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Agent-Based COVID-19 Simulation Model

Model Specification

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Abstract

To simulate solely the spread of SARS-Cov-2 a variety of methods exists, of which many are probably more suited for prognoses than agent-based models. Yet, in order to to evaluate the impact of policies like tracing, individual-based models are required.

We developed an agent based simulation model to reproduce the current outbreak of COVID-19 in Austria that allows for exploratory analysis of tracing in different characteristics. Aim of this work is the presentation of this model and consequent evaluation and comparison of different policies: Can we achieve containment solely by successful tracing or do we need additional policies? How large is the impact of tracing, keeping in mind that a possibly large number of disease progressions are asymptomatic, yet infectious?

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1 Model Definition

We will explain our agent-based COVID-19 model based on the ODD (Overview, Design Concepts, Details) protocol by Volker Grimm et.al. [23, 24].

1.1 Overview

The modelling of the spread of the disease is based on the interplay of four modules.

1. Population. Altogether the agent-based COVID-19 model is based on the Generic Population Concept (GEPOC, see [14]), a generic stochastic agent-based population model of Austria, that validly depicts the current demographic as well as regional structure of the population on a microscopic level. The flexibility of this population model makes it possible to modify and extend it by almost arbitrary modules for simulation of population-focused research problems.

2. Contacts. In order to develop a basis for infectious contacts, we modified and adapted a contact model previously used for simulation of influenza spread. This model uses a distinction of contacts in different locations (households, schools, workplaces, leisure time) and is based on the POLYMOD study [30], a large survey for tracking social contact behaviour relevant to the spread of infectious diseases.

3. Disease. We implemented a module for the course of the disease that depicts the current pathway of COVID-19 patients starting from infection to recovery or death and linked it with the prior two modules.

4. Policies. Moreover, we added a module for implementation of interventions, ranging from contact-reduction policies, hygienic measures, contact tracing to vaccinations. This module is implemented in form of a timeline of events.

1.1.1 Purpose

The agent-based COVID-19 model aims to give ideas about the potential impact of certain policies and their combination on the spread of the disease, thus helping decision makers to correctly choose between possible policies by comparing the model outcomes with other important factors such as socioeconomic ones. In order to fulfill this target, it is relevant that the agent-based COVID-19 model validly depicts the current and near future distribution and state of disease progression of infected people and their forecasts.

In the following overview of the model, we will not state any parameter values to focus on the model concept. A full collection of model parameters including values, sources and justifications is found in Section 1.3.3.

1.1.2 Entities and State Variables

Each person-agent is a model for one inhabitant of the observed country/region. We describe state variables of a person-agent sorted by the corresponding module.

Population. Each person-agent contains the population specific state variables *sex*, *date of birth* ($\cong$ age) and *location*. The latter defines the person-agent's residence in form of latitude and longitude and uniquely maps to the agent's municipality, district and federal state.

Contacts. Independent on how, where and with whom the person-agent has contacts with, it is assigned an individual scalar *contactivity* parameter that models, how many contacts this agent typically has. This parameter is sampled once at the start of the simulation and remains constant for the whole simulation time. Agents with low *contactivity* have, on average, a smaller number of daily contacts. Moreover each person-agent features a couple of contact network specific properties. These include a *household* and might include a

workplace or a *schoolclass*. We summarise these as so-called *locations* which stand for network nodes via which the person-agent has contacts with other agents. As well as person-agents, locations have their own coordinate which uniquely maps to political regions. Assignment of person-agents to *locations* is based on distance of the agent's residence to the position of the *location*. Each day, an agent has a certain number of contacts within each of the *locations*, which essentially leads to spread of the disease. To model contacts apart from these places, every person-agent has an additional amount of leisure time contacts, which are sampled randomly based on a spatially-dependent distribution. Some loactions are themselves summarised in so-called *location-collections*: Multiple *schoolclasses* and one *workplace* representing teachers are summarised into one *school*, multiple *households* and one *workplace* representing care home workers are summarised to one *care-home*. If a location is part of a location collection, some contacts are scheduled across different locations within the collection. The contact network is schematically displayed in Figure 1.

For disease spread, contacts between infectious and susceptible agents are important. Hereby the disease is transmitted with a certain probability (see Section 1.1.4).

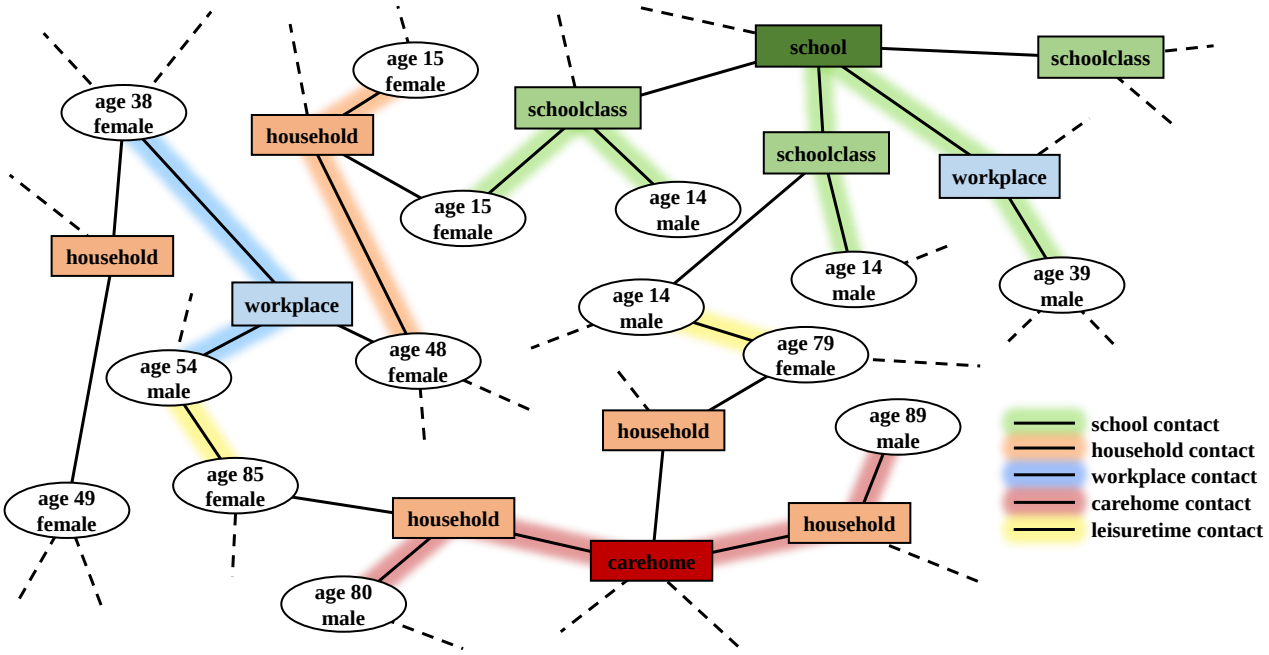

Figure 1: Contact network of agents in the agent-based COVID-19 model. Regular contacts between agents occur via locations (schoolclasses, workplaces and households), location-collections (schools, carehomes), while random leisure time contacts extend the standard contact network.

