

Instructor Notes

Title: “Ethics Within Epidemics”: The Study of an Epidemic

Discipline and courses: Philosophy, in particular, Contemporary Moral Problems (PHIL 132). It could also be used in Introduction to Philosophy (PHIL 233).

Degree of difficulty: I (introductory)

Duration: 4-6 MWF classes. This is a rough estimate since it hasn't been run yet.

Deliverables and evaluation: The instructor is encouraged to make individual decisions on how much or how little of this module to use. These decisions greatly affect the appropriate deliverables. Typical deliverables would be one or two short written reports and/or an in-class presentation. Discussion, numeric tables, computed measures, and conclusions arising from the simulation could be presented as a written report or could be presented in class as, say, a PowerPoint presentation.

Additional Exercises (open ended questions):

Can you think of two or three more quantitative measures that a public health agent (or parent) might like to know about a disease that is going epidemic?

Example responses: What is the mortality rate of the disease? How contagious is it? How long does it last? How sick does it make you? What treatments are appropriate? What is the cost of treatment?

Discuss the tension between the welfare of a society vs the freedom of the individual. Is it reasonable to require individual confinement or the use of protective devices during an epidemic if such requirements protect the public?

Discussion notes on the Tuskegee Study:

The Tuskegee Syphilis Study (TSS) was riddled with mistakes. We can separate these mistakes into two groups, scientific mistakes and ethical mistakes. Today we would call this study a part of biomedical research, the branch of science that studies life processes and environmental issues with a goal of preventing diseases and ameliorating suffering, usually in humans. Such research can focus on different issues but can be divided into basic or non-therapeutic research and therapeutic research. The goal of the first is to achieve more knowledge about a particular disease, for example, while the goal of the second is to stop or mitigate that disease. (1) Was the goal of the TSS basic or therapeutic or some combination of the two? (2) List the scientific mistakes and explain why they are mistakes from a scientific perspective. (2) List and explain the ethical mistakes made in the study. (3) Are any of the ethical problems with the study issues that are part of the Black Lives Matter movement? (4) If so, explain how and why.

Instructor Notes on the simulation

Organize the class into teams of two, each team runs the simulation ten times. If class size is n , this gives $n/2 * 10$ runs of the simulation. Note and point out that $n/2$ teams running the simulation ten times each is the same as one team running the simulation ($n/2 * 10 = 5*n$) times. Here is an example. Imagine that we have 22 students. We then divide by 2, which gives us 11 teams. Each team runs the simulation ten times, so we multiply our 11 teams by 10 simulation runs each, which results in 121 simulations.

The students will run the dice experiment and record the distribution of the infected number, the mean, and standard deviation. We will give them printed copies of the included worksheet or they can use an Excel spreadsheet to record their results and to calculate mean and sd.

Example Run of Simulation with dice. These are the results of physically rolling a die and recording what happened.

Index case: 5, i.e. rolled the die and got a five

Day	Visit to	Who is Infected	Total infected to date
1	5	5	1
2	6	6	2
3	2	2	3
4	5		
5			

Three people were infected. On day 4 the infected person in room 2 visited the immune person in room 5 and that ended the chain. On day 5 no one in the home was infected.

Now suppose a class of 30 students was divided into 15 pairs and each pair repeated the above simulation ten times. They would bring their results to class and their combine experience could be summarized as:

Number Infected	Frequency	Relative freq
2	38	0.25
3	43	0.29
4	43	0.29
5	19	0.13
6	7	0.05
Total	150	1.00

The frequency would be the number of times out of 150 trials that the number of infected to the left were observed. The relative frequency would be the frequency divided by the total. In this case the total is 150 so the relative frequency of two people being infected is $38/150 = .25$. When the number of repetitions is large one would be justified in thinking of the relative frequency of an outcome as the approximate probability of that outcome. As an example, there is a 29% chance that the infection will burn out when four people have been infected.

The average called the mean (in statistics there are many averages) is calculated by multiplication of the observed and the frequency, adding up all of these products and then dividing by the total number of observations. For example:

Num Infected	Freq	product
2	38	76
3	43	129
4	43	172
5	19	195
6	7	42
total		614

The mean is $614 / 150 = 4.09$. On average, 4 people were infected and then the illness burnt out.

