The Anatomy of Simulated Covid-19 Epidemics in

Multiple Interacting Populations and Spaces

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ABSTRACT

CovidSIMVL is an agent-base simulation tool that models complex interactions of multiple spaces with populations that have different movement characteristics based on their roles in these Universes. The totality of the Universes make up the Multiverse, whose complex behaviour can be studied in detail.

The simulation model is built on three abstract layers: the first the action of the virus on the agent, following the temporal dynamics model of Xi, He[123]. The second layer is the interaction between agents that can be in the classic states of susceptible, incubating, pre-symptomatic, symptomatic, and inert. The rules governing these interactions are based on stochastic movements based on mingle factors, and the Hazard Radius of an agent, which if large, makes the agent more susceptible or more likely to infect, as contact likelihood is increased. Hazard Radius is a reflection of the population density of a space and the mobility of the agent.

The third level of interaction is that of populations that move in and out of different Universes according to schedules that can be set for individuals as class members or uniquely. The population description encompasses notions of work, of susceptibility, or time spent in a space, of the level of activity (Mingle Factor) of the individual in the space which has its own baseline of activity level.

In this paper, we introduce the specifications for a particular trial of CovidSIMVL, encompassing 100 agents in various roles and family structures, moving from Universe to Universe according to a daily repeated schedule (the system permits explicit deviations). The Multiverse consists of a school with classroom, project, playground, lunch, and teacher’s lounge; in addition, there is a Long Term Care facility with permanent residents, staff, visitors, and a bar, with staff and clients drawn from the population. The Universe HOME is one in which only members from the same family transmit to one another.

We run CovidSIMVL for this context with two sets of parameters: the first, OutOfBox, is with all mingleFactors set to 10; the second, HOMEWeighted, sets the Long Term Care MingleFactor to 0.1 and the HOME and Bar values to 80.

CovidSIMVL is an OpenSource public domain system freely available under GNU License framework at github/ecsendmail/MultiverseContagion. It runs on a browser like Chrome, Edge, Safari.

Using devtools and console.log, we record all infections as they happen. With this, we further develop the concepts of average time between infections (which we name “theta”) [TR004] and the metric of efficiency Q, derived from the shape of transmission trees [TR005], to the analysis of the Multiverse.

In this article, we describe the detailed progression of these two trials, using theta and Q, and the time related frequency of transmission in specific Universes, to show how one differs from the other, and which Universes are the generators of new transmitters, and thus the perpetuators of the epidemic.

INTRODUCTION

Typically, equation based models fit historical data to predict trends into the future, where the key assumptions are a population uniformly distributed subject to random transmission of the infective agent. These dynamic models do well when populations and times are large, but do not model complex movements of persons in and between different types of social environments very well.

CovidSIMVL is an agent-based model which supports three levels of simulation: the temporal dynamics of viral growth within persons, the interaction between agents that are susceptible and those who are transmitters, and the interaction of populations that share common spaces in time-varying patterns.

The classic paradigm for simulation applies to Covid epidemics as much as to many complex systems: that simple rules governing behaviour at each level, when put together, create dynamic systems whose behaviour is not easily predictable from component rules. Studying real complex systems offer many problems which simulations can avoid by creating and observing many variations of these systems, with the ability to record granular detail at will.

BACKGROUND

We have posted two articles about CovidSIMVL and its dynamics as seen in a single fixed Universe. The first of these addresses the relationships between the population density and agent mingling activity as determinants of the intensity of progression of an epidemic. Here, the population density is expressed as the Hazard Radius of an agent, given that the arena for the model is a fixed 800x600 pixel frame. The Mingle Factor affects the stochastic random walk of an agent – the higher it is, the more likely the agent is to cover the arena, and to encounter other agents.

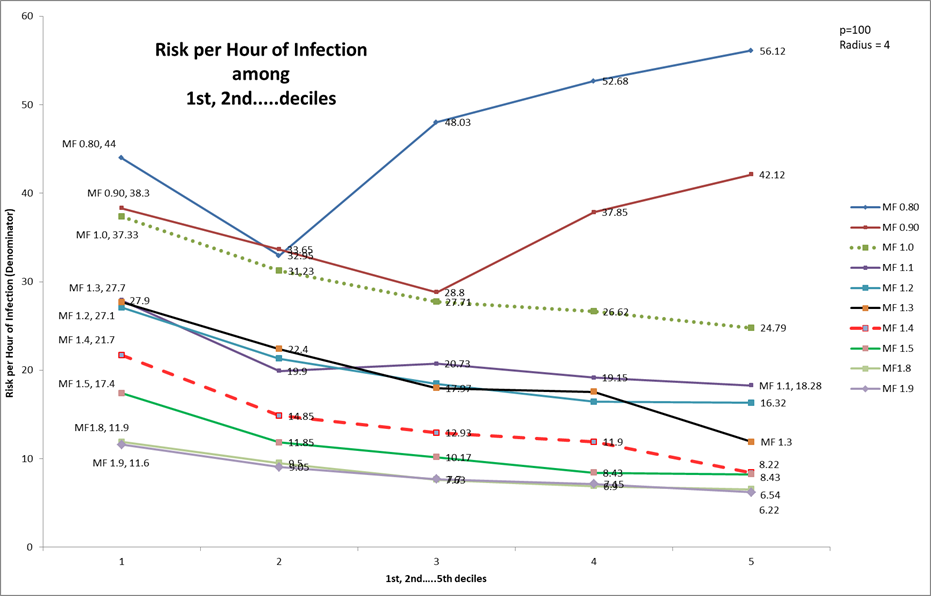
Clearly, the larger the Hazard Radius, the more likely a susceptible agent is to be contacted by a transmitter, and similarly, the larger the Hazard Radius of a transmitter, the more likely it is to contact a susceptible. This is a proxy for population density as well as susceptibility (which would act to change the Hazard Radius of a particular agent).

