Development of an interactive, agent-based local stochastic model of COVID-19 transmission and evaluation of mitigation strategies illustrated for the state of Massachusetts, USA

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Abstract

Since its discovery in the Hubei province of China, the global spread of the novel coronavirus SARS-CoV-2 has resulted in millions of COVID-19 cases and hundreds of thousands of deaths. The spread throughout Asia, Europe, and the Americas has presented one of the greatest infectious disease threats in recent history and has tested the capacity of global health infrastructures. Since no effective vaccine is available, isolation techniques to prevent infection such as home quarantine and social distancing while in public have remained the cornerstone of public health interventions. While government and health officials were charged with implementing stay-at-home strategies, many of which had little guidance as to the consequences of how quickly to begin them. Moreover, as the local epidemic curves have been flattened, the same officials must wrestle with when to ease or cease such restrictions as to not impose economic turmoil. To evaluate the effects of quarantine strategies during the initial epidemic, an agent based modeling framework was created to take into account local spread based on geographic and population data with a corresponding interactive desktop and web-based application. Using the state of Massachusetts in the United States of America, we have illustrated the consequences of implementing quarantines at different time points after the initial seeding of the state with COVID-19 cases. Furthermore, we suggest that this application can be adapted to other states, small countries, or regions within a country to provide decision makers with critical information necessary to best protect human health.
Author summary

In this work we presented a local agent-based geographic model for the epidemic spread of COVID-19 with and without quarantine measures. The model is implemented as an interactive Microsoft Windows application, as a web tool online (summaries only), and the source code is freely available at GitHub. In this article, the model is presented for the state of Massachusetts (United States), but can be easily adopted to other administrative districts, areas and territories where the demographics and population characteristics of the reported cases are known. After calibration, the model predicts the morbidity and mortality of the epidemic as it spreads with different quarantine parameters, which lead to reduction of social contact probabilities between individuals. The model outputs for different quarantine start dates and durations are then summarized and compared to actual disease incidence. These summaries demonstrate the effectiveness of the early quarantine measures on the reduction of the number of new infections and deaths. The model framework can also be adopted for use in future decision making process for government and health officials as plans to cease or ease quarantines continue to evolve using the interactive application.

Introduction

The epidemic of a novel coronavirus was first detected in the city of Wuhan in the Chinese province Hubei on December of 2019 [1] [2] [3] [4]. Despite the unprecedented efforts from Chinese authorities including the complete lockdown of the entire city of Wuhan on January 22, 2020 the virus has rapidly spread to all continents except Antarctica. The World Health Organization (WHO) officially declared the coronavirus a global pandemic on March 11, 2020 [5], only three months after the first case was detected. The novel coronavirus is now officially named SARS-CoV-2 and the disease caused by it has been called COVID-19 [6] to distinguish from SARS-CoV and the corresponding severe acute respiratory syndrome (SARS) pandemic from 2003 [7] [8]. Despite the much lower case-fatality rate, SARS-CoV-2 has caused morbidity and mortality orders of magnitude higher than severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) combined [9]. As of May 13, 2020, more than 4.1 million infections have been reported worldwide, with more than 287,000 deaths due to complications of COVID-19 [10]. As of May, 2020 there is neither an effective virus-specific treatment, nor Food and Drug Administration (FDA) approved vaccine available for SARS-CoV-2 [11] [12] [13] [14]. As such, social distancing and quarantine are the only available measures to reduce the transmission and prevent overwhelming the capacity of existing healthcare systems. Starting at the epicenter of Hubei province [15] in January, 2020, governments around the world have implemented society lockdown measures of varying degrees [16] [17] [18] [19] [20]. Since such measures remain the only available tools to control the spread of the pandemic, it is critical to understand the transmission dynamics of SARS-CoV-2 in the population. This would allow for the prediction of COVID-19 cases and deaths over time under different mitigation strategies, which could be implemented to reduce morbidity and mortality; as well as the allocation of limited resources to medical providers.

