



ENHANCEMENTS OF PEST RISK ANALYSIS TECHNIQUES

A report comparing the advantages and disadvantages of different approaches for creating a generic integrated model for pest spread and impacts

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PROJECT OVERVIEW: PRATIQUE is an EC-funded 7th Framework research project designed to address the major challenges for pest risk analysis (PRA) in Europe. It has three principal objectives: (i) to assemble the datasets required to construct PRAs valid for the whole of the EU, (ii) to conduct multi-disciplinary research that enhances the techniques used in PRA and (iii) to provide a decision support scheme for PRA that is efficient and user-friendly. For further information please visit the project website or e-mail the project office using the details provided below:

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Explanation of the Contents of the Deliverable

During the execution of task 2.5, it became apparent that two types of models had to be created: (i) models simulating pest spread and (ii) a generic integrated framework reflecting the relationships between the spread and impact models and between spread, impacts and the other key factors, e.g. climatic suitability, that influence the magnitude and distribution of impacts. Therefore it was decided that it would be more logical if the description of the work undertaken on the two different types of model is placed in separate deliverables. Accordingly, D2.6 contains a review of the different approaches for modelling pest spread and a detailed description of the spread models that have been developed with instructions for their use and several worked examples. D2.7 contains the description of the generic integrated framework, including a comparison of advantages and disadvantages of different approaches. It outlines the relationships between the spread and impact models and between spread, impacts and the other key factors, e.g. climatic suitability, that influence the magnitude and distribution of impacts. It is closely linked to D3.3 that provides a decision support scheme for mapping endangered areas.

PREFACE

An assessment of the likelihood and extent of spread is an integral part of pest risk analysis (PRA). However, in PRAs, spread is generally assessed by expert judgement, and few tools, if any, are provided to risk assessors to model spread as a dynamic process in space in the PRA area. In PRATIQUE, an attempt has been made to evaluate existing spread models, adapting and developing them for PRA and linking them to maps of host distribution, climate and potential economic impacts. This report documents the results of these attempts. We do not claim here that we have succeeded in producing a generic method for modelling spread that can easily be applied to assessing the spread of new invaders. This was our objective, but the result is more modest than that. We have developed a suite of spread models that covers different aspects of the dynamic spatio-temporal process of pest range expansion and we have programmed these models in the computer language R to make it as straightforward as possible for risk assessors to run and build familiarity with the models. Examples are provided to help the users. We hope that as experience increases in the use of these models it will be easier to identify the models that are most useful to risk assessors and which parameter values can be used as “default values” for new species. Although these models have been presented and tested at a meeting of pest risk assessors in Hammamet, Tunisia on 23rd-26th November 2010 and detailed examples are presented in this document, further work is required with a larger range of species and a greater number of risk assessors to clarify their role in PRA. The models presented here are only likely to become widely adopted when risk assessors have gained sufficient familiarity with them, and feel comfortable with the parameter estimates for well known species, the parameter estimation process for new species and the interpretation of the simulation outputs. This will need further time and effort.

During the preparation of the models described in this guide, we have benefited from discussions with colleagues in the PRATIQUE project.

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1 Introduction

1.1 Background

The assessment of pest impacts in a PRA is based on the area of potential establishment (equivalent to the fundamental niche) and needs to estimate the endangered area (the area where economic impacts are expected). Assuming that the pest is present throughout the area of potential establishment, impacts can be estimated for this worst case scenario. However, to provide more realistic estimates, risk assessors need to take into account the time a pest takes to invade these areas. The generic spread module has been developed for this purpose. This module can therefore be used to investigate the dynamic process of the invasion increasing the accuracy of the impact assessment and providing valuable information for surveillance and management as appropriate. Within the integrated model it can be seen as an intermediate step between risk mapping which defines the area of potential establishment map and impacts (Fig. 1.1). The spread module is closely linked to the EPPO decision support scheme (DSS) for PRA: the answers to some questions can be used to estimate some of the model parameters and, in turn, the outputs of the module can provide additional information to help answer some questions (see this linkage in section 5). A DSS for mapping endangered areas is provided in PRATIQUE Deliverable 3.3. The spread models are included at Stage 4 of this DSS to enable the invasion process to be modelled dynamically if required.

The spread module is a new tool that allows risk assessors to quantify the potential spread of the pest in time and space, contributing greater precision to the assessment of impacts.

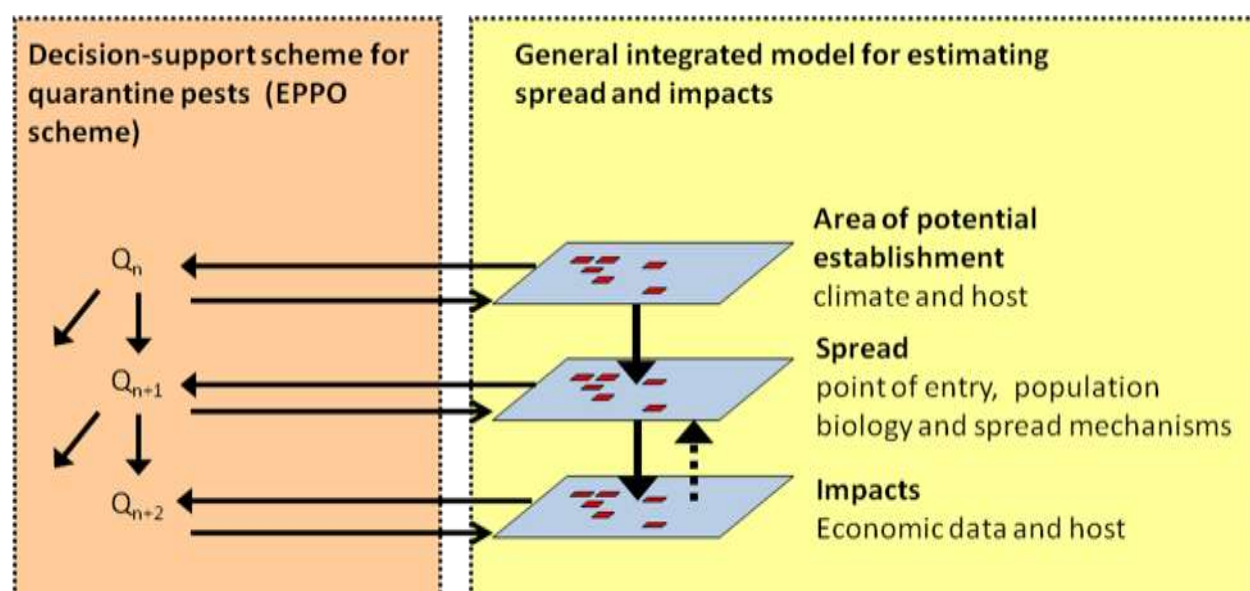


Figure 1.1: Representation of the linkage between the EPPO DSS for PRA and the general integrated model, and the interactions between the area of potential establishment, spread and impacts within the general integrated model.

1.2 Objective

The objective of this spread modelling section is to describe different approaches for developing a generic spread module and to present the different models that have been developed. The application to various case study pests representing a variety of taxa (plant, insect, nematode and pathogen) is also included. Based on the experience with these case studies, recommendations for the use of the modules and guidance on the situations when spread modeling is appropriate are provided.

Note that references to the EPPO DSS for PRA concern the new version developed within PRATIQUE.

1.3 Structure of the spread modelling section

In chapter 2, the different approaches for modelling spread are described. Two types of models are presented:

- those that take the geographical distances into account (“spatial process models”)
- those which ignore distances (“temporal process model”).

In chapter 3, the spread models are described in detail in order to provide all technical and scientific information necessary for a risk assessor to apply the module.

In chapter 4, the application of the spread module to several species is presented. This part focuses not only on the estimation of the parameters and how to apply the models but also on the difficulties and the feedback received from experts on the consistency of the models’ outputs.

In chapter 5, recommendations are given about the choice of the models and the linkage to the GIF is presented.

In chapter 6, some conclusions are drawn about the efficiency and the constraints to the use of the spread module in a PRA.

2 Approaches for modelling spread

2.1 Introduction

How to model spread?

The expansion of population distribution is often characterized by the radial spread rate determined by the distance between the outside border at two different time steps. This spread rate can readily be mapped to present a forecast of the future population expansion. This is perhaps the simplest way to model spread. The potential spread of a population over the landscape is the cumulative result of the movements of individuals. These movements can

occur by either active or passive dispersal. Spread models should describe the overall spread potential resulting from these different dispersal mechanisms, and, for each mechanism, different modelling approaches are possible. These models may be simple or detailed, stochastic or deterministic and may represent population density, space and time as discrete or continuous (Turchin 1998). The reaction-diffusion model is commonly used in ecology (Turchin 1998, Shigesada & Kawasaki 1997). This model, derived from the discrete random walk theory, simulates how population density varies in space and time. The solution of the two-dimensional diffusion equation is the Gaussian distribution (Shigesada & Kawasaki 1997). This distribution has a thin tail since the population density decreases at a rate below the exponential with increasing distance. This means that, although the probability of very long distance dispersal is not zero, the population mainly disperses over short distances. For a distribution with a fat tail, e.g. a Cauchy distribution, the population density decreases at a rate above the exponential with increasing distance and therefore a much larger proportion of the population is predicted to disperse over long distances. More generally, dispersal kernel models redistribute the population in space without changing the total population density and should be combined with a growth model. Spread models based on such dispersal kernels, allowing both short and long distance dispersal, are probably the most detailed. Although spread models normally take into account geographical distance when assessing the likelihood of dispersal at particular places, other models can be applied to predict the changes in the population density over time and test hypotheses regarding the locations where the population is likely to occur.

Previous attempts to develop generic spread models

Many spread models have been developed to predict the potential spread of invasive species (e.g., Shigesada & Kawasaki 1997, Murray 2002, Robinet 2006, Pitt 2008, Carrasco 2009), but the user generally needs strong modelling, mathematical and computer skills. Moreover, these models are often developed for a particular species, using some specific functions to describe particular processes involved in the species dynamics. The number of parameters and the amount of data required to estimate these parameters is usually high. Some specific experiments are usually required to collect the required data. Although such spread models are useful for some species, it is not realistic to recommend the development of such sophisticated models to any species within the PRA process. Therefore, the development of generic spread models has become essential to assess more easily and more rapidly the spread potential of the species. To our knowledge, only a few attempts have been made to create generic spread models and non-modellers may have some difficulties to apply these models and estimate the parameters for any species. For instance, the models developed by Carrasco (2009), although applied to three species (two insects and one bacterium), appear to be relatively specific because a mark-release-recapture experiment was necessary to fit the dispersal kernel model, and a phenology model was also developed. The number of parameters required for these models is relatively high (more than 10 parameters for the simpler model and some values were “assumed”) and may not be convenient for risk assessors who are generally

not familiar with modelling approaches. The models developed by Pitt (2008), under the name Modular Dispersal in GIS (MDiG) were designed to simulate insect dispersal in a realistic landscape taking into account local diffusion, long distance dispersal, growth and mortality rates. Despite the great interest to model spread in a GIS environment, this approach has not been designed to assist a risk assessor in a PRA and may be still too complex. This model has only been applied so far on one insect (the Argentine ant, *Linepithema humile* (Mayr)) and one plant (the butterfly bush, *Buddleja davidii*).

What is novel here?

None of the models developed within the spread module is novel from an ecological point of view, except for model 5 (the 2Dt dispersal kernel). Making these simple ecological models available and useful to the PRA user community by generalizing them (for instance by putting densities on a 0-100 scale) and linking them with the area of potential establishment (e.g. provided by CLIMEX) is entirely novel. For the first time, these simple ecological models are now made available to risk assessors in a –relatively user-friendly format and cast in the context of PRA. In this sense, the effort is comparable to CLIMEX when it was first proposed (Sutherst & Maywald, 1985). The concept of insect population modelling based on thermal time and reduction functions for stress factors was not new at all at the time (mid 1980s). However, the idea of generalizing the modelling framework (putting densities or growth indices on a scale 0-100), making a framework for calculating a growth (GI) and ecoclimatic index (EI) by integrating weekly indices and linking it to a world climatic data for input of forcing functions and to presence/absence data for calibration was completely novel. For the spread module, the objective is somewhat similar.

An important input: the area of potential establishment

The main input required for developing a spread model is the area of potential establishment for the species. This area defines the maximum extent of the potential spread of the species. It is also called the fundamental niche and methods for modelling and mapping this area are provided in deliverable 3.3. In the area of potential establishment both the biotic (e.g. the presence of host plants) and abiotic factors (e.g. climate and soil) are suitable for pest establishment. Climatic modelling and mapping of the area of potential establishment can be undertaken using CLIMEX which combines correlative and deterministic techniques (Kriticos et al., 2005; Stephens et al. 2007; Robertson et al., 2008; Potter et al., 2009; Watt et al., 2009ab), correlative models such as Bioclim, Domain, Maxent, Climate Space Model, Envelope Score, Environmental Distance, GARP (Busby, 1991; Carpenter et al, 1993; CIFOR, 1996; Ward, 2007; Pearson, 2007; Pearson et al. 2007, Philipps et al. 2006; Philipps, 2007; Boston & Stockwell, 1994), and mechanistic models such as Ecocrop, phenology and generic infection models (provided in NAPPFast, Magarey et al.2007 and <http://www.nappfast.org/userman2.html>). All of these models can provide the climatic suitability layer needed to run a spread model. However, the CLIMEX model “Compare locations” is an integrated model combining correlative and mechanistic approaches and it provides outputs with biological meaning (notably the Ecoclimatic Index and

the Growth Index). The second step consists of combining this area of suitable climatic conditions with the additional factors required for establishment, e.g. host plants as described in D3.3. The spread models can be applied to determine which parts of the area of potential establishment are likely to be infested at particular times. The model outputs can then be used to help assess impacts.

Data requirement

Data availability is critical in determining the extent to which the spread module can be applied. The spread models vary in their data requirements but, if critical data are lacking, it may not be appropriate to apply any of the spread models presented. The model requirements are listed in chapter 5. The spread module can only be applied once the area of potential establishment has been defined.

Spatial distance in spread models

As far as possible, the outputs of the spread model should be spatially explicit, enabling spatially informed decision making. One of the options outlined below is completely spatially explicit. However, some of the models just predict temporal processes and ignore the spatial component (assuming that all the area of potential establishment has already been invaded). Although these models do not actually describe the spatial processes, the outputs can still be shown on a map. Both approaches are presented below. Since the models are applied over grid cells, the basic spatial area unit is called a “cell” hereafter (see chapter 3 for more details).

Excluded models

Network spread models have been investigated but have not been included in the spread module. This type of model describes the connection between specific points and can therefore take into account human mediated dispersal between hotspots (Jeger et al., 2007; Robinet et al., 2009, Xu et al. 2009, Harwood et al. 2009). This alternative, and potentially complementary, approach to modelling spread is particularly relevant for movement through human agency along specific pathways. For example, some pathogens mainly spread via waterways (e.g. the potato brown rot bacterium, *Ralstonia solanacearum*), and a kernel approach is not appropriate (Breukers et al., 2006, 2008). However it was decided not to include this type of model because it cannot be readily applied in a generic framework and requires data on intra-country commodity movement that are obtainable in the USA (Magarey et al., 2011) but are rarely available in Europe.

2.2 Approach 1: temporal process models

In this approach, the geographical distance between the locations is ignored. Two models have been developed based on the same graph (Fig. 2.1) that defines the speed at which an invasive pest colonizes the area of potential establishment. The curve is defined by several parameters estimated for each

species. The meaning of this curve is however different in both models. For model 1 (a population dynamics model based on a simple logistic growth model (SLG), see section 3.3.2.1), this curve represents the pest density in percentage of the carrying capacity (K) in each cell, assuming that all the cells within the area of potential establishment are invaded by a small amount of population (N_0) at an initial time ($t=0$). This first model assumes that the pest has been introduced to all the cells in the area of potential establishment. It provides temporal and spatial information allowing the risk assessor to determine the cells where the species population can grow rapidly if introduced. This model provides a population density at different time steps in the future and thus can be used as part of an assessment of economic impact assuming the worst case (all cells initially invaded). For model 2 (Temporal spread over cells integrated with impacts based on a logistic growth model with economic variables (LG-Econ), see section 3.3.2.2), this curve represents the percentage of cells invaded in the area of potential establishment. The locations of these invaded cells are selected according to various scenarios based on economic values (see section 3.3.2.2). In this case, the model simulates the presence or absence of the species in each cell and does not provide a population density. When the population progress curve reaches 100%, the pest is considered to have invaded every cell in the area of potential establishment.

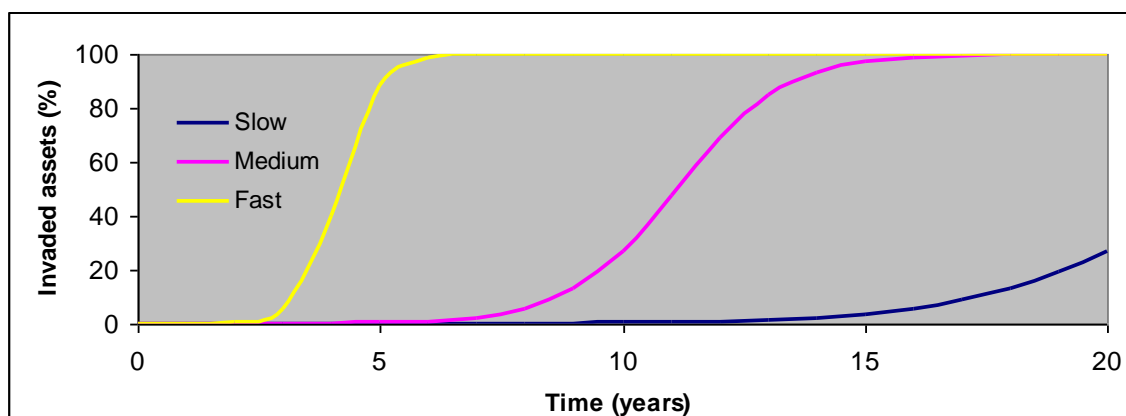


Fig. 2.1: Possible scenarios for the speed of an invasive pest spreading throughout the area of potential establishment based on slow, medium and fast invasion assumptions. In practice, there is no pre-defined curve. In model 1, the speed is determined by the growth potential (based on G_I and \square_{max}) and the Y axis represents the population density expressed as a percentage of the carrying capacity. In model 2, the speed is defined by the relative rate of spatial increase and the Y axis represents the percentage of invaded cells in the area of potential establishment.

Note that this approach does not actually model the spread of the species and therefore does not require precise knowledge or a prediction of the point of entry.

The advantages of temporal process models are that unlike spatial process models they:

- (1) are easy to understand and transparent for risk assessors
- (2) can be conducted quickly, with less complications arising from missing data than the spatial approach (see below)
- (3) do not give the impression of false accuracy (which can be implied by spatial models)
- (4) can be used to roughly assess the range of potential impact

2.3 Approach 2: spatial process models

The other approach to modelling spread entails an explicitly spatial approach employing spatially explicit models to predict pest spread over the area of potential establishment. There are many spatially explicit spread models, from the simplest, which does not take population densities into account (model 3, based on radial range expansion (RR)), to the most complex (model 5 based on a dispersal kernel (DK)). These models all predict the invasion of new locations based on their distance from previously invaded areas. In this second approach, the entry point or points need to be defined. Since model 3 is very simple (see section 3.3.3.1), only model 5 is described below (see also section 3.3.3.3).

For model 5, a dispersal kernel is used to calculate the annual dispersal from an infested source area to a new area that can be nearby or far away. The dispersal kernel is simply a two dimensional probability distribution, connecting “mother” areas to “daughter” areas in space. This model, although derived from a 1-dimensional space kernel (Clark et al. 1999), is based on a novel mathematical construct in 2-dimensional space (Van der Werf et al., unpublished).

Three theoretical dispersal kernels are shown in Fig. 2.3. Two models are normal, i.e. bell shaped with thin tails, but differ in scale. The third model has fat tails. The thickness of the tails is not conspicuous in Fig. 2.3, but appears very clearly when the cumulative distribution over space is drawn (Fig. 2.4). Fat tails produce “jumps” in species distribution and daughter foci that may be far away from their source. Two parameters are used to define these curves: p , the shape parameter mainly defines the thickness of the probability distribution tail, and u , the scale parameter which mainly governs the distance. With both of these parameters, this model can potentially simulate all kinds of spread (short or long distance spread). In addition to this dispersal function, this model combines a growth model based on the CLIMEX GI.

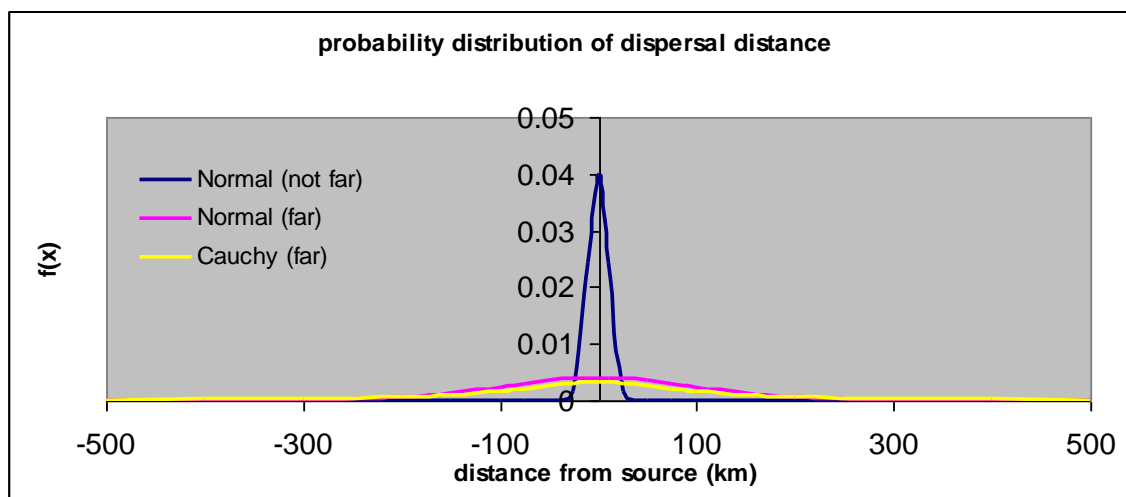


Fig. 2.3: Three theoretical dispersal kernels (spatial probability distributions) showing the pest dispersal distance after one year

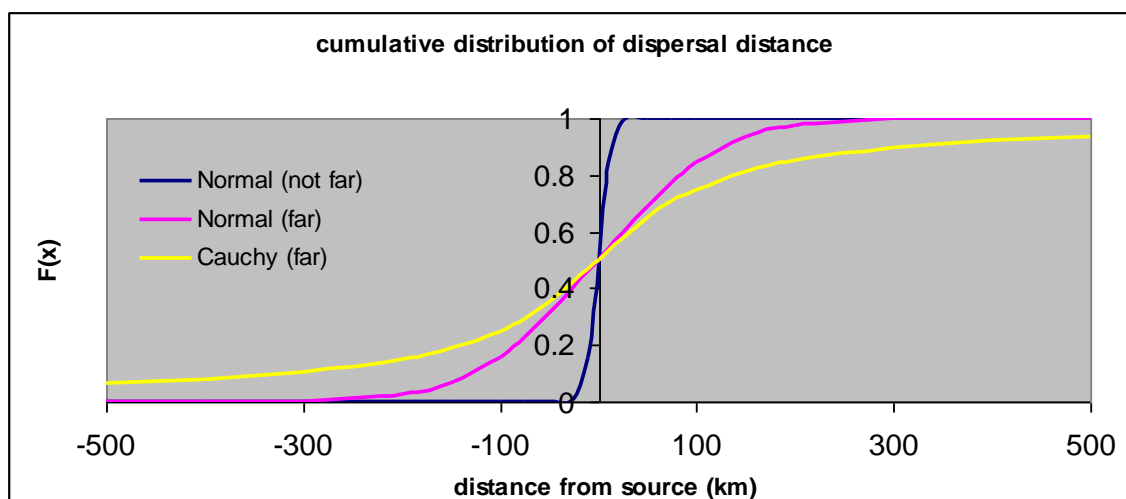


Fig. 2.4: Three theoretical dispersal kernels (spatial probability distributions) showing the cumulative distribution of pest dispersal distance after one year

The result of the second approach (where the geographic distance is used to simulate the spread) is a series of maps through time, showing the projected time course of pest invasion, given the point of entry. To visualize the inherently unpredictable nature of long distance spread, a stochastic version of the dispersal kernel model has been developed. When the point of entry is not known (e.g. because the species is not yet present in the PRA area), then risk assessors can choose this point at random or select likely points of entry such as airports or ports to investigate differences in colonisation speed. If the point of entry is already known, scenarios can be used to visualize the formation of daughter foci and spread from additional points of entry.

As for the first approach, where the geographic distance is ignored, it is essential to search for the data needed to choose the dispersal kernel and parameterise the models.

The advantages of spatial process models are that:

- (1) The output is a time series of spread maps enabling spatial interpretation and analysis
- (2) Although time consuming, this type of output enhances the precision of the pest risk assessment

2.4 Coding platform

Prototypes can be built in a variety of computer languages to create a platform for testing concepts and algorithms. The language R (R Development Core Team 2009) was chosen because it can be freely downloaded, it can be coded transparently and uses high level calculations. Although the generic spread module is closely linked to the EPPO DSS for qualitative risk assessment, it has not been included in the Capra system currently developed by EPPO. Future work could enhance user-friendliness and link the spread module more closely to CAPRA.

The spread module is not yet available online. Risk assessors who wish to use and test this module can request the code from the authors (e.g. christelle.robinet@orleans.inra.fr).

2.5 Test species

The models developed for the generic spread module were tested on selected case study pests. Seven species from different taxonomic groups (plants, insects, nematodes and pathogens) were tested in greater depth to explore a variety of possible dispersal patterns and thus benefit from all these different modelling experiences. Among them, two important species for the EU were tested: the western corn rootworm, *Diabrotica virgifera virgifera*, and pine wood nematode (*Bursaphelenchus xylophilus*).

3 Tutorial on the spread module

3.1 General presentation of the spread module

The spread module consists of a suite of models. Each model is based on a different set of assumptions. Consequently, each model will give a different picture of the spread process. This immediately shows that the results of the models should not be seen as accurate predictions. Rather, they are scenarios that depict what is likely to happen if the process of spread obeys the rules that are captured in the models included here. These rules are very simple. The spread models are intended as quick assessment tools, and as a result they are simple and crude. However, they are not necessarily less accurate than more elaborate models. The key thing is that the user of the models should be aware of the principles and assumptions of each model and interpret the results with due caution, in the light of the credibility of the model simplifications and the quality of the parameter values.

The module consists of five models. Two of the five model the increase of a pest population in time. The three others depict the increase of a pest population in time and space. All models are run on a map of Europe, resulting in a spatial representation despite the underlying process in the first two models being purely temporal.

The first model is called Simple Logistic Growth (SLG). It assumes that a pest is present throughout Europe and that in each cell (a rectangular area on the map) its population density starts at a low value. Subsequently, the population in each cell increases over time according to a logistic S-shape curve, initially representing exponential growth but plateauing when the maximum population is approached. The user can specify the maximum yearly multiplication factor of the species within a cell. The user can also specify the initial value in each cell, expressed as a percentage of carrying capacity. Input maps are needed for the area of potential establishment for the species. For the current implementation of the spread module, we have based these input maps on CLIMEX because this software provides not only an index for long term survival (EI) but also on potential growth (GI).

The second model is called Logistic Growth with Economic Values (LG-Econ). This model simulates the number of infested cells on the map according to a logistic function. While the logistic function is mathematically the same as in the first model, the meaning is completely different. Here, the process is the increase in the number of infested cells. Density within the cells is not considered. The user should specify a relative rate of increase for the invasion process of the cells. The relative rate specifies the proportionate increase per year. Three scenarios are available for adjusting *where* the newly invaded cells are located on the map. This may be random, or it may be based on the economic values represented in each cell on the map. If the most valuable cells are invaded first, this represents a *worst case*. Otherwise, if the least valuable cells are invaded first, we have a *best case*. Clearly, the worst and best cases provide the extremes of possible outcomes. The user can explore the effect of specifying different relative rates of increase and different initial proportions of invaded cells.

The third model is called Radial Rate expansion (RR). This simple model accepts one or more points of entry from the user plus a radial rate of population expansion (km/year). The population's range then expands according to the prescribed radial rate.

The fourth model is called Random Radial Rate Expansion (Rand-RR). It uses the radial rate expansion concept to calculate the outer edge of the potentially invaded area, but it uses the Igecon model (random case) to calculate which cells in this potentially invaded area are actually infested. This model accepts as parameters the points of entry and a radial rate of population expansion, as well as parameters for the Igecon model: the initial proportion of invaded cells in the risk area and the relative rate of increase in the number of invaded cells.

The fifth model is a true population growth and dispersal model (DK). It combines a logistic process for population increase within cells (as in the first model) with a probability distribution of dispersal distance. This probability distribution is called a kernel. The model requires entry points and initial population densities at these points, yearly multiplication factors within cells and two parameters that define the dispersal kernel. One is a scale parameter, which represents the width of the kernel. The other parameter represents the fatness of the tails of the kernel. Fat kernels have a higher probability of long distance dispersal, and result in much faster spread. As the fifth model is much more computation intensive than previous models, it takes longer to run (minutes). Two versions are available: a deterministic version (dispk) and a stochastic version (dispksto). In the latter version, both population growth and dispersal are simulated, but dispersal is based on probabilities. While this refinement is biologically realistic and interesting allowing the species to make some jumps, it makes the model very slow. It takes hours or even days to run for the whole of Europe, especially at 10 km resolution.

As indicated, the different models provide different, and often complementary, perspectives on the process of spread. We recommend that users play with the models to get familiarity and then explore the projected trends in dynamics with alternative model approaches.

The module is programmed in the computer program R, which can be downloaded freely from the internet¹. The spread module was initially applied on the grid used in CLIMEX (regular grid in decimal degrees). However, a second version was developed in a metric system (ETRS 1989 LAEA) at a resolution of 10 km by 10 km to allow interaction with risk maps for a projection adapted to Europe. Only the last section of the tutorial is dedicated to this metric version since the functions are basically the same. The main difference is in the format of input files and the need to adjust some parameters to this spatial resolution. In both version, it is possible to export the output result in the LAEA projection to combine it with other maps (e.g. using the software MCAS).

Section 3.2.3 summarizes how the spread module R code should be operated on a PC. Section 3.3 describes how the six models are implemented in the R code, and how these models should be run. In section 3.4, we provide a supplement for the metric version.

3.2 First steps in the spread module

This tutorial is associated with the R SpreadModule code version 21 (May 30th, 2011) for the decimal degree version (DD version), and version 8 (May 30th, 2011) for the metric version.

¹ <http://cran.r-project.org/>

3.2.1 Required datasets

The spread module is part of a generic integrated model. It requires several inputs:

1) Climatic suitability (obligatory) (“ClimexOutput.txt”)

Two variables are needed:

- a variable indicating whether the species can potentially establish (values from 0 to 100, or 0 to 1)
- a variable indicating how the populations can grow (values from 0 to 100).

In the spread models we have used two outputs from CLIMEX respectively: the ecoclimatic index (**EI**) and growth index (**GI**). The EI indicates the favourability of the climate for long-term survival of the species (from 0 if not favourable to 100 in case of ideal conditions) and GI indicates the overall potential for population growth (see Sutherst et al. 2007 for further details,

<http://www.hearne.com.au/attachments/ClimexUserGuide3.pdf>).

Note that in the spread module:

- GI is rescaled so that the max(GI) over the area of interest = 100.
- it is possible to use other datasets than these CLIMEX indexes as long as the range of values and the meaning are the same.

2) Habitat distribution (optional) (“habitat”)

A raster indicating the habitat distribution (based on hosts, soil or a combination of both) can be used (values from 0 to 100, or 0/1). In this case, the species cannot disperse in areas where its habitat is absent. In practice, we assume that EI=0 and GI=0 at these locations.

3) Economic data (optional; just for one model) (“econ”)

A raster indicating the economic value (€ / km²) represented by the host can be used. This dataset is required for only one model (LG-Econ). If the units are different, e.g., € /ha, it is possible to convert them by directly applying a multiplicative factor (*mult*) (see the following chapter for more details). These data should already take into account the proportion of land covered by the host. If not, you can assume that a given proportion of the area within the host distribution is actually covered by the host. In this case, you should also use the multiplicative factor to ensure that the data represent the economic value of the host per km².

Note that:

- The **spatial resolution** of the spread module is the resolution of the climatic suitability dataset (except for the metric version, see chapter 3.4). This dataset should be composed of locations (defined by their latitude and longitude in **decimal degrees**) and values for EI and GI at these points. In this guide, we will refer either to the **locations** or to

the **cells** (rectangles centred at these points), with the ensemble of all the cells covering the whole study area.

- **Raster files** can be easily exported from GIS software. Be sure that the coordinate system is the same as in CLIMEX (decimal degrees, WGS 1984). In ArcGIS, for instance, select the required layer, then click right on the mouse, select “Data”, then “Export data” and choose the GRID format. Two folders are generated: one folder with the name you entered (the folder you need) and another one called “info” (not needed).
 - If you want to include habitat distribution in the models, you should:
 - export this dataset as previously described and call this exported file “**habitat**”
 - copy and paste the raster for habitat distribution (only the folder “habitat”) into the spread module folder
 - If you want to apply the model associated with economic values, you should:
 - export this dataset as previously described and call this exported file “**econ**”
 - copy and paste the raster for economic values (only the folder “econ”) into the spread module folder

Note that, in the DD version, habitat and economic can be in any raster format (GRID but also .tif or .asc for instance).

3.2.2 Procedure to get the required files

3.2.2.1 CLIMEX file

The spread module needs outputs from CLIMEX (the ecoclimatic index EI and the growth index GI).

- If no CLIMEX model is available, then it is not possible to apply the spread module (current version – May 2011).
- If a specific CLIMEX model is available, then consider the following instructions.

Use CLIMEX² compare locations (1 species) with **grid data**, for the area of interest (e.g., Europe). **Do not use the CLIMEX grid data for the world** because GI will be rescaled over the world instead of rescaled over the PRA area, inducing some errors, and, due to the amount of points, the code may crash for some models. Then, export the CLIMEX file:

- click on the “Run” button
- click on the “Save to file” button, then select “new”
- select the model variables: Latitude, Longitude, EI, GI (Comma-delimited), and “Save” (Fig. 1a)
- find the exported file in the folder “models” of CLIMEX, copy this .csv file and paste it in the spread module folder of your study species

² These instructions are valid for CLIMEX version 3

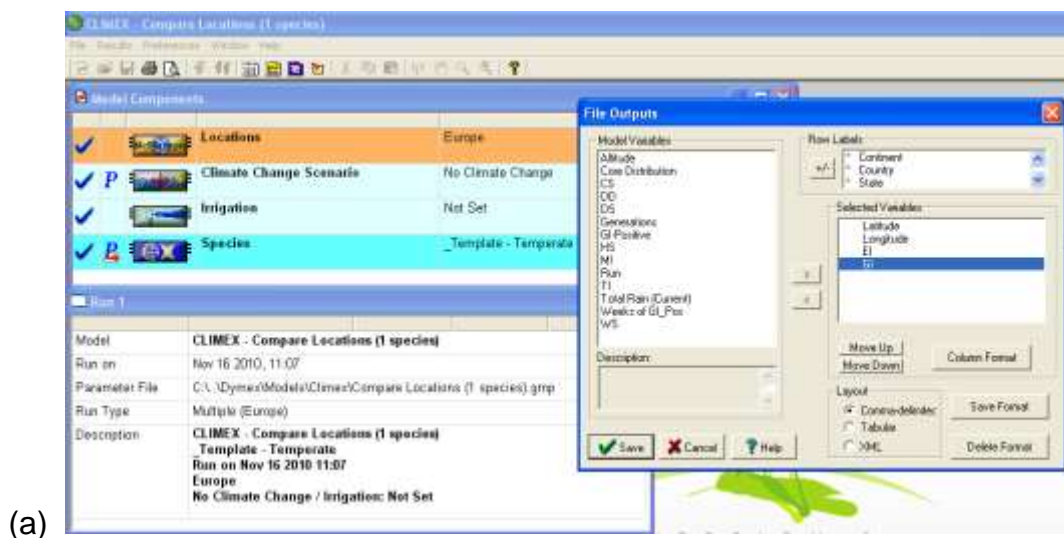
Then you have two options:

Option 1: you directly use this file. In this case:

- rename this csv file: “**ClimexOutput.csv**”

Option 2: you want to use a reworked file, providing only the coordinates, EI and GI. This option is useful when you want to work on these data before applying the spread module. In this case:

- open this file with Excel (all the data are in the first column) (Fig. 1b)
- select the whole first column (A) and go to “Data”, “Convert”, then select “Delimited”, and “Comma” for the separator. *The preview already shows you the result. Check that all the data appear correctly. Decimals should be written with dots and not commas.*
- delete the 4 first columns (Continent, Country, State, Location) and keep only **Latitude, Longitude, EI and GI** columns. **You must always keep them in this order, otherwise significant errors will occur. If your columns are not in this order, change them.**
- delete the first empty lines and the header line (Fig. 1c)
- **save as a .txt file, but use either MS-DOS (.txt) or ANSI (.txt).**
- call this file: “**ClimexOutput.txt**” (you must respect capital letters) (Fig. 1d). This is the .txt file which will be imported in R (these points will define the grid cells).



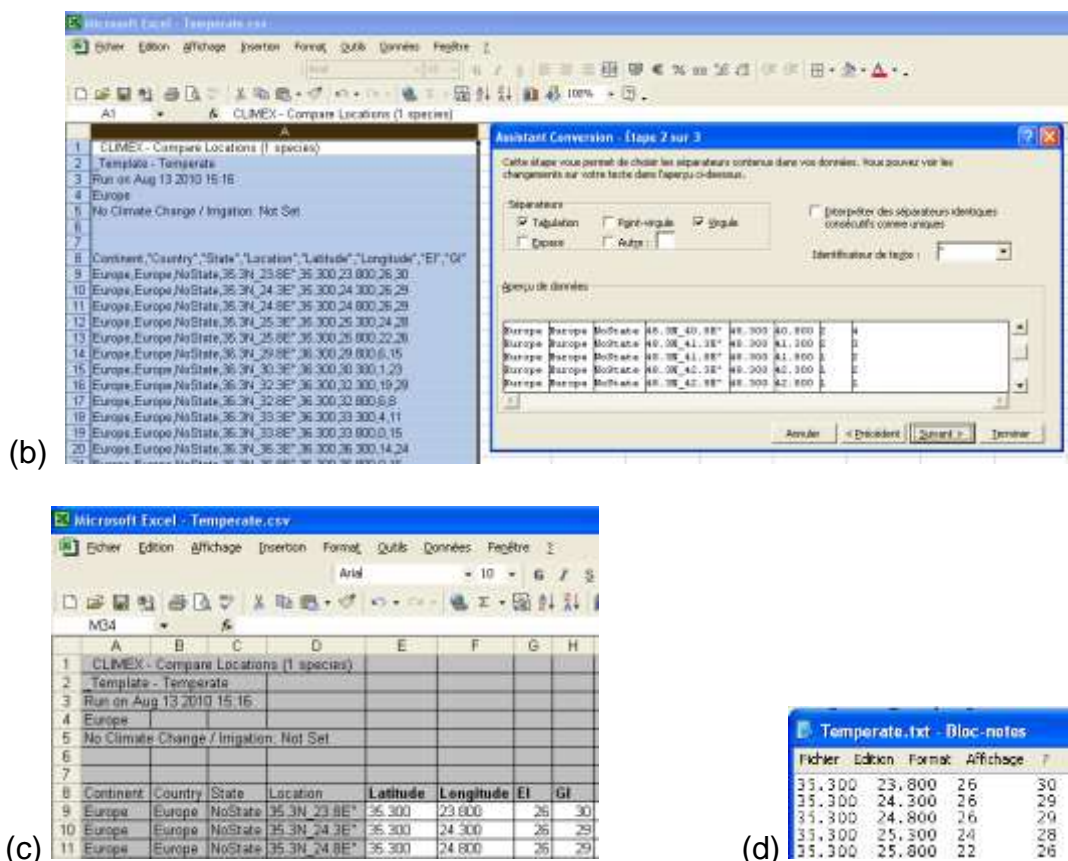


Figure 3.2-1: (a) Exporting the CLIMEX file. (b) csv file exported from CLIMEX and opened in Excel and the procedure to separate the columns. (c) the same file after the separation of the columns. Grey cells are the cells that should be deleted. (d) txt file that should be imported into R.

3.2.2.2 Habitat and economic files

- If habitat and economic files are already used for mapping endangered areas (see PD No. 3.3), then these maps can be exported from MCAS.
 - In the metric version of the spread module, these maps can be used directly. Just rename them correctly (“habitat” and “econ”).
 - In the decimal degree version, open R and write:

```
library(sp)
library(raster)
library(rgdal)
projWGS84="+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs
+towgs84=0,0,0"
projETRS89="+proj=laea +lat_0=52 +lon_0=10 +x_0=4321000
+y_0=3210000 +ellps=GRS80 +units=m +no_defs"
prj=as.character(expression(PROJCS["ETRS_1989_LAEA",GEOGCS["GCS_
ETRS_1989",DATUM["D_ETRS_1989",SPHEROID["GRS_1980",6378137.0,2
98.257222101]],PRIMEM["Greenwich",0.0],UNIT["Degree",0.0174532925199
```

```
433]],PROJECTION["Lambert_Azimuthal_Equal_Area"],PARAMETER["False
_Easting",4321000.0],PARAMETER["False_Northing",3210000.0],PARAMET
ER["Central_Meridian",10.0],PARAMETER["Latitude_Of_Origin",52.0],UNIT["
Meter",1.0]))
r <- raster(choose.files())
# find your .asc file
projection(r)=projETRS89
plot(r)
mask=raster(xmn=-20, xmx=70, ymn=30, ymx=80, crs=projWGS84)
# here you can adjust the spatial extent you need
res(mask)=0.5
rproj=projectRaster(r,mask)
plot(rproj)
writeRaster(rproj,"name_of_the_export_file.tif",format="GTiff")
# => in this last command, put a name for the output file, either habitat or econ
```

- If these maps are not available from risk mapping (MCAS), then the risk assessor can obtain host distribution data from the McGill University (Canada) website:

<http://www.geog.mcgill.ca/landuse/pub/Data/175crops2000/ArcASCII-Zip/>

If the host species is found there, the risk assessor should download the corresponding file (either “harea”, the percentage of land covered by the species within the cell, or “yield”, the production in tons per ha). Then, unzip the file, open the .asc file with a text editor (notepad for instance), delete the first blanks at the beginning of the 7 first lines (before “ncols”, ... and before the first value) and save the changes. Then open R and,

- in the metric version, write:

```
library(sp)
library(raster)
projWGS84="+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs
+towgs84=0,0,0"
projETRS89="+proj=laea +lat_0=52 +lon_0=10 +x_0=4321000
+y_0=3210000 +ellps=GRS80 +units=m +no_defs"
prj=as.character(expression(PROJCS["ETRS_1989_LAEA",GEOGCS["GCS_
ETRS_1989",DATUM["D_ETRS_1989",SPHEROID["GRS_1980",6378137.0,2
98.257222101]],PRIMEM["Greenwich",0.0],UNIT["Degree",0.0174532925199
433]],PROJECTION["Lambert_Azimuthal_Equal_Area"],PARAMETER["False
_Easting",4321000.0],PARAMETER["False_Northing",3210000.0],PARAMET
ER["Central_Meridian",10.0],PARAMETER["Latitude_Of_Origin",52.0],UNIT["
Meter",1.0]))
r = raster(choose.files())
# find your .asc file
mask=raster(nrows=500, ncols=450, xmn=2500000, xmx=7500000,
ymn=1000000, ymx=5500000, crs=projETRS89)
res(mask)=10000
```

```
projection(r)=projWGS84
q = projectRaster(r,mask)
res(q) = 10000
ymin(q) = 1000000
ymax(q) = 5500000
xmin(q) = 2500000
xmax(q) = 7500000
plot(q)
writeRaster(q,"name_of_the_export_file.tif",format="GTiff")
# => in this last command, put a name for the output file, either habitat or econ
```

- in the decimal degree version, write:

```
library(sp)
library(raster)
r = raster(choose.files())
# find your .asc file
r2 = aggregate(r,fact=6,method="bilinear")
# to have a resolution of 0.5° (30 min = 6 * 5 min of the origin file)
# it usually takes a while for the calculation, be patient
res(r2) = 0.5
ymin(r2) = -90
ymax(r2) = 90
xmin(r2) = -180
xmax(r2) = 180
projWGS84="+proj=longlat +ellps=WGS84 +datum=WGS84 +no_defs
+towgs84=0,0,0"
mask=raster(xmn=-20, xmx=70, ymn=30, ymx=80, crs=projWGS84)
# here you can adjust the spatial extent you need
res(mask)=0.5
q = crop(r2,mask)
plot(q)
writeRaster(q,"name_of_the_export_file.tif",format="GTiff")
# => in this last command, put a name for the output file, either habitat or econ
```

- If these maps are not available neither from MCAS nor from McGill University, risk assessors could find them from other sources, but in this case, they need to be able to convert them into the correct format since we cannot provide a universal procedure here.

Note for the economic file: in the McGill university database, it is possible to derive an economic file. You should make the following calculation: 100 * yield [ton/ha] * area [% covered by the species] to obtain the number of tonnes per km² of land. Then, for model 2 (see section 3.3.2.2), you can use this file and attribute a constant economic value for each tonne (*mult*).

3.2.3 The R code



The code for the spread module is written in the file called “Prog-SpreadModule.R”. You can load this code with the statistical language software R. It is a free software program you can download at: <http://www.r-project.org> (click on “CRAN” on the left column, select the closest location to you, then consider only the part at the top, and select for instance “Windows”, then “base”, and “Download R x.xx.x for Windows” – versions 2.10.1 and 2.11.1 were used for the testing).

3.2.3.1 Required files for the spread module

The following files are provided for the spread module:

File name	Description
SpreadModule.RData	A blank R file where the simulations should be done
Prog-SpreadModule.R	The code you should load in R
europel.txt	Countries’ border required for the maps
elev.asc	Elevation raster (meters above sea level)
raster_1.3-11.zip sp_0.9-66.zip rgdal_0.6-28.zip	Libraries needed by R, also available on the R project website. You should install them only once and then simply call them each time you open R. See section 3.2.

The following files should be supplied by the end user:

File name	Description
ClimexOutput.txt or.csv	Climatic suitability (derived from CLIMEX)
habitat	Raster file of the habitat distribution (host, soil, ...)
econ	Raster file for the LG-Econ model only
presence.txt	Entry points, see section 3.3.3.3, dispersal kernel models

The first file (ClimexOutput) is obligatory and the others optional.

CAUTION: All these files should be placed in the same folder. If you are assessing several species, you should create several folders and duplicate non-specific files in these folders.

3.2.3.2 To start with the spread module

1) Open the SpreadModule.RData file in the spread module folder of your study species (do not use the R icon on the desktop otherwise you will have to change the working directory where R works).

2) The R code used for the spread module calls some raster files, e.g. to take into account the maximum elevation limit for the species occurrence, host distribution, or economic value. Therefore, you should load some specific libraries. If they are already installed on your computer, go to step 3. If not, go to “Packages”, then “load the package file from a zip file”, and select “sp_0.9-66.zip”. Do the same thing for “raster_1.3-11.zip” and “rgdal_0.6-28.zip”.

3) write in the R console:

```
> library(sp)
> library(raster)
> library(rgdal)
```

4) say if you have a direct output from CLIMEX (.csv, option1):

```
> climexcsv = T
or if not (you should provide a re-worked .txt file as described previously,
option 2)
> climexcsv = F
```

5) give the elevation limit (for instance 1000 m hereafter)

```
> elevmax = 1000
or, if you do not want to have an elevation limit, write:
> elevmax = F
```

6) Then, if you have a raster file for the habitat distribution and want to take it into account, write:

```
> habitatfile = T
If this is not the case, write:
> habitatfile = F
```

7) You should tell the raster format of the habitat file (if used). If it is a tif format, then you should write:

```
> habitatformat=".tif"
If it is an asc format, then you should write:
> habitatformat=".asc"
If it is a GRID format (arcGIS specific format), a folder with many files will
be generated. In this case, you should write:
> habitatformat=NULL
```

8) **LOAD THE R CODE**: click on “File”, “open a R source code”, find the file Prog-SpreadModule.R, open. It takes a few seconds (be patient). Then the information concerning the spread module is given. If you want to display this information later, just type:

> `printinfo()`

The prompt > appears just after this and then you can type the commands to run the models (see section 3.3 for the command lines that need to be typed to call the models).

If the habitat distribution is provided, then the CLIMEX EI and GI values are considered to be 0 where the host is absent. If an elevation limit is provided, then, above the limit, EI and GI values are also considered to be 0.

You can plot several maps: the risk area map (where $EI > 0$), the rescaled GI, and the habitat (if available) using the following commands respectively:

> `plotRA()`

> `plotGI()`

> `plohabitat()`

The map legend is given on the R console when calling the functions.

If you have the coordinates of infested locations and you want to know the number of infested cells, you should create a new file and enter longitude (1st column) and latitude (2nd column) in decimal degrees, and save it as a text file in your working directory. The first line should not give the name of the columns but directly the values. Then, you can use the following function:

> `pointtocell("name_of_your_file.txt")`

to obtain the number of infested cells.

3.2.3.3 Some basic notes about the use of R

- You can save the workspace. In this case R will keep in memory all the functions and the values saved in variable names. If you open this R file later, you will just need to call the libraries and you can continue working as if R has not been closed.
- If you want to save the commands you have written in the R console, you should save the history (use the file menu). Then you can open this history file (with a text editor for instance) and find all the commands you typed in R.
- When you call a function (see section 3.3), you can change the order of the parameters. If you do not write a given parameter with its value, then R will take the default value (arbitrary but constant value) for this parameter.
- T means true, F means false, NA means "Not a Number", NULL means no value.
- R differentiates lower case and capital letters, therefore you should always include appropriate capital letters otherwise R will not recognise the names of variables or files.
- The decimal is a dot and not a comma.

3.2.4 Quick launch

If you want to test the models rapidly, follow the steps below, copy the commands and paste them into the R console. They are given as examples; you should change them according to the specific case you are interested in. This is a summary of the commands. For more details, read the following sections.

- 1- Obtain the CLIMEX dataset (or other climatic suitability datasets)
 - 2- Obtain the habitat distribution if required
 - 3- Obtain economic data if required (for one model only)
- and place them in the spread module folder.

R commands:

```
library(sp)
library(raster)
library(rgdal)
climexcsv = T
elevmax = F
habitatfile = T
habitatformat= ".tif"
# LOAD THE R CODE (do not forget this important step)
res = slg(N0=0.1,lmax=10,t=5)
res = lgecon(N0=0.1,r=2,t=5, econraster=F,mult=1,sim=10)
res = radial(RR=80,t=5,coord=c(-5,39))
res = radialrand(RR=200,t=4,N0=0.1,r=1,coord=c(30,47))
res = dispk(N0=1, t=10, lmax=40, p=50, u=100, presencefile=F,nentry=1)
```

Note that you should type: zero and not the capital letter O when writing N0; little L and not the number 1 when writing lmax.

3.2.5 WARNING

These models should be considered as **scenarios**. The outputs of the models are not predictions to be trusted blindly. These predictions depend closely on the validity of the assumptions and parameter estimates. **You**, the user, are responsible for these estimates and a prudent interpretation of the model results. The models developed for the spread module are tools for risk assessors to obtain a spatial representation of the potential spread of the study species. To some extent, they are designed to summarize on a map the basic biological knowledge available on spread and allow the user to test several values for the parameters to mimic uncertainty and see how this affects the potential spread. None of these model scenarios will give the same results because their assumptions are different. It is thus recommended to test several models to obtain a range of possible outcomes, and eventually to

select the most suitable models according to the species spread behaviour, data availability and the degree of confidence that you place on the model assumptions and the parameter estimates.

3.3 Description of the models (Decimal Degree version)

This tutorial is associated with the R SpreadModule code version 21 (May 30th, 2011) for this DD version.

This section describes the models and the parameters. Risk assessors should first collect data to estimate the value of the parameters. In this section, the models and the meaning of the parameters are described but no guidance on how to estimate the parameters is provided here because there is no universal method. However, examples of parametrisation are given in chapter 4.

3.3.1 How to map uncertainty

It is generally difficult to find a single value for the parameters, because there is very often a range of possible values or a range of values resulting from this uncertainty. In this R code program, you can only enter a single value for each parameter each time you run the model, but it is advisable to test several values, one by one, within the possible range to explore the range of potential outcomes for a chosen model.

More precisely, *to illustrate the uncertainty*, you should plot **three maps**: the best case, the most likely case and the worst case, taking, in turn, the parameter values (within their potential range) corresponding to the slowest spread, the most likely spread and the most rapid spread simulations. If the spread module is applied by only one expert, then we recommend testing the most likely values - 10% and + 10% for all the parameters to obtain the best and worst cases. If there are large uncertainties in the estimates, you can use +/- 50% instead of 10%. If the spread module is applied by a group of experts, then each expert should provide his/her best estimates and the most likely case will then be provided by the mean, the best case by the minimum and the worst case by the maximum parameter value.

3.3.2 Temporal process models

In these models, we ignore the distance between the cells and the dispersal from one cell to another. There is no link between the cells. Here we make no assumption about the initial distribution (e.g. entry points).

3.3.2.1 Model 1: Population dynamics model (SLG)

“Simple Logistic Growth model” or “Temporal spread within cells”

We assume that the same initial population density N_0 (%) is introduced in all suitable cells (where the CLIMEX $EI > 0$) and then we simulate the “spread” or more precisely the population growth within each cell according to a logistic function. The output map will show all the areas which are the most suitable for population growth within the area of potential establishment. This model provides a population density for the worst case (i.e. all suitable cells are invaded) and the output is particularly useful for indicating areas where the highest population densities are likely to occur, a key factor to take into account in economic impact assessments (see recommendations in section 5.4).

Table 1: List of parameters for model 1(SLG)

<i>Parameter</i>	<i>Unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
N_0	%	0-100	1	Biological or user choice	Population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K)
λ_{max}		≥ 1	7	Biological	Maximum year to year multiplication factor (“finite growth rate”) that a population could achieve under optimal conditions assuming unlimited space
t	year	≥ 1	1	End user choice	The time horizon for the simulations (year) to calculate the spread
<i>movie</i>	Logical	T or F	F	Graphic	If <i>movie</i> = T (true), then you will see the map for each time from 1 to t , clicking on the figure each time. If F (false), then only the map at time t will be plotted

export	Logical	T or F	F	End user choice	If <i>export</i> = T (true), then the output will be exported in a tif file.
name	Character		SLG-DD-output	End user choice	If <i>export</i> = T (true), then the name given here will be the name of the exported tif file.

Note that the parameter λ_{\max} is written lmax in R.

We apply a logistic function to calculate the population abundance (%) in each suitable cell at time t :

$$N_t = \frac{N_0 \exp(rt)}{1 + N_0(\exp(rt) - 1)/100} \quad (\text{Eq 1})$$

$$\text{with } r = GI * \ln(\lambda_{\max}) / 100 \quad (\text{Eq 2})$$

The growth index (GI) provided by CLIMEX can potentially range from 0 to 100 and provides an indication of the potential growth based on climate. However, in many cases, GI does not reach 100. To adjust this parameter to the “real” population growth observed in the PRA area, this parameter was rescaled to range effectively from 0 to 100 and the specific intrinsic rate of natural increase r is equal to $\ln(\lambda_{\max})$ where $GI=100$.

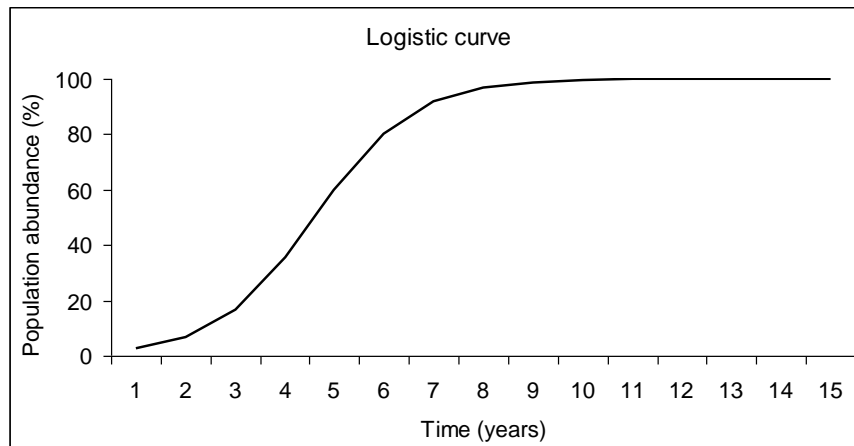


Figure 3.3-1a: Curve used in the simple logistic growth model to calculate the population abundance in grid cells.

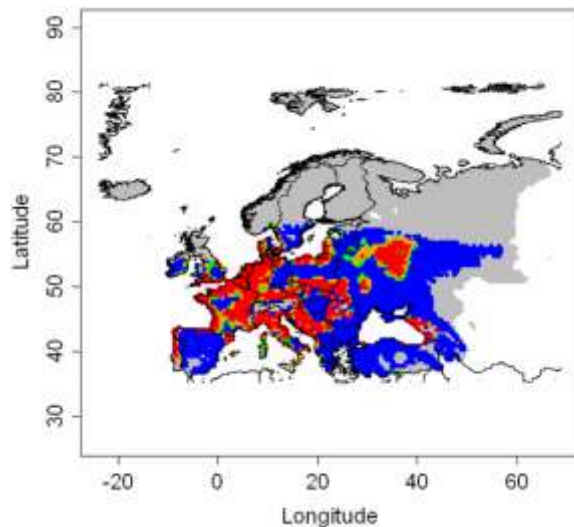


Figure 3.3-1b: Example of an output for the simple logistic growth model. Grey dots represent cells where $EI = 0$, blue dots where $0 < N_t \leq 25$, green dots where $25 < N_t \leq 50$, orange dots where $50 < N_t \leq 75$, and red dots where $75 < N_t \leq 100$. This example was generated for $t = 20$, $N_0 = 5 \cdot 10^{-5}$, $\lambda_{\max} = 40$.

In R, write:

```
res = slg()
```

and press enter to run this model with default values, or if you want to use other parameter values, you can write for instance:

```
res = slg(N0=0.1,lmax=10,t=5)
```

You will see the result on a figure. Grey dots represent cells where $EI = 0$, blue dots where $0 < N_t \leq 25$, green dots where $25 < N_t \leq 50$, orange dots where $50 < N_t \leq 75$, and red dots where $75 < N_t \leq 100$. The following commands allow you to produce several results:

<code>res\$slg</code>	the corresponding population abundance (%)
<code>res\$ntot</code>	the total number of cells considered in the model
<code>res\$nRA</code>	the number of cells included in the risk area ($EI > 0$)
<code>res\$sum0</code>	the number of cells where $N_t = 0$
<code>res\$sum25</code>	the number of cells where $0 < N_t \leq 25$
<code>res\$sum50</code>	the number of cells where $25 < N_t \leq 50$
<code>res\$sum75</code>	the number of cells where $50 < N_t \leq 75$
<code>res\$sum100</code>	the number of cells where $75 < N_t \leq 100$

To export the output:

```
res = slg(N0=0.1,lmax=10,t=5,export=T,name="SLGresult")
```

In this case, the output will be exported in a tif file called SLGresult.tif in the working directory. The projection of this raster file is Lambert Azimuthal Equal Area (ETRS 1989 LAEA), a European metric projection used in risk mapping (see WP3 and the metric supplement, section 3.4). This file can be combined to other risk maps using MCAS (see WP3).

We do not recommend exporting the file at first because it takes a long time to create the raster file and export it, and problems arise if you export the file

several times with the same name. The best approach is to play with the model first and then, when the results are satisfactory and you want to work on this output, you can export it (as mentioned above).

3.3.2.2 Model 2: Temporal spread over cells integrated with impact (LG-Econ)

“Logistic Growth model based on Economic values”

In this model, we use a logistic function to calculate the percentage of the cells invaded at time t .

We assume that an initial population abundance N_0 is introduced and then we simulate the invasion based on various scenarios.

- worst case scenario: cells with the highest economic value are invaded first
- best case scenario: cells with the lowest economic value are invaded first
- random case scenario: cells are invaded at random

This model, like the simple logistic growth model, uses logistic growth. However, it is conceptually a very different model (see recommendations on the model choice in section 5.4). Whilst the logistic equation in the simple logistic growth model represents the S-shaped growth of a population *within each grid cell*, the Logistic growth model based on economic values represents the S-shaped increase in the *number of invaded grid cells* over time. It therefore operates over a much greater scale. This model has the same parameters as the simple logistic growth model, r and N_0 , however, its interpretation is different. In this case, r is the relative rate of increase in the number of invaded grid cells per unit of time. This model is useful to obtain a range of economic impact (see section 5.4).

Table 2: List of parameters for model 2 (LG-Econ)

<i>Parameter</i>	<i>Unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
N_0	%	0-100	1	Biological or End user choice	Initial percentage of the risk area invaded at time $t=0$
r	year ⁻¹	0-100	1	Biological	Relative rate of spatial increase per year
t	year	≥1	1	user choice	The time horizon for the simulations (year) to calculate the spread

econraster	Logical	T or F	F	Data availability	If T, then the code will use the raster “econ” provided by the end-user to obtain the values at required points. If F, then values are either derived from the host distribution if hostraster=T, or chosen at random between 1 and 100 if hostraster=F.
econformat	Character		NULL	Data availability	If econraster = T (true), then the format of the economic file should be given. If it is a GRID format, then it should be NULL. If it is another raster format, then write the extension of the file, e.g. “.tif”.
habitat raster	Logical	T or F	F	Data availability	If no economic raster is available, economic values are derived from habitat abundance.
valperhost	€/host abundance	> 0	NULL	Economic variable	The value (€/host abundance per km ²) should be provided if economic values are derived from host abundance.
mult		> 0	1	Data availability	Multiplicative factor to convert the values given in the raster file

					into the required unit: €/ km ²
sim		≥1	1	End user choice	Number of replicate simulations for the random case.
export	Logical	T or F	F	End user choice	If <i>export</i> = T (true), then the output will be exported in a tif file.
name	Character		LGECON-DD-output	End user choice	If <i>export</i> = T (true), then the name given here will be the name of the exported tif file.

In R, write:

```
res = lgecon()
```

and press enter to run this model with default values, or if you want to use other parameter values, you can write for instance:

```
res = lgecon(N0=0.1,r=1,t=5,sim=10)
```

You will see the results of the 3 cases on a figure. Grey dots represent cells where EI=0, orange dots where EI>0, and red dots invaded cells (among those where EI>0). The following commands allow you to obtain several results:

```
res$ntot    the total number of cells considered in the model
res$nRA     the number of cells included in the risk area (EI>0)
res$ninv    the number of cells invaded
res$pniche  the percentage of cells invaded within the risk area
res$worst   the accumulated economic values for the worst case
res$best    the accumulated economic values for the best case
res$rand    the accumulated economic values for random case
             (min, 1st qu., median, mean, 3rd qu. , and max)
res$econvalues economic values used by the model
```

To export the output:

```
res = lgecon(N0=0.1,r=1,t=5,sim=10,export=T, name="LGECONresult")
```

In this case, the output for each of the three scenarios will be exported in tif files in the working directory (files called LGECONresult_best, LGECONresult_rand and LGECONresult_worst respectively for the best, random and worst scenarios). The projection of this raster file is Lambert Azimuthal Equal Area (ETRS 1989 LAEA), a European metric projection used in risk mapping (see WP3 and the metric supplement, section 3.4). This file can be combined to other risk maps using MCAS (see WP3). The value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the

cell is not within the area of potential establishment and the value -9999 means that data is missing.

To know how many cells are covered by some points of pest presence, you can use the following function:

`pointtocell("name_of_your_file.txt")`

You should enter the name of the file containing the longitude (column 1) and latitude (column 2) in decimal degrees. This file should be located in the working directory. For each point, the function determines the cell where it is located within the area of potential establishment. If the point is located outside the area of potential establishment, then the corresponding cell is the closest one within this area.

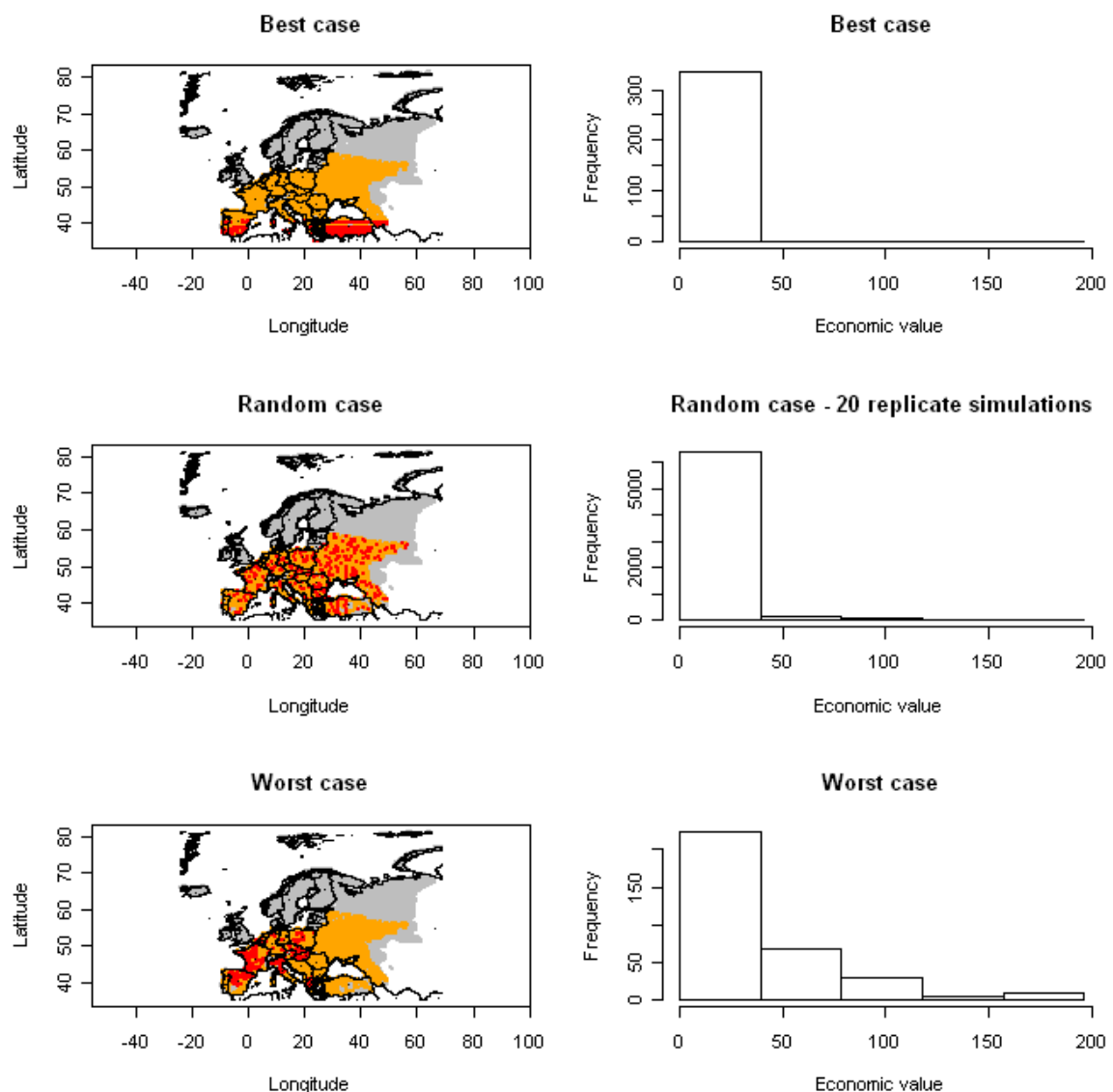


Figure 3.3-2: Example of an output for the logistic growth model based on economic values. Grey dots represent the cells where $EI=0$, orange dots where $EI>0$, and red dots the invaded cells. Economic values are expressed in monetary units per raster cell. These are defined by the user in the input file "econ".

3.3.3 Spatial process models

In these models, we take into account the entry points and the distance between the cells to describe the dispersal capability of the species.

3.3.3.1 Model 3 : Radial range expansion model (RR)

This model determines the potential spread of a species introduced in the PRA area based on a parameter for the radial rate of expansion (see section 5.4 for the recommendations). The model output runs within the area of potential establishment based on climatic suitability ($EI > 0$).

We used the following formula to calculate the distance d in km between two points (x_1, y_1) and (x_2, y_2) in decimal degrees:

$$d = \frac{20000}{\pi} \arccos \left(\sin \left(\frac{\pi}{180} y_1 \right) \sin \left(\frac{\pi}{180} y_2 \right) + \cos \left(\frac{\pi}{180} y_1 \right) \cos \left(\frac{\pi}{180} y_2 \right) \cos \left(\frac{\pi}{180} (x_2 - x_1) \right) \right) \quad (\text{Eq 3})$$

For the map projection in a metric system, we chose the origin of the x-axis to be $x = 20^\circ$ East, and we used the following formulae:

$$x_{km} = \frac{40000}{360} (x - longref) \cos \left(\frac{\pi}{180} y \right) \quad (\text{Eq 4})$$

$$y_{km} = \frac{40000}{360} y$$

These complicated formulas are needed because the earth is not flat, but a sphere.

Table 3: List of parameters for model 3 (RR)

<i>Parameter</i>	<i>Unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
RR	km/yr	> 0	20	Biological	Radial rate of range expansion per year
t	year	≥ 1	1	End user choice	The time horizon for the simulations (years) to calculate the spread
coord	Decimal degrees	Similar to the range of ClimexOutput	At random in the risk area	Place of introduction place or user choice (test)	The entry point(s) or a simulation of an introduction at

					this place.
figkm	Logical	T or F	T	Graphic	If T (true), then <i>figdd</i> should be F, and the figure will be in a metric system.
figdd	Logical	T or F	F	Graphic	If T (true), then <i>figkm</i> should be F, and the figure will be in a decimal degrees.
export	Logical	T or F	F	End user choice	If <i>export</i> = T (true), then the output will be exported in a tif file.
name	Character		Radial-DD-output	End user choice	If <i>export</i> = T (true), then the name given here will be the name of the exported tif file.

Note that entry points should be chosen from within the area that is climatically suitable for establishment ($EI > 0$). If the point is outside this area, the code will select the closest point in the suitable area.

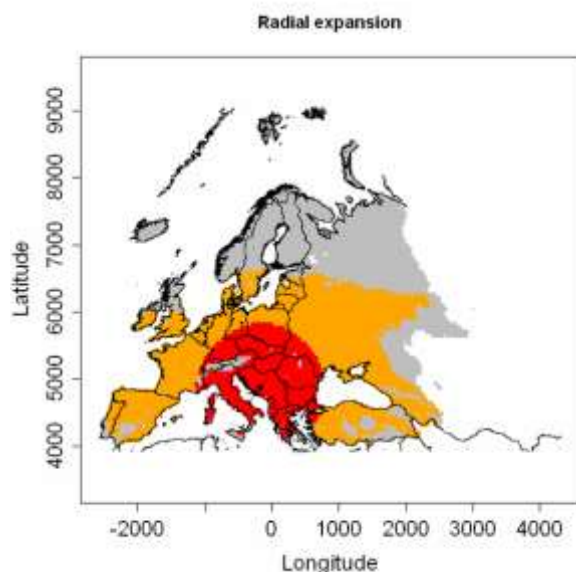


Figure 3.3-3: Radial expansion model for $t = 16$, $RR = 60$ km/year based on an entry point in former Yugoslavia (black dot). Grey dots represent the points where $EI = 0$, orange dots represent the suitable area ($EI > 0$) not invaded and red dots the invaded cells based on the spread rate given by the user.

In R, write:

```
res = radial()
```

and press enter to run this model with default values, or if you want to use other parameter values (e.g. a radial rate of 80 km/year, and a simulation time of 5 years), you can write for instance:

```
res = radial(RR=80,t=5)
```

In the previous case, the entry point is selected at random within the area where $EI > 0$. In case, you want to provide the coordinates of this entry point, write:

```
res = radial(RR=80,t=5,coord=c(-5,39))
```

The first value in coord is the longitude and the second one the latitude of the entry point in decimal degrees. Note that you can enter several entry points. In this case, write longitude(point1), latitude(point1), longitude(point2),latitude(point2),... as follows:

```
res = radial(RR=80,t=5,coord=c(-5,39,-6,42))
```

You will see the result on a figure. Grey dots represent the points where $EI = 0$, orange dots represent suitable area ($EI > 0$) not invaded and red dots invaded cells. The following commands allow you to have several results:

```
res$radial latitude (col1), longitude (col2), EI (col 3), GI (col 4)  
of invaded points
```

```
res$ntot the total number of cells considered in the model
```

```
res$nRA the number of cells within the risk area ( $EI > 0$ )
```

```
res$ninv the number of cells invaded
```

```
res$pniche the percentage of cells invaded within the risk area
```

To export the output:

```
res = radial(RR=80,t=5,coord=c(-5,39,-6,42),export=T, name="Radialresult")
```

In this case, the output will be exported in a tif file called Radialresult.tif in the working directory. The projection of this raster file is Lambert Azimuthal Equal Area (ETRS 1989 LAEA), a European metric projection used in risk mapping (see WP3 and the metric supplement, section 3.4). This file can be combined to other risk maps using MCAS (see WP3). The value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the cell is not within the area of potential establishment and the value -9999 means that data is missing.

3.3.3.2 Model 4: Hybrid of logistic growth and radial rate expansion (Rand-RR)

"Random radial range expansion"

This model combines a randomised version of the temporal spread over cells model (LG-Econ) with the radial expansion model (RR) to take into account the distance from the entry point(s). Since this model is based on the random selection of the cells (in-between the best and worst cases), it does not require economic data inputs. It is therefore an advantage in terms of data availability. Invaded cells are chosen at random within the area given by the radial expansion model which makes the spatial distribution more realistic and

credible. The distance and the projection in a metric system are calculated using Eqs 3-4. This model is useful to take into account that the population may not spread over all the area defined by the radial expansion rate. It provides more information than model 3.

Table 4: List of parameters for model 4 (Rand-RR)

<i>Parameter</i>	<i>Type or unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
<i>N₀</i>	%	0-100	1	Biological	Initial percentage of the risk area invaded at time $t=0$
<i>r</i>	year ⁻¹	0-100	1	Biological	Relative rate of spatial increase per year
<i>RR</i>	Km/yr	> 0	20	Biological	Radial rate of range expansion per year
<i>t</i>	year	≥1	1	End user choice	The time horizon for the simulations (year) to calculate the spread
<i>coord</i>	Decimal degrees	Similar to the range of ClimexOutput	At random in the risk area	Introduction place or end user choice (test)	The entry point(s) or a simulation of an introduction at this place.
<i>figkm</i>	Logical	T or F	T	Graphic	If T (true), then <i>figdd</i> should be F, and the figure will be in a metric system.
<i>figdd</i>	Logical	T or F	F	Graphic	If T (true), then <i>figkm</i>

					should be F, and the figure will be in a decimal degrees.
export	Logical	T or F	F	End user choice	If <i>export</i> = T (true), then the output will be exported in a tif file.
name	Character		Radialrand-DD-output	End user choice	If <i>export</i> = T (true), then the name given here will be the name of the exported tif file.

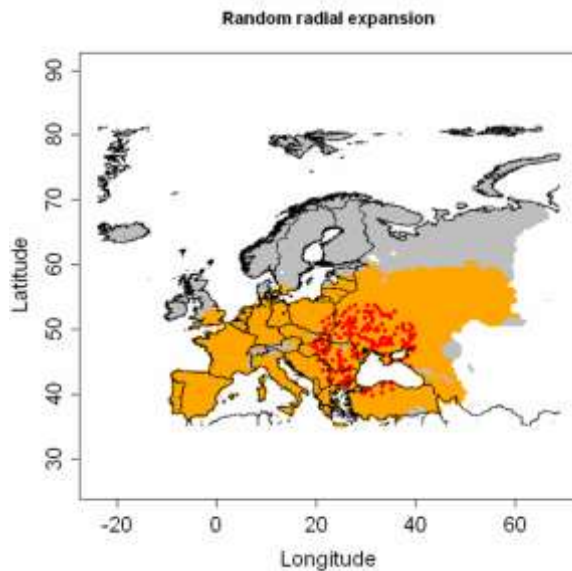


Figure 3.3-4: Random radial expansion model for $t = 4$, $RR = 200$, $N_0 = 0.1$, $r = 1$, $coord = c(30,47)$. Grey dots represent the points where $EI = 0$, orange dots represent suitable area ($EI > 0$) not invaded and red dots invaded cells.

