

Impact of climate change on the spread of pests and diseases in Scotland

Project Final Report



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Authors: Adam Kleczkowski^{1*}, Matthew Castle², Glyn Jones³, Vincent Keenan¹, Crawford Revie¹ and Oleg Sheremet¹

¹University of Strathclyde, 16 Richmond Street, Glasgow, G1 1XQ

²University of Cambridge, Downing Street, Cambridge, CB2 3EH

³Fera Science Ltd., Sand Hutton, York, YO41 1LZ

*Corresponding author

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1 Executive Summary

1.1 Aim

The aim of the project was to construct a framework which allows studying the effects of climate change on emergence and spread of plant and tree pests and diseases and to apply it to selected pests and diseases.

1.2 Methods

The project involved three elements. Firstly, a novel modelling framework was constructed which combined epidemiological and economic modelling. The framework was implemented as a desktop and a web app, with a user-friendly front end. Secondly, we used a literature review to obtain estimates of epidemiological parameters and economic values (both market and non-market). The assumptions were discussed with an expert panel. Finally, we used the framework to study predictions of spread and economic impact of three pests which are currently not in the UK, i.e. *Xylella* spp., *Liberibacter* (Zebra chip disease) and bark beetles, to estimate the infestation progress and the resulting losses to the plant and tree market and non-market value over the period until 2050. Sensitivity analysis was used to illustrate uncertainty associated with the predictions

1.3 Results

All three pests are shown to have a high probability of invading, spreading and causing large losses in the period 2019-2050. Firstly, *Xylella* spp. was used as an example of a system where both market and non-market values are affected. In this case, we only considered its effects on oak and ignored the costs of statutory control measures and their impact on trade; we found average loss of £50m per year over 32 years (15-20% of the total value of oak lost in this period). The disease quickly fills in the area where climatic conditions are suitable, and the total area is increasing with the climate change. Secondly, in order to illustrate how the model can be used to estimate the potential losses in an agricultural setting, Zebra chip disease on potatoes was considered. Percentage losses of value due to the pest were found to be highly uncertain (from 5% to 87%); using 40% figure (based on proportion of potatoes used for chipping and processing) we predict up to 90% of the area affected as early as 2030 and the average loss of £40m per year (representing 15% of the total value). Finally, bark beetle impact on spruce was used to demonstrate the sensitivity of the predictions to climate responses. We found average losses of £50m per year with major damage in years 2025-45 and up to 50% of forest area affected. However, we also found that the results were highly sensitive to assumptions about the response of the pest to increase in summer temperature.

1.4 Conclusions

The project demonstrates how a combination of literature review, expert elicitation and modelling can be used to predict the economic losses due to pests and pathogens that are not yet in the UK. The study also identified key knowledge gaps for all the species and demonstrated how the model can be used to identify key parameters and processes to which the prediction is mostly sensitive.

Note that the results in this report are provided for illustration purposes only and are not based on rigorous parameter estimation.

2 Introduction

The invasion of plant pests and diseases is among the most important side effects of a tightly integrated global economy. To design an appropriate response to such invasive species, the decision makers need to be able to rapidly, transparently and consistently assess the extent of the outbreak and its economic impact. The decision-making process can significantly be enhanced by the availability of a flexible modelling framework that quantifies economic, social, environmental, political, technical and legal considerations associated with pests and disease spread.

In 2017 the Department for Environment, Food and Rural Affairs (Defra) and the Forestry Commission UK commissioned a team from FERA Ltd and the universities of Stirling (later Strathclyde), York and Salford to develop such a modelling framework that can be used to study a response to actual or potential pest or disease incursion in the UK and other forests (Defra ITT project 7338 “Developing a plant health outbreak decision support framework”, Jones et al., 2018). In 2018, the Scottish Plant Health Centre commissioned a new version of the framework to include a capacity to analyse the effects of climate change on spread of plant pests and diseases.

The aims of the framework are to:

- Rapidly, transparently and consistently assess the implications of the outbreak and its economic impact.
- Assess future costs and benefits of control measures, taking into account uncertainties; this also includes an option of “doing nothing”.
- Be user-friendly and fast.
- Allow rapid response while using a mechanistic model.

For this project, the DEFRA framework was significantly extended as follows:

- 1 Front end has been completely redesigned and parallel computation introduced to speed up calculations.
- 2 The model has been extended to include non-forest systems (hosts, pests and pathogens) and in particular to cover selected aspects of agricultural systems.
- 3 We have used a literature search to assess how the key parameters and values at risk are expected to vary with the climate change. The analysis has been carried out for a selection of pests and diseases, both present and which can be arriving under selected climate change predictions. The approach also required a construction of a simplified climate and weather model (including emulators and transfer functions).
- 4 The DEFRA tool assumed that the epidemic has been initiated. We have modified the model to incorporate the future probability of arrival.
- 5 The original program did not include weather and climate influence on the processes it described. We have modified the model in three areas:
 - a. An emulator was constructed to capture the essential features of both long-term (IPCC UKCP09 predictions for the mean temperature anomaly for model RCP8.5) and short-term (daily average temperature data).
 - b. The rate of spread was modified to depend on the monthly temperature through a transfer function.
 - c. The availability of susceptible hosts was modified to depend on long-term changes, selectable through the user input.

Project outputs include:

- 1 A web-based application.
- 2 A report outlining the methodology.
- 3 A review of literature on climate influence on selected host/pest/pathogen combinations – Appendix A.
- 4 A set of scenarios for selected host/pest/pathogen combinations – Appendices B-D. The case of *Ips typographus* was selected instead of the originally planned *P. ramorum* study due to more information being available and its potential impact on spruce cultivation.
- 5 An extensive and completely rewritten user guide – Appendix E.

2.1 *Limitations of the approach*

The framework currently has a range of limitations:

- Spread is not explicitly spatial as the model assumes full mixing. The model does not include any spatial heterogeneity in spread and damage or costs;
 - The model can still be used for horizon scanning and scenario testing when there is a particular uncertainty about the parameters (as here) as well as for rapid early guidance until a more detailed model is developed and parameterized.
 - The model can be used if we want relative figures for scales of effort.
 - The spatial elements of the spread become particularly important at larger scales. Although in this project we use the model to describe the spread in the whole UK, the simplicity of the model makes it applicable under the uncertainty even if the details of the spread might not be captured in detail.
- The population age structure is assumed to be constant;
 - The model is particularly suitable for situations when the host population has a stable age structure, or when the pests/pathogens do not distinguish between different ages, or when maturation occurs very quickly (as for annual crops).
- There is a strong dependence on the size of initial outbreak, particularly for systems where the pest is currently not present, making the results dependent on highly uncertain parameters;
 - The model allows exploration of the parameter uncertainty and its effects on the future spread.
- Some stochastic elements are included (temperature) but no demographic stochasticity;
 - The model can be reliably used to describe the dynamics of pests/pathogens in situations where the number of plants involved is large.
- The rate of spread of pests/pathogens is assumed to depend on average monthly temperature only and not on measures like degree-days, or on humidity, rainfall, etc.
 - The model is particularly suitable for temperature-dependent infections/infestations such as insect vectors, although less for humidity governed pathogens like *Phytophthora* spp.
- The model currently does not include cryptic and latent classes.
 - The model can be used if the latent (cryptic) periods are relatively short, or if detection is relatively quick.
- In the current version the uncertainty associated with the climate predictions is not implemented, i.e. the parameters in the model above are assumed to be constant between realisations.
 - As the RCP8.5 simulations results are given for other quantiles than the median, it would be possible to include them in the model in the future, but it was deemed to be unnecessary due to large uncertainties otherwise present in the case scenarios.

2.2 Recommended applications

Given the balance of assumptions and scope of this tool, we feel that it could be used to:

- answer broad questions concerning the future threats of different pests and pathogens in relative terms (e.g. pest “X” is likely to cost 10 times as much to manage as this other pest if it were to arrive);
- explore initial feasibility options for the scale of control necessary for a specific well-documented pest/pathogen;
- provide rapid, early stage assessment of the likely impact of certain pests and pathogens;
- engage with stakeholders to illustrate the effects of climate change and control strategies.

We also stress that for detailed management advice for a specific pest or pathogen a bespoke epidemiological model should be developed and parameterised.

3 The general approach

The mathematical and computer model itself is part of a framework incorporating parameter elicitation, decision of model structure and uncertainty, followed by evaluation of results, see figure 1. The computer package is a user-friendly decision-support system implemented in Shiny (GUI version) which can run either online (hosted on an R/Shiny server, either at shinyapps.io or a self-hosted server) or locally from within RStudio. The current version also supports parallel computing (using available cores) which significantly speeds up computations.

The elicitation box illustrates the procedures that can in general be used to obtain model structure and parameters. In this project, we primarily used literature to obtain the parameters; in the previous project on which the modelling approach is based (under separate funding), we also used expert survey and expert workshop, as well as data to estimate the rates of spread.

The modelling box captures the key elements of the approach, with model structure and parameters described in the following section, whereas parameter values and their uncertainty as well as model results are addressed in the Case Studies section. Finally, we use expert workshop to present and evaluate the model. We also used feedback from experts to iterate the drafts of this report.

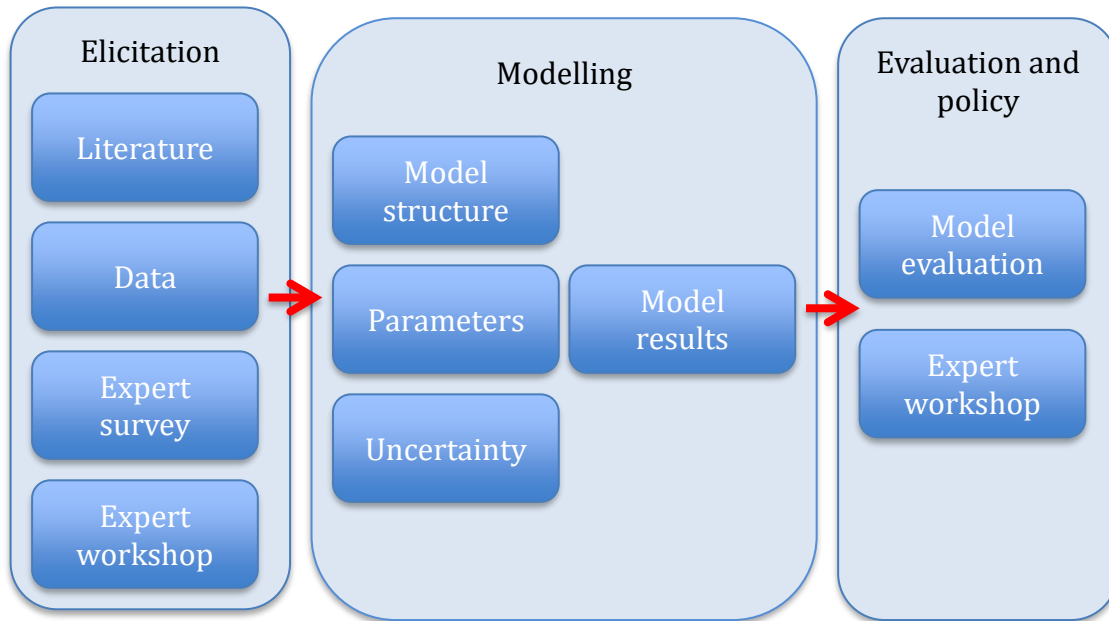


Figure 1. Decision support and analysis framework.

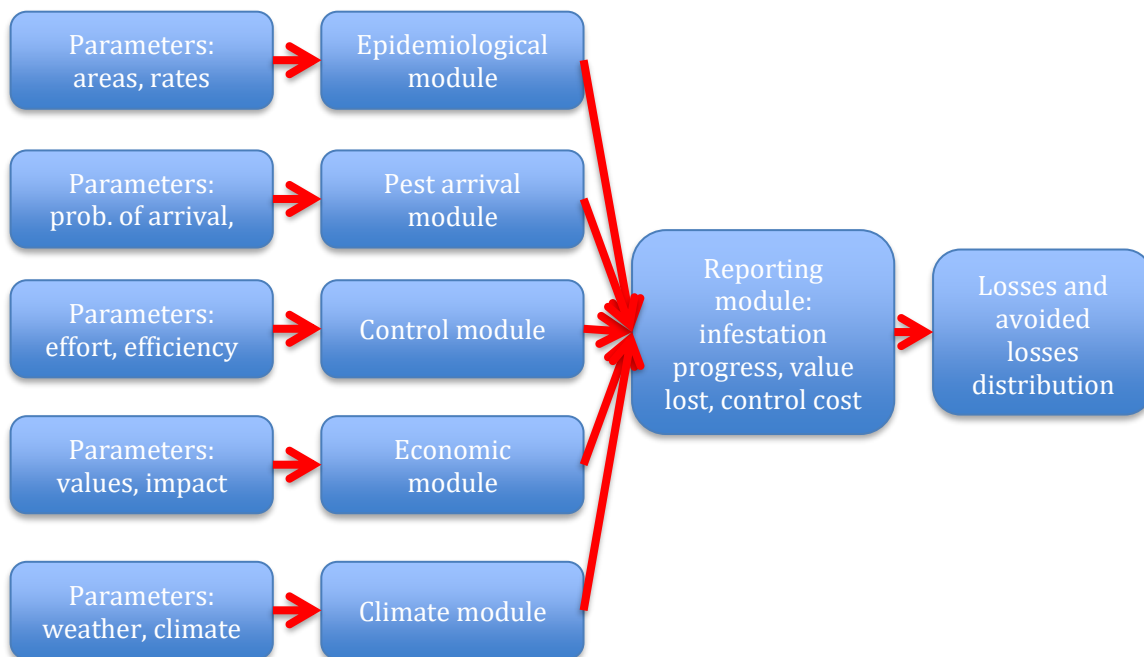


Figure 2. The structure of the model.

The model consists of six elements: (i) the epidemiology module, including areas and regions, (ii) the pest arrival module, (iii) the control module, (iv) the economic module, (v) the weather and climate module, (vi) the reporting module, see figure 2. The five boxes on the left list inputs into the different elements of the model, and the box on the right represent the outputs.

4 Modelling framework

4.1 General modelling structure

The underlying epidemiological model is a discrete-time Susceptible-Infected-Removed-Vaccinated (SIRV) model, commonly used in human, animal, plant and forest epidemiology, which captures the dynamics of both pest and pathogen spread.

The basic unit in the model is considered to be area expressed in hectares; the area is split into four classes, unaffected and susceptible (S), infested/infected and infectious (I), removed by control measures (e.g. by clear-cutting or a ban on continuation of growth, (R) and treated by preventive measures (spraying, vaccination, planting of resistant varieties, (V). Only plants in the infested area are capable of causing further disease.

The time step is currently taken as one month and parameters are given in units of per year. The time step is a compromise between accuracy of the model and speed of calculations.

Each time step consists of the following sub-steps:

1. The weather and climates sub-step;
2. The arrival sub-step;
3. The epidemiological sub-step;
4. The control sub-step;
5. The extinction sub-step.

For clarity, sub-steps 1.-2. are discussed after the epidemiological model which introduces the key concepts.

4.2 The epidemiological model

The epidemiological part of the model is applied first and given by:

$$\left. \begin{aligned} S^*(t+1) &= S(t) - b \frac{S(t)I(t)}{krN} \\ I^*(t+1) &= I(t) + b \frac{S(t)I(t)}{krN} \end{aligned} \right\} \text{Infection step}$$

with the values at the end of the previous step given by $S(t)$ and $I(t)$, whereas the temporary values in the current step are given by $S^*(t+1)$ and $I^*(t+1)$. N is the total area of host plants and r is the proportion of host plants in this area which are genetically susceptible to the infestation/infection. K represents one of the mechanisms by which climate change is deemed to act on the model, with the overall population of genetically susceptible plants, rN , being modified by a scale factor that represents the proportion of host area that is climatically suitable (a detailed discussion of the climate effect is given later in the report).

