Mathematical Model for the Transmission of Smallpox from European Colonists to Native American Populations

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Introduction

During the conquest and colonisation of the Americas by Europeans throughout the XVIth century, it is estimated that 90% of American indigenous populations were decimated. Although initial population sizes and the magnitude of population decline are disputed, most scholars agree that epidemic disease was by far the leading cause of death. A number of diseases including chicken pox, measles, bubonic and pneumonic plague, typhus, cholera, mumps, small pox and pertussis (whooping cough) were introduced into populations that had no previous exposure, and therefore no immunity to them. Smallpox, in particular, was a deadly disease in Europe that had not reached the Americas until colonisation, where it devastated the Native American populations.

Smallpox is caused by the viruses Variola minor and Variola major. The virus is transmitted through direct person to person contact, through the air, and through shared fomites (such as blankets etc.). The virus is highly transmissible: Individuals sharing a household with an infected individual have a 1 in 2 chance of getting infected. After contraction, patients undergo an incubation phase which lasts 7-12 days, during which they show no signs of infection, and are not infectious. Patients then start showing generic immune response symptoms for 3-4 days such as nausea, chills, vomiting and high fevers. Sometimes symptoms are particularly aggravated and include convulsions, bad dreams, and delirium. This phase is followed by the characteristic skin eruptions of scarlet coloration. The disease lasts about a month and results in death in about ¼ of cases. Death can occur a few days after the rash, after a week of rash, or before rash had even appeared. However, if an individual survives, they have gained immunity from smallpox for the rest of their lives.

In Europe, smallpox has been a major cause of morbidity and mortality since the Middle Ages, and at its height was responsible for one in ten of all deaths. The first outbreak of smallpox in the Americas closely followed the arrival Christopher Columbus: two outbreaks hit the island Hispanola in 1507 and 1518. Some historians estimate that this outbreak contributed heavily to the population in Hispanola dropping from 300,000-1,000,000 inhabitants in 1492 to 500 in 1541. During the following century, epidemics hit every South American country and Caribbean island: Cuba in 1518, Puerto Rico in 1519, Mexico in 1520, and Peru in 1424, each time bringing devastation: at least half of the population of Natives died with each outbreak. The true extent of Native deaths (and of original population size) caused is a subject of some controversy as it is brings to surface the question of whether the colonisation of the Americas by the Europeans constituted a genocide. Nevertheless, all estimates remain high, from 9/10 of populations dying within six months to ⅓ within 10 years. In addition to being directly responsible for thousands of deaths, smallpox demoralized the Natives' spirit; especially when their tribal leaders would fall to the disease. This was an important part in the Europeans' success in America.

