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RESEARCH ARTICLE

Machine Learning Model for Predicting Number of COVID-19 Cases in Countries with Low Number of Tests

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Abstract:

Background:

The COVID-19 pandemic has presented a series of new challenges to governments and healthcare systems. Testing is one important method for monitoring and controlling the spread of COVID-19. Yet with a serious discrepancy in the resources available between rich and poor countries, not every country is able to employ widespread testing.

Methods and Objective:

Here, we have developed machine learning models for predicting the prevalence of COVID-19 cases in a country based on multilinear regression and neural network models. The models are trained on data from US states and tested against the reported infections in European countries. The model is based on four features: Number of tests, Population Percentage, Urban Population, and Gini index.

Results:

The population and the number of tests have the strongest correlation with the number of infections. The model was then tested on data from European countries for which the correlation coefficient between the actual and predicted cases R^2 was found to be 0.88 in the multi-linear regression and 0.91 for the neural network model

Conclusion:

The model predicts that the actual prevalence of COVID-19 infection in countries where the number of tests is less than 10% of their populations is at least 26 times greater than the reported numbers.

Keywords: Machine learning, Model, COVID-19 cases, Healthcare systems, Testing, RNA viruses.

Article History

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1. INTRODUCTION

The SARS-CoV-2 or COVID-19 outbreak was declared a global health emergency on 30th January, 2020, by the WHO. COVID-19 is a member of the coronavirus family enveloped positive sense single-stranded RNA viruses. It is thought that COVID-19 transitioned from animal to human hosts in the Huanan seafood market in Wuhan in the province of Hubei, China [1]. The virus spread rapidly initially within China and then worldwide. COVID-19 was declared a pandemic on 11th March, 2020, by the World Health Organization. As of April 25th, 2021, there have been almost 100 million confirmed cases worldwide. Yet PCR (polymerase chain reaction), which can detect the genetic material of the virus, is the most accurate

technique for identifying the COVID-19 infection [2]. COVID-19 has exposed several inequalities. In the scramble to obtain medical resources, poorer countries have been left behind. Governments of low- and middle-income countries have struggled to provide sufficient funds to obtain medical resources, such as COVID-19 tests [3]. Furthermore, more geopolitically powerful countries have been accused of hoarding supplies leaving poorer countries unable to access sufficient tests [4]. With a disparity in the number of COVID-19 tests available, we aim to provide a prediction model based on machine learning that mitigates the reliance on clinical tests.

Machine learning has been utilized in contact tracing as a diagnostic and prognostic tool in vaccine and treatment development as a method to forecast and predict COVID-19 cases and deaths [5 - 11]. It has the potential to reduce the strain on healthcare systems that have been heavily burdened

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by the COVID-19 pandemic. For example, machine learning has been used to predict a positive COVID-19 infection in a PCR test [12]. The prediction is based on 8 binary features, including age, sex, contact with individuals known to have had COVID-19, and the appearance of five clinical symptoms. In addition, Sun et al. developed a model to predict the severity of a COVID-19 infection [13]. Furthermore, the model has been utilized to predict the prevalence of COVID-19 patients between one and six days in advance in 10 Brazilian states [14].

In this work, we have built multilinear regression and neural network models to predict the number of COVID-19 cases as of 15/03/2021. The models have been trained on the US States data and tested against the number of infections in the European countries. Then, both the models have been used to predict COVID-19 infection cases in countries with a low number of tests. The model was based on four features: the number of tests, population, urban population, and the Gini index. The model suggests that the actual number of infections is at least 10 times higher than the reported number of infections.

Uncertainties from different sources are not considered in this study; first, the ML model parameter uncertainty, which requires different techniques to be placed, such as Bayesian Neural Networks (<https://arxiv.org/abs/2107.03342>). This uncertainty is not considered since the DNN used for this study does not deliver certainty estimates or suffers from over- or under-confidence. Second, uncertainty data sources, since the data used in the analysis performed provide neither uncertainty in the PCR tests nor the estimation of the number of populations. Additionally, the PCR test uncertainty used in the US data, used in training, was different from the corresponding uncertainty for the tests used in other countries, and thus was used for the inference. Moreover, different COVID-19 variants significantly change the uncertainty rates, which can be a topic of future studies.

