



Zika Virus Spreads

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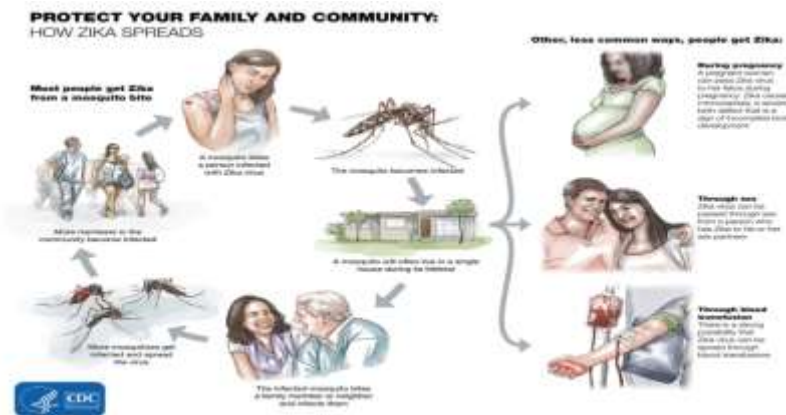
ABSTRACT

The Zika virus, a mosquito-borne pathogen, emerged as a significant global health concern in recent years. This abstract explores the factors contributing to the spread of the Zika virus and its potential implications for public health. The transmission dynamics of the virus involve the *Aedes* species of mosquitoes, primarily *Aedes aegypti* and *Aedes albopictus*, which have a wide geographical distribution. Human mobility and climate conditions play vital roles in the spread of the virus to new regions, making it essential to understand the patterns of dissemination. Additionally, vertical transmission from infected mothers to their fetuses raises concerns about congenital Zika syndrome and related birth defects. This abstract also delves into the challenges faced in controlling the spread of the virus, such as limited diagnostic tools, vaccine development, and the need for effective mosquito control strategies. Enhanced surveillance, public awareness, and international collaboration are crucial in mitigating the impact of Zika virus outbreaks. By examining the factors influencing its spread, this abstract seeks to foster a deeper understanding of the Zika virus and facilitate more proactive and comprehensive approaches to disease control and prevention.

Key Word: Life Cycle, Zika, SIR model, Vensim

Introduction

Zika is a virus transmitted to humans primarily through contact with infected mosquitoes. Although Zika has not been associated with death, infections may become symptomatic and have symptoms such as rash, fever, muscle and joint pain, or headaches for 3-7 days. CDC provides a diagram that shows the spread of ZIKA virus.



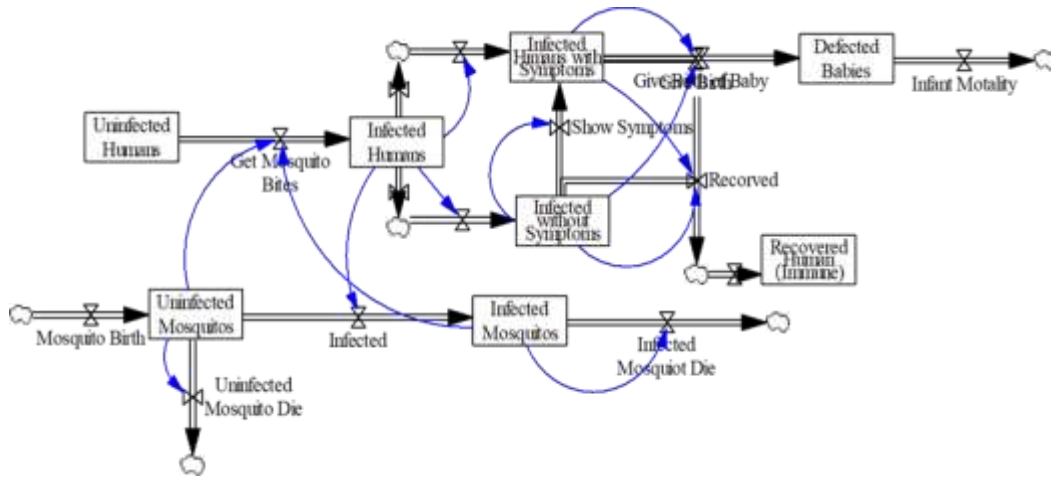
The Zika virus can cause major birth defects and other problems in pregnant women. Also, Zika greatly increases the mortality rate of infants born with zika related defects. The Zika virus transmission model includes two major parts: human and mosquito sub-models. During this research we first created two sub-models: human host sub-model Model and mosquitos host sub-model. Finally, we combined these two sub-models into one Zika transmission model.

