ARENA Analysis of the Spread of COVID-19 in a Population

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Abstract

The purpose of this report and study is to understand how a virus can be spread through a small populated system and how preventative measures can impact the spread. Further purposes are to understand how long spread would take and what the implications of health infrastructure are on the mortality rate of the citizens of the system. The implications of this study can be expanded to a larger scale like that of a state, region, or even nationally to understand what areas have higher risk factors such as population per square foot, political views on vaccines, economy, vaccine access, and more. Our results show that the rate of spread can be impacted by the choice of vaccination and masking. Other attributes that also have an impact are age and the amount of interaction one had with others in the system. The methods we use in this study involve an ARENA Simulation Model with various parameters to simulate the arrivals of citizens in the system and the cycling of citizens as the disease is spreading. Follow up methods include statistical analysis and verification of the implementation.

Background

The problem at hand is the spread of a pandemic level virus that has advanced from a classroom to a small populated system. We specifically chose to analyze COVID-19 data from the past two years. We chose a population that starts out with a low probability of getting infected. Once one person gets infected, the probability of infection increases. However, one's risk of infection can be reduced by the precautionary measures like masking, vaccination, and limitation of exposure. If infected, individuals can either recover at home or the hospital depending on severity of their symptoms. Individuals at the hospital still face a chance of death at the hospital due to supply chain and capacity constraints of the hospital. We will recycle living entities that are still susceptible to infection through the system to mimic living in a city where others are infected.

The flow of the report will be as follows: We will walk through the various blocks or modules that we need to use in ARENA and their purposes. We will review the intricacies of each block's customizations like arrival distributions, conditional expressions, and other pertinent information. Within each of these sections we will describe why we chose the

parameters and then present a snippet of our final chosen simulation. From there, we will move to our results and its implications. We will also discuss other parameters that we tested and why we chose against those. Finally, we will wrap up with a summary of our findings and how this can be adopted to larger uses given more time.

Problem at Hand

CDC and other governmental officials want to understand what variables and permutations of variables will impact the spread of the disease at hand. In order to control the spread of a virus, it is important to understand what the biggest factors are that impact it. The goal of the simulation is to not only show the impacts of not taking precautions like vaccines and masks, but also understand what factors play the biggest role in the spread of the pandemic. Using a Monte Carlo simulation allows us to use repeated random sampling to determine how quickly the spread would be in three months, starting on September 1st, 2021.

Part I: ARENA Model & Assumptions

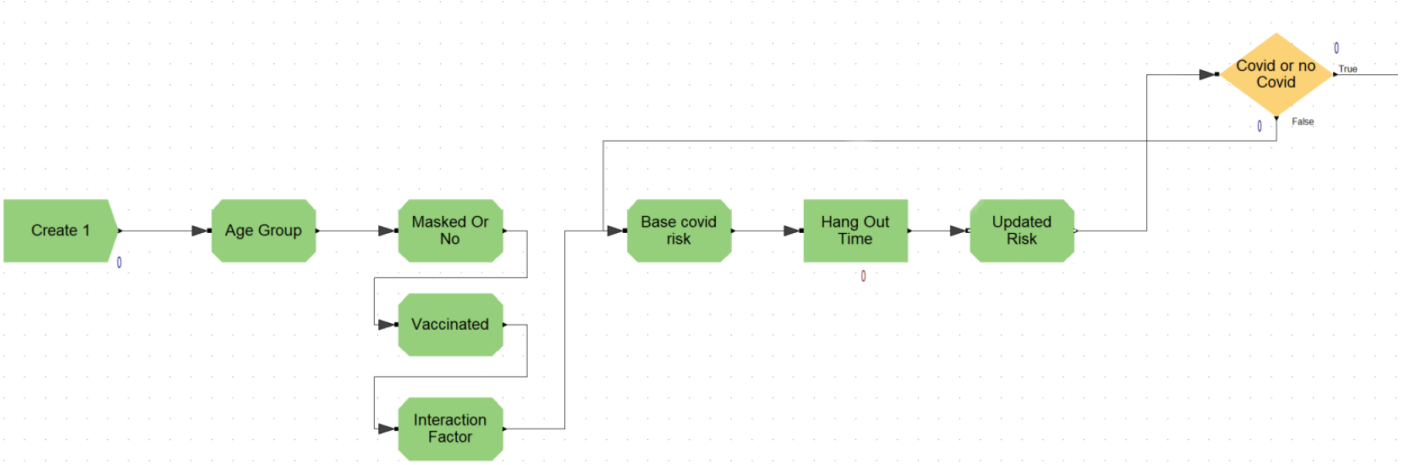


Exhibit 1: Beginning Flow of Model - For assumptions below, *Title* indicates the name of the block in the ARENA snapshot above. Please use the below notes to follow along with the model.

