

A Modified Model of Zika Virus Spread with Saturated Incidence Rate: Modelling and Stability Analysis

by Universitas Internasional Semen Indonesia

Submission date: 17-Mar-2022 08:22PM (UTC-0500)

Submission ID: 1786752257

File name: SSRN-id3813831.pdf (1.34M)

Word count: 2958

Character count: 15665

A Modified Model of Zika Virus Spread with Saturated Incidence Rate: Modelling and Stability Analysis

PUJI ANDAYANI*, LISA RISFANA SARI

Department of Informatics, Universitas Internasional Semen Indonesia

Abstract: *In this paper, we studied the population behaviour in the Zika virus spread system. Several authors have discussed the mathematical model of the spread of the Zika virus. This paper will modify the transmission pattern that is inhibited by the presence of educational factors for vulnerable populations to inhibited the transmission rate. The model consists of five nonlinear differential equations and it is reduced to three nonlinear equations. Then we analyzed the equilibrium points and reproduction number, to describe the stability of the system. Analytically, the disease-free equilibrium it can be ascertained that the mortality indicates that the disease-free balance is locally asymptotically stable when the reproduction number is less than one. Otherwise, the endemic equilibrium point is locally asymptotically stable. Numerical analysis is also performed to show the equilibrium behaviour of the system on certain parameters. The first section in your paper.*

Keywords : *Zika Virus, Endemic, Incidence Rate*

1. Introduction

Zika is a type of vector-borne disease caused by a type of mosquito, namely *Aedes Aegypti* (Andayani, Dynamical Analysis for A Simple Model of Zika Virus Transmission, 2019) . On February 1, 2016, Zika was declared an international emergency problem by WHO, because the worst thing happened to many pregnant women who gave birth with microcephaly (Perkins, Siraj, Ruktanonchai, Kraemer, & Tatem, 2019). Andayani (Andayani, Azmi, & Sari, Comparing Vector-host and SEIR models for Zika Virus Transmission, 2018) has studied a simple borne vector model that applies the Zika virus problem. The model made is a simple model with 5 non-linear equations and a bilinear transmission rate. The conditions that make it disease-free have been acquired, so are the endemic conditions.

Indonesian researchers feel the need to study the pattern of Zika virus spread because the mosquitoes that cause Zika also live in Indonesia. Zika virus infection is almost similar to the dengue virus, so the presence of this infection is often not detected. The Indonesian people are still wary of the possibility of contracting the

Corresponding author : puji.andayani@uisi.ac.id

Zika virus, given reports that this infection has been found in Indonesia and a carrier vector exists in Indonesia, namely the *Aedes Aegypti* mosquito which also carries dengue fever and Chikungunya. In 2015, the Eijkman Jakarta Institute (Aminah, 2016) succeeded in isolating the Zika virus in Indonesia. In fact, from the survey results, it turned out that in 1981 Australian researchers had reported a Zika virus patient after traveling to Indonesia. This is very dangerous if the virus attacks again in Indonesia. If it attacks pregnant women, it can cause hydrocephaly, which is the size of the baby's head smaller than normal. On January 15, 2016, the US government through the US Centers for Disease Control and Prevention 1 (Services, 2017) (Agusto, Bewick, & Fagan, 2017) provided travel warnings for residents who were pregnant or planning to become pregnant to postpone travel to countries infected with the Zika virus. In urban areas, the presence of mosquito transmission causes the Zika virus epidemic. After being traced, the Zika virus is not only caused by mosquitoes but can also be caused by sexual transmission. The persistence of virus in testes and semen has been described and the window of sexual transmission remains unclear, which raises concerns about Zika infection during pregnancy (Suryanto, 2011) (Andayani, Dynamical Analysis for A Simple Model of Zika Virus Transmission, 2019) (Molles, 2002).

The mathematical model of Zika virus transmission has been studied in previous studies, assuming closed individual interactions, the spread of the virus through sexual intercourse, blood transfusion, and laboratory exposure. The occurrence rate in the model is bilinear. When an individual's grief is very high, the number of occurrences may also be high. So that the bilinear rate is not quite right. The psychological effect of the alert individual after seeing other infected individuals is an inhibiting factor. In this research, it will be developed by changing the incidence rate of bilinear to be saturated (Xiao & Ruan, 2007). In his second study, Andayani (Andayani, Azmi, & Sari, Comparing Vector-host and SEIR models for Zika Virus Transmission, 2018) compared the pattern of Zika virus spread in the conditions where the mosquito grows in the area with the conditions when humans become infected due to traveling. This study discusses the conditions

where the disease spreads in the area where the mosquito that causes Zika is present.

