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1 Model Description

We use the computer software Netlogo (Wilensky, 1999) to implement our model. Netlogo is an easy to use and popular environment for creating agent-based models (ABMs) (Gilbert, 2008). We chose Netlogo due to the increasing popularity of the platform with agent-based modellers and its ability as a medium to high/large scale modelling platform. It does, however, have disadvantages, one of the biggest being the speed of the program. When modelling simulations with a small number of agents Netlogo works well, however, once the number of agents gets large enough the simulation slows down.

Our model is an agent-based model for COVID-19 spread in the Irish population. An agent-based model for the spread of infectious diseases typically has four main components: disease, society, transportation and environment (Hunter et al., 2017). The disease component is structured to resemble an SEIR (susceptible, exposed, infected, and recovered) type compartmental model with the agents moving between the four state relating to infectiousness. Our society component is created to simulate a specific population using real census data to create a realistic synthetic population for Ireland, however, to save computing time we use a scaling factor so each agent represents 100 people in Ireland. The model includes transportation with agents moving between their current location and desired destination using predetermined destinations or destinations selected using a gravity model. The environmental component includes the Irish counties from the CSO that agents can move between. The model is a scaled up model of the county level agent-based model for Ireland (Hunter et al., 2020) and the town level agent-based model for Ireland (Hunter et al., 2018).

The following sections provide a detailed description of the model. We use the ODD (Overview, Design concepts, Details) protocol for our model description (Grimm et al., 2010).

2 Purpose

The purpose of the model is to simulate the spread of COVID-19 in Ireland with the aim of determining how different interventions strategies and different levels of agent movements affect the outbreak

3 Entities, state variables and scales

- **Agents/Individuals:** The model has one type of agent. The agents represent people in Ireland. The state variables for each agent include characteristics such as age, gender and economic status. Tables 1 - 2 shows the full list of variables for each agent.
- **Spatial Units:** Each grid cell or patch in Netlogo represents a county in Ireland. The state variables for each grid cell within the model are listed in Table 3.
- **Environment:** The Netlogo world is a two dimensional grid where the squares that make up the grid are referred to as patches. Patches in our model represent a county. All agents that are in a county at a given time are physically in the same location. However, agents will keep track of their location within that county. There are four possibilities for agents locations within a county: home, work, school, or the community. Who an agent comes into contact with depends on that location. For example, if an agent is at home, they know they are at home and will only come into contact with other members of their household who are also at home. Agents in the community within a county will come into contact with other agents in that county in the community but will not come into contact with all agents in the community. The probability of two agents in the community coming into contact is dependent on their shared social networks. If two agents from the same household are in the community there is a larger probability of them coming into contact than two agents who are in the same workplace or school who in turn have a larger probability of coming into contact than two agents who have no other connection. The probabilities of coming into contact with other agents are determined to match as best as possible with the POLYMOD data (Mossong et al., 2008), which measures contact patterns by age group and location for a number of countries. All agents within a county patch have access to information about the patch they are in, including the number of primary and secondary schools in the county. As well as the real world distances between the center of that county and all other counties in the model.

Environmental variables within the model include time, day of the week and week number. Each time step in the model represents two hours in a day. Seven days will make up one week. The first week in the year is considered week 1. Weeks are tracked to take into account summer vacation for students. Agents determine where they are moving based on

the time. The model is affected by the day of the week, as agents will act differently on a weekend versus a weekday. The week number also affects the model; students will not attend school in the summer and will treat everyday as a weekend.

4 Process overview and scheduling

The model proceeds in discrete time steps that each represent two hours. The model runs until there are no longer any agents who are exposed or infected. Using the language to describe an agent-based model from the ODD protocol (Grimm et al., 2010), an ABM can be broken down into a number of submodels. In other programming languages or programming tasks these submodels might be considered a function and are run in a specified order each time step. In this ABM every time step the following submodels are run: clock, vaccinate_schedule, lockdown_move or move depending on the lockdown status of the country, infect, recover, isolate_contacttrace, update-global-variables, find-R. Submodels are described in Section 8.

5 Design Concepts

- **Basic Principles:** We base the infection part of the model on an SEIR (susceptible, exposed, infected and recovered). It is a model that is widely used within infectious disease modelling. The idea is that when a susceptible agent come into contact with an infected agent there is a certain probability that the agent will become exposed to the disease. This probability is determined using the R_0 for the disease. R_0 is the basic reproductive number and is defined as the expected number of individuals infected by one infectious individual in a completely susceptible population. It can be broken down into three components, number of contacts per unit time (c), the transmission probability per contact (p) and the duration of the infectiousness (d). The relationship can be seen in Equation 1 (Thomas & Weber, 2001).

$$p = \frac{R_0}{cd} \quad (1)$$

Of the four variables in the equation, R_0 , c , p , and d , three are known or can be estimated from our model, allowing us to determine the value for p .

