Social Networks, Compartmental Models & COVID-19

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Abstract

The purpose of our research was to accurately model the spread of the disease COVID-19. To do this, we used the Susceptible-Infectious-Recovered (SIR) model and applied it to several types of social network graphs in the programming language R. We adjusted the average number of edges between nodes, mirroring the number of close contacts an individual can spread the disease to, which allowed us to simulate non-pharmaceutical interventions that governments used to limit the spread of the virus.

The SIRS model

A common model in epidemiology is the SIR model. It is a compartmental model, meaning that each individual in the population must be a member of one of the model's compartments. In the most basic cases, the compartments are Susceptible (the individual can contract the disease), Infectious (the individual has the disease and can spread it to others), and Recovered (the individual is immune to the disease)[1, 2]. To more accurately reflect COVID-19, we decided to adapt the SIR model to the SIRS model. The SIRS model takes into account the fact that individuals may become susceptible to the disease again after recovery, meaning that they do not have lifelong immunity.
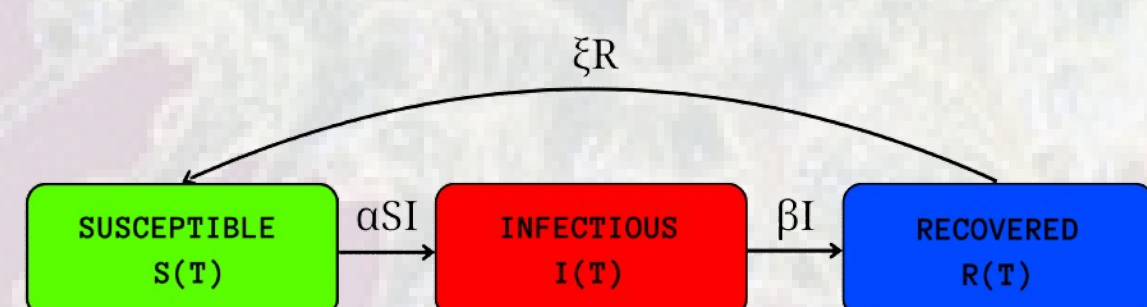

Figure: An illustration of the compartments of the SIRS model.

Graph Generation

Social network graphs can be used to model the spread of diseases by using nodes and edges to represent individuals and the relationships between them. The average number of people infected individuals may come into contact with is represented by the degree distribution. Epidemic modelling with these networks means that governments can decide what measures to take based on predictions of what a disease will do next [3].
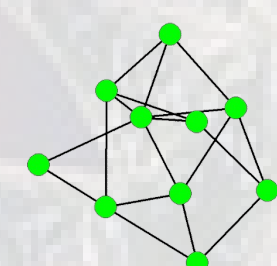

Figure: An example of a simple social network

Random network generation allow scientists to create random graphs, where each node has a random number of edges with other randomly selected nodes [4].

In the Erdős–Rényi model, graphs with a fixed set of vertices and edges are all equally likely [4]. There are 2 main variants of this model. In the G(n, M) variant, a graph is chosen uniformly at random from the collection of all possible graphs that have n nodes and M edges. In the G(n, p) model, a graph is made by connecting nodes randomly. Each edge has probability p to be included in the graph, independent of other edges [4].
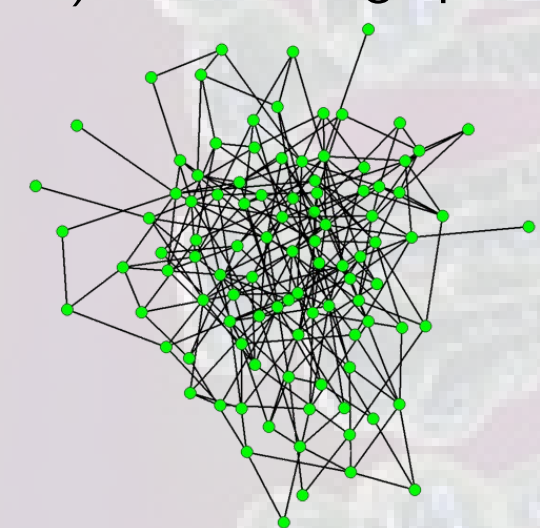

Figure: Graph generated with the Erdős–Rényi model.

