Early estimates of COVID-19 infections in small, medium and large population clusters

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Abstract

Since its emergence in December 2019, COVID-19 has rapidly developed into a pandemic with many countries declaring emergency conditions to contain its spread. The impact of the disease, while has been relatively low in the Sub Saharan Africa (SSA) so far, is expected to be devastating given the less developed and fragmented health care system in the continent. In addition, most emergency measures such as border closings, cancellations of inbound flights, social distancing, and promotion of hand hygiene may not be as effective due to the clustered way people live in large as well as smaller population centers. As SSA waits for the start of large epidemics as seem in other regions, there exist acute need for estimates of the potential impacts of the disease once it gets strong hold in the region. To address this need, we developed a mathematical model with key parameters obtained from recent studies, to estimate the number of infections with in the first 90 days of the transmission under 54 scenarios of population sizes, initial number of cases, and coverage of contact tracing and isolation. Our results show that if implemented early, 80% contact tracing may “flattens the curve” of local epidemics, brings the pandemic to a manageable level for all population sizes we assessed. In countries with limited

workforce, hospital resources and ICU care, a robust contact tracing program could yield in outcomes that prevent several millions of infections and thousands of deaths across the continent.

Introduction

Since its emergence in December of 2019, SARS-CoV-2 virus has continued to spread in many regions with 824 thousand confirmed cases and more than 41 thousand reported deaths worldwide in 206 countries and territories by March 31, 2020 [1]. The rapid progression of the number of infections and deaths due to SARS-CoV-2 has taken many by surprise, with many of its characteristics related to its transmissibility under continuous update [2]. While the disease is still actively spreading in many regions of the world, researchers are working to quantify transmission parameters [2–7], and make estimates of infections and resulting deaths under different scenarios [8–11]. However, these studies are either too specific to certain geographies [10,12] or are too general to handle realistic scenarios [8,11] in the context of Sub Saharan Africa where majority of the population live in rural and semi urban areas with poor physical interconnections. To overcome this problem and make estimates of infections in clusters of population with different sizes, we developed a mathematical based model with Susceptible-Exposed-Infectious-Removed states, with parameters obtained from recent studies, and based on 54 scenarios of initial number of cases, coverage of contact tracing, and population size, more suited to realities in resource poor, less inter-connected regions around the world.

Methods

We developed a process-based model with four human compartments: Susceptible, Exposed, Infectious, and Removed (S-E-I-R). Susceptible individuals get infected by the virus and progress to the exposed state E at a rate determined by the force of infection Λ. The force of

infection is determined by the length of the infectious period ($1/\gamma$) and the basic reproduction number R_0 - the mean number of secondary infections from a single infected individual introduced into a fully susceptible population, a fixed value in this study. Once exposed, infected individuals stay in that state for the duration of the incubation period ($1/\xi$) and subsequently progress to the infectious state *I*, where they stay for the length of the infectious period ($1/\gamma$) until they are removed either through isolation or recovery. In our model, contact tracing coverage of θ is assumed to affect those that are in the infectious state where those affected will be transitioned to the removed state *R*. We assumed a mean time to isolation after start of the infectious period ($1/\varphi$, where $0 < 1/\varphi < 1/\gamma$). The model has a stochastic process where the infection dynamics is determined using the following system of Ordinary Differential Equations.

$$\frac{dS}{dt} = -\Delta S \quad (1)$$

$$\frac{dE}{dt} = \Delta S - \xi E \quad (2)$$

$$\frac{dI}{dt} = \xi E - \theta\varphi I - (1-\theta)\gamma I \quad (3)$$

$$\frac{dR}{dt} = \theta\varphi I + (1-\theta)\gamma I \quad (4)$$

where $\Delta S \sim Poisson\ (\Lambda S)$ and (5)

$$\Lambda = \gamma \frac{I}{N} R_0 \quad (6)$$

We let the number of new infections to come from a Poisson distribution with the mean given by the force of infection Λ times the number of susceptible populations, *S*, at time *t*.

