Considering Elite Network Patterns in Application to Infectious Disease Spread

Karl F. Vachuska

Abstract

Anecdotal evidence suggests the elite may be more likely to contract an infectious disease during a pandemic, especially earlier on. In this paper, I propose general patterns for how the elite may experience contact differently and then utilizing mathematical models, simulate how those general patterns may affect infection rates among the elite and general population during a pandemic.

Introduction

In this paper, I will consider contact networks in the context of the elite as it is relevant to infectious disease spread. During the COVID-19 Pandemic, celebrities were infected with Coronavirus at a seemingly disproportionate rate, especially early on. I consider a novel hypothesis in that the modern emergence of “wealth work” has led to elite populations being subject to higher initial infection rates. Through mathematical models and simulations, I demonstrate that this is a plausible effect. I additionally find more substantial evidence indicating that wealth work may accelerate overall initial infection rates. Analyzing empirical data, I find some evidence that counties with more wealth work had higher initial infection rates.

Celebrities and Coronavirus

During the very early stages of the COVID-19 Pandemic in the Western Hemisphere, numerous celebrities, including professional athletes, actors, and politicians, had announced testing positive for the disease. While transmission of the disease was widespread, even in the most infected parts of the western world early on in the pandemic (mid-March 2020), only approximately 0.02% of the population had contracted the disease. This raises the question, are celebrities/elites more likely to contract Coronavirus earlier in the Pandemic, and if so, why?

For several reasons, the question of whether or not elites are more likely to get Coronavirus is challenging to create evidence for or against statistically. This is because it is hard to measure “fame” or “eliteness” objectively. Additionally, a complete list of who has Coronavirus is unavailable, for obvious reasons of medical confidentiality, so we primarily must rely on people publicly announcing they have tested positive for Coronavirus. An additional confounding factor is that not everyone who has Coronavirus may be tested for it, leading to a selection bias in that celebrities who have Coronavirus may receive tests for it at a higher frequency than non-celebrities.

A simplistic statistical attempt to estimate the number of famous people estimated that between 1 in 10,000 and 1 in 2,000 people in the English-speaking world are famous. (Arbesman 2013) Taking the higher estimate, 1 in 2,000 people or (0.05% of the population). Between the United States and the United Kingdom, the two English-speaking countries with the highest number of Coronavirus cases as of March 16th, 2020, there was a total of slightly over 5,000 confirmed cases of Coronavirus. Between these two countries, there were at least ten people with Wikipedia articles who were residents of the country. This suggests that approximately 1 in 500 people who have confirmed cases of Coronavirus have Wikipedia articles, a disproportionately higher percentage, even compared to the most liberal estimates for the number of famous people. This statistical investigation is relatively simple but provides some primary evidence that celebrities were more likely to get Coronavirus earlier on in the pandemic.

Elite Networks

Past research has found that celebrities tend to have social ties to other celebrities, and celebrities tend to have low degrees of separation from one another. (Gilad, Ravid and Currid-Halkett 2013) In general, individuals tend to have social ties to individuals who are of similar economic and social class to themselves. (McPherson et al 2001) Additionally, social networks tend to have high degrees of clustering. (Watts and Strogatz 1998)

Since social networks are meant for the transmission of information, social networks cannot wholly explain the transmission of disease, since interpersonal or merely proximal contact does not reflect social networks. Instead, there may be a significant difference between the two. While celebrities' social networks often include other celebrities, or merely other people with high economic and social class, evidence suggests celebrities may have a high degree of contact with people of lower social and economic classes, due to their high level of financial expenditure, and the subsequent broad and miscellaneous services they receive from various workers of lower classes.

“Wealth Work” is one of the most rapidly growing categories of occupations. (Autor and Salomans 2019) Wealth work includes jobs such as “yoga instruction, sommelier services, pet care, and many forms of personal training and counseling”. (Autor 2019) Wealth Work, as the name suggests, involves performing “in-person services for affluent consumers”. (Autor 2019) Notably, individuals who perform wealth work have about average earnings. In summary, wealth workers are of low

to middle-income status and have in-person contact with affluent individuals as part of their occupation. As it applies to considering how an infectious disease spreads, wealth work is a very viable possibility between which disease may be transmitted between worker and consumer. Wealth work is rapidly growing, accounting for 52% of new work. (Autor and Salomans 2019)

Utilizing network analysis and SIR model simulations, I consider several hypotheses for why elite individuals, people with very high socioeconomic status and power, are more likely to get Coronavirus earlier in the Pandemic. The simplest hypothesis is that elites have more extensive immediate social networks as well as higher degrees of centrality in social networks. Another hypothesis is simply that celebrities have a greater number of “bridges”, or social ties serving as the only link between otherwise vastly disconnected social network clusters. I hypothesize “wealth work” plays a critical role in why celebrities/elites are more likely to get Coronavirus as well as, more importantly, rapidly accelerating the spread of the disease.

