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Modelling in Plant Health

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Abstracts

Presentations

Introduction to the workshop

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The European Food Safety Authority (EFSA; http://www.efsa.europa.eu/) was established by the Regulation (EC) No 178/2002 in 2002 and introduced a separation of risk assessment and risk management. EFSA provides scientific advice to EU policy-makers through 10 Scientific Panels and an overarching Scientific Committee. EFSA has ca. 400 staff which support > 1500 scientific experts. EFSA publishes ca. 500 scientific opinions per year.

The EFSA 2020 Strategy “Trusted science for safe food” sets out EFSA’s strategic objectives and way forward for meeting the challenges and opportunities ahead to protect European consumers against risks related to the food chain https://www.efsa.europa.eu/en/corporate/pub/strategy2020). EFSA’s driving values are: scientific excellence, independence, openness, innovation and cooperation. EFSA seeks to invest in key assets and capabilities, such as data, expertise & capacity building and risk assessment methodologies.

For EFSA, trust in its work is vital. The value of the scientific advice is linked directly to the level of trust people have. Trust is something that has to be earned. Building trust at EFSA is by ensuring that the science is of the highest scientific standard and is transparent about the processes used for risk assessment. This is challenging, especially when dealing with 500 million citizens, sharing different cultures and with a perception of food-related risks that may vary from country to country. Communication plays a key role.

EFSA seeks collaboration with individual experts, national and international organisations in the field of food safety and plant health. Specifically, EFSA and EPPO, the European and Mediterranean Plant Protection Organisation, have increased their collaboration in plant health in the last years, and started cooperating since 2011, to avoid duplication of work and enhance collaboration. In 2014, a Joint Workshop on Data collection and Data sharing in plant health took place. The current Joint Workshop on Modelling in Plant Health is another result of our collaboration with the aim to explore how models can support risk assessment of plant pests and decision making. This workshop welcomes 150 participants, including 40 speakers from all across Europe and abroad. Finally, other forms of cooperation are going to be realized in the coming period in order to foster collaboration and common activities in the area of plant health.

Models used in quantitative risk assessment in plant health

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Quantitative methods are increasingly used in risk assessment, including those developed for plant health. Despite the constraints imposed by time, expertise and other resources, mathematical models can assist in analysing plant trade pathways for entry, and the subsequent patterns of establishment and spread of plant pests at different temporal and spatial scales. Methods are available for quantifying and partitioning the uncertainties associated with each stage of an assessment and for the evaluation of options for reducing risk. Less developed are methods for quantifying impact, or consequences, of the introduction and spread of a plant pest, especially when environmental considerations are taken into account. The further development and uptake of models for risk assessment in plant health depends critically on initial engagement with those responsible for making consequent regulatory decisions and the ways in which quantified risks are communicated.

Modelling potential establishment hotspots of exotic pests of high significance "flying under the radar" in USA

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A modeling approach is being developed by APHIS to understand the risk of high significance exotic pests that are "flying under the radar" (i.e., they are not currently the target of detection efforts). Exacerbating this risk is the fact that being undetected may contribute to increased likelihood of introduction. A key to the management of this risk is to identify what species are more likely to fit the aforementioned under the radar group. However, we need to learn first what areas are at highest risk of pest establishment under current patterns of trade/transportation and host availability. In the model, pest establishment is a function of probability of entry, host availability, probability of optimum propagule pressure, and climate suitability. Establishment is estimated for a variety of forest and crop ecosystems on a cell by cell basis using a lattice of 10x10km cells. The criterion for cell size is to contain initial biological spread to within each cell. To address the high uncertainty inherent in the model (exacerbated by its spatial resolution) a hotspot analysis is conducted on each establishment map.. Initial hotspot analysis conducted on the continental United States showed large amounts of overlap among establishment hotspots involving different pathways (country of origin x commodity) and host availability. This finding may indicate the potential to coordinate multiple surveillance efforts in the overlapping hotspot area. Currently we are analyzing the interaction and potential implications that different transportation pathways (air, maritime, truck) may have between hotspots. Identification of establishment hotspots may facilitate the optimization of resources dedicated to surveillance. This is particularly beneficial in large diverse countries or regions. The potential application of this modeling approach to other regions of the world is discussed.

Pest Risk Modelling in Australasia

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It can be argued that Australia is the birthplace of computer-based bioclimatic modelling, which underpins the majority of our pest risk modelling methods. Since the mid-1980's Australia and New Zealand's innovation sectors have created some of the most important research tools for assessing and managing pest risks across the biosecurity continuum. Self-organising maps have been applied to analyse invasive pest assemblages to estimate pre-border invasion threats. CLIMEX was developed as a generic modelling framework to estimate climate suitability patterns for invasive species. It has applications across the continuum, identifying and distinguishing establishment and transient pest risks: informing incursion responses (where could the pest spread to, in what seasons is it likely to be active, and what assets are threatened). These climatic niche models have been integrated into bioeconomic models to help inform appropriate policy responses. Population dynamics models have been used to explore detailed questions about eradication and pathway management (e.g. the sustainability of winter window treatment regimes in the face of climate change). In this presentation I outline some of these tools and their applications and comment on the patterns of adoption in Australasia and elsewhere.

From sessile to free-moving hosts: modelling in support of animal health risk assessment

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Animals health risk assessments indeed also rely to expanding extend on any different kind of expert or forecasting models. Beyond the classic modelling studies grounded in spatio-temporal population ecology, complexity of daily risk analysis problems in Animal Health motivate more sophisticated system modelling. We will illustrate the observation using examples from recent EFSA mandates. The apparent difference to problems in the Plant Health remit is the scenery set by motile hosts. The moving and dispersing animals create a dynamically shaping landscape of habitat for the spreading pathogen of interest. Moreover, the pathogens may not need abiotic or biotic vehicles other than their hosts to achieve transmission. We will dig into that difference and bring its relevance to a relative size. Finally, we address interesting views on models in risk assessment maybe turning the seemingly differences into useful equivalencies. Lessons learnable from over-the-fence conclude the presentation.

Challenges faced by risk managers - can models help?

