COVID-19 Paper corrections

# Reviewer 1

## 1. COMMENT

English is very bad

## RESPONSE

We have used myspell and Grammar Check utilities for this.

## 2. COMMENT

In each equations relation typos exist missing of dots etc.

## RESPONSE

Corrected.

## 3. COMMENT

Why this method is so important?

## RESPONSE

## 4. COMMENT

Replace Covid-19  by COVID-19

## RESPONSE

Corrected.

## 5. COMMENT

Improve conclusion and presentation.

## RESPONSE

1) A flowchart showing the proposed technique has been added at the beginning of section 2.

2) We have performed additional experiments using different values for the number of chromosomes and the maximum number of allowed generations and two new figures have been added in the revised text. Also, the added text in the **Experimental Results** section reads:

“*Additional experiments were performed to evaluate the parameters used in the proposed method. The figure* [*fig:Average\_chromosomes*](#fig_Average_chromosomes) *shows the average error of the proposed method with 2 constructed features for all experiment countries. In these experiments, a varying number of chromosomes was used from 100 to 1000. As expected, the proposed method reduces the average error as the number of chromosomes increases. This means, however, that the execution time of the method increases as well as the memory that will be needed to store the computational structures. Therefore, the value of 500 used in the proposed method for the number of chromosomes is a good compromise between speed and efficiency of the proposed technique.*

*Regarding the number of generations of the genetic algorithm, similar experiments were done with this number between 50 and 400. The results of these experiments are shown in graph* [*fig:Average\_generations*](#fig_Average_generations)*. Again, increasing the number of generations seems to reduce the error, although the reduction is not as drastic as it was with the increase in chromosomes. Again the choice of 200 made for the number of generations in the experiments appears to be a fair compromise.”*

*3)*Additional statistical tests have been performed and the following paragraph has been added in the “Experimental Results” section

*“The Wilcoxon signed-rank test was used to compare the total test error for the prediction of COVID-19 cases in different countries of the proposed method (FC1, FC2, and FC3) with the respective total test error for ADAM, MLPPSO, and MLPGEN optimization methods. The results obtained with those statistical tests are shown in Figure* [*fig:boxplot\_cases*](#fig_boxplot_cases)*. We also compared the average error in predicting deaths per country of the proposed method (FC1, FC2, and FC3) with the average error for ADAM, MLPPSO, and MLPGEN optimization methods using the Wilcoxon signed-rank test. The results obtained with those statistical tests are shown in Figure* [*fig:boxplot\_deaths*](#fig_boxplot_deaths)*.*

”

*4)* The conclusion section has been changed to the following:

“*In this paper, the use of a feature construction technique to predict the cases of COVID19 disease and also to predict the mortality due to it was presented. The prediction was made on widely available data for 10 randomly selected countries. The proposed method constructs new features from existing ones using Grammatical Evolution and evaluates them using a radial basis network (RBF). After the evaluation, the best resulting features are used to train an artificial neural network. The results of the proposed methodology were compared with those of other artificial neural network training techniques and in all cases there was a dramatic reduction in the network's error for both case number prediction and mortality prediction. Furthermore, the more artificial features are created, the lower the neural network error. Future research should include the physical interpretation of the generated features in relation to the nature of the problem. Also, future improvements of the method may include:*

1. *Incorporation of more advanced stopping rules for the genetic algorithms of the two phases.*
2. *Usage of another machine learning models instead of the RBF network to evaluate the constructed features.*
3. *Usage of parallel techniques to speed up the feature creation process.*
4. *Use of the technique on data that will also contain demographic characteristics of each country, in order to establish whether there is a correlation of the rate of cases or mortality with any particular characteristic of some countries.* ”

## 6. COMMENT

Recent large number of relevant work on covid like:

* Taylor Series Expansion Method To Compute Approximate Solution For Nonlinear Dynamical System
* On The Iterative Methods For Solving Fractional Initial Value Problems: New Perspective

## RESPONSE

The following paragraph and the appropriate references has added in the Introduction section:

“*Furthermore, a series of recent works have been proposed to model the dynamics of COVID-19 virus using fractional derivatives [*[*covid\_fractional1*](#LyXCite-covid_fractional1)*,* [*covid\_fractional2*](#LyXCite-covid_fractional2)*,* [*covid\_fractional3*](#LyXCite-covid_fractional3)*] or the work of Huzaifa et al [*[*ebola\_fractional*](#LyXCite-ebola_fractional)*], that was used for another virus, the Ebola virus.*”

# Reviewer 2

## 1. COMMENT

In order to improve the fluency of the paper, the author can add a flowchart to the method description section to explain the relationship between the various algorithm modules.