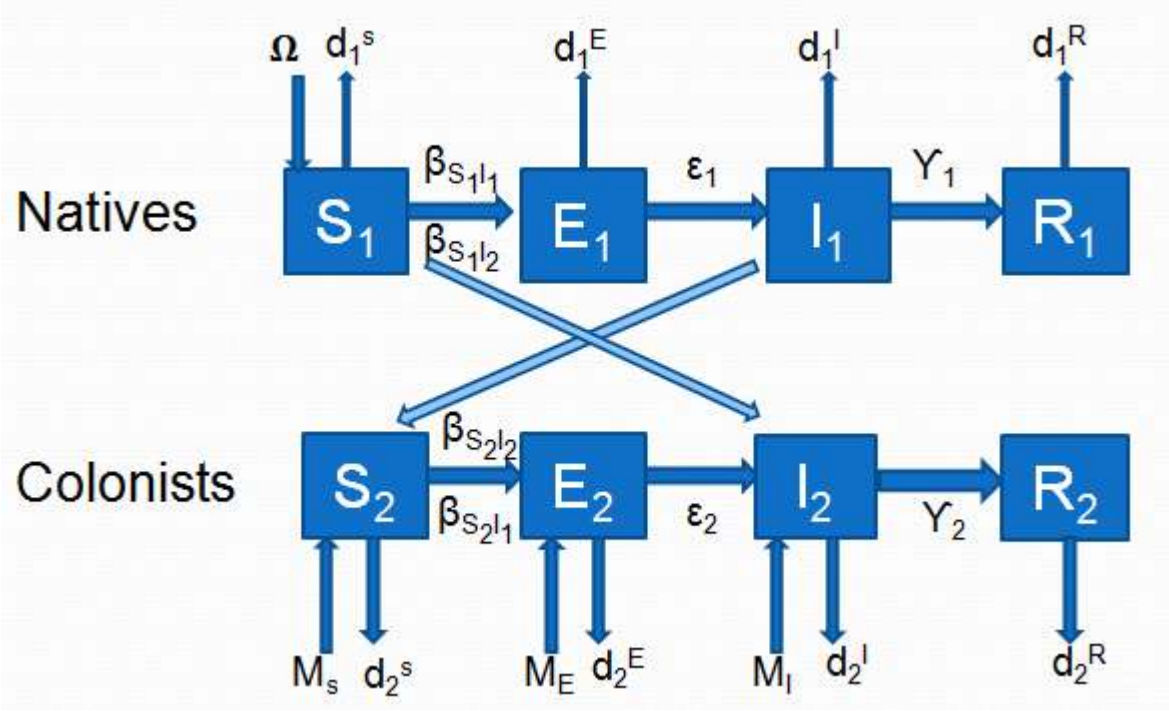
The disease was carried by Colonists who had previously had the disease in Europe and did not suffer from it. In some cases, they showed no sign of infection because they had been infected earlier in life and were no longer susceptible. It is also likely that some susceptible Colonists died from smallpox during their journeys to the New World. However, the former was probably why the disease was able to survive the transoceanic voyages until landing in the Americas.

Smallpox was the first disease which was mathematically modeled, by Bernoulli in 1760. Since then it has been modeled in different circumstances, for example to examine the effect of a bioterrorist attack using this deadly virus. However, devastating as it was, the transmission and spread of smallpox from Europeans to Native Americans has never been modeled. In the present analysis, we model the spread of smallpox from a small number of Colonists to a moderate sized Native population, similar to that of Hispanola.

Materials and Methods

1. *The model*

Figure 1: Mathematical model for the spread of smallpox from Colonists to Natives



Ω = Birth Constant
M_S = Susceptible Immigrants
M_E = Exposed Immigrants
M_I = Infected Immigrants
d_i= Death rate
$\beta S_i I_j$ = Infection rate
Υ_i= Recovery rate
ε_i= Rate of progression from exposed to infectious stage

Individuals can be in one of four stages. They start off as susceptible (S) and become exposed (E) upon contact with an infected individuals at a rate β_{SiIi}, which depends on the numbers of susceptible and infected in the population. After a period of latency where they are infected but not yet infectious, they progress to the infectious stage (I) at a rate ε. They then move to the recovered (R) stage at a rate Υ. During any stage individuals can die (d); the rate of death is higher for infected than for any other group. An important characteristic of this model is that the population is divided into two groups, Natives (subscript 1) and colonists (subscript 2). While Natives are born at a rate Ω into the susceptible group, Colonists arrive into the population through immigration (M), and can do so into any of the groups S, E or I. Differential equation representing the changes in this population are:

$$\frac{dS1}{dt} = \Omega - S_1 I_1 \beta_{S_1 I_1} - S_1 I_2 \beta_{S_1 I_2} - S_1 d_1^{s}$$

$$\frac{dS2}{dt} = M_s - S_2 I_2 \beta_{S_2 I_2} - S_2 I_1 \beta_{S_2 I_1} - S_2 d_2^{s}$$

$$\frac{dE1}{dt} = S_1 I_1 \beta_{S_1 I_1} + S_1 I_2 \beta_{S_1 I_2} - E_1 \varepsilon_1 - E_1 d_1^{E}$$