To achieve this goal, multiple approaches can be implemented that are typically driven by the quality and precision of the available data. The most commonly reported data for epidemics are the incidence of new cases and deaths represented as a time series over the fixed intervals (e.g. days or weeks) aggregated across multiple regions and reporting sources [21] [22] [23]. This aggregated data can be used for incidence curve reconstruction, modeling, and prediction when more detailed information about each infected individual is not available [24] [25] [26] [27] [28]. Such models are called
compartmental models [29] where the study population is divided into groups while individuals within each group are assumed to have the same characteristics of interest (e.g. susceptible, infected, vaccinated, or immune). The compartmental models are formulated via a defined system of differential equations that allows for both deterministic and stochastic formulations to quantify the uncertainty of the model fit. Those models provide insight into the underlying epidemic dynamics and allow for the prediction of future trends in incidence under different transmission scenarios, including interventions such as social distancing, quarantines, and vaccinations. Another approach are the agent-based models [30] [31] [32] [33], which utilize a synthetic population, that attempts to realistically represent the social interactions in time and space between individuals with different characteristics and infection status [32]. Compared to compartment models, agent-based models rely on detailed data about the study population, making them more computationally intensive while allowing for more realistic simulations of human transmission pathways.

An example of an agent-based model that has been successfully applied to study respiratory diseases, including the efficacy of quarantine measures for containment of SARS-CoV-2 is the FluTE model [31] [34]. The FluTE model is based on the assumption that the synthetic study population is parsed in social subgroups and the interactions between them are modeled at different community levels (household, neighborhood, work), age groups, time of the day, and other characteristics. In this work, we propose a localized, agent based model using incidence data from Massachusetts, USA. The proposed model incorporates the infected individuals that are reported in the beginning of an epidemic for a given area and their personal characteristics such as the date the infection was confirmation, geographic location, and demographic characteristics. Thus, by using a limited amount of information, such as the populations of each zip code and number of reported cases, a robust simulation is generated with time series data of predicted disease morbidity and mortality. Furthermore, by incorporating different quarantine strategies, the reduction in the number of new cases and deaths can be estimated for each locale depending on their unique characteristics. Since this model uses limited input data that are publicly available and is implemented in the form of an interactive web application, we believe that this tool could represent a widely adaptable format for state and local governments and health officials to make informed decisions as they consider easing or ceasing mandatory quarantines. Once effective treatments and vaccines become available, this framework could also be used to allocate treatment resources and plan vaccination campaigns tailored to fit different geographic regions. The reported demographics data can also be depersonalized in accordance to HIPAA regulations [35] to make the use of the model versatile and not to violate the privacy of individuals.

Materials and methods

The Model Structure

The model stochastic simulations are generating the infected individuals at different times and stages. Those individuals are indexed by $k$ and have individual characteristics presented below:

$$Q_k = \{(x_k, y_k), t_{inf_k}, det_k, stg_k, age_k, rad_k, p_{cont(k)}, cont_k, R_0(k), sever_k, dur_k, st_k(t)\}. \quad (1)$$

The characteristics of each individual $Q_k$ are determined and updated within the simulation process and have the following details:

- $(x_k, y_k)$ - the Cartesian coordinates (in pixels) of the individual $Q_k$ that do not change within the simulation process after they are introduced;
- \textit{tinf}_k – the time of infection onset for the individual \( Q_k \) which is measured in relation to the simulation baseline time denoted as 0;

- \textit{det}_k – the detection time variable measured in days that corresponds to a period from an infection acquisition until the proper diagnosis and reporting of individual \( Q_k \);  

- \textit{stg}_k = (\textit{stg}_{1(k)}, \textit{stg}_{2(k)}, \textit{stg}_{3(k)}) – the vector of durations of three disease infection stages measured in days that characterize the severity of the disease. It is assumed that \( \textit{stg}_{1(k)} + \textit{stg}_{2(k)} + \textit{stg}_{3(k)} = \textit{det}_k \);

- \textit{age}_k – the age of the individual \( Q_k \) at the time of the infection onset;

- \textit{rad}_k – the distance (in meters) up to which the individual \( Q_k \) is able to infect the nearby individuals;

- \( p_{\text{cont}(k)} \) – the probability that during each day the individual \( Q_k \) has any contacts which lead to new infections;

- \( \textit{cont}_k = (\mu_{\text{cont}(k)}, \sigma^2_{\text{cont}(k)}) \) – the individual-specific parameters that define the distribution of the number of successful infection transmissions to other individuals within a given day. This number is generated randomly for each day \( t \), provided that the individual has any transmissions on the given day (according to the contact probability \( p_{\text{cont}(k)} \)).

