

# A Simple Stochastic Model of Disease Spread in a Small Population

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## Abstract

This paper presents a continuous time Markov Chain (CTMC) model of disease spread in a small population, such as a classroom, small office, or a household. Simulation results are given.

## 1. Introduction

This paper presents a stochastic model of disease spread in a small population ( $N < 100$ ). It is an extension of one of the models presented in [5].

The model describes diseases spread by direct contact, such as viral or bacterial infections. The basic idea is that one infected individual enters a small population (household, daycare, or office) and the disease spreads. The quantities of interest are the time until the disease is detected and how many individuals are infected by this time.

The model presented in this paper is novel for three main reasons: its simplicity (there are only two environmental parameters and three disease parameters), its portability (it could be applied to several environments and diseases), and its focus on small populations.

Section 2 describes the basic model. Section 3 contains simulated values and sensitivity analysis for the parameters in the model. Section 4 introduces the idea of response time, i.e. once the disease has been detected, how much time the administration has to respond before everyone is infected. Section 5 contains a concrete example of disease spread and Section 6 describes future work.

## 2. The Basic Model

### 2.1. Model Description

Using the idea of [6], there are three stages of the disease and the first two stages last for an independent, exponentially distributed amount of time with rate  $\mu_i$ ,  $i = 1, 2$ . When

an individual contracts the disease he is in stage 1, asymptomatic and non-contagious; he then moves to stage 2, asymptomatic and contagious; and then moves to stage 3, symptomatic. As soon as the first individual reaches stage 3, i.e. as soon as the first person shows symptoms, we assume the disease is detected.

There are  $N$  people in a building and one is infected (stage 1). Each pair of individuals interacts at rate  $\lambda$ , i.e. after an independent exponential rate  $\lambda$  amount of time. If a contagious individual (stage 2) interacts with a healthy individual, then with probability  $\rho$ , the healthy individual contracts the disease. The quantities of interest are the expected time until the disease is detected and the expected number of infected individuals by the time of detection.

## 2.2. The Continuous Time Markov Chain

Because of the exponential assumptions, the model is described by a continuous time Markov chain (CTMC)  $X_t$ . Let  $S_t^i$  be the number of stage  $i$  individuals at time  $t$ ,  $i = 1, 2, 3$ . Then  $X_t$  is the 3-tuple  $(S_t^1, S_t^2, S_t^3)$  described by the rates:

$$\begin{aligned} q[(s_1, s_2, 0), (s_1 + 1, s_2, 0)] &= s_2 \lambda \rho (N - s_1 - s_2) & (2.1) \\ q[(s_1, s_2, 0), (s_1 - 1, s_2 + 1, 0)] &= s_1 \mu_1 \\ q[(s_1, s_2, 0), (s_1, s_2 - 1, 1)] &= s_2 \mu_2 \\ q(i, j) &= 0 \quad \text{otherwise} \end{aligned}$$

Note that the process stops as soon as the first person reaches stage 3; hence  $S_t^3$  equals 0 or 1 (for  $0 \leq t \leq T$ ). We comment on the derivation of the above rates. Let  $s_i$  be the number of stage  $i$  individuals,  $i = 1, 2$ . The  $(N - s_1 - s_2)$  healthy individuals each interact with a contagious individual at rate  $s_2 \lambda$  (and contract the disease with probability  $\rho$ ). Thus, the rate of new infection is  $s_2 \lambda \rho (N - s_1 - s_2)$ . Each stage 1 individual enters stage 2 at rate  $\mu_1$ , so the stage 2 rate of increase is  $s_1 \mu_1$ . Similarly, each stage 2 individual enters stage 3 at rate  $\mu_2$ , so the stage 3 rate of increase, i.e. the rate of detection, is  $s_2 \mu_2$ .

Let  $T$  be the time of detection, i.e. the time that the first individual shows symptoms of the disease. Then  $S_T^1$  and  $S_T^2$  are the number of stage 1 and stage 2 individuals, respectively, at the time of detection. We are interested in estimating  $ET$ ,  $ES_T^1$ , and  $ES_T^2$ .

