

Technological University Dublin [ARROW@TU Dublin](https://arrow.tudublin.ie/)

[Articles](https://arrow.tudublin.ie/scschcomart) **School of Computer Science** School of Computer Science

2023

Assessing The Impact of Contact Tracing With an Agent-Based Model for Simulating the Spread of COVID-19: The Irish Experience

Elizabeth Hunter Technological University Dublin, elizabeth.hunter@tudublin.ie

Sudipta Saha Health Research Board, Ireland

Jwenish Kumawat HSE, Dublin, Ireland

See next page for additional authors

Follow this and additional works at: [https://arrow.tudublin.ie/scschcomart](https://arrow.tudublin.ie/scschcomart?utm_source=arrow.tudublin.ie%2Fscschcomart%2F217&utm_medium=PDF&utm_campaign=PDFCoverPages)

Part of the [Computer Engineering Commons,](https://network.bepress.com/hgg/discipline/258?utm_source=arrow.tudublin.ie%2Fscschcomart%2F217&utm_medium=PDF&utm_campaign=PDFCoverPages) and the [Medicine and Health Sciences Commons](https://network.bepress.com/hgg/discipline/648?utm_source=arrow.tudublin.ie%2Fscschcomart%2F217&utm_medium=PDF&utm_campaign=PDFCoverPages)

Recommended Citation

Hunter, Elizabeth; Saha, Sudipta; Kumawat, Jwenish; Carroll, Ciara; Kelleher, John; Buckley, Claire; McAloon, Conor; Kearney, Patricia; Gilbert, Michelle; and Martin, Greg, "Assessing The Impact of Contact Tracing With an Agent-Based Model for Simulating the Spread of COVID-19: The Irish Experience" (2023). Articles. 217.

[https://arrow.tudublin.ie/scschcomart/217](https://arrow.tudublin.ie/scschcomart/217?utm_source=arrow.tudublin.ie%2Fscschcomart%2F217&utm_medium=PDF&utm_campaign=PDFCoverPages)

This Article is brought to you for free and open access by the School of Computer Science at ARROW@TU Dublin. It has been accepted for inclusion in Articles by an authorized administrator of ARROW@TU Dublin. For more information, please contact [arrow.admin@tudublin.ie, aisling.coyne@tudublin.ie, vera.kilshaw@tudublin.ie.](mailto:arrow.admin@tudublin.ie,%20aisling.coyne@tudublin.ie,%20vera.kilshaw@tudublin.ie) <u>ெ ெ</u>

This work is licensed under a [Creative Commons Attribution-Share Alike 4.0 International License](https://creativecommons.org/licenses/by-sa/4.0/). Funder: This work was partly supported by the ADAPT Centre for Digital Content Technology which is funded under the SFI Research Centres Programme (Grant13/RC/2106_P2) and is co-funded under the European Regional Development Funds

Authors

Elizabeth Hunter, Sudipta Saha, Jwenish Kumawat, Ciara Carroll, John Kelleher, Claire Buckley, Conor McAloon, Patricia Kearney, Michelle Gilbert, and Greg Martin

Contents lists available at [ScienceDirect](https://www.elsevier.com/locate/health)

Healthcare Analytics

journal homepage: www.elsevier.com/locate/health

Assessing the impact of contact tracing with an agent-based model for simulating the spread of COVID-19: The Irish experience

Eliz[a](#page-2-0)[b](#page-2-2)eth Hunter ª,*, Su[d](#page-2-4)ipta Saha ʰ, Jw[e](#page-2-5)nish Kumawat ˤ, Ciara Carroll ^d, John D. Kelleher ^e, Claire Buckley ^{[f](#page-2-6)}, Conor McAloon ^{[g](#page-2-7)}, Patri[c](#page-2-3)a Kearney ^f, Mic[h](#page-2-8)elle Gilbert ^c, Greg Martin ^h

^a *ADAPT Research Centre, Technological University Dublin, Grangegorman, Dublin 7, D07 H6K8, Ireland*

^b *Health Research Board, Dublin 2, Ireland*

^c *HSE, COVID-19, Contact Management Programme, 1 Heuston South Quarter, St. Johns Road, Dublin 8, Ireland*

^d *HSE Public Health, Area A; Dr Steevens' Hospital, Dublin 8, D08W2A8, Ireland*

^e *ADAPT Research Centre, Maynooth University Hamilton Institute, Maynooth University, Maynooth, CO Kildare, W23 A3HY, Ireland*

^f *School of Public Health, University College Cork, Cork, Ireland*

^g *School of Veterinary Medicine, University College Dublin, Dublin, D04 W6F6, Ireland*

^h *Health Protection Surveillance Centre, Mountjoy, Dublin, D01A4A3, Ireland*

ARTICLE INFO

Keywords: Contact tracing Agent-based model COVID-19 Descriptive analytics Epidemiology Simulation

A B S T R A C T

Contact tracing is an important tool in managing infectious disease outbreaks and Ireland used a comprehensive contact tracing program to slow the spread of COVID-19. Although the benefits of contact tracing seem obvious, it is difficult to estimate the actual impact contact tracing has on an outbreak because it is hard to separate the effects of contact tracing from other behavioural changes or interventions. To understand the impact contact tracing had in Ireland, we used an agent-based model that is designed to simulate the spread of COVID-19 through Ireland. The model uses real contact tracing data from the first year of the COVID-19 pandemic. We found that without contact tracing, and everything else held constant, a larger number of cases, hospital admissions, ICU admissions and deaths would have occurred. The model suggests that without contact tracing deaths from COVID-19 in Ireland during the first year of the pandemic could have increased by 80% (this equates to approximately 5,768 agents in the model). This modelling study is an important step in highlighting the impact that contact tracing had on the course of the COVID-19 pandemic. Although we use a model for Ireland, this method is applicable to any country or region.

1. Introduction

The public health approach to mitigating the impact of infectious disease outbreaks and epidemics has relied on contact tracing since it was first introduced in the 1930s to slow the spread of syphilis [[1\]](#page-10-0). In order to prevent transmission chains, case investigation and contact tracing are crucial steps in supporting patients and warning contacts to isolate so as to not spread the infection further [\[2\]](#page-10-1). Since its introduction, contact tracing has been used for many different disease outbreaks including Ebola, severe acute respiratory syndrome, and COVID-19 [[3\]](#page-10-2). Experts argue that non-pharmaceutical interventions (NPIs) such as contact tracing remain indispensable even when interventions, such as vaccines, are widely available [[4\]](#page-10-3).

Globally, testing and contact tracing was central to the public health response to COVID-19, with unprecedented resources being allocated worldwide to strengthen testing and tracing capabilities [[5\]](#page-10-4). However, during the COVID-19 pandemic, government policies on contact tracing varied widely across the world. Country responses to contact tracing can be categorised into no tracing, limited tracing, and extensive tracing [\[6\]](#page-10-5). Ireland and several countries such as China, Australia, and Japan carried out extensive contact tracing.

In Ireland in early 2020 in response to the COVID-19 pandemic, a scalable national contact tracing program, the contact management program (the CMP), was rapidly developed. Working closely with regional public health departments, the CMP ensured that cases and contacts were managed in an organised and consistent process [[6](#page-10-5)]. To implement the CMP, 3,384 contact tracers were hired and trained in Ireland during the first year of the pandemic. Most of these individuals had no previous experience in public health, thus the formation and ongoing operation of the CMP represented a significant public health expenditure [[6\]](#page-10-5). It is, therefore, important to quantitatively assess the effectiveness of contact tracing as a public health tool, even if generally contact tracing is deemed to be cost efficient. If we know the effectiveness of the contact tracing program that was implemented

Corresponding author. *E-mail address:* elizabeth.hunter@tudublin.ie (E. Hunter).

