Overview

We used a spatially explicit individual-based model to track a simulated COVID-19 epidemic unfolding in a refugee camp over discrete timesteps that correspond to days. The infection starts in one individual, and is transmitted probabilistically among individuals as they interact during daily activities. The parameters that describe the population and the camp simulate the Moria refugee camp on Lesbos, Greece. The parameters that describe disease progression and transmission are drawn from the literature on COVID-19. The parameters that describe individuals' movements about the camp are heuristic, but our qualitative predictions hold under other reasonable sets of parameter values. We modelled epidemics with no interventions, and epidemics where interventions or combinations of interventions were used to reduce disease transmission. To assess the effect of interevtions, we compared the peak number of infected individuals, the time to peak infection, and the total number of individuals infected, with interventions and in the baseline case.

Throughout this manuscript, we use "Moria" to refer the Moria refugee camp, and "camp" to refer to the camp in our model. We use "person" or "people" to refer to people in Moria, and we use "individuals" to refer to individuals in the model population.

The population

The model population is comprised of 18,700 individuals. Each individual is characterised by its age, sex, condition, and disease state. Condition describes whether an individual is healthy or has a pre-existing condition that increases the risk of severe infection or mortality from COVID-19 (i.e.,). Age, sex, and condition are fixed characteristics. Each individual is assigned an age, sex and condition that matches a randomly selected person from the medical records of the Moria camp. Disease state describes the progression of a COVID-19 infection in an individual, and thus changes over time. The initial disease state for all individuals is "susceptible."

The camp

Each individual is a member of a household that occupies either an isobox or a tent. Isoboxes are prefabricated housing units with a mean occupancy of 10 individuals. Tents have a mean occupancy of 4 individuals. A total of 8100 individuals occupy isoboxes, and 10,600 individuals occupy tents. The exact occupancy of each isobox or tent is drawn from a Poisson distribution, and individuals are assigned to isoboxes or tents randomly without regard to sex or age. This is appropriate because many people arrive at Moria travelling alone, and thus isoboxes or tents may not represent family units.

The entire camp covers a 1 x 1 (e.g., km) square. Isoboxes are assigned to random locations in a central square that covers one half of the area of the camp. Tents are assigned to random locations in the camp outside of the central square. There are 144 toilets evenly distributed throughout the camp. Toilets are placed at the centres of the squares that form a 12 x 12 grid covering the camp. The camp has one food line. The position of the food line is not explicitly modelled.

In Moria, the homes of people with the same ethnic or national background are spatially clustered, and people interact more frequently with others from the same background as themselves. To simulate ethnicities or nationalities in our camp, we assigned each household to one of eight "backgrounds" in proportion to the self-reported national origins of people in the Moria medical records. For each of the eight simulated backgrounds, we randomly selected one household to be the seed for the cluster. We assigned the x nearest unassigned households to that background, where x is the number of households in the background. Thus, the first background occupies an area that is roughly circular, but other backgrounds may occupy crescents or less regular shapes.

Disease Progression

If an individual becomes infected, the infection progresses through a series of disease states (figure #). The time from exposure until symptoms appear (*i.e.*, the incubation period) is drawn from a Weibull distribution with a mean of 6.4 days and a standard deviation of 2.3 days (Backer et al. 2020). In the first half of this period, the individual is "exposed" but not infectious. In the second half, the individual is "pre-symptomatic" and infectious. Fractional days are rounded to the nearest day in discrete-time simulations. After the incubation period, the individual enters one of two states: "symptomatic" or "1st asymptomatic." All children under the age of 16 become asymptomatic (ref), and others become asymptomatic with probability 0.178 (Mizumoto et al. 2020). Individuals remain in the symptomatic or 1st asymptomatic states for 5 days, and are infectious during this period. After 5 days, individuals pass from the symptomatic to the "mild" or "severe" states, with age- and condition-dependent probabilities following Verity and colleagues (2020) and Tuite and colleagues (preprint). All individuals in the 1st asymptomatic state pass to the "2nd asymptomatic" state. Individuals are infectious in these states. On each day, individuals in the mild or 2nd asymptomatic state pass to the recovered state with probability 0.37 (Lui et al. 2020), and individuals in the severe state pass to the recovered state with probability 0.071 (Cai et al., preprint). Recovered individuals are not infectious, and are not susceptible to reinfection. We do not model deaths explicitly, but this is unlikely to affect the dynamics of the epidemic if neither recovered nor dead individuals are infectious.

