Final Phase Epidemic Risk Model *v1.0.0*

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Model definition and state transition diagram

The definition of our model's compartments and state transition diagram inherits intuitions from the literature and adds some variations to better serve to our research goal *(30-33)*. In Figure S1, we show the state transition diagram with compartments as nodes and edges labelled with transition probabilities. Table S1 summarizes the characteristics of compartments with a description of the configurations for simulations.

The first compartment is for **Susceptible (S)** individuals, which could be infected when, in the contact network, a directly connected peer is in an infected state. Infection propagation is modelled starting with a general transmission probability empirically evaluated with respect to the reference scenario (i.e., scenarios considered are: 10, 30, or 50% of total infected at the end of the epidemic (infection attack rate)). This general transmission probability represents the infectivity of a full viral dose, which is present in individuals developing acute symptoms (Acute Infected compartment, discussed in the following). The transmission probability is reduced for individuals in different conditions, namely incubating the infection and with mild or no symptoms.

Logically following the Susceptible state, we have included the **Incubating Infected (II)** state. A state representing the disease incubation time has a long tradition in deterministic and stochastic models in epidemiology *(32)*. Among compartmental models, the standard SEIR dubbed it Exposed *(35)*, which became Latent in other SLIAR models, specifically referring to incubating but not infectious persons *(15, 36)*. Others, like *(37)*, studying the 2002-2003 SARS epidemic, did not consider a specific state for those incubating the disease being not infectious. Instead, they defined an Asymptomatic compartment as the first stage for all susceptible cases turned infected. In that state, persons are infectious and could possibly be quarantined or develop a fully symptomatic state. With respect to our research goal, both these two standard approaches were not suitable. There is no purpose in our model to specify an incubating not infectious state, because irrelevant for the study of the dynamics of infectious individuals being isolated or free to roam their contact network. On the other hand, regarding the current COVID-19 epidemic, some epidemiologists analyzing a sample from the Chinese outbreak have reached the conclusion that individuals could develop infectivity in the incubation period *(19)*. Being this possibility relevant for our study, we have included the Incubating Infectious (II) state with the specific meaning of modelling the time period of infectivity during the disease incubation.

The distinction between symptomatic and asymptomatic infected individuals was originally introduced by *(12)* as an extension of the standard SEIR model, by postulating the fundamental assumption that only the symptomatic cases withdraw with some probability to a restricted place (e.g., home confined, hospitalized). Most recent epidemic models, conveniently customized, are based on that distinction *(35)*. Following the introduction of the two classes for the symptomatic and the asymptomatic cases, models have attempted to manage the different social impacts. In *(35)*, the two new classes are added to represent different forms of social distancing: Generic quarantine for the asymptomatic and specific isolation for the symptomatic. The quarantine

compartment is useful for modelling the dynamic of the contagion when a social distancing policy is enforced by the public health authority (e.g., national/federal state, regional/local authority) in order to limit contacts between casual susceptible persons and undiagnosed infected individuals, untested and often asymptomatic. Differently, symptomatic infected are supposed to be diagnosed and strictly isolated, for example in a medical facility or hospital, within a certain time frame from the outset of symptoms or after a positive test. With respect to our goal, the quarantine state is not strictly needed to study the final phase of the epidemic. What matter most to us is to account for the ability to spread the contagion of all undiagnosed infected individuals, both in case they are free to move or in a regime of limited movements, with respect to those whose infectivity has been diagnosed and contained. Consequently, in our model, we have included two states called **Mild Infected (MI)** and **Acute Infected (AI)** as key for our research goal, because most of current uncertainty about the real extent of the epidemic relies on the former class, whether official communications from national emergency task forces and international organizations refer to the latter. Then we added a single **Contained (C)** state for those individuals infected and isolated. For our research goal, the Contained compartment serves the purpose of modelling those whose ability to spread is greatly reduced by means of personal containment measures, with respect to others without limitations (or only subject to a general social distancing policy).

We make the hypothesis that public health authorities as well as information networks and the press and, in general, public opinion makers, in the final phases of the epidemics will be primarily influenced by the dynamics of the Acute Infected and the Contained classes, as recorded by official statistics, and will be unable to account for risks brought by the mostly unknown Mild Infected class.