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Plant health risk managers take decisions on phytosanitary measures that, alone or in combination, will reduce risks to an acceptable level, phytosanitary measures being "any legislation, regulation or official procedure having the purpose to prevent the introduction or spread of quarantine pests[1]". Risk managers, and organisations such as EPPO which make recommendations to risk managers, face a number of key challenges: how to allocate resources, how to assess and compare risks, and how to choose the best combination of measures against each risk. Decisions must be made without undue delay; rapidly, in the case of a response to a new outbreak, if the opportunity for eradication or successful containment is not to be lost. Often decisions must be made in the face of considerable uncertainty and with limited opportunity or resources for gathering data to reduce that uncertainty. Choosing the optimum size of a buffer zone is an example. A buffer zone is "an area surrounding or adjacent to an area officially delimited [as infested or as free from a pest] in order to minimize the probability of spread of the target pest into or out of the delimited area, and subject to phytosanitary or other control measures, if appropriate[2]". When EPPO carries out Pest Risk Analyses and develops Standards on National Regulatory Control Systems, an appropriate size of buffer zone may be recommended, along with measures to be taken within the buffer zone. With limited data available these decisions have been difficult and have sometimes been challenged. Models ("simplified descriptions of a system, process, etc., put forward as a basis for theoretical or empirical understanding[3]") could in principle help formulate such recommendations, but in practice their use to date has been rather limited. The presentation will consider constraints on making more use of models, and ways in which risk managers and modellers can work together to overcome those constraints.

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[1] International Standard for Phytosanitary Measures number 5, the Glossary of Phytosanitary Terms
[2] International Standard for Phytosanitary Measures number 5, the Glossary of Phytosanitary Terms
[3] Oxford English Dictionary

A quantitative approach to EFSA pest risk assessment - case studies

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A quantitative method for pest risk assessment and the identification and evaluation of risk reducing options is currently under development by the EFSA Plant Health Panel. The method is used by the Panel when responding to requests for scientific opinions regarding risks posed by specific plant pests which can cause harm to plants, plant products, ecosystem services or biodiversity in the EU. The new approach is adaptive, when conditions for the assessment are changing, mechanistic and population based by connecting all steps and sub-steps in the assessment via the abundance of the pest and by integration of risk reducing options (RROs), and quantitative by combining knowledge and uncertainty, with increased consistency by using quantities measurable in the real world. A strategy has been developed to communicate the results of the risk assessment in a clear, comparable and transparent way, with the aim to provide the requestor of the risk assessment with a useful answer to the question(s) posed to the EFSA Plant Health Panel. To conduct the assessment, scenarios are defined that allow the comparison between different situations, e.g. comparison of a scenario under current regulation against a scenario where the pest is deregulated and RROs are removed, or against a more stringent scenario where additional RROs are imposed. This new approach has been applied to four pilot studies – *Ceratocystis platani*, *Cryphonectria parasitica*, *Ditylenchus destructor*, and Flavescence doree - and some of the results and their innovative communication will be shown in this presentation.

A model for quantitative pathway analysis of plant pest introduction to the EU territory by trade

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A quantitative pathway model is provided to support risk assessment for plant pest introduction into EU territory on a range of edible plant commodities. The model simulates the distribution of an imported infested/infected commodity to and within the EU from source countries and the result is broken down by month of arrival and by EU NUTS2 region. The model has two modules: Module 1 is a trade pathway model, linked to a Eurostat database of five years of monthly trade volumes for each specific commodity into the EU28 from all source countries and territories, including any sources in the EU itself. Infestation levels based on interception records, commercial quality standards or other available information determine the proportion of traded commodity that is infested entering, and transshipped within, the EU; Module 2 allocates commodity volumes to processing, retail use and waste streams across the EU NUTS2 regions based on population densities and the locations of fruit and vegetable processing enterprises. Transfer potential to domestic host crops is a function of the distribution of imported infested product and area of domestic production in the NUTS2 regions, pest dispersal potential, and seasonality in pest susceptibility in domestic crops in the regions. The output of Module 1 of the model is a distribution of the estimated volumes of infested produce arriving in Member States. In Module 2, this infested produce is distributed to the NUTS2 region across the EU28, by month or annually, and by relating this to the accessible susceptible domestic crop, risk is expressed as a potential volume of infested fruit leading to potential pest contact with an area of susceptible domestic host crop. The model was developed using a series of cases studies agreed with the funding body, EFSA. These pests had limited host ranges but the model is now being extended for use with more polyphagous species in the context of the EC FP7 DROPSA project. This involves *Drosophila suzukii,* as well as some other EPPO alert-list pests yet to be selected.

Modelling the probability of transfer of a pest from an imported commodity

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International trade of agricultural products provides a major pathway for the unintentional spread of pests. In the EU, regulated pests are frequently intercepted on produce (cut flowers, fruit and vegetables) imported from third countries. For frequently-intercepted pests in the Netherlands, a calculation was made of the percentage of infested commodities that were intercepted and the number of infested commodities that entered despite import inspections. It was estimated that the majority of infested commodities were not intercepted because of limitations in detection. Biological and trade chain information were used to develop a generic model of pest transfer. Transfer was defined as the probability of a pest to move from an imported commodity to a place suitable for establishment. Seven variables/questions were considered to be relevant for transfer. For each question, the assessor employs either a pre-defined rating or a probability reflecting their own belief. The model calculates the probability of transfer dependent on the rating level/probability chosen for each of the seven questions. Transfer probability was most sensitive to (i) the stage of the pest at arrival, (ii) immature stages developing into adults and (iii) pests reaching suitable sites. Cases with low transfer probabilities confirmed that high numbers of interceptions do not necessarily imply high risk. The model is available as an Excel workbook with six pest/commodity case studies.

A pathway model for wood pests to support risk assessment and decision making on trade regulation

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Travel and trade are the main drivers of the introduction of exotic species into new areas. To explore the role of wood trade in the potential introduction of tree pests, we developed a pathway model and calculated the exposure of trees in Europe to tree pests. The model describes the import, inspection and treatments of wood, as well as the trade among European countries and processing to sawn wood, final product and residues. The model quantifies the frequency of escape of the pest from wood, and the transfer to host trees. This model was designed to be generic, but for illustration, it was applied to round wood of oaks coming from the United-States of America potentially carrying the oak wilt fungus, *Ceratocystis fagacearum* (not present in Europe yet) and to round wood and sawn wood of conifers coming from China potentially carrying the pine wood nematode, *Bursaphelenchus xylophilus* (detected in Portugal in 1999). We show that this pathway model can be used to identify the points along the pathway which mainly contribute to the exposure and to test the effectiveness of various risk reduction options. Pathway modelling is a promising tool to study entry pathways of alien tree pests. First, it is useful to target the data which are necessary to collect to better assess the exposure. Then, it can assist plant health managers in pest risk analyses and support decision makers in their decisions about trade regulation and associated conditions.