The exponential growth rate, b , can be reparameterised in terms of a doubling time, T_2 , i.e. time needed for the initial population area to double. Then,

$$b = \frac{\ln(2)}{T_2}.$$

The doubling time might be an easier quantity to estimate and to communicate to the stakeholders. The rate of spread, $b(e, T)$, is assumed to depend on the control effort, e under one of the control strategies (see below). It also depends on temperature, T (see below for details).

The model allows recovery from all classes to the susceptible class. This corresponds to natural recovery, or to replanting with susceptible plants, or return to original planting following a quarantine. Currently this is implemented by returning a proportion of area from each class of I, R and V to class S at the end of the simulation step.

4.3 Control module

The control step is applied after the epidemiological step. The measures currently implemented include three options:

- Removal of infested/infected plants, for example by clear-felling (control method 1);
- Removal of both infested/infected plants and susceptible plants, for example by replacing them with resistant varieties, in which case the 'value lost' as described below represents a difference in profit between the susceptible and the resistant varieties (control method 2);
- Spraying leading to reduction in the rate of spread (control method 3).

Note that the control method 2 is a replacement for the original method that affected susceptible plants only.

The equations describing different control options are given below. The effort is specified by a proportion of the total area that can be treated per unit of time (year), or the current infested/susceptible area, whichever is smaller. It is assumed that once the pest/disease is eradicated, control effort stops. It is also assumed that control is implemented in a single block of time, with start and end times to be specified by the user. Currently the control strategies cannot be mixed. The state of the variables after the control is applied is given by

$$I_{t+1} = I_{t+1}^* - c \cdot \min\left(I_{t+1}^*, eN\right) \quad \text{Control step}$$

$$R_{t+1} = c \cdot \min\left(I_{t+1}^*, eN\right) \quad \text{Control effect.}$$

for the case when only infected plants are treated, and

$$\left. \begin{aligned} S_{t+1} &= S_{t+1}^* - a \times \min\left(S_{t+1}^*, e \times \left(\frac{S_{t+1}^*}{S_{t+1}^* + I_{t+1}^*}\right) \times N\right) \\ I_{t+1} &= I_{t+1}^* - a \times \min\left(I_{t+1}^*, e \times \left(\frac{I_{t+1}^*}{S_{t+1}^* + I_{t+1}^*}\right) \times N\right) \end{aligned} \right\} \quad \text{Control step}$$

$$V_{t+1} = a \times \min\left(S_{t+1}^*, e \times \left(\frac{S_{t+1}^*}{S_{t+1}^* + I_{t+1}^*}\right) \times N\right) + a \times \min\left(I_{t+1}^*, e \times \left(\frac{I_{t+1}^*}{S_{t+1}^* + I_{t+1}^*}\right) \times N\right) \quad \text{Control effect.}$$

if both susceptible and infected plants are treated.

Here a is the rate at which the susceptible and infested areas are treated and moved to the ‘resistant’ class, and c is the rate at which the infested area is treated and moved to the ‘removed’ class. e represents the control effort. Then, eN represents the maximum area treated per year and is selected if the infested/susceptible area is larger; otherwise, the infested/susceptible area is chosen. For the purpose of cost calculations, eN is used to represent the area treated, independently of the infested/susceptible areas; this calculation reflects a situation in which effort is applied to the whole area.

For method 3, the rate depends on effort as

$$b(e) = \frac{b}{1 + he}$$

with h determining the reduction of the rate due to effort (e.g. spraying).

The model does not include the effect of replanting with susceptible material or loss of immunity. Thus, there are no transitions from infested, vaccinated and removed class back to the susceptible class.

4.4 Threshold for eradication

As a result of control methods implemented, the amount of infested material in the model reduces at each control sub-step. It is thus possible to eradicate the infestation, but in a deterministic model the level at which the infestation agent is considered to be extinct needs to be specified separately. As the model describes areas rather than individual trees or plants and thus ignores effects associated with demographic stochasticity, the populations are assumed to be equal to zero if they drop below a certain threshold which can be set by a user. Currently the threshold is set as an inverse of the planting density, representing the condition that an infestation level of less than a single plant or a tree, will be made extinct.

4.5 Arrival module

In the model, the introduction of infestation can occur in two ways. Firstly, the pest or pathogen can already be present at the start point of the simulations. Thus, at $t = 0$,

$$\begin{aligned} S(0) &= krN - I_0, & I(0) &= I_0 \\ V(0) &= 0, & R(0) &= 0 \end{aligned}$$

where I_0 is the initial infested area. If the pest is not present, $I_0 = 0$.

Secondly, the pest or pathogen might be arriving after the start point of the simulations, so that initially the host population is pest- and disease-free. Also, even if pest is already present, there could be future incursions in addition to the initial infestation. In the model, at each time step, a small additional area of infestation is created with a probability which changes in time. This additional area is assumed to represent a single plant, tree, or field, and can be related to the threshold for eradication (see the description of threshold above).

To model the continuing pest incursions we use a non-stationary Poisson process, with the probability varying over time given by a gamma function. The gamma function depends on two parameters, the average arrival time, \bar{t} , and the shape parameter, S . If $S = 1$, then the function describes an exponential decay in time; increase in S leads to a more peaked distribution. Alternatively, if $S = 0$ the model defaults to a constant probability per time (a stationary Poisson process). The gamma function offers the model flexibility in specifying the

shape of the arrival time distribution and there is a single "tuning" parameter that allows us to specify this shape. If we think that there is a constant unchanging probability of arrival over time (e.g. if a fixed proportion of all shipments into the country carry a pest) then we can model that by using $S = 0$ and the constant probability. If we are very confident that the pest will arrive in 5 year's time with a little uncertainty on either side then we can also model that using high values of S ; equally if we think that a pest will arrive in 5 years but we are very uncertain, we can use smaller values of S to capture this uncertainty.

The average number of incursions per year also needs to be specified. Figure 3 shows examples of the time dependence and samples of the arrivals; this mechanism allows some degree of stochasticity into an otherwise deterministic dynamics.

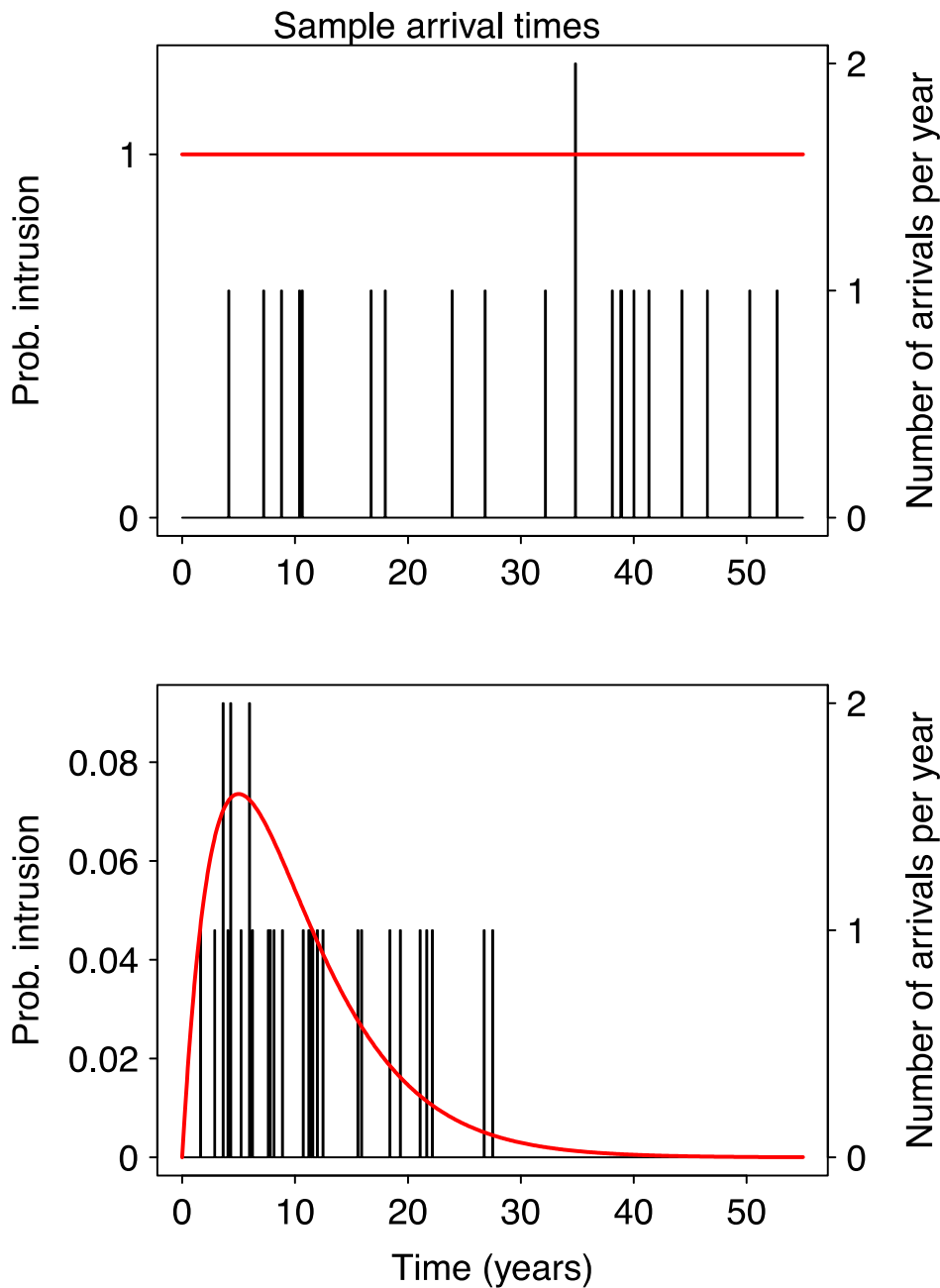


Figure 3. Arrival probability as a function of time, with a sample of arrival events; (a) constant arrival probability and (b) gamma-shaped arrival probability. Average number of arrivals is 0.5 per year and for the gamma function, $S = 2$. Red line shows the dependence on time for the probability of intrusion, black lines show the number of new infestation events per given month.

Note that in the current implementation of the model, the arrivals do not go extinct due to demographic stochasticity and thus always contribute to the spread; this represents the ‘worst-case scenario’ in which every arrival becomes established. This is particularly relevant for situations in which we have a flat arrival probability which would mean that we can never drive the disease to extinction under the default extinction threshold parameterisation.

4.6 Weather and climate module

4.6.1 Data sources

The climate data were obtained from:

<https://www.metoffice.gov.uk/research/collaboration/ukcp>

which provides the following disclaimer:

The data on this web site are available under the Open Government Licence, see

<http://www.nationalarchives.gov.uk/doc/open-government-licence/>

Header length	16
Area	312500.0 737500.0
Baseline	1981-2000
Data Source	Land probabilistic projections
Data Type	cdf
Scenario	RCP 8.5
Show Labels	TRUE
Software Version	WPS-1.0.6-DP-1.0.6-CV-1.0.2
Spatial Representation	25km grid
Temporal Average Type	Monthly
Time Period	all
Time Slice Type	1-year time slices
Variable	Mean air temperature anomaly at 1.5m (Å°C)
Year Maximum	2100
Year Minimum	1961

The weather data were obtained from <https://www.meteoblue.com/en/historyplus>

history+ offers historical weather simulation data, with a spatial resolution between 4 and 30 km, not measurement data. Starting in 1984, the historical weather data are available in hourly steps or daily aggregations with a spatial resolution of 30 km, whereas higher resolution data are available since 2008 for nearly every place on Earth.

4.7 Parameter dependence

We choose to incorporate the effects of climate change by allowing the epidemiological parameters to vary in time according to the local weather and climate conditions. The rate of spread of the pathogen, b , is affected by the short-term weather predictions whilst the proportion of susceptible plants, K is deemed to be affected by the longer term climatic variation.

Existing models for climate and weather exist (UKCP09 and Meteoblue), however these highly detailed and complex models require significant processing power and time to run. In order

to produce a modelling tool that is fit for purpose and that can produce results quickly we have constructed a simplified climate and weather model.

The underlying climate model captures the essential features of more complicated and realistic models while providing flexibility, speed and simplicity of the calculations. Two data sets were used to construct the model:

1. The UK Climate Projections (UKCP09). Mean temperature anomaly (difference in temperature compared with 1985) for model RCP8.5 was used to predict the future trends. Monthly model predictions were created for Central Scotland for 1985-2100 and the model is using the median value for each month.
2. The daily average temperature data for 1985-2019 were obtained from MeteoBlue for a location in Scotland (Glasgow). This data set is based on weather simulations but rigorously checked against the past data (for details see MeteoBlue website, <https://www.meteoblue.com/en/products>).

The model simulations start at 1985 which is where the records from the MeteoBlue web site are available. The program uses artificial (random) data and not the actual data for the period 1985-2019.

The model consists of two parts. The weather module uses a full simulation with a monthly resolution. The climate module uses only the baseline average temperature change. Thus,

$$T(t) = T_{base} + T_{slow}(t) + T_{fast}(t) + T_{month}(t) + T_{rand}(t)$$

$$T_{slow}(t) = \frac{c_1}{1 + \exp(-c_2(t - c_3))} - c_4$$

$$T_{fast}(t) = \frac{Ac_5}{1 + \exp(-c_2(t - c_3))} \times \sin(2\rho(t - c_6)) \times \left(1 + c_7 \sin\left(2\rho \frac{t - c_8}{c_9}\right)\right)$$

$$T_{month}(t) = B \left(1 + \frac{c_{10}}{1 + \exp(-c_2(t - c_3))}\right) \times \sin(2\rho(t - c_6))$$

$$T_{rand}(t) \sim c_{11} N(m = 0, S = 1)$$

with $T_{base} = 8.78$ representing the average baseline temperature in 1980s, T_{slow} representing the slow (decadal) change in the RCP8.5 anomaly, T_{fast} representing the fast (yearly) change in the RCP8.5 anomaly, T_{month} representing the natural variation at yearly time scale, and T_{rand} is the random component. Note that the weather results for the emulator are sampled at monthly interval and compared here with daily records for Glasgow.

Parameters $c_1 - c_{10}$ were estimated by comparing the RCP8.5 anomaly and the daily weather records with simulations.

Figure 4 shows the different components of the weather and climate change, as represented by the emulator, compared to the detailed model results (RCP8.5) and the weather record for 1985-2019. The emulator predictions are in strikingly good agreement with the more sophisticated RCP8.5 model predictions and offer a significant improvement in terms of speed and ease of use.

