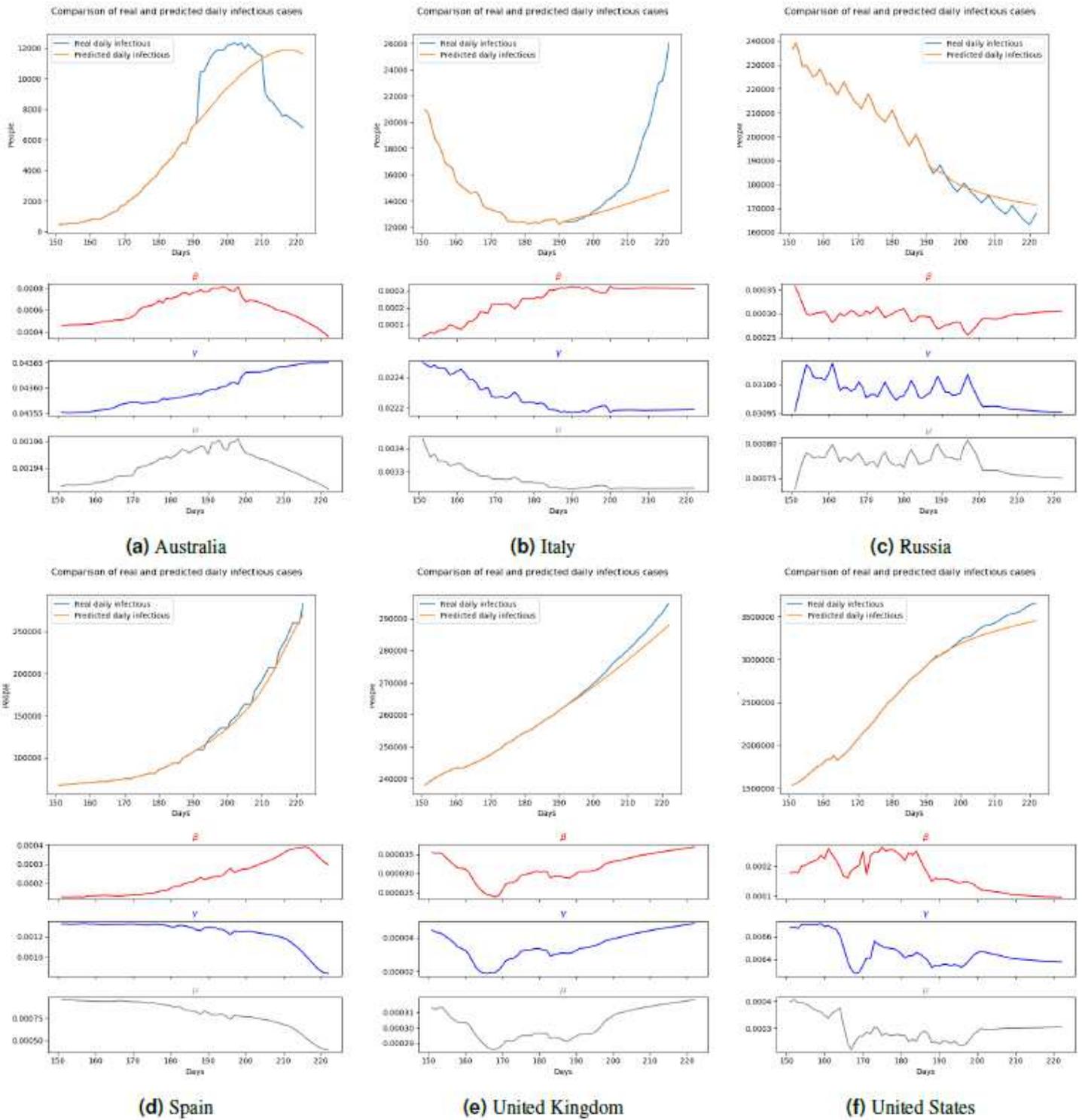


Figure 12

Forecasting results with transition rates of 192th-222nd day (Aug. 1st 2020 - Aug. 31st 2020) using data of 182nd-191th day (Jul. 22nd 2020 - Jul. 31st 2020)

