

New Infection Model for Foliar Fungal Plant Pathogens

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Abstract: Epidemiological models for plant diseases are very important for prediction, control and estimation of the infection incidence. Such models are fundamentally characterized by the influence of some meteorological variables. In this paper, we design a new model to predict incidence of infection by pathogens in function of the mixed effects of temperature and wetness. These deeply influential parameters are estimated and adjusted with regards to the disease caused by various infectious pathogens. In addition, we show that it is primordial to introduce bound constraints on the model's location parameters. This allows to perform a more accurate minimization of the sum of residuals. The proposed optimization procedure is based on the trust-region method. Our methodological approach is simple and easy to implement for the prediction and / or control of diverse plant infections. In order to show its efficiency, our model is validated and compared for different plant diseases adapted from several studies published in the literature. As a matter of comparison, the results of goodness of fit demonstrate that our new model outperforms the other reported models.

Keywords: Plant disease, Epidemic Models, Temperature and wetness duration, Fitting, Nonlinear optimization

Introduction

The design of disease models for plant infections is the only rigorous way for disease forecasting and control (Delignette-Muller 2009; Krause and Massie 1975). In this spirit, the infection propagation must be adequately described by mathematical models that are conceived in order to express the interaction between some environmental variables that can be measured and studied in laboratory, greenhouse, field experiments or simulated (Krause and Massie 1975; Madden and Ellis 1988; SHRUM 1978; Waggoner 1974). Note that, in the areas of crop physiology and agricultural meteorology the temperature, the surface wetness, the humidity and the rainfall, are the most commonly considered environmental variables (Wang and Engel 1998; YAN and HUNT 1999; Yin et al. 1995).

In this paper, we consider two important issues: The design of a suitable infection model for plant pathogens, and the foundation of an original methodology for fitting. Specifically, we provide a model that can be efficiently applied to plant infections with regard to the mixed effects of the temperature and the wetness duration. Moreover, our model has good merits compared with other published models (Duthie 1997; Furuya et al. 2009; Grove, Madden, and Schmitthenner 1985; Sharma et al. 2014). One of these merits is that its whole parameters have an intrinsic biological meaning, which describes the scale, the shape, and the location of the disease response.

A second merit concerning our approach is that in contrast to many other epidemic models reported in the literature for which the location parameters are predetermined or empirically fixed or even absent in the model (Duthie 1997; Erincik et al. 2003; Sharma et al. 2014); these fundamental biological parameters are considered as unknown variables that should be determined from the fitting procedure. As a result, based on the introduced methodology, the proposed model is applied to various plants and infectious pathogens with comparison to some important well-known models in the literature (Furuya et al. 2009; Grove et al. 1985; Sharma et al. 2014). Moreover, it is shown that our original least-square procedure with bound constraints

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introduced in this paper, leads to efficient and better fitting for three kinds of plants with different fungal infections based upon experimental data sets. In all the case studies, our model is shown to be very competitive and outperforms the well-known reported models.

The reminder of the paper is organized as follows. In Section 2, we introduce the epidemic model for plants infection under mixed effects of temperature and wetness. Section 3 provides a fitting method for the parameters estimation. In section 4, the proposed models are validated using simulation results with comparison to some reported works in the literature. Finally, concluding remarks are presented in Section 5.

Plant Diseases Model

We consider a mixed effects modeling for plant disease with regard to the relative infection response subject to the effect of the most influential environmental variables represented by the temperature and the wetness duration.