HARMVECT-a simulation-based tool for pathway risk maps of invasive arthropods in Belgium

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HARMVECT is a tool simulating the introduction of arthropods into Belgium. Via simulations of the potential introduction pathways the tool calculates risk indices which are used to generate pathway risk maps for Belgium. An essential approach is the tool's design in guiding the user in dividing the complex arrival of the arthropod into potential pathways (e.g. trade host commodities, human transfer, natural spread, import), which in their turn are further subdivided into individual pathway-segments based on decisive aspects like e.g. transport mode and origin of the transport course. The manageable and singular segments are then used to specify the detailed data the user has to gather and feed to the tool. This data is used to simulate the arthropod's introduction and calculate risk indices related to arrival via the various pathway segments; risks are based on propagule pressure. The tool generates 2 types of pathway risk maps: (a) a Point-Of-Entry pathway risk map (POE); this map, generating concentrated hotspots, is based on entry at the national borders, and (b) a Point-Of-Appearance pathway risk map (POA); this map is successive to the POE and visualizes the locations and level at which undetected propagules of the arthropod are exposed to the outside environment throughout Belgium. In conclusion, the tool produces a risk map for the arthropod's potential establishment, which is generated by combining the POA with a climate-suitability and host-availability map.

Economic strategies to minimise the probability of introduction of invasive pathogens through trade

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Widespread movement of plant products across continents, countries and businesses is an increasing source of invasive pathogens (Dehnen-Schmutz et al. 2010). Plant nurseries are key businesses in the plant trade network, selling millions of trees per year. One of the main problems nurseries face are uncertainties in the market demand. These hamper the growers' ability to accurately plan the number of plants needed to satisfy the demand at any given time. As a consequence, importing plants for demand satisfaction is the norm, even for common and endemic species. Increasing the size and frequency of imports translates in an increase in the probability of introducing new diseases (EPPO 2007). Here, we develop a model of the dynamics of plant growth linked to economic variables to investigate how production-importing processes within nurseries affect the probability of introducing invasive pathogens. Our research leads to three key results: 1) as demand variability increases, the probability of introducing new pathogens increases; 2) optimum profit is determined by the production and import costs ratio, which is linked to the number of imports and thus, the probability of introducing diseases, and 3) holding unsold trees for future sales can reduce the probability of introducing new diseases. These results contribute to the knowledge advancement of pathogen dispersal through trade, allowing policy makers and stakeholders develop more robust disease control strategies.

Bioeconomic modelling of spatial spread and control of forest epidemics: Policy-driven and voluntary strategies

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Understanding how both publicly-owned and private forest sectors respond to pest and disease threats and to incentives aimed at controlling them requires a joint consideration of economic and epidemiological processes. Recently there has been significant progress in designing new mathematical models synthesising epidemiological, economic and behavioural elements driving disease spread and control and capturing the resulting series of inter-connected spatial interactions between environmental and economic dynamics. In this talk I will showcase two approaches to spatial disease control, a policy-mandated ring treatment and an incentive-driven shortening of rotation length for controlling tree pathogens. We first use a combination of a network model and the net-benefit analysis to compare different compulsory ring control strategies to find a set of bioeconomic conditions under which one of the three main strategies is optimal, treating a large number of individuals, treating a small number of individuals in a well-defined neighbourhood of a detected case, and allowing the disease to spread unchecked. We find that the choice of the optimal strategy is governed mainly by a relative cost of the preventive treatment, but the details of the local control strategy, and in particular the optimal size of the control neighbourhood, are determined by the epidemiology of the disease. We subsequently consider a model in which spatial control is not driven by policy but spontaneously arises by voluntary actions of forest owners. This strategy of leaving land managers to deal with new disease works for highly damaging and fast spreading pathogens only; this can be extended by providing suitable subsidies. For both strategies, we study the sensitivity of local control strategies to limited information available to decision makers regarding parameters or network structure. We show that local measures can cope with small level of uncertainty but subsequently collapse with a threshold-like behaviour. Our work demonstrates a potential for bioeconomic modelling to address problems in which human actions based on limited information are responsible for success or failure of disease control for plants and trees. I will end with outlining implications for designing control strategies in different zones depending on the distance to the current front of disease.

Spread model of bacterial canker of kiwifruit in Europe

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We examined the applicability of the dispersal kernel model from the generic spread model toolbox developed in the former EU project PRATIQUE. It was already tested for some well studied insect pests. The model based on a CLIMEX file to define species climatic needs and limitations and runs with the spread module package in R. Aim of our work was the model adaptation for further organisms including bacterial pathogens within the EU project DROPSA ("Strategies to develop effective, innovative and practical approaches to protect major European fruit crops from pests and pathogens"). We applied the model to bacterial canker of kiwifruit Pseudomonas syringae pathovar actinidiae (Psa) biovar 3. Psa was observed in 2008 in kiwi orchards in Italy and spread within 4 years into the main kiwifruit growing areas in Europe. We picture the area of potential establishment and the predicted spread with regard to the spread history. Challenges of parameter setting for a bacterial pest to comply with model requirements will be discussed.

Modelling the dispersal of *Monochamus galloprovincialis*, the vector of the pine wood nematode, and assessing the effectiveness of clear-cutting measures

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Following the detection of a pine wood nematode outbreak, Implementing Decision 2012/535/EU imposes eradication measures for at least four years, mainly consisting of the establishment of: i) clear-cuts with a radius of 500 m around the infested plants and ii) intensive surveillance within a radius varying from 6 to 20 km around the infested zone. To estimate the effectiveness of these measures, a simulation model was developed and calibrated using experimental data specifying the dispersal capabilities of the insect vector *Monochamus galloprovincialis.* These data were obtained in the laboratory (on a flight mill) and *in natura* (mark-and-recapture experiments) in the context of the Landes de Gascogne forest (David, 2014 and David *et al.*, 2014), one of the forest areas most exposed to the risk of introduction of the pine wood nematode in France. The simulations that were then carried out under different scenarios (preventive or curative) showed that the clear-cuts currently requested by European and French regulations would not be effective in a landscape configuration of continuous plantations of maritime pine. Indeed, with the recommended radius of 500 m, at best 11% of nematode transmissions by the insect vector would be avoided. Moreover, to obtain a pine wood nematode transmission rate lower than 0.1%, it would be necessary to implement clear-cuts with a radius of 15 - 38 km (Anses, 2015). These simulations, carried out in the context of a continuous forest, should however be supplemented by a scenario involving highly fragmented pine forests. In this regard, it would be interesting to include biological data from Spanish forest managers, as they are directly involved in implementing nematode eradication measures in this type of landscape. Alternative management measures to control the spread of the pine wood nematode were also assessed by the Working Group.