In R, write:

`res = radialrand()`

and press enter to run this model with default values, or if you want to use other parameter values, you can write for instance:

`res = radialrand(RR=200,t=4,N0=0.1,r=1)`

In the previous case, the entry point is selected at random within the area where $EI > 0$. In case, you want to provide the coordinates of this entry point, write:

```
res = radialrand(RR=200,t=4,N0=0.1,r=1,coord=c(30,47))
```

The first value in coord is the longitude and the second one the latitude of the entry point in decimal degrees. You can enter several entry points. In this case, write longitude(point1), latitude(point1), longitude(point2),latitude(point2),... as follows:

```
res = radialrand(N0=0.1,r=0.5,RR=80,t=5, coord=c(0,37,5,50))
```

You will see the result on a figure. Grey dots represent the cells where $EI = 0$, orange dots represent suitable area ($EI > 0$) not invaded and red dots invaded cells. The following commands allow you to display several results:

```
res$radialrand    latitude (col1), longitude (col2), EI (col 3), GI (col 4) of  
invaded cells  
res$ntot         the total number of cells considered in the model  
res$nRA          the number of cells within the risk area (EI>0)  
res$ninv         the number of cells invaded  
res$pniche       the percentage of cells invaded within the risk area
```

To export the output:

```
res = radialrand(N0=0.1,r=0.5,RR=80,t=5, coord=c(0,37,5,50),export=T,  
name="Radialrandresult")
```

In this case, the output will be exported in a tif file called Radialrandresult.tif in the working directory. The projection of this raster file is Lambert Azimuthal Equal Area (ETRS 1989 LAEA), a European metric projection used in risk mapping (see WP3 and the metric supplement, section 3.4). This file can be combined with other risk maps using MCAS (see WP3). The value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the cell is not within the area of potential establishment and the value -9999 means that data is missing.

3.3.3.3 Model 5: Dispersal kernel models (DK)

These types of model require: a population growth model, a dispersal kernel (2Dt in this case) and the proportion of population engaged in dispersal. Two versions have been developed: a deterministic version where the population spread relies on probabilities, and a stochastic version, where the dispersal distance is chosen at random in the probability distribution and several replicate simulations are required to obtain a representative population spread. See section 5.4 for the recommendations.

The dispersal kernel in 2 dimensions is given by:

$$f(r) = \frac{1}{u^2 p \pi} \frac{\Gamma\left(\frac{p+1}{2}\right)}{\Gamma\left(\frac{p-1}{2}\right)} \frac{1}{\left(1 + \frac{1}{p} \frac{r^2}{u^2}\right)^{\frac{p+1}{2}}} \quad (\text{Eq 5})$$

where r is the distance between two points calculated with eq 3.

For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses at long distance) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail) (Clark et al. 1999).

To account for the shrinkage due to the earth curvature (the length of the ring at distance r is less than that of a ring in the plane at distance r), we included a correction and finally used the following formula to calculate the probability to disperse at a distance r .

$$k(r) = \frac{r}{20000/\pi} \frac{1}{\sin\left(\frac{r}{20000/\pi}\right)} f(r)$$

To see the shape of the kernel, write:

```
> plotkp(u=50,p=5,xmax=200,color="blue")
```

and eventually:

```
> plotkp(u=5,p=5,xmax=200, add=T,color="red")
```

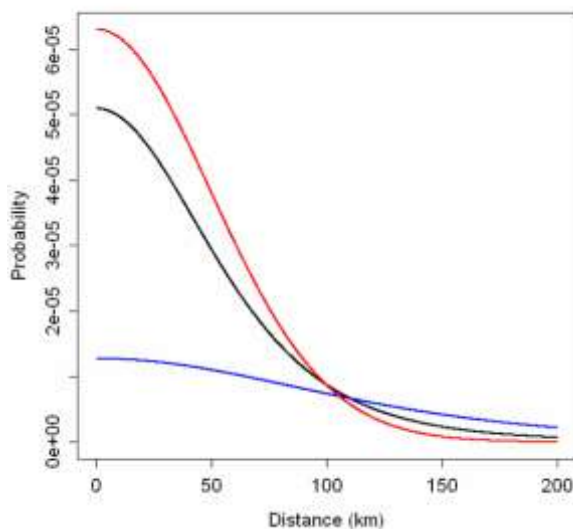


Figure 3.3-5: Dispersal kernel with $p = 5$ and $u = 50$ (black), $p = 100$ and $u = 50$ (red), $p = 5$ and $u = 100$ (blue).

Depending on the knowledge of the locations and population densities where the species is present in the PRA area the model operates in three ways:

- (1) the risk assessor knows the points where the species is present and the population density at a given time $t = 0$ (initial condition for the model): the corresponding file should be a text file with three columns. **Column 1 is longitude, column 2 latitude in decimal degrees, and column 3 the population density** (in % of the carrying capacity, between 0 and 100). Note that in this case no formula should be entered in this file. For instance if the population density is $1.7 \cdot 10^{-7}$ at time $t = 0$, the risk assessor should enter 1.7e-7 in the file (3rd column). This file should be named “**presence.txt**” and placed in the folder containing the R file “SpreadModule.Rdata”.

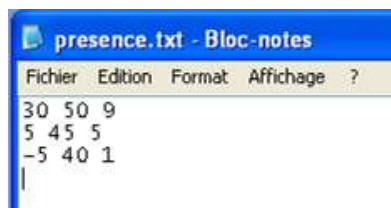


Figure 3.3-6: Presence file with three points and initial population densities (9, 5 and 1%). You should press enter at the end of the last line and save it.

- (2) The risk assessor knows only the points where the species is present and can provide a single arbitrary value N_0 for the population density at these locations before calling the function: the corresponding file should be a text file with two columns. Column 1 is longitude and column 2 latitude in decimal degrees. This file should be named “**presence.txt**” and placed in the folder containing the R file “SpreadModule.Rdata”.
- (3) The risk assessor does not know the points where the species is present or the species is not present in the PRA area. In this case, no presence file should be provided and the model will randomly select some presence points (the risk assessor can choose the number of presence points with the parameter *nentry*). If the risk assessor wants to test entry at some precise points (e.g. introduction at some ports or airports), he can create a presence file and consider these points as in case (2).

This model cannot be used when the annual spread rate is smaller than the CLIMEX grid resolution.

3.3.3.3.1 Deterministic model

Description of the model:

- the presence file is first transformed into a vector associated with the grid points. This vector contains either false/true values to identify the points where the species is present (in cases 2 and 3) or the population density at each grid point (= 0 when there is no point where the species is present near the grid point, and the mean population density if there is more than one point near the grid point);

- for each time step between 1 and t , we select the grid points where $EI > 0$ and the initial points where the species is present as potential source points (to limit the calculations). For each of these potential source points, we calculate the distance from this point to all the grid points, apply the dispersal kernel and integrate this kernel over space (multiplying these dispersal probabilities by the area of the cells). We finally multiply these probabilities by the density of the population engaged in dispersal and accumulate these values. Then, we add non-dispersing individuals. The distance and the projection in a metric system are calculated using Eqs 3-4.

- We assume that individuals die if they disperse into a cell where the $EI = 0$.

- We apply the growth model (logistic model) to this new population distribution.

- This result provides the population expansion after one time step. Then we repeat these calculations until the time step t .

Table 5: List of parameters for the deterministic version of model 5(DK)

<i>Parameter</i>	<i>Unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
N_0	%	0-100	NULL	Biological	Population abundance at time $t = 0$ expressed as a percentage of the maximum population abundance (carrying capacity K). If NULL then the file presence.txt should be provided.
λ_{max}		≥ 1	7	Biological	Maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

<i>P</i>		0-1	1	Biological	Proportion of the population engaged in dispersal
<i>p</i>	Degree of freedom	≥ 2	50	Biological	Shape parameter of the $2Dt$ dispersal kernel (number of degrees of freedom)
<i>u</i>	km	> grid resolution	100	Biological	Scale parameter of the $2Dt$ dispersal kernel
<i>t</i>	year	≥ 1	1	End user choice	The time horizon for the simulations (year) to calculate the spread
<i>presencefile</i>	Logical	T or F	T	End user choice	If T (true), a presence file should be provided. If F (false), then provide the number of entry points (<i>nentry</i>) to be selected at random in the suitable area and the population density N_0 .
<i>nentry</i>		≥ 1	NULL	End user choice	The number of entry points to select at random within the risk area ($EI > 0$) if no presence file is provided
<i>figkm</i>	Logical	T or F	T	Graphic	If T (true), then <i>figdd</i> should be F, and the figure will be in a metric system

figdd	Logical	T or F	F	Graphic	If T (true), then <i>figkm</i> should be F, and the figure will be in a decimal degrees
--------------	---------	--------	---	---------	---

In this model, the parameter P represents the proportion of individuals engaged in dispersal. Although there is an option to alter the value of this parameter, it is advisable to keep $P=1$ (the default value).

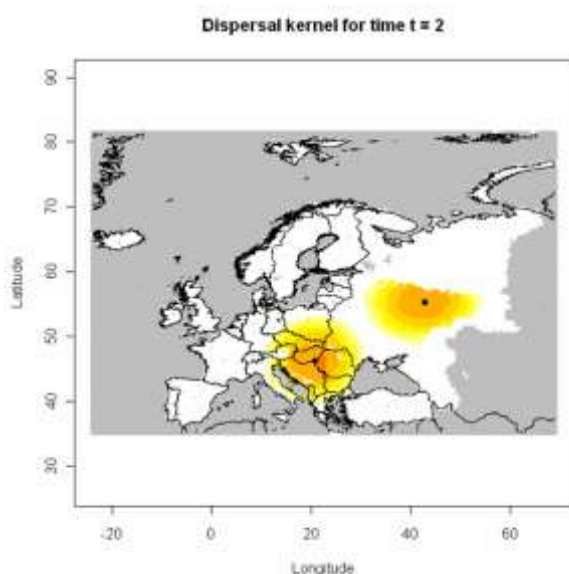


Figure 3.3-7: Output of the dispersal kernel model ($N_0=2$, $lmax=7$, $t = 2$, $u = 100$, $p = 50$, $nentry=2$) in decimal degrees.

In R, write:
`res = dispk()`

and press enter to run this model with default values, or if you want to use other parameter values, you can write for instance:

`res = dispk(t=10, lmax=40, p=50, u=100, figkm=T, figdd=F)`

N_0 and $nentry$ are not required if you provide some entry points (if you provide a "presence.txt" file, these values are automatically used whatever values you enter here). If you want to have a figure in decimal degrees, write `figdd=T` (T means true), and if you want a figure in a metric system, write `figkm=T` (otherwise write = F, F means false). You will see the result on a figure. The colors are going from white for a population density $< 10^{-6}$ to yellow, orange and red for a population density $\geq 10\%$. Grey represents missing values (no CLIMEX data). The following commands allow you to have several results:

- `res$dispk` a vector indicating the population density on the grid
- `res$ntot` the total number of cells considered in the model
- `res$nRA` the number of cells within the risk area ($EI > 0$)
- `res$iniv` the number of cells invaded (where the density is above 1)
- `res$pniche` the percentage of cells invaded within the risk area

This model is much more computation intensive than previous models. Therefore, the simulation time is much longer. Note that increasing the year t

will increase the time for calculation. You will see the year for which the calculations are running on the screen at any time of the calculation (click on the R console window to update the value). The map on the R graphics screen will be refreshed for each time between 1 and t .

If you want to define a threshold for the population abundance (%) above which you consider that the area is invaded, and see the resulting map, you should type:

```
plotkernel(res$dispk,res$presence, figkm=F,figdd=T,  
legend=F,threshold=0.01)
```

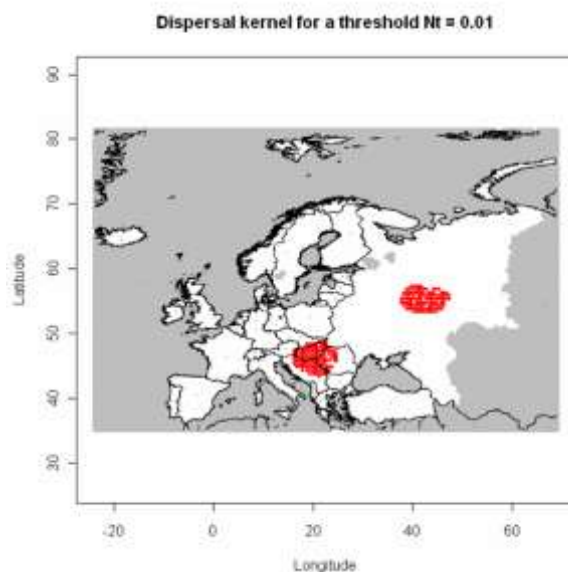


Figure 3.3-8: Figure 3.3-7 with a threshold = 0.01%. The population abundance (%) is above this threshold in red cells.

Note that you can also use this function to plot the map resulting from the dispersal kernel model. In this case, provide no value for threshold:

```
plotkernel(res$dispk, res$presence, t=10, legend=T, threshold=NULL,  
figkm=F,figdd=T)
```

To export the output:

Since it takes a long time to obtain the output for this model, the exportation procedure is slightly different from the other models. Here, the model should be called as above, and then, in a second step, the following function should be called:

```
exportkernel(res$dispk, name="Kernelresult")
```

In this case, the output will be exported in a tif file called Kernelresult.tif in the working directory. The projection of this raster file is Lambert Azimuthal Equal Area (ETRS 1989 LAEA), a European metric projection used in risk mapping (see WP3 and the metric supplement, section 3.4). This file can be combined to other risk maps using MCAS (see WP3). The values given by this file represent the population density expressed as a percentage of the carrying capacity at time t defined by the end user.

3.3.3.3.2 Stochastic model

This model is similar to the previous one, except that we choose at random where the individuals disperse according to the dispersal probabilities provided by the 2Dt kernel. The number of random jumps from one cell is equal to the population density (rounded to the unit). Generally, several hundred replicate simulations should be done to provide a reasonable indication of the invasion probability.

The time needed for the simulations is relatively long. This time closely depends on the number of cells within the area of potential establishment and the number of replicate simulations. For instance, for the Colorado beetle and the corresponding CLIMEX model, the calculations take 2h25min for only 10 replicate simulations and $t=15$ years. Although this version is available, it has not been widely tested and, until now, it is recommended to use the deterministic version as a priority.

Table 6: List of parameters for the stochastic version of model 5(DK)

<i>Parameter</i>	<i>Type or unit</i>	<i>Range</i>	<i>Default value</i>	<i>Type of parameter</i>	<i>Description</i>
N_0	%	0-100	Given in the file presence.txt	Biological	Population abundance at time $t = 0$ expressed as a percentage of the maximum population abundance (carrying capacity K)
λ_{max}		≥ 1	7	Biological	Maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

<i>P</i>		0-1	1	Biological	Proportion of the population engaged in dispersal
<i>p</i>	Degree of freedom	≥ 2	50	Biological	Shape parameter of the $2Dt$ dispersal kernel (number of degrees of freedom)
<i>u</i>	km	> grid resolution	100	Biological	Scale parameter of the $2Dt$ dispersal kernel
<i>t</i>	year	≥ 1	1	user choice	The time horizon for the simulations (year) to calculate the spread
<i>sim</i>		≥ 1	200	user choice	The number of replicate simulations. Since the model is stochastic, it is necessary to make several simulations and calculate the average result.

<i>presencefile</i>	Logical	T or F	T	user choice	If T (true), a presence file should be provided. If F (false), then provide the number of entry points (<i>nentry</i>) to be selected at random in the suitable area and the population density N_0 .
<i>nentry</i>	number	≥ 1	null	user choice	The number of entry points to select at random within the risk area ($EI > 0$) if no presence file is provided
<i>figkm</i>	Logical	T or F	T	Graphic	If T (true), then <i>figdd</i> should be F, and the figure will be in a metric system
<i>figdd</i>	Logical	T or F	F	Graphic	If T (true), then <i>figkm</i> should be F, and the figure will be in a decimal degrees

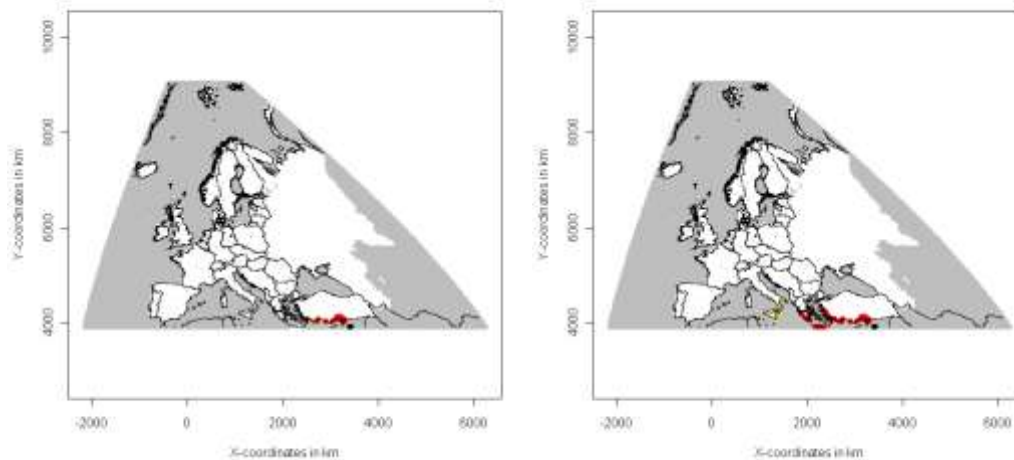


Figure 3.3-9: Output of the stochastic version (left) and deterministic version (right) for $t = 3$, $u = 100$, $p = 50$, $sim=200$, and the CLIMEX model of the Queensland fruit fly.

In R, write:

```
res = dispksto()
```

and press enter to run this model with default values, or if you want to use other parameter values, you can write for instance:

```
res = dispksto(N0=1, t=1, p=50, u=100, nentry=1, figkm=T, figdd=F, sim=10)
```

N_0 and $nentry$ are not required if you provide some entry points (if you provide a "presence.txt" file, these values are automatically derived whatever values you enter here). If you want to have a figure in decimal degrees, write $figdd=T$ (T means true), and if you want a figure in a metric system, write $figkm=T$ (otherwise write = F, F means false). You will see the result on a figure. The colors are going from white for a population density $< 10^{-6}$ to yellow, orange and red for a population density $\geq 10\%$. Grey represents missing values (no CLIMEX data). The following commands allow you to have several results:

res\$dispksto a vector indicating the population density relative to the grid

res\$ntot the total number of cells considered in the model

res\$nRA the number of cells within the risk area ($EI > 0$)

res\$ninv the number of cells invaded (where the density is above 1)

res\$pniche the percentage of assets invaded within the risk area

Note also that increasing the number of simulations will increase the time for calculation. You will see the number of simulations done on the screen at any time of the calculation (click on the R console window to update the value).

3.4 Supplement for the metric version

This tutorial is associated with the R SpreadModule code version 8 (May 30th, 2011) for the metric version.

The spread module was initially developed on a regular grid in latitude and longitude (0.5° x 0.5°), directly derived from the CLIMEX dataset. Since the generic integrated model developed by the PRATIQUE project aims to combine various types of GIS datasets (notably including host distribution), it was decided to choose a single coordinate system: the metric projection, Lambert Azimuthal Equal Area (ETRS 1989 LAEA) and a single spatial resolution, 10 km x 10 km, for all the maps. Maxime Dupin helped the spread modeller team to develop this metric version so that it is completely compatible with the files used or generated in risk mapping (WP3).

Therefore, this supplement devoted to the metric version aims to guide the users using this version of the spread module and to describe the changes. The main advantage for the end-user is the possibility to work in the same projection as the projection used in risk maps (WP3). As well as the DD version, it is possible to export the outputs in a tif file that can be used in MCAS and integrated in Decision Support Scheme for Mapping Endangered Areas (Deliverable 3.3).

Since the estimation of some parameters depends on the spatial resolution, it is necessary to carefully check the calculations and update the estimations when switching from the DD version to the metric version, and vice versa.

The CLIMEX file:

Similarly to the non metric version, you can also use the output of CLIMEX (csv file; **climexcsv = T**) directly or a modified file providing only latitude, longitude, EI and GI (in this order) (txt file; **climexcsv = F**).

Be careful to use the meteorological dataset: CRU_WRLD_V2_1.mm

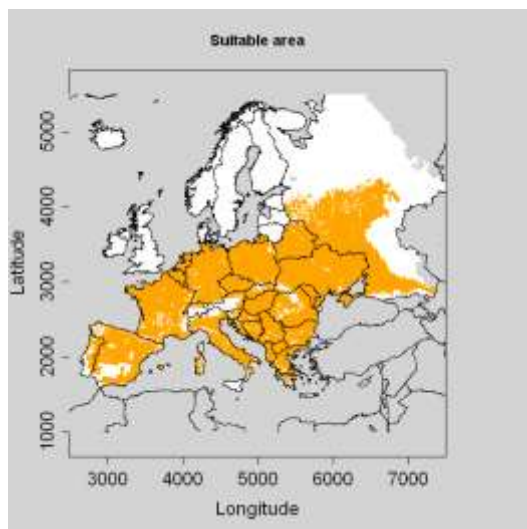
- click on MetManager icon on the locations line, add/edit/remove sequence
- click on "new"
- select CRU_WRLD_V2_1.mm
- find Europe CRU HD V2_1, then click on OK
- click on OK

The spatial resolution of the meteorological dataset should be absolutely 0.5° everywhere (even around the longitude 0°). By using the meteorological dataset CRU_WRLD_V2_1.mm some problems can be avoided.

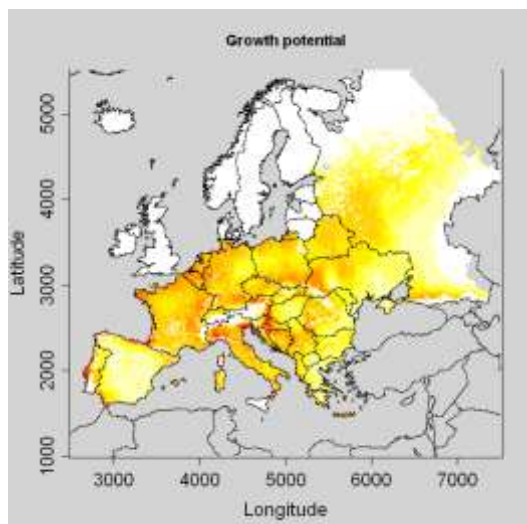
Description of the metric version

```
library(sp)  
library(raster)  
library(rgdal)  
climexcsv = T  
elevmax = F  
habitatfile = T  
habitatformat = ".tif "  
# load the R code
```

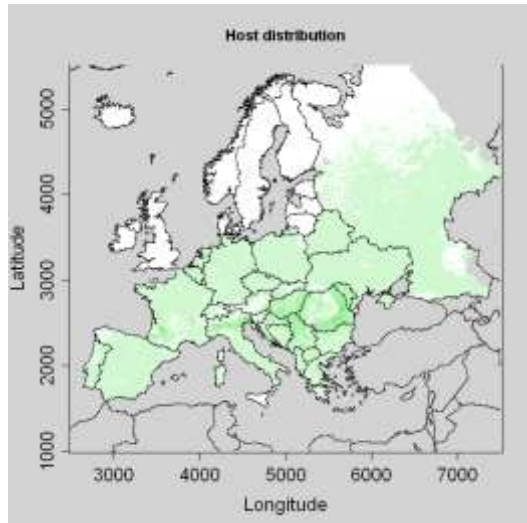
plotRA()



plotGI()



plohabitat()



```
> printinfo()
[1] "
[1] "----- For this specific case study: -----"
[1] "The grid resolution is 10 km"
[1] "The area of a cell is 100 km²"
[1] "The number of suitable cells is: 45670"
[1] "The total number of cells is: 225951"
[1] "The number of missing values in the CLIMEX dataset is: 117615"
[1] "The number of missing values in the host distribution is: 87160"
[1] "The total number of missing values (CLIMEX or host) is: 130798"
[1] "
[1] "
[1] "----- Type the commands below to call the functions -----"
[1] "
"
```

Note that in this version, you do have not the choice of viewing the map in decimal degrees or in a metric system (the variables `figdd` and `figkm` do not exist anymore in this version) because the map is always projected in the ETRS 1989 LAEA metric system.

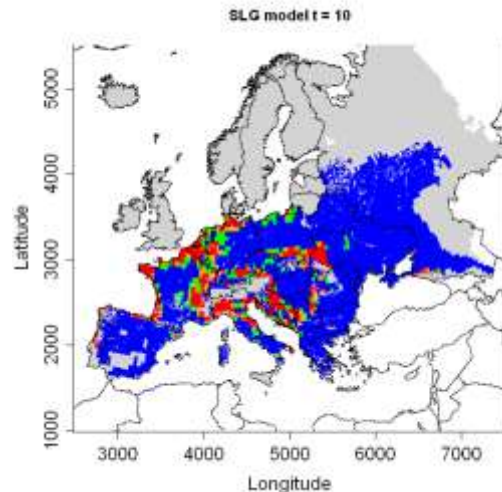
3.4.1 Temporal process models

3.4.1.1 Model 1: Population dynamics model (SLG)

“Simple Logistic Growth model”

In this metric version, nothing has changed to call the function:

```
res = slg(N0=1.6*10^(-7),lmax=40,movie=F, t=10)
```



Exporting the output

```
res = slg(N0=1.6*10^(-7),lmax=40,movie=F, t=10, export=T, name="SLGoutput")
```

We do not recommend exporting the file at first because it takes a long time to create the raster file and export it, and problems arise if you export the file several times with the same name. The best approach is to play with the model first and then, when the results are satisfactory and you want to work on this output, you can export it (as mentioned above). Missing values (NA in the exported file) coming from both the CLIMEX dataset and the habitat distribution (if used). The data represent the percentage of the carrying capacity of the species (0-100).

Warning: the parameter estimates should be updated

$$N_0 = 100 * \frac{n_0}{K} \text{ with}$$

$K = \text{area_cell (km}^2\text{)} * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2\text{)}$

Therefore, we have:

$$K = (10*10) \text{ (cell area in km}^2\text{)} * 0.20 \text{ (host proportion)} * 200e6$$

$$n_0 = 100$$

$$\Rightarrow \underline{\underline{N_0 = 5e-8}}$$

3.4.1.2 Model 2: Temporal spread over cells integrated with impact (LG-Econ)

“Logistic Growth model based on Economic values”

In this metric version, there are also three cases for the economic data file. We can use:

- (1) a raster of economic values of the habitat in LAEA projection at the 10 km resolution. In this case, the value should be the value in euros of the crop for each cell. If this value is in another unit, you should use the multiplicative factor *mult* in the function to make conversion. For instance, if the value is euros per km², then you should simply put *mult* = 100 (to have per cell of 10 km * 10 km).
- (2) a raster of habitat density. In this case, the value, *valperhost*, should be given per km² assuming that habitat is everywhere.
- (3) random values

`res = lgecon(N0=0.0388,r=0.45,econraster=T,econformat= ".tif ",t=16,mult=1, sim=1)`

Warning: the parameter estimates should be updated

$$N_0 = 100 * n_0 / K$$

with n_0 , the number of invaded cells at $t = 0$, and K the number of suitable cells.

We assume that only one cell is invaded at the beginning (only one infested location).

The number of suitable cells is found when calling the module's information: `printinfo()`. We have 45670 suitable cells.

Thus, the initial density for the logistic function is: $N_0 = 100 * \frac{1}{45670} = 0.0022$,

i.e. one cell colonized out of the 45670 cells with $EI > 0$.

=> **N0 = 0.0022**

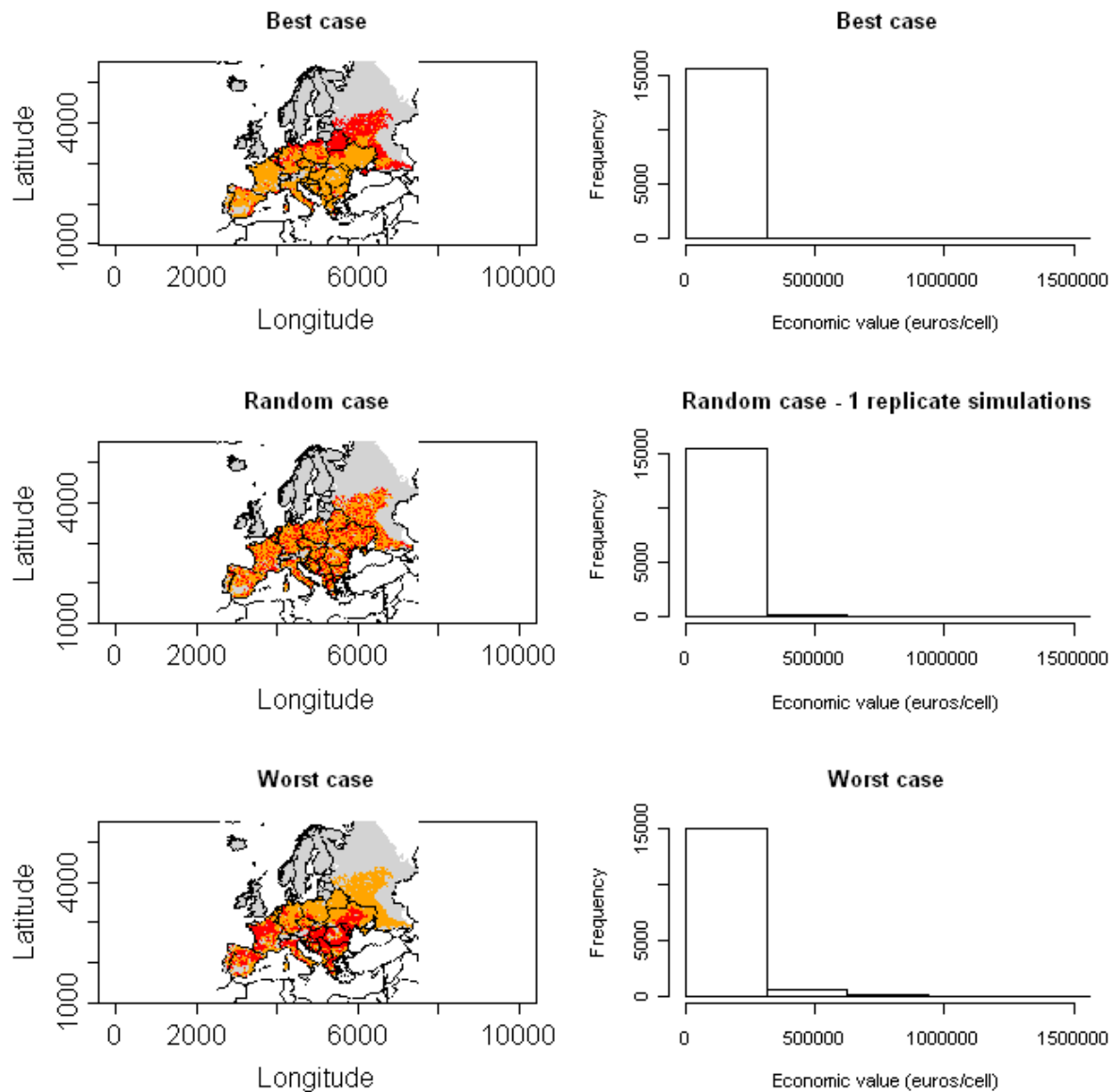
We roughly estimated that the colonized area in 2008 covered approximately 1/3rd of the risk area (=> 45670 / 3 = 15223 infested cells in 2008 over the

$$\ln\left(\frac{15223}{45670 - 15223}\right) = \ln\left(\frac{1}{45670 - 1}\right) + 16r$$

45670 grid cells (K)).

$$r = \frac{1}{16} \left(\ln\left(\frac{15223}{30447}\right) - \ln\left(\frac{1}{45669}\right) \right) = 0.62 \text{ yr}^{-1}$$

=> **r = 0.62**



Exporting the output

`res = lgecon(N0=0.0388,r=0.45,econraster = T, t=16, mult=1, export=T, name="EconOutput")`

In this case, three files are exported:

- name_best: file for the best case scenario
- name_worst: file for the worst case scenario
- name_rand: file for the random case scenario (cumulating the number *sim* of replicate simulations)

In these files, the value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the cell is not in the area of potential establishment and the value -9999 means that data is missing.

To know how many cells are covered by some points of pest presence, you can use the following function:

```
pointtocell("name_of_your_file.txt")
```

You should enter the name of the file containing the longitude (column 1) and latitude (column 2) in km (ETRS 1989 LAEA projection). This file should be located in the working directory. For each point, the function determines the cell where it is located within the area of potential establishment. If the point is located outside the area of potential establishment, then the corresponding cell is the closest one within this area.

3.4.2 Spatial process models

3.4.2.1 Model 3: Radial range expansion model (RR)

A function to transform the decimal degrees in LAEA projection system, in km

The following function has been added to find the coordinates of a point in LAEA (km):

```
proj(20.3,44.82)
```

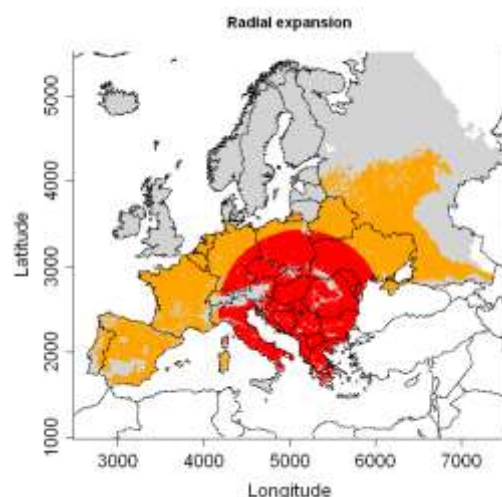
The first value is the longitude and the second one is the latitude in decimal degrees. This function converts the coordinates of the introduction point to the required projection coordinates.

If you need the inverse function, use:

```
projinv(5020,2090)
```

the first value should be the longitude in km and the second value the latitude in km (LAEA projection). The function returns the coordinates of this point in decimal degrees.

```
res = radial(RR=60,t=16,coord=c(5134.207, 2468.253))
```



Exporting the output

```
res = radial(RR=60,t=16,coord=c(5134.207, 2468.253), export=T,  
name="RadialOutput")
```

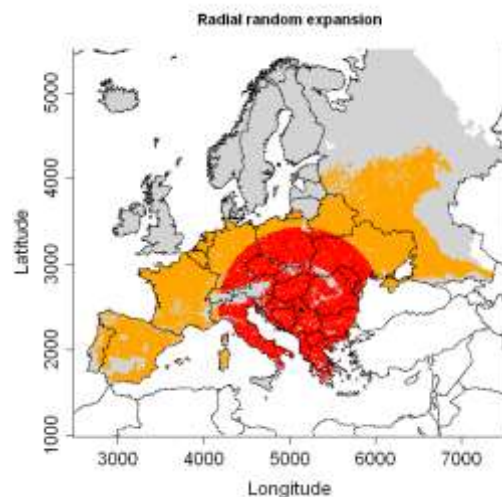
In this case, the value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the cell is not in the area of potential establishment and the value -9999 means that data is missing.

3.4.2.2 Model 4: Hybrid of logistic growth and radial rate expansion (Rand-RR)

“Random radial range expansion”

Exporting the output

```
res=radialrand(N0=0.0388,r=0.45,t=16,RR=60,coord= c(5134.207,  
2468.253),export=T,name=“HybridOutput”)
```



In these files, the value 1 means that the cell is invaded, the value 0 means that the cell is within the area of potential establishment but not invaded, the value -1 means that the cell is not in the area of potential establishment and the value -9999 means that data is missing.

Warning: the parameter estimates should be updated

=> **N0 = 0.0022**

=> **r = 0.62**

3.4.2.3 Model 5: Dispersal kernel models (DK)

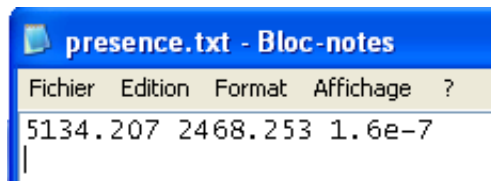
Note that the dispersal kernel can theoretically be used in the metric version of the spread module, but there is a technical problem that is impossible to solve until now: the calculation time. The number of cells is 13 times higher in the metric version than in the DD version (with a 0.5° resolution) for the dispersal kernel (17,298 in the DD version vs 225,951 cells in the metric version). For *Diabrotica virgifera virgifera*, for instance, the number of cells within the area of potential establishment is 16 times higher in the metric version than in the DD version (with a 0.5° resolution) for the dispersal kernel (3,326 in the DD version vs 54,792 cells in the metric version). Since the time

increases exponentially with the number of cells within the area of potential establishment (potential source points), it is almost impossible to use this model in practice. Therefore, this model is described hereafter but it is recommended **not to apply the dispersal kernel model in the metric version.**

Exporting the output

Since this last model takes a long time for the simulations, a separate function has been coded to export the outputs.

You should first create the presence file (if you need) and call the function:



```
presence.txt - Bloc-notes
Fichier  Edition  Format  Affichage  ?
5134.207 2468.253 1.6e-7
|
```

```
res = dispk(N0=NULL, t=1,lmax=40, p=5,u=60, presencefile=T, nentry=NULL)
```

Then call another one to export:

```
exportkernel(res$dispk,name="KernelOutput")
```

Warning: the parameter estimates should be updated

=> **N0 = 5e-8**

Note that the stochastic version is not available in the metric version because of the very long time required for the simulations.

4 Case studies

The spread module was tested by risk assessors within PRATIQUE and at an EPPO Workshop in Hammamet, Tunisia on 23rd-26th November 2010 on species of particular interest to the EU. Although 10 species have been tested, only the seven most well worked cases are presented in detail in this section. The first example, the western corn rootworm, *Diabrotica virgifera virgifera*, was chosen because it is well known, has spread widely in Europe and has been used as a case study in other PRATIQUE deliverables. The second example, the citrus longhorn beetle, *Anoplophora chinensis*, was used to train the participants of the EPPO workshop on PRA in Hammamet on 23rd-26th November 2010. The third insect example is the Asian longhorn beetle, *Anoplophora glabripennis*. Some nematode species have also been tested: the root-knot nematode, *Meloidogyne enterolobii*, and the pine wood nematode, *Bursaphelenchus xylophilus*. For this latter species, the generic spread model is more precisely applied to the damage it causes (pine wilt disease) because the climatic constraints are mainly associated with disease expression. In addition, for this particularly important example, a more detailed and specific spread model has been applied to Europe in order to identify the entry points from which the nematode and the disease could spread the most rapidly across Europe (see Robinet et al. 2011). The generic spread module is also applied to one plant species, the water hyacinth, *Eichhornia crassipes*, and the pathogen responsible for pitch canker disease, *Gibberella circinata*.

There is no universal method to estimate the parameters since the method will depend on the data available. Therefore the objective of this chapter is to provide examples on how the parameters can be estimated and how the spread models can be applied.

As already mentioned (section 3.3.1), the uncertainty can be represented by three maps showing respectively the best case, the average case and the worst case scenarios. In this chapter, these uncertainty maps (3 scenarios) are explicitly given for the pine wood nematode, and for other species (e.g. the western corn rootworm, two *Anoplophora* species, the root-knot nematode, and the water hyacinth), some maps are also provided to show the effect of changing the value of some parameters.

4.1 Insects

4.1.1 Western Corn Rootworm, *Diabrotica virgifera virgifera*

The Western Corn Rootworm was chosen as the first example for the spread models in order to show how the values of the parameters can be obtained and how the spread module can be applied. As already mentioned, it is recommended to test several values for the parameters iteratively within the possible range.

Modelling was based on the guidance for the Spread Module, given in chapter 3, and the R-code Version V21.

4.1.1.1 Information on *D. virgifera virgifera*

- **Climatic suitability (obligatory) (“ClimexOutput.txt”)**

We used a CLIMEX model initially developed by Philippe Reynaud (ANSES, France) and Darren Kriticos (CSIRO, Australia). The CLIMEX parameters are given in Table 11 of PRATIQUE Deliverable 3.3 (DSS on Mapping Endangered Areas) and the results for EI and GI are shown in fig. 4.1.1-1). Our study area is Europe.

- **Habitat distribution (optional) (“habitat”)**

This map was derived from a McGill University, Canada dataset (Monfreda et al., 2008) (see description under 3.2.2.2). A combined map of grain and forage maize indicating the total maize area in Europe was applied (see DSS on Mapping Endangered Areas and fig. 4.1.1-2).

- **Economic data (optional; just for one model-“econ”)**

The economic data were derived from Monfreda et al. (2008, see description under 3.2.2.2).

Although the role of topography was discussed in the infested areas of southeast Europe by Baufeld & Enzian (2005) suggesting that *D. virgifera virgifera* is not able to fly regularly above altitudes of 900 m, Meinke et al. (2009) stated that the data on topography are not very clear. It can be assumed that the beetle is able to reach areas where maize is grown and that elevation maybe more a limitation for growing maize (Baufeld, pers. comm. 2011). **We therefore did not include an elevation limit** in this case study.

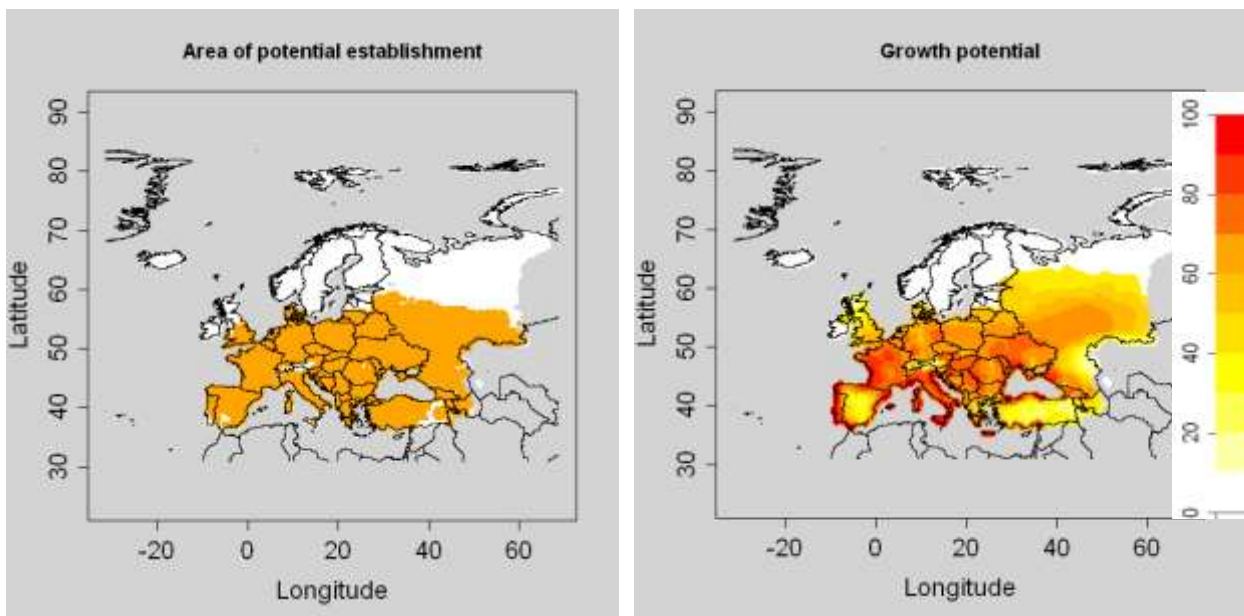


Figure 4.1.1-1: Area of potential establishment on the left (in orange: suitable cells, EI>0 and host present; in white: non suitable cells, in grey: no data) and growth potential (rescaled GI; on the right) for *D. virgifera virgifera* in Europe based on a CLIMEX model by Philippe Reynaud and Darren Kriticos; EI = Ecoclimatic Index, indicates, how favourable the climate is for the long term survival of the species; GI=Growth Index indicates the overall potential for the population growth.

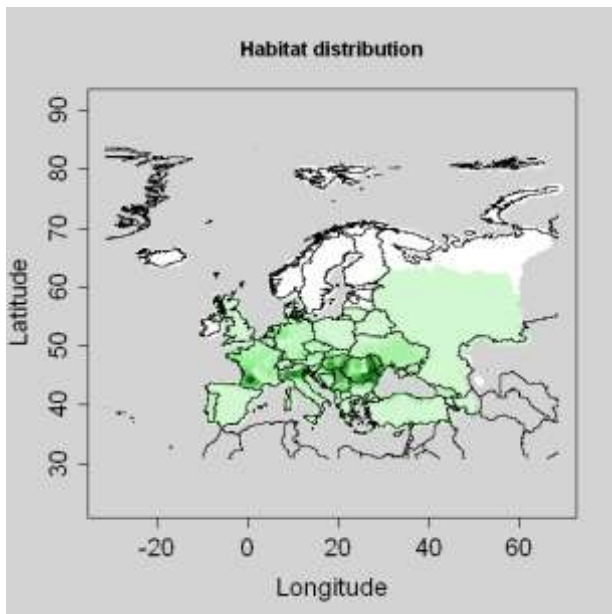


Figure 4.1.1-2: Habitat distribution in Europe based on the area grown with maize (grain maize and forage maize) in 2000 (source: Monfreda et al. (2008); graduated colors from white (no host) to dark green (max=91%). Grey means no data).

4.1.1.2 Model 1: Population dynamics model (SLG)

- **Starting population N_0**

This parameter is defined by:

$$N_0 = 100 * \frac{n_0}{K}$$

with n_0 the number of introduced individuals, e.g. 100, in each suitable cell, and K the carrying capacity (the maximum number of individuals in a cell).

In Hungary and Italy, the beetle abundance reached 1.5×10^6 and 2.5×10^6 beetles / ha of maize respectively (the abundance is related to the conditions for maize growth, which are superior in Italy due to better water availability in the soil; personal comm. Peter Baufeld, JKI, and Zsuzsanna Dancsházy, Directorate of Plant Protection and Soil Conservation, Hungary 2010). Based on these data, the maximum number of beetles was assumed to be 200 / m² of maize.

If we assume that 20% of the grid cells is grown with maize (i.e. where maize is present), then:

$$K = \text{area_cell (km}^2\text{)} * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2\text{)}$$

The mean area of the cell is given when loading the code.

In this example, this area = 1579 km².

$$\Rightarrow K = 1579 \text{ (km}^2\text{)} * 0.2 * 200 \text{ (/m}^2\text{)} * 10^6 \text{ (m}^2\text{/km}^2\text{)} = 6.3 * 10^{10} \text{ beetles/cell}$$

$$\Rightarrow N_0 = 100 * 100 / 6.3 * 10^{10} = 1.6 * 10^{-7} \%$$

- **Multiplication factor λ_{\max}**

According to Hemerik et al. (2004), the maximum yearly multiplication factor for *D. virgifera virgifera* in the countries of the former Yugoslavia is around 40 (see the column for R_0 , which is the finite growth, in the table below) for northern regions the values are much lower (e.g. 8 for the Netherlands). Kruegener et al. (2011) calculated a multiplication factor of 7.5 for German conditions. Since λ_{\max}

represents the multiplication factor under optimal conditions, we chose the value of 40 as a worst case scenario and also tested a lower value (10) to represents the conditions in other parts of Europe. This maximum yearly multiplication factor is the value of the multiplication factor where GI is the highest within the PRA area (or, equivalently where rescaled GI = 100). In other areas, the multiplication factor decreases with decreasing GI, down to 0 where GI = 0 (or, equivalently where rescaled GI = 0).

Table 3 The velocity of population expansion of *D. virgifera* as calculated in km year⁻¹ for several locations in Europe, using the model of van den Bosch et al. (1992)

Location	Longitude (E)	Latitude (N)	Mean R ₀	Velocity Eqn (3)	Velocity Eqn (4)
Belgrade	20.4	44.8	39.0	27.1	93.2
Copenhagen	12.5	55.6	12.6	22.5	60.5
De Bilt	5.2	52.1	8.1	20.5	49.0
Zagreb	15.9	45.8	42.6	27.4	95.9
Oslo	10.6	59.9	0.5	–	–

- **Time frame t**

Here we can choose any time t (in years) because we do not assume an entry point at the time $t = 0$. For instance, we have used $t = 10$ and 18 years (which represents the time interval between the first finding of *D. virgifera virgifera* in Serbia in 1992 and 2010).

Results

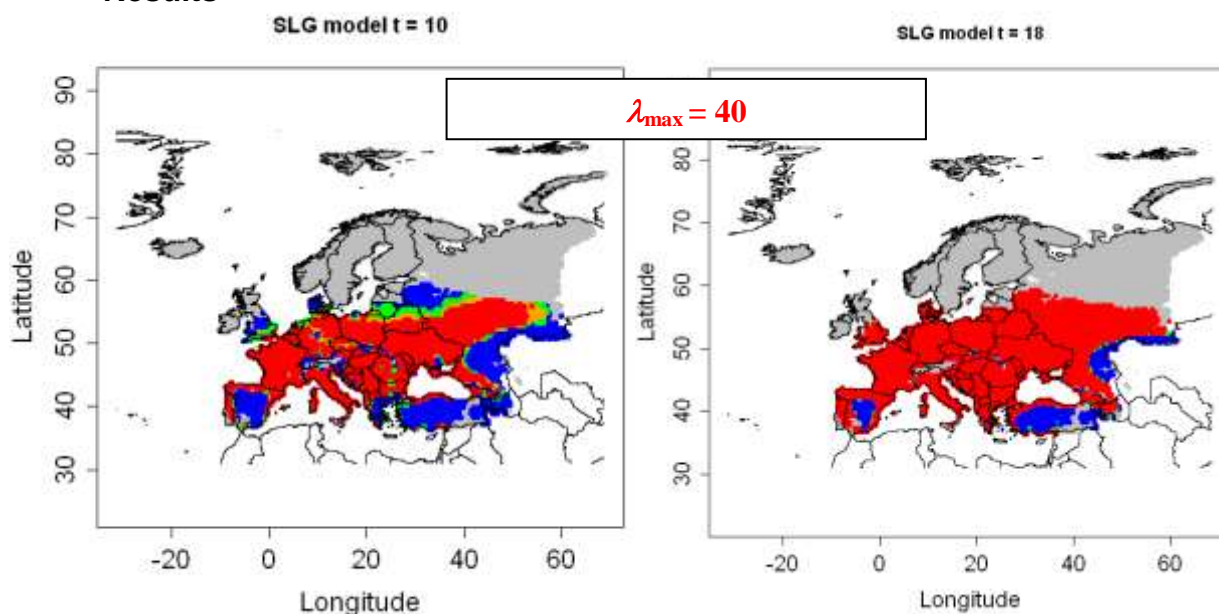


Figure 4.1.1- 3a: Output of the SLG model for *Diabrotica virgifera virgifera* for $t=10$ and 18 years and $\lambda_{max} = 40$, based on a CLIMEX model from Philippe Reynaud and Darren Kriticos (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data, and N_t is the population density expressed as the percentage of the carrying capacity K).

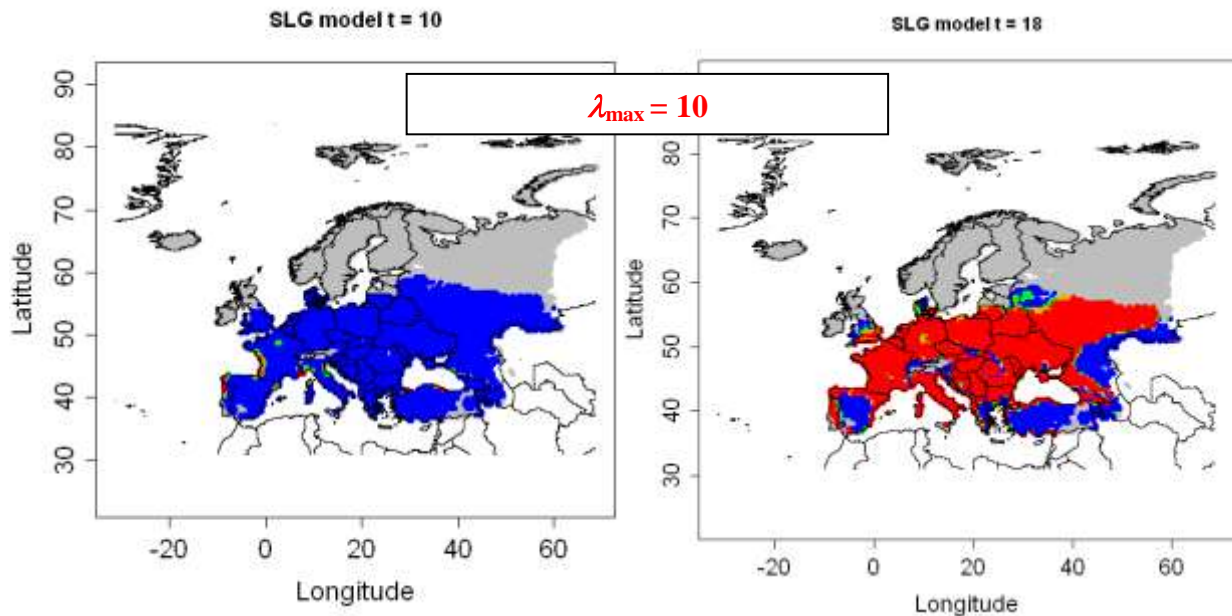


Figure 4.1.1- 3b: Output of the SLG model for *Diabrotica virgifera virgifera* for t=10 and 18 years and $\lambda_{\max} = 10$, based on a CLIMEX model from Philippe Reynaud and Darren Kriticos (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data, and N_t is the population density expressed as the percentage of the carrying capacity K)

4.1.1.3 Model 2: Temporal spread over cells integrated with impact (LG-Econ)

- N_0

This parameter is defined by: $N_0 = 100 * n_0 / K$

n_0 is the number of invaded cells at $t = 0$, and K , the number of suitable cells. We assume that only one cell is invaded at the beginning (only one infested location).

The number of suitable cells is obtained by the following command: `printinfo()`. We have 3326 suitable cells.

Thus, the initial density for the logistic function is: $N_0 = 100 * \frac{1}{3326} = 0.0301$, i.e. one cell colonized out of the 3326 cells with $E_i > 0$ and host present.

- **Relative rate of spatial increase r**

To determine the relative rate of increase in the number of invaded grid cells per unit of time we based our estimate on comparing the area of potential establishment (Fig. 4.1.1-1; to obtain this map, you can type `plotRA()`) and the actual distribution of *D. virgifera virgifera* in 2010 (Fig. 4.1.1-4), knowing that the first detection of the beetle was in 1992.

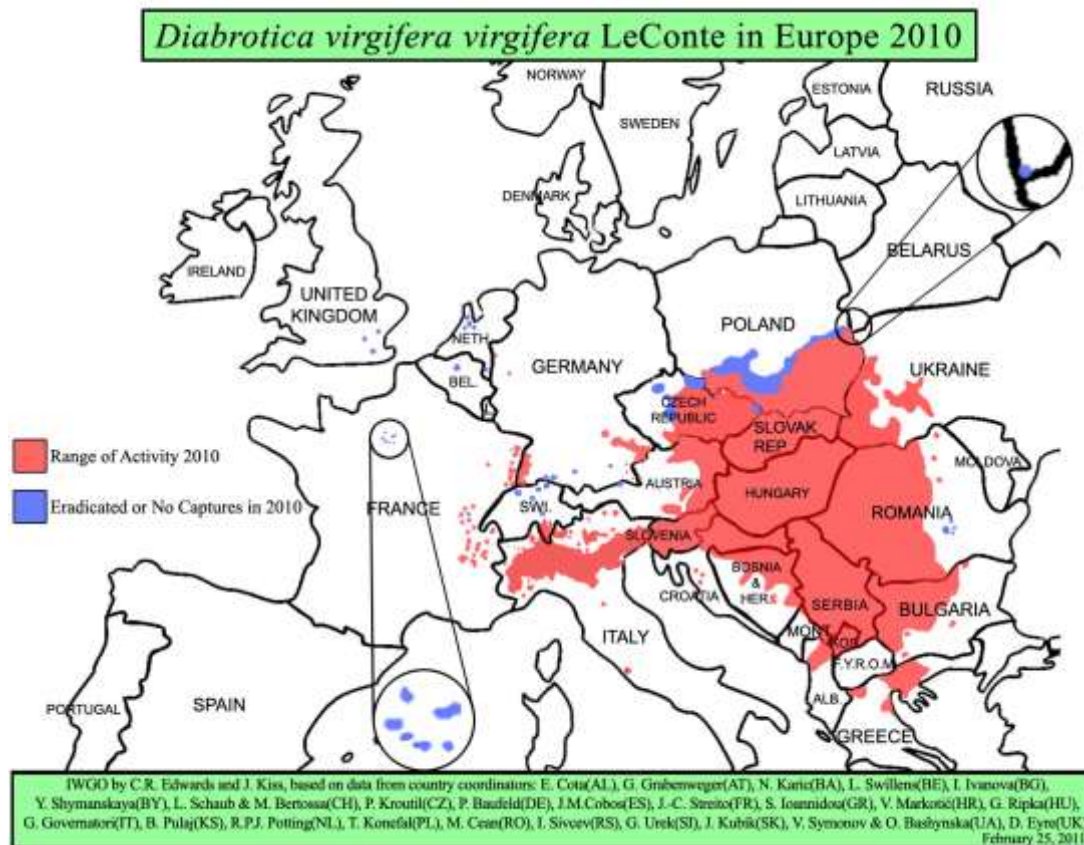


Figure 4.1.1-4: Distribution of *Diabrotica virgifera* in 2010 (Purdue University, <http://extension.entm.purdue.edu/wcr/>)

We estimated that the area colonized in 2010 covered approximately $1/3^{\text{rd}}$ of the risk area ($\Rightarrow 3326 / 3 = 1109$ infested cells in 2010 over the 3326 grid cells (K)). Then we applied the logistic growth formula on a logit scale to estimate the parameter r .

$$\ln\left(\frac{n_t}{K - n_t}\right) = \ln\left(\frac{n_0}{K - n_0}\right) + r \cdot t \quad \text{with } n_t, \text{ the number of invaded cells at time } t$$

Taking $t = 18$ years (time between 2010 and 1992), we obtain:

$$\ln\left(\frac{1109}{3326 - 1109}\right) = \ln\left(\frac{1}{3326 - 1}\right) + 18r$$

$$r = \frac{1}{18} \left(\ln\left(\frac{1109}{2217}\right) - \ln\left(\frac{1}{3325}\right) \right) = 0.41 \text{ yr}^{-1}$$

- **Time frame t**

We consider $t = 18$ years (between 1992-first detection- and 2010-latest map available in Europe, see fig. 4.1.1-4).

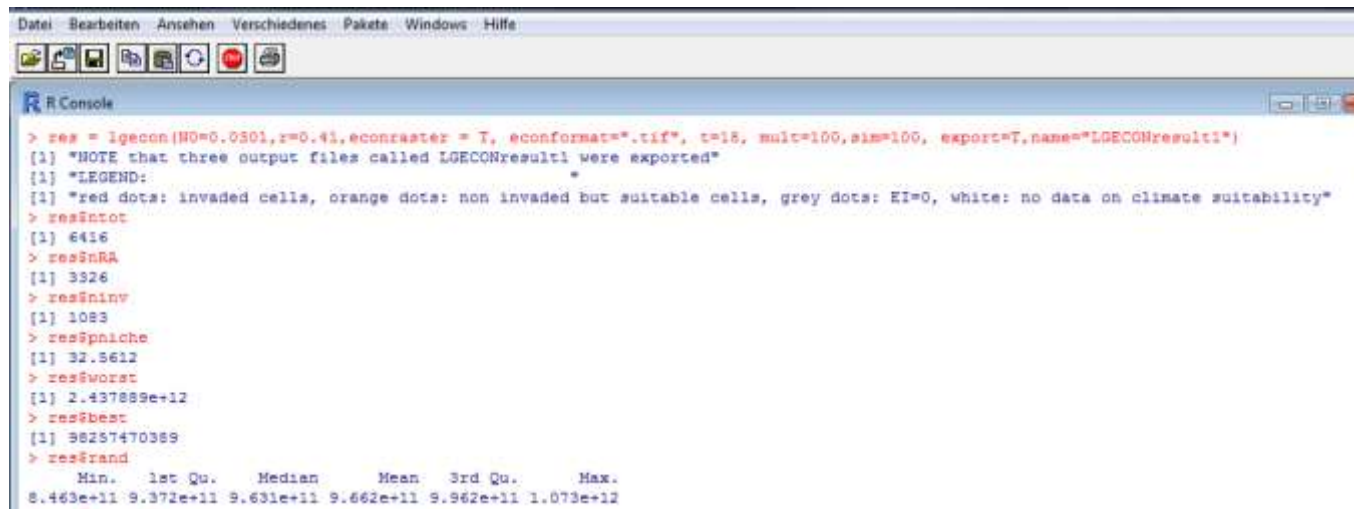
- **Economic data on host plants econraster**

We put econraster = T (true) and econformat=".tif", because we have economic values (€/ha) in a raster file called "econ.tif". These data were derived from the McGill University, (Canada) website:

<http://www.geog.mcgill.ca/landuse/pub/Data/175crops2000/ArcASCII-Zip/>. See also section 3.2.2.2.

- **mult**
We put 100 to convert €/ha into €/km².
- **sim**
We put for instance sim = 100 replicate simulations for the random case scenario.

Results



```
Datel Bearbeiten Ansehen Verschiedenes Pakete Windows Hilfe
R Console
> res = lgecon(N0=0.0501,r=0.41,econraster = T, econformat=".tif", t=18, mult=100,sim=100, export=T,name="LGECONresult1")
[1] "NOTE that three output files called LGECONresult1 were exported"
[1] "LEGEND:
[1] "red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data on climate suitability"
> resIntoc
[1] 6416
> resInRA
[1] 3326
> resInInv
[1] 1083
> resSpniche
[1] 32.8612
> res$worst
[1] 2.437889e+12
> res$best
[1] 38257470389
> res$rand
      Min.   1st Qu.   Median     Mean   3rd Qu.    Max.
8.463e+11 9.372e+11 9.631e+11 9.662e+11 9.962e+11 1.073e+12
```

Figure 4.1.1 - 5 (a): Output of the LG-Econ model for *Diabrotica virgifera virgifera*

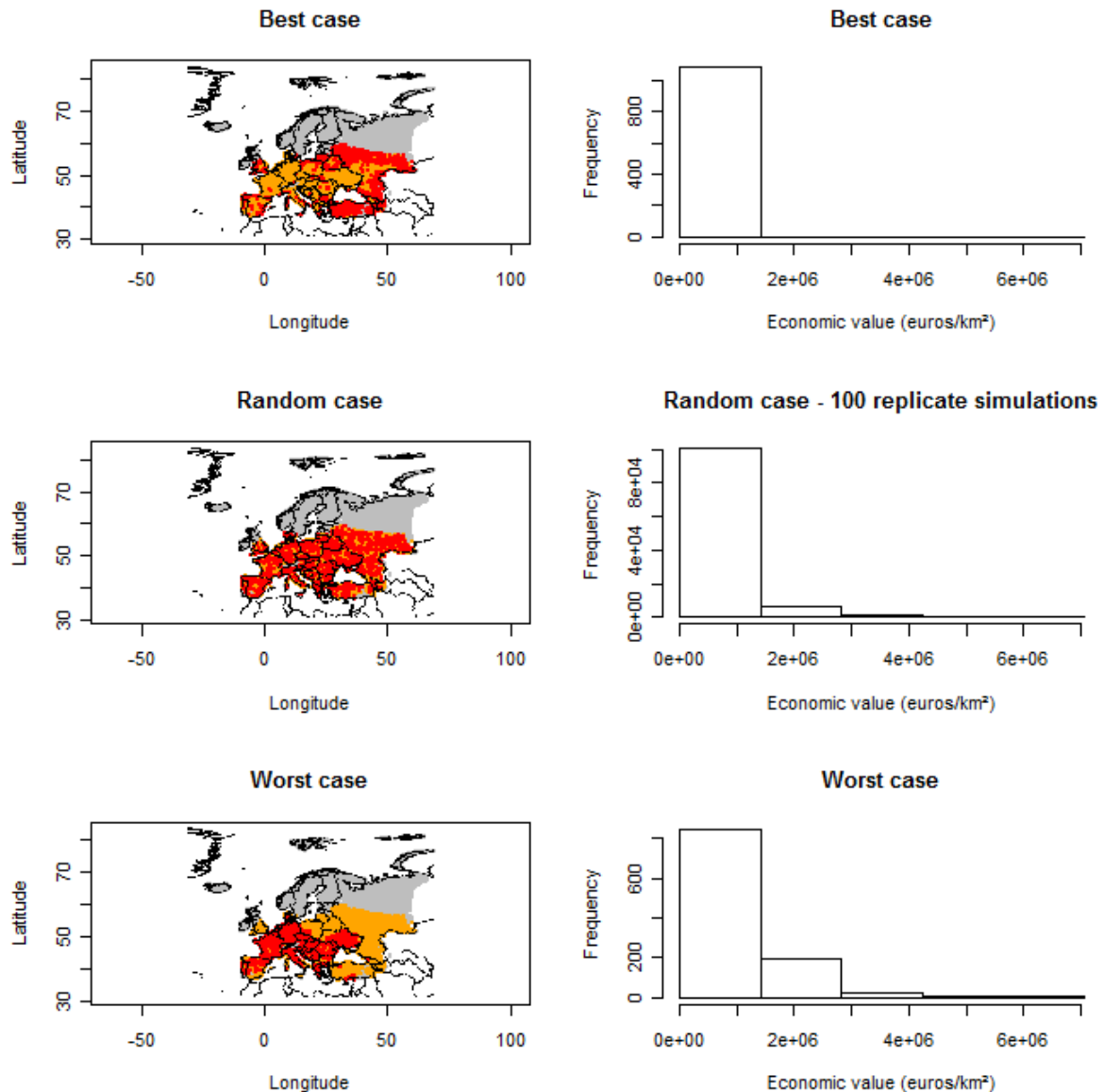


Figure 4.1.1-5 (b): Output of the LG-Econ model for *Diabrotica virgifera virgifera* based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos for t=18 years (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0 or no host, white: no data on climate suitability).

4.1.1.4. Model 3: Radial range expansion model (RR)

- **Radial rate of range expansion per year *RR***

According to Baufeld & Enzian (2005): “The spreading of the WCR ranged from 60 to 100 km per year without any measures (natural spread) [...] The maximum spreading rate is reached by WCR in the succeeding year only if continuous maize is available in the infested area.”

Wessler & Fall (2010) summarized the spread rates observed in Europe:
 “Baufeld (2003) analysed the rate of spread of the WCR in Europe and assumes the rate of spread to range from 60 to 100 km/year if there are no containment measures. MacLeod et al. (2004) assume the same range for the maximum and

the minimum rates and a typical rate at 80 km/year for the purpose of their analysis. Experts at the Wageningen workshop on the WCR (2007) agreed on a consensus for modelling WCR spreading at a rate of 20 km/year in areas where the proportion of maize is less than 50% and 60 km/year in areas where the proportion of maize is higher than 50%.”

Therefore, we considered a spread rate of 60 to 100 km /year.

- **Time frame t**

We consider $t = 18$ years (between 1992, first detection, and 2010, the latest map available in Europe at the time).

- **Entry point coord**

D. virgifera virgifera was first observed near the city of Belgrade (Serbia) (EPPO 2004). So we considered the entry point to be at approximately N 44.82°; E20.30°.

Result

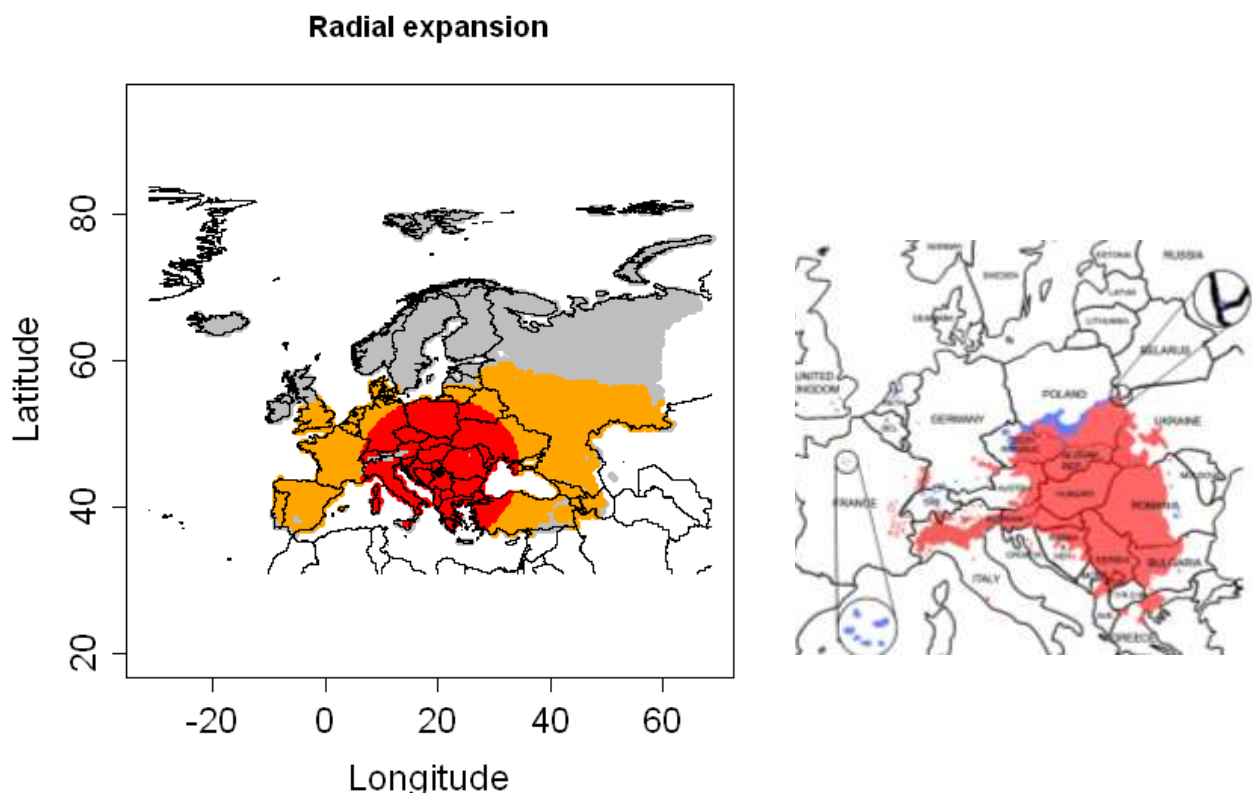


Figure 4.1.1-6: Output of the radial expansion model for *Diabrotica virgifera virgifera* for $t=18$ and an entry point near Belgrad (Serbia), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos; RR = 60 km/year (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data). Right map shows spread of *D. virgifera virgifera* in Europe in 2010 according to Purdue University¹.

¹ <http://extension.entm.purdue.edu/wcr/>

With the Radial Range Expansion model the spread of *D. virgifera virgifera* in Europe over 18 years after detection in Serbia was mapped showing that it has spread a little further compared to the spread map of 2010 for the species. The difference could be due to the application of control measures in some countries.

4.1.1.5. Model 4: Hybrid of logistic growth and radial rate expansion (Rand-RR)

The required parameters were previously estimated (see above):

- **RR, coord:** same as radial expansion model
- **N_0, r, t :** same as LG-Econ model

Result

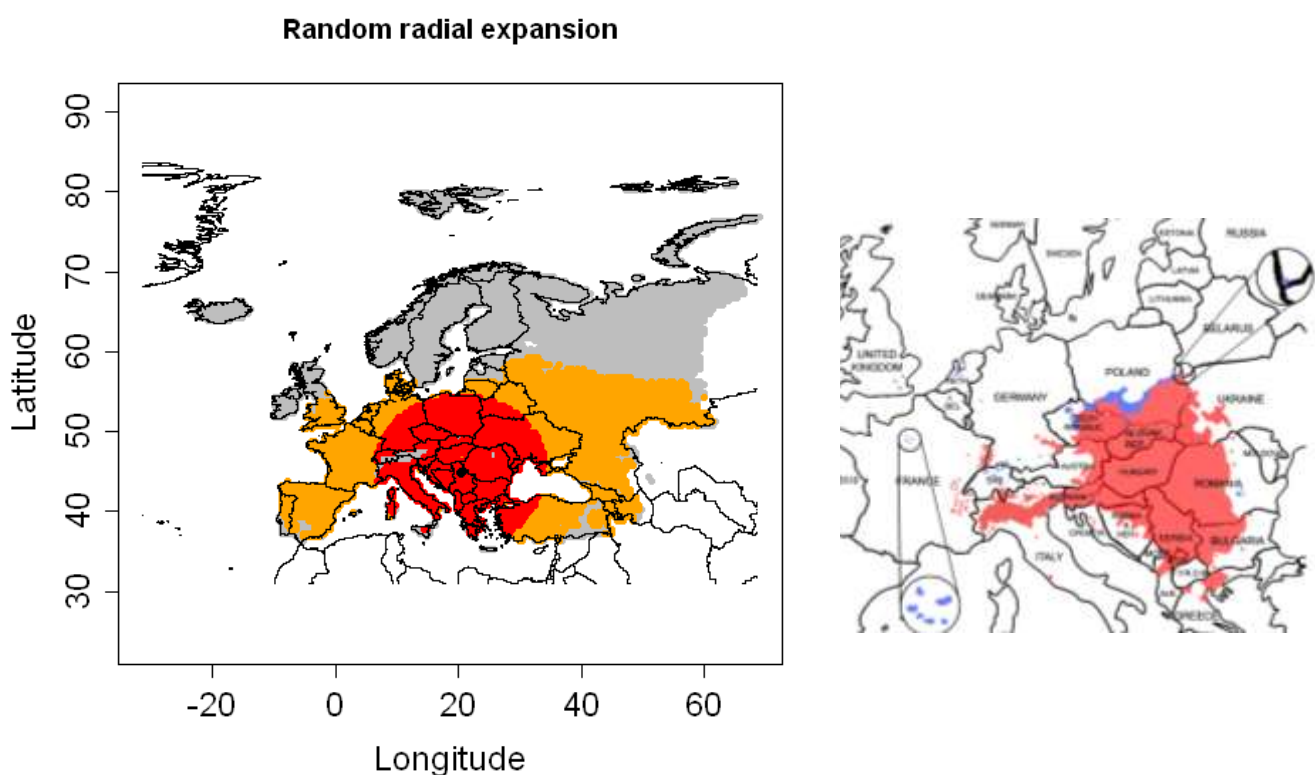


Figure 4.1.1-7: Output of the Rand-RR model for *Diabrotica virgifera virgifera* for $t=18$ and an entry point near Belgrade (Serbia), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos; $RR = 60$ km/year (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$ or no host, white: no data). The map on the right shows the spread of *D. virgifera virgifera* in Europe in 2010 according to Purdue University.

With the Random Radial Range Expansion model the spread of *D. virgifera virgifera* over 18 years after detection in Serbia was shown to have spread a little further compared to the spread map of 2010 for the species. The difference could be due to the application of control measures in some countries.

Compared to the Radial Range Expansion results in fig. 4.1.1-7 there is hardly any difference because, in this example, the number of invaded cells is high enough to cover all the area of potential invasion defined in model 3.

4.1.1.6. Model 5: Deterministic version of the dispersal kernel model (DK)

- **Starting population N_0**

Since we have the entry point near the city of Belgrade (Serbia) (radial expansion model: N44.82°, E20.30°) and the initial population abundance (simple logistic growth model: $N_0 = 1.6 \cdot 10^{-7}$), we entered $N_0 = \text{NULL}$ and instead provide a presence file:



Figure 4.1.1-8: presence file for *D. virgifera virgifera*

- **presencefile**

Since we created a presence file, we put presencefile = T

- **Multiplication factor λ_{\max}**

This parameter was already estimated for the simple logistic growth model: $\lambda_{\max} = 10$ and 40 (see above)

- **Shape parameter of the dispersal kernel p**

Since we suspect a large number of individuals to disperse far away, we use a small p (and thus a thick tail kernel). We consider $p = 5$.

- **Scale parameter of the dispersal kernel u**

We took a scale between 60 and 100 km.

- **Time frame t**

We consider $t = 18$ years (between 1992, first detection and 2010, the latest spread map available for Europe).

- **Entry point(s) n_{entry}**

Because we have a presence file, we do not give a value for this parameter, so $n_{\text{entry}} = \text{NULL}$.