## 2.3. Summary of Model Notation and Parameters

- $N$  = Total number of people.
- $\lambda$  = rate of contact.
- $\rho$  = probability of disease spread. If a contagious individual interacts with a healthy individual,  $\rho$  gives the probability that the healthy individual contracts the disease.

- $\mu_i$ . Each infected individual spends an exponential amount of time with mean  $\mu_i^{-1}$  in stage  $i$ ,  $i = 1, 2$ .
- $X_t$ . The system is described by the CTMC  $X_t = (S_t^1, S_t^2, S_t^3)$ , where  $S_t^i$  is number of stage  $i$  individuals at time  $t$ .
- $T$  = time of detection.
- $S_T^1$  = total number of stage 1 individuals by time of detection.
- $S_T^2$  = total number of stage 2 individuals by time of detection.

### 3. Sensitivity Analysis

In this section and throughout, expected values and variances are approximated from simulations of 10, 000 iterations. This section considers the sensitivity of the main values ( $ES_T^1, ES_T^2$ , and  $ET$ ) to changes in the parameter values. It also includes a comment about the large variation in the process.

First we make a note concerning the parameters  $\lambda$  and  $\rho$ . In a modeling context,  $\lambda$  and  $\rho$  are two separate parameters; however, in sensitivity analysis they are not. As can be seen from the rate equations (2.1) the value that matters is the product  $\lambda' = \lambda\rho$ . In fact,  $\lambda'$  can be viewed as the effective rate of contact, the rate at which individuals interact long enough for the disease to be spread with probability 1. This section considers changes in  $\lambda'$ . An increase in  $\lambda'$  can be viewed either as a separate increase in  $\lambda$  or  $\rho$ , or as a simultaneous increase in the two parameters.

Table 1 gives approximations for expected values ( $ES_T^1, ES_T^2$ , and  $ET$ ) computed at different parameter values (all tables and figures are included at the end of the paper). The expected number of infected ( $ES_T^1, ES_T^2$ ) should be increasing in  $\lambda'$  and  $N$ . These relationships are apparent from the rate equations (2.1), but also they make intuitive sense. With more total people, there are more people who can contract the disease. And as people interact more ( $\lambda$  increases) or the probability of transfer increases ( $\rho$  increases), the disease will spread to more people. It is also reasonable that increasing  $\mu_1$  or  $\mu_2$  should tend to decrease the expected number of infected (by the time of detection), since increasing either parameter will decrease the time until detection. These relationships are illustrated in Table 1.

The expected time until detection ( $ET$ ) should be inversely related to  $N$ ,  $\lambda'$ ,  $\mu_1$ , and  $\mu_2$ . Increasing  $N$  or  $\lambda$  will increase the number of infected; and more infected individuals means there are more people who could eventually show symptoms. Although, these are only secondary effects. Increasing  $\lambda'$  or  $N$  will directly increase  $ES_T^1$ ; however, it is  $\mu_1$  and  $\mu_2$  which control how quickly these individuals pass to stage 2 and eventually stage 3 (when detection occurs). Thus, we expect that changing  $\mu_i$ ,  $i = 1, 2$ , would have a greater effect on  $ET$ . In fact, Table 1 supports these hypotheses. Increasing  $\lambda'$  by orders of magnitude only slightly decreases  $ET$ ;  $ET$  is more sensitive to changes in  $N$ ; and it is the most sensitive to simultaneous changes in  $\mu_1$  and  $\mu_2$ .

**Table 1. Expected Values ( $ES_T^1$ ,  $ES_T^2, ET$ ) vs.  $\lambda'$  and  $N$** 

		$\lambda' = .01$			$\lambda' = 1$			$\lambda' = 10$					
		$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$			
N		3.03	2.45	155	5.76	3.34	139.31	6.21	3.73	136.47	6.31	3.68	133.79
10		7.23	3.37	149.49	13.34	4.92	129.56	14.49	5.31	129.91	14.64	5.31	123.10
20		20.33	5.46	133.01	37.44	8.05	122.48	41.1	8.43	117.5	41.35	8.63	115.67
50		43.23	7.72	122.59	78.06	11.13	114.54	87.13	11.91	109.74	87.81	12.14	114.58

