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BRIEF REPORT

UPDATE Predicting the evolution and control of the COVID-19 pandemic in Portugal

[version 2; peer review: 2 approved]

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Abstract

Coronavirus disease 2019 (COVID-19) is a worldwide pandemic that has been affecting Portugal since 2 March 2020. The Portuguese government has been making efforts to contradict the exponential growth through lockdown, social distancing and the usage of masks. However, these measures have been implemented without controlling the compliance degree and how much is necessary to achieve an effective control. To address this issue, we developed a mathematical model to estimate the strength of Government-Imposed Measures (GIM) and predict the impact of the degree of compliance on the number of infected cases and peak of infection. We estimate the peak to be around 650 thousand infected cases with 53 thousand requiring hospital care by the beginning of May if no measures were taken. The model shows that the population compliance of the GIM was gradual between 30% to 75%, contributing to a significant reduction on the infection peak and mortality. Importantly, our simulations show that the infection burden could have been further reduced if the population followed the GIM immediately after their release on 18 March.

Keywords

COVID-19, Pandemic Control, Predictive modeling, Simulation, Social Isolation, Mathematical model

This article is included in the Pathogens gateway.

Open Peer Review

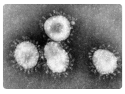
Approval Status ✔ ✔

	1	2
version 2 (update) 09 Sep 2020	✔ view	✔ view
version 1 23 Apr 2020	? view	? view

1. **Elves Heleno Duarte**, National Health Direction Ministry of Health, Cambridge, UK
2. **Kamal Shah**, University of Malakand, Chakdara, Chakdara, Pakistan

Any reports and responses or comments on the article can be found at the end of the article.

This article is included in the Emerging Diseases and Outbreaks gateway.



This article is included in the Coronavirus (COVID-19) collection.

Corresponding authors: Ricardo J. Pais (rjpais@bioenhancersystems.com), Nuno Taveira (ntaveira@ff.ulisboa.pt)

Author roles: Pais RJ: Conceptualization, Formal Analysis, Investigation, Methodology, Software, Writing – Original Draft Preparation; **Taveira N**: Conceptualization, Data Curation, Investigation, Methodology, Supervision, Validation, Writing – Review & Editing

Competing interests: No competing interests were disclosed.

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First published: 23 Apr 2020, **9**:283 https://doi.org/10.12688/f1000research.23401.1

UPDATE **Updates from Version 1**

As relevant new data on the evolution of COVID-19 pandemic in Portugal give new insights and challenged our model. We have decided to take these data (up to 19 August 2020), improve our model and provide a retrospective insight on the evolution and control of this outbreak in Portugal. We believe that this new version may help to have a better understanding on the evolution of COVID-19 pandemic in Portugal and provide a simple approach to guide on the control and prevention of future outbreaks.

Any further responses from the reviewers can be found at the end of the article

Introduction

Coronavirus disease 2019 (COVID-19) is already considered a world pandemic which is starting to have dramatic effects in Europe, where, as of 27 of March, 265,421 cases have been reported[1,2]. COVID-19 infection in Portugal has been growing exponentially with an average rate of 34±13% new cases per day from 2 March and is far from reaching the peak by the end of March. As of March 27, 4268 infection cases and 76 deaths have been reported[2]. The highest infection burden is found in Porto (317 cases, 7.4%) and in Lisbon (284 cases, 6.7%) but the disease is present throughout the entire country. As in other countries, infection occurs mostly in individuals' with ≥40 years of age (71.9% males; 69.3% females). Death occurs mostly in males (64.5%) all with ≥50 years of age.

Predictive models estimate that the peak of SARS-CoV-2 infection globally would be between mid-April and May, with an estimated total of 48 million people infected[3]. As with most other countries, the Portuguese national health care system cannot deal with the increasing demand of care due to limited ventilators and care units[3]. Therefore, the Portuguese government together with the National Health Directorate (DGS) declared a state of emergency and adopted interventive populational measures through Government-Imposed Measures (GIM) on 18 March 2020 in an attempt to drop the peak of infections even if at the cost of prolonging the infection time. These measures are based on the lockdown of people at home, social distancing and adopting protective antiseptic policies such as the usage of masks. Lockdown was implemented to assure compliance of the population, expect for people that maintain basic services such as medical and food distribution staff.