Results for $\lambda_{\max} = 10$

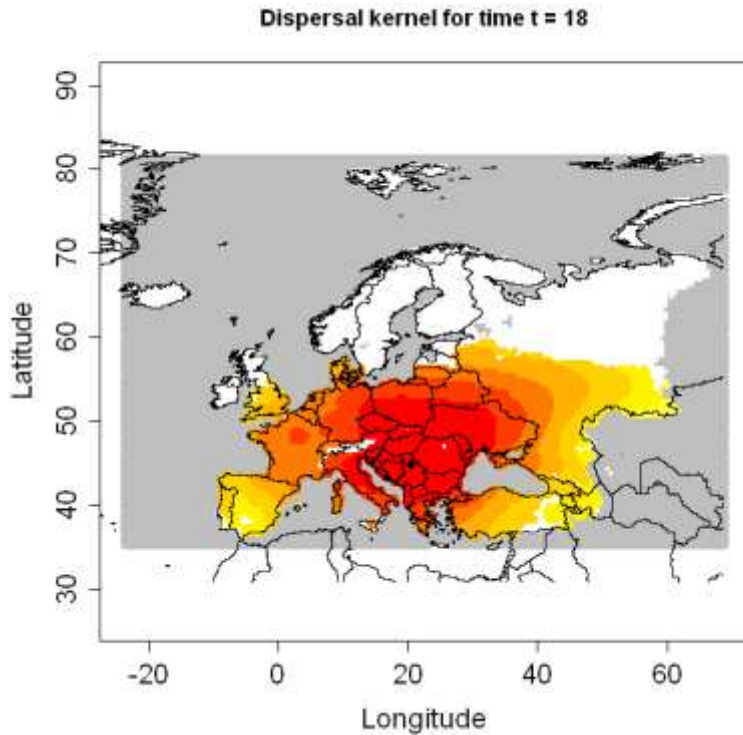


Figure 4.1.1-9a: Output of the dispersal kernel model for *Diabrotica virgifera virgifera* ($u = 60$ km, $t=18$ years, $\lambda_{\max} = 10$), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos (N_t : population abundance (%); graduated colors from white ($N_t < 10^{(-6)}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data.

A map was created where the population abundance is above a given threshold (here 25% and 15% of the carrying capacity), shown in figure 4.1.1-9b.

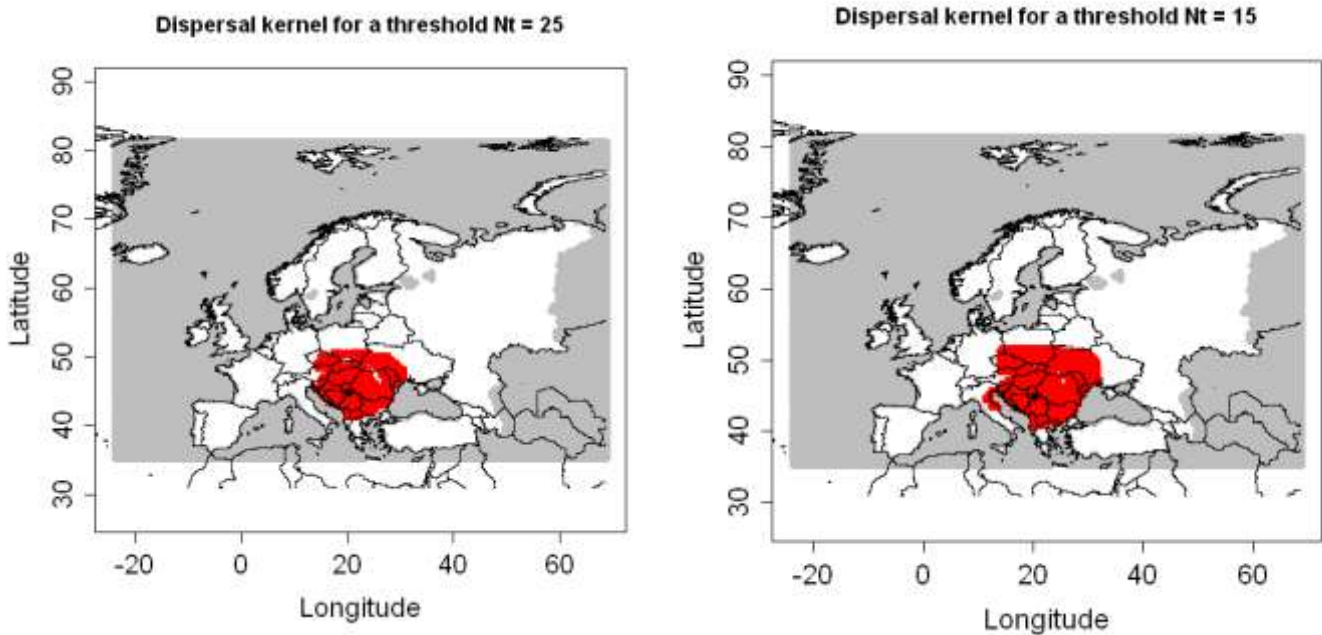


Figure 4.1.1-9b: Output of the dispersal kernel model for *Diabrotica virgifera virgifera* ($u = 60$ km, $t=18$ years, $\lambda_{\max} = 10$) with a given threshold ≥ 25 and 15% (red dots: cells where $N_t > =$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

For capturing the uncertainty of the scale parameter “u” we also applied a higher value of 100 km. The result is shown in figure 4.1.1-10.

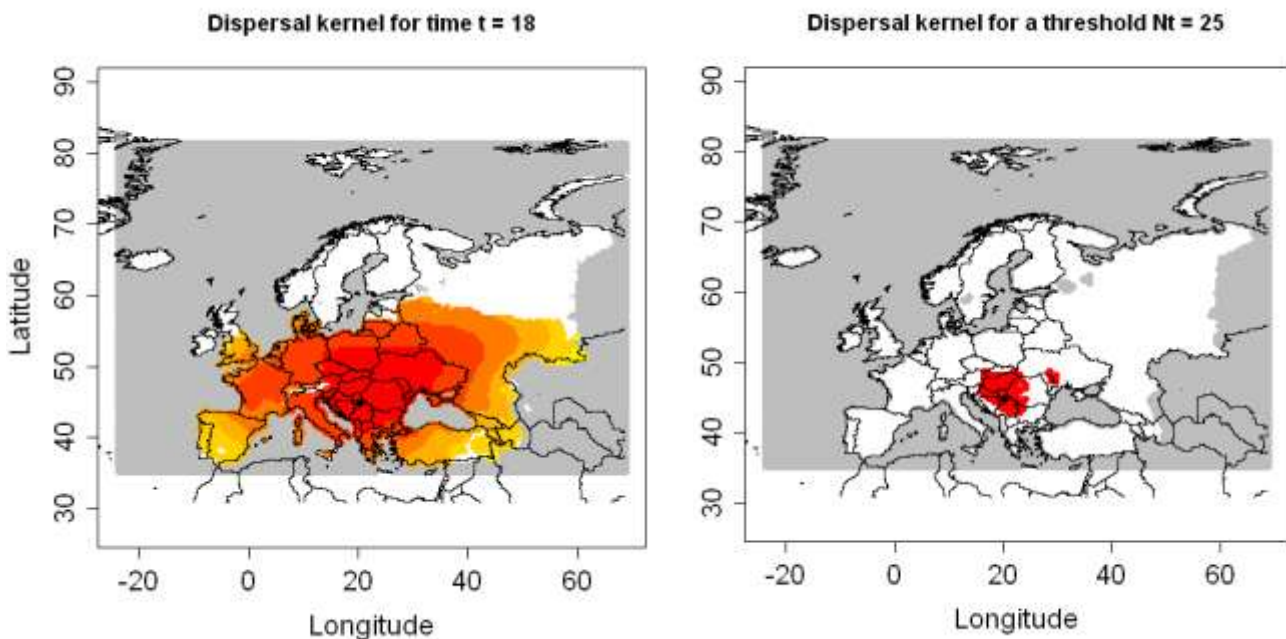


Figure 4.1.1-10: Left map: Output of the dispersal kernel model for *Diabrotica virgifera virgifera* ($u = 100$ km, $t=18$ years, $\lambda_{\max} =10$), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data. Right map: Output of the dispersal kernel model with a given threshold $\geq 25\%$.(red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

For $u=100$ km (figure 4.1.1-10) the beetle spread further but this results in a smaller area with population abundance compared to $u=60$ km.

Results for $\lambda_{\max} = 40$

The application of the higher value for the yearly multiplication λ_{\max} is shown in figures 4.1.1-11 and 4.1.1-12.

The results for the higher multiplication factor (worst case scenario, $\lambda_{\max} =40$) suggest an almost complete coverage of the area of potential establishment 18 years after the start of spread with high abundances of the beetle ($\geq 25\%$ of the carrying capacity, which was assumed to be about 2 million beetles per hectare) for both the lower and higher scale parameter “u”. This is not in accordance with the observations made in Europe and leads to the conclusion that the multiplication factor of $\lambda_{\max} =40$ (derived from Serbian conditions) is too high.

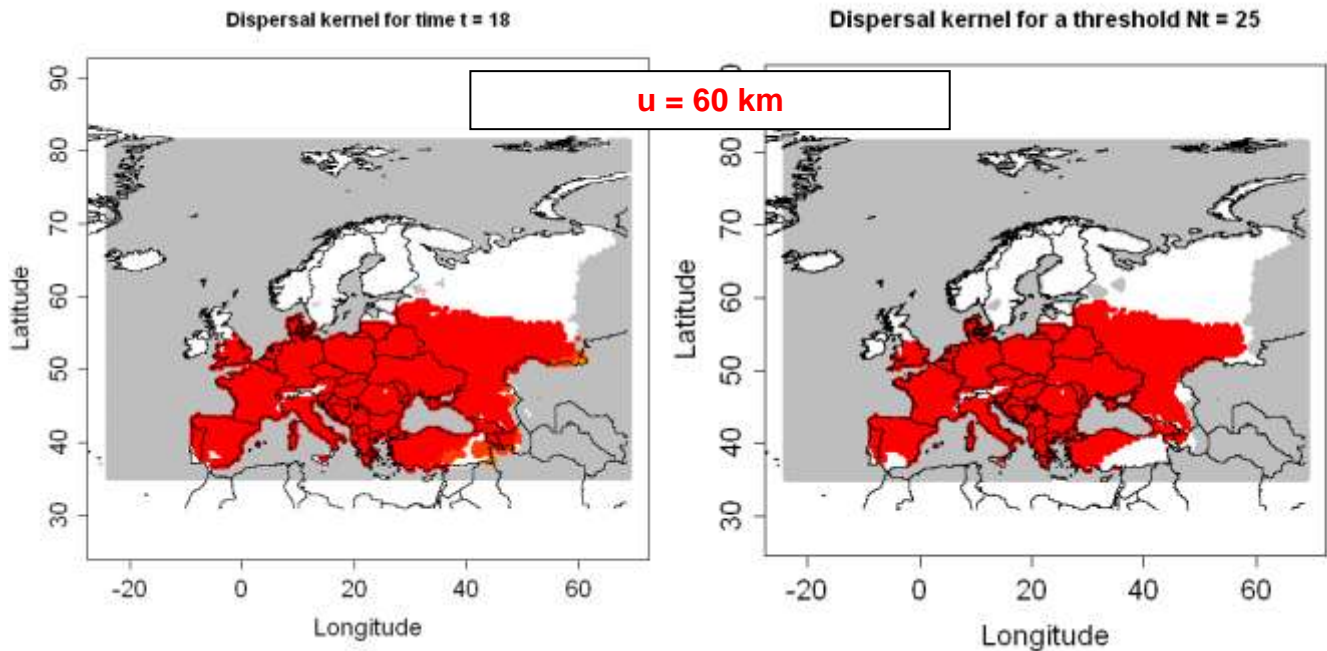


Figure 4.1.1-11: Left map: Output of the dispersal kernel model for *Diabrotica virgifera virgifera* ($u = 60$ km, $t=18$ years, $\lambda_{max}=40$), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).
Right map: Output of the dispersal kernel model with a given threshold $\geq 25\%$. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

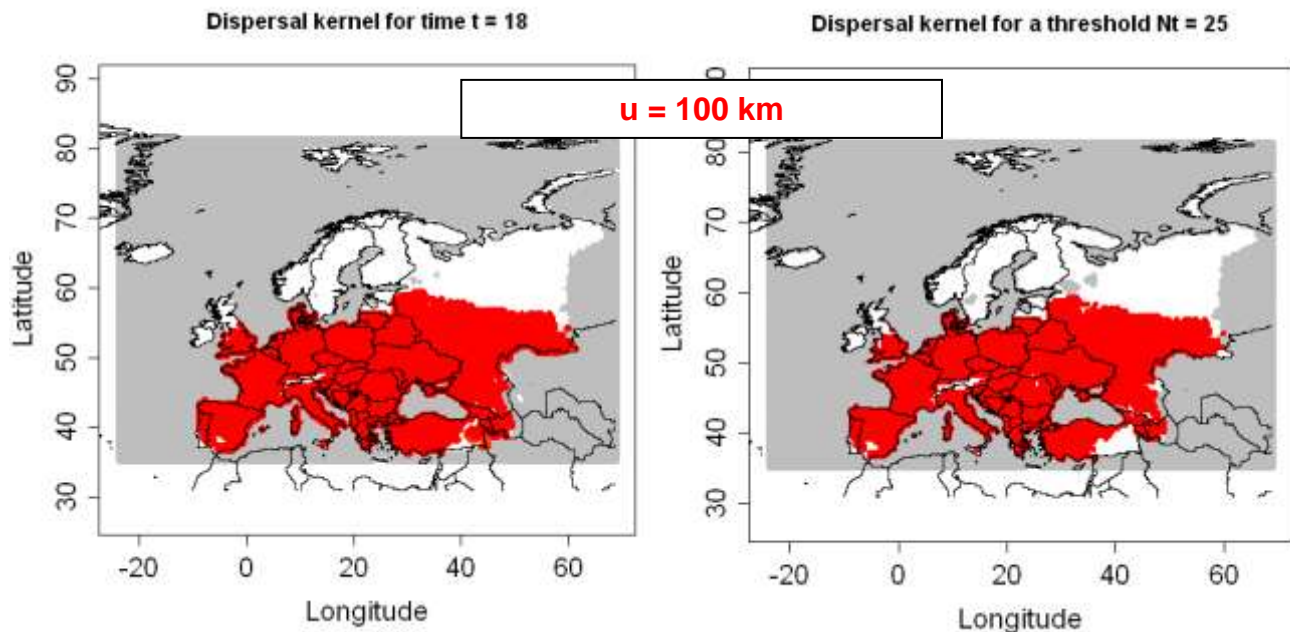


Figure 4.1.1-12: Left map: Output of the dispersal kernel model for *Diabrotica virgifera virgifera* ($u = 100$ km, $t=18$ years, $\lambda_{max}=40$), based on a CLIMEX model provided by Philippe Reynaud and Darren Kriticos (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).
Right map: Output of the dispersal kernel model with a given threshold $\geq 25\%$. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

4.1.1.7 Summary

The application of the spread models to simulate the spread of *D. virgifera* in Europe showed that it is possible to map the spread quite well in accordance with the observed spread rates in Europe over the past 18 years. In this example, the time t is the number of years between the detection of the species and the latest available map allowing us to compare both maps and evaluate how well the model compares with what actually happened. However risk assessors may be more interested in future simulations and choose a higher value for t .

Model 1 (population dynamics model) shows the area where high population abundance is expected, i.e. those cells with optimal climatic and habitat conditions. With the multiplication factor $\lambda_{\max} = 40$, after 10 years most parts of Europe are already predicted to be infested with a high population abundance but with, the $\lambda_{\max} = 10$, this will happen much later (after 18 years).

Model 2 (Temporal spread over cells integrated with impacts) shows the areas with lowest and highest economic value that *D. virgifera virgifera* could potentially invade. It also provides a range of possible economic impacts.

With Model 3 (Radial Range Expansion Model) and Model 4 (Random Radial Range Expansion Model) the spread of *D. virgifera virgifera* compared quite well to the actual spread maps for the beetle in 2010.

Model 5 (Dispersal Kernel Model) provided realistic spread mapping results for the lower value of λ_{\max} ($=10$). While λ_{\max} had a strong influence on the result, varying the scale parameter “ u ” had little effect.

Although *D. virgifera virgifera* has been in Europe for several years and much effort has been directed to analyse the biology and the dispersal behaviour of the beetle, keydata are still lacking leading to difficulties and uncertainty in some parameter estimations.

Summary of the commands for modelling the spread of *Diabrotica virgifera virgifera*

```
library(sp)
library(raster)
library(rgdal)
climexcsv = F
elevmax = F
habitatfile = T
habitatformat=".tif"
# load the R code
plotRA()
plotGI()
plothabitat()

res = slg(N0=1.6*10^(-7),lmax=40,movie=F, t=10)

res = lgecon(N0=0.0301,r=0.41,econraster = T, econformat=".tif", t=18,
            mult=100,sim=100,name="LGECONresult1")

res = radial(RR=60,t=18,coord=c(20.3,44.82),figkm=T, figdd=F)

res = radialrand(N0=0.0301,r=0.41,RR=60,t=18,coord=c(20.3,44.82),
                export=T,name="RRrand1")

res = dispk(N0=NULL, t=18,lmax=10, p=5,u=100, presencefile=T, nentry=NULL,
            figkm=F,figdd=T)
plotkernel (res$dispk,threshold=25,figkm=F,figdd=T)
```

4.1.2 *Anoplophora chinensis* (Citrus longhorn beetle)

This document, prepared by Hella Kehlenbeck, provides a case study for modelling the potential spread of the Citrus longhorn beetle *Anoplophora chinensis* in Europe. The objective of the case study is to test the models and to provide an example and guidance for the estimation of the required parameter values for this invasive insect that damages trees. Modelling has been performed with the R-code Version V17. Three of the five models were applied: the Population Dynamics Model (Model 1), the Radial Range Expansion Model (Model 3) and the Dispersal Kernel Model (Model 5). Due to the lack of economic data on the host plants of *A. chinensis*, the Logistic Growth model based on Economic Values (model 2) was not used here. Information and data on *A. chinensis* are mainly based on a Pest Risk Assessment conducted in 2008 (Van der Gaag et al, 2008), on information provided on the EPPO website on *A. chinensis* (see references) and Van der Gaag et al. (2010).

The case study was supported and reviewed by Dominic Eyre (Fera, UK) and Marc Kenis (CABI, CH) as experts on *A. chinensis*.

4.1.2.1 Information on *A. chinensis*

A. chinensis is a longhorn beetle whose larvae bore inside living hosts. It is a major wood boring pest of fruit trees, including *Citrus*, in China, Japan and Korea.

Host range and host distribution

A. chinensis is polyphagous on many deciduous trees: amenity trees and many natural forests in northern and southern Member States are at risk. *A. chinensis* can attack plant species of more than 20 plant families. In Italy, plant species belonging to 22 genera are attacked. Host plants include *Acer*, *Betula*, *Corylus*, *Fagus*, *Prunus*, *Citrus*, *Malus*, *Platanus*, *Populus*, *Pyrus*, *Rosa*, *Ulmus* and *Salix* and suitable habitats are widespread in the EU. For this case study, therefore, we used the percentage of land covered by broadleaf forest (from Päivinen et al., 2001) see figure 4.1.2-1).

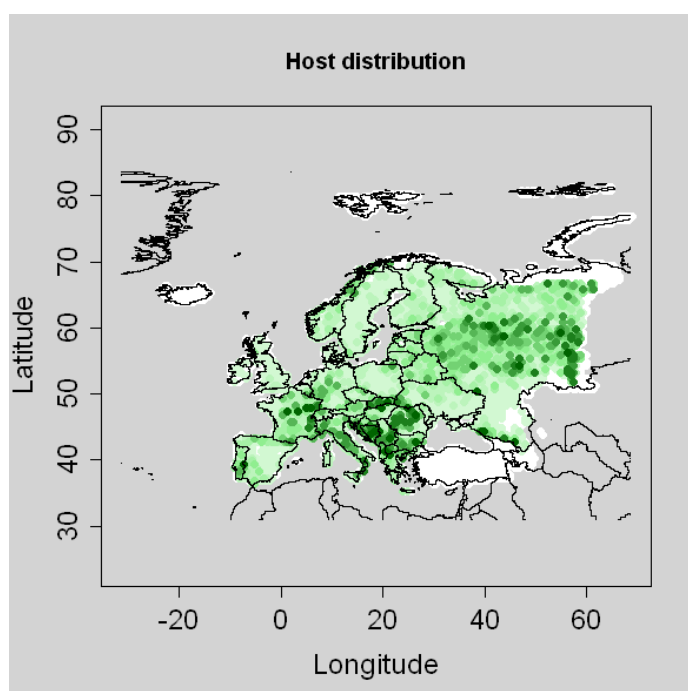


Figure 4.1.2-1: Host plant distribution for *Anoplophora chinensis* in Europe based on the percentage of area covered with broadleaf forest distribution according to Päivinen et al., 2001 (graduated colors from white (no host) to dark green (max=91%). Grey means no data).

Findings in Europe

A population of *A. chinensis* is present in four areas of Lombardy in northern Italy (detected in 2000, the outbreak covers one area of approximately 100 km² and three areas of 2 km² each) although it is under official control. Other detections were in France (detected in 2003 and eradicated) and in the Netherlands detected in 2007 (where eradication was declared in 2010). *A. chinensis* has been intercepted in several European countries (UK, Netherlands, Germany, France, Switzerland).

Pathways

There is a history of *A. chinensis* being transported from Asia into the EU via plants for planting, especially with bonsai. In the Netherlands, 1.6 to 2 million Acers were imported per year during the period 2005 – 2007. Dutch importers and growers estimate the total value of these plants (wholesale price) at about 3 – 6 million euro. They also estimate that 30 – 70 % of all Acers imported into the EU from China, Japan and Korea are imported via the Netherlands. The total import of Acers from these countries into the EU was assessed to be about 4 million plants with a total value of about € 6 –12 million.

Climatic suitability in Europe

A CLIMEX study conducted by the Netherlands in 2004 (De Boer, 2004) indicated that it was unlikely that *A. chinensis* could establish in North Western European countries. A UK PRA had concluded that it was unlikely that *A. chinensis* could establish in the UK based on a comparison of climate data from one of the warmest parts of the UK and areas where *A. chinensis* is known to be present and the presumption that a maximum of two years was needed to complete its life cycle (Baker & Eyre, 2006). However, the finding in the Netherlands with summer temperatures comparable to those in the warmest parts of the UK and a life cycle of three years shows that *A. chinensis* can establish in the Netherlands and probably also in the UK. Additionally, findings of breeding populations in Italy, France and the Netherlands, have shown that *A. chinensis* is able to establish in various climatic regions of the EU. Adults are not active at temperatures below about 10°C.

CLIMEX file

An updated CLIMEX model output file for *A. chinensis* was provided by Dominic Eyre on 7th October 2010. This new model includes the findings of the beetle in the more Northern parts of Europe in the Netherlands, France and the UK. Figure 4.1.2-2 shows the environmental index and figure 4.1.2-3 the risk area and the growth potential for *A. chinensis* according to this new CLIMEX model.

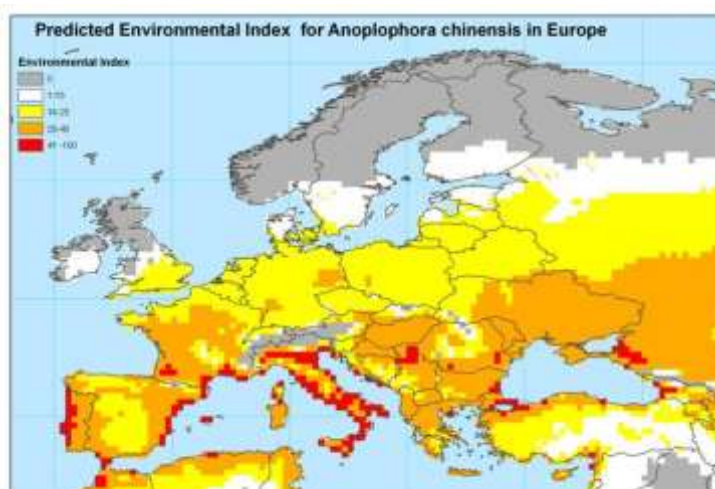


Figure 4.1.2-2: Environmental Index for *Anoplophora chinensis* in Europe based on a CLIMEX model by Dominic Eyre (7th October 2010).

Reproduction strategy

In Southern Europe, *A. chinensis* has a life cycle of 1-2 years and populations will build up much faster than in Northern European countries.

No information is available about the number of female and male beetles that is needed to start a new population. The presence of only one male and one female beetle at the same location and at the same time may be sufficient to start a new population. Findings of trees in France and the Netherlands with exit holes close to a nursery with trees from Eastern Asia suggest that only a few beetles are needed to infest new areas. However, this is very uncertain as information is lacking about the number of beetles that were actually present when eggs were deposited on these trees.

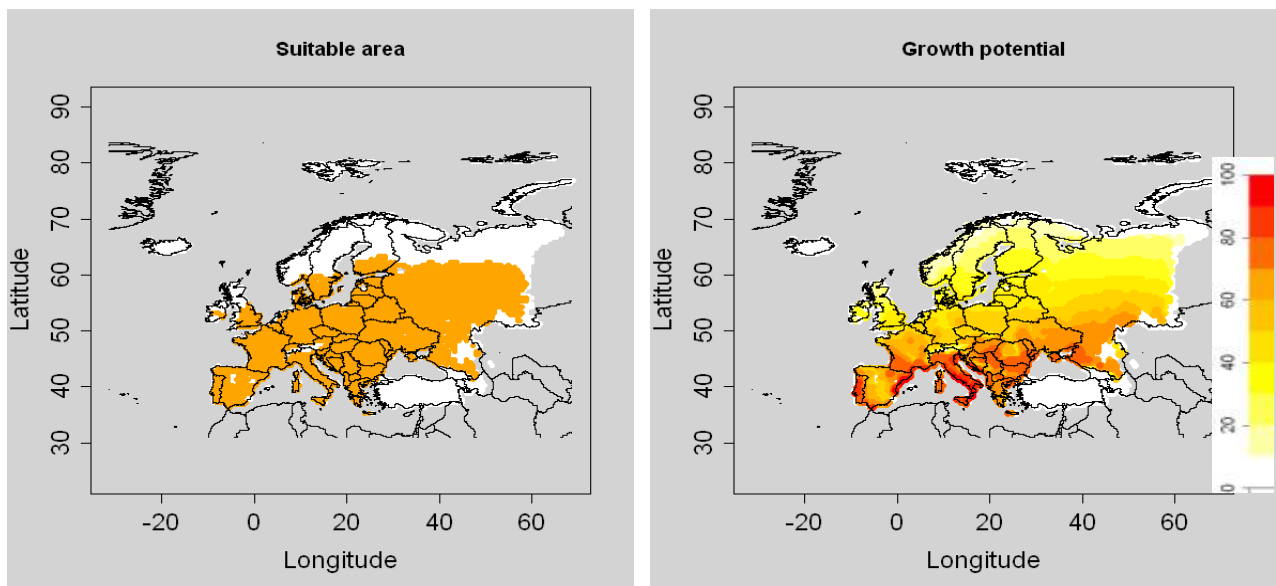


Figure 4.1.2-3: Suitable area (on the left; orange dots: $EI > 0$ and host present, white dots: $EI = 0$ or host absent, grey: no data) and growth potential (adjusted GI; on the right) for *A. chinensis* in Europe based on a CLIMEX model by Dominic Eyre (7th October 2010; EI = Ecoclimatic Index, indicates, how favourable the climate is for the long term survival of the species; GI = Growth Index indicates the overall potential for the population growth).

Natural spread:

Adult *A. chinensis* are considered to behave like the related species, *A. glabripennis*, in that they usually do not fly further than 400 m. Natural spread from the infested area in Italy (Lombardy) is therefore likely to proceed slowly. It is thought that *A. chinensis*, like *A. glabripennis*, will usually stay near the tree from which it emerged:

In France, two *Acer* trees were infested next to the nursery that had imported infested plants from eastern Asia.

In the Netherlands, *Acer* trees were infested within 30 m of the nursery that had imported infested plants. The infested trees were found during the winter of 2007/2008 while the pest had probably already been introduced in 2002.

Thus, *A. chinensis* will probably spread slowly by natural means. At high population densities *A. chinensis* may fly more than 2 km and may spread more rapidly. However, it is

likely to take several years for populations to build up to high densities at new outbreak sites in the EU.

Human assisted spread:

A. chinensis could spread by human assistance in several ways

- a) By trade in infested trees - *A. chinensis* has been introduced into new areas by movement of infested plants over large distances (from Eastern Asia to Europe and the USA). If areas become infested in which plants are grown for trade, *A. chinensis* can be moved over large distances within the PRA area.
- b) As a contaminant on transport vehicles
- c) By movement of infested wood

Topography or elevation limits

No information is available on the elevation limits for *A. chinensis*, therefore they were not considered.

4.1.2.2 Model 1: Population dynamics model (SLG)

For this model we assume that an initial population abundance N_0 (%) is introduced in each suitable cell (cells where $EI > 0$) and then we simulate the “spread” or more precisely the growth within each cell according to a logistic function. The output map shows the areas which are the most suitable for population growth assuming introduction.

- **Starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

Calculation:

$$N_0 = 100 * \frac{n_0}{K}$$
 with n_0 the number of introduced individuals, in each suitable cell, and
 K the carrying capacity (the maximum number of individuals in a cell).

$K = \text{area_cell (km}^2\text{)} * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2\text{)}$,
or

$K = \text{area_cell (km}^2\text{)} * \text{host_plant_density (/km}^2\text{)} * \text{max_population_density (/host plant)}$

Relevant information and data

Details of an outbreak in the Netherlands (from the PRA, 2008): The Netherlands observed 1 – 7 exit holes on infested Acer shrubs and trees (see table in the PRA). The Acer tree had 7 exit holes and 18 larvae of *A. chinensis* were found inside the trunk. If all these 18 larvae will complete their development, the number of beetles per tree would be 25. Therefore an estimate of a carrying capacity of 25 beetles per tree (and perhaps a lower number for shrubs) seems plausible. The number of exit holes was obtained from living trees, meaning that the beetles did not kill the trees or shrubs.

The CABI Crop Protection Compendium states that: ‘Across all regions, there was a mean of 3.8 holes per [citrus] tree although means between regions varied from 2.2 to 5.9 holes per tree’.

We assume the maximum population density (max_population_density) to be 5- 25 beetles per host plant

Host trees and shrubs per ha:

50 - 100 trees or shrubs / ha, i.e about 50% hosts of *A. chinensis* = 25 – 50 host plants/ha

Calculation of the capacity K:

$K_1 = 5 \text{ beetles/shrub} \times 25 \text{ hosts/ha} \times 100 \text{ ha (transfer ha to km}^2) \times 1579 \text{ km}^2 \text{ (grid cell)}$

$K_1 = 19.737.500 = 1.97 \times 10^7 \text{ beetles/grid cell}$

$K_2 = 25 \text{ beetles/shrub} \times 50 \text{ hosts/ha} \times 100 \text{ ha (transfer ha to km}^2) \times 1579 \text{ km}^2 \text{ (grid cell)}$

$K_2 = 197.375.000 = 1.9 \times 10^8 \text{ beetles/grid cell}$

Calculation of N_0

Starting number of beetles (= n_0) : can be very low, just 2 beetles (one female and one male) per grid cell could be sufficient

$N_0 = 100 \times \text{starting number } n_0 / K = \%$

$N_0 = 100 \times (2 \text{ beetles per grid cell} / 1,97 \times 10^7 \text{ beetles/grid cell}) -$

$100 \times (2 \text{ beetles per grid cell} / 1.9 \times 10^8 \text{ beetles per grid cell})$

$N_0 = 0,00001\% (=1.0 \times 10^{-5}) \text{ to } 1.0 \times 10^{-6}$

$N_0 = 1.0 \times 10^{-6} \% - 1.0 \times 10^{-5} \%$

- **The multiplication factor λ_{max}**

λ_{max} is the maximum year to year multiplication factor (“finite growth rate”) that a population could achieve under optimal conditions assuming unlimited space

Relevant information and data

In Lombardy, data on the eradication of infested trees showed that within 5 years the number of infested trees reached 2240. Given that two beetles (one male and one female) were the initial population, and assuming that there were 5 – 10 beetles/plant, the multiplication factor over these 5 years would have been 5600 – 11200. The multiplication factor for one year (λ_{max}) can be calculated in the following way:

$$\lambda_{max} = 5600^{1/5} - 11200^{1/5}$$

$$\lambda_{max} = 5.6 - 6.45$$

$$\lambda_{max} = 6$$

- **Time frame t**

$t = 10 - 30 \text{ years}$

Results:

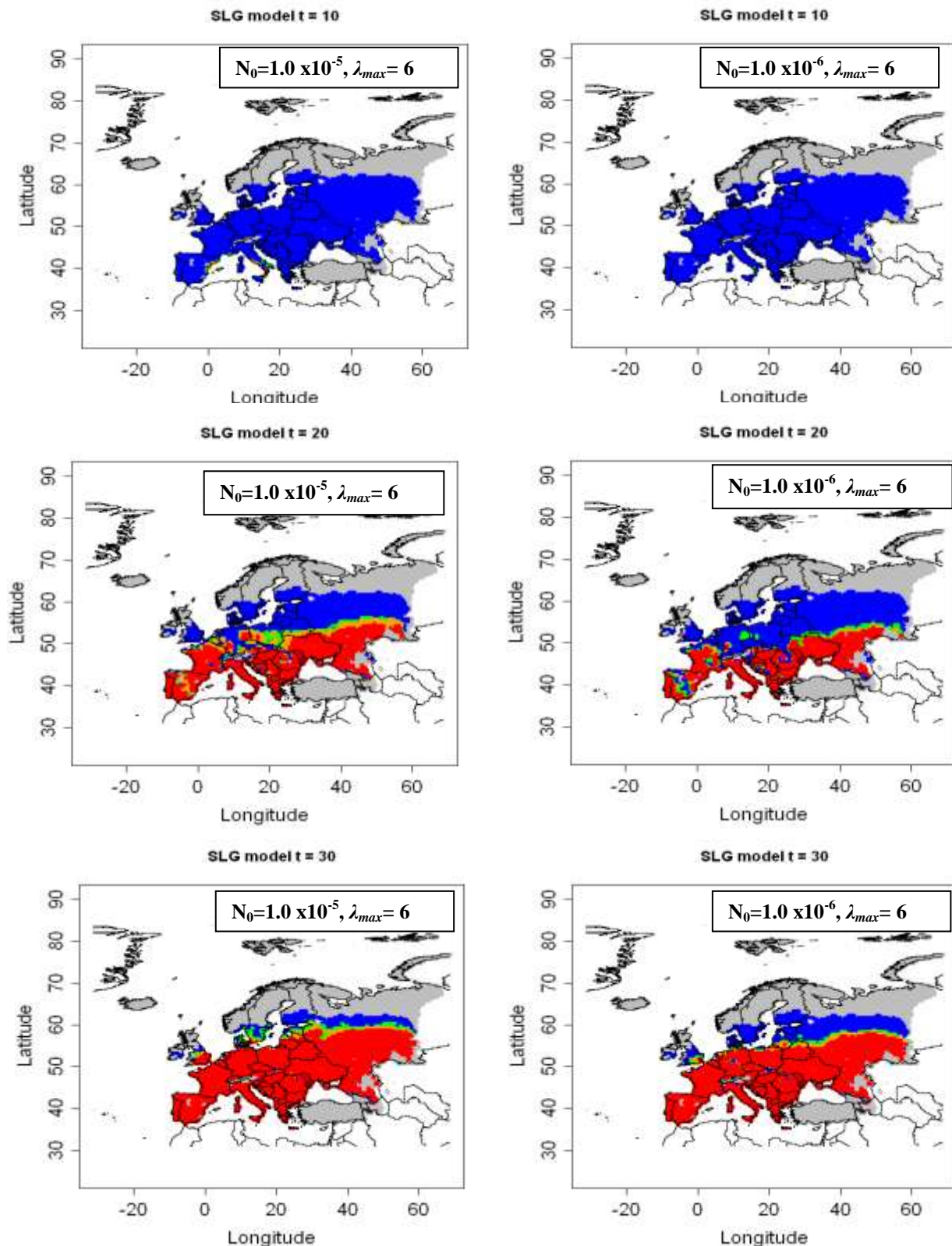


Figure 4.1.2-4: Output of the SLG model for *A. chinensis* for 10, 20 and 30 years, for two different estimates of N_0 , based on the CLIMEX model from Dominic Eyre (blue dots: $0 < Nt \leq 25$, green dots: $25 < Nt \leq 50$, orange dots: $50 < Nt \leq 75$, red dots: $75 < Nt \leq 100$, grey dots: $Nt=0$, white: no data). Left pictures: $N_0=1.0 \times 10^{-5}$; right pictures: $N_0=1.0 \times 10^{-6}$

The results of the simulation with the SLG model in figure 4.1.2-4 show the area where the species can grow rapidly and therefore become a more important problem compared to other places.

4.1.2.3 Model 3: Radial range expansion model (RR)

This model aims to determine the potential spread of a species introduced in the PRA area based on the radial rate expansion parameter. The model output is overlapped with the niche map ($EI > 0$).

- **Radial rate of range expansion per year (RR)**

Relevant information and data

The initial introduction of *A. chinensis* to Italy (Lombardy at approximately N45°00; E09°00) may have happened 10-20 years before the pest was first discovered in 2001 and it is very likely that repeated introductions occurred

The furthest boundary of an infested municipality was approximately 28km from the site where the outbreak was first discovered in the spring of 2007 (see map below). This would be in accordance with the estimate of 1km/year (10-20 years before 2001 plus 6 years until 2007 -> 28km /16years or 28 km/26 years). There has been an eradication programme in place since the discovery of the pest (since 2001) and it is not known how far the pest would have spread without this programme.

RR will be tested with 1 km/year and also with 2 km/year.

- **Time frame t**

t = 30 – 60 years

- **Entry point(s) or simulation of an introduction at a place (coord)**

Northern Italy: coord (9,45); France (0,50); Netherlands (8,53)

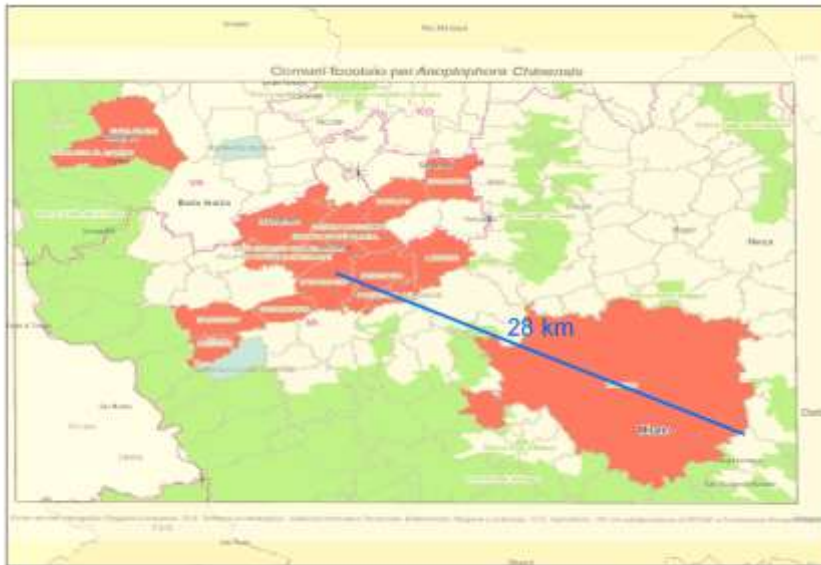


Figure 4.1.2-5: Infested area with *Anoplophora chinensis* in Lombardia Italy . Red Areas show the municipalities where the Citrus longhorn beetle is present; in blue marked areas only adult beetles were found. Infestation was first observed near Milano in 2000 and this map shows the presence of the pest in 2007 (source: http://www.eppo.org/QUARANTINE/anoplophora_chinensis/chinensis_IT_2007.htm) .

Results:

Radial range expansion after 30 years with one entry point in Northern Italy

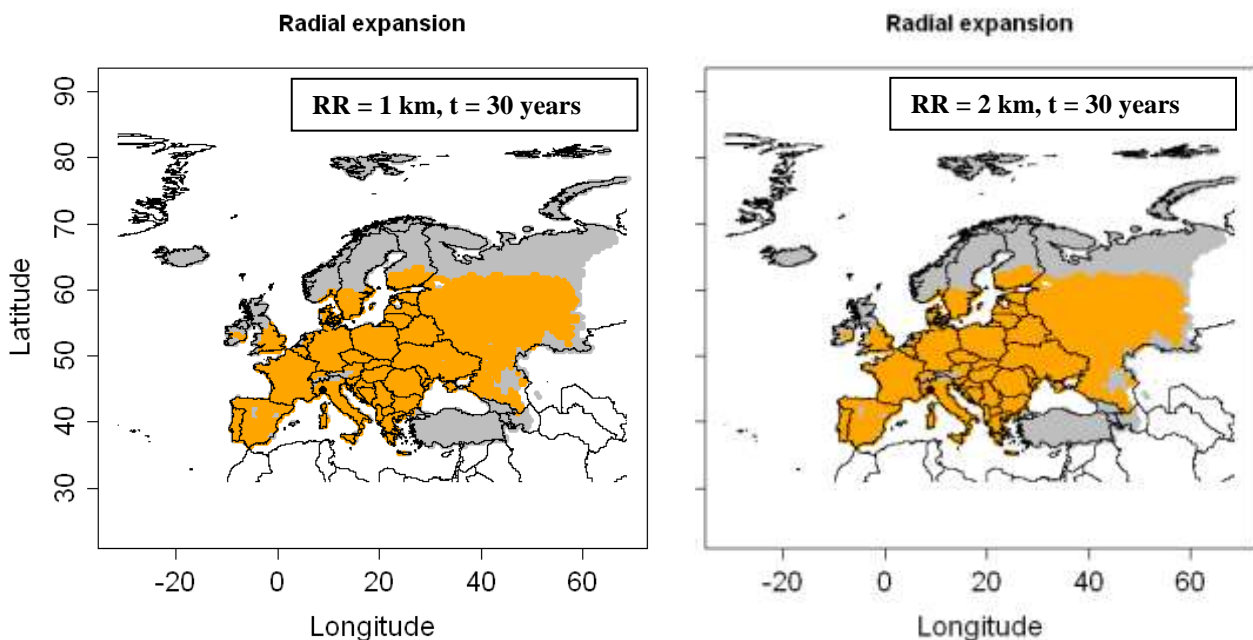


Figure 4.1.2-6: Radial range expansion of *A. chinensis* for $t=30$ years, an entry point in Northern Italy based on a CLIMEX model by Dominic Eyre. Left picture: $RR = 1$ km /year; right picture: $RR = 2$ km/year; (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data).

The outputs of the model are not very different for $u = 1$ and $u = 2$ km/yr (Fig. 4.1.2-6). It shows that the uncertainty for u does not have a significant effect on the results.

Radial range expansion after 60 years with one entry point in Northern Italy

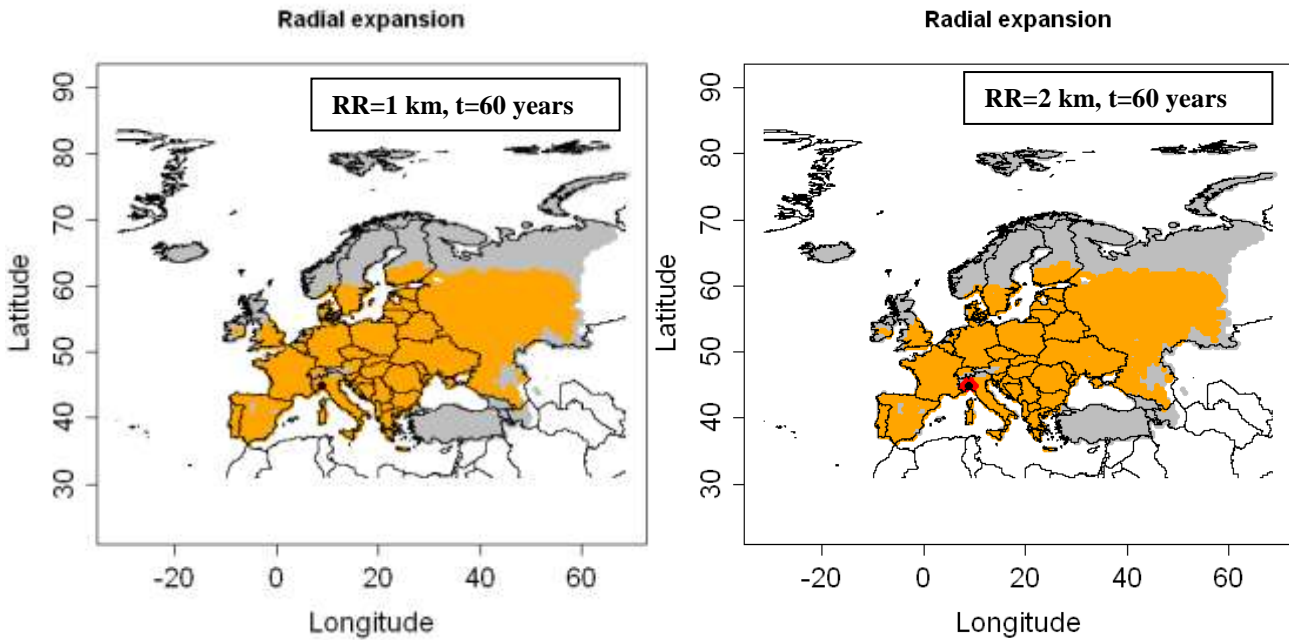


Figure 4.1.2-7: Radial range expansion of *A. chinensis* for $t=60$ years, an entry point in Northern Italy based on a Climex model by Dominic Eyre. Left picture: $RR = 1$ km /year; right picture: $RR = 2$ km/year; (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data).

Radial range expansion after 60 years with two and three entry points

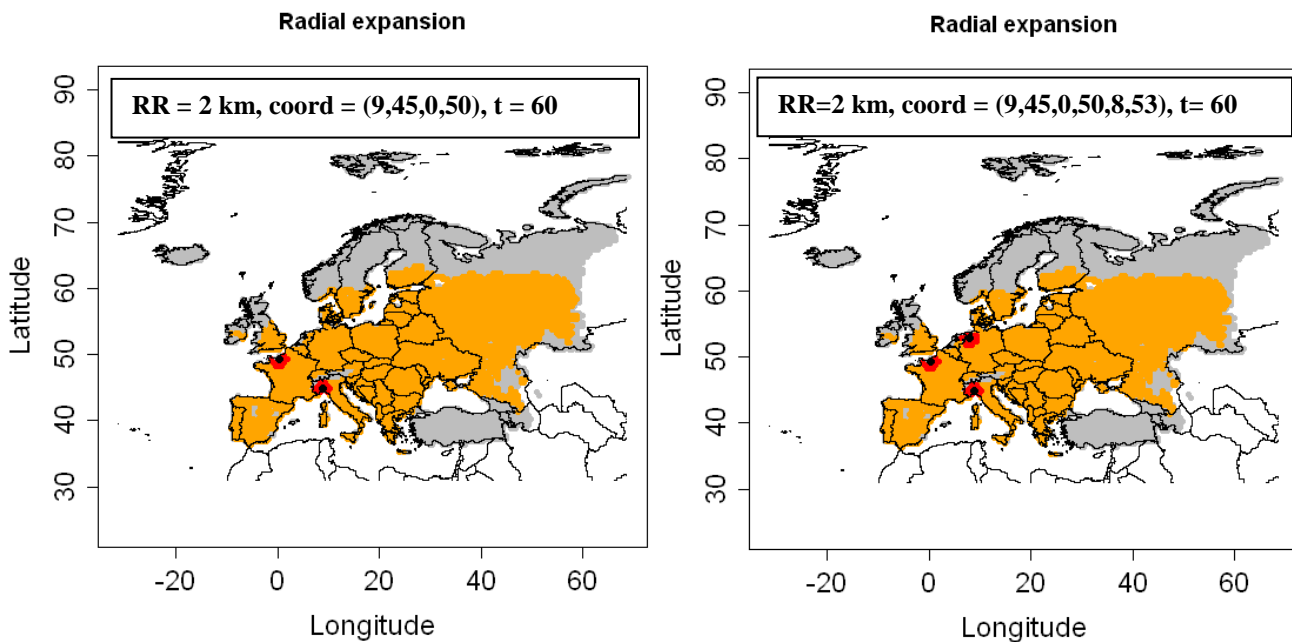


Figure 4.1.2-8: Radial range expansion of *A. chinensis* for $t=60$ years, two entry points (left picture: Northern Italy and France) and three entry points (right picture: Northern Italy, France and Netherlands) based on a CLIMEX model by Dominic Eyre. RR = 2 km/year; (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0 or host absent, white: no data).

4.1.2.4 Model 5 : Deterministic version of the dispersal kernel model (DK)

This type of model combines a population growth model and a dispersal kernel ($2Dt$) and it considers the proportion of the population that is engaged in dispersal.

- **Starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

$N_0 = 1.0 \times 10^{-6} \% - 1.0 \times 10^{-5} \%$ (see 2.1.1)

- **Multiplication factor λ_{max}**

λ_{max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

$\lambda_{max} = 6$ (see 2.1.1)

- **Shape parameter (p) of the $2Dt$ dispersal kernel**

(number of degrees of freedom or the proportion of the population engaged in long or short distance dispersal)

For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses further than 3σ) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail; individuals disperse at short distance).

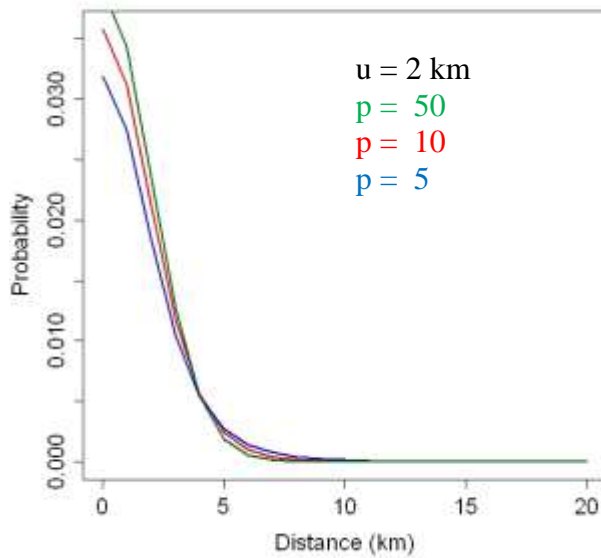


Figure 4.1.2- 9: Dispersal kernel with $p = 50$ (green graph, short distance spread), $p = 10$ (red graph) and $p = 5$ (blue graph, long distance spread) and $u = 2$ km.

Based on the information on *A. chinensis* we assume that only a small number of beetles will be engaged in long distance dispersal (see above under natural spread). We therefore do not use a “small” p (e.g. 1 or 5) but test the Dispersal Kernel Model with a “medium” p and compare $p=10$, $p=30$ and $p=50$.

- **Scale parameter (u) of the 2Dt dispersal kernel for the distance in km**

Here we use $u = 2$ km (derived here from 3.1.1)

- **Presence file**

The presence file contains the coordinates for the entry point and N_0 .

In this case the average $N_0 = 5.5 \times 10^{-6}$ was used.



Results:

Results for $p=10$

Dispersal kernel for time $t = 10$

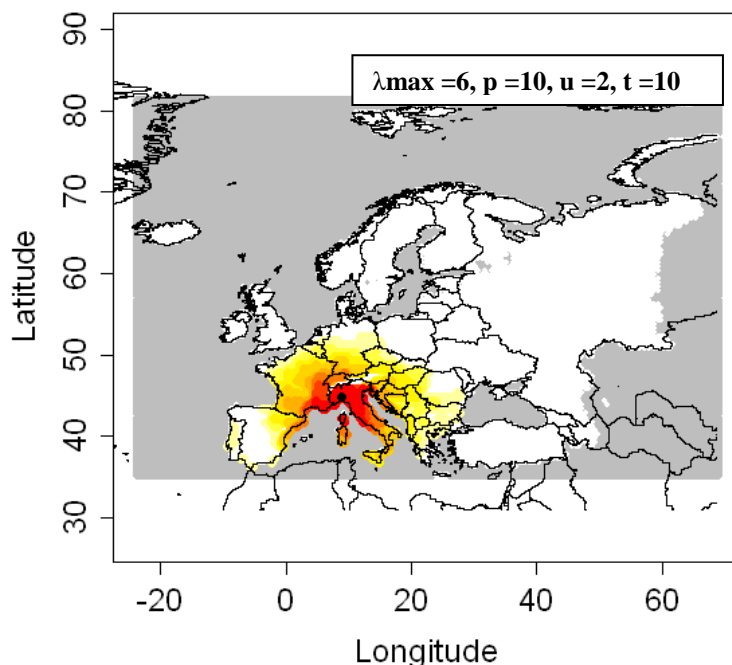


Figure 4.1.2-10: Output of the dispersal kernel model for *A. chinensis* based on a CLIMEX model by Dominic Eyre; $N_0 = 5.5 \times 10^{-6}$; $p=10$, $u=2$, $t=10$ years (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Dispersal kernel for a threshold $N_t = 25$

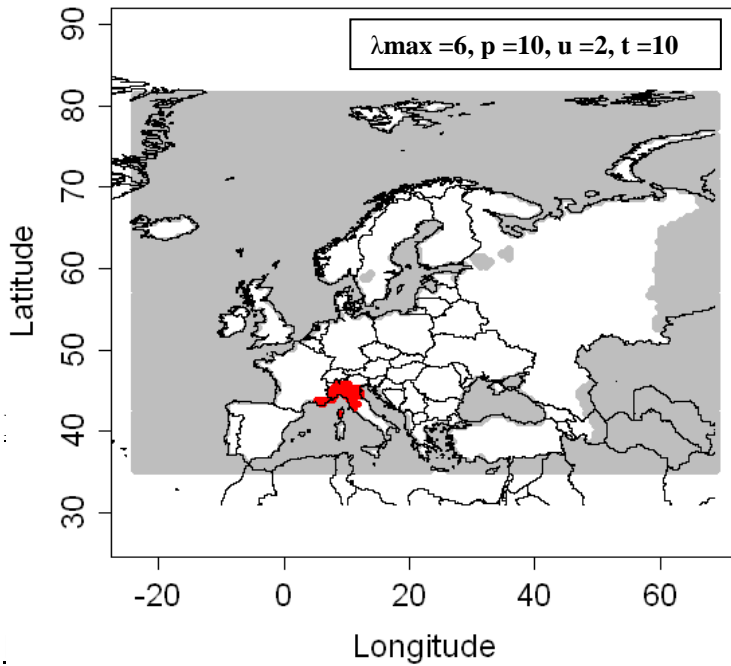


Figure 4.1.2-11: Output of the dispersal kernel model for *A. chinensis* (figure 4.1.2-10) with a threshold = 25%. $N_0 = 5.5 \cdot 10^{-6}$; $p=10, u=2, t=10$ years. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Dispersal kernel for time $t = 10$

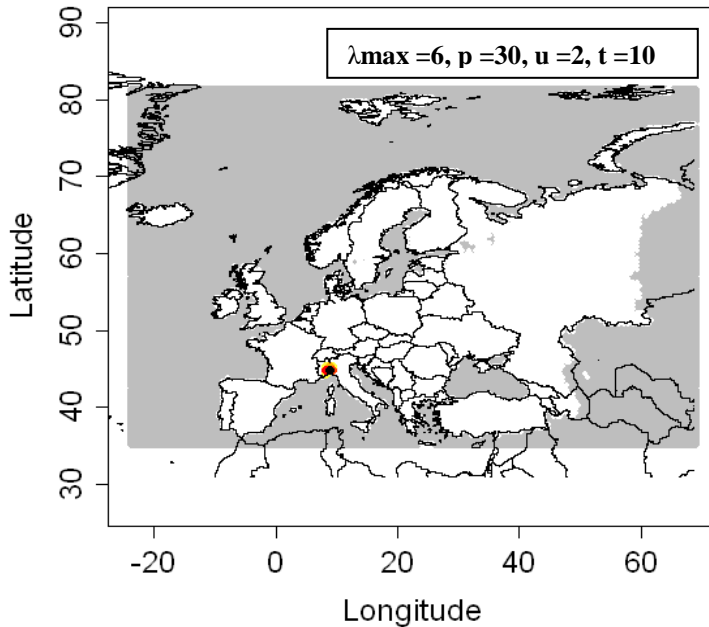


Figure 4.1.2-12: Output of the dispersal kernel model for *A. chinensis* based on a CLIMEX model by Dominic Eyre; $N_0 = 5.5 \cdot 10^{-6}$; $p=30, u=2, t=10$ years (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Dispersal kernel for a threshold $N_t = 25$

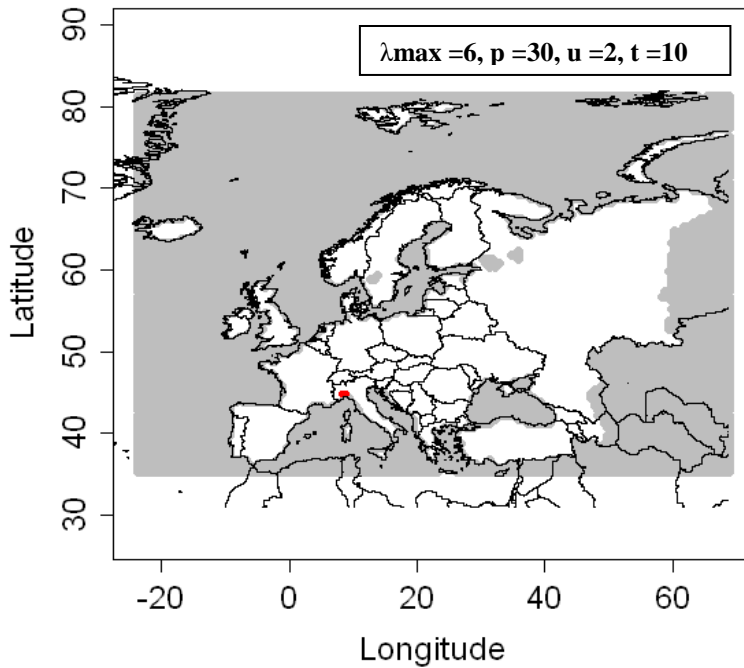


Figure 4.1.2-13: Output of the dispersal kernel model for *A. chinensis* (figure 4.1.2-12) with a threshold = 25%. $N_0 = 5.5 \cdot 10^{-6}$; $p=30$, $u=2$, $t=10$ years. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Results for $p=50$

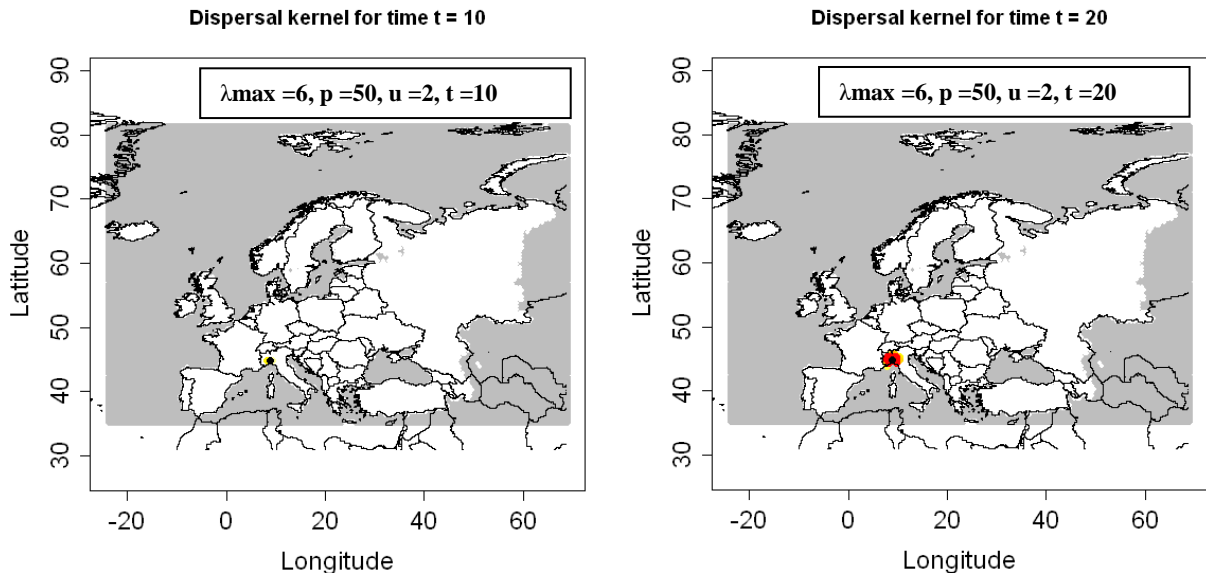


Figure 4.1.2-14: Output of the dispersal kernel model for *A. chinensis* based on a CLIMEX model by Dominic Eyre; $N_0 = 5.5 \cdot 10^{-6}$; $p=50$, $u=2$, $t=10$ years (left picture) and 20 years (right picture); N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data.

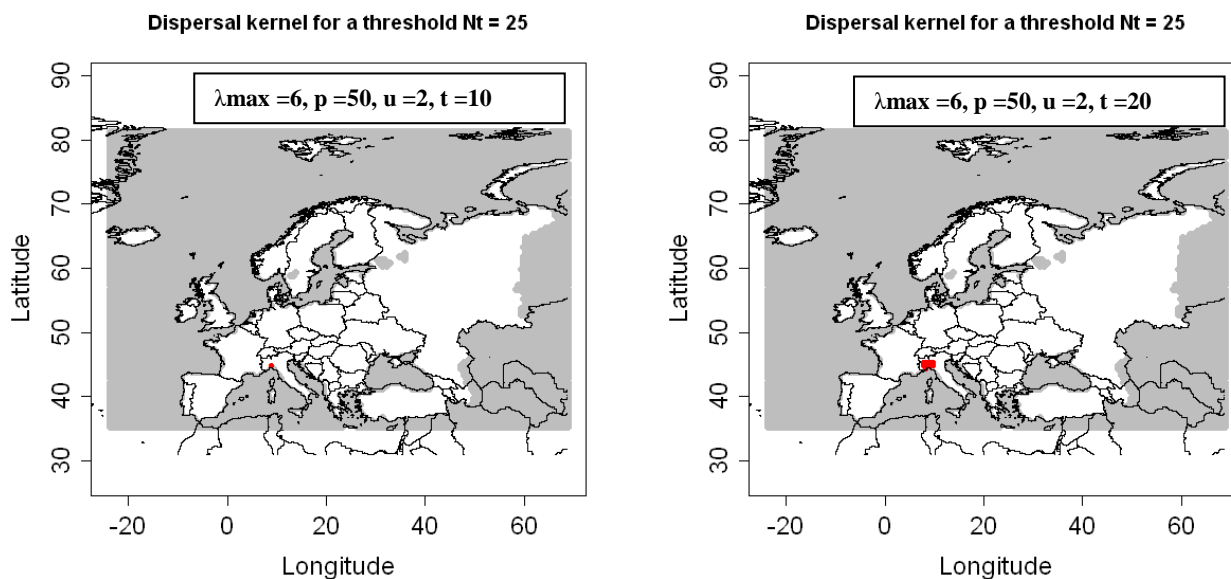


Figure 4.1.2 -15: Output of the dispersal kernel model for *A. chinensis* (figure 4.1.2-14) with a threshold = 25%. $N_0 = 5.5 \cdot 10^{-6}$; $p=50$, $u=2$, $t=10$ years (left picture) and 20 years (right picture) . The population abundance (%) is above this threshold in red cells (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

4.1.2.5 Summary

The application of the generic spread models to the Citrus longhorn beetle showed that the spread of the beetle could be mapped with reasonable results by the Radial Range Expansion Model and the Dispersal Kernel Model. According to literature and data from China and Italy the beetle disperses slowly by natural means and this was clearly displayed by the resulting maps, showing the areas at risk.

Additional information is provided by the Simple Logistic Model. Due to the assumptions underlying this approach that every suitable grid cell is invaded at the same time the result shows the temporal spread within cells. It therefore shows clearly which areas are expected to have high beetle abundances after different time intervals providing useful information for identifying locations where the highest impacts are to be expected.

The Radial Range Expansion Model only requires few parameters (starting population, radial range expansion per year and starting point(s) for the infestation). For *A. chinensis*, these could be derived from the literature and outbreak data from Italy. The application of this model approach is straightforward and the assisting experts felt quite comfortable with its outcome.

The Dispersal Kernel Model also leads to reasonable results, which are more visible by mapping the area above a defined threshold (N_t) for the abundance (N) after a specific time (t). However, in this case, the results depend on the choice of the shape parameter (p) of the $2Dt$ kernel. The application therefore requires some testing and "playing" with the model" and in the future more guidance on the most appropriate values for the given species (and how to derive them) should be provided.

Feedback from experts after reviewing the case study

The Radial Range Expansion per year (Model 3) was felt to result in more sensible results compared to the output of the Dispersal Kernel (Model 5) which from the point

of view of the experts results in a faster spread than they would have expected from their experience. The dependency on the chosen parameters is seen to be more critical for the Dispersal Kernel Model since this more sophisticated approach needs more testing to select the most appropriate parameters (e.g. the shape parameter p).

Summary of the commands for modelling the spread of *Anoplophora chinensis*

```
library(sp)
library(raster)
library(rgdal)
elevmax = F
hostfile = T
# load the R code
plothost()
plotRA()
plotGI()
res = slg(N0=1.0*10^(-5),lmax=6,movie=F, t=20)
res = radial(RR=2,t=60,coord=c(9,45,0,50),figkm=T, figdd=F)
res = dispk(N0=NULL, t=10,lmax=6, p=50,u=2, presencefile=T, nentry=NULL, figkm=F,figdd=T)
plotkernel (res$dispk,threshold=25)
```

4.1.3 *Anoplophora glabripennis* (Asian longhorn beetle)

This case study document, prepared by Hella Kehlenbeck, provides an example on applying the generic models for spread of invasive species developed within the frame of the EU project PRATIQUE to the potential natural spread of the Asian longhorn beetle *Anoplophora glabripennis* in Europe. The objective of the case study is designed to test the models and to provide an example with guidance for the estimation of the required parameter values for this invasive tree pest. It is also intended to support the Pest Risk Assessment on *A. glabripennis* for the EFSA funded project PRIMA PHACIE.

The Modelling has been done with the R-code Version V17.

Three of the five models were applied: 1. the Simple Logistic Growth Model, 2. the Radial Range Expansion Model and 3. the Dispersal Kernel Model.

Information and data on *A. glabripennis* are based on expert input, a datasheet developed within PRIMA PHACIE (first interim report on PRIMA PHACIE, Annex, 1b) and information gathered during Risk Assessment Method testing (within PRIMA PHACIE). Dominic Eyre (Fera, UK) kindly provided a CLIMEX model which provides the basis for the area of potential establishment and the population development within the models.

The case study was supported and reviewed by the PRATIQUE *A. glabripennis* experts Andrea Battisti and Massimo Faccoli as well as the PRIMA PHACIE case study group for *A. glabripennis* with its coordinator, Alan MacLeod.

4.1.3.1. Information on *A. glabripennis*

Natural spread potential

Adult beetles are capable of flying several hundred metres or more in a single flight to locate host trees. *A. glabripennis* tends to fly farther to find suitable host trees when no host trees are present in the surrounding area, whereas, when host trees are densely planted, little dispersal by adult *A. glabripennis* occurs (Huang, 1991).

Mark-release-recapture experiments showed that adults of the Asian longhorn beetle can disperse 1 to 3 km during their life span, although most remain near the tree where they emerge (Bancroft & Smith, 2005; Smith et al. 2001, Smith et al., 2004). Smith et al. (2004) recaptured 98% of the marked beetles within 920 m from the release point.

The average annual population dispersal distance measured by Wen et al. (1998) was 106.3 m, and this dispersal was positively correlated with wind velocity and temperature. However, a mean dispersal distance of 266 m has been recorded using the mark–release–recapture method (Smith et al., 2001). Further mark–release–recapture studies demonstrated that, although 72% of beetles were recaptured within 300 m of release points, some beetles were recaptured up to 2600 m away (Smith et al., 2004). In these studies, beetle dispersal from release trees was positively associated with the abundance of beetles at the release tree and smaller female beetles moved greater distances and were more attracted to taller trees (Bancroft & Smith, 2005).

A study of the outbreak in New York / New Jersey suggests that a low density introduction of *A. glabripennis* occurred and remained localized and undetected for many years and spread slowly until the beetle density on hosts became unsustainable at which time adults dispersed hundreds of metres to over 1 km (Sawyer, 2007). Sawyer & Panagakos (2008) reported estimated dispersal distances of ALB at three infested areas in New York and New Jersey of 2.25 km in 7 years, 2.25 km in 5 years and 1.6 km in 4 years leading to a medium range of 0.4 km per year. If suitable host trees are abundant, a population of ALB may remain highly localized for years, reproducing on few trees in a limited area (a few hundred metres in radius).

In *A. glabripennis* infested areas in Europe; all infested trees were found within an area with a radius of 200 – 500 m at the end of 2004 (Hérard et al., 2005). The infestation size in Cornuda (Northern Italy) had reached 4.1 ha in October 2010 (detection in 2009) leading also to an area with distances of about 200 - 300 m (Battisti et al. 2010). These observations indicate that beetles do not fly over long distances in these areas. Beetles will possibly fly over longer distances at high population densities or low host plant densities.

A. glabripennis is likely to spread locally in the short term, especially where host trees are abundant. Development is slow; it may take one or more years to complete a generation. It would take many years (decades) for *A. glabripennis* to spread by natural means over much of Europe.

Human-mediated spread potential, which is the most important pathway for long distance dispersal of *A. glabripennis*, is not considered by the modeling approach used here.

Host range and host distribution

Anoplophora glabripennis can adapt to feed and develop on many tree species. In Asia, North America and Europe various species from many different families have been reported (Lingafelter & Hoebeke, 2002; Hérard *et al.*, 2006; Sawyer 2008). The main hosts include species from *Acer*, *Populus*, *Salix* and *Ulmus* (Lingafelter & Hoebeke, 2002; Williams *et al.*, 2004; Haack 2006).

The complete development of *A. glabripennis* in Europe has been recorded on *Acer*, *Aesculus*, *Alnus*, *Betula*, *Carpinus*, *Fagus*, *Fraxinus*, *Platanus*, *Populus*, *Prunus*, *Salix* and *Sorbus* with *Acer* being the most commonly infested genus followed by *Betula*, *Salix*, *Aesculus* and *Populus* (Hérard *et al.* 2006; 2009). In a risk analysis of 1997 MacLeod (1997) reported the following species as hosts: *Acer dasycarpum* – silver maple, *A. negundo* – box elder, *A. platanoides* – Norway maple, *A. pseudoplatanus* – sycamore, *A. saccharinum* – silver maple, *A. saccharum* – sugar maple, *A. truncatum* – a maple in N. China, *Aesculus hippocastanum* – horse-chestnut, *Morus alba* – white mulberry. Within Europe *Acer* species, especially *A. negundo*, *A. platanoides* and *A. pseudoplatanus*, as well as some *Populus* *ssp.*, *Salix* *ssp.* and *Aesculus hippocastanum* are widely spread.

Anoplophora glabripennis is highly polyphagous and its major hosts are present in many European countries in urban areas. Hosts also occur widely in the natural environment. Some hosts are grown across large areas for forestry or to a lesser extent within mixed and natural forests. According to Schröder *et al.* (2006) all broadleaved trees (including fruit trees) are potential hosts of *A. glabripennis*. We therefore used the percentage of land covered by broadleaf forest for the spread modeling (see figures 4.1.3-1 and 4.1.3-2).

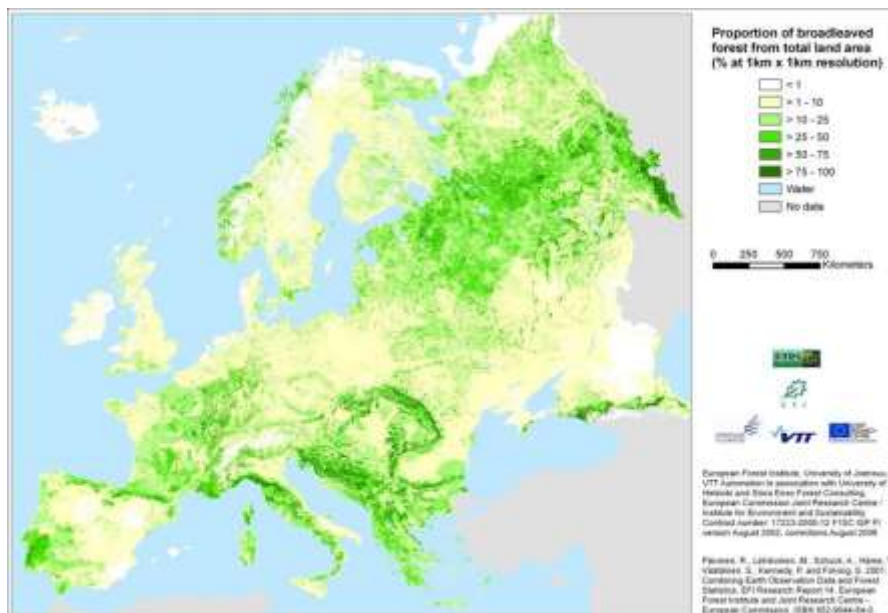


Figure 4.1.3-1: Proportion of broadleaved forest from total land area (% at 1 km by 1 km resolution; Päivinen *et al.* 2001).

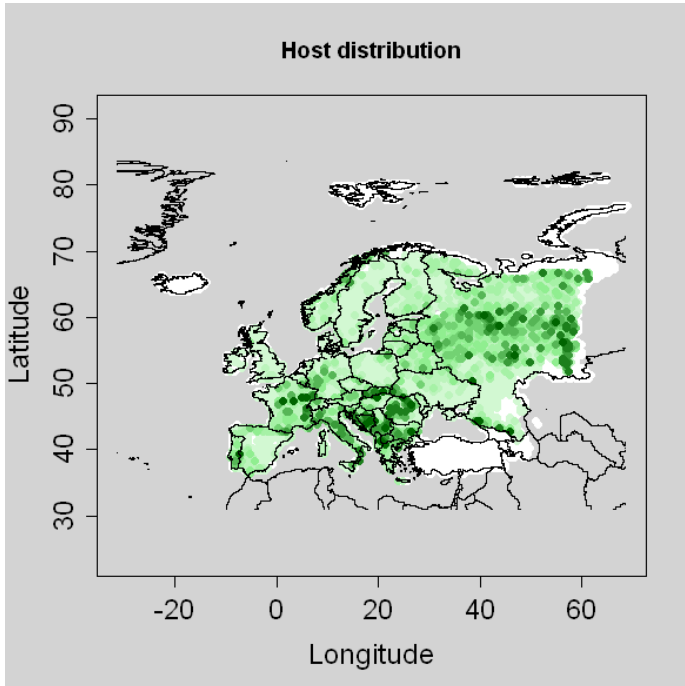


Figure 4.1.3-2: Host plant distribution for *Anoplophora glabripennis* in Europe based on the percentage of area covered with broadleaved forest according to Päivinen et al. 2001 (graduated colors from white (no host) to dark green (max=91%). Grey means no data).

Findings of *A. glabripennis* in Europe

(to be used as starting points for the modeling; source: EPPO reporting service, different years; coordinates for the locations were collected from the Internet/Google Earth)

Austria

- First finding in 2001 in Braunau am Inn (48°15'53"N,13°2'11"E (48.27,13.04))

France

- first finding in 2003 in Gien (Loiret) 47°41'N, 2°38'E (47.68,2.63))
- 2004 finding in Saint-Anne-sur-Brivet (Loire-Atlantique, Western France) 47°27'38"N, 2°0'8"W (47.46,2.002)
- 2008 finding in Strasbourg (Hérard, et al. 2009)

Germany

- first finding in 2004 in Neukirchen am Inn (near Passau, Bavaria, Southern Germany), 48°31'N,13°22'E (48.51,13.37)
- 2005 finding in Bornheim (near Bonn, Northrhine-Westfalia, Western Germany) 50°46'N,7°0'E (50.77,7.0)

Italy

- first finding in 2007 in Corbetta (Lombardia region, near Milano) [45°28'0"N, 8°55'0"E](#)
- in 2009 in Cornuda (Treviso region; 45°50'N, 11°59'E (45.83,11.98))
- in 2010 new spot in Maser (about 5 km from Cornuda, Battisti et al. 2010) 45°49'N 11°59'E (45.82,11.98)

Netherlands

- First finding in 2010 in the municipality of Almere, 52°23'N, 5°13'E (52.38,5.22)

Climatic suitability in Europe

MacLeod *et al.* (2002) reported that *A. glabripennis* would find the climate in many regions of Europe suitable for establishment, if biotic factors were appropriate. Detailed modelling using CLIMEX (by MacLeod and Eyre, 2010, within PRIMA PHACIE) also suggests that large areas of Europe provide suitable climatic conditions for the development of *A. glabripennis*. A complete generation could develop within 1 year in parts of the southern EU, whilst development over much of central and northern EU could take place within 2 - 3 years. The occurrence of outbreaks in Austria, France, Germany and Italy confirms establishment is possible in southern and central EU. Further north in Europe populations may be transient, depending on sufficient summer temperatures. Given that there has been an ongoing outbreak in Austria, perhaps since 2000, and in France, possibly since 2003, and outbreaks in Germany and Italy, and findings in live trees more recently in the Netherlands (2010), there is no doubt that climate in Europe is suitable for *A. glabripennis* development and that the beetle could establish and spread within the EU.