Although the Zika virus was discovered in 1947, its first human case was not detected and documented until 1952. Zika can be spread through several means, however, the main transmission is from infected *Aedes* species mosquitoes. The virus can also spread through sex with an infected person, childbirth, or through blood transfusion. Unlike other viruses there is no vaccine or specific treatment for the zika virus. The best way to prevent the spread of Zika virus transmission is to protect oneself from exposure to mosquito bites. In addition, because zika can be spread sexually, using condoms and abstinence can be other means of preventing Zika transmission. Zika is diagnosed through a blood or urine test. Even though people may develop symptoms from Zika, most people do not get very sick, and death is rare. Most infections also tend to develop some type of immunity against future infections. The largest health risks concerning the Zika virus involve pregnant women and infants affected by the virus. Zika has been linked to major

birth defects in women such as microcephaly, Guillian-Barre syndrome, and other major birth defects. Congenital Zika Syndrome is a pattern of defects and disabilities associated with Zika recognized by the CDC. Developing a Zika Transmission model will help us study how Zika affects the health of affected populations specifically pregnant women and infected newborns. This is important for understanding the full spectrum of the health issues presented by the spread of the Zika virus in human populations.

Initial Diagram for Zika Model

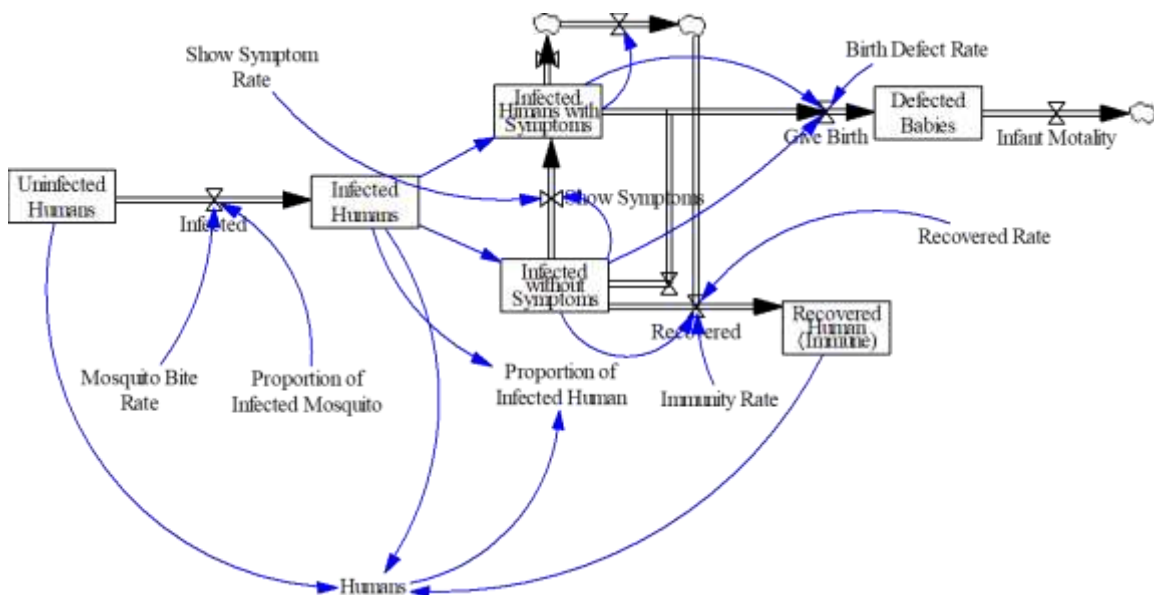
Since life expectancy of human is much longer than mosquito's, we ignored the new birth of human. However, the new birth of mosquitos is significant and cannot be ignored. We use Vensim PLE to create our diagrams.