Agents will come into contact with other agents based on how they move through the environment and in the case when a contact results in an agent becoming exposed the agent will then progress from exposed to infected and finally to recovered. The transitions between states is determined by the natural history of COVID-19. As we are modelling COVID-19 we know that people who are infected become infectious prior to developing

symptoms thus we include a presymptomatic period for agents that occurs a given number of days before developing symptoms. Additionally, there are a number of subtypes of infected agents who are infectious. The agents can be asymptomatic, isolating, not isolating, waiting for a test or tested.

The model uses a gravity model to determine agent movements. Agents movements that are not predetermined (moving to home, school or work at given times) are determined based on an inverse relationship with the distance to the location and proportionally to the population density of the location. Agents are pulled to locations where there are already a lot of other agents and pushed away from locations that are far away. During weekends and summer holidays agents who are students move using the gravity model.

To scale the model up to a model for the entire Irish population we use a scaling factor. The scaling factor assumes that we can equate 100 similar people in the population to one agent. The scaling factor is further discussed in Section 6.1.

- **Emergence:** The emerging result from the model is the course that the infection takes. Based on the type of agent that is initially infectious, the other agents that come into contact with the infectious agent and how long the contact lasts, patterns can emerge for how an outbreak will spread. For example, if a student is infected compared with an unemployed agent, the student will likely come into contact with more susceptible agents every day it attends school leading to a larger outbreak. Agents decisions to stay home when sick can also have a major effect on how the outbreak occurs.
- **Adaptation:** Agents reproduce observed behaviors based on a set of rules given to them. For example, on weekends agents will move from one location to another a certain percentage of the time. If an agent becomes sick they will adapt their behavior in that they can decide to go about their day as normal or to stay home. Agents can also adapt their behaviour based on their vaccination status. With vaccinated agents more likely to be in the community mixing with other agents.
- **Sensing:** As they move through the environment, agents will sense if there are agents within their networks in the same area who they may come into contact with. Additionally, infected agents will sense if other agents that are close to them are susceptible so that they can potentially infect them.
- **Interaction:** The model assumes direct interaction between agents. If two agents occupy the same space (both agents are on the same Netlogo patch) they may be in contact with each other. If an agent comes into contact with another agent is determined by their location in the county (home, work, school or community) and if the other agent is in their

network. An interaction may lead to the infection of an agent if one is susceptible and one is infected.

- **Stochasticity:** Agent movements in the model are partially random. Weekend movement for all agents, summer movement for students and everyday movements for unemployed, stay at home, retired, and sick and disabled agents as well as everyday movements for agents who are not essential workers and are in lockdown are all determined stochastically. Agents will stay where they are $x\%$ of the time and $(1-x)\%$ of the time they will move to a selected location selected using a gravity model.

Additionally stochasticity in the model is seen in the spread of the infectious disease through the population. When an infectious agent comes into contact with a susceptible agent there is a certain probability that determines if the susceptible agent will become exposed. Once exposed the length of time that an agent will remain exposed before becoming infectious is determined by a probability distribution. Similarly the length of time an agent stays infectious is determined by a probability distribution.

- **Observation:** Every run of the model, data is collected on the number of agents who are newly infected that day, susceptible, exposed, infected and recovered at each time step. Additionally we collect the effective R value, the number of agents who are infected and infected with each variant, the number of agents who are infected and were infected in different locations (home, work, school and the community). The number of agents infected by 10 year age bands. The number of agents who are vaccinated, the number of agents who are vaccinated and are infected and the number of agents who are vaccinated and infected with each variant and the number of agents who are infected in each county.

6 Initialization

There are two steps to the initialization process, the first is creating the agents and the world and is only done once. After it is run once, the *world* in Netlogo is saved and is reloaded in for each run. The second initialization process involves loading in the saved world, setting global model parameters and setting initial conditions.

6.1 Scaling Factor

In order to simulate the spread of COVID-19 through the entire population of Ireland we use a scaling factor to map the agent population to the Irish population in order to reduce the amount of computing time and memory required to run the model. The scaling factor reduces the number of agents in the model. We use a factor of 100 so that every 1 agent in the model represents 100 people in Ireland. Tests of the scaling factor show that if the number of infected and exposed agents in the scenario being modeled is at least one order of magnitude

greater than the scaling factor then the model produces results similar to a non scaled model.

