Effects of the 'Bubble' Contact Network Structure on Disease Dynamics

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Modelling Real World Problems

Date: 28th May 2021

Introduction

1.1 Broad Introduction into the Study Topic and Context

During recent years we have witnessed a number of significant outbreaks of infectious diseases, the most recent being COVID-19. With the coronavirus viral epidemic posing a considerable threat to human health and wellbeing, governments around the world have set out to devise rules and guidelines to prevent or delay the spread of coronavirus. These guidelines include washing hands thoroughly and regularly, keeping 1.5 meter distance, quarantining, and more. Beyond these basic measures, governments have been experimenting and introducing new measures potentially reducing infection rates.

A prominent example of experimentation with Corona prevention measures occurred in Belgium, where the government introduced 'corona bubbles' to ease social restrictions in May 2020. This rule employs a different approach than most European governments. It does not enforce a fixed number of people an individual can meet in one day, ex. in the Netherlands receive max. 2 visitors a day (Government of the Netherlands, 2021), but requests Belgian citizens to form permanent, unchanging "bubbles" - households with which to interact. The Guardian described this measure as: "two sets of four people make a "corona bubble", who can visit each other's homes" (2020).

1.2 Research Topic

Corona 'bubbles' are meant to reduce coronavirus infection rates by trapping the infection in small groups of people. However, the size of the bubble matters and 'leakages' often occur when members interact with people outside of their designated contacts. In Belgium in May 2020, the recommended size of a COVID 'bubble' was four people because it matched the country's capacity to do contact tracing if someone fell ill (The Guardian, 2020).

Understanding the disease dynamics is key to developing effective interventions to control or prevent an epidemic such as coronavirus. In particular, studying patterns of social contacts can help establish the rate and extent of viruses spread in a population. This information is crucial to developing concrete government regulations - for example, the recommended size of a social 'bubble'.

This paper provides an analysis of the effects of the adjusted bubble contact network structure on COVID dynamics, as well as proposes an optimal threshold size for a bubble under which the spread of the virus is mitigated. A model that limits the interaction of a node in a network within its two chosen individuals (forming an adjusted bubble) is designed and investigated. A total of 3 scenarios are explored, with the bubble sizes ranging from 2 to 4 people in total.

For each scenario, changes in epidemic dynamics and pattern formations are observed and recorded to report our findings. This information allows the threshold size of the bubble, at which the infection does not spread through the network, to be investigated. We expect to

find that smaller sizes of bubbles to have a large impact on virus spread in a graph trapping the infection at an early stage, while larger sizes of bubbles (3 or 4 people) to increase the spread of the disease and lead to extensive transmission in the whole network.

Material and Methods

2.1 Data Set, Network, and Model Description

2.1.1 Data and Network Description

The Haslemere data set is used as the basis for the network created in the scope of this investigation. This dataset provides a list of close geographical contacts on the basis of which a node will choose a 'bubble friend' in the simulation - someone to form a social bubble with. The network is then formed from this data set by adding edges between individuals in accordance with the size of the bubble for this scenario. The network is undirected.

For the purposes of this investigation, the bubble size refers to the number of edges one node is allowed to have. For a bubble of size 3, one node is connected to two other nodes; however, these two other nodes are not necessarily connected to each other. This differs from the real-life Belgian model, as this describes a bubble in which everyone within that bubble has to be connected. A visual presentation can be seen in *Figure 0.* below. This adaptation was made because an implementation of these isolated bubbles would leave no room for any infection to continue. This is because other real-life factors, such as chance interactions in a grocery store or on public transport, that further the infections are not implemented in this model.

In Red:

Definition of a 'bubble' in this investigation

Definition of a 'bubble' under Belgian law
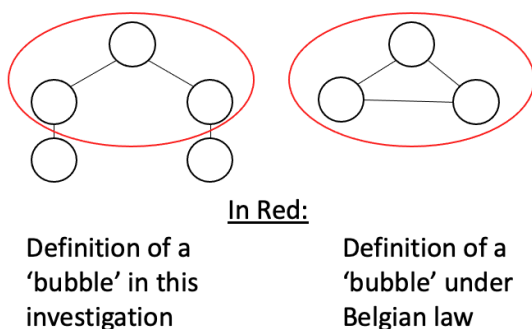
Figure 0.: Belgian definition of a bubble and adapted definition

In order to reduce possible type A uncertainties and increase statistical significance that the dynamics observed and data collected is less due to chance, every data point is an average of 30 trials. This means for every experiment, a new network is created. This includes making new random edges between nodes according to implemented bubble size, and a new selection of the initial ten infected individuals I(0).