**1a.**  $\mu_1 = \mu_2 = .01$

		$\lambda' = .01$			$\lambda' = 1$			$\lambda' = 10$					
		$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$			
N		0.48	1.39	19.26	2.96	2.47	15.78	5.74	3.46	14.04	6.31	3.63	13.96
10		1.10	1.66	17.52	7.00	3.35	15.07	13.36	4.91	13.15	14.59	5.26	12.76
50		3.08	2.34	16.47	19.78	5.16	13.54	38.28	7.74	11.95	41.06	8.39	11.33
100		6.88	3.10	15.24	43.12	7.71	12.38	79.62	11.43	11.64	86.95	11.97	10.95

**1b.**  $\mu_1 = \mu_2 = .1$

		$\lambda' = .01$			$\lambda' = 1$			$\lambda' = 10$					
		$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$	$ES_T^1$	$ES_T^2$	$ET$			
N		0.05	1.04	2.05	0.46	1.38	1.86	3.01	2.40	1.58	5.69	3.55	1.41
10		0.11	1.09	1.92	1.07	1.65	1.79	7.15	3.48	1.54	13.43	4.98	1.32
50		0.25	1.18	1.81	3.18	2.41	1.57	20.23	5.41	1.41	37.81	7.76	1.22
100		0.57	1.40	1.90	7.15	3.24	1.57	42.00	7.40	1.27	79.07	11.58	1.13

**1c.**  $\mu_1 = \mu_2 = 1$

Table 1: Expected number of infected ( $ES_T^1$ ,  $ES_T^2$ ) and the expected time of detection ( $ET$ ) for different parameter values.