2. MATERIALS AND METHODS

The data were obtained from several official sources, such as from the World Bank World Development Indicators [16 - 19], government websites and publications [20 - 22], Worldometer [23], and from Our World in Data [14]. The data were extracted, standardized, and compiled into a single file. Although several features were considered, only four were included in the model owing to a lack of availability of data and low correlation with COVID-19 cases recorded. The four features used were Population, Tests, Gini Index, and % Urban Population. As the model first needed to be trained on the US States and then tested on European countries, data for all factors included would need to be available for both. This considerably limited the number of features that could be incorporated into the models. Several other factors were also considered, for example, median age and percentage of the population that always wears a face mask. However, median age was excluded from the model as it correlated poorly with the number of infections. The mask-wearing variable was excluded as the proportion of the populations that always wore masks was measured differently between the training and test

countries and likely with all other countries for which the models were used to make predictions.

Data used to train the model covered the period from the beginning of the pandemic to February 2021. Later time period data were not used owing to the vast differences among countries not only in terms of the starting date and accessibility of vaccines but also the rate of vaccination. These discrepancies would make predictions for other countries inaccurate. The data used to test the model covered the period up until March 15th, 2021. A later date was considered for the test data than for the training data as most European countries started vaccination after the US.

Although the intention was originally to train the data on Indian states as well as the US states to allow for different models for the developing and developed countries, India was excluded owing to the high prevalence of the new B. 1.617 variant, which has increased transmissibility [24]. Although replacing India with Russia as an additional training data set was considered, the lack of data available made this unfeasible.

Some pre-processing steps had to be taken to clean the data before it could be used for the machine learning algorithm. First, the relevant features and information were extracted from the .csv file, where the data were stored; after that, all commas were removed from individual data points to make sure python could parse them correctly. The data were then normalized via a min-max-scaler, which places all data points between 0 and 1. For each data point in a feature, the MinMaxScaler deducts the smallest value in the feature and then divides this answer by the range, which is the difference between the original maximum and original minimum. The MinMaxScaler retains the original shape of the distribution, thus preserving the information embedded into the initial data set. However, it is important to note that this also means that the MinMaxScaler does not reduce the importance of outliers. Finally, the pre-processing procedure was completed by removing data samples that had missing values for some of their features. This is to make sure that all data can be used for training the model, as missing values can cause errors and unwanted variations within the procedure.

Two different types of machine learning algorithms were used for the analysis of the data multi-linear regression and a multi-layer perceptron artificial neural network (ANN). The multiple linear regression model was built using the Scikit-learn library [16]. The neural network code operated Keras architecture from the Tensorflow library [25] was used to construct the model. The ANN utilizes 1 output layer, 1 input layer, and 3 dense hidden layers (Fig. 1).

All dense layers use the Rectified Linear Unit (ReLU) as an activation function, which is defined as follows:

$$\begin{cases} 0 & \text{if } x \leq 0 \\ x & \text{if } x > 0 \end{cases}$$

The slope is always 0 for negative inputs and always 1 for positive inputs. ReLU was used as it is computationally less intensive and faster than most other activation functions, such as sigmoid and tanh.

The mean squared error (MSE) function is used to calculate the loss in the current iteration of the neural network. This function takes the absolute error of all points and calculates their mean. MAE is calculated via the following equation:

$$MSE = \frac{\sum_{i=1}^n |y_i - x_i|^2}{n} = \frac{\sum_{i=1}^n |e_i|^2}{n}$$

MSE was used because it is a commonly used metric and relatively robust to outliers suitable for the data used in this study.

The neural network contains a few hyperparameters that had to be set manually before the training. These hyperparameters are chosen by using a random grid search technique. The choice of the ReLU activation function, the number of hidden layers, and the number of nodes in each layer are examples of hyperparameters.