The last compartment of our model is the traditional **Recovered/Removed (R)**, which accounts for all individuals that end the epidemic process and have acquired immunization or deceased. In this work, we do not consider the case of re-infection and temporary immunization. One reason is because we explicitly aim to focus on the last period of the first epidemic wave and the potential risks due to undiagnosed infected, therefore we assume that even in case of temporary immunization, the rate of re-infections would be not particularly relevant in that specific time frame. Another reason is that at present, to the best of our knowledge, the possible temporary immunization for COVID-19 patients is still a hypothesis investigated by medical researchers and epidemiologists.

Table S2 lists the state transition probabilities showed in Figure S1 with a description and the values used for simulations. In Figure S2 the state transition diagram is presented with simulation values and assumptions described in Table S2 (e.g., we do not consider the case of AI individuals spontaneously recover without being diagnosed and contained, and the corresponding direct link between states AI and R has been removed).

Model execution

The execution of the model is described in Algorithm 1. Each iteration represents a time step in simulation time. At every time step, each node is selected in random order and, if in state S its state is checked with respect to peers, or if in other states, according to time periods specific of states II, MI, AI, and C. The probability of a node S to become infected depends on infected peers II, MI and AI, independently (μ is the reduction factor to account for reduced viral dose of II and MI). For simplicity, we have not listed here the variation tested with the C class also

infectious. The list of parameters for the initialization of simulations has been presented in Table S3.

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Algorithm 1: Time-discrete multi-agent model execution

Input: Adjacency matrix (A_i,j), selecting random seeds, attributing the T_{II} , T_{MI} , T_{AI} , $T_{C|MI}$ and $T_{C|AI}$ to each nodes according to defined distributions.

for t in Timesteps:
  for i in A_i,j:
    At each timestep t, for all nodes in A_i,j, run the model according to the current node's state.

Case S:
  if i in state S:
    for j in A_i,j and in states (II,MI,AI):
      for each peer in state AI
        With probability p_trans change the state to II.
      end for each
      for each peer in state MI
        With probability μp_trans change state to II.
      end for each
    end for

Case II:
  if i in state II:
    Remain in II for T_II(i) = gamma(α, t_II_mean/α) steps.
    if rand[0,1) < MI/(MI+AI) then change state to MI.
    else change state to AI.

Case MI:
  if i in state MI:
    Remain in MI for T_MI(i) = norm(T_{MI}) steps.
    if rand[0,1) < P(MI,C) then change state to C.
    else change state to R.

Case AI:
  if i in state AI:
    Remain in AI for T_AI(i) = gamma (α, t_AI_mean/α) steps.
    When T_AI(i) expires then change state to C.

Case C:
  if i in state C:
    if at t-1 i changed state from MI:
      Remain in C for T_C(i) = norm(T_C) steps, then move to R.
    elif at t-1 i changed state from AI:
      Remain in C for T_C(i) = norm(T_C) steps, then move to R.
  end for

Case R:
    if i in state R:
      Remain in R.