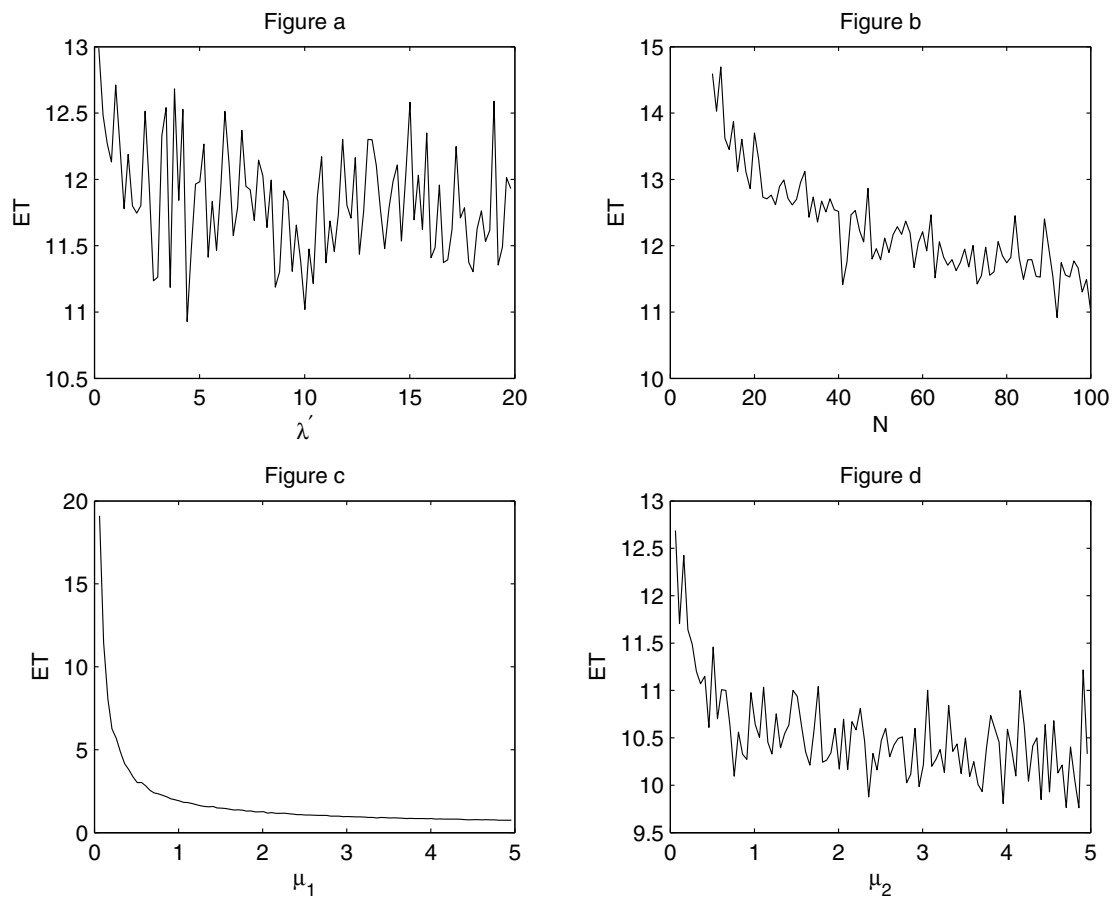


Figure 1: Expected time of detection vs.  $(\lambda', N, \mu_1, \mu_2)$ . The default values are  $\lambda' = 1$ ,  $N = 50$ , and  $\mu_1 = \mu_2 = .1$ . For example, in Figure a,  $\lambda'$  varies, but  $N = 50$  and  $\mu_1 = \mu_2 = .1$ .

Figure 1 further explores these relationships concerning  $ET$ . The figure presents plots of  $ET$  versus  $\lambda'$ ,  $N$ ,  $\mu_1$ , and  $\mu_2$ . These plots illustrate that  $ET$  is the most sensitive to changes in  $\mu_1$ , in fact  $ET \approx \frac{C}{\mu_1}$ . They also illustrate that none of  $\lambda'$ ,  $N$ , or  $\mu_2$  strongly effect  $ET$ . It is surprising that  $\mu_2$  does not have a stronger inverse relationship with  $ET$ . The rationale is that  $\mu_1$  controls the number of stage 1 individuals that pass to stage 2, and only stage 2 individuals will eventually show symptoms. No matter how large  $\mu_2$  is, if there are no stage 2 individuals, then no one can pass into stage 3. Thus, the value of  $\mu_1$  will limit the impact that  $\mu_2$  will have on  $ET$ . In other words, for a fixed  $\mu_1$ , increasing  $\mu_2$  beyond a certain value will not cause  $ET$  to drop significantly; however, over a certain range,  $ET$  is decreasing in  $\mu_2$ . These ideas are displayed in Table 2. For example with  $\mu_1 = .01$  ( $N = 50$ ,  $\lambda' = 1$ ), for  $\mu_2 \in [.1, 10,000]$ ,  $ET \approx 100$ .

**Table 2. The Impact of  $\mu_2$  on  $ET$** 

$\mu_2$	$\mu_1 = .01$	$\mu_1 = .1$	$\mu_1 = 1$
.001	162.79	38.78	22.57
.01	118.48	17.25	4.14
.1	101.67	12.52	1.93
1	100.17	10.69	1.34
10	100.87	9.89	1.10
100	99.67	9.83	1.01
1000	99.90	9.80	1.02
5000	100.27	10.31	1.01
10,000	100.37	10.18	0.98

Table 2: Expected time of detection ( $ET$ ) vs.  $\mu_1$  and  $\mu_2$ . In all cases,  $N = 50$ ,  $\lambda' = 1$ .

There is large variation in the process, i.e. the variances of  $T$ ,  $S_T^1$ , and  $S_T^2$  are often quite large (relative to the mean). Thus, a single realization of the process produces values which can be quite far from the mean. Tables 3 and 4 give the variance of the number infected and time of detection, respectively, along with the coefficient of variation in parentheses.

## 4. Response Time

### 4.1. Introduction

It is assumed that as soon as the first person shows symptoms that the disease is detected. The question of how much time the administration has to react once the disease is detected is still unanswered. This section attempts to answer that question by defining the notion of response time: the amount of time from the first individual showing symptoms until everyone is infected. It is possible that everyone is already infected before the first individual shows symptoms, and this would correspond to a zero response time. We define the random variable  $T^*$  as:

$$T^* \equiv \max\{T, \text{time until everyone is infected}\}.$$

Response time is defined as  $T^* - T$ .

