Supplementary Methods and Results Empowering the crowd: Feasible strategies to minimize the spread of COVID-19 in informal settlements

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Model

We consider a stochastic model governed by the following set of differential equations:

$$\dot{S}_i = -\lambda_i S_i \tag{1}$$
$$\dot{E}_i = \lambda_i S_i - \delta_E E_i \tag{2}$$
$$\dot{P}_i = \delta_E E_i - \delta_p P_i \tag{3}$$
$$\dot{A}_i = (1-f)\delta_p P_i - \gamma_A A_i \tag{4}$$
$$\dot{I}_i = f\delta_p P_i - ((1-g_i-h_i)\gamma_I + h_i\eta + g_i\alpha)I_i \tag{5}$$
$$\dot{H}_i = h_i\eta I_i - \gamma_H H_i \tag{6}$$
$$(\dot{R/D})_i = \gamma_H H_i \tag{7}$$
$$\dot{R}_i = \gamma_A A_i + (1-g_i-h_i)\gamma_I I_i \tag{8}$$
$$\dot{D}_i = g_i\alpha I_i \tag{9}$$

where

$$\lambda_i = \sum_{j=1}^{n} \beta_{ij} \frac{P_j + A_j + I_j + H_j}{N_j} \tag{10}$$

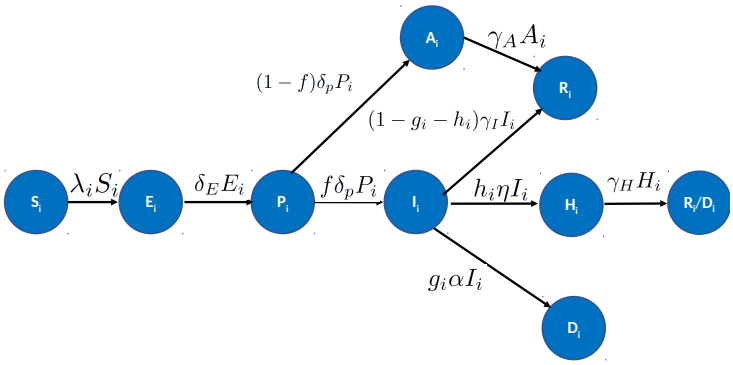

Figure 1: **Diagram of the model.** The model considers the following compartments: susceptible (S), exposed (E), presymptomatic (P), asymptomatic (A), symptomatic (S), recovered (R) and dead (D). In our model, individuals requiring ICU care immediately after the symptomatic period would die, and those requiring hospitalization are considered infectious for a longer period. To model the latter type of individuals, we included the compartment H. Since the fate of individuals in the H compartment is uncertain if health care is not available, we run simulations considering two limiting possibilities, either all the individuals in H are recovered, or all die. This is indicated in the model with the variable R/D.

with $\beta_{ij} = \tau C_{ij}$, τ being the probability of infection for a contact with an infected person, and C_{ij} is the average number of contacts of an individual of class i with an individual of class j. The rest of parameters are described in Table [Table], and the model is illustrated in Fig. . In the following, to simplify the notation we define $\kappa_i = ((1-g_i-h_i)\gamma_I + h_i\eta + g_i\alpha)$.

Parametrization of the contact matrix

We estimated the average number of contacts of individuals of class i in the camps, $\bar{c}_i$, and we parametrized the contact matrix assuming that, in a well-mixed population, these contacts will be distributed among classes relative to the fraction of individuals within each class, i.e.

$$C_{ij}^0 = \bar{c}_i^0 N_j / N, \tag{11}$$

with N the total population size. A well-mixed population will be considered the null model, and parameters derived under the null model assumptions are indexed with the superscript 0, e.g. the null contact matrix is C_{ij}^0. The type

of interventions that we consider, aim to reduce either the average number of contacts a class i (e.g. self-isolation) or the accessibility of class i to class j (e.g. shielding strategies). We model the first type of intervention introducing the parameter ϵ_{ij}, representing the fraction of the average number of contacts observed in the null model that prevail after the intervention: $\bar{c}_i = \epsilon_{ij}\bar{c}_i^0$. Similarly, we model the second type of intervention with the matrix m_{ij}, representing the fraction of population j visible to population i after the intervention. The contact matrix resulting from management strategies can therefore be written with respect to the null model as:

$$C_{ij} = \epsilon_{ij} m_{ij} \bar{c}_i^0 N_j/N = \epsilon_{ij} m_{ij} C_{ij}^0 = M_{ij} C_{ij}^0, \tag{12}$$

and the matrix M_{ij} will be called the managament matrix. Given this parameterization, we substitute it in the explicit expression of λ (Eq. **??**) to obtain a model including management strategies

$$\lambda_i = \frac{\tau}{N} \sum_{j=1}^{n} \epsilon_{ij} \bar{c}_i^0 m_{ij} \left(P_j + A_j + I_j + H_j\right) \tag{13}$$

Derivation of the transmissivity

Overall strategy To estimate the probability of infection if there is a contact between a symptomatic and an infected individual (parameter τ) we proceed as follows [Ref]: 1) Define the infected subsystem, i.e. all equations that include compartments where individuals can get infected. 2) Linearize the subsystem in the disease free equilibrium. 3) Find the next generation matrix (NGM) with large domain (K_L) by writing the linear system as: $\dot{\boldsymbol{x}} = (\boldsymbol{T} + \boldsymbol{\Sigma})\boldsymbol{x}$, here $\boldsymbol{x}$ is a vector containing all states where individuals can get infected, $\boldsymbol{T}$ contains all terms corresponding to transmission and $\boldsymbol{\Sigma}$ all terms corresponding to transitions between compartments. Then: $\boldsymbol{K} = -\boldsymbol{T}\boldsymbol{\Sigma}^{-1}$. 4) The parameter τ can be estimated relating the ominant eigenvalue of the NGM to an estimation of the basic reproduction number obtained from the literature.

Estimation of the Next Generation Matrix

We start considering the subsystem containing the infectious population:

$$\dot{E}_i = \lambda_i S_i - \delta_E E_i \tag{14}$$

$$\dot{P}_i = \delta_E E_i - \delta_p P_i \tag{15}$$

$$\dot{A}_i = (1-f)\delta_p P_i - \gamma_A A_i \tag{16}$$

$$\dot{I}_i = f\delta_p P_i - \kappa_i I_i \tag{17}$$

$$\dot{H}_i = h_i \eta I_i - \gamma_H H_i. \tag{18}$$

For the sake of simplifying the notation, let us consider the following ordering of the variables in the vector $x = (E_1, ..., E_M, P_1, ..., P_M, A_1, ..., A_M, I_1, ..., I_M, H_1, ..., H_M)$, with M the number of population classes. We are interested in the parametrization of the null model, which will serve as a baseline to estimate the parameter τ, which is unknown, and that does not change when interventions are introduced. For the null model, Eq. 13 becomes

$$\lambda_i = \frac{\tau}{N} \sum_{j=1}^{n} \bar{c}_i^0 \left(P_j + A_j + I_j + H_j\right).$$

Following this notation, the linearized system can be written in the form $\dot{\boldsymbol{x}} = (\boldsymbol{T} + \boldsymbol{\Sigma})\boldsymbol{x}$, where:

$$\boldsymbol{T} = \tau \begin{bmatrix} \mathbf{0} & \boldsymbol{\Theta} & \boldsymbol{\Theta} & \boldsymbol{\Theta} & \boldsymbol{\Theta} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \end{bmatrix} \tag{19}$$

is the transmission matrix, with $\boldsymbol{\Theta} = \mathrm{diag}(p_i \bar{c}_i^0)\boldsymbol{U}$, $p_i = N_i/N$, and $\boldsymbol{U}$ being the all-ones matrix of size M. The transition matrix is

$$\boldsymbol{\Sigma} = \begin{bmatrix} -\delta_E \boldsymbol{I} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \delta_E \boldsymbol{I} & -\delta_p \boldsymbol{I} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & (1-f)\delta_p \boldsymbol{I} & -\gamma_A \boldsymbol{I} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & f\delta_p \boldsymbol{I} & \mathbf{0} & -\mathrm{diag}(\kappa_i)\boldsymbol{I} & \mathbf{0} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \eta\,\mathrm{diag}(h_i)\boldsymbol{I} & -\gamma_H \boldsymbol{I} \end{bmatrix} \tag{20}$$