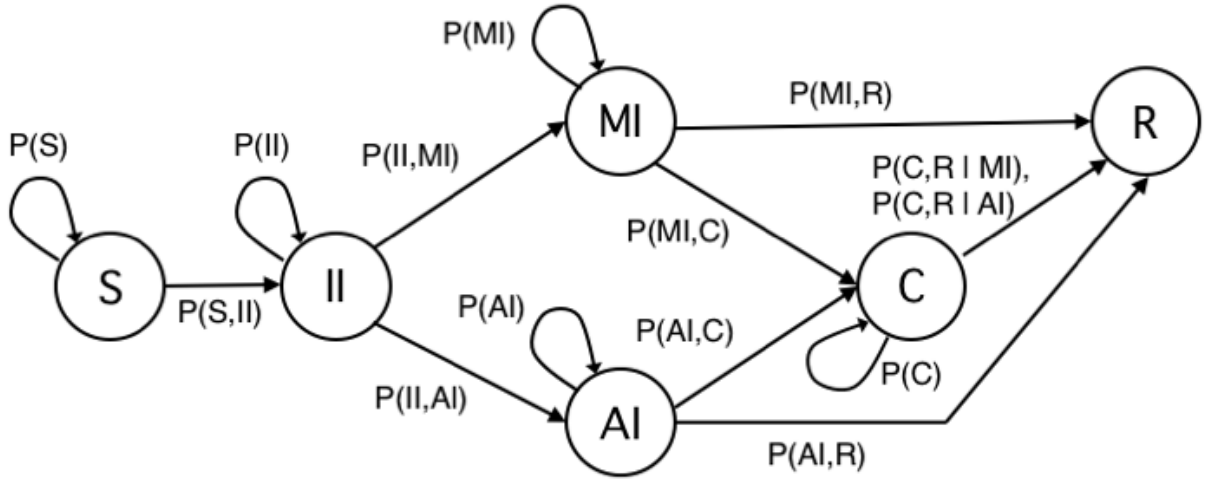

Fig. S1: State transition diagram.

The model consists of six states: *S* (Susceptible), *II* (Incubating Infected), *MI* (Mild Infected), *AI* (Acute Infected), *C* (Contained), and *R* (Recovered/Removed).

For sake of clarity, transition probabilities are showed with a notation different from typical epidemiologic studies, which adopt Greek letters. Here a probability is showed with a single parameter when meant to be the probability to remain in current state (e.g., P(S) is the probability of an agent to remain susceptible); instead, it is showed with two parameters to denote the probability to change state (e.g., P(II,AI) is the probability of an incubating infected node to move in the acute infected state). For all transitions except one, the diagram is a discrete-time memoryless Markov chain. The exception is the state transition from Contained (C) to Recovered (R), which depends on the previous transition, because from epidemiologic studies and medical reports of the COVID-19 pandemics *(15)*, the probability distribution of the recovery time has clearly distinct ranges for individual with mild or acute infection. Choosing a single state C has been done to keep the model as simple as possible, the trivial solution would have been with two distinct C states, for Mild and Acute individuals, with no advantage for our study.

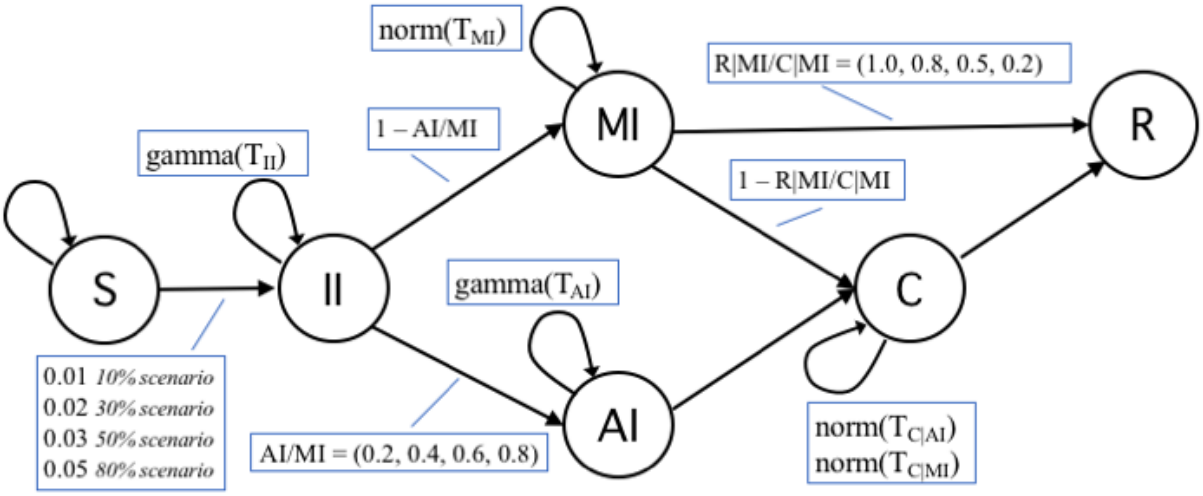

Fig. S2: Main settings for simulations.
In simulations, it has been excluded the case of AI individuals directly moving to Recovered/Removed without being diagnosed and contained. Although that case certainly happened in current outbreaks, we have not found any reliable estimate of its prevalence and considered it as a minor event, with respect to the overall system dynamics.
Specifications in text boxes represent the settings for the specific transitions. In some cases, they are indicated as a probability distribution over a time period (e.g., gamma(T_{II})), as lists of alternative values that have been tested (e.g., 0.01, 0.02, and 0.03 for the transmission probability of Susceptible individuals), or as complements (e.g., 1-R|MI/C|MI, meaning the corresponding list 0.0, 0.2, 0.5, 0.8). For simplicity, in some cases (i.e., for state S, and edges AI-C and C-R), the value has been omitted, being the probability of the complementary state transition, given by the only other outgoing edge of the origin node.