$$\frac{dE2}{dt} = M_E + S_2 I_2 \beta_{S_2 I_2} + S_2 I_1 \beta_{S_2 I_1} - E_2 \varepsilon_2 - E_2 d_2^{E}$$

$$\frac{dI1}{dt} = E_1 \varepsilon_1 - I_1 \Upsilon_1 - I_1 d_1^{I}$$

$$\frac{dI2}{dt} = M_I + E_2 \varepsilon_2 - I_2 \Upsilon_2 - I_2 d_2^{I}$$

$$\frac{dR1}{dt} = I_1 \Upsilon_1 - R_1 d_1^{R}$$

$$\frac{dR2}{dt} = I_2 \Upsilon_2 - R_2 d_2^{R}$$

2. *Disease Free and Endemic Equilibrium*

One of the first steps in the analysis of infectious disease modeling is the determination of R_0 values. These values can be interpreted as thresholds, where if $R_0 > 1$ then the disease in question persists and if $0 < R_0 < 1$ then the disease dies out. Although there are numerous methods to calculate these values, most of these would require extensive calculations due to the complexity of the model.

Disease free equilibrium

The Jacobian at the disease-free equilibrium method would yield, after simplification, the determination of Eigen-values of a 4 by 4 matrix. This technique in our case would involve solving for λ^4, a fourth degree polynomial expression.

$$\det\begin{bmatrix} -\varepsilon_1 - d_1^E - \lambda & 0 & S_1\beta_{S_1I_1} & S_1\beta_{S_1I_2} \\ 0 & -\varepsilon_2 - d_2^E - \lambda & S_2\beta_{S_2I_1} & S_2\beta_{S_2I_2} \\ \varepsilon_1 & 0 & -\gamma_1 - d_1^I - \lambda & 0 \\ 0 & \varepsilon_2 & 0 & -\gamma_2 - d_2^I - \lambda \end{bmatrix}$$

Since the disease-free equilibrium is:

$$(\frac{\Omega}{d_1^S}, \frac{M_S}{D_2^S}, 0, 0, 0, 0, 0, 0) = (S_1, S_2, E_1, E_2, I_1, I_2, R_1, R_2)$$

The Jacobian matrix with the equilibrium values would yield:

$$\det\begin{bmatrix} -\varepsilon_1 - d_1^E - \lambda & 0 & \frac{\Omega}{d_1^S}\beta_{S_1I_1} & \frac{\Omega}{d_1^S}\beta_{S_1I_2} \\ 0 & -\varepsilon_2 - d_2^E - \lambda & \frac{M_S}{D_2^S}\beta_{S_2I_1} & \frac{M_S}{D_2^S}\beta_{S_2I_2} \\ \varepsilon_1 & 0 & -\gamma_1 - d_1^I - \lambda & 0 \\ 0 & \varepsilon_2 & 0 & -\gamma_2 - d_2^I - \lambda \end{bmatrix}$$

Endemic equilibrium

Another technique used to uncover R_0 is by method of endemic equilibrium. The first step is to determine the endemic equilibrium values for the infected population variables, namely, I_1 and I_2. The differential equations presented previously are all set equal to zero, since the system is in equilibrium, and all variables are solved for in terms of constants.

