

Development of Equation to Estimate Basic Reproduction Number of Plant Disease in Case of Different Host Distribution

Jirathun Thaweewattananont, Usa Humphries, Frank van den Bosch

Abstract: Distribution of susceptible host between agricultural fields is a factor that effect to plant epidemic. The plant epidemic can be described by the basic reproduction number. From its definition, the high value of basic reproduction number can represent high epidemic. The equation is developed to estimate the basic reproduction number to represent the epidemic. To develop the equation, four factors such as the number of spore that the infected host can produce in the infected period, the probability that healthy host become infected host when it receive spore, the probability that the spore land in the distance r and the distribution of susceptible host are considered. Then, Checking the developed equation by using stochastic process. Because the difficulty of real data. The Gillespie's Algorithm is used to select the event that will happen in stochastic process and consider 180 cases of parameter. The results show that all the correlation coefficient of the basic reproduction number from two method has more than 0.85. that is the basic reproduction number from the developed equation has a very strong relationship with the basic reproduction number from the stochastic process.

I. INTRODUCTION

Plant epidemic is the progress of disease in time and space which needs three suitable factors such as susceptible host, pathogen, and environmental conditions. Plant disease is occurred when inoculum from the infected host spread to susceptible hosts. The distance of dispersion is estimated to 2 inches up to hundreds of kilometers. The inoculum can be spread by several ways, for example, wind, water, insect, human, etc. The environmental factors like wind and water disperse the inoculum in various range which depends on wind spend or stream. Whereas, any infectious vectors or insects spread plant disease with the attached inoculum on themselves. Moreover, human's activities can also assist to spread the epidemic such as transportation of crop products [1].

Dispersion with high range of distance leads to two main agricultural fields which separately far from each other become infected when one main field infected [5].

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Jirathun Thaweewattananont, Department of Mathematics, Faculty of Science, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

Usa Humphries, Department of Mathematics, Faculty of Science, King Mongkut's University of Technology Thonburi (KMUTT), Bangkok, Thailand.

Frank van den Bosch, Department of Environment & Agriculture, Centre for Crop and Disease Management, Curtin University, Bentley 6102, Perth, Australia

Wild or agricultural susceptible host between these separated fields are factors of dispersion since the different susceptible host distribution affect to plant epidemic. In consequence, the ability of infection from the source to the other field depends on the susceptible host distribution between them [6].

The characteristic of inoculum's dispersion is modelled by dispersal function which based on experimentally measured dispersal gradients or the physical theories [2]. For the disease that produce large propagules that aggregated in mucilage commonly are dispersed by rain or other water resources and dispersal distance generally less than one meter [3]. As a result, the model that expressed this dispersion is in the negative exponential form [4].

Therefore, this paper aims to study the relationship between host distribution and invading of disease. The Poisson Cluster Process is used to generate host distributions which represent almost real distribution in nature. Then, developing the equation to describe the relationship between distribution and epidemic by investigate the basic reproduction number. This relationship will be useful to determine the epidemic behavior when the characteristics of the host distribution is detected.

II. BASIC REPRODUCTION NUMBER MODEL

Basic reproduction number is used to indicate plant epidemic, which define by the expected number of secondary infected host that infect from one initial infected host in complete susceptible population [7]. From the definition, the high value of R_0 can represent high epidemic. There are four factors which are considered such as the number of spore that the infected host can produce in the infected period (θ), the probability that spore land in the distance r , the probability that healthy host become infected host when it received spores (ρ) and the distribution of host. Since parameters θ and ρ are specific in each disease, both of them are assumed them which equal to 1. The probability that spore lands in the distance r can be calculated by dispersal function which depends only on distance r , $D(r)$. In this paper, the negative exponential dispersal function is considered and the derivation of $D(r)$ is shown below.

The negative exponential dispersal function is

$$D(x, y) = \frac{\alpha^2}{2\pi} e^{-\alpha\sqrt{x^2+y^2}}$$

Transformation of dispersal function into polar coordinate as



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$$D(r) = \frac{\alpha^2}{2\pi} \int_0^{2\pi} r e^{-\alpha r} d\theta = \alpha^2 r e^{-\alpha r} \quad (1)$$

Then, considering distribution of host by O-ring statistic which describes the density of host distribution at the distance r . The O-ring statistic is function that depends on the distance r which defines as

$$O(r) = \frac{\lambda}{2\pi r} \frac{dK(r)}{dr} \quad (2)$$

From the equation (2), λ represents density of host distribution and $K(r)$ is Ripley's K-function which defines as

$$K(r) = \frac{\text{expected number of point in circle radius } r}{\lambda}$$

Since, the circle area with distance r is considered the equation to calculate R_0 can be calculated from the equation

$$R_0 = \theta \rho \int_0^{\infty} 2\pi r D(r) O(r) dr \quad (3)$$

The basic reproduction number from the model is denoted by R_0^{model}

III. STOCHASTIC PROCESS

To examine on the basic reproductive number model, the real data are necessary for model validation. Since the lack of experimental data, the stochastic process is considered instead of the data. For the detail of stochastic process, firstly generating the host distribution for using as sample 50

distributions. Each distribution contains 150 susceptible hosts and consider in stochastic process one by one. Secondly, denote a source of infection. Thirdly, calculate the rate of event such as the rate of infection of each host and rate of death of source of infection.