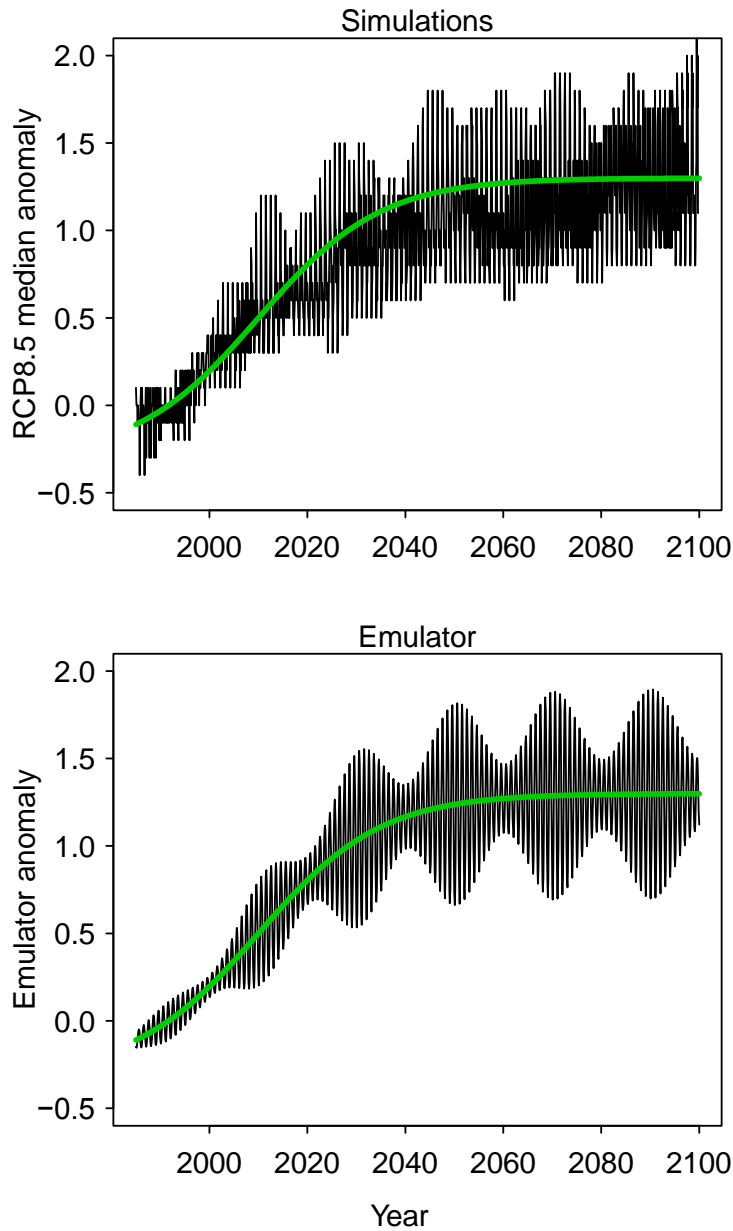


Figure 4. The RCP8.5 anomaly (black lines) from the IPCC simulations (top graph) compared with the emulator results bottom graph). The slow (decadal) change is superimposed on the record (green thick line; right column) and is used to model long-term changes in the availability of susceptible hosts.

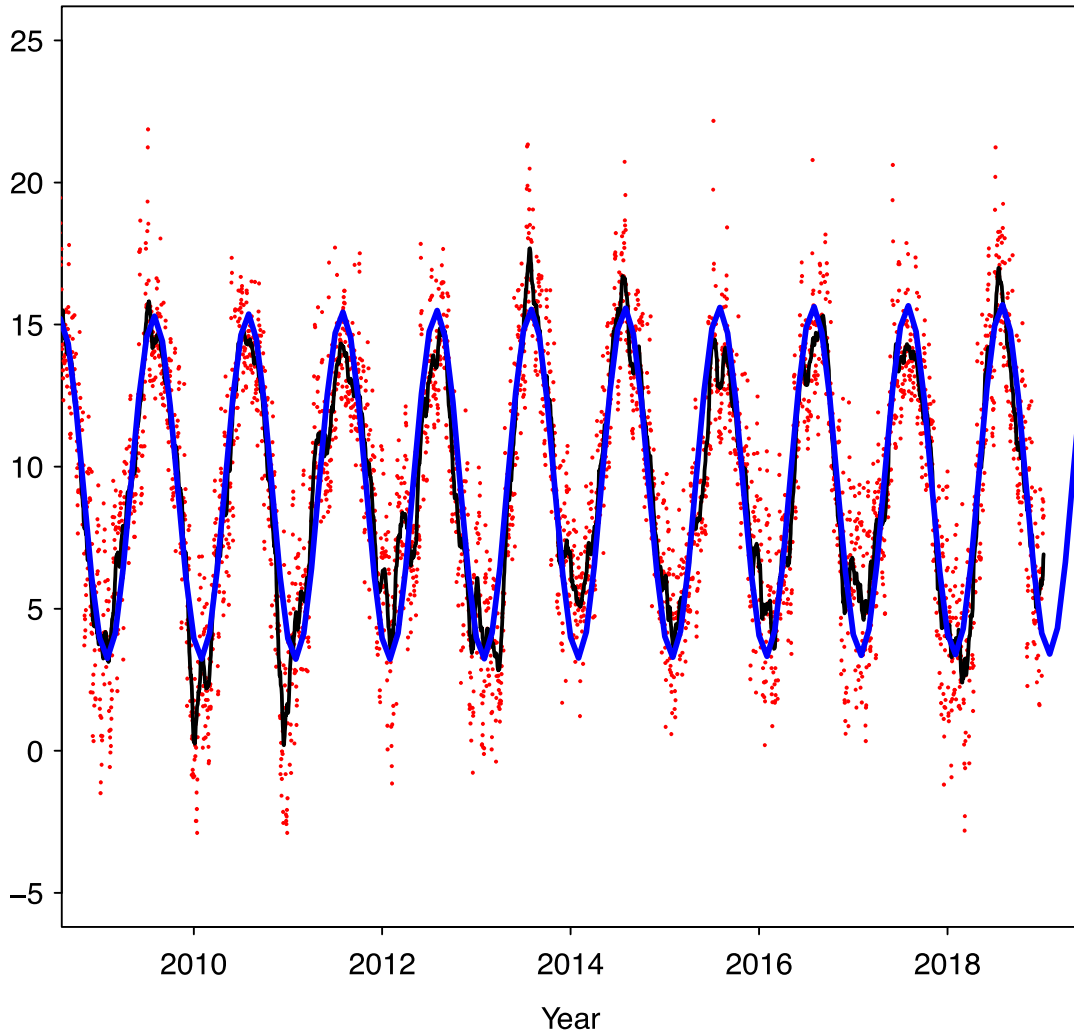


Figure 5. The short-term variability in the weather record (Meteoblue model) for the last 10 years is represented by the daily mean temperature data (small red dots) and the 30-days running mean (black line). The emulator representation of the data is shown as its smooth part, $T_{base} + T_{slow}(t) + T_{fast}(t) + T_{month}(t)$ (blue line).

4.8 Transfer functions and climatic susceptibility

The emulator successfully captures the key features of the temperature changes at different time scales, ranging from daily and monthly variability to decadal changes in the anomaly. It also assumes that not only the variability in the temperature record, but also a range of changes will increase over the period considered here.

The next required step is to specify how the changes in temperature affect the parameters of the epidemiological model, the task achieved by *transfer functions*.

The model implemented here considers two cases. Firstly, we assume that the rate of spread, \mathcal{D} , is affected by the monthly temperature record. This reflects the fact that many pests and pathogens have clearly defined temperature ranges and will not spread or spread slower outside this range. In this case, the transfer function is given by a bell-shaped function, see Figure 7, which captures the key features of temperature response for many known pathogens. The formula is given by

$$b(T) = b_{\min} + (b_{\max} - b_{\min}) \times \exp\left(-\frac{|T - T_{\text{thresh}}|^a}{aT_{\text{width}}^a}\right).$$

where b_{\min} determines the baseline rate, b_{\max} is the rate value at the peak, T_{thresh} is the location of the peak, T_{width} determines the width of the relationship, and a is the shape parameter, with $a \geq 2$ (the higher the value, the more “hat-like” relationship is).

Figure 7 shows an example of the transfer function for the short-term weather change and the corresponding effect on the rate (with $T_{\text{thresh}} = 25$, $T_{\text{width}} = 5$, $a = 8$. The pest can only effectively spread in the months when the temperature exceeds $\sim 18.5^\circ \text{C}$ (marked on the plot). Here we can see that as the average temperature trend increases over the decades, the number of years that contain months that exceed the critical level for successful spread of the pest increases in frequency until we see invasion every year after about 2018.

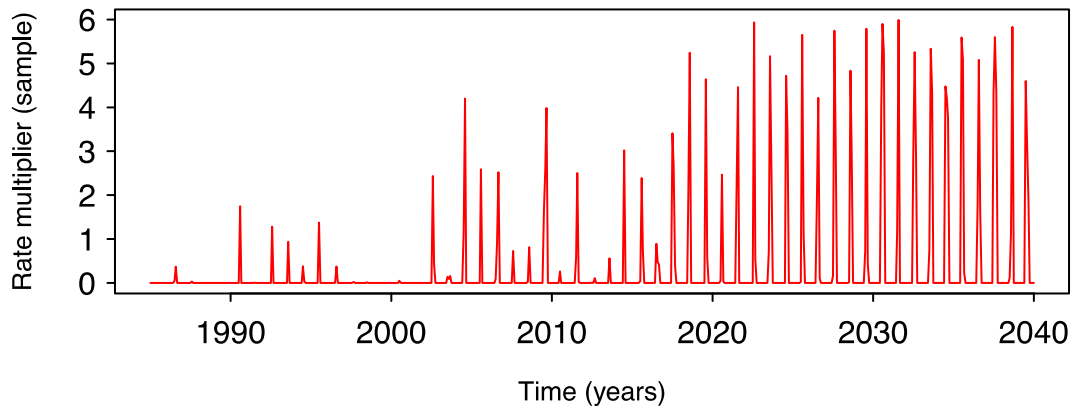
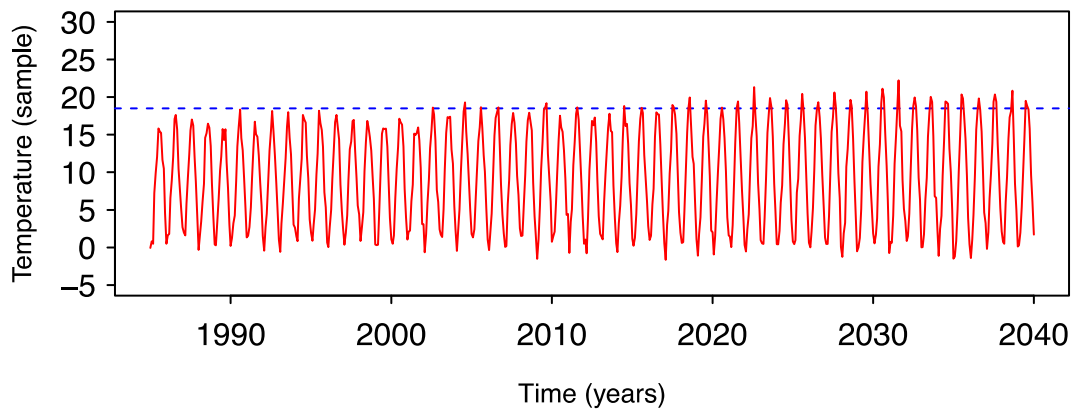
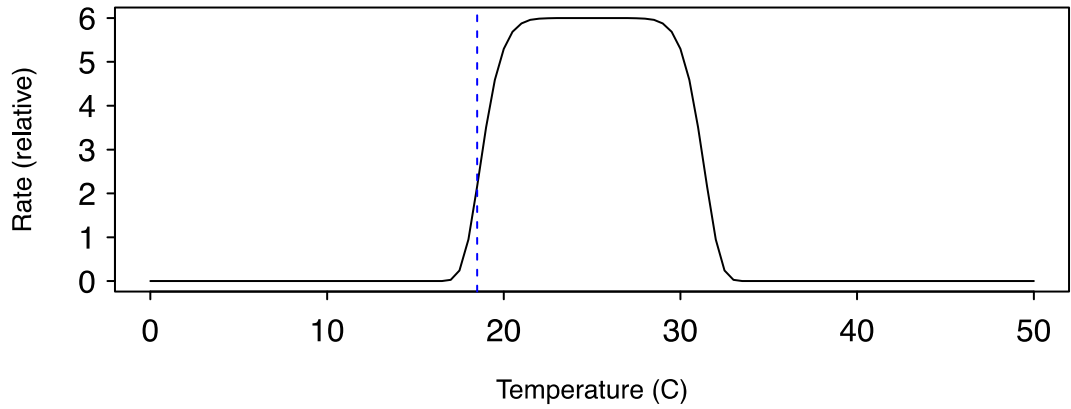


Figure 7. Top figure: The transfer function for the monthly weather component. Middle figure: a sample run of temperature, with the threshold marked by a horizontal line. Bottom figure: The corresponding rate multiplier, showing months in which, the temperatures were high enough to cause pest spread.

Secondly, we assume that the proportion of the total area with susceptible trees is being modified by a scale factor that represents the proportion of host area that is climatically suitable. This represents:

- change in local weather to alter pest survivability and growth (only weather effects rather than climate due to the short life span of the pest).
- change in accessible host range i.e. the proportion of the entire host population (N) that has a suitable environment. Given that the model is not spatially explicit this is how we can incorporate space. This means that the relationship over time should not just be increasing; we should be able to allow for the proportion of Scotland for example that is suitable for a particular pest to decrease over time too. For rapidly spreading invasive species weather would be more important. For slower spreading endemic pests climate would be more relevant.
- change in host abundance or host area due to environmental changes. This would reflect changes to N due to weather/climate.

The coefficient K is given by a piecewise-linear function which increases (or decreases) in time in a way specified by the user.

We propose that the function is given by

$$K(t) = \begin{cases} K_{\min} & ; t < t_{\text{low}} \\ K_{\min} + (K_{\max} - K_{\min})x \frac{t - t_{\text{low}}}{t_{\text{high}} - t_{\text{low}}} & ; t_{\text{low}} < t < t_{\text{high}} \\ K_{\max} & ; t > t_{\text{high}} \end{cases}$$

where the parameters t_{low} and t_{high} give the threshold times for changes to climatic suitability.

Thus, for example if the multiplier K is equal to 0 (below a lower threshold), the pest cannot become established (as there are no susceptible plants), and if it is equal to 1 (above the upper threshold), the pest can affect the maximum number of plants given by rN see Figure 8. The lower bound does not need to be 0, but the upper bound needs to be smaller than 1.

Figure 8 shows an example for the climatic suitability for the case when initially the climatic conditions are not suitable; the suitable area starts to increase in year 2020 and reaches the maximum level in 2040.