- \( R_0(k) \) – the individual’s reproduction number. This variable stores the number of individuals that is infected by \( Q_k \) during the infection period \( \textit{det}_k \). The average of those reproduction numbers across individuals and simulations are used to estimate the basic reproduction number \( R_0 \) [36] which is a characteristic of the entire epidemic;

- \textit{sever}_k – the disease severity variable for the individual \( Q_k \) that takes three values, where 1 corresponds to lethal, 2 corresponds to severe, and 3 corresponds to mild; the disease severity does not change for a given individual after it is determined randomly from a trinomial distribution;

- \textit{dur}_k – the disease duration from the infection onset to cure (or death) in days, which is generated randomly based on the \textit{sever}_k parameter;

- \textit{st}_k(t) \) - the status of the individual \( Q_k \) at a given day \( t \). The status of the individuals within the simulation is expected to change over time and is expected to take the following values:

  - \( \textit{st}_k(t) = 0 \) – the individual is detected based on the external information i.e. from the reported data that are used as the model input;
  - \( \textit{st}_k(t) = 1 \) - the individual is infected but has not been identified as such yet;
  - \( \textit{st}_k(t) = 2 \) – the individual has been infected and detected as such, which has also implied the individual’s isolation (quarantine).
  - \( \textit{st}_k(t) = 3 \) – the individual has recovered and is immune;
  - \( \textit{st}_k(t) = 4 \) – the individual has deceased.

In the beginning of the simulations the model utilizes multiple local epidemic epicenters \( E = \{E_1,E_2,\ldots,E_I\} \). Those epicenters serve as the model initial conditions and represent the introductory geographic points for the index cases that are introduced into the susceptible population. The epicenters can either correspond to the actual address...
coordinates for those places where the initial outbreaks were detected or to the centers of the corresponding aggregated geographic units. The latter may be the case, if either the exact infection acquisition locations are not known, or the privacy concerns prevent the inclusion of such data into the model. In the latter case the centers of the aggregated geographic units are taken as epicenters \( E_i \) for each \( i = 1, 2, \ldots, \mathcal{L} \).

The local epicenters in the model are defined by a pair of geographic coordinates \((\text{Lat}_i, \text{Long}_i)\) and by an epicenter-specific region radius \( R_i \) which is defined in meters. Therefore, for \( i = 1, 2, \ldots, \mathcal{L} \) the epicenter region is defined by a triplet:

\[
E_i = ((\text{Lat}_i, \text{Long}_i), R_i) .
\]  

(2)

The epicenter regions are defined from the surveillance epidemiological data. As the initial conditions in addition to the local epicenters the model incorporates the areas of high density \( P = \{P_1, P_2, \ldots, P_J\} \) for \( j = 1, 2, \ldots, J \), where each \( P_j \) represents a large city or a densely populated area and which is also defined by a triplet:

\[
P_j = ((\text{Lat}_j, \text{Long}_j), R_j) .
\]  

(3)

In the model the reporting times (days) for the initial index cases for each epicenter \( i \) precede the modeled epidemic starting time which corresponds to the baseline time slot \( t = 0 \). Therefore, the reported time slot indexes across the epicenters \( E_i \) are denoted as \( s = 1, 2, \ldots, \mathcal{S} \) with the corresponding times \( t_1, t_2, \ldots, t_\mathcal{S} \). The earliest reported cases and their dates are used for the model input with indexes \( s = 1, 2, \ldots, \mathcal{S} \) such that \( \tilde{S} < \mathcal{S} \) and the corresponding times \( \tilde{t}_1, \tilde{t}_2, \ldots, \tilde{t}_\tilde{S} \). The corresponding number of confirmed and reported infections for each local epicenter \( E_i \) up to and including the time \( \tilde{t}_s \) for \( s = 1, 2, \ldots, \tilde{S} \) is denoted as \( n_i(\tilde{t}_s) \). The corresponding set of infected and reported (i.e. with the status \( s_{ik} = 1 \)) individuals across all epicenter is denoted as:

\[
D = \{\tilde{Q}_1, \tilde{Q}_2, \ldots, \tilde{Q}_{\mathcal{S}}\} ,
\]  

(4)

where \( k = 1, 2, \ldots, \mathcal{K}_{\tilde{S}} \) is the global index for initial cases across all times \( \tilde{t}_1, \tilde{t}_2, \ldots, \tilde{t}_{\tilde{S}} \) and \( \mathcal{K}_{\tilde{S}} \) is the total number of the initial index cases that is simulated within the model based on the input data. The tilde notation for \( \tilde{Q}_k \)'s in \( D \) emphasizes the link to the model input data.