The Mingle Factor, again, increases the likelihood of contact between agents. It is easy to see that if the Mingle Factors are reduced to zero in the middle of an epidemic, no new infections would occur.

The first article reports on conjoint values of HzR (Hazard Radius) and mF (MingleFactor) that give rise to R0 values at the point either of extinction (no further transmitters) or at 50% of the population infected. From these relationships, one can set simulation parameters for different intensities of Covid epidemics.

In addition, the concept of Risk per Hour (perhaps better termed “theta”) is a measure of the average time (in generations) between infections, at various points in the epidemic. Thus, theta-10 would be the average number of generations for the first 10% of transmissions, and theta-20 would be the average generation count for the first 20%, and so on. Since we use a population of 100, a 10% transmission is the same as 10 agents becoming infected in that period. Theta is, to put it another way, the number of hours between infections within the time period in which 10%, 20% etc of agents are infected.

It was shown that although Mingling Factor changes the base theta-10 values (higher Mingle Factors produce lower theta-10s), the slope of the theta values as the epidemic progresses from theta-10 to theta-50 and theta-60 is a reflection of the intensity of the epidemic. A declining value (downslope) indicates that the epidemic is increasing in intensity, whereas an upward slope reflects an epidemic slowing down and heading to self-extinction. This is illustrated in the following graph, taken from the first article.



The second article looks further into the stochastic morphology of the chains of transmission that are generated in the course of a single source epidemic in a fixed Universe. It is intuitively obvious that rampaging epidemics have many transmitters simultaneously active, and therefore require fewer generations to infect the simulated population, whereas epidemics that run to extinction with partial population penetration must have fewer simultaneously active transmitters, and take more generations to cover the same population infected.

We developed the notion of a Transmission Tree, since the simulation can capture every transmission between agents, and the time of the transmission. The concept was developed of the shape of the Transmission Trees in terms of the depth (longest path), average depth (over all path lengths), the breadth expressed as the number of leaves (which is the same as the number of distinct paths).

To quantify the aggressiveness of the epidemic (the more simultaneity, the shorter the total generations needed, the more agents are infected), we proposed two measures that combined all these factors. The most sensitive, which we adopt, is simply termed Q, and is defined as:

|  |  |
| --- | --- |
| Q = | (Leafs/AvD)/Gen\*100 |
|  |  |



This table shows that as the Mingle Factor and R0 (for 50% population infection) increases, the value of Q increases, in bands, and that these bands reflect the morphology of the Transmission Tree in the metric Leafs/AverageDepth fairly well.

We will apply these metrics to the subject of this article, which is an exploration of the dynamics of Covid-19 epidemics where multiple interacting populations of various structures move between different types of spaces (which we term Universes) that have their own intrinsic mingling factors.

DESCRIPTION OF THE OUT-OF-BOX TRIAL

In the first trial, the simulation is configured as programmed and specified in the .CSV files, without altering any run-time parameters (specifically, Hazard Ratio and MingleFactor). The default Hazard Ratio as an initial setting for every agent is 5, and the MingleFactor for each Universe is set to 10.

We now describe the structure of the 9 Universes, and then the population structures, and then the schedule of movement of the agents.

This set of Trials is created to simulate the areas of a school, and interactions between the students, teachers, their families who may work as staff in a Long Term Care facility, and a bar, and these agents may also be visitors to Long Term Care, and be clients of the bar.

There are 9 Universes in this Trial called U0 to U8. The names assigned to them are:

U0 Classroom 1

U1 Project/Lab Room

U2 Lunchroom

U3 Playground

U4 Classroom 2

U5 Teacher’s Lounge

U6 LTC (Long Term Care)

U7 High Mingle site (Bar, reception, party)

U8 HOME

HOME is a unique Universe, in that transmissions among agents who are in the HOME universe only take place between members of the same family.

There are agents in Long Term Care who do not leave U6, and there are agents in U6 who are not parts of existing families.

Each Universe can be assigned its own intrinsic Mingle Factor at run time, and this acts as a multiplier to the move generated for each agent in the Universe, each such agent having their own Mingle Factor, which may be related to their role in that facility, as set in the population file.

The population of 100 agents is set up in the Population.csv file. As configured, these look like:



The Family Structure

We begin by enumerating the social roles (total 100)

1. Students 3 x 10 in groups A, B, C
2. Teachers 6
3. Grandparents 7
4. LTC residents 28 of which 10 are associated with families
5. LTC staff 14
6. High-mingle site (Bar) staff 10
7. Spouse community work 5

The family structures are complex and we have created 19 families in this community. Before we enumerate them, the general structure of a family is:

1. Heads of family (one or two) with social roles
   1. May be two-person eg Teacher + LTC staff
   2. May be single-person
   3. May be grandparents only (two-person with social role)
2. May have children (0 to 4)
3. May have multi-generational (grandparents not heads of family)
4. May have LTC resident as part of family (grandparents, aunts)

The 19 families have been carefully defined and structured with the use of analog tools (poker chips, pins, paper clips, checkers pieces, anchor bolts, etc). The enumeration of the families follows, in no particular order:

F0 LTC(S), BAR, A, C LTC(S) – staff, BAR – bar staff, A,C – student groups A,C

F1 T, BAR, LTC(R), C T – teacher, LTC(R) – LTC resident

F2 T, LTC(S), LTC(R),G,B,C G – grandparent

F3 LTC(S),BAR,B,C,LTC(R),LTC(R)

F4 G,G,B Grandparents as head of family with one grandchild

F5 T,BAR,A,C

F6 T,LTC(S),A,A,B,C,G,G,LTC(R) biggest family unit – four kids, 2 grandparents, one LTC res

F7 BAR, LTC(S), A,B,B

F8 BAR,LTC(S),A,C

F9 BAR,LTC(S),A,C

F10 BAR,S,G,A,C Bar worker, spouse, grandparent, two children

F11 LTC(S), S Long Term Care staff, spouse – no kids

F12 LTC(S),S

F13 LTC(S),S, LTC(R) this will be among the visitors to LTC

F14 LTC(S), S, LTC(R), LTC(R)

F15 T,LTC(S), G, LTC(R)

F16 BAR,LTC(S),A,B,B three kids, two in same group

F17 BAR, LTC(S), A,B,C

F18 T,B, LTC(R) single parent (teacher), one child, one LTC resident

This microcosm is tightly coupled between the workers who are teachers, LTC staff, and BAR workers (BAR being a place-holder for high-mingle spaces). With so many being in the same family units, this scenario may have a higher rate of crossover transmission between the school and LTC unit not just because of frequenting the high-mingle bar, but also because of the family units, which have most LTC workers with children, and/or spouses who are teachers or work in the HIGH-MINGLE bar.

This information is incorporated in the Population.csv file, which specifies the movements between Universes for each agent, according to the following overall schedule.



This is a single day 24-hour schedule, repeated over and over. However, the capability has been built in to CovidSIMVL to specify different DDHH for movements to take place.



Clearly, this is a deterministic rather than a stochastic schedule. We can easily modify this to be more probabilistic in one of two ways: first, to provide an alternative set of Universes to move to anytime there is a departure for an agent from a Universe; second, to introduce stochastic elements into length of stay, so it might be for example, 4 hours +/- 5%; third, both. For now, most of the non-determinism in CovidSIMVL is in the viral growth dynamics, and the distances moved at each generation.

Whether this pattern of movement is reasonable, too restricted, or too broad is difficult to verify. This is a pattern, and others can be specified, but a true set of movements can be at best a snapshot obtained with great difficulty, without any guarantee of generalizability. Our approach is to try a reasonable configuration, and to be open to any others proposed.

The population.csv file is the technical specification for the movements for each person, and has a structure like this.



These are the .csv lines for the students (agents) 0,1,2 which are the pIDs. The “sno” column is the “STOP number” for the agent, and these must be present, and in order. The ETA is the time of arrival at the universe “@U” and the ETD is the time of departure from that universe “@U” to the new Universe “>U”. Note that when at HOME (U8) the mF is high (8) so family members may contact one another.

The Role is either “R”, or “A”, or “T”. The first, “R”, means that they are “resident” in that universe for the time they are there, and the second “A” means “Attached” as a staff member would be, and “T” would be for “Transient” visitors, shoppers, guests at bars, etc. In general, these are meant to convey different levels of activity. However, each line has its own MingleFactor, which describes the activity level of the agent in that Universe.

For example, a person may be a staff member in LTC, during which the MingleFactor (mF) may be high, say >6. Then in the bar, they may be quiescent, and have an mF of 3. As a visitor to LTC, they may be a volunteer, in which case they might have an mF of 4, and at home they might after 11 have an mF of 1.

Since mF influences the extent of contact with another agent in the same Universe, this fine level of detail can be applied to classes of persons, as well as to specific individuals. CovidSIMVL has the capability of tracking all movements, and transmissions. The movement algorithm generates a proposed move, using a Pareto distribution, then modifies it by the individual mF and the Universe mF for a final position, which is in turn modified if it goes outside the fixed arena.

Note that the FamKey needs to be specified just for the first line of a new agent.

Finally, we come to the Case file, another .csv file. This describes the initial agents that are infective, and the system permits the user to invoke additional case files during a run. The format is simple, but has to include the viral load, and the number of days since the agent was infected, in order to comply with viral dynamics.

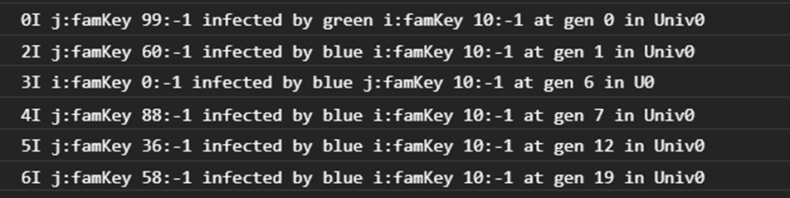


The operations for running CovidSIMVL using the .csv files are found in the /docs directory of the gothub repository github.com/ecsendmail/MulitverseContagion, which contains documentation of how to operate the system. This is an open source, public domain software under the framework of the GNU License.

RUNNING THE TRIAL

The trial “Out-Of-Box” was run by invoking the index.html file in the repository, and then opening the two .csv files which were loaded from the repository into a local directory. The browser used was Chrome, and devtools was invoked by right-click and selecting “inspect” in the window.