The Basic “Wealth-Work” Graph

As a principle, most human networks, particularly social networks, have a high degree of clustering. (Watts and Strogatz 1998) Further, individuals tend to have ties to individuals with similar socioeconomic status to themselves. As such, I organize all the graphs I create with socioeconomic status as a foundational

attribute of all actors, applied to graphs via nodes having a predetermined “order”. I additionally ensure an essential high degree of clustering in graphs, applied in a similar way to how Watts and Strogatz (1998) generate their small-world graphs. I apply “wealth work” to my graphs via actors having a probability of connections to non-neighboring actors proportional to their socioeconomic status. Later on, I introduce variations of this where non-neighboring actors they can connect to must be of specific socioeconomic class, but in this most general case, I allow it to be to any non-neighboring actors.

Henceforth, I shall refer to “actors” as “nodes”, “ties” as “edges” or “connections” and “networks” as “graphs”.

How to generate the Basic Wealth-Work graph:

Step 1: Take N nodes such that all nodes are ordered and map to the set of natural numbers from 1 to N

Step 2: Now, connect each node to it’s nearest K neighbors on each side. The inner $N - 2K$ nodes on either side should now have $2K$ edges each. The K nodes on either end though will have only between K and $2K - 1$ edges however.

Such a graph where $N = 20$ and $K = 3$ would look like the following:

Step 3: Next, add edges to nodes separated by atleast K units in the order to the graph at probability p where $p = c \times \frac{(\max(i,j))^2}{n^2}$ where i and j are the unique values associated with the two nodes.

The following resulting graph would be one in which there is a quadratic association between a node's associated value and having connections to nodes they are not neighbors with.

*1 here denotes the highest ranked node, 20 denotes the lowest.

This fits the general nature of wealth work and how it is structured within contact networks. While individual's contact networks are generally highly clustered and strongly organized along socioeconomic status, individuals with the highest socioeconomic status are disproportionately likely to consume personal services and are subsequently more likely to have contact with increasing numbers of people outside of their relative socioeconomic status. A quadratic distribution for income is very sensible, since there are many people with low to middle-income spending capacities but significant percentages of people still exist with incomes 5-

10 times that of the median. (Other variations of p can of course be created for this type of graph, but for this case this function is most suitable)

Now, I will present several variations of this type of graph:

For the purposes of simplicity, all other graphs will continue following the completion of Step 2 in the original variation above.

Simple Small-World Variation

This variation is very similar to the Newman-Watts variation of the small-world network. (Watts and Strogatz 1998; Newman 2003)

Step 3: Add edges between nodes where they do not exist to the graph at probability p where p is constant.

For $p = .25$ this is what a graph may potentially look like

*1 here denotes the highest ranked node, 20 denotes the lowest.

This variation is somewhat distinct from the original small-world network, besides not consisting of a ring lattice initially, in that rather than “rewiring” edges I am adding in new edges without deleting any of the original ones.

Elite-Clustering Variation

Step 3: Take the Q nodes with the highest order and add in edges to them, so that they are connected to their L closest neighbors on either side (where $L > K$), rather than simply their K closest neighbors.

For $Q = 5$ and $L = 5$, this would produce the following graph

*1 here denotes the highest ranked node, 20 denotes the lowest.

This scenario is analogous to one in which a subset of actors in a network have more connections than the rest of the actors while maintaining a high degree of clustering. Some evidence suggests that elite individuals simply have more connections while still tending to only have connections with the individuals of the

same socioeconomic status. This models that scenario fairly purely. Notably, this graph has no randomization to it and is completely determined by the specific parameters.

Poor Wealth-Worker Variation

Step 3: Next, add edges to nodes separated by atleast K units in the order to the graph at probability p where $p = c \times \frac{(\max(i,j))^2}{n^2}$ where $\min(i,j) < B$.

For $B = 10$ the following is a what a possible graph may look like:

*1 here denotes the highest ranked node, 20 denotes the lowest.

The role of the limiting value B is to ensure that non-neighboring edges connect specifically to nodes at the bottom. This is analogous to the scenario as posed by the service industry broadly, where service workers tend to have low socioeconomic status serving individuals of very high socioeconomic status.