Table 1: Parameters and assumptions used to run the scenarios

All time units are in days

Parameter	*Value / Distribution*	Source
Incubation period, 1/ξ (μ, shape)	Weibull (2.45, 6.28)	Lauer et al.
Basic reproduction number, R_0	2, 2.5 or 3	Kucharski et al.
Infectious period, $1/\gamma$	5	Davies et al.
Time to isolation after contact traced, 1/φ	One half the incubation period	Assumed
Coverage of contact tracing and isolation, θ	0, 0.5 or 0.8	Assumed
Initial number of cases	50 or 100	Assumed
Cluster population size	100k, 1M or 3M	Assumed

Because estimates of R_0 and length of the infectious period cannot be viewed in isolation, we made sure we used estimates in their proper context and paired R_0 and length of infectious period estimates from similar sources when available. Accordingly, we used parameters obtained from two studies by the same modeling group to run our model [7,12]. We run all scenarios based on the cluster sizes: 100 thousand, 1 million and 3 million populations in consideration of population clusters most common in the SSA context, yielding in a total of 54 scenarios. All model simulations were performed using the Partially Observed Markov Process (Pomp) package available in R, with all scenarios run based on Monte Carlo sample of parameter values from their corresponding distributions.

Results

The effects of contact tracing

Our results show a cluster of 100k with 50% coverage of contact tracing and isolation will have an estimated 7k (95% CI 60-15k), 38k (95% CI 65-56k), 76k (95% CI 285-84k) cases for R_0 values of 2, 2.5 and 3 respectively (Fig 1, S1 Fig.), in the 90 days after the start of the epidemic, while these figures could have been 48k (95% CI 14k-79k), 85k (95% CI 53k-90k) and 94k (95% CI 83k-95k) with no contact tracing assumed (Fig 1, S2 Fig.). Improving the contact

tracing and isolation to 80% will drop the total number of infected cases to just 2k (95% CI 35-12k), 18k (95% CI 45-51k) and 52k (95% CI 71-81k) depending on the basic reproduction number assumed (Fig 1, S3 Fig., S1 Table).