2. Theoretical Framework and Hypothesis Development

Referring to Andayani (Andayani, Azmi, & Sari, Comparing Vector-host and SEIR models for Zika Virus Transmission, 2018) and Kaddar (Kaddar, 2019), we constructed a model of the Zika virus transmission with a saturated incidence rate which is developed to represent interventions of individual behavior rate in the transmission of the virus. The model represents the following nonlinear in differential equations:

$$\begin{aligned}
 \frac{dS_h}{dt} &= \Lambda_h - \frac{\beta_1 S_h I_h}{1 + \alpha_1 I_h} - \beta_2 S_h I_v - \mu_h S_h, \\
 \frac{dI_h}{dt} &= \frac{\beta_1 S_h I_h}{1 + \alpha_1 I_h} + \beta_2 S_h I_v - \gamma I_h - \mu_h I_h, \\
 \frac{dR_h}{dt} &= \gamma I_h - \mu_h R_h, \\
 \frac{dS_v}{dt} &= \Lambda_v - \beta_3 S_v I_v - \mu_v S_v, \\
 \frac{dI_v}{dt} &= \beta_3 S_v I_v - \mu_v I_v.
 \end{aligned} \tag{1}$$

Where $S_h(t)$, $I_h(t)$, $R_h(t)$, $S_v(t)$, $I_v(t)$ stands for susceptible human, infected human, recovered human, susceptible mosquitoes, and infected mosquitoes respectively. In this study, we assume all of the parameters are positive, where Λ_h denotes the growth rate of a human, Λ_v denotes the growth rate of mosquitoes, β_1 is the rate of direct transmission of the disease, β_2 is the rate of transmission from mosquitoes to human, β_3 is the probability of transmission from human to mosquitoes, γ for the per capita recovery rate of the infective population, μ_h means the death rate of a human, μ_v means the death rate of mosquitoes, respectively. Then, by simplifying the computation, we reduce model (1) become the following equation:

$$\begin{aligned}\frac{dS_h}{dt} &= \Lambda_h - \frac{\beta_1 S_h I_h}{1 + \alpha_1 I_h} - \beta_2 S_h \left(\frac{\Lambda_v}{\mu_v} - S_v \right) - \mu_h S_h, \\ \frac{dI_h}{dt} &= \frac{\beta_1 S_h I_h}{1 + \alpha_1 I_h} + \beta_2 S_h \left(\frac{\Lambda_v}{\mu_v} - S_v \right) - \gamma I_h - \mu_h I_h, \\ \frac{dS_v}{dt} &= \Lambda_v - \beta_3 S_v \left(\frac{\Lambda_v}{\mu_v} - S_v \right) - \mu_v S_v.\end{aligned}\tag{2}$$

Initial conditions of model (2) are

$$S_h(0) \geq 0, \quad I_h(0) \geq 0, \quad S_v(0) \geq 0.\tag{3}$$

Furthermore, the total dynamic of human population is

$$\frac{dN_h}{dt} = \Lambda_h - \mu_h N_h.\tag{4}$$

With given initial condition (3), it is ensure that $N_h(0) \geq 0$. So that, the total population $N_h(t)$ will be positive and bounded for all finite time $t > 0$. The total vector population is

$$\frac{dN_v}{dt} = \Lambda_v - \mu_v N_v.\tag{5}$$

The equilibria of the system (2) are disease free equilibrium (DFE) and endemic equilibrium(END).

2.1. Disease-Free Equilibrium

The DFE is $DFE = \left(\frac{\Lambda_v}{\mu_v}, 0, 0 \right)$, then the dynamics of the system is describe by analyzing the quantity of basic reproduction number R_0 , as follows,

$$R_0 = \frac{\Lambda_h(\beta_2\beta_3\Lambda_v + \beta_1\mu_v^2)}{\mu_h\mu_v^2(\mu_h + \gamma)}.\tag{6}$$

Lemma 3.1. *If $R_0 < 1$, then the disease-free equilibrium (DFE) is locally asymptotically stable, otherwise it is unstable.*

Proof. The local stability of DFE can be verify by linearize the Jacobiam matrix of the system (2) around DFE.