<https://doi.org/10.1016/j.health.2023.100229>

Received 1 March 2023; Received in revised form 14 July 2023; Accepted 14 July 2023

2772-4425/© 2023 The Author(s). Published by Elsevier Inc. This is an open access article under the CC BY-NC-ND license [\(http://creativecommons.org/licenses/by-nc-nd/4.0/\)](http://creativecommons.org/licenses/by-nc-nd/4.0/).

during COVID-19, policymakers can use this evidence to inform their decisions for management of future pandemic.

Traditionally, there are a number of measures that have been used to study the effectiveness of contact tracing. These are either process measures (e.g., index patents referred for contact tracing, contacts per index, positive contacts identified, time to notify contacts), outcome measures (e.g., incidence rates in the community, diagnoses in contacts), or related measures (e.g., index patients and contacts satisfaction with contact tracing, contacts, proportion of total infections in contacts) [\[7\]](#page-10-6). During the COVID-19 pandemic, contact tracing has been evaluated by comparing programmatic adaptations within tracing interventions [\[8\]](#page-10-7). The CMP has used a number of such methods to assess the impact of contact tracing looking at cases with contact tracing successfully recorded, close contacts identified and time to notify contacts [[6](#page-10-5)].

While the CMP had an impact on the COVID-19 cases in Ireland, the extent of this impact has not been ascertained with analyses conducted to date. Although measures such as the number of positive cases whose contacts were traced give an idea of the potential chains of infection that were broken, we cannot compare what happened during the COVID-19 pandemic to the corresponding real-world scenario with no contact tracing because such a scenario does not exist. Although it is possible to compare what happened in other countries or at different points of the pandemic where contact tracing strategies might have been different or non-existent, there will of course be other confounding differences in these scenarios. For example, the restrictions put in place or the number of cases could affect the comparison. Infectious disease models can help us to quantify the impact of different interventions by simulating scenarios in which those interventions were not employed.

There are several types of models that are used to understand infectious disease epidemiology, each with their own set of advantages and disadvantages [[9](#page-10-8)]. Historically, the most common types of infectious disease models are equation-based compartmental models, commonly known as the SIR (susceptible, infected, recovered) model. These models are typically made up with a set of differential equations that define the movement between compartments, from susceptible to infected or infected to recovered [\[10](#page-10-9)]. These models have been shown to capture the general dynamics of an outbreak and thus are widely used. However, SIR models make strong simplifying assumptions, for example, within each compartment (i.e., susceptible, infected, recovered) all individuals in the population are modelled so as to be homogeneous and to mix homogeneously. Although this homogeneous assumption can be made in some scenarios, the heterogeneity in a population is often vital to understand how an infectious disease will spread [[11\]](#page-10-10). Thus, alternative model types have been implemented that better take into account this heterogeneity. Some models are designed to use agecohorts [\[12](#page-10-11)[,13](#page-10-12)], or transportation between subpopulations [\[14](#page-10-13)], or treat an outbreak as a hierarchical tree of infectors and infectees [[15\]](#page-10-14).

Another model type that is being used more often in infectious disease modelling is agent-based models [[4](#page-10-3),[16,](#page-10-15)[17\]](#page-11-0). Agent-based models are a type of computer simulation that are made up of agents and an environment. Agent behaviours and interactions are determined by a set of coded rules [[18\]](#page-11-1). They are useful when considering individual actions or behaviours that drive a phenomenon such as in the spread of an infectious disease. The models are able to trace chains of infection between agents making them particularly suitable for looking at the impact of certain interventions such as contact tracing.

The existing literature for contact tracing modelling includes a number of different modelling types. Several studies have investigated the effectiveness of contact tracing strategies for different infectious diseases including COVID-19 using mathematical or equation-based models [[19](#page-11-2)[–25](#page-11-3)]. Other studies use branching tree models [[15\]](#page-10-14), while others use household transmission models [[26\]](#page-11-4) and others use agent-based models [[27,](#page-11-5)[28\]](#page-11-6).

Although model types might differ, across the contact tracing models there are a number of characteristics that the models share or that can be used to differentiate between models. We found that the majority of existing models that have been used to understand the impact of contact tracing on various diseases are typically done as exploratory and theoretical studies. One common characteristic of existing models is that they do not model a specific population [[29\]](#page-11-7), and thus do not take into account factors of the population such as the age structure of the population, social norms or socioeconomic status that might impact the outcome of the outbreak [[22\]](#page-11-8). However, there are some models that consider a specific outbreak on a specific population [[20,](#page-11-9)[27\]](#page-11-5) looking forward to predict how contact tracing might impact the outbreak, while others consider the disease more generally and look at the impact of contact tracing across a number of different diseases [\[15](#page-10-14),[19\]](#page-11-2). Model calibration is often done using data from the literature for disease parameters $[19,22]$ $[19,22]$ $[19,22]$ or from a real outbreak $[20,21]$ $[20,21]$ $[20,21]$ and estimates for different contact tracing scenarios. No modelling studies that we found calibrated their models using real contact tracing data from an outbreak. While these existing models are useful in understanding how contact tracing might impact an outbreak, the effectiveness of contact tracing can vary based on a number of factors not related to the disease including, social, political and ethical issues such as the approach of the public health personnel, the cooperation of the community and the availability and accessibility of testing [[1\]](#page-10-0). Thus, to learn as much relevant information as possible from a model, it is important to have a model that is designed using the specific characteristics of a population. Additionally, the models that are based on real outbreaks [[20,](#page-11-9)[27](#page-11-5)] tend to be prospective models looking at how contact tracing and other strategies might impact an outbreak in the future. There is a gap in the literature for models that are used to better understand a situation that happened. Looking back at the decisions made during the COVID-19 pandemic will help to determine what methods should be used in the event of another global pandemic or even a more local outbreak.

We propose using a country specific agent-based model that was designed to simulate the spread of COVID-19 in Ireland [[30\]](#page-11-11) to determine the effectiveness of contact tracing in Ireland during the first year of the COVID-19 pandemic (from March 2020 through February 2021). The model uses real data about the contact tracing program that was implemented in Ireland as an input to generate realistic estimates. Although we use Ireland as a case study in this paper, we present the use of a detailed country specific agent-based model to assess the impact of contact tracing as a methodology that can be used by other countries or regions. In the next section we provide a brief description of the model used, we then discuss the experiments run, and present the results and analysis.

2. Methods

2.1. Model description

The model used for the contact tracing study is presented in detail in a previous paper [\[30](#page-11-11)]. Here we provide a brief description of the model but for a better understanding see [\[30](#page-11-11),[31\]](#page-11-12). The model is an agentbased model that was created to simulate the spread of COVID-19 in Ireland. There are four main components that make up an agent-based model for the spread of an infectious disease: environment, society, transportation, and disease [\[32](#page-11-13)]. The model in [[30\]](#page-11-11) uses Irish data from the Irish Central Statistics Office (CSO) to create the environment, society, and transportation components the simulation is run on. The environment is made up of 31 counties (e.g., Cork County, Meath County) and city/county areas (e.g., Dublin City, Cork City) that are defined by the CSO. To create the society, we use census data to create a synthetic population where 1 agent is equal to 100 real people and the agent population in each county corresponds to the real population for that county in terms of its distributions of age, sex, economic status (e.g. student, working, retired, etc.), household size, household type (e.g. single, couple, couple with children, etc.) and number and age of children per household (under 15, 15 and older, both under

and over 15) [\[33](#page-11-14)]. Agent transportation is determined using either a gravity model (that simulates agents' movements in the community, with agents more likely to move to locations that are nearby and more likely to move to locations that are densely populated) or using agents' commuting movements, to work and school, based on the POWSCAR data [\[34](#page-11-15)]. This data provides information for the number of people commuting from one region in the country to another. Agent mixing patterns are calibrated to match contact rates in the POLYMOD study [[35\]](#page-11-16). The POLYMOD study provides a matrix of contacts by age groups, for example it provides information such as the average number of contacts individuals in age group 10–14 has with age group 60–64 in a community setting per day. The disease component of the model is set to mimic the spread of COVID-19 and several parameters, including R_0 , are taken from the literature to drive the model [[31\]](#page-11-12).