The time index that corresponds to individual day within the model is denoted as \( t \) and is equal to 0 at the model baseline. The simulation baseline time \( t = 0 \) corresponds to the latest reporting time \( \tilde{t}_{\tilde{S}} \) of the earliest reported cases that are used for the model input. The actual infection times for those index cases precede the selected baseline simulation time \( t = 0 \) due to the infectivity periods generated for those index cases prior to their reporting. The actual simulation starting time that accounts for the infectivity periods is denoted as \( t = T_{\text{min}} \) and is smaller than the baseline time \( t = 0 \). This simulation starting time \( t = T_{\text{min}} \) is generated within the model, while the baseline time \( t = 0 \) is defined by the data and is defined by the largest index within the set of calibration indexes \( s = 1, 2, \ldots, \mathcal{S} \). The largest simulation time \( t = T_{\text{max}} \) is determined by the model user based on the desired length of prediction. The initial set of index cases \( D \) from (1) defines the model initial cases that are allocated across the local epicenters (2) at times up to the baseline time \( t = 0 \).

Based on the model geographic characteristics (2) and (3) and the initial set of reported individuals \( D \) from (4) the new lists \( \mathcal{L}(t) \) of of modeled individuals are simulated for time slots \( t \in [T_{\text{min}}, T_{\text{max}}] \) where \( T_{\text{max}} - T_{\text{min}} + 1 \) is the total number of the simulated time slots. The simulated lists \( \mathcal{L}(t) \) have the following format:

\[
\mathcal{L}(t) = \{Q_1, Q_2, \ldots, Q_{\mathcal{K}(t)}\} .
\]  

(5)
where the value of \( K(t) \) is defined by the simulation at every simulation time step \( t \in [T_{\text{min}}; T_{\text{max}}] \). During this procedure the input set individuals \( D \) defined in (4) is allocated between the different epicenters and time slots within the lists \( L(t) \) defined by (5). The allocations of the set \( D \) is performed during the time slots \( t \in [T_{\text{min}}; \tilde{t}_S] \) where \( \tilde{t}_S < T_{\text{max}} \).

### The Overall Model Flow

The entire modeling process can be summarized via the following steps:

- The model input time interval is determined by fixing the first \( \tilde{S} \) reporting indexes out of the total \( S \) where \( \tilde{S} < S \). Those indexes correspond to the reporting time slots \( \hat{t}_1, \hat{t}_2, \ldots, \hat{t}_S \). This completely defines the list of reported index cases \( D \) from (4) that are used as the model initial conditions. The baseline time of the model \( t = 0 \) is assumed to correspond to \( \hat{t}_S \).

- The individuals from the reported set \( D \) that are defined in (4) are assigned to the local epicenters of the future epidemic \( E_i \) for \( i = 1, 2, \ldots, I \) based on the available (from the input data) geographic distribution.

- The geographic data about the areas of high density \( P_j \) for \( j = 1, 2, \ldots, J \) are incorporated into the model.

- The model is initialized with the index cases from \( D \). Based on those index cases that are defined in (4) the initial infection time \( T_{\text{min}} \) is determined. This step is necessary to incorporate the infection times that have been present before the first reporting time \( \hat{t}_1 \) into the model.

- The final time point of the stochastic simulations \( T_{\text{max}} \) is define by the user based on the desired study and prediction goals.

- The initial list of infected individuals \( L(T_{\text{min}}) \) is initialized at time \( T_{\text{min}} \) only with the earliest model input cases from the list \( D(T_{\text{min}}) \).

- The infected list of individuals \( L(t+1) \) for the time slot \( t+1 \) is generated sequentially for all \( t \in [T_{\text{min}}, T_{\text{max}} - 1] \) based on the list of individuals \( L(t) \) from previous time slot \( t \) and the individual’s characteristics within the list \( L(t+1) \) are updated at this time step \( t+1 \). The details of the new infection generations are provided in \( \text{SI Appendix} \).