Secondly, the R_0 technique follows after the assertion that if I_j (each infected population) variables are positive at the endemic equilibrium, then the disease persists.

$$\bar{I}_j > 0$$

Suppose in a simpler case, that an endemic equilibrium value is found for the infected population variable:

$$\bar{I}_j = A - B$$

$$A - B > 0$$

$$A > B$$

$$\frac{A}{B} > 1$$

$$R_0 = \frac{A}{B} > 1$$

Note that by similar deduction, we come to the conclusion that:

$$\overline{I_j} < 0 \Rightarrow R_0 < 1$$

This is a very useful result since the model studied in this research yielded the following endemic equilibrium values for I_1 and I_2.

$$I_1 = \frac{\Omega\varepsilon_1}{\left(\varepsilon_1 + d_1^E\right)\left(\gamma_1 + d_1^I\right)}$$

(Note that I_1 can be inserted in the next equation by substitution)

$$(I_2)^2\left[(\beta_{S,I_2})(\gamma_2 + d_2^I + \frac{d_2^E\gamma_2}{\varepsilon_2} + \frac{d_2^E d_2^I}{\varepsilon_2})\right] + (I_2)\left[\left(\beta_{S,I_2}\right)\left(-M_S - M_I + \frac{M_1 d_2^E}{\varepsilon_2} - M_E + \frac{I_1 d_2^E\gamma_2}{\varepsilon_2}\right) + \left(\beta_{S,I_1} I_1\right)\left(\gamma_2 + d_2^I + \frac{d_2^E d_2^I}{\varepsilon_2}\right) + \left(d_2^S\right)\left(\gamma_2 + d_2^E + \frac{d_2^E\gamma_2}{\varepsilon_2} + \frac{d_2^E d_2^I}{\varepsilon_2}\right)\right] + \left[\left(\beta_{S,I_1} I_1\right)\left(-M_S - M_I + \frac{M_I d_2^E}{\varepsilon_2} - M_E\right) + \left(d_2^S\right)\left(-M_I - \frac{M_I d_2^E}{\varepsilon_2} - M_E\right)\right] = 0$$

The complexity of the second equations makes it very difficult to isolate I_2. Hence, to simplify the analysis of R_0, we can keep the two endemic equilibrium functions and use them to determine if the disease will persist or die out without actually calculating R_0. From now on in, the determination of the endemic equilibrium values will be referred to as the R_0 test.

Since I_2 is a quadratic polynomial and will necessitate the calculation of a square root, we only need to consider the biggest root. Namely for: $a (I_2)^2 + b (I_2) + c = 0$

$$I_2 = \frac{-b + \sqrt{b^2 - 4ac}}{2a}$$

Hence for the R_0 test, if $I_1 > 0$ or $I_2 > 0$ then the disease persists, or if $I_1 < 0$ and $I_2 < 0$ the disease will die out. It can be noted that this is equivalent to saying that if the biggest endemic infected variable is negative at the equilibrium (i.e. $\max\{ I_1 , I_2 \} < 0$), then the disease dies out, otherwise it will spread.

An immediate observation can be made regarding I_1. Since all parameters are positive, as seen previously, I_1 will always be positive. The result will be that the disease will propagate no matter what values are given. The upcoming graphs for the model simulations will support this conclusion.

Another useful result derived from R_0 test is its ability to predict the behavior of the model. When analyzing the model, it can be seen that changing parameters that will increase the I_1 and I_2 values will enhance the spread of the infection and accelerate the devastation of the susceptible native population.

3. Calibrating the model

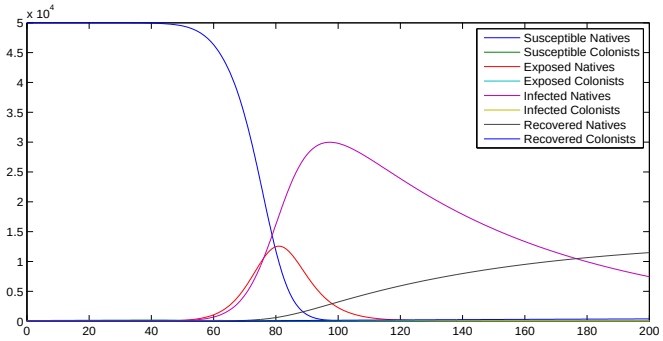
In order to carry out simulations in MATLAB, parameters of the model were given values. Historically documented parameters were used as much as possible and realistic values were estimated, where necessary. A Native population size of 50000 was selected, and we calculated the current world average birth rate. Death rate was chosen to ensure population renewal in the absence of disease. We decided Colonists would arrive in a small group of 100, and varied the number of infected among the 100. In the event of contact with an infected individual, one has a ½ chance of becoming infected. Furthermore, those infected have a ¼ chance of dying from the disease. The exposed state lasts 7-12 days, and the full course of disease lasts one month. Estimates were converted to daily rates for simulations (see Appendix 1: MATLAB script).