The disease component of the model follows the same structure as the SEIR population level model that was used by decision-makers in Ireland during the COVID-19 pandemic [\[36](#page-11-17)]. Agents can have a disease status of susceptible, exposed, infectious, or recovered. Agents who are exposed will move from exposed to either be infectious and pre-symptomatic or infectious and asymptomatic. If the agents are presymptomatic, they will become symptomatic after a predetermined period of time. All infectious agents will be infectious for a predetermined period of time before recovering. When an agent is infected and symptomatic they are either waiting to get tested and then tested, quarantining or not quarantining. Agents who are getting tested or quarantining will restrict their movements while agents not quarantining will move as usual. The values for the length of time that an agent is in each of these categories as well the portion of infected and symptomatic agents who are waiting for a test, quarantining and not quarantining are determined from the literature and for the COVID-19 model can be found in [\[31](#page-11-12)].

During each run of the model a certain number of infectious agents are ''tested'' and are informed of their COVID-19 status. The model is designed to simulate a given period of the actual pandemic in Ireland and so a number of parameters of the model (e.g., days an agent is presymptomatic, days an agent is infectious and the percent of infected agents who take part in contact tracing) are fitted to real rates as recorded during that period of time. The implementation of the model also includes the ability to turn-on/off several interventions designed to slow the spread of the virus. These interventions are based on those that were used in Ireland during the pandemic. The model allows for a number of interventions including allowing schools to open and close, a lockdown to occur that results in a certain percent of agents working from home and agents reducing movements, contact tracing, and vaccinations. The model can also be adjusted so that agents reduce their movements without a lockdown. As we aim to investigate the impact of contact tracing in Ireland using our model the next section discusses the contact tracing intervention in the model in more detail. To see more detail of the implementation of the other interventions (school closures, lockdowns and vaccinations) see [\[31](#page-11-12)].

2.2. Contact tracing

Agent-based models are a useful tool to estimate the impacts of contact tracing as they can directly simulate and track contacts between individuals (agents) within the model. We are then able to see how isolation of the contacts or a percent of contacts of an infected agent will impact the spread of COVID-19. The model allows for contact tracing to be turned on or off. This allows the user to determine if contact tracing is happening in their scenario. If contact tracing is turned on in the model, to simulate contact tracing within our model, when an agent tests positive, the model determines if the agent takes part in contact tracing or not. Contact tracing is only done in the model for agents who test positive and not for infectious agents who have not been tested in the model. We estimate the probability that an agent will take part in contact tracing using the percent of cases in Ireland where

contact tracing was completed for a given month. Thus, the proportion traced changes each month. For example, if 80% of cases in Ireland participated in contact tracing then the model uses a probability of 80% to determine if an agent that has tested positive will participate in contact tracing. If an agent does participate in contact tracing, then their close contacts, agents who are part of their home, school, work or extended family networks, while infectious will be notified. If an agent is notified a probability determines if the notified agent participates in contact tracing and isolates. For this probability we use the percent of close contacts identified that got a COVID-19 test as a proxy. The isolation done by contacts when contact tracing is turned on in the model is in addition to any quarantining/isolating the agents do once they are symptomatic.

2.3. Schedule

Agent-based models are run using discrete time steps. Our model is run with 12 time-steps per day and 84 time-steps per week. Having multiple time steps per day allows for more realistic agent movements throughout the model. During night hours agents will remain at home and will not mix within the community, while during the day agents will follow set schedules based on their economic status. On weekdays, students will go from home to school at a given time-step then remain at school before returning home at a given time-step. Workers will follow a similar schedule to students, whereas non-working agents will move throughout the community during the daytime. On weekends, students and workers will also move through the community. The model will start at a given week in the year and keeps track of the weeks to follow the school schedules. Between weeks 26 and 34, and between weeks 51 and 52 schools are closed to simulate summer and Christmas holidays.

2.4. Model output

The main output from the agent-based model that is used in the contact tracing study is the total number of newly infectious agents who have COVID-19 on a given day in the model daily incidence or new cases of COVID-19 in the model. At the start of each day in the model the number of new cases is reset to 0, then each time an agent who is in an exposed state moves from exposed to infectious the count of new cases is increased by 1. At the end of the day in the model, the total number of new cases is reported.

Although hospitalisations, ICU admissions, and deaths are not directly incorporated in the model, they are important in understanding the impact of COVID-19 on the Irish healthcare system. Thus using the daily incidence produced as output from the model, we estimate the hospitalisations, ICU admissions, and deaths. For the first year of the COVID-19 pandemic we take the actual recorded monthly rates of hospitalisations and ICU admissions in Ireland and the monthly case-fatality rate in Ireland as determined by the date of death. The denominator used to calculate case-fatality, hospital and ICU admission rates was the number of new cases notified. These rates therefore represent the proportion of new cases that were admitted to hospital or to ICU or that died. These rates can be found in [Table](#page-5-0) [1](#page-5-0) and were calculated from data reported in the Health Protection Surveillance Centre's COVID-19 Detailed Statistics Profile, hospitalisation rates, ICU admission rates and case fatality rates using the number of PCR-confirmed cases, hospitalisations, ICU admission and deaths per month [[37\]](#page-11-18).

Combining the actual rates with the outputs of the model under different intervention scenarios we calculate two things: (1) a monthly number of hospitalisations, ICU admissions and deaths, and (2) a daily number of hospitalisations, ICU admissions and deaths. For the monthly estimates we sum the number of new cases from the model for each month the model is run and then multiply by the rates in [Table](#page-5-0) [1](#page-5-0). This gives us monthly estimates for hospitalisations, ICU admissions and deaths based off the number of cases simulated in the model. For

Table 1

Monthly rates of hospitalisations, ICU admissions and deaths in the first year of the COVID-19 pandemic. *Source:* Data from [\[37\]](#page-11-18).

example, if a given run of the model predicts there were 100 cases of COVID-19 in Ireland in March 2020, using the rate in [Table](#page-5-0) [1](#page-5-0) we would estimate that these cases resulted in 29 hospitalisations, 5 ICU admissions and 4 deaths. The daily estimates are taken by multiplying the rates for the month by the number of new cases simulated from the model each day.

2.5. Experiments

The model is run to simulate the first year of the COVID-19 pandemic in Ireland. We start the model from 1st February 2020. Although no cases were notified in Ireland until 29th February 2020 [[38\]](#page-11-19), we begin our model on 1st of February for a number of reasons. The first is this allows for the model to have a burn-in period and for the dynamics of the system to take over from the initial conditions. While the initial conditions are important in an agent-based model, there can be initialisation bias in agent-based models that may over or underestimate the outcomes. A burn-in period helps to mitigate this [\[39](#page-11-20)]. Additionally, it is possible that the initial infected case in Ireland had already infected others before they were identified, or other cases were infectious but not yet identified. Starting the model before the first identified cases helps to stabilise the model and takes into account these different possibilities.

The simulation is run where we include contact tracing and where we do not include contact tracing but everything else in the model is held constant. This allows us to compare the results between the two scenarios and estimate the impact that contact tracing had on the COVID-19 pandemic in Ireland. [Table](#page-6-0) [2](#page-6-0) shows the values for each month for the percent of cases where contact tracing was complete in Ireland and the percent of contacts who were tested. Anonymous aggregate data on cases and close contacts collected in the CovidCare Tracker were used to determine the proportion of cases with contact tracing completed, and the proportion of close contacts who attended for testing. These data have been reported on since the implementation of the CMP, for monitoring and evaluation of the program to ensure alignment with the object of the HSE as defined in the Health Act 2004.[1](#page-5-1)[2](#page-5-2) These are used as proxies in the model for the probabilities of a case taking part in contact tracing and a notified contact participating in contact tracing respectively. In March and April 2020 and January 2021, no close contacts were referred to testing. In March and April 2020 test supplies were limited and in January 2021 due to the high

number of cases in Ireland testing close contacts was temporarily paused. As there was a recommendation for close contacts to isolate in January 2021 we assume the same percent of contacts will isolate as they had in December thus in the model 78% of close contacts will isolate in January. Agent-based models are stochastic; thus each model run will produce different results. In order to accurately capture the model results, for each scenario (contact tracing and no contact tracing) we run the model 30 times and average the results across the 30 runs. We determined that 30 runs were necessary using the methodology outlined in [[40](#page-11-21)].