“console” was chosen in devtools, so that the transmission details are displayed, which were copied into an Excel spreadsheet at the end of the run. It looks like this:



As the mF was the same for each Universe out of the box, the simulation was expected to go to completion, and to end after relatively few generations. The model as programmed does not remove symptomatic agents from general circulation, nor place them into hospital or transition them to death, or to quarantine. Thus, this simulation is set for mild cases with no mitigation.

At the end of the run, the console.log was analyzed as discussed below, using the tools. Screen shots were captured, as shown here. The last transmission is at generation 683 from console.log.



There’s a lot going on here. First, the top left boxes in gray show that the run stopped on Day 41 Hr 17, with 9 survivors (Green), and 91 Oranges (Inert after 10 days symptomatic).

The rightmost charts show the cumulative status on each day for the entire population of 100 agents. The top is the typical SEIR graph, with two Y-axes….the right showing Yellows (incubating), and Reds (symptomatic), while the left Y-axis shows Greens (susceptibles), Blues (pre-symptomatic infectious) and Orange (inert – next phase of Red).

This SEIR chart shows the symptomatic cases in red peaking at Day 20, and the susceptibles (green) reaching 50% at about Day 12. A closer examination of the red curve reveals 2-3day plateaus around days 21, 26, 30 and 33, lasting for 2-3 days each. These plateaus are interesting in that if there were no new cases in this period, the graph for cases (reds) should be falling, so plateaus imply maintenance of new cases at a lower and possibly constant daily rate. If the rates were increasing, the daily cases would be increasing, and the curve would be rising, not flat.

Looking at the charts for each Universe, the right hand Y-axis shows the scale for the counts for Reds (positive cases). In the LTC Universe6, the scale is 0 to 40, and the peak is before Day 20, with a value near 30. The Bar Universe7 has a scale of 0 to 15 with a peak of 12 before Day 20. The only other Universe with a large count of reds is Universe8 HOME, with a scale of 0 to 40 and small peaks around Days 18, 23 and 28.

The plateaus in daily cases might be therefore closely associated with the HOME infections, where these peaks on Days 18,23 and 28 happen to compensate for falling rates in LTC U6 and Bar U7.

Despite the initial seed of 5 students as transmitters (pID 10 to 14) the detail charts show that subsequent transmission among the student and teacher population is not high(see Universes 0 to 5). Recall that in examining the individual Universe charts, the graph shows daily tallies of populations moving in and out of these spaces, who are there for just a few hours each day.

If we scan the change in the Green bars in the school Universes, we see that their numbers are at 50% on approximately Day 20 (look at the left Y-axis for Green numbers). These show the daily count of them, but not where the losses have taken place. For that, we have to rely on the detailed console.logs.

In contrast to the school Universes, the LTC U6 drop to 50% around Day 10, and for the U7 Bar and U8 HOME, around Day 15, scanning the charts visually. These show that the attrition (infection) must be fastest and highest for LTC U6, then for U7 and U8, and lastly for the school Universes. This should be reflected in a more detailed analysis of the console.logs.

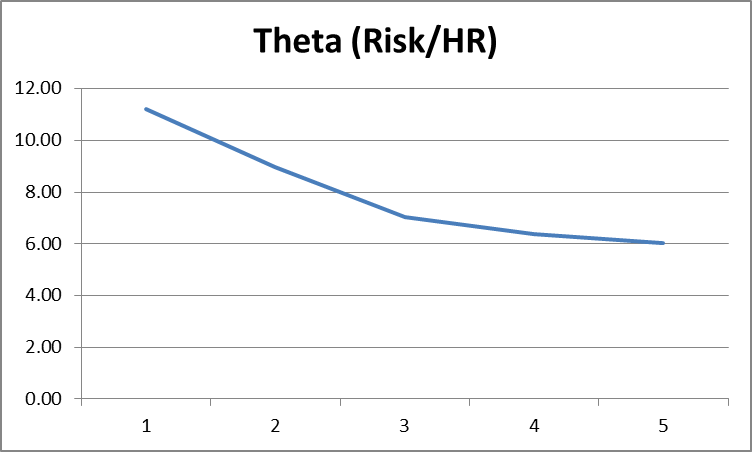
The crossover point for the green (susceptibles) and reds (positive cases) represent the Day on which these two groups have the same numbers. From visual inspection of LTC U6, this happens on Day 12 with a count of around 10 Greens and 8 Reds. This means that on that day, when there were 8 cases, only 10 Greens were left of the original 36. In fact, at the 50% point for the Greens (susceptibles), only a few Reds were present. This is the hallmark of an aggressive epidemic, in which the pre-symptomatic and asymptomatics are dominating.

The same analysis can be applied to the other Universes, especially U7 and U8.

We now turn to a more quantitative examination of the progression of this Multiverse epidemic, using tools we have developed in previous studies, regarding the speed of transmission (theta values) and the characteristics of the transmission trees (Q-values).

Out-Of-Box Trial and Theta Values

Theta is the Risk Per Hour of infection, which is computed by the count of generations for the first 10%, 20% etc. of transmissions. This can be done for the Multitverse of all the Universes seen as a whole population.



The first two columns are derived from the console.log trace. From this we get the table of Theta values and the graph with the downslope showing the acceleration with time of the epidemic, but slowing.

Next, we look at the school Universes from the console.log (sorted by U).

Theta-n is the number of generations to reach n% of infections, and for a population of 100, n can be considered the number of agents to be infected.