In the above sections, the process is stopped once the first individual passes to stage 3 (time  $T$ ). But now the process continues to run until  $T^*$ , and thus we need to keep track of the stage 3 individuals since they can also cause new infections. A slight modification

**Table 3. Variation in the Number Infected vs.  $\lambda'$  and  $N$**

		$\lambda' = .01$		$\lambda' = .1$		$\lambda' = 10$	
		$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$
N							
10	4 (.66)	2 (.58)	3 (.52)	3 (.28)	3 (.46)	2.7 (.26)	2.8 (.45)
20	14 (.52)	5 (.66)	7 (.56)	7 (.18)	7 (.50)	7 (.18)	6.8 (.49)
50	113.8 (.52)	15.8 (.73)	20 (.56)	20.2 (.11)	19.1 (.52)	17 (.10)	17 (.48)
100	578.3 (.56)	35.7 (.77)	43.8 (.59)	75 (.10)	38 (.52)	41 (.07)	41 (.53)

**3a.  $\mu_1 = \mu_2 = .01$**

		$\lambda' = .1$		$\lambda' = 1$		$\lambda' = 10$	
		$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$
N							
10	0.5 (1.47)	0.42 (.47)	2.36 (.62)	2.96 (.30)	3.11 (.51)	2.89 (.27)	2.98 (.48)
20	1.54 (1.13)	1.14 (.64)	5.30 (.69)	9.77 (.23)	7.36 (.55)	6.85 (.18)	6.78 (.50)
50	8.64 (.95)	3.04 (.75)	15.28 (.76)	52.27 (.19)	18.93 (.56)	24.07 (.12)	19.32 (.52)
100	37.70 (.89)	6.33 (.81)	36.96 (.79)	294.12 (.22)	43.01 (.57)	73.75 (.10)	39.35 (.52)

**3b.  $\mu_1 = \mu_2 = .1$**

		$\lambda' = .1$		$\lambda' = 1$		$\lambda' = 10$	
		$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$	$VarS_T^1$	$VarS_T^2$
N							
10	0.05 (4.47)	0.05 (.22)	0.36 (.43)	3.59 (.63)	2.55 (.67)	3.05 (.31)	3.2 (.50)
20	0.09 (2.73)	0.13 (.33)	1.07 (.63)	15.78 (.56)	5.45 (.67)	9.46 (.23)	7.07 (.53)
50	0.31 (2.23)	0.36 (.51)	3.69 (.80)	120.55 (.54)	15.97 (.74)	67.31 (.22)	18.49 (.55)
100	0.81 (1.58)	0.69 (.59)	7.42 (.84)	560.93 (.56)	32.92 (.78)	295.61 (.22)	45.92 (.59)

**3c.  $\mu_1 = \mu_2 = 1$**

Table 3: Variance and coefficient of variation, in parentheses, of the number infected ( $S_T^1, S_T^2$ ) for different parameter values.

**Table 4. Variation in the Time until Detection vs.  $\lambda'$  and  $N$**   
**4a.  $\mu_1 = \mu_2 = .01$**

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	10,880 (.67)	10,917 (.75)	9415.6 (.71)	9259.1 (.72)
20	10,765 (.69)	9249.4 (.74)	10,409 (.79)	9833.5 (.81)
50	9820.4 (.75)	10,029 (.82)	9834.7 (.84)	10,799 (.90)
100	8737.8 (.76)	9801 (.86)	10,064 (.91)	10,958 (.91)

**4b.  $\mu_1 = \mu_2 = .1$**

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	148.38 (.63)	121.34 (.70)	116.77 (.77)	112.63 (.76)
20	145.37 (.69)	106.84 (.69)	107.79 (.79)	104.71 (.80)
50	138.78 (.72)	99.86 (.74)	90.58 (.80)	90.73 (.84)
100	103.41 (.67)	93.87 (.78)	101.51 (.87)	86.66 (.85)