Vector behaviour and plant defence influence vector-borne pathogen spread: assessing risks of enhanced spread of *Xylella fastidiosa* from grapevines with novel defensive traits

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Development of resistance traits in agricultural crops is often a critical component of integrated disease management strategies. In contrast, tolerance traits—traits that reduce disease symptom severity without reducing pathogen populations in a host plant—may actually increase the risk of pathogen spread through a host population. At the same time, vector preference for hosts based on host infection status can have strong impacts on disease spread. Theoretical work from our group predicts that the precise form of defense—whether resistance or tolerance—will influence the spread of a vector-borne pathogen depending on whether vectors prefer or avoid feeding on diseased hosts. Specifically, when vectors avoid feeding on diseased hosts, resistance traits will reduce spread whereas tolerance traits will enhance spread, relative to a fully susceptible host population. The vector-borne bacterial pathogen *Xylella fastidiosa* causes Pierce's Disease in grapevines and has lead reduced productivity and increased insecticide use in grapevines in California. In response, a diverse array of novel defensive traits have been developed to more effectively manage Pierce's Disease. While these new traits reduce disease severity, it remains unclear how these traits influence bacteria populations, that is, if these traits confer resistance or tolerance. At the same time, the dominant sharpshooter vectors of *X. fastidiosa* avoid feeding on diseased grapevines, increasing the risk of enhanced pathogen spread in tolerant host populations. We are currently evaluating the effects of two promising novel defensive traits on transmission of *X. fastidiosa* by sharpshooters. In this talk, I will present our theoretical work on the interactive effects of host defense and vector preference, our on-going experimental work to test these predictions, and our efforts to bridge theoretical and experimental work to aid in assessing epidemic risks prior to commercial release of novel defensive traits in agricultural crops.

Exploiting the high resolution JRC-MARS European climatic dataset for pest risk mapping

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When modelling the potential distribution of an invasive pest, or areas at risk from spread of a pest already present, climate data with a high temporal and spatial resolution are an invaluable resource. The European Commission's Joint Research Centre runs a programme called Monitoring Agricultural Resources (MARS). The MARS datasets have been made publicly available under the name Agri4Cast and provide a unique source of Europe-wide daily climate data. These data, available from 1975 to the end of the previous year (currently 2015), are interpolated from over 5,000 weather stations to a 25 x 25 km resolution. All geographical Europe is included, and coverage extends to the Mediterranean area of the Middle East and North Africa. The climatic parameters available include temperature (daily minima and maxima), sunshine, wind speed, rainfall and relative humidity at five different times of day. As well as the potential for use in simple climate modelling, selected parameters can be imported into CLIMEX for more sophisticated analyses. Case studies of how the MARS data have been used by the UK NPPO to date are presented, for the insects *Thaumetopoea pityocampa*, *Hyphantria cunea* (both Lepidoptera) and *Popillia japonica* (Coleoptera). The case studies will include some methods of representing uncertainties where there is a lack of thresholds in the published literature, conflicting data, and only air temperature data are available to model a soil-dwelling organism.

Relative roles of climatic and spatial factors in the geographical range of citrus black spot

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Citrus black spot (CBS), caused by *Phyllosticta citricarpa*, is one of the most damaging fungal diseases of citrus worldwide. Correlative and process-based models were used to estimate the potential geographical range of CBS, but with contradictory results. None of these models considered spatial effects, so hierarchical Bayesian models with climatic and spatial factors were implemented here. CBS distribution in South Africa (1950 and 2014) and WorldClim climate data were used. Moran's I and Geary's C analyses revealed a strong spatial dependence of CBS. Descriptive analysis showed that CBS emerged in South Africa in areas with summer rainfall and later spread to arid regions. Non-spatial models of CBS distribution, including climatic covariates or principal components, were compared with their spatial counterparts including a geostatistical component. Bayesian inference by INLA was used and the geostatistical effect was implemented by the stochastic partial differential equation approach. Spatial models outperformed non-spatial models in the 1950 dataset. Problems of model convergence were detected in 2014 due to the strong spatial structure of CBS. Spatial models with principal components for 1950 had better classification accuracy of CBS distribution in 2014 than non-spatial ones. Thus, models based solely on climate may underestimate the potential geographical distribution of CBS.

Mechanistic modelling of root rot, wind and bark beetle dynamics in Finland

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The changing climate is most likely increasing the risk of disturbances in forest management in the Nordic countries. Currently, the Norway spruce (*Picea abies*) dominated forests face three major threats: root rot caused by Heterobasidion species complex, wind and European spruce bark beetle (Ips typographus). Norway spruce stands infested with root rot are more prone to the heavy winds. In these stands, the infected trees lack the full support of a root system compared to the healthy, non-infected trees. The windthrown trees are the optimal habitat for bark beetle reproduction and can further lead to serious bark beetle outbreaks. In such areas, the overall economic losses can be significant. However, silvicultural choices can affect the disturbance agent dynamics, and the most suitable forest management practices are therefore of great importance.
The purpose of this research was to develop three separate mechanistic models, each representing single disturbance agent dynamics (Honkaniemi et al. 2014, Honkaniemi et al. manuscript, Honkaniemi et al. manuscript). The models were combined with MOTTI tree stand growth simulator (Salminen et al. 2005) to analyse the effect of different forestry management options on the damage risks as well as to compare the financial justification of various control methods. The new software system can be used to include quantitative risk analysis in forest management simulations and further aid decision support and policy making.

Application and use of insect phenology modelling for regional and global pest risk assessments

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Insects cannot internally regulate their own temperature and depend on the temperature to which they are exposed. The relationship between temperature and the insect life-history (development, survival, reproduction, etc.) can be well described by process-based phenology models. These models can be used to identify environments where pests might persist to predict their risks of establishment and population growth potential. The International Potato Center has developed a novel approach and software, named Insect Life Cycle Modeling (ILCYM), to support the development of process-based temperature-driven and age-stage structured insect phenology models based on temperature-dependent life-table data and to apply these models for insect species distribution and risk mapping. ILCYM is an open-source computer-aided tool built on R and Java codes and linked to uDig platform, which is a basic geographic information system (GIS) to help ILCYM's users in analyzing and visualizing the risk assessment maps. The software has three main modules: the model builder, the validation and simulation module, and the potential population distribution and risk mapping module. Phenology models and risk maps on global and regional scales have been developed for a wide range of pests. The modeling steps in ILCYM will be explained and examples given to apply this approach for pest risk assessments under current and future climates.