For small numbers, such as U0, the number of generations to reach its one and only infection is 396. That is its theta.

For U1, it takes 62 generations to reach the first infection, and 135 to reach the second infection. Thus, the theta-1 value is 62, theta-2 is 67 (135/2), and theta-3 is 68 (203/3).

Thus, for larger numbers, we can use theta-n%, and for smaller numbers, we would use theta-k.

For U3, theta-1 is 180, theta-2 is 186 (371/2), theta-3 is 180 (539/3), and theta-4 is 171 (683/4).

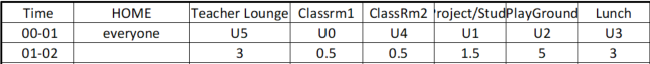
For U4, theta-1 is 178, and theta-2 is 173 (346/2).

The following Table shows these values and their relationship.



The simulation shows that in spite of the larger numbers of agents in Playground (U2) and Lunchroom (U3) with 2 cohorts each of 30 sharing the space, the theta-k values are “worse” for Project/Lab (U1), in the sense that the lower the theta value, the smaller the generation count between infections. From this, the smaller the inter-generation count, the more frequent the transmission, and thus, the epidemic is more aggressive in Universes with smaller theta values.

A possible explanation for U1 having smaller theta values is that the Playground (U2) and Lunchroom (U3) are used for one hour each cohort, whereas the students spend more time in the other rooms. The lower theta-k for the Project/Lab (U1) can be further predicted by the mF used when students arrive in these rooms:

The Project/Lab (U1) is assigned a MingleFactor three times higher than the two Classrooms. Thus, we see here the complexity of detailed simulated spaces: duration of exposure, activity, and density all matter.

Turn now to the LTC, which leads in the speed of progression of transmissions.

Here, we use theta-n% since the numbers are larger and we want to know the time between transmissions within the space.

There are 55 transmissions.

10% is 5.5, round to 6 gen 148

20% is 11 gen 182

30% is 16.5, round to 17 gen 214

40% is 22 gen 253

Theta-10% is 24.7

Theta-20% is 16.5

Theta-30% is 12.6

Theta-40% is 11.5

Recall that the lower theta is, the faster the speed of transmission, being the time between transmissions.

In this simulation, the Bar is relatively harmless. Only five transmissions took place within U7.

Theta-1 is 164

Theta-2 is 126

Theta-3 is 94

Theta-4 is 105

All rather safe, compared to the theta of <10 for LTC.

The situation for HOME transmissions between family members is interesting. The 10 families involved have four repeats – F07 with three, and F2, F8 and F17 with two each. Referring back to the Family Structure, these are not the largest families, which are F06 with 9, and F2 and F3 with 6 members each.

A member of F06 (pID 25) did get infected in generation 47, but this did not lead anywhere. To understand this, we turn to the Transmission Tree(s) for this trial.

Transmission Tree and Intensity of the Epidemic

The initial conditions were set for five transmitter agents, so we end up with five distinct transmission trees, each rooted at one of the initial infected agents, pID 10-14. They look like this:

Each entry is <generation;susceptible;U>

Recall that each row of the Transmission Tree (in its path-representation) is a path of the tree, which represents a chain of transmission from an index case to the leaf of the tree, from which no further transmissions take place in this simulation.

Note that pID=25 from the largest family F06, is in the tree rooted at pID=13, and had one immediate descendant, which led to two leaves. Such is the nature of stochastic transmissions.

The previous article on Transmission Trees presented the metric Q that takes the shape of the tree, as well as the time involved, and the number of distinct agents infected, to be an estimate of the aggressiveness of the epidemic, with **higher numbers being a faster** expanding epidemic.

We work through the example of the largest tree, rooted at pID=12, and leave the others to the reader.



The values of Q for the other trees are:

Root 10 T/E 17.06 Q 18.96

Root 11 T/E 15.94 Q 16.64

Root 12 T/E 16.10 Q 28.12

Root 13 T/E 4.21 Q 0.67

Root 14 T/E 8.08 Q 2.69

Note the asymmetry in the size of tree that follow from the initial seed of transmitters, and the heterogeneous property of the path lengths, which vary from a high of 6 in Tree 12 to lows of 1 in both Tree 10 and Tree 11.

Indeed, it appears not just natural, but inevitable, that stochastic approaches to the modelling of contagion-based epidemics should end with trees that are not uniform in shape, where some nodes, near the root, give rise to many leafs, while others wither. For example, in tree 12, node 12 gives rise to all 35 new infections, and node 75, an immediate descendant of node 12, is the ancestor of 14 chains and 28 new infections, while pID=13 (also an initial seed) only yields 4 new infections in total.

From this simulation (and many others), it would appear that a stochastic approach predicts an inherent asymmetry in path generation, and that so-called super-spreader persons may be artifacts of the natural probabilistic progression of a contact-based epidemic.

This simulation trial also presents the inherent asymmetry in spaces with different mingling characteristics visited by varying mixes, and the notion that some time-based occupations of these spaces would give rise to more transmissions than others is also borne out as a natural consequence of stochastic behaviours.

For example, in the span between generations 396 to 399 (3 hrs) there were 4 infections in U6; between 248 to 255 (7hrs) there were 5 infections in U6; between 301 to 311 (10 hrs) there were 6 infections.