Based on the lists \( L(t) \) at every time slot \( t \in [T_{\text{min}}; T_{\text{max}}] \) the infected modeled population summaries can be computed and summarized. In particular, the total number of currently infected but not identified individuals (i.e. those with the status \( st(t) = 1 \)) is saved into \( Inf(t) \) variable for every \( t \). The total number of treated or quarantined individuals (i.e. with the status \( st(t) = 2 \)) is saved into \( Treat(t) \) variable for every \( t \). The total number of recovered individuals (i.e. with the status \( st(t) = 2 \)) is saved into \( Recov(t) \) variable for every \( t \). The total number of deceased individuals (i.e. with the status \( st(t) = 4 \)) is saved into \( Dead(t) \) variable for every \( t \). Those numbers are used in the model calibration procedures, epidemiological summaries and in the model predictions. The model input utilizes only the first \( \tilde{S} \) reported indexes with the corresponding reported times \( \hat{t}_s \) for \( s = 1, 2, \ldots, \tilde{S} \) with the total number of reported indexes equal to \( S \) and \( \tilde{S} < S \). The remaining reported indexes \( \tilde{S} + \tau, \tilde{S} + \tau + 1, \ldots, S \) for some integer \( \tau \) are divided into the two groups:

\[
\{ \tilde{S} + \tau, \tilde{S} + \tau + 1, \ldots, S \} \quad \text{and} \quad \{ S + 1, S + 2, \ldots, S \}.
\]
The first group of the reported indexes from (6) is used for the model calibration and estimation of the unknown parameters. The second group of the reported indexes from (6) is used to evaluate the quality of the model predictions. The Massachusetts surveillance data that are used for the model calibration, validation and predictions are freely available at the Massachusetts Department of Public Health web site [37]. The first reported date which corresponds to the time index \( \tilde{t}_1 \) in the model is March 13, 2020. The latest reported date that is used for the model input is March 26, 2020 which corresponds to the time index \( \tilde{t}_{\tilde{S}} + \tau \) in the model. The time indexes that correspond to \( \tilde{t}_{\tilde{S}+\tau} \) and \( \tilde{t}_{\tilde{S}} \) are April 14, 2020 and April 22, 2020 respectively. The parameter optimization is performed by minimizing the sum of squared differences between the model-produced outputs and the calibration data by using the Nelder–Mead numerical minimization method [38]. The additional details about the model formulation, parameterization, and calibration are summarized in the [S1 Appendix](https://doi.org/10.1101/2020.05.17.20104901).

After the model calibration is performed various quarantine and transmission intervention strategies can be investigated as a build-in function within the calibrated model. Those intervention strategies are based on the assumption that the probability of contacts decreases with the increase in quarantine measures. The social contact probabilities can also be adjusted within the model settings and are either estimated or defined manually for both non-quarantine and quarantine settings.

### The model availability

The model has been implemented in multiple environments which include the implementation for Microsoft Windows and as a web prediction tool [39] [40] (summaries only). In addition to that the model application is freely available under the terms of the MIT license [41] and the sources are available on GitHub [42]. The current model implementation has been calibrated based on the state of Massachusetts (United States) incidence data [37]. The proposed framework and the code are fairly general and can be adopted for other areas and territories where the demographics of the incidence cases and population characteristics are known with at least some geographic precision, and where the rapid evaluations of social distancing measures have to be quantified.

