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Network Modeling of Infectious Disease: Transmission, Control and Prevention

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Network Modeling of Infectious Disease: Transmission, Control and Prevention

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ABSTRACT

Many factors come into play when it comes to the transmission of infectious diseases. In disease control and prevention, it is inevitable to consider the general population and the relationships between individuals as a whole, which calls for advanced mathematical modeling approaches.

We will use the concept of network flow and the modified Ford-Fulkerson algorithm to demonstrate the transmission of infectious diseases over a given period of time. Through our model one can observe what possible measures should be taken or improved upon in the case of an epidemic. We identify key nodes and edges in the resulted network, which will help determine an improved plan of disease prevention. This solution has been implemented through a Java code.

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1. **Introduction**

Many factors come into play when it comes to the transmission of infectious diseases. The actual way a disease is spread can be either through direct (person-to-person) or indirect (airborne, animals, etc.) contact. Further, whether or not a person gets infected depends on their hygiene habits and their exposure to an infected person. Therefore, in disease control and prevention, it is inevitable to consider the general population and the relationships between individuals as a whole. Mathematical modeling is necessary to make sense of those relationships

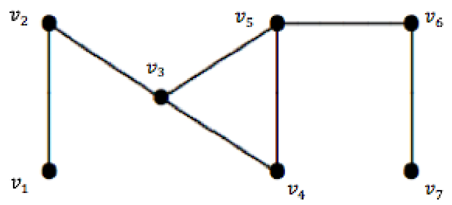
Our goal is to use the concept of network flow and a modified Ford-Fulkerson algorithm to demonstrate the transmission of infectious diseases over a given period of time. The model uses five years of data on Hepatitis B retrieved from the CDC, but ultimately could use data on any disease for future study. Through our model, one can observe what possible measures should be taken or improved upon in the case of an epidemic. In order to take a given time period into consideration, we construct our network in a recursive manner so that the dynamic nature of evolution is reflected in one physical structure.

1.1. Basic Graph Theory

The graphs used in this project are not the ones seen in algebra and calculus classes, but instead they are much more abstract. The easiest way to describe the definition of a graph is "points connected by lines". Therefore, it is possible to use graphs to model a wide variety of things. Unless otherwise specified, the definitions discussed in this section are from David Guichard's book, *An Introduction to Combinatorics and Graph Theory* [1]. Study of graph theory dates back to the early 1700's with the famous Seven Bridges of

Konigsberg problem. Euler, one of the most prolific mathematicians of all time, solved this problem and opened up a totally new field of mathematics while doing so.

By definition, a graph G consists of a pair (V, E) where V is the set of vertices, and E is the set of edges. Vertices are points while edges are lines that connect two vertices. It is common to write $V(G)$ to represent the vertices of a graph G and $E(G)$ for the edges of the same graph. Furthermore, the graph used in this project is a simple graph, meaning that there are no loops or multiple edges. Loops are edges that connect a vertex back to itself, and multiple edges are edges that share the same endpoints. The edges of a simple graph are written as a set of two element sets. For example,



$(\{v_1, v_2, v_3, v_4, v_5, v_6, v_7\}, \{\{v_1, v_2\}, \{v_2, v_3\}, \{v_3, v_4\}, \{v_3, v_5\}, \{v_4, v_5\}, \{v_5, v_6\}, \{v_6, v_7\}\})$ creates the simple graph pictured above.

The edges of a graph can also have a direction. These graphs are called directed graphs, or digraphs, and their edges are written as an ordered pair of vertices. The first value of the ordered pair is the origin and the latter is the endpoint. We use a digraph for this project. Another name for a directed edge in a digraph is arc, which is typically represented as an arrow when constructing a graph. It is possible to have two directed edges such as (u, v) and (v, u). This notion is separate from the concept of a multiple edge as the two arcs are distinct. Directed graphs can be classified as simple or complex depending on whether or not they have multiple edges or loops. Like graphs, digraphs are simple if they contain neither. A practical example of a digraph is a map of airplane routes. Vertices are airports and edges flight path from one airport to another.

1.2. Flow Network

A network is a directed graph with a designated source s and sink (target) t. Each arc e in a network has a positive capacity - commonly denoted $c(e)$. The flow of a network is a function f from the arcs to $\mathbb{R}$ such that $\forall\ e, 0 < f(e) < c(e)$ and the sum of the flows in and out of a vertex are equal. This last characteristic applies to all vertices of a network except for the sink and source. The value of a flow f that is at least as large as any possible flow of a particular network is called the maximum flow. Maximum flow marks the overall efficiency of a network, making it a critical value. A cut in a network is a set C of arcs such that every path from the sink to the source uses at least an arc in C. The term "cut" naturally comes from the important fact that if the edges in C are removed from the network, there is no longer any path from s to t. The capacity of a cut, $c(C)$, is equal to the sum of the capacities, which can be positive or negative depending on the orientation, of all the arcs in C. The cut with the smallest capacity is referred to as the minimum cut, which plays a large role in this project [1].