Most forecasting models are based on the number of cases reported and do not take into account the effects of these government-imposed measures and behavioral change. Thus, accessing the compliance degree and predicting how much is necessary for the control of SARS-CoV2 infection would be a useful tool for fighting COVID-19 pandemic. Recently published mathematical modelling studies of COVID-19 transmission have already provided useful insights that can be used to guide public health measures and resource allocation to better control this pandemic[4–7]. However, most parameters of statistical models have been estimated with high degree of uncertainty, resulting in predictions with wide intervals of confidence[4,6]. Compartmental models such as susceptible, infected and resistant (SIR) models are deterministic approaches based on solving nonlinear systems of Ordinary Differential Equations (ODE) that have been successful in describing complex dynamics of virus infection in populations, including COVID-19 in several countries[7–11]. Here, we provide a simple SI model that describe the dynamics of transition of COVID-19 in Portugal during the first 21 days, explain the evolution of SARS-CoV-2 infection dynamics up to 19 of August and predicts the degree of compliance of GIM by the Portuguese population.

Methods

Basic transmission dynamics of COVID-19 was modelled using a simple mathematical model based on a system of two ordinary differential equations (ODE) developed specifically for this purpose (Equation 1 and Equation 2). The equations reflect the number of people infected (I) and susceptible (S) to infection per unit of time (dI/dt and dS/dt). In this model, we accounted for the reported average time of duration of infection (τ) of 14 days[4,11]. The model was calibrated by adjusting the rate constant (k) to approximate the total infection value reported by the DGS at 17 March. No further fitting was performed in this model. The compliance of GIM by different fractions of the population was modelled through the variation of parameter α in Equation 1 and Equation 2. We considered that these protective measures (GIM) were 97% effective based on recent meta-analysis estimates, accounted through model parameter β[12]. The ODEs were encoded and solved using PLAS software version 1.2.0.120, where a series of simulations were carried scanning various values of the α parameter[13]. Simulations were carried with the initial two cases reported by the DGS and considering only the population of the grand Lisbon and Porto areas (total of 6.5×10^6) since they represent most of the susceptible population (see Figure 2). For simulations, we used the numerical solver based on the Adams/BDF method, implemented in the LSODA routine of PLAS software. Because a serological screening study made by the Portuguese Nacional Institute of Health (http://www.insa.pt/) found a 6-fold higher infected due to untested asymptomatic exposed to SARS-CoV-2, we have considered this ratio to estimate the reported symptomatic infected by the DGS. Further analysis, computations and plots were conducted using Python 3 in the Jupiter Notebook ipython 7.8.0 programing environment under Anaconda distribution version 4.7.12. Data regarding the daily evolution of number of total infected in Portugal by COVID-19 was collected from the DGS web site (https://covid19.min-saude.pt/ponto-de-situacao-atual-em-portugal/) from 2 March to 19 August 2020 (see *Source data*, Table S1 and Figure S1)[14]. The model is available as *Extended data*.

$$\frac{dI}{dt} = k(1-\alpha)SI + \alpha k\beta SI - \frac{1}{\gamma}I \qquad \text{(Equation 1)}$$

$$\frac{dS}{dt} = -k(1-\alpha)SI - \alpha k\beta SI \qquad \text{(Equation 2)}$$

Results and discussion

Simulation of the first 18 days with our model was able to describe the exponential increase of the number of confirmed cases reported by the DGS between 2 and 18 March 2020 (Figure 1). The predicted peak time for this scenario was 49 days which would be by the 21 of April. This is within the estimated range predicted by statistical modelling of US, Italy and Korea scenarios[3]. Further, the predicted numbers of cases for the end of March if no measures were taken would be around 42,000. This is also in agreement with the number released by the DGS to the social media based on statistical modelling. Thus, the model presented here is consistent with the forecasting made by conven tional models, reinforcing the confidence on our model capacity to generate predictions.