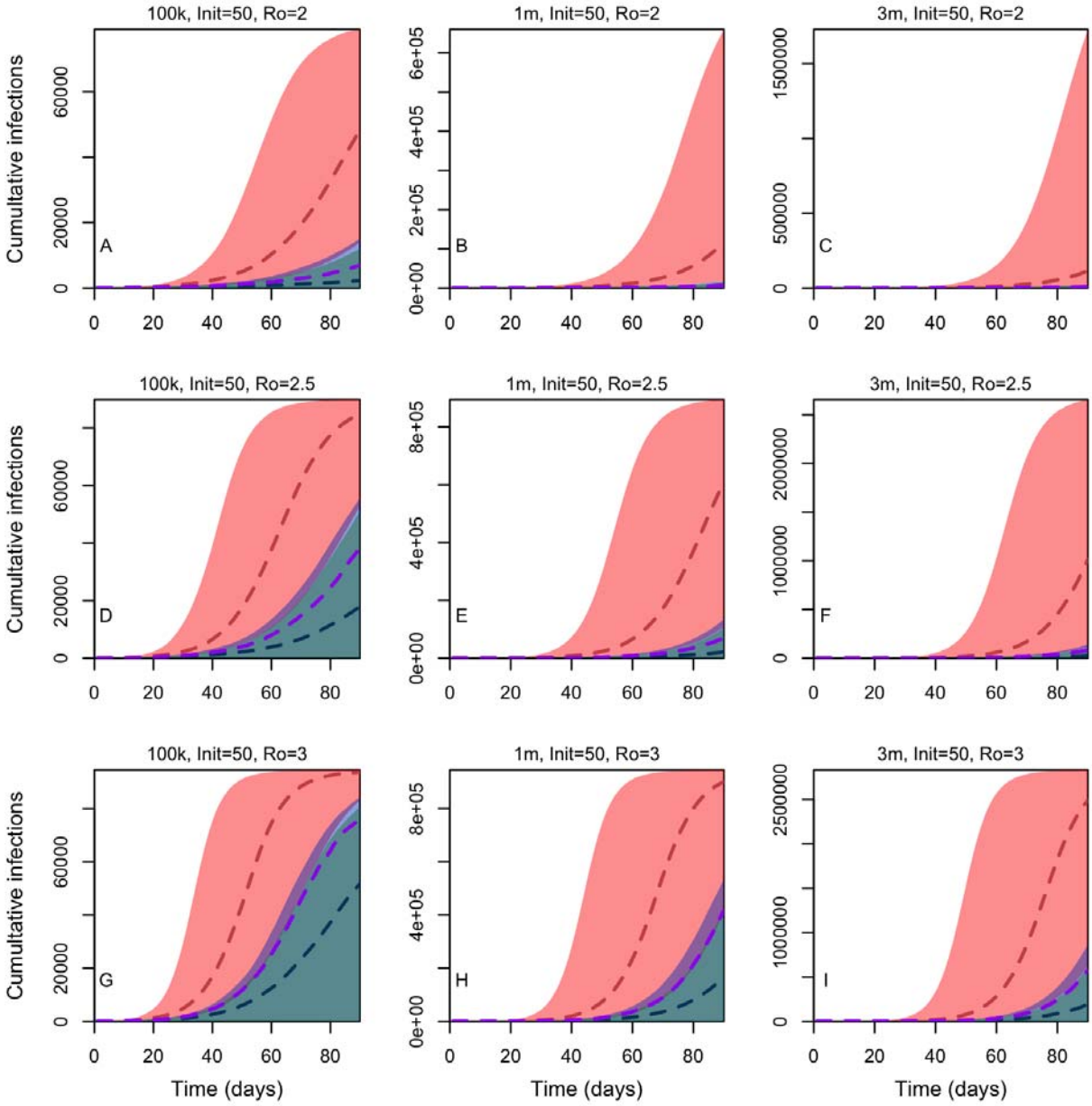

Fig 1: Cumulative number of infections in the initial 90 days with 0% (red), 50% (blue), and 80% contact tracing (green) and 50 initial cases, assuming Ro=2, 2.5 and 3 (top to bottom respectively) for the three population sizes (left to right). Broken line shows the median value and corresponding regions show the 95% confidence interval.

Similarly, by the end of the first 90 days, a cluster of 1M with 50% coverage of contact tracing and isolation will have an estimated 7k (95% CI 92-17k), 70k (95% CI 103-135k), 416k (95% CI 379-532k) cases for R_0 values of 2, 2.5 and 3 respectively (Fig 1, S1 Fig). Compare with 117k (95% CI 18k-659k), 608k (95% CI 108k-894k) and 900k (95% CI 409k-945k) if no contact tracing was assumed (Fig 1, S2 Fig.). With 80% contact tracing and isolation implemented, the number of infected cases would go down to 2k (95% CI 27-15k), 21k (95% CI 38-103k) and 166k (95% CI 78-419k) for basic reproduction number R_0 values of 2, 2.5 and 3 respectively (Fig 1, S3 Fig.).

For larger cluster of 3M population, 50% coverage of contact tracing and isolation yielded in an estimated 8k (95% CI 42-20k), 81k (95% CI 103-141k), 575k (95% CI 274-867k) cases for R_0 values of 2, 2.5 and 3 respectively (Fig 1, S1 Fig.), while there would be 116k (95% CI 13k-1727k), 1M (95% CI 113k-2.66M) and 2.5M (95% CI 623k-2.8M) respectively if no contact tracing was assumed (Fig 1, S2 Fig). With 80% contact tracing and isolation implemented, these figures would go down to 2k (95% CI 45-17k), 25k (95% CI 43-100k) and 192k (95% CI 108-611k) for basic reproduction number R_0 values of 2, 2.5 and 3 respectively (Fig 1, S3 Fig).

The effects of early intervention

In addition to the effects of contact tracing, our results show dramatic differences in outcomes due to the timing of contact tracing. With 80% contact tracing implemented at the time of 50 infections instead of when 100 infections occurred, number of infections could be lowered by 2k (95% CI 20-11k), 7k (95% CI 22-20k), and 10k (95% CI 50-26k) for basic reproduction number R_0 values of 2, 2.5 and 3 respectively (Fig 2). The effects are even more dramatic when we consider a population size of 1M and 3M. With 80% of contact tracing assumed, implementing

contact tracing earlier would bring the differences to 2k (95% CI 25-17k), 12k (95% CI 30-93k), and 69k (95% CI 52-218k) for 1M size cluster, and 2k (95% CI 10-15k), 13k (95% CI 47-116k) and 134k (95% CI 37-408k) for 3M size cluster basic reproduction number R_0 values of 2, 2.5 and 3 respectively (Fig 2).

