Welcome to Zombie University

ISYE 6644 - Simulation

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1 Abstract

Modeling the spread of a fictional zombie virus provides an interesting scenario for examining the complexities of epidemic transmission. Using the EpiModel package in R can create a dynamic network to simulate complex interactions in a zombie outbreak. This project reviews several scenarios through Susceptible-Infected (SI) and Susceptible-Infected-Recovered (SIR) models through the stochastic network model feature in EpiModel. The goal was to explore how fast a fictional homogeneous and heterogeneous population would be infected and how much a cure and vaccines would deter the spread of the virus.

2 Scenario

The glass breaks. A gasp goes through the room. Inspired by zombie media, a student at University A has accidentally created and released a zombie virus in a lab! Thanks to this, a new epidemic is quickly infecting staff and students. Luckily for University A students, University B visitors have been brought in to rescue the university! [1] However, can they concoct a cure and save as the zombified members in time?

3 Literature Review

One of the biggest obstacles in research for this topic was the fact that since zombies are fictional, there is no real data or anything concrete about the undead. This made finding any academic research or data to use as the model basis quite difficult. Thus, some inspiration on the zombie behavior would come from fictional zombie media. Some factors to consider included the nature of zombies, how susceptible humans are to zombie bites, immunity, cures, and external influences. However, while there were some generally agreed upon traits, the interpretations of zombies vary across media for narrative purposes. While predominantly portrayed as aggressive antagonists, there have also been instances where zombies were protagonists and thus portrayed with more humanistic traits. Another big barrier was that the creation process of zombies was also inconsistent or extremely vague. An example would be that in the recent hit video game/TV series, "The Last of Us" [1], zombies were created through fungal infection. Other media simply attributed the process to unknown pathogens or even magical/mythological processes found in historical folklore [2].

In general, zombies are portrayed as undead humans that desire to eat and infect other humans in the process. Interestingly, while academic literature does not exist specifically on zombies, it was found that some previous modeling on zombie apocalypse had been performed by students [5]. This was done by solving ordinary differential equations (ODEs) based on the SIR model. The authors discuss scenarios such as latent infection, quarantine, recovery without immunity, and targeted attempts at eradicating zombies. However, the authors similarly expressed that there was no consistent agreement on the exact zombie creation process and zombie behavior. Instead, they chose to model zombie behavior on what they called "the classical pop-culture zombie", which was slow and had a strong desire to consume human flesh.

To combat this lack of consistent source material, similar diseases were explored. One of the major considerations was rabies, which similarly transmitted infection through bites from animals. The World

[1] As Dave may say, University A are probably UGA students while University B are Georgia Tech students.

Health Organization describes two types of rabies behavior, furious and paralytic [9]. The furious rabies symptoms describe patients displaying hyperactivity and erratic behavior. Assuming that a zombie-like virus was to occur similar to rabies, zombies would follow this pattern of being highly infectious, erratic, difficult to cure, and would lack the strength/intelligence to coordinate their attacks. In addition, it is also described that Post-exposure prophylaxis (PEP) was a possible treatment if symptoms had not yet appeared, and vaccinations were the most efficient strategy to mitigate transmission. This is further supported by modeling done in a study about rabies transmission in China [7], where Ruan models the transmissions in a Susceptible-Infected-Exposed-Recovered model (SEIR). They noted that the current rabies vaccination was actually highly effective, but vaccine coverage was poor, which is why the rates of transmission were persistent.

Considering both fictional and similar diseases, it was decided for this project to simulate a highly infectious zombie-like virus and cause an outbreak that would draw inspiration from pop culture but be more grounded in what may occur in a true epidemic. This allowed for similar epidemic research to be used as the basis and combats the inconsistencies on zombies in the media. This meant modelling a highly infectious disease that would spread quickly like rabies and explore possibilities such as an effective vaccination intervention and a cure.

In addition, three epidemiological models are used to simulate the spread of a fictional zombie virus. The SI model, the simplest, divides the population into the Susceptible (S) and the Infected (I). Here, people move from susceptible to infected with no chance of recovery, representing a scenario where individuals permanently become zombies. Another variation is the SIS model, which adds a layer of complexity by allowing infected individuals to recover but will continue to be susceptible. However, this project will use the SI model with a vaccine intervention instead of SIS to simulate how effective a vaccine would be to prevent or prolong the apocalypse. Finally, the SIR Model introduces Recovered (R), allowing infected people to permanently recover from the disease through immunity and cure [4].

4 Methodology

4.1 Package Choice

To explore something new and to try something more dynamic, the EpiModel package in R was chosen for this simulation. [3] EpiModel's network model is based on exponential-family random graph models (ERGMs) [4]. ERGMs are typically used in social network modeling, as they allow dynamism in simulating disease transmissions in a network. Unlike deterministic models, this dynamic network model accounts for changing interactions within the population. This creates more realistic depiction of nodal interactions. However, they tend to be expensive to model, require strong previous knowledge/data for accurate results, and are limited to a single network structure [8].

Despite the drawbacks, this provided a chance to try a different modeling structure for this epidemic. Previous literature/modeling were done through continuous deterministic models, typically with homogeneous populations. EpiModel allowed nodal attributes, which meant that that it provided a chance to try out a dynamic network along with introducing some heterogeneity into the population to see what kinds of results could arise. The dynamic network in the EpiModel library could allow simulation of the zombie virus to imitate the random spread in a contained location. EpiModel is also able to accommodate modeling SI, SIS, and SIR models, which gave flexibility to explore scenarios. For example, it was discovered that vaccine interventions could be implemented.

4.2 Model Setup

As stated above, previous modeling has mostly focused on homogeneous populations, and for this project, introducing some variation in the population was of interest. In horror movie tropes, there is often "the one who gets killed immediately" and some people are considered to be more likely to survive than others. This is true even in real life epidemics, where portions of the population are of higher-risk due to variations of age, health conditions, etc. To introduce a variability on skewing the odds, the population was split into two groups, where one group would carry a higher risk of infection. Three different scenarios were also selected for two variations in populations: The SI base model, an SI model with a vaccine intervention, and finally,

an SIR model with a cure and immunity. To have a baseline for comparison, both homogeneous (single risk population) and heterogeneous populations would be modeled for these three scenarios. It should be noted that the network was held static in terms of population size in these scenarios for simplicity, but notably death would be a major factor for zombie aggression and human resilience.