6.2 Creating the World

The steps for creating the world in Netlogo are as follows. The model is setup using data sets from the Irish Central Statistics Office (CSO). We use county level data. Agents are added to the county based on the closest census data to the year being modelled. Census data is produced every five years with the two most recent data set from 2016 census. The number of agents in the simulation will be approximately the number of people living in Ireland divided by 100. The following steps are used in populating the model with agents and are performed for each individual small area:

- Each household is assigned a type (single, couple, couple plus others, couple with children, couple with children plus others, single parent, single parent plus others, or other) and a family id that links all agents in the same household.
- Adults are added into each household. One agent is added to households with types single, single parent, and other. Two agents are added to the households with type couple.
- Adults in each household are assigned a sex and age based on a probability distribution determined from the CSO census age, sex tables for the relevant county.
 - The age categories provided by the CSO are by year until 19 after which ages are reported in ranges of five years, for example ages 20-24 or ages 60-64, and then anyone over 85 is combined into one age bracket. To have all ages represented in our model in each age bracket we randomly assign individuals one of the five ages represented in that bracket.
 - Couples are assigned opposite genders and ages within 10 years of each other.
- If a household type includes children a probability distribution determined from the relevant census data is used to determine if all children in the house are under 15, over 15, or both over and under 15.
- Data from the family units with children by size and age of children table is used to determine the probability that each household with type child has 1, 2, 3, 4 or 5 children in the household.
- Children are added into each household.
- Children are assigned a sex and age based on a probability distribution extracted from the relevant census data and the type of children the household is assigned to (under 15, over 15 or both under and over 15).

- If the total number of agents populating a county is not equal to the total number of agents who should be in the area based on the scaled down CSO data, additional agents are added and randomly assigned to households of types couple plus others, couple with children plus others, single parent plus others, or other.
- All agents are assigned an economic status based on CSO data.
 - Agents over 65 are assigned to retired.
 - Agents between the ages of 5 and 14 are assigned to student.
 - Agents between the ages of 15 and 18 are first assigned to student. If there are more agents aged 15 to 18 in the county than the number of students in the same age categories then the agents are assigned to looking for first job. If there are still more agents aged 15 to 18 they are then assigned an economic status of work, unemployed or sick/disabled following the distribution for these categories for the relevant county.
 - Adult agents under 65 are assigned to work, looking for first job, unemployed, sick/disabled, or stay at home following the distribution for these categories for the relevant county. Agents are only assigned to stay at home if they are part of a couple.
 - Agents under the age of 5 are assigned to student if they have no stay at home parent. If they have a stay at home parent then a probability determines if the agent will be assigned to student.
- Agents with an economic status of work are assigned to a workplace based on commuting data. The data is used to determine the probability that an agent in a given electoral division (CSO area one step above small areas) will commute to any other county.
- Agents aged 13 and up with an economic status of student are assigned to a secondary school based on a distance function. The closer the secondary school to the student the greater the probability the student will attend the school.
- Agents aged 4 to 12 with an economic status of student are assigned to a primary school based on a distance function. The closer the primary school to the student the greater the probability they student will attend the school.
- Agents aged 3 and below with an economic status of student are assigned to a pre-school closest to their home patch.
- When all agents in the region are assigned a workplace or school, social networks are created.
 - Agents create a family network with all other agents in their household.

- Agents create a work network with all other agents that work in the same workplace.
- Students create a school network with all other agents in their school and a class network with other agents in the school who are the same age as them.
- Students create a small school network which is a smaller class network made of only agents their own age. The size of this small school network is determined from a global parameter.
- Extended family networks are created so that to help capture the spread of the virus between children and grandparent carers. The number of agents over 69 who take care of grandchildren is input into the model. This number of agents then set the variable `grandparent_care` to true and determine the number of hours that they care for grandchildren each week. These agents are then matched with households in their county who have at least one child under the age of 15. All agents in both households are assigned to an extended family network.

6.3 Setting Global Parameters

There are a number of global parameters that need to be defined before the model is run. These parameters are determined from a number of different sources or can be changed to investigate the affect changing the parameter has on the model output. Table 4 shows the parameters, their explanation, examples of values for the parameters and sources for the parameter values.