The Ford-Fulkerson algorithm is a systematic way to find the maximum flow and minimum cut of a network. The algorithm works as follows [2]:

- Find a directed path from the source to the sink, such that the flow on each of the forward edges can be improved and the flow on each of the backward edges is non-zero. Such a path is called an "augmenting path".
- Improve the flow, from the source to the sink, along the augmenting path.
- Repeat the above steps until no more augmenting path exists. Then the resulted flow is maximum and a minimum cut is identified at the same time.

Note that, since in every step the value of the flow strictly increases by a positive integer (if all original capacities are positive integers), the above process terminates in finitely many steps. Also, note that the maximum flow of a network is equal to the capacity of the minimum cut.

1.3. Motivation

Studying disease prevention and transmission is the key to healthier lives for everyone. According to the CDC's website [3]:

- With better health, children are in school more days and are better able to learn. Numerous studies have found that regular physical activity supports better learning. Student fitness levels have been correlated with academic achievement, including improved math, reading and writing scores.
- With better health, adults are more productive and at work more days. Preventing disease increases productivity—asthma, high blood pressure, smoking and obesity each reduce annual productivity by between $200 and $440 per person.
- With better health, seniors keep their independence. Support for older adults who choose to remain in their homes and communities and retain their independence ("aging in place") helps promote and maintain positive mental and emotional health.

Thus, it is clear that continuously learning and developing our knowledge of disease is beneficial for everyone. Our motivation for pursuing this project comes from the potential usefulness in this learning. There are so many different diseases in the world, and just as quickly as some diseases are eradicated, more are being discovered. Also, many strands of certain diseases keep evolving to become immune to our medicines and vaccines originally designed to dispose of them. Because of these constant changes, it is important to keep studying. This is where mathematical modeling comes into play. With our model, we hope to provide a tool that can be modified as needed, depending on the disease being studied.

1.4. Mathematical modeling

Flow network has been a popular model for numerous practical problems such as public transportation (where nodes denote bus stops and arcs denote one way streets), financial flow (where the flow between nodes represents the real current flow between different entities), assignment problems (where the nodes and arcs represent the work assignment and the ordering of individual assignments). In our study of the transmission of infectious diseases, each node can represent a single person, a group of people, or a region. The directed arc between nodes simply denotes the interaction between the corresponding people or regions. The capacities assigned to these arcs essentially measures the scale of interactions between those people/regions. We will use different copies of the same structure to mimic the evolution of the disease and its transmission through time. The maximum flow of such a network would imply the scale of the transmission.

2. **Methods**

2.1. Data Collection

Although the model could use information gathered from any type of illness/disease, we illustrate our methodology through studying Hepatitis B. Hepatitis B is a liver disease that is transmitted through bodily fluids from an infected person to an uninfected person. The most common forms of transmission are from mother to child during birth, sexual contact, and sharing needles, syringes, or other injection equipment. The CDC collects data on all types of diseases, but they have a clear chart of surveillance data of Hepatitis B covering five years from 2010-2014 [4]. This is our main source of data for the model. For our calculations, we needed infection rates of Hepatitis B throughout regions of the continental United States. To do this, we took the number of reported cases from each state and gathered it into the table along with the state's population for that year. Then, we found the total population and total number of cases for each region and divided them by each other to find the rate for each region. That is,

$$regional\ infection\ rate = \frac{\sum number\ of\ cases}{\sum populations}$$

The data was then gathered into tables in Microsoft Excel. As an example, here is the data gathered for the year 2010 [4][7]:

Hepatitis B by Region 2010			
SOUTHEAST	Population	Number	Rate
Alabama	4779736	68	
Arkansas	2915918	66	
Florida	18801310	297	
Georgia	9687653	165	
Kentucky	4339367	136	
Mississippi	2967297	33	
North Carolina	9535483	113	
South Carolina	4625364	59	
Tennessee	6346105	150	
Virginia	8001024	97	
West Virginia	1852994	88	
TOTAL	73852251	1272	1.72236E-05
			172
MIDEAST			
Delaware	897934	0	
Maryland	5773552	67	
New Jersey	8791894	77	
New York	19378102	139	
Pennsylvania	12702379	72	
TOTAL	47543861	355	7.46679E-06
			75
NEW ENGLAND			
Connecticut	3405565	22	
Maine	1274923	13	
Massachusetts	6349097	13	
New Hampshire	1235786	5	
Rhode Island	1048319	0	
Vermont	608827	2	
TOTAL	13922517	55	3.95044E-06
			40
GREAT LAKES			
Illinois	12419293	135	
Indiana	6080485	75	
Michigan	9938444	122	
Ohio	11353140	95	
Wisconsin	5363675	54	