2.1.2 Model Description

The SI model is used to model the spread of infection in the network. The foundation of the SI model lies in several equations defined by the number of susceptible individuals S(t) and the number of infected individuals I(t) which are both functions of time. The susceptible are not infected at *t*, but are able to be infected. The infected are infected at *t* and can transmit the disease.

We did not include the R(t), the number of removed people as a function of time, as this would not be relevant in serving our goal in this investigation. This is because we are aiming to model and analyze strategies for the prevention of the spread, focusing on how the behaviour of the general population under the "bubble rule" affects the total number of infected people I(*t*).

2.1.3 Limitations of the Model

One significant aspect that is not included in this model is the spread through chance interactions that occur routinely, such as while grocery shopping or using public transport. Another limitation of the model is that we are using contact within 50 meters as an opportunity to create a connection which will be a part of a bubble, which does not necessarily represent realistic social connections.

2.2 Variables and Parameters

Biological	Mathematical
Person	Node
Connection	Edge
Reproduction Number/R0	Probability of Transmission

Figure 1.: Translation of Biological and Mathematical Interpretations

Independent Variable
The bubble size ranges from 1 - 5 in discrete steps of one; this is defined as the number of contacts one person can have, in other words, the number of edges one node can have.

Dependent Variable
The total number of infected individuals in the network.

Controlled variables
- Probability of Transmission = 0.2
- Exceptions (individuals who break the rules) = 0
- Total number of individuals in the Network = 576
- Initial number of infected individuals I(0) = 10

The probability of transmission was controlled, so that for every infected node in contact with a susceptible node there was a probability of 0.2 of disease transmission. The other controlled variable was the exclusion of exceptions; all individuals followed: $number\ of\ edges\ of\ an\ individual \leq imposed\ bubble\ size$. Furthermore, the constancy of population is static as there are no births (new node additions to network) and no deaths (node deletions of network). There are 576 nodes in the network. The initial number of infected subjects S(0) is 10. Therefore the initial number of susceptible subjects S(0) is 566.

Results

3.1 Effects of Bubble Size on Disease Spread

In this section, diagram representations of the SI model are presented. Plotting the progression of the number of susceptible and infected individuals over time demonstrates how the topology of the graph influences the spread of the disease. This allows for time to be another independent variable, so that the network dynamics of the number of infected individuals per time unit can be investigated. In each figure, the blue line represents the number of susceptible individuals, the red line represents the number of infected individuals in each time step.

The representation of a graph with a certain bubble size at the final step 30 demonstrates the scale and distribution of the infection in the given graph. It allows to see the formed clusters of infected individuals, as well as the outreach of the infection.

For the below graphs, the susceptible individuals are represented by the color blue and infected individuals are represented by the color red.