The model is described by:

$$y(t, w) = f(t, w) + \varepsilon \quad (1)$$

Where the function f is expressed as

$$f(t, w) = \left(1 - \frac{1}{((h_1(t-t_1)^{f_1})+1)}\right) \left(1 - \frac{1}{((h_2(t_c-t)^{f_2})+1)}\right) \left(1 - \frac{1}{(h_3(w-w_1)^{f_3}+1)}\right) \quad (2)$$

The involved quantities under study are

- y is the measure of the relative infection on a scale from 0 to 1 (or score response tacking values in the interval $[0 ; 1]$).
- t is the temperature (in Celsius).
- w is wetness duration (in hours).
- ε is the model residual or perturbation error represented by an unknown random normal variable

The parameters of the model are defined by

- h_1, f_1, h_2, f_2 , and h_3, f_3 are the shape paramerters.
- t_1, t_c , and w_1 are the location paramerters such that
 - t_1 : minimum temperature required for infection (in Celsius)

$$t_1 = \min(t | y \neq 0)$$

- t_c : maximum temperature required for cure (in Celsius)

$$t_c = \max(t | y \neq 0)$$

- w_1 : minimum wetness duration for infection (in hours)

$$w_1 = \min(w | y \neq 0)$$

It is worth mentioning that by construction of the model, the location parameters intrinsically satisfy the fact that for all (t, w) we have $y(t_1, w) = y(t_c, w) = y(t, w_1) = 0$.

Proposition 1.

The function f take its values in the interval $[0,1]$ if and only if $h_1 > 0, h_2 > 0, f_1 > 0, f_2 > 0, f_3 > 0, h_3 > 0$.

Proof: The condition $h_1 > 0, h_2 > 0, h_3 > 0, f_1 > 0, f_2 > 0$, and $f_3 > 0$ results from the fact that the functions f do not go to infinity at the boundary of the domain $[t_1, t_c] \times w_c$

Parameters Estimation

The proposed parameters estimation for our model is based on likelihood principle which under some statistically legitimate assumptions (independence of measured values, normal distribution of the residual), this leads to fit a given model to the observed data based upon the least square procedure.

In the sequel, we consider the sample data of measured temperature $T := \{t_1, \dots, t_n\}$ and the set of measured wetness duration $W := \{w_1, \dots, w_n\}$ with their corresponding observed relative infection $Y := \{y_1, \dots, y_n\}$. Then, in order to fit the model to the sample data Y by estimating the involved parameters, one has to find the best parameters $h_1, f_1, h_2, f_2, h_3, f_3, t_1, t_c, w_1$ that are effectively the optimal solution to the following nonlinear least square optimization (Sum of Squares Error (SSE) minimization)

$$SSE := \min_{h_1, f_1, h_2, f_2, h_3, f_3, t_1, t_c, w_1} \|y - \hat{y}\|^2 \quad (3)$$

The estimate model $\hat{y} = f(t, w)$ is entirely described by the function f ;

The above optimization problem can be solved more efficiently if one can include some information from the sets T and W . In fact, the useful information is to take into account the following underlying constraints

$$\begin{cases} t_c^- \leq t_c \\ t_i^- \leq t_i^+ \\ w_i^- \leq w_i^+ \end{cases} \quad (4)$$

Hence, we add natural bounds from the data sets by integrating the lower bound on t_c and the upper bounds respectively on t_i and w_i .

In the following, it is show how to obtain the previous introduced bounds.

Proposition 2. In order to fit the data sets (Y, T, W) , the following bounds must hold

$$\begin{cases} t_c^- := \max_{y_i \neq 0}(t_i) \\ t_i^+ := \min_{y_i \neq 0}(t_i) \\ w_i^+ := \min_{y_i \neq 0}(w_i) \end{cases} \quad (5)$$

Proof. The argument line is straightforward from the construction of the model.

Now, considering **Proposition 1**, the constrained nonlinear least square optimization problem under consideration for fitting the proposed model to the sample data (Y, T, W) is adequately formulated as:

$$\min_{h_1, f_1, h_2, f_2, h_3, f_3, t_1, t_c, w_1} \|y - \hat{y}\|^2 \quad (6)$$

Subject to

$$\begin{cases} h_1 > 0, f_1 > 0, h_2 > 0, f_2 > 0, a > 0, b > 0 \\ t_c^- \leq t_c \leq t_c^+ \\ t_i^- \leq t_i \leq t_i^+ \\ w_i^- \leq w_i \leq w_i^+ \end{cases} \quad (7)$$

Were, one can set t_c^+, t_i^- and w_i^- to some empirical or trivial meteorological extremum values. For instance, set $w_i^- = 0h$ and more or less $t_c^+ = 40 C^\circ, t_i^- = 0C^\circ$.