Infection Dynamics

Infections can be transmitted from infectious to susceptible individuals in four ways: within households, at toilets, in the food line, or as individuals move about the camp. Let p_{idw} denote the probability that susceptible individual i becomes infected on day d by transmission route w, where $w \in \{h,t,f,m\}$ indicates transmission within the household, at toilets, in the food line, or as individuals move about the camp, respectively. The probability that susceptible individual i becomes infected on day d is thus

$$p_{id} = 1 - \prod_{w \in \{h,t,f,m\}} (1 - p_{idw}). \tag{1}$$

Infection within the household. On each day, each infectious individual in a household infects each susceptible individual in that household with probability p_h. Thus, if individual i shares its household with h_{cid} infectious individuals on day d, then

$$p_{idh} = 1 - (1 - p_h)^{h_{cid}}. \tag{2}$$

We set $p_h = 0.5$ in our baseline model.

Infection at toilets. We assume that every individual visits the toilet nearest its household 3 times per day. On each visit, it interacts with the individual in front of it and the individual behind it in the toilet line. If a susceptible and an infectious individual interact, then the infection is transmitted with probability p_a. Thus, the probability that susceptible individual i is infected at the toilet on day d is

$$p_{idt} = 1 - \sum_{j=0}^{6} \binom{6}{j} \left(1 - \frac{t_{cid}}{t_{id}}\right)^{6-j} \left(\frac{t_{cid}}{t_{id}}\right)^{j} (1 - p_a)^j, \tag{3}$$

where t_{cid} and t_{id} are the numbers of infectious individuals and of all individuals, respectively, that share a toilet with individual i on day d. In our baseline model, we set $p_a = 0.1$ following Fang and colleagues (2020).

Infection in the food line. The food line forms 3 times per day. We assume that only individuals without symptoms (i.e., susceptible, exposed, pre-symptomatic, asymptomatic, and recovered) attend food lines. Food is delivered to individuals with symptoms by others, without interaction (e.g., food might be left outside homes). We assume that each individual without symptoms attends the food line once per day on 3 out of 4 days. On other occasions, food is brought to that individual by another individual without additional interactions. For example, food might be brought by a member of the same household, or by a neighbour with whom the individual would otherwise interact (see below). If an individual attends the food line, it interacts with the individual in front of and the individual behind it in the line. Thus, the probability that susceptible individual i is infected in the food line on day d is

$$p_{idf} = \frac{3}{4}\left(1 - \sum_{j=0}^{2} \binom{2}{j} \left(1 - \frac{n_{yd}}{n_{zd}}\right)^{2-j} \left(\frac{n_{yd}}{n_{zd}}\right)^{j} (1 - p_a)^j\right), \tag{4}$$

where n_{yd} is the number of infectious individuals without symptoms (i.e., pre-symptomatic and asymptomatic) in the camp on day d, and n_{zd} is the total number of individuals without symptoms in the camp on day d.

Infection as individuals move about the camp. Individuals move about outside their households, and interact with individuals from other households as they move. We assume that each individual occupies a circular home range centred on its household, and uses all parts of its home range equally. Two individuals may interact if their home ranges overlap. If individuals i and j have home ranges with radii r_i and r_j, respectively, and the distance between their households is d_{ij}, then area of overlap in their home ranges is

$$a_{ij} = r_i^2 \, \mathrm{acos}\left(\frac{d_{ij}^2 + r_i^2 - r_j^2}{2d_{ij}r_i}\right) + r_j^2 \, \mathrm{acos}\left(\frac{d_{ij}^2 - r_i^2 + r_j^2}{2d_{ij}r_j}\right)$$

$$-\frac{1}{2}\sqrt{(-d_{ij} + r_i + r_j)(d_{ij} + r_i - r_j)(d_{ij} - r_i + r_j)(d_{ij} + r_i + r_j)}.$$

(5)

The proportion of time that individuals i and j spend together in the area of overlap is

$$s_{ij} = \frac{a_{ij}}{\pi r_i^2}\frac{a_{ij}}{\pi r_j^2},$$

(6)

and the relative encounter rate between individuals i and j is

$$\frac{s_{ij}}{a_{ij}} = \frac{a_{ij}}{\pi^2 r_i^2 r_j^2}.$$

(7)

To obtain the interaction rate between individuals i and j from the relative encounter rate, we scale by a factor g_{ij} to account for ethnicity or country of origin. In particular, $g_{ij} = 1$ if individuals i and j have the same background, and $g_{ij} = 0.2$ otherwise. Furthermore, we scale the interaction rate such that two individuals with the same background that share an identical home range with a radius of 0.02 interact on average one time per each day. Thus, the daily rate of interaction between individuals i and j is

$$f_{ij} = 0.02^2 \frac{a_{ij}}{\pi r_i^2 r_j^2} g_{ij}.$$

(8)