To set the stage of our simulation, the starting population has zero COVID-19 cases at that point in time, but there is an existing strain of the virus present and there are effective vaccinations distributed. This can be similar to certain periods of time the past two years where there were zero new cases on a singular day but spikes of cases in the following days. Our simulation begins with entities entering our system, using a **CREATE** module that has a homogenous poisson arrival distribution. The interarrival time is two hours, as we wanted to mimic a small town where the citizens are moving through the system. The max arrival is 100 entities and they are cycled through to keep the population realistic.

When the entities enter the system they go through a series of four **ASSIGN** modules to receive their attributes. The first is *Age Group*; research shows that susceptibility and recovery from COVID-19 is affected by the person's age[5], so we assigned the entity a value of one to four based on the age groups: 75 and older, 50-75, 35-50 and 25-35, respectively. The likelihood of the entity belonging to each group is based on the breakdown of the U.S. population. This attribute is modeled as a discrete distribution: `Discrete(0.1,1, 0.52, 2, .80, 3,1.0,4)`[17]. The other attributes are based on the entity's way of moving through the system that could increase or decrease their likelihood of catching the virus. *Masked or No* refers to if the entity wore a mask. In the U.S. 56% of the population[15] favored wearing a mask and that provided us with a Bernoulli distribution: 1 if the entity wears a mask and 0 if they do not: `Discrete(.56,1,1.0,0)`. Our next attribute is vaccinations, as we simulated in Fall of 2021 when vaccinations were available and administered. Entities are assigned a 1 if they were vaccinated and 0 if they were not. Approximately 53% of the population was vaccinated with two doses [15]. Hence, we utilized a Bernoulli distribution, `Discrete(.53,1,1.0,0)`. The last attribute is an interaction factor, where entities are assigned a 1 for highly sociable and 0 for not sociable. The purpose of this is to mimic the U.S. population where people are willing to take the risk to socialize during the pandemic, hence increasing the risk of spreading the virus. We utilize a Bernoulli distribution with a 70% chance of being "highly sociable" as we witnessed in the past year that most of the U.S. was against the idea of isolation.

All of the previously mentioned attributes will increase or decrease the likelihood of the entity catching COVID-19, but there is a base risk for how infectious the virus is in the system. This base risk can increase if there are more cases of COVID-19. We use an **ASSIGN** block to set this value to `1 + Count_I`, where *Count_I* is a variable of positive cases at TNOW minus the cases that are in the hospital or quarantining at home. After this **ASSIGN** block, entities go through a *Hang Out Time* **PROCESS** block. This is to simulate time passing in the system where entities are existing in the system and facing potential risks of exposure. This is modeled with a Triangular distribution: `TRIA(5,7,12)`. After the entities pass time in the system, they go through the *Updated Risk* **ASSIGN** block. The entity's base risk attribute is re-evaluated based on a combination of mask status, vaccination status, interaction factor, and the initial base risk. The equation is:

```
BaseRisk - (BaseRisk*.8*(VaccinationStatus==1)) +
(BaseRisk*.8*(VaccinationStatus==0)) - (BaseRisk*.8*(Masks==1)) +
(BaseRisk*.80*(Masks==0)) + (BaseRisk*.30*(InteractionFactor))
```

. Masks and vaccines are 80% effective at preventing the spread of the virus, so the risk decreases if the person wore a mask or was vaccinated[4,18]. However, if the entity does not wear a mask or get vaccinated, the updated risk increases by the same factor. The interaction factor increases the

entity's risk by an arbitrary factor of 30%. With the updated base risk attribute, entities then go to a **DECIDE** block to determine if the entity gets infected with COVID-19. If *COVID or No COVID* evaluates to false, the entity cycles back to the *Base Risk* **ASSIGN** block, to simulate them still remaining in the system and remaining susceptible to the virus. If the **DECIDE** block evaluates to true, the entity moves on to the second part of the model. The equation for the **DECIDE** evaluation is: `((UpdatedRisk < 100 && UpdatedRisk > 0)*(UpdatedRisk)) + ((UpdatedRisk > 100)*(MN(100,UpdatedRisk))) + ((UpdatedRisk < 0)*(MX(0,UpdatedRisk)))`. This equation evaluates based on the Updated Risk while protecting against edge cases (in the event of the factors causing a risk over 100 or under 0).

