

An extended SIR model incorporating population classes

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Motivation

The aim of this model is to provide a solid basis to explore the impact of a possible COVID-19 outbreak in Syrian refugee camps. The model should have sufficient complexity to bring reliable results while being sufficiently general to embrace the diversity of situations that exist in the different camps.

In our modeling approach, we need to take several key distinctions between the Syrian context and the high income country contexts in which previous COVID-19 models have been developed into account. The lack of access to healthcare makes consideration of a “hospitalized” compartment meaningless; it will be omitted from our model and we will assume that all cases requiring hospitalization will die. Since we expect increased disease severity in Syrian refugee compared to high income country populations, epidemiological parameters found in the literature from high income countries should be reconsidered. Since there is no existing data on COVID-19 outbreaks in similar settings, a careful sensitivity analysis of the model under different scenarios must be performed. The social contexts of Syrian refugee camps suggest social interaction and contact be compartmentalized by age. Any interventions to mitigate a COVID-19 outbreak in Syrian refugee camps should therefore take these and other relevant considerations of their social contexts into account. Since the most feasible interventions are related to shielding strategies, the complexity of living conditions should be considered in models of these interventions.

To address some of these challenges, our model incorporates the concept of *population class*, a subset of the population that we distinguish because it either has different epidemiological parameters (e.g. proportion requiring hospitalization), a significantly different frequency of contact with individuals in other classes, or both. Population classes allow us to generalize previous models that considered stratification of population by classes [REF] or locations [REF], that we can implicitly model via different subsets of parameters. This approach will allow us to model the impact of potential mitigation measures, such as shielding vulnerable members of the population, and controlling their contact with potential carers.

Description of the model

The model considers a generic population class i , whose dynamics is described by the model:

$$\dot{S}_i = -\lambda_i S_i \quad (1)$$

$$\dot{E}_i = \lambda_i S_i - \delta_E E_i \quad (2)$$

$$\dot{P}_i = \delta_E E_i - \delta_P P_i \quad (3)$$

$$\dot{A}_i = (1 - f)\delta_P P_i - \gamma_A A_i \quad (4)$$

$$\dot{I}_i = f\delta_P P_i - ((1 - g_i - h_i)\gamma_I + h_i\eta + g_i\alpha)I_i \quad (5)$$

$$\dot{H}_i = h_i\eta I_i - \gamma_H H_i \quad (6)$$

$$\dot{R}_i = \gamma_A A_i + (1 - g_i - h_i)\gamma_I I_i \quad (7)$$

$$\dot{R}_i/\dot{D}_i = \gamma_H H_i \quad (8)$$

$$\dot{D}_i = g_i\alpha I_i \quad (9)$$

where all the compartments S_i (susceptible), E_i (exposed, latent), P_i (*infectious, pre-symptomatic*) A_i (infectious, asymptomatic), I_i (infectious, symptomatic), H_i (cases requiring hospitalization), R_i (recovered), R_i/D_i (recovered/dead), and D_i (dead) are class-specific. The model is illustrated for a single class in Fig. 1.

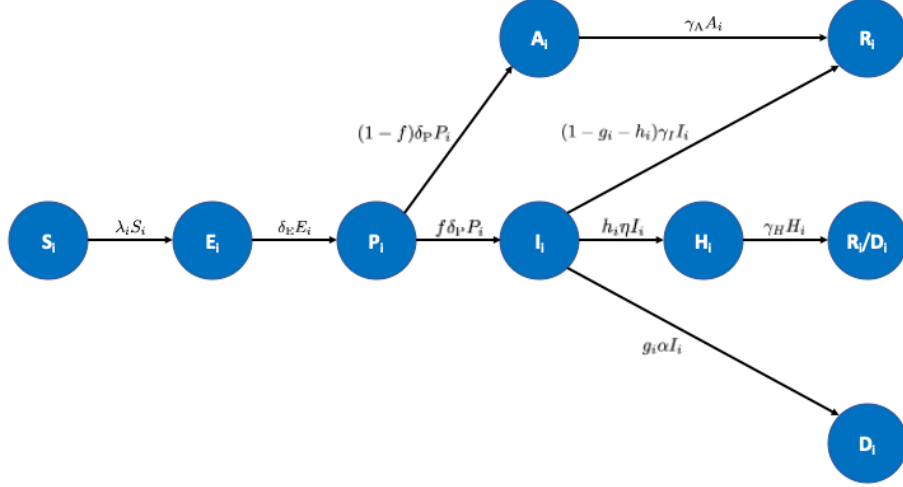


Figure 1: **Schematic representation of the model.**

Some of the parameters are also class-specific and are labelled with the subindex i : the fraction of symptomatic cases that will be severe enough to require hospital admission but not severe enough to require ICU admission, h_i , and the fraction of symptomatic cases that will be severe enough to require ICU admission for survival, g_i .

The following parameters are independent of class: the fraction of infectious cases that are symptomatic, f , the duration of the latent period, $\frac{1}{\delta_E}$, the duration of the pre-symptomatic period, $\frac{1}{\delta_P}$, the duration of infection, $\frac{1}{\gamma_I}$, time from symptom onset to hospitalization, $\frac{1}{\eta}$, time from symptom onset to critical care/death, $\frac{1}{\alpha}$, and duration of hospitalization, $\frac{1}{\gamma_H}$.