Disease. In order to model the spread of the disease each person-agent has a couple of health states that display the current status of the agent. They stand for certain points within the patient pathway of an infected person and enable or disable, respectively, certain person-agent actions. The disease states relevant for the simulation dynamics are *susceptible*, *infected*, *infectious*, *detected*, *severity* and *infectiousness*. The prior three are boolean states, that can either be true or false, and multiple of them can be true at a time. The meaning of these attributes is self-explanatory: for example an agent with attribute *detected=true* is detected by a SARS-CoV-2 PCR or antigen test. Note, that we don't consider false positive tests in the model. To decide about the progression of the person-agent's disease a state *severity*, which can be *undetected*, *mild*, *severe* or *critical*, is

sampled as soon as the person-agent becomes infected. Disease state *undetected* states that the agent will have no (asymptomatic) or very mild symptoms, so it is not going to be detected by the standard test regime, states *severe* and *critical* indicate that the person-agent is going to require hospital care. As soon as *infectious=true* the person-agent's contacts become infectious based on a continuous infectiousness curve that depends on the date of infection and the disease severity state (see Figure 2).

To make generation of simulation output easier, we sometimes make use of derived parameters such as *undetected* (=*infected*$\wedge\neg$*confirmed*) or additional book-keeping variables such as infectious contacts per infected. Stating all these would make this documentation unhandy and difficult to read though.

Anyway, more on the influence of the state variables and how they change is described in Section 1.1.4.

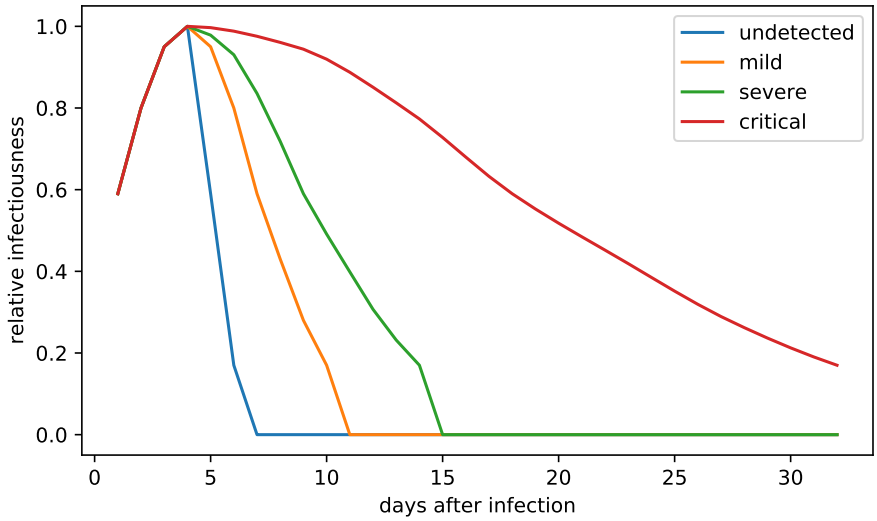

Figure 2: Relative infectiousness n-days after infection dependent on the *severity* state.

Policies. Policies apply either to *locations* or to person-agent-behaviour directly and require additional agent properties. All *locations* except for households are defined *open* or *closed* which marks whether this place is available for having contacts. For person-agents the variable *quarantined* is applied to mark agents isolated not only via a positive test but also due to tracing measures.

For the sake of simplicity of speech we furthermore address mentioned parameters as attributes for the corresponding agents. I.e. an agent with *infectious* set to true will be denoted as "*infectious* agent".

1.1.3 Scales

Unlike other agent-based models it is not possible to validly run the model with a smaller number of agents (e.g. one agent represents 10 or 100 persons in reality) as certain contact-network parameters do not scale this way (average school size,...). Consequently, one simulation run always uses agents according to the size and structure of the full population.

1.1.4 Process Overview and Scheduling

Like the underlying population model, the agent-based COVID-19 model can be interpreted as a hybrid between a time-discrete and a time-continuous (i.e. event-updated) agent-based model:

The overall simulation updates itself in daily time steps, wherein each step is split into three phases. In the first phase each agent is called once to plan what it aims to do in the course of this time step. In the second phase, each agent is, again, called once to execute all planned actions for this time step in the defined order. In the third step, a recorder-agent keeps track of all aggregated state variables.

On the microscopic scope, each person-agent is equipped with its own small discrete event simulator. In the mentioned planning phase, each agent schedules certain events for the future which may, but not necessarily must, be scheduled within the current global time step. In the second phase, the agent executes all events that are scheduled for the currently observed time interval, but leaves all events that exceed this scope untouched.

This strategy comes with the following benefits:

- In contrast to solely event-based ABMs, the event queue is distributed among all agents which massively increases the speed for sorting (a solely event-based ABM with millions of complex agents would not be executable is feasible time).
- Moreover, in contrast to solely event-based ABMs, usage of daily transition probabilities/rates instead of transition times is possible as well.
- In contrast to solely time-discrete ABMs, agents can operate beyond the scope of time steps and sample continuous time-intervals for their state-transitions.

We shortly describe all actions that are scheduled and executed by one person-agent within one time step sorted by the specified module.

Population. As briefly described in [14], agents trigger birth and death events always via time- and age-dependent probabilities that apply for the observed time step (i.e. the observed day). If one of these events triggers, the agent samples a random time instant within the current time step and schedules the event. Note that in contrast to the basic population model, immigration and emigration events are disabled in the agent-based COVID-19 model due to closed borders in reality.

Contacts. Also contact specific events are scheduled and executed within the scope of only one time step. We summarize all contact events planned and executed within one timestep in Table 1.

Table 1: Contacts sampled within one time-step. In addition to the depicted conditions, *quarantined* agents don't have any contacts outside their household, *hospitalised* agents don't sample contacts at all. Moreover, Poi stands for the poisson distribution, c for the individual *contactivity* and dlc, dsc and dwc for *daily leisuretime, school* and *work contacts*

condition(s)	**contact type**	**number of contacts per time-step**	**sampling method**
	household contact	size of household - 1	one with every member
	leisuretime contact	$Poi(c \cdot dlc)$	random in whole agent list, based on regional distribution
agent has *schoolclass* $\wedge$ *schoolclass* is open $\wedge$ *schoolclass* is not quarantined	*school* contact	$Poi(c \cdot dsc)$	fraction randomly in own class, rest randomly in whole school
agent has *workplace* $\wedge$ *workplace* is open $\wedge$ *workplace* is not quarantined $\wedge$ *workplace* **is not** part of *location collection*	*workplace* contact	$Poi(c \cdot dwc)$	randomly in *workplace*
agent has *workplace* $\wedge$ *workplace* is open $\wedge$ *workplace* is not quarantined $\wedge$ *workplace* **is** part of *school* or *carehome*	*school/ carehome workplace* contact	$Poi(c \cdot dwc)$	randomly in whole *school/carehome*
household is part of *carehome* $\wedge$ *carehome* is open $\wedge$ *carehome* is not quarantined	*carehome* contact	$Poi(c \cdot dwc)$	randomly in whole *carehome*

Contact partners for leisure time are drawn based on an origin-destination matrix on municipality resolution. The latter has been gathered from mobile data (see Tables 3-4).