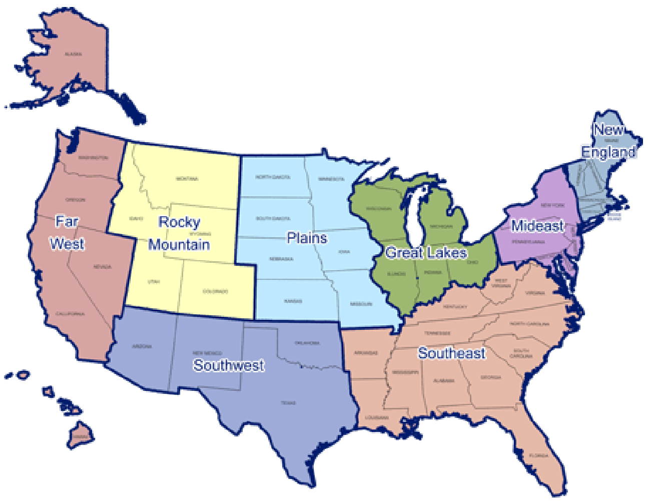
TOTAL	45155037	481	1.06522E-05
			107
PLAINS			
Iowa	3046355	15	
Kansas	2853118	11	
Minnesota	5303925	23	
Missouri	5988927	67	
Nebraska	1826341	12	
North Dakota	672591	0	
South Dakota	814180	2	
TOTAL	20505437	130	6.33978E-06
			63
SOUTHWEST			
Arizona	6392017	26	
New Mexico	2059179	5	
Oklahoma	3751351	115	
Texas	25145561	394	
TOTAL	37348108	540	1.44586E-05
			145
ROCKY MOUNTAINS			
Colorado	5029196	46	
Idaho	1567582	6	
Montana	989415	0	
Utah	2763885	8	
Wyoming	563626	3	
TOTAL	10913704	63	5.77256E-06
			58
FAR WEST			
California	38041430	252	
Nevada	2700551	41	
Oregon	3831074	42	
Washington	6724540	50	
TOTAL	51297595	385	7.50523E-06
			75

The table continues for years 2011-2014. Since the model requires integers in order to successfully run the algorithm, each rate was then multiplied by 10^7 and rounded up or down accordingly. The results of these calculations can be found in the following table:

Region	2010	2011	2012	2013	2014
Southeast	172	86	178	197	181
Mideast	75	77	64	59	60
New England	40	67	72	64	40
Great Lakes	107	76	98	103	89
Plains	63	60	27	56	37
Southwest	145	86	69	55	53
Rocky Mountains	58	32	39	40	40
Far West	75	49	43	46	34

2.2. Network Setup

Our model, simply put, is a series of copies of a network representing the status of the country in different years. Each node represents a different region of the continental United States, and adjacency was based on whether or not boundaries touched, as seen in the map. Since the boundaries of these regions do not change, that is how we are able to simply copy the same network up to five times. The network starts with the source connecting to every regional node in phase one. Then, within the phase, the region nodes connect to each other accordingly. These connections go both ways in order to model interaction appropriately. For example, since the Southeast and Great Lakes are adjacent, there are two edges between them: (SE, GL) and (GL, SE). A parameter is used to represent the capacity of the edges between adjacent regions, the value of which we



may manipulate as needed for analysis. This variable ultimately represents the amount of interaction between the regions. A lower value means less interaction and a higher value means more interaction.

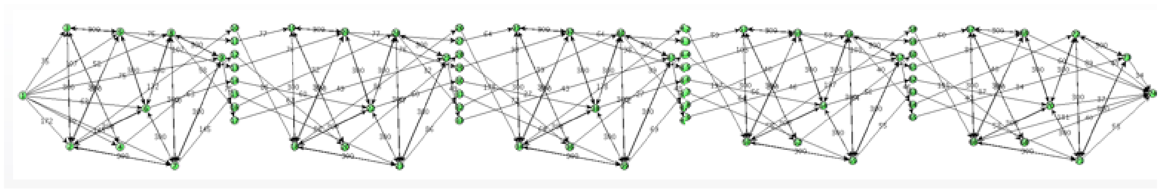
The next part of the network is the “evo” nodes. These are the eight nodes between phases to account for change in infection rate between years. There is a unique evo node for each region because this is also how a region is connected to its copy in future phases. The model supports calculations on a model that represents up to five years of data. In theory, the model could support more phases, but we are limited to the data that was available. As stated previously, the data comes from rates of Hepatitis B from 2010 through 2014. These numbers are used for the capacities of edges that connect a vertex to its evo node. Thus, the capacity of the edge leaving the evo node is different from the capacity of the edge coming in. These changes in capacities make the amount of years (or phases) included in the network critical to the results. At the end of the final phase, or year, instead of connecting back to an evo node, each region then connects back to the sink. This gives us the complete network on which to perform the algorithm.