The Barabási–Albert model is a scale free model [5], which means there are hubs (nodes with a very high number of connections to other nodes) rather than all the nodes forming connections at random. This occurs due to preferential attachment, where nodes with more edges are more likely to form new edges with other nodes as the graph is generated.
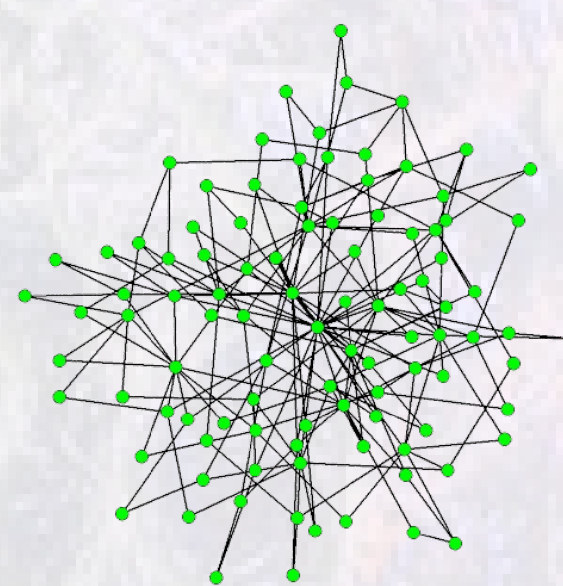

Figure: Graph generated with the Barabási-Albert model

The stochastic block model is another example of a random graph generation model, but it is characterised by nodes being in subsets known as communities that are connected by particular edge densities. In other words, edge densities may be higher within rather than between these communities [6].
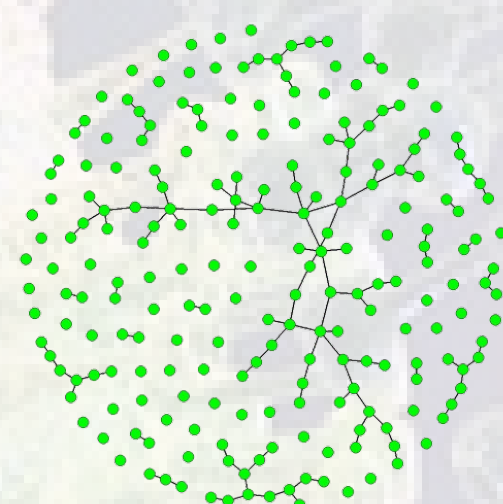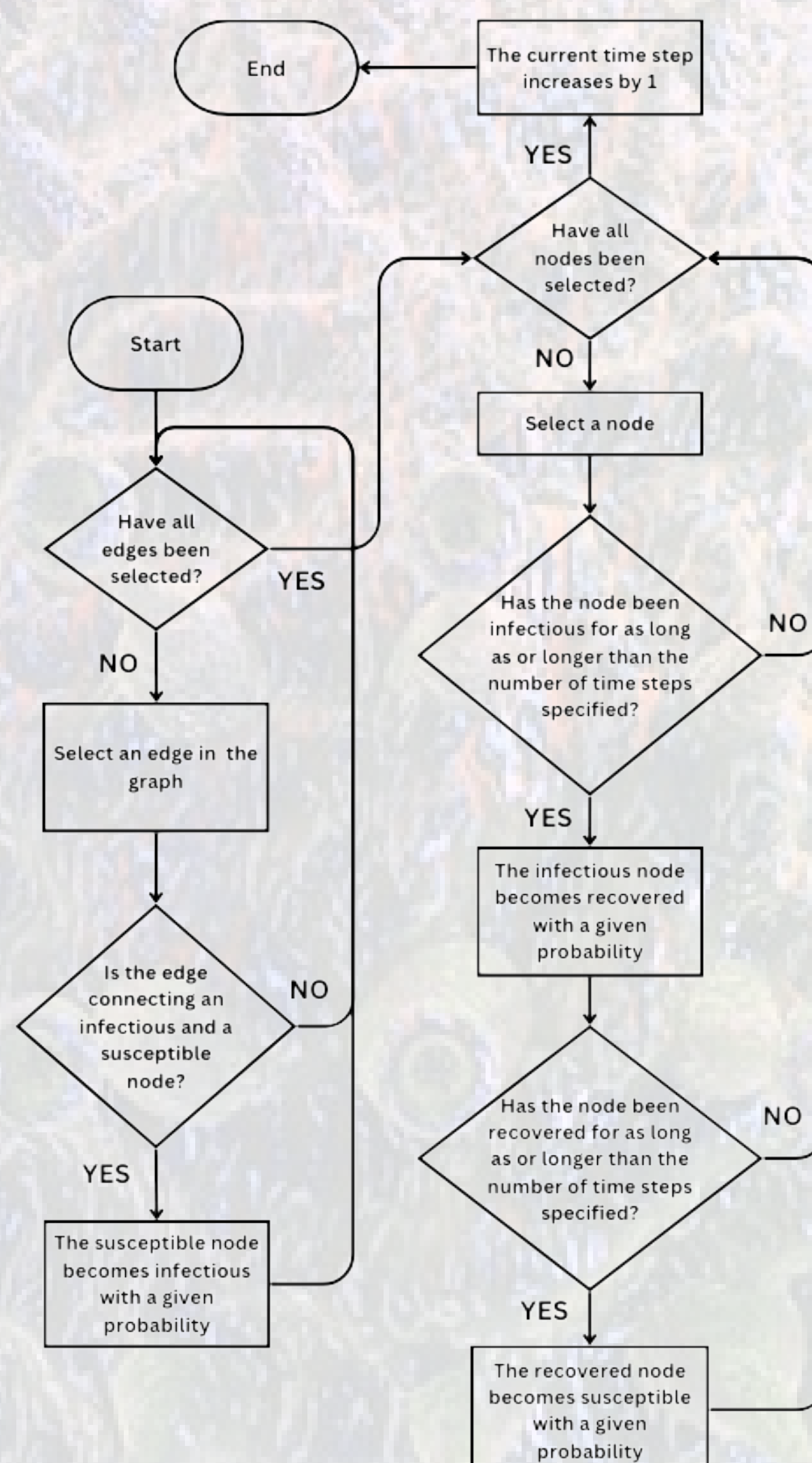