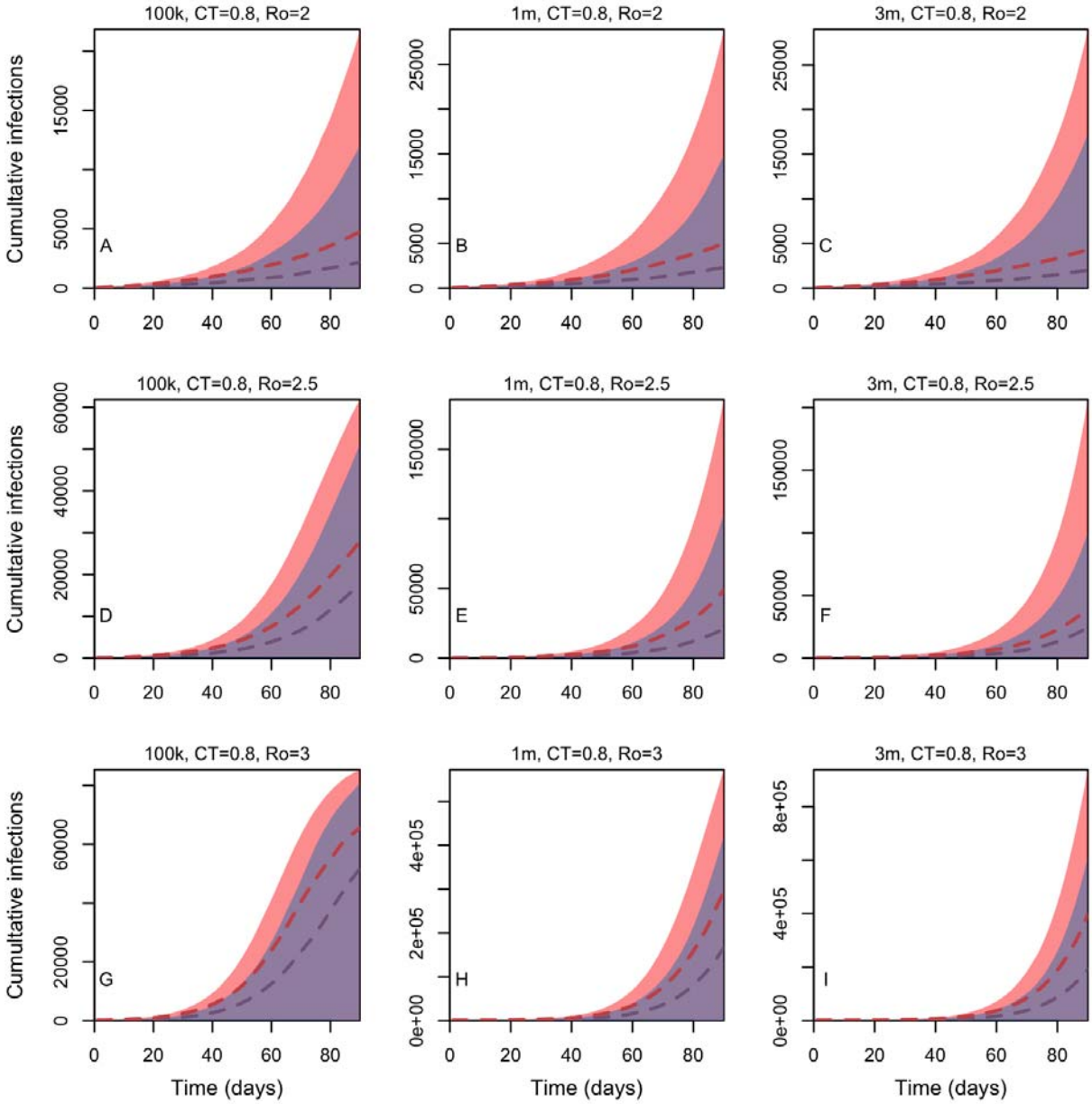

Fig 2: Cumulative number of infections in the initial 90 days with 50 (blue) and 100 (red) initial cases and 80% contact tracing, assuming Ro=2, 2.5 and 3 (top to bottom respectively) for the three population sizes (left to right). Broken lines show the medians and corresponding regions show the 95% confidence interval.