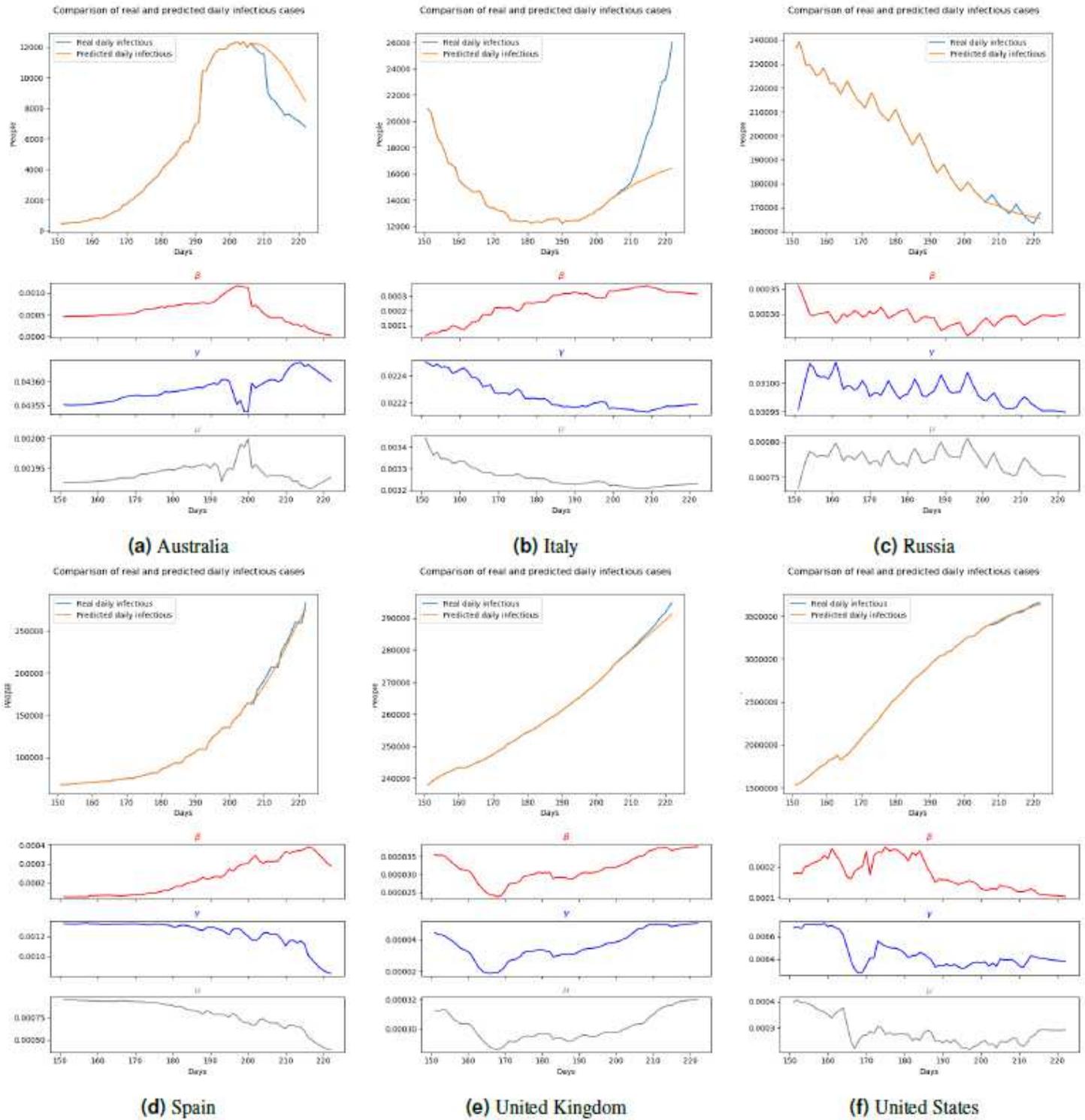


Figure 13

Forecasting results with transition rates of 207th-222nd day (Aug. 16th 2020 - Aug. 31st 2020) using data of 197th-206th day (Aug. 6th 2020 - Jul. 15th 2020)

COVID-19 Current Infectious Map



Total Infectious
71,704,885.0

Current Infectious
21,242,914.0

Recovered
46,856,914.0

Deceased
1,605,017.0

Rank	Country	Total population	Total infection	Current infection	Recovered	Deceased
1	Monaco	-	15,780	2,336	8,822	322
2	Slovenia	-	133,794	34,230	95,416	1,148
3	North Macedonia	-	2,1026	32,201	48,736	2,086
4	Canada	-	35,141	849	33,851	441
5	Lebanon	-	5,263	887	1,319	88
6	Bahrain	-	7,649	1,432	5,943	163
7	Cuba	-	11,354	946	9,371	137
8	Denmark	-	133,942	17,226	117,719	3,940
9	Costa Rica	-	5,047	36,438	112,822	1,895
10	Israel	-	7,273	40,996	213,344	3,133

