The program that we ran was written in R and simulated an SIR (susceptible infected recovery) situation. We began by assuming that a single node was infected. In each step the program determined through probability if the connected nodes were then infected. The program ran until no nodes were infected. We ran the simulation one hundred times for each node and computed the average number of nodes infected by the original infected node. We determined that if the probability of infection was less that 37%, then the disease would likely die out within one or two steps. This percentage is known as the epidemic threshold and the average infected nodes were calculated using this probability.

We computed standard centrality measures from the network with the following results. It should be noted that for some of the centrality measures a tie was produced. In those cases we listed the individuals alphabetically.

We created a network of the faculty in the mathematics department at the United States Military Academy. A node represents a single individual. Edges represent shared office space or shared classroom space. Our goal is to understand how a disease, such as a cold or flu virus, spreads among faculty that share offices or classrooms. We created the network below for analysis and simulation.

The data for this was taken from the Fall 2012 classroom list and the Fall 2012 phone list (for office data). Some changes were made to the classroom schedule after this list was made. We decided to stick with the original list since there were additional changes made mid semester. There were a few mislabeled offices in the phone list which we rectified. We defined an office to mean the room where a faculty member’s working desk is located. There are 73 vertices in the graph.

We modeled the network that exists among the teaching staff at the United States Military Academy. We used the network to study a hypothetical disease outbreak among the staff using a computer simulation. We used this information to understand the nature of how the disease might spread. We also used classic network science methods together with the simulation results to determine which faculty members would be likely to infect the greatest number of people.

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