Anyway, planned contacts are always scheduled for the beginning of the new time-step. Hence, interaction between agents is actually limited to the discrete time steps of the simulation. This guarantees, that the states of both involved agents do not differ between the time of the planning of the event and its execution.

Disease. First of all, it is important to mention that the model is not parametrised by a reproduction number R_0 or R_{eff}, but by a contact-specific probability for a transmission in case of a contact. Nevertheless, the agent-based model provides the opportunity to generate estimates for R_0 and R_{eff} by its original definition: the average number of secondary infections of an infected agent. Hence, what comes as model input for many traditional SIR models becomes a model output for the agent-based COVID-19 model.

In case of a contact, *infectious* agents spread the disease to *susceptible* agents with a certain *infection probability*. This probability calculates as a product of three different factors:

$$P(\textit{transmission}) = \textit{base infectivity} \cdot \textit{infectiousness}(t) \cdot \textit{infection intensity}(t, \text{region}).$$

The *base infectivity* relates to R_0 of the disease and stands for the base probability of an infection if not reduced by any other factor. Based on the time and severity of the disease, the infectious agent has a current *infectiousness*. The third factor is a location/region dependent relative *infection intensity* parameter used to calibrate e.g. seasonality effects of adherence.

Anyway, an infectious contact triggers the start of the newly-infected agent's patient-pathway. This pathway describes the different states and stations an agent passes while suffering from the COVID-19 disease and can be interpreted as a sequence of events of which each triggers the next one after a certain sampled duration.

We show this infection strategy in a state chart in Figure 3 and describe how to interpret this figure by explaining the initial steps in the pathway in more detail: As soon as a person-agent becomes infected, its *infected* state is

set to *true*, its *susceptible* variable is set to *false*, and its *severity* parameter is drawn from a given distribution. Moreover, a *latency period* is sampled according to a distribution as well. The corresponding "Infectious" event is scheduled for the sampled time instant in the future. As soon as this "Infectious" event is executed, the *infectious* parameter is set to *true* and a parallel branch that updates the *infectiousness* is started. After the "Finish Incubation" event, the first branch in the patient's pathway decides whether the agent continues being detected by the standard test-regime, or continues undetected due to mild or nor symptoms at all. All other elements of the pathway follow analogously. All branches are evaluated with age-class-dependent probabilities (see Section 1.3.3).

In most cases (i.e. if the agent does not die for any other non-COVID related reason - see Population module), the final state of every agent's disease pathway is the *Recovery/Removal* event with either sets the agent resistant (it is not *susceptible* anymore, or renders it deceased with a certain death-by-COVID probability that depends on the agent's disease severity. Consequently, the model differs between COVID-caused and COVID-affected deaths.

Policies. Every policy is modelled as a global event occurring before the planning phase of any of the simulation time steps. Policies are timed-events that are fed into the model as an event-timeline (see Figure 4). The elements of this timeline may include real policies like closure or opening of locations, start of tracing, vaccination rounds (for a full list, see Table 7), but may also contain incidents that change the model behaviour but are not directly related to policies, such as raising hygiene awareness or seasonality. The most outstanding feature of the model is clearly its ability to model contact tracing policies, since agents are aware of all other agents with which they had contacts. Using simple housekeeping arrays, these can be logged for a certain period of time and used for detection and isolation of contact partners.

Due to the huge flexibility of this strategy, the pool of available policies that can be added and combined in simulation scenarios is huge. In Table 7 the reader finds those which have been included to the canonical main-version of the model and which used for the most fundamental research problems. Some popular model extensions are shortly explained at the end of this document.

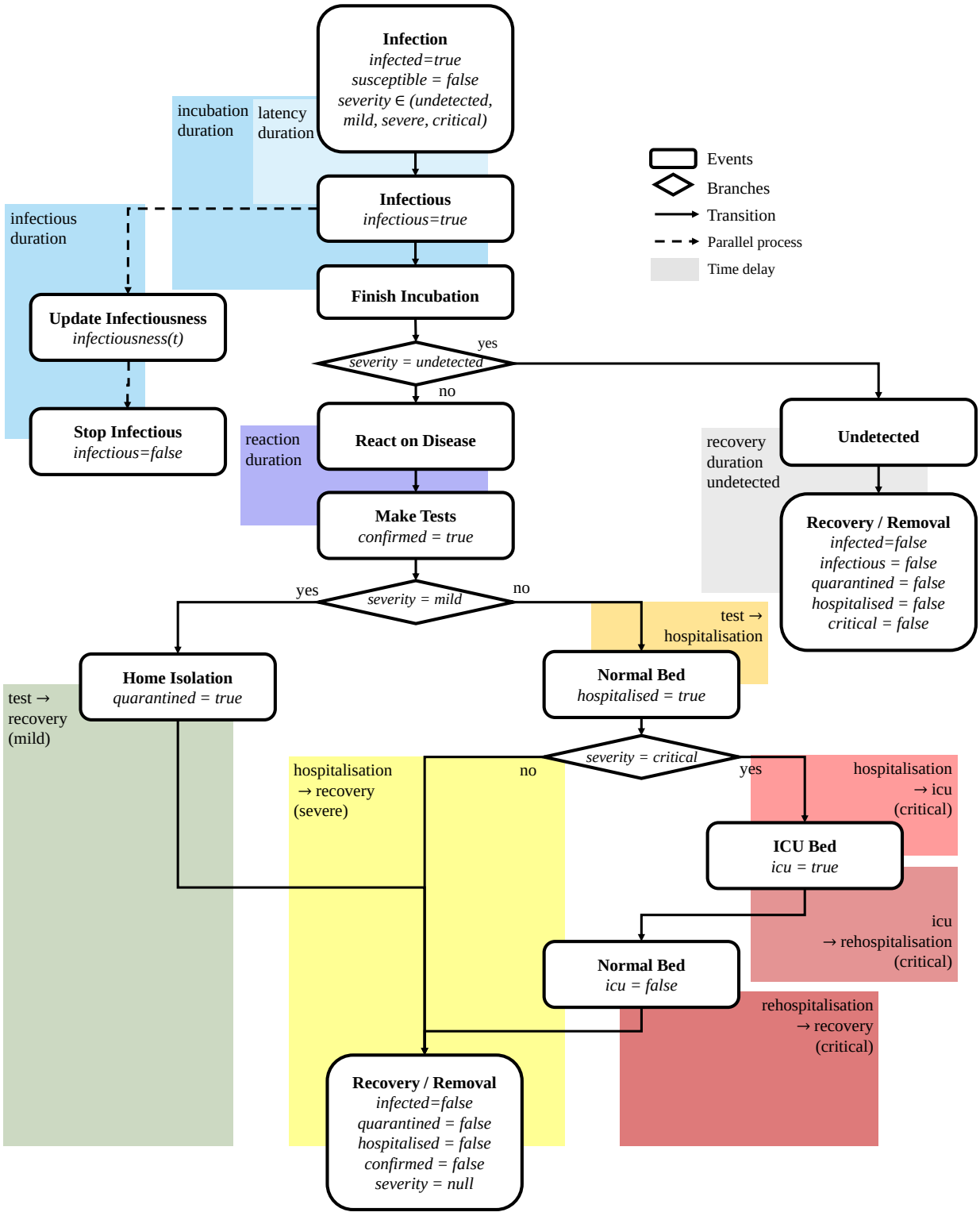

Figure 3: State chart of the patient pathway of a person-agent in the agent-based COVID-19 model. Only those state variables that are changed by the corresponding event are labelled, all others remain at the current value. The initial state of all infection-specific state variables is *false* or *null*, except from *susceptible* which is initially *true*.