Physiologically based model to assess the probability of establishment of plant pests including a case study on *Pomacea spp*.

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Pest risk analysis requires the identification of areas for potential establishment of a pest to assess the risk posed to agriculture and the environment. Pest abundance is considered as a predictor of the magnitude of impacts in the invaded habitat in the area for potential establishment. Maps representing the potential distribution of pest abundance and the suitable habitats potentially affected by the pest provide key information supporting risk managers in their decision making process.

Spatially explicit Physiologically-based Demographic Models (PBDMs) are a powerful tool to assess the potential establishment of invasive alien species including plant pests. They provide an appropriate level of mechanistic synthesis for predicting pest population phenology, age structure and abundance dynamics as a function of the spatial and temporal variability of environmental forcing variables. They may also include bottom-up effects of plant growth and development on herbivore dynamics and, in some cases, the top-down action of natural enemies. PBDMs are able to capture relevant ecosystem complexity across wide geographic areas and at different levels of resolution using a modest number of measurable parameters. This modelling approach is also very efficient in generating scenarios of potential establishment and spread of invasive alien species considering climate change.

A PBDM supporting risk assessment of the invasive apple snail *Pomacea maculata* detected for the first time in Europe in 2010 (Ebro Delta, Spain) has been developed. Apple snails have been reported as a highly invasive species in wetlands and freshwater ecosystems worldwide causing significant impacts on the flora and fauna of the habitats where it is established. Based on this mechanistic model the potential distribution and abundance of the apple snails in Europe have been obtained and overlapped with the distribution of wetlands, freshwater ecosystems and protected areas potentially subjected to apple snails' invasion in Europe. Mapping suitable habitats for the apple snails has required an accurate screening of high resolution wetlands and freshwater datasets available at the European level. Finally, the Natura2000 sites map has been used to determine protected areas in Europe that include wetlands and freshwater ecosystems which will be more at risk if the apple snails will spread.

The modelling elements in a new methodology by EFSA to assess environmental impact of plant pests

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The assessment of the risk posed by plant pests to the environment (environmental risk assessment, ERA) is a component of increasing importance for Pest Risk Analysis. Available methods for assessing the environmental risks of plant pests that have previously been used in pest risk assessment were reviewed and the limitations identified by the review led to the definition of the new EFSA methodology for ERA.

Emphasizing the importance of assessing the consequences on both the structural (biodiversity) and the functional (ecosystem services) aspects of the environment, the EFSA approach includes methods to link the population abundance with the impact. The method also considers the resistance, resilience of the receiving environment and the management in the assessed area.

A list of questions has been provided for the assessor to evaluate the consequences for structural biodiversity and for ecosystem services in the risk assessment area. To ensure the consistency and transparency of the assessment, a rating system has been developed based on a probabilistic model, taking also into account the uncertainty of the results.

Currently a new quantitative methodology is developed in EFSA for pest risk assessment. In order to harmonise the ERA approach with the new methodology, modelling elements could be introduced to support a fully quantitative ERA. These could include models defining the pressure of the invading population as well as models putting into relation the population pressure and the state of the receiving environment, thus resulting in the impact of the pest on ecosystem services and biodiversity components.

Model-based identification and optimization of key parameters for sharka management strategy

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Strategies for disease control are often based on expert opinions rather than on the formal demonstration that they are, at least in theory, effective. An alternative and promising approach consists in modeling both the epidemic processes and control measures in order to optimize disease management. In this way, the most influential parameters can be identified, and alternative control strategies can be proposed and tested in silico in order to assess their potential efficiency. To this end, we developed a spatially-realistic stochastic model simulating disease dynamics and management. We used this model to carry out generic sensitivity analyses with parameter ranges large enough to encompass values that are typical of many perennial plant diseases and of their management. These analyses revealed the importance of the latent period duration. Then, we specifically scrutinized the main processes affecting sharka epidemics, caused by Plum pox virus, a quarantine pathogen of prunus trees (especially apricot, peach and plum) in many areas of the world (Rimbaud et al., 2015). Using realistic parameter ranges given the present knowledge of sharka epidemiology, another sensitivity analysis on the most promising control parameters enabled the theoretical economic optimization of sharka management strategy. The identified optimized control strategies are discussed with the organizations responsible for sharka control in order to help the design of durable and cost-effective strategies.

Modelling epidemiological and economic consequences of *Flavescence dorée* to Austrian viticulture

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The first disease outbreak of *Flavescence dorée* (FD) was detected in Styria in 2009; its vector *Scaphoideus titanus* was found in the same vine growing region 5 years before. In the frame of a national research project ("VitisCLIM") the spread and the economic impact of FD towards the Austrian viticulture was simulated. It was an interdisciplinary approach involving plant health and pest risk assessment experts as well as economists and stakeholders. Model input parameters were gained through a literature search and field surveys. Moreover, specific statistical data from the region were available to incorporate also geographic and topographic data from two different model domains with FD outbreaks. A stochastic Monte-Carlo simulation model was implemented, in order to model the spread of FD and *S. titanus* and in addition the spread of FD as a function of the efficiency of different intervention strategies. An Input-Output (IOA) analysis was used to assess the potential economic impact of the disease. The model results confirm the importance of scenario adapted pest control and of the early detection of FD. It shows the potential of uncontrolled grapevine arbours with high vector population densities to act as disease reservoirs and thereby having a significant role in the spread of the disease. The potential losses calculated vary from zero to more than 5 Mio € depending on the different intervention strategies.

Disease control strategies: a modelling case study

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Cassava is a key staple crop for subsistence growers in East Africa, where it is often relied upon for food security. Cassava Brown Streak Disease is a major threat to this, causing yield loses of up to 75%. One dispersal mechanism for the pathogen is the informal trade of planting material, which can be particularly difficult to regulate. Creating a mathematical model of the system, we show that this trade is likely to be vital to long-range dispersal of the pathogen, while the vector of the pathogen is more important in local amplification of the disease. An agricultural police unit is currently being set up in Uganda to try and restrict the informal trade of untested material, and our model suggests that any such efforts will reduce the dispersal rate of disease. However, to effectively reduce disease other control methods are required. One such method in the early stages of establishment in Tanzania and Uganda is the clean seed system, for distribution of disease-free, improved planting material. A key consideration is the importance of informal trade of the improved material between growers, extending the reach of the introduction of clean seed beyond the direct beneficiaries. We show that restrictions in trade cannot always be effectively combined with clean seed systems; the success or otherwise of restrictions depends on the introduction strategy used.

