COVID-19 INDIVIDUAL BASED MODEL WITH INSTANTANEOUS CONTRACT TRACING

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1. Overview

The individual based model (IBM) is for simulating the spread of COVID-19 in a city and to analyse the effect of both passive and active intervention strategies. The model includes demographic data, which control both the dynamics of the interactions of individuals as well as the the outcome of the disease. The disease is spread via interaction between individuals which are remembered to facilitate contact-tracing. Intervention strategies such as self-quarantining, testing and contact-tracing can then be analysed.

2. Demographics

The demographics of the model are based upon UK-wide data for 2018 from the Office of National Statistics (ONS). Individuals are put in one of 3 categories: child (0-17 years), adult (18-64 years) and elderly (65+). Every individual is part of household which forms an important part of each persons daily interactions. We use household size data from the ONS.

3. Interaction Network

Interactions between individuals are modelled via membership of numerous networks which represent peoples daily interactions. The membership of different networks leads to

Demographic Parameters		
Name	Description	Value
`n_total`	Total population simulated	100,000
`uk_pop_0_17`	UK population 0-17 years old (millions)	14.05
`uk_pop_18_64`	UK population 18-64 years old (millions)	40.22
`uk_pop_65`	UK population 65+ years old (millions)	10.04
`uk_house_1`	UK households with 1 person (thousands)	8,198
`uk_house_2`	UK households with 2 person (thousands)	9,609
`uk_house_3`	UK households with 3 person (thousands)	4,287
`uk_house_4`	UK households with 4 person (thousands)	3,881
`uk_house_5`	UK households with 5 person (thousands)	1,254
`uk_house_6`	UK households with 6 person (thousands)	596

Mean daily interactions	
Age-Group	Value
children (0-17 years)	15
adults (18-64 years)	13
elderly (65 years+)	7

Work-place Network Parameters		
Name	Description	Value
`mean_work_interaction_child`	mean number of connections for children	10
`mean_work_interaction_adult`	mean number of connections for adults	7
`mean_work_interaction_elderly`	mean number of connections for elderly	3
`child_network_adults`	fraction of adults in child network	0.2
`elderly_network_adults`	fraction of adults in elderly network	0.2
`daily_fraction_work`	fraction of daily work connections made	0.5
`prob_network_rewire`*	probability of rewiring a connection in the Watts-Stogatz small-world network	0.1

age-group assortativity in the interactions. Previous studies of social contacts for infectious disease modelling has estimated the mean number of interactions that individuals have by age group (Mossong, 2008). We estimate mean interactions by age-group by aggregating this data

Our model contains 3 types of networks. One to represent households, one work-place (for children this would be school) and one random daily interactions.

3.1. **Household Network.** Each individual is assigned to live in a household, with the proportion of people in each household taken from the UK household data (see demographics section). Each day, each person has an interaction with everybody within their household. Elderly people are assumed to live in either 1 or 2 person household with other elderly people, with the ratio of elderly 1 and 2 person households being the same as the general population. Children are assumed to live in household with two adults (so they can only live in 3/4/5/6 person households). The proportion of 3/4/5/6 person with children is the same as the those with adults only.

3.2. **Work-place Network.** Each individual is part of a single work-place network. The work-place networks are Watts-Strogatz small-world networks. There is one network for each age group, with the child and elderly network containing a small proportion of adults (i.e. teachers and carers). When constructing the work-place networks we randomly sort the individuals, so there is no link between the household interactions and the local interactions on the small-world network. Every day each person interacts with a random subset of their connections on their work-place network.

Random Network Parameters		
Name	Description	Value
mean_random_interaction_child	mean number of connections for children	2
mean_random_interaction_adult	mean number of connections for adults	4
mean_random_interaction_elderly	mean number of connections for elderly	3
sd_random_interaction_child*	s.d. number of connections for children	2
sd_random_interaction_adult*	s.d. number of connections for adults	4
sd_random_interaction_elderly*	s.d. number of connections for elderly	3

The difference in the number of interactions for each age group is due to the overall number of daily interactions that each group have

3.3. **Random Network.** In addition to the recurring structured networks of households and work-places, we include a number of random interactions as well. These interactions are drawn each day and are independent of the previous days connections. The number of random connections an individual makes is the same each day (without interventions) and is drawn at the start of the simulation from a negative-binomial distribution. This variation in the number of interactions introduces "super-spreaders" in to the network who make much larger numbers of interactions than the average.