2.3. Coding

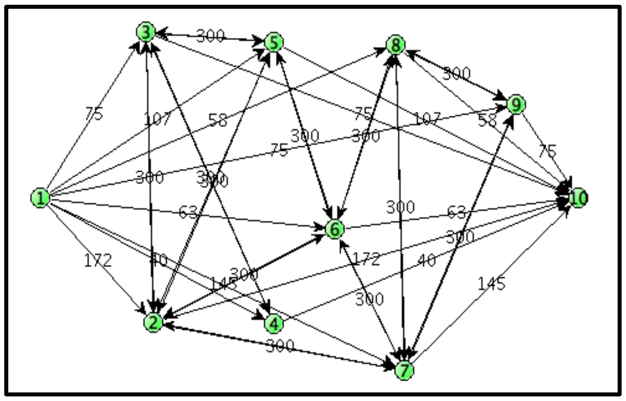
The calculations for this project are done using a Java source file. We retrieved a code, which we modified in several ways to fit our needs, that implements the Ford Fulkerson algorithm over an adjacency matrix. An adjacency matrix is a square matrix and a common way to represent graphs in coding. The rows and columns represent the vertices of the graph where the first row and the first column represent the first vertex (in our case the source), the second row and column representing the second vertex, and so on. The values in a standard adjacency matrix are zeros and ones [5]. One means there is a vertex from node A to node B while zero means no edge exists between those nodes. However, in our code, the values that would be one in the adjacency matrix are the value of the capacity of the edge between two nodes. We use a variable in these cases so that the value can be easily modified when need be, which is one of the significant modifications made.

In addition to the adjacency matrix, there is also a matrix for the evo nodes. The values in this matrix are the rates from the data collected in the tables. This matrix is implemented to mark the edges and their capacities between a region and its evo node. This matrix is not square like the traditional adjacency matrix; it is a 5×8 matrix. It is just a way of storing the values for the infection rates in a logical way where each row has a rate for each region for that particular year and each subsequent year is listed below it. There is a section of code that expands the original adjacency matrix in order to create the additional phases. For each year that is added in to the model, the new matrix has to include the proper amount of phases along with the evo nodes between the years. This is where it retrieves the values from this matrix to mark the capacities of the edges between regions and their evo nodes.

Another key addition to the code was printing out the minimum cut. Since the minimum cut is a set of information key to gathering results, it was necessary to make sure it was provided along with the maximum flow. This was easily accomplished with a couple lines of code that retrieved the edges identified in the minimum cut and printed them out.



The Ford-Fulkerson algorithm already finds the minimum cut along with the maximum flow, so no changes to the actual algorithm were necessary.



Several classes were also added in order to make a GUI, graphical user interface, of the network. GUI's are key for codes like this because it allows the user to interact with the product of the code without having to actually manipulate the code themselves [11]. These GUI classes worked together in order to generate the image shown. As you can see, it provides a network including all five years (also included is an image of the network at 1 year). The user is able to drag the nodes around in order to better observe if needed. Being able to actually see the network was key to understanding the effects of the changes made when gathering our results.

Perhaps the most essential of these GUI classes is GraphData. This class creates one environment to input data for the network where it can be accessed by both the GUI classes and the class for the algorithm. This class also allows multiple networks to be saved in the code. This is vital because the user can change/manipulate a copy of a network while still saving the original and avoids many potential errors.

3. Results and Discussion

The results and observations for this project came from three major modifications to the network: changing the variable, "isolating" regions, and introducing treatment. The first modification is simple to understand. We would simply change the value of the variable in the adjacency matrix and record the maximum flow and minimum cut. This was performed on models for one, two, three, four, and five years. The second modification is referred to as “quarantine”. Essentially, one region (vertex) was removed from the network before running the algorithm. Finally, we further changed the network by simulating treatment. This was done by changing the infection rate of a region to 0 in each possible year while still allowing interaction with other regions. Of course, these are ideal scenarios since it is unlikely that treatment would be provided to an entire region and immediately heal all who were infected. In all these situations, the maximum flow measures the extent of how much the disease has spread, so the smaller the flow, the better. The minimum cut is the set of edges that are identified as the most important to focus on for that particular scenario.