Specific Wealth Worker Variation

Step 3: Next, assign the label of “worker” to nodes with probability q where the nodes rank $i < B$

Step 4: Connect each “worker” node to higher ranked node j at probability $p =$

$$c \times \frac{(\max(i,j))^2}{n^2}$$

A potential graph would look like this:

*1 here denotes the highest ranked node, 20 denotes the lowest.

This variation of the graph seeks to most accurately represent the concept of “wealth work”, where specific wealth workers serve large numbers of affluent consumers.

Model Comparison

The SIR model is one of the most commonly used mathematical models of infectious disease spread. In my simple version, all nodes are either S (Susceptible),

I (infected), or R (Recovered). A Susceptible node can become Infected in the next step with probability $1 - (1 - p)^x$ where x is the number of nodes that it is tied to that are infected, and p is the probability of transmission. Otherwise, a susceptible node remains susceptible in the next step with the complementary probability, $(1 - p)^x$. An infected node becomes recovered in the next step with probability 1. A recovered node remains recovered in the next step with probability 1.

For a very large graph, we can somewhat simply express the number of infected nodes through a small number of steps M , in the scenario such that the graph is so large and M is so small such that the probability any two randomly selected nodes on have values within $(M \times K) + ((M - 1) \times K)$ is effectively zero.

I will denote the expected number of nodes that have been infected at or by time M as $E[G_M]$

Time 1, or Step 1, for the purposes here, will be defined as in which the disease is introduced into the network, and exactly one node is infected.

An important expression I will additionally be using is $E[W_M | K = K_i]$ which describes the number of infected nodes at or by time M for a graph W with a large number of nodes such that the *only* edges that exist are to the nearest K_i nodes on either side. This hypothetical graph is equivalent to how any of our graphs would be at the conclusion of Step 2.

It's obvious that $E[W_1 | K = K_i] = 1$

And is fairly trivial that $E[W_2|K = K_i] = p \times 2K_i$ when the probability of transmission is p

For any higher number of M it's fairly complicated to express an exact solution.

Subsequently, for my purposes, it is simpler to merely state that for all M ,

$$E[W_M|K = K_i + l] \geq E[W_M|K = K_i] + (p \times M \times 2l)$$

This is a fairly useful bound for arbitrary purposes, since as $M \rightarrow \infty$ or as $p \rightarrow 1$

$$E[W_M|K = K_i + l] \rightarrow E[W_M|K = K_i] + (p \times M \times 2l)$$

For the Basic Wealth World graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i$, $c = c_{BWW}$, the disease is transmitted at probability p_i , and when M is small:

$$E[G_M|K = K_i, c = c_{BWW}, p = p_i] =$$

$$E[W_M|K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j|K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{BWW} \times p_i)^k \times (E[W_{M-j-k+1}|K = K_i] - E[W_{M-j-k}|K = K_i])$$

where

$$F(k) = \int_0^1 \frac{1}{3} + \frac{2}{3} x_1^3 \times \int_0^1 (f(x_2, x_1) \dots \times \int_0^1 (f(x_{k-1}, x_{k-2}) \times \int_0^1 \int_0^1 (f(x, x_{k-1}) \times f(x, x_k)) dx dx_k dx_{k-1} \dots$$

and

$$f(x, x_i) = \begin{cases} x_i^2 & \text{if } x_i > x \\ x^2 & \text{if } x_i \leq x \end{cases}$$

For the Small World graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{SW}$, the disease is transmitted at probability p_i , and when M is small:

$$E[G_M | K = K_i, c = c_{SW}, p = p_i] =$$

$$E[W_M | K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} (N \times c_{SW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])$$

For the Elite Clustering graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, Q = Q_{EC} \times N, L = L_{EC}$, the disease is transmitted at probability p_i , and when M is small:

$$E[G_M | K = K_i, Q = Q_{EC} \times N, L = L_{EC}, p = p_i] =$$

$$(1 - Q_{EC}) \times E[W_M | K = K_i] + (Q_{EC}) \times E[W_M | K = K_i + L_{EC}]$$