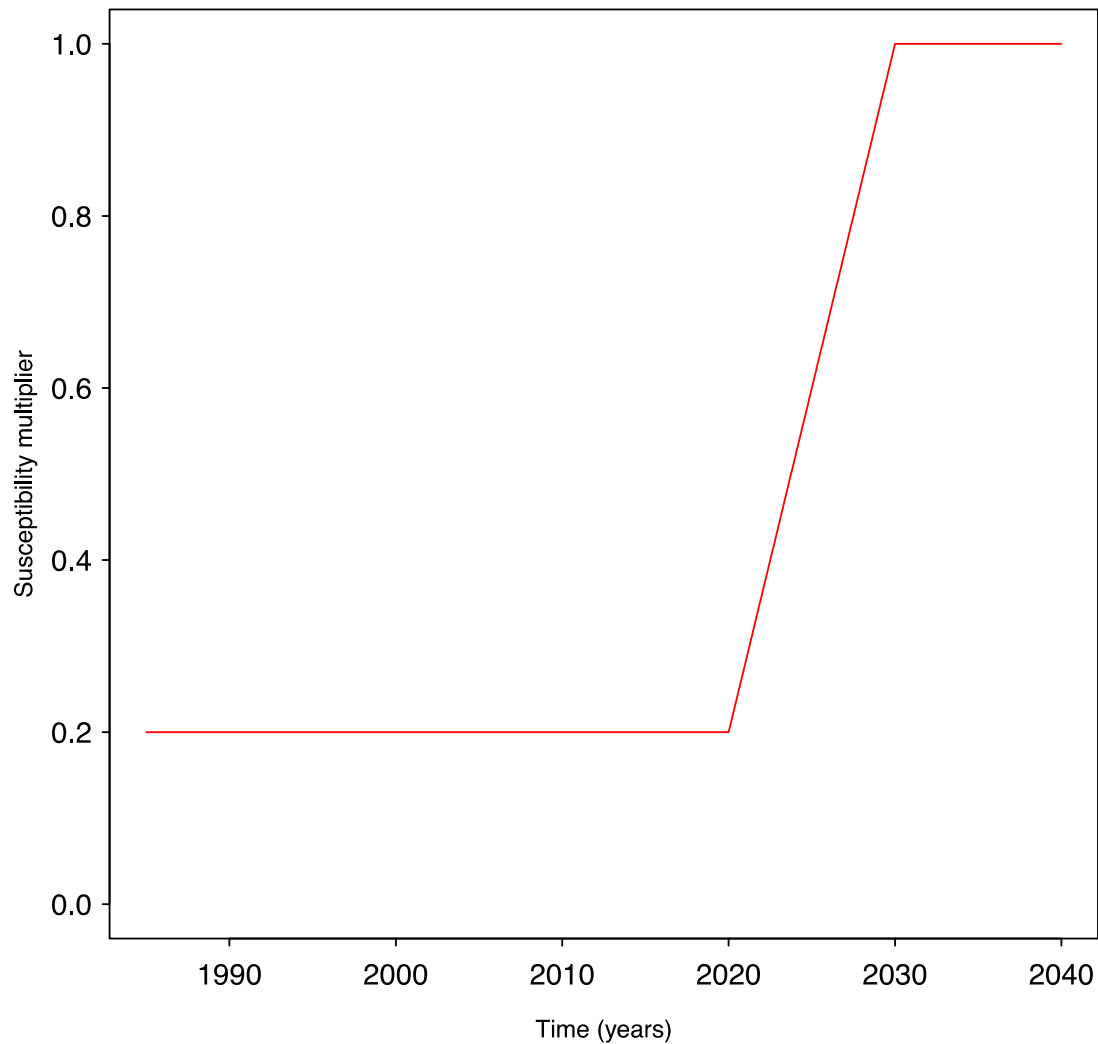


Figure 8. The susceptibility multiplier, K as a function of time.

The response of pests and pathogens to climate changes is potentially very complicated and pest and host specific, with limited data available to structure a model and parameterise it.

4.9 Economic module

The cost-benefit analysis is performed based on the valuation of ecosystem services of the plants, i.e.

- Market values:
 - Production value, e.g. timber
- Non-market values:
 - Carbon sequestration
 - Air pollution removal
 - Landscape value
 - Recreational values
 - Flood protection
 - Biodiversity
 - Health protection/reduction

and on costs of control. The individual values are entered independently and expressed as GBP per ha; they are multiplied by the relevant acreage to produce the total value at any given time. The values are all combined into a single number representing the estimate of the total value and the Net Present Value is calculated using an appropriate discounting factor (as specified in the Green Book).

The following scenarios can be addressed in the model:

1. Healthy-infested plants only: This is the simplest setting in which there are only two states, S and I, with S areas worth the baseline amount, and I areas worth the reduced amount. Example is provided by the *Xylella* infestation, in which plants continue to be infested, but represent a lower value due to defoliation and restrictions on recreation.
2. Healthy-infested-removed, with R class representing areas that were infested but are now lost due to removal or ban on production. In this scenario, the plants in the R class have zero value; thus the value of S and I classes represent the difference compared to the R class. Example: Bark beetle infestation in which infested plants are removed; the reduction in the timber value captures the need to separately process infested trees.
3. Healthy-infested-removed-resistant, with the V class (analogous to vaccinated in a standard SIRV model) representing areas that were healthy but are now treated or replanted with resistant varieties. In this scenario, the V class has the same value as the S class, assuming that the treatment/replanting has no effect on the usefulness of the plants. Example is provided by treatment of healthy trees for ash dieback or spraying large areas of the forest, or cutting down the susceptible trees and replanting with resistant varieties which have the same ability to supply the ecosystem services.
4. Similar to 3., but with the V class treated in the same way as the R class, i.e. representing zero value. In that case, the value of the S class represents the differential between the value of fully healthy crop/trees and the value of the replacement. Examples include usage of resistant varieties which have a lower yield or value, or replacing seed potato growth with ware.

Costs of treatment are assumed to be constant per area treated, i.e. eN .

Net Present Values of benefits and costs are evaluated over time, depending on the current status of infestation/infection and control effort, using a discount rate as specified in the UK Government "Green Book", i.e. 3.5% for years 1-30 and 3% for >30 years. Cumulative NPVs are used in assessing the effectiveness of the control measures. Thus,

$$C_{t+1} = \begin{cases} eN; & I_{t+1} \neq 0, t \in [t_{start}, t_{stop}] \\ 0; & \text{otherwise} \end{cases}$$

$$D_{t+1} = \begin{cases} \sum_i v_i (g_i I_{t+1} + R_{t+1}) & \text{if infected plants are removed} \\ \sum_i v_i (g_i I_{t+1} + r_i V_{t+1}) & \text{if both infected and susceptible plants are treated} \end{cases}$$

$$\text{Value lost}_T = \sum_{t=0}^T \frac{1}{(1+d)^t} (D_{t+1} + C_{t+1})$$

with

v_i	value of ecosystem service i
g_i	reduction in the value of ecosystem service i of infected plants (removed worth 0)
r_i	reduction in the value of ecosystem service i of treated plants
d	discount factor.

where c_{t+1} represents the costs associated with the time step $t+1$; similarly c_{t+1} represents damages at that time; value lost is then computed as a Net Present Value of the costs and damages by the time T . D_t represent the level of damages caused by the pest/pathogen.

The use of the cumulative Net Present Value requires an explanation. The damages and costs are calculated in each period, i.e. with a monthly resolution, for a period of 32 years (2019-2050, inclusive). The future values are discounted, using the recommended discount rate(s), and subsequently added to produce a total figure up to a given time. Thus, to use an illustrative example, let the loss of the value of Ecosystem Services be £1m every month for 384 months (32 years, 12 months each). Without discounting, the total figure over this period will therefore be £384m, with an average of £12m per year. The discounting procedure reduces the future value of the losses, so that the actual NPV will be smaller; in our example it will be equal to £231m, i.e. £7.2m per year. In more realistic examples, the losses will be determined by pest or pathogen spread and therefore will change over time.

4.10 Parameter values and their uncertainty

In order to address the uncertainty in the parameters and processes, the model is solved repeatedly using different values of parameters drawn from a distribution. Thus, although the model dynamics is currently purely deterministic (except when weather is included), the variation in parameters will translate into the distribution of outcomes.

Each parameter is drawn from a triangular distribution which is currently assumed to be symmetric and thus the user can select the lowest and the upper limit (when the two are equal this means no uncertainty in the given parameter). The parameters are assumed to be uncorrelated.

For the purpose of comparison between the scenario without control and with control, the random numbers are reused. Thus, a pair of two simulation runs is created, one without control being implemented, and one with the appropriate control, but they have the same set of parameters (except weather stochastic realisations). This allows a direct comparison of the effect of control, conditioned on all parameters being the same.

4.11 Reporting module

The model including control options is run a user-specified number of times; each run corresponds to a different selection of random parameters. The simulations are repeated for the case with no control options (effort set to zero), to obtain a benchmark corresponding to the “do nothing” case. The results are then presented to the user in a graphical way, with a median, 50% and 95% confidence limits. The source-code version which runs in RStudio allows the user to create custom plots.

The key graphs include:

1. The infestation progress over time.
2. The progress of losses (damages plus costs) over time.
3. The avoided losses distribution.
4. The removal progress – area moved to R class.

The avoided losses are defined as a difference between the NPV of losses calculated for the case without control (“do nothing”) and the NPV of losses calculated for the case with the specified control strategy. Thus, a negative value of the avoided losses means that the combination of costs and damages with control exceed the damages when doing nothing; this suggests that no action should be implemented. Conversely, a positive outcome suggests that control is cost beneficial.

Thus, for example, b will be drawn from a triangular distribution and then a pair of simulations will be carried out, one of which will include appropriate control measures. The losses will be calculated for both cases and a difference will then give an estimate of the avoided losses for this pair. This process will be repeated, yielding a distribution of avoided losses.

The main feature of this method is that if there is no effect of control, the value of avoided losses will always be equal to 0, even if the losses with and without control are randomly distributed.

4.12 Parallel computations

The ensemble method requires a large number of replicated runs to correctly address the uncertainty; this leads to long execution runs which are particularly difficult for the interactive version. The program is able to use the ability of modern computer processors to run the simulations in parallel on a multi-core architecture.

The ability to use the parallel computation is regulated in two ways. Firstly, there is a variable, *allowParallel* which is settable in the scenarios. When a variable *allowParallel* is set to 1, it enables parallel computation; there is an initial lag in starting the program when compared to the non-parallel option (when *allowParallel*=0), but it then carries out simulations much quicker. Both the initial start up time and the speed depend on the number of cores available on the computer (up to 16, which is the optimal number suggested by benchmarking using a Linux computer with 48 cores).

Unfortunately, due to an MS Windows bug, it is sometimes not possible to run the model in the parallel mode in RStudio on a Windows computer; *allowParallel* must be set to 0.

4.13 Scenarios

A complete set of all the parameters (including those used internally in the program and unused parameters) is called a Scenario and can be saved in a CSV file. This file can be investigated and modified in MS Excel or a compatible program and then input back into the simulation program. This allows a creation of several Scenarios, as well as helping with maintaining security of sensitive information related to the parameter choices. Thus, the model equations can be made public, but the parameter estimates and detailed model assumptions can be loaded only when the program is run and then discarded.

The CSV file must follow exactly the format of a sample Scenario included in the package. In particular, the order of the columns and the first two rows must be kept exactly. Different rows can be added with scenarios which then can be selected from within the program.

Appendix A: Review of the climate and weather influence on selected pests and pathogens

In this section we provide a literature review that was subsequently used to guide the parameterisation of the model in Case Studies listed in Appendix B.

The effect of climate change will be seen on both host plants and pathogens via impacts on their genomes, physiology, and environmental spread, which in turn will influence the

outcome of the plant-pathogen interactions – though climate change can have positive, negative or neutral impact on individual plant-pathogen interactions. Nevertheless, all sides of the plant-environment-pathogen triangle of the plant disease will be affected, and so climate change will add an extra layer of complexity to the task of plant protection (Pertot, Elad, 2012). Because a plant disease is the result of interaction between a susceptible host plant, a virulent pathogen and the environment, climate change will certainly affect plant diseases. The changes associated with global warming (i.e., increased temperatures, changes in the quantity and pattern of precipitation, increased CO₂ and ozone levels, drought, etc.) thus, may affect the incidence and severity of plant disease and influence the further co-evolution of plants and their pathogens (Pertot, Elad, 2012; Pautasso et al., 2012). Moreover, pathogens that have evolved at higher latitudes may be able to tolerate a wider range of temperatures. These pathogens usually live in climates cooler than their physiological optima; therefore, warming is expected to enhance their fitness and the risk of epidemics of the diseases with which they are associated (Elad, Pertot, 2014 and references therein).

For example, the increased mean winter temperatures, the shift in precipitation from summer to winter and the tendency toward heavier rain, which have been noted in central Europe, favour infection by several *Phytophthora species* and thus increased incidence of root rot in forest trees (Pertot, Elad, 2012). Next, dryer conditions will lead to lower expression or lower efficiency of disease resistance genes in some plants (e.g. bacterial diseases in rice), but will also reduce the possibility of spread for certain fungal infections, such as pine needle disease *C.rubicola*, which is a wet- and cool-weather disease. Similarly, higher temperature may be beneficial for the northward latitudinal spread of some trees and simultaneous increase in spread areas of pests for which those trees are host plants. And higher CO₂ content may induce plant structural changes and also higher fecundity and expansion of fungal pathogens affecting conifers, such as *Colletotrichum gloeosporioides* or needle blight or *P. cinnamomi*. Another example is the spread of pathogens with more frequent hurricanes, such as an assumed immigration of soybean rust to the USA via Hurricane Ivan, though for this pathogen a drier future climate will probably slow its movement across country (Garreth, 2014).

There will be direct effects of climate change on pathogens. Summarizing the effect of higher annual temperatures, higher CO₂ levels, and changes in relative humidity, it is possible to expect that: (i) increased air temperature would result in a poleward expansion of the geographical range of pathogens and in more generations per year; (ii) elevated winter temperatures would increase survival and hence the amount of initial inoculum in many pathosystems; (iii) the longer growing seasons that will result from global warming will extend the amount of time available for pathogen reproduction and dissemination; (iv) and that greater continental dryness during summer would reduce risk of infection by pathogens that require leaf wetness or saturated soils for infection; (v) pathogen fecundity has been shown to increase in the presence of elevated levels of CO₂, thereby accelerating evolution in response to climate change (Kudela, 2009; Elad, Pertot, 2014).

Climate change may directly affect several aspects of the biology of host plants, including their phenology, sugar and starch contents, nitrogen and phenolic contents, root and shoot biomass etc. Any change in any of these areas may influence infection and colonization by pathogens. On the other hand, abiotic stress may induce the activation of general defence pathways in plants, which increase resistance, but also increase the susceptibility of the plant to certain pathogens. Drought may impair the production of plant defence substances or growth, favouring the progress of the pathogen, but at the same time several diseases are less severe when the availability of moisture is limited. Higher CO₂ concentration will result in higher leaf area and total biomass, and many foliar pathogens can take advantage of the more humid microclimate caused by denser plant growth and the higher availability of host tissue. Thus pathogen infection rates of these pathogens usually increase at higher CO₂ levels (Pertot, Elad, 2012).

Increased levels of CO₂ and ozone in the atmosphere may have also indirect effects on the plant diseases via affecting microbial communities in soil and the functioning of the microbial ecosystem. It may, in turn, affect plant growth and the plants' ability to withstand attacks by pathogens. Higher concentrations of atmospheric CO₂ may also lead to an increased plant resistance to certain viruses (Elad, Pertot, 2014).

In case of vector-borne diseases, climate influences the spatial distribution, susceptibility to infection, the spread of infection within the host as well as intensity of transmission to a new host, and seasonality of diseases transmitted by vectors (Kudela, 2009). In particular, in a warmer climate the risk of infection may be higher because the vector populations will be larger by the time of crop planting.

Taking into account all the above effects of climate change, plant protection under the changing conditions will be a very complex task. As noted by Pertot and Elad (2012), under worst-case scenarios, several crops may require more fungicide spray treatments or higher application rates, thus increasing costs for farmers, prices for consumers, but also soil and water pollution and the likelihood of the development of fungicide resistance. At the same time, temperature can directly influence the degradation of chemicals and alter plant physiology and morphology, thus possibly reducing the efficiency of anti-disease treatments. So more attention will be attracted to the possibilities of changing or adapting agronomic practices (such as crop rotation, tillage, fertilization, irrigation, seed selection) or development of biocontrol agents and methods in order to cope with an increased risk of diseases (Juroszek and von Tiedemann 2011).

Xylella fastidiosa

As described in Bosso et al (2016b), *Xylella fastidiosa* is a xylem-limited bacterium that affects several economically important plants. Pathogenic strains of *X. fastidiosa* were first recognized in North and South America and Asia in the 1990s. This bacterium was first observed in Europe near Gallipoli (Apulia Region), southern Italy, in October 2013, and since its initial outbreak it has spread across the region and northward at a rate of approximately 20km per year, causing considerable damage to olive groves. *X. fastidiosa* is transmitted by various species of sap-sucking hopper insects and in Apulia it is vectored to olive trees by the spittlebug, *Philaelus spumarius*. The species *X. fastidiosa* were subdivided into six subspecies (*X. fastidiosa*, *pauca*, *multiplex*, *sandyi*, *tashke* and *morus*), but only two of them, *fastidiosa* and *multiplex*, are formally considered valid names.