3.1. Effect of variable

The purpose of the parameter in the network is to simulate a certain amount of interaction between the regions. The smaller the variable’s value, the less interaction and vise versa with a higher value. We ran the algorithm with the parameter set to a certain value over a model for each amount of possible years. Then, we would increase the value by 10 and repeat the process. We started this calculation with the parameter set to 10 and increased its value until there was no longer any change in the maximum flow or minimum cut. In models for all possible number of years, there is a point where the variable’s value stopped having an impact on the output of the algorithm.

In models for one year and two years, the variable actually doesn't affect the maximum flow. Regardless of the value, the maximum flow and minimum cut show no change. This can be observed in the table:

	1 Year	
Value	Max Flow	Minimum Cut
10	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
20	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
30	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
40	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
50	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
	2 Years	
Value	Max Flow	Minimum Cut
10	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)
20	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)
30	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)
40	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)
50	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)

What this table is telling us is that if someone were to look at the effects of a disease for only a year or two, interaction between regions is not as important as what is going on within each region.

In models for three, four, and five years, the results turn out to be the same. Unlike the one and two year models, though, interaction plays a more important role. The variable stops having an impact on the maximum flow and minimum cut when it reaches a value of 28, which looking back at the table with the infection rates is one greater than the smallest rate. This smallest rate also happens to occur in the third year of data, so it explains why the same results occur for the four and five year models, as well. The results are shown in the following table. One can easily observe how the maximum flow increases by one as the parameter increases by one, while the minimum cut stays the same. The last change to the maximum flow and minimum cut occur when the variable reaches 28.

	3,4,5 years	
Value	Max Flow	Minimum Cut
26	463	(30,38);(31,39);(18,26);(27,35);(21,29);(4,12);(24,31);(33,41);(19,20)
27	464	(30,38);(31,39);(18,26);(27,35);(21,29);(4,12);(24,31);(33,41);(19,20)
28	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
29	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)

These results demonstrate how interaction plays a role when studying the long term scenarios, but only to a certain point. There is only one edge that represents interaction between two regions is in the minimum cut. We can know this without having to look at the picture of the network because the edges between nodes and evo nodes have a constant difference in their labels. By process of elimination, that makes $(19,20)$ the key edge of interaction. This edge represents the interaction from the Mideast region to New England. If this edge is removed from the network, New England is no longer influenced by the rest of the network, creating a disconnect. Though this result may seem counterintuitive, it validates that cancelling this channel of interaction is important. Further analysis of the minimum cut after the parameter reaches a value of ≥ 28 shows that all of the included edges are between the regions and their respective evo nodes. This is because every region, through a series of vertices, forms a direct path from the source to the sink. It is also important to note that these edges all involve the evo nodes between years two and three. Thus, if someone wanted to take action against the disease, that time would be the best time. This further emphasizes the importance of mathematical modeling because what may be the best option may not always be the most obvious.

3.2. Quarantine

The quarantine of a region was simulated by disconnecting an it from the network one region at a time. As to be expected, each time a particular node is removed, the overall maximum flow decreases, which makes sense because there are less infected people in the network. Minimum cuts turned out to be very similar to the normal model, but edges involving the region under quarantine are absent. The following table displays the results from running the algorithm with this change. Note that the results listed next to a specific region were the output when that region was under quarantine.

	1 Year	
Region	Max Flow	Minimum Cut
Southeast	563	(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
Mideast	660	(1,2);(1,4);(1,8);(1,7);(1,6);(1,5);(1,9)
New England	695	(1,2);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
Great Lakes	628	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,9)
Plains	672	(1,2);(1,4);(1,8);(1,7);(1,3);(1,5);(1,9)
Southwest	590	(1,2);(1,4);(1,8);(1,3);(1,6);(1,5);(1,9)
Rocky Mountains	677	(1,2);(1,4);(1,7);(1,3);(1,6);(1,5);(1,9)
Far West	660	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5)
Normal	735	(1,2);(1,4);(1,8);(1,7);(1,3);(1,6);(1,5);(1,9)
	2 Years	
Region	Max Flow	Minimum Cut
Southeast	418	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24)
Mideast	429	(1,4);(13,21);(14,22);(17,25);(15,23);(16,24);(10,18)
New England	464	(13,21);(3,11);(14,22);(17,25);(15,23);(16,24);(10,18)
Great Lakes	428	(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)
Plains	444	(13,21);(3,11);(17,25);(15,23);(4,12);(16,24);(10,18)
Southwest	418	(13,21);(3,11);(14,22);(17,25);(4,12);(16,24);(10,18)
Rocky Mountains	472	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(10,18)
Far West	455	(13,21);(3,11);(14,22);(15,23);(4,12);(16,24);(10,18)
Normal	504	(13,21);(3,11);(14,22);(17,25);(15,23);(4,12);(16,24);(10,18)