Optional: further work with this simulation. If a professor wants to explore running this simulation with a larger hotel and/or more runs of the simulation a short explanation of a computer simulation can be given and the program OneHouse(n, r) can be ran. An R script for this simulation is included below. More information on using this script will be furnished upon request.

Sample Output: The beauty of a simulation written in computer code is that you can instantly adjust the size of the simulation. Imagine 20 people living in the building. Run 250 simulations.

```
> RESULTS <- OneHouse(20, 250)
```

```
SHOW RESULTS
```

Number Infected At die-out	% of time This occurred
2	6%
3	12%
4	15%
5	18%
6	11%
7	13%
8	8%
9	7%
10	5%
11	5%
12	1%
13	0%

Interpretation: in 6% of the simulation runs the disease died out with only two people being infected. Each row of the above table is similar. For another example we read above that 11% of the runs the disease died out with a total of six people infected. The most people ever infected

was 12 persons and this happened 1% of the time. Students may find this surprising, usually expecting more persons to be infected before die-out.

In this run the average number of people infected before die out was 5.948 with a standard deviation of 2.54 persons.

This model assumes everyone has same chance of being infected. That may not be the case. Some may have more robust natural resistance to infection, some may have less contact with other persons, etc.

R code for simulation. Words after # symbol are comments

```
> OneHouse
function(npeople=6, simsize=20) {
# default house size is 6, default number of repetitions is 20
#
# clear and previous results
results <- c()
#
while (length(results) < simsize ) {
history <- c() #initialize history
x <- sample(1:npeople,1); n <- 1 # pick index case
history <- c(history,x) # store index in history
repeat { y <- sample(1:npeople,1) # pick person to visit
while (y == x ){
y<-sample(1:npeople,1) # be sure you are not visiting yourself
}
if (y %in% history) { # if person has been visited you are done
with this run

break
}
n<-n+1; history[length(history)+1] <- y # store who was visited
x <- y }
results <- c(results,n); cat( "\n")
}
return(results)
}
```

Sample Use and output

```
> catnap <- OneHouse(6,150)
> table(catnap)
catnap
 2  3  4  5  6
30 38 55 20  7
> round(prop.table(table(catnap)),2)
catnap
 2    3    4    5    6
```

```

0.20 0.25 0.37 0.13 0.05
> mean(catnap)
[1] 3.573333
> sd(catnap)
[1] 1.095118

```

Breaking news: I have just worked out a version of the manual simulation using dice that modifies the infection parameters by assuming that an infected person can infect others for two days instead of one day. I went to a house of 12 rooms and so used a pair of dice. With a pair of dice we can generate random integers 1-12 inclusive. The notation for recording the progress was the primary challenge. This is what I came up with:

Index Case: roll the dice to determine the index case. The result was 2 so 2 is the first case, the index case.

Notation will be (old infected | new infected) followed by a list of who each visited. For example:

(| 2) 10 : meaning no old infected (residual infected) and 2 is newly infected. The 10 means that 2 visits 10 who becomes infected. Next day

(2 | 10) 1, 8 : 2 is residual infected, 10 is newly infected. By rolling the dice it is determined that person 2 visits 1 and person 10 visits 8 (determined by rolling the dice). Verify that 1 and 8 can be infected, i.e. are not immune or currently infected.

(10 | 1, 8) 10 is residual infected, 1, 8 new infected. They went visiting: 12, 2, 12 which means that 10 visited 12 and 1 visited 2 and 8 visited 12. What's the result of that visiting? 12 becomes infected but 2 was already infected so the next day looks like,

(1, 8 | 12) and by now you see that 1 and 8 are residual and 12 is newly infected. They (1, 8, 12) go to visit, visits determined by rolling dice, and when I ran this the visits were to 10, 2, 8. Ten is already infected, two is already infected, eight is already infected so next day there are no new infected. The display is

(12 |) And so on. When I finished this it went on for 11 days then died out. Persons 6, 7, and 9 were never infected, everyone else was infected at some point. If you run the same simulation typically you will get different results because of the randomness built into the process.

There is of course no requirement to run this simulation in the “infective phase last two days” mode, but it was fun. Could you modify the procedure to simulate an epidemic in which there are 20 people in the house and the infective phase last three days? Hint: there are dice made from icosahedrons, 20 sided regular polyhedral.

Notice that increasing the number of days that a person can transmit the virus is increasing the number R_0 which results in more infected persons.