The mean numbers of connections were chosen so that the total number of daily interactions matched that from the social interaction studies. The split between work and random interactions was chosen to be lower in children. Each day a list is made which contains all individuals who make random interactions and each person is repeated by the number of interactions they make. This list is then randomly shuffled and interactions are made between adjacent pairs on the shuffled list.

4. Infection Dynamics

The disease is spread by interactions between infected and susceptible individuals. The probability of transmission is determined by the the status of the infector and the age of the susceptible. Note that the type of interactions (i.e. household, work or random) or the length of the interaction (currently not modelled) is not used in deciding the likelihood of transmission. From early studies of coronavirus and analyses of other epidemics, we know that immediately after become infected an individual is not infectious. The level of infectiousness increase with time and peaks typically 5-7 days after the initial infection before decreasing. Following (??), we model the infectiousness of the time of infection using a gamma function, and the infectiousness on day t after infection is calculated by integrating the gamma function from $t-1$ to t. It has been observed that some people who are infected with coronavirus remain completely asymptomatic and assume that these people are less infectious then those who go on to develop symptoms. Note, there is a difference between somebody who is asymptomatic who will never go on and develop symptoms, as opposed to somebody who is pre-symptomatic who will go on and develop

Infection Parameters			
Symbol	Name	Description	Value
R	`infectious_rate`	mean number of people infected by each infected person	2.5
A_{sym}	-	relative infectious rate of symptomatic	1
A_{asym}	`asymptomatic_infectious_factor`	relative infectious rate of asymptomatic	0.25
μ_i	`mean_infectious_period`	time of peak infectiousness (i.e. the mean of the gamma p.d.f.)	6 days
σ_i	`sd_infectious_period`	width of infectiousness curve (i.e. the s.d. of the gamma p.d.f.)	2 days
s_{child}	`relative_susceptibility_child`	relative susceptibility of child to adult	0.1
s_{adult}	-	-	1
s_{elderly}	`relative_susceptibility_elderly`	relative susceptibility of elderly to adult	1.7
-	`n_seed_infection`	number of individual randomly infected at start of simulation	10

symptoms. The second factor that comes into whether the disease is transmitted is how susceptible the uninfected person is. Data from China show that the children are far less susceptible to the disease than adults and that elderly people are more susceptible, which we model by a simple multiplicative factor based upon the age group of the susceptible. The final formula for the probability of the virus being transmitted in a single interactions as

$$\lambda(t, a_s, b) = \frac{R s_{a_s} A_b}{\bar{I}_{a_s}} \int_{t-1}^{t} f_\Gamma(u; \mu_i, \sigma_i^2) \mathrm{d}u, \tag{1}$$

where $f_\Gamma(u; \mu_i, \sigma_i^2)$ is the p.d.f. of a gamma distribution with mean μ and variance σ^2; t is the number of days since the infector become infected; a_s is the age group of the susceptible; b is an indicator of whether the infector is asymptomatic; and, the other terms are parameters which are in the Infectious Parameters table.

The epidemic is seeded by randomly infecting a small number of individuals at the start of the infection. The infection was assumed to take place on immediately before the simulation starts.

5. Disease Dynamics

Upon infection, an individual enters a disease progression cascade where the outcome and rates of progression are dependent upon age of the infected person (figure 1). The first split is that only a fraction of individual who will develop symptoms, where a fraction (ϕ_{asym}) remain asymptomatic. Those who are asymptomatic are infections (at a lower level, see Infection Dynamics section) and will move to a recovered state after a time

($\tau_{\text{a,rec}}$) drawn from a gamma distribution. Once an individual is recovered we assume that they have immunity and cannot be reinfected.