Results

R_0 test and model behaviors

Figure 2 models the disease with the parameters that were introduced previously. The R_0 test yielded the following endemic values: $I_2 = 7.07\ (10^7)$ and $I_1 = 333.1$

Figure 2



It is important to note that the following models held all parameters constant except for the ones that were tested. Hence to have an accurate understanding of parameter effects, the results must be compared to those of the first model above and not with each other.

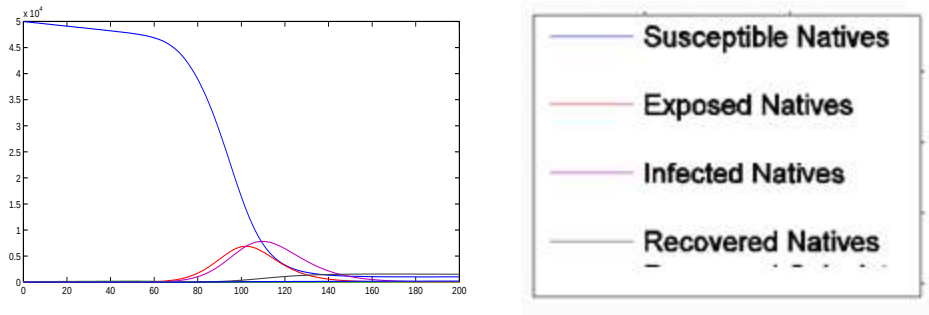
1) Parameter Changes: Death rates of the infected and exposed multiplied by 10

The first test was to increase the death rates of the exposed and infected populations. This had proven to reduce the amount of infected and exposed individuals at the equilibrium. Intuitively, this makes sense since if the exposed and infected populations die faster; they're not able to spread the

disease for as long of a period thus slowing down the spread of the disease. The susceptible native population depicted in *figure 3* clearly shows relative stability for a longer period before the disease spread takes over. Although the disease spread is slower at earlier stages in this simulation, the end result is devastating since it can be seen that almost no natives are able to recover from the disease. The R_0 test values were weaker in this case hence coinciding with the fact that the disease spread was weaker even though the disease killed faster.

R_0 test values: $I_2 = 9.06\ (10^6)$ and $I_1 = 47.3$

Figure 3

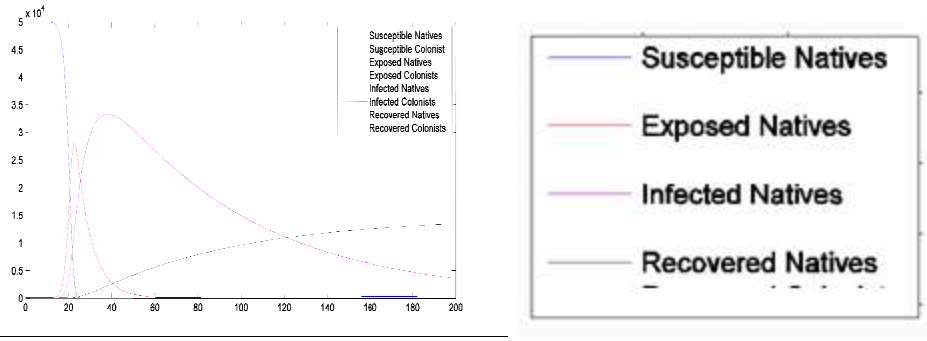


2) Parameter Changes: Transmissibility increased/reduced tenfold

The increase in the transmissibility (by a factor of 10 in the parameters) showed to be the deadliest parameter change since it yielded the strongest I_2 value. *Figure 4a)* coincided with this finding since it showed the fastest decent in susceptible native population and the quickest increase in exposed and infected natives out of all simulations.