For the network population size, 500 nodes was selected as the population size. Due to the limitations of run time and model complexity, it was not possible to directly model a university campus, which often would be more than tens of thousands of students. It was nevertheless a large enough sample size that provided some insight into possible behaviors. In addition, an overall mean degree of 1.5 was selected to ensure a highly connected network and a strong chance for a large number of nodes to be connected to multiple nodes at once. This would allow large groups of humans to be connected and display good potential for highly infectious zombies to attack and bite multiple victims at a time.

In the overall code structure, the network was initialized with $n = 500$. The network is fed a formation term that can be adjusted to contain items of interest that would represent the network formation. Target statistics are used to constrain the network according to the formulation of the network, and dissolution coefficients are used to parameterize the duration of partnerships/edges that would then be used to estimate coefficients for an initial model fit. A duration of 3 time steps was selected to allow for quick connection and dissolution to indicate how zombies would quickly claim their victims and move on to their next potential victim. After the coefficients then allows model diagnostics to be performed for any potential adjustments required to be made in case of a poor fit.

4.2.1 Code for Homogeneous Population

```
n = 500
nw <- network_initialize(n = n)
formation <- ~edges
target.stats <- 3*n/4

coef.diss <- dissolution_coefs(dissolution = ~offset(edges),
duration = 3)
est <- netest(nw, formation, target.stats, coef.diss)
```

4.2.2 Code for Heterogeneous Population

The code is essentially the same as the homogeneous population, with the addition of a vertex attribute to label the nodes into different groups and a node term in formation formula. Additionally, a constraint was added that at least half of group 1's interactions would be intergroup, which meant that they would only interact with those classified in the same group as them. This allowed for some mixing of group interactions, but also reflected that in the likely scenario of a zombie apocalypse, people would likely keep to people they are familiar with and share a similar risk tolerance.

```
n = 500
nw_het <- network_initialize(n = n)
nw_het <- set_vertex_attribute(nw_het, attrname = "group",
value = rep(1:2, each = n/2))
formation_het <- ~edges + nodematch("group")
target.stats_het <- c(3*n/4, n/4)
coef.diss_het <- dissolution_coefs(dissolution = ~offset(edges), duration = 3)
est_het <- netest(nw_het, formation_het, target.stats_het, coef.diss_het)
}
```

4.2.3 Other Parameters

The two risk groups were assigned separate infection rates to model a more realistic situation with varying innate immunity. A Poisson distribution was brought into the picture to obtain a realistic probability between the two population groups through ppois in R. By ascertaining a hundredth of the population in both group

1 and 2 to get infected per time step, the cumulative infection probability was determined from 40% or less of group 1's population, and 70% or less of group 2's population. These probabilities were calculated out as approximately 12.47% and 26.50% respectively. Hence, we would expect group 2 to be more susceptible to infection. This setup assumes that up to a chosen fraction of a hundredth of the population are being infected for sure. With these cumulative probabilities being close to a quarter, it suggests that the majority of the population would fail to be turned. However, due to the higher number of edges and quick edge dissolution, nodes quickly latch on and off to create a rampant infection spread over multiple exposure windows.

For the second model that would account for vaccine intervention, the efficacy was determined to be 90% [7] and made effective after 30 time steps had passed. It should be noted that this efficacy was applied the same to both groups at the same time. Finally, the third model introduced recovery rates where it would model how effective a cure would turn zombies back into humans. For group 1, this was 5%, and for group 2, it was 1%. This assumes that group 2, who are more susceptible to infection, would recover slower than group 1.

In the code for the models, in order to sample from the Poisson distribution multiple times, a for loop was used to do to sample from the distribution three times, and then each sample had three runs to make a total of nine simulations. The limited runs are due to the runtime limitations, as the model is more complex and requires longer runtime. This is the based structure that is used for all models. Initial number of zombies are set as $i.num = 5$ to represent a small student lab size. The time frame of the simulation was selected to be 100 time steps, with the exception of the SIR model, which is at 200 time steps. The reason for the extended time frame is that the recovery/cure creates some interesting behavior that takes a bit more time to play out.

4.3 SI Model

This is the apocalyptic scenario where University A students are infected with no intervention or immunity. It answers the question of how long students can hold out for before everyone turns into a zombie. In the homogeneous model, if a hundredth of a population is certain to be zombified, the cumulative probability is calculated for 40% or less of this infected population at around 12.47%.In the heterogeneous model, there is a second group where 70% or less of this infected population at around 26.50%.

4.3.1 Code for Homogeneous Population

```
for (i in 1:3){
  param <- param.net(inf.prob = ppois(n/100*0.4,n/100))

  init <- init.net(i.num = 5)
  control <- control.net(type = "SI", nsteps = 100, nsims = 2, ncores = 5)
  sim <- netsim(est, param, init, control)
  results_SI[[i]] <- as.data.frame(sim, out = "mean")
}
```

4.3.2 Code for Heterogeneous Population

The only lines of code that changes for the heterogeneous population are the parameters and initialization, where group 2 has a different infection probability and two people from group 1 and three people from group 2 are initialized as zombies.

```
param <- param.net(inf.prob = ppois(n/100*0.4,n/100),
                   inf.prob.g2 = ppois(n/100*0.7,n/100))

init <- init.net(i.num = 2, i.num.g2 = 3)
```

4.4 SI Model with Vaccine

In this scenario, University A is unable to discover a cure, but miraculously, someone was able to modify a usable vaccine to give a fighting chance to those who are still uninfected. In reality, this is likely the

most realistic scenario. As seen with the past COVID-19 pandemic, it is highly difficult for a disease to be "cured", and diseases are attempted to be eradicated through thorough vaccination campaigns.[6] Here, two more parameters are set up to include the intervention efficacy at 90% which would start after 30 time steps.