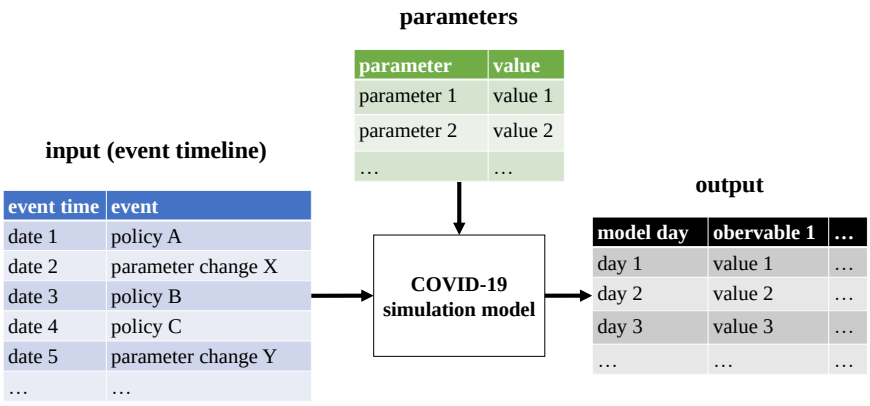

Figure 4: Event-timeline as the input of the simulation model in contrast to standard model parameters.

1.2 Design Concept

1.2.1 Basic Principles.

Increasing the level of detail from a standard epidemiological model for simulation of disease waves to a model that is capable of dealing with various different policies is a huge step with respect to model complexity. It excludes the use of macroscopic strategies and requires modelling of a contact network and contact behaviour. Consequently a detailed demography, spatial components and stochasticity need to be introduced to the model which come with a huge number of additional parameters and parameter values.

Hence, we were very careful that the agent-based model is designed as simple as possible yet tracking the most important features for evaluation of certain policies. Hereby, many details within the pathway of an infected person and, in particular, lots of details within the personal daily routine are simplified to avoid indeterminable model parameters and unpredictable model dynamics.

1.2.2 Emergence.

In addition to the classic emergence of nonlinear epidemiological effects, analysis of the effects of interaction between different measures is one of the key objectives of the model. For example, seemingly unconnected policies like *school closure* and *contact reduction for the 65+* might lead to unexpected effects when applied simultaneously. More generally speaking, the model displays that the individual effects of applied policies do not add up linearly.

1.2.3 Sensing.

Agents' perception of reality is one of the key problems of modelling COVID-19 as no agent is actually aware of its own disease and, more importantly, infectiousness until symptoms occur. Therefore, agent parameters can be distinguished into two sets: the ones the agent is aware of (e.g. *detected*, *hospitalised*), and the ones it is not (e.g. *infected*, *infectious*).

Interestingly, besides the individual perception of agents and the perception of an omniscient observer, there is also a third level of perception included into the model: the perception of the general public. While an individual

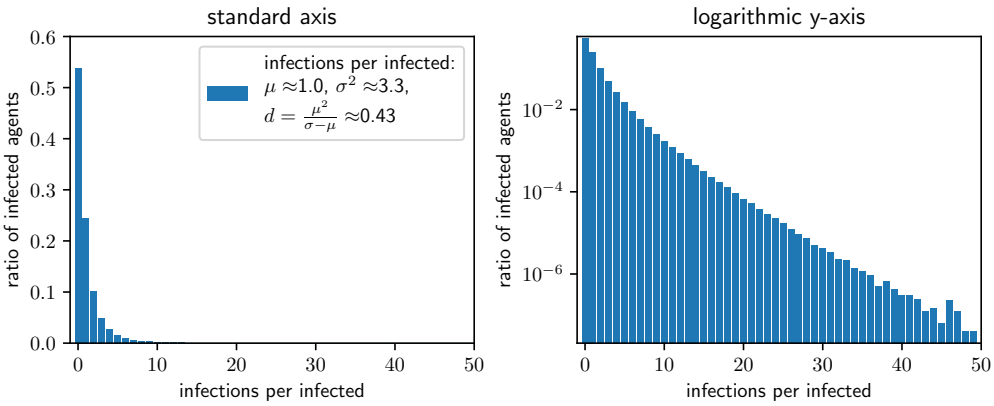

Figure 5: Infections per infected of a fully unconstrained epidemic wave. Note, that such a scenario causes the average number of secondary infections per infected tracked over the whole time-frame (here calculated as μ) to be slightly smaller than 1. The dispersion factor d can be estimated by the stated formula considering mean and variance of the distribution.

agent knows about its symptoms, the public is not yet aware of this additional infected case, until the person-agent has reacted on the disease, has had itself tested and eventually becomes *confirmed*. Consequently, the levels of perception can be sorted with regards to their amount of knowledge:

$$\text{omniscient observer} > \text{person-agent} > \text{general public}.$$

1.2.4 Interaction.

Interaction between agents only occurs in form of contacts at *locations* or *leisure time*. The features provided by the underlying population model make it possible to investigate contacts on a very local level. As described before, *leisure time* contacts are weighted by their regionality, but also *school* and *workplace* contacts depict locality: Using specified latitude and longitude for locations, it is possible to assign person-agents with distance-dependent probabilities (see Section 1.3.1). Consequently, interactions between agents follow a spatially-continuous locally-biased contact network.

1.2.5 Stochasticity.

Basically all model processes, including the initialisation, contain sampling of random numbers. Therefore, Monte Carlo simulation is applied, results of runs are averaged and also their variability is assessed (see Section 2.1).

Yet, besides being time-consuming to flatten, the stochasticity of the model is actually its key strength. It allows to model heterogeneity and skewness of the infection-network which distinguishes the model from classic macroscopic approaches. This specifically refers to the way, how contacts are modeled: Since the person-agent's *contactivity* is initially drawn from a Gamma distribution, the contacts sampled via Poisson distribution result in a so-called Gamma-Poisson mix, which is by definition Negative-Binomial distributed. This strategy allows to directly parametrise the skewness of the contact network to published information on the dispersion factor of COVID-19 clusters (see Figure **??**.