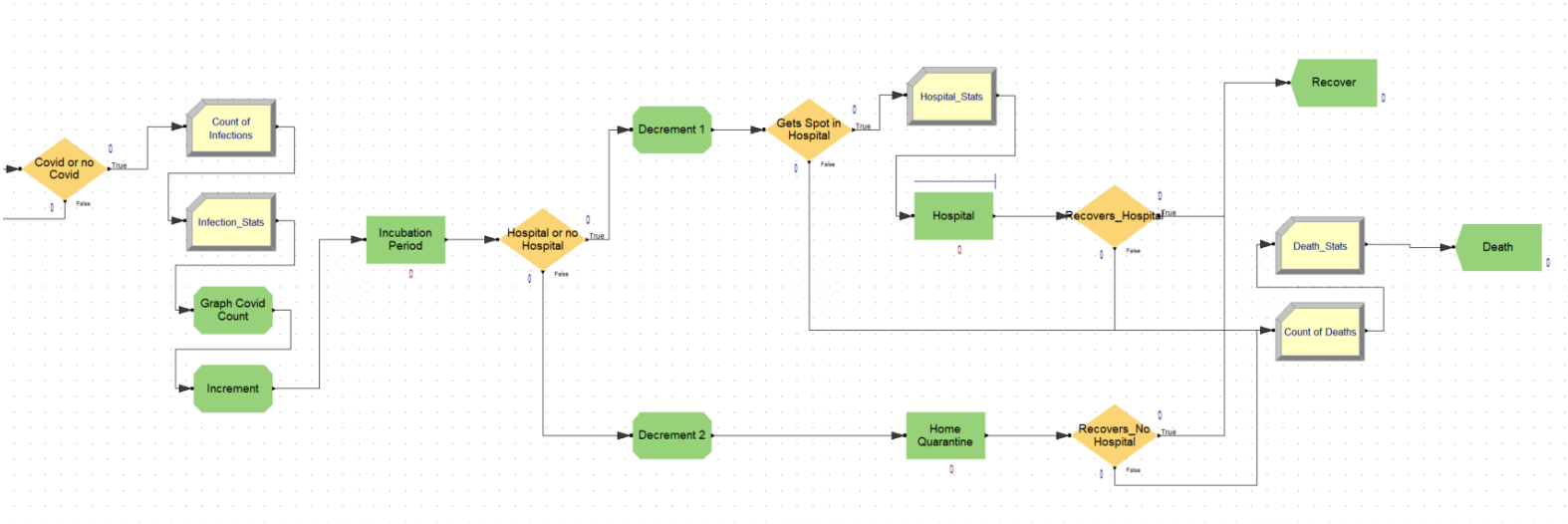


Exhibit 2: End Flow of Model

Following the true path of the *COVID or NO COVID* block, we have several **ASSIGN** blocks that help us calculate our metrics. The *Graph COVID Count* is utilized to build graph analytics on the total number of entities that were infected. This value is expected to increase consistently over time. The *Counter Increment*, *Counter Decrement*, and *Counter Decrement 2* help us maintain the *Count_I* variable that represents the number of entities infected at TNOW. These blocks increment after an infection and decrement after the entity isolates at home or goes to the hospital, as at that point the entity is no longer an active risk to spread the infection.

After passing through the **ASSIGN** blocks, the infected entities then experience the *Incubation Period* **PROCESS** block. This simulates time passing in the system while the virus infects the entity but the symptoms have not shown as of yet. This is a constant delay of three days. After incubation, the *Hospital or no Hospital* **DECIDE** block determines if the entity's

symptoms are severe enough that they will need to go to the hospital. This is a two-way by chance decision based on the age and vaccination attributes. From our research [16], 1% of vaccinated entities will go to the hospital. If the entity is unvaccinated, then their age makes a larger impact. Their percent by chance is 17% if the entity is above 75, 14% if the entity is between 50-75, 5% if the entity is between 35-50, and 1% if the entity is between 25-35. The final evaluation of this block is:

```
(1*(VaccinationStatus==1)) +
(17*(VaccinationStatus==0)(AgeGroup==1)) +
(14*(VaccinationStatus==0)(AgeGroup==2)) +
(5*(VaccinationStatus==0)(AgeGroup==3)) +
(1*(VaccinationStatus==0)(AgeGroup==4))
```

. If the evaluation is true, the entity moves to another **DECIDE** block to determine if they will be accommodated at the hospital due to capacity constraints at the hospital. This block looks ahead to the *Hospital* **PROCESS** Block for the number of entities in the queue waiting for a resource, in this case a critical care bed. The fixed capacity of this resources is three. This value was scaled to our population from the research that large city hospitals have a critical care unit of 21-30 beds[10]. If `NQ(Hospital) < 3`, then the entity goes to the hospital. If the queue is too long, the entity is not able to receive the needed care and moves to the *Death* **DISPOSE** block. The hospital is represented as a seize-delay-release **PROCESS** block modeled as a Triangular distribution: `TRIA(2,5,10)` [2]. This represents the length of time they will be treated in the hospital. Afterwards, they face another **DECIDE** block to determine if they recover or die from the disease. Our research found that 83% [11] of individuals suffering from COVID-19 recovered, so this was a 2-way by chance decision. Entities who recover travel to the *Recover* **DISPOSE** block as they are now immune from the virus and will have no impact on the other entities in the system. Entities who do not recover move to the *Death* **DISPOSE** block.