4.4.1 Code for Homogeneous Population

```
for (i in 1:3){
  param <- param.net(inf.prob = ppois(n/100*0.4,n/100),
                     inter.eff = 0.9,
                     inter.start = 30)

  init <- init.net(i.num = 5)
  control <- control.net(type = "SI", nsteps = 100, nsims = 3, ncores = 5)
  sim <- netsim(est, param, init, control)
  results_SIV[[i]] <- as.data.frame(sim, out = "mean")
}
```

4.4.2 Code for Heterogeneous Population

Similar to the SI model, the only changes are adding group 2 with a different infection probability and two people from group 1 and three people from group 2 are initialized as zombies.

```
param <- param.net(inf.prob = ppois(n/100*0.4,n/100),
                   inf.prob.g2 = ppois(n/100*0.7,n/100),
                   inter.eff = 0.9,
                   inter.start = 30)

init <- init.net(i.num = 2, i.num.g2 = 3)
```

4.5 SIR Model

This final scenario follows a typical zombie media hero pop-culture plot. University B has swooped in, using their simulation powers to have predicted the zombie apocalypse in advance and arrive with a cure already made. It is in fact so powerful, it not only cures the zombies, it also makes them immune from turning back into the undead once again. The University B students begin their work of infiltrating the infected University A campus where they begin immunizing and saving the University A students from certain doom. As there is a higher chance of recovering, this would model how long it would take to completely cure humanity of the disease. Here, the recovery rates for group 1 and group 2 were set as 5% and 1% respectively. This assumes that group 2 recovers slower as they are more susceptible to be infected. No students are initialized as recovered at the start.

4.5.1 Code for Homogeneous Population

```
for (i in 1:3){
  param <- param.net(inf.prob = ppois(n/100*0.4,n/100),
                     rec.rate = 0.01)

  init <- init.net(i.num = 5, r.num = 0)
  control <- control.net(type = "SIR", nsteps = 200, nsims = 3, ncores = 5)
  sim <- netsim(est, param, init, control)
  results_SIR[[i]] <- as.data.frame(sim, out = "mean")
}
```

4.5.2 Code for Heterogeneous Population

Once again, the main changes are adding group 2 with a different infection and recovery probability and two people from group 1 and three people from group 2 are initialized as zombies.

```
param <- param.net(inf.prob = ppois(n/100*0.4,n/100),
                   inf.prob.g2 = ppois(n/100*0.7,n/100),
                   rec.rate = 0.05,
                   rec.rate.g2 = 0.01)

init <- init.net(i.num = 2, i.num.g2 = 3, r.num = 0, r.num.g2 = 0)
```

5 Results and Discussion

For each model and scenario, the the number of susceptible, infected, and recovered are plotted across the entire duration of the simulation. The thick lines of the graphs represent the range of values received throughout the simulation, and a mean line is plotted through to represent the average value. As well, network graphs at various time points of the simulation are included to illustrate infection spread and different edge connections throughout the simulation.

5.1 SI Model

5.1.1 Homogeneous Population

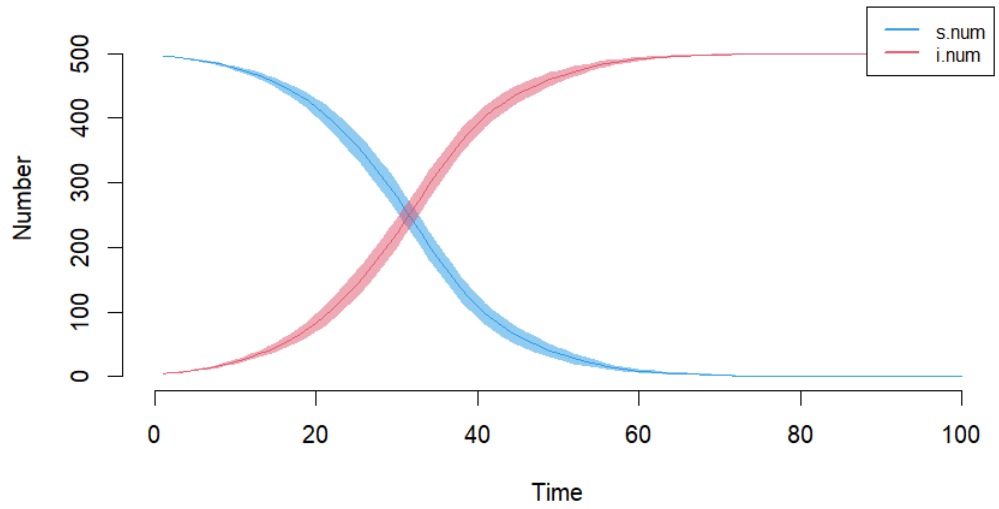
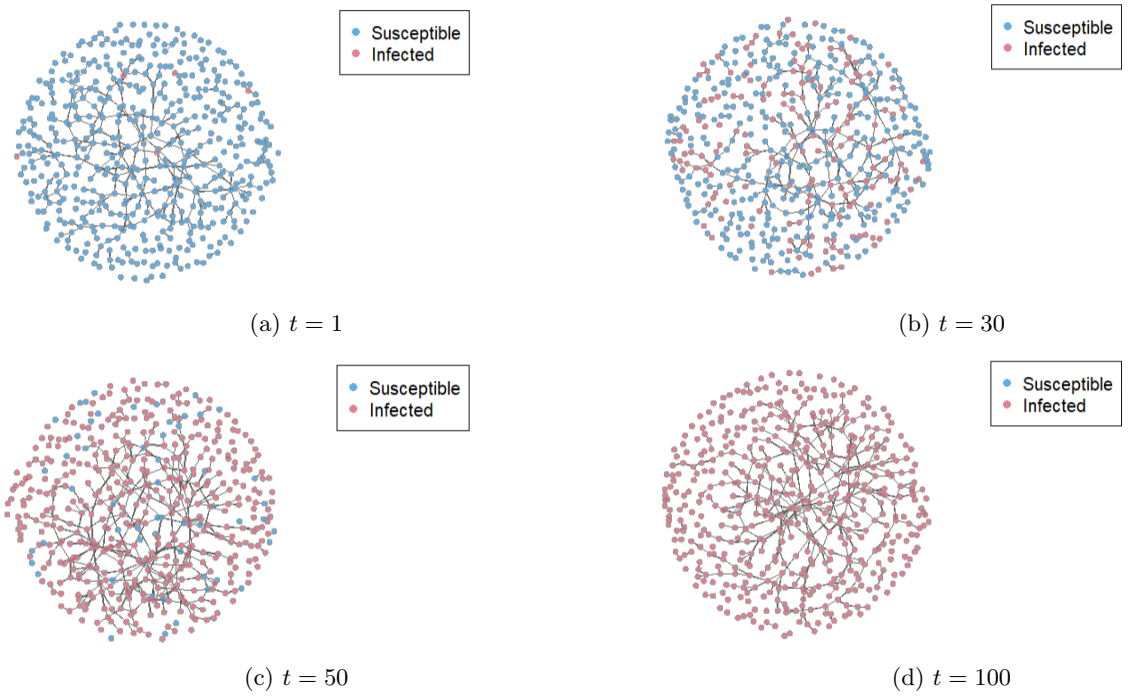