Importantly, our results show that the GIM had an immediate impact on diminishing the exponential increase of the number of infected cases and this depends on the percentage of the population that is in compliance with such measures (Figure 2). This is evident by the increasing deviation of the reported number of cases relative to the unperturbed simulation (0%) with time. The evolution of the number of cases reported by DGS between 18 and 25 March fit between the simulation curves corresponding to 30% and 40% of model perturbation on parameter α This suggests that the estimated percentage of the Portuguese population that have been start following the GIM was between 30% to 40%. From simulations, we identify other intervals (e.g. 50–60% and 70–75%) that are compatible with the reported data form DGS between April to August 2020, regarding observed peaks of infection and hospitalizations (Figure 2, Table 1). For 19 august, the computed total infections and deaths for the 70–75% interval is 30,664 - 91,426 and 1,004 - 2,995, respectively. This is within the range of the reported values by the DGS for this day (54,701 and 1,786, respectively)[14], making our model consistent with the reported data by the DGS. Together, these results indicate that GIM compliance degree shifted from 30–40% to 70–75% suggesting a gradual compliance degree of the Portuguese population.

Based on the fraction of hospitalized and mortality reported by the DGS on 27 March 2020, together with our model

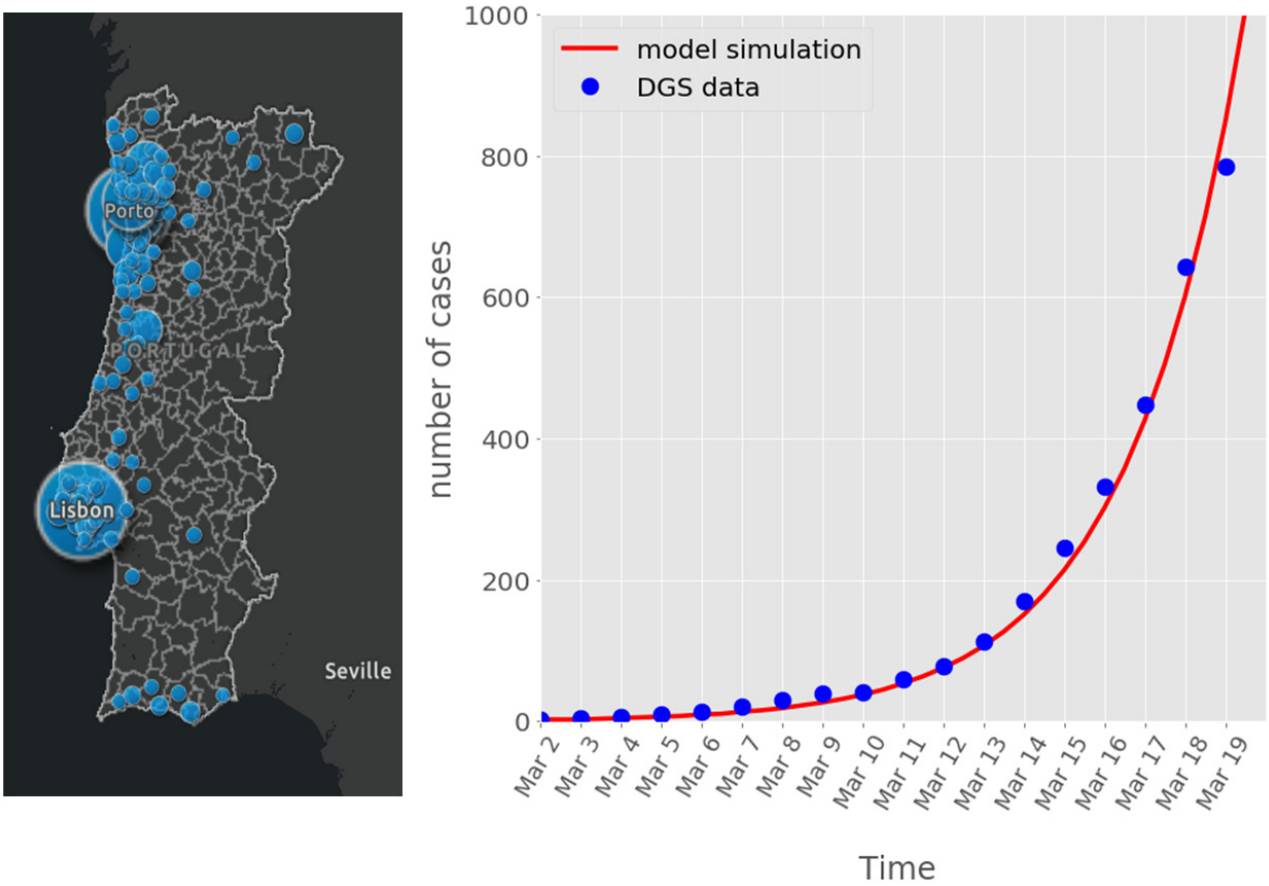

Figure 1. COVID-19 spreading on Portuguese population up to 19 of March. Left, the distribution of confirmed cases on 19 March are depicted in the map. Right, evolution of the cases between 2 and 19 of March. Lines indicate simulation using the mathematical model and blue dots correspond to the confirmed cases reported by DGS.