If the *Hospital or No Hospital* **DECIDE** block evaluates to false, the entity quarantines at home. This **PROCESS** module simulates time passing in the system where an entity is isolated away from others in the system. The time is evaluated as a Triangular distribution: `TRIA(3,8,14)` [12]. Following their quarantine, similar to the *Hospital* process flow, the entity faces the *Recovers_No Hospital* **DECIDE** block to determine if they recover from COVID-19. This is also a two-way by chance, based on the 95% recovery rate we found in our research [12]. Entities with a true evaluation will go to the *Recover* **DISPOSE** black and a false evaluation will send entities to the *Death* **DISPOSE** block.

Our model only has two **DISPOSE** blocks. The *Death* **DISPOSE** block is when the entity contracts COVID-19 and dies either in home quarantine or the hospital. They are disposed of

and removed from the system population. The *Recover* **DISPOSE** block receives entities that successfully recover after contracting the virus. These entities are no longer susceptible to the virus as human immunity is approximately three months and our simulation is for a full duration of three months. So they too are removed from the system.

Throughout our model there are several **RECORD** blocks. These have no impact on the entity or flow of the model, but are included to aid in the data collection of the system.

Assumptions

Throughout the model build and output analysis process, we dictated our assumptions and areas to improve upon in a future iteration of this simulation. Starting with the assumption on vaccination status, this was a Bernoulli distribution with an assumption that the second phase of COVID-19 had been released to the larger population and vaccinations were already administered to those who were inclined to take it. We utilized a static statistic of the percent vaccinated in Fall 2021. However, we also assume that the protection from the vaccine remains the same over time during the entire three month period. Additionally, while there could be a correlation between age and success with recovering from COVID-19, our model assumes a static risk factor depending on four categories of age. Similarly to age, research shows that pre-existing conditions or disease account for a large percentage of hospital cases of COVID-19[3].Gender also played a role as the mortality was higher in women as age increased[17]. We made the assumption that these factors do not increase or decrease one's success in recovering once getting infected with COVID-19.

In regards to the decision to go to hospital or isolate at home, we made a static assumption solely on age and vaccination status that dictates the "severity of the symptoms". If one is not vaccinated, the risk was based on age to increase and decrease the need to go to the hospital. If one is vaccinated, there was a much smaller chance of going to the hospital. We assume that these are the only factors while in reality, insurance, socioeconomic status, personal beliefs, and more impact this decision as well. In the other case, the entities that decided to self-isolate were assumed to die in isolation and would not instead be taken to the hospital in an emergency, which may be less realistic. Finally, the reporting of COVID-19 cases is also up to individuals or if they get hospitalized. Hence, there is variability in the actual number of infections due to this biased information source.

Part III: Simulation Replication Parameters

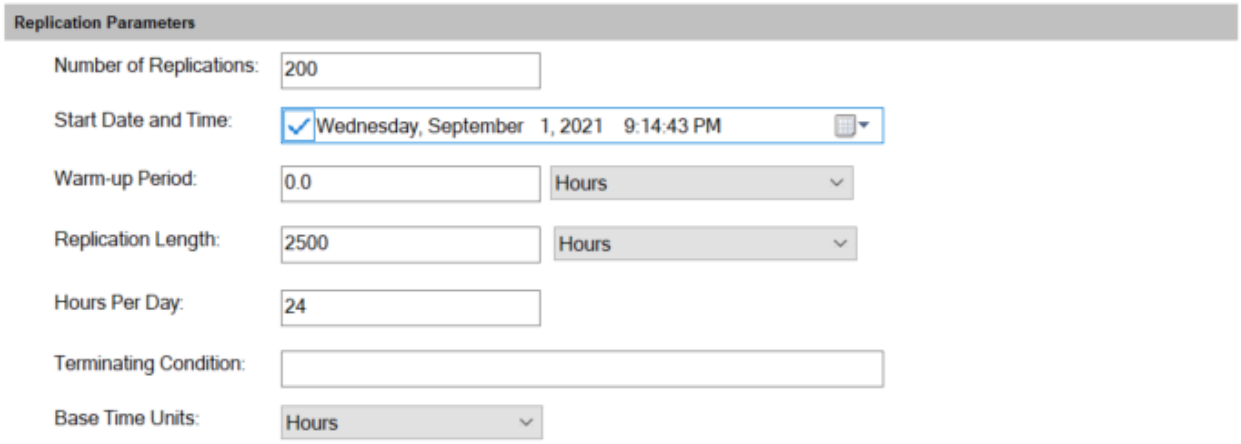


Exhibit 3: Simulation Replication Parameters in Run Setup

For an initial study, 200 replications are recommended. We did not have a warm up period so we can simulate and include the first positive case of COVID-19 that kicks off our simulation. To offset the bias this introduces, we had long run durations of three months. Additionally, since we were in the student version of ARENA, we were limited in the number of entities that could enter the system and chose 100 entities.