Figure 1: SI model with homogeneous population

The graph suggests that the number of zombies are about equal to humans after around 30 time steps. The increase in infection is exponential, which means that likely after the susceptible and infected numbers cross around $t = 30$, it reaches a state where likely the zombies will take over disproportionately at rapid speed. Numbers appear to plateau around 60 time steps, where the zombies have completely taken over. Thus, University A have a very small chance of survival unless intervention occurs before the zombies begin to take over the population rapidly.



(a) $t = 1$ (b) $t = 30$

(c) $t = 50$ (d) $t = 100$

Figure 2: SI homogeneous model network at various times

The network graphs show the progression of infection and how the nodes are connected. As desired by choosing a high mean degree, there are several nodes that are interconnected with several other nodes all at once, which allow for many pathways where the infection could spread. We see that by $t = 30$, about a little more than half the network is already infected, and by $t = 50$, the lone survivors are barely holding out. At the end of the simulation at $t = 100$, everyone has become a zombie.

5.1.2 Heterogeneous Population

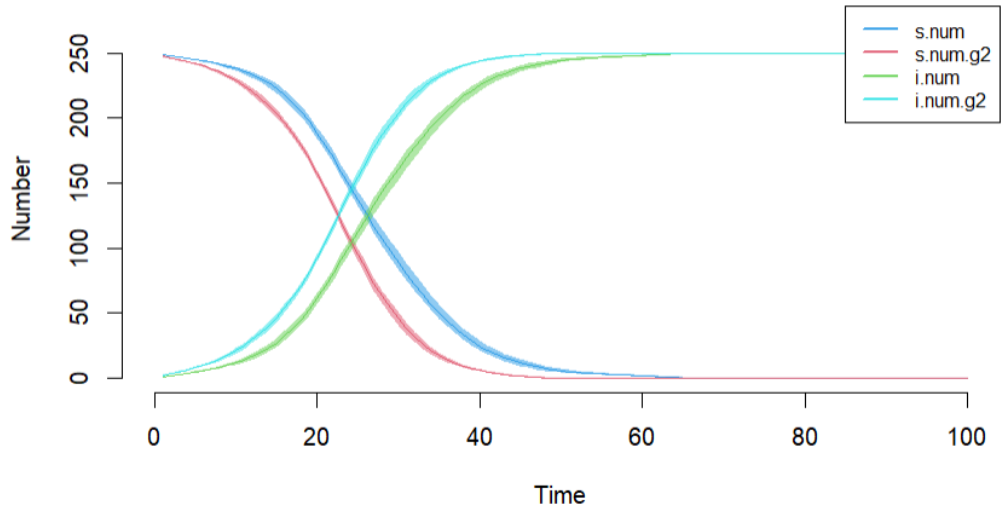
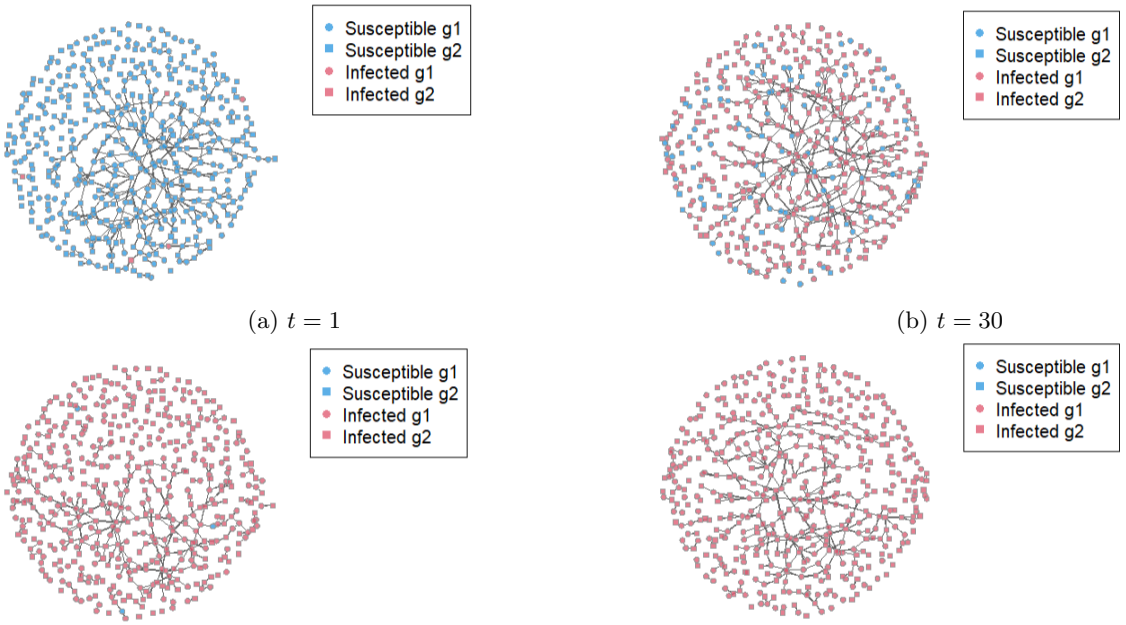