State Variables	Description
Who	Unique Agent Id
Age	0 - 95
Sex	Male, Female
Familyid	Connects family members
Extendedfamily_id	Connects extended family members
Small_area	Region of town agent lives in
Adult?	Is the agent an adult. True/False
Home_patch	The Netlogo patch where the agent's home is located
Infant	Is the child an infant. True/False
Econ_stat	Economic Status of the agent. Work, Student, Retired, Unemployed, Looking for First Job, Stay-at-home, Sick/Disabled
Work_patch	Coordinates of the agent's workplace
Workplace	ID of workplace
Essential	Is the agent an essential worker or working during lockdown
School	ID of school agent attends
Family_network	Other agents in the agent's family
extendedfamily_network	Other agents in the agent's extended family (grandparents)
Work_network	Other agents in the agent's workplace
Class_network	Other agents in the agent's school who are the same age
School_network	Other agents of any age in the agent's school
School_small_network	A small number of agents in the agents class network
Small_network	Variable used to create school small network
grandparent_care	Does the agent take pat in grandparent care
grandparent_care_hours	Care hours assigned to the agent
grandparent_day	Number of days the agent takes care of grandchildren
Location	Where is the agent in the small area Community, Work, School, Home
Sick?	Is the agent sick? True/False
Immune?	Is the agent immune? True/False
Exposed?	Is the agent exposed? True/False
Infectious?	Is the agent infectious
Isolate?	is the agent isolating
Nisolate?	Is the agent not isolating even though sick
Tested?	Has the agent been tested positive?
Asymptomatic?	Is the agent asymptomatic?
Presymptomatic	Is the agent presymptomatic?
Vaccinated	Is the agent vaccianted? True/False
Variant	What variant is the agent infected with alpha/delta
Individual_infectivity	Base infectivity plus any modifiers to an agents infectivity (variant, asymptomatic, vaccianted etc)
Individual_movement	Modifier for an individual agent's movement. Are they more or less likely to stay home
Complication	Will the agent have severe case
Home_sick	Likelihood that an agent will stay home when infected.
Asymptomatic_delta	Is the agent immune to symptomatic infection from the delta variant
Asymptomatic_alpha	Is the agent immune to symptomatic infection from the alpha variant
Immunity_alpha	Is the agent completely immune to alpha variant
Immunity_delta	Is the agent completely immune to the delta variant
Days_sick	Number of days the agent has been sick
Days_exposed	Number of days the agent has been exposed
Days_presymp	The days until an agent is presymptomatic
Tick_exposed	The time the agent was first exposed
Ticks_exposed	The length of time the agent has been exposed
Tick_sick	The time the agent first moved from exposed to sick

Table 1: State Variables for agents model

State Variables	Description
Where_sick	Where was the agent infected? Community, Work, School, Home
Immunity	The immunity the agent has to the disease. Values between 0 and 1
Dest-patch	The location the agent is moving towards
Patchon	The patch that the agent is currently on
Num_contacts	List of the number of contacts an agent had had each time step
Avg_contacts	The average number of contacts the agent has had
Contact?	was the agent in contact with an infectious agent
Close_contact?	Was the agent in contact with an infectious agent in their network
Infectedby	Other agent who the agent was infected by
Numinfected	Number of agents the agent infected
contactby	What infectious agent came into contact with the agent
close_contact	Is the agent identified as a close contact
family_contact	Is the agent identified as a family contact
isolate_length	How long will the agent isoalte
tick_notified	The time the agent is notified they are a close contact

Table 2: State Variables for agents model continued

State Variables	Description
sm_area	The small area ID for the Netlogo patch from the CSO data
town_name	Name of the town that the small area is part of
county	Name of the county
primary_count	Count of primary schools in the small area
secondary_count	Count of secondary schools in the small area
distances	List of real world distances to other small areas
otherpatches	List of the small area IDs of the other patches
moveprob	The probability that the agents on the patches will move to another patch based on the distance
other_ed	List of other small areas in the town. List should only be included for one patch in the town All other patches in the town should have a value of 0.
turtsted	List of agents in the town

