PEER REVIEW HISTORY

ARTICLE DETAILS

TITLE (PROVISIONAL)	Modeling COVID-19 Transmission in Africa: Country-wise Projections of Total and Severe Infections Under Different Lockdown Scenarios
AUTHORS	Frost, Isabel; Craig, Jessica; Osena, Gilbert; Hauck, Stephanie; Kalanxhi, Erta; Schueller, Emily; Gatalo, Oliver; Yang, Yupeng; Tseng, Katie; Lin, Gary; Klein, Eili

VERSION 1 – REVIEW

REVIEWER	Josiah Mushanyu University of Zimbabwe, Zimbabwe
REVIEW RETURNED	21-Oct-2020

GENERAL COMMENTS	The model developed in this paper is tractable and fits well with settings in most African countries. An improvement of this model to capture superspreading events in COVID-19 disease transmission dynamics will also be an interesting area for consideration of future work.

REVIEWER	Lin Zhang University of Minnesota, USA
REVIEW RETURNED	10-Nov-2020

GENERAL COMMENTS	Review Report for the Article Modeling COVID-19 Transmission in Africa: Country-wise Projections of Total and Severe Infections under Different Lockdown Scenarios The paper uses a dynamic model of SARS-CoV-2 transmission to estimate the COVID-19 case burden for all African countries under four scenarios: no intervention, moderate lockdown, hard lockdown, and hard lockdown with continued restrictions after lift of lockdown. While the considered issue is important, the analysis conducted lacks many details. Following are my detailed comments. 1. For the dynamic model: Explanation and reasoning should be provided for the set of differential equations. In addition, symbol 'RR' in not defined in the text above and symbol '$IIHH$' should be $IIss$ instead. 2. For the epidemiological parameters: There is no description of the LHS model used to estimate the uncertainty or reference of the method. 3. For the assumed four scenarios: Not clear where these percentage numbers on

	transmission changes come from. How much uncertainty in these estimates of transmission reduction and resumption percentage? How robust will the analysis results be to small variation in these estimates? 4. For reweighting the parameters: Not clear how the parameters were weighted by age and HIV/TB distributions among populations. Do the authors obtain parameter estimates for each age and HIV/TB group and then take the weighted average? 5. The decimal point looks weird in many places, e.g. Page 9 Line 16 and throughout the Result and Discussion sections.

VERSION 1 – AUTHOR RESPONSE

Reviewer: 1
Dr. Josiah Mushanyu, University of Zimbabwe
Comments to the Author:
The model developed in this paper is tractable and fits well with settings in most African countries. An improvement of this model to capture superspreading events in COVID-19 disease transmission dynamics will also be an interesting area for consideration of future work.

We thank Dr. Mushanyu for these comments. We completely agree that superspreading events appear to be key in the transmission of COVID-19, though they were unfortunately beyond the scope of this piece of work. We have included the following on page 14 of the conclusion: 'Superspreading events are likely to play a key role in the transmission of SARS-CoV-2 and, though beyond the scope of this model, this is an important consideration for future work.'

Reviewer: 2 **Please see attachment for this reviewer's report**
Dr. Lin Zhang, University of Minnesota
Comments to the Author:
Please see the attachment.

The paper uses a dynamic model of SARS-CoV-2 transmission to estimate the COVID-19 case burden for all African countries under four scenarios: no intervention, moderate lockdown, hard lockdown, and hard lockdown with continued restrictions after lift of lockdown. While the considered issue is important, the analysis conducted lacks many details. Following are my detailed comments.

Many thanks to Dr. Zhang for these insightful comments, we agree that this is an important issue and answer the questions raised in more depth below.

1. For the dynamic model: Explanation and reasoning should be provided for the set of differential equations. In addition, symbol 'RR' in not defined in the text above and symbol 'IIHH' should be IIss instead.

Many thanks for spotting these typographical errors – R has now been included in the text description of the equations and IH has been replaced with IS. This model is adapted from a published model, Lin G, Bhaduri A, Strauss AT, et al. Explaining the Bomb-Like Dynamics of COVID-19 with Modeling and the Implications for Policy. medRxiv 2020. In line with these comments we have edited the following text to describe the model (p8 of the methods section):