For the Poor Wealth Worker graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{PWW}, B = b_{PWW} \times N$ the disease is transmitted at probability p_i , and when M is small:

$$E[G_M | K = K_i, c = c_{PWW}, B = b_{PWW} \times N, p = p_i] =$$

$$E[W_M | K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{PWW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])$$

where

$$F(k) = \int_0^1 g(x_1) \times \int_0^1 (f(x_2, x_1) \dots \times \int_0^1 (f(x_{k-1}, x_{k-2}) \times \int_0^1 \int_0^1 (f(x, x_{k-1}) \times f(x, x_k)) dx dx_k dx_{k-1} \dots$$

and

$$f(x, x_i) = \begin{cases} x_i^2 & \text{if } \min(x_i, b_{PWW}) > x \\ x^2 & \text{if } x_i \leq x, x < b_{PWW} \\ 0 & \text{if } x_i \leq x, x > b_{PWW} \end{cases}$$

and

$$g(x) = \int_0^1 f(x, x_i) dx_i = \begin{cases} \frac{1}{3} + \frac{2}{3}x^3 & \text{if } x < b_{PWW} \\ b_{PWW}x^2 & \text{if } x > b_{PWW} \end{cases}$$

For the Specific Wealth Worker graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{SWW}, q = q_{SWW}, B = b_{SWW}$ the disease is transmitted at probability p_i , and when M is small:

$$E[G_M | K = K_i, c = c_{SWW}, q = q_{SWW}, B = b_{SWW}, p = p_i] =$$

$$E[W_M | K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{SWW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])$$

where

$$F(k) = \sum_1^{Fib_{k+2}} \int_0^1 \left(\int_0^1 f_{\alpha_k}(x, x_1) dx \right) \times \int_0^1 f_{\alpha_{k-1}}(x_3, x_2) \dots \times \int_0^1 f_{\alpha_1}(x, x_k) dx dx_k dx_{k-1} \dots$$

where α_i can equal 1, 2 or 3, but in the finite sequence $\alpha_1, \alpha_2, \alpha_3, \dots$, a 1 can only be immediately followed by a 2, a 2 can only be immediately followed by 1 or 3, a 3 can only be immediately followed

by 1 or 2. Additionally, α_1 must equal 1 or 3. The number of possible sequences follows the Fibonacci numbers.

The finite sequence $\alpha_1, \alpha_2, \alpha_3, \dots$ is unique in each iteration of the summation

Further,

$$f_1(x, x_i) = \begin{cases} x_i^2 & \text{if } x < \min(x_i, b_{SWW}) \\ 0 & \text{if } x > \min(x_i, b_{SWW}) \end{cases}$$

and

$$f_2(x, x_i) = \begin{cases} 0 & \text{if } x < x_i \\ x^2 & \text{if } x > x_i \end{cases}$$

and

$$f_3(x, x_i) = \begin{cases} 0 & \text{if } x < x_i \\ 0 & \text{if } x > x_i, x_i > b_{SWW} \\ q_{SWW}x^2 & \text{if } x > x_i, x_i < b_{SWW} \end{cases}$$

Additionally, it is possible to calculate infection rates for “elite” nodes for each graph. These solutions are very similar for the most part and are listed in the appendix.

These solutions suggest implications for the rate we can expect infections to spread across different graph variations early on, as well as in an early number of steps how disproportionality infected elite nodes will be. While maintaining a consistent number of total edges across all variations, I would expect the ratio between Elite nodes’ and Average nodes’ infection rates to generally be highest in

the Elite Clustering variation, presuming a low value for Q_{EC} . For the Elite Clustering Variation, the ratio essentially scales with $(K_i + L)/K_i$ and M , thus easily allowing Elite nodes to be infected at a much faster rate than the average node.

While these equations provide exact solutions to estimating how the disease may spread through an infinitely large network, real simulation on finite sized graphs can provide potentially more realistic insight on disease spread:

For all graphs I set $N = 10000$, and $K = 3$. I further assign $c = .001$ for the Basic Wealth Work graph, and subsequent parameters are all assigned according to give each graph variation an equal number of expected edges.

For each variation I generated 100 random graphs, and simulated disease spread with probability $p = .5$ for 10 trials starting with randomly selected node to be infected in each graph, totaling 1000 simulations.

The following figure depicts the percentage of nodes that are or have been infected by step:

The SWW and PWW graphs have highest initial infection rates. Their infection rates are eventually outpaced by that of the BWW and SW graphs which have less variation in the shortest distance between any two nodes, thus allowing infection to reach all nodes fairly quickly. While the SWW and PWW graphs can more rapidly infect a larger number of nodes, it takes longer for infection to reach all nodes in these variations. In the EC graph, infection is extremely slow, directly attributable to nodes only connecting to neighboring nodes, and thus infection only moving by limited increments.