The model starts with three agents infectious with COVID-19 and two exposed but not yet infectious. One of the infectious agents is asymptomatic and one is pre-symptomatic. All other agents are susceptible as there was no prior immunity to COVID-19 at the start of the pandemic. These initial conditions were chosen so that the model showed sustained transmission and would produce a peak in April and May 2020 similar to the peak that occurred in Ireland at that time.

As we aim to simulate the COVID-19 pandemic in Ireland, we implement several interventions throughout the year that are intended to mimic what occurred in Ireland. The interventions are school closures, lockdowns, vaccinations, and reduction in agent movements. [Table](#page-6-1) [3](#page-6-1) shows the date changes occurred in the model and what the status of each intervention is at that time. The mixing column shows the rate of community mixing that determines how often the agents will enter the community. This parameter has been calibrated so that the simulated pandemic with contact tracing included roughly matches what happened in the real pandemic and was the only parameter that was calibrated to match the real data. [Fig.](#page-6-2) [1](#page-6-2) shows the number of newly notified cases per day recorded in Ireland between February 2020 and March 2021 and the number of new cases per day that the model simulates during this time period. The root mean squared error between the simulated and real cases from February 2020 to March 2021 is 759.81 and the correlation coefficient is 0.82 suggesting a strong relationship between the two sets of data. However, if we calculate the root mean squared error from February 2020 through December 2020, we get a root mean squared error of 315.96 and a correlation coefficient of 0.88 suggesting an even stronger match between the data. This shows the model is well calibrated in general and specifically through December 2020. The potential cause of the worse calibration from January 2021 is that in January 2021, because of the high number of cases, close contacts were no longer tested, and the surge of cases resulted in reporting delays. Both of these could have an impact on calibration. As the cases simulated from the model appear to match the real cases, we take this as evidence that the contact tracing scenario we are modelling is close to what happened in Ireland during the COVID-19 pandemic. This allows us to make the assumption that the results from our scenarios when we remove contact tracing from the model may be similar to what would have happened in Ireland if no contact tracing had occurred.

3. Results

To assess the impact that contact tracing had in the first year of the COVID-19 pandemic in the Republic of Ireland, we present the results of modelling the experiments discussed in the previous section. We first look at the number of cases simulated in each scenario and then on measures that are proxies for burden on the health system (hospital admissions and ICU admissions) and finally present the difference in estimated deaths between the two scenarios.

3.1. Cases of COVID-19 in Ireland

[Fig.](#page-7-0) [2](#page-7-0) shows the total number of cumulative cases between the scenarios with contact tracing versus without. In the first few months of the pandemic, the difference between the two scenarios is small, but after August 2020 the difference begins to increase. There appears to

¹ [https://www.irishstatutebook.ie/eli/2004/act/42/section/7/enacted/en/](https://www.irishstatutebook.ie/eli/2004/act/42/section/7/enacted/en/html#sec7) [html#sec7](https://www.irishstatutebook.ie/eli/2004/act/42/section/7/enacted/en/html#sec7)

² Data available in reports prepared by CMP, approved by HSE Senior Staff, sent to NPHET and subsequently published on DOH website – [https://www.gov.ie/en/collection/691330-national-public-health-emergency](https://www.gov.ie/en/collection/691330-national-public-health-emergency-team-covid-19-coronavirus/)[team-covid-19-coronavirus/.](https://www.gov.ie/en/collection/691330-national-public-health-emergency-team-covid-19-coronavirus/)

Fig. 1. New Notified Cases per day recorded in Ireland and simulated by the model from February 2020 to March 2023.

Table 2

Percent of cases with completed contact tracing and percent of contacts who attended a PCR test. Used as a proxy in the modelling for the probabilities of a case taking part in contact tracing and a notified contact participating in contact tracing respectively. A value of N/A means that contacts were not referred to tests during that month. *Source:* Data from Ireland's CovidCare Tracker.

	% of cases with contact tracing complete	% of close contacts referred for a PCR test who attended
Mar-20	81%	N/A
Apr-20	64%	N/A
$May-20$	68%	78%
$Jun-20$	58%	83%
Jul-20	75%	81%
Aug- 20	82%	86%
$Sep-20$	88%	89%
$Oct-20$	79%	90%
$Nov-20$	84%	81%
$Dec-20$	87%	78%
Jan-21	82%	N/A
Feb-21	77%	82%
$Mar-21$	81%	90%

Table 3

Restrictions and changes in agent mixing that were implemented in the model. The normal mixing rate is the mixing rate determined when calibrating the model to the POLYMOD study data and represents the expected mixing if the agents are not adapting their behaviour because of the infectious disease outbreak.

be a more rapid increase in the difference between the two scenarios, in October 2020 and January 2021. By the end of February 2021 in the model, there were approximately 300,000 more cases in the scenario with no contact tracing compared to the scenario with contact tracing.

These changes appear to correspond to the peaks in different waves of the pandemic in Ireland which can be seen in [Fig.](#page-7-1) [3](#page-7-1) showing the total number of newly infectious cases per day by scenario. This suggests that contact tracing had an important role in reducing the size of the peaks of each wave during the first year of COVID-19. In other words, contact tracing did help to flatten the curve, particularly during peaks of the outbreak when a large percentage of healthcare capacity is being utilised, and thereby protected the health services. The cases of COVID-19 are the main output of the model and the output that is used to derive the rest of the measures presented in the next sections (Hospital and ICU Admissions, and Deaths). As the outputs presented here are averages, over a set of 30 runs, we also present the standard deviations for new cases per day at each time point in [Fig.](#page-7-2) [4](#page-7-2) to provide a better understanding of the variability across the simulations. In the figure it appears that the highest variability in the model results occurs at the peaks of the outbreak when there is a higher average number infected.

3.2. Hospital and ICU admissions

[Fig.](#page-8-0) [5](#page-8-0) shows the cumulative number of hospitalisation and ICU admissions in each scenario. From [Fig.](#page-8-0) [5](#page-8-0) it can be seen that in the no contact tracing scenarios we seem more hospitalisations. The differences between the two scenarios is 16,005 more hospitalisations and 1,678 more ICU admissions. These are large numbers that could lead to the Irish health care system becoming overwhelmed. To put in perspective, Ireland's ICU capacity is amongst the lowest in the industrialised world with five ICU beds per 100,000 in 2019, equating to approximately 215 ICU beds [[41\]](#page-11-22). By comparison, France has 16 ICU beds per 100,000 and Germany has 28.

Interestingly, looking at hospitalisations and ICU admissions it is apparent that there were certain times during the pandemic where contact tracing seemed to have a larger impact on the difference in the number of hospitalisations and ICU admissions when the rate of admissions increases more rapidly in the scenario without contact tracing. This can be seen to some extent in the first few months of the pandemic (March to May 2020) and then again during the peak of the second wave (September and October 2020) and much more noticeably during the peak of the third wave (January and February 2021). In fact, the difference in the number of hospitalisations and the ICU admission between the contact tracing and no contact tracing scenarios in January 2021, 5,494 more hospitalisations and 572 more ICU admissions without contact tracing, is over a third of the total difference between the scenarios. As the month with the most cases of COVID-19 was also January, this makes sense and shows the critical importance of contact tracing even when case numbers are high.