We assume that only individuals without symptoms interact in their home ranges. Thus, the rate at which individual i interacts with infected individuals in its home range on day d is

$$q_{id} = \sum_j \mathrm{I}(j, d) f_{ij},$$

(9)

where I(j,d) is an indicator function that returns 1 if individual j is pre-symptomatic or asymptomatic on day d and returns 0 otherwise, and the summation runs over all individuals in the model that do not share a household with individual i. The probability that susceptible individual i becomes infected on day d while moving about its home range is thus

$$p_{idm} = 1 - e^{-q_{id}p_a}.$$

(10)

In our baseline model, we assume that females and individuals under the age of 10 use home ranges with radius 0.02, and that males over the age of 10 use home ranges with radius 0.1.

Baseline and interventions

We modelled four different interventions that might be imposed on the baseline model, alone and in combinations: transmission reduction, lockdown, sectoring, and remove-and-isolate.

Transmission reduction. Behaviours including wearing facemasks, frequent handwashing, and maintaining a safe distance from others can reduce the risk of COVID-19 transmission (refs). To simulate transmission reduction interventions, we scaled the per interaction transmission probability p_a in equations (3), (4), and (10) by a factor v_t. In Moria, there is approximately one tap per 42 people, so frequent handwashing (e.g., greater than 10x per day, as in Jefferson et al. 2009) may be impossible. Due to the high population density in Moria (~20,000 people km^{-2}), maintaining safe distances among people may also be difficult or impossible. However, people in Moria have been provided with facemasks. We simulated a population in which all individuals wear facemasks outside their homes by setting v_t = 0.32 (Jefferson et al. 2009).

Lockdown. Some countries have attempted to limit the spread of COVID-19 by requiring people to stay in or close to their homes (ref). This intervention has been called "lockdown." We simulated a lockdown in which most individuals are restricted to a home range with radius r_l around their households. We assumed that a proportion w_l of the population will violate the lockdown. Thus, for each individual in the population, we set their home range to r_l with probability (1- w_l), and to 0.1 otherwise. By manipulating r_l and w_l we simulated lockdowns that are more or less restrictive and/or strictly enforced.

Sectoring. The camp in our baseline model has a single food line, where transmission can potentially occur between two individuals from any parts of the camp. This facilitates the rapid spread of COVID-19 infection. A plausible intervention would be to divide the camp into sectors with separate food lines, and require individuals to use the food line closest to their households. To simulate this sectoring intervention, we divide the camp into an n x n grid of squares, each with its own food line. We replace equation (4) with

$$p_{idf} = \frac{3}{4}\left(1 - \sum_{j=0}^{2} \frac{2}{j}\left(1 - \frac{n_{iyd}}{n_{izd}} \right)^{2-j} \left(\frac{n_{iyd}}{n_{izd}} \right)^{j} (1 - p_a)^j \right), \tag{11}$$

where n_{iyd} is the number of infectious individuals without symptoms (i.e., pre-symptomatic and asymptomatic) served by the same food line as individual i on day d, and n_{izd} is the total number of individuals without symptoms served by the same food line as individual i on day d.

Remove-and-isolate. Managers of some populations, including Moria, have planned interventions in which people with COVID-19 infections and their households will be removed from populations and kept in isolation until the infected people have recovered. To simulate such remove-and-isolate interventions, we conduct simulations in which in each individual with symptoms (i.e., symptomatic, mild case, or severe case) is detected with probability b on each day. If an individual with symptoms is detected, that individual and its household are removed from the camp. Individuals removed from the camp can infect or become infected by others in their household following equation (2), but cannot infect or

become infected by individuals in other households by any transmission route. We assume that individuals are returned to the camp 7 days after they have recovered, or if they do not become infected, 7 days after the last infected person in their household has recovered. By setting different values of b, we can simulate remove-and-isolate interventions with different detection efficiencies.

Simulations

In each simulation, we initialised the model population and camp structure as described above, and we randomly selected one individual to enter the exposed state. We simulated the epidemic by iterating days, and we tracked the disease state of each individual over time. We ran each simulation until all individuals in the population were either susceptible or recovered, at which point the epidemic had ended. We recorded the maximum number of infected individuals, the time to peak infection, and the proportion of the population that became infected in each simulation. When remove-and-isolate simulations were in place, we also recorded the peak number of individuals in isolation, to help assess the plausibility of the intervention.

Figure #. Disease progression.