This constrained optimization problem can be solved using nonlinear programming methods such as the classical Gauss-Newton with its many variants, Trust-Region, Interior Points method. These methods work well in practice, if the initial starting points are well-guessed or can be close to the optimal solution.

Models Validation and Numerical Results

Here, we perform a comparison study with the most well-known nonlinear models related to fungal infection that are based upon the combined effects of wetness duration and temperature.

These models can be categorized as follows

- Beta model :

$$f(t, w) = a(t - t_1)^b (t_c - t)^c w^d \tag{8}$$

- Duthie's model :

$$f(t, w) = \frac{s(h+1)h^{(h-1)^{-1}-1} \exp(g(h+1)^{-1}(t-f))}{1 + \exp(g(t-f))} \tag{9}$$

- Polynomial model :

$$\log\left(\frac{y}{1-y}\right) = a_0 + w(a_1 + a_2 t + a_3 t^2 + a_4 t^3) \tag{10}$$

In order to fit our model, we have applied Trust Region method to solve the optimization problem. Matlab implements this method via the function fit. The chosen initial conditions t_1^0 , t_c^0 and w_1^0 for the temperature and the wetness, are close to the proposed bounds on t_1 , t_c and w_1 . For the others initial parameters we have selected values between 0 and 1.

In the simulation results, we have considered *SSE* index accuracy, which indicates close estimates to the real observed disease values *y*.

Note that the goodness of the fit greatly depends on the statistical measures of performance. Hence, we have also validated our model via the well-known statistical goodness of fit indicators R^2 and its adjusted value R_a^2 , which show the tendency to the linear relationship between the predicted and observed values as they become closer to the 1 (perfect fit).

The simulation results in Tables 1.and 2. Show that the two proposed models are more effective than the other reported models (8)(9)(10). It can be seen that our performance factors are better since they provide a better fit and significantly outperform these alternative models.

Table 1. Different infection model based on published studies relating fungal infection to temperature and wetness duration

Pathogen	Host	Model	Ref	Goodness of fit			
				R^2	R_a^2	<i>SSE</i>	<i>RSSE</i>
Powdery mildew	Picrorhiza kurrooa	Beta	(Analytis 1977; Erincik et al. 2003; Mio and Amorin 2002; Sharma et al. 2014)	0.81	*	*	*
Puccinia allii	Spring onion	Dutie	(Duthie 1997; Furuya et al. 2009; Wu et al. 1999)	0.9501	*	*	*
Spinach White Rust	spinach	Polynomia 1	(Madden and Ellis 1988; Sullivan, Damicone, and Payton 2002)	0.8917	0.8909	*	*

Table 2. Parameters estimation for the model (2) with their corresponding goodness of fit

Pathogen	Host	Ref	Parametre									Goodness of fit			
			h_1	h_2	h_3	f_1	f_2	f_3	t_1	t_c	w_1	R^2	R_a^2	<i>SSE</i>	<i>RSSE</i>
Powdery mildew	Picrorhiza kurrooa	(Sharma et al. 2014)	7.25e-08	3.31	0.009	10.78	866.3	1.84	29	38	0.1	0.9687	0.9521	0.0893	0.077
Puccinia allii	Spring onion	(Furuya et al. 2009)	0.4417	0.03653	1.602	2.1	6.002	3.4	1.872	27.38	0.6469	0.9549	0.9308	0.1728	0.1073
Spinach White Rust	spinach	(Sullivan et al. 2002)	1.74e-4	0.00134	1.03e-3	5.35	2.97	2.953	4.285	30.65	1.3e-4	0.9003	0.8913	0.7510	0.0919