Figure: Graph generated with the stochastic block model

Methodology

We used R to combine the SIRS model and social networks. At the start, the user selects the type of graph generation and the values of several variables such as the total number of nodes and the probability of infection. The following flowchart illustrates the algorithm at each time step.

Results

Graph number	1	2	3
Generation Type	Erdős–Rényi	Barabási–Albert	stochastic block
Number of nodes	750	750	750
Prob_infection	0.2	0.2	0.2
Prob_recovery	0.3	0.3	0.3
Recovery time	14	14	14
Susceptibility time	90	90	90
Edge density	0.0097944	0.0053298	0.0035427
Number of edges	2751	1497	917
ρ	328	293	4
τ	31	27	14

Table: ρ is the maximum number of infectious nodes in a given time step and τ is the time step at which the number of infectious nodes is maximum.

The table illustrates how different graph generation algorithms result in graphs of various edge densities.
The Erdős-Rényi graph has the highest edge density as it represents a network with no measures taken to limit the number of contacts between nodes.
The Barabási-Albert graph has a lower edge density as it represents a scenario where most people follow lockdown procedure.
The stochastic block model graph has the lowest edge density as it represents an ideal lockdown scenario, where every member of the population obeys the restrictions.
Accordingly, the number of edges in the Erdős-Rényi graph is the highest, followed by the Barabási-Albert graph and then the stochastic block model graph.

Conclusions

The Erdős-Rényi model was used to generate a graph which represents a situation where no government interventions have taken place and all individuals have a large number of contacts. This resulted in the number of infectious individuals increasing rapidly, as the high edge density means one infectious individual can spread the disease to many susceptible individuals, who can in turn infect many others.

The Barabási-Albert graph illustrates a scenario where a lockdown causes individuals to reduce their close contacts, but a small number of individuals violate regulations, forming hubs around them where edge density is higher. Initially disease spread is low, however once a node at the centre of a hub becomes infectious, it is able to infect a large number of other individuals. Only 5% fewer individuals were infected compared to the Erdős-Rényi model, showing lockdowns are ineffective when violated, even by a small number.

The stochastic block model depicts a "perfect" lockdown scenario where all population members significantly reduce contact, with some nodes isolated to reflect individuals self-isolating. This scenario shows a slower disease spread and lower maximum infected nodes. This is consistent with real observations, as individuals still mixed with others for food shopping, exercise, and healthcare, allowing an avenue of transfer for the disease.

To summarise, the disease spreads more rapidly if there is a large number of contacts between nodes. Therefore, non-pharmaceutical interventions such as lockdowns are effective at limiting the spread of COVID-19, provided they are adhered to by the majority of the population.

References

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