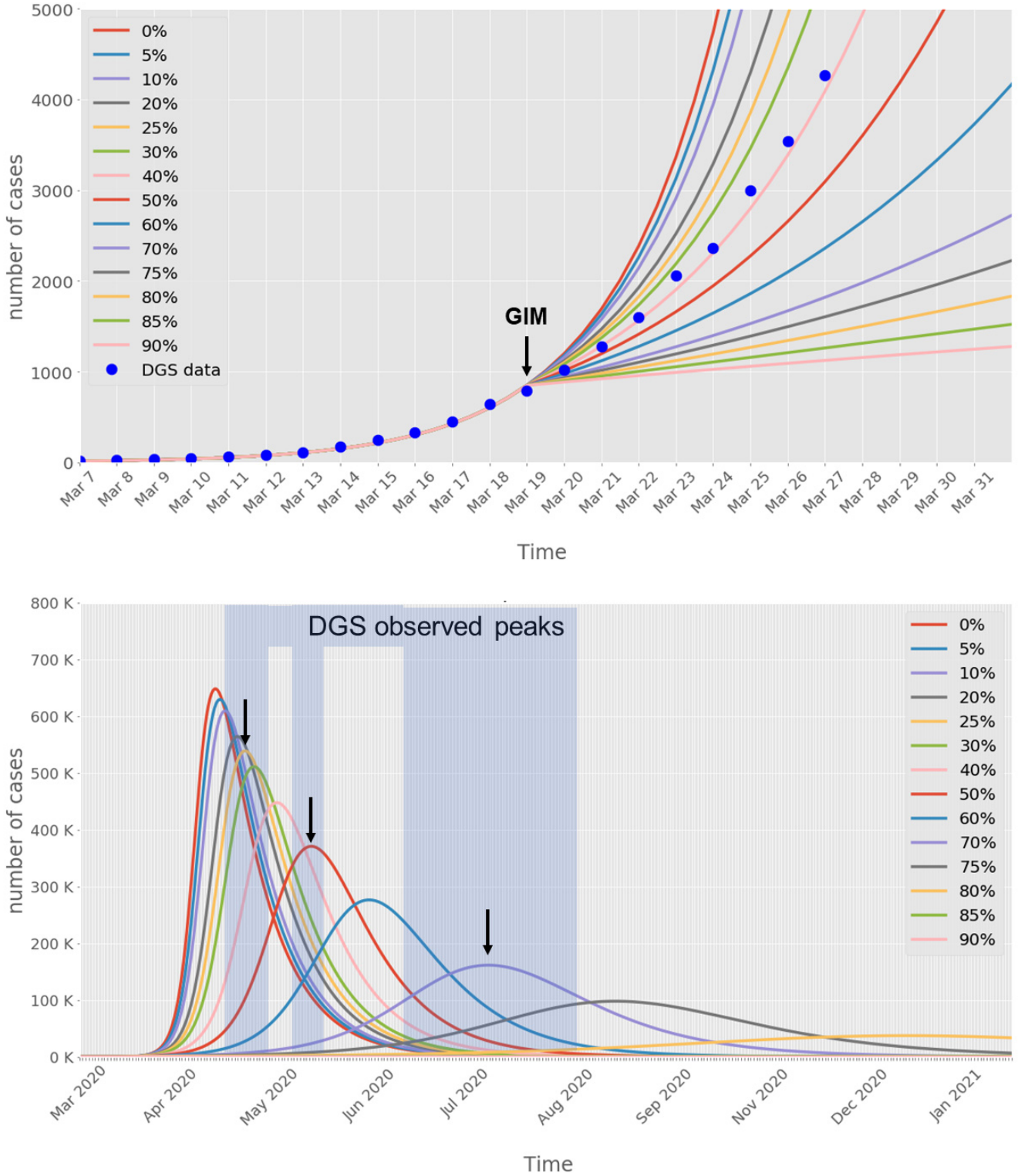

Figure 2. Simulation of the transmission dynamics of SARS-CoV-2 infection on Portuguese population with different percentages of compliance of Government-Imposed Measures (GIM). Above, predicted total infected population in the month of March. The starting of the measures is depicted by GMM and the arrow indicates the time of change. Below, Predicted peak of infection. Observed peaks of SARS-CoV-2 infection by the DGS are indicated by arrows and their intervals in blue. These peaks were collected based on reported new cases and hospitalizations due to SARS-CoV-2 infection up to 19 August 2020 (available in figure S1 as extended data[14]).