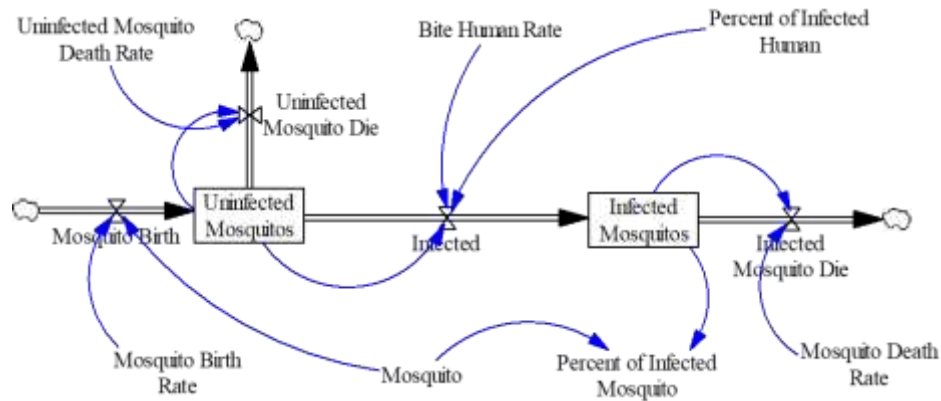
The life cycle of the Zika virus is more complex than a simple SIR model as the virus serves hosts to two species. In the creation of our model, we break down the interaction between mosquitoes and humans. The virus is transmitted from infected host to uninfected host, regardless of species. Thus all species serve as vectors for the virus. Infected mosquito carries the disease from one human to another (acting as a “vector”), while infected humans transmit the virus to uninfected mosquitos, however in contrast to the human host, the mosquito vector does not suffer from the presence of the virus.

We refine our model to a detail Human Sub-Model and a detail Mosquito Sub-Model.