Where $\boldsymbol{I}$ and $\mathbf{0}$ are the identity and null matrices of size M, and $\kappa_i = ((1 - g_i - h_i)\gamma_I + h_i\eta + g_i\alpha)$. We next compute the inverse of the transition matrix

$$\boldsymbol{\Sigma^{-1}} = \begin{bmatrix} -\frac{1}{\delta_E}\boldsymbol{I} & \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ -\frac{1}{\delta_p}\boldsymbol{I} & -\frac{1}{\delta_p}\boldsymbol{I} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ -\frac{(1-f)}{\gamma_A}\boldsymbol{I} & -\frac{(1-f)}{\gamma_A}\boldsymbol{I} & -\frac{1}{\gamma_A}\boldsymbol{I} & \mathbf{0} & \mathbf{0} \\ -f\,\mathrm{diag}(\frac{1}{\kappa_i})\boldsymbol{I} & -f\,\mathrm{diag}(\frac{1}{\kappa_i})\boldsymbol{I} & \mathbf{0} & -\mathrm{diag}(\frac{1}{\kappa_i})\boldsymbol{I} & \mathbf{0} \\ -\frac{f\eta}{\gamma_H}\mathrm{diag}(\frac{h_i}{\kappa_i})\boldsymbol{I} & -\frac{f\eta}{\gamma_H}\mathrm{diag}(\frac{h_i}{\kappa_i})\boldsymbol{I} & \mathbf{0} & -\frac{\eta}{\gamma_H}\mathrm{diag}(\frac{h_i}{\kappa_i})\boldsymbol{I} & -\frac{1}{\gamma_H}\boldsymbol{I} \end{bmatrix} \tag{21}$$

The NGM with large domain can now be found by $\boldsymbol{K_L} = -\boldsymbol{T}\boldsymbol{\Sigma}^{-1}$. hHowever, as we know that each individual that gets infected first will become an exposed individual (E compartment), we can calculate instead the NGM with small domain, $\mathbf{K}_\mathrm{S}$ that only consists of the E compartment [Heffernan]. We do this by removing from T the rows that correspond to the other compartments and from Σ^{-1} the columns.We then find:

$$\boldsymbol{K_S} = \tau \left[\left(\frac{1}{\delta_P} + \frac{(1-f)}{\gamma_A} \right) \boldsymbol{\Theta} + \mathrm{diag} \left(\frac{f}{\kappa_i} (1 + \frac{h_i \eta}{\gamma_H}) \right) \boldsymbol{\Theta} \right].$$

Estimation of τ

The reproduction number can be obtained from the maximum of the absolute value of all eigenvalues of $\boldsymbol{K_S}$, i.e. $R_0 = |\lambda_1|$. In our model all parameters are known except the probability of infection per contact, τ. We estimate the probability distribution of τ generating realizations of R_0 and $\tilde{K_S} = K_S/\tau$ assuming a well mixed population as null model and solving for τ:

$$\tau = \frac{R_0}{|\tilde{\lambda}_1^0|}, \tag{22}$$

where $|\tilde{\lambda}_1^0|$ is the maximum of the absolute values of all eigenvalues of $\tilde{K_S}$, when the contact matrix is estimated under the null model, i.e. $\bar{c}_i = \bar{c}_i^0$.

Parametrization of the interventions

Safety zone

In the following, we analyse the effect of creating a safety zone to isolate certain fraction f_S of the population, mostly vulnerable. In practice, this is made dividing the camp in two areas, a "green" zone (denoted g) for vulnerable population and an "orange" zone (o) for the remaining population. These two populations could eventually interact via a "buffering" zone under controlled conditions. In particular, we will consider that members of both populations will meet in an open space, maintaining 2m of distance and using contention measures such as masks, reducing the infectivity an 80% [Ref], i.e. $\hat{\tau} = 0.2\tau$. In addition, only a limited number of members c_{fam} will be allowed to interact per each individual in the green area per day. Finally, in some interventions we considered that individuals visiting the buffering zone will have a health check (e.g. temperature measurement), aimed at excluding symptomatic patients from the buffering zone. In the model, this intervention reduces the transmission probability of individuals from the I and H compartments to zero in this zone.