	3,4,5 Years	
Region	Max Flow	Minimum Cut
Southeast	378	(20,28);(30,38);(31,39);(27,35);(21,29);(24,32);(33,41)
Mideast	373	(1,4);(30,38);(31,39);(18,26);(21,29);(24,32);(33,41)
New England	397	(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Great Lakes	388	(20,28);(30,38);(31,39);(18,26);(27,35);(24,32);(33,41)
Plains	437	(20,28);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Southwest	395	(20,28);(30,38);(18,26);(27,35);(21,29);(24,32);(33,41)
Rocky Mountains	432	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(33,41)
Far West	421	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32)
Normal	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)

As to be expected, isolating each region results in a smaller maximum flow. In this case, the rates and the amount of connections a region forms play a role in how much the maximum flow is affected. For instance, the Southeast consistently has one of the largest changes in maximum flow. With infection rates of 172, 86, 178, 197, and 181, it makes sense that removing these from the network makes a huge influence. The Southeast also connects to multiple other regions, so taking these connections out of the network also results in a smaller maximum flow. Similar reasoning can be applied to regions like the Southwest and Great Lakes.

For the most part, the minimum cuts contain edges that are in the minimum cut for the control model. In the three, four and five year models, since they are again all the same, it further supports the key idea that the crucial time to take action in this network lies between years two and three.

There is one region, the Mideast, whose minimum cut has a different edge, though. In all three tables, it contains the edge (1,4), which is the edge connecting the source to New England. The reason is simple; when the Mideast is cut off from the network so is New

England since its only connection to the rest of the network is through the Mideast. This is also why the Mideast's isolation results in a much smaller maximum flow since both regions are cut off at the same time.

3.3. Treatment

In order to model treating the disease in a certain region, we changed the capacity of a vertex's edge to its evo node to 0 but kept the edges of interaction the same. In other words, the region's infection rate was reduced to 0. In the previous two data collection methods, the algorithm runs over a changed network with each possible amount of phases. This time, the algorithm always goes over a network with five phases, but treatment is introduced in each of the five phases for each region. Overall, the results stemming from this modification prove that the earlier treatment is introduced, the better, which is logical. Also, many edges included in the minimum cut are the same edges from previous results.

	In Year 1,2,3	
Region	Max Flow	Minimum Cut
Southeast	352	(60,68);(62,70);(65,73);(61,69);(63,71);(51,59);(56,64)
Mideast	400	(20,28);(30,38);(31,39);(18,26);(21,29);(24,32);(33,41)
New England	397	(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Great Lakes	388	(20,28);(30,38);(31,39);(18,26);(27,35);(24,32);(33,41)
Plains	437	(20,28);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Southwest	395	(20,28);(30,38);(18,26);(27,35);(21,29);(24,32);(33,41)
Rocky Mountains	432	(20,28);(30,38);(31,39);(18,26);(27,35);(24,32);(33,41)
Far West	421	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32)
normal 5 year model	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)

The table above includes the results of the algorithm for when treatment was introduced in the first year, the second year and the third year. Since the results are the same, the maximum flow and minimum cut are even more important. Without any regions being treated, the maximum flow is 464. If there is a large difference between that and the maximum flow for when a certain region is treated, this is a key region to look at. With that being said, it is easy to observe that the Southeast and Great Lakes regions create the largest impact on the maximum flow. Therefore, it would be wise to select one of these two regions to treat before any of the others. Though there are potentially many reasons why these regions stand out, an easy one to discern comes from their infection rates. Both of these regions, the Southeast especially, have consistently higher rates than the other regions, so it is easy to conclude that their treatment would result in the biggest differences in maximum flow.

As for the minimum cuts, the Southeast is the only region, such that after its treatment, the minimum cut is completely different from the normal model. As discussed before the edges in the minimum cut for the normal model involve edges between vertices and their evo nodes between years two and three. In the minimum cut after treating the Southeast, however, the edges are all between vertices and their evo nodes between years four and five. As demonstrated previously, the Southeast is a pivotal region in the network. By treating the Southeast most of the key edges identified by the normal minimum cut are dealt with. Therefore, the minimum cut for when the Southeast is treated includes other edges from later on. The other resulting minimum cuts just further support the idea that the key time to take action is between years two and three.