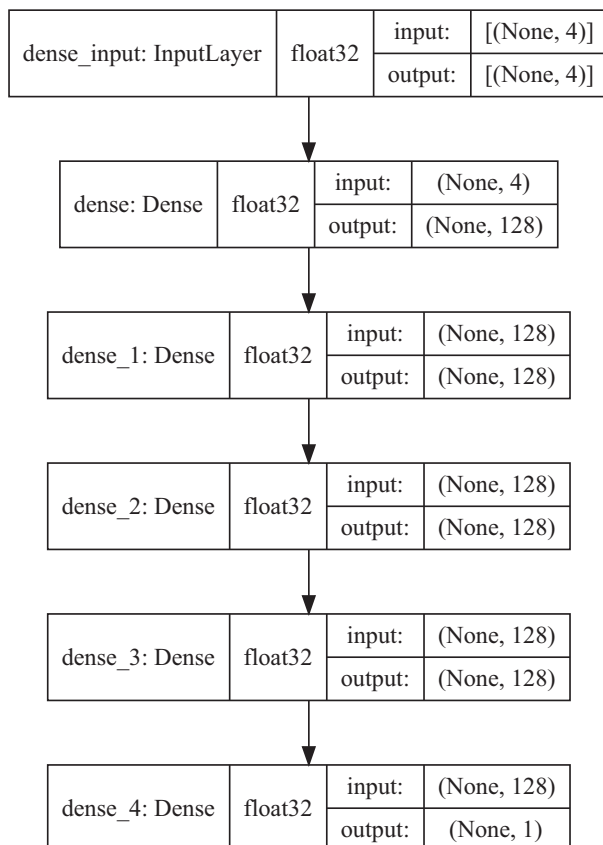


Fig. (1). Artificial neural network architecture.

3. RESULTS AND DISCUSSION

Since the start of the COVID-19 pandemic, the US has conducted over 400 million COVID-19 tests, making the country a rich and reliable source of information [15]. For this reason, the data from all US states were used to train our machine learning models. To evaluate the models, they were tested against the data from the European countries. Finally,

the models were used to make predictions for the number of COVID-19 cases in countries that have conducted low numbers of tests. The following countries were used as an example of low-testing countries: Nepal, Vietnam, Mongolia, Kenya, Ghana, Zambia, Iran, Paraguay, and Ecuador.

3.1. Features Analysis

The features currently utilized in the models are as follows: Population, Tests, Gini index, and % Urban population. To observe their collinearity, the number of cases was plotted against these features for the US states (Fig. 2).

The population and the number of tests conducted both show a strong correlation with the prevalence of COVID-19 cases with R^2 values of 0.95 and 0.81, respectively (Fig. 3) (AB)), and p-values of zero. However, a much lower correlation was obtained for the Gini index and percentage urban population with R^2 values of 0.12 and 0.16, and p-values of 0.01 and 0.003, respectively. The features that are currently utilized in the models were selected based on their strong correlation with the number of cases. Other features, such as Median age, % of people wearing a facemask outside, and Number of lockdown days, were not used as low correlation was found between these features and the number of cases, and because the data were incomplete for a number of these features. Adding these features to the models would have resulted in a higher error.

3.2. Multilinear Regression

A multiple linear regression model was built and trained on the US States data according to the following equation:

$$Y = Ax_1 + Bx_2 + Cx_3 + Dx_4 + K \rightarrow \quad (1)$$

Where, Y denotes the number of cases; A , B , C and D are the regression coefficients obtained from least square fitting; x_1, x_2, x_3 and x_4 are the independent variables (population, number of tests, Gini index, and % of the urban population, respectively), and K is the y-intercept.

The model shows a very strong correlation between the predicted and actual prevalence of COVID-19 cases for both the US States data (the training dataset) and the European data (the test dataset) (Fig. 3).

For the US data, the calculated slope is 1.00 with an intercept of zero and R^2 of 0.95. For the European data, the correlation coefficient R^2 is 0.88, and the slope and the intercepts are 1.49 and 12k, respectively, which indicates that the predicted prevalence of infections for the EU is generally higher than the reported. This could result from the differences in the behavior and commitment of the people toward the governmental rules in the US and the EU.

To understand the contribution of each feature to the prediction model, we report the estimated regression coefficients for each of the four features. The calculated coefficients are 0.87, 0.13, -0.01, and -0.03, for the population, number of tests, Gini index, and % urban population, respectively.