### Results

Within the model multiple epidemic progression scenarios can be considered; three different quarantine strategies are presented in this manuscript as an illustration of the model input and outputs. Other quarantine scenarios can be produced and customized by the user within the interactive application. The first scenario corresponds to the quarantine date on March 29, 2020 i.e. the early reduction in contact probabilities and social distancing between individuals. The second scenario assumes the implementation of the quarantine measures on April 6, 2020, and the third scenario assumes the implementation of the quarantine measures on April 13, 2020. The point estimates and the prediction bands have been produced by replicating each of the three scenarios and taking the median values across 500 model runs for the point estimates and 5-th and 95-th percentiles for the 90% prediction intervals. The results are summarized in Tables [1] and [2] for the model-predicted cases and deaths, respectively. For example, the summaries from Table [1] can be compared after one month of the baseline date i.e. on April 26, 2020. For the first scenario the model predicts 24,039 cumulative cases (with the 90% PI (20,665; 27, 296)), for the second scenario the model predicts 56,587 cumulative cases (with the 90% PI (46,944; 66, 401)), and for the thirds scenario the model predicts 123,351 cumulative cases (with the 90% PI (100,113; 144,018)). Compared to the quarantine start date in the second scenario, the first scenario results...
in 58% reduction in cumulative cases on April 26, 2020, in 63% reduction in cumulative cases on May 26, 2020, and in 65% reduction in cumulative cases on June 26, 2020. Compared to the quarantine start date in the third scenario, the first scenario results in 81% reduction in cumulative cases on April 26, 2020, in 87% reduction in cumulative cases on May 26, 2020, and in 88% reduction in cumulative cases on June 26, 2020. Based on the model outputs the earliest quarantine measures and the reduction in contact probabilities can be extremely beneficial in mitigation of the outbreak consequences. The analogues summaries for the model-predicted death across the three scenarios are summarized in Table 2. Compared to the quarantine start date in the second scenario, the first scenario results in 52% reduction in cumulative deaths on April 26, 2020, in 63% reduction in cumulative deaths on May 26, 2020, and in 65% reduction in cumulative deaths on June 26, 2020. Compared to the quarantine start date in the third scenario, the first scenario results in 70% reduction in cumulative deaths on April 26, 2020, in 86% reduction in cumulative deaths on May 26, 2020, and in 88% reduction in cumulative deaths on June 26, 2020.

| Scenario | Quarantine Date | April 26, 2020 | May 26, 2020 | June 26, 2020 |
|----------|-----------------|----------------|---------------|---------------|
| First    | March 29, 2020  | 24,039 (20,665; 27,296) | 32,692 (27,361; 38,221) | 36,767 (30,288; 43,976) |
| Second   | April 06, 2020  | 56,587 (46,944; 66,401) | 89,727 (72,843; 106,797) | 105,464 (84,859; 127,796) |
| Third    | April 13, 2020  | 123,351 (100,113; 144,018) | 245,255 (197,748; 294,750) | 307,128 (243,184; 362,104) |

The model is presented via the graphic user interface (GUI) application for Microsoft Windows as well as the as web prediction tool [39] [40] (summaries only) that can be used for the geographic visualization of various epidemiological curves and geographic visualization of cases in the state of Massachusetts. Users can work with the tool and utilize the available model customizations. The appearance of the GUI for MS Windows application is presented in Fig [1].

The presented application does not require installation and can be launched directly by running the executable file. The tool allows the parameters optimizations and the visual animated simulations of the model outputs and their comparison with the reported data. The user can interactively customize the most important simulation parameters, change the duration of prediction, and adjust manually the locations of high population density. This allows the user to consider multiple scenarios of the epidemic spread. In addition, the user has flexibility to re-run the model multiple times either step by step or entirely for all time slots. The user can scroll via each day of the recently completed simulation to see the visualized results of that specific day and choose which epidemiological curves to include in the summary graphs. The modeled cases and other summaries are saved into the comma-separated values (csv) files after the end of each simulation. The tool also provides the estimate of the population basic reproduction number $R_0$ for each simulation run together with the corresponding 90% confidence intervals. The estimates for $R_0$ are provided based on the quantiles of the individual’s reproduction numbers $R_{0(k)}$ across multiple individuals $k$ both before and
after the quarantine date that is defined by the user. The resulting distribution of the individual’s reproduction numbers $R_0(k)$ from the tool before and after the quarantine are summarized in Fig 2.