	In Year 4, 5	
Region	Max Flow	Minimum Cut
Southeast	352	(60,68);(62,70);(65,73);(61,69);(63,71);(51,59);(56,64)
Mideast	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
New England	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Great Lakes	444	(60,68);(62,70);(58,66);(65,73);(63,71);(51,59);(56,64)
Plains	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Southwest	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Rocky Mountains	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)
Far West	464	(20,28);(30,38);(31,39);(18,26);(27,35);(21,29);(24,32);(33,41)

The table above displays the results of the algorithm when treatment is introduced to the regions in the fourth or fifth year. This data further supports the claim that the earlier treatment is introduced the better because most of the regions' results saw no change from the normal model. These regions are marked in blue in the table. This is also to be expected because, as mentioned previously, the key time to take action as identified by the minimum cuts is between years two and three, so most of the time, waiting until after four or five years is too late.

Another important notion within this set of results is that again the Southeast and Great Lakes regions are singled out. In this situation, they are the only ones where treatment in the fourth or fifth year makes an impact on the maximum flow and minimum cut. This influence is because of the minimum cuts, which are the same minimum cut from introducing treatment to the Southeast in the first, second, or third years. Since the edges all involve the evo nodes between the fourth and fifth years, it is consistent with what one would naturally assume. In addition, the maximum flow when treating the Southeast is the same as before. This shows that treating the Southeast will create a large impact on the network regardless of when treatment is provided. On the other hand, the maximum flow for the Great Lakes region increased significantly proving that it is better to treat this region sooner rather than later, but later is better than never.

4. **Conclusion**

In this project we use a network flow model and the Ford-Fulkerson algorithm to analyze the transmission of disease. With the algorithm implemented though a Java program, we were able to easily study multiple copies of the model in order to incorporate time. Focusing on data gathered by the CDC on Hepatitis B, we were able to identify the best ways to fight the disease. First, interaction between regions is important, but analysis of the parameter revealed that interaction only affects the model up until a certain point. We also discovered that when looking at Hepatitis B, the Southeast is a key region. It consistently had a large impact on the network when it was treated or isolated. Furthermore, the model revealed that the most important time to take action against Hepatitis B in this model is between two and three years after the beginning of the model, not right away as one may assume. This ultimately shows how imperative mathematical modeling is to this type of study because it reveals what the human eye may not be able to see. Though our model only focuses on the transmission of Hepatitis B, our model can be used to study any other disease in the future.

References

[1] D. Guichard, An Introduction to Combinatorics and Graph Theory, https://www.whitman.edu/mathematics/cgt_online/cgt.pdf

[2] Class Nodes, University of British Colombia, http://www.ugrad.cs.ubc.ca/~cs490/sec202/notes/flow/Flow%20Intro.pdf

[3] CDC, National Prevention Strategy: America's Plan for Better Health and Wellness, https://www.cdc.gov/features/preventionstrategy/

[4] CDC, Surveillance for Viral Hepatitis – United States, 2014, https://www.cdc.gov/hepatitis/statistics/2014surveillance/index.htm

[5] Weisstein, E., Adjacency Matrix, http://mathworld.wolfram.com/AdjacencyMatrix.html

[6] Java Program to Implement Ford–Fulkerson Algorithm, Sanfoundry: Technology Education Blog, http://www.sanfoundry.com/java-program-implement-ford-fulkerson-algorithm/

[7] Fairfax, A., U.S. State Population Changes for 2010 to 2011, http://censuschannel.net/cc/news/u-s-state-population-changes-for-2010-to-2011-1309

[8] 2012 State Population Census Estimates, Governing: The States and Localities, http://www.governing.com/gov-data/state-census-population-migration-births-deaths-estimates.html

[9] State Population Census Estimates: 2013 Births, Deaths, Migration Totals, Governing: The States and Localities, http://www.governing.com/gov-data/census/census-state-population-estimates-births-deaths-migration-totals-2013.html

[10] List of US States by Population: 2014, Wikipedia, https://simple.wikipedia.org/wiki/List_of_U.S._states_by_population

[11] The Importance of User Interface Design, Art Vision, https://artversion.com/blog/importance-of-user-interface-design/