Table 3: State Variables for each Netlogo patch in the model

Global Parameters	Description	Value or Range	Citation
prop-newvariant	Proportion of cases that are the new variant	0.2	Range from 0 to 1
newvariant_infectiousness	the infectiousness multiplier of the new variant	1.6 (Delta variant)	
infectivity	Baseline parameter to determine if an infectious agent will pass on the virus on contact with a susceptible agent	0.007	Formula from (Thomas & Weber, 2001)
R0	Parameter not directly in the model but used to determine infectivity	3.73	(More et al., 2020)
ssn	size of small school network	5	Derived to match (Mossong et al., 2008)
start_week	week of the year the model starts in	1-52	
class_cont	Baseline number that determines if a student comes into contact with another student their age while in school	0.002	Derived to match (Mossong et al., 2008)
school_cont	Baseline number that determines if a student comes into contact with another student in their school while in school	0.001	Derived to match (Mossong et al., 2008)
school_sn_cont	Baseline number that determines if a student comes into contact with another student in their small school network while in school	0.03	Derived to match(Mossong et al., 2008)
work_cont	Baseline number that determines if an agent comes into contact with another agent in their work network while at work	0.05	Derived to match(Mossong et al., 2008)
community_cont	Baseline number that determines if an agent comes into contact with another agent not in their network while in the community	0.003	Derived to match(Mossong et al., 2008)
community_work	Baseline number that determines if an agent comes into contact with another agent in their work or class network in the community	0.75	Derived to match (Mossong et al., 2008)
stay_at_home_rate	how often an agent stays at home when not in the work or community	0.6	Derived to match (Mossong et al., 2008)
work_from_home_rate	percent of working agents going to work and not working from home if there is a lockdown	0.2	(Redmond & McGuinness, April 2020)
percent_asymptomatic	percent of infected assumed to be asymptomatic	0.5	Range from (Gleeson et al., 2021)
percent_isolation	percent of infected agents assumed to go immediately in to isolation	0.13	Range from (Gleeson et al., 2021)
percent_nisolation	percent of infected agents who will not isolate	0.12	Range from (Gleeson et al., 2021)
u13_communityclassmodifier	modifier for community contacts between under 13 year old students	0.133	Derived to match (Mossong et al., 2008)
u13_communitymodifier	modifier for community contacts for those under 13	0.037	Derived to match (Mossong et al., 2008)
s1319_communityclassmodifier	modifier for community contacts between 13 and 18 year old students	0.04	Derived to match (Mossong et al., 2008)
s1319_communitymodifier	modifier for community contacts for those between 13 and 18	0.0185	Derived to match (Mossong et al., 2008)
u13_ssnmodifier	modifier for small school network contacts for under 13 year olds	6	Derived to match (Mossong et al., 2008)
u13_schoolmodifier	modifier for school network contacts for under 13 year olds	2	Derived to match (Mossong et al., 2008)
u13_classmodifier	modifier for class network contacts for under 13 year olds	5	Derived to match (Mossong et al., 2008)
asyp_reduction	modifier for the reduction in infectivity for asymptomatic agents	0.25	Range from (Gleeson et al., 2021)
child_reduction	modifier for the reduction in infectivity for children	0-1	
isolate_reduction	modifier for the reduction in infectivity for isolating agents	0.05	Range from (Gleeson et al., 2021)
exposedperiod	Days that an agent is exposed but not yet showing symptoms	5.9	Range from (Gleeson et al., 2021)
infectiousperiod	Days that an agent is infectious and showing symptoms	7	Range from (Gleeson et al., 2021)
presymptomaticperiod	Days an agent is infectious but presymptomatic	1	Range from (Gleeson et al., 2021)
waittotest	Days between symptoms and a positive test	5.15	(More et al., 2020)
lockdown	Are there movement restrictions?	TRUE/FALSE	
secondary_school_closed	Are secondary schools closed?	TRUE/FALSE	
primary_school_closed	Are primary schools closed?	TRUE/FALSE	
vaccinate?	Is vaccination included in the model	TRUE/FALSE	
grandparents_care_count	count of over 70s taking care of grandkids	948	Percent from (TILDA, 2019)
per_contacttrace	percent or tested agents who are contact traced	0-1	
per_ct_tested	percent of agents who are identified as contacts who isolate	0-1	

Table 4: Global parameters for the model

Additionally there are a set of global variables that are essential to the running of the model but are defined by the model itself. For example, a variable *students* that records all agents who are students in the model, or *week* records the week of the year that is being simulated. Table 5 lists these variables.

Global Variables	Description
twns	A list of towns in the region
students	A list of agents who are students
workers	A list of agents who are workers
non-workers	A list of adult agents who are not working (retired, unemployed etc.)
stay-at-home	A list of agents who are stay at home parents
infants	A list of agents who are infants (under 1 year)
town_patches	A set of patches or gridcells that represent the counties in the model
time	time of the day in the simulation (0-11)
day	day of the week in the simulation (1-7)
week	week in the year of the simulation (1-52)

Table 5: Global parameters for the model

6.4 Setting Initial Conditions

The initial conditions of the model are set to make the start of the simulation as realistic as possible. Initial conditions need to be given for the following categories. The categories of agents are set to match those in the population SEIR model for Ireland (Gleeson et al., 2021).

- exposed agents
- presymptomatic agents
- infectious agents
- asymptomatic agents
- isolating agents
- tested agents
- not isolating agents
- recovered agents
- effectively vaccinated agents by age group
- percent of agents infected with new variant

These numbers should be scaled down using the scaling factor before being used as inputs in the model.