R_0 test values: $I_2 = 8.23\ (10^8)$ and $I_1 = 333.1$

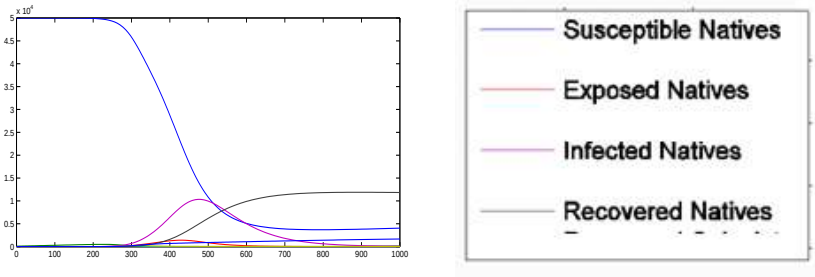
Figure 4a



However, the inverse changes (i.e. the reduction of transmissibility by a factor of 10), showed to greatly reduce the speed of the spread of the disease. *Figure 4b)* depicts a shrunken population of exposed and infected individuals. Note that this parameter change yielded the weakest I_2 value of all R_0 parameter tests.

R_0 test values: $I_2 = 4.32\ (10^6)$ and $I_1 = 333.1$

Figure 4b

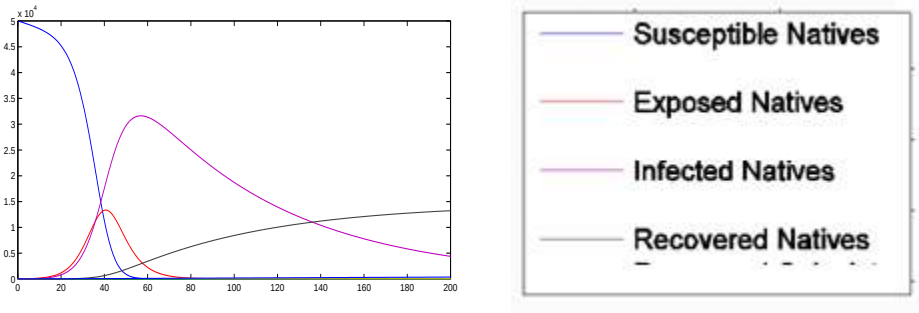


3) Parameter Changes: Immigration of Europeans increased tenfold

Another test performed was one on the effects of the increase in immigration of Europeans. At the beginning, the increased immigration model shown in *figure 5* behaved very similarly to the model of *figure 2*. However, the disease was seen to start spreading sooner in this simulation. At later time values, the difference between the two models was negligible and behaved very similarly. The intuition of the results is sound due to the fact that a faster immigration rate of sick Europeans would mean that the disease would start spreading faster.

R_0 test values: $I_2 = 2.77\ (10^8)$ and $I_1 = 333.1$

Figure 5

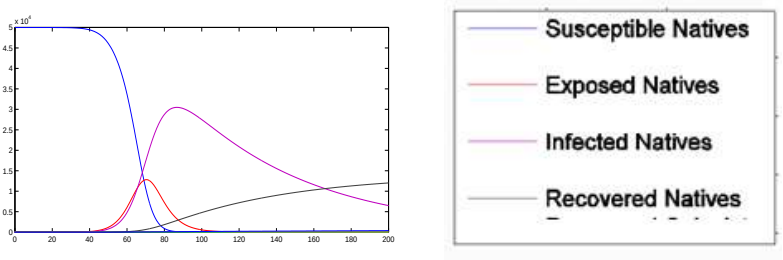


4) Parameter Changes:

The increase in initial European populations had the effect of accelerating the process of the first model. The endemic equilibrium values for the R_0 test are the same as the original model, but *figure 6* shows that the disease spread and fall of susceptible natives happened sooner.