Appendix A

FordFulkseron.java [6]

```
package edu.georgiasouthern.math.fordfulkerson;
import java.awt.Point;
import java.awt.event.WindowAdapter;
import java.awt.event.WindowEvent;
import java.util.HashSet;
import java.util.Iterator;
import java.util.LinkedList;
import java.util.Queue;
import java.util.Set;

import edu.georgiasouthern.math.jgraph.GraphFrame;
import edu.georgiasouthern.math.jgraph.GraphUtilities;

public class FordFulkerson {
    private int[] parent;
    private Queue<Integer> queue;
    private int numberOfVertices;
    private boolean[] visited;
    private int[][] residualGraph;
    public FordFulkerson(int numberOfVertices) {
        this.numberOfVertices = numberOfVertices;
        this.queue = new LinkedList<Integer>();
        parent = new int[numberOfVertices + 3];
        visited = new boolean[numberOfVertices + 3];
    }
    public boolean bfs(int source, int goal, int graph[][]) {
        boolean pathFound = false;
        int destination, element;
        for(int vertex = 1; vertex <= numberOfVertices; vertex++) {
            parent[vertex] = -1;
            visited[vertex] = false;
        }
        queue.add(source);
        parent[source] = -1;
        visited[source] = true;
        while (!queue.isEmpty()) {
            element = queue.remove();
            destination = 1;
            while (destination <= numberOfVertices) {
                if (graph[element][destination] > 0 &&  !visited[destination]){
                    parent[destination] = element;
                    queue.add(destination);
                    visited[destination] = true;
                }
                destination++;
            }
        }


        if(visited[goal]) {
            pathFound = true;
        }
        return pathFound;
    }
    public int fordFulkerson(int graph[][], int source, int destination) {
        int u, v;
        int maxFlow = 0;
        int pathFlow;
        residualGraph = new int[numberOfVertices + 1][numberOfVertices + 1];
        for (int sourceVertex = 1; sourceVertex <= numberOfVertices;
sourceVertex++) {
            for (int destinationVertex = 1; destinationVertex <=
numberOfVertices; destinationVertex++) {
                residualGraph[sourceVertex][destinationVertex] =
graph[sourceVertex][destinationVertex];
            }
        }
        while (bfs(source ,destination, residualGraph)) {
            pathFlow = Integer.MAX_VALUE;
            for (v = destination; v != source; v = parent[v]) {
                u = parent[v];
                pathFlow = Math.min(pathFlow, residualGraph[u][v]);
            }
            for (v = destination; v != source; v = parent[v]) {
                u = parent[v];
                residualGraph[u][v] -= pathFlow;
                residualGraph[v][u] += pathFlow;
            }
            maxFlow += pathFlow;
        }
        Set<Point> minCut = new HashSet<Point>();
        for(v = 0; v <= numberOfVertices; v++) {
             for(u = 0; u <=  numberOfVertices; u++) {
                  if (visited[v]==true && visited[u]==false && graph[v][u]>0) {
                            minCut.add(new Point(v, u));
                   }
             }
        }
        //output the min cut
        Iterator<Point> it = minCut.iterator();
        while (it.hasNext()) {
             Point p = it.next();
             System.out.println("(v, u) = (" + ((int) p.getX()) + ", " + ((int)
p.getY()) + ")");
        }
        return maxFlow;
    }
    public int[][] getResidualGraph() {
             return residualGraph;
       }
       public static void main(String...arg) {
        int[][] graph;
        int numberOfNodes;
        int source;
        int sink;
        int maxFlow;
        Graph graphData = GraphData.num2;
        numberOfNodes = graphData.numOfNodes + (graphData.numOfStages - 1) * 2
* graphData.numOfNodes + 2;
        source = graphData.source;
        sink = numberOfNodes;//GraphData.num1.sink;
        graph = GraphData.computeMatrix(graphData);//GraphData.num1.matrix;
        int[][] newGraph = new int[graph.length * 2][graph.length * 2];
             for(int i = 0; i < graph.length; i++) {
             for (int j = 0; j < graph[i].length; j++) {
                    newGraph[i][j] = graph[i][j];
             }
        }
        int w = graph.length;
             for(int i = 0; i < graph.length; i++) {
```

```
                        for (int j = 0; j < graph[i].length; j++) {
                        newGraph[i+w][j+w] = graph[i][j];
                    }
                }
                final GraphFrame frame = GraphFrame.showFrame();
                    //display a new graph
                    GraphUtilities.createNewGraph(frame.getGraphPanel(), graph);
                    GraphUtilities.labelGraphEdges(frame.getGraphPanel(), graph);
                    //frame.getGraphPanel().layoutGraph3();
                    GraphUtilities.setNodesPositionsWithStages(frame.getGraphPanel(),
graphData);
                    frame.addWindowListener(new WindowAdapter() {
                            public void windowClosing(WindowEvent we) {
                                    String coords =
GraphUtilities.getNodesPositions(frame.getGraphPanel());
                                    System.err.println(coords);
                                }
                            });
                FordFulkerson fordFulkerson = new FordFulkerson(numberOfNodes);
                maxFlow = fordFulkerson.fordFulkerson(graph, source, sink);
                System.out.println("The Max Flow is " + maxFlow);
                //scanner.close();
            }
        }
```