Figure 3: SI model with heterogeneous population

When adding in the group dynamics, the graph shows that the number of group 1 zombies would overtake humans after around 25 time steps while group 2 zombies overtake humans right after 20 time steps. As expected, group 2 with the higher infection probability reaches the halfway point faster. Notably, while the groups reach that point at different time steps, the pattern of how quickly the infection rate grows remains quite similar as seen by how the lines for group 2 simply appear shifted. This may be due to the fact that some intergroup interactions were allowed, and further testing of differences in intergroup interactions may yield stronger differences in patterns between groups.



(a) $t = 1$ (b) $t = 30$

(c) $t = 50$ (d) $t = 100$

Figure 4: SI heterogeneous model network at various times

The network graphs here show similar results as the network graphs for the homogeneous population, but notable at $t = 30$, we can see the most of the human survivors remaining are actually from group 1, which indicates how much quicker the group 2 population is zombified.

5.2 SI Model with Vaccine

5.2.1 Homogeneous Population

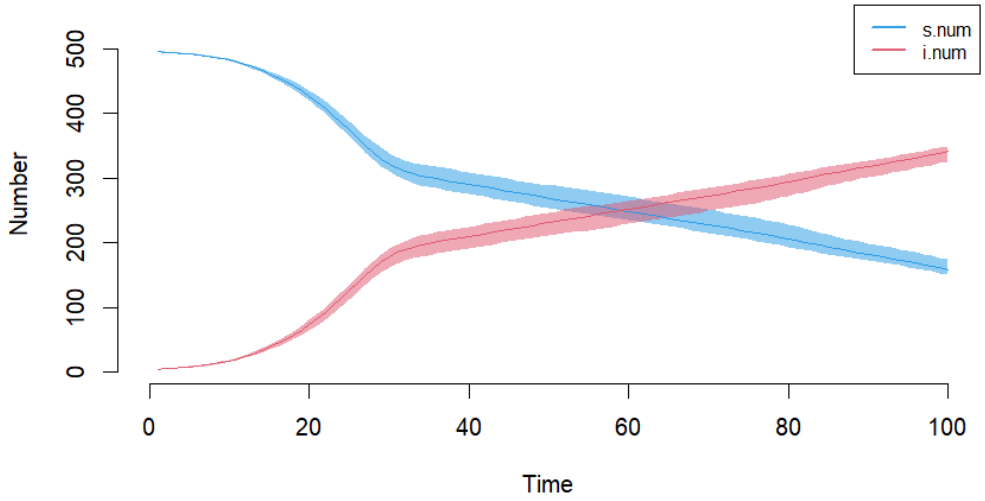
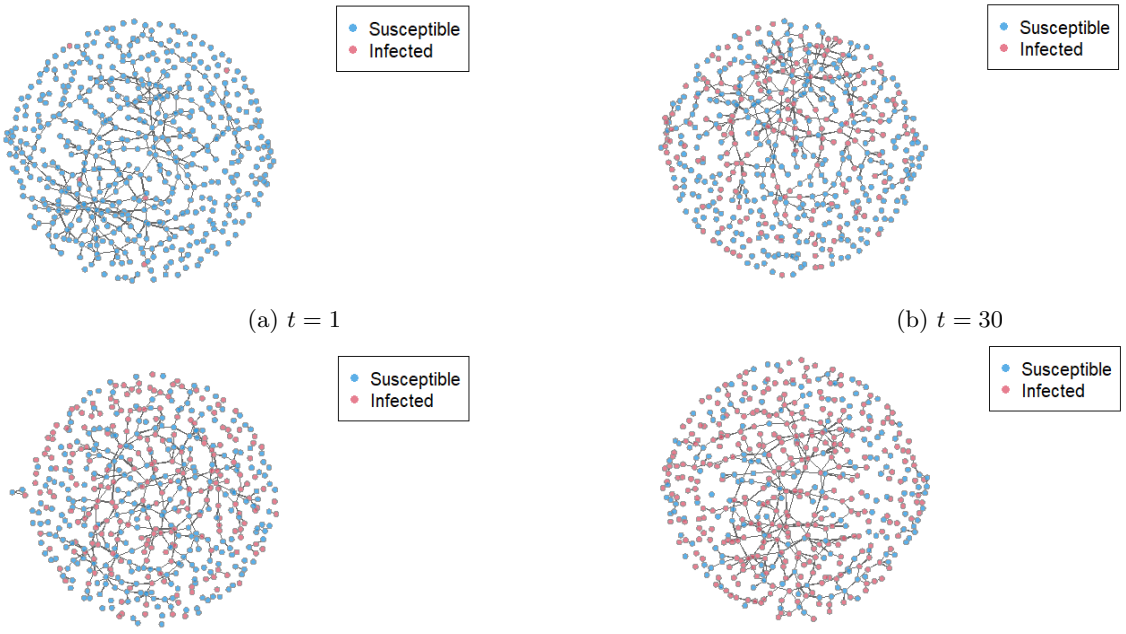


Figure 5: SI with vaccine model with homogeneous population

From the SI model, it would seem like the number of zombies would overtake humans after around 30 time steps without an intervention. However, in this graph, the vaccine instead slows down the infection rate, where the halfway point takes place at around 60 time steps instead. However, this does not stop the infection transmission, it merely acts as a delay to buy more time. Unless more drastic steps are taken, the entire population will still be infected. In addition, it should be noted the lines are particularly thick here, indicating that there is a much higher variation of response here, which means that the introduction of a vaccine can cause more uncertainty in how the exact numbers will likely play out. This makes sense, as who is able to receive the vaccine fast enough before being infected has a certain level of randomness to it, which can cause varying results.