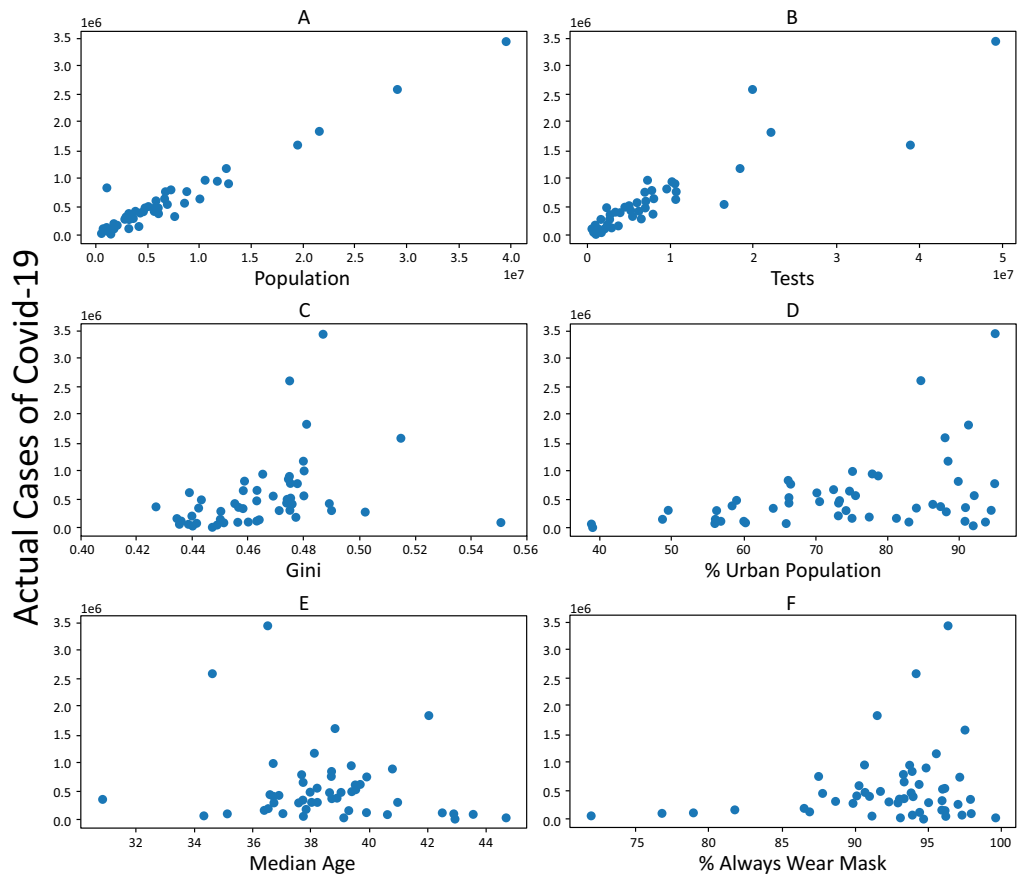


Fig. (2). COVID-19 cases vs.. (A) Population; (B) Number of tests; (C) Gini index; (D) % Urban population; (E) Median age; (F) % of population that always wears a mask. Each point represents a state.

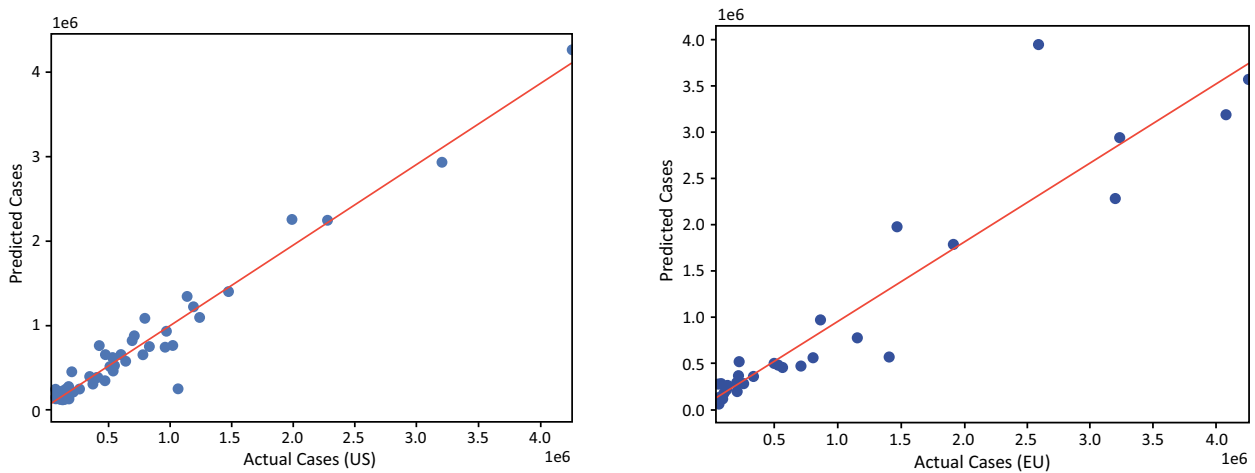


Fig. (3). To the left, the predictions vs.. observed cases for US data (Slope: 1.00; Intercept: 0; R^2 : 0.95). To the right, the predictions vs.. observed cases for European data (Slope: 1.49; Intercept: 12K; R^2 : 0.88).