## RESPONSE

A flowchart showing the proposed technique has been added at the beginning of section 2.

## 2. COMMENT

How to determine the experimental parameters in Table 2.

## RESPONSE

We have performed additional experiments using different values for the number of chromosomes and the maximum number of allowed generations and two new figures have been added in the revised text. Also, the added text in the **Experimental Results** section reads:

“*Additional experiments were performed to evaluate the parameters used in the proposed method. The figure* [*fig:Average\_chromosomes*](#fig_Average_chromosomes) *shows the average error of the proposed method with 2 constructed features for all experiment countries. In these experiments, a varying number of chromosomes was used from 100 to 1000. As expected, the proposed method reduces the average error as the number of chromosomes increases. This means, however, that the execution time of the method increases as well as the memory that will be needed to store the computational structures. Therefore, the value of 500 used in the proposed method for the number of chromosomes is a good compromise between speed and efficiency of the proposed technique.*

*Regarding the number of generations of the genetic algorithm, similar experiments were done with this number between 50 and 400. The results of these experiments are shown in graph* [*fig:Average\_generations*](#fig_Average_generations)*. Again, increasing the number of generations seems to reduce the error, although the reduction is not as drastic as it was with the increase in chromosomes. Again the choice of 200 made for the number of generations in the experiments appears to be a fair compromise.”*

## 3. COMMENT

In Table 3, the test results of the ADAM algorithm have a large gap with the actual results, and we think this may be because the experimental parameters set are not ideal.

## RESPONSE

The following text has been added in the “**Experimental Results**” section of the revised manuscript:

“*Also, the Adam method appears to achieve worse results than the PSO and the Genetic algorithm methods and this is expected, since this method is a local optimization technique while the PSO and the Genetic algorithms are global optimization methods.*”

## 4. COMMENT

In Table 3 and Table 4, it can be seen that the experimental algorithm is not good for Brazil's prediction effect. What's the reason for this?

## RESPONSE

The following text has been added in the “**Experimental Results**” section:

“*From the execution of the above experiments, it is clear in principle that the efficiency of the methods depends to a great extent on the country in question. In some countries the test error is high and in others quite low. This is probably due to the different course of the number of cases and the mortality rate in each country separately. For example, if one looks at the experimental results for Brazil, one will find that all the methods present a relatively high error. This may be due to the large and abrupt changes that the disease has had in this country, as shown in figure* [*fig:BrazilJohnHopkins*](#fig_BrazilJohnHopkins)*, which shows the course of deaths in this country and is available from Johns Hopkins University. However, even in this country using the proposed methodology there was a large reduction in approximation error of 90%.* ”

## 5. COMMENT

The authors' discussion of the experimental results is not sufficient.

## RESPONSE

Additional statistical tests have been performed and the following paragraph has been added in the “Experimental Results” section

*“The Wilcoxon signed-rank test was used to compare the total test error for the prediction of COVID-19 cases in different countries of the proposed method (FC1, FC2, and FC3) with the respective total test error for ADAM, MLPPSO, and MLPGEN optimization methods. The results obtained with those statistical tests are shown in Figure* [*fig:boxplot\_cases*](#fig_boxplot_cases)*. We also compared the average error in predicting deaths per country of the proposed method (FC1, FC2, and FC3) with the average error for ADAM, MLPPSO, and MLPGEN optimization methods using the Wilcoxon signed-rank test. The results obtained with those statistical tests are shown in Figure* [*fig:boxplot\_deaths*](#fig_boxplot_deaths)*.*

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