Table 1. Predicted ranges (upper and lower values) for several SARS-CoV-2 infection indicators under three GIM compliance scenarios (percentages).

Indicators	30–40%	70–75%	90%
Total Infected	885,725 – 928,703	456, 446 – 572,624	847
Total death	14,674 – 16,754	5,288 – 9,056	23
Infected (on peak)	447,876 – 511,341	97,877 – 161,413	702
Hospitalized (on peak)	37,148 – 42,412	8,118 - 13,388	58
Expected peak occurrence	26 Apr – 4 May 2020	10 Jul – 20 Aug 2020	No peak.

predictions, we computed several infection indicators for these intervals (Table 1).

Our model analysis indicates that current government-mandated measures together with compliance changes shifted at least two times the expected peak of infections, causing a substantial reduction in the infection numbers (Figure 2, Table 1). Based on our model, the predicted peak in the number of cases without any interventive measures would be around 650 thousand, whereas current degree of compliance (70–75%) have resulted in a decrease around one half of expected cases, hospitalizations and deaths (Table 1) Because we used a 6-fold ratio for asymptomatic infected individuals that have not went through testing pipeline, the total infected up to the end of 2020 is estimated to be around 2.7 –3.4 million people, assuming a 70–75% tendency of GIM compliance. This corresponds to about 1/3 of Portuguese population, suggesting that GIM should continue in 2021 to prevent a secondary outbreak. Our simulations also indicate that the SARS-CoV-2 infection could be further reduced if the population had a degree of compliance over 90% starting from 17 of March (Table 1, Figure 2). This scenario would result in much less total mortality and hospitalization requirements on peak in comparison to the current trend (Table 1, Figure 2). Meanwhile, percentages >75% comes with the burden of prolonging the time of pandemic control over a year, which can be economically unbearable. Thus, the ideal solutions would be between 70–90% compliance of the GIM. The results obtained during simulations are available as *Extended data*, Table S2[14].

Although our model precisely described the exponential curve and explains the shift in the temporal evolution of DGS data, it has limitations that may compromise the exact values of predictions. The fact that we only assume two compartments (susceptible and infected) considering the main populated cities (Lisbon and Porto) as one is huge approximation that neglects regional dynamics. Thus, the model is just an approximation that reflects an average trend and may fail to explain regional observations. In this model we also neglected many important parameters of infection transmission such as age groups, types of social interactions, contact dependent probability, and viral load dependent probability[15]. The inclusion of these parameters would definitely make the model more realistic. However, this data is not available for the Portuguese case and these models require accurate processing of data curation for suitable validation. We have bypassed these limitations by aggregating all of these parameters into one constant, which was fitted to the available data. Overall, the predictions shown here should be taken as semi-quantitative estimates within an upper and lower case-scenario.

Conclusions

In this work we demonstrate the potential of modelling the dynamics of SARS-CoV-2 infection as a useful support tool for predicting the impact of corrective measures as well as estimating the degree of compliance of the GIM by the population. Government-mandated measures on the Portuguese population effectively prevented COVID-19 from reaching dramatic numbers in Portugal but still could be substantially improved to reduce the infection peak. Our estimates and approach may help in guiding additional measures to control the COVID-19 evolution and future epidemies.

Data availability

Source data

Figshare: Modelling COVID-19 evolution and control in Portugal: Code and data from 2 to 27 of March 2020. https://doi.org/10.6084/m9.figshare.12136446.v1[14].

This project contains the following source data used in the present study:

- Table S1 (CSV). (The number of confirmed cases in Portugal officially reported by the DGS.)

Extended data

Figshare: Modelling COVID-19 evolution and control in Portugal: Code and data from 2 to 27 of March 2020. https://doi.org/10.6084/m9.figshare.12136446.v1[14].