Part IV: Statistical Tests and Verification of Blocks

Once the simulation is complete, we can calculate the mean, standard deviation, and confidence interval of the 200 independent replications. Starting with the number of infections, the mean confidence interval with 95% confidence is between 17.7 and 19.3, or 18.52± 0.81. On average approximately 18 entities would be infected over 3 months. However, our standard deviation is 5.85, which is high relative to the mean. This indicates that there was high variability in the number of infections over the 200 replications. The expected number of infections is approximately 25, based on research of smaller populations[8]. Hence, our infection rate is lower than the average for most replications. In regards to the death rates, the confidence interval with 95% confidence is between 8.12 and 8.14, or 8.13 ± 0.00972. This indicates that the average death rate, which is the ratio of deaths to number of infections, is approximately 8%. Interestingly, the standard deviation is a very small spread of 0.07. This could indicate that the relative death to infection rate had some consistency through the replications. Finally, the mean confidence interval with 95% confidence is between 1.29 and 1.62, or 1.455 ± 0.167. On average, 1.46 entities die each run. Since there cannot be a partial death, the average deaths per run is 2 people. The standard deviation is 1.2 which does indicate variability

considering the average is very close to the standard deviation. Combining the average death rate of 8% and the number of deaths at 2,we can assume that the outliers with large numbers of infections on the right end of Figure VI are skewing the death rate higher, unproportionally to the number of infection rates. Compared to the expected death count of less than 1 in 100 entities since the expected death rate in the U.S. is 0.3%, our death rate is reasonable as we have a small population and it is challenging to simulate less than 1 death per run overall.

Age Group	Expected Infections	Observed Infections	$\frac{(Oi - Ei)^2}{Ei}$
Under 35	5	3.80	0.29
35-50	6	5.19	0.11
50-75	8	8.90	0.10
Above 75	0.9	2.01	1.37
$\chi 02$:	1.87		
$\chi 0.05,3$	7.81		

Exhibit 4: Chi Square Test

We performed a Goodness of Fit Chi-Squared Test of the normality of the distribution of the infections over the age groups within the simulation. We assumed an average infection rate of 25% in smaller populations across the U.S[8]. This would mean that our average infection rate for 100 entities would be 25. However, since our research did not include children, our expected infections is 20 to exclude the age demographics that were not researched in this simulation. From that expected infection rate and value of 20, we then determine the expected infections broken down by age bracket (bins) from a normal distribution, which represents the expected distribution of infection counts. Our alpha α was .05 and our degrees of freedom was k-1 which was 3. From the above test, our χ_0^2 was less than the critical value of 7.81, and therefore we accept the null hypothesis that our data follows a normal distribution in its spread of infection counts across the population by age.

An important note is while this test allows us to accept normality, there is still a high variance in the number of infections in each simulation. Combining these two thoughts, one can assume that the spread of the infections, even if there was a high number of them in a specific replication run, is normally distributed.