The intervention implies a reduction in the number of contacts between classes of the green zone and the orange zone, but not in the mean number of contacts that each individual has per day, therefore $\bar{c}_i$ does not vary. We model this redistribution of the contacts with the parameter ϵ_{ij} as follows:

$$\begin{aligned} \epsilon_{ij} &= \rho c_{\mathrm{fam}}/\bar{c}_i \quad (i,j \text{ in different areas}) \\ \epsilon_{ij} &= 1 - \rho c_{\mathrm{fam}}/\bar{c}_i \quad (i,j \text{ in same area}). \end{aligned}$$

If we assume that the relatives from the orange zone visiting the buffering zone are always different, $f_{\mathrm{o,fam}} = c_{\mathrm{fam}} \frac{N_{\mathrm{g}}}{N_{\mathrm{o}}}$ will be the fraction of the orange population susceptible of visiting the buffering zone and we define ρ as:

$$\rho = \begin{cases} 1 & \text{if } i \in \mathrm{g} \\ f_{\mathrm{o,fam}} & \text{if } i \in \mathrm{o} \end{cases}$$

[1]

The next step is to model the probability of interaction between a member of the class i and the class j, depending on whether they belong to the same or a different area. Since in the intervention classes are constrained to interact in the demarcated areas, once one individual is within a given area she will observe an increased likelihood of finding members of the classes permitted to visit that area with respect to the null model. In particular, the proportion N_i/N of individuals for class i in the null model will become N_i/N_{X} with N_{X} the total number of individuals in the area $X = \{\mathrm{o}, \mathrm{g}\}$. This leads to the following factors for m_{ij}:

$$\begin{aligned} m_{ij} &= \left(\tfrac{N_i}{N_{\mathrm{X}}}\right) / \left(\tfrac{N}{N_i}\right) = \frac{N}{N_{\mathrm{X}}} \quad (i, j \text{ in same area } X) \\ m_{ij} &= \left(\tfrac{N_i}{N_{\mathrm{Y}}}\right) / \left(\tfrac{N}{N_i}\right) = \frac{N}{N_{\mathrm{Y}}} \quad (i \in X \text{ and } j \in Y) \end{aligned}$$

Estimation of the infectivity of the isolated and evacuated populations

To estimate the infectivity of the population isolated we depart from the following assumptions. Firstly, the population class taking care of the isolated individuals belong to the one of adults with no comorbidities, and we considered a number N_{care} of carers having c_{care} contacts per day and carer with the isolated population. More specifically, these individuals should not be symptomatic (nor death), and we denote the number of individuals fulfilling this requirements with N_{exp} (number of exposed). To continue with, we considered that the number of symptomatic individuals exceeding the isolation capacity $\tilde{N}$ are fully infectious (note that we use a tilde to denote variables related to the isolated population). In addition, the occupancy of the isolation beds is distributed among classes proportionally to the number symptomatic individuals that each class contributes, i.e. $\tilde{N}_j = \tilde{N} \left(I_j / \sum_j I_j \right)$. Finally, symptomatic individuals developing symptoms that would require a hospitalization, are either evacuated or they become fully infectious. The rationale behind the latter choice

[1] [APG: Double check implementation] Note that it could be considered that this function saturates if every member of the orange zone eventually visits the buffering zone:

$$\rho = \begin{cases} 1 & \text{if } i \in \mathrm{g} \\ f_{\mathrm{\o,fam}} \left(1 - \mathrm{H}(f_{\mathrm{o,fam}} - 1) \frac{f_{\mathrm{o,fam}} - 1}{f_{\mathrm{o,fam}}} \right) & \text{if } i \in \mathrm{o} \end{cases}$$

with the Heaviside function $\mathrm{H}(f_{\mathrm{o,fam}} - 1) = 1$ if $f_{\mathrm{o,fam}} \geq 1$.

is that, if an individual requires a more dedicated care, the available means in the camps to protect the population from these patients would be insufficient. In particular, it is unlikely that this person can stay alone in a tent. We model the evacuation considering a parameter $\epsilon = 0$ if evacuation is put in place and $\epsilon = 1$ otherwise.