1.2.6 Observation.

Inspired by [31], a recorder-agent takes care about tracking and aggregating the current status of the simulation. At the end of each global time step, all person-agents report to the recorder-agent which furthermore keeps track of all necessary aggregated model outputs. This includes for example *confirmed active cases*, *confirmed cumulative cases*, *hospitalised agents*, *undetected agents*, *incubating agents*, *recovered agents*, *agents in a certain hospital*, or *average-number of contacts per infectious agent*. If required, numbers can also be tracked with respect to age, sex, regional level and/or contact-location.

1.3 Details

Clearly, Section 1.1 could only outline the basic concepts of the model and left a lot of technical and modelling details necessary for a reproducible model definition open. In particular, this refers to the highly non-trivial initialisation process of the model. Hereby, two problems occur that require completely different approaches. The first problem considers the generation of the person-agents, locations and hospitals in the first place. The second problem deals with the initialisation of the status quo of the distribution of the disease states of the agents for the specified initial date.

1.3.1 Initialisation of Person-agents, Locations and Hospitals.

A lot of problems that deal with the sampling of the initial population have already been solved in the original GEPOC model [14]. In particular this refers to the Delaunay-triangulation-based sampling method for locations. We apply this method to merge information from the national statistics institute and the global human settlement layer [21]. Consequently, besides initialisation of the disease states which is described in the next section, only new methods for location- and hospital-generation had to be implemented.

In general, locations and location collections are initialized in a two step mechanism. First, the location / location collection is created with a certain capacity. Secondly, the location / location collection is filled with agents / locations using a regional distribution. Similar to the sampling algorithm for leisure time contacts, an origin-destination matrix on district level gathered from mobile phone data is used in the following way:

1. Filter the agent list for all agents that are suitable for being assigned to the location.
2. Given a certain location in district x and municipality xx, draw a random district y according to the distribution in the matrix.
3. If $x \neq y$, pick a randomly chosen agent from district y. If this fails, return to 2.
4. If $x = y$, a Bernoulli experiment decides to either pick a random agent from xx or from somewhere else in x. If this fails, return to 2.

For location collections, we follow more-less the same strategy, with suitable locations instead of agents. We go into more detail about sampling and filling having a look at the specific location types:

Households are initialised given a discrete distribution of their sizes and household members. We hereby distinguish between five groups: children ($age < 18$), male and female adults ($18 - 64$) and male and female retired (65+). The number of households is created on demand, so that every person-agent can be assigned a household eventually. Household coordinates are drawn according to the same algorithm as creation of person-agents. and they are filled, as explained above. After a household is successfully filled, all coordinates of all household members are set manually to the coordinate of the household.

Workplaces[1] are initialised with a certain capacity by a *workplace-sampler* based on district-level data about branches of industry. Given the district, the coordinate is sampled re-using the mentioned sampler for person-agent coordinates. Note, that the workplace is hereby also assigned a certain occupation which will be required for sampling of *carehome* and *school workplaces*. Filling of workplaces works analogous to households, yet coordinates of person-agents remain unchanged.

Schools and schoolclasses are initialised based on known distributions w.r.t. average school size and number of pupils in total. We distinguish between schools for children below 14 and older. A *school-sampler* iteratively generates school and a assigns a random number of new created schoolclasses (triangular distribution) wit fixed capacity. The process is repeated until the sum of all schoolclass capacities matches the known number of pupils in reality. In a next step, each school is assigned one of the created workplace with branch "teaching" and the school's coordinate is set to the coordinate of the workplace. In a next step, classes are filled with the same algorithm as workplaces. Clearly, the number of model agents in the group of agents below 18 is larger than the number of pupils. Consequently, we force distribution of all 6 to 14 year old agents, and distribute as many 15 to 18 year old agents as possible. All remaining 15 to 18 year old agents are considered to be working or unemployed.

Care-homes are generated with a fixed size and providing space for a fixed number of inhabitants. Analogous to schools, every carehome is assigned a workplace with the corresponding branch and coordinates are harmonized. Furthermore, suitable households are assigned using the mentioned filling algorithm.

Finally, hospitals are generated based on publicly available data. This includes capacities (beds, intensive-care units) as well as their location (latitude and longitude).

1.3.2 Initialisation of the Disease State

The spread of SARS-CoV-2 displays probably better than any other system, that the most dangerous enemy is the invisible one. While confirmed infected persons are detected and well known, they hardly contribute to the spread of the disease – they are already isolated properly, and most infections occur even before the onset of symptoms.

Consequently, it is not possible to simply "start" the simulation with a certain number of confirmed cases, acquired for example from official internet sources. Valid values for pre-symptomatic (e.g. persons within latency and incubation period) and asymptomatic persons need to be acquired as well – yet, this number is hardly measurable in reality.

In order to solve this problem, a three stage concept, henceforth denoted as initialisation phase, was designed to generate a feasible initial state for a certain time t_0:

1. **Initialise-Simulation.** The agent-based COVID-19 model is set up with a small number of initially infected agents (40 was found to be the most stable and useful option). This number corresponds to an estimated count of initial infection clusters in the country, but actually hardly influences the outcome. Furthermore, the agent-based simulation is run and interrupted by a state event, namely if the cumulative number of *confirmed agents* in the model is greater or equal to a specific value $C(t_{-1})$. Hereby, t_{-1} refers to a self chosen point in time and $C(t_{-1})$ to the reported number of positive tests in reality until t_{-1}. Hereby t_{-1} must be chosen properly so that the reported number of positive tests is large enough to be representative yet before implementation of any policies.

   As soon as the simulation is interrupted by the state-event, the timelines of simulation and reality are synced: t_{-1} in reality becomes t_{-1} in the simulation.

[1] Workplaces should not be confused with total companies. They rather represent the different teams where the members are in regular contact with each other.

The initialise-simulation is continued, considering all policies that have been implemented in reality, until, finally, t_0 is reached. Properly calibrated by a calibration routine (see Section 1.3.4), the initialise-simulation contains approximately the same cumulative number of *confirmed agents* as the corresponding reported number in the real system.

The initialise-simulation is finished by exporting parts of the final state of the simulation. This refers to all households that contain either infected or recovered agents which are finally written into a file. Hereby, an initial population is generated that contains not only a valid approximation of the confirmed cases, but also a valid estimate for the unknown pre-symptomatic and asymptomatic persons, a correct distribution of their future planned events and a correct household distribution as well.

2. **Fine Tuning.** Even with best calibration routines (see Section 1.3.4) it is not possible to perfectly match the model output with the status quo in reality, in particular w.r.t. regional distribution. Therefore, a bootstrapping algorithm was implemented that corrects the small differences between the initialise-simulation output and the real data (confirmed cases, hospitalisation, intensive-care units and recoveries per region) to make sure, that the initial state of the actual simulation matches the current state precisely. This step can be omitted, if matching the current state precisely is not required.

3. **Load Households.** Finally, the actual simulation is initialised with the previously recorded and fine-tuned agents from the initialise-simulation. To be precise, this process does not only include agents themselves, but also the *households* these agents live in. Hereby, the fundamental network structure from the initialise-simulation can be maintained.

1.3.3 Parametrisation

With respect to parametrisation, we will distinguish between model input and model parameters.