Graphs and Visuals

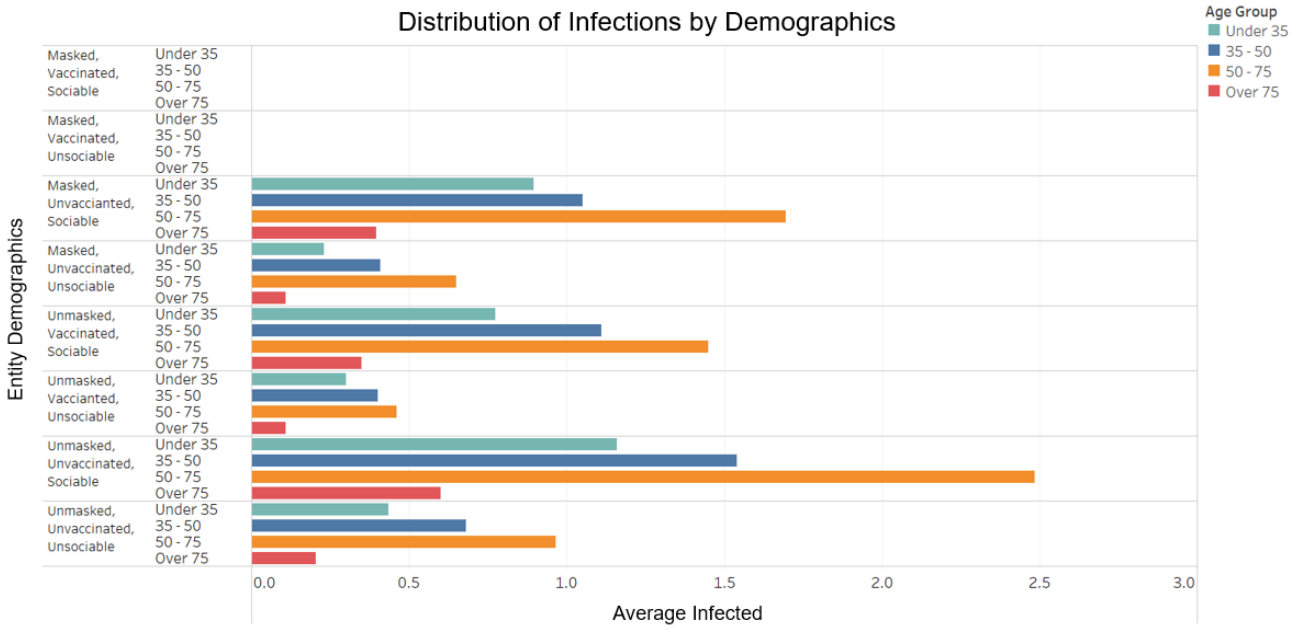


Figure I: Distribution of infections categorized by entities' demographics. The average number of infections are categorized above by different demographic groups of entities within the age groups. The demographic groups consisting of masked and vaccinated entities show no infections regardless of how sociable they are.

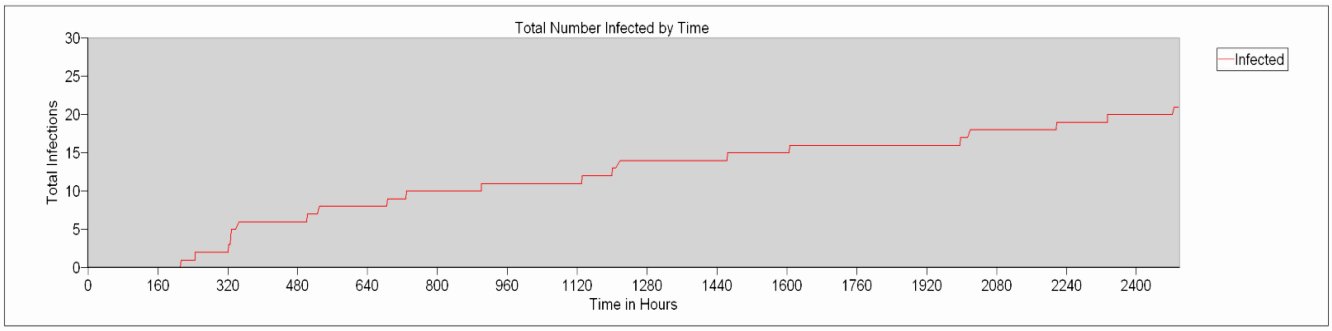
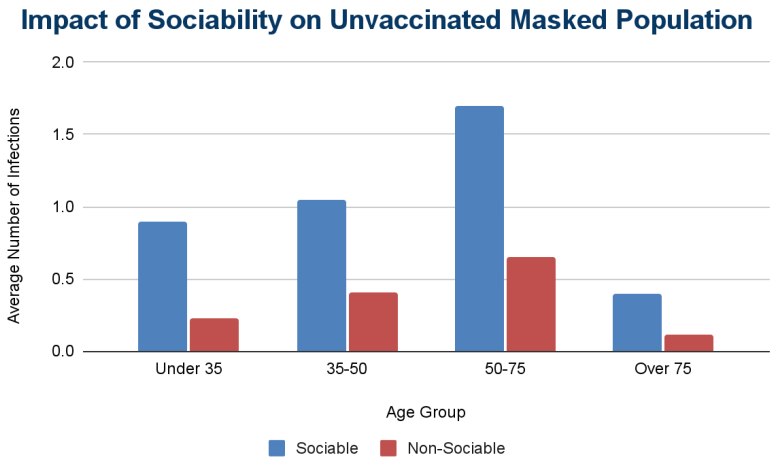
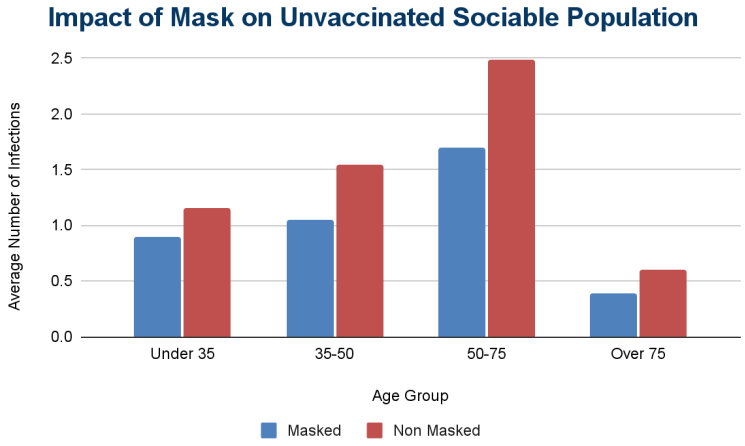


Figure II: Total number of infections over time during the simulation. The x-axis is in hours to simulate ~three months. We can infer a correlation between the number infected in the system and the risk of getting COVID-19 by including the number infected at TNOW in the base risk as an entity went through the system.