Table S1
Model's compartments with description of characteristics and assumptions for simulations.

Symbol	Compartment	Description
S	Susceptible	The initial state for all individuals in the model except the ones seeding the epidemic. At each discrete time step, individuals interact through the contact network with directly connected peers and could become infected with a certain probability that depends on the number of infected peers and their infected state (II, MI, AI, or, but only for some simulations, C).
II	Incubating Infected	Incubating infected are Susceptible individuals that become infected after the contact with an infected peer. The reason for this state in our model is because there is the possibility that infectivity, although reduced with respect to the symptomatic state, develops in this phase, according to the current medical literature. This is the state assigned to the initial seeding nodes in simulations. Individuals stay in this state according to a probability distribution within a time range (in time steps) derived from the literature.
MI	Mild Infected	Infected persons showing no symptoms or mild symptoms easily interpreted as common cold or flu, or due to the mildness of the condition, reluctant to self-quarantine and look for medical assistance. Persons in this state are assumed to have a reduced biological infectivity with respect to those that develop full acute symptoms. On the other hand, we assume no restriction to the contact network, being them free to entertain all usual social relations or interact with cohabitants (e.g., relatives, roommates). MI individuals could at some point in time be diagnosed and contained or remain undiagnosed until spontaneous recovery. The probability to move to state C is one of the unknown of the model and has been simulated by considering different possibilities. Instead, the probability to move to state R depends on the probability distribution within a time range derived from the literature.
AI	Acute Infected	Infected persons that developed full symptoms and are infectious with the full viral dose. Susceptible individuals have the highest probability to become infected when in contact with AI individuals. On the other hand, we assume that all AIs receive a diagnose within a given time frame, and as a consequence move to state C. The possibility that AI individuals are not diagnosed and thus contained exists in practice, of course, and the state diagram shows the corresponding probability. However, in this work, we have

		considered that case as not relevant for the outcome and discarded.
C	Contained	Infected person that have been diagnosed and then isolated. Our working assumption is that contained individuals have all their social ties removed from the contact network. This is not true in reality, because, for example, hospital propagation especially to medical personnel is certainly not negligible and in some case the seed of new outbreaks. However, we have considered the case of no propagation from individuals in state C as the reference case for simulations. This simplification certainly results in an underestimation of new infections, either MI or AI. We have run some simulations with different probabilities of infection also from C individuals to qualitatively evaluate the possible impact, although at present clear estimates of the prevalence of infections developed from isolated individuals seems still unconfirmed. We have also run simulations starting with the simplified assumption that no MI becomes contained. This represents the *worst-case scenario* for our analysis, the one with the largest number of undiagnosed and not contained infected persons. Beside this case, we have produced simulations with increasing rates of MIs that become detected and thus contained, for example as a consequence of screening campaigns for the asymptomatic population introduced with the emergency response policy.
R	Recovered/Removed	This is the final state of the transition diagram reached by all individuals in our model and depends on the probability distribution within a time range, different in case of MI and AI.

Table S1
State transition probabilities and values used in simulations.