EPIDEMIC DRIVERS

In a complex interacting set of spaces (Universes), some naturally have more conditions conducive to rapid spread than others (LTC vs Classroom2), which can be identified by their Q metrics. For the less contagious Universes, they must be supplied with more transmitters as earlier ones go past their viral best-by dates. These are Universes that lead in transmissions and the creator of new ones that feed into the others. We can identify these by their velocity graphs, as follows.

These charts show, for selected Universes, the relationship between time and the percentage increase of new cases per day over the previous day.

The clustering makes it clear that U6 rises first, followed closely by U8, then the school rooms, with the Teacher Lounge and Bar the latest in terms of days since the start of the trial.

This kind of information is useful, as it shows the places that are the drivers where new transmitters are created, and the places that lag behind and transmit new cases as a result of the activity in the lead spaces.

Here, it is no surprise that the LTC and HOMEs are the first places where transmissions take place. In the case of LTC, the residents are densely situated with the staff and visitors, and have long exposure times to one another.

In the case of the HOMEs, everyone (except LTC residents) go home, and the mF level for agents are set high, so family members get the opportunity to contact and transmit to one another.

Perhaps it is less expected that the bar as a high mingle Universe should be the laggard, peaking at almost 40 days. A closer examination shows that U7 has an average of 6.6 agents present and a maximum of 13. Since the initial see of transmitters are students, and they don’t frequent the bar, the active transmitters would have to come from teachers or LTC staff. So even if the bar has a higher mF than the classrooms, the transmitters and the prolonged opportunity to mix gives the schools a higher infection velocity than the bar.



Indeed, if we look at the first 25 transmissions, we see that 14 of them occurred in U6 (LTC), 5 at HOME (U8), 5 at school (two in U1, and one each in U2, U3 and U4) while only one transmission happened in the Bar, by pID=31 (a Teacher).

The first school transmission was in U1, in generation 62 which is on the 3rd day.

Of the first 10 infections, all but one were by the initial seeds (pID 10 to 14), and only one was in a school space. The others were either at HOME or in LTC, as visitors.

This shows the power of population density (LTC) and mF (HOME).

COMPARING THE OUT-OF-BOX TRIAL TO OTHERS

In what follows, we will briefly look at the metrics for some other simulations using the same population structure, but changing the mF for selected Universes, to see whether we can change the Universes that are more aggressive as sources of new transmissions, and thus are ht spots that fuel the overall contagion.

Using the metrics developed, we will compare the first simulation trial to another in which the run-time parameters are:

* U6 LTC mF set to 0.1
* U7 Bar mF set to 80
* U8 HOME mF set to 80

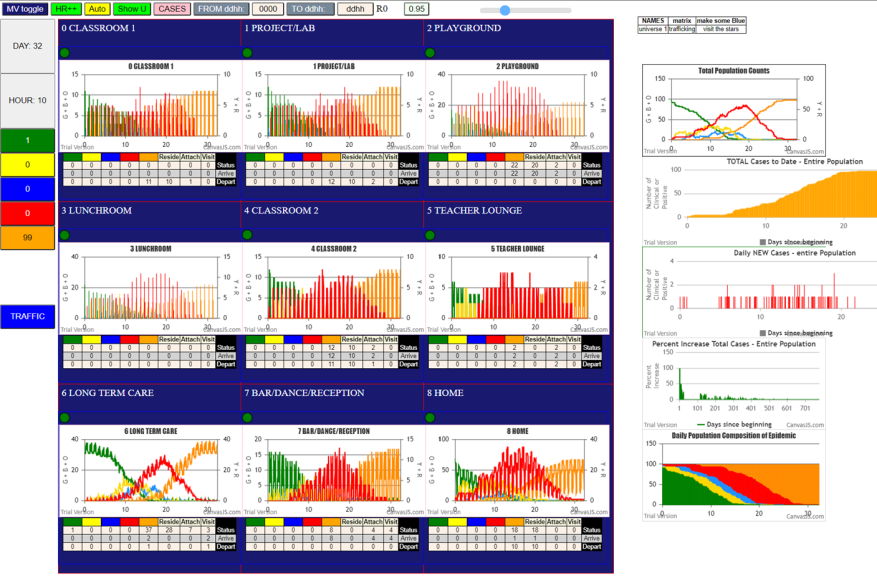
We will call this the “HOME Weighted Trial”.

We will compare them with respect to the metrics developed in the CovidSIMVL simulation model for complex interacting spaces and populations, namely:

* theta (average time between transmissions at various points in the epidemics)
* Q (showing aggressiveness of the epidemic using Transmission Trees)
* the relative drivers of the epidemic among the Universes

THE HOME-WEIGHTED TRIAL

This is the console.log of the trial, in generation order, as transmissions occurred, plus the screen capture of the multiverse at the end of the trial, which left one survivor after 32 days and 10 hours.





The SEIR curve on the top right shows that the number of symptomatics (red) peaked around day 20. The last transmission was generation 486, around 20 days, the rest of the 32 days given to the time between symptom appearance and becoming inert (orange).

COMPARISONS OF THETA between HOME-weighted and OUT-OF\_BOX

These are the Theta-% and theta-k values for the Ou-of-Box trial overall and in its component universes, using the console.log as the time between transmissions.

The corresponding Theta-% and theta-k (where numbers are small) are as follows.



Recall that theta is the average time between transmissions, so the smaller, the worse the epidemic. In this regard, Out-of-Box is overall similar to Home-weighted, ranging from 11.20 to 6.02 from Theta-10% to Theta-50% in the first, with Home-weighted having 10.60 to 6.90 respectively.