R_0 test values: $I_2 = 7.07\ (10^7)$ and $I_1 = 333.1$

Figure 6



Note that figures 2, 5 and 6 all have models that behave very similarly. This is also analogous to the similarity in values of the R_0 test. The main differences are the times at which the disease spread starts.

Discussion

In this paper, we modeled the American smallpox epidemic which followed the arrival of the Europeans. We focused on a small Native American population of 50,000 (a little smaller than the island of Hispanola) after the arrival of 100 Europeans. Congruent with historical accounts, simulations based on our model clearly led to Native populations being decimated. The model and simulations showed that smallpox was so infectious and deadly that it could easily result in the death up to ⅔ of individuals in a small population within 3 months.

The most notable aspect of this model is the subdivision of our population, which is crucial to the realistic modeling of smallpox spread from Colonists to Natives. Indeed, we chose a population of 50,000 Natives into which a small number of Colonists (100) arrive. Very few immigrants are infected, yet disease rapidly spreads through the Native population. The population subdivision allows us to account for different rates of contact dynamics between and within groups. Indeed, transmission rates β_{Sili} depend on numbers of susceptible and infected individuals but also on rates of contact between them and risk of transmission. Our model allows for higher contact within groups than between them, and higher rates of transmission to Natives than to Colonists (as we know that many Colonists had some resistance). Although they were highly infectious, transmission rates from Colonists to Natives were low because they did not come into close contact regularly. Native to Native transmission rates on the other hand were very high, both because of increased viral shedding and because of high rates of contact between them. Spread of disease within Natives was exacerbated by behaviours such as sleeping and eating together.

Our simulations generated results consistent with historical accounts, 2/3 of our small Native population died within 200 days (approx 6 months). Simulations emphasized the fact that the contagiousness and amount of contact, or in other words the transmissibility of the disease, was the most detrimental factor. It can also be noted that an increase death rate of those infected, or the decrease of transmissibility would yield the best outcome by only delaying or softening the inevitable pandemic. Depending on how much the transmissibility parameters were changed prior to simulations, the outbreaks could have been deferred by a few months.

The immigration rate and the initial population of Europeans had negligible effects on the outcomes of the simulations. The only thing that can be concluded is that the introduction of fewer infectious Europeans in a susceptible village could have potentially bought a few extra weeks before the disease would manifest itself.

Our model nevertheless has several important limitations. Firstly, it is limited in time and space to allow for the mass-action laws to stand. Because of the huge size of the continent, human dispersal, and therefore time it would take colonists to reach different areas, we decided to model an outbreak in a small population after arrival of 100 Europeans. The situation is more akin to the arrival of the first explorers than to the decades of immigration which caused a series of smallpox outbreaks across the continent. Our model could not take into account the gradual increase in immigration rate from the Old World to the New World. The introduction of an increase in immigration rate by a polynomial rate of immigration would have been complex, but it is certain that it would have made things worse for the natives who already had no chance of fighting off the disease with so few Europeans. Furthermore, the model does not take into account birth rates among the Europeans, nor does it allow for reproductive mixing between the populations – which is known to have happened. The model also does not into take account the contribution of the slave trade to smallpox transmission.