It should be noted that if vaccination is not administrated early enough, there is a chance that it will not impact the infection rate whatsoever, this is because at that point, the infected numbers are increasing so quickly that it causes very little impact. In testing, it was found that if vaccine intervention could come in before the susceptible and infected numbers cross, it would create enough impact as shown here.



(a) $t = 1$ (b) $t = 30$

(c) $t = 50$ (d) $t = 100$

Figure 6: SI with vaccine homogeneous model network at various times

As seen in the network graphs, the infection spread is noticeably slower compared to the base SI model. At $t = 30$, majority of the population is still human, and even by $t = 100$ at the end of the simulation, there is still a significant portion of human survivors.

5.2.2 Heterogeneous Population

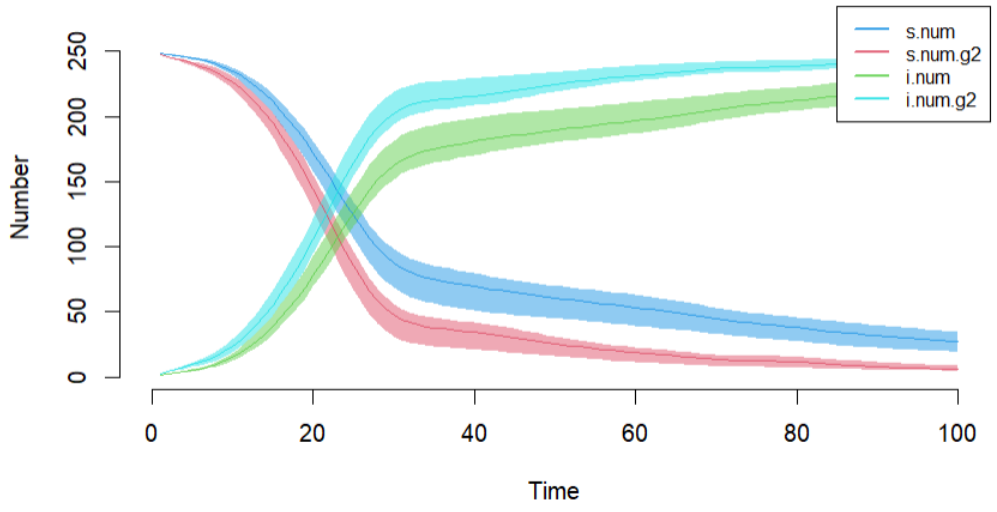
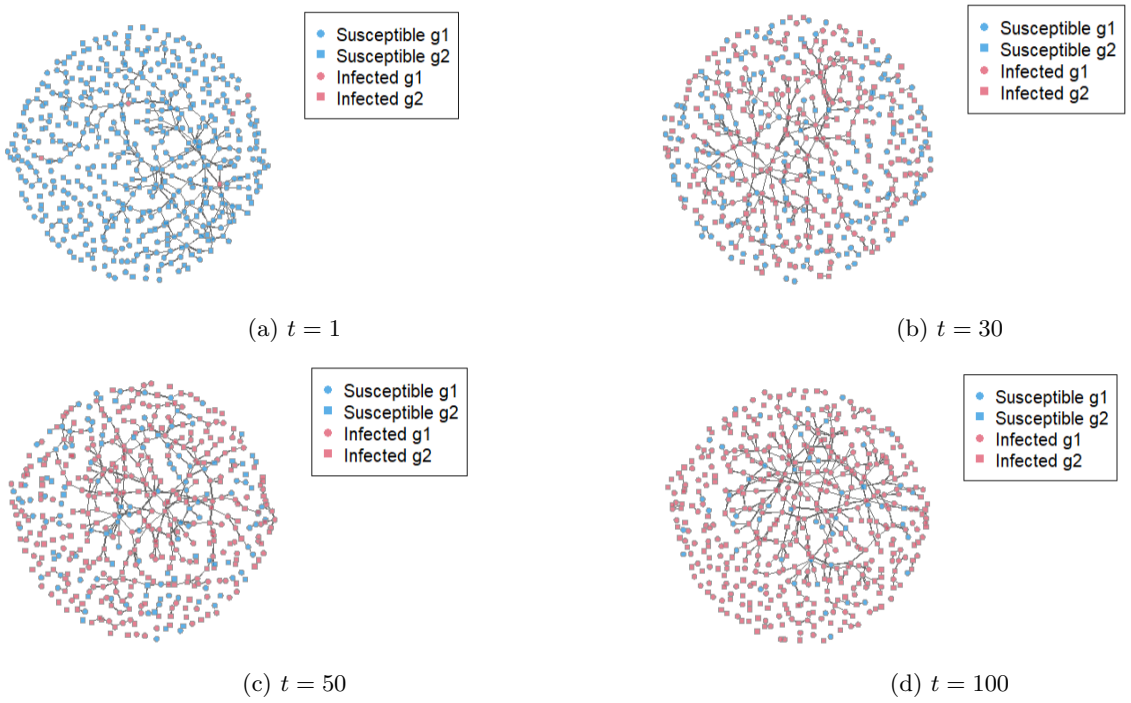


Figure 7: SI with vaccine heterogeneous Model

When adding in the group dynamics, the model suggests that the number of group 1 zombies would overtake humans right before 25 time steps. By around 35 steps, the slope begins to flatten, and nearly

everyone is infected. Group 2 zombies overtake humans right after 20 steps and the slope flatten at around 35 steps. Once again, there is more variability in the simulation runs as shown by the thicker lines and the pattern of infection is similar across both groups.



(a) $t = 1$ (b) $t = 30$

(c) $t = 50$ (d) $t = 100$

Figure 8: SI with vaccine heterogeneous model network at various times

The network graph for the heterogeneous model shows how much stronger the infection has spread compared to the homogeneous model. With just half of the population at a higher risk, there are definitely more zombies compared at similar time points of the homogeneous model. While the vaccination has slowed down the infection slightly compared to the base SI model with a heterogeneous population, it does not to have as strong of an impact as the vaccine did for the homogeneous population. This indicates that introducing various high risk factors will probably require faster preventative action to slow down infection transmission and even more drastic measures such as quarantining human survivors may have to be implemented to have a stronger impact.