$$J(DFE) = \begin{pmatrix} -\mu_h & -\frac{\beta_1\Lambda_h}{\mu_h} & -\frac{\beta_2\Lambda_v}{\mu_v} \\ 0 & \frac{\beta_1\Lambda_h}{\mu_h} - (\mu_h + \gamma) & \frac{\beta_2\Lambda_v}{\mu_v} \\ 0 & \frac{\beta_3\Lambda_v}{\mu_h} & -\mu_v \end{pmatrix}. \quad (7)$$

The characteristic polynomials of the Jacobian (7) as follows,

$$P(END) = (\lambda + \mu_h)(\lambda^2 + a_1\lambda + a_0), \quad (8)$$

Where,

$$a_1 = \mu_v + (\mu_h + \gamma) - \beta_1 N_h; \quad a_0 = a_1\mu_v - (\mu_v^2 + \beta_2\beta_3 N_h N_v).$$

Three eigenvalues are corresponding to equation (8). An eigenvalue $-\mu_h$ and two other eigenvalues can be obtained by identifying the characteristic polynomials. By the 2 fundamental mathematics computation, if $a_1 > \frac{(\mu_v^2 + \beta_2\beta_3 N_h N_v)}{\mu_v}$ then it is satisfy the condition $a_0 > 0$ and $a_1 > 0$. So that, the polynomial (8) has three negative real parts eigenvalue. Then the DFE is locally asymptotic stable. Then, the polynomial (8) has one real part positive eigenvalue and two complex eigenvalues with zero real part. Then it established the DFE is locally asymptotically stable.

2.2 Endemic Equilibrium

In this section, we consider the stability of endemic equilibrium (END) of model (2). The Endemic equilibrium is $END = (S_h^*, I_h^*, S_v^*)$ with,

$$S_h^* = \frac{\Lambda_h \mu_v (1 + \Lambda_h + \alpha_1 I_h^*) (\mu_v + \beta_3 I_h^*)}{\varphi_2 I_h^{*2} + \varphi_1 I_h^* + \mu_h \mu_v^2}, \quad I_v^* = \frac{\beta_3 \Lambda_v I_h^*}{\mu_v (\mu_v + \beta_3 I_h^*)},$$

$$\varphi_2 = \beta_1 \beta_3 \mu_v + \beta_3 \alpha_1 (\beta_2 \Lambda_v + \mu_h \mu_v); \quad \varphi_1 = \beta_1 \mu_v^2 + \beta_2 \beta_3 \Lambda_v + \mu_h \mu_v (\beta_3 + \alpha_1 \mu_v).$$

If $I_h^* \neq 0$ then substitute S_h^*, I_v^* to the system (1), we have the following polynomials,

$$f(I_h^*) = b_2 I_h^{*2} + b_1 I_h^* + b_0, \quad (10)$$

Where,

$$b_2 = \beta_3 (\mu_h + \gamma) (\beta_3 \Lambda_v + \beta_2 \Lambda_v \alpha_1 + \mu_h \mu_v \alpha_1),$$

$$b_1 = \varphi_1 (\mu_h + \gamma) - \beta_3 \Lambda_h (\beta_2 \alpha_1 \Lambda_v - \beta_1 \gamma),$$

$$b_0 = \mu_h \mu_v^2 (\mu_h + \gamma) - \beta_2 \beta_3 \Lambda_h \Lambda_v - \beta_1 \Lambda_h \mu_v^2.$$

By using elementary calculus theory (Zill & Wright, 2013) (Hirsch, Smale, & Devaney, 2013) it established that polynomial (10) has only one positive root if and only if $\mu_h \mu_v^2 (\mu_h + \gamma) < \beta_2 \beta_3 \Lambda_h \Lambda_v + \beta_1 \Lambda_h \mu_v^2$.

Lemma 4.1. *If $R_0 > 1$, then there only one positive solution of END.*

Proof. Let see equation (10). If $R_0 > 1$, then we have $b_0 < 0$. According to (Hirsch, Smale, & Devaney, 2013), by simple mathematical analysis we can find that $a_1 < \sqrt{a_1^2 - 4a_2 a_0}$. By substituting the previous result to equations (10), it is provided there only one positive solution of END.