The ‘population’ feature has a score close to one, and thus is the major contributor to the prediction model. The scores for

the % Urban population and Gini are negative, which suggests that these features are not significant for the regression model.

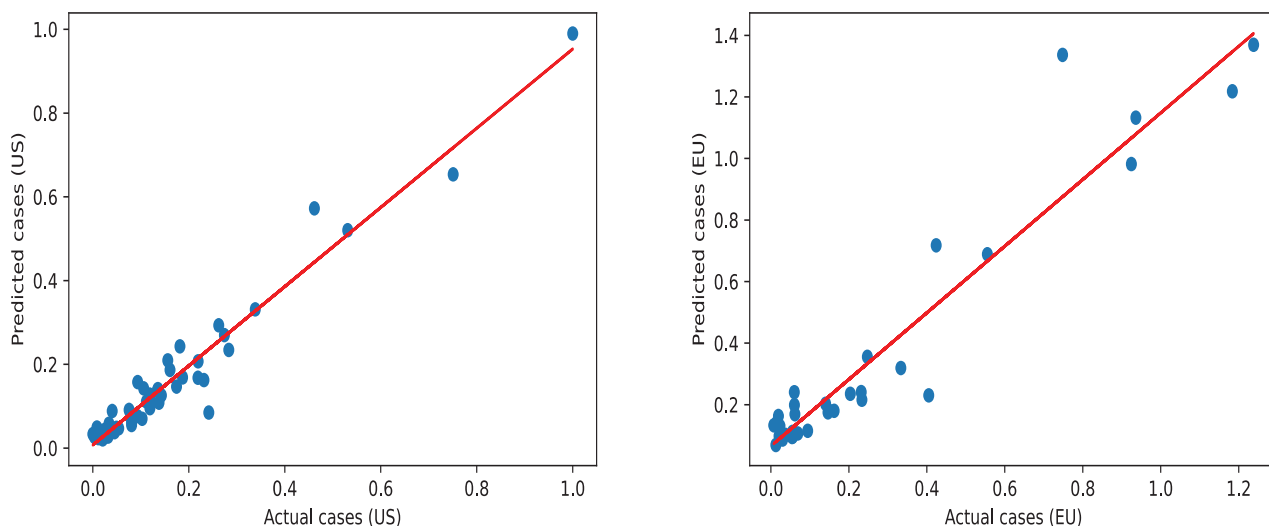


Fig. (4). (A) the predictions vs.. observed cases for US data (Slope: 0.95; Intercept: 0.0; R^2 : 0.95); (B) the predictions vs.. observed cases for European data (Slope: 1.57; Intercept: 45K; R^2 : 0.81).

3.3. Neural Networks

The neural network model is mainly considered to account for possible non-linearities in the Gini index and the percentage of urban populations. A fully connected Deep Neural Network (DNN) is trained and tested with US and EU datasets, respectively. The input layer of the network consists of 128 nodes and is followed by four hidden layers with 128 nodes and an output layer with a single node. The number of nodes of the output layer corresponds to the number of classes. Each layer has a random weight and bias initialization based on the normal distribution initializer, which is necessary to set the first set of numbers of weights and biases and thus initiate the training procedure. The ReLU function has become the default activation function for many types of neural networks because such models are easy to train, and often achieve good performance.

The DNN model is trained with an objective function (loss function) that must be minimized. The Mean Squared Error (MSE) is used as a loss function, and Stochastic Gradient Descent (SGD) optimizer is employed to find the best values for the DNN parameters by minimizing the loss function iteratively over the dataset. The number of iterations (epochs) is chosen to be 100 epochs. The network is trained using data

from US states and tested using data from European countries using the same set of features as in the case of multilinear regression, namely Population, Tests, Gini, and the Percentage of urban population. The testing results are illustrated in Fig. (4), which quantify the correlation between the predicted number of infections and the number of infections recorded. The slopes are 0.95 and 0.80, the R^2 values are 0.95 and 0.91, and the mean absolute error is 0.03 and 0.06 for the US and EU datasets, respectively. These measurements suggest that the model fits the observed data by learning the relationships between the input variables.