Based on the input of initial conditions, agents are assigned randomly to the infectious categories (infectious, asymptomatic, isolating, tested, and not isolating). If variants are being considered we then assign a given number based

off of the percent of agents infected with the new variant to be infected with that variant. We then half the number of exposed agents from the initial condition and randomly assign this number of agents who are not already infectious to exposed. Again we assign a given number of these exposed agents to be infected by a new variant based on the proportion of cases that should be the new variant. The other half of the exposed agents we assign to those in households of agents who were assigned infectious. The variant these exposed agents will be infected with is determined by the variant the infectious agent in their household has. This is to make a more realistic starting scenario as it is more likely that those who are infectious will expose someone in their own household than someone in the community. The number of agents who are randomly assigned to exposed, represents community transmission. Similarly, when assigning the recovered agents we first select for every sick agent one agent who is not already infectious or exposed and is in their network and then the remainder of the recovered we assign randomly to agents in the model.

Each agent has their own internal model that determines how long they are exposed before infectious and how long they are infectious. If the internal model begins on the day the model starts for the agents who are assigned sick or exposed from the initial conditions this would be the equivalent to the agents all becoming exposed or infected on the first day which means they will all be simultaneously exposed for the entire exposed period and infectious for the entire infectious period which is not realistic and effects the momentum of the outbreak. To account for this we use an exponential distribution to initialize the number of days agents are infectious or exposed with a mean equal to the mean infectious or exposed days for the disease.

The initial conditions also account for the number of vaccinated agents with a certain number of agents in each age group becoming vaccinated. Based on vaccine effectiveness data the agents can be completely immune to the virus, immune to symptomatic infection (but still able to be asymptomatic) or immune to severe disease (but still able to be symptomatically infectious). The model can also be set up to take into account differences in vaccine effectiveness by variant with the agents having multiple parameters for immunity to variant 1 and variant 2.

7 Input Data

The model uses input data from a projected vaccination schedule to determine the number of agents who are vaccinated each day. Each day the number of agents who are expected to be vaccinated by age group is read into the model and the corresponding number of agents is assigned to be vaccinated. Additional information is included to assign a given number of those agents to fully immune, immune to symptomatic infection and immune to severe infection.

8 Submodels

The following submodels are run to simulate the infectious disease outbreak. Some submodels are run every time step while others are run when certain conditions are met. For example, the clock submodel is run every time step while the choice between the Move or Lockdown_move submodels is determined by the global parameter lockdown. If lockdown is true than the submodel Lockdown_move will be called if it is false the submodel Move will be called.

- **Clock:** The clock submodel keeps track of the time, day and week of the model. The time is the determined as the modulus of ticks and 12. When the time goes back to 0 the day is increased by one. If the day is 8, the week is increased by one and the day goes back to 1.
- **Vaccine_Schedule:** The vaccine schedule submodel reads in the input file describing the number of individuals who should be vaccinated per day and assigns vaccination status to agents accordingly. If vaccination is being considered in the model, every day in the model at the end of the day for each age group a certain number of agents defined by the input data will be vaccinated and immune to severe infection. These agents will set their individual movement parameter to 1 which means that they will not modify their movements. Then a number of agents who were vaccinated will be immune to symptomatic disease (they can still become infected but will be asymptomatic) and will set their asymptomatic variable to true. The number of agents that are in this category is determined by the vaccination input. Finally, a number of agents, determined from the vaccination input file, who are immune to asymptomatic disease will also be immune to all disease and will set their immunity to 1 so that they will can not be infected by other agents.

If variants are included, then agents will set an asymptomatic variable true for each variant and an immunity variable for each variant.

- **Move:** In the model agents move in one step between their current location and their desired destination. Some movements are predetermined by the model's rules others are determined using a gravity model. A gravity model is used to determine agents movements throughout the country. This is an alternative to the simple random movements used in earlier models. Random selection of the agents next destination is a naive model that was acceptable under the assumptions of a small town or city but when the area over which agents can travel increases to say a county this assumption of random movement does not hold as well. For example, in a small town moving to the other side of the town is much more likely than moving from one side of the county to the other. To account for this a gravity model is used to determine movements. Gravity models are a type of transportation model that is similar in formula to Newton's gravitation model. A traditional gravity model gives the interactions between two location pairs and determines those interactions based on the characteristics

of a location and the distance between locations (Rodrigue et al., 2006). In the model, agents move between home and school or work at certain predetermined times and will return home at predetermined times. On weekends, summers for students, and after school or work hours agents will move through the community and these movements are determined by the gravity model. The probability of an agent moving to another county is proportional to the population density of the county, a county with more agents is more attractive, and inversely proportional to the distance to the county from the agents current location, counties that are farther away are less attractive.