Discussion

We developed a stochastic S-E-I-R mathematical model with parameters from recent published works, to estimate infections within the first 90 days of initial cases for scenarios more realistic to many African settings in terms of population size and capacity to carry out effective contact tracing. Our estimates show effective contact tracing could bring down the number of infections and associated deaths to manageable levels when implemented early. Our results confirm the significant positive role contact tracing play as the most reliable non-pharmaceutical intervention against SARS-Cov-2 [8,11].

While the virus is spreading around the world at a fast pace, Sub-Saharan Africa is anticipating a start of epidemic levels disease and death rates, having reported only 3725 confirmed cases in 42 countries by April 1, 2020 [1]. Though each African nation's situation may be unique, patterns of population settlement and physical connectedness, as well as living conditions in most countries can be generalized into one of isolated rural, semi-rural or large urban settlements, the latter with a possibility slam area. Our classifications of population centers into three sizes of 100k, 1M and 3M thus follows this assumption in consideration of most common population settlement patterns in SSA.

To decide which scenario to choose, each country should consider the current existing risk of importing new cases, best estimate number of identified cases, the strength of the field epidemiology work, coverage of facemask [13], strength of social distancing measures taken and population density. Those countries with a potential for simultaneous clusters of cases around

new epicenters, contact tracing and isolation should be accompanied by travel restrictions between clusters to prevent importation of cases.

The effect of increased contract tracing and isolation is not only lowering the total attack rate and mortality, but also delaying the time to the peak transmission slowing build-up of cases, thus allowing hospitals and healthcare systems mobilize their workforce and resource supplies in this emergency situation. This so-called "flattening the curve" scenario will allow critical resources, including health care workers, hospital beds, and medical equipment and supplies, to be utilized efficiently leading to more lives saved. While we have not included explicit estimates of mortality, based on the 2.84% mortality rate in Wuhan [11], we estimate 510 to 1335 (95% CI) and 1192 to 1902 (95% CI) deaths averted with 50% and 80% contract tracing coverage implemented.

Sub Saharan Africa's large young population is expected to lead to relatively lower mortality rates given the observed larger mortality rates among older population [11]. In addition, the overall low population density in rural areas should allow natural distancing, thus mitigating the impact of the SARS-CoV-2 pandemic [7,14]. On the other hand, weak health systems, poor access to sanitation, overcrowded cities and slums make social distancing a challenge and negatively impact the spread of the virus. Population face mask utility can support the social distancing needed to decrease transmissibility of SARS-CoV-2 [15] especially in urban centers where people may find it hard to keep distances. We have modeled our estimate based on three basic reproduction number R_0 values, three cluster sizes and three initial cases. SSA countries

and regions are advised to take their situation into account [16] when they use estimates from these scenarios.

The large differences in the number of infected individuals between scenarios initialized with 50 cases and 100 cases (Fig 2) demonstrate the effect of early action preventing large transmissions and lowering the size of the epidemic. This suggests a need for countries to quickly undertake extensive training of field epidemiologists to identify and isolate contacts of those who are diagnosed with SARS-CoV-2. Currently, Africa has the lowest testing rate of any part of the world. Since testing is a necessary precondition for contact tracing and isolation, countries should scale up their testing, contact tracing and isolation capacities within the short window of opportunity that remains to minimize the local impact of the pandemic.

Our model is highly sensitivity to certain parameters, especially the infectious period of a person given the reproduction number. This means that letting the length of infectious period vary within a distribution could have widened the range of estimated infections. We will continue to update our estimates when new evidence on the key parameter assumptions emerges.

Our model is not without limitations. We have not considered clinical and sub-clinical infections separately, which may have overestimated the force of infection. Also, we have accounted for contract tracing by using a constant proportion of the incubation period, unlike others who have used using distribution-based time to isolation [8]. We have assumed that contact tracing will be completely effective with no onward transmission from those individuals suspected of the disease, which may not be realistic given the less optimal process of identifying suspects, and

putting them in safe isolated location in many African countries. Thus, our results many have overestimated the impact of contact tracing as implemented on the ground. In addition, our assumptions of the initial number of cases may not be realistic given evidences large number of unobserved infections [10]. Finally, the fact that our model does not have age structure has limited our capacity to include mortality estimates.

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