3.4. Prediction of COVID-19 Cases

The reported infections and their corresponding predicted values (using linear regression and NN) are shown in Table 1. Furthermore, according to the training dataset, the US has performed 361 million tests, which is equal to approximately 110% of the US population. Thus, we reported the predicted number of cases for European and other countries with a low number of tests as these countries have had tests equal to 1.1 multiplied by their respective populations (columns 6-8 of Table 1). Although the number of tests for the EU countries is increased by 30%, the slopes of the linear regression and the NN models are increased only by 5% and 11%, respectively.

Table 1. The predicted number of COVID-19 cases for test countries.

Country	Actual No. of Tests	Reported No. of Infections	Predictions (Multilinear Regression)	Predictions (Neural Network)	Tests = 110% of Population	Predictions (Multilinear Regression)	Predictions (Neural Network)
Albania	506676	117474	210493	171218	3163148	239234	358221
Austria	6033827	495464	713692	498778	9946648	770166	762327
Belgium	10110146	808283	906281	527839	12787487	957884	650472
Bosnia and Herzegovina	702920	142160	263250	223023	3593094	295191	392963
Croatia	1431342	251174	317183	273416	4496184	352885	437758
Cyprus	2563270	39651	56012	149468	1334864	44094	503521

(Table 1) contd....

Country	Actual No. of Tests	Reported No. of Infections	Predictions (Multilinear Regression)	Predictions (Neural Network)	Tests = 110% of Population	Predictions (Multilinear Regression)	Predictions (Neural Network)
Czechia	9665502	1402420	851078	546321	11795219	895219	805890
Denmark	20418687	220459	526270	420297	6387490	406445	662516
Estonia	1038888	86086	65321	82105	1459877	69132	373473
Finland	3596402	67334	375604	152357	6101438	409848	521883
France	57231533	4071662	5455817	3026689	71912361	5758992	3671764
Germany	46319641	2578835	6752524	3338496	92369061	7397418	4629496
Greece	5856618	221147	796133	479660	11425943	871592	707136
Hungary	4104415	524196	734001	437445	10607413	816269	701647
Ireland	3720861	225741	362195	333602	5473973	387925	643442
Italy	44623304	3223142	4982964	2681373	66439272	5340019	3382223
Latvia	1670193	93959	98590	147075	2058635	103506	503588
Lithuania	2218746	205644	194128	127608	2965009	204527	352468
Luxembourg	2248588	57877	-6932	72753	696387	-23384	217924
Moldova	771763	204463	332354	106253	4430108	373454	358590
Netherlands	6970400	1157192	1244594	613274	18877627	1396911	1250356
Norway	4115415	80440	364594	176433	5996009	392747	609492
Poland	10668987	1917527	2962379	1413123	41599229	3346222	2136684
Portugal	8480932	814257	820324	557283	11193380	868501	764967
Romania	6774562	862681	1520347	768489	21062036	1700082	1141785
Serbia	3149048	516277	680907	450877	9583870	760126	681613
Slovak Republic	2200380	337960	466872	341250	6007649	513081	374066
Slovenia	976907	200579	159814	210357	2287053	173893	374025
Spain	40292390	3183704	3879261	2147433	51444247	4101208	2654842
Sweden	6627544	712527	721451	364833	11157720	786554	892642
Switzerland	5387481	570645	661132	390075	9568835	719229	683189
UK	103053938	4258438	6078592	3409492	74949540	5988545	3816487
Ukraine	7328468	1467548	3314135	1525414	47903633	3803081	2476377

The negative value reported for Luxembourg is a result of the very low population and the relatively high urban population and Gini index.

Table 2. The predicted number of COVID-19 cases for countries whose total tests were equal or less than 10% of their population.

Country	Actual No. of Tests	Reported No. of Infections	Predictions (Multilinear Regression)	Predictions (Neural Network)	Tests = 110% of Population	Predictions (Multilinear Regression)	Predictions (Neural Network)
Afghanistan	465731	55985	3034780	404687	41845929	3422007	509312
Algeria	230861	115410	3327210	349522	47358359	3768219	470700
Chad	119517	4328	1317840	158913	17541564	1480872	219913
DRC	159469	27077	6681106	779441	95469624	7572999	1110283
Egypt	2824316	191555	7770111	1100450	110426880	8777033	1318575
Guatemala	1411568	183014	1316936	194200	18264429	1474642	164909
Honduras	714929	178925	776194	98998	10720729	869826	85309
Indonesia	16610468	1430000	20837478	3404783	297688125	23467745	3339198
Mozambique	454528	64516	2372216	270953	33402640	2680538	387939
Pakistan	9530000	609964	16699868	2557415	238221850	18839920	2686825
Papua New Guinea	112995	2269	792772	127738	9653720	882052	176443
Syria	103566	16556	1357616	136954	18777149	1532360	158446
Yemen	62990	2908	2313264	271150	32078114	2612855	369019

All the numbers are reported up to /03/15/2021.