The example of the summary graphs for the model-produced outputs for the second scenario from Tables 1 and 2 are presented in Fig 3, which contains the four combined graphs available in the “Statistics” tab in the top right corner of the tool. Those graphs within the tool can be produced by setting the “Max Simulation Time” and “Forecast Day” fields to July 15, 2020 and by running the model 500 times by using the “Daily Forecast Evaluation” button. The 500 runs are necessary to produce the median predictions and the corresponding 90% uncertainty prediction bands across those runs by taking the 5-th and the 95-th percentiles across those situations for each time slot. Those graphs include the cumulative numbers of reported cases and deaths, together with the currently hospitalized patients and unreported cases. The graphs also include the reported data in blue. The calibration time period is highlighted in blue and is bounded by vertical bars.
Fig 2. The distribution of the individual’s reproduction numbers $R_{0(k)}$. The example of the tool output for the distribution of the individual’s reproduction numbers $R_{0(k)}$. The output graph contains the estimated probability density function of the individual’s reproduction numbers $R_{0(k)}$ together with the cumulative distribution functions both before and after the quarantine implementation date.

Discussion

In this work the local agent-based modeling framework for respiratory diseases has been presented. This framework incorporates the reported geographic incidence data that are typically available from surveillance, which include individual’s age, infection status, and the severity of the disease. The model accounts for the latent period of the individual’s infection before detection and proper reporting as well as for different disease severity levels. The framework also allows to incorporate the exact geographic addresses of individuals (if available) or the random geographic distribution of individuals within those aggregated districts where they are reported in case of privacy concerns. The model allows to perform predictions with different levels of social isolation between individuals and quarantine measures. Those measures are implemented at different times to compare different quarantine scenarios. As expected, there was a decrease in the cumulative incidence and deaths inversely proportional to the date quarantine was implemented; which resulted in approximately 50-80% reduction in cases and deaths depending on the scenario.

Compared to complex agent-based models, the compartmental models are based on the assumptions of homogeneous mixing and can be parameterized by a relatively small set of rates and initial conditions. The main challenges for the compartmental models are the determination of the compartment types that are used in the model, the assignment of individuals between compartment i.e. the specifications of the set of rules that assign each particular individual to each type of compartments, and the determination of the parameters of interest which can either be postulated from external sources or estimated from data. The agent based models, due to their inherited complexity, incorporate separate individuals with multiple different characteristics and parameters per individual. This adds another layer of parameterization flexibility, but also introduces another layer of modeling challenges, since the number of individual’s characteristics within the model is determined by the modeler. Ideally, the
Fig 3. The model-produced predictions. The median of the model-produced 500 runs together with the corresponding 90% uncertainty prediction bands for different model outputs. The top left graph includes the cumulative numbers of reported cases. The top-right graph summarizes the cumulative subset of the reported cases that have deceased. The bottom graphs summarize the number of hospitalized and unreported patients in the given moment of time. The reported data are displayed in blue for visual comparison.

The model has to be: 1) flexible enough to incorporate the possible social and geographic characteristics of individuals and to provide the way to realistically represent the social interactions and the disease transmission mechanisms; 2) simple enough to avoid the problems with parameterization, but able to capture the actual transmission patterns with the goal of predictions and intervention studies; 3) utilize the available surveillance and public health data in the best possible way. The best possible way in this context means, that all the information from the data that can be used to answer the questions of interest are utilized, while the number of assumptions within the model beyond the information available from the data is the smallest possible that is necessary to implement the model.

In the case of COVID-19, an epidemic which has quickly evolved into a pandemic, the local epidemic developments in every region are expected to have different dynamics influenced by multiple region-specific factors. Thus, an agent based model which utilizes local settings is likely superior to a global agent-based model in this setting and can be implemented with minimal inputs as long as local data are available. In this example, we chose regional data for the state of Massachusetts, however we believe this framework and interactive tool could be adopted and useful for small or middle size countries or other administrative districts within a larger country, that have comparable reporting and data quality across different administrative regions.
Conclusion

In this paper, we have presented a novel, localized agent-based model that can be used within minimal input data, which is publicly available and tailored to the population distributions of Massachusetts, USA. After calibration the model provided a good estimation of the actual incidence, hospitalizations, and death rates, with the added benefit of estimating the number of undetected infections in the population. Given the necessity for making decisions of easing or ceasing quarantines that are specific to a state or county based on their reported case counts, adaptation of this framework could prove to be very useful with efforts to reopen the economy, while quantifying the disease burden posed by such decisions. In addition, this model could be used for future outbreaks of other novel respiratory diseases to protect public health and possibly designed tailored interventions of treatment and vaccination campaigns.

Supporting information

S1 Appendix. Model Details The details about the model formulation, parameterization, and calibration.

References

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