**4c.  $\mu_1 = \mu_2 = 1$**

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	2.09 (.71)	1.51 (.66)	1.12 (.67)	1.02 (.72)
20	1.73 (.69)	1.36 (.65)	1.1 (.68)	0.98 (.75)
50	1.67 (.71)	1.09 (.66)	1.14 (.76)	0.99 (.82)
100	1.48 (.64)	1.1 (.67)	0.87 (.73)	0.89 (.83)

Table 4: Variance and coefficient of variation, in parentheses, for time until detection ( $T$ ) for different parameter values.

of the rates (2.1) gives

$$q[(s_1, s_2, s_3), (s_1 + 1, s_2, s_3)] = (s_2 + s_3)\lambda\rho \left( N - \sum_{i=1}^3 s_i \right) \quad (4.1)$$

$$q[(s_1, s_2, s_3), (s_1 - 1, s_2 + 1, s_3)] = s_1\mu_1$$

$$q[(s_1, s_2, s_3), (s_1, s_2 - 1, s_3 + 1)] = s_2\mu_2$$

$$q(i, j) = 0 \quad \text{otherwise}$$

It is possible that once an individual realizes that he is sick, then he will remove himself from the population, i.e. he will go home sick. If symptomatic individuals remove themselves from the population then number of stage 3 individuals will not enter the rate equations. In this case, the rate of new infections is given by:

$$q[(s_1, s_2, s_3), (s_1 + 1, s_2, s_3)] = s_2\lambda\rho \left( N - \sum_{i=1}^3 s_i \right) \quad (4.2)$$

The above two cases can be generalized. Instead of stage 3 individuals definitely staying or leaving the population, they remain in the population with probability  $p_r$ . This

requires introducing a fourth stage, individuals who have left the population.<sup>1</sup> The rates are:

$$q[(s_1, s_2, s_3, s_4), (s_1 + 1, s_2, s_3, s_4)] = (s_2 + s_3)\lambda\rho \left( N - \sum_{i=1}^4 s_i \right) \quad (4.3)$$

$$q[(s_1, s_2, s_3, s_4), (s_1 - 1, s_2 + 1, s_3, s_4)] = s_1\mu_1$$

$$q[(s_1, s_2, s_3, s_4), (s_1, s_2 - 1, s_3 + 1, s_4)] = s_2p_r\mu_2$$

$$q[(s_1, s_2, s_3, s_4), (s_1, s_2 - 1, s_3, s_4 + 1)] = s_2(1 - p_r)\mu_2$$

$$q(i, j) = 0 \quad \text{otherwise}$$

With  $p_r = 1$  rates (4.3) are equivalent, after reformulation, to rates (4.1); with  $p_r = 0$  they are equivalent to rates (4.2).

With  $p_r < 1$  it is possible that some individuals will never contract the illness. If all of the infected move to stage 4, then the system would only contain stage 4 individuals and healthy individuals, consequently, no more transitions would be possible (and thus  $T^*$  would be infinite). The following fact is obvious:

$$Pr(T^* < \infty) = 1 \quad \text{iff } p_r = 1. \quad (4.4)$$

## 4.2. Simulated Values

Because of Fact 4.4, we simulate values for response time when  $p_r = 1$ . Simulated values related to response time are contained in Tables 5, 6, and 7. Tables 5 and 6 give the expected value and variance, respectively, of response time at different parameter values. Table 7 contains estimates of the probability of a zero response time (the percentage of iterations when  $T^* = T$ ). It is possible that when the first individual shows symptoms everyone is already infected, hence there will be zero response time.

The expected response time is decreasing in  $\lambda'$ ; similarly, the probability of a zero response time is increasing in  $\lambda'$ . These relations make sense since a high  $\lambda'$  means that the disease will quickly spread and thus by the time the first individual shows symptoms, most people will at least be in stage 1.