<u>Bubble Size 2</u>

In this scenario, the virus spread is mitigated at an early stage as seen in *Figures 2 and 3.*, with the disease being contained mostly within the pairs of people. *As can be seen in Figure 3*, the number of infected people and the number of susceptible people are almost horizontal straight lines with a slight toward each other - the rate of infection is very slow.
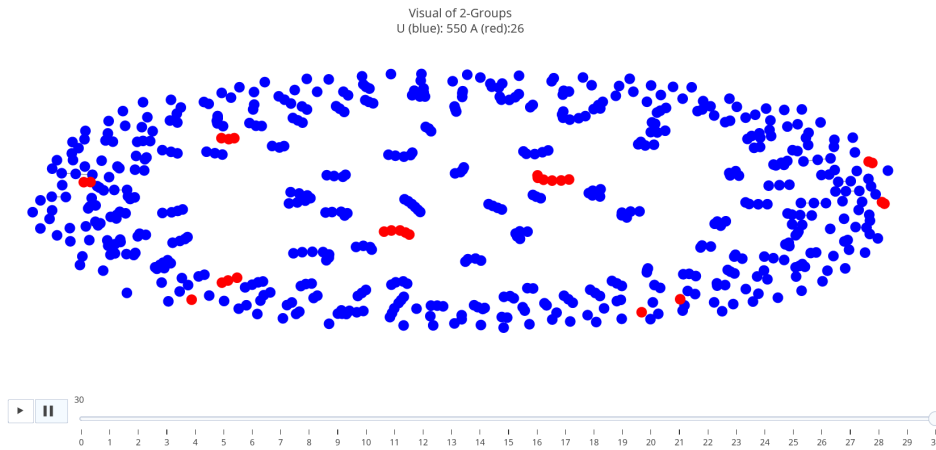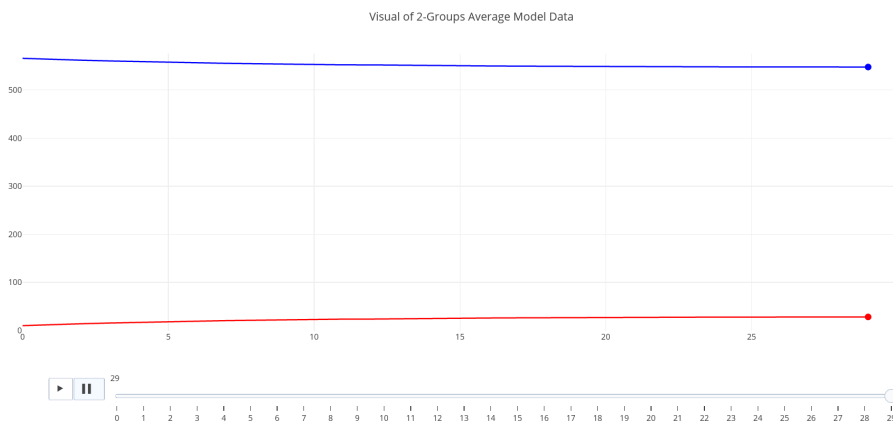

Figure 2.: Network with Bubble Size 2 at time step 30

Figure 3.: Network Dynamics with Bubble Size 2

In this scenario, the virus spread is moderate as seen in *Figures 4 and 5*. While the virus reaches a significant part of the population, it does not reach some less connected nodes who only managed to make one social connection in this network, creating separated bubbles. As can be seen in *Figure 3*, the number of infected people and the number of susceptible people increase and decrease at a fairly steady pace, respectively.
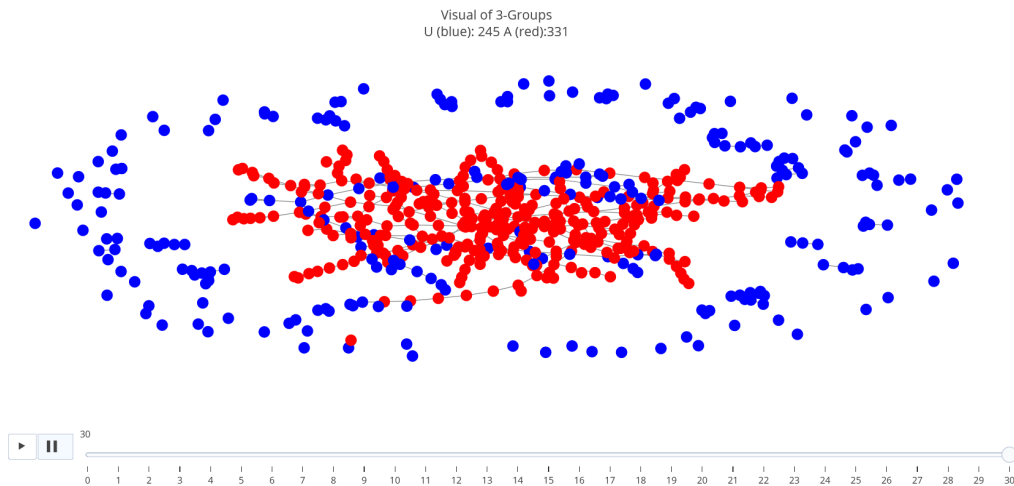