‘The model follows a modified SEIR structure (Figure 1) with seven unique compartments to describe the epidemiology of SARS-CoV-2. This is adapted from the model structure previously described in Lin et al. 2020.[18] This model is adapted from the Kermack and McKendrick compartmental model according to the disease dynamics that have been reported for COVID-19. The model assumptions are described in further depth in [18], but in brief, we assume susceptible individuals that become infected have an incubation period; and some asymptomatic or mildly symptomatic individuals are neither tested nor counted as confirmed cases. Susceptible individuals, S, are those in the population that can become infected with the virus. They become exposed, E, to SARS-CoV-2 by encountering infected individuals in the population at rate β_1 for asymptomatic individuals or β_2 for symptomatic individuals. We assume that individuals that are asymptomatic or mildly symptomatic have a lower transmission rate, β1, than more symptomatic individuals, β2 .[18] Exposed individuals incubate the virus at rate μ (calculated as the inverse of the incubation period). A proportion of these individuals, θ, become symptomatically infected while the rest become contagious with mild or no symptoms, C. Of the symptomatically infected individuals, a proportion, h, have severe symptoms, to the extent that they will require hospitalization if available, IS, and the rest have moderate or non-severe symptoms, IN. Asymptomatic or mildly symptomatic, moderately symptomatic, and severely symptomatic individuals recover (or otherwise become non-contagious), R, at rates γ_1, γ_2, and γ_3, respectively. It is assumed that recovered individuals are immune from becoming re-infected during the time period of the study. Severely infected individuals may also die, D, at rate δ.’

2. For the epidemiological parameters: There is no description of the LHS model used to estimate the uncertainty or reference of the method.

We have edited the following description of the LHS technique (page 9 of the methods):

‘To assess the uncertainty of the parameter ranges on model estimations, we used Latin Hypercube Sampling (LHS), a stratified sampling technique that efficiently analyzes large numbers of input parameters by treating each parameter as a separate random variable [18]. LHS is a type of Monte Carlo sampling which treats each input parameter as a separate random variable and is able to efficiently analyze large sets of input parameters. The parameter distribution is stratified into equiprobable intervals and then each of these intervals is sampled once, without replacement. These random samples of each of the input parameters are then collated into an input vector. This process is highly efficient as each parameter is only used once and the model is then run to derive distribution functions for each of the output variables. The probabilistic nature of this technique allows it to be conveniently used within a statistical framework. Stochastic sampling of the parameters with LHS was based on an estimation of parameter ranges obtained from the literature (Table 1). From the parameter sampling, we were able to calculate the 95% confidence interval (CI) for all compartment values over the temporal domain.’

3. For the assumed four scenarios: Not clear where these percentage numbers on transmission changes come from. How much uncertainty in these estimates of transmission reduction and resumption percentage? How robust will the analysis results be to small variation in these estimates?

We considered the uncertainty in the parameter values and ran all sets of assumptions with the upper and lower bounds shown in Table 1, this gives rise to the upper and lower bounds shown in the shaded regions of figures 2 and 3. However, the sensitivity of each intervention to the assumptions is not included. This model is adapted from a published model, Lin G, Bhaduri A, Strauss AT, et al. Explaining the Bomb-Like Dynamics of COVID-19 with Modeling and the Implications for Policy. medRxiv 2020 and in this paper the sensitivity of the model to different parameter values is explored

in more depth.

The numbers that describe change in transmission were to some extent selected as reasonable numbers to demonstrate the potential relative impact of measures to reduce transmission, such as a lockdown, for different periods of time. The nature of the lockdowns implemented by different African countries showed extensive variation and are likely to have had different effects on transmission in highly heterogeneous environments. This being the case, and in light of the lack of data on the exact impact on transmission of different measures in African countries, we have used a representative figure, which we hope will help policymakers, researchers and other interested parties as they think about the impact of different measures to mitigate the pandemic.

4. For reweighting the parameters: Not clear how the parameters were weighted by age and HIV/TB distributions among populations. Do the authors obtain parameter estimates for each age and HIV/TB group and then take the weighted average?

To weight the parameters based on the HIV/TB distribution we used population data from the World Bank (with the exception of Eritrea for which population data came from IndexMundi) indicating the fraction of the population in the under 64 years age category. Those of 64 or more years of age were modelled as before, however those under 64 were split into healthy individuals and those affected by TB and/or HIV/AIDS according to the Global Burden of Disease tool (Institute for Health Metrics and Evaluation (IHME). GBD Compare. Seattle, WA: IHME, University of Washington, 2015. Available from http://vizhub.healthdata.org/gbd-compare. (Accessed 15th July 2020)). In the affected group the only parameter that was changed was the progression to severe disease (κh), which was doubled to 0.404 (upper bound tripled to 0.606 and lower bound of 0.202), for populations with HIV/AIDS and/or TB, based on estimates for mortality from South Africa (Davies M-A. HIV and risk of COVID-19 death: a population cohort study from the Western Cape Province, South Africa. medRxiv;:1–21. And National Institute for Communicable Diseases. Covid-19 Sentinel Hospital Surveillance Update. 2020.).

This is described in detail on page 8 and edits have been added in response to this comment improve clarity.

5. The decimal point looks weird in many places, e.g. Page 9 Line 16 and throughout the Result and Discussion sections.

We have corrected this throughout.

Many thanks to reviewers and editors for these comments. We hope to have addressed them here but please do not hesitate to contact me for any further clarifications.

Yours sincerely,

Isabel Frost

VERSION 2 – REVIEW

REVIEWER	Lin Zhang University of Minnesota, USA
REVIEW RETURNED	29-Jan-2021

GENERAL COMMENTS	The reviewer completed the checklist but made no further comments.