Moreover, the local stability of END can be verifu by linearize the Jacobian matrix around END as follow.

$$J(END) = \begin{pmatrix} -\frac{\beta_1 I_h^*}{1 + \alpha_1 I_h^*} - \beta_2 I_v^* - \mu_h & -\frac{\beta_1 S_h^*}{1 + \alpha_1 I_h^*} + \frac{\beta_1 S_h^* I_h^* \alpha_1}{(1 + \alpha_1 I_h^*)^2} & -\beta_2 S_h^* \\ \frac{\beta_1 I_h^*}{1 + \alpha_1 I_h^*} + \beta_2 I_v^* & \frac{\beta_1 S_h^*}{1 + \alpha_1 I_h^*} - \frac{\beta_1 S_h^* I_h^* \alpha_1}{(1 + \alpha_1 I_h^*)^2} - \mu_h - \gamma & \beta_2 S_h^* \\ 0 & \beta_3 \left(\frac{\Lambda_v}{\mu_v} - I_v^* \right) & \beta_3 I_h^* - \mu_v \end{pmatrix}. \quad (11)$$

The characteristic polynomials of the Jacobian (11) is

$$P(\lambda) = \lambda^3 + c_2 \lambda^2 + c_1 \lambda + c_0.$$

Where,

$$c_2 = \frac{1}{\Delta} (\Delta (\beta_3 I_h^* + \mu_v + \gamma + 2\mu_h + \beta_2 I_v^* + \beta_1 I_h^*) - 2\alpha_1 \beta_1 I_h^* - \beta_1 S_h^*),$$

$$c_1 = \frac{1}{\Delta} (\varphi + \varphi_2 (\gamma + \mu_h) \beta_2 I_v^* + \gamma \mu_h + \mu_h^2 - \beta_2 \beta_3 S_h^* N_v)$$

$$+ \sqrt{\Delta} \left((\gamma + \mu_h + \mu_v) \beta_1 I_h^* + \beta_1 \beta_3 I_h^{*2} \right) + (\mu_h \beta_1 (I_h^* - S_h^*) - \beta_2 \beta_3 S_h^* I_h^* - \mu_v \beta_1 S_h^*),$$

$$c_0 = \frac{1}{\Delta} (\mu_h (\Delta (\varphi - \beta_2 \beta_3 S_h^* N_v) + \sqrt{\Delta}) (\mu_v \beta_1 S_h^* + \beta_2 \beta_3 I_h^*) - \mu_v \beta_1 S_h^*) + \Delta (\varphi_1 \gamma) + \sqrt{\Delta} \beta_1 \beta_3 \gamma I_h^{*2} + \mu_v \gamma \beta_1 I_h^*$$

Then we can concern to the following Lemma.

Lemma 4.2. *The END is locally asymptotically stable if only $c_1 > 0$.*

Proof. Let's see polynomial (12). By Calculus the polynomial (12) have three negatives real part eigenvalues are negatives. The condition $\Delta\varphi + \sqrt{\Delta}\beta_1\beta_3I_h^{*2} + \mu_v\beta_1I_h^* > \Delta\beta_2\beta_3S_h^*N_v + \beta_1\beta_3S_h^*I_h^* + \beta_1S_h^*(\mu_h + \gamma)$ is qualify of $c_1 > 0$. In addition, the condition of $c_1 > 0$ is also established that $c_1 > 0$ and $c_1 > 0$, it provided that EN is locally asymptotically stable.

3. Research Method

A mathematical model of the Zika virus has been analyzed in the research of (Andayani, Dynamical Analysis for A Simple Model of Zika Virus Transmission, 2019). Andayani (Andayani, Dynamical Analysis for A Simple Model of Zika Virus Transmission, 2019) developed the model of vector-host to describe human transmission. The infection of that model is expressed by using a bilinear incidence rate. It is assumed the transmission rate is corresponding to the number of the population without reasoning the constraints which occur during the transmission process. The transmissions between population are influenced by many things, one of them is changes in individual behaviour. Considering this, Kaddar (Kaddar, 2019) developed the SIR model with a saturated incidence rate. The mathematical model that has been constructed is analyzed by dynamical analysis, by computing the equilibrium point, and its analysis. In the end, the numerical simulation is also shown to ensure the analytical result.

4. Result and Discussion

In this part, we will discuss the numerical simulation of the model (2). This numerical simulation is presented to clarify the analytical computation. The fourth order RungeKutta method (Kincaid & Cheney, 2002) was used to solve it. Then we consider the following Table 1.