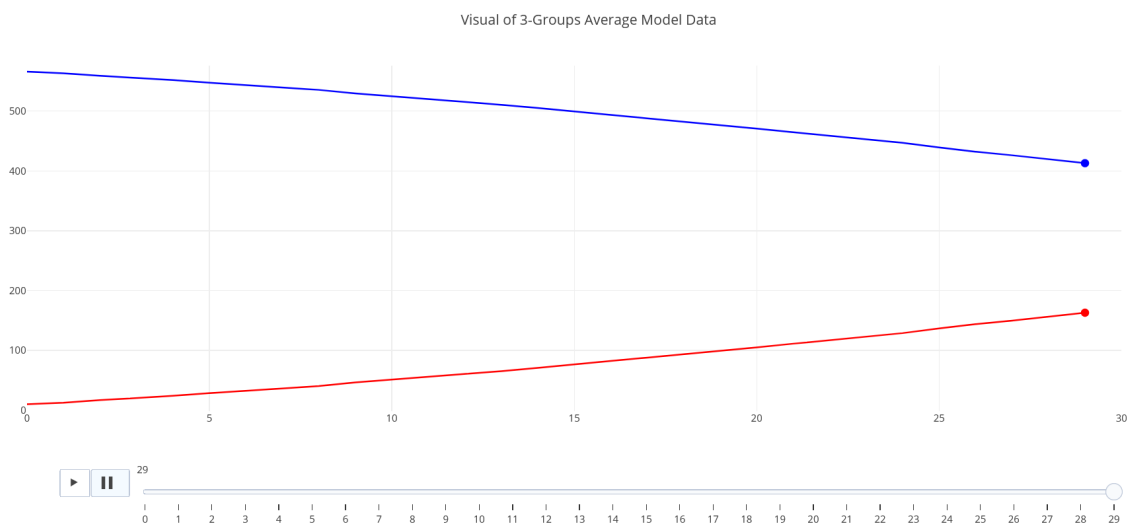*Figure 4.: Network with Bubble Size 3 at time step 30*

Figure 5.: Network Dynamics with Bubble Size 3

Bubble Size 4

In this scenario, the virus spread is severe as seen in *Figures 6 and 7*. The virus reaches the overwhelming majority of the population with the exception of isolated nodes - those that have not formed connections. As can be seen in *Figure 3*, the number of infected people and the number of susceptible people increase and decrease dramatically, respectively.
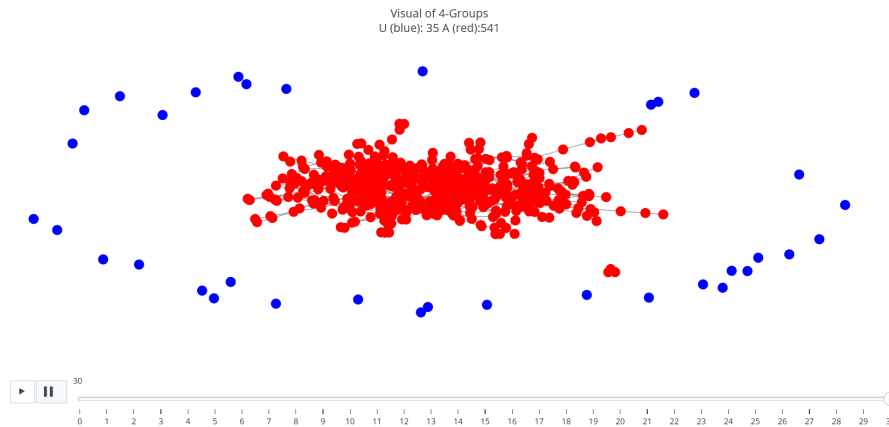

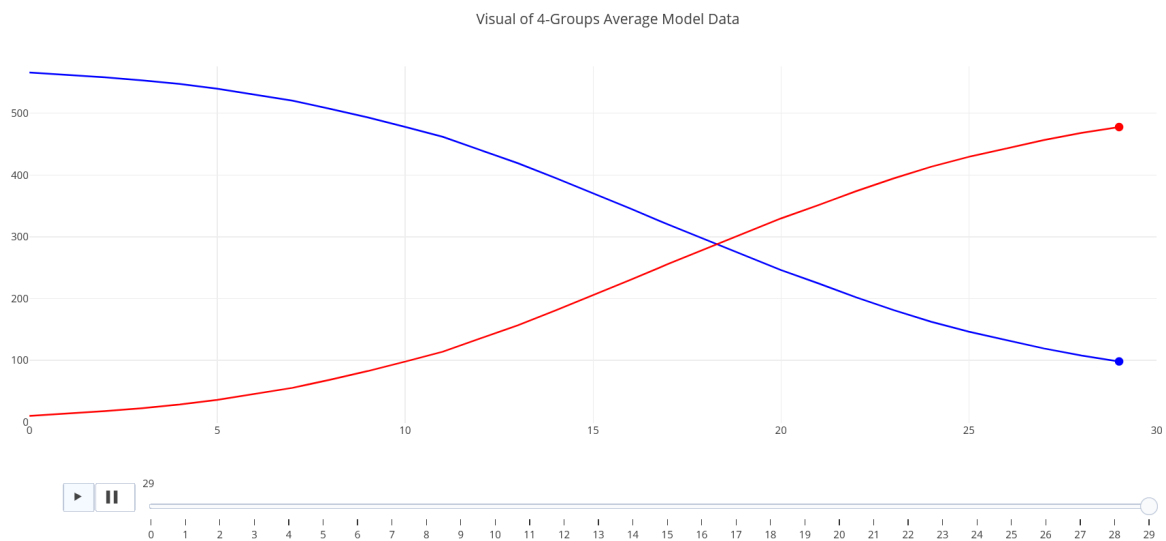*Figure 6.: Network with Bubble Size 4 at time step 30*