Battisti (2010, pers. comm.) states that beetles would not be active and fly below temperatures of about 10°C. Roden et al (2008) exposed larvae to low temperatures of -25°C to -40°C for 24 hours and observed that a high percentage of larvae (95%) survived the treatment and that, of those, 25 to 45% even completed their development and mated. The authors assume that ALB is freeze tolerant and that the northern distribution of the beetle will not be limited by winter temperatures but by host availability and summer temperatures.

CLIMEX file

A CLIMEX model for *A. glabripennis* was provided by Dominic Eyre. Figure 3 shows the risk area and the growth potential for *A. glabripennis* according to this model.

Reproduction strategy

The majority of the area where establishment is possible in the EU suggests that development would actually take 2 years (in contrast to the situation in China). This is due to the summer temperatures of Europe generally being cooler than in China, although this will vary depending on which locations are compared. The number of generations per year will have an influence on the reproduction rate and population densities. With a two or three year development cycle, the population will not grow as fast compared to a one-year-life-cycle. However, in 2003 a shortened life cycle of 1.5 years in Germany and elsewhere in Europe was reported due to the hot summer temperatures (T. Schröder, JKI, personal communication).

Topography or elevation limits

T. Schröder (personal communication) considers the Alps to be a natural barrier. We therefore applied an elevation limit for *A. glabripennis* of 2000 m.

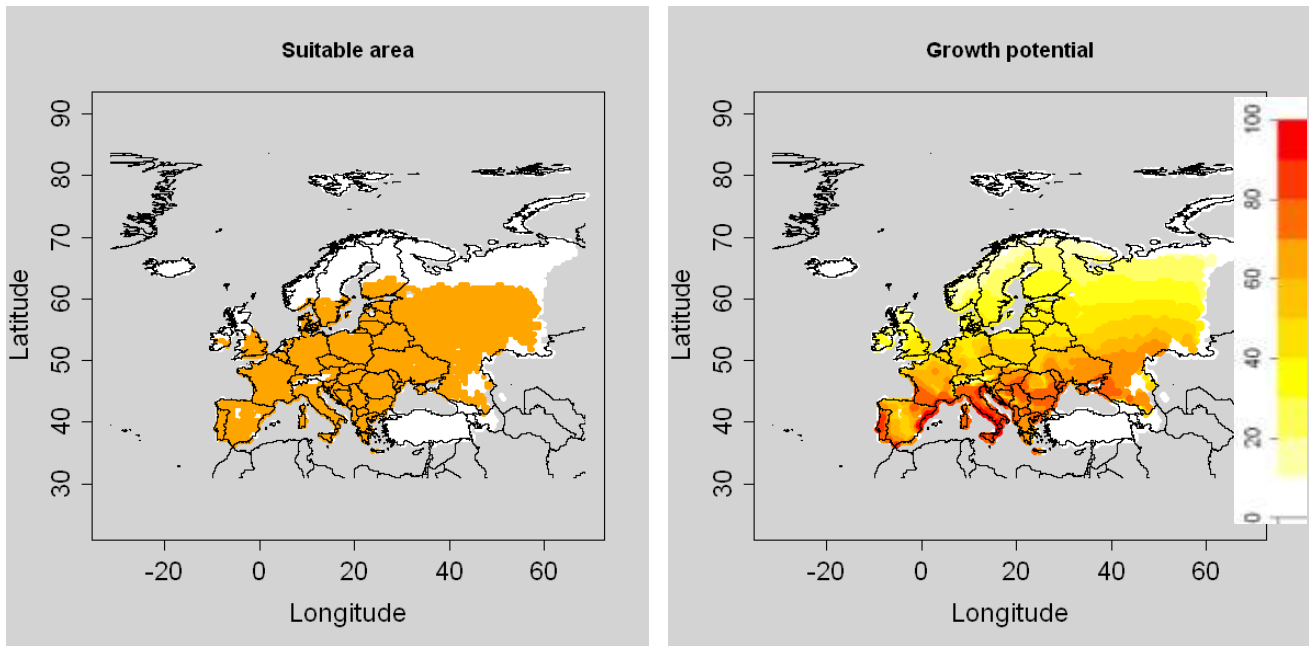


Figure 4.1.3-3: Suitable area (on the left; orange dots: EI>0, white dots: EI=0, grey: no data) and growth potential (GI; on the right) for *A. glabripennis* in Europe according to a CLIMEX model provided by Dominic Eyre. (EI = Ecoclimatic Index indicates, how favourable the climate is for the long term survival of the species; GI=Growth Index indicates the overall potential for the population growth).

4.1.3.2 Model 1: Population dynamics model (SLG)

For the SLG, it is assumed that an initial population abundance N_0 (%) is introduced in each suitable cell (cells where $EI > 0$) and then we simulate the “spread” or more precisely the growth within each cell according to a logistic function. On the output map, we will see areas which are the most suitable for population growth if some individuals were introduced there.

- **Starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

Calculation:

$$N_0 = 100 * \frac{n_0}{K}$$
 with n_0 the number of introduced individuals, in each suitable cell, and K the carrying capacity (the maximum number of individuals in a cell).

$K = \text{area_cell (km}^2) * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2)$,
or
 $K = \text{area_cell (km}^2) * \text{host_plant_density (/km}^2) * \text{max_population_density (/host plant)}$

Relevant information and data

In Italy, trees were observed with 10 to 20 exit holes (Battisti, pers. comm.). However, these numbers maybe much higher in single cases: Hérard et al. (2009) reported one sycamore maple tree (8 m tall with a triple trunk) in Italy (2007, Corbetta) that permitted 339 individuals to develop. At the same location three birches were found with together 32 exit holes and 74 living larvae, leading to about 100 individuals on these three *Betula* trees.

In the Netherlands (in November 2010) 16 exit holes and three larvae were detected on one *Acer* tree.

We assumed the maximum population density (max_population_density) = 10 – 20 beetles/host tree (Information by Andrea Battisti, UPAD, Italy)

Host trees and shrubs per km²

On a 5 x 5 km grid in Italy there are about 12.000 suitable trees (=12.000/25 trees/km² = 480 host trees / km²; according to Andrea Battisti for Italy)

Calculation of the capacity K:

$K_1 = 10 \text{ beetles/host tree} \times 480 \text{ hosts/km}^2 \times 1579 \text{ km}^2 \text{ (grid cell)}$

$K_1 = 7.579.200 = 7.58 \times 10^6 \text{ beetles/grid cell}$

$K_2 = 20 \text{ beetles/host tree} \times 480 \text{ hosts/km}^2 \times 1579 \text{ km}^2 \text{ (grid cell)}$

$K_2 = 15.158.400 = 1.5 \times 10^7 \text{ beetles/grid cell}$

Calculation of N_0

Starting number of beetles (= n_0) : can be very low, just 2 beetles (one female and one male) per grid cell could be sufficient

$N_0 = 100 \times \text{starting number } n_0 / K = \%$

$N_0 = 100 \times (2 \text{ beetles per grid cell} / 7.6 \times 10^6 \text{ beetles/grid cell}) -$

$100 \times (2 \text{ beetles per grid cell} / 1.5 \times 10^7 \text{ beetles per grid cell})$

$N_0 = 2.6 \times 10^{-5} \% \text{ to } 1,3 \times 10^{-5} \%$

- **Multiplication factor λ_{max}**

λ_{max} is the maximum year to year multiplication factor (“finite growth rate”) that a population could achieve under optimal conditions assuming unlimited space

Relevant information and data

In Northern Italy within 5 years the number of infested trees reached 430 (Battisti, pers. comm.). Given that two beetles (one male and one female) were the initial population, and assuming, that there have been 10 – 20 beetles/tree, the multiplication factor over these 5 years would have been 2150 – 4300. The multiplication factor for one year (λ_{max}) can be calculated in the following way:

$\lambda_{max} = 2150^{1/5} - 4300^{1/5}$

$\lambda_{max} = 4.6 - 5.3$

$\lambda_{max} = 5$

- **Time frame t**

$t = 20 - 30 \text{ years}$

Results

Results for SLG Model for 20 and 30 years and two different estimates for N_0
Figure 4.1.3.4 shows the results of the Simple Logistic Growth Model for 20 and 30 years.

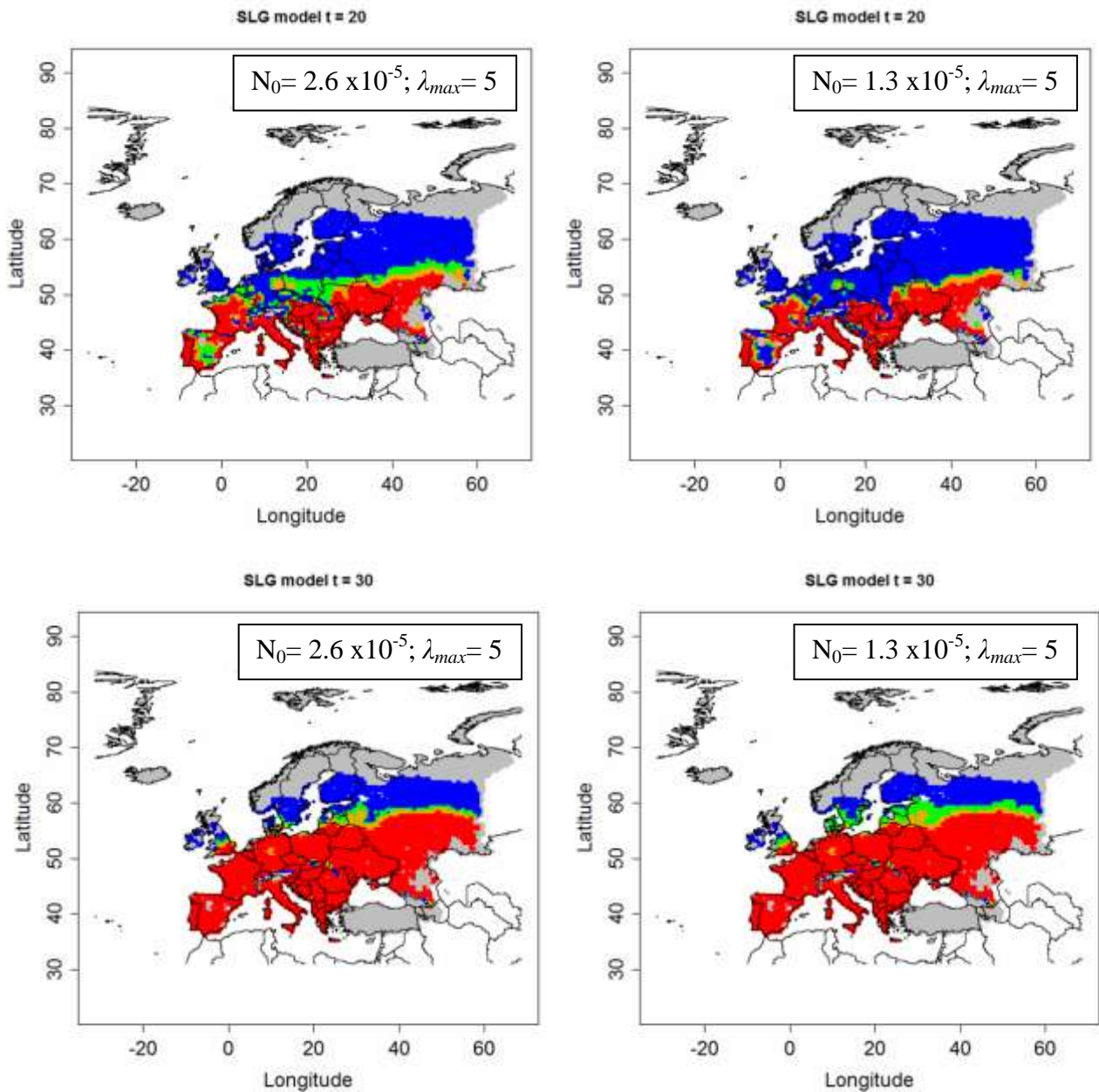


Figure 4.1.3-4: Output of the SLG model for *A. glabripennis* for 20 and 30 years, based on the CLIMEX model from Dominic (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data). Left pictures: $N_0=2.6 \times 10^{-5}$; right picture: $N_0=1.3 \times 10^{-5}$.

Information provided by the Simple Logistic Model: due to the assumptions underlying this approach that every suitable grid cell is invaded at the same time the result shows the temporal spread within cells. It therefore clearly shows which areas

are expected to have high beetle abundances after different time intervals indicating where the highest impacts / consequences are to be expected.

4.1.3.3 Model 3: Radial range expansion model (RR)

This model aims to determine the potential spread of a species introduced in the PRA area based on the radial rate expansion parameter. The model output is overlapped with the niche map ($EI > 0$).

- **Radial rate of range expansion per year (RR)**

RR = 1.5 km/year (estimated by Andrea Battisti)

Relevant information and data

Fight distances of ALB adults have been observed in the range of up to 3 km although most remain near the tree where they emerged. Smith et al. (2004) recaptured 98% of the marked beetles within 920 m from the release point. In infested areas in Europe trees with symptoms occurred within an area of a radius of 200-500 m.

Sawyer & Panagakos (2008) assumed dispersal distances of ALB at three infested areas in the USA of 2.25 km in 7 years, 2.25 km in 5 years and 1.6 km in 4 years leading to medium range of 0.4 km per year. If suitable host trees are abundant, a population of ALB may remain highly localized for years, reproducing on few trees in a limited area (a few hundred meters in radius). If food resources decline beetles may disperse more widely.

The chosen value of 1.5 km/year is assumed to capture the range of distances between several hundred metres and more than 2 km.

- **Time frame t**

$t = 40 - 60$ years

- **Entry point(s) or simulation of an introduction at a place ($coord$)**

Northern Italy (Treviso region): coord (11,46.15)

Results

Radial range expansion of *A. glabripennis* after 40 years

Results for the radial range expansion after 40 years are shown in figure 4.1.3-5. The map shows the very local spread of *A. glabripennis* which is expected based on the information available and the parameters chosen.

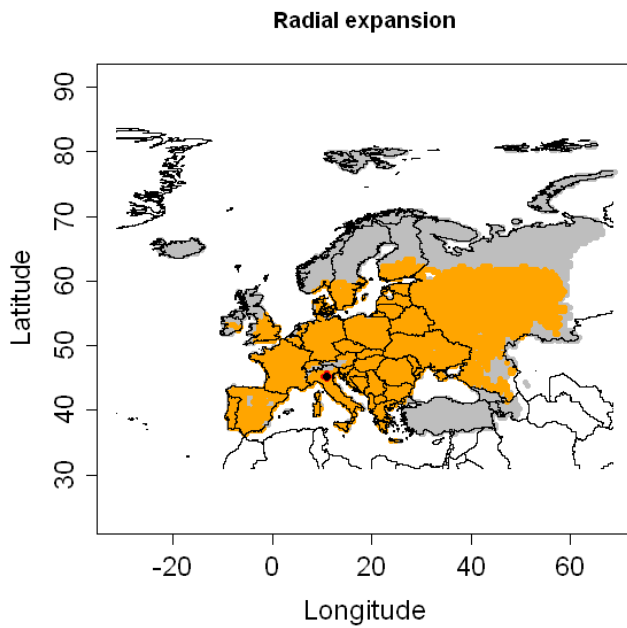


Figure 4.1.3-5: Radial range expansion of *A. glabripennis* for t=40 years, an entry point in Northern Italy based on a CLIMEX model by Dominic Eyre. RR = 1.5 km /year (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0 or host absent, white: no data).

Radial range expansion after 60 years

Figure 4.1.3-6 shows the results for the radial range expansion after 60 years. As expected the species has spread only a short distance compared to figure 4.1.3-5.

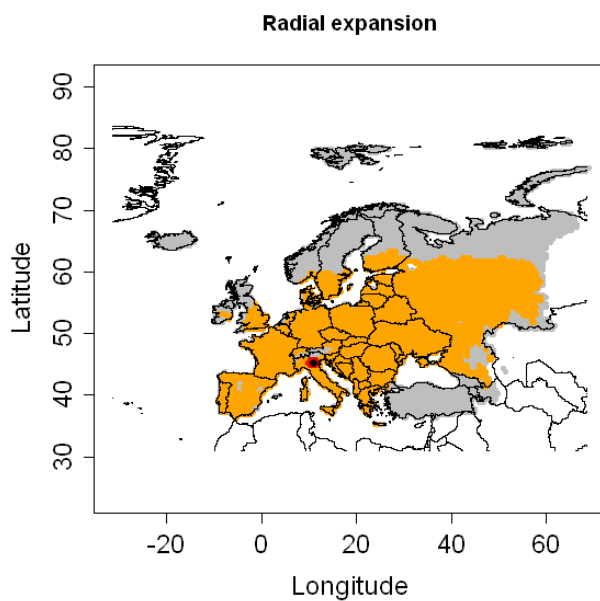


Figure 4.1.3- 6: Radial range expansion of *A. glabripennis* for t=60 years, an entry point in Northern Italy based on a CLIMEX model by Dominic Eyre. RR = 1.5 km /year (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0 or host absent, white: no data).

4.1.3.4 Model 5: Deterministic version of the dispersal kernel model (DK)

This type of model requires: a population growth model, a dispersal kernel (2Dt in this case) and the proportion of population engaged in dispersal.

The dispersal kernel is given by:

$$f(r) = \frac{1}{u^2 p \pi} \frac{\Gamma\left(\frac{p+1}{2}\right)}{\Gamma\left(\frac{p-1}{2}\right)} \frac{1}{\left(1 + \frac{1}{p} \frac{r^2}{u^2}\right)^{\frac{p+1}{2}}}$$

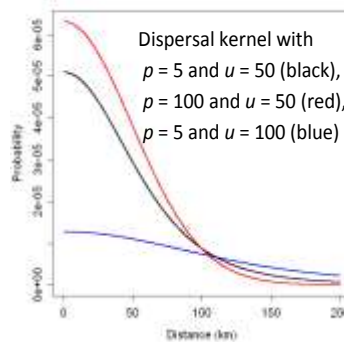


Figure 4.1.3-7: Dispersal kernel with different shape parameters for the proportion of individuals engaged in dispersal (p ; "small" $p \sim$ long distance; "large" $p \sim$ short distance) and scale parameter for the distance in km (u)

where u is the scale parameter, p the shape parameter and r the distance between two points. This kernel has a variance of:

$$\sigma^2 = 2 \frac{p}{p-3} u^2 \xrightarrow{p \rightarrow +\infty} 2u^2$$

For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses further than 3σ) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail; individuals disperse at short distance)

- **Starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

$N_0 = 2.6 \times 10^{-5} \% - 1,3 \times 10^{-5} \%$ (see 3.1.1)

- **Multiplication factor λ_{\max}**

λ_{\max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

$\lambda_{\max} = 5$ (see 3.1.2)

- **Shape parameter (p) of the 2Dt dispersal kernel**

(number of degrees of freedom or the proportion of the population engaged in long or short distance dispersal)

For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses further than 3σ) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail; individuals disperse at short distance).

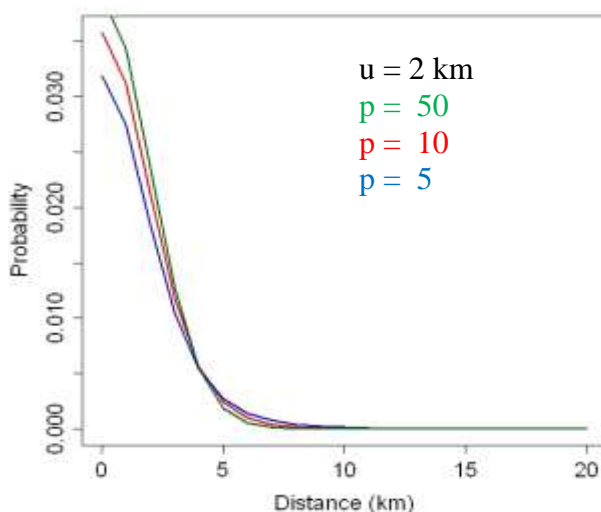


Figure 4.1.3-8: Dispersal kernel with $p = 50$ (green graph, short distance spread), $p = 10$ (red graph) and $p = 5$ (blue graph, long distance spread) and $u = 2$ km.

Based on the information on *A. glabripennis* we assume that only a small number of beetles will be engaged in long distance dispersal (see above under information on spread). We therefore do not use a “small” p (e.g. 1 or 5) but test the Dispersal Kernel Model with a “medium” p and compare $p=30$, $p=40$ and $p=50$.

- **Scale parameter (u) for the distance in km of the 2Dt dispersal kernel**

Here we use $u = 1.5$ km (derived here from Model 3)

- **Presence file**

The presence file contains the coordinates for the entry point and N_0 .



Results

Testing different values for the shape parameter p of the 2Dt dispersal kernel (affecting long and short distance dispersal) and two different values for the starting population N_0 , starting point in Italy

Results for $p=30$

Figure 4.1.3-9 and 4.1.3-10 show the results of the simulated spread of *A. glabripennis* over 20 years, starting in Northern Italy (coordinates see within the presence file) for $p=30$, two different values for N_0 and a scale parameter u of 1.5 km.

The abundance of the beetle above a threshold of 25% of the carrying capacity after 20 years (figure 10) does not show a difference between the two different values for N_0 . Based on the estimated parameters, *A. glabripennis* would spread over Northern Italy and move further to the North including small areas of Switzerland and Southern Germany.

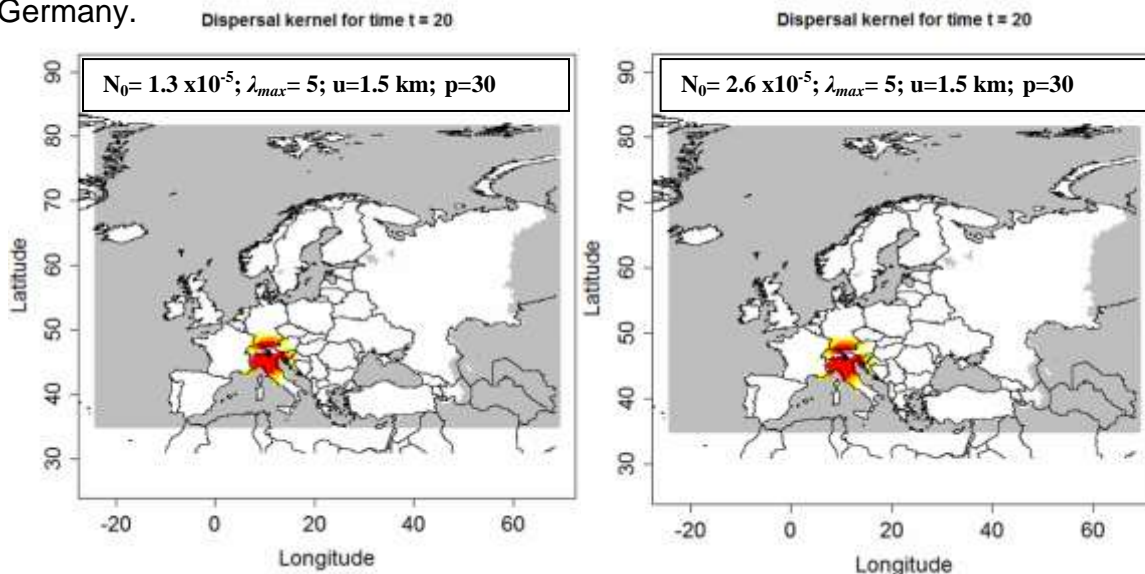


Figure 4.1.3-9: Output of the dispersal kernel model for *A. glabripennis* based on a CLIMEX model by Dominic Eyre; $p=30$, $u=1.5$ km, $t=20$ years; left picture: $N_0 = 1.3 \cdot 10^{-5}$; right picture: $N_0 = 2.6 \cdot 10^{-5}$; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

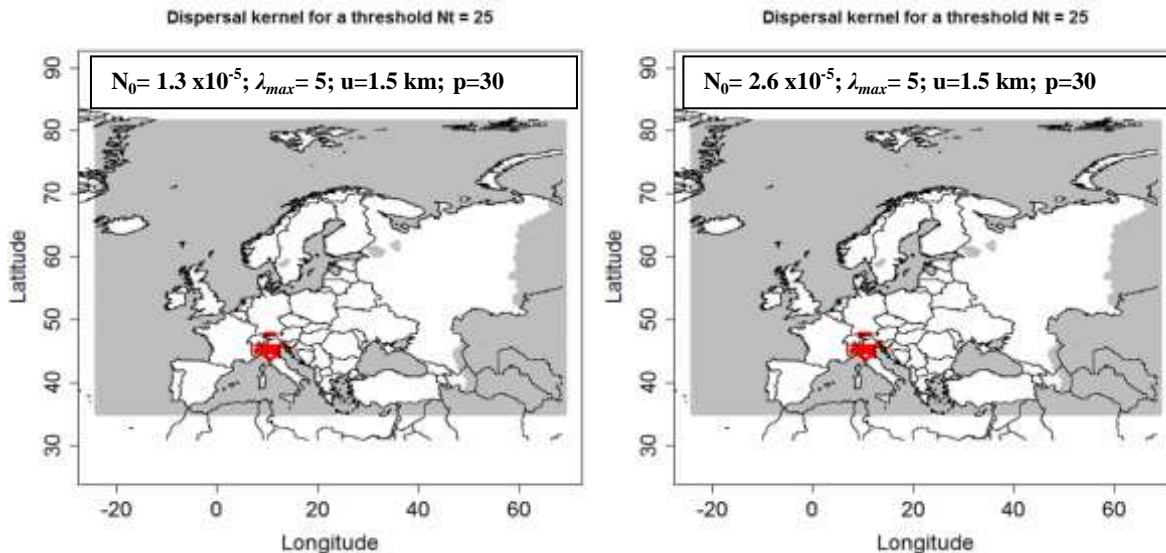


Figure 4.1.3-10: Output of the dispersal kernel model for *A. glabripennis* (figure 4.1.3-9) with a threshold = 25%. $p=30$, $u=1.5$, $t=20$ years, left picture: $N_0 = 1.3 \times 10^{-5}$; right picture: $N_0 = 2.6 \times 10^{-5}$. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

Results with $p = 40$

The results for $p=40$ (for only one value for N_0) are included below in figure 4.1.3-15. The simulated spread of *A. glabripennis* over 20 years is, as expected, reduced compared to $p=30$, due to the effect of the shape parameter p (see above, page 10). Under these assumptions the beetle would only spread in parts of Northern Italy.

Results with $p = 50$

Figures 4.1.3-11 and 4.1.3-12 show the results of the simulated spread of *A. glabripennis* over 20 years, starting in Northern Italy (for coordinates see the presence file) for $p=50$, two different values for N_0 and a scale parameter u of 1.5 km.

The abundance of the beetle above a threshold of 25% of the carrying capacity after 20 years (figure 4.1.3-12) is similar for the two different values for N_0 . Based on the estimated parameters and especially due to the chosen value for $p=50$, the simulated spread of *A. glabripennis* after 20 years only covers very small parts of Northern Italy.

Testing of a (worst case) scenario with $u = 3$ km

Figures 4.1.3-13 and 4.1.3-14 show the results of the simulated spread of *A. glabripennis* over 20 years, starting in Northern Italy (for coordinates see 5.1.5 in the presence file) with a higher scale parameter u ($u=3$ km) for distance in the dispersal kernel compared to the lower distance used before ($u = 1.5$ km).

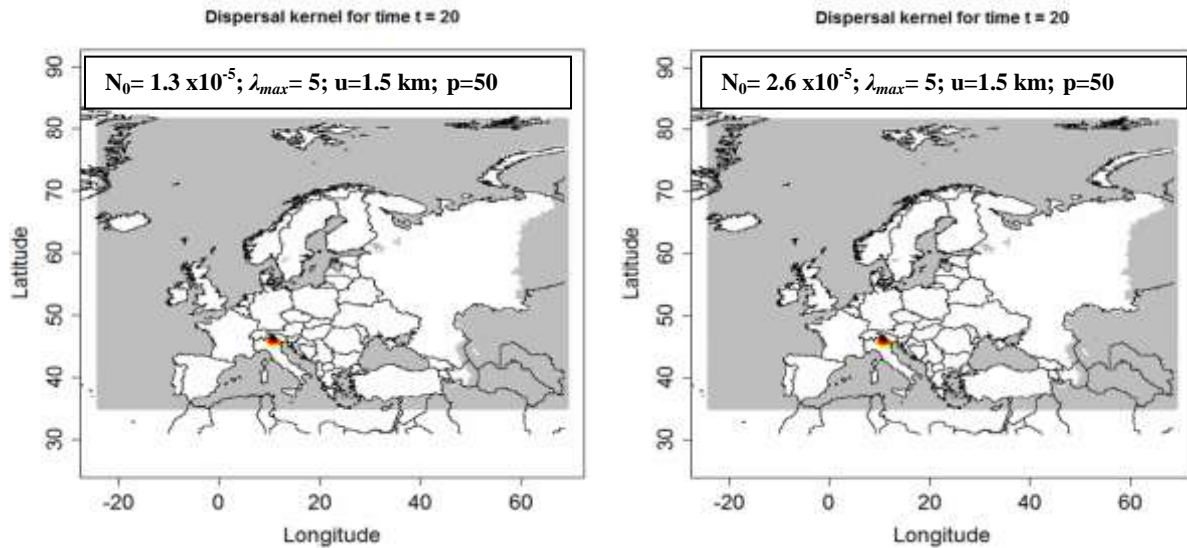


Figure 4.1.3-11: Output of the dispersal kernel model for *A. glabripennis* based on a CLIMEX model by Dominic Eyre; $p=50$, $u=1.5$ km, $t=20$ years; left picture: $N_0 = 1.3 \times 10^{-5}$; right picture: $N_0 = 2.6 \times 10^{-5}$; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

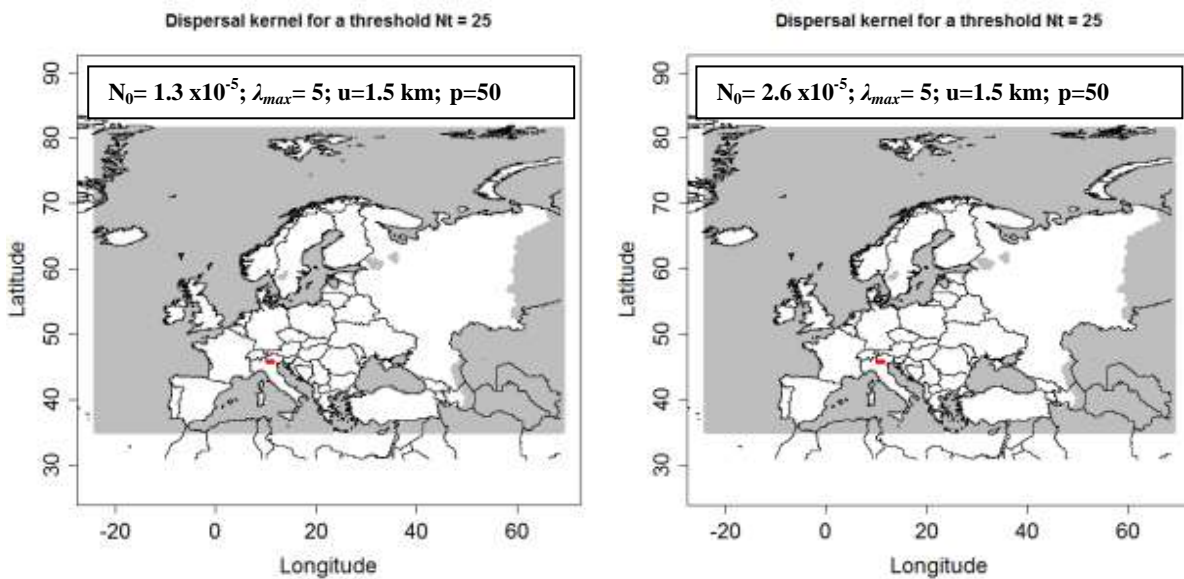


Figure 4.1.3-12: Output of the dispersal kernel model for *A. glabripennis* (figure 11) with a threshold = 25%. $p=50$, $u=1.5$, $t=20$ years, left picture: $N_0 = 1.3 \times 10^{-5}$; right picture: $N_0 = 2.6 \times 10^{-5}$. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

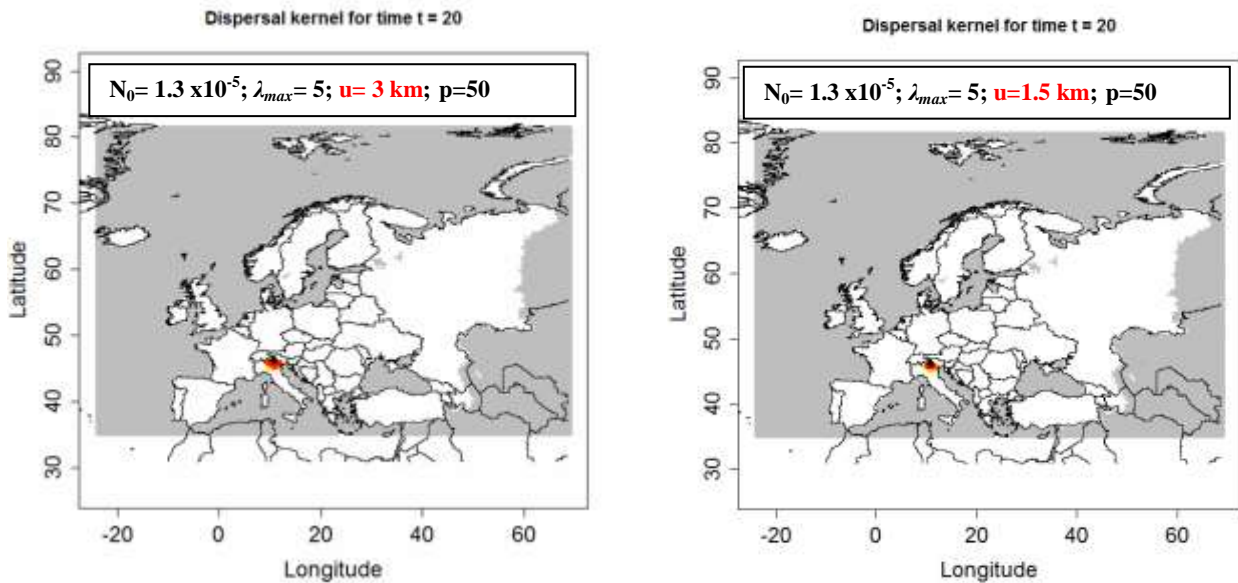


Figure 4.1.3-13: Output of the dispersal kernel model for *A. glabripennis* based on a CLIMEX model by Dominic Eyre; $N_0 = 1.3 \times 10^{-5}$, $p=50$, $u=3$ km (left picture) and $u=1.5$ km (right picture), $t=20$ years; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

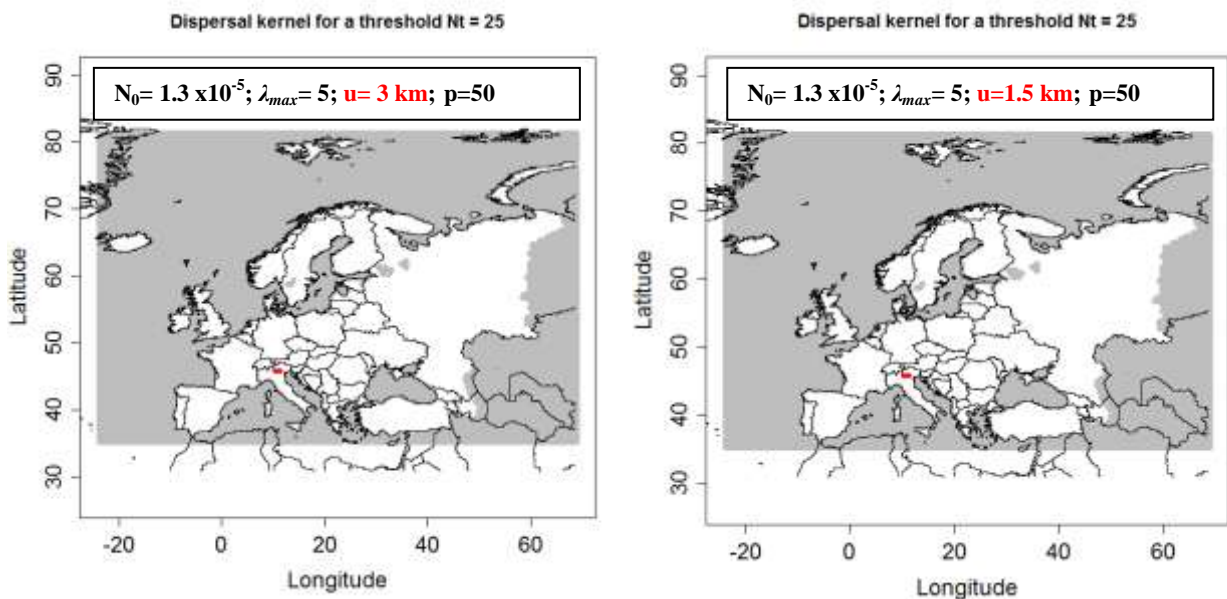


Figure 4.1.3-14: Output of the dispersal kernel model for *A. glabripennis* (figure 4.1.3-13) with a threshold = 25%. $N_0 = 1.3 \times 10^{-5}$, $p=50$, $u=3$ km (left picture) and 1.5 km (right picture), $t=20$ years. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

According to figure 4.1.3-13 the beetle would have been expected to spread further with the assumption of $u=3$ km compared to $u=1.5$ km. But, the abundance of the beetle above a threshold of 25% of the carrying capacity for $u=3$ km after 20 years (figure 4.1.3-16) does not show a difference between the two different values for u . This means that although for $u=3$ km the beetle disperses further, at the places that are located farther from the starting point, the abundance of the beetle (N_t) is below

25%. It would be reasonable to compare lower values ($< 25\%$) for the carrying capacity threshold to see if more areas could be affected assuming $u=3$ km.

Based on the estimated parameters *A. glabripennis* would only spread to a very small part of Northern Italy for both u -values.

Modeling the spread of *A. glabripennis* for different starting points (Netherlands, Germany and Italy)

Results for $p=40$

Figure 4.1.3-15 shows the maps for the spread modeling over 20 years for different starting points in Europe (Netherlands (Almere), Germany (Neukirchen) and Italy (Treviso region) for a shape parameter of the dispersal kernel $p = 40$.

The German starting point (Neukirchen am Inn) is located near the southern border of Germany. In this case, the simulated spread of *A. glabripennis* would also reach small parts of the southern neighbouring country, Austria. For the other starting points (Netherlands and Italy) there is no overlap with the neighbouring countries.

Results for $p=50$

Figure 4.1.3-16 and 4.1.3-17 show the spread modeling over 20 years for different starting points in Europe (Netherlands (Almere), Germany (Neukirchen and Bornheim) and Italy (Treviso region) for $p = 50$.

Expectedly the areas above the threshold (figure 4.1.3-17) are smaller compared to $p=40$ and spread is more limited for all starting points with the application of a shape parameter $p=50$.

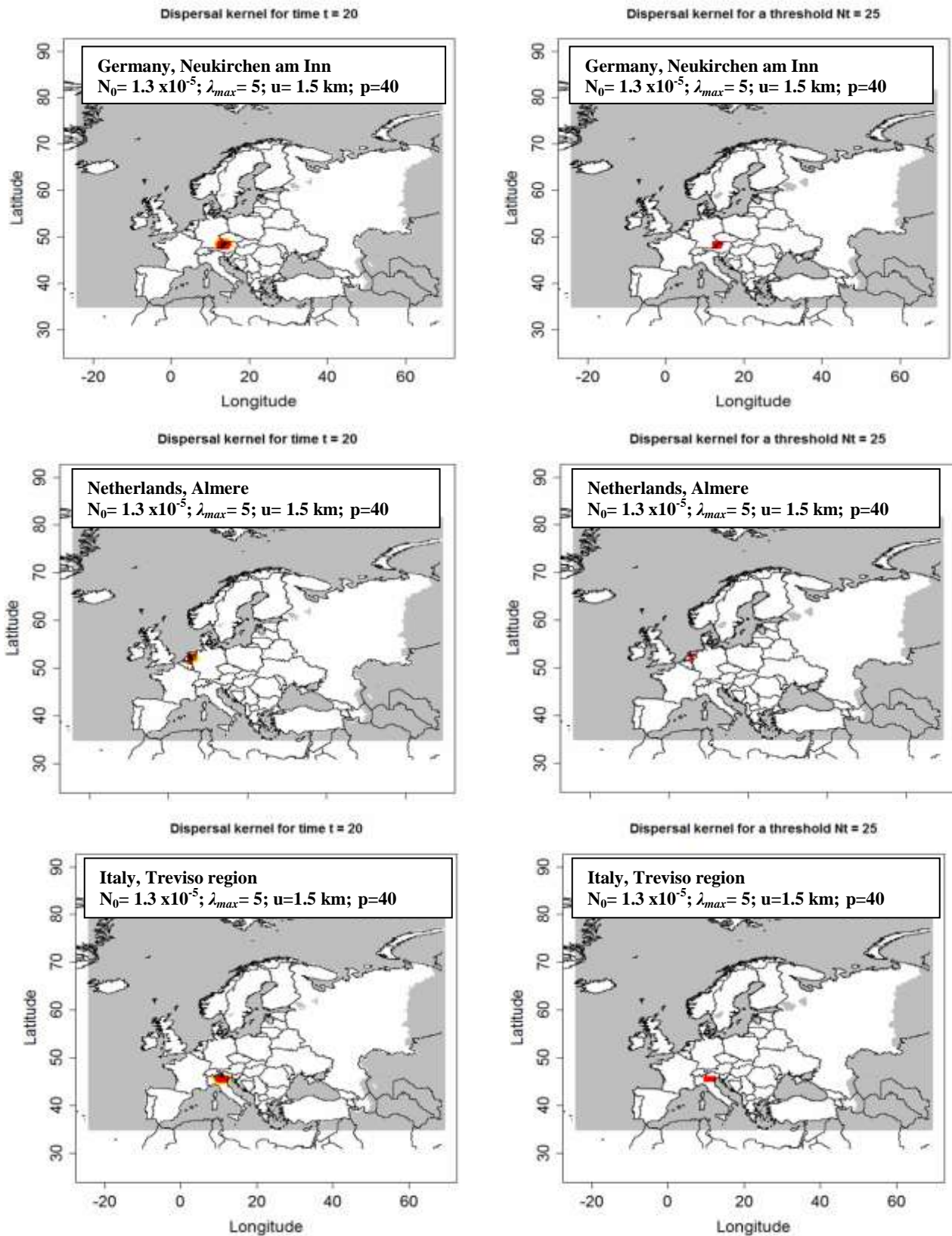


Figure 4.1.3-15: Left: Output of the dispersal kernel model for *A. glabripennis* for different starting points, based on a CLIMEX model by Dominic Eyre; $N_0 = 1.3 \times 10^{-5}$, $p = 40$, $u = 1.5$ km, $t = 20$ years; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data); Right: Output of the dispersal kernel model for *A. glabripennis* (left) with a threshold = 25%. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

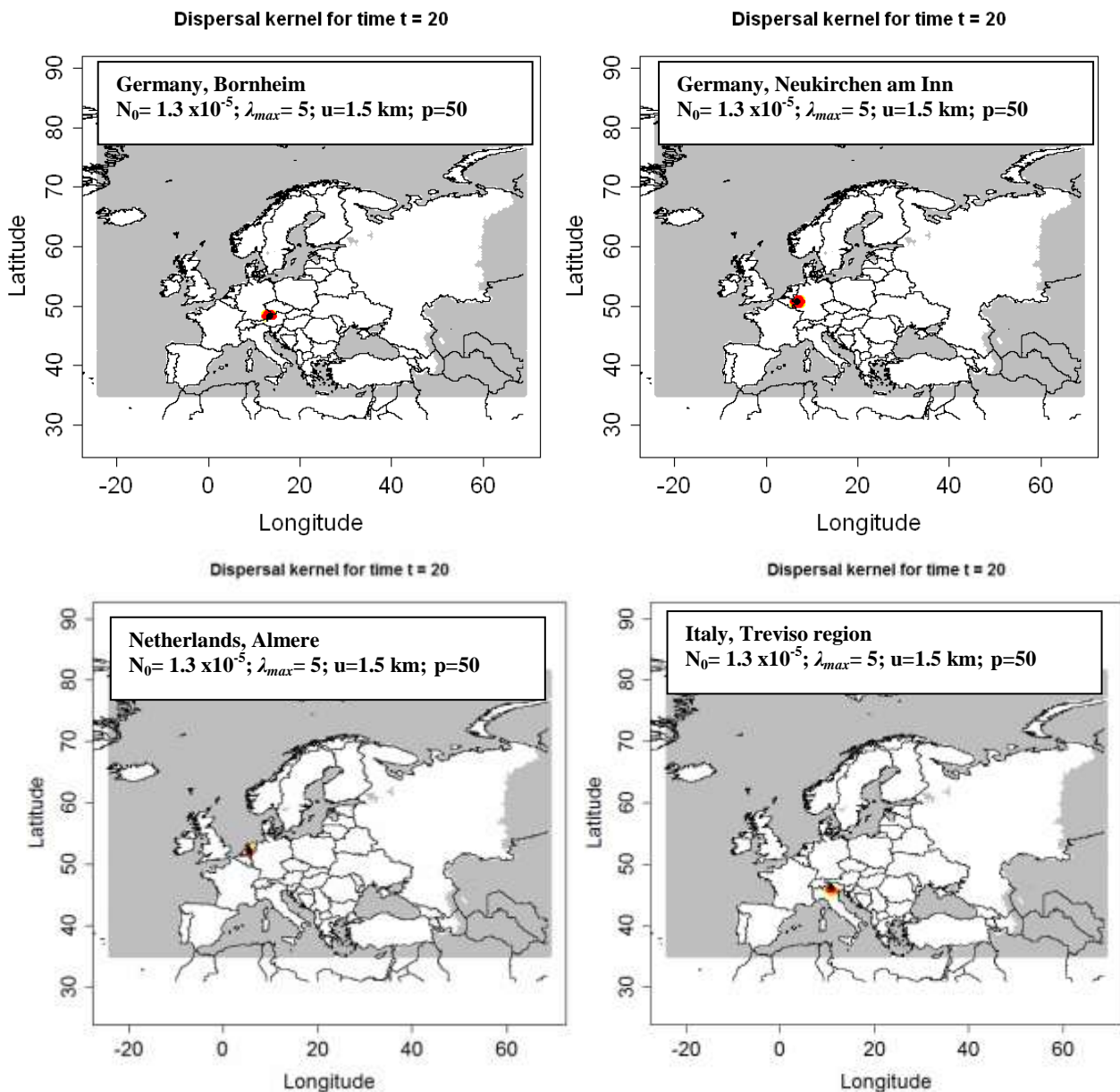


Figure 4.1.3-16: Output of the dispersal kernel model for *A. glabripennis* for different starting points in Europe, based on a CLIMEX model by Dominic Eyre; $N_0 = 1.3 \times 10^{-5}$, $p = 50$, $u = 1.5$ km, $t = 20$ years; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

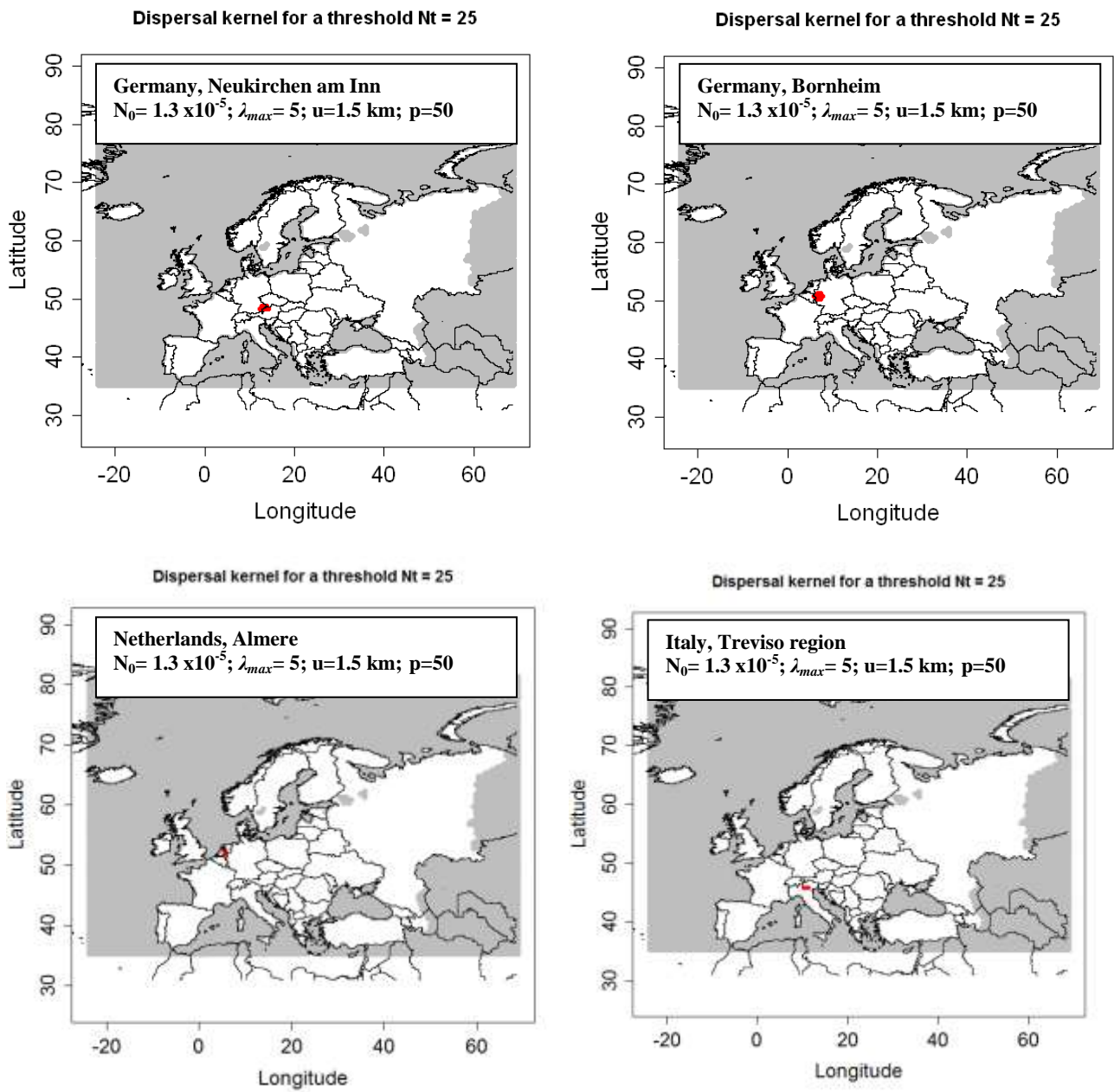


Figure 4.1.3-17: Output of the dispersal kernel model for *A. glabripennis* (figure 4.1.3-16) with a threshold = 25%. $N_0 = 1.3 \times 10^{-5}$, $p = 50$, $u = 1.5$ km, $t = 20$ years; The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data).

Modeling the spread for different starting points (Netherlands, Germany, France and Italy) over a period of 30 years

Results for p=40 and t=30

Figure 18 shows the results of the spread of *A. glabripennis* over a period of 30 years for different starting points in Europe for p=40.

By applying these parameters, *A. glabripennis* would spread over parts of western and central Europe (France, Germany, Italy, the Netherlands, Belgium, Austria, Czech Republic, Slovenia, Croatia, parts of Hungary and Slovakia).

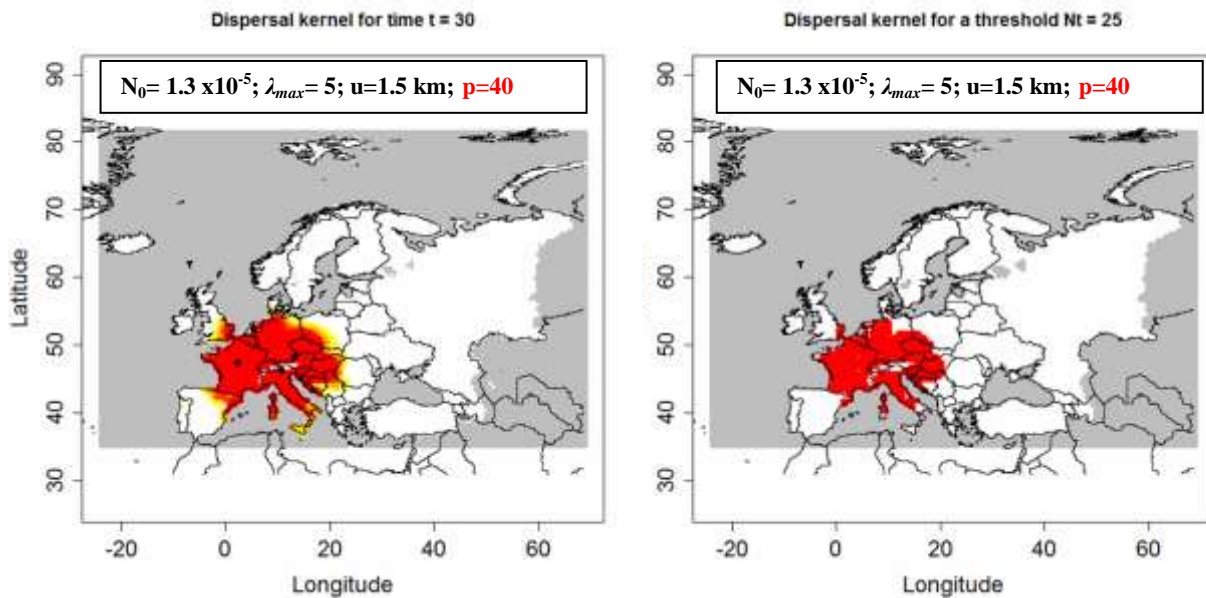


Figure 4.1.3-18: Left: Output of the dispersal kernel model for *A. glabripennis* for different starting points, based on a CLIMEX model by Dominic Eyre; $N_0 = 1.3 \times 10^{-5}$, $p=40$, $u=1.5$ km, $t= 30$ years; (Nt: population abundance (%); graduated colors from white (Nt < 10^{-6}) %) to yellow, orange and red (Nt $\geq 10\%$). Grey means no data); Right: Output of the dispersal kernel model for *A. glabripennis* (left picture) with a threshold = 25%. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt \geq threshold, white: cells where Nt < threshold. Grey means no data).

Results for p=50 and t=30

Figure 4.1.3-19 shows the results of the spread of *A. glabripennis* over a period of 30 years for different starting point in Europe for p=50.

When using p=50 as a shape parameter of the dispersal kernel, the spread kernels of the different starting points do not overlap and *A. glabripennis* spreads within France, parts of Germany, Northern Italy, the Netherlands, Belgium, Austria, Czech Republic and parts of Slovenia.

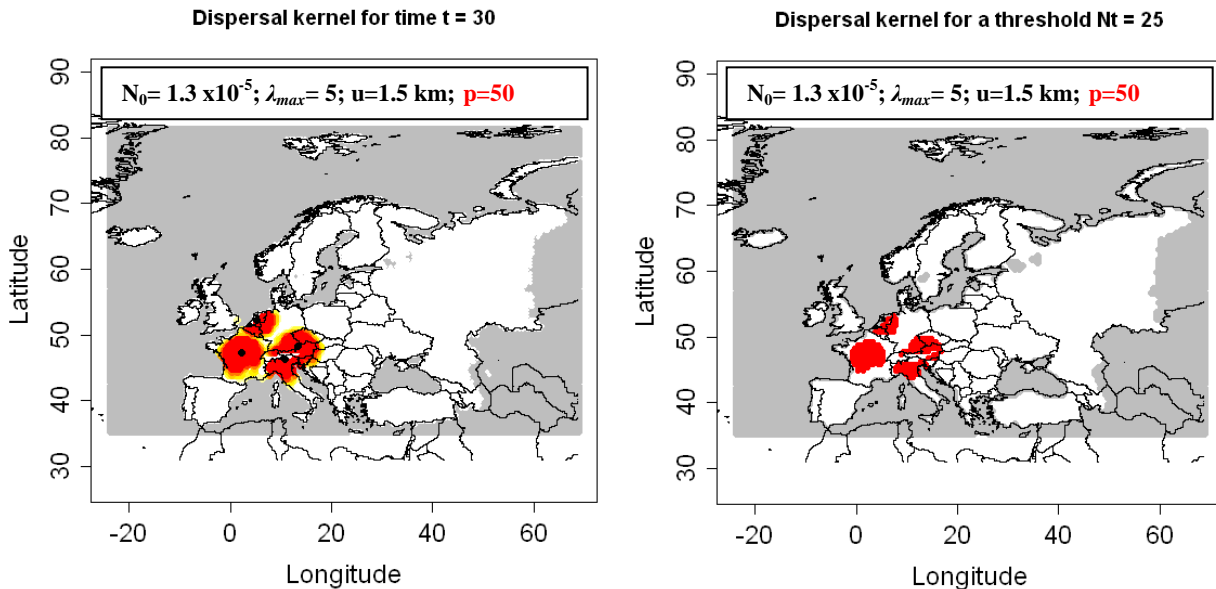


Figure 4.1.3-19: Left: Output of the dispersal kernel model for *A. glabripennis* for different starting points, based on a CLIMEX model by Dominic Eyre; $N_0 = 1.3 \times 10^{-5}$, $p=50$, $u=1.5$ km, $t=30$ years; (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data); Right: Output of the dispersal kernel model for *A. glabripennis* (left) with a threshold = 25%. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Discussion of results for different parameter values

Parameter values for the dispersal kernel model were varied to take into account the different data and information that were available from the literature and experts.

By altering the parameters used for the dispersal kernel model we showed that the changes in N_0 (1.3×10^{-5} or 2.3×10^{-5}) as well as the different values for the scale parameter u ($u=1.5$ or $u=3$) lead to quite similar results in the extent of the spread and the abundance of ALB. However, changes in the shape parameter (p) of the dispersal kernel ($p=30$, $p=40$, $p=50$) resulted in relatively big differences, showing the high sensitivity of this model to the parameter p . Taking the longer time frame of $t=30$ years into account, it is assumed that a value of $p=50$ better reflects the short distance dispersal of the ALB compared to $p=40$ and especially $p=30$. Additional testing for $p=60$ is recommended.

Additionally expert judgment on the most reasonable modeling output should be included.

4.1.3.5 Summary

The application of the generic spread models to the Asian longhorn beetle showed that the spread of the beetle could be mapped with reasonable results by the Radial Range Expansion Model and the Dispersal Kernel Model. According to the data and literature from Italy, USA and China the beetle disperses slowly by natural means and this was clearly displayed within the resulting maps, showing the areas at risk.

Additional information is provided by the Simple Logistic Model: due to the assumptions underlying this approach that every suitable grid cell is invaded at the same time the result shows the temporal spread within cells. It therefore highlights

which areas are expected to have high beetle abundances after different time intervals and this can be used to identify the locations where the greatest consequences are to be expected.

The Radial Range Expansion Model only requires a few parameters (starting population, radial range expansion per year and starting point(s) for the infestation). For *A. glabripennis*, these were derived from outbreak data from Italy and from the literature.

The Dispersal Kernel Model also leads to reasonable results, which are best visible by mapping the area above a defined threshold (N_t) for the abundance (N) after a specific time (t). However, in this case, the results depend on the choice of the shape parameter (p) of the 2Dt kernel. The application therefore requires some testing and "playing" with the model". For *A. glabripennis* the mapping of spread with a shape parameter $p=50$ was assumed to lead to the best results in comparison to literature data but expert judgment and additional testing for p -values above $p=50$ would be appropriate.

Feedback from experts after reviewing the case study

Massimo Faccoli suggested to test the models without any host plant restriction since he argued that the applied broadleaf forest distribution would not really take account of the situation that the beetle mainly occurs in urban areas on ornamental trees planted in or near to towns and villages and not in natural forestry areas (this has been observed in Italy and as well in Asia). Therefore he would not consider the absence of broadleaf forests as a limiting factor for the ALB spreading in the models.

Dominic Eyre commented on the spread rate mapped and from his point of view it is faster than expected in the figures 4.1.3-9 and 4.1.3-10 as well as in 4.1.3-18 and 4.1.3.-19. This corresponds to what has already been discussed above for the different values for the shape parameter p .

Summary of the commands for modelling the spread of *Anoplophora glabripennis*

```
library(sp)
library(raster)
library(rgdal)
elevmax = 2000
hostfile = T
# load the R code
plohost()
plotRA()
plotGI()

res = slg(N0=1.3*10^(-5),lmax=5,movie=F, t=20)
res = radial(RR=1.5,t=60,coord=c(11.5,45.6),figkm=T, figdd=F)
res = dispk(N0=NULL, t=1,lmax=5, p=50,u=1.5, presencefile=T, nentry=NULL, figkm=F,figdd=T)
plotkernel (res$dispk,threshold=25, figkm=F, figdd=T)
```

4.2 Nematodes

4.2.1 Root-Knot Nematode, *Meloidogyne enterolobii*

This document, prepared by Hella Kehlenbeck, provides a case study example on applying the generic models for the spread of invasive species developed within the framework of the EU project PRATIQUE to the potential spread of the root-knot nematode *Meloidogyne enterolobii* in Europe. The objective of the case study is to test the models and to provide examples with guidance for the estimation of the required parameter values for an invasive nematode damaging a broad range of host crops in Europe. The case study was conducted with the help of Zhenya Ilieva (PPI, Bulgaria), expert on *Meloidogyne*, who also provided data and reviewed the document.

Modelling is based on the Guide for the Spread Module, Version 0.21, and the R-code Version V17, both dating from November 23rd, 2010 (see chapter 3).

4.2.1.1. Information on *M. enterolobii*

M. enterolobii is a tropical root-knot nematode that induces root galls and can cause significant damage to a large number of vegetable and ornamental crops in protected and field cultivation. Further information can be derived from the EPPO Alertlist: (http://www.eppo.org/QUARANTINE/Alert_List/nematodes/meloidogyne_enterolobii.htm).

Natural spread potential

The capacity of *M. enterolobii* for natural movement is very low and is comparable to other *Meloidogyne* species. According to Tiilikkala *et al.* (1995), free-living second-stage juveniles can move 1-2 m at maximum per year.

Human-assisted spread potential

M. enterolobii can easily be spread throughout the EU with infested rooted plants or soil. It can also be spread by farm machinery moving between different fields. Human assisted spread within the EU is very likely to occur through the trade in infested rooted host plants and soil.

The nematode has been found several times in imported plant material (ornamentals such as *Rosa* sp., *Ficus* sp., *Cactus* sp. from Africa and Asia). The most relevant pathways are traded host plants or cuttings with roots (with or without soil). Recent findings of *M. enterolobii* in imported ornamentals in the Netherlands show that the concentration of the pest on the pathway at origin can be high: imported *Rosa* sp. (from South Africa and China) and *Brachychiton bidwilli* (from Israel) were heavily infested. In a root sample of *Brachychiton bidwilli*, 12,360 eggs, 4,380 juveniles and 200 females were found (source: NPPO of the Netherlands).

Host range and host distribution

The host range of *M. enterolobii* includes a large number of horticultural and agricultural crops (Britto *et al.*, 2004a,b,c; 2007; Cetintas *et al.*, 2007). Amongst these are tomatoes, cucumbers, bell peppers, eggplants, beans, onion, potatoes, roses and a number of other ornamentals.

Findings of *M. enterolobii* in Europe
(to be used as starting points for the modelling)

- France
M. enterolobii has been reported from a cold greenhouse in France (Concarneau, Brittany) (Blok *et al.*, 2002).
- Switzerland
M. enterolobii has been reported from two greenhouses in Switzerland, where it is still present (Kiewnick, 2008).
- Netherlands
In the Netherlands, *M. enterolobii* has been intercepted approximately 10 times (from 1991 to 2007) in imported plant material from Asia, South America and Africa.

Climatic suitability in Europe

Based on the current distribution, *M. enterolobii* needs a relatively high temperature to develop, i.e. within the tropical-Mediterranean temperature range. These conditions are present outdoors in the southern part of Europe and in greenhouses in the northern part. Although the precise temperature requirements of *M. enterolobii* have not yet been studied, it is likely that the northern limit to its range in Europe is comparable to *M. incognita*. The northern limit to the current area of distribution for *M. incognita* outdoors is likely to be just south of Paris (Karssen, 2002; Ritter, 1972). In Northern European countries, *M. enterolobii* will probably not be able to establish or cause major problems in field grown crops. It will probably only be able to establish in greenhouses.

The species has often been found in mixed populations with *Meloidogyne incognita*, *M. arenaria* and *M. javanica* (Diop, 1994, Carneiaro *et al.*, 2001, Brito *et al.*, 2004(a); Brito *et al.*, 2004(c); Brito *et al.*, 2007; Brito *et al.*, 2008; Centinas *et al.*, 2008; etc.). All of these root-knot nematodes are widespread in the EU (CABI, 2007). We therefore decided to use the available data on the temperature limits of the following parthenogenetic nematode species: 1) *M. javanica* - a nematode with a more opportunistic life strategy and 2) *M. incognita* - a nematode with more of a K strategy (Evans & Perry, 2009) for *M. enterolobii*.

CLIMEX file

According to the assumptions made above, two different CLIMEX models were constructed by Zhenya Ilieva: one for *M. javanica* and another for *M. incognita*. Figures 4.2.1-1 and 4.2.1- 2 show the area of potential establishment (EI, suitable area) and the growth potential (GI) for the two *Meloidogyne* species according to these models.

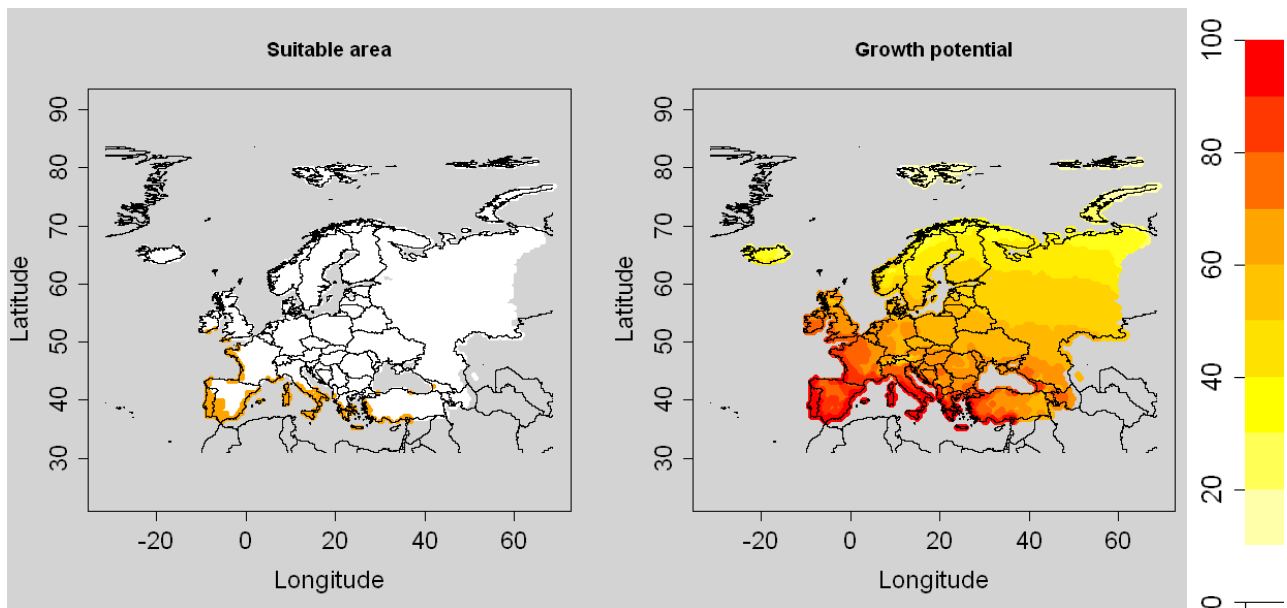


Figure 4.2.1-1: Suitable area (area of potential establishment, on the left; orange dots: EI>0, white dots: EI=0, grey: no data) and growth potential (GI; on the right) for *M. javanica* in Europe based on a CLIMEX model by Zhenya Ilieva

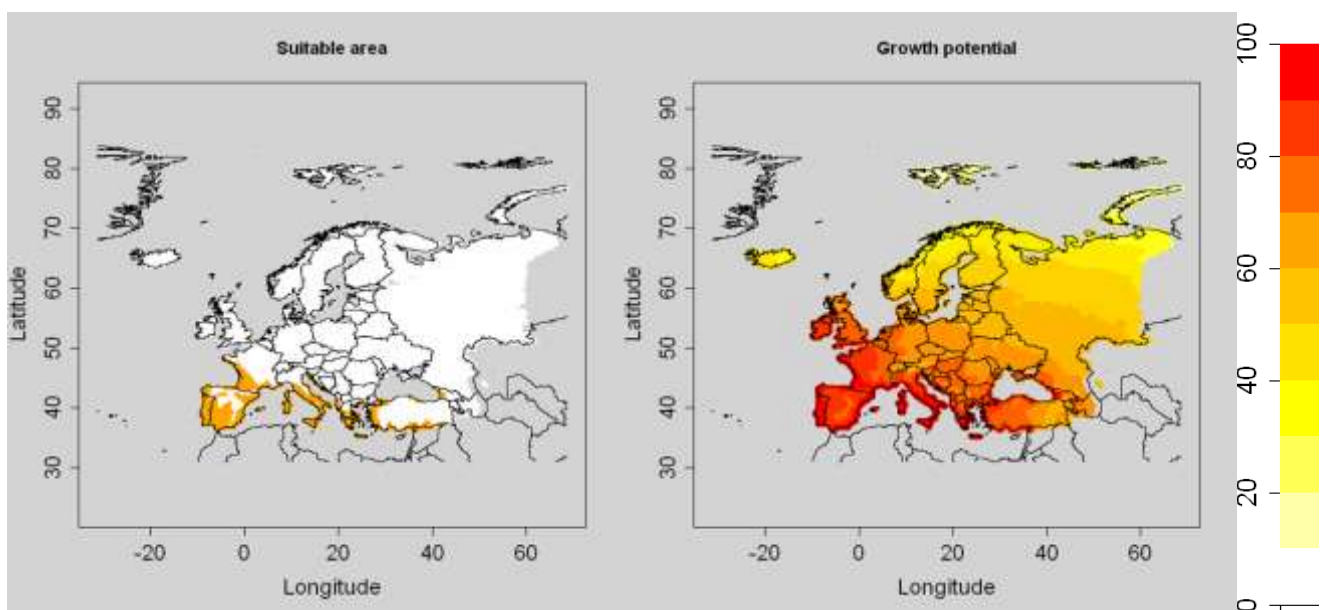


Figure 4.2.1-2: Suitable area (area of potential establishment, on the left; orange dots: EI>0, white dots: EI=0, grey: no data) and growth potential (GI; on the right) for *M. incognita* in Europe based on a CLIMEX model by Zhenya Ilieva

Based on the two CLIMEX models the number of suitable cells is given below:

Meloidogyne javanica:

[1] "The number of suitable cells is: 246"

[2] "The total number of cells in SLG, LG-Econ, radial, rand-radial is: 6416"

[3] "The total number of cells in the grid used by the dispersal kernel model is: 17298"

Meloidogyne incognita:

[1] "The number of suitable cells is: 402"

[2] "The total number of cells in SLG, LG-Econ, radial, rand-radial is: 6416"

[3] "The total number of cells in the grid used by the dispersal kernel model is: 17298"

Soil conditions in Europe

Soil is a very important factor that influences the potential distribution and spread of *Meloidogyne* species and needs to be taken into account when mapping the area of potential establishment. According to Braasch et al. (1996), *Meloidogyne* spp. can occur on a wide range of soil types, but their association with crop damage is mainly observed in sandy soils. Clay content above 30% and sand content below 30 % result in a denser soil structure that is generally considered unfavourable for root-knot nematodes (Greco and Di Vito, 2009). Both observations indicate that areas with such types of soils in the EU are at high risk from *M. enterolobii*, assuming the climate is suitable and hosts are available. These sandy soils are present throughout the EU (see figure 4.2.1-3 with Dominant Surface Textural map throughout Europe, Maxime Dupin). It is possible to create a 0/1 raster file to define the area where the soil is favourable (1) or not (0), and use it as the habitat file. However, here we use another approach. The models presented below only consider the CLIMEX dataset, and then, it is recommended to combine the soil maps to the outputs of the spread models in MCAS to define more precisely the potential distribution of *Meloidogyne enterolobii* (see procedures set out in the DSS for mapping endangered areas (PRATIQUE Deliverable 3.3).

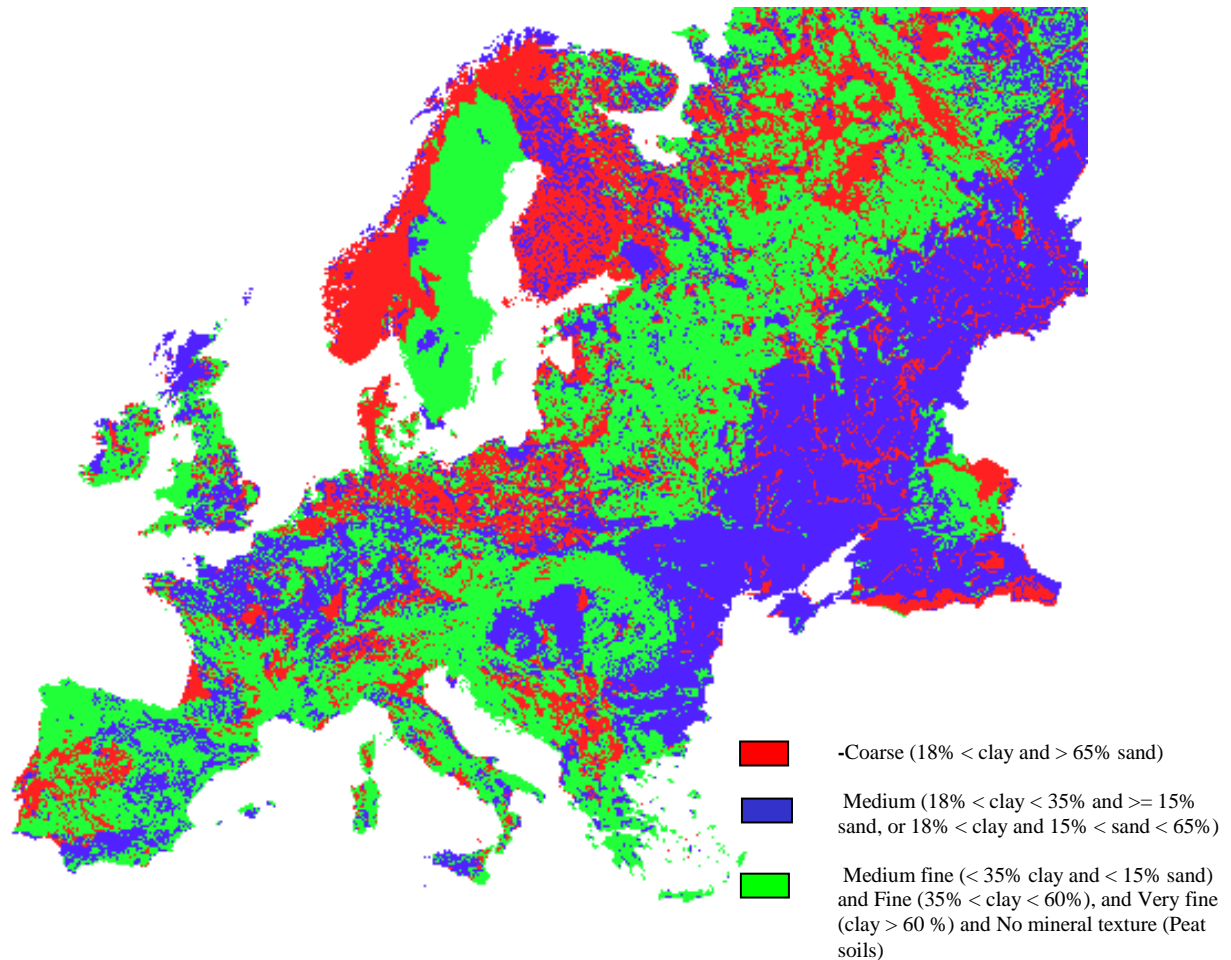


Figure 4.2.1-3: Dominant Surface Textural map throughout Europe (source: European Soil Database version 2 (JRC, 2010) http://eusoils.jrc.ec.europa.eu/ESDB_Archive/raster_archive/ESDBv2_ETRS_LAEA_raster_archive.html)

Reproduction strategy

M. enterolobii reproduces by obligate mitotic parthenogenesis and is a polyploid organism ($2n=44-46$). Therefore, one second-stage juvenile can start a new population as it reproduces without sex (Yang & Eisenback, 1983). Within a greenhouse, it completes one generation every 4-6 weeks. Under field conditions in southern Europe, the maximum number of generations is estimated (at 20°C with a 6 week generation time) at about 4-6 per year (Karssen & Moens, 2006). *Meloidogyne* spp. females are able to lay 100 – 500 eggs (Enneli & Toros, 1995, CABI, 2007).