Classical model parameters specify scalar or array-typed model variables that are initialised at the beginning of the simulation and, if not changed by certain model events, keep their value for the entire simulation time. Examples are the infection probability of the disease, the age-dependent death rate of the population, or the distribution parameters of the recovery time.

In contrast to model parameters, the model input consists of an event-timeline that describes at which point in time a certain incident changes the behaviour of the model. This incident usually refers to the introduction of a policy, e.g. closure of schools or start of tracing, but may also refer to instantaneous changes of model parameters which are related but cannot be directly attributed to policies, e.g. the increase of compliance among the population to increase hygiene.

In the following, we state lists of used parameters and parameter-values including corresponding sources and/or justifications. They are found in Tables 2 to **??**. Table 7 states a list of possible event-timeline elements that can pose as the model's input.

Table 2: List of population specific parameters

parameter	description	value	source
birthrates, *deathrates*, *initial population*, *regional distribution*	parameters used by the underlying population model	see source	rates and population tables from Austrian National Statistics Institute [9]. Maps from the Global Human Settlement Project [20] and [4].

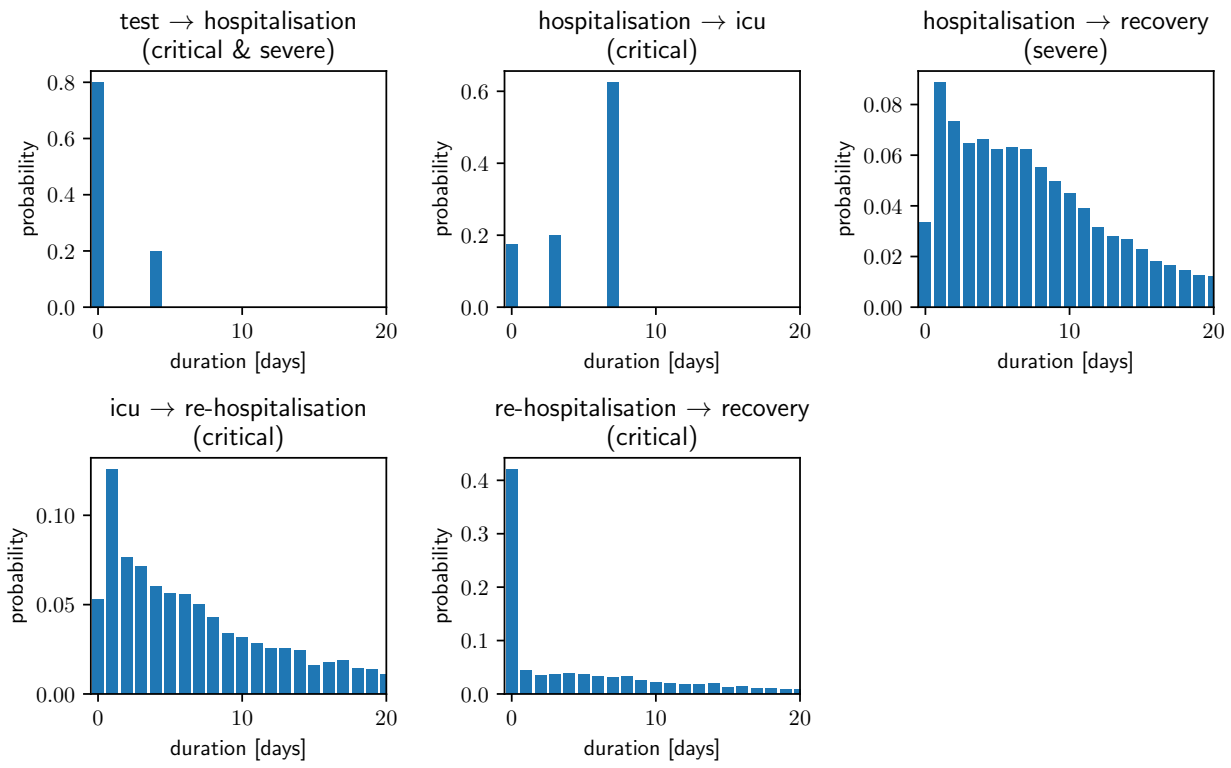

Figure 6: Duration distributions between different disease states regarding hospitalisation.

1.3.4 Calibration

Clearly, there is no valid data available for direct parametrisation of the *base infection probability* parameter which is (next to *infection intensity* and the) the most fundamental of the three factors that decide about a transmission in case of a direct contact. First of all, this parameter is hardly measurable in reality and moreover strongly depends on the definition of "contact". Consequently, this parameter needs to be fitted in the course of a calibration loop.

The calibration experiment is set up as follows:

1. We vary the parameter *infection probability* using a bisection algorithm.
2. For each parameter value, the simulation, parametrised without any policies, is executed ten times (Monte Carlo simulation) and the results are averaged.
3. The average time-series for the *cumulative confirmed cases* is observed and cropped to the beginning upswing of the epidemic curve, to be specific, all values between 200 and 3200. In this interval the growth of the curve can be considered as exponential.
4. The cropped time-series is compared with the corresponding time-series of real measured data in Austria, specifically the confirmed numbers between March 10^{th} and 20^{th} 2020 (source EMS system, [2]).
5. Both time-series are compared w.r.t. the average doubling time of the confirmed cases. The difference between the doubling times is taken as the calibration error for the bisection algorithm.

Note: As the sample standard deviation of each observable of the runs has been observed to be at most a fifth of the sample mean, the iteration number of nine for the Monte Carlo simulation has been considered to be sufficient for calibration purposes w.r.t. the ideas in [15, 26].

After calibrating the infection probability parameter, also the parameters of the input timeline of the initialisation-simulation needs to be calibrated to the policies applied in the real system. For this, we split the events in the policy timeline into three types:

- Events that can be modelled and parametrised directly (e.g. closure of schools)
- Events which impact needs to be estimated (e.g. reduction of leisuretime contacts)
- Events that do not directly related to policies, but represent other influences. These are summarized as *infection intensity* events.

We do not regard the first two events in an automatic calibration routine, but model and parametrise them as well as possible using given information about active policies and expert opinions. To guarantee the fit of the model, we focus on iteratively adding events of the third type.

Analogous to the *base infectivity*, this is done iteratively using a bisection algorithm as well.

1. Define a date x of the first *infection intensity* event.
2. Vary the region-dependent (federal-states/ or districts) value of the event using a bisection strategy, knowing, that 1 is an upper and 0 is a lower bound of the parameter value.
3. Evaluate the impact of the event, by comparing the modelled detected cases (Monte Carlo simulation) with the officially reported ones on $x + 14[d]$.
4. After sufficiently many iterations, set $x \leftarrow x + 14[d]$ and continue with the next time-period, until the current day (i.e. the day where we want to start the actual simulation) is reached.

2 Model Implementation

Simulation of agent-based models like the agent-based COVID-19 model is a huge challenge with respect to computational performance. As the model cannot be scaled down, almost 9 Million interacting agents need to be included into the model in order to simulate the spread of the disease in Austria.