The simultaneous increase in  $\mu_1$  and  $\mu_2$  increases the expected response time and decreases the probability of a zero response. This makes sense since increasing  $\mu_i$  means that individuals move through the stages quicker and thus show symptoms faster. Hence by the time the first person shows symptoms there will still be several individuals who have not yet contracted the disease. The question of interest for response time is how quickly the disease is spreading (controlled by  $\lambda'$ ) relative to how quickly an infected individual will show symptoms (controlled by  $\mu_i$ ). Thus the values of interest are the ratios  $\frac{\lambda'}{\mu_i}$ ,  $i = 1, 2$ .

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<sup>1</sup>Stage 4 individuals are in stage 3 of the disease but they have removed themselves from the population; stage 3 individuals are in stage 3 of the disease and they remain in the population able to infect others.

Table 5. Expected Response Time vs.  $\lambda'$  and  $N$ 

		$\lambda' = .01$		$\lambda' = .1$		$\lambda' = 1$		$\lambda' = 10$	
		$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$
10	160.01	63.39	140.97	2.50	136.50	.0448	136.86	.0005	.0005
20	148.58	53.36	131.55	2.86	127.81	.0587	127.22	.0009	.0009
50	136.63	39.41	120.58	2.32	119.30	.0752	116.53	.0008	.0008
100	126.48	29.75	115.90	2.05	112.47	.0724	112.38	.0013	.0013

**5a.**  $\mu_1 = \mu_2 = .01$

		$\lambda' = .01$		$\lambda' = .1$		$\lambda' = 1$		$\lambda' = 10$	
		$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$
10	18.58	62.01	16.21	6.44	13.95	0.27	13.82	.005	.005
20	17.90	43.91	14.71	5.29	13.35	.27	12.88	.0055	.0055
50	16.41	27.72	13.90	3.92	12.26	.2194	11.68	.0074	.0074
100	15.58	19.66	12.67	2.98	11.53	.19	11.26	.0066	.0066

**5b.**  $\mu_1 = \mu_2 = .1$

		$\lambda' = .01$		$\lambda' = .1$		$\lambda' = 1$		$\lambda' = 10$	
		$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$	$ET$	$E(T^* - T)$
10	2.03	57.17	1.87	6.23	1.62	.63	1.41	.0275	.0275
20	1.97	37.06	1.75	4.45	1.49	.5386	1.30	.0275	.0275
50	1.90	19.87	1.64	2.79	1.38	.3882	1.24	.0235	.0235
100	1.84	12.54	1.53	1.97	1.27	.30	1.16	.0201	.0201

**5c.**  $\mu_1 = \mu_2 = 1$

Table 5: Expected Times ( $ET, E(T^* - T)$ ) for different parameter values.

**Table 6. Variation of Response Time vs.  $\lambda'$  and  $N$**

<b>6a. <math>\mu_1 = \mu_2 = .01</math></b>				
$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	2105.9 (.7)	37.20 (2.44)	.12 (7.70)	.0002 (26.75)
20	1052 (.6)	36.11 (2.10)	.15 (6.54)	.0004 (20.52)
50	443.16 (.53)	20.16 (1.94)	.19 (5.84)	.0003 (19.96)
100	209.25 (.49)	12.17 (1.70)	.15 (5.38)	.0004 (15.67)

<b>6b. <math>\mu_1 = \mu_2 = .1</math></b>				
$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	500.43 (.36)	21.90 (.73)	.42 (2.37)	.001 (7.22)
20	158.06 (.29)	10.67 (.62)	.3340 (2.14)	.001 (6.68)
50	40.61 (.23)	4.27 (.53)	.18 (1.95)	.002 (5.86)
100	18.50 (.22)	2.04 (.48)	.11 (1.75)	.001 (5.41)

<b>6c. <math>\mu_1 = \mu_2 = 1</math></b>				
$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	402.35 (.35)	5.12 (.36)	.22 (.73)	.005 (2.43)
20	101.64 (.27)	1.57 (.28)	.11 (.61)	.003 (2.12)
50	14.99 (.19)	.43 (.23)	.04 (.52)	.002 (1.89)
100	4.14 (.16)	.19 (.22)	.022 (.49)	.001 (1.75)

Table 6: Variance of response time ( $T^* - T$ ), with the coefficient of variation in parentheses, for different parameter values.