Detail Human Sub-Model

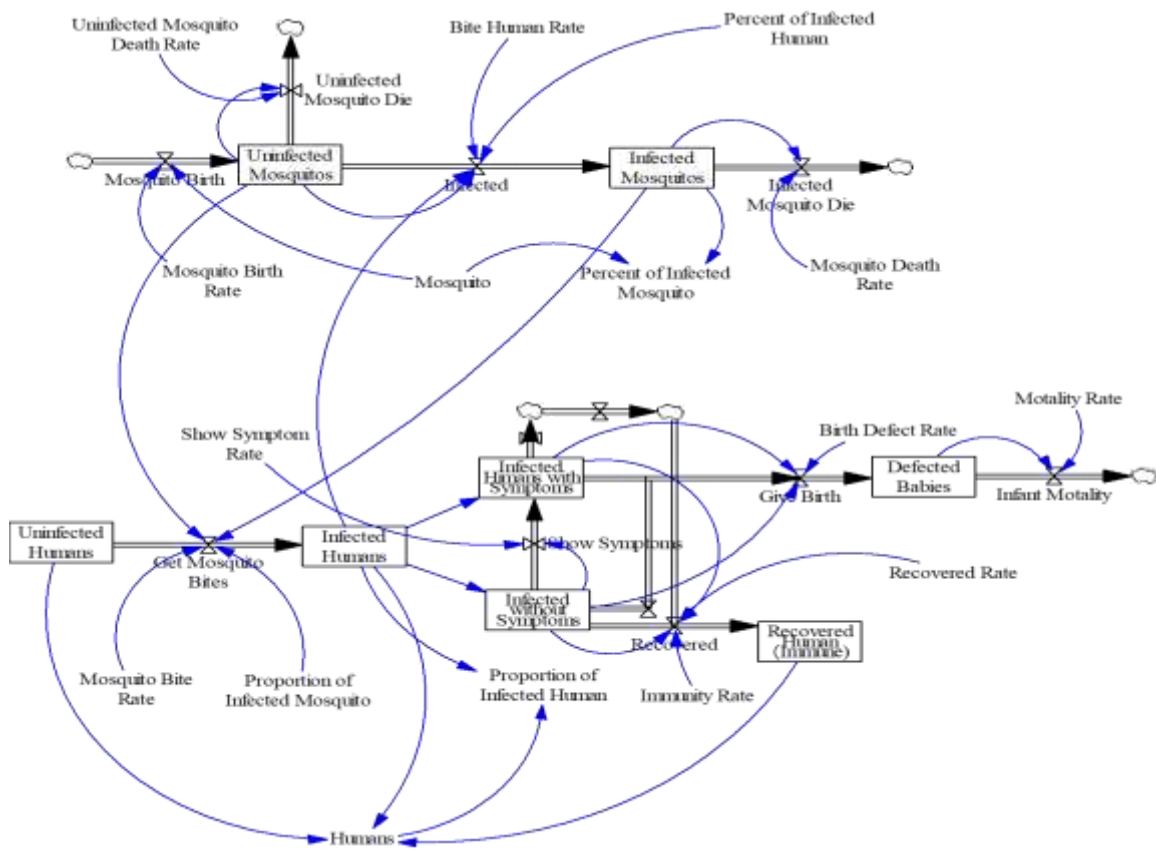


Detail Mosquito Sub-Model



Detail Zika Model

Finally, we combine Human sub-model and Mosquito Sub-Model, we have a Zika Transmission Model



Our main objective is to investigate the transmission. In particular, the relationships between human and *Aedes* mosquito populations. In this research we only concentrate on mathematics of Zika virus lifecycle and the relationships during transmission.

In this research, we need to make some assumptions. As we mentioned before, we ignored the birth of humans since human life expectancy is much longer than that of mosquitos. We also assume there are no immigration, and human death, and the incubation period is short enough to be negligible. The variables of this research are Uninfected Humans, Infected Humans, Recovered Humans, Defected Babies, Uninfected Mosquitos, and Infected Mosquitos. We want to know how Zika spread, and its transmission will affect the zika related birth defects in infants.

Notations we used in this research:

UH: Uninfected Humans, who are susceptible to the virus

IH: Infected Humans, who have zika and spread disease to mosquitos.

RH: Recovered Humans, who are recovered from zika.

UM: Uninfected Mosquito

IM: Infected mosquitos that carry zika virus.

mbr: Mosquito bite rate

rr: Recovery rate

bdr: Birth defect rate

br: Mosquito birth rate

dr: Mosquito death rate

ihp: Infected human percentage: percentage of infected humans

imp: Infected mosquito percentage: percentage of infected mosquitoes

inf: infant mortality rate

Each variable within the research can be written using differential equations in respect to time.

The change in Uninfected Humans can be expressed as

$$\frac{dUH}{dt} = -mbr * imp * IM$$

The change in Infected Humans can be expressed as

$$\frac{dIH}{dt} = mbr * imp * IM - rr * IH$$

The change in Recovered People can be expressed as

$$\frac{dR}{dt} = rr * IH$$

The change in Defected Babies can be expressed as

$$\frac{dDB}{dt} = bdr * IH - inf * DB$$

The change in Uninfected Mosquitos can be expressed as

$$\frac{dUM}{dt} = br * (UM + IM) - UM * mbr * ihp * IH - UM * dr$$

The change in Infected Mosquitoes can be expressed as

$$\frac{dIM}{dt} = UM * mbr * ihp * IH - dr * IM$$

Rewriting the equations using the difference equation for approximating differential equations for use in excel produces