5.3 SIR Model

5.3.1 Homogeneous Population

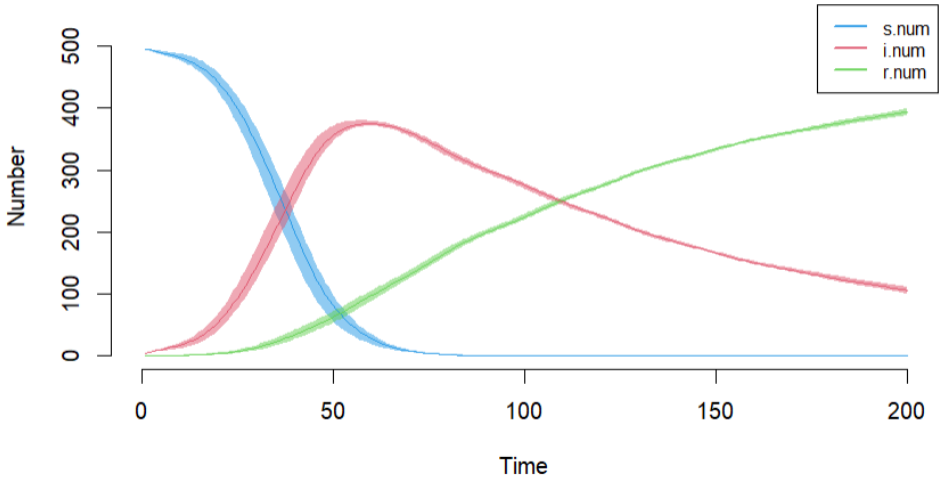
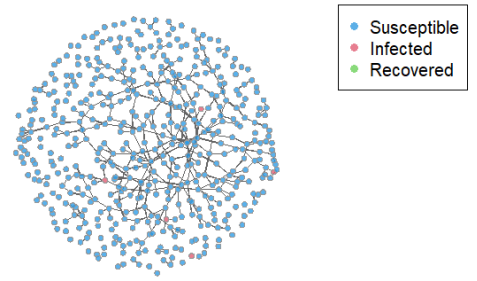
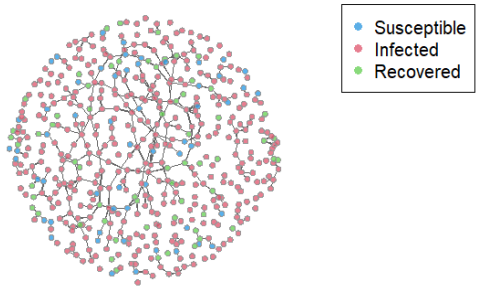


Figure 9: SIR model with homogeneous population

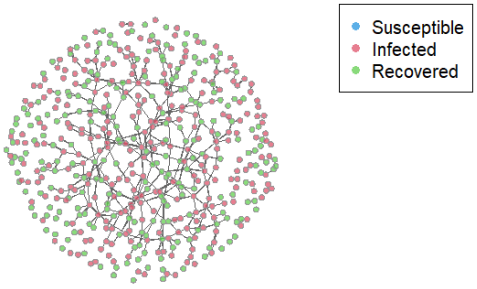
The model shows that the number of zombies equal to the number of humans at around 30 time steps. However, the rate of the cure reaching the population really begins hitting its stride just before 40 time steps. This begins to lower the number of infected, which creates a peak at around 350 zombies. Since the cure is able to reverse zombies, the infection slope begins decreasing just after 50 time steps and the recovery rate rises as susceptible and previously infected humans become cured and immune. While the simulation time frame University B is then able to successfully save the University A students.



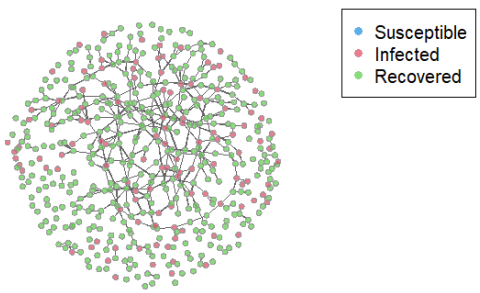
(a) $t = 1$



(b) $t = 50$



(c) $t = 100$



(d) $t = 200$

Figure 10: SIR homogeneous model network at various times

In these network graphs, it is seen that by $t = 50$, almost half of the population is infected, but there is a scatter of susceptible and cured humans. These create the process for the cure to spread around, and by $t = 100$, the blue susceptible humans are completely cured or infected, and the cure appears to have spread further across the network. By the end of the simulation, majority of the population is cured, and the epidemic of zombies look to be likely completely cured and eradicated.