If we consider “elite” nodes to be nodes in the top 1% of the order, we can compare how quickly elite nodes would contract the disease generally, as well as relative to the average node.

The following figure depicts the percentage of elite nodes that are or have been infected by step:

Again, the SWW and PWW graphs have faster initial infection rates, but the BWW and SW graphs outpace them later on. While little distinction in infection rate existed between the BWW and SW graphs for all node, for “elite” nodes BWW clearly has a generally higher infection rate. The EC graph again is moving extremely slowly.

The following figures display the ratio of elite node’s probability of being or having been infected relative to the average node’s probability of being or having been infected by step:

As my equations suggested, the Elite Clustering variation has the highest ratio of Elite node's infection rate to average node's infection rate. The Basic Wealth World variation and Specific Wealth Worker variation additionally, both have high ratios, close to 2:1 in early steps. The Small World Variation and the Poor Wealth Worker variation have generally equal or less than equal rates of Elite node infection rate relative to average nodes.

Empirical Analysis

The New York Times has compiled a dataset of the number of Coronavirus cases for the entire United States by day. Utilizing this dataset, I computed exponential regressions for the March 11th through March 25th, 2020 timeframe for all counties that had one to five confirmed cases on March 11th. I choose this timeframe to minimize the confounding impact of shelter-in-place orders on growth rates. (The first statewide shelter-in-place went into effect on March 19th, Coronavirus symptoms show up typically at least 5 days after infection, and test

results take 1-2 days in order for a potential case to be “confirmed”) Combining this growth rate datapoint with data from the 2014-2018 American Community Survey estimates, I tested my hypotheses.

As Table One shows, the interaction between the percent of occupations in personal service and income inequality is positively associated with counties’ Coronavirus growth rate. As greater income inequality suggests greater stratification by income within the community, counties with higher income inequality and more personal service jobs would presumably tend to have more consumption of personal services (and subsequent contact). That consumption of personal services would further presumably be concentrated among higher-income individuals, given the higher income inequality.

Discussion

This paper proposes different patterns that may arise from and/or characterize the stratification/presence of elite nodes in a contact network. I initially emphasize “wealth work” as a possible explanation for why elite individuals may get infected earlier on in an infectious disease pandemic. My simulations find some supporting evidence for this, demonstrating “wealth work” characteristics, as represented in my “Specific Wealth Worker” graph, does lead to higher infection rates among “elite” nodes at early steps. However, this ratio seems somewhat limited, and my simulations indicate any differences in infection rates of substantial magnitude are likely better explained by an “elite clustering”

phenomenon wherein elite individuals simply have more massive clusters than non-elite individuals. My simulations do suggest that “wealth work” characteristics may generally accelerate the spread of infectious disease, which I find empirical support for in analyzing county-level COVID-19 data. While I broadly propose different elite contact network characteristics, I examine them separately, and further research should better explore the interaction between these patterns.

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Appendix

Here are the following expected number of “elite” nodes that have been infected. In order to maintain consistency, I will define elite nodes in the same way generally, as I did for “Elite Clustering” graph, nodes that are within Q from the top, where , $Q = Q_{EC} \times N$

For the Basic Wealth World graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{BWW}$, the disease is transmitted at probability p_i , and when M is small:

$$E_E[G_M | K = K_i, c = c_{BWW}, p = p_i] =$$

$$E[W_M | K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{BWW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])$$

where

$$F(k) = \int_{1-Q_{EC}}^1 \frac{1}{3} + \frac{2}{3} x_1^3 \times \int_0^1 (f(x_2, x_1) \dots \times \int_0^1 (f(x_{k-1}, x_{k-2}) \times \int_0^1 \int_0^1 (f(x, x_{k-1}) \times f(x, x_k)) dx dx_k dx_{k-1} \dots$$

and

$$f(x, x_i) = \begin{cases} x_i^2 & \text{if } x_i > x \\ x^2 & \text{if } x_i \leq x \end{cases}$$

For the Small World graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{SW}$, the disease is transmitted at probability p_i , and when M is small:

$$\begin{aligned}
& E_E[G_M | K = K_i, c = c_{SW}, p = p_i, Q = Q_{EC} \times N] = \\
& (Q_{EC}) \times E[W_M | K = K_i] \\
& + \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} Q_{EC} \times (N \times c_{SW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])
\end{aligned}$$

For the Elite Clustering graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, Q = Q_{EC} \times N, L = L_{EC}$, the disease is transmitted at probability p_i , and when M is small:

$$\begin{aligned}
& E_E[G_M | K = K_i, Q = Q_{EC} \times N, L = L_{EC}, p = p_i] = \\
& (Q_{EC}) \times E[W_M | K = K_i + L_{EC}]
\end{aligned}$$