The set predetermined movements are as follows:

- Agents who are working leave their home on the fourth time step of the day, which would be equivalent to between 8am and 10am, arrive at work over one time step, spend 4 time steps (8 hours) at work and then return home.
- Students also leave on the fourth time step but only spend 3 time steps (6 hours) at school.
- Stay at home agents who have children in primary school travel with their children to school on the 4th time step and then return home during the same time step. Between the fourth and seventh time step (when students return home from school) stay at home agents move throughout the model: at each step if an agent is at home they have a 50% chance of staying at home. If not at home, an agent has a 50% chance of picking a new destination with the gravity model and moving there. At the 7th time step of the day the stay at home agents will go to their child’s school and then travel home.
- Stay at home agents who do not have a child in primary school move throughout the model using the gravity model between the fourth time step and the seventh time step the same way stay at home parents move when they are not travelling with their children to school or home.
- Agents younger than 4 who are not assigned to a preschool move with their stay at home parent throughout the day.
- Agents who are unemployed, looking for their first job, retired or sick/disabled move throughout the town with the gravity model between the 4th and 10th time steps of the day unless they are involved in grandparent care. If they are involved in grandparent care they will set their location to home for the number of ticks they are assigned to grandparent care.
- If an agent is infected with the disease simulated within a model then their behaviour is affected. Infected agents have a certain probability of staying home.

- All agents will move throughout the town on the weekends using the gravity model.
- After each move agents will make note of which other agents they have come into contact with using their social networks.
 - * If an agent is at home they will come into contact with all other agents in their family network who are also at home.
 - * If an agent is at school they will come into contact with other agents also in school who are in their class network a given percentage of the time, and with other agents also in their school who are in their school network a given percentage of the time. (The user of the model sets the percentage chance of contact but the chance that an agent comes into contact with another agent in their class network should be higher than the chance they come into contact with a member of their school network)
 - * If an agent is at work they will come into contact with other agents in their work network a given percent of the time.
 - * If an agent is in the community they will come into contact with other agents in the same county who are also in the community a given percent of the time. This percent is determined by the social networks the agents are in. There can be a different chance for agents in the same family network, class network, school network, work network and agents who are not in each others social networks, this is set by the user.
- **Lockdown move:** A separate movement algorithm is created for situations where the movement of agents is restricted. The movements during lockdown are determined by a number of parameters: the percent of agents working, the stay at home rate, if primary schools are closed and if secondary schools are closed. All agents who are not working and all students whose schools are closed will stay in their own county. The stay at home rate will determine how often these agents will leave their homes. If the stay at home rate is 0.1 they leave the house for 10% of the day. Agents do not change their behaviour between weekdays and weekends. Agents can have stay at home rate modifiers where their behaviours differ from the whole. For example, an unvaccinated agent might move around the community 75% less than a vaccinated agent.

If primary or secondary schools are open then the appropriate aged agents will attend school as they would in the *move* submodel. However, upon completion of school they will not spend time in the community but will return home. Weekends the student agents will behave as the other agents in the model spending time between home and the community.

Agents who are workers will either be classified as essential workers or workers working from home. Initially essential workers are assumed to be 20% of workers based off of (Redmond & McGuinness, April 2020) but

based off of different levels of lockdown restrictions in the model the “essential workers” category can expand to include previously non-essential worker agents who are returning to work. Agents who are returning to work go to work as they would in the *move* submodel but will return home after work, and on weekends they behave the same as the other agents who have not returned to work.

- **Infect:** When an infected agent comes into contact with a susceptible agent, the infected agent will determine if they will infect the susceptible agent based on the infection rate, a variable chosen at the start of the simulation but that will be modified by a number of factors including, the infectious state of the agent (asymptomatic, isolating etc.), the variant the infectious agents is infected with and the vaccinated status of the susceptible agent. If infected with a more infectious variant, the infected agent will have a higher infection rate but if the agent is asymptomatic or isolating they will have a lower infection rate. If the susceptible agent is vaccinated they may either be completely immune, immune to symptomatic infection (in which case if infected they will only become asymptomatic) or immune to severe disease (which will not impact the infectivity of the agent). If the infected agent determines it will infect the susceptible agent, the susceptible agent will change their health status from susceptible to exposed, will be infected by the variant the infectious agent has and take on the corresponding infectivity, record the location of infection (home, work, school or community), and determine the number of days they will be exposed using a random-exponential distribution with a mean of 5.9 which corresponds to the length of time an individual is exposed but not yet showing symptoms. Agents will also determine the amount of time they are exposed before they become infectious but presymptomatic.