Hoddle (2004) used *X. fastidiosa* records collected in California to project a distribution model CLIMEX to the rest of the world. The model was developed using the climatic response of this plant pathogen from the native geographic range. The main prediction was that cold temperatures would not allow *X. fastidiosa* to colonize northern France and the northern and central areas of grape production in Spain and Italy. Bosso et al (2016a) developed a MaxEnt model (described at http://biodiversityinformatics.amnh.org/open_source/maxent/) for *X. fastidiosa* in Italy based on Apulia records. The Maxent model predicted a high probability of *X. fastidiosa* occurrence in Apulia, Calabria, Basilicata, Sicily, Sardinia and coastal areas of Campania, Lazio and south Tuscany.

Precipitation of the driest and wettest months were found to be the main variables influencing model performance. Based on the model predictions, *X. fastidiosa* had a high probability of colonizing areas characterized by: (a) relatively low altitude (0–150 m a.s.l.); (b) precipitation in the driest month <10 mm, wettest month ranging between 80 and 110 mm and warmest quarter <60 mm; (c) mean temperature of coldest quarter ≥8°C; (d) agricultural areas comprising intensive agriculture, complex cultivation patterns, olive groves, annual crops associated with permanent crops, orchards and vineyards; forest (essentially oak woodland); and Mediterranean shrubland.

Further study (Bosso et al., 2016b) showed that, first, *X. fastidiosa* spread in the Mediterranean basin is unlikely to be affected by climate change, as the region is already suitable for the disease; and second, further spread into northern parts of Italy or France, or further northwards is unlikely. However, this model was calibrated by the data of *Xylella*'s current spread in southern Italy, which limits the precision of model forecast for other climatic zones. It is therefore possible that under certain climate change scenarios *X. fastidiosa* range would increase to include parts of Northern Europe.

Godefroid et al (2018) used the historic data on *Xylella* spread in the native and invaded environments, combined with climate conditions predicted by MIROC5 model, to generate future disease spread and severity using a Cumulative Link Model and a Species Distributed Model implemented in R (packages 'ordinal' and 'dismo'). Their simulations also concluded that subspecies *X. pauca* would be approximately limited by the Mediterranean basin, and the conditions for *X. multiplex* may become favourable in most of Europe up to southern England, except for elevated areas and cold northern regions. Accounting for the fact that the subspecies *X. multiplex* is associated to economically important plants such as almonds and olives, and may also colonize multiple ornamental plants, the impact of *Xylella* spread will likely be significant.

DEFRA (2017) provides an updated and extended analysis of the risk of *X. fastidiosa* arrival and establishment in the UK. They confirm an earlier assessment that *X. fastidiosa* was unlikely to moderately likely to establish (in part, because cold winters and unreliable snow cover that limit overwinter survival) and that its potential to cause economic, environmental and social impacts was small. These risk ratings were primarily based on models MaxEnt and CLIMEX and on climatic suitability because hosts and vectors are present. However, the degree of uncertainty about those conclusions is very high because the species is so variable, is still spreading and the actual limits to its distribution are so poorly known. So both models are regarded as providing rather imprecise predictions.

White et al (2017) developed a spatial model of *Xylella* spread in Italy in the early stage of invasion. Besides predicting the pattern of spread, the model allows to evaluate different disease control strategies; we used the results of the model to guide our estimation of the doubling time for *X. fastidiosa*.

As cited by Godefroid et al (2018), it was shown that there is a so-called 'cold cure phenomenon', when grapevines recovered from symptoms of *Xylella* following multiple exposures to temperatures below -8°C during several hours. Furthermore, it was suggested that areas experiencing more than 2-3 days with minimal temperatures below -12.2°C are at low risk of *X. fastidiosa* incidence. However, DEFRA (2017) cites evidence that the subspecies *X. fastidiosa multiplex* may be the principal risk to the UK, since it seems to be not as much affected by low temperatures as other subspecies and is also found in temperate climates as far north as south-eastern Canada. It is still not clear though if this cold tolerance is an inherent *Xylella* feature or rather a result of the host-pathogen interactions.

Zebra chip disease

Zebra chip disease of potato is a serious pest of potato in North and Central Americas and New Zealand, first documented in late 1990s-early 2000s. According to USDA data, zebra chip disease is a quality issue for growers (with a potentially high economic impact) and does not constitute a health risk for the general public. It is caused by the bacterium *Liberibacter solanacearum* which is spread very effectively by the tomato-potato psyllid (*Bactericera cockerelli*). This psyllid is absent from the EU at the moment. In November 2016 symptoms of zebra chip were reported for the first time anywhere in the EU by Spanish authorities in the autonomous region of Cantabria, though the disease levels were low with only 0.5% tubers with symptoms (DEFRA, 2018).

Psyllid populations are likely driven, both locally and regionally, by environmental factors such as temperature, rainfall, host quality, etc. Studies conducted under controlled conditions, demonstrated that potato psyllids are able to survive for several hours when exposed to sub-freezing temperatures. The outbreak of psyllids can be controlled with the use of both insecticides and biological control agents, such as some larvae, insects, parasitoids, and a fungus (USDA, 2014).

Havercort and Verhagen (2008) analysed the effects of climate change on potato diseases and pests and concluded that a higher disease pressures should be expected. On one side, pests and disease vectors (e.g. psyllids) multiply faster at higher temperatures and also will have a longer period for multiplication. On the other side, overwinter survival rate for insects hiding in host plants will also increase (Kanters, 2018). Horton et al (2015) noted that there are two factors that limit northward expansion of psyllids: first, overwintering in northern latitudes would require the psyllid to be cold-hardy enough to survive winter temperatures; and second, relatively limited availability of host plants on which the psyllid can survive between the end of over-wintering and the emergence of potato in spring. Future warmer and more humid environment or emergence of a 'bridge' overwintering host plant may weaken the restrictive effect of these factors.

Bark beetle

According to Lausch et al (2011) and references there, there are more than 150 species of the bark beetle in Europe. Perhaps the most important is *Ips typographus*, which infests spruce trees across the continent. It is considered a secondary pest, in the sense that it finds favourable conditions to thrive only in damaged and dying host trees. Storms and heavy winds, snow damage, emissions from environmental pollutants, or water shortage as a result of extreme weather conditions all lead to damaged spruce trees that can serve as the ideal breeding grounds for *I. typographus* but which can easily favour an outbreak given the right weather conditions. Once they have reached high population levels, the *I. typographus* are even able to attack and kill healthy trees and thus are capable of causing the mortality of apparently-healthy trees over millions of hectares of forest.

During its development, the spruce bark beetle comes through several stages, and the whole generation development from the copulation to the adult has duration of 7–11 weeks. Adults finish maturation in the spring prior to their dispersal flight. These flights are initiated in response to air temperatures of 20°C. The number of generations per year is dependent upon temperature.

There is a broad consensus that global warming is changing both the temporal and spatial dynamics, and the pattern, frequency and population dynamics of *I. typographus*. In particular, rises in temperature are leading to changes in the number of generations per year and their survival through winter periods, as well as an increase in the susceptibility of the host vegetation.

For example, in the northern part of its range, the beetle has one generation a year, but it can complete two generations per year further south (so-called multi-voltinism). In Central European lowlands it frequently completes two generations per year and has been reported to reach three generations in recent climatically favourable years. A first generation having a high rate of reproduction means the beginning of a large second generation, which will produce many offspring flying in the next season.

Jönsson et al (2007) in their literature overview commented that the temperature increase will have both direct and indirect impacts on the population of the bark beetle. In particular, the existing research results show that first, higher temperature increases the probability of appearance and survival of a second generation of the bark beetle in a year, and the risk of lethal bark beetle attacks on living spruce trees increases with beetle population size. And

second, summers may become hotter and drier, and especially drought stress is a major factor undermining resistance of spruce trees to attacks by *I. typographus*.

Jönsson et al (2007) also provided a detailed summary of the bark beetle development dynamics, which is summarized below.

For beetles hibernating in the bark of the trees, a thermal requirement for spring swarming (i.e. for the emergence following the hibernation period) between 48 and 126 degree-days (above +5°C) has been recorded, whereas a heat sum of 110 to 170 degree-days was recorded for beetles hibernating in the soil.

Swarming activity has been recorded at temperatures above 16°C and below 30°C (e.g. Lobinger, 1994). Mass swarming has, however, only been recorded when daily maximum temperature exceeds 20°C, according to reviews by Christiansen and Bakke (1988) and Wermelinger (2004). The swarming is followed by a temperature dependent pre-oviposition period of one to three days (Wermelinger and Seifert, 1999).

For successful attacks on living trees, 3-4 consecutive days above the temperature threshold for swarming is required (Wermelinger, 2004). For daily maximum temperatures above 20°C this occurs on average 9-15 days after the first day exceeding 20°C.

During the oviposition period, a maximum of four to five eggs are produced per female per day at 25–30°C, whereas it takes two days to produce one egg at 12°C (Wermelinger and Seifert, 1999). However, the extension of the egg-laying period also depends on the attack density, with fewer eggs being produced at higher densities. At low densities the oviposition may continue for 20 days at 25°C (Anderbrant and Lofqvist, 1988), but at higher densities, each female spends a shorter time in the brood tree and half of the egg clutch is produced within the first two to four days (Anderbrant, 1990). So on average, mass egg development starts in seven days after the spring swarming.

Then two to four weeks after the spring swarming, about 90% of the parent beetles leave the brood tree. The timing is influenced by weather and attack density (Anderbrant et al., 1985). Approximately one third of these beetles produce a second brood (Anderbrant, 1989).

Interestingly, they commented that the second brood is usually of minor importance compared to the first brood (Anderbrant, 1989), and is even less significant for the population growth in regions with two or three generations per season (Wermelinger and Seifert, 1999).

The development time from egg to adult bark beetle is influenced by the temperature conditions within the brood tree. According to literature reviews by Annila (1969) and Harding and Ravn (1983), the temperature sum needed for the complete development varies between 460 and 1170 degree-days (above +5°C), though the median is within the range of 625–750 degree-days.

After completed development, summer swarming and the production of a second generation can take place. The summer swarming is assumed to take place when the daily maximum temperature reaches +20°C after the date of completed development.

The factors leading to cessation of flight activity (i.e. summer swarming) in late summer are not well understood, but inhibition of summer swarming has been suggested to be triggered by cold spells below a mean temperature of 10–15°C in autumn (Annila, 1969).

Lausch et al (2011, 2013) studied the spread of the beetle in the Bavarian Forest National Park during 1990-2007. Based on the existing literature, they considered the impacts of biotic and abiotic habitat factors on the beetle. Those factors were grouped into five sets of variables: 1)

climatic factors that affect the mobility, larval development, proliferation and the spread of the *I. typographus* (temperature, potential duration of sunshine, potential solar radiation); 2) the topography of the terrain, which plays an important role in the spread of the beetle (aspect, slope, elevation, height differences); 3) soil types that affect the vitality of the spruces, thus leading to a potential increase in *I. typographus* infestation; 4) structure and composition of forest (distance to woods of different ages, percentage of spruces in the previous year, diameter of spruce trees); 5) spatial configuration of the previous year's infestation (distance to affected areas, area and perimeter of deadwood spruce etc.). As it turned out, the importance of some of these factors remained approximately unchanged over the time and stages of the *I. typographus* outbreaks, while others varied in importance. Among the abiotic factors, the most important factor is the absolute elevation of the forest. Unlike the results from other studies, slope and slope orientation are not crucial for the model. Among the climate variables, the duration of sunshine and the potential solar radiation were not important. The impact of annual average temperature was not consistent: it was important during the periods of peak spread (higher temperatures had strong positive impact), but there were also periods when the model favoured lower mean temperatures. Such an ambiguous effect of the mean temperatures on the probability of beetle outbreaks was observed in other studies as well. Among the biotic factors, the soil and forest composition variables did not come out as very important for the analysis. However, the distance to the sites of infestation from the previous year, as well as the distance to and area of the deadwood from the previous years are among the most important factors influencing the distribution and dispersal of the *I. typographus*. Gilbert et al (2005) and Eriksson et al (2006) came to similar conclusions in their research. Their studies showed that the number and size of damaged trees affect the number of *I. typographus* that end up colonizing the forest.

Aukema et al (2008) modelled with a spatial-temporal autologistic regression the dependence between climatic, spatial, and temporal characteristics of the mountain pine beetle outbreaks in British Columbia, Canada in 1970s-1980s and the probability of beetle spread. The climatic variables included temperature maximums and minimums over the year, average daily temperature, numbers of warm and cold days, and accumulated degree days. The temporal variables indicated the presence of the beetle outbreaks at the measurement points (i.e. model cells) in the previous three years, and the spatial variables counted the number of neighbouring infected cells. The main results are that, first, the presence of mountain pine beetle outbreaks in the closest neighbouring cells (within the distances of ca. 18km from a cell's centre) is the best predictor of a cell's chances to host an outbreaking population (coefficient 1.452); second, the presence of beetle outbreaks in the previous two years are also highly significant factors (coefficients 0.700 and 0.502); and third, the probability of outbreak is inversely related to the number of severe cold days during winter (coefficient -0.033, i.e. negative impact on larvae survival), and positively correlates with a higher number of warm days during the summer months when the beetles are most active (coefficient 0.036, i.e. positive impact during the flight period as well as additional low-water stress for the host trees). Although the effect of the mean temperature is less clear due to either collinearity of variables or a possibly non-linear effect of the temperature on the outbreak probability, the authors nevertheless comment that higher temperatures may generate spatial synchrony of beetle spread from several disjoint locations over large regions.

Carroll et al (2004) is another study that looked at the impact of the climatic variables on the dynamics of the mountain pine beetle (*Dendroctonus ponderosae*) infestation area in the British Columbia. They observe that due to continuing global temperature increase more earlier climatically unsuitable (i.e. northern, relatively colder) areas become infested by the pine beetle. At the same time, perhaps due to excess warming, some earlier infested areas become less suitable for the pine beetle populations and the degree of infestation there decline. A possible explanation is that heat accumulation during summer forces beetle populations into partial multi-voltinism (i.e. when segments of the population have more than one generation per year), which in turn will lead to better overwintering of different stages of beetle

development (eggs, pupae etc.) and so to lesser flight synchrony and mass attack success in the following year. Nevertheless, the authors comment that while in the past the pine beetle outbreaks collapsed due to localized depletion of suitable host trees and the adverse effects of low temperatures, current climatic conditions may lead to an insufficient decline of the beetle population following an outbreak.

A related observation was made by Ste-Marie (2015), who summarized the experience of studying the mountain pine beetle and counteracting its outbreaks in British Columbia, Canada, since 2000. As she noted, a century-long wildfire management practice created forest with very homogeneous, even-aged stands of large mature trees, which turned out to be an almost ideal habitat for the mountain pine beetle. In recent years, a c. 1.1C increase in average temperatures and absence of cold events in the area since 1995-96 resulted in dramatic increase in beetle spread and area of killed forest.

Wermelinger and Seifert (1999) studied reproduction of the spruce bark beetle in the laboratory under different temperatures in the range 12-33°C. They fit different models for the daily oviposition rate, combined with beetle development, sex ratio, and mortality data, and find that the optimal temperature range for the beetle population expansion is 25-29°C. Under such conditions females both lay maximum number of eggs and produce 2-3 sister broods. Temperatures above 30°C lead to a rapid decline of beetle population.