Probability	Description	Values
P(S)	p. to remain susceptible. It is fitted empirically according to the scenario considered, 10/30/50 of total infected resulting at the end of the epidemic with respect to the whole population. P(S) = 1- P(S,II)	0.99 for the 10% scenario 0.98 for the 30% scenario 0.97 for the 50% scenario
P(S,II)	p. to get infected (infection rate). Empirically evaluated, same as P(S). P(S,II) = 1- P(S)	0.01 for the 10% scenario 0.02 for the 30% scenario 0.03 for the 50% scenario
P(II)	p. to remain in incubation state. The probability is defined as the probability distribution over the time range T_{II}	For each node, gamma distribution, gamma(T_{II}), with T_{II} in [2,14] with k = 3 and mean = 8
P(II,MI)	p. to move from the incubation state II to the Mild Infected state. This is the main unknown of this model	Simulations have been run with different frequency values for MI:AI=(0.8:0.2, 0.6:0.4, 0.4:0.6, 0.2:0.8)
P(II,AI)	p. to move from the incubation state II to the Acute Infected state (mostly undiagnosed).	Related to P(II,MI), simulations have been run with frequency values corresponding to 1-MI/AI
P(MI)	p. to remain in state Mild Infected. The probability is defined as the probability distribution over the time range T_{MI}	For each node, normal distribution, norm(T_{MI}), with T_{MI} in [2,7]
P(MI,C)	p. to move from Mild Infected to Contained. It measures the odds of an MI individual to be diagnosed or tested as infected and thus isolated. Our assumption is that the standard case for MI is not to be diagnosed/tested	Our working assumption and worst case scenario is to consider P(MI,C)=0, meaning no MI is isolated. We also run some simulations to test the effect of diagnosing and containing a certain proportion of MI (i.e., 20, 50, and 80% with respect to the MI undiagnosed, are the proportions tested). These are hypothetical values, we are not aware of reliable estimates.
P(MI,R)	p. to recover for a MI individual. The probability depends to P(MI) and P(MI,C)	P(MI,R)=1-(P(MI)+P(MI,C)) For each node, when the number of time steps calculated for P(MI) expires, the state changes from MI to R (under the assumption of P(MI,C)=0)

P(AI)	p. to remain in state Acute Infected before being Contained. The probability is defined as the probability distribution over the time range T_{AI}	For each node, gamma distribution, gamma(T_{AI}), with T_{AI} in [2,7], with k = 3 and mean = 3
P(AI,C)	p. to move from Acute Infected state to Contained. It depends on the value of P(AI)	P(AI,C)=1-P(AI) For each node, when the number of time steps calculated for P(AI) expires, the state changes from AI to C
P(AI,R)	p. to move spontaneously recover from acute infection without being diagnosed. We assume this case as non-existent	P(AI,R)=0
P(C)	p. to remain in Contained state. The evaluation of this probability is different for nodes arrived in state C from MI or from AI, being the time intervals completely distinct for the two cases. The probability then is defined as the probability distribution over two time ranges $T_{C\|MI}$ and $T_{C\|AI}$	For each node, normal distribution, norm($T_{C\|MI}$), with $T_{C\|MI}$ in [2,5] if the node was previously in state MI, or norm($T_{C\|AI}$), with $T_{C\|AI}$ in [14,30] if the node was previously in state AI.
P(C|MI,R)	p. to recover from contained state being mild infected. It depends on the value of P(C) evaluated with respect to $T_{C\|MI}$	P(C|MI,R)=1-P(C) for $T_{C\|MI}$ For each node, when the number of time steps calculated for P(C) expires, the state changes from C to R
P(C|AI,R)	p. to recover (or decease) from contained state being acute infected. It depends on the value of P(C) evaluated with respect to $T_{C\|AI}$	P(C|AI,R)=1-P(C) for $T_{C\|AI}$ For each node, when the number of time steps calculated for P(C) expires, the state changes from C to R
P(R)	p. to stay in Recovered/Removed state. By design of our model, this is the final, fixed state. For simplicity, it was not shown in the state transition diagram	P(R)=1.0

Table S3.
Parameters used in simulations.

Parameter	**Value**
Network size	1000
Seed nodes	5
Timesteps	150
Probability of transmission (full viral dose)	0.01 (10% S.) 0.02 (30% S.) 0.03 (50% S.) 0.05 (70% S.)
Reduction factor (reduced viral dose)	$\mu = 0.5$
Latency time (timesteps)	mean=8 [2,14]
Infectious time - Acute Infected	mean=3 [2,7]
Infectious time - Mild Infected	[2,7]
Isolation period - Acute Infected	[14,30]
Isolation period - Mild Infected	[2,5]
Acute Infected : Mild Infected	(0.2, 0.4, 0.6, 0.8)
Mild Infected Contained : Not Contained	(0.0, 0.2, 0.5, 0.8)