These high demands exclude most of the available libraries and software for agent-based modelling including AnyLogic [22], NetLogo [33], MESA [28], JADE [12] or Repast Simphony [32]. Most of these simulators cannot be used as their generic features for creating live visual output generates too much overheads.

Consequently, we decided to use our own agent-based simulation environment ABT (Agent-Based template, see [3]), developed in 2019 by dwh GmbH in cooperation with TU Wien. The environment is implemented in JAVA and specifically designed for supporting reproducible simulation of large-scale agent-based systems.

The next section contains more technical details about the implementation.

2.1 Technical Implementation Details

The implementation of the agent-based COVID-19 model uses JAVA 11 and applies the *UniformRandomProvider* random number generator (RNG) by Apache Commons [1]. This RNG implements a 64 bit version of the Mersenne Twister [29] and exceeds the standard RNG of JAVA, a simple Linear Congruential Generator, in both performance and quality.

The simulation itself is always executed in a Monte Carlo setting and several runs with different RNG seeds are averaged. Due to the huge number of agents, a Law-of-Large-Numbers-effect can be observed (similar to [13] Chapter 5.2), and the standard deviation of the model output is always comparably small. Consequently, Monte Carlo replication numbers of 10 to 20 are usually enough to estimate the mean sufficiently well (we apply the algorithms from [15, 26]).

3 Features and Limitations

Due to the highly flexible policy timeline, the model is capable of testing and combining lots of different policies in different characteristics at different times. Hence, it can easily depict almost any specified policy announced in reality, if estimates for the policy parameters are available.

The latter statement particularly refers to combination of policies: although the model correctly depicts the epidemiological impact of the combination of policies, the social impact needs to be parametrised manually. For instance, the causal relation between closed schools and intensified parent-children contacts needs to be parametrised and is not given by the model dynamics.

Unfortunately, as the model cannot be scaled down, a huge number of agents lead to long computation times, and the necessity of Monte Carlo simulation for flattening of stochastic results increases the time required to get simulation output even further. Consequently, the simulation's capabilities of dealing with multi-variate calibration problems are limited. Consequently, the model is well capable but unhandy to generate (short-time) prognoses.

4 Model Extensions

Since the model is actively used within decision support in Austria, a couple of model extensions needed to be implemented on direct demand. In this section, we roughly explain the most important of these extension modules.

4.1 Vaccination Planner

Purpose. By Summer 2020, the model has been used to council the Austrian vaccination planning board. Hereby the model was put in the loop of an optimization routine to generate an optimal vaccination prioritization plan. The reader is referred to [25] for more information.

Model. We regarded five target groups for *vaccination round events* (elderly, mid-age, young, health-care workers, vulnerable). To depict the latter, additional relevant co-morbidities were distributed among the agents.

Data. We used freely available published data from different sources. The reader is referred to [25].

4.2 Tourism

Purpose. In the time span of the big COVID-19 waves in Austria, the fraction of SARS-CoV-2 infected persons travelling to Austria from other countries has been negligible small due to strict quarantine laws. Yet, over the summer months, case numbers in Austria reached very low levels, so that imported cases could not be neglected anymore. To maintain our duty to calculate short time prognoses for the ministry of health we added a tourism module.

Model. Each model time-step a certain number of randomly chosen uninfected agents are set to infected. This infection happens without any infectious contact with infected agents within the country, thus modelling disease transmissions outside the system boundaries.

Data. We used freely available tourism data from the national statistics institute Statistik Austria [5] and calibrated the total number of imported cases.

4.3 Mass-Testing

Purpose. In winter 2020 the Austrian government started a "mass-test" initiative in which a broad cross-section of the country's inhabitants were tested for SARS-CoV-2 infections. Hereby, undetected and spreading CoV infected person should be made visible and put under quarantine. Our goal was providing estimates for the impact of this policy.

Model. Mass tests are modelled as an additional event type that can be used in the event timeline as model input. As soon as the event is triggered, a certain number/fraction of inhabitants is tested for SARS-CoV-2. If an unconfirmed/pre-symptomatic infected agent is found hereby, it is set to confirmed and isolated.

Data. We used official data for test sensitivity and test specificity and varied the number of participants.

4.4 Mutants

Purpose. By Spring 2021, different more infectious variants of the virus start to spread around the world, in specific the B.1.1.7 lineage replaced the previous variants in Austria. To model this replacement process, different virus variants have been implemented.

Model. A transmission occurs with a virus-strain-dependent probability and the virus strain is transmitted. An additional event to introduce a new strain in the country was implemented.

Data. We calibrated the excess infectivity of the strain from publicly available variant-surveillance data sources in Austria provided by AGES [2].

4.5 SEIR→ SEIRS

Purpose. By Spring 2021 first data about re-infections became available. Since, the question about impact of the immunization level of Austria are highly important, the possibility for re-infections could not be neglected anymore.

Model. A recovery from the disease renders the agent immune for a limited time-span only.

Data. The model was calibrated to official data for re-infections (Epidemiologisches Meldesystem by AGES [2]).

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Table 3: List of contact specific parameters (1/2). Note that all parameter values are specified for the standard model without policies. The Γ-distribution is given as $\Gamma(k, \theta)$.

parameter	description	value	source
contactivity (henceforth *ct*)	individual parameter to scale the average number of contacts per day, to ensure the skewness of the contact-network	$X \sim \Gamma(0.6, 1/0.6)$	calibrated to match a network dispersion factor of 0.43 as published in [6]
leisure time contacts per day	number of leisure time transmission-relevant contacts of an agent per day	$X \sim Poi(ct \cdot 6.11)$	based on the results of the POLYMOD study [30]
workplace contacts per day	number of transmission-relevant contacts at work (if assigned) of an agent per day. Same values used for care-home contacts.	$X \sim Poi(ct \cdot 5.28)$	based on the results of the POLYMOD study [30]
school contacts per day	number of transmission-relevant contacts at school (if assigned) of an agent per day	$X \sim Poi(ct \cdot 4.64)$	based on the results of the POLYMOD study [30]
contact in other class probability	probability of a pupil to draw a contact partner from the whole school and not only its own class	10%	Estimate
household sizes and structure	distribution of household sizes and structure	see source	distribution and structure from freely accessible tables for household statistics from the Austrian National Statistics Institute [9]
school class sizes	Capacity of school classes	20 for schools with pupils below 14, 23 otherwise	gathered from a publication of the Austrian National Statistics Institute [10]
school sizes	The actual number of schools and pupils were gathered to calculate the average number of classes per school. Based on this average, the class-capacities of schools in the simulation are sampled with triangular distribution.	$X \sim Tri(\mu/3, \mu, 5\mu/3)$, with $\mu = \frac{pupils}{schools}$	counts gathered from a publication of the Austrian National Statistics Institute [10]. Bounds for triangular distributed were estimated.
workplace sizes	discrete distribution of workplace sizes	see source	gathered from a survey [11] by the Austrian National Statistics Institute
workplace branches	Industrial branch parameter of the *workplace*. We distinguish 21 branches according to the top level code of the ÖNACE 2008 norm. Two additional branches, care-home workers (Q.86) and teachers (P.85.2-4), were added for obvious reasons	see source	Austrian National Statistics Institute (see [7] for federal-state data, data on district level behind paywall)
care-home units	The actual number of care-homes w staff and residents were gathered to calculate the number of care-home units given a maximum capacity of 20 residents	see source	counts gathered from freely accessible tables from the Austrian National Statistics Institute [8]