The contacts between agents that drive the infections are determined by the agent’s location (home, school, work, or the community), and age. If an agent is at home they will come into contact with any other agents in their family who are also at home. If an agent is at work they will come into contact with other agents at work in their work network at a rate defined by the work contact global parameter. If an agent is at school they will come into contact with other agents at school in their school, class and small school networks. The rate of contact between agents in each school network are determined by the work contact school contact, class contact and school small network contact parameters as well as the school modifier parameters for agents under 13 at school. If an adult agent is in the community they will come into contact with agents in their work network who are also in the community at a rate determined by the community work parameter and other agents not in their networks at a rate determined by the community contact parameter. Students will come into contact with agents in their class network at a rate determined by the community work parameter and the community class modifier for their age group and will come into contact with agents in the community

not in their network at a rate determined by the community contact rate and their community age modifier. The contact rates and modifiers can be found in Table 4 and are all determined to match contact rates from the POLYMOD study by location (Mossong et al., 2008). Regardless of if a susceptible agent is infected when they come into contact with an infectious agent, the susceptible agent will record that they came into contact with the infectious agent. If they are infected the susceptible agent will record if they are a close contact based on if they are in the infectious agent's networks or not. The infectious agent will keep a list of all other agents they have come into contact with.

Agents who are exposed and who have been exposed for the length of time that they will be exposed without showing symptoms will change their health status from exposed to sick. They will determine the number of days that they will remain sick by drawing from a random exponential distribution with a mean equal to the infectious period defined in Table 4.

The agent will also determine if they are asymptomatic: one of the global parameters discussed in Section 6.3 will determine the percent of infected individuals that will be asymptomatic and the agents will use this as a probability. If a random draw from a probability distribution is less than the percent of infected who are asymptomatic than the agent will be asymptomatic. If they are not asymptomatic a given percent of agents will be isolating and another percent will be not isolating. If the agent is isolating their movements in the model will be restricted where they will not leave their home. If an agent is not isolating or asymptomatic another random draw from a probability distribution determines if they will be considered not isolating and will not adjust their behaviours. The percent of agents that are isolating and not isolating are found in Table 4.

- **Recover:** When the agent switches from exposed to infected the agent will use a probability distribution to determine the number of time steps before they are recovered/immune. If an infected agent has been infected for the length of their infectious period they will change their state from sick to immune and cannot become infected again and can no longer infect other agents.

If an sick agent has not reached the length of their infectious period they will determine if they have been tested for COVID-19. If the agent is not asymptomatic, isolating or not isolating the agent will draw from a random normal distribution with a mean of the global parameter defining the length of time to wait for a test and a standard deviation of one day. If the number drawn is less than or equal to the days that the agent has been sick in the model then they will set the tested flag to true and isolate for the remainder of their infectious period. If the agent tested the recover submodel will then call the contact trace submodel discussed in the next section.

- **Contact_trace:**

For any agent that tests positive, the agent will go through the list of those agents they have contacted. If any of the contacts are in the infectious agent's family network they will ask those contacts to set a variable `close_contact` to TRUE, a variable `family_contact` to TRUE and the variable `tick_notified` to the current value for ticks. If any of the contacts are in the agent's extended family network they will ask those contacts to set a variable `close_contact` to TRUE, a variable `extendedfamily_contact` to TRUE and the variable `tick_notified` to the current value for ticks. Agents who are students and test positive will ask any contacts who are in their school small network or class network to set a variable `close_contact` to TRUE and the variable `tick_notified` to the current value for ticks. Similarly, agents who are workers and test positive will ask any contacts in their work network to set a variable `close_contact` to TRUE and the variable `tick_notified` to the current value for ticks.

- **isolate_contacttrace:**

The isolate contact trace submodel is where the close contacts of tested agents who were identified in the `contact_trace` submodel are told to isolate. An agent with the variable `ticks_notified` equal to current ticks and `family_contact` equal to TRUE will isolate for 14 days if a random number generated between 0 and 1 is less than the percent chance that the agent who infected the agent will take part in contact tracing, this percent can be an input from the user. Any agents with variable `ticks_notified` equal to current ticks and `family_contact` equal to FALSE but `close_contact` equal to TRUE will isolate for 14 days if a random number generated between 0 and 1 is less than the percent chance that the agent who infected the agent will take part in contact tracing multiplied by the percent chance that the agent will follow contact tracing guidelines, this percent can also be an input from the user.

If an agent is isolating due to being a close contact and they have not become sick after 14 days they will stop isolating.

- **Update Global Variables:** At the end of each time step, all global variables are updated. The counts and percent of susceptible, exposed, infected and recovered agents are all calculated. The average number of contacts across all agents in the model is calculated by taking the average of each agent's contacts.

- **Find-R:** A submodel to determine the estimated effective reproduction number in the model. The reproduction number of an infectious disease is the average number of secondary infections in a fully susceptible population. We calculate the effective reproduction number by having each infectious agent remember the number of agents they infected. We then average this number across all infected and immune agents to find the effective reproduction number.

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