It is in U6 (LTC) and U8 (HOME) that the differences appear. In Out-Of-Box, U6 takes the lead in the epidemic and this is shown in its U6 Theta-% values from 24.67 to 9.57 from Theta-10% to Theta-50% which shows an accelerating progress, while the HOME-weighted U6 values go from 39.00 to 13.67, longer in every segment.Q

It is even more remarkable in U8 (HOME), where in Out-Of-Box the Theta-10% to Theta-50% values go from 23 to 41.6, relatively long compared to the dramatically short intervals of 1.67 to 5.13 in the HOME-weighted trial.

This is of course, behaving as it should. The other Universes (the school spaces, the bar) have theta-k values in the 50s and higher in both cases, which should tell us that in this set of parameters and movements, these spaces are not significant in the continuation of the epidemics.

COMPARISONS OF Q (based on Transmission Tree topology) between the two models

As we have shown in theta measures, both epidemics are aggressive, and so our expectation of Q values are that they should be similar. Since they are derived from the Transmission Trees, we have created them for HOME-weighted, and they can be compared to those for the Out-Of-Box.





We can see that, in comparison to Out-of-Box, there is a more even distribution across the initial transmitter agents in terms of their descendants, except for pID=14, whereas for Out-of0Box, there were three main trees and two small ones. The more even the distribution, in general, the more simultaneity, and therefore the more rapid the spread.

The Q-values, derived from the shapes of the trees in relation to the generations and size of the trees (the number of unique agents in a tree) can be compared as follows. Recall that the higher the Q measure, the more rapid and diverse the progress of the epidemic.



There are three major differences between OutOfBox and HomeWeight. The first is that OutofBox needed 683 generations to transmit to the population of 100 with 9 survivors, with an initial seed of 5 infectives. This is a net new transmission of 86 new infections. HOMEWeight only needed 486 generations to transmit to 94 susceptibles (there was one survivor). Thus, HOMEWeight was a faster and more penetrating epidemic.

The TREE values for Q were created by assuming a higher root node for which Root 10, 11, 12, 13 and 14 are its descendants. By summing the various components from the sub-trees, the Q value for the whole TREE for OutOfBox and HomeWeight were computed. As shown above, HOMEWeight has a higher Q value, which means it is more effective as an epidemic compared to OutOfBox.

The third differences between the two epidemics is that OutOfBox had 3 balanced sub-trees 12, 12, 18, 2 and 4 distinct paths) while HOMEWeight had trees of 15, 20, 9, 11 and 5 distinct paths. The first had 48 distinct paths, the second 60….this means that there was more simultaneity in the HOMEWeight trial.

This means that not all the distinctions must be due to the differences in parameter settings, because the balance of tree structure reflects the stochastic nature of the contagion. Where probability plays a role in how the next contacts occur, there is only the Law of Large Numbers to rely on – that while a small number of outcomes might be due to chance alone, a large number will reflect the true average outcome.

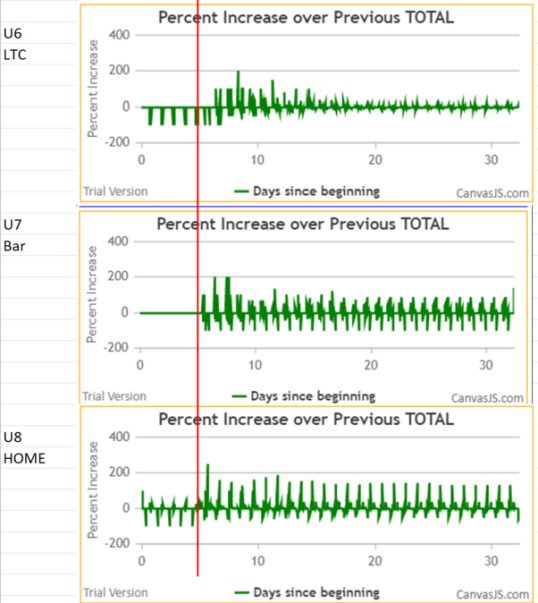
COMPARISONS OF DRIVERS IN THE COMPLEX SYSTEM

One of the fundamental reasons for simulation is that complex systems composed of simpler parts may exhibit unexpected behaviours not easy to predict knowledge of the parts. Thus, in this complex system of school, LTC, bar (high-mingle recreational area) and HOME, which are the generators of new transmitters, and which are dependent?

We have already seen that theta is a measure that shows quantitatively the relative differences between U6 (LTC) and U8 (HOME) in the two trials, and that in OutOfBox, LTC had significantly smaller theta values (time between infections) than U8. In HOMEWeighted, we set parameters to make LTC relatively immobile, while we overloaded the MingleFactors of both U7 and U8.

What we saw was that while U8 had the smaller theta in HOMEWeighted, U6 was still an active place for transmissions, despite a very low intrinsic mF. One reason for this may be the nature of staff and visitors moving in and out, as CovidSIMVL introduces them into random positions when they arrive at LTC on their schedules, and this is a form of mingling activity created not by the movement inside the space, but by the external arrival of agents.