Showing 1 to 10 of 10 entries Previous 1 2 3 4 5 10 Next

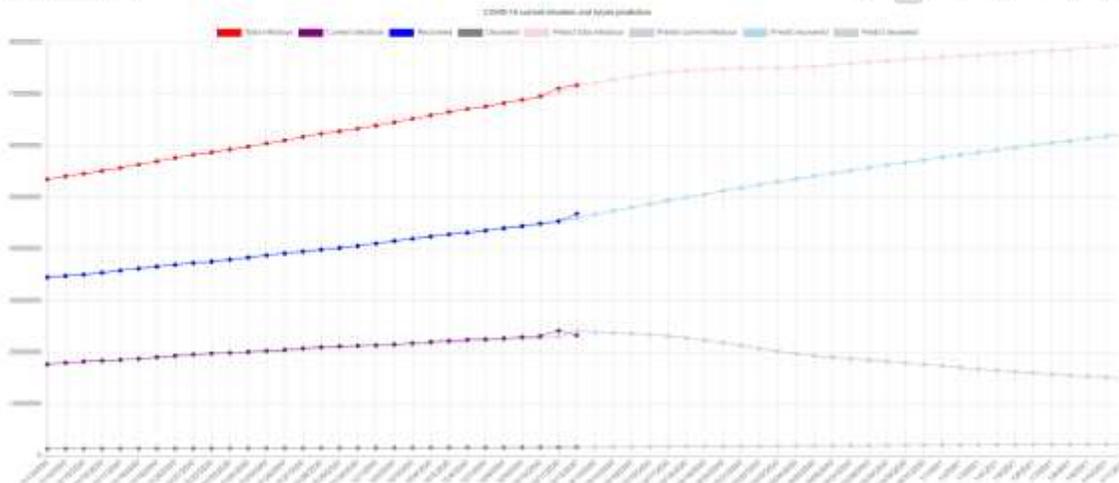


Figure 14

Homepage of web user interface. Note: The designations employed and the presentation of the material on this map do not imply the expression of any opinion whatsoever on the part of Research Square concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. This map has been provided by the authors.

From to

Show 10 entries

Search:

No.	Day	Total infectious	Current infectious	Recovered	Deceased
1	22 / 01 / 2020	555.0	510.0	28.0	17.0
2	23 / 01 / 2020	654.0	606.0	30.0	18.0
3	24 / 01 / 2020	941.0	879.0	36.0	26.0
4	25 / 01 / 2020	1,434.0	1,353.0	39.0	42.0
5	26 / 01 / 2020	2,118.0	2,010.0	52.0	56.0
6	27 / 01 / 2020	2,927.0	2,784.0	61.0	82.0
7	28 / 01 / 2020	5,578.0	5,340.0	107.0	131.0
8	29 / 01 / 2020	6,167.0	5,908.0	126.0	133.0
9	30 / 01 / 2020	8,235.0	7,921.0	143.0	171.0
10	31 / 01 / 2020	9,927.0	9,492.0	222.0	213.0

Showing 1 to 10 of 1,326 entries

Previous Next

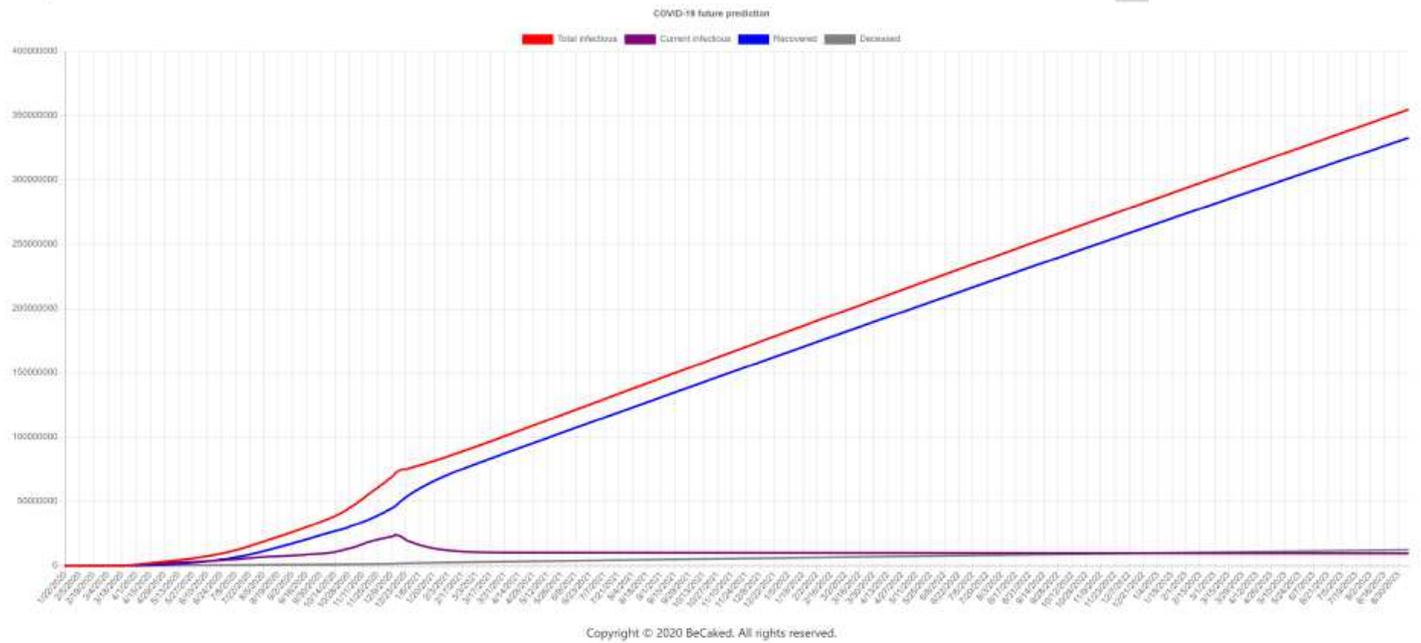


Figure 15

Long-time forecasting page