$$UH(t + \Delta t) = UH(t) + \Delta t * (-mbr * imp * IM)$$

$$IH(t + \Delta t) = IH(t) + \Delta t * (mbr * imp * IM - rr * IH)$$

$$R(t + \Delta t) = R(t) + \Delta t * (rr * IH)$$

$$DB(t + \Delta t) = DB(t) + \Delta t * (bdr * IH - inf * DB)$$

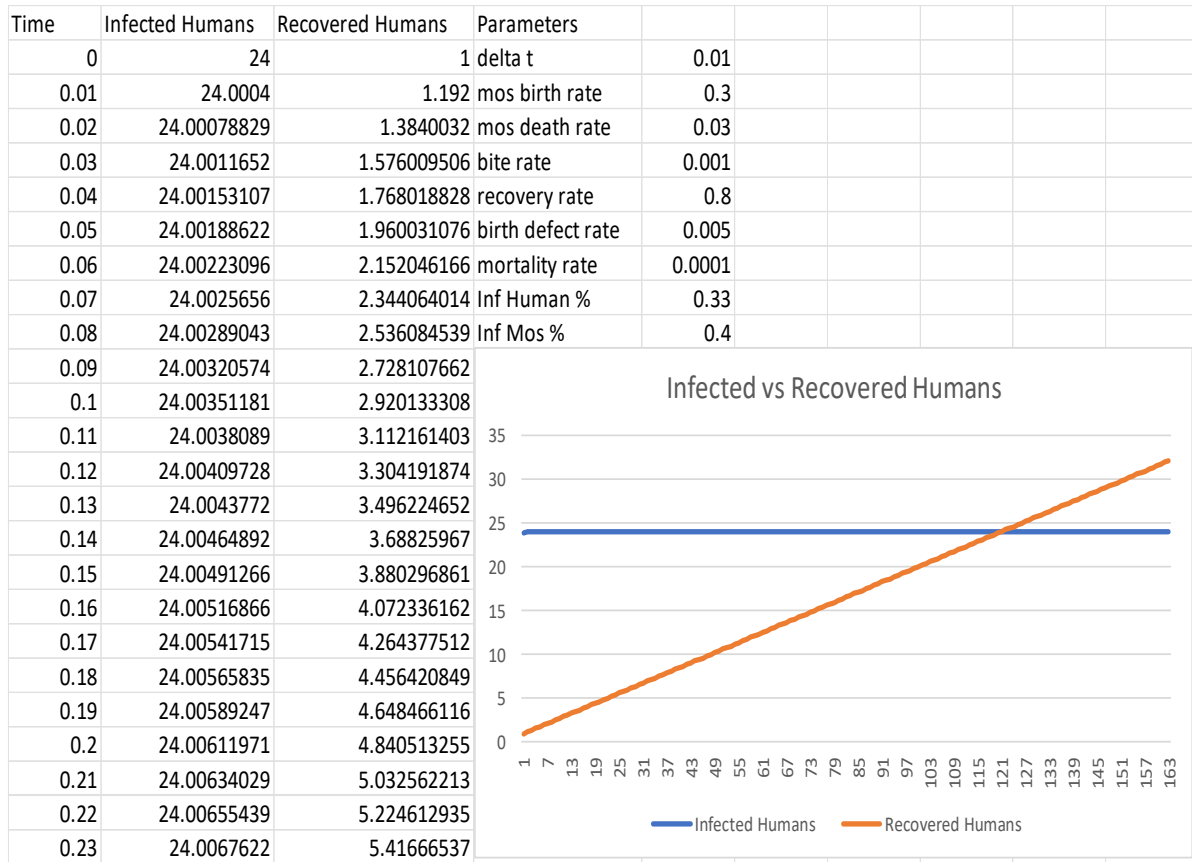
$$UM(t + \Delta t) = UM(t) + \Delta t * (br * (UM + IM) - UM * mbr * ihp * IH - UM * dr)$$