For individual who will develop symptoms, they start by being in the pre-symptomatic state, where whilst they will be able to transmit the disease to others, they will not be showing any symptoms. This is important for modelling interventions because individuals in this state would not be able self-isolate unless they had been contact-traced (or there was a complete shutdown). After a time (τ_{sym}) drawn from a gamma distribution, the individual develops symptoms, at which case interventions can be triggered such as self-isolation, testing and contact-tracing. Whilst most individuals will only develop mild symptoms, a fraction (ϕ_{hosp}(age)) will go on to require hospitalisation, where the probability of requiring hospital treatment is age-dependent. Those of don't require hospitalisation will recover after a time (τ_{rec}) drawn from a gamma distribution, whilst those who require hospital treatment enter after a time (τ_{hosp}) drawn from a Bernoulli distribution of either 1 or 2 days. Once entering hospital, a number of interventions can take place. We assume that a clinical diagnosis can immediately decide whether the patient is a case so that contract-tracing can be commenced straight away. Of those who enter a hospital, a fraction (ϕ_{death}(age)) will die with the rest recovering. The time to death (τ_{death}) and recovery (τ_{death}) are both drawn from gamma distributions.

The disease state transitions are shown in (figure 1) and the model parameters are in the table Disease Dynamics Parameters.

6. Passive Interventions

The model has the ability to model both passive and active interventions. Here we define an active intervention to be one involving contact-tracing with all other interventions being classed as passive. Interventions are designed to reduce the rate of transmission, however, have the side-effect of potentially quarantining significant numbers of people. We also model the testing process to estimate the number of tests required by different intervention strategies.

6.1. **Hospitalisation.**

Upon hospitalisation, a patient immediately stops interacting with both their household and work-place networks. We also reduce the number of random interactions that they have. One aspect of the disease transmission that we are missing is that within hospitals and interactions with healthcare professionals.

6.2. **Self-Isolation upon Symptoms.**

. The next type of intervention we model is self-isolation upon flu-like symptoms. In addition to those infected by coronavirus, we infect a random a sample of the population each day with non-coronavirus flu-like symptoms. Upon experiencing symptoms, a put a fraction of patients in to self-quarantine immediately. Quarantine is modelled by not interacting with your work-place network and having a much reduced number of connections on your random network. On entering self-quarantine, a coronavirus test is ordered for the following day and a result is delivered the day after. Given the patient is already presenting symptoms, we assume that the test will be 100%.