4.2.1.2 Model 1: Population dynamics model (SLG)

For the SLG it is assumed that an initial population abundance N_0 (%) is introduced in each suitable cell (cells where $EI > 0$) and then we simulate the “spread” or more precisely the growth within each cell according to a logistic function. On the output map, we will see areas which are the most suitable for the population growth if some individuals were introduced there.

Estimates of parameters

- **The starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

Calculation:

$N_0 = 100 * \frac{n_0}{K}$ with n_0 the number of introduced individuals, in each suitable cell, and

K the carrying capacity (the maximum number of individuals in a cell).

$K = \text{area_cell (km}^2) * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2)$,
or

$K = \text{area_cell (km}^2) * \text{host_plant_density (/km}^2) * \text{max_population_density (/host plant)}$

Relevant information and data

There is a difference between the carrying capacity on different hosts but here we will take the maximum abundance on tomato plants (Britto et al. 2007b) –395559 eggs and juveniles per plant (respectively per 1 m²).

We therefore assumed the maximum population density ($\text{max_population_density/host plant}$) = 396000 eggs and juveniles per plant.

Calculation of the carrying capacity K :

After Britto et al. 2007b

K per m ² Pf per tomato plant at the end of the season	K per km ²	K per grid cell 1579 km ²
3.96x10 ⁵	3.96x10 ¹¹	6.24x10 ¹⁴

$K = 396,000$ nematodes/plant; 1 tomato plant / m² = 396,000 nematodes/m²

$K = 396,000$ nematodes/m² x 10⁶m² (transfer m² to km²) x 1579 km² (grid cell)

$K = 6.24 \times 10^{14}$ nematodes / grid cell

Calculation of N_0 :

The starting number of nematodes ($=n_0$) for a new population can just be one second-stage juvenile. *M. enterolobii* females are able to lay 100 – 800 eggs (Karssen, pers. comm., 2009).

Here we take the number of eggs/juvenile found in samples (Starting number of nematodes $n_0 = 56,740$ nematodes (see above, this is based on the number of eggs and juveniles found and approximately 200 eggs per female).

$N_0 = 100 \times \text{starting number } n_0 / K = \%$

$N_0 = 100 \times 56740 / 6.24 \times 10^{14} = 9.09 \times 10^{-9}$

$N_0 = 9.1 \times 10^{-9} \%$

Capturing uncertainty

For capturing the uncertainty, we also tried models with half and double the initial density respectively: $N_0 = 4.5 \times 10^{-9} \%$ and $N_0 = 1.82 \times 10^{-8} \%$.

- **The multiplication factor λ_{max}**

λ_{max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

Relevant information and data:

Starr et Jeger (1985) investigated the overwintering of several populations of tropical root-knot nematodes and found that the average survival was 8.9% with a maximum of 33% in some of the populations. In our case if we used max Rf = 109.2 (Kleinwick et al., 2009) at the end of the season and 8.9% winter survival, then $\lambda_{max} = 9.7$

- **Time frame: 10 and 20 years**

Results:

Results for SLG Model based on CLIMEX Model on *M. javanica* for 10 and 20 years

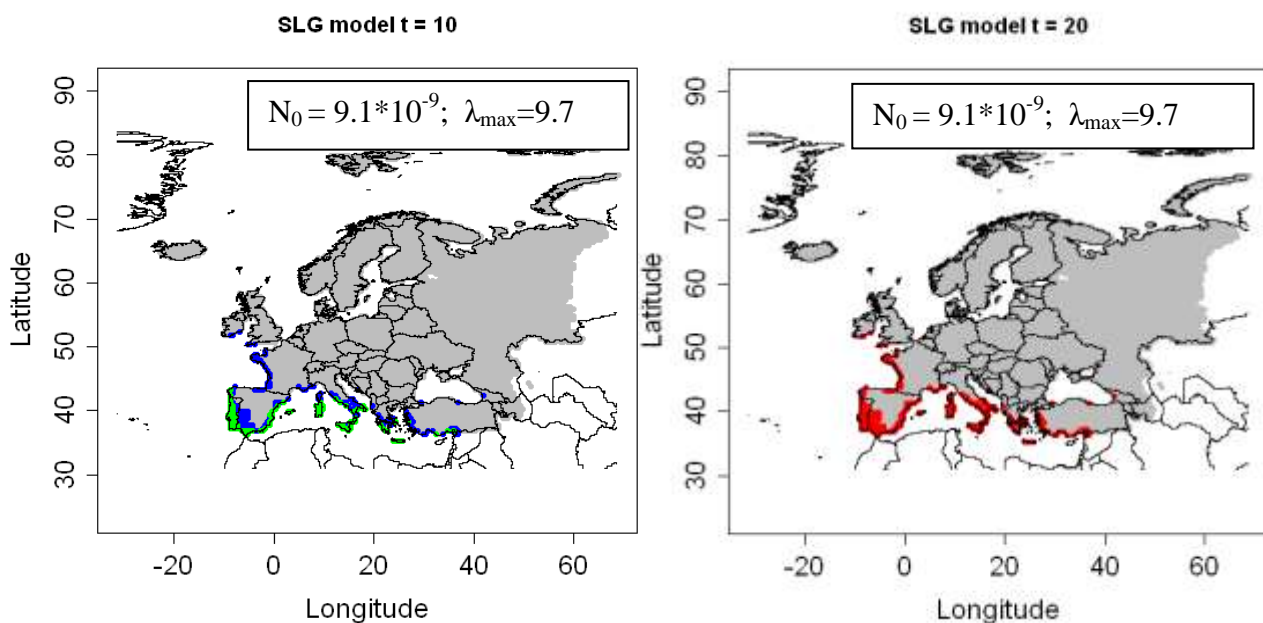


Figure 4.2.1-4: Output of the SLG model for *M. javanica* for 10 and 20 years, based a CLIMEX model by Zhenya Ilieva (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Sensitivity analysis / capturing uncertainty: SLG for different N_0 -values

The sensitivity analysis shows (figures 4.2.1-5 and 4.1.2-6), that the value of N_0 affects the results only for the time frame of 10 years. After 20 years all the suitable areas are already infested – independently of the N_0 -value. To find out if this will happen, different time frames could be tested (e.g. 15 years).

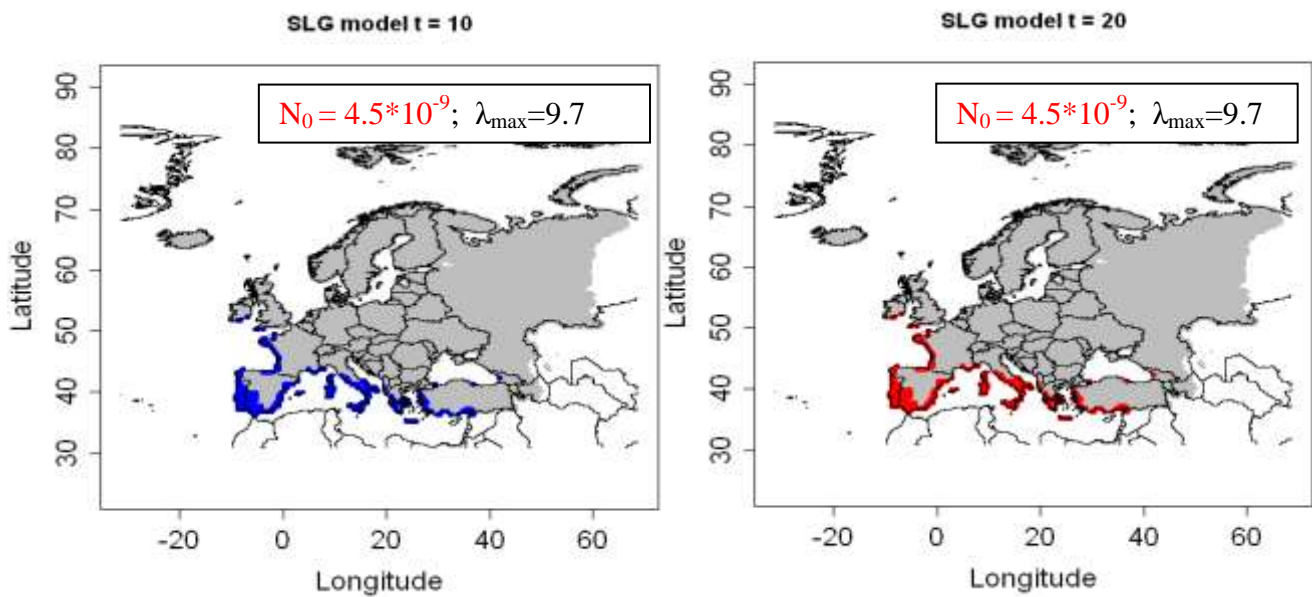


Figure 4.2.1-5: Output of the SLG model for *M. javanica* for 10 and 20 years with a lower value for N_0 , based on a CLIMEX model by Zhenya Ilieva (blue dots: $0 < Nt < = 25$, green dots: $25 < Nt < = 50$, orange dots: $50 < Nt < = 75$, red dots: $75 < Nt < = 100$, grey dots: $Nt=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=4.5*10^(-9),lmax=9.7, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=4.5*10^(-9),lmax=9.7, t=20)`

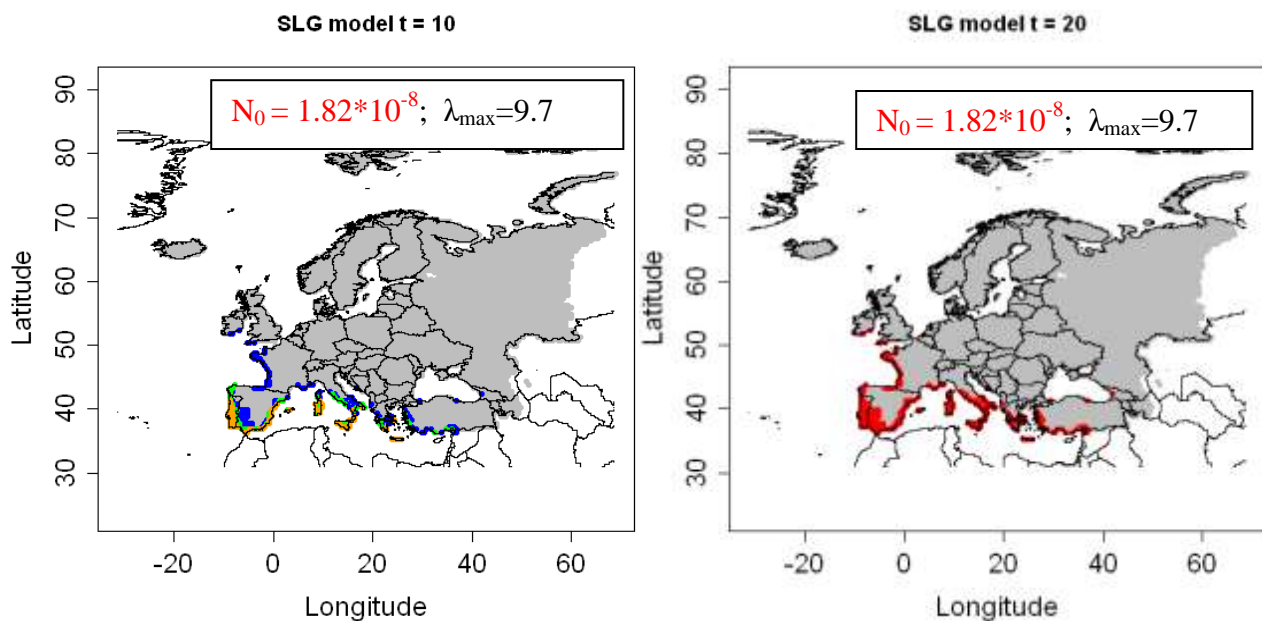


Figure 4.2.1-6: Output of the SLG model for *M. javanica* for 10 and 20 years with a higher value for N_0 , based on a CLIMEX model by Zhenya Ilieva (blue dots: $0 < Nt < = 25$, green dots: $25 < Nt < = 50$, orange dots: $50 < Nt < = 75$, red dots: $75 < Nt < = 100$, grey dots: $Nt=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=1.82 *10^(-8),lmax=9.7, t=10).`

Right Picture: 20 years; R:> `res = slg(N0=1.82*10^(-8),lmax=9.7, t=20)`

Sensitivity analysis / capturing uncertainty: SLG for different λ_{\max} - values

The sensitivity analysis shows (figures 4.2.1-7 and 4.2.1-8), that using SLG model with half and double λ_{\max} - values affects the results only for the time frame of 10 years. After 20 years all the suitable areas are already infested – independently of the λ_{\max} – values.

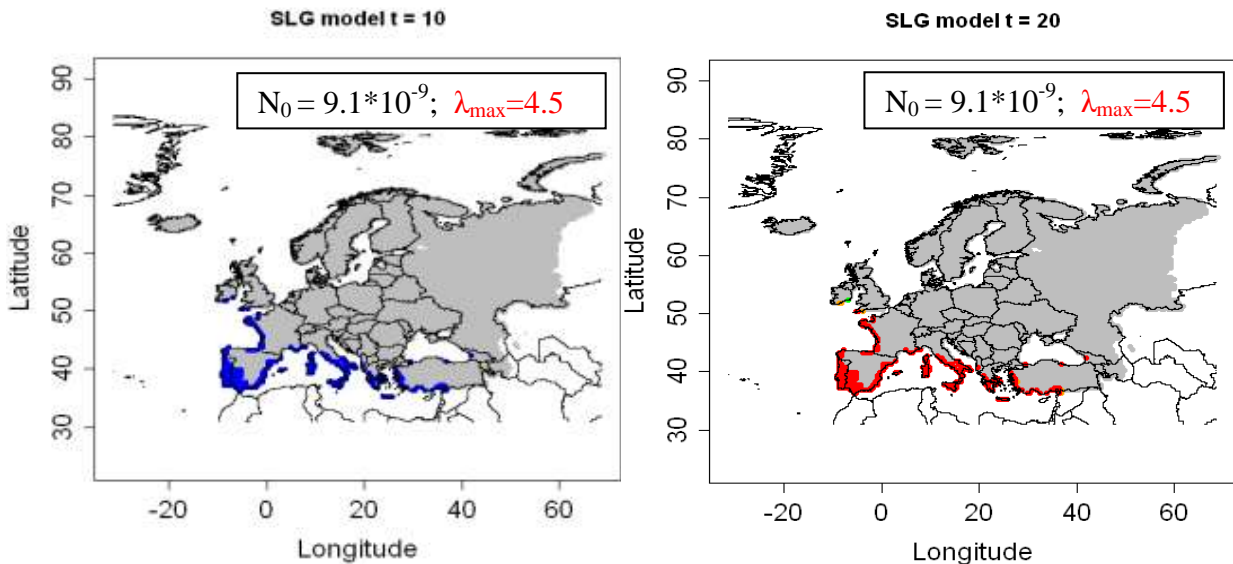


Figure 4.2.1-7: Output of the SLG model for *M. javanica* for 10 and 20 years with a lower value for λ_{\max} , based on a CLIMEX model by Zhenya Ilieva (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=9.1 * 10^(-9),lmax=4.5, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=9.1 * 10^(-9),lmax=4.5, t=20)`

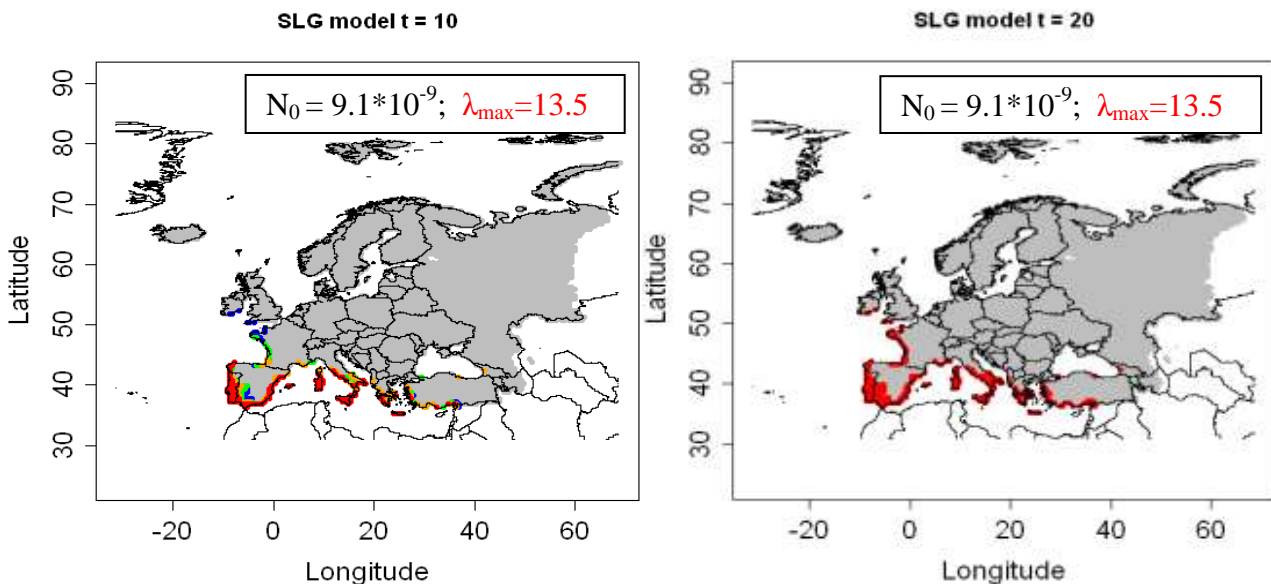


Figure 4.2.1-8: Output of the SLG model for *M. javanica* for 10 and 20 years with a higher value for λ_{\max} , based on a CLIMEX model (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=9.1 * 10^(-9),lmax=13.5, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=9.1 * 10^(-9),lmax=13.5, t=20)`

Results for SLG Model for CLIMEX Model on *M. incognita* for 10 and 20 years

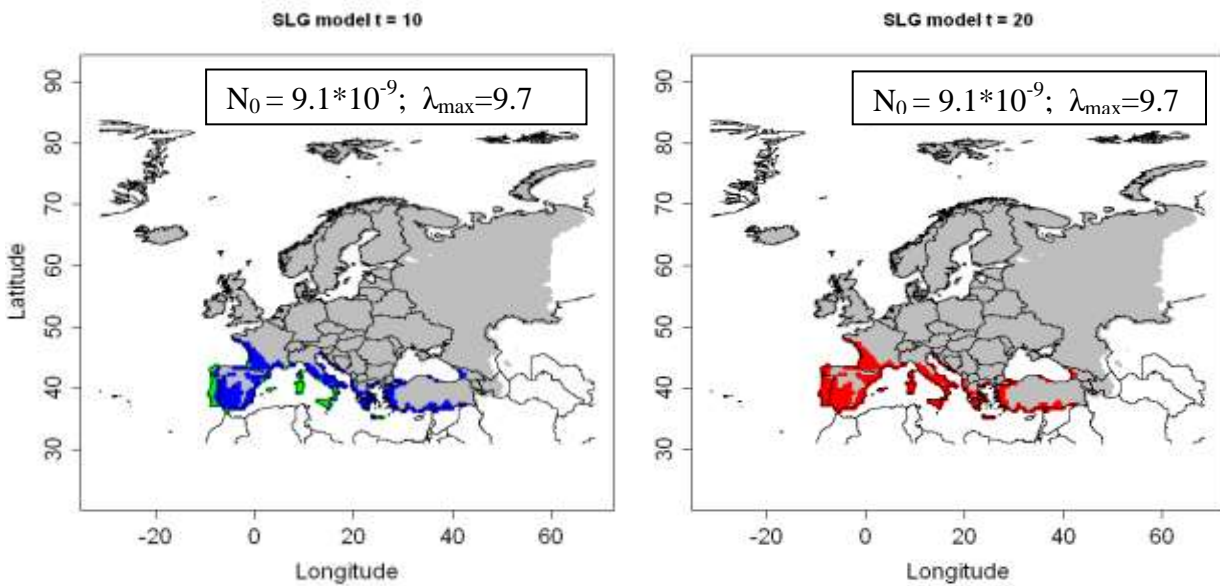


Figure 4.2.1-9: Output of the SLG model for *M. incognita* for 10 and 20 years, based on a CLIMEX model by Zhenya Ilieva (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=9.1*10^(-9),lmax=9.7, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=9.1*10^(-9),lmax=9.7, t=20)`

Sensitivity analysis / capturing uncertainty: SLG model different λ_{max} -values

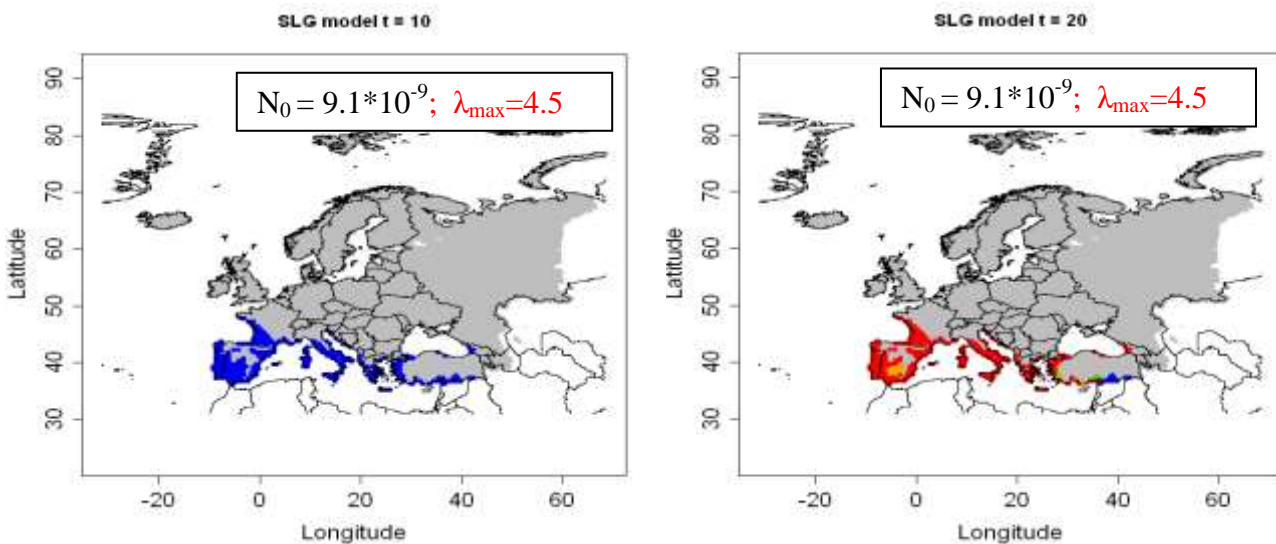


Figure 4.2.1-10: Output of the SLG model for *M. incognita* for 10 and 20 years, based on a CLIMEX model (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=9.1*10^(-9),lmax=4.5, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=9.1*10^(-9),lmax=4.57, t=20)`

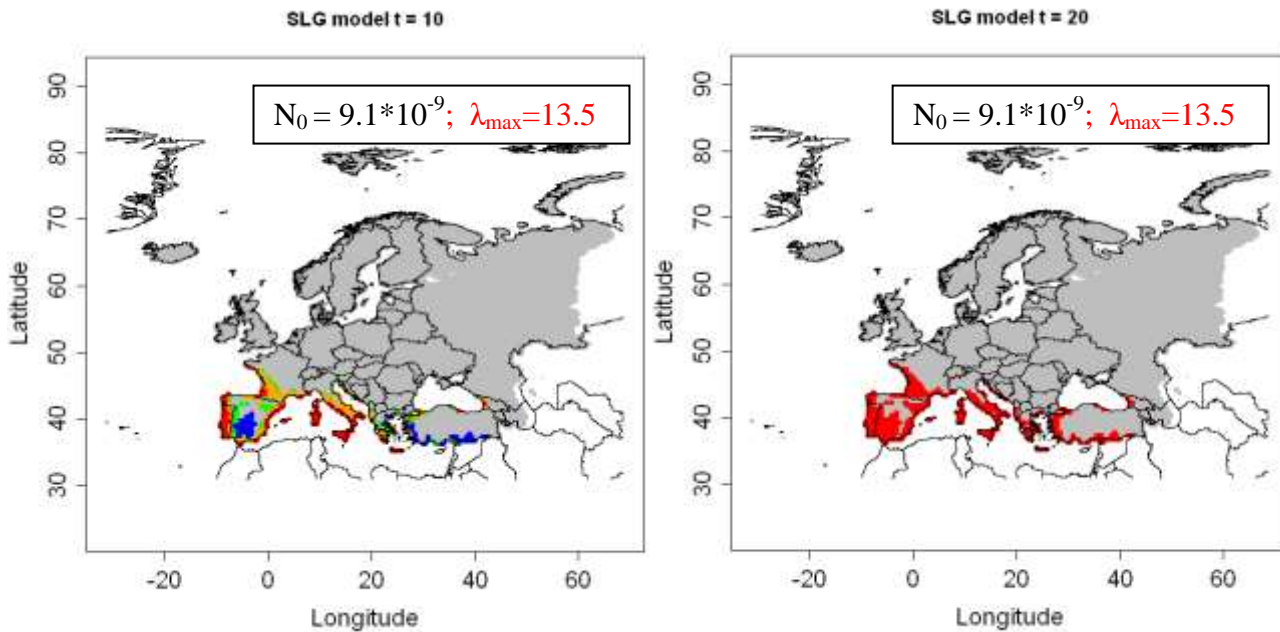


Figure 4.2.1-11: Output of the SLG model for *M. incognita* for 10 and 20 years, based a CLIMEX model by Zhenya Ilieva (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 year ; R:> `res = slg(N0=9.1*10-9,lmax=13.5,7, t=10)`

Right Picture: 20 years; R:> `res = slg(N0=9.1*10-9,lmax=13.5, t=20)`

Feedback on the SLG results by the expert Zhenya Ilieva

The model gives an indication of the population densities that might develop assuming the pest has been introduced to all grid cells in the area of potential establishment with equal initial densities and without any control measures.

The model outputs are principally dependent on the CLIMEX Ecoclimatic Index and, because of the small amount of information about development rate on other suitable hosts for *M. enterolobii* and its presence in the soil and thus subject to a microclimate that is very different to that measured at weather stations, the accuracy is likely to be low. When selecting appropriate initial densities, it is important to take into account the likelihood that at very high initial densities the plant could die and in so doing have a major effect on population density.

Using this model with half and double N_0 - or λ_{max} - values resulted in different number of invaded cells after 10 years but there was no difference after 20 years of simulation for both CLIMEX models (for *M. javanivca* and *M. incognita*). The results for the 20th year seem overestimated.

The method is not very suitable for sedentary parasitic nematodes.

4.2.1.3 Model 3: Radial range expansion model (RR)

This model aims to determine the potential spread of a species introduced in the PRA area based on the radial rate expansion parameter. The model output is overlapped with the niche map ($EI > 0$).

Estimates of parameters

- **Radial rate of range expansion per year:**
RR = 20 km/year
This value reflects both natural and human assisted spread.
Considering uncertainty:
RR= 10 km/year and RR = 30 km / year were tested.
- **Time frame**
t = 10 – 20 years
for the period of 10-20
- **Entry point(s)** or simulation of an introduction at a place
 - France in Brittany (most western point) with coord = (-3.917, 47.867)
 - Switzerland (see above, findings in Europe): tropical *Meloidogyne* spp. are unlikely to survive outdoors
 - Southern Spain (-5,37)

Results

Results of the radial range expansion based on the CLIMEX model for *M. javanica*

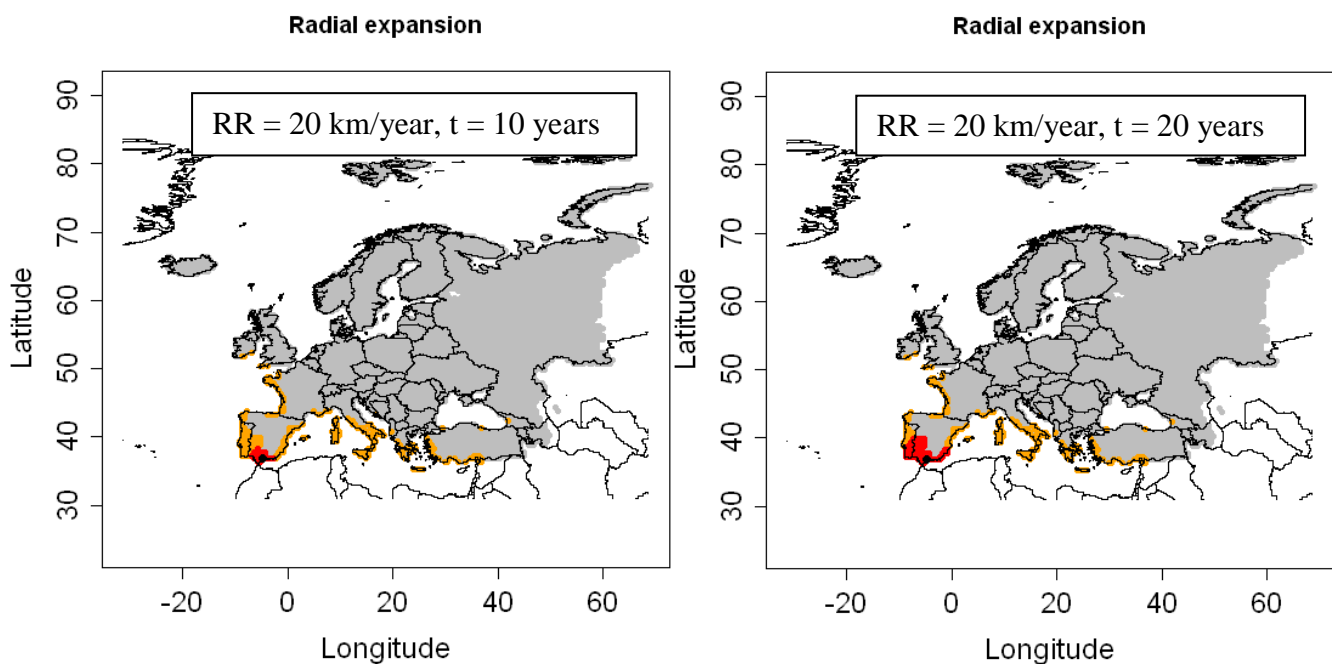


Figure 4.2.1-12: Radial range expansion of *M. enterolobii* for t=10 and 20 years, RR=20km/year and an entry point in Southern Spain based on the CLIMEX model for *M. javanica* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data)

Left picture: 10 years, R:> *res = radial(RR=10,t=20,coord=c(-5,37))*

right picture: 20 years, R:> *res = radial(RR=20,t=20,coord=c(-5,37))*

Sensitivity analysis / capturing uncertainty: testing of different RR-values

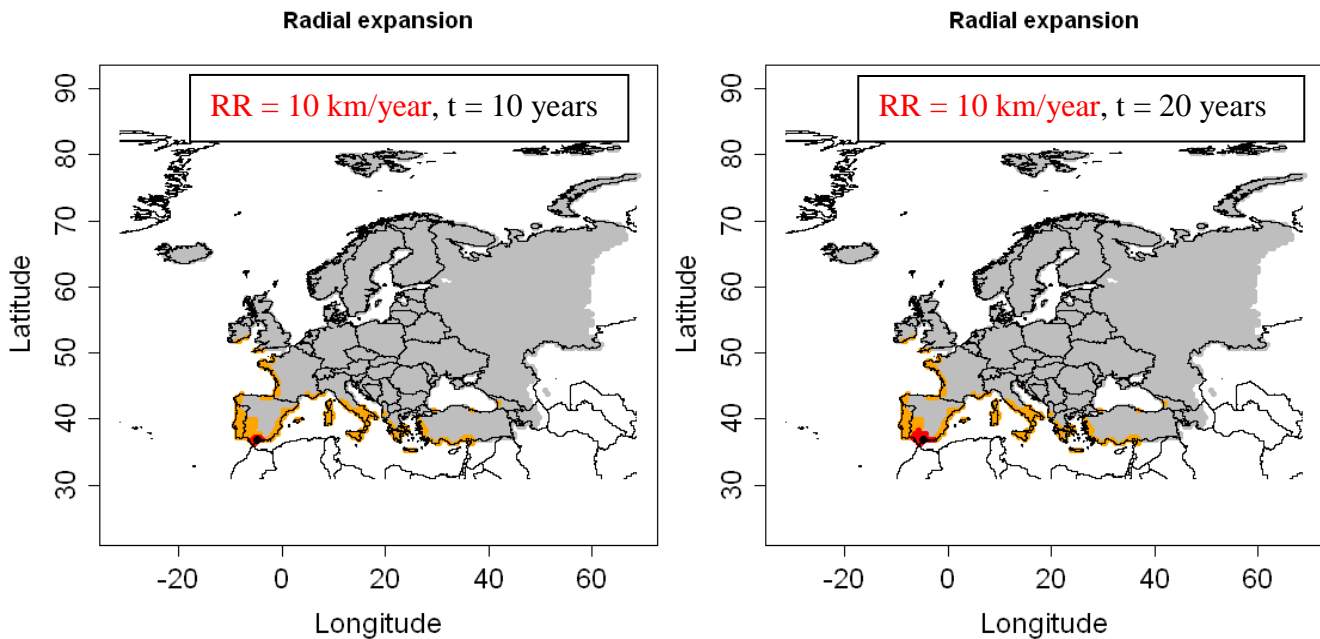


Figure 4.2.1-13: Radial range expansion of *M. enterolobii* for t=10 and 20 years, RR=10km/year and an entry point in Southern Spain based on the CLIMEX model for *M. javanica* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data)

Left picture: 10 years, R:> `res = radial(RR=10,t=10,coord=c(-5,37))`
 right picture: 20 years, R:> `res = radial(RR=10,t=20,coord=c(-5,37))`

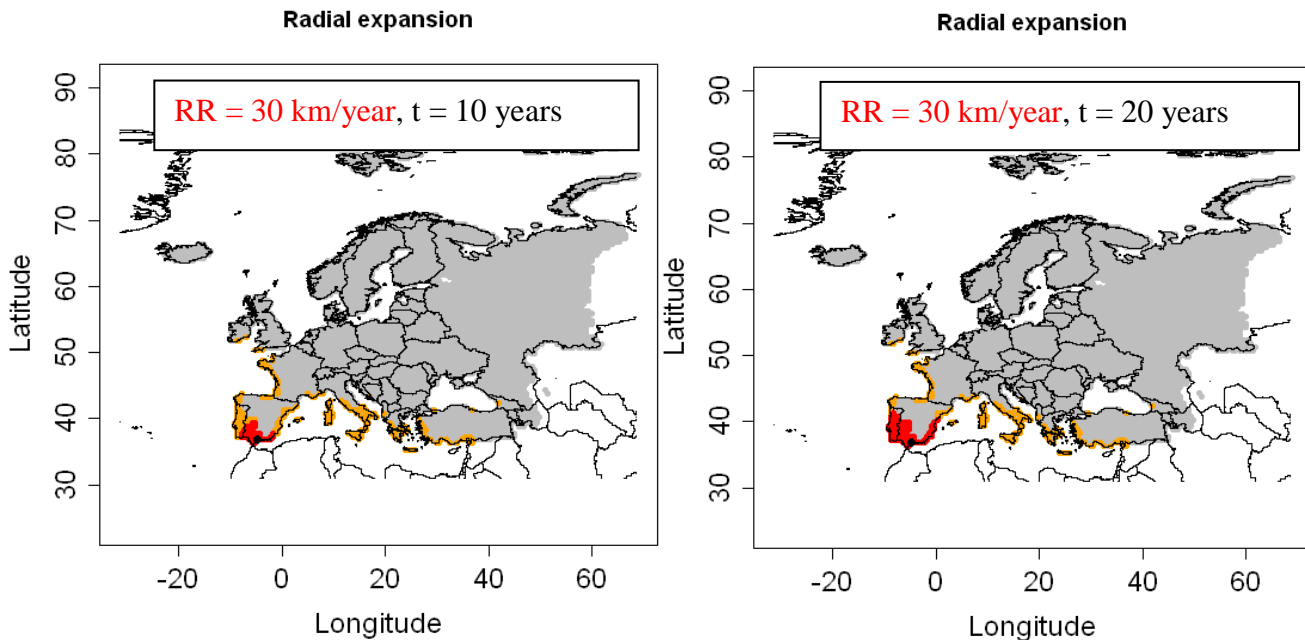


Figure 4.2.1-14: Radial range expansion of *M. enterolobii* for t=10 and 20 years, RR=30km/year and an entry point in Southern Spain based on the CLIMEX model for *M. javanica* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data)

Left picture: 10 years, R:> `res = radial(RR=30,t=10,coord=c(-5,37))`
 right picture: 20 years, R:> `res = radial(RR=30,t=20,coord=c(-5,37))`

Results of the radial range expansion based on the CLIMEX model for *M. incognita*

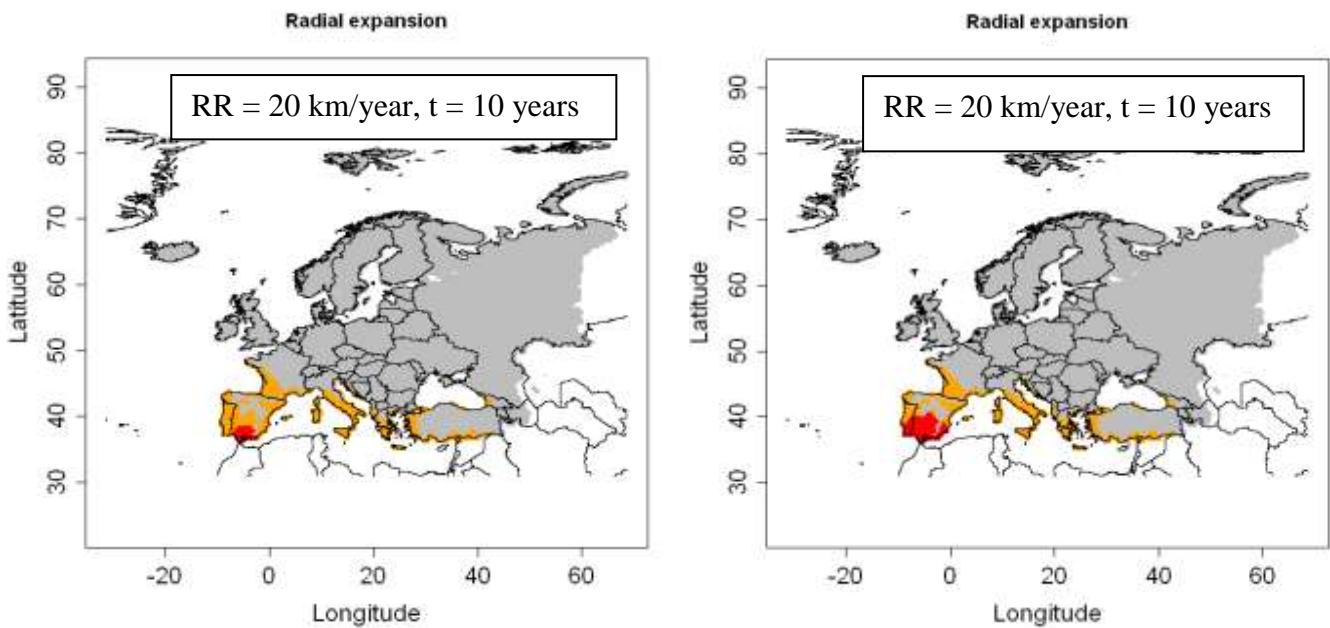


Figure 4.2.1-15: Radial range expansion of *M. enterolobii* for $t=10$ and 20 years, $RR=20$ km/year and an entry point in Southern Spain based on the CLIMEX model for *M. incognita* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data)

Left picture: 10 years, $R:> res = radial(RR=20,t=10,coord=c(-5,37))$

right picture: 20 years, $R:> res = radial(RR=20,t=20,coord=c(-5,37))$

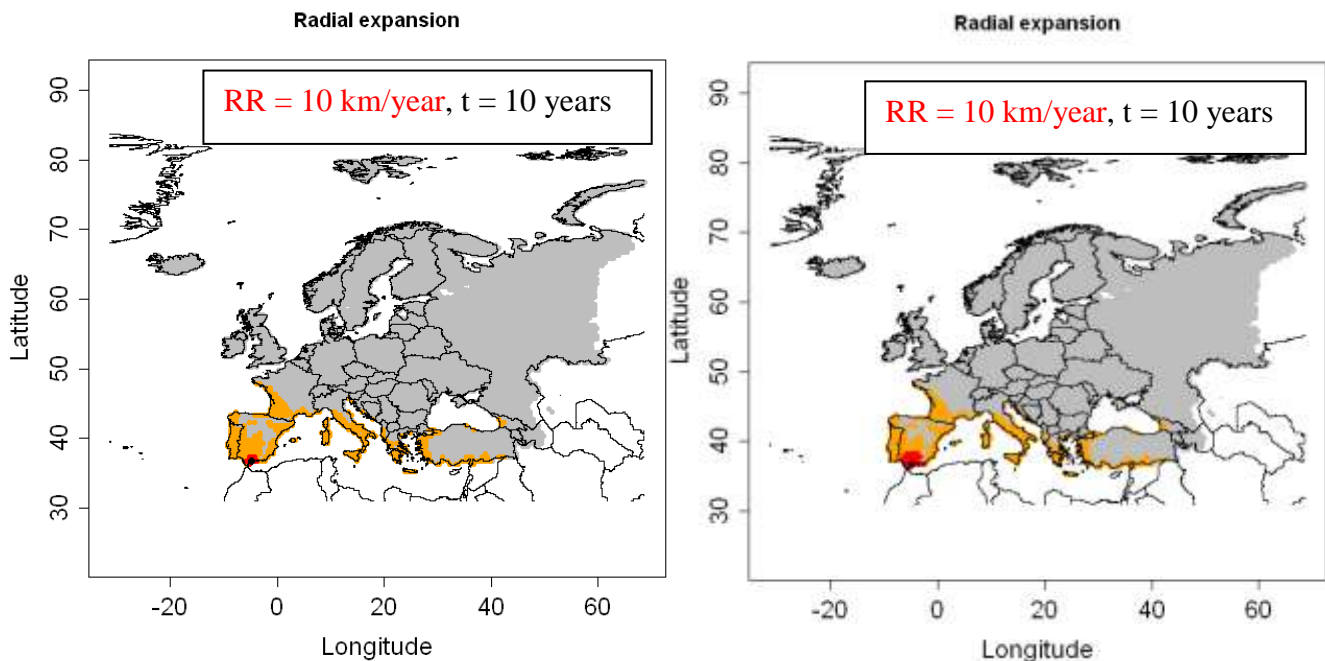


Figure 4.2.1-16: Radial range expansion of *M. enterolobii* for $t=10$ and 20 years, $RR=10$ km/year and an entry point in Southern Spain based on the CLIMEX model for *M. incognita* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data)

Left picture: 10 years, $R:> res = radial(RR=10,t=10,coord=c(-5,37))$

right picture: 20 years, $R:> res = radial(RR=10,t=20,coord=c(-5,37))$

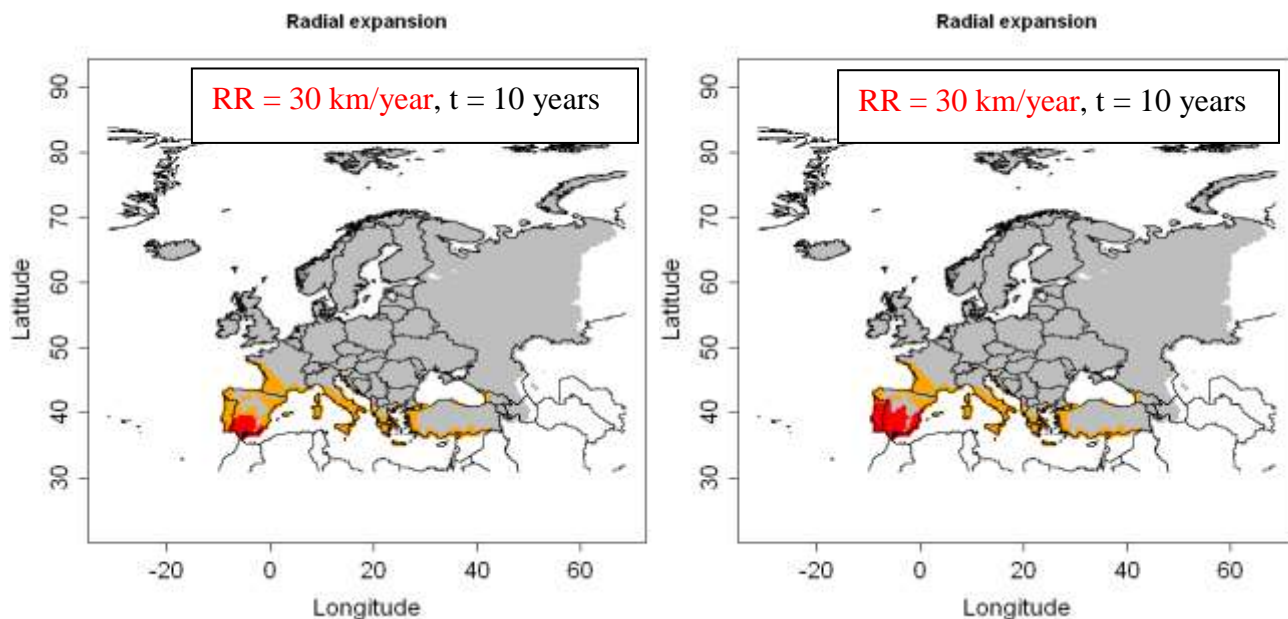


Figure 4.2.1-17: Radial range expansion of *M. enterolobii* for $t=10$ and 20 years, $RR=30\text{km/year}$ and an entry point in Southern Spain based on the CLIMEX model for *M. incognita* (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data)

Left picture: 10 years, $R:> \text{res} = \text{radial}(RR=30,t=10,coord=c(-5,37))$

right picture: 20 years, $R:> \text{res} = \text{radial}(RR=30,t=20,coord=c(-5,37))$

Feedback on the results of the radial range expansion by the expert Zhenya Ilieva

This scenario gives more realistic information about the potential spread of *Meloidogyne enterolobii*. Root-knot nematodes do not have a great dispersal potential and the range of 20 km per year is mostly due to human assisted spread (by shoes, machinery and devices). Intensity of occupation of potential territory in all variants is slower than in the SLG model type and more realistic if we consider only short distance spread of the species.

Again this model gives the worst scenario with continuous suitable hosts all over the climatically suitable area without any control measures.

4.2.1.4 Model 5: Deterministic version of the dispersal kernel model (DK)

This type of model requires: a population growth model, a dispersal kernel ($2Dt$ in this case) and the proportion of population engaged in dispersal.

Estimates of parameters

- **The starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

$$N_0 = 9.1 \times 10^{-9} \%$$

Three different values for N_0 were tested :

“normal” value $N_0 = 9.1 \times 10^{-9} \%$

Higher value $N_0 = 1.82 \times 10^{-8} \%$.

Lower value $N_0 = 4.5 \times 10^{-9} \%$

- The multiplication factor λ_{\max}
 λ_{\max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

$$\lambda_{\max} = 9$$

- **Shape parameter of the 2Dt dispersal kernel p**
(number of degrees of freedom)
For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses further than 3σ) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail; individuals disperse at short distance).

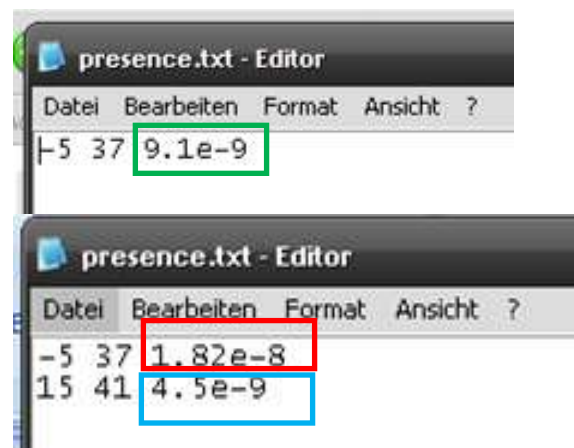
- short distance dispersal if only natural spread: $p=50$
- long distance dispersal if we also take transport of plant material into account: $p=10$

Test first the default value $p=50$, then also $p=10$

- **Scale parameter for the distance of the 2Dt dispersal kernel (u)**

Here we use $u = 20$ km (see Radial Range Expansion Model, as well 10 km and 30 km)

- **presence file**
The presence file contains the coordinates for the entry point and N_0



Results

Results based on the CLIMEX model for *M. javanica*

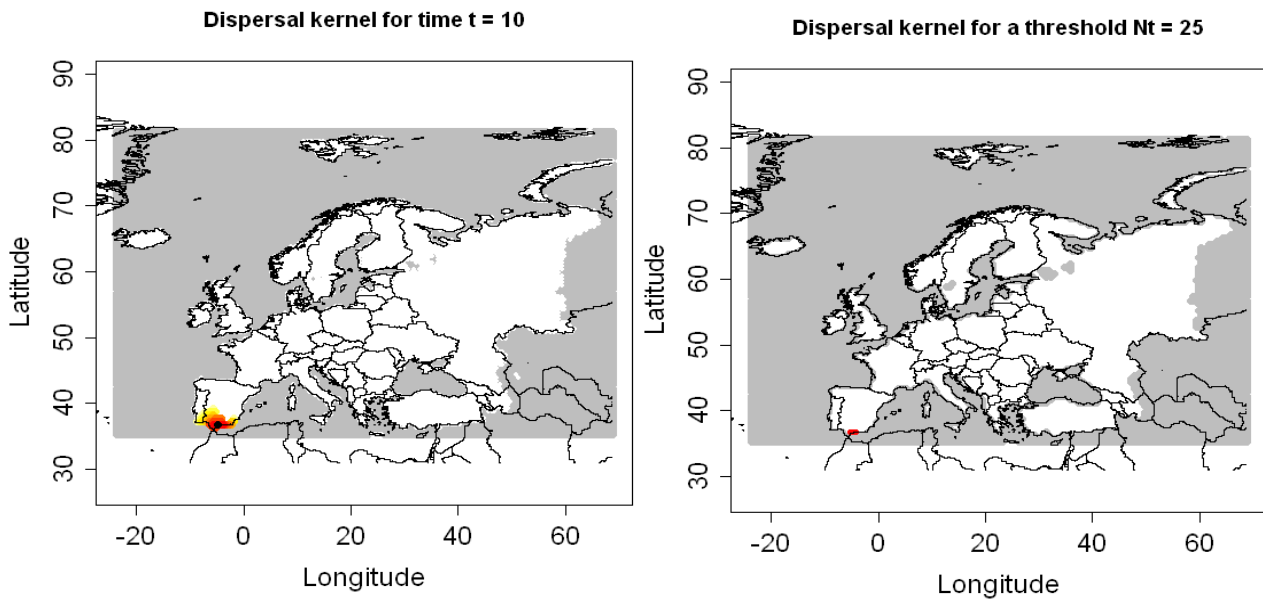


Figure 4.2.1-18: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and $\lambda_{max} = 9.7$ for 10 years ($R:> res = dispk(t=10, lmax=9.7, p=50, u=20)$). Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt ≥ 10%). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt ≥ threshold, white: cells where Nt < threshold. Grey means no data)

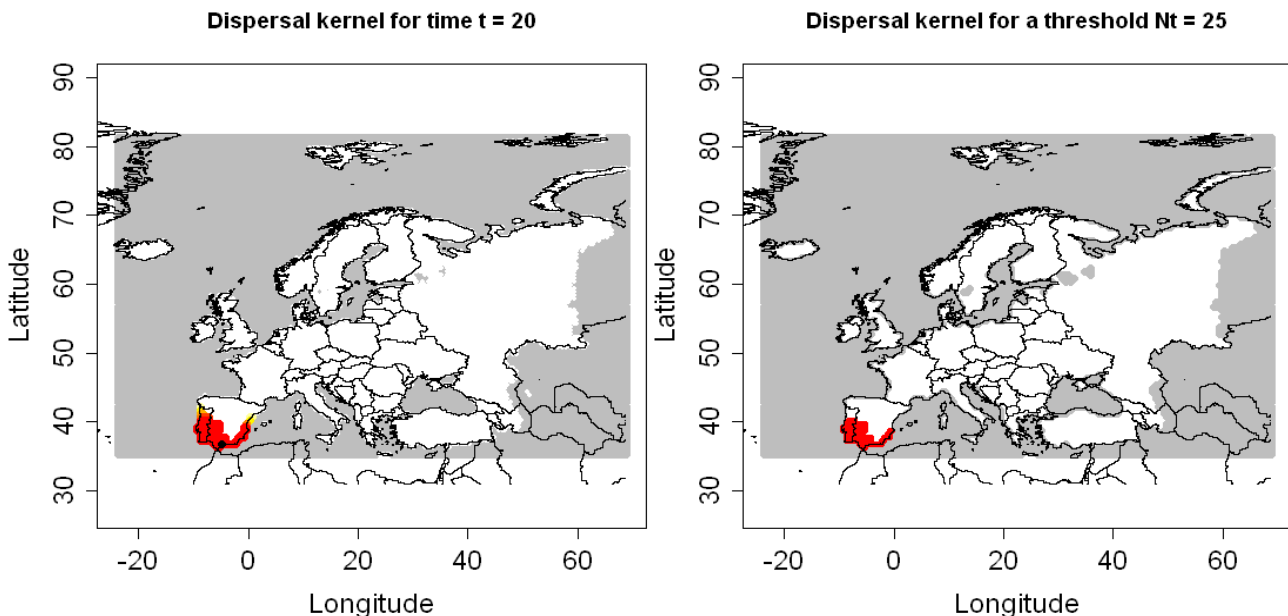


Figure 4.2.1-19: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and $\lambda_{max} = 9.7$ for 20 years ($R:> res = dispk(t=10, lmax=9.7, p=50, u=20)$). Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt ≥ 10%). Grey means no data); Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt ≥ threshold, white: cells where Nt < threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test a lower value for λ_{\max} (4.5)

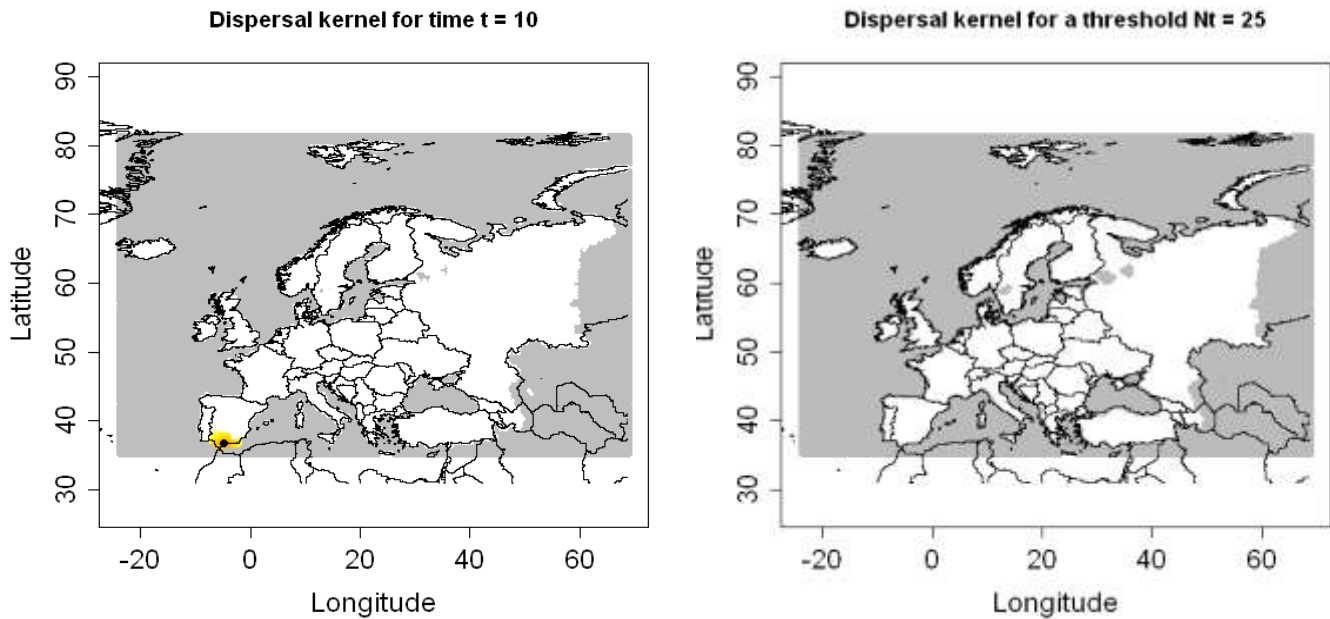


Figure 4.2.1-20: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and a lower $\lambda_{\max} = 4.5$ for 10 years ($R:> res = dispk(t=10, lmax=4.5, p=50, u=10)$). Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10^{-6} %) to yellow, orange and red (Nt $\geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt \geq threshold, white: cells where Nt < threshold. Grey means no data)

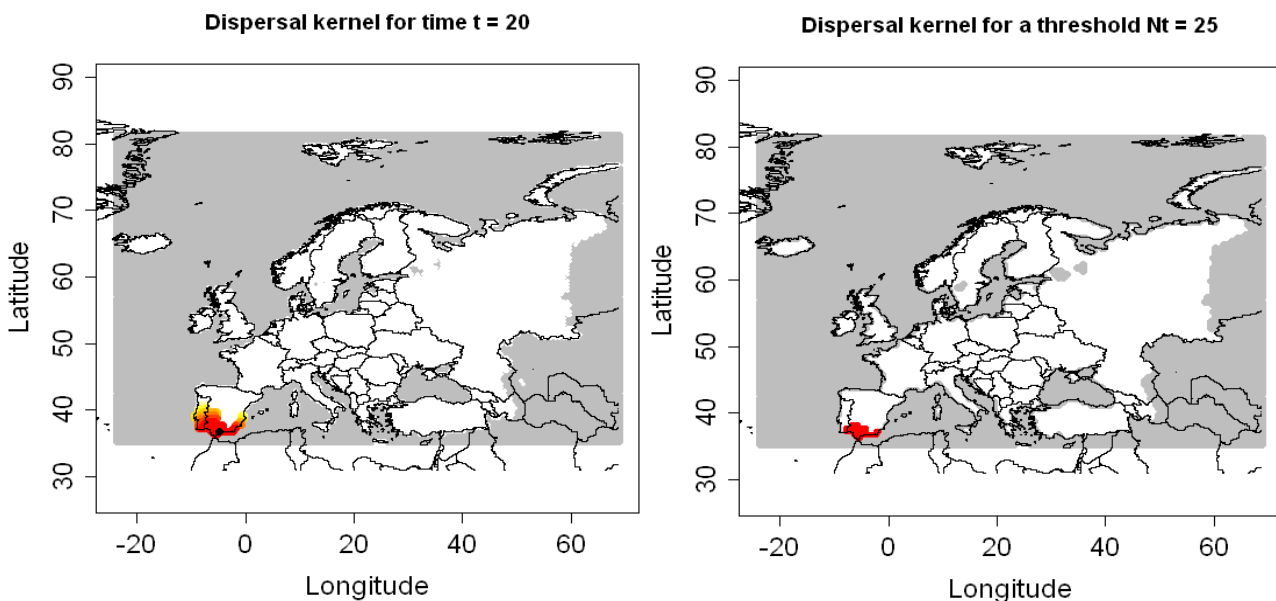


Figure 4.2.1-21: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and a lower $\lambda_{\max} = 4.5$ for 20 years ($R:> res = dispk(t=10, lmax=4.5, p=50, u=20)$). Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10^{-6} %) to yellow, orange and red (Nt $\geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt \geq threshold, white: cells where Nt < threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test a higher value for λ_{\max} (13.5)

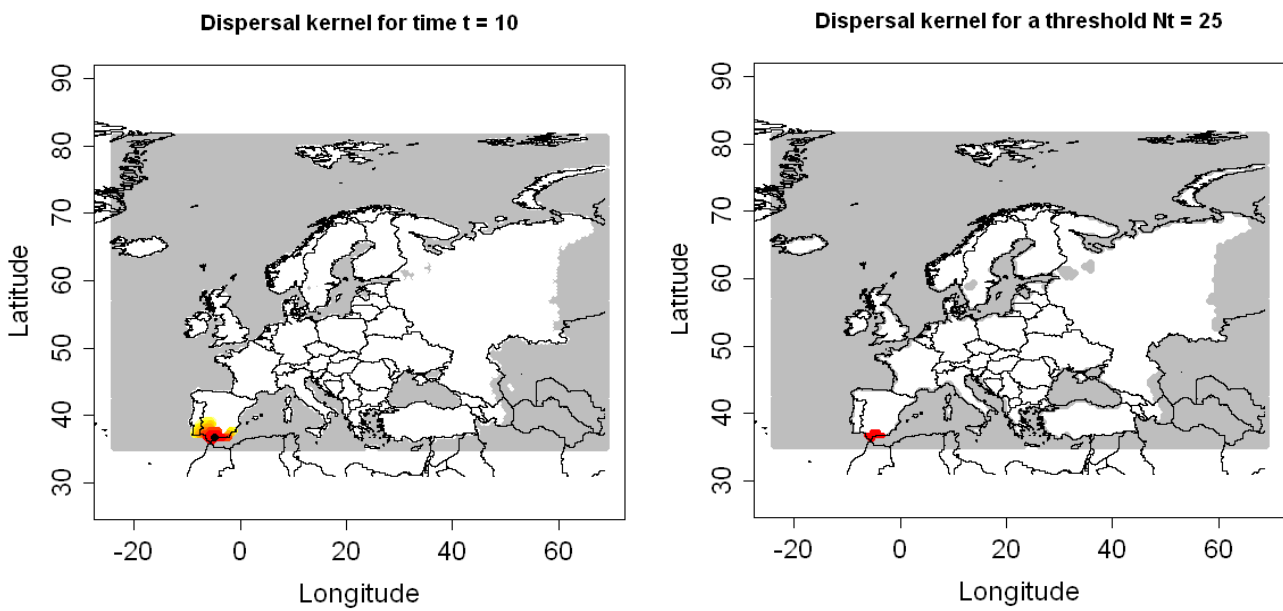


Figure 4.2.1-22: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and a higher $\lambda_{\max} = 13.5$ for 10 years; $R:> res = dispk(t=10, lmax=13.5, p=50, u=20)$. Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt >= 10%). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt >= threshold, white: cells where Nt < threshold. Grey means no data)

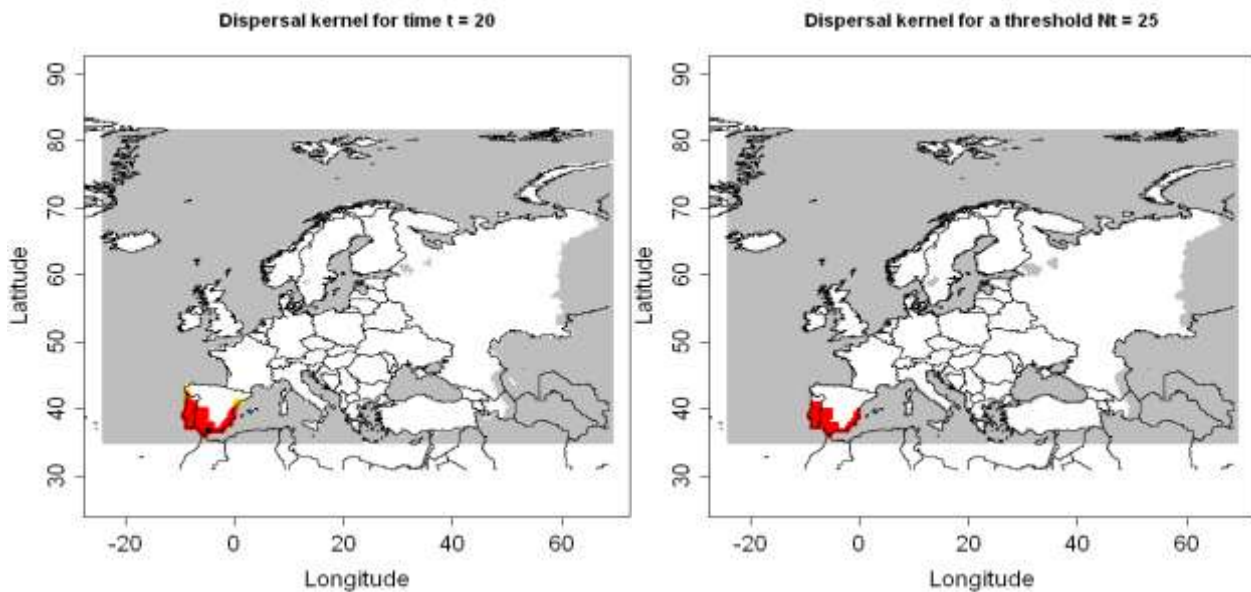


Figure 4.2.1-23: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$ and a higher $\lambda_{\max} = 13.5$ for 20 years; $R:> res = dispk(t=20, lmax=13.5, p=50, u=20)$. Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt >= 10%). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt >= threshold, white: cells where Nt < threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test of lower and higher values for N_0

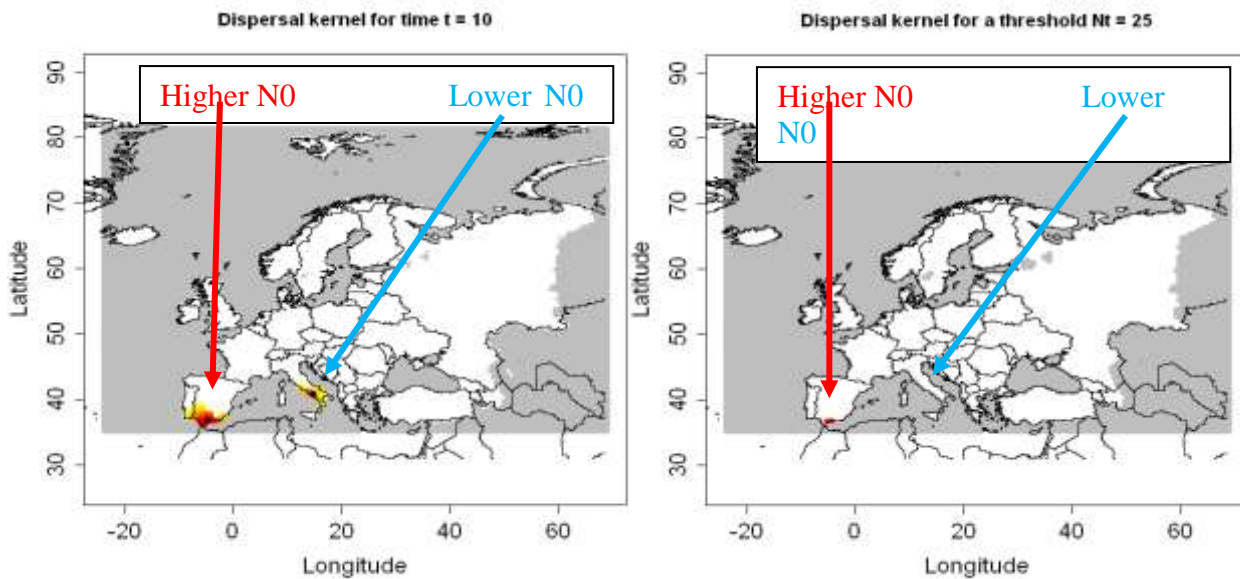


Figure 4.2.1-24: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica* with two different starting point: Spain with a higher $N_0 = 1.82 \cdot 10^{-8}$ and Italy with a lower $N_0 = 4.5 \cdot 10^{-9}$ for 10 years; $R:> res = dispk(t=10, lmax=9.7, p=50, u=20)$. Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

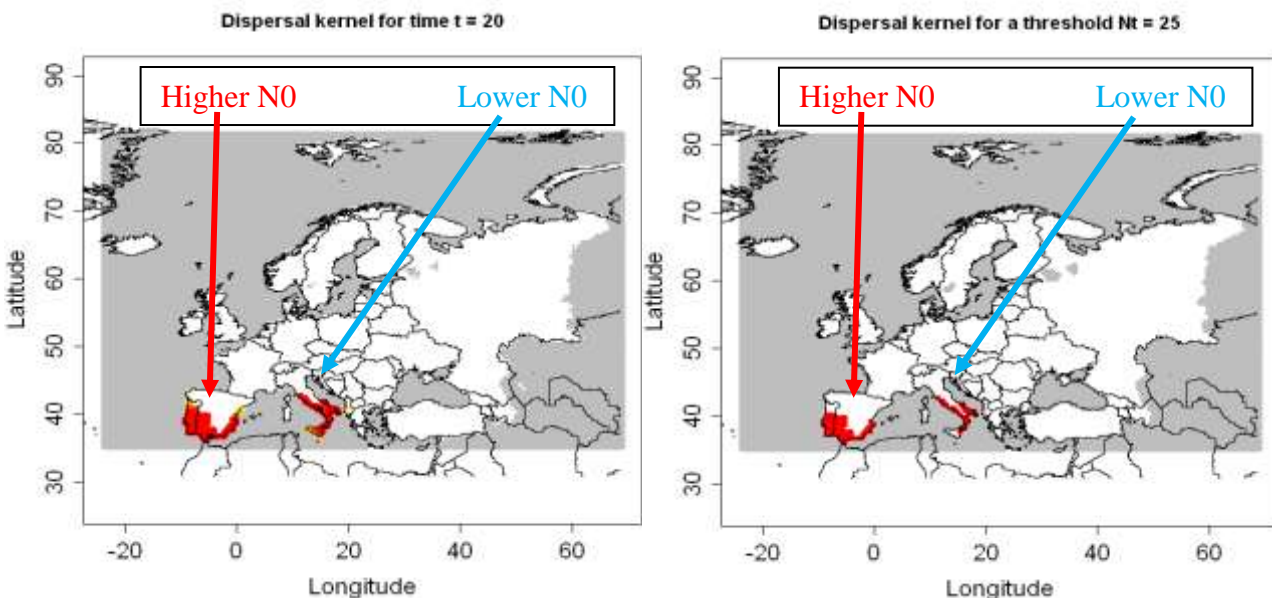


Figure 4.2.1-25: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica* with two different starting point: Spain with a higher $N_0 = 1.82 \cdot 10^{-8}$ and Italy with a lower $N_0 = 4.5 \cdot 10^{-9}$ for 20 years; $R:> res = dispk(t=20, lmax=9.7, p=50, u=20)$. Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test a higher value for u

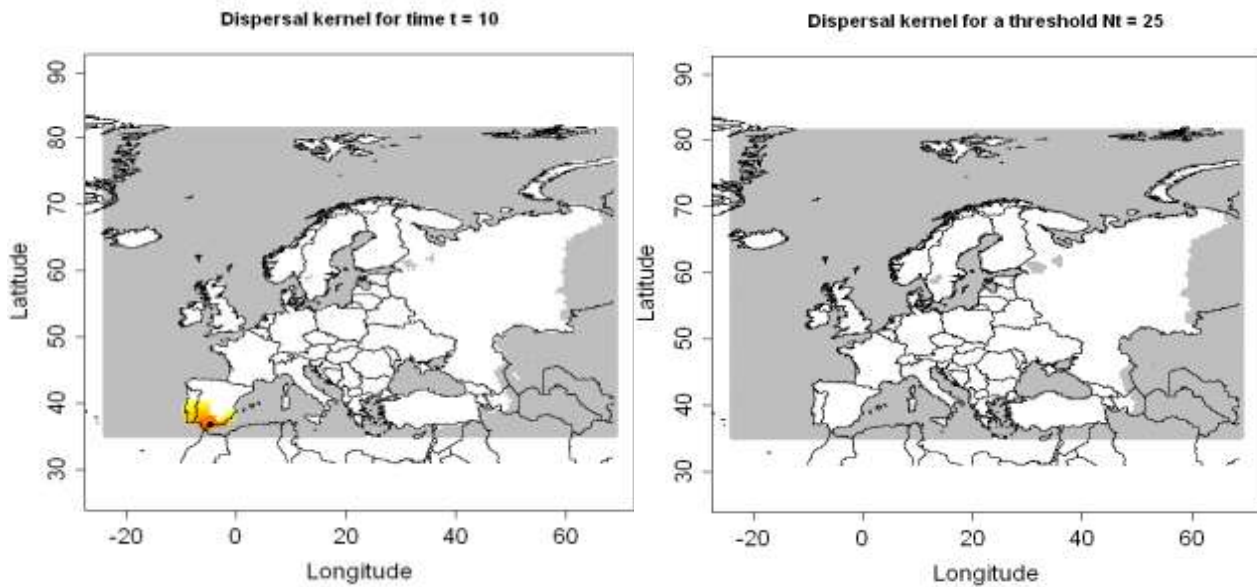


Figure 4.2.1-26: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$ and $u = 30$ km for 10 years; R:> `res = dispk(N0=NULL, t=10,lmax=9.7, p=50,u=30, presencefile=T, nentry=NULL, figkm=F,figdd=T)`.