Jönsson et al (2007) modelled the effect of a climate change-induced temperature rise on the population dynamics of *I. typographus* for southern Sweden. They considered three scenarios, with the annual average temperature staying at its current level (from 10°C in May to 17°C in July-August) or increasing by either 2-3°C or 5-6°C by the end of the century. The results of the simulations predict that under climate change the spring swarming would start approximately 23 and 39 days earlier compared to the status quo, and the second generation will completely develop 28 and 50 days earlier. That is, elevated temperatures would increase the probability of a summer swarming, as well as the probability that the second generation will reach maturity before winter. Consequently, while the summer swarming (i.e. a second generation) would occur 1-4 times during a 30-year period under the current conditions, at higher annual temperatures there would on average be more than 20-25 years with a second generation during a 30-year period, or even every year under the hottest scenario.

But there is also a negative effect of too hot climate on the beetle population. The increased frequency of days with temperatures exceeding the upper threshold for flight activity of *I. typographus* (i.e. above 30°C) implies that the probability of the summer swarming being delayed for one or a few days will correspondingly increase. An increased number of days with temperatures above 30°C will also have a negative effect on the development of *I. typographus* by decreasing the developmental rate of the brood (Wermelinger and Seifert, 1998). Also, temperatures under the bark surface exposed to direct sunlight can easily reach well above the lethal levels of ca. 50°C (Annala, 1969), thus adding significantly to the mortality of immature stages.

Appendix B: Case study 1 - *Xylella* spp. on UK oak

This case study illustrates the potential for the model to capture the risk of a disease that is currently not present in the UK but can become prevalent with climate change. We were unable to find sufficiently reliable estimates of the rate of spread of this pathogen that could be used to estimate its potential spread on hosts relevant for the UK or Scotland, or the ecosystem values and pathogen impacts. However, the model allows us to use the existing information (from Italy) and to address this uncertainty in a quantitative way.

The time horizon is assumed to be 2019-2050 and the model is run 250 times; no control option is currently included in the model.

Parameter	Value	Comments
Doubling time	12 months	Focal spread ca 20km per year in Italy. Unknown in UK conditions; vectors are potentially present everywhere, so spread can be quick. Assumed one year doubling time which captures the expansion in Italy 2013-15.
Total area	167,000 ha	Total area of oak in the UK
Susceptibility	Maximum 60-90%	Assuming most oak trees will be susceptible but some are resistant
Average incursion time and shape	10 years average; shape parameter 1.5 (scalar)	Assuming that the probability of incursion is relatively low at present, but quickly increases – representing the increase in the incidence of <i>Xylella</i> in Southern Europe, with the maximum around 6-7 years from now and slow decay as susceptible hosts in Southern Europe are removed.
Average number of successful incursions per year	0.5	Assumes that on average a successful incursion occurs every 2 years.
Area infected in each incursion	0.05ha	Equivalent to one tree assuming the density of 200 trees per ha.
Weather dependence	No spread below 9.5°C	Vectors are active May-October; this setting ensures that for the current climate emulator spread occurs in that period only.
Long-term climate dependence	From 20% to 100% of the susceptible area	Representing the change of the area in which the bacteria can survive, from South-East England to most of the UK. Assumed here to occur over the period 2030-2050
Ecosystem values: Timber	£1,000 per ha per yr	Estimate based on data from Defra; reduction in value of 100% assuming dead trees are not worth anything
Ecosystem values: Biodiversity	£283 per ha per yr	Based on the total value for oak in GB of £302m (Defra). Proportions for different ecosystem service based on Willis et al (2003). Loss 100%
Ecosystem values: Recreation and landscape	£389 per ha per yr	As above

Ecosystem values: Carbon	£424 per ha per yr	As above
Ecosystem values: Air pollution	£283 per ha per yr	As above

Rate of spread and values are assumed to be varying by $\pm 50\%$.

The assumptions for the climate variables are illustrated in Figs. B.1 and B.2. The assumptions underlying the arrival model and the initial results are shown in Fig. B.3.

Brief discussion of results: The initial invasion and spread is relatively slow, as the number of incursions and the area of each incursion are small (each incursion is assumed to be a single tree). There is a significant uncertainty in the initial spread, as shown in Fig. B.4, but subsequently spread largely follows the availability of susceptible trees (cf. Fig. B.3 top graph with Fig. B.2, bottom right graph). The NPV of cumulative damages reaches ca £1.5b in 2050, an average loss of £50m per year over 32 years (2019-2050). This estimate is a reasonable one, as the total Ecosystem Services value of all oak trees in the UK is estimated at ca £300m per year, and thus the loss represents ca 15-20% of the total value.

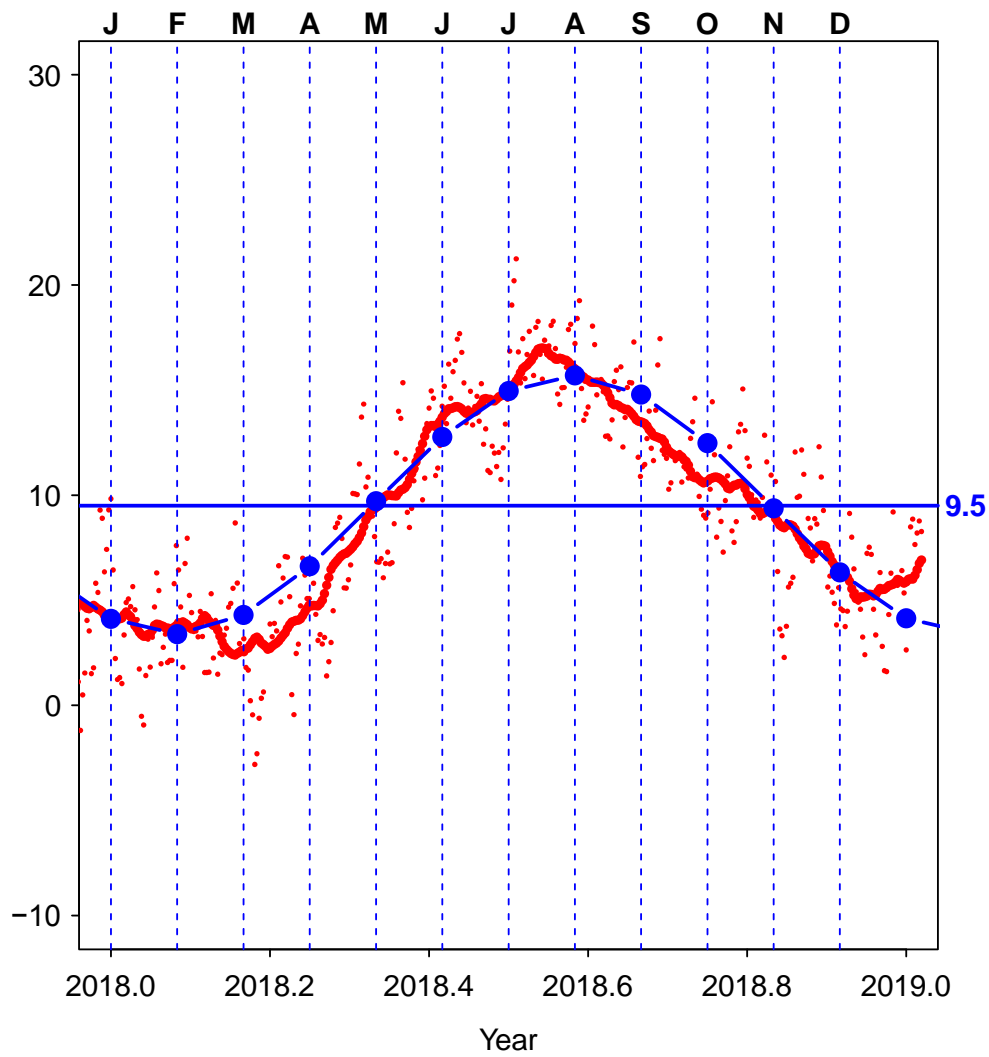


Figure B.1. The average daily temperature (Meteoblue; small red dots) and 30-days running mean of the average daily temperature (red line) compared with the deterministic component of the emulator model (blue line with dots). Vertical line marks months and the horizontal line points to the low threshold for the weather transfer function. The spread will be confined to May-October period as determined by the average daily temperature and the parameters for the rate transfer function.

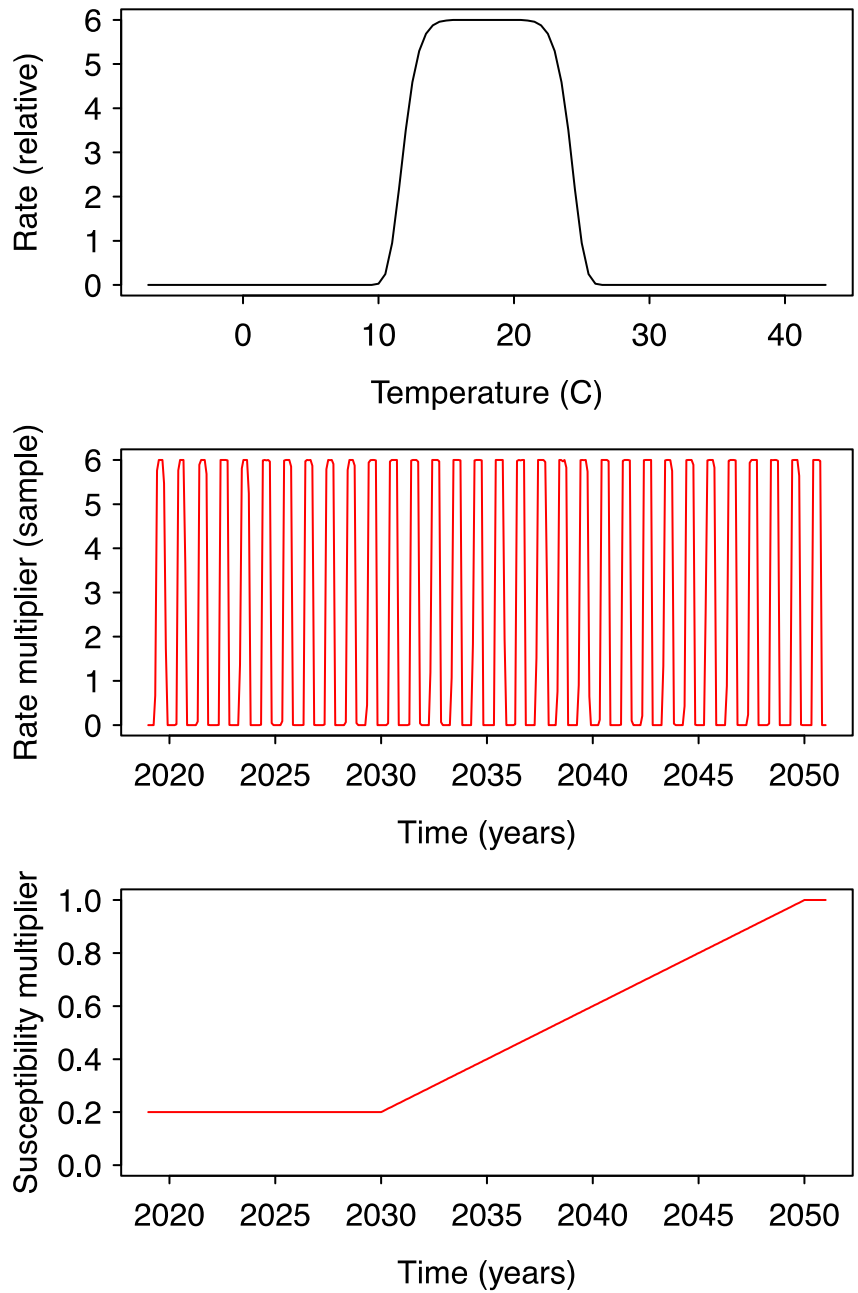


Figure B.2. Assumptions for the climate variables for the Xylella model. Top two figures: short-term weather variability reflects the spread limited to May-October. Bottom figure: long-term climate shift from 20% of the potentially susceptible area (12-18% of the total area) in the next 10 years to 100% of the potentially susceptible area (60-90% of the total area).

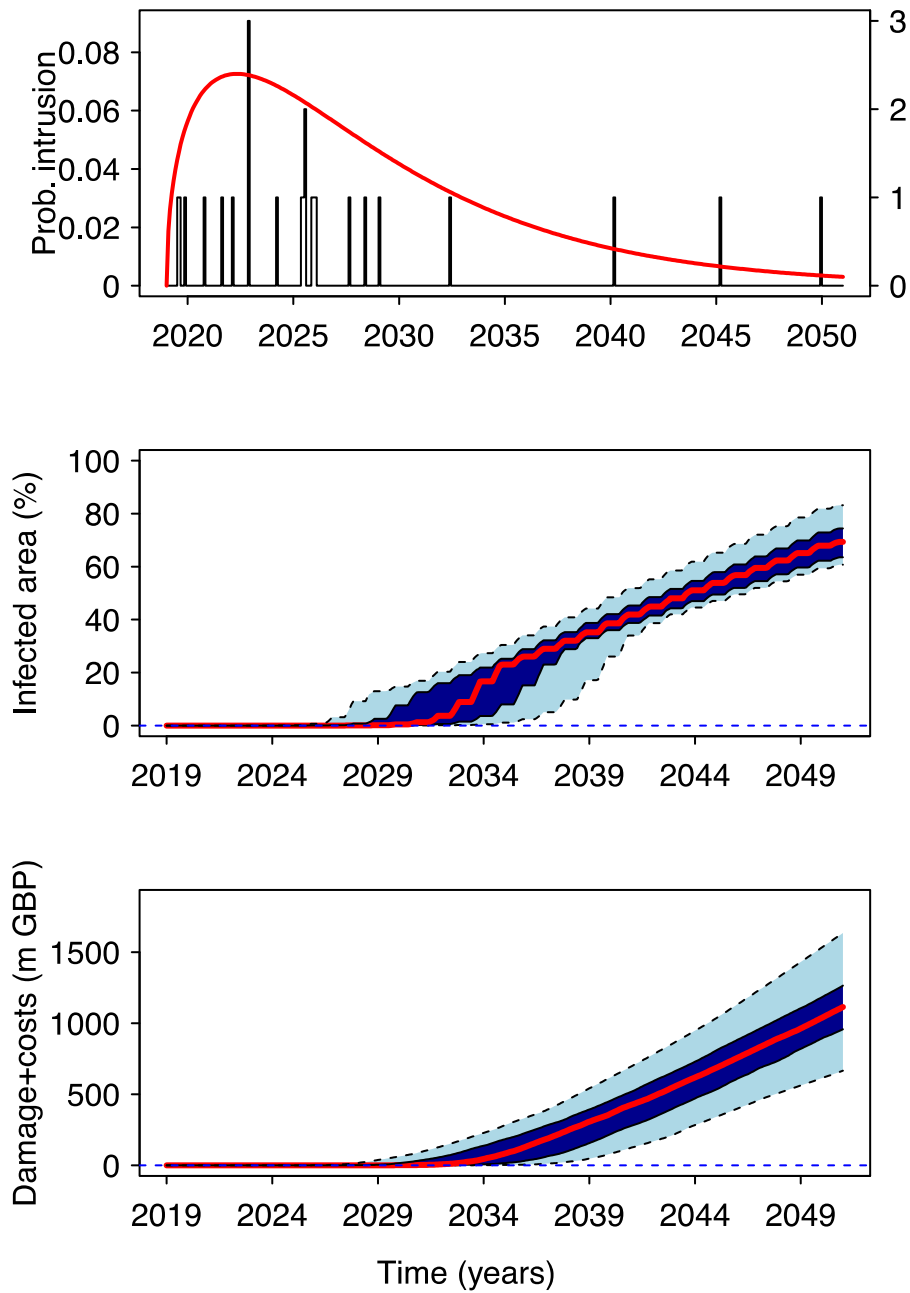


Figure B.3. Top graph: The time dependence of the probability of incursions (red line) with a sample of arrival times (black lines) – 10 arrivals over 50 years. Middle graph: The time dependence of the percentage infected area. Bottom graph: The time dependence of the cumulative NPV of losses. Red line: median, dark blue region: 50% confidence intervals; light blue region: 95% confidence intervals.