* Where no test data could be found, 03/15/2021 data up till 05/15/2021 were used.

Using the same training dataset, we predicted the number of infections in selected countries where the number of tests is

less than 10% of their populations (Table 2). The average number of the predicted infections is higher than that reported

by 26 times for the linear regression model and 4 times for the NN. The discrepancy between the results from multilinear regression and NN models in Table 2 is due to the overfitting feature of the NN. The overfitting indicates that the generalization of the NN model is rather limited. This is due to the minimal dataset, *i.e.*, 52 entries used for the training procedure, which is not enough for the NN model to avoid overfitting.

CONCLUSION

Both the multilinear regression and neural network models predicted the number of COVID-19 cases with a fair degree of accuracy on the European test data set. Considering Table 1, the number of cases predicted by the models was close to the number of cases reported for some countries, such as Italy, Poland and Slovakia. Yet, in most cases, the model predicted more cases than they were reported. The models were trained on data from the US country that tested extensively. Therefore, it seems that due to limited testing in most countries, the number of cases reported was a gross underestimation of the actual number of infections. This disparity was most pronounced in countries that were not testing extensively. The predicted number of infections for these countries was 26 times higher than the reported numbers on average. Therefore, the models can be effective tools for estimating the prevalence of COVID-19 infection in countries where sufficient testing is not available or where it is suspected that governments may not be entirely transparent about the number of COVID-19 infection.

LIST OF ABBREVIATIONS

MSE	=	Mean Squared Error
DNN	=	Deep Neural Network
SGD	=	Stochastic Gradient Descent

ETHICS APPROVAL AND CONSENT TO PARTICIPATE

Not applicable.

HUMAN AND ANIMAL RIGHTS

Not applicable.

CONSENT FOR PUBLICATION

Not applicable.

AVAILABILITY OF DATA AND MATERIALS

The authors confirm that the data supporting the findings of this study are available within the manuscript.

FUNDING

None.

CONFLICT OF INTEREST

The authors declare no conflict of interest, financial or otherwise.

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Declared none.