For the Poor Wealth Worker graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{PWW}, B = b_{PWW} \times N$ the disease is transmitted at probability p_i , and when M is small:

$$\begin{aligned}
& E_E[G_M | K = K_i, c = c_{PWW}, B = b_{PWW} \times N, p = p_i] = \\
& E[W_M | K = K_i] \\
& + \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{PWW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])
\end{aligned}$$

where

$$F(k) = \int_{1-Q_{EC}}^1 g(x_1) \times \int_0^1 (f(x_2, x_1) \dots \times \int_0^1 (f(x_{k-1}, x_{k-2}) \times \int_0^1 \int_0^1 (f(x, x_{k-1}) \times f(x, x_k)) dx dx_k dx_{k-1} \dots$$

and

$$f(x, x_i) = \begin{cases} x_i^2 & \text{if } \min(x_i, b_{PWW}) > x \\ x^2 & \text{if } x_i \leq x, x < b_{PWW} \\ 0 & \text{if } x_i \leq x, x > b_{PWW} \end{cases}$$

and

$$g(x) = \int_0^1 f(x, x_i) dx_i = \begin{cases} \frac{1}{3} + \frac{2}{3}x^3 & \text{if } x < b_{PWW} \\ b_{PWW}x^2 & \text{if } x > b_{PWW} \end{cases}$$

For the Specific Wealth Worker graph variation, the number of nodes that have been infected at or by time M , given N is very large, $K = K_i, c = c_{SWW}, q = q_{SWW}, B = b_{SWW}$ the disease is transmitted at probability p_i , and when M is small:

$$E_E[G_M | K = K_i, c = c_{SWW}, q = q_{SWW}, B = b_{SWW}, p = p_i] =$$

$$E[W_M | K = K_i]$$

$$+ \sum_{j=1}^{M-1} E[W_j | K = K_i] \sum_{k=1}^{M-j} F(k) \times (N \times c_{SWW} \times p_i)^k \times (E[W_{M-j-k+1} | K = K_i] - E[W_{M-j-k} | K = K_i])$$

where

$$F(k) = \sum_1^{Fib_{k+2}} \int_{1-Q_{EC}}^1 \left(\int_0^1 f_{\alpha_k}(x, x_1) dx \right) \times \int_0^1 f_{\alpha_{k-1}}(x_3, x_2) \dots \times \int_0^1 f_{\alpha_1}(x, x_k) dx dx_k dx_{k-1} \dots$$

where α_i can equal 1, 2 or 3, but in the finite sequence $\alpha_1, \alpha_2, \alpha_3, \dots$, a 1 can only be immediately followed by a 2, a 2 can only be immediately followed by 1 or 3, a 3 can only be immediately followed

by 1 or 2. Additionally, α_1 must equal 1 or 3. The number of possible sequences follows the Fibonacci numbers.

The finite sequence $\alpha_1, \alpha_2, \alpha_3, \dots$ is unique in each iteration of the summation

Further,

$$f_1(x, x_i) = \begin{cases} x_i^2 & \text{if } x < \min(x_i, b_{SWW}) \\ 0 & \text{if } x > \min(x_i, b_{SWW}) \end{cases}$$

and

$$f_2(x, x_i) = \begin{cases} 0 & \text{if } x < x_i \\ x^2 & \text{if } x > x_i \end{cases}$$

and

$$f_3(x, x_i) = \begin{cases} 0 & \text{if } x < x_i \\ 0 & \text{if } x > x_i, x_i > b_{SWW} \\ q_{SWW}x^2 & \text{if } x > x_i, x_i < b_{SWW} \end{cases}$$

Table One

March 11th-March 25th Coronavirus Growth Rate by County

	(1)
	Exponential Growth Rate
Population	8.58e-08*** (5.49)
Population Density	0.0000295** (3.24)
Population X Population Density	-1.09e-11 (-1.20)
Personal Service Occupations	-0.518* (-2.15)
Income Inequality	-2.281 (-1.51)
Personal Service Occupations X Income Inequality	1.141* (2.16)
Per Capita Income	0.0000220*** (4.49)
Per Capita Income X Per Capita Income	-2.53e-10*** (-4.07)
Constant	1.781* (2.57)
Observations	163
Adjusted R-squared	0.491

t statistics in parentheses

* p<0.05, ** p<0.01, *** p<0.001