Total Cases

Fig. 2. Total cumulative cases recorded in the simulations with contact tracing and no contact tracing from February 2020 to March 2023.

Fig. 3. New Infectious Cases per day recorded in the simulations with contact tracing and no contact tracing from February 2020 to March 2023.

Fig. 4. Standard deviation of new cases per day at each model time step.

3.3. Deaths

[Fig.](#page-8-1) [6](#page-8-1) shows the total number of deaths based on the number of cases in the model for both the contact tracing and no contact tracing scenarios.

From [Fig.](#page-8-1) [6](#page-8-1) we can see that over the course of the first year of the pandemic contact tracing potentially saved a large number of deaths. The difference in deaths between the two scenarios by March 2021 is 5,768, which would be approximately 0.11% of the current Irish population. Without contact tracing there could have been an approximately 80% increase in deaths in the first year of the pandemic (March 2020 through February 2021). These additional deaths due to COVID-19 in the non-contact tracing scenario, would have a large impact on the number of deaths per year. In 2020 there were 31,765

(a) Hospital Admissions

(b) ICU Admissions.

Fig. 5. Total cumulative hospitalisations and ICU admissions recorded in the simulations with contact tracing and no contact tracing.

Total Deaths

deaths in Ireland, due to both COVID-19 and other causes [[42\]](#page-11-23), adding in the difference in deaths the model finds if no contact tracing occurred from March to December 2020 there would be 2,619 additional deaths which would mean that in 2020 total deaths would have increased from 31,765 to 34,384, which equates to an 8% increase in deaths in 2020.

4. Discussion

Our results show that when contact tracing is included in the agent-based model we observe significant decreases in cases, hospital admissions, ICU cases, and deaths. The model shows that in the first year of the pandemic, if no contact tracing had occurred, there was a potential to have had approximately 16,000 more hospitalisations, and 1,600 more ICU admissions, and nearly one third of these admissions would have occurred in January 2021. The model also shows that there could have been over 5,000 additional deaths due to COVID-19 in the first year of the pandemic. However, the number of deaths were calculated based on the mortality rates during a given month of the pandemic. It is likely that more COVID-19 deaths would have occurred if the health care system was overwhelmed due to higher admissions resulting in a reduction in quality of care for many patients. Additionally, this estimated difference in deaths is only those that are attributed directly to COVID-19. It is likely that there would be an even higher number of excess deaths from other non COVID-19 related conditions due to a more limited access to healthcare. Our model results show that contact tracing seems to have the biggest impact at the peaks of the outbreak. Thus, based on our results it would seem important for contact tracing to continue during peaks of the virus, even though at these times it is often tempting for contact tracing to be scaled down so that the resources used in the contact tracing program can be allocated somewhere else. However, we do note that the success of a contact tracing program or any intervention, is likely due to a number of interdependent factors including the population's adherence to the intervention as well as potential government support. Contact tracing in Ireland leaned heavily on a well-trained cohort of contact tracers working to a detailed script that was regularly updated given the changes in public health guidelines. While the majority of people were well-informed, it was nevertheless the case that guidance and recommendations were updated regularly and differed for different age cohorts and people exposed or infected in different settings. By phoning people and talking them through the advice and guidance we could be sure that each person was getting the most up-to-date advice. This was particularly important given some of the restrictions that were placed on peoples' movements.

The results we found were consistent with the literature where a number of modelling studies have found that contact tracing does result in a reduction of cases and is an important tool in slowing the spread of COVID-19. The effectiveness of contact tracing apps were assessed using an agent-based model [[43\]](#page-11-24) and it was determined that while contact tracing apps can reduce infection rates, if testing capacity is limited the contact tracing apps can create a substantial increase in demand for testing which can be counterproductive if symptomatic cases are not prioritised. Another study used a continuous-time agestructured branching process model to determine the impact of contact tracing and found that a high-quality rapid contact tracing is effective in reducing the spread of COVID-19 if it is combined with support for people in quarantine and isolation [[44\]](#page-11-25). However, our study is unique in that we are not assessing the impact of potential different contract tracing strategies but attempting to determine the impact that contact tracing had on the course of the COVID-19 pandemic in Ireland during the first year of the COVID-19 pandemic. Our model uses a synthetic population created to match the Irish population, implements a set of COVID-19 restrictions that are consistent with what was done in Ireland in 2020, and determines the level of contact tracing in the model based

on the level of contact tracing done in Ireland at a given time of the year. The modelling results showed that there could have potentially been an increase in deaths from COVID-19 of approximately 80% in the first year of the pandemic (March 2020 through February 2021) if contact tracing did not occur. In perspective, the additional deaths from COVID-19 simulated in the model when no contact tracing occurs would be equivalent to an 8% increase in the total deaths (both from COVID-19 and from other causes) that actually occurred in 2020 in Ireland. The finding of an increase in mortality due to COVID-19 is in line with an Irish study showing that from 11 March to 16 June 2020, there was an increase in observed mortality in Ireland and that this increase in mortality was due to COVID-19 [[45\]](#page-11-26). It then follows that if there was no contact tracing leading to an increase in cases, additional deaths would have occurred. The study also found that the increase in mortality was less than the total number of COVID-19 deaths in the period, this was likely due to people who were infected with COVID-19 close to the end of life who would have died regardless of COVID-19 infection [\[45](#page-11-26)]. This would suggest that it is possible that the number of COVID-19 deaths the model predicts might not all be excess mortality in a year.

There are a number of limitations of our study. While models are often used to predict the impact of interventions and our model was calibrated to match the COVID-19 pandemic in Ireland, all models make assumptions and are inherently wrong but that does not mean a model is not useful. The model we use introduces some assumptions and limitations. We use a model that has a scaled population where 1 agent equates to 100 people and has been previously validated and tested [[30\]](#page-11-11). However, the scaling could impact the model results in a number of ways. For example, if the contact rates generated by a scaled down population are underestimated because of a lower population density, this could impact the transmission of the virus. This is accounted for in the model in that the contact rates for the agents are generated so that they match real world contact data. Therefore, even if there are fewer agents, the agents still have the same number of contacts that they would if there was a full population. It was shown in [[30\]](#page-11-11) that the scaling factor did not change the average results but increased variation. Some of the other assumptions that we make are due to available contact tracing data. The data Ireland has collected was collected for clinical purposes and not for evaluating contact tracing. This led to the assumption that we make in using the percent of contacts that received a test as a proxy for the percent of contacts who isolated. This assumption was made because of the data that was available. As we are not sure of the actual portion of contacts who isolated the assumption could lead to either an under or overestimate. It could be an underestimate of those who isolated as it is possible that there were individuals who isolated when they were told that they were a contact but did not get a test or an overestimate if those who got tested did not adhere to isolation. The availability of data led to a further limitation of the study where all agents are equally likely to isolate if they are a contact. Agent-based models have the ability to apply different behaviours by individuals or groups and while it is likely that certain groups were more likely to isolate when told they were a contact, we do not include different likelihoods for isolation for different agent groups due to the data being aggregated at the population level. However, we feel this is an acceptable assumption as a study of compliance in Ireland determined that the only socio-demographic characteristic that had an association with non-compliance was age [[46\]](#page-11-27). The results might differ if we had contact tracing data that was broken down by age groups but due to data availability we were not able to incorporate this into the model. Future work could look at adjusting the chance of isolation based on age to determine the impacts this may have on the model results. Additionally, the contact tracing in the model is done in a way where contacts are notified and then isolate immediately when an agent participates in contact tracing. This could lead to an underestimation of cases in the contact tracing scenario as in the real world it would take a number of days for the contacts to be notified and in that time they