$$IM(t + \Delta t) = IM(t) + \Delta t * (UM * mbr * ihp * IH - dr * IM)$$

Results

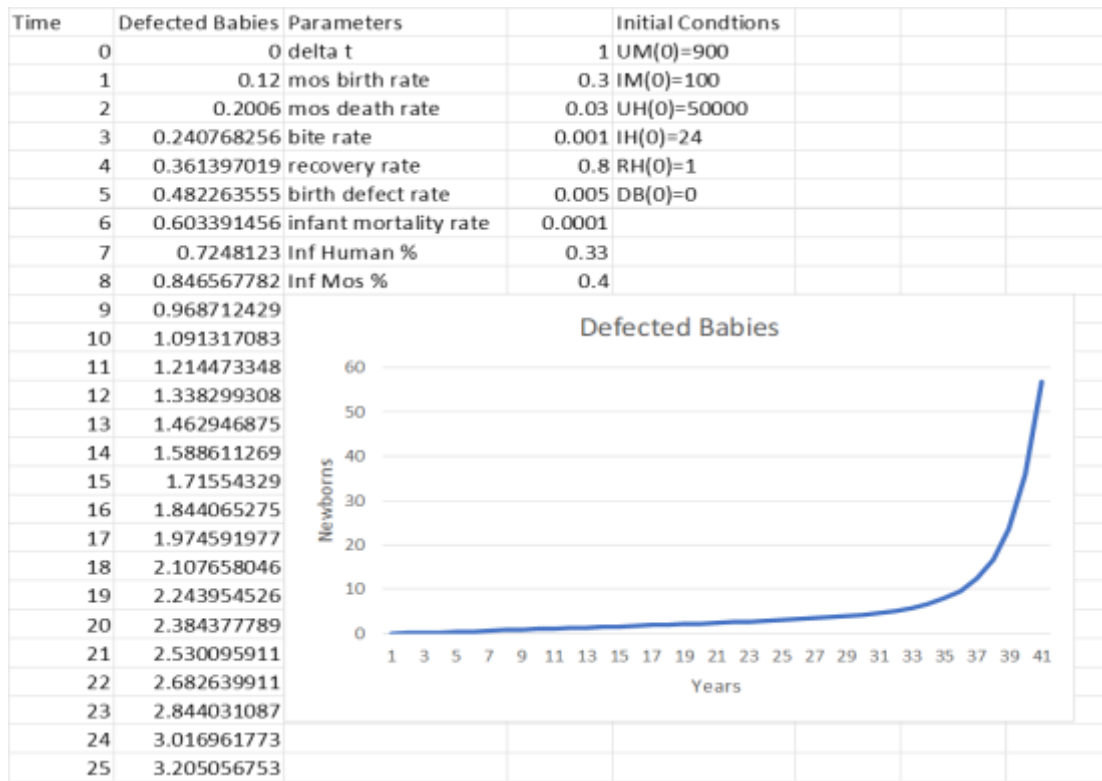
In creating this model, we specifically seek to follow transmission spread to track birth defects in pregnant women. In doing so, we specifically seek the spread of transmission from the mosquito to human transmission. However, there are other ways uninfected humans can contract zika. In many cases, Zika patients are asymptomatic. According to study by the Wuhan Institute of Virology, between sixty and eighty percent of Zika patients are asymptomatic. (Wang) When analyzing the graphs, the infected population does not seem to ever decrease or increase drastically. This can possibly be accredited to the true unknown number of individuals who have zika at one time. The issue with these untracked cases is the true danger in Zika virus

transmission. To further understand the threat of undocumented zika cases, we compared our infected and recovered populations to see their relationship. Further investigation showed that although humans recover from zika, infections may remain the same in the right conditions. This could be caused by undocumented cases of zika; however, these individuals may be asymptomatic and never pose a threat to humans but still carry the zika virus.