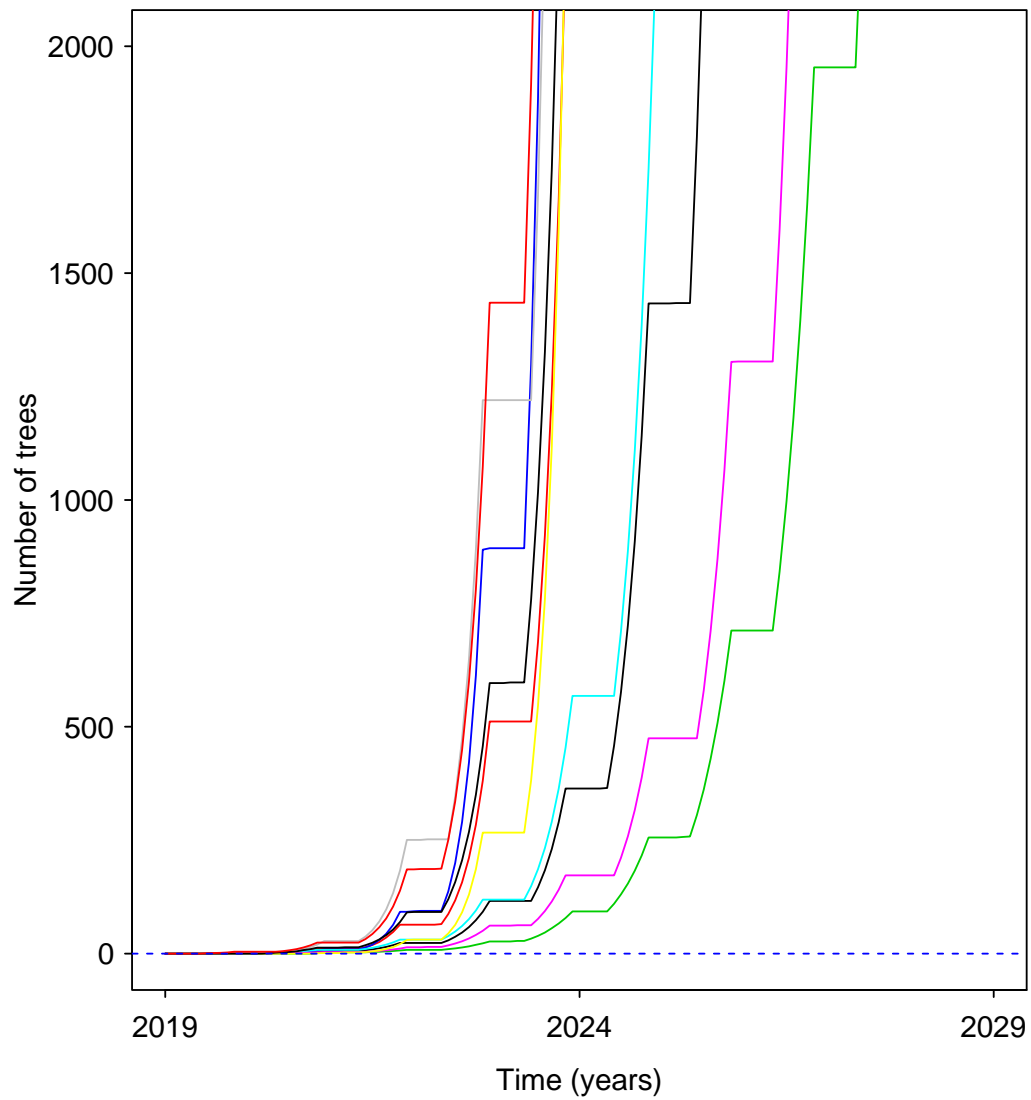


Figure B.4. The initial 10 years of the expected number of infected trees, for 10 replicates (lines with different colour); the density of trees is assumed to be 10 per ha. Periodicity in the growth (with active spread May-October and dormancy November-April) is clearly seen in individual runs. These figures can only be obtained by downloading the data from the model as a CSV file and plotting them separately.

Appendix C: Case study 2 - Zebra chip on UK potatoes

In this case study, we illustrate how the model can be used to estimate the potential losses in an agricultural setting. The rates of spread and the potential damage to the potato production in the UK could not be estimated with any reasonable accuracy. We therefore use the model to establish the sensitivity of the results to different assumptions about the rate and the impact on the industry.

The time horizon is assumed to be 2019-2050 and the model is run 250 times; no control option is included.

Parameter	Value	Comments
Doubling time	12 months, but with wide range of the rate	Unknown in UK conditions; vectors are potentially present everywhere, so spread can be very quick. There is evidence from the US about a very fast spread, but no quantitative data.
Total area	116,200 ha	Total area of potato production in the UK (2016 for which the last detailed data are available; GB Potato Market Intelligence); area harvested 120k ha according to <i>Agriculture in the United Kingdom 2017</i> .
Susceptibility	80-100%	Most potato species are susceptible (Munyaneza et al. 2011).
Average incursion time and shape	10 years average; shape parameter 1.5 (scalar)	Similarly to <i>Xylella</i> , we assume that the probability of incursion is relatively low at present, but quickly increases – representing the increased risk of importing infected material; subsequent decay due to expectation of successful control.
Average number of successful incursions per year	2	More likely to be imported than <i>Xylella</i> due to less stringent control and air-borne/insect nature. Assuming on average 2 incursions per year.
Area infected in each incursion	10 ha	Average farm size in the UK is ca 60 ha; assuming this holds for potato-producing farms, with 6 years rotation, the average field size is 10ha. Assume a single field infected in each incursion.
Weather dependence	No used	No clear data available, so assumed spread throughout the year.
Long-term climate dependence	Not used	No clear data available, so assumed susceptibility constant.
Production value and loss	£5,000 per ha per yr	Average price for potatoes in the UK is £150-200 per t (2016), with average yield 45 t/ha/yr and large volatility (<i>GB Potato Market Intelligence</i>). The

	<p>Worst case scenario: 40% loss, i.e. infected crop worth 60%</p> <p>Most likely scenario: 5% loss.</p>	<p>gross profit margin is estimated as £5,000 per ha per yr (<i>Nix Farm Management Pocket Book, 2017</i>)</p> <p>In the UK, 12% of the production is for chipping and 29% for processing; if both are assumed to be lost, the percentage will be 41%, but could be as high as 100% if potatoes for consumption are affected as well.</p> <p>5% loss as reported in New Zealand; lab study estimated 49.9-87.2% yield loss.</p> <p>No other losses are considered here; potential other factors include: ban on exports, loss at processing companies, loss of jobs.</p>
Other ecosystem services	£0	

Rate of spread and values are assumed to be varying by $\pm 50\%$.

The initial results are shown in Fig. C.1.

Brief discussion of results: The initial invasion and spread is relatively slow, as the number of incursions and the area of each incursion are small. There is a significant uncertainty in the spread particularly between 5-20 years from now, as shown in Fig. C.1, reaching the estimated 80-100% area after ca 18 years.

Assuming 40% loss, the NPV of cumulative damages reaches ca £1.2b in 2050 which corresponds to an average loss of £40m per year over 32 years (2019-2050). This figure can be compared with the total value of the potato production in the UK of £600-700m per year, with the losses representing 15% of this value. This is less than 40%, as for most of the years the production will be disease-free and hence the losses will only be happening later in the period.

100% loss (i.e. all potato production lost) corresponds to £3.5b total over 32 years, £100m average per year. Conversely, 5% loss will lead to £175m total loss over 32 years, £5.5m per year.

However, there is a high uncertainty around these values due to unpredictability of the spread.

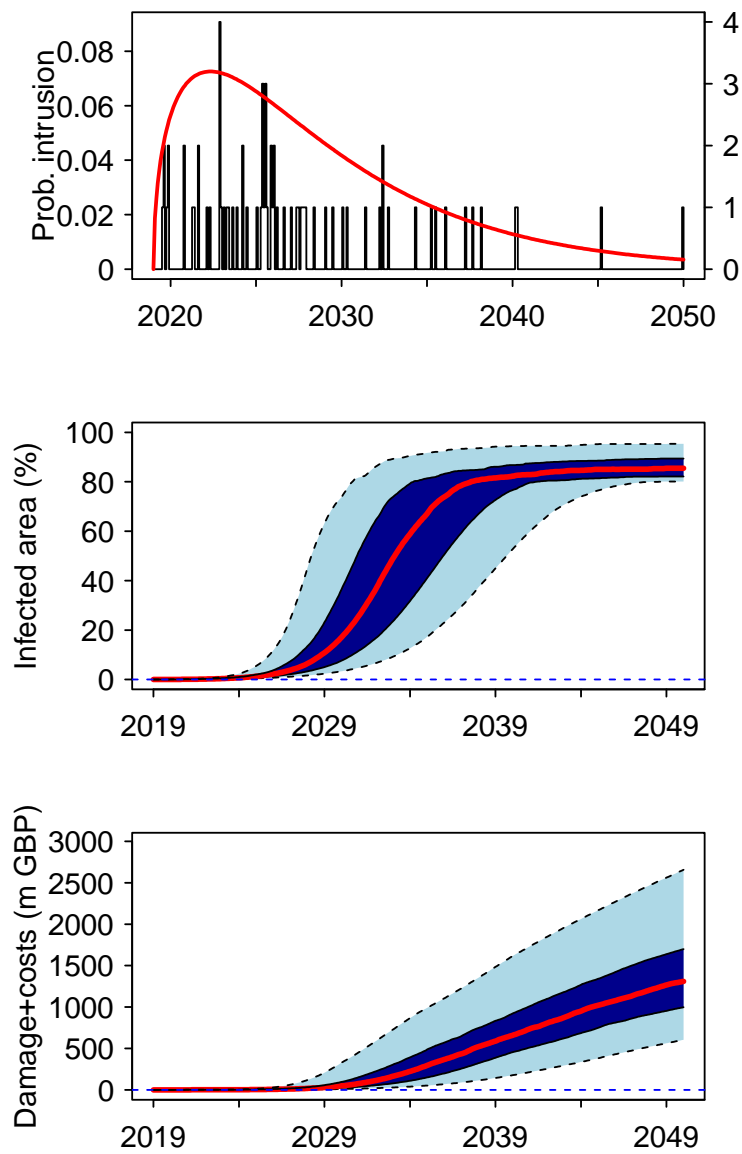


Figure C.1. Top graph: The time dependence of the probability of incursions (red line) with a sample of arrival times (black lines) – 10 arrivals over 50 years. Middle graph: The time dependence of the percentage infected area. Bottom graph: The time dependence of the cumulative NPV of losses. Red line: median, dark blue region: 50% confidence intervals; light blue region: 95% confidence intervals.

Appendix D: Case study 3 - *Ips typographus* on spruce

This case study is selected to demonstrate the response of a pest to short-term variations in temperature. We selected *I. typographus* firstly for its potential impact on timber production in the UK and particularly in Scotland, secondly for the availability of evidence, and thirdly for its clear dependence on climatic forcing.

Parameter	Value	Comments
Doubling time	6 months	<p>Dispersal tends to be local, particularly at low densities; long distance flights can take place. Some control measures like removal of fallen trees could reduce the number of generations and slow down spread.</p> <p>Establishment requires high numbers (Allee effect); often follows other events like windthrow. These effects are not taken into account here.</p> <p>At high densities the spread might be faster due to the pheromone release which attracts the beetles.</p>
Total area	726,000 ha	Total area of Sitka and Norway spruce in the UK is 726,000 ha (Sitka 665,000 and Norway spruce 61,000 ha); data from Forest Research - Forestry Facts & Figures
Susceptibility	Max 40-60%	<p>Currently ca. 40% are young trees, potentially unaffected by <i>Ips</i>. However, over time these trees are likely to become susceptible; the assumption here is that we will keep replanting the forests keeping the same proportion of young trees. Additionally, assume some level of natural resistance.</p> <p>Data from Forest Research - Forestry Facts & Figures</p>
Average incursion time and shape	Uniform	Given high levels of infestation in parts of Europe, a constant probability distribution.
Average number of incursions per year	10	<p>The pest is well established in parts of Europe. This assumes that on average ten incursions occur every year and the pest becomes established; however, the spread can only occur if the weather conditions are right.</p> <p><i>Ips</i> is believed to having been intercepted at the UK ports at a rate ranging from few to over a hundred cases per year</p>
Area infected in each incursion	0.2 ha	Typical gap size of a windthrow in the UK (Quine and Bell, 1998)

Weather dependence	No spread below 16°C and above 30°C, with significant increase above 20°C	Development at temperatures exceeding 10°C. Flights take place >15 °C. Mass swarming has, however, only been recorded when daily maximum temperature exceeds 20°C.
Long-term climate dependence	From 50% to 100% of the susceptible area	This reflects a climatic gradient in the UK under which about 50% of the land currently exceeds 500 degree days above 10°C. An increase of 1 degree on average will significantly affect day-degrees and hence make large parts of Northern England and Scotland suitable.
Ecosystem values: Timber	£1,000 per ha per yr Infected timber worth 90%	Estimate based on data from Defra/FC; reduction in value of 60% reflecting the need to collect timber from infected/dead trees before the optimal rotation Loss 10%
Ecosystem values: Biodiversity	£146 per ha per yr	From Willis et al (2003). Loss 100%
Ecosystem values: Recreation and landscape	£190 per ha per yr	Source as above Loss 100%
Ecosystem values: Carbon	£280 per ha per yr	£70-489; using the average of £280. Source as above Loss 100%
Ecosystem values: Air pollution	£470 per ha per yr	Source as above Loss 100%

Rate of spread and values are assumed to be varying by $\pm 50\%$.

The assumptions for the climate variables are illustrated in Fig. D.1; note that the time axis is extended to include the period from 1985 onwards. The assumptions underlying the arrival model and the initial results are shown in Figs. D.2.

Brief discussion of results: Although the pest invades at a relatively high rate (as indeed reported), the establishment and spread are limited by the requirement that the temperature exceeds 16°C for spread and 20°C for mass swarming. As illustrated in Fig. D.1, these conditions have only been met sporadically in the period 1985-2019, but can occur more frequently and for longer within the next 10-20 years leading to very fast spread covering all Sitka spruce population in the south of the UK. Further, as the climate warms up, the range of availability will move north and the *Ips* infestation will follow. Cumulative losses might reach £1.5b over 32 years from 2019, average ca £50m per year.

We also use the *Ips* system to illustrate the level of the sensitivity of the results to the details of the climate response (transfer function), Fig. D.3. Small changes in the width of the temperature response which shifts the low-temperature threshold at which the pest can spread results in large changes in the prediction of outbreaks. Unfortunately, this information is often very difficult to obtain.

Note also that the assumption is that the spread will occur in months with such high temperatures *only*, hence relatively infrequently. In reality, the spread will continue following such months, even in months with lower temperatures; such 'memory' effects are not included in the model.