REFERENCES

- [1] Walach H, Hockertz S. Wuhan Covid19 data – more questions than answers. *Toxicology* 2020; 440: 152486. [http://dx.doi.org/10.1016/j.tox.2020.152486] [PMID: 32387286]
- [2] Zitek T. The Appropriate Use of Testing for COVID-19. *West J Emerg Med* 2020; 21(3): 470-2. [http://dx.doi.org/10.5811/westjem.2020.4.47370] [PMID: 32302278]
- [3] Spearman P. Diagnostic testing for SARS-CoV-2/COVID19. *Curr Opin Pediatr* 2021; 33(1): 122-8. [http://dx.doi.org/10.1097/MOP.0000000000000972] [PMID: 33278110]
- [4] Kavanagh MM, Erondu NA, Tomori O, *et al.* Access to lifesaving medical resources for African countries: COVID-19 testing and response, ethics, and politics. *Lancet* 2020; 395(10238): 1735-8. [http://dx.doi.org/10.1016/S0140-6736(20)31093-X] [PMID: 32386564]
- [5] Habib N, Rahman MM. Diagnosis of corona diseases from associated genes and X-ray images using machine learning algorithms and deep CNN. *Inform Med Unlocked* 2021; 24: 100621. [http://dx.doi.org/10.1016/j.imu.2021.100621] [PMID: 34075341]
- [6] Reyana A, Kautish S. Corona virus-related Disease Pandemic: A Review on Machine Learning Approaches and Treatment Trials on Diagnosed Population for Future Clinical Decision Support. *Curr Med Imaging* 2021.
- [7] Magar R, Yadav P, Barati Farimani A. Potential neutralizing antibodies discovered for novel corona virus using machine learning. *Sci Rep* 2021; 11(1): 5261. [http://dx.doi.org/10.1038/s41598-021-84637-4] [PMID: 33664393]
- [8] Ban Z, Yuan P, Yu F, Peng T, Zhou Q, Hu X. Machine learning predicts the functional composition of the protein corona and the cellular recognition of nanoparticles. *Proc Natl Acad Sci USA* 2020; 117(19): 10492-9. [http://dx.doi.org/10.1073/pnas.1919755117] [PMID: 32332167]
- [9] Duan Y, Coreas R, Liu Y, *et al.* Prediction of protein corona on nanomaterials by machine learning using novel descriptors. *NanoImpact* 2020; 17: 100207. [http://dx.doi.org/10.1016/j.impact.2020.100207] [PMID: 32104746]
- [10] Findlay MR, Freitas DN, Mobed-Miremadi M, Wheeler KE. Machine learning provides predictive analysis into silver nanoparticle protein corona formation from physicochemical properties. *Environ Sci Nano* 2018; 5(1): 64-71. [http://dx.doi.org/10.1039/C7EN00466D] [PMID: 29881624]
- [11] Papa E, Doucet JP, Sangion A, Doucet-Panaye A. Investigation of the influence of protein corona composition on gold nanoparticle bioactivity using machine learning approaches. *SAR QSAR Environ Res* 2016; 27(7): 521-38. [http://dx.doi.org/10.1080/1062936X.2016.1197310] [PMID: 27329717]
- [12] Zoabi Y, Deri-Rozov S, Shomron N. Machine learning-based prediction of COVID-19 diagnosis based on symptoms. *NPJ Digit Med* 2021; 4(1): 3. [http://dx.doi.org/10.1038/s41746-020-00372-6] [PMID: 33398013]
- [13] Sun L, Song F, Shi N, *et al.* Combination of four clinical indicators predicts the severe/critical symptom of patients infected COVID-19. *J Clin Virol* 2020; 128: 104431. [http://dx.doi.org/10.1016/j.jcv.2020.104431] [PMID: 32442756]
- [14] Lalmuanawma S, Hussain J, Chhakhuak L. Applications of machine learning and artificial intelligence for Covid-19 (SARS-CoV-2) pandemic: A review. *Chaos Solitons Fractals* 2020; 139: 110059. [http://dx.doi.org/10.1016/j.chaos.2020.110059] [PMID: 32834612]
- [15] Hasell J, Mathieu E, Beltekian D, *et al.* A cross-country database of COVID-19 testing. *Sci Data* 2020; 7(1): 345. [http://dx.doi.org/10.1038/s41597-020-00688-8] [PMID: 33033256]
- [16] The World Bank, World Development Indicators, Urban Population. <https://data.worldbank.org/indicator/SP.URB.TOTL.IN.ZS?view=chart2019>.
- [17] The World Bank World Development Indicators. 2019. <https://data.worldbank.org/indicator/SP.URB.TOTL.IN.ZS?view=chart>
- [18] The World Bank World Development Indicators. 2019. Population total <https://data.worldbank.org/indicator/SP.POP.TOTL?view=chart>
- [19] The World Bank World Development Indicators.

- [20] <https://data.worldbank.org/indicator/SI.POV.GINI?view=chart2019>. U.S. Census Bureau. 2020. <https://www.census.gov/content/dam/Census/library/publications/2020/acs/acsbr20-03.pdf>
- [21] U.S. Census Bureau. 2010. Percent Urban and Rural in 2010 by State <https://www.census.gov/programs-surveys/geography/guidance/geo-areas/urban-rural/2010-urban-rural.html>
- [22] U.S. Department of Health & Human Services. 2021. <https://healthdata.gov/Health/COVID-19-Community-Profile-Report/gqxm-d9w9>
- [23] Worldometer. COVID Live Update 2021. <https://www.worldometers.info/coronavirus/#countries>
- [24] Bansal R, Kumar A, Singh AK, Kumar S. Stochastic filtering based transmissibility estimation of novel coronavirus. *Digit Signal Process* 2021; 112: 103001. [<http://dx.doi.org/10.1016/j.dsp.2021.103001>] [PMID: 33613017]
- [25] Rampasek L, Goldenberg A. TensorFlow: Biology's Gateway to Deep Learning? *Cell Syst* 2016; 2(1): 12-4. [<http://dx.doi.org/10.1016/j.cels.2016.01.009>] [PMID: 27136685]

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