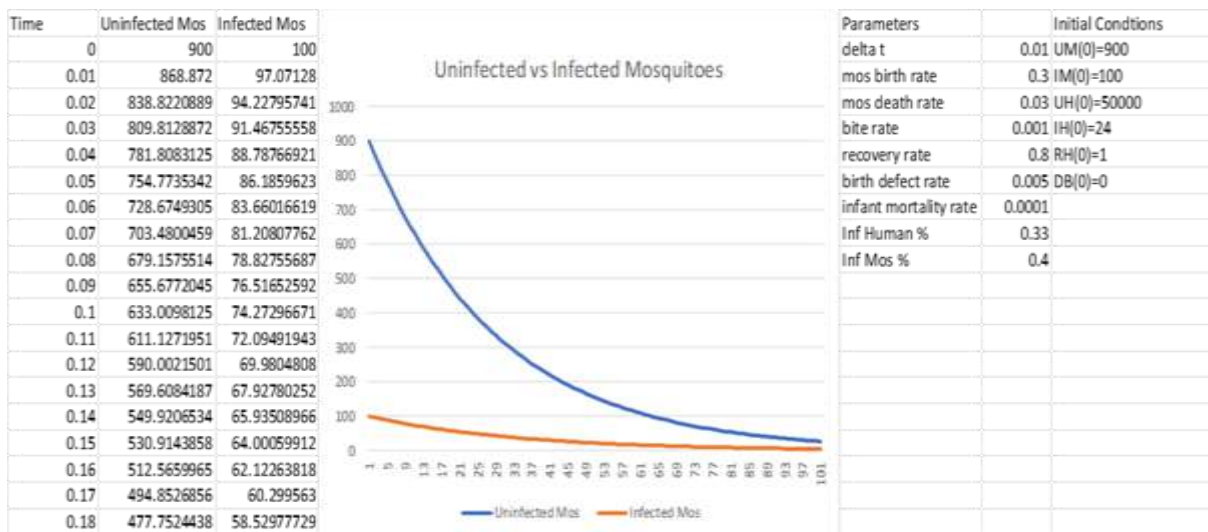


With an increased number of undocumented Zika infections, the likelihood and frequency of zika- related birth defects could increase. Research has shown that Zika has been fatal in rare infant cases. Therefore, the more undocumented zika infections raise the potential for humans to conceive children that are at high risk for zika related- birth defects or even infant mortality due to zika- related infection. We used the model that we created to predict how zika infections would affect the number of defected babies over time.

In this observation we changed our step interval to mimic a longer time period. We wanted to see the how undocumented zika cases in humans could affect the number of infants with birth defects. Unchecked, Zika virus has the potential to become a serious issue. Zika has escaped the radar of being a serious health issue due to lack of serious human infection. While humans simply recover from zika over time, undocumented infections could exponentially increase in zika-related birth defects over time.



Our simulation shows that although initially defected babies are nearly nonexistent, over time the increase of defected babies could have some exponential increase due to zika infections in humans. There are several simple solutions that can be attempted to reduce Zika infections to combat related birth defects. These solutions all vary due to the nature of our zika transmission model. The model we have created for Zika is a multi-host model with both humans and mosquitoes acting for vectors. More developed Zika models attribute for even more hosts. Mosquitoes can transmit the Zika virus to other species such as monkeys, orangutans, zebra, elephants, rodents, etc. (Wang) A model with more variables could produce significant more zika transmission throughout a given community. In other models, weather can significantly change the spread of transmission. The seasonal effects that weather can bring to regions can affect a variety of variables. For instance, in both North and South America, the presence of the Aedes mosquito along with favorable weather patterns have helped provide seasons where zika can transmit more through communities. (Wang) This can be attributed to several factors such as mosquito births, travel, lack of testing and many more factors. In our given model, the relationships between all mosquitoes, both uninfected and infected are heavily based upon human interaction. Given a model with different variables that affects species environment or increase hosts/ vectors could drastically change the transmission of zika in community.



In the future, there are several steps that should be taken to fight the Zika epidemic. Zika has been around for more than 70 years; however, it was not deemed to be an alarming threat to global health until recent years. (Wang) The World Health Organization d. More research needs to be done to document and better understand the true nature of the virology of Zika. This research can be done to help us better develop treatments and possible vaccines for the Zika virus, Vaccines could prove to be an effective tool for combating Zika infections due to the large amount of people who are deemed asymptomatic with Zika infection. In reducing the number of people who are infected with Zika, asymptomatic or symptomatic, we can immediately decrease the number of not only Zika related birth defects but also deaths in infants due to Zika. This common practice has been used for centuries to reduce initial infection and the spread of infections in communities. Previous research done on prior coronaviruses allowed for a swift vaccine to be created in the situation of the Covid-19 pandemic. The creation of those vaccines did not stop the spread of Covid-19 but was effective in controlling the pandemic. The same concept can be used to help control and understand Zika virus transmission before it evolves into a major global health issue.

Conclusion

There are a few major global health issues that have occurred in the last 25 years that have shaped world history. As humans evolve, so do viruses. If humans take heed to the potential global health issues before they become serious, we can use dynamic computer modeling to be proactive in finding cures and treatment for infectious diseases. There are a host of ways to attack an infectious disease model. We can use these and many other tools of dynamic computer modeling to help create treatments and vaccines that are effective in combatting infectious diseases.

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