The charts for activities of the Universes also reflect their temporal relationships, in that one Universe shows peaks before the others. Consider the following chart for HOMEWeighted and OutOfBox

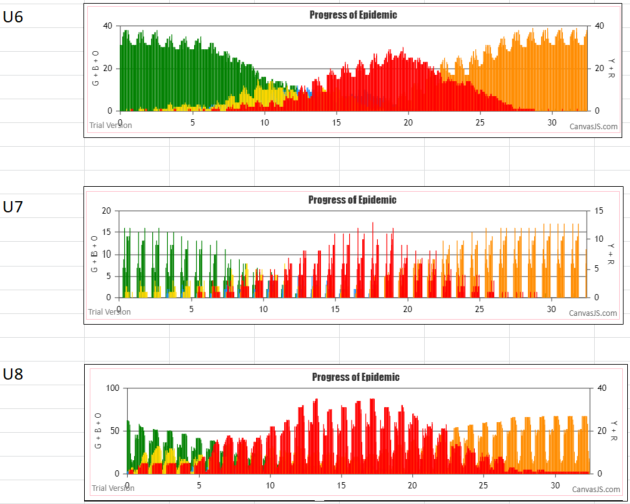
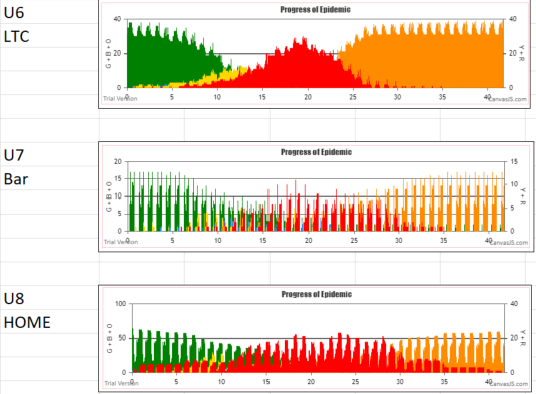


OutOfBox HOMEWeighted

These show the increments of symptomatic cases as the percentage from that of the previous interval, based on the arrivals and departures of agents to these Universes. Thus they increase and decrease as persons leave and the population decreases.

In OutOfBox trial, clearly Bar trails LTC and HOME, and the increase in LTC happens just slightly ahead of HOME, while in the HOMEWeighted trial, clearly LTC trails behind HOME and Bar in their peaking.

Another way to look at this is in the SEIR curves

OutOfBox HOMEWeighted

It is reasonably clear that in HOMEWeighted, the LTC curve trails the other two, while in OutOfBox, LTC is at the same pace or slightly ahead.

Another way to discover which Universe is fueling the epidemic is to return to the console.logs by generation, and see what Universes have the most transmissions at various points in the trial.

OutOfBox HOME Weighted

1st 10 – LTC 5, HOME 4 1st 10 – HOME 10

1st 20 - LTC 10, HOME 5, School 4 1st 20 - HOME 15, LTC 2, School 2

1st 25 - LTC 14, HOME 5, School 1st 25 - HOME 16, School 5, LTC 3

This gives a good estimate of which Universe is generating new transmitters at this point in the epidemic, but of course the supply of susceptibles in a Universe will determine additional transmissions as the epidemic progresses.

DISCUSSION

Through control of simulation parameters and dynamics, we are able to examine very closely the behaviour and metrics of contagion-based epidemics. In CoivdSIMVL, the viral growth model as described in Xi, He has been used to make this Covid-19 relevant.

The simulation model has been extended in CovidSIMVL to a multiverse of interacting Universes, each with their own base level of mingling activity. The population of agents have specifications that control their movement to various Universes for periods of time, with different MingleFactors in different Universes. Family structures are supported, such that at HOME (Universe 8), only members of the same family can transmit to one another.

The ability to control and record in detail the stochastic processes of contact within Universes that operate at different rates for different agents allows us to create two important metrics. The first is theta, the average number of generations between transmissions, for both the Multiverse, and for individual universes. With theta, and the trend for theta values as the epidemic progresses, we can estimate the velocity of the epidemic as a whole and in component spaces.

The other metric is Q, a measure of the efficiency with which an epidemic is acting, based on the breadth, depth and duration of the transmission paths that are combined to make the Transmission Tree for the epidemic. With this, we can again estimate the degree of severity and penetration of an epidemic as it progresses.

There is no such thing as one epidemic, but there are contexts in varying degrees of inclusion. CovidSIMVL is a flexible tool that can model interacting spaces with population movement and mingling properties at varying levels of detail.

In simulation models of traffic, or of shipping, or of a plant, we don’t have to reproduce the system exactly in order to study its behavior. The envelope of solutions that a simulation model can provide is larger than the specific situations for which the model is constructed. The purpose of the simulation model is to understand the behaviour of the complex system in terms of its components, and to try different parameters and observe results at levels of detail that cannot be done in the reality of one time and one system.

This is what CovidSIMVL does as a simulation tool – to provide the range of parameters and detailed observations that give insight into how the physical system is behaving, as we observe it often in parts. For example, the question of heterogeneity of the Covid-19 spread, the concept of super-spreaders and super-spreading events can be shown in CovidSIMVL as a stochastic system, to be an artifact of probability. This is an insight that we obtain through simulation that cannot be obtained by the equation-base approach to Covid-19 prediction modlling, with its assumptions of uniform distribution and random spread of the virus.

The operation of the simulation model to give theta values of the average time between infections leads us to insights about how theta relates to mingling and population density, and how the theta trend tells us about the direction the epidemic is heading, in whatever contexts we are studying. It would be totally expected that what happens with Covid-19 is that some sub-epidemics are self-extinguishing, while others are holding steady, and others yet are expanding. The CovidSIMVL model of interacting complex spaces allow us to gain a quantitative notion of the relative importance of different Universes in the ecology of interacting spaces and populations.