COVID-19 Paper corrections

# Reviewer 1

## 1. COMMENT

English is very bad

## RESPONSE

(Spell Check Grammar Check )

## 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

## 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

## 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

## 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

## 5. COMMENT

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

## RESPONSE