This project contains the following extended data:

- model_code (TXT). (Code used for the model.)
- Table S2 (CSV). (Results obtained during simulation.)

- Python-code (MD). (Python code used with this model.)

Data are available under the terms of the Creative Commons Attribution 4.0 International license (CC-BY 4.0).

Acknowledgments

Eng. Pedro Fernandes for the critical discussions' and advices on the modelling approach. The CiiEM (Egas Moniz) for hosting institution and supporting publication fees.

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Current Peer Review Status: ✔ ✔

Version 2

Reviewer Report 18 September 2020

https://doi.org/10.5256/f1000research.29123.r71065

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✔ **Elves Heleno Duarte**
Department of Genetics, National Health Direction Ministry of Health, Cambridge, UK

Pais & Taveira made an outstanding effort and addressed concerns raised by both reviewers. The current version (v2) is, therefore, a significant improvement over the previous version.

Notably, the authors now conveyed the idea of estimating the strength of the lockdown in Portugal, during early COVID-19 pandemic. Moreover, the authors improved simulations by taking the estimated number of asymptomatic cases into account. Also, they discussed their predicted number of SARS-CoV-2 infection in the light of newly published data by the Portuguese authorities.

It would be great if the authors could define (biologically or epidemiologically) the parameters A (alpha) and B (beta) (equations 1 and 2). The authors should include, if possible, a citation to the sentence 'This is also in agreement with the number released by the DGS to the social media based on statistical modelling'. The closing punctuation is missing after 'The evolution of the number of cases reported by DGS between 18 and 25 March fit between the simulation curves corresponding to 30% and 40% of model perturbation on parameter α'.

Finally, I advise re-writing the sentence 'For 19 august, the computed total infections and deaths for the 70–75% interval is 30,664 - 91,426 and 1,004 - 2,995, respectively.' The current version is quite confusing as readers may interpret '70–75% interval' as the confidence interval. It should be clear that these values represent the percentage of lockdown.

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genetics, bioinformatics, epidemiology, medical entomology, Wolbachia, and host-microorganism interactions

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Reviewer Report 14 September 2020

https://doi.org/10.5256/f1000research.29123.r71064

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Kamal Shah
Department of Mathematics, University of Malakand, Chakdara, Chakdara, Pakistan

The authors have revised their paper correctly. I recommend its indexing.

Competing Interests: No competing interests were disclosed.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard.

Version 1

Reviewer Report 09 July 2020

https://doi.org/10.5256/f1000research.25829.r64347

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Kamal Shah
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Coronavirus disease 2019 (COVID-19) is a worldwide pandemic that has been affecting Portugal since 2 March 2020. The Portuguese government has been making efforts to contradict the exponential growth through social isolation measures. In this regard, the authors have developed a mathematical model to predict the impact of such measures in the number of infected cases and peak of infection. They have estimated the peak to be around 2 million infected cases by the beginning of May if no additional measures are taken. The model shows that current measures effectively isolated 25-30% of the population, contributing to some reduction in the infection peak. Importantly, their simulations showed that the infection burden can be further reduced with a higher isolation degree, providing information for a second intervention. The considered study is interesting in this regard and has the potential to give some sound information about COVID-19.

The work is good but there are some issues to be addressed:

1. Provide the existence of the model.

2. What is the feasible region for the considered model?

3. Also, simulate the model for a long time that is months, 40 days, etc.

4. What techniques for numerical simulation have been used?

5. Some relevant and recent work in this regard also must be included. Please see these examples of recent work:
On a comprehensive model of the novel coronavirus (COVID-19) under Mittag-Lefer Chaos, Solitons and Fractals xxx (xxxx) 109867[1]
Qualitative Analysis of a Mathematical Model in the Time of COVID-19 , BioMed Research International 2020, Article ID 5098598, 11 pages[2]
Statistical analysis of forecasting COVID-19 for upcoming month in Pakistan, Chaos, Solitons and Fractals 138 (2020) 109926[3]
Study of Transmission Dynamics of Novel COVID-19 by Using Mathematical Model." (2020). Archive.[4]

I recommend its publication in this journal strongly.