might become infectious and transmit to others. However, based on our model calibration, the contact tracing scenario is a close match to what happened in Ireland. [Fig.](#page-6-2) [1](#page-6-2) shows the calibrated model matches well through January 2021. However, we only consider reported cases in the calibration, this is likely an underestimate of the cases that occurred and therefore is a potential underestimate of total cases of COVID-19 and the impact of contact tracing. It was decided to only consider reported cases as we have a reliable estimate for reported cases but do not have such a reliable estimate for the unreported cases. Although we do have a tested state for agents that signifies that they are both infected and tested, we did not use this state for initial calibration. This is for simplification purposes as testing strategies varied within the first year of the pandemic in Ireland, thus to appropriately calibrate to this variable we would need to do a more in depth analysis of the testing strategies in Ireland and vary the number of agents that test based on this analysis. Future work could focus on reviewing the testing strategies and calibrating the model to tested cases and estimating the impact of COVID-19 on the reported cases within the model. We also do not consider that even in the no contact tracing scenario some portion of contacts may have isolated if they found out through word of mouth that they were exposed. If this occurred it could reduce the number of cases that we found in the no contact tracing scenario. In the study we only look at the number of cases, hospitalisations, ICU admissions and deaths attributed to COVID-19. These numbers are calculated using monthly rates from what occurred in Ireland from March 2020 through February 2021 and provide a good estimate for the contact tracing scenario, however, it is possible that the rates would be different if there was no contact tracing. For example, if hospitals began to be overwhelmed it is likely the criteria for hospital admission or ICU admission would change. If this was the case the numbers presented in this paper for the no contact tracing scenario would be incorrect. However, we feel that using the same rates allows for a good comparison between the contact tracing and no contact tracing scenarios with all else held constant. Estimating hospitalisations, ICU admissions and deaths based on model output and not directly in the model has a potential impact on the model results as we do not have differences in length of infection based on severity. This could potentially have an impact on the number of agents each sick agent infects. A mild case might have less time to infect other agents than a more severe case. However, for our initial analysis of contact tracing we did not include this difference in severity for the sake of simplicity in modelling. Furthermore, although it is known that the risk of being hospitalised or dying from COVID-19 changes with age, we only applied the overall rates of hospitalisations, ICU admissions and mortality to the data. As the contact tracing scenario is calibrated to the real data, using the average rates for all ages should give us an approximation of the admissions and deaths, but if the mix of ages of those infected in the non contact tracing scenario varies from the contact tracing scenario we might be over or underestimating hospital admissions and deaths. We also do not take into consideration many other factors that would further show the benefits of contact tracing. As mentioned previously deaths would likely be higher due to the health care system becoming overwhelmed. Additionally, we keep the same implementation of restrictions for both scenarios for consistency. This is a limitation to the study as if there was no contact tracing occurring lockdowns might have lasted longer or other interventions been put into place that would reduce cases, however, again we feel that it is important for a first comparison to keep all other parts of the model constant. One factor that might impact the effect contact tracing seems to have in the model is that contact tracing increases the number of agents who are isolating and testing. Thus, there is a question of if the change in cases due to contact tracing is due to identifying and targeting close contacts or just due to an increase in agents who are isolating as isolating agents cannot come into contact with other infectious agents while they are isolating. Future work can be done to determine if the change in cases is just due to an increase

in isolating agents. However, even if the change in cases is simply due to an increase in agents isolating, this would still be a positive impact of contact tracing and would help to better understand how contact tracing impacts an outbreak.

This modelling study is an important step in highlighting the impact that contact tracing had on the course of the COVID-19 pandemic in Ireland. Modelling can and has been used to predict the impact an intervention will have before it is implemented but it is also just as important to look back and understand the impacts of the interventions that were implemented. We clearly show that contact tracing allows for a break in the chain of infections and reduces cases, deaths and the burden on the hospital system. Future work will be done to assess the impacts of contact tracing in different scenarios and improve upon the study in a number of ways. Work can be done to include dynamic lockdowns and other restrictions in the model where lockdowns are entered based on thresholds allowing for an understanding of how much longer lockdowns would have been if contact tracing had not occurred. More work can be done to fully assess the impact of contact tracing not just on cases, deaths and admissions but the social and economic impact as well. While contact tracing has long been recognised as an important tool to control the spread of infectious diseases, the risks of contracting the disease in question needs to be balanced with the potential unintended consequences of isolation of those identified as part of the contact tracing process. Such effects include inability to earn and support dependants, inability to access services such as shops, negative effects on mental health from loneliness, increased occurrence of domestic violence, etc. Each case of COVID-19 has a cost in treatment or days lost from work. The total impact of COVID-19 on a population could be estimated using Disability Adjusted Life Years (DALYs). This would give an idea of both the impact or cost of deaths from COVID-19 and the impact of disability from COVID-19 and would be comparable across scenarios. DALYs could then be used to determine the optimal level of effort put into contact tracing based on DALYs averted. To do this, additional functions would need to be put into the model including deaths by age group as well as a measure of disabilities caused by COVID-19. Longer lockdowns due to higher cases would also result in a larger economic impact. However, while the contact tracing programme in Ireland was labour intensive and expensive, the authors would argue that the net benefit was substantial. The decision to take aggressive non-pharmaceutical interventions (including contact tracing) was due in part to the importance of protecting the hospitals (and ICU bed) capacity. By ''flattening the curve'' the CMP was able to relieve pressure on the hospitals and interrupt the chain of transmission that translated into lives saved. The work can also be applied to other infectious diseases, for example, contact tracing will likely be important in the current Mpox outbreaks and will likely play a role in ring vaccination strategies used to slow the spread of the virus.

Data availability

Data will be made available on request.

Funding

This work was partly supported by the ADAPT Centre for Digital Content Technology which is funded under the SFI Research Centres Programme (Grant13/RC/2106_P2) and is co-funded under the European Regional Development Funds.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

The authors wish to acknowledge the Irish Centre for High-End Computing (ICHEC) for the provision of computational facilities and support.