Figure 7.: Network Dynamics with Bubble Size 4

<u>Combined Graph</u>

Figure 8. aims not to examine the dynamics of the number of infected individuals over time, but per bubble size. In other words, here time is not an independent variable but a constant variable. Hence, the x-axis is the bubble size and the y-axis is the number of infected people after 30 time steps. The number of infected individuals after 30 time steps is displayed because at this time step the number of infected individuals start to approximately level off for all bubble sizes.

As seen in *Figure 8.*, there is a strong positive linear correlation between bubble size and the number of infected individuals at time step 30. This means that there is no specific bubble size threshold value above or below which the number of infected individuals drastically increases or decreases.
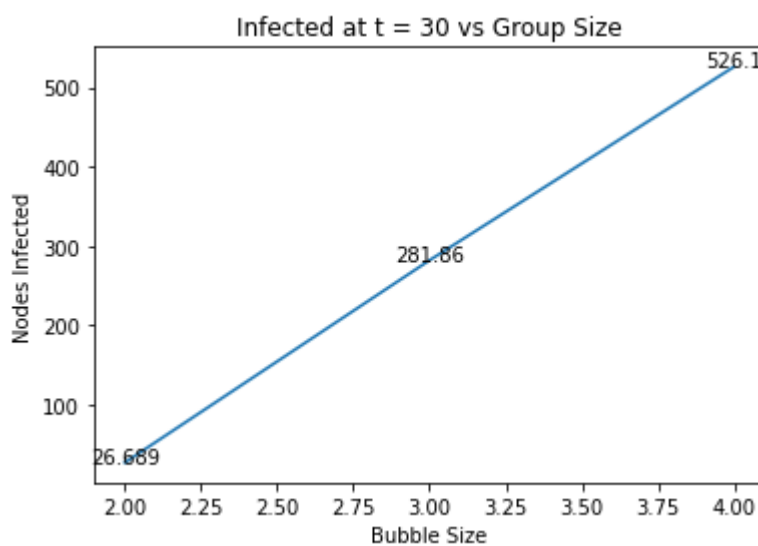