The rate of infection of host i denoted by

$$r_{inf} = \beta e^{-\alpha d_i} \quad (4)$$

The death rate of source of infection denoted by

$$r_{dead} = \mu \quad (5)$$

From the equation (4) and (5), β is the transmissibility rate of host and μ is the death rate of infected host. Then, use the Gillespie's Algorithm to select which event will happen. If there is the new infected host, then remove it from the host distribution and back to the third step. If the source of infection died, then count the number of infected hosts that are removed. Repeat these step 50 times. Then, change the source of infection, back to the third step and do the same process until all of host was considered as source of infection. Finally, the middle of 95% confidence interval to be R_0^{sto} of the host distribution is denoted, and there are 180 cases of parameter considered to get more results which used to compare with R_0^{model} . The parameters that use for simulation are shown in TABLE 1.

Table. 1 All of parameter and their values

Parameter	Notation	Value
Number of spore that the infected host can produce in the infected period	θ	1
Probability that healthy host become infected host when it received spores	ρ	1
Exponent of negative exponential dispersal function (0.5 step size)	α	13.5 – 23.0
Transmissibility rate of host	β	0.001, 0.01, 0.1
Death rate of infected host	μ	0.001, 0.01, 0.1

In simulation, value of exponent of negative exponential dispersal function is varied from 13.5 - 23.0 to guarantee that the spore land in the unit square area at least 99%.

IV. RESULTS

There are two value of basic reproduction number, one from the model (R_0^{model}) and the other from stochastic process (R_0^{sto}). The correlation coefficient is used to show that the model can estimate value of basic reproduction number. Some the result is shown in Figure 1.

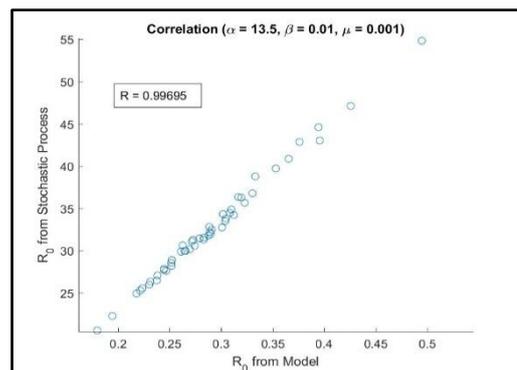


Fig. 1 Correlation graph of basic reproduction number with $\alpha = 13.5$, $\beta = 0.01$, $\mu = 0.001$

From figure 1, each point represents the basic reproduction number of each host distribution which horizontal axis is the basic reproduction number from the model (R_0^{model}) and vertical axis is the basic reproduction number from the stochastic process (R_0^{sto}).



The correlation coefficient of this case is equal to 0.99695, which show that these two method has a very strong relationship. After that, all correlation coefficient is collected to draw histogram and show in Figure 2.

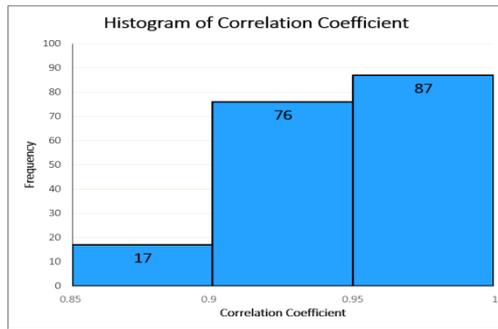


Fig. 2 Histogram of correlation coefficient of all cases

In Figure 2, there are 17 cases of parameters which give correlation coefficient between 0.85 and 0.90, 76 cases give value between 0.90 and 0.95, and 87 cases give value between 0.95 to 1. Since all cases give correlation coefficient more than 0.85, the basic reproductive number equation and stochastic process has a strong relationship.

V. CONCLUSIONS

Plant epidemic is an important problem in agriculture caused by the inoculum that spread far away from source of infection by weather and carrier factors. The susceptible host is one of carrier that can disperse epidemic from the infected field to the remote area. The basic reproduction number is important quantity in the study of epidemics which can be represent the effects of spatial host distribution. Therefore, studying the effect of host distribution is one of important role to manage invading of disease.

The model is developed to estimate the basic reproduction number and compared with data that simulated by using stochastic process. Then, using the correlation coefficient to check relationship between these two methods with 50 host distributions and 180 cases of parameter.

In conclusion, the model has a very strong relationship with the basic reproduction number since their correlation coefficient always higher than 0.85. However, the value of estimated basic reproduction number be different with basic reproduction number from stochastic process, it possible that some factor must be conclude in the basic reproductive number equation to give nearly results to stochastic process.

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