Table 4: List of contact specific parameters (2/2). Note that all parameter values are specified for the standard model without policies.

parameter	description	value	source
regional sampling of leisure time contacts	leisure time contact partners are sampled based on origin-destination matrices on municipality level	Average fraction of all stays of persons from municipality X within municipality Y for all municipalities X and Y of Austria	gathered from mobile phone data evaluated for January 2020
regional distribution of schools, workplaces and carehomes	schools, workplaces and carehomes are created based on known information about workers, teachers and carehome employees per district. The actual coordinate in the district is sampled using the sampling algorithm of the underlying population model		see Table 2 and *workplace branches* in Table 3
regional assignment of schools, workplaces and carehomes	inhabitants of schools, workplaces and carehomes are assigned based on origin-destination matrices on district level	Average fraction of all stays of persons from district X within district Y for all district X and Y of Austria	gathered from mobile phone data evaluated for January 2020

Table 5: List of disease specific parameters (1/2).

parameter	description	value	source
base infection probability	probability that a contact between a susceptible and an infected agent leads to a transmission.	$\alpha = 0.057$	calibrated based on the doubling rates in Austria before introduction of policies (see Section 1.3.4).
infection intensity	Location and region dependent factor that scales the infection probability in case of a contact. Usually modified by calibration using *infection intensity events*.	Base setting: Same for all regions, 1 in all locations except households, 5 in households	see Section 1.3.4.
infectiousness curve	models the virus load in an infectious agent as a severity-dependent function of time, that scales the infection probability in case of a contact	see Figure 2	merged information about the shedding duration from [17] and qualitative information about the shape of the curve from [**?**]
incubation time	time between infection and symptom on-set	scaled β distribution with $min(X) = 2[d]$, $max(X) = 14[d]$, $\mathbb{E}(X) = 5.1[d]$	based on [27]
reaction duration	time between symptom on-set and testing of the agent which furthermore leads to its confirmation and home isolation	Updated regularly, most recent values $X \sim \text{Gamma}(1.75, 1.45)[d]$	processed from officially reported data (Epidemiologisches Meldesystem [18])
delays (mild, severe, critical)	durations between different points in the disease pathway of agents. That is: test $\rightarrow$ recovery, test $\rightarrow$ hospitalisation, hospitalisation $\rightarrow$ icu, icu $\rightarrow$ re-hospitalisation, hospitalisation $\rightarrow$ recovery, re-hospitalisation $\rightarrow$ recovery	see Figure 6	gathered from Austrian hospitalization records (not public, see also [16])
recovery time unconfirmed	time between symptom on-set and recovery for unconfirmed persons (usually asymptomatic)	$Tri(1, 5, 7)[d]$	based on expert opinions
recovery time home-quarantined	time between test and recovery for confirmed infected persons with mild disease	$Tri(7.5, 10.5, 15.5)[d]$	based on expert opinions

Table 6: List of disease specific parameters (2/2).

parameter	description	value	source
detection probability	probability of an infected person to get detected by a test	continuously updated; current values:[8, 34, 45, 39, 41, 42, 28, 25, 43, 68]% for 10 year age-classes	Age distribution is gathered by comparison of Austria's age pyramid with the distribution of the confirmed cases. The overall detection probability for Mar-Jul is calibrated to 35% as suggested by a Austrian trial in autumn 2020 [5].
hospitalisation probability	age-dependent probability that a detected patient requires hospitalisation	2020, continuously updated; current values: [6, 1, 2, 2, 7, 10, 26, 48, 61, 53]% for 10 year age-classes	Distribution is based on comparison of the age distribution of confirmed cases with the age distribution of hospitalised cases (Epidemiologisches Meldesystem [18]).
icu probability	probability that a hospitalised agent becomes critical (needs an intensive care unit)	16.6%	calibrated for Austrian ICUs with data from the ministry of internal affairs
death-by-COVID-19 probability - unconfirmed	probability that an unconfirmed infected agent dies due to COVID-19	0%	No data is available. Moreover, unconfirmed COVID-19 cases are typically asymptomatic.
death-by-COVID-19 probability - mild	probability that a non-hospitalized (mild) infected agent dies due to COVID-19	continuously updated; current values: [0.0, 0.0, 0.0, 0.0, 0.1, 0.5, 1.9, 6.1, 18.1],]% , for 10 year age-classes	Distribution is based on comparison of the age distribution of confirmed non-severe and non-critical cases with the age distribution of fatal cases (Epidemiologisches Meldesystem [18]).
death-by-COVID-19 probability - severe	probability that an infected agent requiring a normal bed (severe) dies due to COVID-19	continously updated; current values: [0.0, 0.0, 0.0, 0.0, 0.0, 1.0, 11.3, 16.8, 25.8]% ,for 10 year age-classes	Distribution is based on comparison of the age distribution of confirmed severe cases with the age distribution of fatal cases (Epidemiologisches Meldesystem by AGES [18]).
death-by-COVID-19 probability - critical	probability that an infected agent requiring an ICU bed (critical) dies due to COVID-19	continuously updated; current values: [0.0, 0.0, 0.0, 0.0, 1.5, 1.2, 8.3, 12.8, 12.5, 42.8]%, for 10 year age-classes	Distribution is based on comparison of the age distribution of confirmed critical cases with the age distribution of fatal cases (Epidemiologisches Meldesystem [19]).

Table 7: List of possible event-timeline elements that can pose for the model's input including their effect and, if available, options for the event parametrisation.

event	description	parameters
infection intensity	Multiplies to the the *infection probability* for contacts in a certain locations or regions. Represents seasonality or adherence caused changes in the infectivity of the disease. This event is usually used for calibration of the model to real-data.	affected location type; affected region; factor to scale the original *infection probability* with
leisure-time contact number reduction event	Based on an age-class (child, adult, retired) and/or region (municipality, districts, federalstates) dependent probability, an agent may "reject" a leisure-time contact with a different agent. As the rejection happens symmetrically, the probabilities multiply.	affected region; age-class-dependent fraction by which daily leisure-time contacts are reduced
location closing event	Fraction of locations of a certain type are closed in this policy.	affected location type; fraction of locations of this type that remain open / are opened
start location tracing event	Starts with location tracing measures. I.e. all members of a newly *confirmed* agent's location are put under preventive isolation for a certain period of time.	affected location type; length of preventive quarantine length
start contact tracing event	Starts with contact tracing measures. I.e. recorded contacts of a newly *confirmed* agent are put under preventive isolation.	fraction of agents capable of recording contacts; length of preventive quarantine length
vaccination round event	Distributes a number of given vaccine doses of a certain type to capable model agents	number of doses; type of vaccine (e.g. first or second dose); target groups; vaccine effectiveness and time delay