Left Picture: (Nt: population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

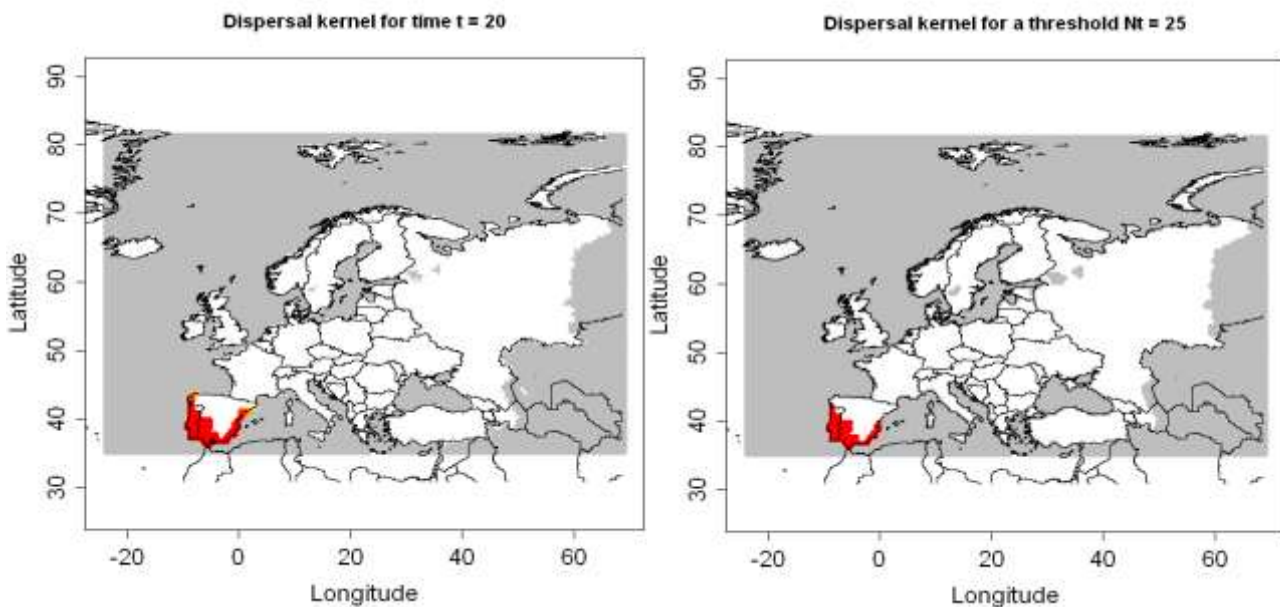


Figure 4.2.1-27: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$ and $u = 30$ km for 20 years; R:> `res = dispk(N0=NULL, t=20,lmax=9.7, p=50,u=30, presencefile=T, nentry=NULL, figkm=F,figdd=T)`

Left Picture: (Nt: population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis: test a small p for taking into account long distance spread

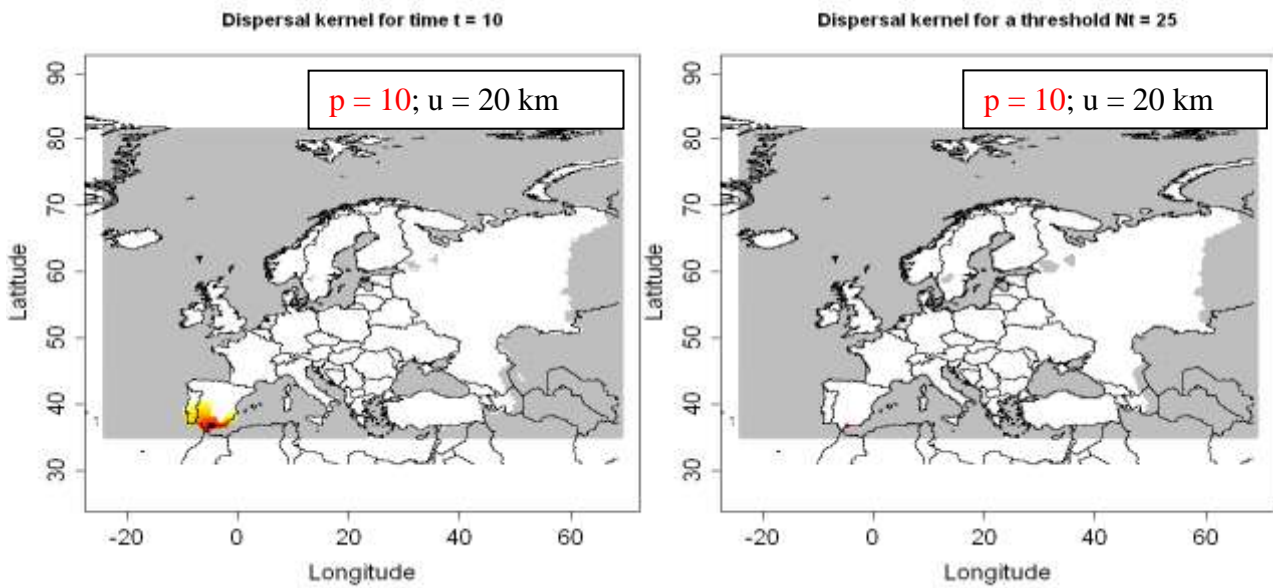


Figure 4.2.1-28: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km and $p=10$ for 10 years; R:> `res = dispk(N0=NULL, t=10,lmax=9.7, p=10,u=20, presencefile=T, nentry=NULL, figkm=F,figdd=T)`
Left Picture: (Nt: population abundance (%); graduated colors from white ($Nt < 10^{(-6)}$ %) to yellow, orange and red ($Nt \geq 10\%$). Grey means no data)
Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $Nt \geq$ threshold, white: cells where $Nt <$ threshold. Grey means no data)

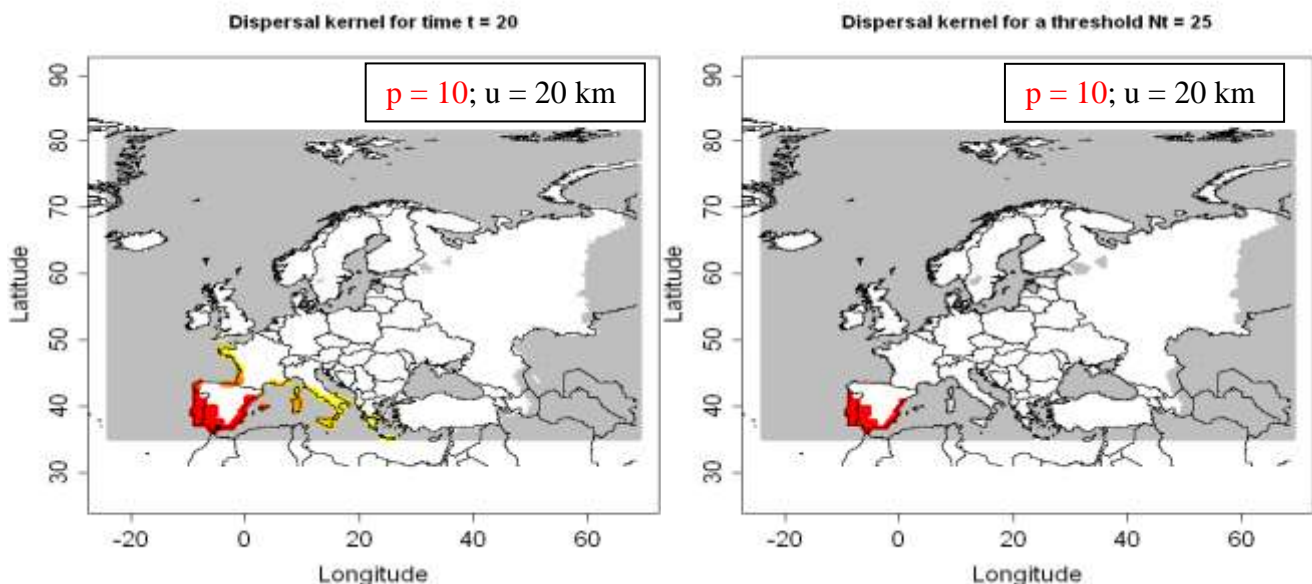


Figure 4.2.1-29: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km and $p=10$ for 20 years; R:> `res = dispk(N0=NULL, t=20,lmax=9.7, p=10,u=20, presencefile=T, nentry=NULL, figkm=F,figdd=T)`
Left Picture: (Nt: population abundance (%); graduated colors from white ($Nt < 10^{(-6)}$ %) to yellow, orange and red ($Nt \geq 10\%$). Grey means no data)
Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $Nt \geq$ threshold, white: cells where $Nt <$ threshold. Grey means no data)

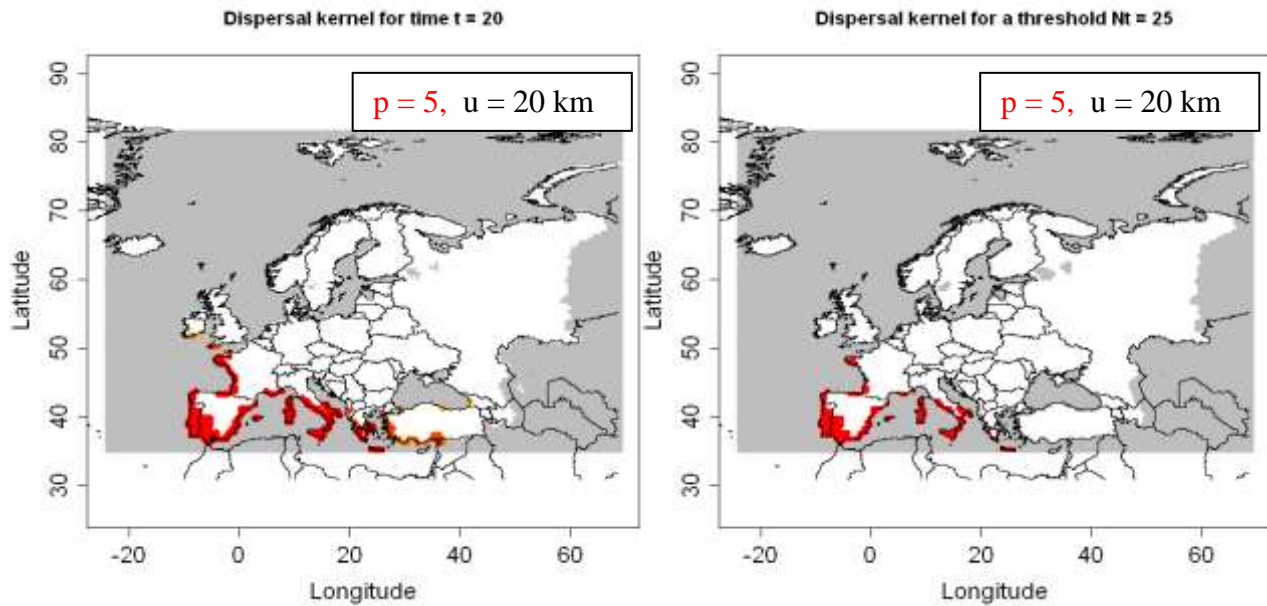


Figure 4.2.1-30: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. javanica*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km and $p=5$ for 20 years; R:> `res = dispk(N0=NULL, t=20,lmax=9.7, p=5,u=20, presencefile=T, nentry=NULL, figkm=F,figdd=T)`

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Results based on the CLIMEX model for *M. incognita*

For *M. incognita* only the medium parameter values for N_0 and λ_{\max} were tested. For p and u one alternative value was tested for each of the two parameters.

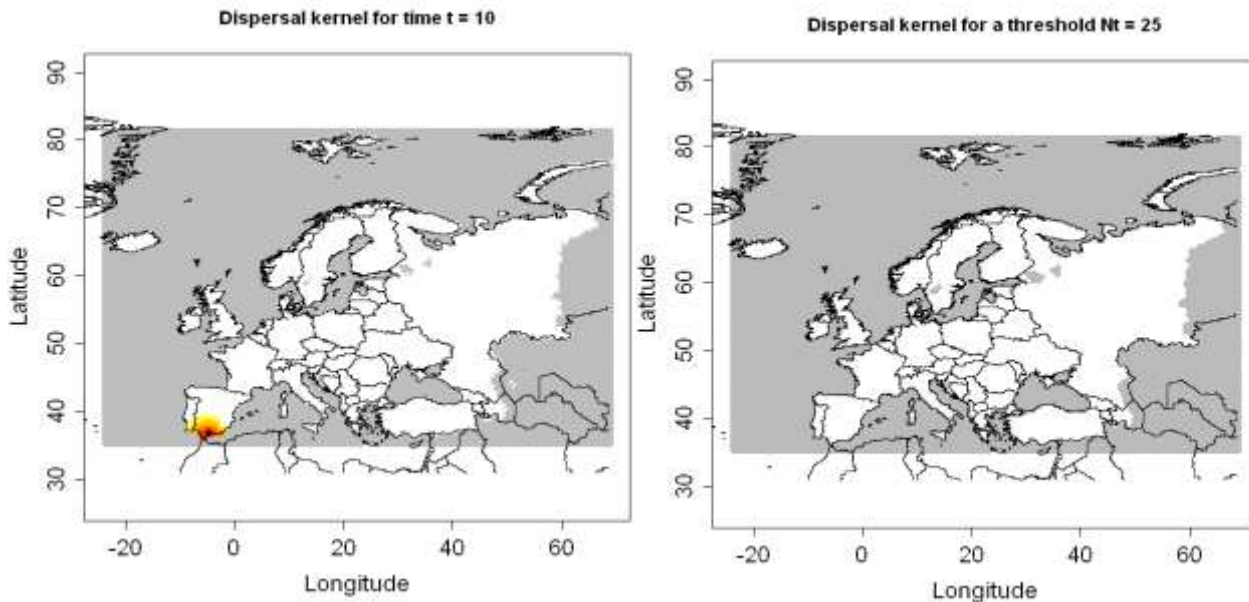


Figure 4.2.1-31: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$ and $\lambda_{\max} = 9.7$ for 10 years ($R:> res = dispk(t=10, lmax=9.7, p=50, u=20)$).

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

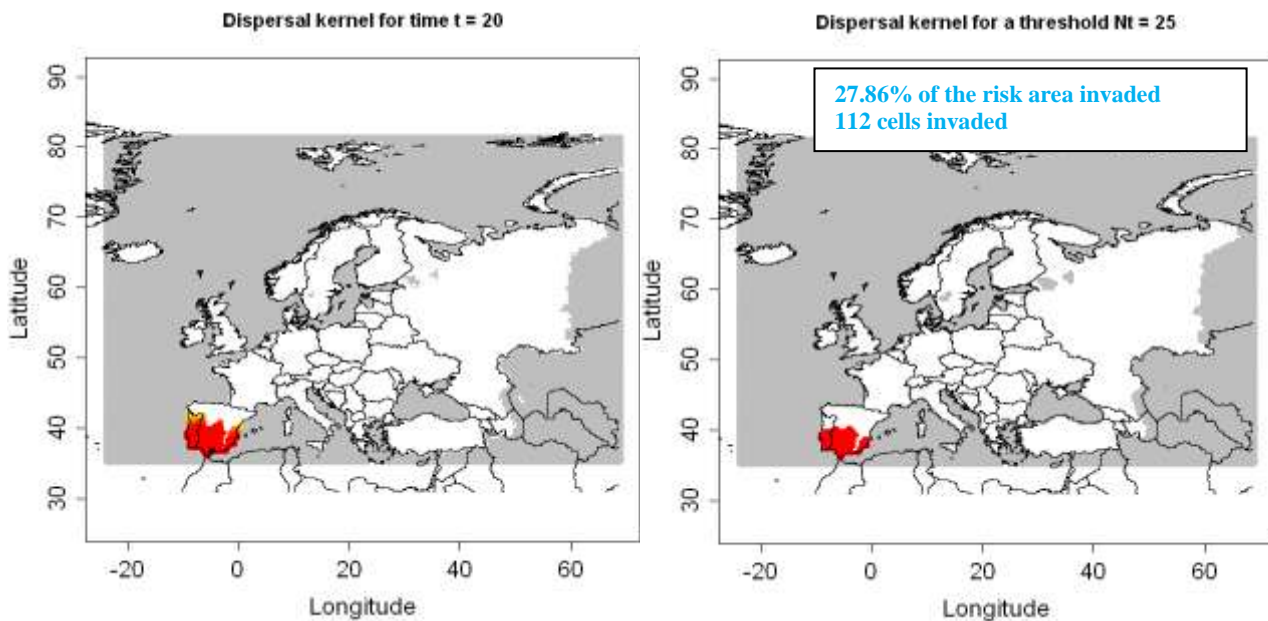


Figure 4.2.1-32: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$ and $\lambda_{max} = 9.7$ for 20 years ($R:> res = dispk(t=20, lmax=9.7, p=50, u=20)$). Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

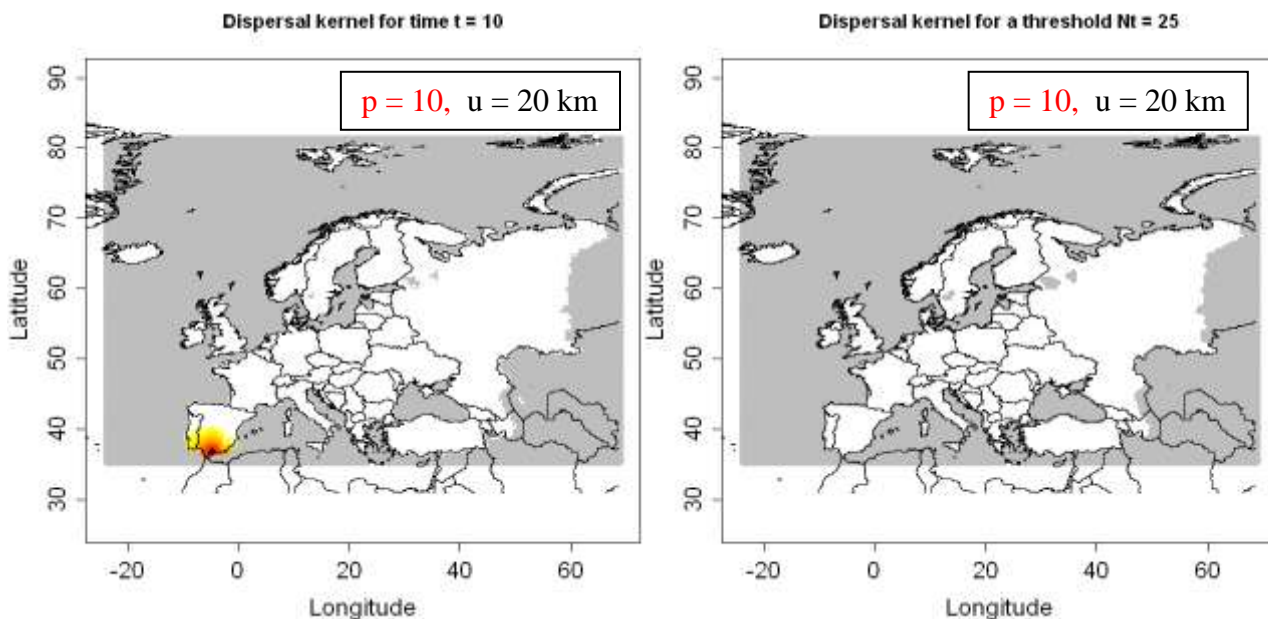


Figure 4.2.1-33: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km and $p=10$ for 10 years; $R:> res = dispk(N0=NULL, t=10, lmax=9.7, p=10, u=20, presencefile=T, nentry=NULL, figkm=F, figdd=T)$. Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

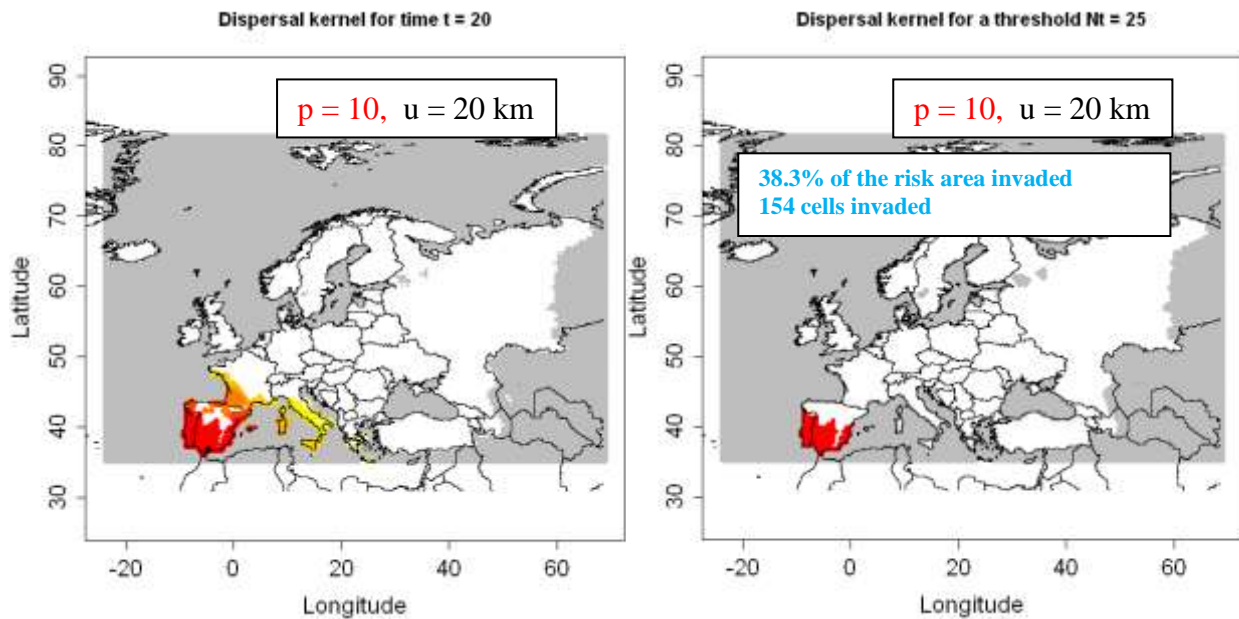


Figure 4.2.1-34: Output of the dispersal kernel model *M. enterocolitidis* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km and $p=10$ for 12 years; R:> `res = dispk(N0=NULL, t=20,lmax=9.7, p=10,u=20, presencefile=T, nentry=NULL, figkm=F,figdd=T)`. Left Picture: (Nt: population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

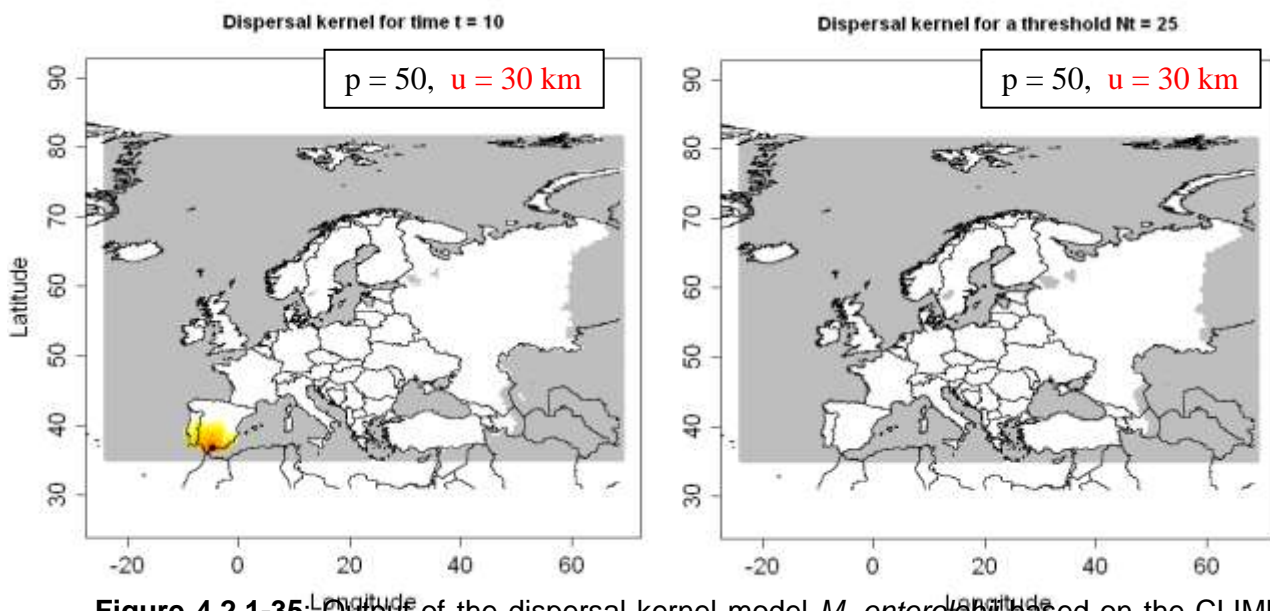


Figure 4.2.1-35: Output of the dispersal kernel model *M. enterocolitidis* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km, $p=50$ and $u=30$ km for 10 years; R:> `res = dispk(N0=NULL, t=10,lmax=9.7, p=50,u=30, presencefile=T, nentry=NULL, figkm=F,figdd=T)`. Left Picture: (Nt: population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

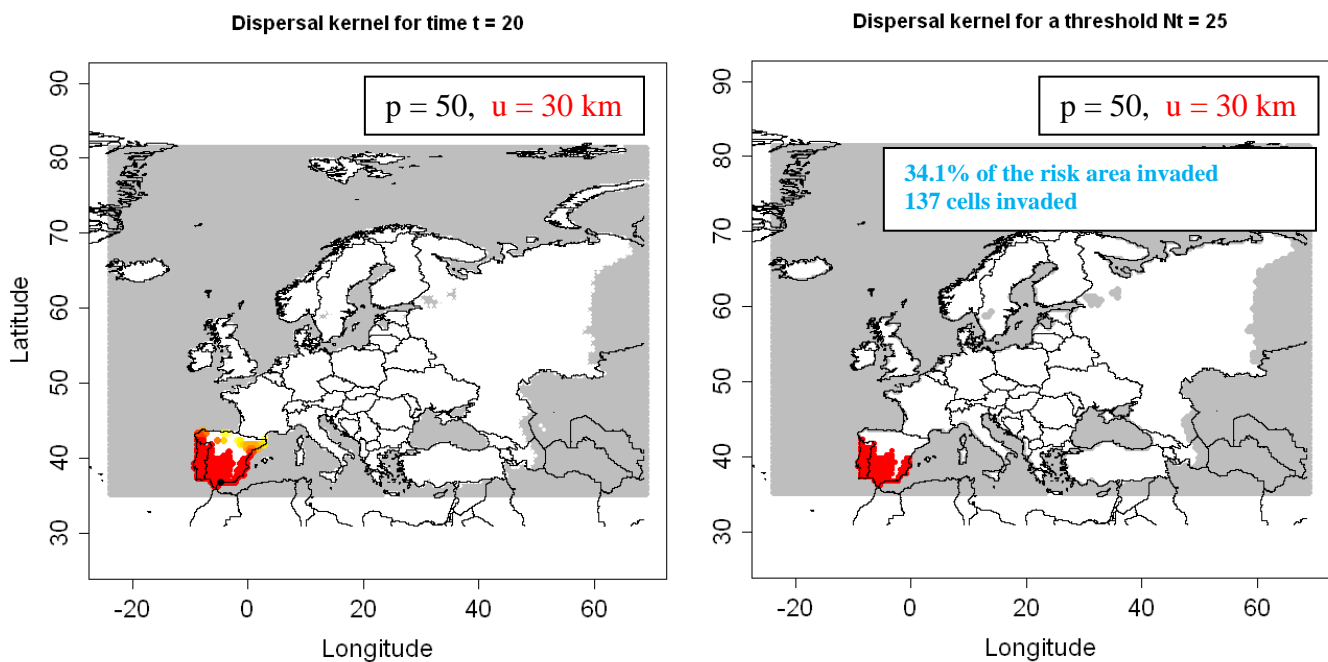


Figure 4.2.1-36: Output of the dispersal kernel model *M. enterolobii* based on the CLIMEX model for *M. incognita*; $N_0 = 9.1 \cdot 10^{-9}$, $\lambda_{max} = 9.7$, $u = 20$ km, $p=50$ and $u=30$ km for 20 years; `R:> res = dispk(N0=NULL, t=20,lmax=9.7, p=50,u=30, presencefile=T, nentry=NULL, figkm=F,figdd=T)`

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data).

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Feedback on the results for the Dispersal Kernel Model by the expert Zhenya Ilieva

The Dispersal Kernel Model gives the most realistic scenario. You can obtain a clearer impression of the intensity of invasion and which part of the endangered area could be invaded for a certain period from a certain entry point. It is obvious that in the case of low initial pest densities damage will appear later and will not be detected for a longer period of time. In such situations, restriction measures on the movement of host plants/host plant products could be effective.

The Dispersal Kernel Model shows a higher sensitivity to changes in the parameters compared to the other tested models concerning not only different N_0 but also more precise levels of invasion in different parts of endangered area. The method clearly differentiates if only short distance dispersal exists ($p=50$) or long distance spread is also included ($p=10$).

4.2.1.5 Summary

Model 1, the SLG model, reflects the Ecoclimatic Index obtained from CLIMEX and gives a rough indication of the population densities of the pest over time without the application of control measures.

Model 3, the Radial Range Expansion Model, provides more realistic maps about the potential spread of *Meloidogyne enterolobii* and the longer distances travelled mostly occur by human assisted spread. The invasion of potential areas is slower than for the SLG model.

The results of Model 5, the Dispersal Kernel Model, are the most realistic. However, the Dispersal Kernel Model shows a higher sensitivity to changes in the parameters compared to the other tested models. The method can be applied to differentiate between short distance dispersal (e.g. $p=50$) and long distance spread (e.g. $p=10$)

Summary of the commands for modelling the spread of *M.enterolobii*

```
library(sp)
library(raster)
library(rgdal)
elevmax = F
hostfile = F
# load the R code
res = slg(N0=9.1*10^(-9),lmax=9.7,t=10)
res = radial(RR=20,t=10,coord=c(-5,37))
res = dispk(N0=NULL, t=10,lmax=9.7, p=50,u=20, presencefile=T,
nentry=NULL, figkm=F,figdd=T)
```

4.2.2 Pine wood nematode and pine wilt disease

This document, prepared by Christelle Robinet, aims to describe the application of the spread module to the pine wood nematode, or more precisely, to pine wilt disease. An illustration on how to map uncertainty is also provided. However, for this important pest, a more detailed and specific spread model has been developed and applied to Europe (see Robinet et al. 2011, for the methodology). Modelling is based on the R-code Version V17 (decimal degree version) dating from November 23rd, 2010.

4.2.2.1 Information on the pine wood nematode

The pine wood nematode (PWN), *Bursaphelenchus xylophilus*, is transmitted by longhorn beetles of the genus *Monochamus*. In Europe, many species are potentially able to carry the pine wood nematode. They are widely distributed although not present in the United Kingdom and Ireland. The nematode was first detected in 1999 in Portugal on maritime pines where it is transported by *M. galloprovincialis* (Mota et al. 1999).

Pine wilt disease (PWD) develops in susceptible species of *Pinus* under suitable climatic conditions (high summer temperature and drought), and the infected tree can wilt and die within weeks of being infested. This disease is caused by the pine wood nematode, but the presence of the nematode in a tree does not necessarily produce the symptoms of pine wilt disease.

Pine wilt disease distribution

Although the disease has been found in the presumed native area of the pine wood nematode, North America, the worst symptoms are observed in invaded countries in Asia (Japan, Korea, China) and more recently (since 1999) in Portugal. Drought and high summer temperature causing water stress in the host trees probably plays an important role in disease development but until now only thresholds defined by a correlation between disease occurrence, summer temperatures (e.g., mean temperature in July or August above 20°C) and the annual rainfall are given in the literature (Rutherford & Webster 1987).

Host range

PWN prefers *Pinus* species, but is also able to attack other Coniferae: *Abies*, *Picea*, *Larix*, *Cedrus* and *Pseudotsuga* (Evans et al. 1996). These genera are considered to be the PWN host plants. In this study, we used the distribution of *Pinus* species kindly provided by the European Forest Institute (EFI, Tröltzsch et al. 2009). All *Pinus* species are not equally susceptible, but this map provides a good indication of the host distribution for the PWN and the beetle vector.

CLIMEX file

The main problem in running the spread models is the absence of a CLIMEX model for pine wilt disease, the pine wood nematode or even for the beetle vector.

There were several options:

(1) use the Mediterranean template of CLIMEX. However, the area where $EI > 0$ is too restrictive.



Fig. 4.2.2-1: CLIMEX Mediterranean template (EI)

(2) use the temperate template of CLIMEX, but the area where $EI > 0$ is probably too large and not appropriate

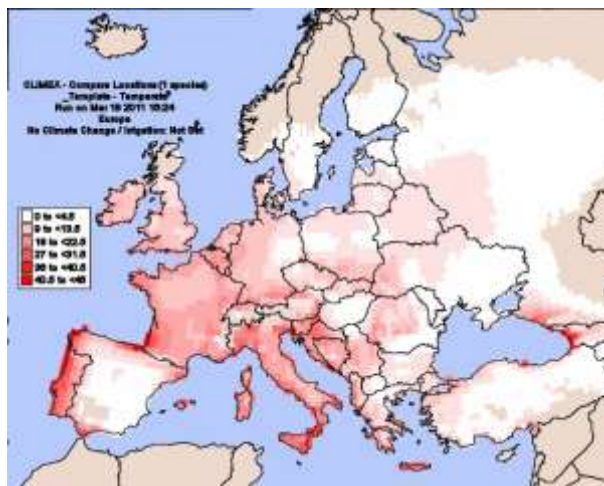


Fig. 4.2.2-2: CLIMEX Temperate template (EI)

The use of CLIMEX templates is however not advisable because it can only poorly predict the climatic suitability for a given species. Unless one template seems appropriate, it is generally recommended to stop and not apply the spread module if a specific CLIMEX model is not available.

(3) adapt the Mediterranean template of CLIMEX for a better fit to Europe

In this case, we removed all the stress indexes and the moisture index. Parameters for the temperature were: DV0 = 13, DV1 = 20, DV2 = 30, DV3 = 35. Parameters for day-degree accumulation above DV0 (MTS=7), DVCS (DVCS=10, *DV4=100), DVHS (DVHS=28) and degree days per generation (PDD=600) were unchanged from the Mediterranean template.

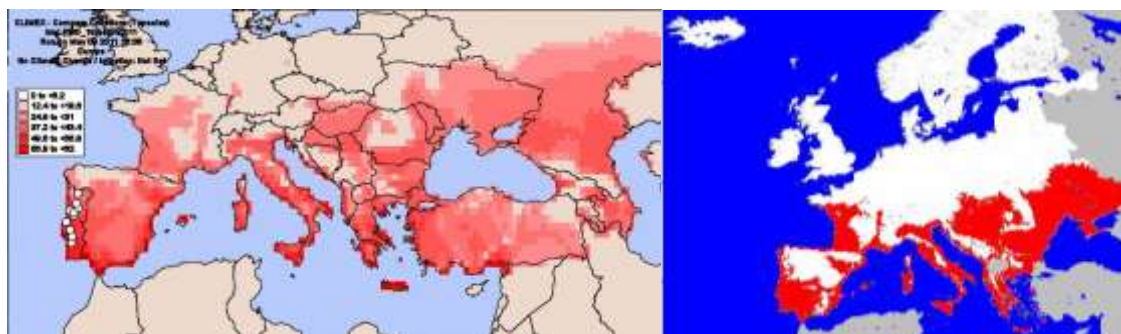


Fig. 4.2.2-3: Adjusted CLIMEX Mediterranean template (EI) (on the left) with presence of PWD (white dots) and the area where the mean July temperature is above 20°C (in red, on the right).

This choice for the CLIMEX model is a compromise between using simple but unrealistic global climate templates, and an adjusted template that is broadly in agreement with the northerly limits of PWD in eastern Asia (Japan, Korea and China). This simple adjusted model is globally in agreement with the map representing the areas where the mean temperature in July is above 20°C (interpolated with latitude, longitude and elevation, based on an average 1979-2008 climate, calculated from daily temperatures given by the European Climate Assessment & Dataset at <http://eca.knmi.nl/> , Fig. 4.2.2-3). Furthermore, it is also consistent with the occurrence of PWD in Asia and North America. **Although this model is used hereafter to apply the spread model, we do not pretend to have developed a CLIMEX model for the pine wilt disease.** We have just created a more appropriate map for PWD than the default climatic templates provided by CLIMEX to illustrate how the spread models can be applied to pine wilt disease.

Note that a specific CLIMEX model will be developed and compared to the process model for prediction of wilt disease in the EU Marie-Curie project TRANZFOR and EU project Re-PHRAME (starting in 2011). Any new CLIMEX model can be used in the future to enhance the predictions of the potential spread.

The following figures represent the maps used in R for the area of potential establishment (Fig. 4.2.2-4 left), the adjusted growth index (Fig. 4.2.2-4 right) and the habitat distribution density (Fig. 4.2.2-5). Information about the spread module is provided by the function `printinfo()` (Fig. 4.2.2.6)

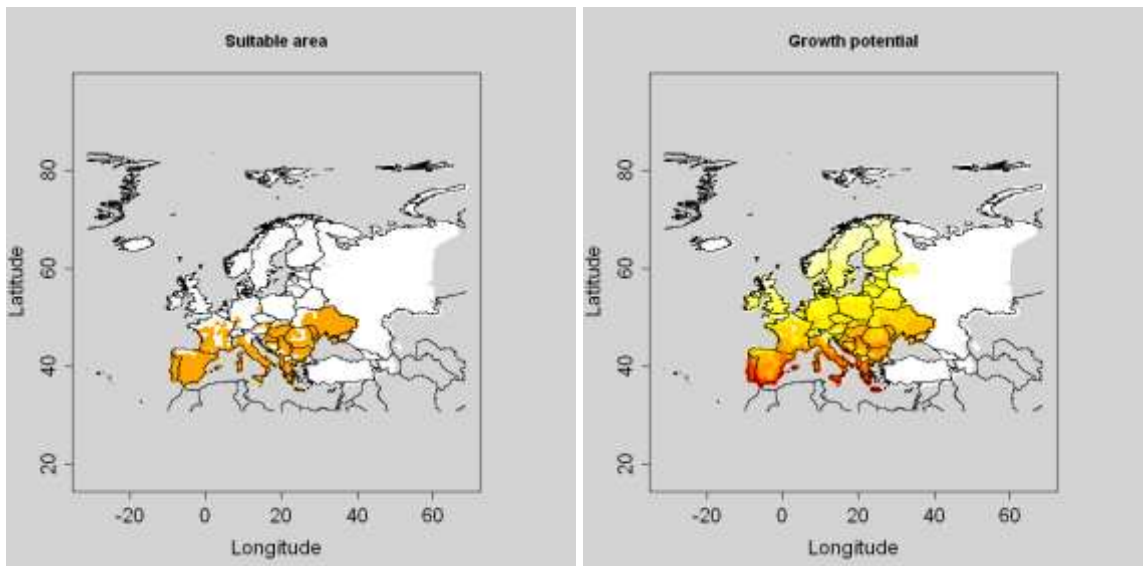


Fig. 4.2.2-4: Risk area on the left. The orange colour represents areas where $EI > 0$ and the hosts are present. Growth potential on the right (adjusted GI) from 0 (light yellow) to 100 (red).

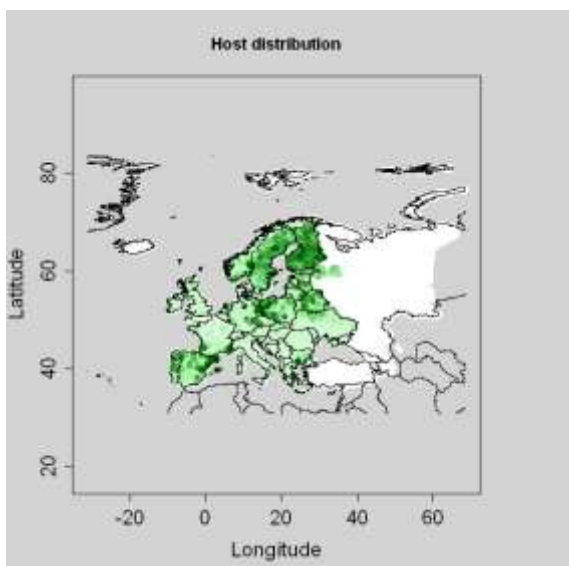


Fig. 4.2.2-5: Habitat distribution represented by the host tree density, or more precisely the proportion of land covered by *Pinus* species from 0 (light green) to 1 (dark green).

```

> printinfo()
[1] "
[1] "----- For this specific case study: -----"
[1] "The grid resolution is: 0.5 decimal degrees"
[1] "The mean cell size: 28 km longitude and 56 km latitude"
[1] "The mean area of a cell is: 1579 km²"
[1] "The number of suitable cells is: 859"
[1] "The total number of cells in SLG, LG-Econ, radial, rand-radial is: 6416"
[1] "The total number of cells in the grid used by the dispersal kernel model is: 17298"
[1] "
[1] "----- Type the commands below to call the functions -----"
[1] "
[1] "
> |

```

Fig. 4.2.2-6: Information provided by the spread module code.

4.2.2.2 Model 1: Population dynamics model (SLG)

Since the number of nematodes can reach a very high level it is difficult to estimate the PWN density. Therefore, we use the density of symptoms (infested trees) as a proxy for the PWN density. This density probably underestimates the PWN density since symptoms are expressed only in susceptible trees.

- **Yearly multiplication factor λ_{\max} :**

In Robinet et al. (2009), the following reaction-diffusion equation was used to simulate the spread and growth of the symptoms in China:

$$\frac{\partial N}{\partial t}(x,y,t) = D.\Delta N(x,y,t) + \varepsilon N(x,y,t)$$

with $\varepsilon = 2.17$; $\exp(\varepsilon)=8.76$

Therefore, if we assume that the maximum growth of the population is similar in China and in Europe, we can take $\lambda_{\max} = 8.76$ as the maximum yearly multiplication factor. To show the uncertainty, we consider this value +/- 10%, $\lambda_{\max} = 7.88$ and 9.64 to test the sensitivity of the model.

- **Initial population abundance N_0 :**

This parameter is defined by:

$$N_0 = 100 * \frac{n_0}{K}$$

with n_0 the number of introduced individuals, e.g. 100, in each suitable cell, and K the carrying capacity (the maximum number of individuals in a cell).

In Rodrigues 2008, there is the following table.

Table 1 Evolution of the number of decline symptomatic trees in the Affected Zone and in the Critical Locations, Comporta e Apostiça. For reference the estimated number of maritime pines, in the Affected Zone, is 7 millions

CAMPAIGN	99/00	00/01	01/02	02/03	03/04	04/05	05/06	06/07
Total number of decline symptomatic trees in AZ ⁽¹⁾	45.531	57.402	46.068	57.061	71.107	95.302	240.097	163.892
Critical Location of Comporta	7,42%	21,88%	49,55%	54,55%	59,82%	64,57%	60,00%	58,33%
Critical Location of Apostiça	14,34%	9,76%	3,15%	7,51%	3,12%	4,66%	5,14%	1,09%
Critical Locations (Total)	21,75%	31,64%	52,70%	62,07%	62,93%	69,23%	65,14%	59,42%
Remaining Affected Zone	78,25%	68,36%	47,30%	37,93%	37,07%	30,77%	34,86%	40,58%

⁽¹⁾ For the sake of comparison, the percentages shown refer to the Affected Zone limits stated on the Regulation n.º 1572/2003, from December, 27th, 258.000 ha.

Since 2005-2006 was the most severe PWN infestation between 1999-2000 and 2006-2007 in terms of number of decline symptomatic trees, we assume that the pine wood nematode reached its maximum density.

In summary, 240 097 trees were infested out of 7 000 000 maritime pines in the 258 000 ha region in Portugal.

Therefore:

$$K = \text{area of the cell (km}^2\text{)} * \text{host plant density (/km}^2\text{)} * \text{max pop density (/ host plant)}$$

$$= 1579 * (7000000/258000 * 10^{(-2)}) * (240097/7000000)$$

$$\underline{K = 14.69}$$

In 1999, 2 sites were initially infested in Portugal but the outbreak covered only one cell. We have assumed that two trees with symptoms was the initial infestation level. Therefore, $n_0 = 2$ and $N_0 = 100 * 2 / 14.69$. So $\underline{N_0 = 13.61 \%}$. For the sensitivity analysis, we consider this value +/- 10%, $N_0 = \underline{12.25 \text{ and } 14.97 \%}$.

- **Time t :**

PWN was discovered in Portugal in 1999 and it spread considerably in 2008 (source: EPPO; Mota et al. 2009), therefore we can take t = 9 years to simulate spread in 2008.

Application:

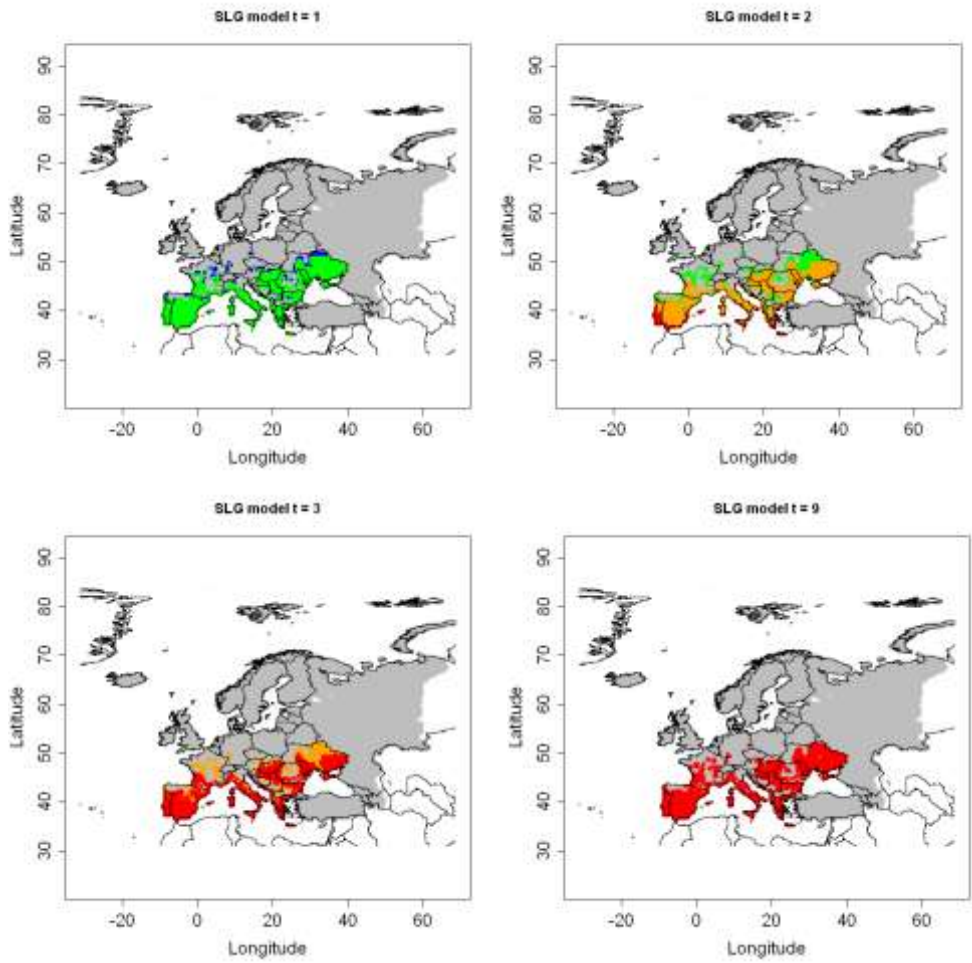
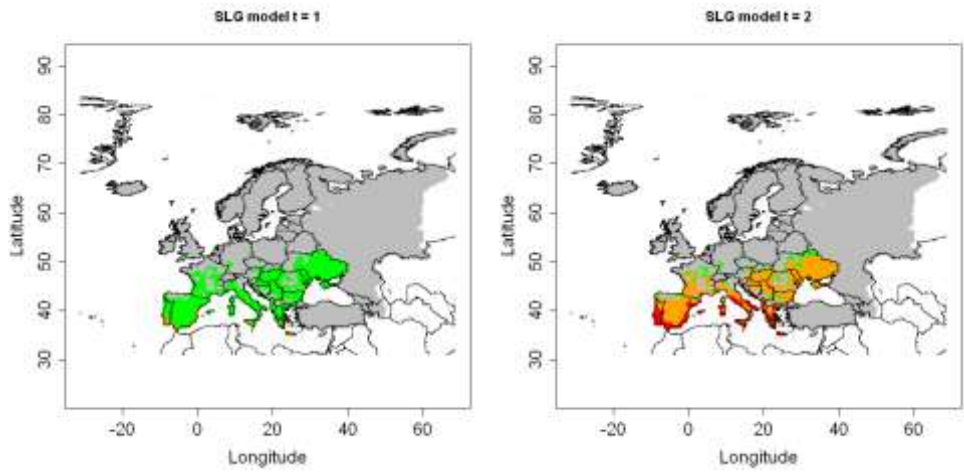


Fig. 4.2-7a: Outputs of model 1 for $t = 1, 2, 3$ and 9 *for the best case.*
 res = slg(N0=12.25,lmax=7.88,movie=F, t=9)



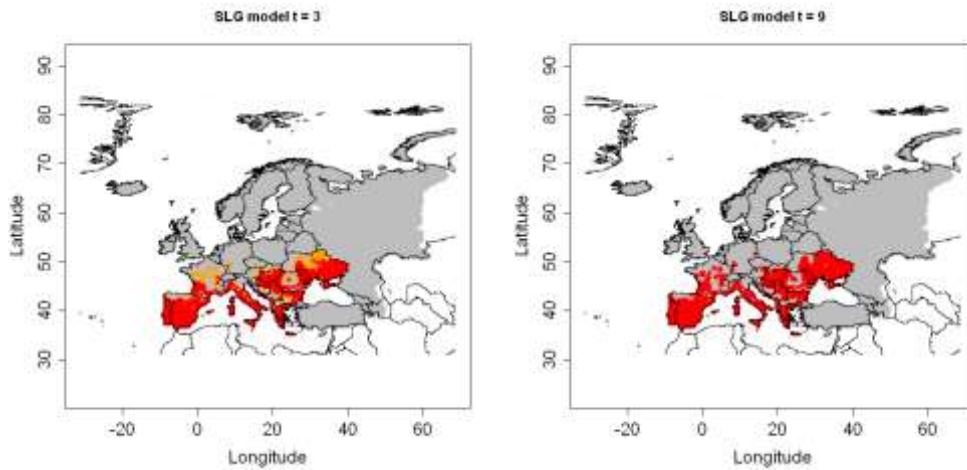


Fig. 4.2.2-7b: Outputs of model 1 for $t = 1, 2, 3$ and 9 *for the most likely case.*
res = slg(N0=13.61,lmax=8.76,movie=F, t=9)

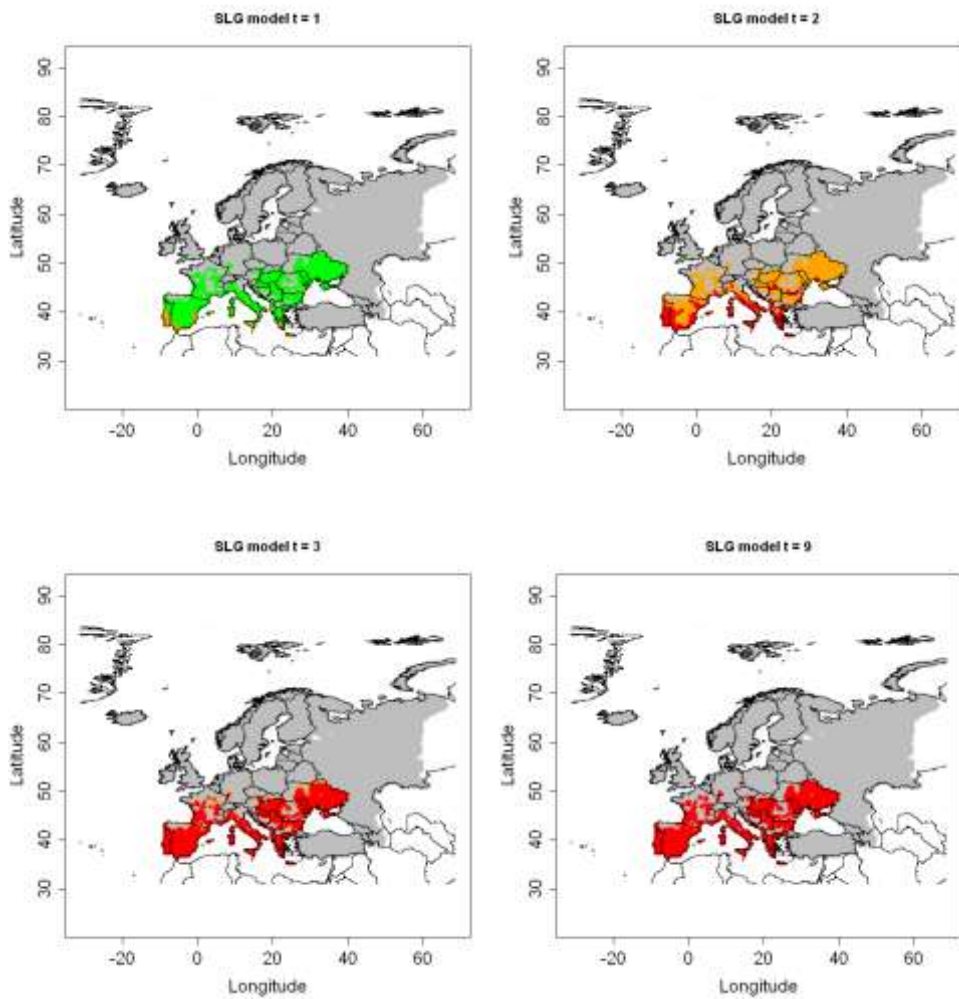


Fig. 4.2.2-7c: Outputs of model 1 for $t = 1, 2, 3$ and 9 *for the worst case.*
res = slg(N0=14.97,lmax=9.64,movie=F, t=9)

This model shows that the most favourable place is southern Portugal and the PWD can grow very rapidly over all the area of potential establishment. The uncertainty does not affect this conclusion.

4.2.2.3 Model 2: Temporal spread over cells integrated with impact (LG-Econ)

- **Initial number of infested cells N_0 :**

This parameter is defined by: $N_0 = 100 * n_0 / K$

n_0 is the number of invaded cells at $t = 0$, and K , the number of suitable cells.

The PWN was discovered at two sites separated by about 3 km (Mota et al 1999); So $n_0 = 2$ cells.

Besides, the number of suitable cells, $K = 859$ (see Fig. 4.2.2-7)

$$\Rightarrow N_0 = 2 * 100 / 859$$

$$\Rightarrow \underline{N_0 = 0.23 \%} \quad (+/- 10 \% : \underline{0.21} \text{ and } \underline{0.25} \text{ to show the uncertainty})$$

- **Relative rate of spatial increase r :**

In 1999, 2 sites were initially infested within one cell. In 2008, 65 locations were infested in Portugal, covering 11 cells. To determine this number of cells, the function “pointtocell” was used.

Besides, the number of suitable cells is 859 (see Fig. 4.2.2-7).

Then we use the formula below to calculate r , with $t = 9$ (corresponding to the year 2008).

$$\ln\left(\frac{N_t}{K - N_t}\right) = \ln\left(\frac{N_0}{K - N_0}\right) + r \cdot t$$

$$\ln\left(\frac{11}{859 - 11}\right) = \ln\left(\frac{1}{859 - 1}\right) + 9r$$

$$r = \frac{1}{9} \left(\ln\left(\frac{11}{848}\right) - \ln\left(\frac{1}{858}\right) \right) = 0.27 \text{ yr}^{-1}$$

$$\underline{r = 0.27 \text{ yr}^{-1}} \quad (+/- 10 \% : \underline{0.24} \text{ and } \underline{0.30} \text{ to show the uncertainty})$$

- **Time t :**

We chose $t = 9$ years (corresponding to the year 2008, since we take $t = 0$ to be 1999).

- **Economic dataset (valperhost):**

We have no precise GIS maps for economic value. From the value at a country scale, we can derive the value per km². If $H(i)$ is the percentage of land covered by host trees (pines) and val is the value for each % of land covered by host tree per km², then we should sum{ $H(i)$ } * val and make it equal to the country value to obtain val (euros per % of cells covered by pines). Finally, we should divide this number by the mean area of a cell (1579 km²). We obtain $valperhost = 8 \text{ €}$ (+/- 10 % : 7.2 and 8.8 to show the uncertainty).

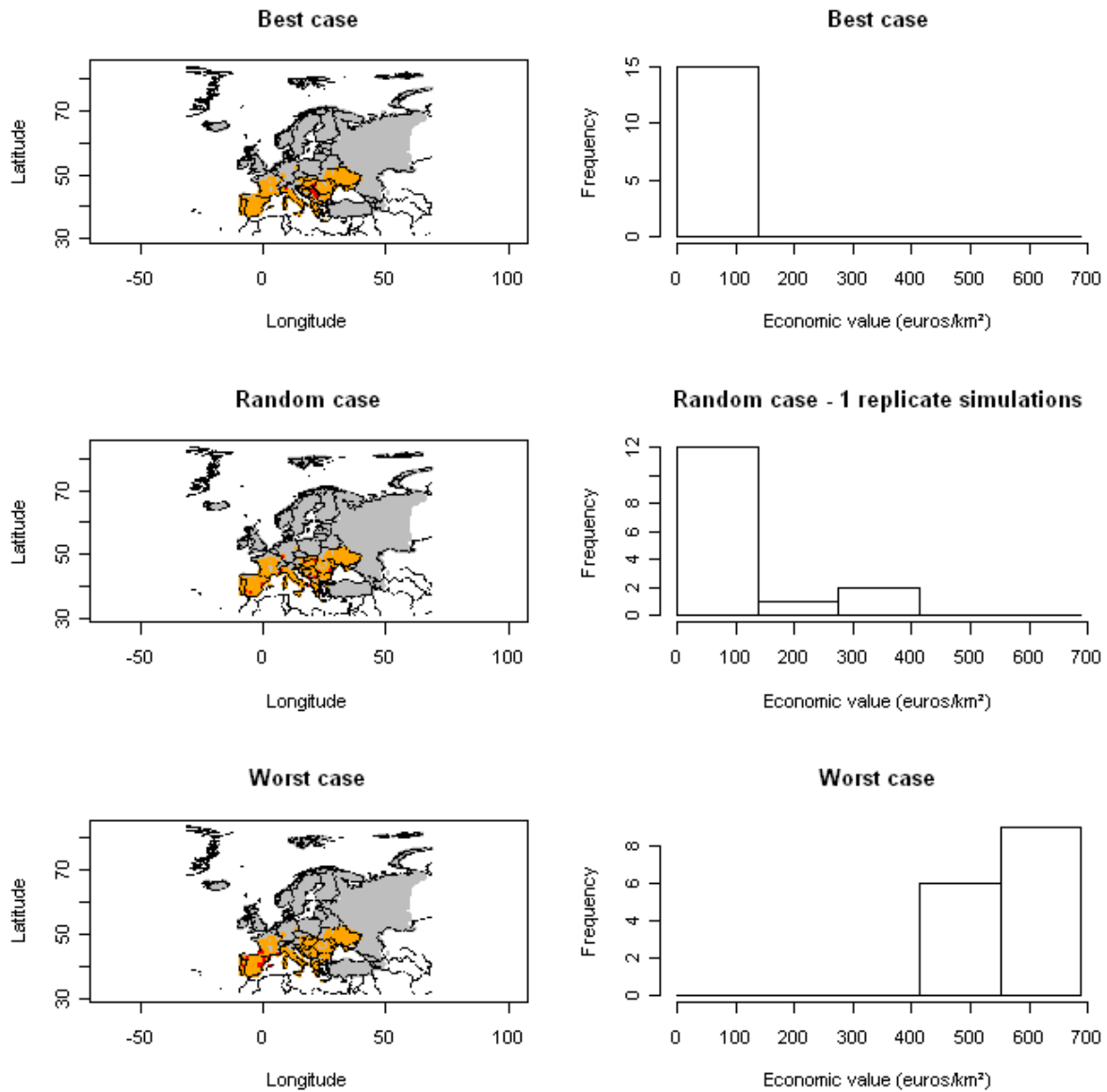


Fig. 4.2.2-8a : Outputs of model 2 *for the best case*. *res = lgecon(N0=0.24,r=0.22,t=9,econraster=F,habitatraster=T,valperhost=7.2)*

Number of invaded cells = 15

Percentage of the niche invaded = 1.7 %

Economic impact = 33 € (best)– 2,135,000 € (random) – 20,038,964 € (worst)

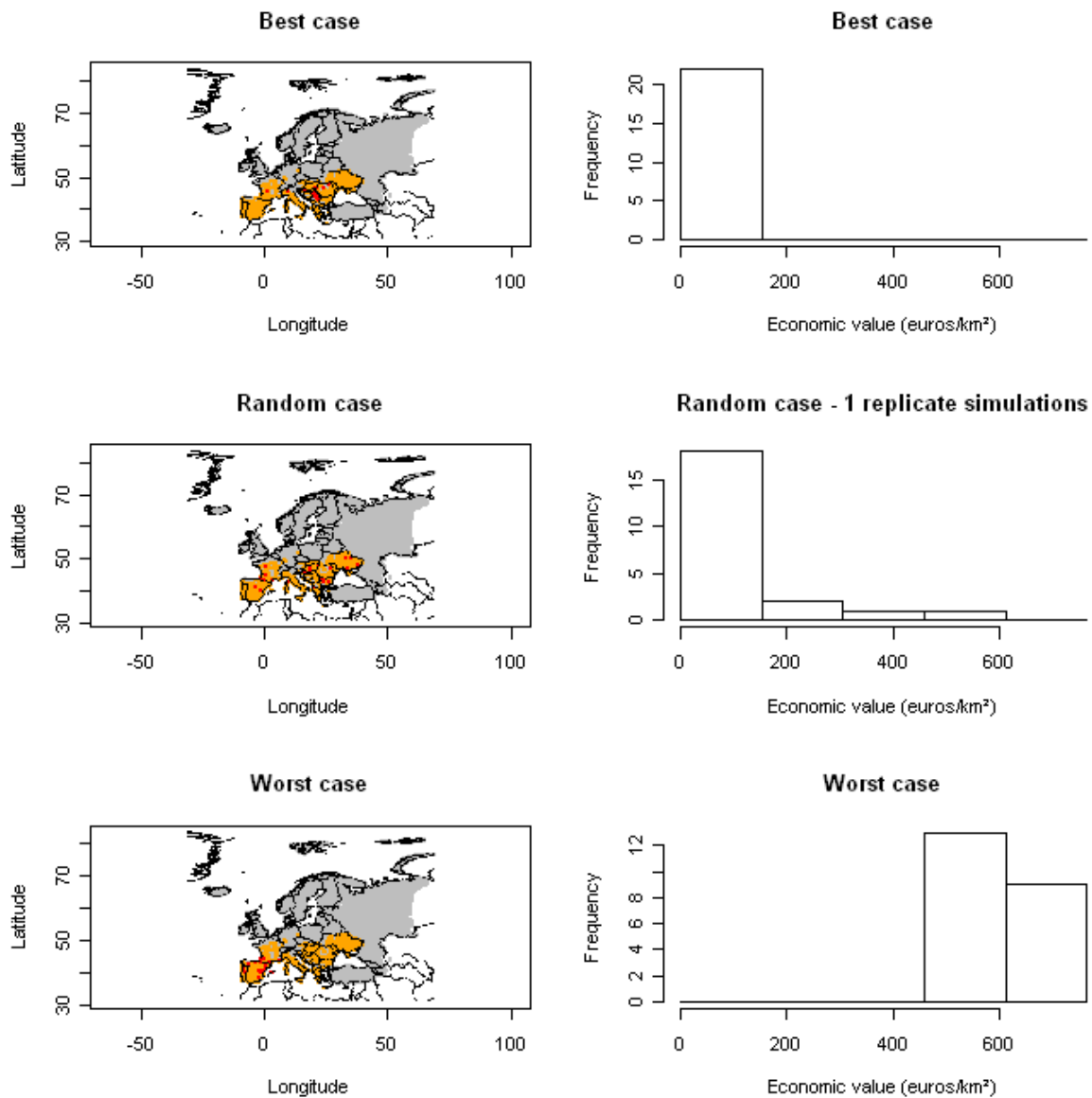


Fig. 4.2.2-8b : Outputs of model 2 *for the most likely case*. *res = lgecon(N0=0.23,r=0.27,t=9,econraster=F, habitatraster=T,valperhost=8)*

Number of invaded cells = 22

Percentage of the niche invaded = 2.5 %

Economic impact = 98 € (best)– 4,831,000 € (random) – 30,857,634 € (worst)

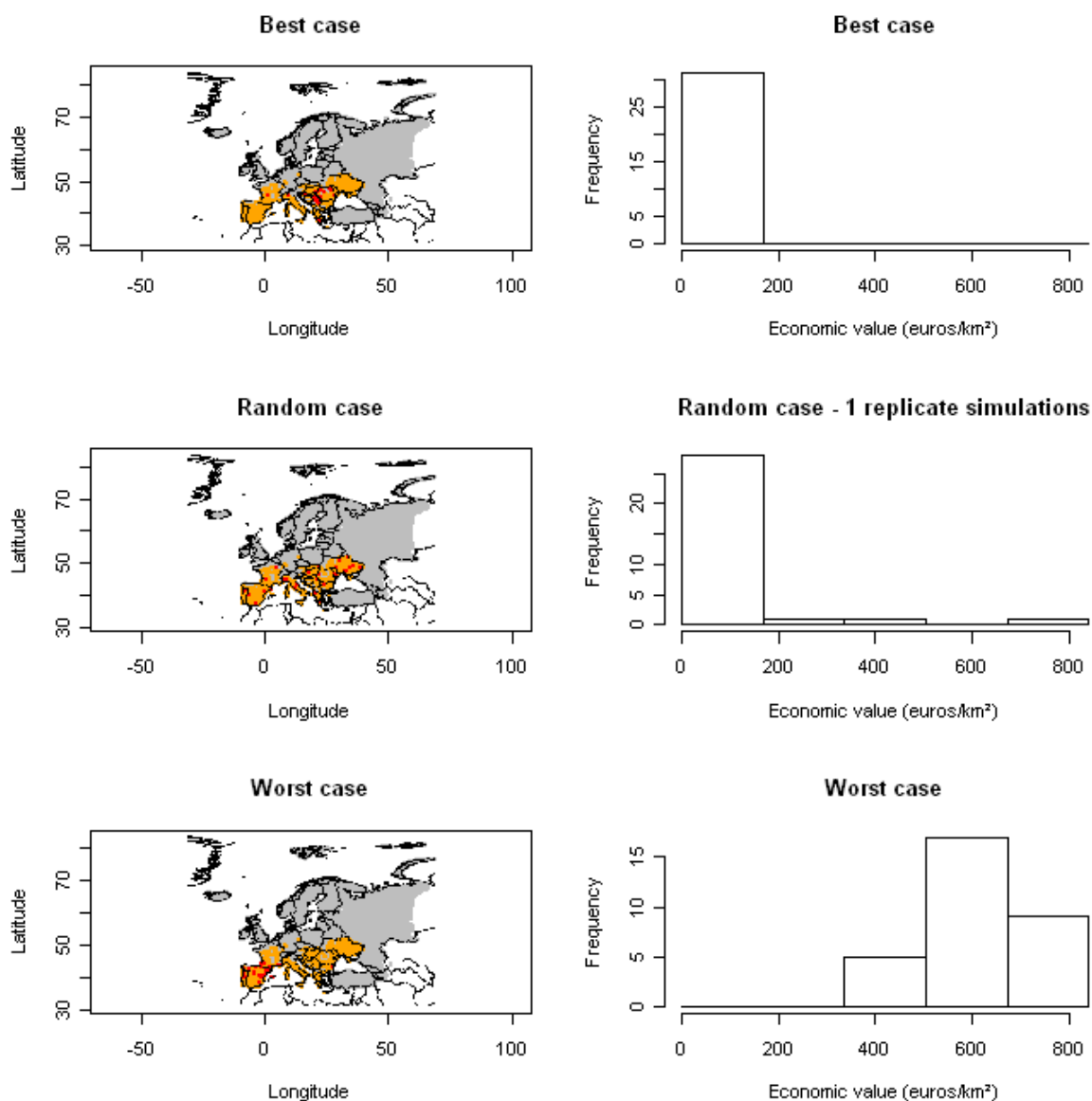


Fig. 4.2.2-8c: Outputs of model 2 *for the worst case*. *res = lgecon(N0=0.25,r=0.30,t=9,econraster=F, habitatraster=T, valperhost=8.8)*

Number of invaded cells = 31

Percentage of the niche invaded = 3.6 %

Economic impact = 367 € (best)– 5,255,000 € (random) – 44,614,853 € (worst)

This model shows that the worst case in terms of economic impact is the presence of the PWN in the Iberian Peninsula. Absolute economic values are not reliable since the economic value is based on a rough estimate of the economic value based on the proportion of cells covered by pines, and an assumption of a constant value over the PRA area and the economic value is set to 0 where data on hosts are missing. The main advantage of this model is to give an idea of the area where the economic impact would be higher and the magnitude of potential spread in terms of the number of invaded cells in this area. It also provides a range of possible economic impacts,

showing whether the PRA area is relatively homogeneous or not concerning the economic impact.

4.2.2.4 Model 3: Radial range expansion model (RR)

- **Radial rate of range expansion RR:**

Short distance spread mediated by longhorn beetles was estimated at 7.5 km per year in China (Robinet et al 2009). In Japan it is estimated from 2 to 15 km/yr, with an average of 6.1 km/yr (Togashi & Shigesada 2006). RR = 6 - 7.5 km/yr (+/- 10 % : 5.4 and 8.2 to show the uncertainty).

- **Time t :**

We can take t = 9 years to obtain simulations in 2008 that can be compared to the real situation (t = 0 in 1999, year of first detection and map available, and the model simulates the spread 9 years later, in 2008 and thus it is possible to compare the simulated spread and the real spread in Portugal).

- **Geographical coordinates coord:**

There were two introduction points in the Setubal Peninsula, approximately at:

Pegoes (38°41'00"N 008°36'43"W)

Landeira (38°35'46"N 008°38'58"W)

Therefore, coord = c(-8.61, 38.70, -8.65, 38.60)

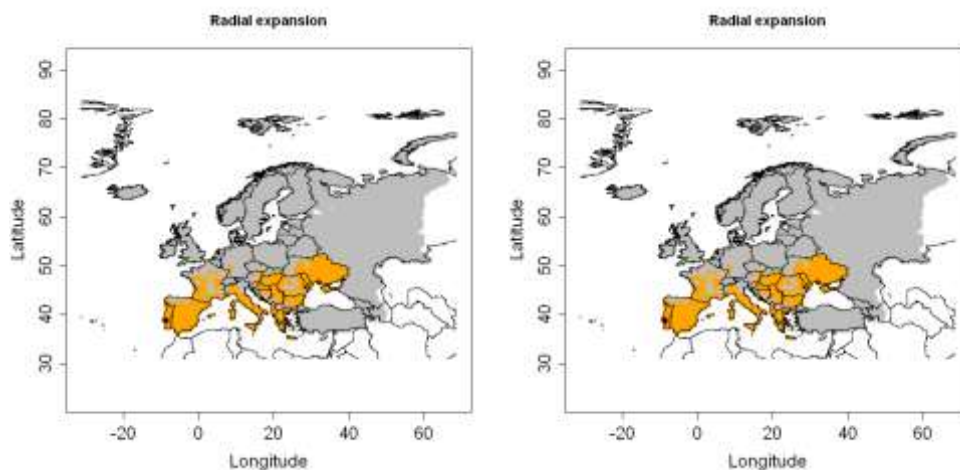


Fig. 4.2.2-9a: Outputs of model 3 for RR = 6 km/yr on the left and RR = 7.5 km/yr on the right, *for the most likely case*. **res = radial(RR=6,t=9,coord=c(-8.61, 38.70, -8.65, 38.60),figkm=F, figdd=T)**

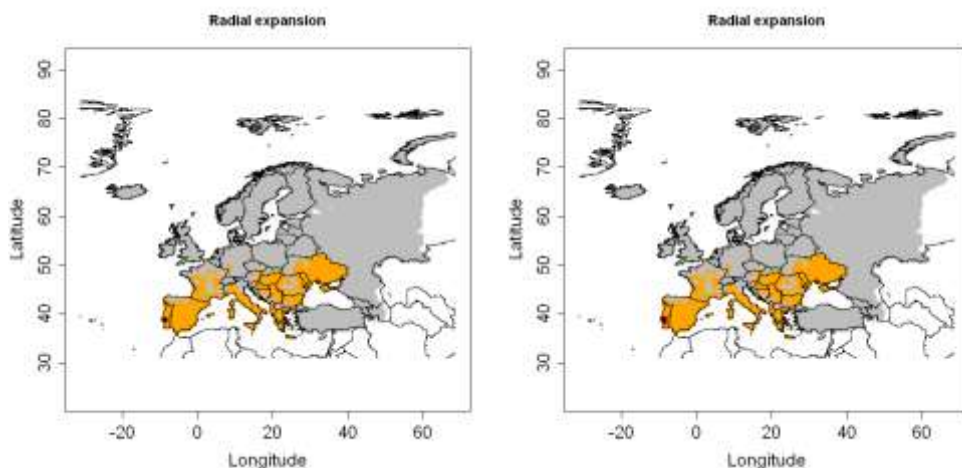


Fig. 4.2.2-9b. Outputs of model 3 *for the best case* (on the left) and *the worst case* (on the right).

This model shows that the PWN cannot spread very fast if only short distance dispersal (e.g. the carrier beetle only disperses on its own) is taken into account. It shows that human mediated dispersal plays the major role in PWN spread.

If we increase the radial spread rate to obtain a satisfactory result for 2008 (i.e. with the infestation covering nearly all Portugal with possible incursions in Spain), we have $RR = 35$ km/yr approximately.

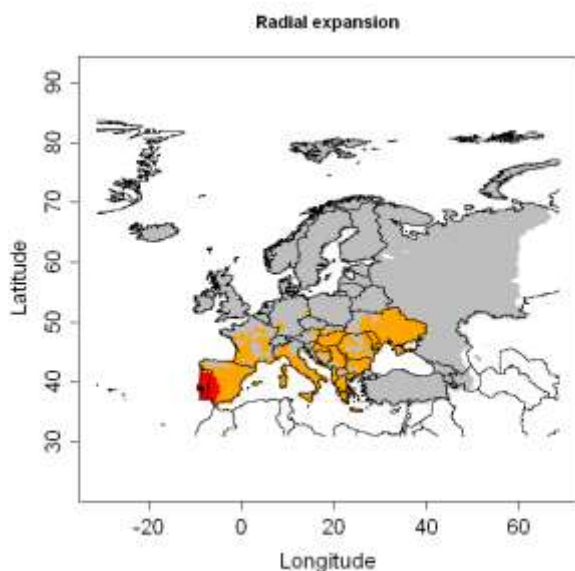


Fig. 4.2.2-9c. Outputs of model 3 for $RR = 35$ km/yr.

Spain is currently less affected than predicted by this map but this is not surprising given the early stage of the invasion process and the eradication strategy employed to contain the pest.

4.2.2.5 Model 4: Hybrid of logistic growth and radial rate expansion (Rand-RR)

Parameters have already been estimated in models 2 and 3. We consider $RR = 35$ km / yr and tested the effects on uncertainty over N_0 and r .

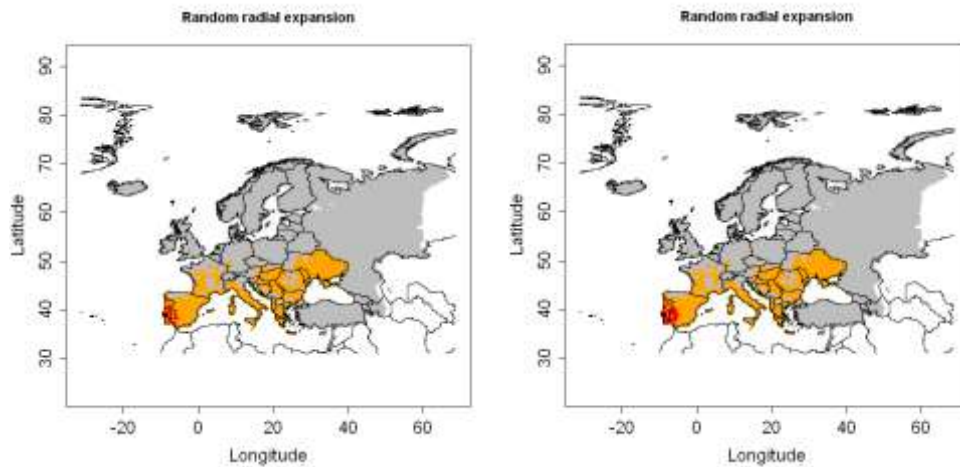


Fig. 4.2.2-10a. Outputs of model 4 *for the best case* (on the left) and *the worst case* (on the right). $res = radialrand(RR=35,t=9,coord=c(-8.61, 38.70, -8.65, 38.60),N_0=0.23, r=0.24,figkm=F,figdd=T)$

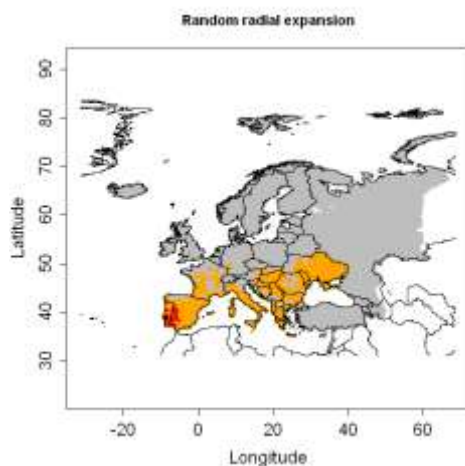


Fig. 4.2.2-10b. Outputs of model 4 *for the most likely case*.

For the best case:

Number of invaded cells = 15

Percentage of the niche invaded = 1.7 %

For the most likely case:

Number of invaded cells = 22

Percentage of the niche invaded = 2.6 %

For the worst case:

Number of invaded cells = 31

Percentage of the niche invaded = 3.6 %

4.2.2.6 Model 5: Deterministic version of the dispersal kernel (DK)

Most of the parameters have already been estimated in model 1 (\square_{\max} , N_0 , t) and 3 ($u \approx RR$).