Modelling for natural enemy distribution and potential efficacy in biocontrol

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Natural enemies play an important role in managing pests and are often used in classical biocontrol programs to manage invasive non-indigenous pests. For the introduction and release of exotic species, many classical biological control programmes have used “climate matching” tools to find climate similarities and differences between the species’ native range of distribution and intended release areas, but which modelling approach gives not a reliable basis for predicting survival and establishment of a species. Temperature-based phenology models based on life-table data derived from constant temperatures studies are developed using Insect Life Cycle Modelling (ILCYM) software and directly connected to GIS mapping to identify those regions in which the parasitoid can potentially establish (establishment index) and to indicate regionally its potential efficacy (number of generations/year and activity) to control its host. Potential release regions for exotic parasitoids are those crop production regions where the pest has been established, causing significant economic damage, and where efficient natural parasitoids are absent. Thus, the establishment, generation and activity indices for the parasitoid are only displayed for those regions in which the pest can potentially establish and cause economic damage. Information will be vital in guiding the understanding and projecting how biological control agents may develop in new regions under current and future climatic conditions.

The neglected importance of network analysis to prevent, manage, and understand crop pest outbreaks

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Networks offer a convenient model to study the spread of pathogens (1). For example, networks mapping all the flight routes connecting the world’s airports have helped unravel the mechanisms behind the 2002-2004 SARS epidemic (2,3). Yet, in plant disease ecology, network analysis is only rarely applied, even if its potential has been recognized (4). Here we show how this could be an important missed opportunity, and that the topological features of spatial networks connecting susceptible crops fields based on their geographical distance can help manage disease outbreaks in face of the many epidemiological unknowns common to quarantine pests. For instance, identifying which and how many nodes (i.e. crop fields) should be treated to 'immunize' a network (5) can provide a clear picture of how realistic and costly it is to set up an effective prevention strategy against different pathogens solely on the basis of their dispersal abilities. Similarly, identifying the individual contribution of nodes to the persistence and transmission of a disease according to network structure and spread simulations (6) can directly inform the prioritization of management interventions, such as preventive cutting or spraying. This is especially compelling in situations where the chances of eradicating a pest from a given area are slim, and where the emphasis instead lies on keeping the disease prevalence as low as possible lest the pathogen makes long-distance jumps to disease-free areas.

FinnPRIO: The Finnish model for ranking invasive pests

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The FinnPRIO model follows the basic structure of a full scale pest risk assessment, i.e. it can be used to separately assess the probabilities of entry, establishment (including spread), and the likely impacts. The model also includes a section for assessing manageability of a pest invasion. The model consists of multiple-choice questions with answer options yielding a different number of points. For each question the most likely answer option and the plausible minimum and maximum options are chosen. The total scores for entry, establishment, impacts and manageability are simulated using a PERT distribution, providing a scale of the scores for each pest and indicating the level of uncertainty associated with the assessment. A score for the likelihood of invasion can also be obtained as the product of the entry and establishment scores. The assessed pests can be ranked according to their entry, establishment or impacts scores, and the likelihood of invasion scores. Ranking can be based on summary statistics, such as median, or upper or lower percentiles of the score distributions depending on the risk manager’s approach. Rankings that consider the entire probability distributions can be obtained using the concept of stochastic dominance. The model has been tested through simulations and by comparing pest rankings produced using the model to those obtained in expert workshops. The results indicate that the model is capable of differentiating pests based on their estimated risk. To date, about 240 pests have been assessed with the model.

BiOR² : a database/software process dedicated to plant pests ranking in France

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Recently, the French Agency for Food, Environment and Occupational Health and Safety (ANSES) was entrusted by the French Ministry for Agriculture to rank a list of plant pathogens in order to achieve pests' categorization. The objective is to prioritize the deployment of resources based on risk and impact of a pest. A new methodology was thus developed: BiOR², which stands for "Biological Organisms data Retrieval and Ranking system". BiOR² associates a database to softwares for multi-criteria analysis. First, the database runs under the database management system (DBMS) PostgreSQL. Its content was collected in a semi-automated manner and consists of 55 tables containing information relative to plants' trade, land use, legislation, pest interceptions and climate classification. The database is linked to a graphic user interface that allows, besides the display of previously entered data, to fill in new data on both host plants and pathogens through a questionnaire. Next, 2800 lines of code enable the link between the available data according to specific criteria and provide a multi-criteria matrix, whose uncertainty can be also quantified by BiOR². A base of 24 criteria, defined according to FAO ISPM N°11 document, covers risk of entry, establishment, spread as well as economic, social and environmental impacts. The ranking is finally achieved through Visual PROMETHEE with the possibility of conducting several scenarios where criteria are assigned different weights. The process was applied to metropolitan France and the French Oversea Departments on respectively 278 and 110 plant pests and pathogens. Results were validated by comparison against results of other models and by a panel evaluation. Overall, BiOR² is intended to be objective, generic, based on sound science, highly adaptable to meet various kinds of questions about the management and impact of pests.

Pest risk ranking model in the Netherlands

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Countries take phytosanitary measures to reduce the probability of introduction (entry and establishment) of new pests. To deploy resources efficiently and to identify weaknesses in the phytosanitary regulatory system, it is important to assess which pests pose a relatively high risk. Therefore, a risk ranking method was developed that takes into account the current phytosanitary measures on the pathways and the potential impact of the pest. The probability of introduction of a pest is assessed by combining four risk criteria: the probability of arrival despite current phytosanitary measures, the probability of transfer, the probability of establishment and the probability of eradication by official measures. The potential impact for crop production is assessed by combining three criteria: the average impact of the pest at field level including yield losses and crop protection costs, the percentage of fields that is expected to become infested on the long term and the economic value of the crop. In addition, three criteria were defined to assess the potential impact for export: the feasibility of the measures that needs to be taken to guarantee pest freedom, the percentage of fields that is expected to become infested and the value of the crop that is exported. The potential impact for the environment is assessed by one criterion which takes into account the severity of the pest or disease and the density of the host plants in the country. For each criterion, four to six rating levels were discriminated and a rating guidance was developed. Thus far, about 100 regulated species have been rated according to the new methodology.