References

- [1] [Allan M. Brandt, The history of contact tracing and the future of public health,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb1) [Am J Public Health 112 \(8\) \(2022\) 1097–1099, Publisher: American Public](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb1) [Health Association.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb1)
- [2] [CDC, Health Departments, 2020, Centers for Disease Control and Prevention.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb2)
- [3] [Thiemo Fetzer, Thomas Graeber, Measuring the scientific effectiveness of con](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb3)[tact tracing: Evidence from a natural experiment, Proc. Natl. Acad. Sci. 118](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb3) [\(33\) \(2021\) e2100814118, Publisher: Proceedings of the National Academy of](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb3) [Sciences.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb3)
- [4] [N. Ferguson, D. Laydon, G. Nedjati Gilani, N. Imai, K. Ainslie, M. Baguelin, S.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [Bhatia, A. Boonyasiri, Z.U.L.M.A. Cucunuba Perez, G. Cuomo-Dannenburg, A.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [Dighe, I. Dorigatti, H. Fu, K. Gaythorpe, W. Green, A. Hamlet, W. Hinsley, L.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [Okell, S. Van Elsland, H. Thompson, R. Verity, E. Volz, H. Wang, Y. Wang,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [P. Walker, P. Winskill, C. Whittaker, C. Donnelly, S. Riley, A. Ghani, Report 9:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [Impact of Non-Pharmaceutical Interventions \(NPIs\) to Reduce COVID19 Mortality](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4) [and Healthcare Demand, Technical Report, Imperial College London, 2020.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb4)
- [5] [Amélie Desvars-Larrive, Elma Dervic, Nina Haug, Thomas Niederkrotenthaler,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Jiaying Chen, Anna Di Natale, Jana Lasser, Diana S. Gliga, Alexandra Roux, Jo](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5)[hannes Sorger, Abhijit Chakraborty, Alexandr Ten, Alija Dervic, Andrea Pacheco,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Ania Jurczak, David Cserjan, Diana Lederhilger, Dominika Bulska, Dorontinë](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Berishaj, Erwin Flores Tames, Francisco S. Álvarez, Huda Takriti, Jan Korbel,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Jenny Reddish, Joanna Grzymała-Moszczyńska, Johannes Stangl, Lamija Hadzi](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5)[avdic, Laura Stoeger, Leana Gooriah, Lukas Geyrhofer, Marcia R. Ferreira, Marta](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Bartoszek, Rainer Vierlinger, Samantha Holder, Simon Haberfellner, Verena](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [Ahne, Viktoria Reisch, Vito D.P. Servedio, Xiao Chen, Xochilt María Pocasangre-](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5)[Orellana, Zuzanna Garncarek, David Garcia, Stefan Thurner, A structured open](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [dataset of government interventions in response to COVID-19, Sci. Data 7 \(1\)](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5) [\(2020\) 285, Number: 1 Publisher: Nature Publishing Group.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb5)
- [6] [Jennifer Martin, Ciara Carroll, Zuneera Khurshid, Gemma Moore, Grainne](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb6) [Cosgrove, Robert Conway, Claire Buckley, Mary Browne, Maureen Flynn, Sarah](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb6) [Doyle, An Overview of the Establishment of a National Contact Tracing Pro](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb6)[gramme: A Quality Improvement Approach in a Time of Pandemic, Technical](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb6) [Report 5:12, HRB Open Research, 2022, Type: article.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb6)
- [7] [Janette Clarke, Contact tracing for chlamydia: Data on effectiveness, Int. J. STD](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb7) [& AIDS 9 \(4\) \(1998\) 187–191, Publisher: SAGE Publications.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb7)
- [8] [Azfar D. Hossain, Jana Jarolimova, Ahmed Elnaiem, Cher X. Huang, Aaron](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb8) [Richterman, Louise C. Ivers, Effectiveness of contact tracing in the control of](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb8) [infectious diseases: A systematic review, Lancet. Public Health 7 \(3\) \(2022\)](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb8) [e259–e273.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb8)
- [9] [Elizabeth Hunter, Brian Mac Namee, John D. Kelleher, A comparison of agent](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb9)[based models and equation based models for infectious disease epidemiology,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb9) [in: Proceedings of the 26th AIAI Irish Conference on Artifical Intelligence and](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb9) [Cognitive Science, 2018.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb9)
- [10] [Herbert W. Hethcote, The mathematics of infectious diseases, SIAM Rev. 42 \(4\)](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb10) [\(2000\) 599–653, Publisher: Society for Industrial and Applied Mathematics.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb10)
- [11] [Shweta Bansal, Bryan T. Grenfell, Lauren Ancel Meyers, When individual](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb11) [behaviour matters: Homogeneous and network models in epidemiology, J. R.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb11) [Soc. Interface 4 \(16\) \(2007\) 879.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb11)
- [12] [Jair Andrade, Jim Duggan, An evaluation of Hamiltonian Monte Carlo perfor](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb12)[mance to calibrate age-structured compartmental SEIR models to incidence data,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb12) [Epidemics 33 \(2020\) 100415.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb12)
- [13] [Alexandra B. Hogan, Kathryn Glass, Hannah C. Moore, Robert S. Anderssen,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [Erratum to: Age structures in mathematical models for infectious diseases, with](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [a case study of respiratory syncytial virus, in: Robert S. Anderssen, Philip](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [Broadbridge, Yasuhide Fukumoto, Kenji Kajiwara, Tsuyoshi Takagi, Evgeny](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [Verbitskiy, Masato Wakayama \(Eds.\), Applications + Practical Conceptualization](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [+ Mathematics= Fruitful Innovation, in: Mathematics for Industry, Springer](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13) [Japan, Tokyo, 2016, p. E1.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb13)
- [14] [Wouter Van den Broeck, Corrado Gioannini, Bruno Gonçalves, Marco Quaggiotto,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb14) [Vittoria Colizza, Alessandro Vespignani, The GLEaMviz computational tool, a](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb14) [publicly available software to explore realistic epidemic spreading scenarios at](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb14) [the global scale, BMC Infect. Dis. 11 \(1\) \(2011\) 37.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb14)
- [15] [Don Klinkenberg, Christophe Fraser, Hans Heesterbeek, The effectiveness of](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb15) [contact tracing in emerging Epidemics, PLOS One 1 \(1\) \(2006\) e12, Publisher:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb15) [Public Library of Science.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb15)
- [16] [Cliff C. Kerr, Robyn M. Stuart, Dina Mistry, Romesh G. Abeysuriya, Katherine](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Rosenfeld, Gregory R. Hart, Rafael C. Núñez, Jamie A. Cohen, Prashanth Selvaraj,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Brittany Hagedorn, Lauren George, Michał Jastrzebski, Amanda S. Izzo, Greer](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Fowler, Anna Palmer, Dominic Delport, Nick Scott, Sherrie L. Kelly, Caroline S.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Bennette, Bradley G. Wagner, Stewart T. Chang, Assaf P. Oron, Edward A.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Wenger, Jasmina Panovska-Griffiths, Michael Famulare, Daniel J. Klein, Covasim:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [An agent-based model of COVID-19 dynamics and interventions, PLoS Comput.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16) [Biol. 17 \(7\) \(2021\) 1–32, Publisher: Public Library of Science.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb16)
- [17] [Jason Thompson, Rod McClure, Tony Blakely, Nick Wilson, Michael G. Baker,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb17) [Jasper S. Wijnands, Thiago Herick De Sa, Kerry Nice, Camilo Cruz, Mark Steven](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb17)[son, Modelling SARS-CoV-2 disease progression in Australia and New Zealand:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb17) [An account of an agent-based approach to support public health decision-making,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb17) [Australian New Zealand J. Public Health 46 \(3\) \(2022\) 292–303.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb17)
- [18] [David Adam, Special report: The simulations driving the world's response to](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb18) [COVID-19, Nature 580 \(7803\) \(2020\) 316–318.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb18)
- [19] [Christophe Fraser, Steven Riley, Roy M. Anderson, Neil M. Ferguson, Factors that](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb19) [make an infectious disease outbreak controllable, Proc. Natl. Acad. Sci. 101 \(16\)](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb19) [\(2004\) 6146–6151, Publisher: Proceedings of the National Academy of Sciences.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb19)
- [20] [Abhishek Pandey, Katherine E. Atkins, Jan Medlock, Natasha Wenzel, Jeffrey P.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb20) [Townsend, James E. Childs, Tolbert G. Nyenswah, Martial L. Ndeffo-Mbah,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb20) [Alison P. Galvani, Strategies for containing Ebola in West Africa, Science 346](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb20) [\(6212\) \(2014\) 991–995.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb20)
- [21] [Joel Hellewell, Sam Abbott, Amy Gimma, Nikos I. Bosse, Christopher I. Jarvis,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21) [Timothy W. Russell, James D. Munday, Adam J. Kucharski, W. John Edmunds,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21) [Centre for the Mathematical Modelling of Infectious Diseases COVID-19 Working](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21) [Group, Sebastian Funk, Rosalind M. Eggo, Feasibility of controlling COVID-19](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21) [outbreaks by isolation of cases and contacts, Lancet. Global Health 8 \(4\) \(2020\)](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21) [e488–e496.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb21)