Control: Population is Unvaccinated and Masked
Variable: Sociable or Not Sociable over Age Groups

Figure III: Impact of sociability on the population that is unvaccinated and masked. There is a direct correlation between being sociable and getting COVID-19. The more sociable the entity is, the higher the risk. The age group 50-75 has the highest average infection rate per replication.



Control: Population is Unvaccinated and Sociable
Variable: Masked or Not Masked over Age Groups

Figure IV: Impact of wearing masks properly on the population that is unvaccinated and sociable. One can notice that there is a direct correlation between wearing a mask and protection from getting COVID-19. Again, the 50-75 age group has the highest infections.

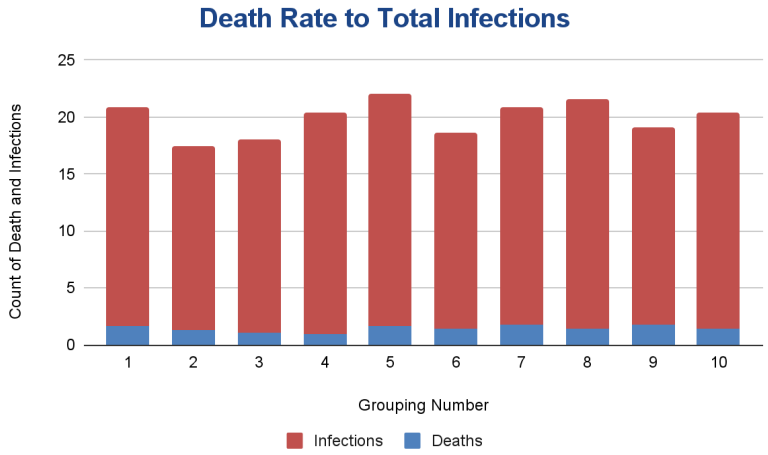


Figure V: Comparison of deaths to number of infections. The number of deaths stayed relatively even over most runs. However, there were some groupings of the independent replications that had more infections but the same amount of deaths, like group number 5. This is not a statistical analysis in regards to "batches" as seen in class, but rather a visually representative way to showcase the 200 independent replications that were observed.

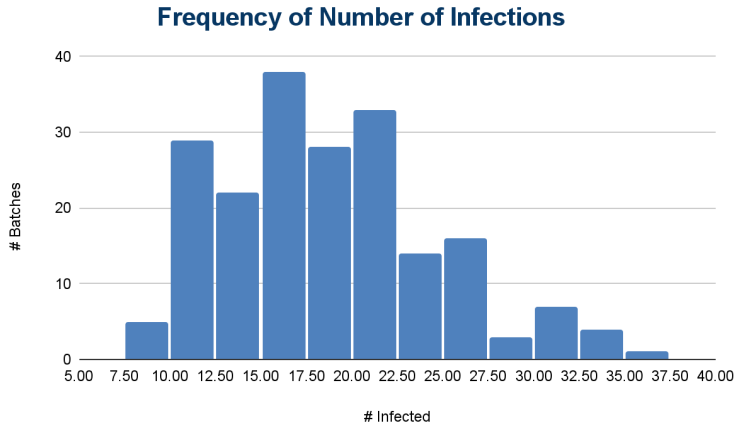


Figure VI: Histogram of infections. The number of infections does not match a normal distribution. It is a right-skewed distribution which indicates that the outlier replications have a larger spread on the right but are closer to the mean on the left.

From the above figures, we have a few additional takeaways that were not represented in the figure footnotes. We record no infections for the population that is vaccinated, masked, and sociable. This is unrealistic as we have seen many vaccinated peers and family members get COVID-19 over the pandemic even if they took minimal risks. Additionally, the 50-75 age group had the largest number of infectious cases regardless of other attributes as seen in the graphs

above. We can infer this is due to the small sample size of 100 entities and that the percent of the population that is above 75 was set to 10%.

Verification of Blocks

We perform a validation and verification analysis of our *Hospital* process. We expect the number of deaths caused by being in the queue too long to be minimal to none as most of the population should be able to get a bed at a hospital. Our research showed from 2020-2022 approximately 80,000 deaths occurred in a two week span due to the ICU being at full capacity[6]. Using that trend in a three month period of our simulation, we would estimate 1 million deaths across the nation. In the one small system that we are simulating, the hospital strain is higher because there is only one hospital. However, in the real simulation output, we do not have any deaths caused by the queue to analyze. This could be attributed to our setup of conditional statements for the wait time in the queue, or that the population is too small for the queue to get big enough to have deaths in the time period we are analyzing.