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2. Shah K, Abdeljawad T, Mahariq I, Jarad F: Qualitative Analysis of a Mathematical Model in the Time of COVID-19.*Biomed Res Int*. 2020; **2020**: 5098598 PubMed Abstract | Publisher Full Text
3. Yousaf M, Zahir S, Riaz M, Hussain SM, et al.: Statistical analysis of forecasting COVID-19 for upcoming month in Pakistan.*Chaos Solitons Fractals*. 2020; **138**: 109926 PubMed Abstract | Publisher Full Text
4. Ud Din R, Shah K, Ahmad I, Abdeljawad T: Study of transmission dynamics of novel COVID-19 by using mathematical model. *Advances in Difference Equations*. 2020; **2020** (1). Publisher Full Text

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Yes

Are sufficient details of methods and analysis provided to allow replication by others?
Partly

If applicable, is the statistical analysis and its interpretation appropriate?
Yes

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Yes

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Applied mathematics, Numerical solutions. Mathematical modeling and analysis.

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 25 Aug 2020

Ricardo Pais

We would like to acknowledge the reviewer for the relevant comments and suggestions. We have considered them all and have revised the manuscript accordingly.

Comment 1
"According to the authors, the model 'predicts the impact of isolation measures towards the expected peak of infection'. I am not convinced this is accurate. I believed the authors used the model to estimate the strength of the measures (i.e. percentage lockdown) and not to estimate the impact of the measures on the spread of SARS-Cov-2"

Reply 1
We agree with the suggestion and have changed the manuscript to convey the idea of estimating the strength of measures, which include the percentage of lockdown, social isolation and usage of masks (see revised version).

Comment 2
"the consistently wrote 'transmission dynamics of COVID-19' and not the correct form 'transmission dynamics of SARS-CoV-2"

Reply 2
We agree with the suggestion and have changed the manuscript replacing COVID-19 with SARS-CoV-2 (see revised version).

Comment 3
"The authors predicted 2 million cases, which I find surprisingly high. Using the optimal isolation percentage (70-75%), the model still predicted over 150,000 cases which are approximately 5-fold higher than the current number of cases in Portugal (~35,000)"

Reply 3
Indeed, our predictions are higher than the reported values. This is because only a small fraction of SARS-COV-2- infected individuals are tested for the virus has only a few patients show symptoms. However, our results are in agreement with the recent serologic study conducted by the National Institute of Health (INSA) from Portugal that found that a total of 300.000 people were exposed to the virus, 6-fold higher than the number of reported cases. By the time we conducted the model calibration and analysis, these results were not known, resulting in the deviation between predictions and reported values. Thus, we have corrected the model accounting for the asymptomatic fraction not tested and other recent data. This resulted in novel results which were compared with new data up to August and presented in the revised manuscript.

Comment 4
"I would like to see the model's prediction using even higher percentages of isolation. This should be also discussed."

Reply 4
We have simulated the model with higher percentages and discuss the results (see revised manuscript).

Competing Interests: No competing interests to disclosure.

Author Response 25 Aug 2020

Ricardo Pais

We would like to acknowledge the reviewer for the relevant comments and suggestions. We have considered them all and have revised the manuscript accordingly.

Comment 1
"Provide the existence of the model"

Reply 1
According to F1000 Research rules for supplementary data, we included the model code, data and the analysis code in python as extended on figshare (see revised version references).

Comment 2
"What is the feasible region for the considered model?"

Reply 2
The recommended feasible region for this model is $10^8 > (S+I) > 10^4$ where initial S + I = city population.

Comment 3
"Also, simulate the model for a long time that is months, 40 days, etc."

Reply 3
We have performed simulations for 500 days for predictions and 17 days for model calibrations. By the time we submitted the paper no more than 27 days of data was available. Indeed, we only used a 17 days simulation for model calibration to estimate a rate constant in the absence of control. Unfortunately, it is not possible to use more data for model calibration since an uncontrolled lockdown was implemented in Portugal immediately after these 17 days of infection. Using more data would actually result in wrong estimates since many people follow the DGS recommendations but others do not. This is why we have simulated a total of 500 days with multiple % of lockdown scenarios towards estimating how much % of lockdown during the evolution of COVID pandemic. However, we now include relevant reported DGS data (up to August) for contrasting with model simulations and predictions (see revised version).

Comment 4
"What techniques for numerical simulation have been used?"