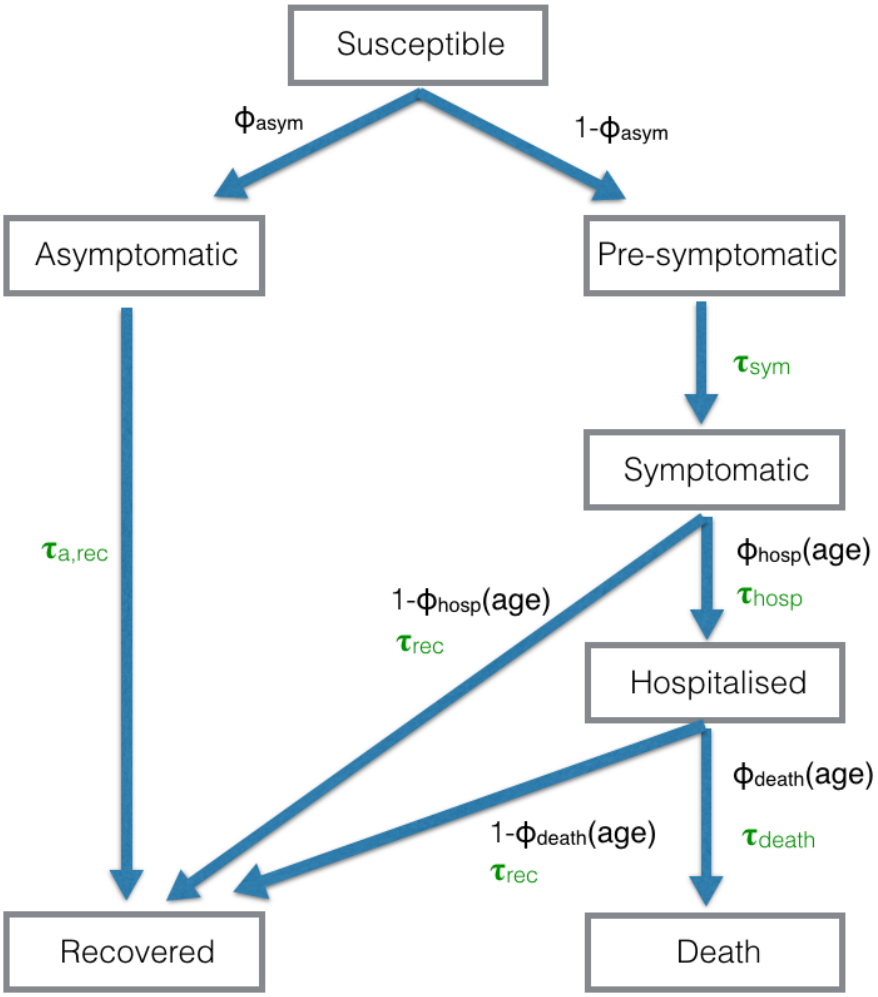

FIGURE 1. The disease status of an individual and the probability and time distribution of transitions. The $\phi_{\text{xxx}}(\text{age})$ variables are the probability of transition to a particular state when there is a choice, where the probability depends upon the age of the individual. The τ_{xxx} are the gamma distributed variables of the time taken to make the transition.

If the result tests positive then the individual remains in quarantine for 14 days (unless they require hospitalisation), otherwise they are released immediately.

Disease Dynamics Parameters			
Symbol	Name	Description	Value
ϕ_{asym}	`fraction_asymptomatic`	fraction of infected who are asymptomatic	0.2
ϕ_{hosp}(child)	`hospitalised_fraction_child`	fraction of symptomatic children hospitalised	0.15
ϕ_{hosp}(adult)	`hospitalised_fraction_adult`	fraction of symptomatic adults hospitalised	0.15
ϕ_{hosp}(elderly)	`hospitalised_fraction_elderly`	fraction of symptomatic elderly hospitalised	0.25
ϕ_{death}(child)	`fatality_fraction_child`	fraction of hospitalised children who die	0.01
ϕ_{death}(adult)	`fatality_fraction_adult`	fraction of hospitalised adults who die	0.04
ϕ_{death}(elderly)	`fatality_fraction_elderly`	fraction of hospitalised elderly who die	0.25
μ_{sym}	`mean_time_to_symptoms`	mean time to symptoms	5.5 days
σ_{sym}	`sd_time_to_symptoms`	s.d. time to symptoms	2.5 days
μ_{sym}	`mean_time_to_symptoms`	mean time to symptoms	5.5 days
σ_{sym}	`sd_time_to_symptoms`	s.d. time to symptoms	2.5 days
μ_{hosp}	`mean_time_to_hospital`	mean time to hospital after showing symptoms	1.6 days
μ_{death}	`mean_time_to_death`	mean time to death once hospitalised	12 days
σ_{death}	`sd_time_to_death`	s.d. time to death once hospitalised	5 days
μ_{rec}	`mean_time_to_recover`	mean time to recover after symptoms/hospital	12 days
σ_{rec}	`sd_time_to_recover`	s.d. time to recover after symptoms/hospital	5 days
$\mu_{\text{a,rec}}$	`mean_asymptomatic_to_recover`	mean time to recover after asymptomatic	15 days
$\sigma_{\text{a,rec}}$	`sd_asymptomatic_to_recover`	s.d. time to recover after asymptomatic	5 days

Passive Intervention Parameters		
Name	Description	Value
mean_random_interaction_child	mean number of connections for children	2
mean_random_interaction_adult	mean number of connections for adults	4
mean_random_interaction_elderly	mean number of connections for elderly	3
sd_random_interaction_child*	s.d. number of connections for children	2
sd_random_interaction_adult*	s.d. number of connections for adults	4
sd_random_interaction_elderly*	s.d. number of connections for elderly	3