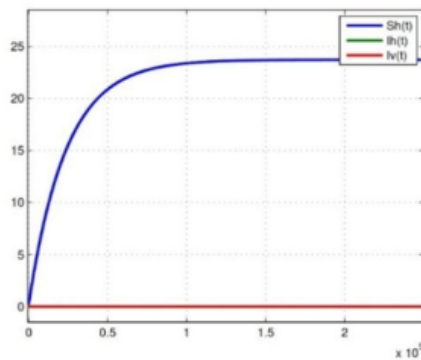
Table 1. The probability of each parameter

Parameter	Probability(value)
-----------	--------------------

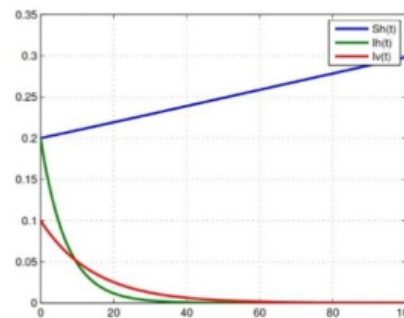
Λ_h	$\mu_h N_h$ (person per - day)
μ_h	$\frac{1}{lifetime} = \frac{1}{65.365} = 0.00004215$ (per - day)
α_1	$0 \leq \alpha_1 \leq 1$ (person per - day)
β_1	$0 \leq \beta_1 \leq 1$ (person per - day)
β_2	$0 \leq \beta_2 \leq 1$ (person per - day)
β_3	$0 \leq \beta_3 \leq 1$ (mosq per - day)
γ	$\gamma = \frac{1}{recoverytime} = \frac{1}{7} = 0.1428$ (per - day)
Λ_v	$\mu_v N_v$ (mosq per - day)
μ_v	$\frac{1}{lifetime} = \frac{1}{14} = 0.0714$ (per - day)

Choose the parameter value $\Lambda_h = 0.001, \Lambda_v = 0.01, \beta_1 = 0.001, \beta_2 = 0.002, \beta_3 = 0.03, \mu_h = 0.00004215, \mu_v = 0.0714, \gamma = 0.1428$.

The Figure 1(a) describe the behaviour of system (2) which satisfy the condition $R_0 < 1$.



(a) $R_0 < 1, t = 100$



(b) $R_0 > 1, t = 250000$

Figure 1. Numerical simulation of system (2)

The Figure 1(a) presented the behaviour of system (2) along 100 days, we can see that the infection of humans and mosquitoes are extinct along 70 days. The second one is to explain the performance of a system (2) over 250.000 days. According to these simulations, we can see that this system will be a free disease in 150.000 days. Another stability phenomenon also occurs in case $R_0 > 1$. Choose the parameter value as follows. According to the above definition, R_0 can be explained to the following :

$$R_0 = \frac{\Lambda_h(\beta_2\beta_3\Lambda_v + \beta_1\mu_v^2)}{\mu_h\mu_v^2(\mu_h + \gamma)} = \frac{\beta_2\beta_3N_hN_v}{\mu_h\mu_v^2} + \frac{\beta_1N_h}{(\mu_h + \gamma)} = R_{01} + R_{02}. \quad (13)$$

Eq.13 shows the transformation of R_0 dispart into R_{01} and R_{02} . R_{01} is a basic reproduction number for the zika virus model without sexual transmission, whereas R_{02} is the basic reproduction number for the zika virus model with sexual transmission, in the absence of mosquitoes in the environment observation. Qualitatively, when the total population is increasing either mosquitoes or human populations, hence the transmission of disease will be faster. To reduce the disease transmission of the zika virus explains the following solutions. Reduce the chances of successful virus transmission from humans to mosquitoes and vice versa. This can be done by using anti-mosquito repellent or curtains. Reduce the chances of success in virus transmission between humans. This can be done by using a condom or reduction of the intensity of sexual interaction with humans infected. Better yet, suspended the sexual interaction with infected humans during which the infected has not been recovered. Reduce the mosquito population in the neighborhood and increase the chance of dying mosquitoes can be done with a 3M Program or fumigation (fogging). Increase the chances of recovery of infected humans, as a means of shortening the time of treatment so quickly for healthy people who are infected and immune from the disease.

5. Conclusion, Implication and Limitation

5.1 Conclusion

In the previous section, we have studied about zika virus transmission. In this section, we summarize the following. Model (2) has two equilibrium points. An uninfected equilibrium, what we called Disease Free Equilibrium (DFE), where the zika virus disease is not present. The second is endemically infected equilibrium or Endemic Equilibrium (END). The analytical analysis of Disease Free Equilibrium (DFE) and Endemic Equilibrium (END) is worked, respectively. The existence of each equilibrium and the linear stabilities are discussed.