The ERIN system to identify, describe and rank new plant health threats in Norway

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The Plant Health Panel of the Norwegian Scientific Committee for Food Safety has developed a system for screening of Emerging Plant Health Risks in Norway (ERIN). The objective of ERIN is to provide a tool that aids to maintain an overview of emerging plant health risks to Norway. It is short. It is not providing a risk assessment in itself, but aims to rank and prioritize plant health threats according a set of criteria defined including an uncertainty score. The basis for the system is a self-initiated task by the Plant Health Panel. The system is designed to deal with organisms newly identified as plant pests, "door knockers" which are potential invasive alien species and unexpected changes for species already present in the country. For the latter case, typical changes considered are change in climate that can trigger change in distribution and behaviour; increased import of a given commodity that can increase entry rate; reduced access to effective plant protection products and resistance development. The system will contain:

- a list of candidate organisms.
- a text describing significant information for each species, inspired by the EPPO Alert list.
- Link or citation to existing international data sheets.
- a summary overview table listing score values for each species.

The overview table is regularly updated by including or removing species. The language is English, in order to simplify utilisation of external sources and facilitate international communication.

The UK Plant Health Risk Register

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The UK Plant Health Risk Register (RR) was developed as a tool for government, industry and stakeholders to screen the results of horizon scanning and new findings and to prioritise actions against pests and diseases which threaten UK plant resources. Primarily focussing on non-native threats, the RR takes into account key aspects of a pest's biology, ecology and damage potential which, combined with trade data, feed into a spreadsheet using simple rules to rate the likelihood and impacts of one of two principal scenarios: "pest is introduced", for pests absent from the UK or "pest spreads to maximum extent", for a pest which is already present in part of the UK. Ratings are given as numeric scores and subject to a review process (with justification for any changes). Expert judgement is used where information is lacking. A 'value at risk' is obtained from economic and environmental data to ensure that risk ratings reflect the value of the host sector to the UK. Ratings in the absence of mitigations are compared with those that take existing actions into account in order to prioritise additional actions, e.g. enhanced regulation. This presentation will give a background on the operation of the RR, how ratings are made, and, using examples, will show how the ratings are used to look at how different mitigation measures can reduce the risks to UK plant health.

A pest risk ranking model for exotic arthropods in the USA

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A primary goal of the USDA-APHIS's Plant Protection and Quarantine (PPQ) division is to protect U.S. agriculture and natural resources from the entry, establishment, and spread of exotic plant pests. We are developing a model for categorizing exotic plant pests across groups (families, feeding guilds) and across host systems (production, natural, urban areas). The model is based on a series of questions which require objective, documented evidence from the scientific literature to answer. Each question is scored based on its power to predict impact, and the final result is given as high, moderate, or low impact. We include uncertainty in the model and allow for alternate answers. We have separate models for arthropods and pathogens. Here, we present the development of the arthropod model.

Modern approaches to surveillance for invading plant pests

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Recent times have seen a significant rise in accidental introductions of exotic plant pests and diseases. These pathogens are a grave threat to crops and natural plant communities. Prominent examples include diseases such as Huanglongbing (HLB) of citrus (syn. Citrus greening), which was first detected in Florida in 2005 and has since spread to practically all commercial plantings throughout the state. The disease now threatens introduction to further citrus producing areas such as California. In Europe, *Xylella fastidiosa* is a major concern to olive, and potentially many other plant species, since its detection in southern Italy in 2013 and has subsequently spread and been found elsewhere in the EU. Early detection of such invaders in new areas is crucial if they are to be successfully eradicated or controlled. Consequently, significant investment has been made into new diagnostic and pest detection technologies and surveillance programs. However, questions remain over how many, how often, where and when to deploy sampling resources for the best chance to detect pests at low prevalence. We discuss recent work using epidemiological modelling to target deployment of expensive sampling resources. We demonstrate how models allow us to quantify the probability to achieve survey objectives and optimally target the use of scare survey resources.

The Agro-Economic Modelling Platform of JRC a tool for assessing plant health impact?

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The Joint Research Centre (JRC) of the European Commission hosts an Agro-Economic Modelling Platform that has become a key instrument for policy analysis in the European Commission. Over the past years the JRC has used economic models for EU agricultural market analysis (productions, prices). Also, the platform of models is used for analysis of economic impacts of new free trade agreements or trade barriers for the agricultural sector. Finally, agro-economic models are increasingly useful for the analysis of environmental policies. For example, agro-economic models have been used recently to estimate the baseline for greenhouse gases emissions in EU agriculture and to simulate how mandatory or voluntary caps in emissions would affect agricultural production, prices and trade.

The platform of agro-economic models use in the JRC includes global equilibrium, partial equilibrium and farm-level models.

In the past years there has been an increased demand for exploring the use of economic models to understand policy decisions related to plant health and plant protection products, as well as the impacts of authorising/banning certain technologies (GMOs, animal cloning). The JRC has been exploring how to introduce yield effects caused by changes in pesticide uses (or elimination of certain families of pesticides) in the global agricultural production and trade. Our models have also been used in the past to estimate the economic impacts of trade conflicts related to the use of certain technologies in different ways by trading partners (animal cloning, GMOs etc).

In this regard, the JRC is now starting to explore the use of agro-economic models for the evaluation of the impact of quarantine pests in the case they would be introduced/and or established in European agricultural regions. In short, we are exploring how to introduce yield shocks in our models to derive the possible impacts of quarantine pests on production, prices, changes in trade flows and eventually in upstream or downstream industries.

What role for meta-analysis in plant health risk assessment?

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A meta-analysis is a “statistical analysis of a large collection of results from individual studies“. Quantitative systematic reviews are generally referred to as “meta-analyses” when a statistical model is applied to a dataset derived from a systematic literature review to estimate some key quantities of interest. Meta-analysis has become an essential technique in human health, and a large number of meta-analyses has been carried out to evaluate and compare the effects of medical treatments, and to weight evidences for hazard identification.

In this talk, I investigate how meta-analysis can be used in plant health risk assessments. First, I show that meta-analysis is a powerful tool for assessing the effectiveness of different risk reduction options for managing plant pest and diseases. The principle is to perform a systematic literature review, and to collect the available experimental data measuring the effects of chemical or biological treatments on a given plant pest or disease. The collected data are then analyzed using a statistical model in order to estimate the effectiveness of the considered treatments and to analyze uncertainties. Second, I discuss the advantages and limitations of this approach, and compare the values of different types of statistical methods. I outline several key practical recommendations for implementing meta-analysis, and I show how this approach can contribute to improve the transparency of scientific opinions.