Reply 4
The numerical solver was based on the Adams/BDF method, implemented in the LSODA routine of PLAS software. This is a general-purpose stiff, variable-step and variable-order solver. We add this information in the methods section (see revised version).

Comment 5
"Some relevant and recent work in this regard also must be included. Please see these examples of recent work"

Reply 5
We have read your suggestions of new modelling work which are quite relevant and innovative for citing as examples of similar modelling approaches applied in the forecasting of SARS-CoV-2 infection dynamics in Pakistan and Wuhan. Thus, we have included these in the new revised version and other recent work as well.

Competing Interests: No competing interests to disclose.

Reviewer Report 09 June 2020

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The work presented by Pais & Taveira is entitled Predicting the evolution and control of the COVID-19 pandemic in Portugal and it aims to describe the spread of SARS-CoV-2 during the first 21 days. The authors used a simple mathematical model assuming 14 days infection period.

According to the authors, the model 'predicts the impact of isolation measures towards the expected peak of infection'. I am not convinced this is accurate. I believed the authors used the model to estimate the strength of the measures (i.e. percentage lockdown) and not to estimate the impact of the measures on the spread of SARS-Cov-2. This would imply a more elaborated study (e.g. case-control study). Indeed the consistently wrote 'transmission dynamics of COVID-19' and not the correct form 'transmission dynamics of SARS-CoV-2'.

The authors predicted 2 million cases, which I find surprisingly high. Using the optimal isolation percentage (70-75%), the model still predicted over 150,000 cases which are approximately 5-fold higher than the current number of cases in Portugal (~35,000). I would like to see the model's prediction using even higher percentages of isolation. This should be also discussed.

Is the work clearly and accurately presented and does it cite the current literature?
Yes

Is the study design appropriate and is the work technically sound?
Partly

Are sufficient details of methods and analysis provided to allow replication by others?
Yes

If applicable, is the statistical analysis and its interpretation appropriate?
Partly

Are all the source data underlying the results available to ensure full reproducibility?
Yes

Are the conclusions drawn adequately supported by the results?
Partly

Competing Interests: No competing interests were disclosed.

Reviewer Expertise: Genetics, bioinformatics, epidemiology, medical entomology, Wolbachia, and host-microorganism interactions

I confirm that I have read this submission and believe that I have an appropriate level of expertise to confirm that it is of an acceptable scientific standard, however I have significant reservations, as outlined above.

Author Response 25 Aug 2020

Ricardo Pais

We would like to acknowledge the reviewer for the relevant comments and suggestions. We have considered them all and have revised the manuscript accordingly.

Comment 1
"According to the authors, the model 'predicts the impact of isolation measures towards the expected peak of infection'. I am not convinced this is accurate. I believed the authors used the model to estimate the strength of the measures (i.e. percentage lockdown) and not to estimate the impact of the measures on the spread of SARS-Cov-2"

Reply 1
We agree with the suggestion and have changed the manuscript to convey the idea of estimating the strength of measures, which include the percentage of lockdown, social isolation and usage of masks (see revised version).

Comment 2
"the consistently wrote 'transmission dynamics of COVID-19' and not the correct form 'transmission dynamics of SARS-CoV-2"

Reply 2
We agree with the suggestion and have changed the manuscript replacing COVID-19 with SARS-CoV-2 (see revised version).

Comment 3
"The authors predicted 2 million cases, which I find surprisingly high. Using the optimal isolation percentage (70-75%), the model still predicted over 150,000 cases which are approximately 5-fold higher than the current number of cases in Portugal (~35,000)"

Reply 3
Indeed, our predictions are higher than the reported values. This is because only a small fraction of SARS-COV-2- infected individuals are tested for the virus has only a few patients show symptoms. However, our results are in agreement with the recent serologic study conducted by the National Institute of Health (INSA) from Portugal that found that a total of 300.000 people were exposed to the virus, 6-fold higher than the number of reported cases. By the time we conducted the model calibration and analysis, these results were not known, resulting in the deviation between predictions and reported values. Thus, we have corrected the model accounting for the asymptomatic fraction not tested and other recent data. This resulted in novel results which were compared with new data up to August and presented in the revised manuscript.

Comment 4

"I would like to see the model's prediction using even higher percentages of isolation. This should be also discussed."

Reply 4
We have simulated the model with higher percentages and discuss the results (see revised manuscript).

Competing Interests: No competing interests to disclosure

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