- [22] [Mirjam E. Kretzschmar, Ganna Rozhnova, Martin C.J. Bootsma, Michiel van](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb22) [Boven, Janneke H.H. M. van de Wijgert, Marc J.M. Bonten, Impact of delays](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb22) [on effectiveness of contact tracing strategies for COVID-19: A modelling study,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb22) [Lancet. Public Health 5 \(8\) \(2020\) e452–e459.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb22)
- [23] [Steven Riley, Christophe Fraser, Christl A. Donnelly, Azra C. Ghani, Laith J.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23) [Abu-Raddad, Anthony J. Hedley, Gabriel M. Leung, Lai-Ming Ho, Tai-Hing Lam,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23) [Thuan Q. Thach, Patsy Chau, King-Pan Chan, Su-Vui Lo, Pak-Yin Leung, Thomas](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23) [Tsang, William Ho, Koon-Hung Lee, Edith M.C. Lau, Neil M. Ferguson, Roy M.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23) [Anderson, Transmission dynamics of the etiological agent of SARS in Hong Kong:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23) [impact of public health interventions, Science 300 \(5627\) \(2003\) 1961–1966.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb23)
- [24] [Ken T.D. Eames, Matt J. Keeling, Contact tracing and disease control, Proc. R.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb24) [Soc. B: Biol. Sci. 270 \(1533\) \(2003\) 2565–2571.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb24)
- [25] [James O. Lloyd-Smith, Alison P. Galvani, Wayne M. Getz, Curtailing transmission](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb25) [of severe acute respiratory syndrome within a community and its hospital, Proc.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb25) [Biol. Sci. 270 \(1528\) \(2003\) 1979–1989.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb25)
- [26] [Niels G. Becker, Kathryn Glass, Zhengfeng Li, Geoffrey K. Aldis, Controlling](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb26) [emerging infectious diseases like SARS, Math. Biosci. 193 \(2\) \(2005\) 205–221.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb26)
- [27] [Adam J. Kucharski, Petra Klepac, Andrew J.K. Conlan, Stephen M. Kissler,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Maria L. Tang, Hannah Fry, Julia R. Gog, W. John Edmunds, Jon C. Emery,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Graham Medley, James D. Munday, Timothy W. Russell, Quentin J. Leclerc,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Charlie Diamond, Simon R. Procter, Amy Gimma, Fiona Yueqian Sun, Hamish P.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Gibbs, Alicia Rosello, Kevin van Zandvoort, Stéphane Hué, Sophie R. Meakin,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Arminder K. Deol, Gwen Knight, Thibaut Jombart, Anna M. Foss, Nikos I. Bosse,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Katherine E. Atkins, Billy J. Quilty, Rachel Lowe, Kiesha Prem, Stefan Flasche,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Carl A.B. Pearson, Rein M.G. J. Houben, Emily S. Nightingale, Akira Endo,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Damien C. Tully, Yang Liu, Julian Villabona-Arenas, Kathleen O'Reilly, Sebastian](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Funk, Rosalind M. Eggo, Mark Jit, Eleanor M. Rees, Joel Hellewell, Samuel](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Clifford, Christopher I. Jarvis, Sam Abbott, Megan Auzenbergs, Nicholas G.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Davies, David Simons, Effectiveness of isolation, testing, contact tracing, and](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [physical distancing on reducing transmission of SARS-CoV-2 in different settings:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [a mathematical modelling study, Lancet Infect. Dis. 20 \(10\) \(2020\) 1151–1160,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27) [Publisher: Elsevier.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb27)
- [28] [Corey M. Peak, Lauren M. Childs, Yonatan H. Grad, Caroline O. Buckee,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb28) [Comparing nonpharmaceutical interventions for containing emerging epidemics,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb28) [Proc. Natl. Acad. Sci. 114 \(15\) \(2017\) 4023–4028.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb28)
- [29] [Isobel Braithwaite, Thomas Callender, Miriam Bullock, Robert W. Aldridge,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb29) [Automated and partly automated contact tracing: a systematic review to inform](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb29) [the control of COVID-19, The Lancet Digital Health 2 \(11\) \(2020\) e607–e621,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb29) [Publisher: Elsevier.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb29)
- [30] [Elizabeth Hunter, John D. Kelleher, Validating and testing an agent-based model](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb30) [for the spread of COVID-19 in Ireland, Algorithms 15 \(8\) \(2022\) 270, Number:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb30) [8 Publisher: Multidisciplinary Digital Publishing Institute.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb30)
- [31] [Elizabeth Hunter, John Kelleher, An ODD-protocol for agent-based model for the](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb31) [spread of COVID-19 in Ireland, Reports \(2022\).](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb31)
- [32] [Elizabeth Hunter, Brian Mac Namee, John D. Kelleher, A taxonomy for agent](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb32)[based models in human infectious disease epidemiology, J. Artif. Soc. Soc. Simul.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb32) [20 \(3\) \(2017\) 2.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb32)
- [33] [\(CSO\) Central Statistics Office, Census 2016 small area population statistics -](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb33) [CSO - Central statistics office, 2018, Publisher: CSO.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb33)
- [34] [CSO, Census 2016 place of work, school or college - census of anonymised](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb34) [records \(POWSCAR\), 2017, Central Statistics Office.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb34)
- [35] [Joël Mossong, Niel Hens, Mark Jit, Philippe Beutels, Kari Auranen, Rafael](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb35) [Mikolajczyk, Marco Massari, Stefania Salmaso, Gianpaolo Scalia Tomba, Jacco](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb35) [Wallinga, Janneke Heijne, Malgorzata Sadkowska-Todys, Magdalena Rosinska,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb35) [W. John Edmunds, Social contacts and mixing patterns relevant to the spread of](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb35) [infectious diseases, PLOS Med. 5 \(3\) \(2008\) 1.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb35)
- [36] [James P. Gleeson, Thomas Brendan Murphy, Joseph D. O'Brien, Nial Friel,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb36) [Norma Bargary, David J.P. O'Sullivan, Calibrating COVID-19 susceptible-exposed](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb36)[infected-removed models with time-varying effective contact rates, Phil. Trans.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb36) [R. Soc. A 380 \(2214\) \(2022\) 20210120, Publisher: Royal Society.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb36)
- [37] [Ordinary Survey Ireland, COVID-19 HPSC detailed statistics profile, 2022.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb37)
- [38] [HSE Health Protection Surveillance Centre, COVID-19 Annual Report 2020, 2022,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb38) [Dublin: HSE HPSC.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb38)
- [39] [Jeon-Young Kang, Jared Aldstadt, Using multiple scale space-time patterns to](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb39) [determine the number of replicates and burn-in periods in spatially explicit](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb39) [agent-based modeling of vector-Borne disease transmission, ISPRS Int. J. Geo-](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb39)[Inf. 10 \(9\) \(2021\) 604, Number: 9 Publisher: Multidisciplinary Digital Publishing](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb39) [Institute.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb39)
- [40] [Elizabeth Hunter, John Kelleher, A framework for validating and testing agent](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb40)[based models: A case study from infectious diseases modelling, in: 34th Annual](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb40) [European Simulation and Modelling Conference, 2020.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb40)
- [41] [Michael Power, National audit critical care capacity - census report 2020, 2020,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb41) [Acute Operations Division, HSE National Clinical Programme for Critical Care,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb41) [Clinical Design and Innovation, HSE.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb41)
- [42] [Central Statistics Office, Vital statistics yearly summary 2021, 2022, Publisher:](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb42) [CSO.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb42)
- [43] [Jonatan Almagor, Stefano Picascia, Exploring the effectiveness of a COVID-19](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb43) [contact tracing app using an agent-based model, Sci. Rep. 10 \(1\) \(2020\) 22235.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb43)
- [44] [A. James, M.J. Plank, S. Hendy, R. Binny, A. Lustig, N. Steyn, A. Nesdale,](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb44) [A. Verrall, Successful contact tracing systems for COVID-19 rely on effective](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb44) [quarantine and isolation, PLOS One 16 \(6\) \(2021\) e0252499, Publisher: Public](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb44) [Library of Science.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb44)
- [45] [Health Information and Quality Authority, Analysis of excess all-cause mortality](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb45) [in Ireland during the COVID-19 epidemic, 2020, p. 35.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb45)
- [46] [Patricia M. Kearney, Danko Stamenic, Katarzyna Gajewska, Margaret B.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb46) [O'Sullivan, Sarah Doyle, Orlaith O'Reilly, Claire M. Buckley, Cross-sectional](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb46) [survey of compliance behaviour, knowledge and attitudes among cases and close](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb46) [contacts during COVID-19 pandemic, Public Health Pract. \(2023\) 100370.](http://refhub.elsevier.com/S2772-4425(23)00096-5/sb46)