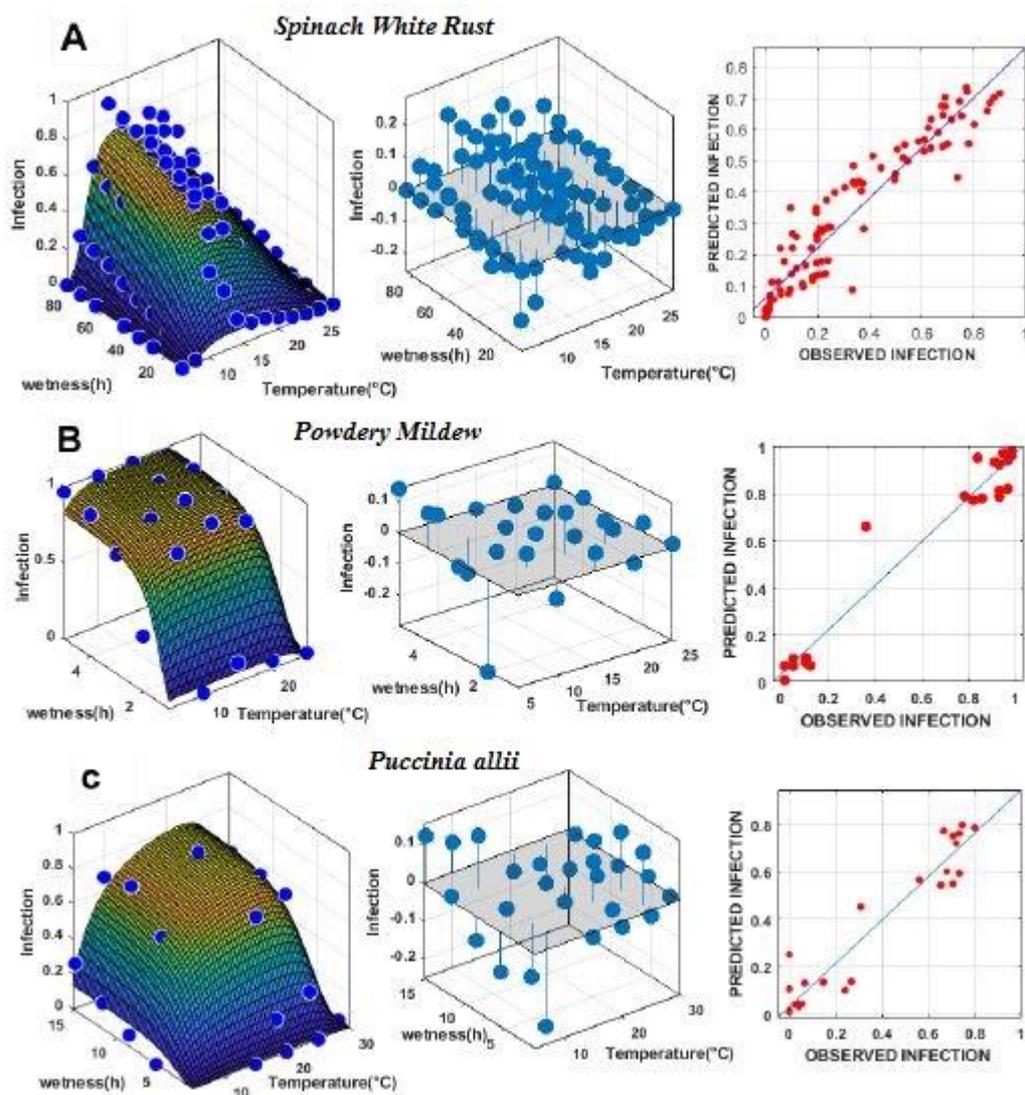


Figure 1. Observed and predicted values of the relative disease using model (2) and Residuals versus the fitted values

Conclusion

The model and the approach provided in this paper are original. It has been shown that accurate modeling for plant disease can be achieved based upon the provided techniques, which can be implemented for simulation analysis, prediction and/or control. Moreover, the comparison study has shown the efficiency of the proposed epidemic model.

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