We created a presence file with the entry points mentioned previously (in model 3), and put N_0 as the initial population density.

```
presence.txt - Bloc-notes
Fichier Edition Format Affichage ?
-8.61222 38.68333 13.61
-8.64389 38.59611 13.61
```

Fig. 4.2.2-11. Presence file.

For the parameter p , we take a low value to simulate long distance spread.

$u = 35$ (RR estimated above)

$p = 5$ (long distance spread)

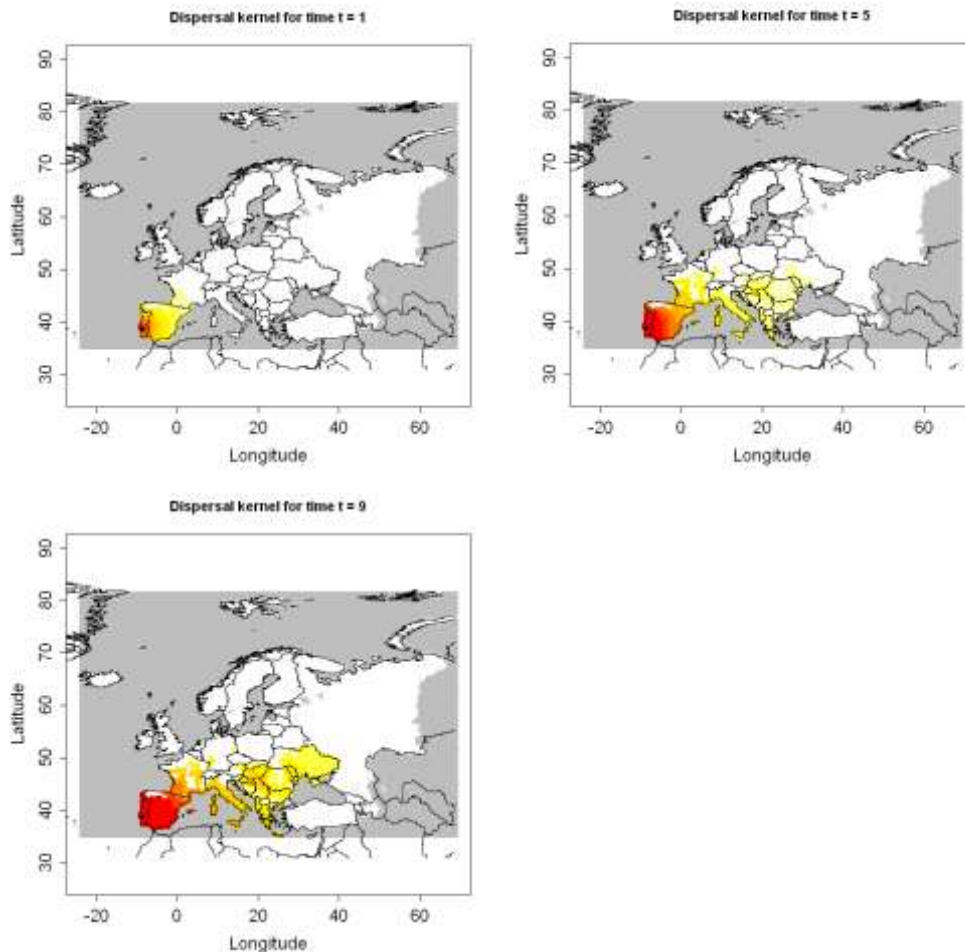


Fig. 4.2.2-12a. Outputs of model 5 for $u = 35$ and $t = 1, 5, 9$. $\text{res} = \text{dispk}(N_0=\text{NULL}, t=9, \text{lmax}=8.76, p=5, u=35, \text{presencefile}=T, \text{nentry}=\text{NULL}, \text{figkm}=F, \text{figdd}=T)$

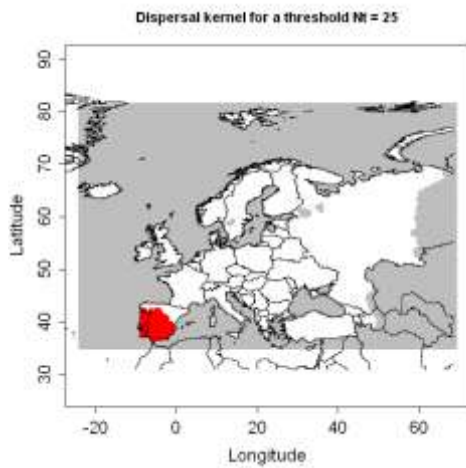


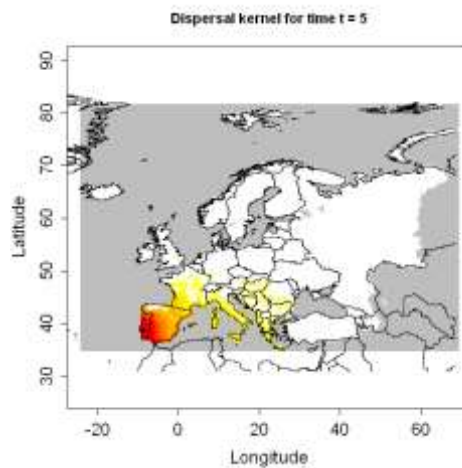
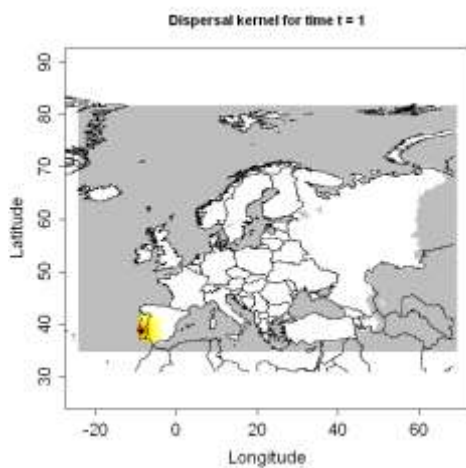
Fig. 4.2.2-12b. Outputs of model 5 for $u = 35$ ($N_t > 25\%$).

`plotkernel(vectpop0=res$dispk,presence=res$presence,figkm=T,figdd=T,t=9,legend=F,threshold=25)`

For comparison, we made simulations for a lower u , based on the initial spread distance found in China:

$u = 7.5$ (RR for short distance spread in China)

$p = 5$ (long distance spread)



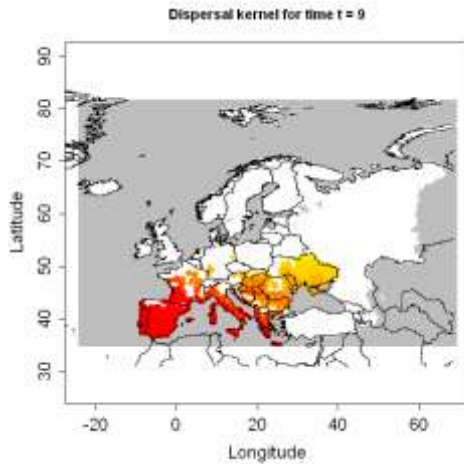


Fig. 4.2.2-13a. Outputs of model 5 for $u = 7.5$ and $t = 1, 5, 9$. `res = dispk(N0=NULL, t=9, lmax=8.76, p=5, u=7.5, presencefile=T, nentry=NULL, figkm=F, figdd=T)`

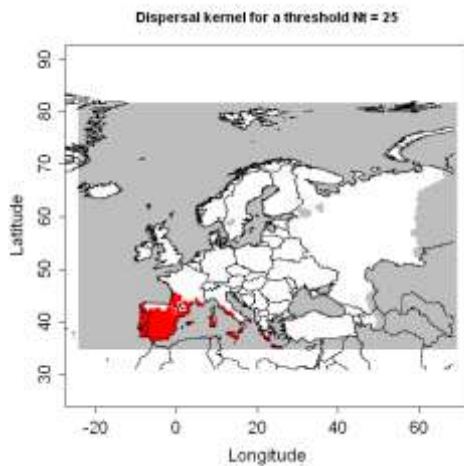


Fig. 4.2.2-13b. Outputs of model 5 for $u = 7.5 (N_t > 25 \%)$. `plotkernel(vectpop0=res$dispk, presence=res$presence, figkm=T, figdd=T, t=9, legend=F, threshold=25)`

When u is decreased, the population does not disperse as far and the population density increases. Therefore, the population density can build up more rapidly and the pest can then spread more rapidly instead of being diluted in the PRA area. Therefore decreasing u seems to increase the spread rate.

This dispersal kernel model assumes that the population can spread continuously from short to long distances whereas, in reality, some places will remain uninfested because man will also move some individuals from one place to another. Thus, there will be some gaps in the distribution and this pattern cannot be simulated by model 5 (nor the previous ones).

4.2.2.6 Summary

In Europe, (a) it is too early in the invasion process to estimate and adjust the parameters based on the observations of spread (b) the rate of spread is likely to have been affected by the strategy undertaken to contain and eradicate the pest.

Model 1 is useful to show how fast PWD can grow and which regions are the most favourable. Model 2 is useful to provide a range of possible economic impacts and indicate the area where the highest impact is expected (although the economic impact predictions are unreliable because economic value is not available at the grid's spatial resolution). Model 3 shows that long distance spread should be taken into account and we can estimate the overall radial spread. Model 4 is very similar to model 3 and probably provides more accurate estimates for potential spread because it is based on the radial range expansion but does not assume that all the cells within this area are invaded. Model 5 is not appropriate to describe long distance dispersal due to human transportation.

Summary of the commands for modelling the spread of pine wood nematode (or more precisely pine wilt disease symptoms)

```
library(sp)
library(raster)
library(rgdal)
elevmax = F
habitatfile = T
  # load the R code
plothabitat()
plotRA()
plotGI()
res = slg(N0=13.61,lmax=8.76,movie=F, t=9)
res = lgecon(N0=0.23,r=0.27,t=9,econraster=F, hostraster=T,valperhost=8)
res = radial(RR=35,t=9,coord=c(-8.61, 38.70, -8.65, 38.60),figkm=T, figdd=F)
res = radialrand(RR=35,t=9,coord=c(-8.61, 38.70, -8.65, 38.60),N0=0.23,
  r=0.27,figkm=F,figdd=T)
res = dispk(N0=NULL, t=9,lmax=8.76, p=5,u=35, presencefile=T, nentry=NULL,
  figkm=F,figdd=T)
plotkernel(vectpop0=res$dispk,presence=res$presence,figkm=T,figdd=T,t=10,le
  gend=F,threshold=25)
```


4.3 Plant

4.3.1 Water hyacinth, *Eichhornia crassipes*

This document, prepared by Hella Kehlenbeck, provides a case study example on the application of the generic models for the spread of invasive species developed within the framework of the EU project PRATIQUE for the potential spread of the Water Hyacinth *Eichhornia crassipes* in Europe. The objective of the case study is to test the models and to provide examples with guidance for the estimation of the required parameter values for an invasive alien plant species relevant for Europe. The case study was conducted with the help of Sarah Brunel (EPPO, Paris), who also provided data and information on the pest. In addition, data were derived from the EPPO PRA on *E. crassipes* of 2008.

The modelling is based on the Guide for the Spread Module, Version 0.21, and the R-code Version V17, both dating from November 23rd, 2010 (see chapter 3).

4.3.1.1. Information on *E. crassipes*

E. crassipes is considered to be one of the worst aquatic invasive plants worldwide. In Europe it already poses a threat in Spain and Portugal, but its distribution is still limited in the EPPO region.

Natural spread potential

The natural spread of up to hundreds of kilometres has been documented in many of the large river systems in Africa and in Spain. Studies in Spain showed that propagule dispersal was highest in September with an average of 4.5 propagules dispersed in 15 minutes. However, such dispersal is confined within to the same catchment.

Human-assisted spread potential

E. crassipes can be accidentally spread by human activities during the maintenance of swimming areas and drainage ditches and attached to fishing gear or to hulls, anchor lines, engines, or other parts of boats both within the same catchment and between catchments. Moreover, existing practices of mechanical waterway maintenance tend to cut off plants and to spread the fragments. These fragments thrive and form new plants, enabling new populations to develop.

Long distance spread is enhanced because Water Hyacinth is intentionally imported as an ornamental aquatic plant for use outdoors.

Host range and habitat distribution, here

The habitats at risk are freshwater bodies and ecosystems which are very common throughout the EPPO region. These have not been included in the spread models. Ideal habitats for *E. crassipes* are slow moving or still freshwater bodies and ecosystems.

According to the CORINE Land Cover nomenclature, the suitable habitats are:

- Continental waters (water courses, water bodies)
- Banks of continental water, Riverbanks / canal sides (dry river beds)

The land cover by country can be explored at <http://www.eea.europa.eu/data-and-maps/figures/corine-land-cover-2006-by-country> . See also PRATIQUE Deliverable 3.3.

Findings of *E. crassipes* in Europe (to be used as potential starting points for the modelling)

The plant is established in Italy, Portugal, and Spain. It is casual (= transient) in France, the Netherlands, Belgium and the UK. *E. crassipes* also occurs in botanical gardens, e.g the Botanic Gardens of Amsterdam (The Netherlands), Cologne (Germany) and in Brno (Czech Republic). It has been reported from Slovakia where it is cultivated during the summer in gardens. It does not thrive in these countries and is replanted every year. It might be more widely spread as it is freely available in shops, markets and on the internet. *E. crassipes* is widely grown as an ornamental in UK glasshouses.

Climatic suitability in Europe

The climatic conditions in southern Europe are very similar to those in its native range but are totally dissimilar to those in northern Europe. Optimal growth occurs at temperatures of 28-30°C (air temperatures) while growth ceases when water temperatures drop below 10°C. The whole Mediterranean area would be suitable for *E. crassipes*. In the more temperate regions of Europe it is more likely that transient populations of the weed may occur. Populations can expand during the summer months, but die back during winter, as in canals in the Netherlands.

CLIMEX file

A CLIMEX model for this species was provided by Sarah Brunel. Figure 1 shows the area at risk and the growth potential for *E. crassipes* according to CLIMEX.

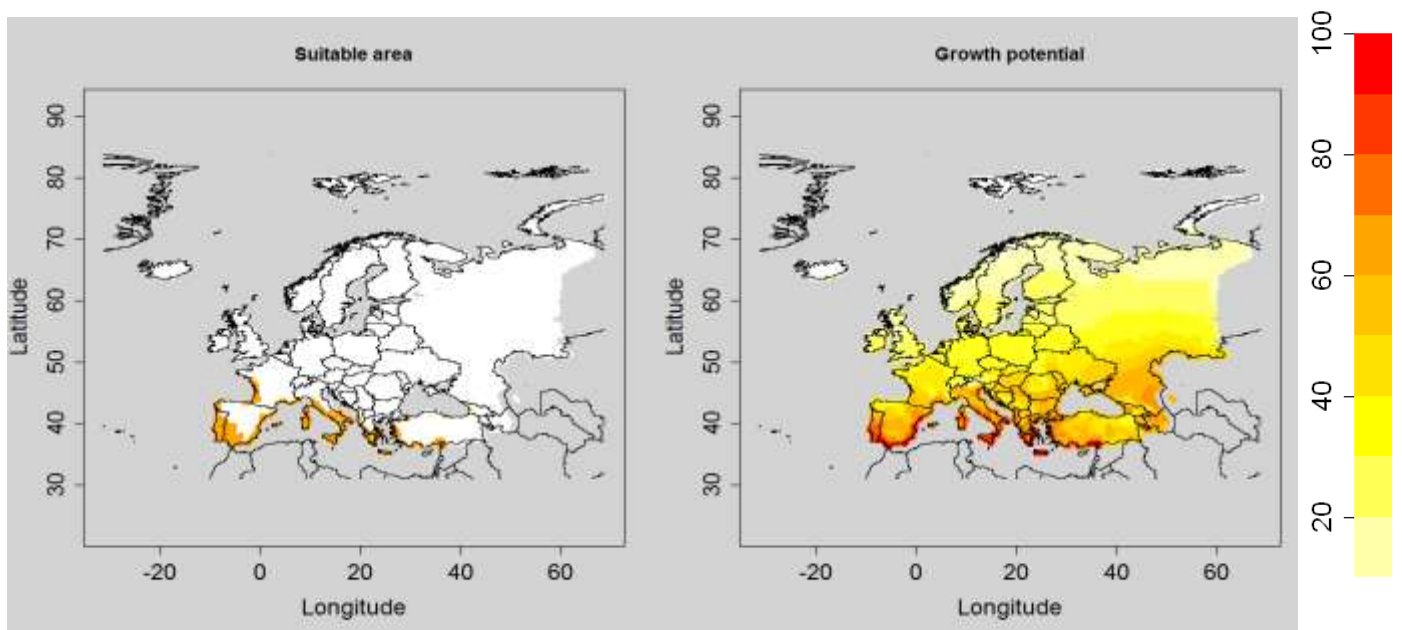


Figure 4.3.1-1: Suitable area (on the left; orange dots: EI>0, white dots: EI=0, grey: no data) and growth potential (GI; on the right) for *E. crassipes* in Europe according to a CLIMEX model by Darren Kriticos and Sarah Brunel.

Based on the CLIMEX model the number of suitable cells for *E. crassipes* is given below:

[1] "The number of suitable cells is: 252"

[2] "The total number of cells in SLG, LG-Econ, radial, rand-radial is: 6416"

[3] "The total number of cells in the grid used by the dispersal kernel model is: 17298"

Reproduction strategy of *E. crassipes*

E. crassipes grows very fast. Another species is not needed to complete the life cycle of the plant and the plant is able to reproduce vegetatively. In Spain (River Guadiana), *E. crassipes* reproduces both vegetatively and sexually and has floral cycles of about 1-2 days; 1-2 months are required to produce mature dehiscent fruits and seeds. Its doubling time can be as little as one week, and depends on water nutrient content and temperature. In the Guadiana river in Spain, doubling time varied between 10 and 60 days.

Each flower of *E. crassipes* produces about 250 long-lived seeds (up to 20 years) that are resistant to the drying up of the water body. Germination occurs once the water body is re-inundated and the plants are then capable of rapid growth through asexual production of daughter plants

It is thought that *E. crassipes* was introduced to a number of countries as a single plant from which infestations have arisen.

4.3.1.2 Model 1: Population dynamics model (SLG)

For the SLG it is assumed that an initial population abundance N_0 (%) is introduced in each suitable cell (cells where $EI > 0$) and then we simulate the "spread" or more precisely the growth within each cell according to a logistic function. On the output map, we will see areas which are the most suitable for the population growth if some individuals were introduced there.

Estimates of parameters

- **The starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

Calculation:

$$N_0 = 100 * \frac{n_0}{K}$$
 with n_0 the number of introduced individuals, in each suitable

cell, and K the carrying capacity (the maximum number of individuals in a cell).
 $K = \text{area_cell (km}^2\text{)} * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2\text{)}, \text{ or}$

$K = \text{area_cell (km}^2\text{)} * \text{host_plant_density (/km}^2\text{)} * \text{max_population_density (/host plant)}$

Relevant information and data:

On a length of 75 km in a river in Africa, 200,000 tonnes of *E. crassipes* has been observed.

Considering an average width of 60 m of the river, the surface area of these 75 km of river was calculated to be 4.5 km². The carrying capacity of this river is therefore calculated to be $K=200000 \text{ ton}/4.5 \text{ km}^2$.

It is assumed that about 5% of the surface is covered with water.

Calculation of the carrying capacity K:

$$K = 44444 \text{ tons / km}^2.$$

$$K = 44444 \text{ tons / km}^2 \times 1579 \text{ km}^2 \text{ (size of the grid cell)}$$

$$K = 7.02 \times 10^7 \text{ tons / grid cell}$$

Calculation of the starting population N_0 :

Initial density $n_0 = 500 \text{ g of } E. \text{ crassipes}$ (or 0,0005 tons)

5% of the surface is covered with water

$$N_0 = 100 \times 0,0005 \text{ t} / 7.02 \times 10^7 \times 0.05$$

$$N_0 = 3,6 \times 10^{-11} \%$$

Capturing uncertainty

For capturing the uncertainty, we also used half $N_0 = 1.8 \times 10^{-11} \%$ and double

$N_0 = 7.1 \times 10^{-11} \%$.

- **The multiplication factor λ_{\max}**

λ_{\max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space

Relevant information and data

According to the literature provided by Sarah Brunel, Water Hyacinth develops during the growing season from 1 kg to about 30 kg within one year.

$$\lambda_{\max} = 30$$

Capturing uncertainty

For the sensitivity analysis we also tested $\lambda_{\max} = 20$ and $\lambda_{\max} = 40$

- **Time frame:** 10 and 20 years

Results

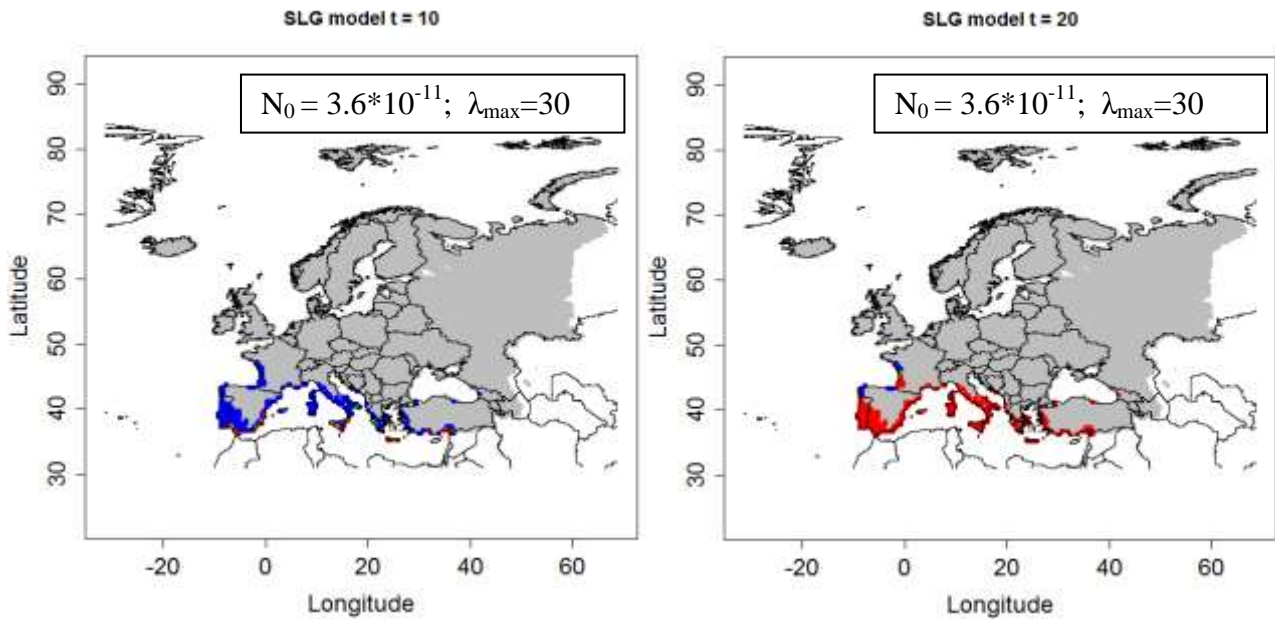


Figure 4.3.1-2: Output of the SLG model for *E. crassipes* for 10 and 20 years, based a CLIMEX model by Darren Kriticos and Sarah Brunel (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 years ; R:> res = slg(N0=3.6*10⁻¹¹),lmax=30, t=10)

Right Picture: 20 years; R:> res = slg(N0=3.6*10⁻¹¹),lmax=30, t=20)

Sensitivity analysis / capturing uncertainty: SLG for different N_0 -values

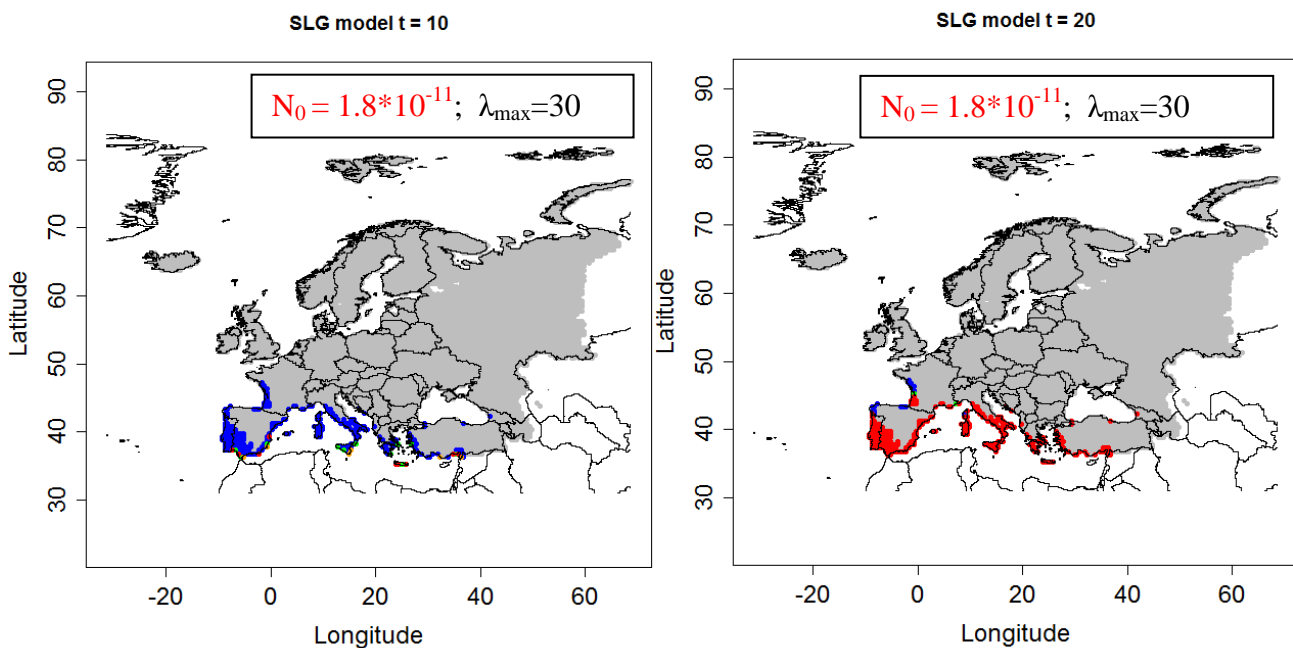


Figure 4.3.1-3: Output of the SLG model for *E. crassipes* for 10 and 20 years with a lower value for N_0 , based a CLIMEX model by Darren Kriticos and Sarah Brunel (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 years ; R:> res = slg(N0=1.8*10⁻¹¹),lmax=30, t=10)

Right Picture: 20 years; R:> res = slg(N0=1.8*10⁻¹¹),lmax=30, t=20)

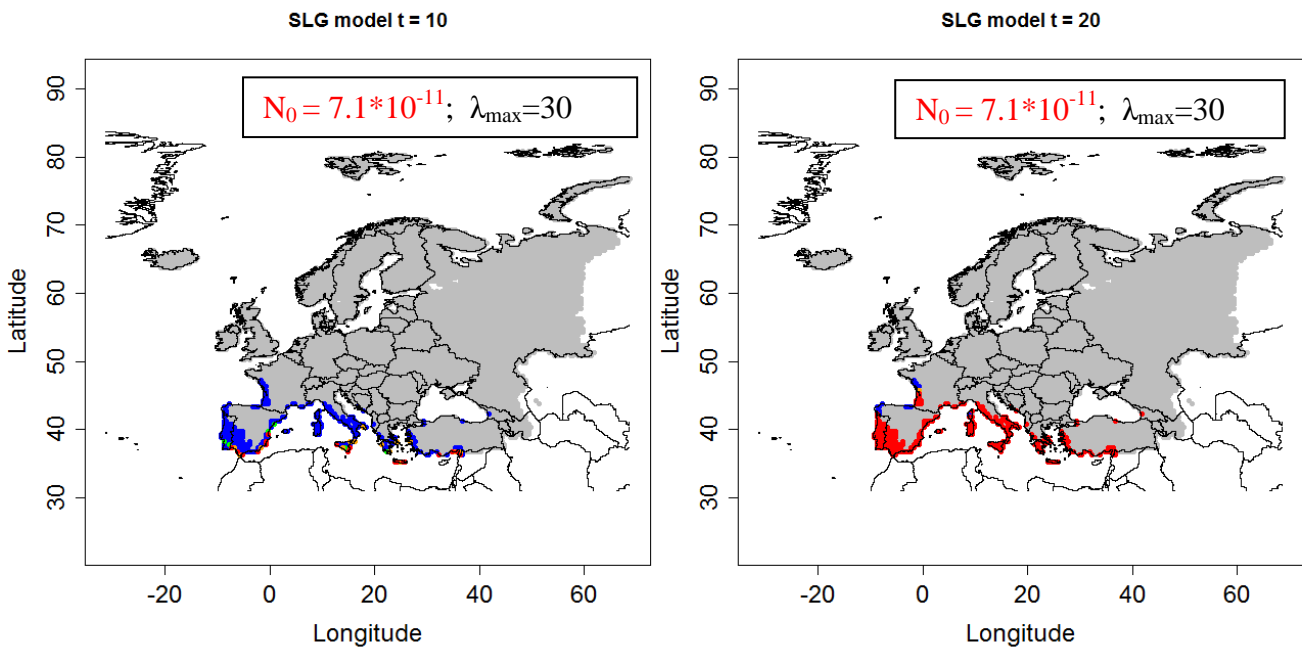


Figure 4.3.1-4: Output of the SLG model for *E. crassipes* for 10 and 20 years with a higher value for N_0 , based a CLIMEX model by Darren Kriticos and Sarah Brunel (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 years ; $R:> res = slg(N0=7.1*10^{-11},lmax=30, t=10)$

Right Picture: 20 years; $R:> res = slg(N0=7.1*10^{-11},lmax=30, t=20)$

Sensitivity analysis / capturing uncertainty: SLG for different λ_{max} - values

The sensitivity analysis shows that changes in λ_{max} - values (figures 4.3.1-5 and 4.3.1-6), factor is much higher compared to changes in N_0 .

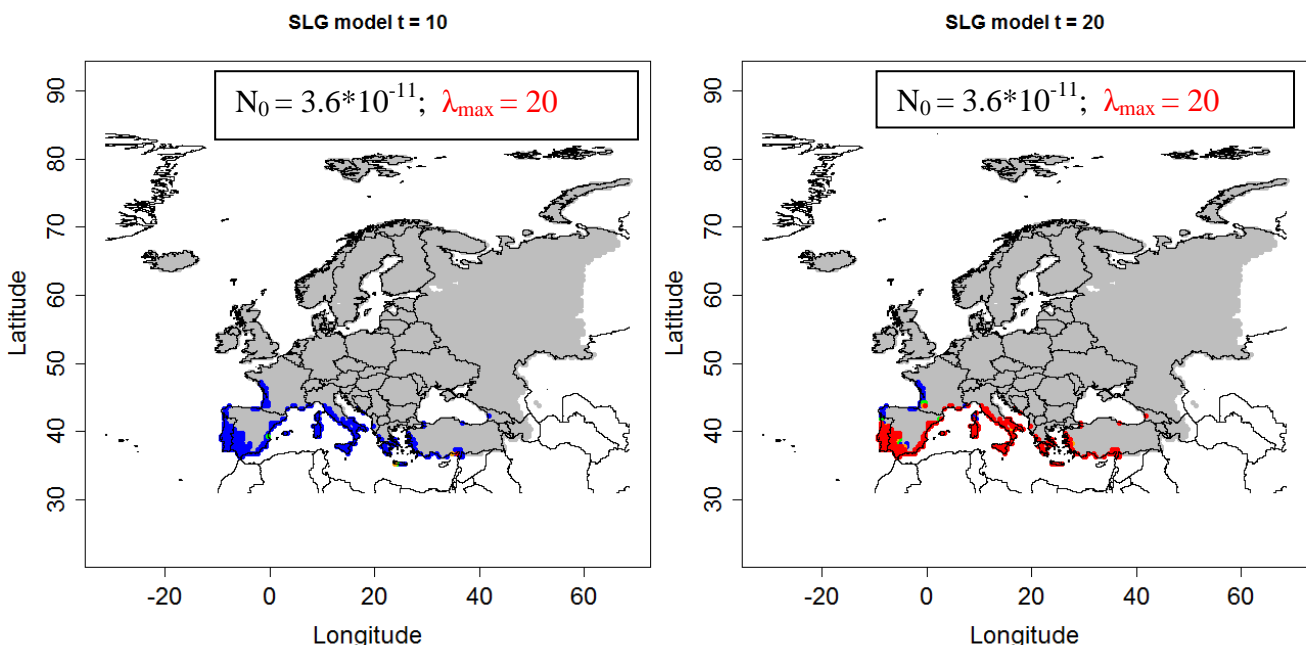


Figure 4.3.1-5: Output of the SLG model for *E. crassipes* for 10 and 20 years with a lower value for λ_{max} , based a CLIMEX model by Darren Kriticos and Sarah Brunel (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 years ; $R:> res = slg(N0=3.6*10^{-11},lmax=20, t=10)$

Right Picture: 20 years; $R:> res = slg(N0=3.6*10^{-11},lmax=20, t=20)$

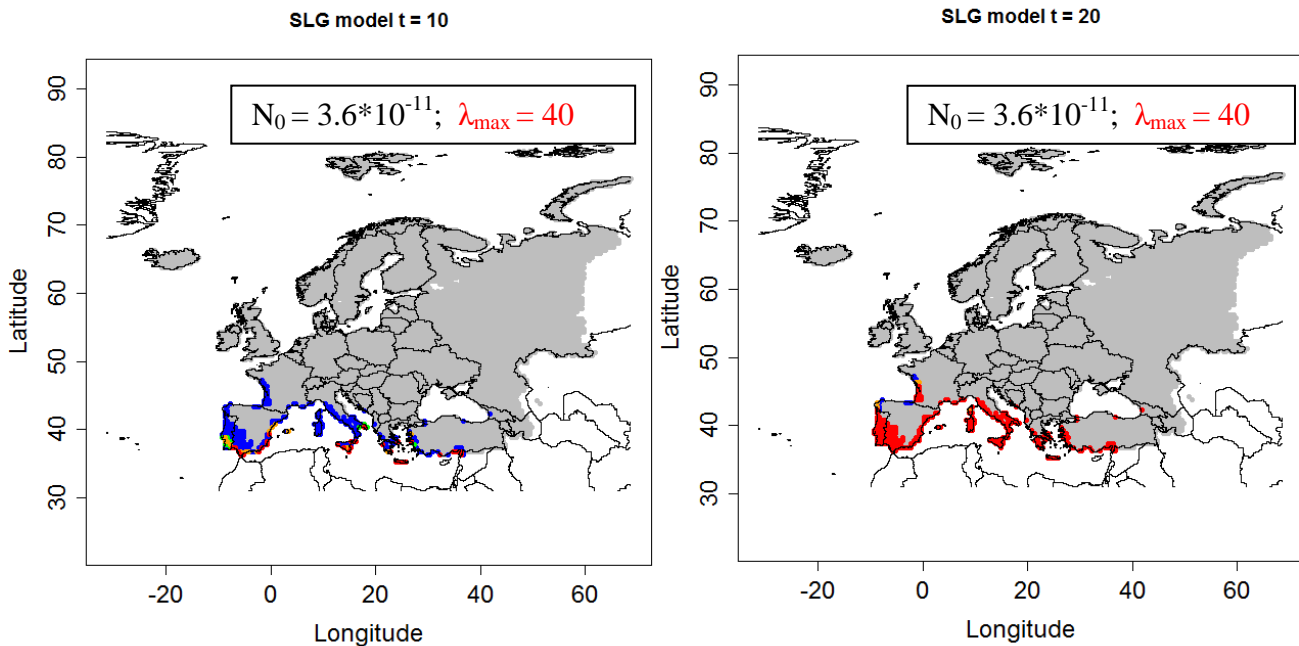


Figure 4.3.1-6: Output of the SLG model for *E. crassipes* for 10 and 20 years with a higher value for λ_{\max} , based a CLIMEX model by Darren Kriticos and Sarah Brunel (blue dots: $0 < N_t \leq 25$, green dots: $25 < N_t \leq 50$, orange dots: $50 < N_t \leq 75$, red dots: $75 < N_t \leq 100$, grey dots: $N_t=0$, white: no data).

Left Picture: 10 years ; R:> res = slg(N0=3.6*10⁻¹¹),lmax=40, t=10)

Right Picture: 20 years; R:> res = slg(N0=3.6*10⁻¹¹),lmax=40, t=20)

Feedback from the expert Sarah Brunel:

The results from the population dynamics model reflects what is expected by the expert.

4.3.1.3 Model 3: Radial Range expansion model (RR)

This model aims to determine the potential spread of a species introduced in the PRA area based on the radial rate expansion parameter. The model output is overlapped with the niche map ($EI > 0$).

Estimates of parameters

- **Radial rate of range expansion per year**

RR = 50 km/year

To consider as well human assisted spread, a value of 100 km / year was used.

Considering uncertainty:

RR= 30 km/year and RR = 70 km / year were tested.

- **Time frame:** t = 10 – 20 years
- **Entry point(s)** or simulation of an introduction at a place
 - Southern Spain (-6.2,38.5), where the species is present

Results

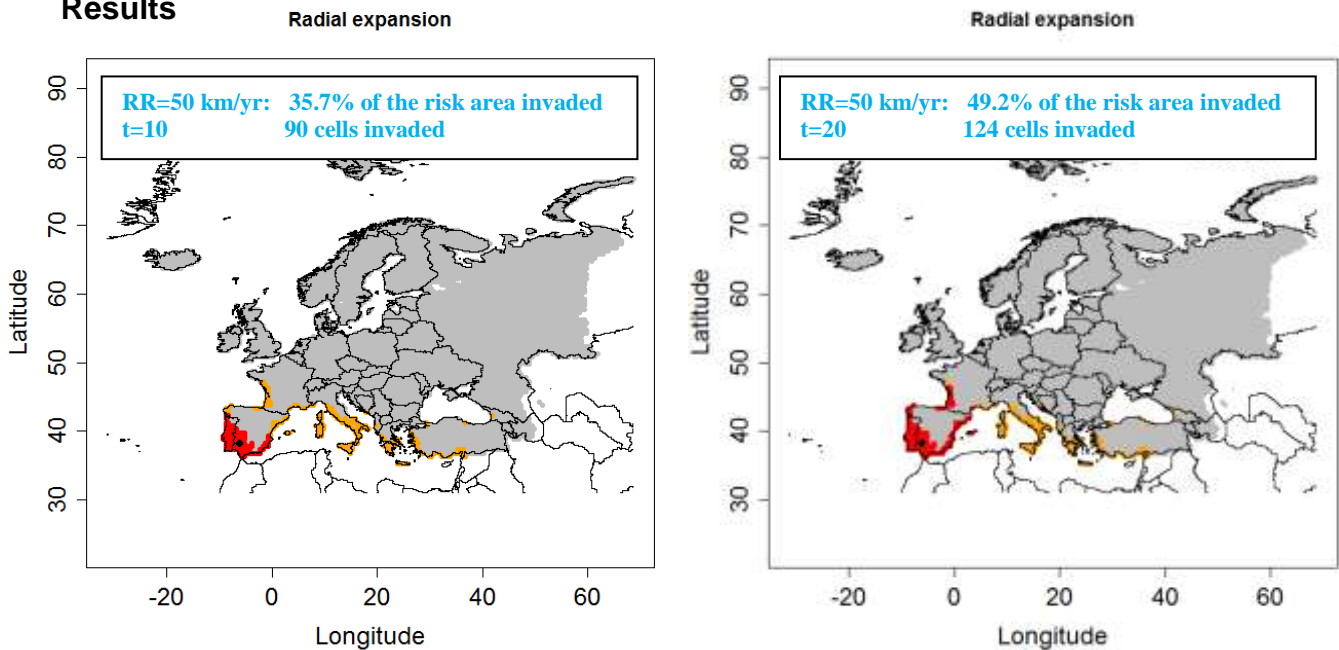


Figure 4.3.1-7: Radial range expansion of *E. crassipes* for $t=10$ and 20 years, $RR=50$ km/year and an entry point in Southern Spain based on a CLIMEX model by Darren Kriticos and Sarah Brunel (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data)

Left picture: 10 years, $R:> res = radial(RR=50,t=10,coord=c(-6.2,38.5))$

right picture: 20 years, $R:> res = radial(RR=50,t=20,coord=c(-6.2,38.5))$

Sensitivity analysis / capturing uncertainty: testing of different RR-values

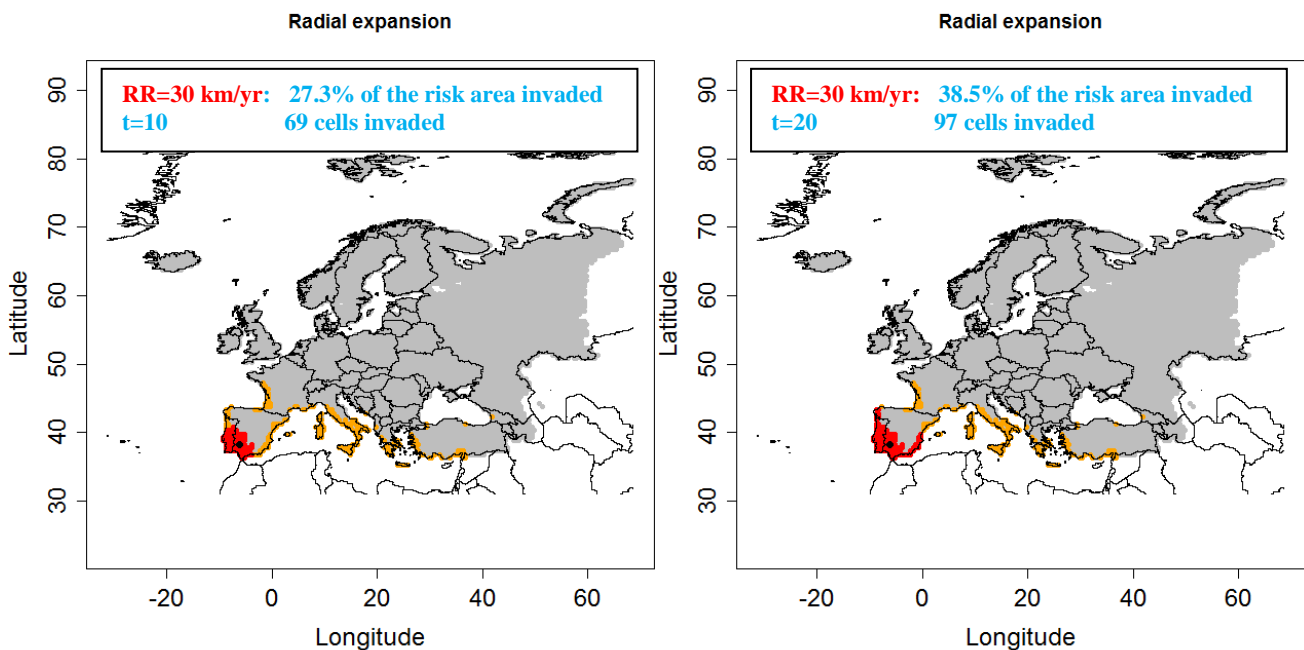


Figure 4.3.1-8: Radial range expansion of *E. crassipes* for $t=10$ and 20 years, $RR=30$ km/year and an entry point in Southern Spain based on a CLIMEX model by Darren Kriticos and Sarah Brunel (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: $EI=0$, white: no data)

Left picture: 10 years, $R:> res = radial(RR=30,t=10,coord=c(-6.2,38.5))$

right picture: 20 years, $R:> res = radial(RR=30,t=20,coord=c(-6.2,38.5))$

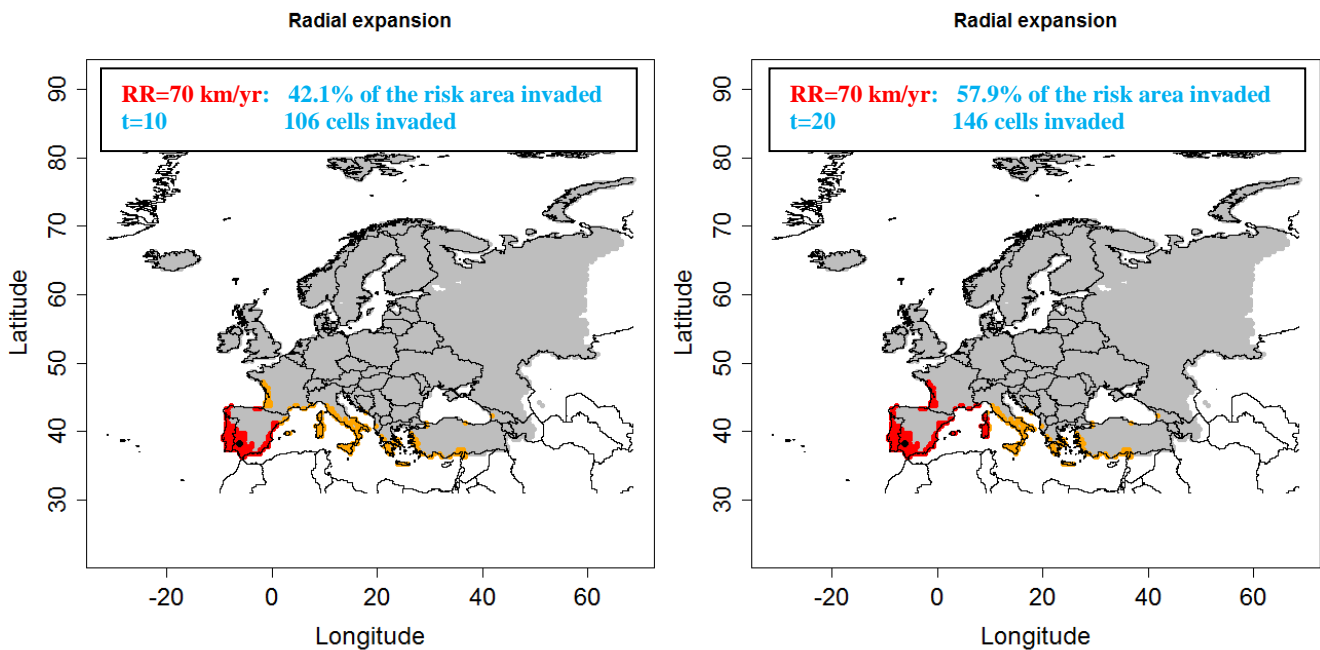


Figure 4.3.1-9: Radial range expansion of *E. crassipes* for t=10 and 20 years, RR=70 km/year and an entry point in Southern Spain based on a CLIMEX model by Darren Kriticos and Sarah Brunel (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data)

Left picture: 10 years, $R:> res = radial(RR=70,t=10,coord=c(-6.2,38.5))$

right picture: 20 years, $R:> res = radial(RR=70,t=20,coord=c(-6.2,38.5))$

Sensitivity Analysis : test 100 km / year to take account long distance, human assisted spread

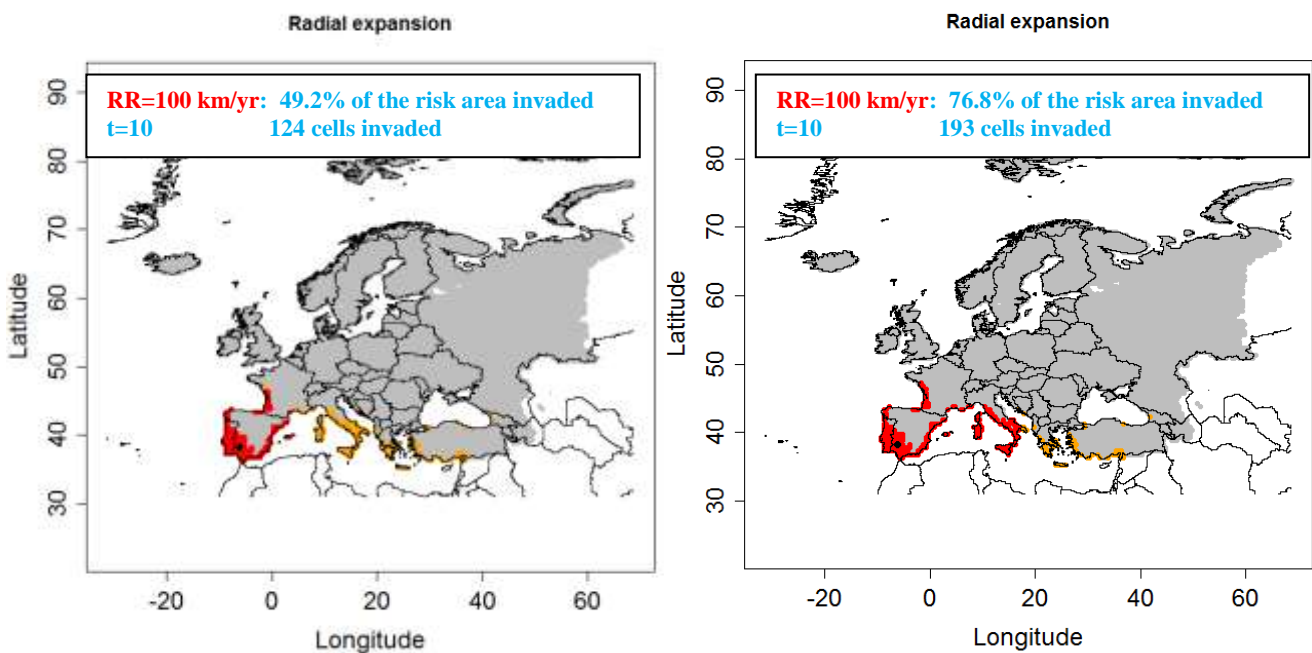


Figure 4.3.1-10: Radial range expansion of *E. crassipes* for t=10 and 20 years, RR=100 km/year and an entry point in Southern Spain based on a CLIMEX model by Darren Kriticos and Sarah Brunel (red dots: invaded cells, orange dots: non invaded but suitable cells, grey dots: EI=0, white: no data)

Left picture: 10 years, $R:> res = radial(RR=100,t=10,coord=c(-6.2,38.5))$

right picture: 20 years, $R:> res = radial(RR=100,t=20,coord=c(-6.2,38.5))$

Feedback on the results of the radial range expansion by the expert Sarah Brunel
The Radial Range Expansion Model maps the spread of *E. crassipes* with acceptable results.

4.3.1.4 Model 5: Deterministic version of the dispersal kernel (DK)

This type of model requires: a population growth model, a dispersal kernel (2Dt in this case) and the proportion of population engaged in dispersal.

Estimates of parameters

- **The starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K).

$$N_0 = 3.6 \times 10^{-11} \%$$

- **The multiplication factor λ_{\max}**

λ_{\max} is the maximum year to year multiplication factor (“finite growth rate”) that a population could achieve under optimal conditions assuming unlimited space

$$\lambda_{\max} = 30$$

- **Shape parameter of the 2Dt dispersal kernel p**

(number of degrees of freedom)

For $p = 1$, this kernel has a Cauchy distribution (thick tail; a large number of individuals disperses further than 3σ) and for $p \rightarrow +\infty$, it has a normal distribution (thin tail; individuals disperse at short distance).

- if we take into account more natural spread we have short distance dispersal if only and apply $p=50$
- if we also take long distance dispersal into account (e.g. with transport of plant material) we apply $p=10$

- **Scale parameter for the distance of the 2Dt dispersal kernel (u)**

Here we use $u = 50$ km (see 4.1.1, as well 30 km and 70 km)

- **presence file**

The presence file contains the coordinates for the entry point and N_0

Three different values for N_0 were tested :

“normal” value $N_0 = 3.6 \times 10^{-11} \%$

Lower value $N_0 = 1.8 \times 10^{-11} \%$

Higher value $N_0 = 7.1 \times 10^{-11} \%$.

Results

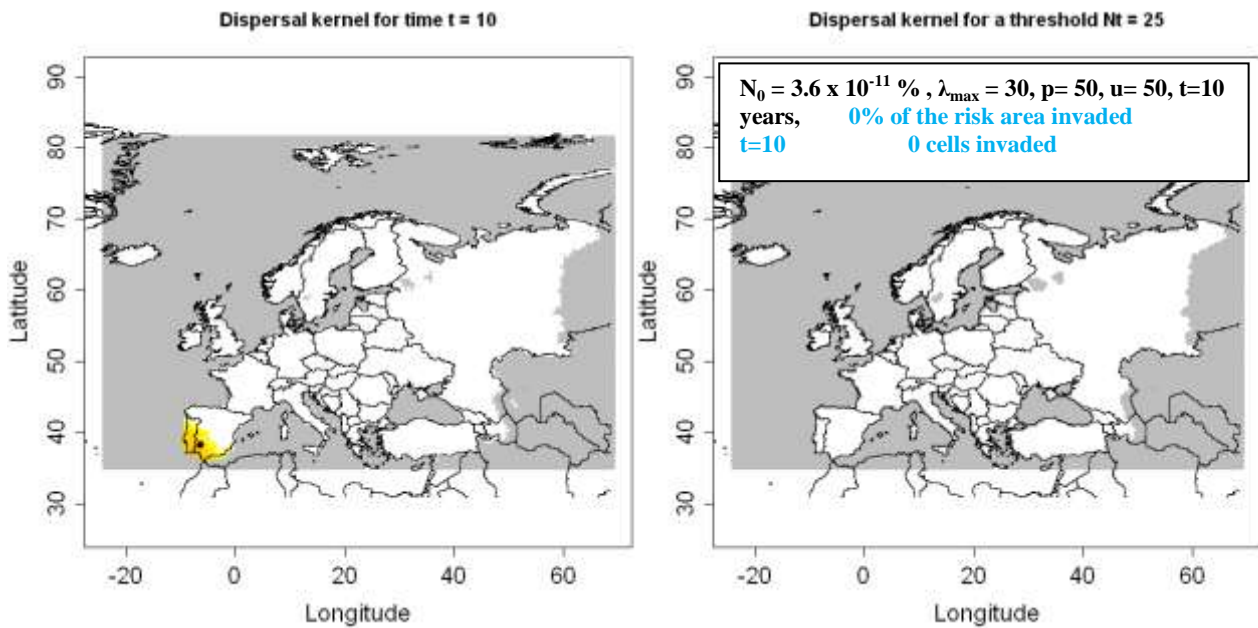


Figure 4.3.1-11: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{\max} = 30$ for 10 years ($R:> res = dispk(t=10, lmax=30, p=50, u=50)$).

Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt ≥ 10%). Grey means no data)

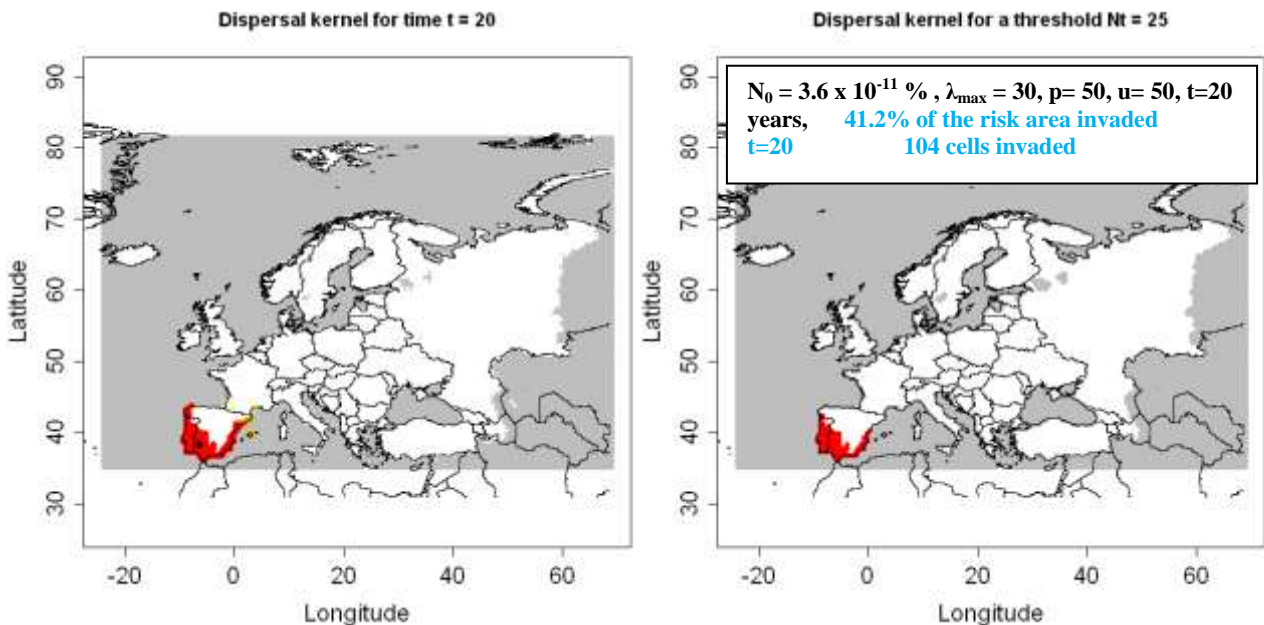


Figure 4.3.1-12: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes*; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{\max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=50, u=50)$).

Left Picture: (Nt: population abundance (%); graduated colors from white (Nt < 10⁻⁶ %) to yellow, orange and red (Nt ≥ 10%). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where Nt ≥ threshold, white: cells where Nt < threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test a lower value for λ_{\max} (20)

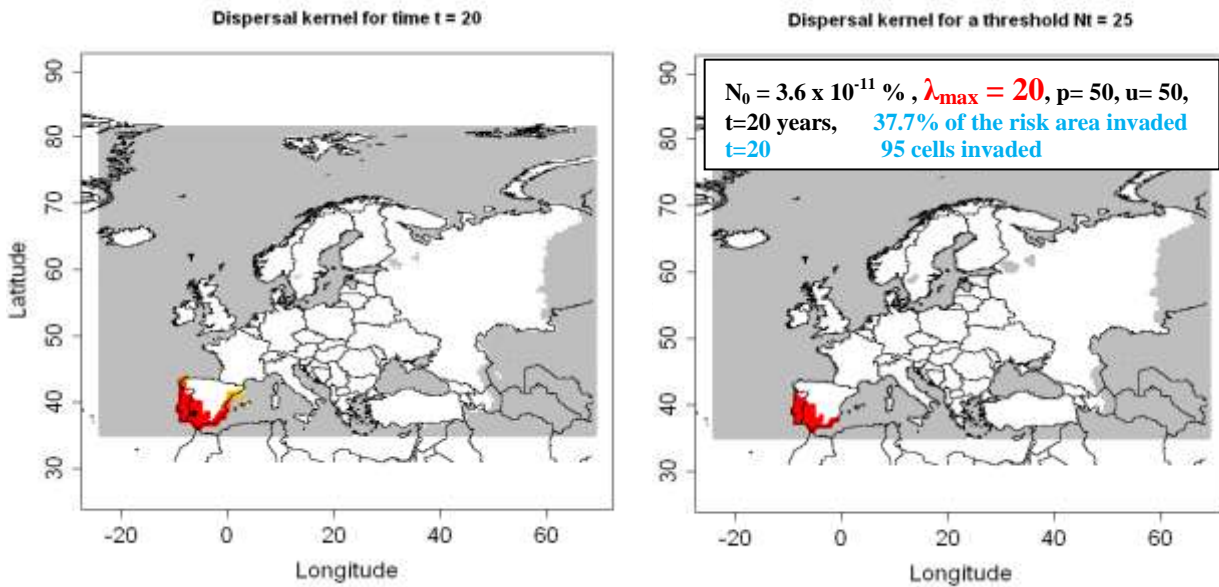


Figure 4.3.1-13: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes*; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{\max} = 20$ for 10 years ($R:> res = dispk(t=20, lmax=20, p=50, u=50)$).
Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{(-6)}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)
Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test a higher value for λ_{\max} (40)

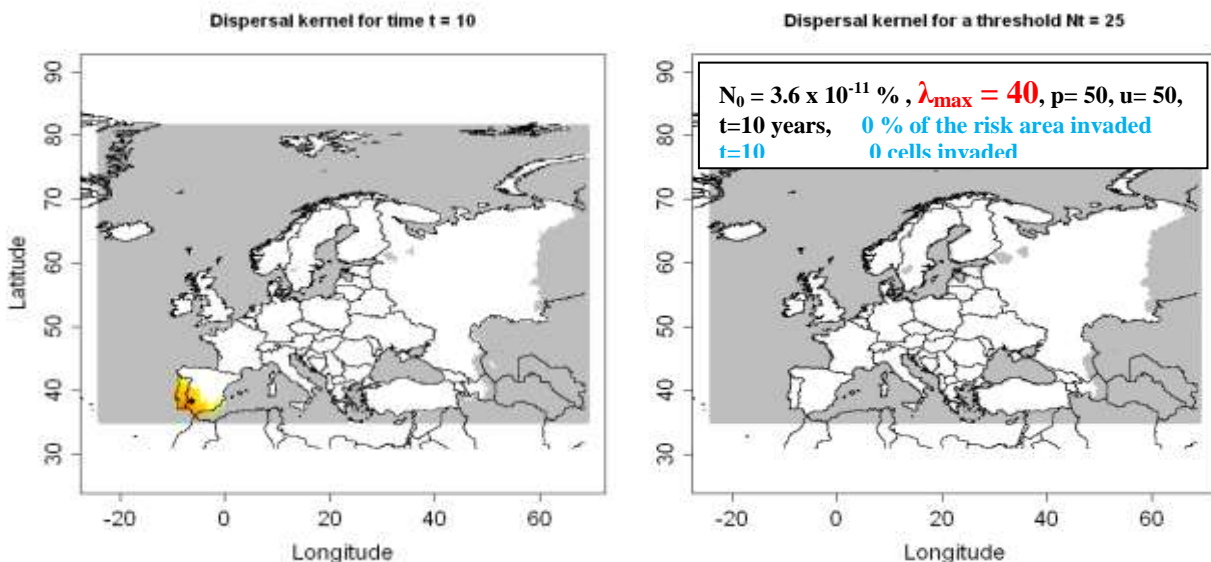


Figure 4.3.1-14: Output of the dispersal kernel model based on the CLIMEX for *E. crassipes* model by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{\max} = 40$ for 10 years ($R:> res = dispk(t=10, lmax=40, p=50, u=50)$).
Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{(-6)}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)
Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

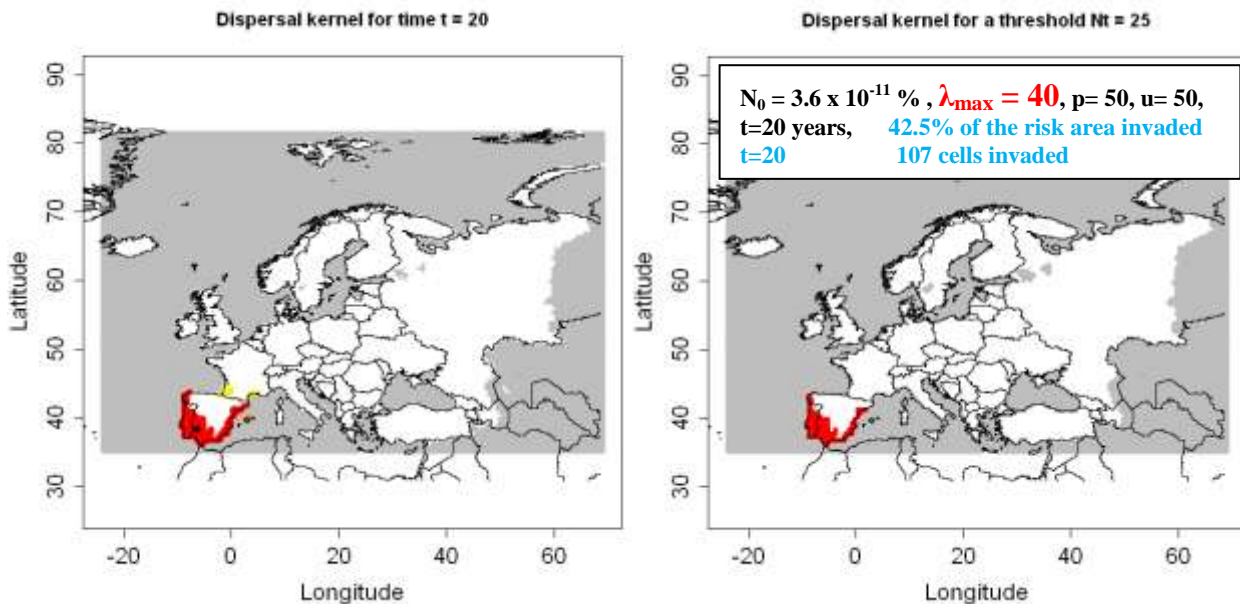


Figure 4.3.1-15: Output of the dispersal kernel model based on the CLIMEX *E. crassipes* model by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{max} = 40$ for 20 years ($R:> res = dispk(t=20, lmax=40, p=50, u=50)$).

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis / capturing uncertainty: test of lower and higher values for N_0

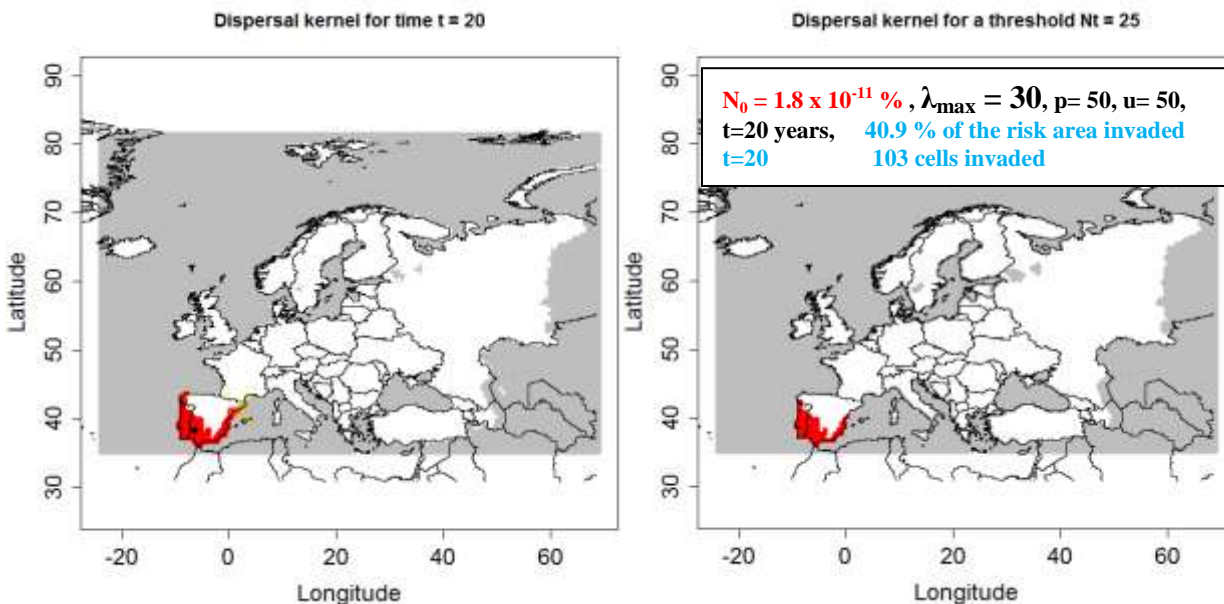


Figure 4.3.1-16: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 1.8 \times 10^{-11}$ and $\lambda_{max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=50, u=50)$).

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

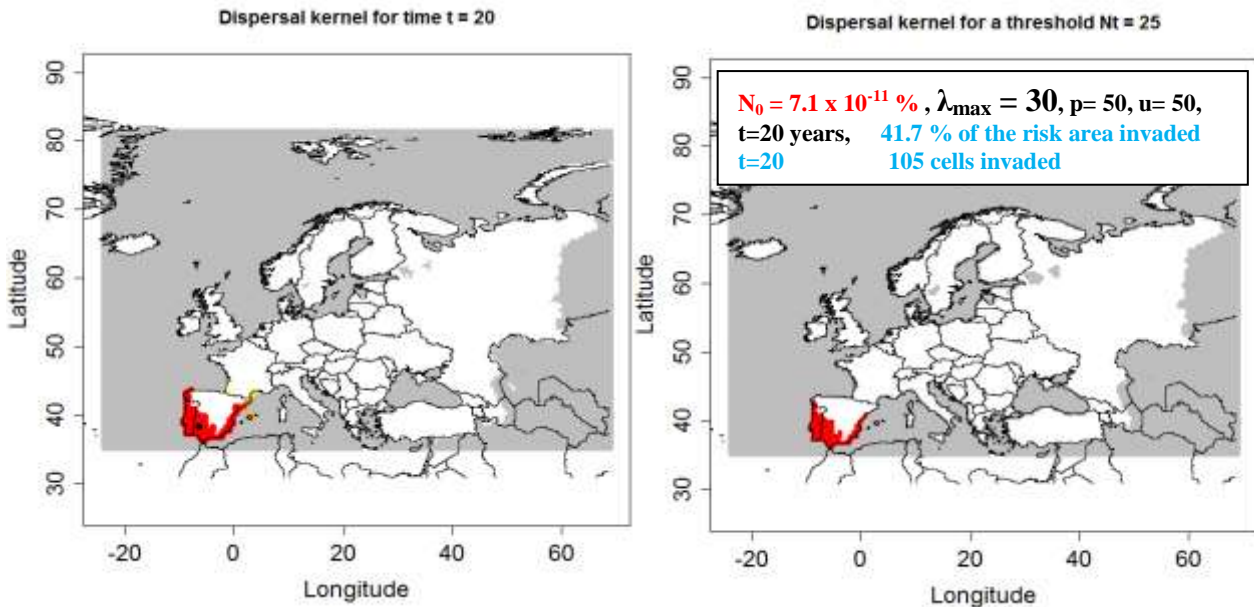


Figure 4.3.1-17: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 7.1 \times 10^{-11}$ and $\lambda_{\max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=50, u=50)$).

Left Picture: (N_t : population abundance (%)); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis: test a small p ($p=10$) for taking into account long distance spread

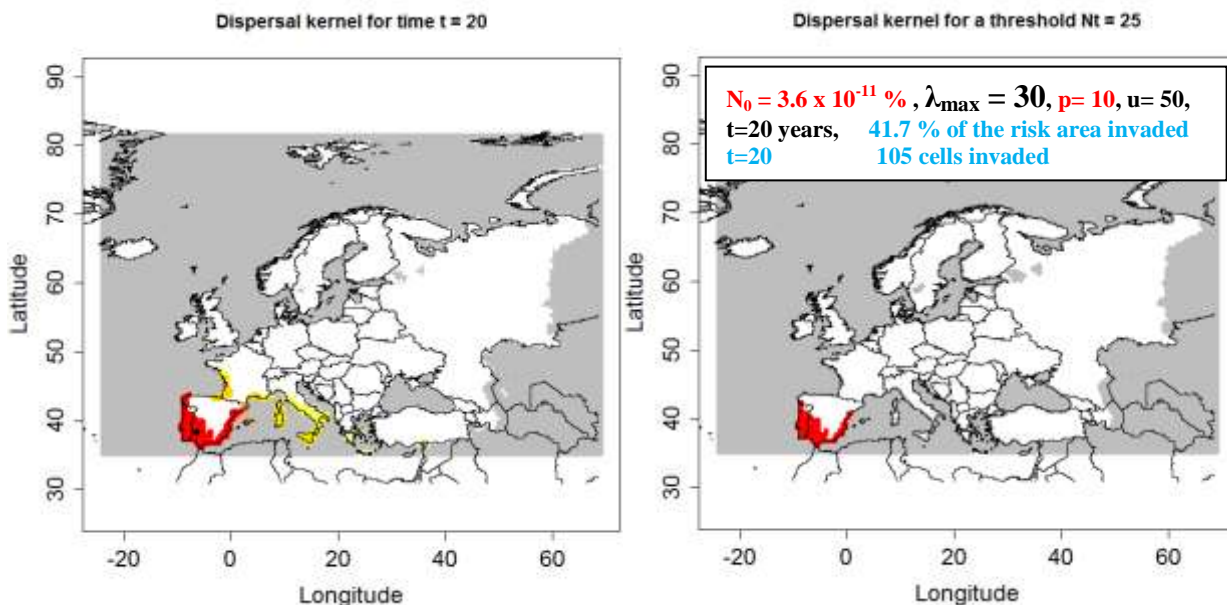


Figure 4.3.1-18: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{\max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=10, u=50)$).

Left Picture: (N_t : population abundance (%)); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data)

Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis: test a higher value for p (p=70)

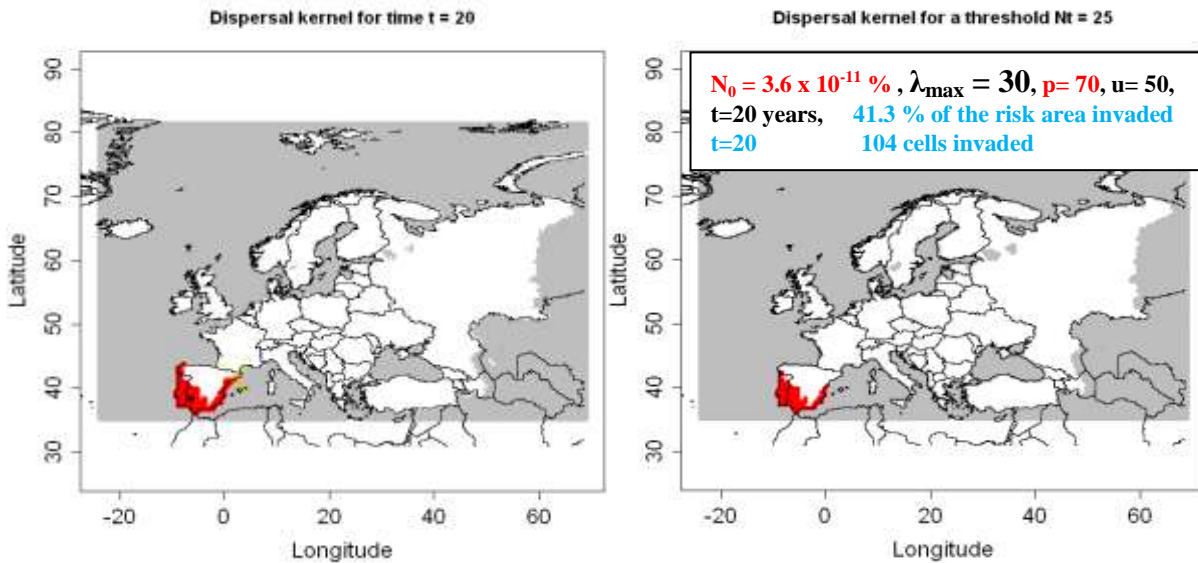


Figure 4.3.1-19: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=70, u=50)$).

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data); Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Sensitivity Analysis: test different values for the scale parameter u (u=30 km and u=70 km)

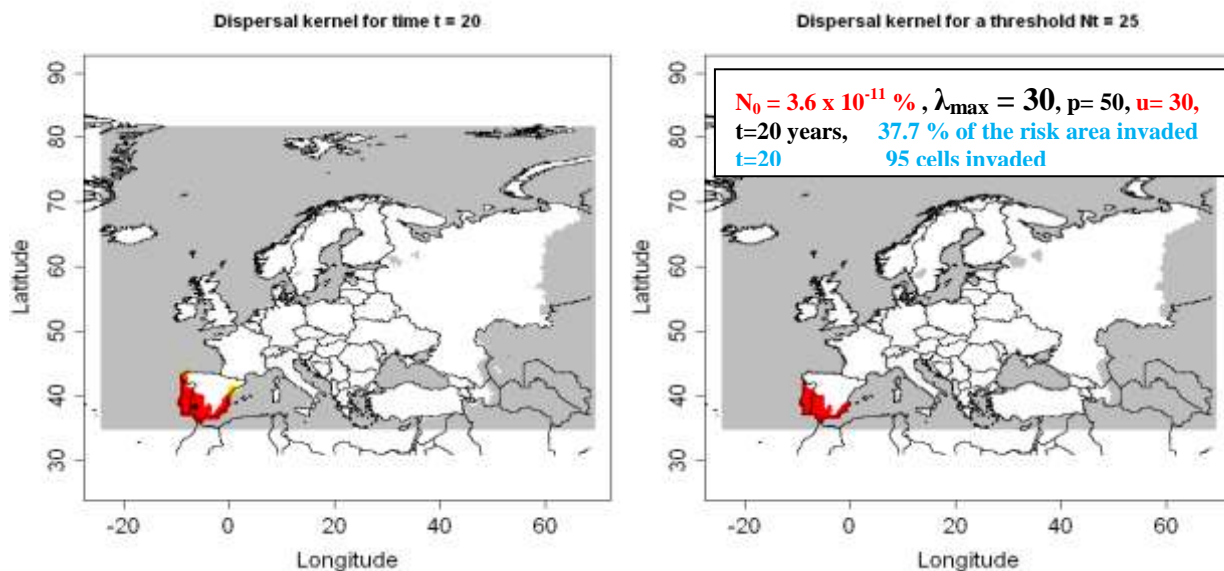


Figure 4.3.1-20: Output of the dispersal kernel model based on the CLIMEX model for *E. crassipes* by Darren Kriticos and Sarah Brunel; $N_0 = 3.6 \times 10^{-11}$ and $\lambda_{max} = 30$ for 20 years ($R:> res = dispk(t=20, lmax=30, p=50, u=30)$).