Continuing with the *Hospital* process, we analyze the resource utilization, which would be the ICU beds. As discussed with the queue, the demand in our simulation never reaches the capacity of three beds and therefore the wait in the queue is nearly zero through all simulations. Therefore, utilization is a small percent of the capacity of beds available at any point in time, at 25.4%. This translates to an average of 4.8 beds seized over each three month simulation. While this would be a good sign in the real world, indicating that the population is not having severe symptoms from COVID-19, we do acknowledge that this was not realistic and would need to have a tighter restriction on capacity of beds.

We estimate total time in the system to ensure that the entities are spending a relatively similar time in the system across processes and queues. Additionally, there are some entities who do not get COVID-19 the first time in the system and therefore were recycled back into the system. This causes more variability for total time in the system as some entities are only in the system for one cycle while others for multiple cycles. Let E[ST] be the total time system time. To calculate this value, we add the average (mean) service times for all Processes, Delays, and Queues. This formula is the following: E[Exposure Time] + E[Incubation Time] + E[Hospital Time] + E[Self Isolation Time] + E[Queue Time]. The E[Total Time] was 1355 hours, the average minimum time in the system was 500 hours, while the average maximum time in the system was 2260 hours. This can indicate that the first case of COVID-19 is after approximately 21 days, while the average case thereafter was roughly in the middle of the simulation at 57 days. The variable WIP, which stored the number of entities in the system at a given time on average was 89 entities which is almost all the entities (100) and is a favorable statistic.

Part V: Impact of Findings

The impact of the findings are beneficial once scaled. While this simulation is for a small population/system, it can allow hospitals and governments to prepare for the spread and provide more resources to cities as needed. For instance, this simulation is for a system that has one hospital, but some cities are privileged to have more hospitals available. Additionally a simulation can show which areas are going to be impacted by shortage of beds so the government can provide funding accordingly. The simulation can also be distributed as public data to show the impact to the public so there is more motivation to get vaccinated and wear masks to protect oneself. Parameters could be adjusted to see the impact on COVID-19 transmission as well. Additionally, with the full version of ARENA, one could simulate larger populations and see the nationwide impact of a longer pandemic that shifts to an endemic, rather than just the start of a pandemic on a system.

Part VI: Challenges

ARENA Parameters

Parameters that were not fully examined in this final ARENA simulation are important to address. With the Hospital Process block, the time in a hospital can be from hours to days. For some COVID-19 patients, all that is needed is IV Fluids and Monitoring to ensure the symptoms are not worsening. On the flip side, others need ventilators, surgery, or other procedures that impact the spread of time spent in hospital. We attempted to have different pathways for these procedures but soon realized that this would be an entire submodel (similar to the Call Model seen in class) on its own that we would not be able to research and develop in this course timeline. The accuracy of the queuing and time in hospital depends on a very accurate Hospital process block and due to the time constraints, our queueing was not as accurate as we would have liked.

As we were also limited by entity size from ARENA's Student version, it was hard to mimic a real population or even scale our simulation to match a larger population. Additionally, not configuring the model dynamically to have changing vaccination rates over time affected the outcome of getting infected and recovery success rates. Lastly, categorizing the age into four groups was realistic to some degree. However, this does not incorporate the difference in risk in children compared to adults as *Under 35* is all in the same category in our model.

One parameter we tested but chose against was the cycling of entities through the system and allowing the "reassignment" of attributes to diversify the population further as

people leave and re-enter the population. However, we could not do this due to the entity limitation and needed to have a static population to perform statistical analysis on.

Project Methodology

Students were all remote. Given the limitations of ARENA's compatibility with MAC computers as well, team members had to work together virtually on Zoom calls. It would be nice to have a future state of ARENA that has a shared "live" version that can be worked out of. In hindsight as well, we do think a stronger programming language like Python may have been a more straightforward approach to create and develop this model.

Part VII: Conclusion

In conclusion, our project sought to simulate the start of a virus, specifically COVID-19, within a small population. Our model had some consistent patterns with the way the virus spreads through the country the past two years. While our model did not incorporate all possibly relevant attributes of an entity (person), it was a good starting point to model a disease spreading through a system. Our modeled death rate was high compared to pandemic data we researched, and we can attribute that to a small sample size and not including all factors that determine the risk of infection, like that of pre-existing conditions and gender. Our high variability in the infection rate does show that we cannot conclude a strong correlation between our attributes and infections, however the data suggests that vaccination and mask usage can be effective preventative measures against COVID-19. We also acknowledge that we had outlier replications that had a very high infection rate compared to the average, which could be thrown out in a future analysis. In a future simulation we would want to have a larger model population to better model accurate infection and death rates, as well as a longer time spread to show the transition to an endemic.

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