Figure 8.: Effect of Bubble SIze on Number of Infected Individuals at t = 30

3.2 Extended Research: Varying Probability of Transmission

In this section the research has been extended by altering the previously controlled (fixed) variable of probability of transmission. In addition to the previous experiments with probability of transmission 0.2, the effect of the bubble size on the number of infected individuals with probability of transmission 0.4 was investigated. Another controlled variable is the number of exceptions to the bubble rule, which stays 0.
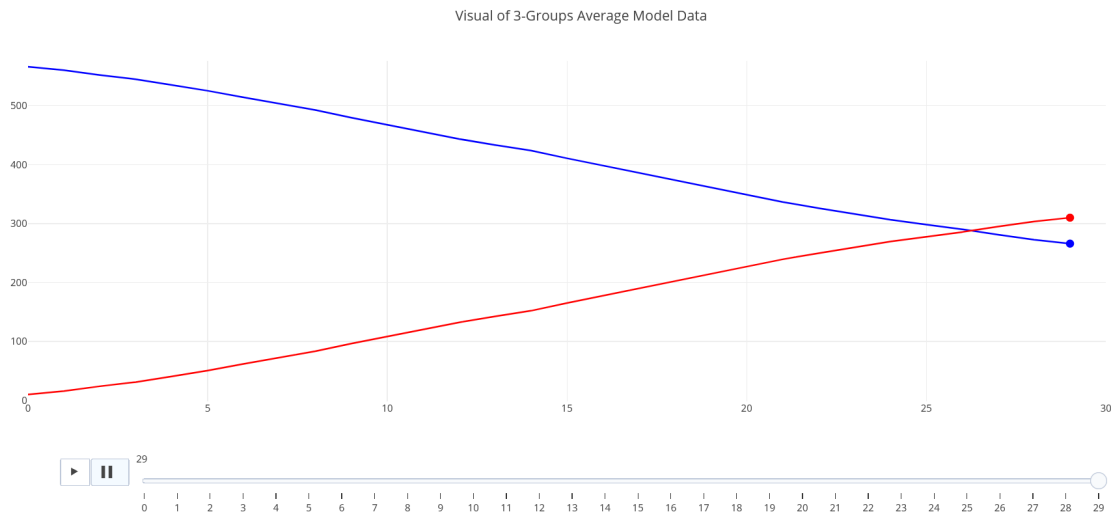
Bubble Size 2

In this scenario, the virus spread has not been impacted by the increase in the probability of transmission. The virus spread is still mitigated at an early stage as seen in *Figure 9*, with the rate of growth of infected individuals being very slow.
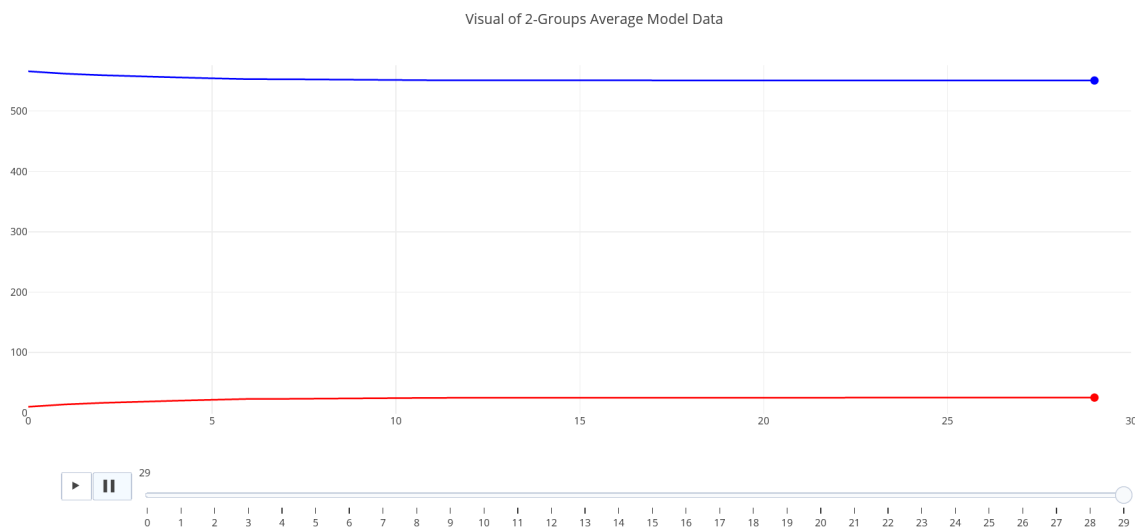
Figure 9.: Network Dynamics with Bubble Size 2 (probability of transmission = 0.4)
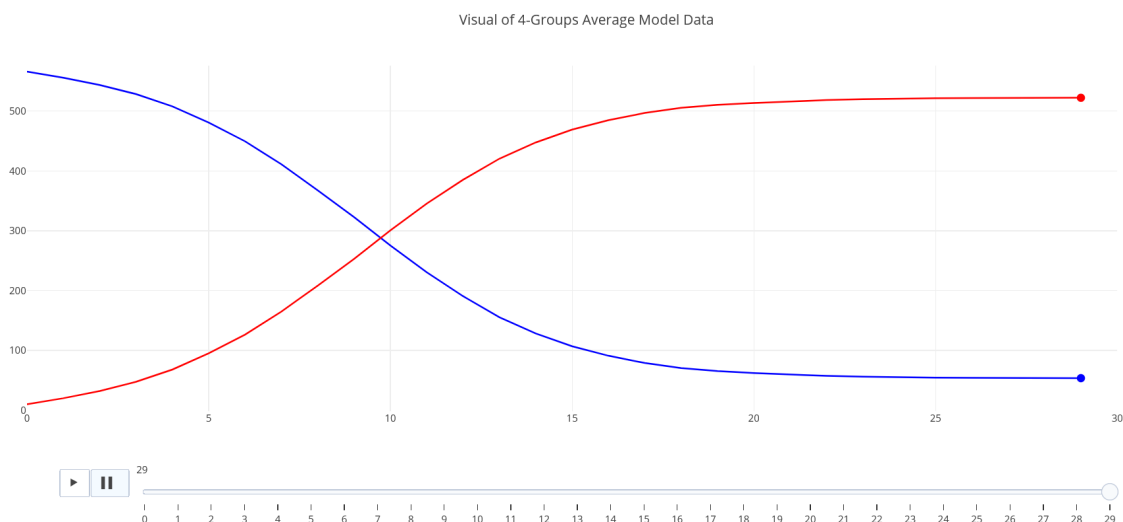
<u>Bubble Size 3</u>