5.3.2 Heterogeneous Population

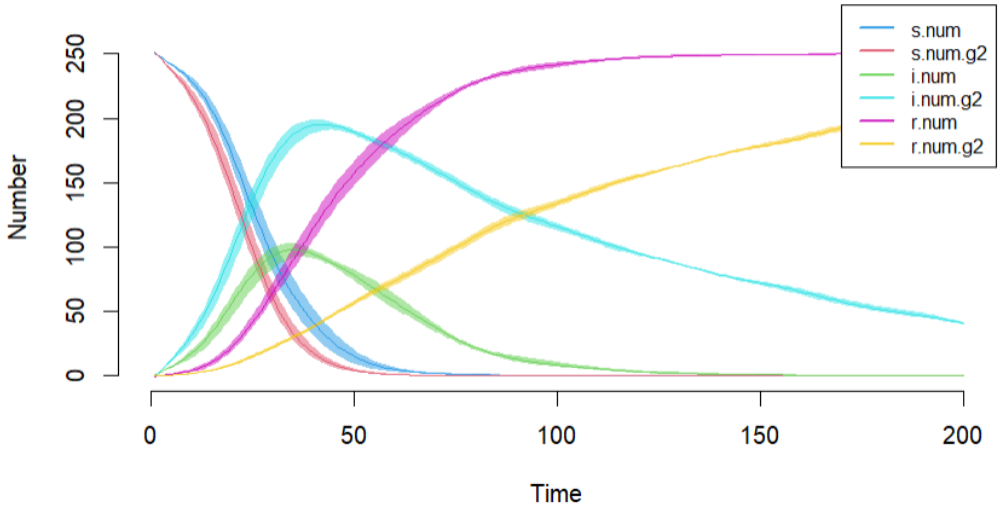
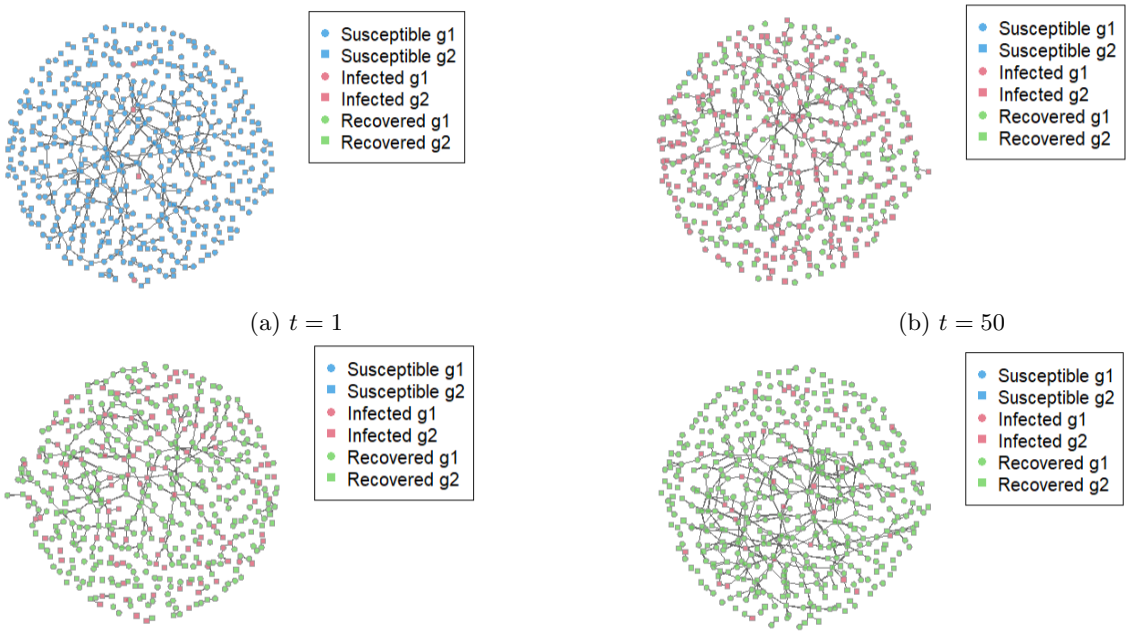


Figure 11: SIR model with heterogeneous population

When the heterogeneous population, the model suggests that the number of group 1 zombies would equal the number of humans at around 30 time steps. However, the cure would overtake the susceptible humans a few steps later, causing it to delay the rate of zombies transformations. This would cause a decrease in the susceptible and infected slopes, with all gradually flattening out after 50 time steps. Group 2 zombies become equal to the number of humans right before 20 time steps but the cure only crosses the susceptible humans at around 40 time steps. In addition, group 2 has a slower recovery rate, so the drops in infection are much less severe and delayed. Interestingly, while the susceptible and infection patterns are quite similar again, the recovery is quite different. This is likely due to the severity in difference of recovery rates.



(a) $t = 1$ (b) $t = 50$

(c) $t = 100$ (d) $t = 200$

Figure 12: SIR heterogeneous model network at various times

In the network graph, compared to the homogeneous population, the cure by $t = 50$ appear to be more widespread, with basically very few susceptible humans left. The ratio of cured humans to the infected zombies is more evenly split, and it can be seen at $t = 100$ and $t = 200$ how quickly the cure has also spread in comparison. Much like how having two groups of various risk factors allowed for a higher infection spread, it also appears to have equally allowed for a higher spread of a cure. The differences seem to suggest that maybe there are strong intragroup connections that allow infection/cures to spread more quickly.

5.4 Future Considerations and Extensions

Future considerations would involve investigating on how to add more nuances into the model to consider other external factors. For example, the existing classification could include a mortality rate to obtain a death toll of how many died as a human or as a zombie. The current model also does not distinguish between the fight versus flight response when encountering a zombie and the chances a human would survive a fight with a zombie. This could possibly spring a decline in infections due to humans breaking away from their infection network or by killing the zombie, or also decrease the human population faster depending on the deadliness of the zombies.

Regarding demographics, gender and age could also affect the risk and infection probabilities. Different ratios of how the groups should be set up and stronger differences in infection and recovery rates could also create more varying results. It should be noted that EpiModel does offer various extensions and the possibility of customized modules to create different nodal attributes, which make these extensions theoretically possible, but this was not explored due to the time constraint of this project.

6 Conclusion

When simulating a zombie virus using EpiModel, there are several challenges and limitations. One of the primary challenges in simulating a zombie virus is the absence of real data and expert background. Considering that zombies are fictional in nature, it is hard to set the target statistics since there is nothing in real world data that could be used as reference material. Media's depiction of zombies tends to exaggerate the zombie's capabilities and each depiction has varying factors on how zombies behave. Due to this lack of

real data, it's impossible to perform data validations regarding the model. This phenomenon is present in all real emerging epidemics as in the beginning stage of a virus, it is difficult for biologists to accurately depict the future of an epidemic, especially if behaves differently from anything that has already been documented. Hence, it is important to note that this research only serves as a base for a potential epidemic, tuned to simulate the effectiveness of each scenario in saving humanity. Overall, the scenarios showed that a rapid spreading disease with a highly connected network would require immediate and drastic action to truly have an impact if a zombie apocalypse broke out. It suggests that time sensitivity is one of the key factors in whether or not humanity survives, and in the absence of a cure, measures must be taken to create delays to prevent strong infection transmissions before everyone becomes a zombie.

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