Another limitation of the model is that it cannot significantly take into account other processes which lead to the death of Natives: other diseases, as well as deliberate extermination. The literature is full of accounts, for example, of characteristics that exacerbated the epidemic among the Natives. The Native way of life was a very harsh one especially for the ones that lived as nomads. This meant that they survived mainly on hunting and foraging. The men were the hunters and gatherers, and as such, tribes could face starvation if they became ill. Another important notion that differentiated the Natives from the colonists is how they handled their sick; the ill were sometimes left with no one to care for them, and in some cases, abandoned and left to die. It is also recorded that the men, when sick, would not stop to rest and continue running, swimming, and hunting until they fell dead. This meant that their immune system had no time to recover and get stronger which is one of the reasons why it is recorded that the smallpox epidemic in North America affected mostly men. The psychological consequences of smallpox are also noted in the literature. Smallpox often raced ahead of the Conquistadores and even killed major leaders, destroying Native spirit.

Finally, we were not able to incorporate inoculation into our model. Inoculation consists in taking scabs from infected individuals, grating them up, and rubbing them into a cut of a smallpox naïve individual. Patients infected through this route do not display such severe symptoms as those infected through inhalation. Infection manifests itself externally and does not affect internal organs. This method saved many lives in Africa and China but somehow seems to have arrived too late in the Americas (especially North America). Although this method still killed up to 10% of patients, it contributed to the eradication of the disease until the vaccine finally eradicated smallpox. The racism that split the Natives and the colonists seems to have gone as far as not only withstanding the knowledge of inoculation but also the spreading of smallpox as a biological weapon which we did not include in our model. What if some colonists had really wanted to spread smallpox to kill off the Natives and take their land? The deliberate inception of disease would have been an interesting effect to model in our simulations. It is documented

that General Armherst used blankets to deliberately transmit smallpox. This is only one recorded event but it is likely that there were other such incidents due to the ease of the spread of infection amongst Natives.

Finally, we were limited in the historical data we were able to obtain. These epidemics happened a long time ago and sources are too few to give an exact picture of the situation. Many of these deaths might have been due to famine (for example if the male hunter is infected by smallpox and unable to hunt then the family has no food) and other diseases which the Natives population had no immunity to. The wars also devastated the population, and combined with these deadly diseases, had a destructive effect on the morale of the Natives.

However, we did reach the conclusion that the disease would spread by inserting one infected native or colonist in a clean population of one village. This means that although we cannot analyse with certitude the time it took for smallpox to ravage the Native population we can see with confidence how damaging it was with the mathematical model. In this paper, we have laid the foundations for a more complete modeling of the spread of smallpox from colonists to Native Americans. A better model might be able to shed some light on this important period of history and possible resolve long-standing controversies on the extent of the devastation caused to Native American populations.

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APPENDIX 1: MATLAB SCRIPT

```
function pdot = smallpox(t,p)
G=5;
MS=2;
ME=0;
MI=0.001;


Bs1i1=0.00001;
Bs2i2=0.00001;
Bs1i2=0.0001;
Bs2i1=0.001;

e=0.14;
s=0.07;

d1s=0.0001;
d2s=0.0001;
d1e=0.0001;
d2e=0.0001;
d2i=0.0025;
d1i=0.01;
d1r=0.0001;
d2r=0.0001;

g1=0.005;
g2=0.03;

S1=p(1);
S2=p(2);
E1=p(3);
E2=p(4);
I1=p(5);
I2=p(6);
R1=p(7);
R2=p(8);

pdot(1,:)= G - Bs1i1.*S1.*I1- Bs1i2*S1.*I2- S1.*d1s;
pdot(2,:)=MS-S2.*I2.*Bs2i2-S2.*I1.*Bs2i1-S2.*d2s;
pdot(3,:)=S1.*I1.*Bs1i1+S1.*I2.*Bs2i2-E1.*e-E1.*d1e;
pdot(4,:)=ME+S2.*I2.*Bs2i2+S2.*I1.*Bs2i1-E2.*s-E2.*d2e;
pdot(5,:)=E1.*e-I1.*g1-I1.*d1i;
pdot(6,:)=MI+E2.*s-I2.*g2-I2.*d2i;
pdot(7,:)=I1.*g1-R1.*d1r;
pdot(8,:)=I2.*g2-R2.*d2r;


end
```