Left Picture: (N_t : population abundance (%); graduated colors from white ($N_t < 10^{-6}$ %) to yellow, orange and red ($N_t \geq 10\%$). Grey means no data). Right picture: with a threshold = 25 %. The population abundance (%) is above this threshold in red cells. (red dots: cells where $N_t \geq$ threshold, white: cells where $N_t <$ threshold. Grey means no data)

Feedback from expert Sarah Brunel and summary of the results for the Dispersal Kernel Model

The application of the Dispersal Kernel Model is felt to be less intuitive compared to the other two tested models. The higher number of parameters and the number of the resulting maps after applying the sensitivity analysis is a little bit confusing.

Table 4.3.1-1 summarizes the results of the sensitivity analysis for the different parameters of the dispersal kernel model. While changes in the starting population N_0 and of the shape parameter p do not lead to changes in the numbers of invaded cells after 20 years, the multiplication factor λ_{max} and the scale parameter reduce the number of invaded cells by 9% by using lower parameter values.

E. crassipes is a species with a rather small range of suitability in Europe (252 suitable cells within the spread module). This could be one reason that the changes in the parameters do not lead to very big changes in the output of the models.

Table 4.3.1- 1: Summary of results from the sensitivity analysis as reflected in the number of invaded cells and percentage of invaded area for a time frame of 20 years

Parameter	Lower value			Higher value		
	Change compared to "normal"	Number of invaded cells	Relative to normal (normal =104)	Change compared to "normal"	Number of invaded cells	Relative to normal
Multiplication factor λ_{max}	- 50%	95	91%	+ 50%	107	103%
N_0	- 50%	103	99%	+ 50%	105	101%
Shape parameter p	More long distance ($p=10$)	105	101%	More short distance ($p=70$)	104	100%
Scale parameter u	- 40%	95	91%	+ 40%	105	101%

4.3.1.5 Summary

The application of Model 1 is useful to show how fast *E. crassipes* can grow without any control measures and which regions are the most favourable ones. Model 3 shows that if long distance spread is taken into account almost the whole suitable area will be invaded after 20 years. Model 5 maps the spread of *E. crassipes* mainly in Spain and Portugal. *E. crassipes* is a species with a rather small range of suitability in Europe. Therefore the range of expansion for this pest is already very limited by the habitat suitability. Changes in parameters do not lead to big changes in the output of the Dispersal Kernel Model.

Summary of the commands for modelling the spread of *E. crassipes*:

```
library(sp)
library(raster)
library(rgdal)
elevmax = F
hostfile = F
  # load the R code
res = slg(N0=3.6*10^(-11),lmax=30,t=10)
res = radial(RR=50,t=10,coord=c(-6.2,38.5))
res = dispk(N0=NULL, t=10,lmax=30, p=50,u=50, presencefile=T,
nentry=NULL, figkm=F,figdd=T)
```

4.4 Pathogen

4.4.1 Pitch canker disease, *Gibberella circinata*

This document was prepared by Christelle Robinet and Annie Yart (INRA Orléans), based on the Guide for the Spread Module Version 0.21 and R-code Version V17, November 23rd, 2010.

4.4.1.1 Information on *Gibberella circinata*

Fungi, Ascomycota, Hypocreales, Nectriaceae.

Teleomorph: *Gibberella circinata* Nirenberg et O'Donnell

Anamorph: *Fusarium circinatum* Nirenberg et O'Donnell

Synonyms: *Fusarium subglutinans* f. sp. *Pini* Hepting, *Fusarium moniliforme* Sheldon var. *subglutinans* Wollenweber, *Fusarium lateritium* f. sp. *Pini* Hepting.

Gibberella circinata is the causal agent of Pitch canker disease which can affect all *Pinus* species but also Douglas fir (*Pseudotsuga menziesii*) (Anon 2009). This disease, causes cankers that girdle branches and is a serious threat to the pine forests because tree mortality may occur after multiple branch infection. Moreover, *Gibberella circinata* may also be soil-borne, cause root rot even on mature trees (Garbelotto et al. 2007) and infect seeds externally or internally (without any symptoms before seed germination).

The anamorph, *Fusarium circinatum*, is a wound pathogen and may occur after mechanical wounds (Sakamoto et al. 2006) as well as after wood boring insect damage (Anonymous 2009). Tree infection occurs by aerial dispersion of conidiospores or by feeding insect vectors (Gordon et al. 2001, Schweigkofler et al. 2004).

Gibberella circinata is officially reported in USA, Mexico, Haiti, South Africa, Japan, Chile, Iraq, Japan, Kyushu, Ryukyu Archipelago, South Africa (EPPO 2005, EFSA 2010), and also in Europe: Spain, France, Portugal and Italy, mainly in coastal areas (Anonymous 2009, EFSA 2010).

Pitch canker has been described in several regions of Spain but always as isolated outbreaks originating from nurseries (EPPO 2005 and 2006a).

It was first reported in France in 2006 on declining pines and Douglas fir (EPPO 2006b) and visual inspection combined with laboratory tests confirmed pest eradication (EPPO 2008). But new isolated outbreaks (Vosges 2008 and Vendée, Côtes d'Armor, EPPO 2009a) were reported and studies were initiated to identify the origin of the infection (EPPO 2009a and 2010).

During the same period, *Gibberella circinata* dieback symptoms in Italy were identified on the basis of morphological and cultural characteristics confirmed with PCR with specific primers (Carlucci et al. 2007) and the fungus was eradicated (EPPO 2009b) while in Portugal its presence on symptomatic plant samples was confirmed by PCR and pathogenicity tests after a first identification based on morphological and cultural characteristics (EPPO 2009c, Bragança et al. 2009).

Host range

Pinus species

Pseudotsuga menziesii

CLIMEX file

A CLIMEX model was applied in Ganley et al. (2009). Parameters' values were used in CLIMEX and the required file was exported (with latitude, longitude, EI and GI). This model fitted well with the observed disease distribution. However, when using a more recent climate (1999-2007) instead of the past climate (1961-1990) or using an increased spatial resolution, the model predicted favourable conditions in larger areas (EFSA 2010). Therefore caution is needed when using this model and interpreting the results of this study.

4.4.1.2. Comments of the difficulties

It is difficult to find quantitative data to estimate K and λ_{max} . There are perhaps several reasons for this:

- the number of spores is extremely high in an infected tree (some millions), so it is impossible to determine the "population density" to estimate K and λ_{max} .
- as a proxy, we could take the number of trees infected by the disease, but we have no clear information on this. Moreover, there is a latent infection period.

It is also difficult to estimate the spread rate because the infection is usually transmitted from one nursery to another one, and because of control actions. There is long-distance dispersal resulting from trade, humans themselves, or machines carrying the pathogen). The disease can also spread by natural means (wind, rain, insect vector) (EFSA 2010). However, trees in nurseries are under surveillance and as soon as an infection is detected, some eradication measures are applied and the invaded area is contained. Based on the invasion history, there is little short distance (spatial extent of the disease from one introduction point) but relatively more long distance spread from one nursery to another (several introduction points). The latent period probably makes it difficult to detect the pathogen before sale and transport. Consequently, it seems that model 3 is not appropriate and model 5 could be tested with small u (few short-distance dispersal events) and small p (thick tail – high proportion of long-distance spread). However this model will not take into account the observations that dispersal occurs mainly between nurseries and it may overestimate spread in Europe.

4.4.1.3. Qualitative assessment of spread

Estimating spread qualitatively is also difficult. The responses to the spread questions in the EPPO DSS for PRA are given below.

4.01 What is the most likely rate of spread by natural means (in the PRA area)?

Note: Natural population spread, increasing the infested area, can result from the movement of the pest by flight (of an insect), wind or water dispersal (except irrigation), transport by vectors such as insects, birds or other animals (internally through the gut or externally on the fur), natural migration, rhizomial growth.

Consider potential vectors of the pest in the PRA area, the presence of natural barriers, and the suitability of the environment. In this question the mean rate of spread should be taken into account to decide on the rating. The maximum spread capacity should be described in the justification text and the corresponding rating may also be given when the assessors considers it important to describe different scenarios.

Spread can be described as distance covered per unit time (e.g. 50 m /year) or in increasing area occupied (e.g. km²) over time.

very low rate of spread, low rate of spread, moderate rate of spread, high rate of spread, very high rate of spread

Level of uncertainty:	Low	Medium	High
Rating guidance			
<p>1) The pest cannot spread naturally (the vector is absent or it can only spread by intervention of man (e.g. grafting or budding)) or the pest has a very low rate of spread (less than 10 m per year)?</p> <p>Yes very low rate of spread</p> <p>No go to 2</p>			
<p>2) The pest has a low mobility (10 m to 1 km per year) that only allows movement within production sites or within sites of suitable habitat?</p> <p>(Spreading to occupy a circular area at a linear speed of between 10 m and 1 km per year would, within 4 years, lead to up to 50 km² being occupied)</p> <p>Yes low rate of spread</p> <p>No go to 3</p>			
<p>3) The pest has a medium mobility (1km to 10km per year)?</p> <p>(Spreading to occupy a circular area at a linear speed of between 1 and 10 km per year would, within 4 years, lead to between approximately 50 km² and 5,000 km² being occupied)</p> <p>Yes moderate rate of spread</p> <p>No go to 4</p>			
<p>4) The pest has a high mobility (between 10 and 50 km per year)?</p> <p>(Spreading to occupy a circular area at a linear speed of between 10 and 50 km per year would, within 4 years lead to approximately 5,000 and 125,000 km² being occupied)</p> <p>Yes high rate of spread</p> <p>Are there natural barriers that would prevent the natural spread of the pest?</p> <p>Yes moderate rate of spread</p> <p>No go to 5</p>			
<p>5) The pest has a very high mobility (more than 50 km/year)?</p> <p>(Spreading to occupy a circular area at a linear speed of 50 km per year would, within 4 years over 125,000km² would be occupied)</p> <p>Yes very high rate of spread</p> <p>Are there natural barriers that would prevent the natural spread of the pest?</p> <p>Yes high rate of spread (or even lower, depending on e.g. the location and dimension of the natural barriers)</p>			

G. circinata

Rating: **moderate rate of spread**

Level of uncertainty : **medium**

The pathogen can disperse with wind or in water splash (larger than 200 m from an infected pine; Blakeslee et al., 1979; Dwinell et al., 1981; Garbelotto et al., 2008) and also with bark beetles. In mark-recapture experiments, bark beetles, *Ips sexdentatus*, were caught at distance up to 4 km (Jactel 1991). However it may not necessarily establish because wounds are necessary for a successful infection (EFSA 2010).

4.02 What is the most likely rate of spread by human assistance (in the PRA area)?

Note: consider the potential for movement with commodities, packing materials, baggage, mail or conveyances, the fact that the species is intentionally dispersed by people and the ability of the pest to be unintentionally dispersed along major transport routes. For intentionally introduced plants consider spread to the unintended habitat.

Mechanical transmission through human activities (by grafting or budding and contamination of hands, clothing and tools used for pruning, cutting, thinning and preparing the soil) commonly occurs over short distances within the place of production. However, since employees often travel long distances to work and contract workers (that visit many production sites) are commonly employed, it is considered that evidence of mechanical transmission indicates the potential for at least moderate spread.

Very low rate of spread, moderate rate of spread, high rate of spread, very high rate of spread

Level of uncertainty:	Low	Medium	High
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Rating guidance

1 Has a pathway that is not natural spread been identified for this pest?

If yes, the rate of increase in the infested area by human assistance is at minimum moderate go to 2

If no, the rate of increase in the infested area by human assistance is very low

2 Can the pest be transmitted by pollen, seed or (other) plants for planting (cuttings, budwood grafted plants, etc.), plant products, with packaging, conveyance machinery?

If yes, the rate of increase in the infested area by human assistance is at minimum high go to 3

If no, the rate of increase in the infested area is moderate

3 Is the pathway on which the pest is likely to be present widely distributed in the PRA area (trade or movement with persons) or is the pest likely to be moved intentionally by persons in the PRA area? (unintentional movement)

If yes, the rate of increase in the infested area by human assistance is very high

If no, the rate of increase in the infested area by human assistance is high

G. circinataRating: **very high rate of spread**Level of uncertainty: **medium**

The pathogen can be moved unintentionally when trees, pine seeds, wood commodities, wood packages, wood bark are transported (EFSA 2010). Only few data are available about this pathway but, due to the location of infected areas, there is some evidence that the pathogen can be introduced by human assistance (e.g., isolated outbreaks found in France – Vosges, Vendée, and Côtes d'Armor, EPPO 2009a).

4.03 Based on its biological characteristics, how likely is it that the pest will not be contained in case of an outbreak within the PRA area?

Note: consider the biological characteristics of the pest that might allow it to be contained in part of the PRA area. For intentionally introduced plants consider spread to the unintended habitat.

very unlikely, unlikely, moderately likely, likely, very likely.

Level of uncertainty:

of Low

Medium

High

Rating guidance (note that that not all criteria in the selected rating have to be satisfied to choose the rating)

very unlikely

Detection

The pest or its symptoms are very visible. It is easy to detect (no hidden stage). Outbreaks are easy to find and to delimit.

Spread

It spreads very slowly. Only one mechanism of propagule dispersal easy to prevent.

Movement of plants and plant product likely to carry the pest are easy to control..

Reproduction

It reproduces very ineffectively, no propagule/seedbank.

Control

Effective plant protection products are available, easy to obtain, inexpensive.

Hosts and habitats

Host plants are very limited (abundance/number of species) around the outbreak area. Limited suitable habitats (i.e. plant is not extremely adaptable and able to grow almost anywhere)

unlikely

Detection

The pest or its symptoms are visible. Detection is possible with little effort. Incursions can be limited.

Spread

Natural spread is slow and spread through mechanical

	<p>transmission is easy to prevent. Movement of plants and plant product likely to carry the pest are easy to control.</p> <p>Reproduction It reproduces in low numbers</p> <p>Hosts and habitats Host plants/habitats are limited (abundance/number of species, see question 3.09) around the outbreak area. The host plant is not present all year around, and the pest does not survive in the absence of the host plant.</p> <p>Control Effective plant protection products are available but restrictions are possible or products are expensive. Cultivation practice is available to contain the pest (e.g. pruning, bagging, burning). It is easy to establish a zone around the outbreak with no host plants or to prevent human spread (strict hygienic measures can be implemented by producers).</p>
moderately likely	<p>Detection The pest or its symptoms are visible with some effort (e.g. microscopy). Early detection is essential for containment success, infection is detectable before spread.</p> <p>Spread Spread is slow. For pest which need a vector, spread can be limited when the vector is controlled. Movements of plants for planting are easy to control but not movement of plant products.</p> <p>Reproduction Reproduction strategy is effective. Survival of the pest as latent infection is possible.</p> <p>Hosts and habitats Host plants/habitats are available around the outbreak.</p> <p>Control Plant protection products would be effective but are not or no longer authorised.</p>
likely	<p>Detection The pest and its symptoms are not visible in the first years of infection. It is present as latent infections or in asymptomatic plants and can spread unseen. Asymptomatic weeds, contaminated irrigation water and crop debris act as reservoirs for the pest.</p> <p>Spread The pest spreads quickly by natural means. When a vector is needed, it is difficult to prevent its spread. For a successful containment, movements of plants and plant</p>

	<p>products likely to carry the pest have to be strictly prohibited.</p> <p>Reproduction The reproductive strategy is very effective.</p> <p>Host and habitats Host plants/habitats are widely distributed (see question 3.09), e.g. in private gardens; all <u>infected</u> plants need to be treated to limit spread.</p> <p>Control No effective treatments are available. To contain the pest host plants have to be eliminated or should not be planted in an area around the outbreak. Human spread over short distance is difficult to prevent (spread by tools...)</p>
very likely	<p>Detection The pest and its symptoms are not visible, at least in the first years of infection. The pest is of a small size, hidden, small eggs in soil, difficult to destroy, long lived individuals, resilient life stages, pest is polyphagous, intensive survey necessary, weeds as alternative hosts, high fecundity, fast life cycle, efficient mate finding.</p> <p>Spread When a vector is needed, it is impossible to prevent its spread. The pest has an effective spreading mechanism, it has already spread effectively when symptoms appear. For a successful containment, movements of plants and plant products likely to carry the pest have to be strictly prohibited.</p> <p>Reproduction Multiple generations are produced in one year, for plants, prolific viable seed production. The pest has an efficient mate finding mechanism.</p> <p>Hosts and habitats The pest has a large host range and host plants/habitats are very widely distributed (see question 3.09), e.g. in private gardens; for plants, long lived seed bank, can grow in a multitude of habitats (i.e. shade tolerant, infertile soil tolerant, drought tolerant, etc.)</p> <p>Control The pest is difficult to destroy with long lived individuals, resilient life stages, No effective treatments are available. To contain the pest host plants have to be eliminated or should not be planted in an area around the outbreak. Human spread over short distance is nearly impossible to prevent (spread by tools...).</p>

G. circinata

Rating: **moderately likely**

Level of uncertainty: **high**

It is particularly difficult to answer to this question. Until now, the pathogen has always been eradicated but there is a risk not to detect the pathogen at the beginning (latent phase). In fact, detection is difficult but eradication after detection seems feasible.

In a sense, it can be **unlikely** that the pest will not be contained because:

- Spread: is slow (spread by natural means)
- Control: cultivation practice is available to contain the pest (burning) and movement of plants and plant product likely to carry the pest are easy to control.

But in another sense, it can be **likely** that the pest will not be contained because:

- Detection: the pest and its symptoms are not visible in the first years of infection. It is present as latent infections or in asymptomatic plants and can spread unseen.
- Reproduction: The reproductive strategy is very effective (but low chance to establish because it requires some wounds)
- Hosts and habitats: Host plants/habitats are widely distributed, e.g. in private gardens; all infected plants need to be treated to limit spread.

This assessment is in agreement with EFSA report (EFSA 2010).

Conclusion on the probability of spread

4.04 Describe the overall rate of spread

Note: The overall rate for spread should combine the assessments of the rate for natural spread and human spread. In most situations the overall rate of spread equals the highest rate of spread given to either question 4.01 or 4.02.

very low rate of spread, low rate of spread, moderate rate of spread, high rate of spread, very high rate of spread

Level of uncertainty:	Low	Medium	High
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The assessor should also give his/her best estimate for the following questions:

4.05 What is your best estimate of the time needed for the pest to reach its maximum extent in the PRA area?

Note: In this question, ignore any containment measures (considered in question 4.03) that may be taken to prevent or contain the spread of the pest. The maximum extent can be considered to be the area of potential establishment defined in question 3.08.

The factors to be taken into account in deciding on the time to reach its maximum extent include:

- The rate of spread,
- The survival and reproductive rate
- The relationship between population density and impact thresholds
- The time taken for impacts to be observed, e.g. through a lag phase
- Climate and land use change

4.06 Based on your responses to questions 4.01, 4.02, and 4.05 while taking into account any current presence of the pest, what proportion of the area of potential establishment do you expect to have been invaded by the organism after **5 years**?

Level of uncertainty:	of	Low	Medium	High
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Go to the next section

G. circinata

Rating 4.04: **very high rate of spread**

Level of uncertainty: **medium**

G. circinata

Rating 4.05: **10 years**

Level of uncertainty: **high**

G. circinata

Rating 4.06: **50%**

Level of uncertainty: **high**

It is also difficult to say because spread seems to occur mainly at long distance between points (nurseries), therefore the area of spread would perhaps remain relatively restricted compared to the area of potential establishment. If we ignore containment measures, the spread will mainly depends on human-mediated transportation, which is a rather random process in the number of transportations and in the geographical areas connected. For these two questions, it seems essential to obtain some simulations from the spread module to define more clearly a range of possible outcomes.

4.4.1.4 Application of the spread module

The main source of information to find the estimates of the parameters is a paper published by Cook & Matheson in 2008. They developed a generic model that combined spread and economic impact. They estimated the parameters based on Zadocks & Shein (1979), refined by expert opinion. Although these estimates may be subject to errors, we based our spread model on them because, at least until now, no other estimates were available to our knowledge.

We used the CLIMEX model developed by Ganley et al. (2009) and the *Pinus* distribution provided by EFI (Tröltzsch et al. 2009) (Fig. 4.4.1-1) to determine the area of potential establishment (Fig. 4.4.1-2) and the adjusted GI map (Fig. 4.4.1-3).

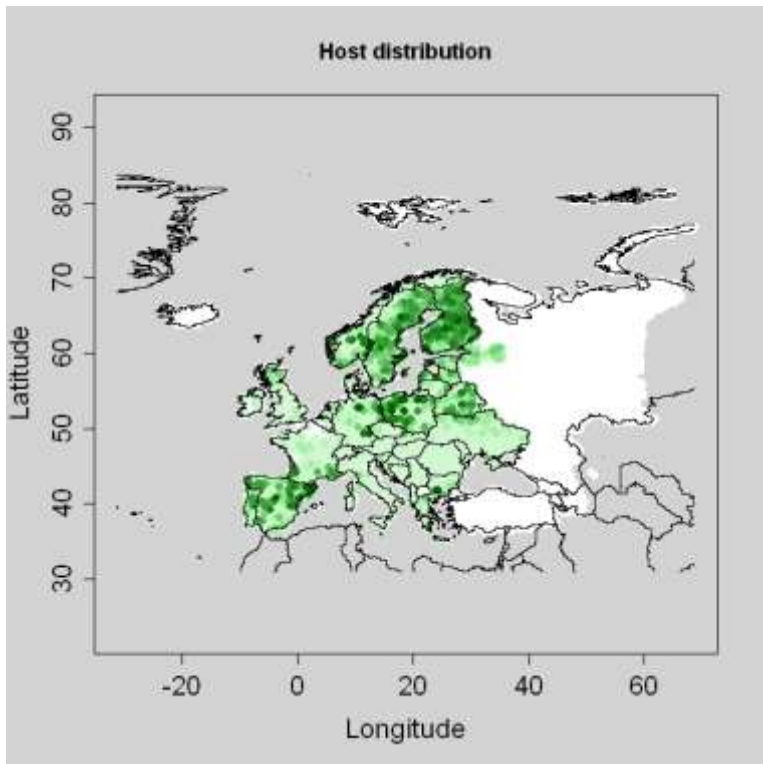


Fig. 4.4.1-1. Proportion of land covered by pines from 0 (light green) to 1 (dark green).

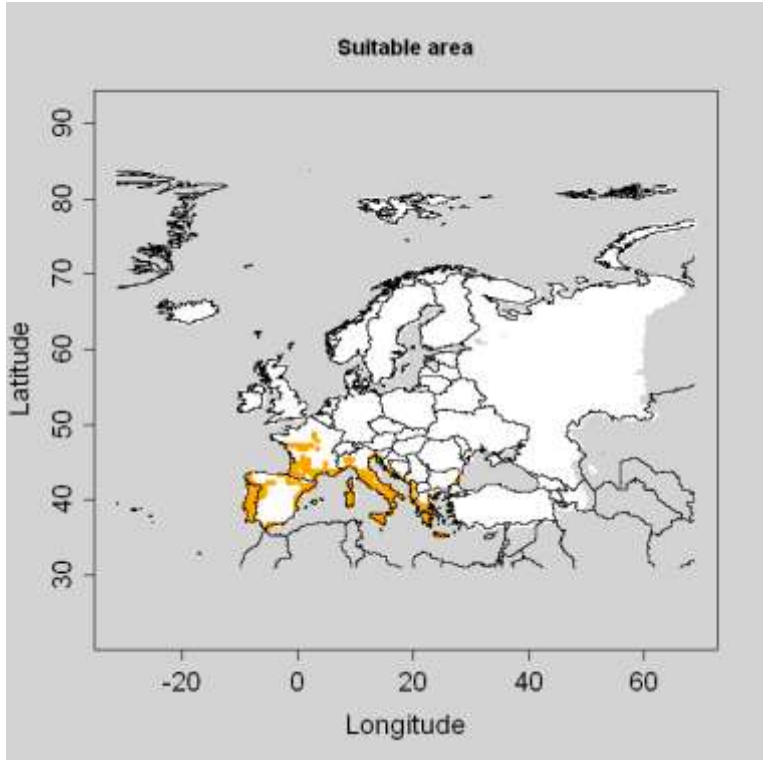


Fig. 4.4.1-2. Area of potential establishment (EI > 0 and presence of host trees).

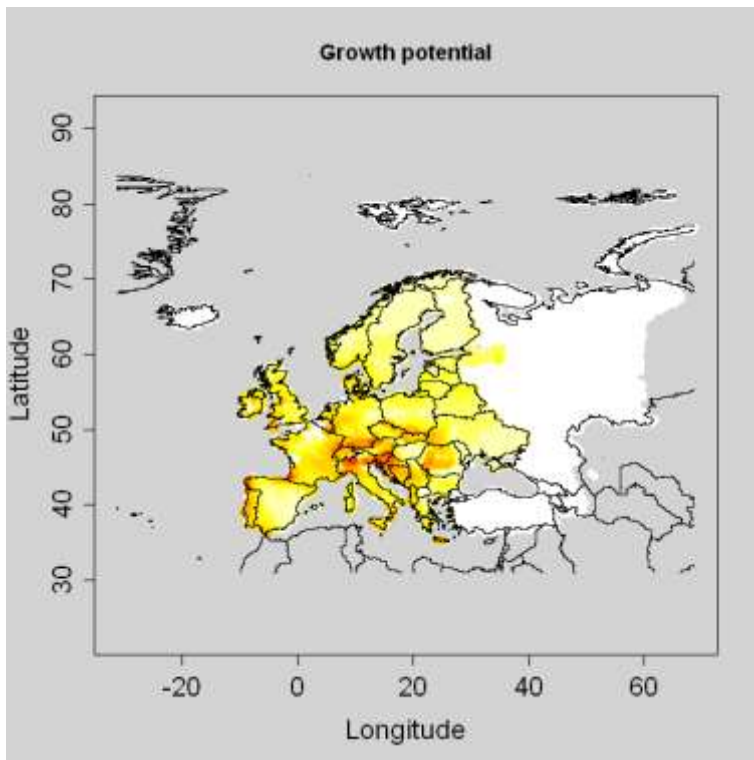


Fig. 4.4.1-3. Adjusted GI from 0 (light yellow) to 100 (red).

4.4.1.5. Model 1: Population dynamics model (SLG)

For this model we assume that an initial population abundance N_0 (%) is introduced in each suitable cell (cells where $EI > 0$) and then we simulate the “spread” or more precisely the growth within each cell according to a logistic function. On the output map, we will see areas which are the most suitable for the population growth if some individuals were introduced there.

- **Starting population N_0**

N_0 is the population abundance for all suitable cells at time $t = 0$ expressed as a percentage of the maximum abundance (carrying capacity K). K can in this case be derived from the maximum number of beetles per tree and by calculating this for a grid cell by taking into account the number of trees per m^2 or ha and the size of a grid cell of 1579 km^2)

$$N_0 = 100 * \frac{n_0}{K} \text{ with } n_0 \text{ the number of introduced individuals, in each suitable cell, and}$$

K the carrying capacity (the maximum number of individuals in a cell).

$$K = \text{area_cell (km}^2\text{)} * \text{proportion_covered_by_host} * \text{max_population_density (/km}^2\text{)},$$

or

$$K = \text{area_cell (km}^2\text{)} * \text{host_plant_density (/km}^2\text{)} * \text{max_population_density (/host plant)}$$

We used the following estimates from Cook & Matheson (2008):

- for n_0 :

$N_{min} = \text{Pert}(1,2,3)$ the pest density immediately upon establishment (supposedly per ha).

We used the most likely value: $n_0 = 2 * 100$

- for K:

$K(N_{max}) = \text{Pert}(10000,55000,100000)$ the carrying capacity per ha

proportion_covered_by_host = mean (host)= 6%

We used the most likely value: $K = 55000 * 100 * 1576$ (area of cell)*0.06 (mean proportion of host)

$K = 5.21 * 10^8$

Therefore $N_0 = 100 * n_0 / K \Rightarrow \underline{N_0 = 3.8 * 10^{-5}}$

- **Multiplication factor λ_{max}**

(λ_{max} is the maximum year to year multiplication factor ("finite growth rate") that a population could achieve under optimal conditions assuming unlimited space. Try to consider how the number of infested trees may have developed from one year to the next or over several years and then calculate the multiplication factor from these data.

From Cook & Matheson (2008): $r = \text{Pert}(0.5,0.75,1.0)$ the intrinsic rate of population growth

Since the required value is the maximum yearly multiplication factor, we considered the higher value of r and calculated:

$\lambda_{max} = \text{exp}(r_{max}) = \text{exp}(1) \Rightarrow \underline{\lambda_{max} = 2.72}$

Results

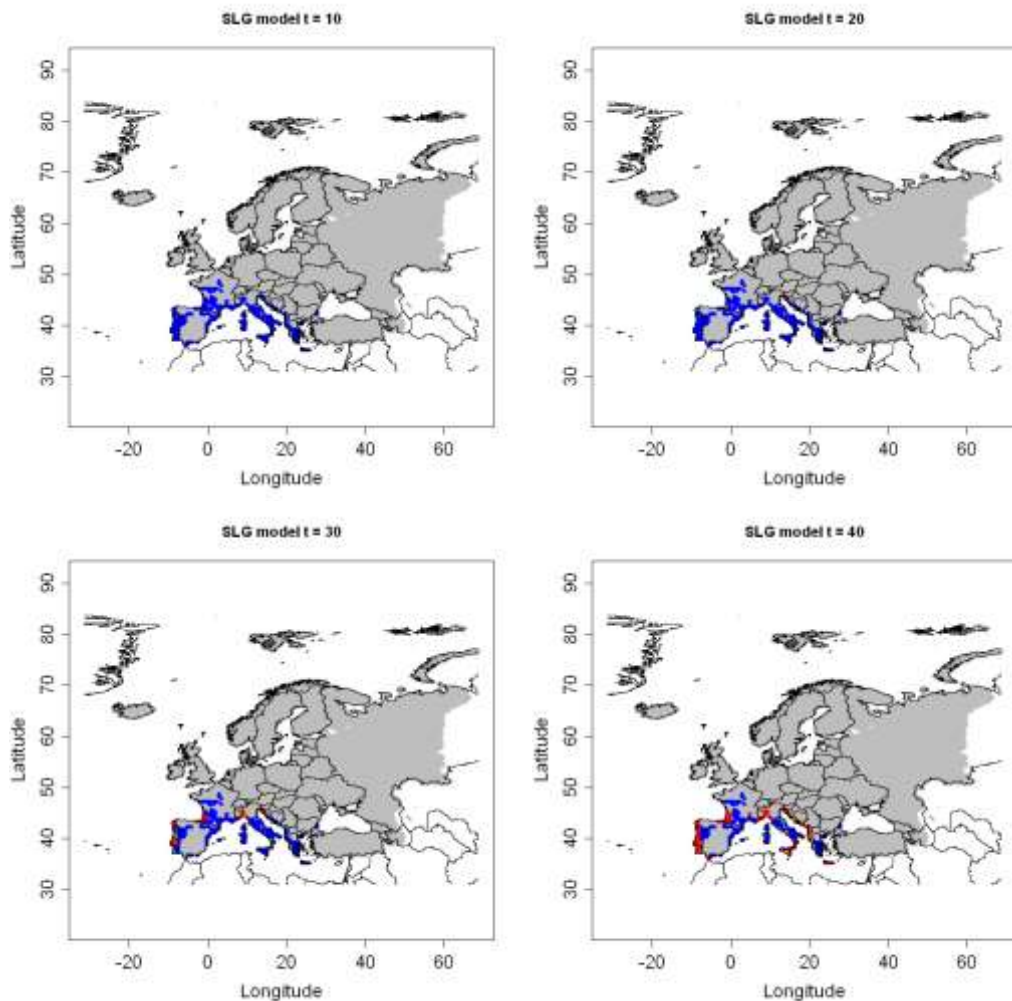


Fig. 4.4.1-4. Outputs of model 1 for $t = 10, 20, 30,$ and 40 .

From these simulations, it seems that the pathogen population needs a long time to start increasing.

4.4.1.6. Model 5: Deterministic version of the dispersal kernel model

This model combines a population growth model and a dispersal kernel ($2Dt$)

- **Starting population N_0**
 $N_0 = 3.8 \cdot 10^{-5}$ (see model 1)
- **Multiplication factor λ_{\max}**
 $\lambda_{\max} = 2.72$ (see model 1)
- **Scale parameter u (km) and shape parameter p**
Since the pathogen cannot disperse at very long distance unless transported by humans, we used an arbitrary small scale parameter ($u = 1$ km) and an arbitrary small shape parameter $p = 2$ (thick tail, long distance).

Results

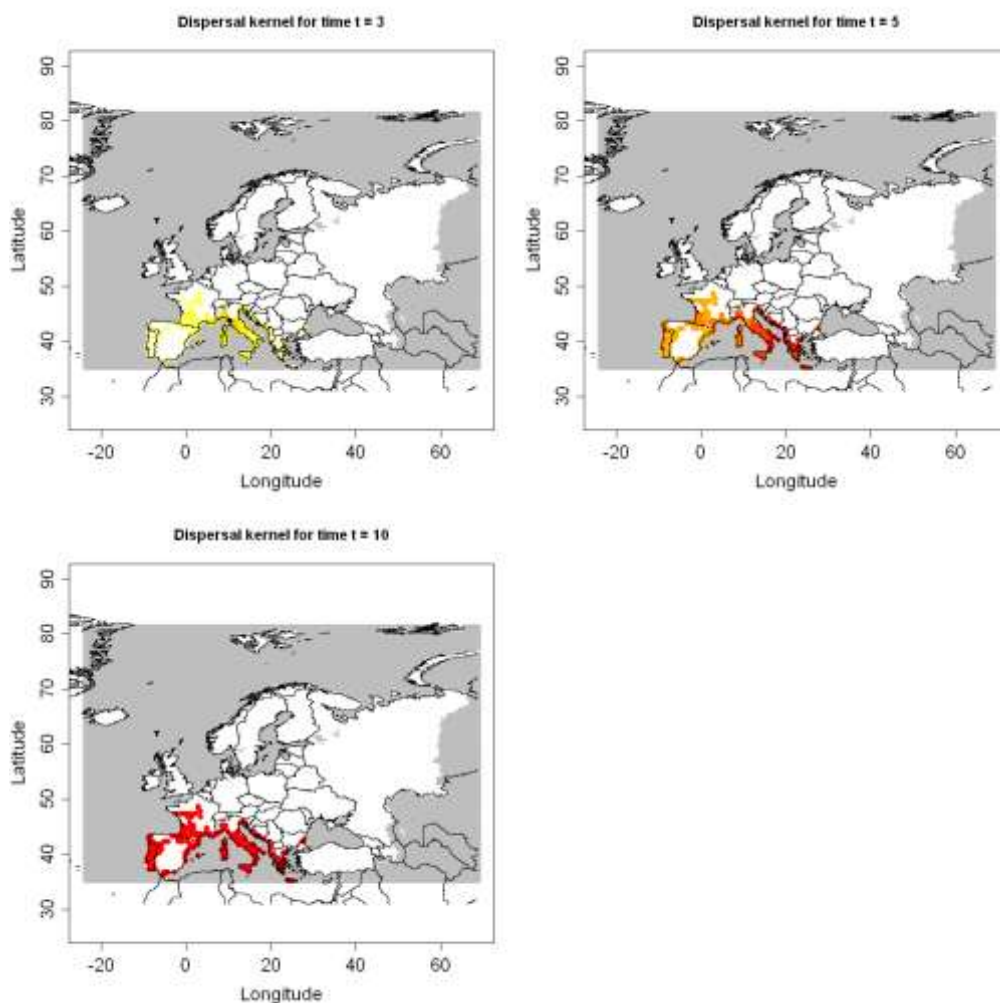


Fig. 4.4.1-5. Outputs of model 5 for $t = 3, 5,$ and 10 .

Despite very small short-distance spread, it seems that the disease could spread very fast across Europe (based on very arbitrary values of the parameters). This model is not appropriate because it does not simulate long distance jumps but a continuous spread from short to long distance spread.

4.4.1.7. Summary

For this pathogen, it was relatively difficult to estimate the parameters for the spread models and also to assess the potential spread qualitatively. Although some values are chosen arbitrarily, the spread module can be used to simulate some possible outcomes and help the risk assessor to answer some of the spread questions in the EPPO DSS for PRA. Model 5 can provide some indications to the answers for:

- question 4.05: it seems that the pest could reach its maximum extent within 10 years.

- question 4.06: after 5 years, around a half of the area of potential establishment could be infested by the pest at relatively high densities.

Caution is however needed in this particular case because of high uncertainties and low performance of the model to simulate long distance jumps.

Model 1 was useful to show that the pathogen population may not build up rapidly. Model 2 was not applied because of the lack of economic data and maps to calculate the relative rate of spatial increase. Model 3 was not appropriate because the pathogen mainly makes some long distance jumps and therefore its spread cannot be simulated through a radial rate of expansion. Model 4 was not applied because it is based on models 2 and 3 (none of them applied).

Summary of the commands for modelling the spread of **Pitch canker disease**, *Gibberella circinata*

```
library(sp)
library(raster)
library(rgdal)
elevmax = F
habitatfile = T
    # load the code
plothabitat()
plotRA()
plotGI()
res = slg(N0 = 3.8*10-5, lmax = 2.72, t = 10)
res = dispk(lmax= 2.72, presencefile=F, N0= 3.8*10-5, nentry=1, p=2, u=1, t = 10)
```

4.5 Conclusion from the case studies

In this report, the application of the spread module to seven species is presented but some work on five others is in process (Table 4.5-1). Based on these examples, it is clear that the spread module can provide reasonable results for species for which extensive data and information are available but the simulations can still provide an important indication of the potential spread when the model parameters are highly uncertain. When it is relatively difficult for the end user to find data to estimate the parameters (Table 4.5-2), approximate values can still be used to assess the time needed to invade the area of potential establishment and the proportion of the area infested within 5 years.

The ease of parameter estimation can differ strongly between the parameters (models) and between pests. Overall, it seems very easy to estimate the radial spread rate RR (model 3) and the radial range expansion model provides good results despite its simplicity. In many cases, it is difficult to estimate the maximum yearly multiplication factor λ_{\max} (model 1) and also the shape parameter p (model 5). Although it may not be so difficult to estimate r (relative rate of spatial increase, model 2), the temporal spread over cells integrated with impacts is only rarely applied because of missing data about economic value of the host.

Consequently, we can draw the following conclusions:

- if a large amount of data is available on the species, applying the spread module can provide good results to determine the potential spread of the species. In this case all the models can be tested.
- if few data are available on the species, the risk assessor can try some arbitrary but reasonable values to obtain a rough indication of the possible spread. Model 1 can be tested to determine whether the population can rapidly grow and to indicate the most favorable areas for the population growth, while models 3 and 5 could be tested to obtain an indication of the potential spread.

Table 4.5-1: Status of testing and feedback of experts

Species tested	Group	Experts	Status	Feedback on results
<i>Diabrotica virgifera</i>	Insect	many contributors	done	reasonable results, rebuild spread in Europe
<i>Anoplophora chinensis</i>	Insect	many contributors	done	reasonable results
<i>Anoplophora glabripennis</i>	Insect	Massimo Faccoli, Andrea Battisti, Dominic Eyre with Hella	done	Results of SLG and RR reasonable, dispersal kernel mapped spread too fast
<i>Saperda candida</i>	Insect	Peter Baufeld with Hella	Parameter estimation done, modeling in progress	--
<i>Agrius planipennis</i>	Insect	Marc Kenis with Hella and Christelle	Parameter estimation in progress	--
<i>Bemisia tabaci</i>	Insect	Ventsislav Ventsislavov (BG) with Hella (and Dominic Eyre)	In process	--
<i>Thrips palmi</i>	Insect	Vladimir Krumov (BG) with Hella	In process	--
<i>Tuta absoluta</i>	Insect	Zhenya and colleague with Hella	In process	--
<i>Meloidogyne enterolobii</i>	Nematode	Zhenya Llieva with Hella and Christelle	done	Results are reasonable
<i>Bursaphelenchus xylophilus / Monochamus</i>	Nematode / Insect	Christelle	done	Problem: no CLIMEX model. Here it is the spread of the disease which is modeled. The models cannot describe long distance jumps, but they can help to assess the potential spread.
<i>Eichhornia crassipes</i>	Plant	Sarah Brunel with Hella, Christelle and Wopke (in Treviso)	done	Models do not really add additional information to mapping on establishment potential
<i>Gibberella circinata</i>	Pathogen	Annie Yart with Christelle	done	Difficult to determine the potential spread. The models cannot describe long distance jumps but they could however help to answer the spread questions in the EPPO DSS for PRA.

Table 4.5-2: Rating of easiness of parameter estimation for different test species and feedback of risk assessors (- = impossible, + = difficult, ++ = less difficult, +++ = quite easy)

Species tested	Group	Parameters						Feedback on parameter estimation
		Carrying capacity K	Yearly multiplication factor λ_{max}	Spread rate RR	Relative rate of spatial increase r	Shape parameter of DK p	Scale parameter of DK u	
<i>Diabrotica virgifera</i>	Insect	++	+	+++	++	+(+)	+++	Many data from literature and experience available
<i>Anoplophora chinensis</i>	Insect	++	++	+++		+	+++	Good expert knowledge
<i>Anoplophora glabripennis</i>	Insect	++	++	+++		+	+++	Good expert knowledge
<i>Saperda candida</i>	Insect	++	+	+		+	+	only little data and literature available
<i>Eichhornia crassipes</i>	Plant	+	+	+		+	+	Difficult and hardly to understand
<i>Meloidogyne enterolobii</i>	Nematode	+++	+	+		+	+	Spread rate takes also human assisted spread into account
<i>Bursaphelenchus xylophilus</i> / <i>Monochamus</i>	Nematode / vector: insect (beetle)	+	+	+	++	+	+	Difficult, human assisted spread hardly to take appropriately into account
<i>Gibberella circinata</i>	Pathogen	+	+	-		+	+	Problems with parameter estimation

5 Recommendations and linkage to the GIF

5.1 When is it appropriate to apply the spread models?

The results show that spread can be modelled and mapped by the generic spread module with good results for the tested pest species.

Spread modelling and mapping is most likely to be useful if:

- the qualitative rating of spread within the EPPO PRA Scheme is not sufficient and quantitative data are needed to indicate when the pest is expected to arrive at particular locations (depending on the entry/starting point).
- additional information on questions within the EPPO PRA scheme is required for questions 4.05 (*What is your best estimate of the time needed for the pest to reach its maximum extent in the PRA area?*) and 4.06 (*Based on your responses to questions 4.01, 4.02, and 4.05 while taking into account any current presence of the pest, what proportion of the area of potential establishment do you expect to have been invaded by the organism after 5 years?*)
- detailed estimates are required to quantify impacts as they build up over time (e.g. infested area per year)
- detailed dynamic information on spread over time is required to design and target surveillance campaigns, contingency plans and phytosanitary measures
- quantitative data are required for the analysis of the costs and benefits of phytosanitary measures (e.g. comparison of spread with and without measures)
- essential inputs to the spread models are already available – the area of potential establishment has already been mapped and the data only have to be transferred to the spread module

Table 5.1 summarizes the inputs required, the model outputs and the recommendations for the spread module. As already pointed out above, all models need a CLIMEX output file and models 1, 2, 4 and 5 also need data on population development (e.g. the carrying capacity of the host plant, a year to year multiplication factor and a rate of spatial increase). If appropriate, an elevation limit should also be estimated.

5.2 Time and expertise for applying the spread models

Table 5.1 shows the datasets and parameters that are required for each model and table 5.2 indicates the time needed to run each model.

Out of the five models, three were found to be relatively straightforward to apply because they require less input data, fewer parameters and run quickly. These are Model 1 (Simple Logistic Growth Model or population development

within cells), Model 3 (Radial Range Expansion Model) and Model 5 (Dispersal Kernel Model).

Two models (Model 2 and Model 4) were more difficult and time consuming to apply. Model 2 (Temporal spread over cells integrated with impact (LG-Econ)) requires data on the economic values of the host plants. For most of the test species these data were not found to be readily available or could not be obtained without considerable effort. In addition, LG-Econ uses the relative rate of spatial increase r parameter which is difficult to estimate correctly. This model was only tested with two species: *D. virgifera virgifera*, a species for which a lot of data are already available - and Pine Wood Nematode, for which fewer data compared to *D. virgifera virgifera* were available. Recommendations are thus very difficult to make.

Like Model 2, Model 4 (Hybrid of logistic growth and radial rate expansion model, (Rand-RR)) requires an estimate of the relative rate of spatial increase r . This requires two species distribution maps at two different time steps. If model 2 has already been applied, the additional time required for model 4 is very low. But, if model 2 has not yet been applied the application of model 4 is likely to be very difficult. Since this model has also only been used for *D. virgifera virgifera* and Pine Wood Nematode, recommendations are also very difficult.

Table 5.1: Datasets and parameters required for each model

Model		Model 1	Model 2	Model 3	Model 4	Model 5
Datasets	CLIMEX output	X	X	X	X	X
	Economic data (GIS map)		X			
Parameters	Carrying capacity K	X				X
	Yearly multiplication factor λ_{max}	X				X
	Relative rate of spatial increase r		X		X	
	Spread rate RR			X	X	
	Shape parameter of DK p					X
	Scale parameter of DK u					X

K: maximum population density per unit area of habitat
 λ_{\max} : maximum multiplicative factor of the population abundance from one year to another in the PRA area
r: rate of spatial increase (to estimate this parameter, maps of the species distribution at two time steps are required)
RR: radial range expansion, typically the rate of spread
u: same as RR as a first estimate
p: requires rough estimates of the proportion of individuals dispersing over long distances (e.g. human assisted spread)

Although other datasets (such as the distribution of hosts or soils) and other parameters (such as the entry point) may be needed to interpret the results and can be included in the models for some case studies, they are not essential and the models can be run without them. In most cases, it is the availability of those datasets and parameters listed in the table above which will determine the choice of the model(s).

Additional data are needed to include population development and/or the spread rate in the models. It can be difficult and time consuming to derive these data from literature or expert consultation. Table 5.2 indicates the time and expertise needed for the different spread models and table 4.5-2 (section 4.5) also includes information on the parameter estimation for the test species.

Table 5.2: Information required, model output and recommendations for the application of the different spread models

Model	Information required			Results / model output	Recommendation
	Data	Time	Expertise		
	all the models require: - data on climatic suitability (CLIMEX-model) - where appropriate, host or habitat distribution data - basic data on population development (carrying capacity and year to year multiplication factor) – except Model 3 - an elevation limit, if appropriate				
Model 1 (SLG)	See the list of pre-requisites above	Little - Medium	Some understanding of population development and dynamics. Interpret with caution (does not model spatial spread).	Population abundance in every cell of the area suitable for establishment	Interesting for identifying areas where high pest abundance (and therefore economic impacts) are to be expected after different time intervals
Model 2 (Econ)	The pre-requisites above + Economic data on host plants + relative rate of spatial increase r (requires maps of the species distribution at two time steps)	Medium Depends on data availability and time for data search	Some understanding of population development and dynamics	Presence/absence of the pest	Currently only applied to <i>Diabrotica virgifera virgifera</i> and pine wood nematode but shows its potential in simulating best case to worst case economic impact scenarios; economic impacts can directly be simulated
Model 3 (RR)	- needs less input + spread rate + start location	Little	Easy to apply if the spread rate is known, simple in its assumptions	Presence/absence of the pest (visualizes the spread rate on a map)	<ul style="list-style-type: none"> • good results for several tested insect species to model the presence / absence of the pest • could be based on the qualitative spread rating by applying the spread rate considered there • easy to apply
Model 4 (Rand-RR)	+ spread rate + start location + relative rate of spatial increase r (requires maps of the species distribution at two time steps)	Little if model 2 and 3 have already been applied Medium if model 2 has not been applied (additional estimation of r)	Easy to apply, calculation of r needed according to the guidance document on the spread module	Presence/absence of the pest	<ul style="list-style-type: none"> • Only applied to <i>Diabrotica virgifera virgifera</i> and PWN • more accurate estimates for the potential spread compared to model 3 because it does not assume that all the cells within the area of the spread rate are invaded (simulation at random)
Model 5 (DK)	+ kernel parameters	Most time compared to others for running the model and testing of parameters	Some understanding of population dynamics as well as of the dispersal kernel	Population abundance	<ul style="list-style-type: none"> • good results for several tested insects for spatial explicit population abundance • results depend on kernel parameters, especially on the shape parameter p. This needs some time and guidance to adjust it for each species

5.3 Decision support scheme on quantitative spread modeling:

1. *“Is it appropriate to map spread?”*

1.1 Is the qualitative rating of spread within the EPPO PRA Scheme insufficient and quantitative data are needed to indicate when the pest is expected to arrive at particular location (depending on the entry/starting point)? **Yes/No**

1.2 Is more detailed information required to answer questions within the EPPO PRA scheme (questions 4.05 (*What is your best estimate of the time needed for the pest to reach its maximum extent in the PRA area?*) and 4.06 (*Based on your responses to questions 4.01, 4.02, and 4.05 while taking into account any current presence of the pest, what proportion of the area of potential establishment do you expect to have been invaded by the organism after 5 years?*))? **Yes /No**

1.3 Are detailed estimates required to quantify impacts as they build up over time (e.g. infested area per year) ? **Yes/No**

1.4 Are detailed dynamic information on spread over time required on spread over time required to design and target surveillance campaigns, contingency plans or phytosanitary measures? **Yes/No**

1.5 Are quantitative data required for the analysis of costs and benefits of phytosanitary measures (e.g. comparison of spread with and without measures)? **Yes/No**

If at least one question has been answered with yes, go to 2.

2. ***“What kind of maps/information/data are already available for the suitability of the PRA area for the organism?”***

2.1 Is a map of endangered areas already available?

If YES, go to 3

If NO, go to 2.2

2.2 Is a CLIMEX model and map already available?

If YES and available for the PRA area, go to 3

If YES but needs to be adjusted for the PRA area, rerun the CLIMEX model and go to 2.3

If NO, go to Annex C and attempt to construct a CLIMEX model and go to 2.3

2.3 Has a CLIMEX model and map been successfully constructed?

If YES, go to 3

If NO, STOP. You cannot apply the spread module

2.4 Is a map of hosts (or habitats) already available?

If YES, you can apply the spread module, go to 3
 If NO, you can apply the spread module but must assume that suitable hosts (or habitats) are available everywhere go to 3

3. “What are the key factors affecting spread of the pest and how much information is available?”

Collect available information from the answers to questions 4.01 – 4.06 from the EPPO PRAScheme, from datasheets or literature and try to either derive a spread rate (km/year) or to indicate whether short or long distance dispersal is relevant for the species.

Spread mechanism	Yes/No	Specify	Short distance (within a range of 1 m – 10 km)	Long distance (move/jump to new areas)
			Yes/No (and/or spread rate)	Yes/No (and/or spread rate)
Active movement		e.g flight of adult beetles		
Passive movement with wind, water, etc		e.g. spore dispersal with splash water		
Human assistance		e.g with vehicles, trade, hithchiking		
Vector needed		e.g. beetle, psyllid, aphid		

Go to 4

4. “How much information is available on the key data for parameter estimation?”

Consider the available information and indicate also the uncertainties of these information

Key data for parameters (for pest and/or vector)	Specify	Information available Yes / No	Uncertainty of available data (low – medium – high)
4.1 spread rate(s) (question 3)	<i>(already done in 3)</i>		
4.2 entry points, locations of observations	e.g. airports and harbours,		
4.3 data on pest densities observed for at least two different years (without eradication or containment measures if possible)	e.g. 5 trees infested trees in one year, 500 trees infested 3 years later		
4.4 data on highest observed pest densities (carrying capacity of host plant or habitat)	e.g. 20 <i>Anoplophora</i> exit holes per tree; 2 - 2.5 Million <i>Diabrotica</i> beetles per ha		
4.5 data on the lowest pest density to establish a new population	e.g. one male and one female		
4.6 distribution maps for two different time steps			

Go to 5

5. “Based on the information, data and maps available for the organism (question 4.1 – 4.6) how easy will the parameter estimation and therewith the modelling be ?”

- **Only yes answers with**
 - low to medium uncertainty
 - very easy and straightforward, all the spread models can be used; go to B 4.2
 - medium to high uncertainty
 - very easy, all the spread models can be used but best, likely and worst case scenarios should be simulated to evaluate the spread uncertainty; go to B 4.2
- **More yes than no answers, with**
 - low to medium uncertainty
 - quite easy, some spread models can be used; go to B 4.2
 - medium to high uncertainty
 - quite easy, some spread models can be used but best, likely and

worst case scenarios should be simulated to evaluate the spread uncertainty; go to B 4.2

- **Same number of yes and no answers,**
 - with low to medium uncertainty
 - possible, some spread models can be used; go to B 4.2
 - with medium to high uncertainty
 - possible, some spread models can be used but best, likely and worst case scenarios should be simulated to evaluate the spread uncertainty; go to B 4.2 or Stop
- **More no than yes answers, yes answers**
 - with low to medium uncertainty
 - it might be possible to apply one or two models, go to B 4.2 or Stop
 - with medium to high uncertainty
 - Impossible, Stop
- **Only no answers**
 - Impossible, Stop

5.4 Recommendations on the different models - When to use which model?

The recommendations based on the initial testing for the different spread models are summarised in Table 5.2. The models differ in their output but also the parameters and data they require (see table 5.1). Therefore the decision on the application of a specific model may depend not only on the expected result (presence/absence of the pest or population abundance) but also the time and expertise that is required for the estimation of the parameters and the data availability.

Model 1 (Simple logistic growth model or population dynamics model, SLG) provides information and data on the temporal development of pest abundance within the grid cells. The output maps can be used for identifying areas where high pest abundance (and therefore economic impacts) after different time intervals may be expected. It can help risk managers to decide where phytosanitary measures should be applied.

Model 2 (Temporal spread over cells integrated with impact, LG-Econ) can be used to simulate best case, worst case and most likely economic impact scenarios. However, these results very much depend on the data that is available on the economic value of the host plants or habitats and they can only provide a very rough estimate of impacts.

Model 3 (Radial range expansion model) just demonstrates the spatial expansion of a species according to its spread rate. Since it does not take population dynamics into account, no data on pest abundances are provided and only the presence or absence of a pest species in a location is mapped. This rather simple model can be based on the qualitative rating of spread in Question 4.01 in the EPPO PRA scheme.

Model 4 (Random Radial Rate Expansion Model, Rand-RR) maps the presence or absence of a species in an area according to its radial range expansion (spread rate) but, in addition, the invasion process is simulated at random and is likely to provide more accurate estimates of the potential for spread because it does not assume that all the cells within this area are invaded. This model does not provide information on the population abundance within the invaded cells. The parameter estimation differs from model 1 and 3 (see table 1) since here the relative rate of spatial increase (r) is used. This parameter can be derived if distribution maps of the species are available for at least two different time steps.

Model 5 (Dispersal kernel model) is the most complex spread modeling approach because it estimates not only the spatial distribution of a pest species but also the pest abundance at a specific time in a specific place. Compared to the other two models it needs more time to run the model, to derive and to adjust the parameters of the dispersal kernel in addition to some understanding of the dispersal kernel. The advantage of the stochastic version is the possibility to simulate some jumps, but a high number of replicate simulations are required to obtain a representative output. When increasing this number of replicates, the stochastic version will converge with the deterministic version. However, one important drawback is the relatively long simulation time.

It is not yet possible to distinguish between groups of species and the appropriateness of the different model types. Since most of the species tested so far have been insects, more testing is needed for the other groups of species.

5.5 Linkage between the EPPO PRA scheme and the generic spread module

The spread module is designed to help pest risk assessors to derive quantitative information on the potential expansion of the geographical distribution of a pest species in the EPPO region. The spread module can use information from the answers to the questions of the spread section and can also help justify the answers to the spread questions. Figure 5.1 summarizes the linkage between the generic integrated framework and the EPPO Decision support scheme for quarantine pest.

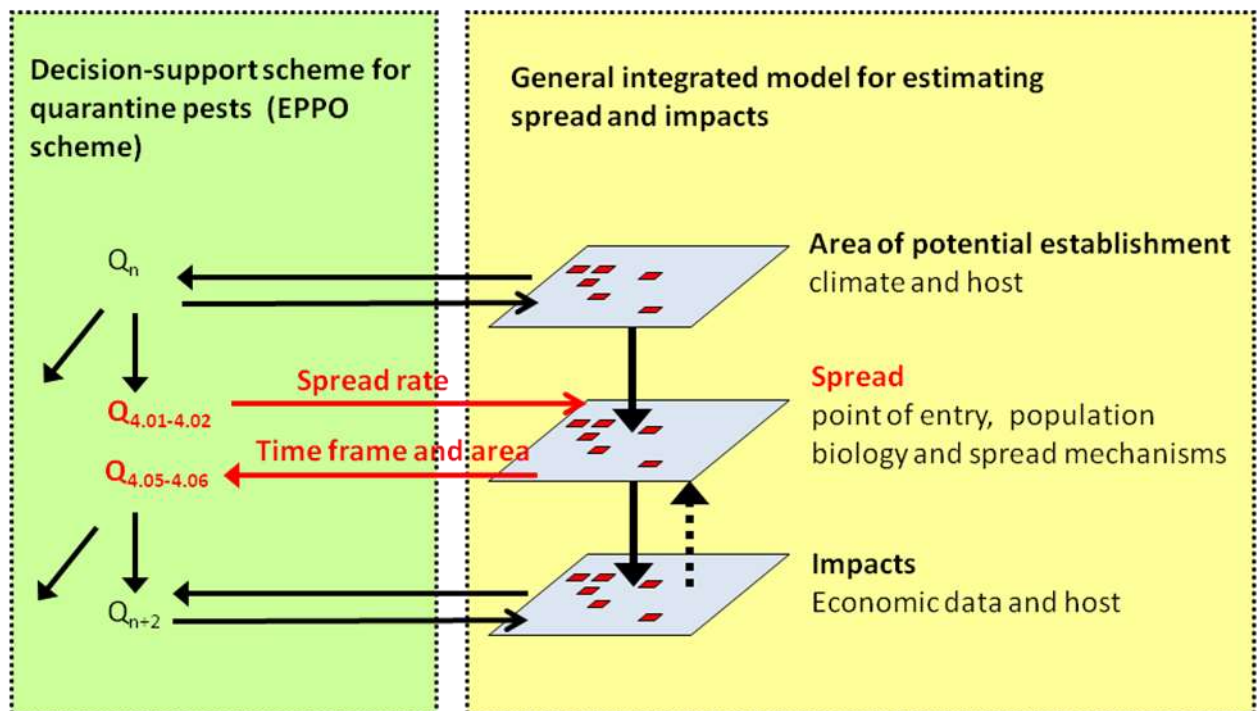


Figure 5.1: Linkage of the generic integrated framework to the EPPO PRA scheme with special consideration of spread questions.

The spread models directly take the area of potential establishment into account since they are based on climate, host plant distribution and soil conditions thus mapping very clearly where and when the pest will spread and build up abundances/densities that may result in damage and economic impact.

These spread models mainly address the natural spread potential of a species and therefore relate to question 4.01 of the revised EPPO PRA scheme. Up to now human assisted spread (which is concerned in question 4.02) has not been included explicitly into the spread module. In fact, the spread models do not differentiate natural and human assisted dispersal. The simulated spread will depend on the data used by the risk assessor to estimate the parameters. If human assisted dispersal is not differentiated from the overall spread of the species, the model will mimic this combined dispersal.

The rating in **question 4.01** (“What is the most likely rate of spread by natural means (in the PRA area)”) takes spread distances into account. The scale within the rating uses quite broad ranges (e.g. 10 m to 1 km/year, 1 - 10 km, 10 - 100 km/year). This may be an advantage if there is little knowledge and data on the spread rate available. Within the spread models spread rates are taken into account with defined values and different values or ranges can be checked against each other and the results be compared.

One of the developed models, the Radial Range Expansion Model, could almost be based directly on the results of the rating within 4.01. It just requires the spread rate per year, one or several starting point(s) and a time frame. For some of the species tested so far (*Diabrotica virgifera virgifera*, *Anoplophora chinensis* and *A. glabripennis*) the output of this model, which is the presence or absence in a location, was – according to the opinion of experts on the given species – reasonable and spread could be mapped with rational results.

Question 4.02 (*What is the most likely rate of spread by human assistance (in the PRA area)?*) provides information on the extent of human assisted spread (very low rate of spread, moderately rate of spread, high rate of spread, very high rate of spread). This result can be taken into account for evidence of human assisted spread rate within the models: if it is very low or moderate we can assume that human assisted spread is more local/regional and the natural spread rate could be increased. In cases where the human assisted spread rate is high to very high it may be assumed that long distance spread with “jumps” to new loci may occur. These “jumps” cannot be directly mapped as separate new locations but they could be considered within the shape parameter p of the Dispersal Kernel Model. The area between the “jumps” would in this case not remain free of the pest but would be modeled as infested areas, which in reality would usually not be the case.

Question 4.03 (*Based on its biological characteristics, how likely is it that the pest will not be contained in case of an outbreak within the PRA area*) considers information about the spread, reproduction, the hosts and habitats. Although the spread module cannot be used directly to answer this question, it can contribute to determine whether the species can spread very quickly or not according to the habitat distribution (models 3, 4, 5), and whether the population can grow rapidly (model 1).

Question 4.05 asks for the time needed for the pest to reach its maximum extent in the PRA area and Question 4.06 considers the potential area where the pest has established after 5 years. For these two questions, which are very difficult to estimate for a risk assessor, the spread module could provide supporting evidence:

Question 4.05:

If you know the average spread rate (km/year), resulting either from natural dispersal (from the answer to question 4.01) or, combined with possible human assisted spread, you can apply the Radial Range Expansion Model. If you know the entry point, or locations where there is a high probability of pest introduction, you can enter the coordinates, otherwise you can use a random entry point within the area of potential establishment to obtain simulations of presence and absence. The time t can be increased until the total area is invaded. The lower t for which all the area of potential establishment is invaded should similar to the time t requested in question 4.05. (See the general prerequisites in Table 5.1 to apply the radial expansion model).

If, in addition to the spread rate (see above), you have data on the population growth rate (yearly multiplication factor), the carrying capacity and some information about the proportion of individuals dispersing at long distance, you can apply the Dispersal Kernel Model. This model requires more time to estimate the parameters and for the simulations, but provides estimated population densities. You should increase the time t until the total area is invaded. The lower t for which all the area of potential establishment is invaded should approach the time t requested in question 4.04. (See the general prerequisites in Table 5.1 to apply the dispersal kernel model).

Question 4.06:

If you know the average spread rate (km/year), resulting either from natural dispersal (take value given in question 4.01) or to some extent combined with possible human assisted spread, you can apply the Radial Range Expansion Model with $t = 5$ years. If you know the entry point, you can enter the coordinates, otherwise you can use a random entry point within the area of potential establishment to obtain simulations of presence and absence. The outputs provide estimates of the number of cells invaded and the total number of cells within the area of potential establishment. The proportion of area invaded at time $t=5$ can then be calculated simply. This value should be similar the proportion of the area requested in question 4.05. See the general prerequisites to apply the radial expansion model.

If, in addition of the spread rate (see above), you have data on the population growth (yearly multiplication factor), the carrying capacity and some information about the proportion of individuals dispersing at long distance, you can apply the Dispersal Kernel Model with $t = 5$ years. This model requires more time to estimate the parameters and for the simulations but provides data on population densities. The outputs provide the number of cells invaded and the total number of cells within the area of potential establishment. The proportion of area invaded at time $t=5$ can then be calculated simply. This value should be similar to the proportion of the area requested in question 4.05. See the general prerequisites to apply the dispersal kernel model.

5.6 Linkage to the Generic Integrated Framework

The spread models are linked to the Generic Integrated Framework (GIF), where data from the PRA process are combined to quantify impacts. Figure 5.2 shows how the spread models are integrated into this process when the data required for spread modelling are available.

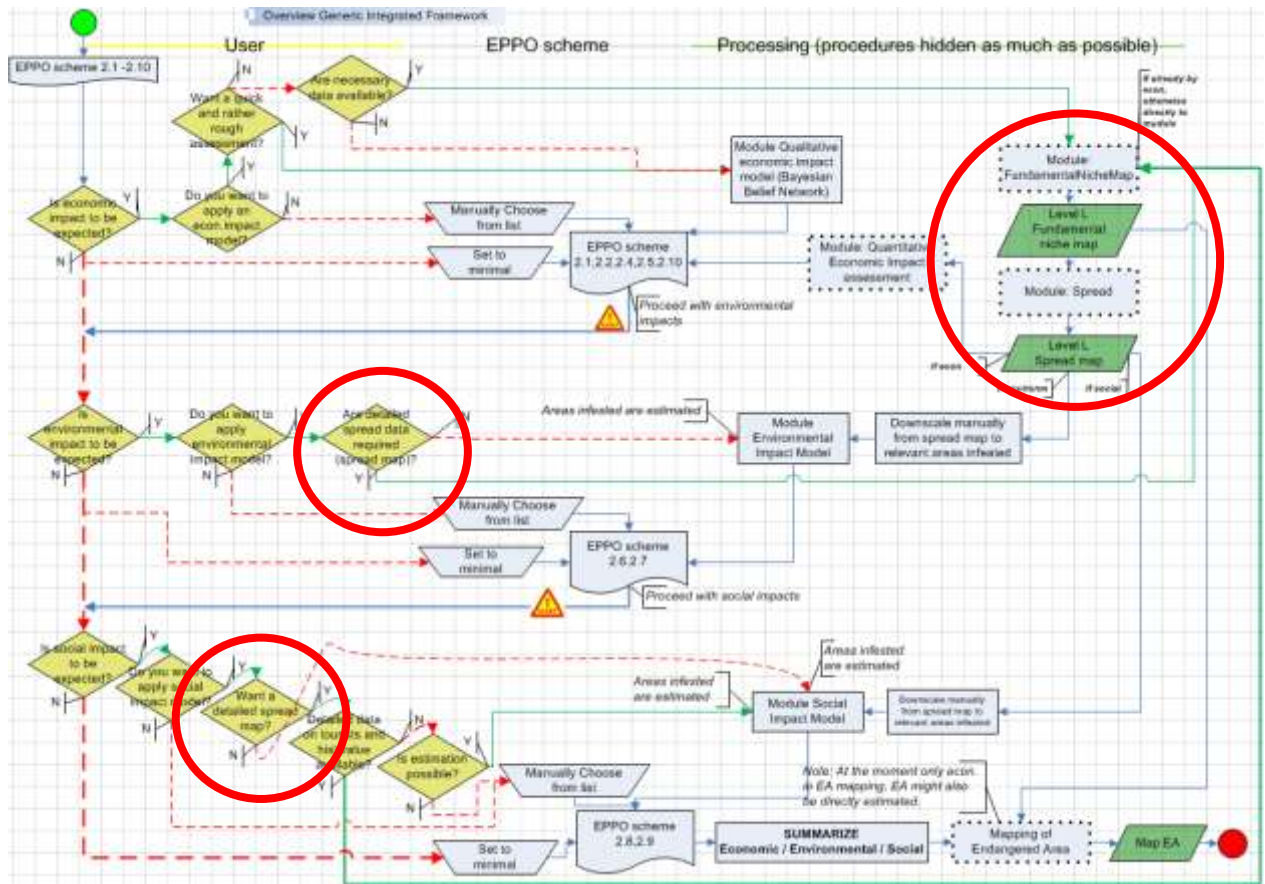


Figure 5.2: Overview on the Generic Integrated framework (GIF) provided by Jan Benninga (29. March 2011)

Figure 5.3 shows the detailed process of mapping the endangered area, where the spread models can be applied after having mapped the establishment area. With Model 1 (see Chapter 3) the pest density within the grid cell can be mapped and this map then shows, after comparison with information on the economic threshold, where economic impacts are to be expected.

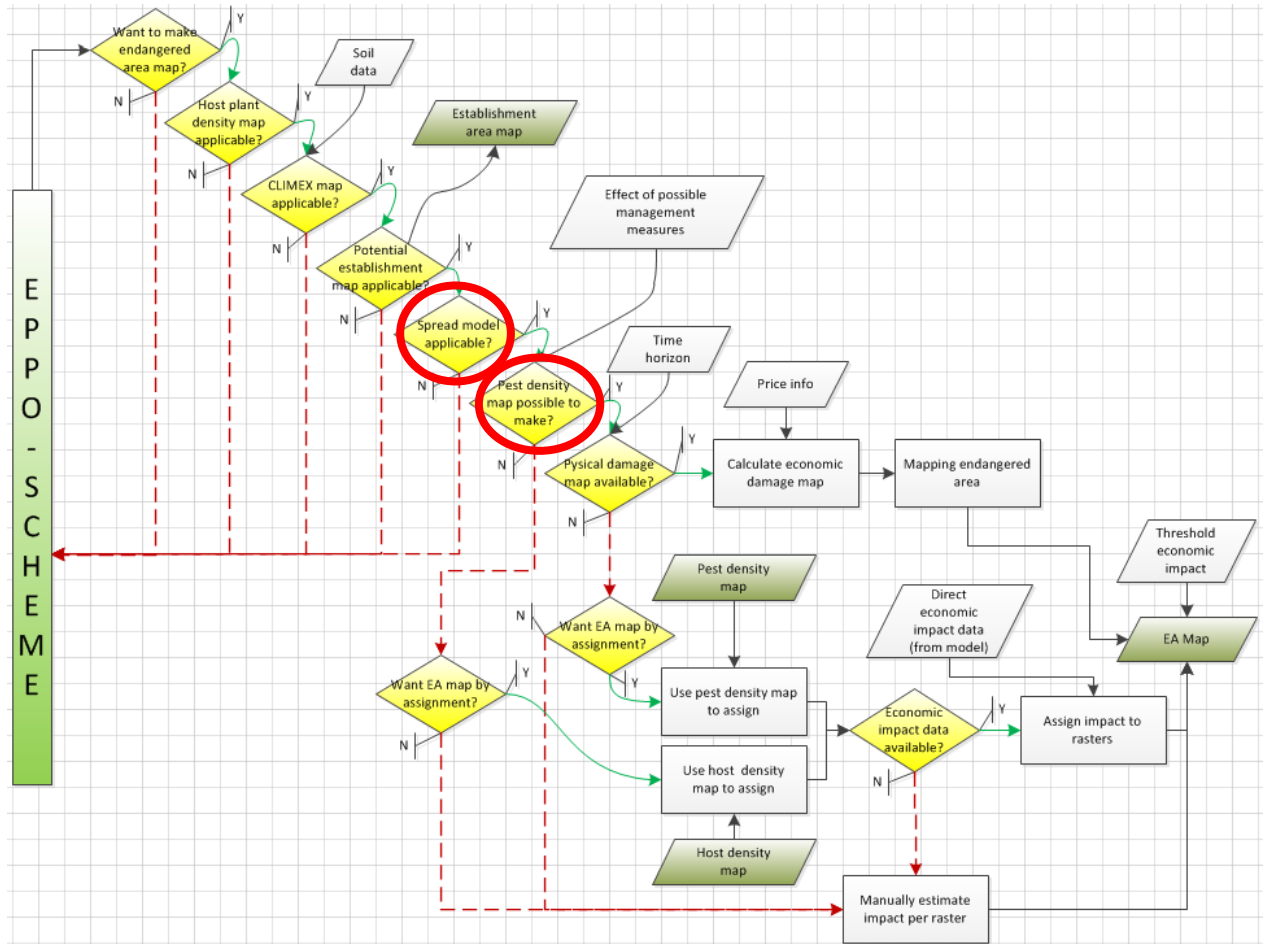


Figure 5.3: Overview on the Process for Mapping the Endangered Area within the Generic Integrated Framework (GIF) provided by Jan Benninga (29. March 2011).

6 Conclusions

A prototype module for pest spread has been provided using various approaches. Five spread models have been applied to a large range of test species and the feedback from the testing phase is reported. The conclusions listed below result from this feedback and also from the comments collected during the EPPO workshop on PRA in Hammamet (Tunisia) in November 2010.

- The **temporal process models**, although not directly linked to the potential for spatial spread, can provide useful outputs for PRAs. Model 1, as already mentioned in this report, can be used to estimate the population density at a future time t and identify areas at greatest risk from economic impacts. This method should be applied when there is little information on spatial spread and economic values. Model 2 is more difficult to apply because high resolution economic values are often missing. However, when applied, this model provides information on the range of possible economic impacts and the locations where these impacts could be highest.
- The **spatial process models** are perhaps the most useful models for risk assessors. Although the most complex (model 5) they may describe the spatio-temporal dynamics better than simple models such as the radial range expansion model (model 3) and its parameters are relatively difficult to estimate. Therefore, in most cases, the simplest model (model 3) may be the most appropriate. Furthermore, this model is closely associated with the EPPO DSS for PRA, notably to the questions concerning the spread rate.
- Although these models do not explicitly differentiate **human mediated dispersal** from natural dispersal (by active flight, wind, vector ...), the simulated spread rate depends on the data used to estimate the parameters. If risk assessors only use natural dispersal information to estimate the parameters, then the model will simulate natural dispersal. If risk assessors use data on dispersal without differentiating natural and human mediated dispersal, the model will simulate this overall dispersal capacity. However, when testing the spread module on some case species, it was found that the possibility for a species to make some long distance jumps without colonizing the area in between is missing. The spatial process models developed here can simulate long distance dispersal but only with continuous spread from the source point to a point at long distance. The gap between them is not simulated by these dispersal models unless establishment is not possible in this area. Consequently when such dispersal pattern appears, it is advisable to develop a model that is specifically adapted to the risks of the species being moved from one place to another one by human agency. There are several options:

(1) consider that human spread can take place at any time, at any distance, so everywhere is at risk

(2) identify the main pathway and apply either a specific network model or a model using the human population density as a risk factor to move the species from one place to another place (see Robinet et al 2011 as an example on the pine wood nematode).

- Although testing the generic spread module with many more **species for each major taxon** is necessary to define more precisely the recommendations and the default values, it was found to be easier to obtain the data to estimate the parameters and apply the models for insects. By contrast, it was very difficult to apply the spread module to a pathogen. When estimating the parameters, problems often appear because the required value is not directly given in the literature and some calculations need to be done to obtain the required value in the correct unit. Therefore an in-depth understanding of the parameters' meaning is crucial to estimate the most likely value. Despite the request of the users, it is not possible to provide a unique method to derive these parameters' values since the method can be different for each case, according to data availability. Examples described in details in this report should nevertheless help risk assessors to see how these values should be calculated.
- There are very often large **uncertainties** in the parameter values. In this generic spread module, only one value can be used for each simulation. To capture uncertainty, three maps should be created: one for the best case scenario, one for the most likely case or intermediate scenario, and one for the worst case scenario. Despite the simplicity of this rule, it is appreciated that identifying these scenarios may be difficult in practice. The range of possible values can be derived from all the experts' judgments or literature data, but also on a standardized rule such as testing the most likely value +/- 10% or 50%. Until now, no precise rule has been defined. The risk assessor probably has a good knowledge of the uncertainty corresponding to his study species and his choice may be better than a standardized rule, but on the other hand, it may be difficult to compare all the maps without a standardized method.
- In this current version, the spread module is constrained by the availability of a **CLIMEX model**, and especially the Ecoclimatic Index, EI (to determine the area where the species can establish at long term) and the Growth Index, GI (to determine how fast the species can grow). In the future, the challenge is to find another way to obtain a proxy for these datasets when a CLIMEX model is not available. The output of the correlative and mechanistic models (see section 2.1) might be used to derive such indexes.
- Until now, the generic spread module is a **separate module** and requires some time and expertise before obtaining the results. The spread module still needs further testing and development to become more closely integrated into the PRA process.

- It is important for the user to recognise that all these models are **scenarios** and the assumptions should always be taken into account when interpreting the results. This generic spread module has been designed to apply to any species and to be used by those with little or no modelling experience. Therefore, most of the models are relatively simple and may not capture the specific spread pattern of a particular species. The module should also be seen as a compromise because detailed and accurate spread models cannot be developed for most species because of the limited information that is generally available.

7 Acknowledgements

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