$N$  does not have a consistent effect on expected response time; however, for several parameter values,  $E(T^* - T)$  is decreasing in  $N$ . An inverse relationship is expected as  $ES_T^i, i = 1, 2$ , are increasing in  $N$ . Surprisingly, the probability of zero response is also decreasing in  $N$ .

### 5. Concrete Example

There are 25 employees in a small office building that interact at a rate of 10 times a day ( $\lambda = 10$ ). One employee comes to work infected with an illness with the following properties: if a contagious worker interacts with a healthy worker, the healthy worker contracts the disease with probability .7 ( $\rho = .7$ ); people become contagious on average one hour after contracting the illness ( $\mu_1 = 24$ ); and on average it takes one day for a contagious individual to show symptoms ( $\mu_2 = 1$ ). Based on 10,000 iterations the simulation model predicts that on average the disease will be detected after 3.5664 hours (variance: .108). After this time, on average 6.05 people will be in stage 1 (variance 14.67) and 16.0294 people will be in stage 2 (variance 46.8). Notice that of the 25 employees, on average, over 22 will be infected by the time the disease is discovered; however, there is high variation in these estimates. With such a large percentage of the

**Table 7 Probability of a Zero Response Time****7a.**  $\mu_1 = \mu_2 = .01$ 

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	.1002	.7688	.9736	.9972
20	.0514	.6978	.967	.9964
50	.0216	.6504	.9548	.9966
100	.0126	.5918	.9478	.9944

**7b.**  $\mu_1 = \mu_2 = .1$ 

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	0	.0958	.7506	.97
20	0	.052	.7112	.9656
50	0	.0194	.6688	.9574
100	0	.0102	.612	.9456

**7c.**  $\mu_1 = \mu_2 = 1$ 

$N$	$\lambda' = .01$	$\lambda' = .1$	$\lambda' = 1$	$\lambda' = 10$
10	0	0	.1	.7626
20	0	0	.0528	.7088
50	0	0	.0182	.6502
100	0	0	.0098	.6022

Table 7: Probability of a zero response time,  $Pr(T^* = T)$ , for different parameter values. When  $T^* = T$ , by the time the first person shows symptoms everyone is infected so the response time is zero.

employees infected by the time of detection, we expect a short response time. In fact, on average there is only 17.71 minutes to respond (variance: .576) and the the probability of zero response is .5874.

## 6. Future Work

In this section we consider possible extensions of the current model. The small population size is essential to the assumption that each pair of individuals interacts at the same rate. As  $N$  increases, this assumption becomes less realistic. To model larger populations, we would use the idea of connected units. Each unit is a small population modeled as above, and there exists a rate of interaction between the units. For example, to model disease spread in a school, each classroom is modeled as a single unit and there is interactions between the classrooms. Similar modeling could be used for large companies which are divided into smaller divisions or interactions between different floors of a building (where each floor is a single unit).

In the current model, as soon as the first person shows symptoms, it is assumed that the disease is detected. It might be more realistic to assume that multiple people have to

show symptoms of the (same) disease before the administration takes notice. The above model could easily be extended to the case where once  $\beta$  people show symptoms, the disease is detected. The rarer and deadlier diseases would have lower  $\beta$ 's. It would be interesting to examine how  $\beta$  affects  $ET$ , for instance. Also,  $\beta$  could be viewed as a policy variable, which gives the threshold at which the administration warns it employees about a possible infection in the office. There is a cost to alerting your employees that a certain disease is spreading: employees might start leaving work. But there is also a cost related to having employees become ill. The administration could establish an optimal threshold  $\beta$  based on this tradeoff.

In the numerical examples dealing with response time, symptomatic individuals remain in the population ( $p_r = 1$ ). It would be useful to examine the effect (on the expected number infected) of decreasing  $p_r$ . Is there a strong enough effect to justify an administration's efforts to push  $p_r$  as close to zero as possible, by forcing sick individuals to go home? This policy at least seems feasible in a grade school setting.

With different interpretations of the stages of the disease and some reformulation, this model could be used in settings outside of the spread of diseases, such as the spread of computer viruses or rumors.

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