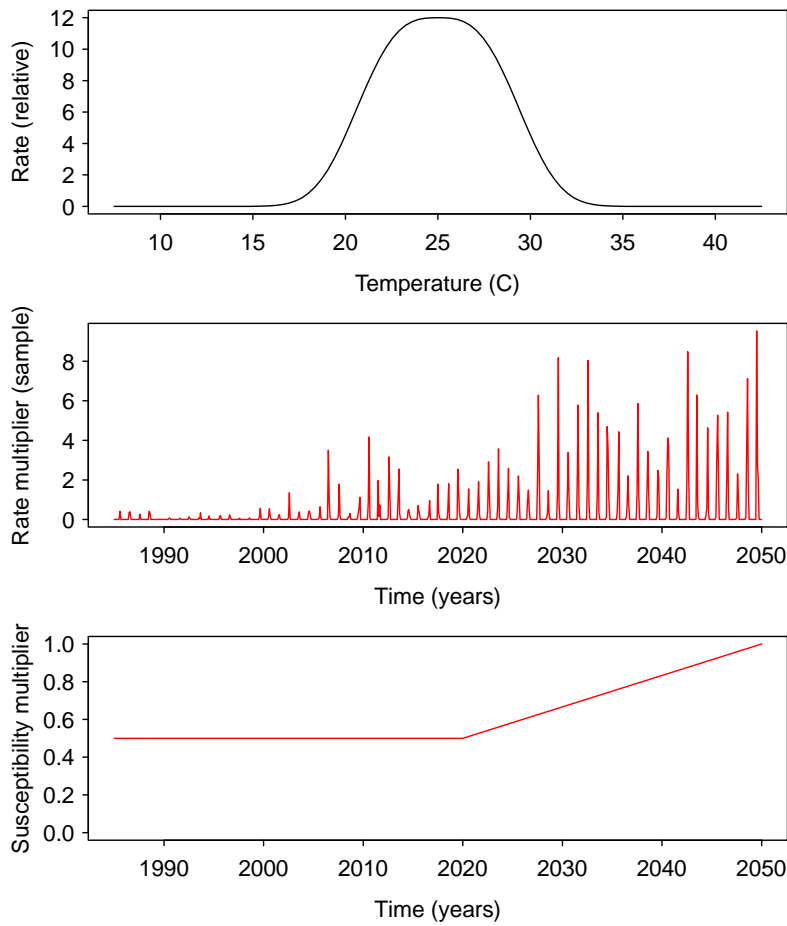


Figure D.1. Assumptions for the climate variables for the Ips model. Top figure: transfer function, i.e. relative rate of spread as a function of temperature. Middle figure: short-term weather variability reflects the increased frequency and amplitude of hot weather events; this figure shows a sample simulation run and hence does not represent the actual weather data. Bottom figure: long-term climate shift from 50% of the potentially susceptible area (20-30% of the total area; representing 50% area of the UK and 40-60% trees being susceptible) to 100% of the potentially susceptible area (40-60% of the total area).

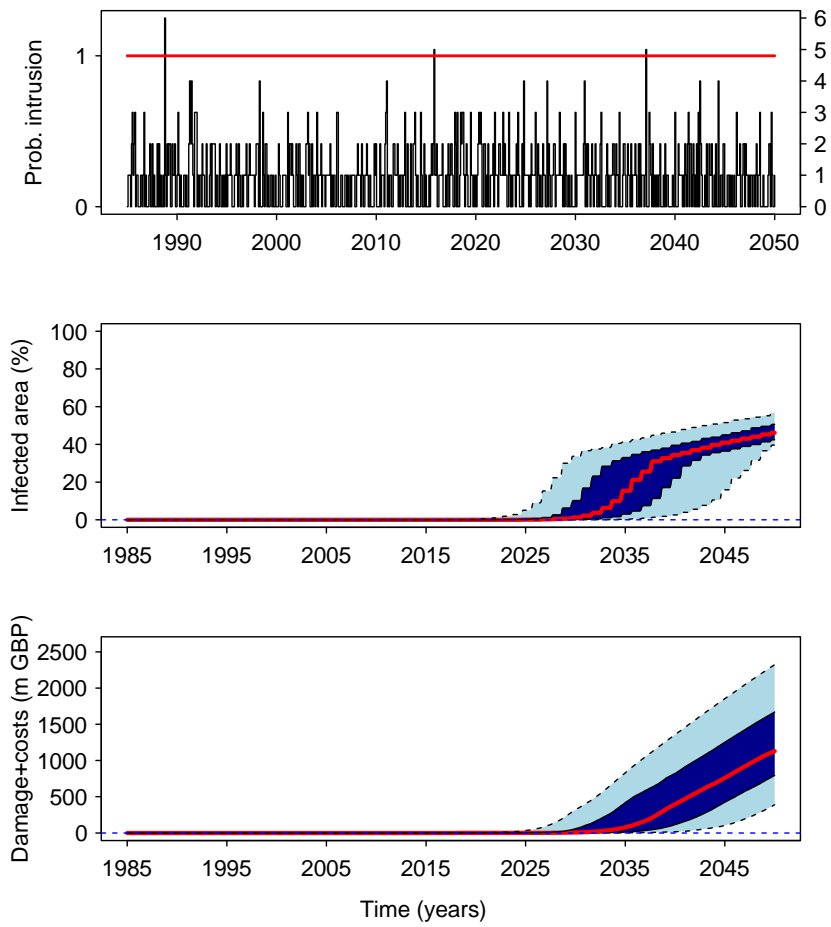


Figure D.2. Top graph: The time dependence of the probability of incursions (red line) with a sample of arrival times (black lines) – 10 arrivals over 50 years. Middle graph: The time dependence of the infested area. Bottom graph: The time dependence of the cumulative NPV of losses. Red line: median, dark blue region: 50% confidence intervals; light blue region: 95% confidence intervals.

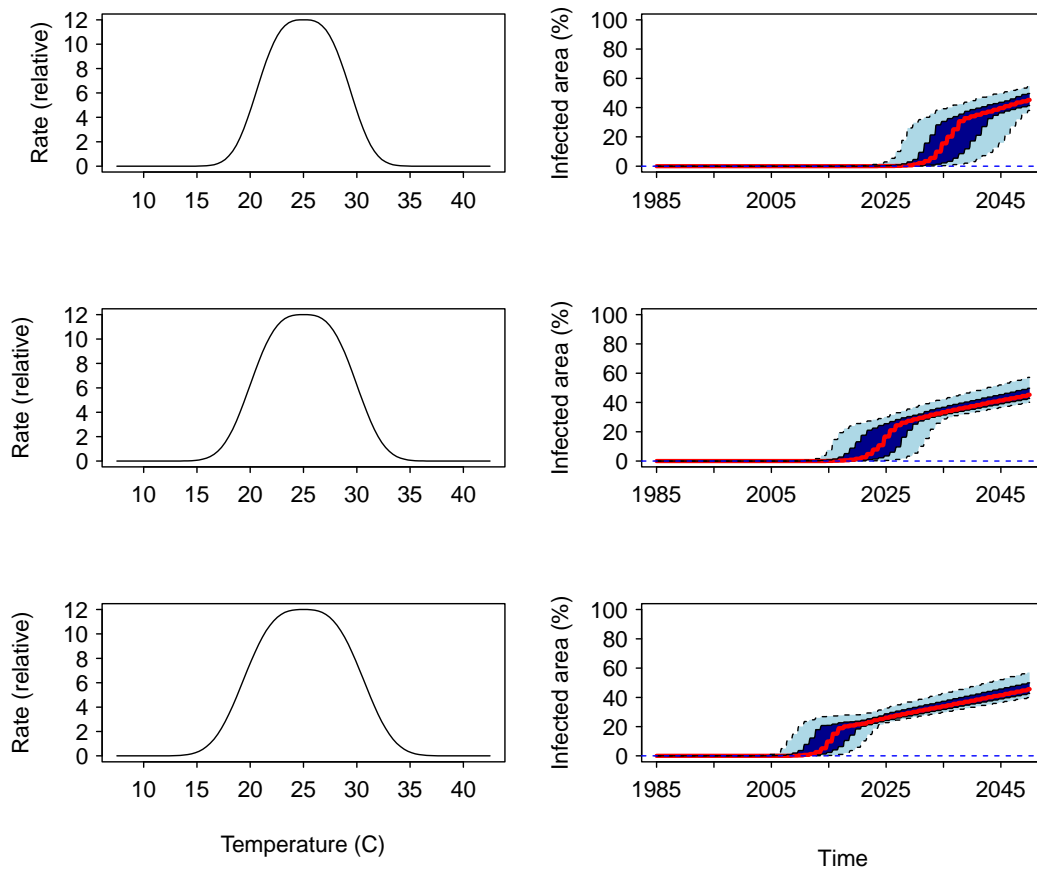


Figure D.3. Left column: The relative rate of spread as a function of temperature for three different values of the width, 3.5°C (top row), 4°C (middle row) and 4.5°C (bottom row); central point corresponds to 25°C and the shape factor is 3. Right column: The corresponding time dependence of the infested area proportion. Red line: median, dark blue region: 50% confidence intervals; light blue region: 95% confidence intervals.

5 References

- Aukema, B.H., Carroll, A.L., Zheng, Y., Zhu, J., Raffa, K.F., Moore, R.D., Stahl, K., Taylor, S.W., (2008). Movement of outbreak populations of mountain pine beetle: influences of spatiotemporal patterns and climate. *Ecography* 31, 348–358.
- Bosso L, Di Febbraro M, Cristinzio G, Zoina A, Russo D (2016a) Potential distribution of *Xylella fastidiosa* in Italy: a maximum entropy model. *Phytopathologia Mediterranea*. doi:10.14601/Phytopathol_Mediterr-16429
- Bosso, L., Di Febbraro, M., Cristinzio, G. et al. *Biological Invasions* (2016b) 18: 1759. Downloaded from <https://doi-org.proxy.lib.strath.ac.uk/10.1007/s10530-016-1118-1>
- Carroll, A. L., Taylor S.W., Regniere J., Safranyik L. (2004). Effects of climate change on range expansion by the mountain pine beetle in British Columbia. In: Shore, T. L. et al. (eds), *Challenges and solutions*. Proc. of the Mountain Pine Beetle Symp., Kelowna, BC, Canada October 30-31, 2003, Information Report BC-X-399, Canadian Forest Service, Pacific Forestry Centre, pp. 223-232.
- CEH news (2018) Downloaded from <https://www.ceh.ac.uk/news-and-media/blogs/uk-preparedness-xylella-fastidiosa>
- DEFRA (2017) Updating the UK Rapid Pest Risk Analysis for *Xylella fastidiosa*. Downloaded from <https://planthealthportal.defra.gov.uk/ph-api/pests/12570/risk-analyses/407/documents/4127/document>
- DEFRA (2018) Pest Alert: Zebra chip disease of potato. Downloaded from <https://planthealthportal.defra.gov.uk/assets/factsheets/Zebra-chip-pest-alert-v8.pdf>
- Elad Y., Pertot I. (2014) Climate Change Impacts on Plant Pathogens and Plant Diseases. *Journal of Crop Improvement*, 28:1, 99-139, DOI: 10.1080/15427528.2014.865412
- Eriksson, M., Lilja, S., Roininen, H., (2006). Dead wood creation and restoration burning: implications for bark beetles and beetle induced tree deaths. *Forest Ecology and Management*, 231, 205–213.
- Garreth K.A. (2014) Climate Change and plant diseases. Downloaded from <http://www.nationalacademies.org/hmd/~media/D8C1AA4BB32E49F1B519F79A95E0E7F9.ashx>
- GB Potatoes: Market Intelligence 2018-19. <https://potatoes.ahdb.org.uk/publications/gb-potatoes-market-intelligence-2018-19>
- Gilbert, M., Nageleisen, L.-M., Franklin, A., Gregoire, J.C., (2005). Post-storm surveys reveal large-scale spatial patterns and influences of site factors, forest structure and diversity in endemic bark-beetle populations. *Landscape Ecology*, 20, 35–49.
- Godefroid M., Gruaud A., Streito J.-C., Rasplus E.-Y., Rossi J.-P. (2018) Climate change and the potential distribution of *Xylella fastidiosa* in Europe. Downloaded from <https://www.biorxiv.org/content/biorxiv/early/2018/03/28/289876.full.pdf>
- Haverkort A.J., Verhagen A. (2008) Climate change and its repercussions for the potato supply chain. *Potato Research*, 51:223-237.
- Hoddle M.S. (2004) The potential adventive geographic range of glassy-winged sharpshooter, *Homalodisca coagulata* and the grape pathogen *Xylella fastidiosa*: implications for California and other grape growing regions of the world. *Crop Protection*, 23:691–699.
- Horton D.R., Cooper W.R., Munyaneza J.E., Swisher K.D., Echegaray E.R., Murphy A.F., Rondon S.I., Wohleb C.H., Waters T.D., Jensen A.S. (2015) A New Problem and Old Questions: Potato Psyllid in the Pacific Northwest. *American Entomologist*, 61 (4), 234-244.
- Jönsson, A., Harding, S., Barring, L., Ravn, H. P. (2007) Impact of climate change on the population dynamics of *Ips typographus* in southern Sweden. *Agricultural and Forest Meteorology*, 146, 70–81.
- Juroszek P., von Tiedemann A. (2011). Potential strategies and future requirements for plant disease management under a changing climate. *Plant Pathology*, 60:100–112.

- Kanters J. (2018) Potato production and climate change. Spudsmart article from March 12, 2018. Downloaded from <https://spudsmart.com/potato-production-climate-change/>
- Kudela, V. (2009) Potential Impact of Climate Change on Geographic Distribution of Plant Pathogenic Bacteria in Central Europe. *Plant Protection Science*, 45, Special Issue: S27–S32. Downloaded from: <https://www.agriculturejournals.cz/publicFiles/13964.pdf>
- Lausch, A., Fahse, L., Heurich, M. (2011) Factors affecting the spatio-temporal dispersion of *Ips typographus* in Bavarian Forest National Park: A long-term quantitative landscape-level analysis. *Forest Ecology and Management*, 261, 233–245.
- Lausch, A., Heurich, M., Fahse, L. (2013) Spatio-temporal infestation patterns of *Ips typographus* (L.) in the Bavarian Forest National Park, Germany. *Ecological Indicators*, 31, pp. 73–81.
- Joseph E. Munyaneza J.E., Buchman J.L., Sengoda V.G., Fisher T.W. and Pearson C.C. (2011) Susceptibility of Selected Potato Varieties to Zebra Chip Potato Disease. *American Journal of Potato Research*, 88:435–440
- Pautasso M, Döring TF, Garbelotto M, Pellis L, Jeger MJ (2012) Impacts of climate change on plant diseases—opinions and trends. *European Journal of Plant Pathology*. Downloaded from DOI: 10.1007/s10658-012-9936-1
- Pertot I., Elad Y. (2012) Climate change impact on plant pathogens and plant diseases. *Bulletin of the EnviroChange Project, Fondazione Edmund Mach*, September 2012.
- Quine, C.P. and Bell, P.D. (1998) Monitoring of windthrow occurrence and progression in spruce forests in Britain. *Forestry: An International Journal of Forest Research*, 71, 87–97.
- Redman, G., J. John Nix Pocketbook for Farm Management, 2017. Agro Business Consultants Ltd
- Ste-Marie, C. (2015) Learning lessons from the mountain pine beetle outbreak in Canada. Presentation at the ICF National Conference, Cardiff, April 2015.
- USDA (2014) Recovery plan for Zebra Chip of Potato. Downloaded from <https://www.ars.usda.gov/ARSUserFiles/opmp/Potato%20Zebra%20Chip%20Recovery%20Plan.pdf>
- Wermelinger, B., Seifert, M. (1999) Temperature-dependent reproduction of the spruce bark beetle *Ips typographus*, and analysis of the potential population growth. *Ecological Entomology*, 24, pp. 103–110.
- White S.M., Bullock J.M., Hooftman D.A.P., Chapman D.S. (2017) Modelling the spread and control of *Xylella fastidiosa* in the early stages of invasion in Apulia, Italy. *Biological Invasions*, 19:1825–1837.

Plant Health Centre
c/o The James Hutton Institute
Invergowrie,
Dundee, DD2 5DA

Tel: +44 (0)1382 568905

Email: Info@PlantHealthCentre.scot
Website: www.planthealthcentre.scot
Twitter: [@PlantHealthScot](https://twitter.com/PlantHealthScot)



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