In comparison with the original research, in this scenario the virus spread has increased significantly as seen in *Figure 10*. The number of infected people and the number of susceptible people increase and decrease at a steadier pace than in the original research, respectively. For example, the value of 100 infected individuals is reached at time step 10 instead of time step 20 in the original research for bubble size 3.

Figure 10.: Network Dynamics with Bubble Size 3 (probability of transmission = 0.4)

<u>Bubble Size 4</u>

In comparison with the original research, in this scenario the virus spread is also even more severe as seen in *Figure 11*. The number of infected people and the number of susceptible people increase and decrease even more dramatically, respectively.

Figure 11.: Network Dynamics with Bubble Size 4 (probability of transmission = 0.4)

Discussion

4.1 Conclusions

For each scenario, changes in epidemic dynamics and pattern formations have been observed and recorded. For bubble size 2, the virus spread was mitigated; for bubble size 3, the virus spread was moderate with the majority of individuals infected at final time step; for bubble size 4, the virus spread is severe with the overwhelming majority of individuals infected. This corresponds with the prediction to find that smaller sizes of bubbles would have a large impact on virus spread in the graph, trapping the infection at an early stage, while larger sizes of bubbles (3 or 4 people) would increase the spread of the disease and lead to extensive transmission in the whole network.

Several conclusions can be drawn from this investigation. Firstly, smaller bubbles within a network were positively correlated with a reduced rate of disease spread, as was predicted. Secondly, increased probabilities of transmission were correlated with an increased rate of disease spread - this reflects the real life situation, in which many variables affect transmission rates. This highlights the relationship between prevention measures and transmission rates. With the change in transmission rates due to all these variables, government regulations also need to be adjusted.

As for the optimal threshold size of the bubble, connecting to 2 other individuals, forming bubbles of size 2, would create the most effective reduction in the spread of disease. This is due to the lowest transmission rate of the disease and the trapping of the infection. However, there is no concrete 'threshold value' per se. This is based on the conclusions drawn from the combined graph (*Figure 8.*) that there is a positive linear correlation between bubble size and number of infected individuals at time step 30. Choosing a threshold value would hold more significance if this relationship would be exponential. *Figure 8.* can be used as a guideline in estimating the infection spreading rates depending on the real life enforcement capabilities.

4.2 Future Research

Changes could be made to our model to allow for further research, especially to include aspects of social dynamics and disease spread which we have not yet modelled. Evolving networks might be more able to model the social patterns that exist in society. Changing connections often or weighting connections differently for example, could all affect infection spread through a network. Reciprocal bubbles, in which people agree on a group of a certain size and only contact this group, could be combined with a slight chance of occasional random connections. This would more closely represent the Belgian restrictions. If bubbles are completely adhered to, significant infection is impossible, as the network is not connected. However, the addition of random connections with low chance might be able to simulate the chance encounters that still allow infection.

In addition, rules are never going to be followed completely. For this reason, 'rebels' who have larger groups, changing connections, or many connections with low risk, all might be modelled, to study the effects of this behavior on the spreading of infection.

On a larger scale, all of these mentioned variables and parameters can be used to manipulate the current network and investigation to achieve results that more closely model specific real-life situations.

In order to generate the files used here, run file displayandanalysis.py

Bibliography

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