Given these assumptions, the number of contacts that the healthy adult population class will have with the isolated population will be $c_{\text{care}} N_{\text{care}}/N_{\text{exp}}$ per individual and day. The expression clearly shows that, increasing the number of carers, the number of isolated individuals, and the number of contacts per day between carers and individuals, will increase the rate of infection. Hence, we expect that, for fixed N_{care} and c_{care}, the positive effects coming from isolating individuals will be less pronounced for increasingly large $\tilde{N}$ values. We further assume that this interaction is regulated following the guidelines introduced for a safety zone, and the infectivity becomes thus reduced by a factor $\xi = 0.2$. Finally, we should note that the probability of finding an isolated individual belonging to class j is equal to $(N_j/N)(\tilde{N}_j/N_j)$, but this probability is equal to one for the healthy adult population (due to their role of carers) and equals zero for the remainder classes (since they have no access to the isolation area).

For simplicity, we assume that there is one carer for each infected person in the class j, $(N_{\text{care},j} = \tilde{N}_j)$, having only one contact per day (c_{care}). Note the convenience of this choice, since if the number of infectious is larger than the number of available individuals to be carers, the ratio $\tilde{N}_j/N_{\text{exp}} > 1$, meaning that more than one contact per day is needed to care that population class. With these considerations, the rate of infection for the healthy adult population class (indexed k) becomes:

$$\lambda_k = \tau \sum_j \xi \frac{\tilde{N}_j}{N_{\text{exp}}} + C_{kj} \frac{P_j + A_j + \Theta(N_I - \tilde{N})(I_j - \tilde{I}_j) + \epsilon H_j}{N_j},$$

where Θ is the Heaviside function and N_I the total number of symptomatic individuals at time t. For the remainder classes $(i \neq k)$ the rate of infection becomes:

$$\lambda_i = \tau \sum_j C_{ij} \frac{P_j + A_j + \Theta(N_I - \tilde{N})(I_j - \tilde{I}_j) + \epsilon H_j}{N_j}.$$

Leftovers

Maximum number of family members permitted

[APG, the following should be reviewed, it is unfinished] We considered until now that people from the orange area visiting the buffering zone will be always different within the same week. An interesting question for management is how to keep the fraction of the orange population using the buffering zone as small as possible to minimize the spread of the infection. This relies on the assumption that, since symptomatic members are excluded from the buffering zone,

increasing this fraction increases the chances for assymptomatic or presymptomatic individuals to visit the buffering zone. As we will see immediately, this observation could be used to improve the management strategies.

To illustrate this point we note that the fraction of the orange population getting in contact with the green population can be estimated through the quantity $0.2\epsilon_{ij}m_{ij}$ ($i \in$ o), which we aim to keep lower than one. Expanding this expression we obtain

$$c_{\text{fam}} < 5\sqrt{\bar{c}_i \frac{N_{\text{o}}}{N}}$$

with a value of ≈ 17 individuals per day for the adult class and assuming 20% of the population shielded. Note that the estimation heavily relies on the efficiency of the protection measures.

The clan's dilemma

In the previous section, we considered that the family members visiting were always different. However, if the population in the camps is structured in large families (hereafter clans) it opens the question of whether it would be more beneficial to keep all members of the same clan in the same area or in different areas. If all members of the same clan live in the same zone, there would be little need to interact with members of the other zone, hence reducing c_{fam}. However, since the capacity of the green zone is limited, shielding whole clans may lead to leaving other clans completely outside of the green zone, even if the strategy may be better to minimize the overall impact in the population. On the other hand, if clans are split, it increases the chances that the same relatives visit the buffering zone several times. Under the assumption that minimizing the number of different people would reduce the probability of infection, this could also be a positive strategy.