5.2 Implication and Limitation

The linear stability of DFE and END was solved by linearized the non-linear equilibrium of system (1) by Jacobian. By compute the eigenvalue of Jacobian and substituting each equilibrium, we can conclude that DFE is local asymptotically

stable if $R_0 < 1$. Otherwise, when $R_0 > 1$, the END is local asymptotically stable. In general, we can avoid the zika virus by using anti-mosquito repellent or curtains, suspended the sexual interaction with infected humans, 3M Program or fumigation (fogging), and treatment so quickly for healthy people are infected and immune from the disease.

Reference

- Agusto, F., Bewick, S., & Fagan, W. 2017. Mathematical Model for Zika virus dynamics with sexual transmission route. *Ecological Complexity* : 61-81.
- Aminah, A. N. 2016. *Gaya Hidup*. Retrieved from Republika Online: <http://www.republika.co.id/berita/gaya-hidup/infosehat/16/02/11/o2d8kc384-lembaga-eijkman-ditugaskan-teliti-virus-zika>
- Andayani, P. 2019. Dynamical Analysis for A Simple Model of Zika Virus Transmission. *Jurnal Matematika Sains* : 19-23.
- Andayani, P., Azmi, R. D., & Sari, L. R. 2018. Comparing Vector-host and SEIR models for Zika Virus Transmission. *J.Exp. Life Sci.* Vol. 8. No. 3 : 161-164.
- Hirsch, M. W., Smale, S., & Devaney, R. L. 2013. *Differential Equations, Dynamical Systems, and Introduction to Chaos*. Elsevier. Oxford.
- Kaddar, A. 2019. On The Dynamics of A Delayed SIR Epidemic Model with A Modified Saturated Incidence Rate. *Electronic Journal of Diferential Equations* : 1-7.
- Kincaid, D., & Cheney, W. 2002. *Numerical Analysis : Mathematics of Scientific Computing*. Thomson Learning.
- Molles, M. 2002. *Ecology Concept and Applications Second Edition*. Mc Graw Hill. Mexico.
- Perkins, A. T., Siraj, A. S., Ruktanonchai, C. W., Kraemer, M. G., & Tatem, A. J. 2019. Model-Based Projections of Zika Virus Infections in Childbearing Women in Americas. *Nature Microbiology*.
- Services, U. D. 2017. *Zika Transmission*. Retrieved from Center for Disease Control and Prevention: <https://www.cdc.gov/zika/transmission/index.html>
- Suryanto, A. 2011. A Dynamically Consistent Numerical Method for SIRS Epidemic Model with Non-Monotone Incidence Rate. *The 7th IMT-GT International Conference on Mathematics, Statistics and its Applications (ICMSA 2011)*.
- Xiao, D., & Ruan, S. 2007. Global Analysis of an Epidemic Model with Nonmonotone Incidence Rate. *Mathematics Bioscience* : 419-429.
- Zill, D. G., & Wright, W. S. 2013. *Differential Equations with Boundary-Value Problems*. Richard Stratton. Boston.

A Modified Model of Zika Virus Spread with Saturated Incidence Rate: Modelling and Stability Analysis

ORIGINALITY REPORT

8%

SIMILARITY INDEX

6%

INTERNET SOURCES

6%

PUBLICATIONS

3%

STUDENT PAPERS

PRIMARY SOURCES

- 1** Puji Andayani. "The effect of social media for a Zika virus transmission with Beddington DeAngelis incidence rate: Modeling and analysis", AIP Publishing, 2019
Publication **3%**
- 2** www.imo.universite-paris-saclay.fr
Internet Source **3%**
- 3** Kevin M. Knight, Soumadwip Ghosh, Sharon L. Campbell, Tyler J. Lefevre et al. "A Universal Allosteric Mechanism for G Protein Activation", Cold Spring Harbor Laboratory, 2020
Publication **3%**

Exclude quotes Off

Exclude bibliography On

Exclude matches < 3%

A Modified Model of Zika Virus Spread with Saturated Incidence Rate: Modelling and Stability Analysis

GRADEMARK REPORT

FINAL GRADE

/0

GENERAL COMMENTS

Instructor

PAGE 1

PAGE 2

PAGE 3

PAGE 4

PAGE 5

PAGE 6

PAGE 7

PAGE 8

PAGE 9

PAGE 10