The transmission rate λ_i depends on the average contacts between the different classes. To determine its value, we define the maximum transmission rates of latent, β_P , asymptomatic, β_A , symptomatic, β_I , and severe (requiring hospitalization), β_H , and the reduction of these transmission values between the class i and class j with the matrix $C_{ij} \in [0, 1]$. This reduction may be motivated by social factors (e.g. different contact patterns of children and adults) or management actions (e.g. a class is shielded from the remaining population). Its value represents the fraction of contacts that the classes i and j have with respect to the mean contacts between two individuals in the whole population. Taking these considerations we define the transmission rate of the class i as:

$$\lambda_i = \sum_j C_{ij} \frac{(\beta_P P_j + \beta_A A_j + \beta_I I_j + \beta_H H_j)}{N_j} \quad (10)$$

where j runs across all classes including the reference class i .

**APG: NOT UPDATED FROM HERE

[Explain assumptions given the data available and the inaccessibility to facilities]

The quarantine variable Q deserves special consideration. In its current form there is a fraction of the population that can be removed at a certain rate. This may make sense in a context in which there is a regulation within the population to become quarantined if certain conditions happen (e.g. being in contact with a symptomatic), in which case the quarantine rate is density-dependent (and hence the term ηQ). On the other hand, if quarantine happens because an external (e.g. WHO agent) remove symptomatics from the camp, the capacity of the agency to remove patients will saturate at some point and it would be more appropriate to model it as a constant or a sigmoidal-like function. In addition, note that in the current form of the model the parameter q is not implemented.

Estimation of parameters

[TO do]

Examples

Shielding vulnerable population

In this example exist only two classes, one vulnerable subpopulations and one healthy, differing in their epidemiological parameters. Then we considered two scenarios, one in which both populations are well-mixed, and a second scenario in which the average number of contacts between the healthy and vulnerable subpopulations are reduced to half the whole population values. The dynamics of both populations for both scenarios are shown in Fig. 2. We observe that the total number of deaths are reduced from 55 to 51.

Socially-structured population with shielding and carers

As a second proof of concept we consider now a more complex example in which the population is divided in three age-levels (young, adults and elderly). Starting population values were proportional to Syrian structure, and total population size is 2000. In addition, within each age-level there are two additional classes, healthy and vulnerable. The fraction of vulnerable population within each age class increases with age. Finally, each class is divided by gender. This leads to 12 population classes and 82 epidemiological variables.

We consider again one scenario in which the population is well-mixed, and where there is one infection starting in the class o adult healthy men. The second scenario considers two contact limitations. Firstly, healthy women have contacts only with their respective partners from the class of healthy men. Considering an average number of contacts in the whole population of 20, we reduce the transmission parameters between these subpopulations to 1/20. In addition, we shield the elderly vulnerable classes (male and female) from all the other subclasses except the one of adult healthy women, which will be considered the carers, again with a parameter 1/20.

The death toll for the different subclasses in both scenarios is shown in Fig. 3. Without shielding there is a 61% more deaths, and it becomes apparent that the reduction comes from the shielded population at age 3.

Leftovers

The basic reproduction number [APG, the following section is wrong]

To estimate the basic reproduction number R_0 we note that it is an adimensional quantity composed of three factors: the transmissibility (i.e. the infection between infected and susceptible given there is a contact), the average rate of contacts and the duration of infectiousness. The first two factors are encoded for each population class in the infection rate λ_i . The duration of infection for each class, τ_i , can be estimated as the inverse of the (weighted) average rates of recovery of symptomatic and assymptomatic compartments for each population class:

$$\tau_i = \left(\frac{\sigma_i \gamma_{Ai} + (1 - \sigma_i)(\gamma_{Ii} + \alpha_{Ii} + \eta)}{\sigma_i + (1 - \sigma_i)} \right)^{-1}.$$

Multiplying for each population class $\lambda_i \tau_i$ and summing up we get that $R_0 = \sum_i \lambda_i \tau_i$, or more explicitly:

$$R_0 = \frac{1}{N} \sum_i \frac{\sum_j C_{ij}(\beta_A A_j + \beta_I I_j + \beta_P P_j)}{\sigma_i \gamma_{Ai} + (1 - \sigma_i)(\gamma_{Ii} + \alpha_{Ii} + \eta)}.$$

Since the β parameters are interpreted as the probability of infection *given* that there is a contact, we considered that these values do not differ from what is found in the literature, and we focus on the values of the matrix C_{ij} as the main difference with respect to more developed human settlements. The rational is that the expected increase in the infection rates is driven by an increase in the average rate of contacts due to the crowded living conditions rather than in an increase of the probability of infection. This approximation will allow us to concentrate in the reduction in the average mean of contacts as the main strategy to control the spread of the infection.

More specifically, we factorize the contacts matrix as $C_{ij} = \bar{C} m_{ij}$ with \bar{C} being the average contacts rate of the population in the absence of infection and m_{ij} the management matrix, representing the reduction in the average contacts rate between class i and j due to an intervention in which both subpopulations reduce their



Figure 2: **Population dynamics of healthy and vulnerable subpopulations.** (Top) Well mixed scenario. (Bottom) Average contact between healthy and vulnerable populations are reduced to half their value. Total number of deaths are reduced from 55 to 51.



Figure 3: **Death tolls for a population with a strong social structure.** (Top) Well mixed scenario. (Bottom) A socially-structured shielding strategy is implemented (see Main Text for details). Note the change in the scale between both figures.

contact. In the absence of any intervention, $m_{ij} = 1 \quad \forall i, j$ so if an estimation of R_0 is given and assuming that $\beta_A = \beta_I = \beta_{\mathbb{I}}$ we can estimate the average contacts rate with the expression:

$$\bar{C} = \frac{NR_0}{\beta} \left(\sum_i \frac{\sum_j A_j + I_j + P_j}{\sigma_i \gamma_{Ai} + (1 - \sigma_i)(\gamma_{Ii} + \alpha_{Ii} + \eta)} \right)^{-1}$$