Model “Success” Depends on the Decision-Making Situation

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I have contributed to at least 11 quantitative modeling efforts for decision making during my career in Plant Protection and Quarantine in USDA. A categorical look at these examples gives insight into both the models and decision-making situations surrounding them. I have categorized them by how easy or difficult was the decision to be made, and whether or not the model was a primary or secondary source of information to the decision maker(s). On that basis, models were apparently most successful (supported the eventual decision) when the problem was an easy one, and the model was primary (5 cases). Models also seemed successful when the decision was difficult but a robust non-quantitative risk assessment was the primary source of support (2 cases). I have no examples of models used secondarily for easy issues, which perhaps indicates that such problems need no such support. Lastly, models seemed much less convincing when they were the primary source of information on a difficult (less straightforward) decision (1 case in support, 3 cases not in support). I do not think those models were less accurate or useful than in the other situations. Rather, when the decision(s) to be made is not straightforward or is contentious, being definitive is difficult for managers, perhaps regardless of model credibility. Considering the decision making situation may help modelers understand how convincing the effort needs to be, as well as prepare them for situations in which decision makers cannot or do not take definitive actions.

Bayesian approach to modelling pest introduction

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Bayesian methods have become another tool in data analysis, though the underlying assumptions are somewhat different when compared to more conventional statistical methods. The Reverend Thomas Bayes is thought to have provided the equation that allows one to combine current knowledge (or beliefs) with new information. In Bayesian statistics, all quantities of interest (parameters) have a distribution, as opposed to the fixed values found in conventional (frequentist) statistics. Key concepts here include the 'prior distribution' (what one thinks the parameter values are), and the 'posterior distribution', which is the result of combing the 'prior' with data. A simple example of how Bayes' Theorem can be used to combine new information with a prior probability is presented.

While simple questions can be solved analytically with Bayes' Theorem, more complicated problems can be formulated as a collection of random variables and their conditional probabilities (Bayesian Network), either as equations or a directed acyclical graph (DAG). This type of question can be answered by using Markov Chain Monte Carlo (MCMC) methods, often using a method called Gibb's Sampling. The computational power of modern computers is used in an iterative procedure, where the current values of the parameters to be estimated are used to the estimate the next set based on the conditional probabilities. This procedure is repeated many times and the resulting set of values is used to describe the distribution of the parameters. BUGS, and OPENBUGS, are programs that allow this type of analysis. BUGS stands for Bayesian Inference using Gibbs Sampling.

Programs that focus on analysis of population structure of different organisms can also be used to study pest populations, and many of these can also use Bayesian methods for analysis of these populations. One example is the program 'Structure' which can be used to answer a number of different questions about population structure based on multi-locus genotype data. Another program that can use similar kinds of data is 'Migrate' which allows one to identify and quantify migration rates between different populations. In addition, several different hypotheses about migration patterns can be tested within 'Migrate' by using Bayes' Factor to compare the different models. Examples of analyses from these programs are presented.

Risk based management of invading plant disease

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Effective control of new and emerging plant disease remains a key challenge. Attempts to eradicate pathogens often involve removal of all plants within a fixed distance of detected infected hosts, targeting asymptomatic infection. Here we develop and test potentially more efficient, epidemiologically-motivated management strategies, using a spatially-explicit, stochastic, epidemic model, previously fitted to data on the spread of citrus canker in Florida. A risk based strategy, ranking hosts for potential removal based on the number of secondary infections they are expected to cause, significantly outperforms constant radius removal. However, the risk based strategy is not transparent to stakeholders, since removals depend in a complex fashion on past patterns of pathogen spread. This motivates a variable radius strategy, in which removal radii are fixed at the start of the epidemic, but vary for each host according to a “rule of thumb”. This strategy has intermediate performance. Both strategies are robust to changes to disease spread parameters and patterns of susceptible hosts. However, improved control has a cost, with efficiency degrading if epidemiological parameters are incorrectly characterised. This focuses attention on gaining maximal information from past epidemics, understanding model transferability between locations and adaptive management strategies that can change over time.

EFSA’s activities and plans around sharing and designing Risk Assessment Models

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Recently models used by EFSA over the last 15 years have been brought together in a new EFSA community: the Knowledge Junction. The models can be shared and cited by anyone and registered users can upload their own model or tool. A selection of these tools are also available as web applications so registered users can select a model, upload their data, run the analysis, tweak parameters and view the results. This new community platform makes all the models EFSA has used available to people interested in food and feed risk assessment. The Knowledge Junction runs on the EU-funded Zenodo research-sharing platform where uploaded items get a unique Digital Object Identifier to make them citable. Submissions go beyond models and can include reports, datasets, images, videos, laboratory outputs, software, tools, models, code, protocols, study quality appraisal schemes, FAQs. The contents can then be cited and re-used by EFSA’s scientists and any others preparing new risk assessments. Models and tools with added value to the risk assessment community and stakeholders will gradually be made available as web applications. Additional functionalities that will be added to the Knowledge junction in collaboration with the Member State authorities include a research and development platform open for the risk assessment community where models can be re-engineered and combined adding the possibility to crowd source innovation as piloted in separate projects.

Models for policy advice – white elephant or an elephant in the room

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The bilateral "issues" arising, when risk modelling and decision support interact (e.g. through risk assessment) are well acknowledged and manifold statements exist how this could be a constructive process of cross-fertilisation towards satisfying the needs. Nevertheless, practical experience may often remind either the white elephant, something value-laden and costly that the receiver cannot get rid of, or the elephant in the room, something solving at hand but not recognised at all. Maybe nobody knows for sure how to avoid either or of these creatures – but they exist. Using famous historic examples from Animal Health I want to make them lively and bring up some feeding thoughts from literature.

Posters

Pest risk mapping based on spatial and temporal distribution of crop production

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We suggest a method that ranks production areas of a certain crop species according to the relative probability of pest invasion, using information on the spatial distribution of the crop species during the past 5-10 years. The results are presented as risk indices on a 0.5 × 0.5 km grid. The relative probability of pest invasion is assessed flowingly. 1) The probability of pest entry to a cell, in a given year is assumed to depend linearly on the area of the studied crop species in the cell, in that year. 2) The probability of pest spread to the surrounding cells is modeled with a Cauchy dispersal kernel. 3) The probability of pest survival in a cell, in a given year is assumed to depend on the presence of the studied crop species, so that if it is not present in the cell, in that year, the probability is assumed to decrease according to a predetermined proportion. 4) The probability of pest invasion in a cell is assumed to accumulate over the years, so that the probability of invasion at the end of year t (resulting from steps 1-3) is used as the baseline for calculating the probability for the year t+1. Using this method we estimated the areal pest risk to carrot production in Finland, and compared the risk indices to presence-absence data of *Candidatus* Liberibacter solanacearum on carrot fields. Preliminary analysis indicates that the carrot fields in the cells with high index values are more likely to be infected with Ca. L. solanacearum.

A transmission model for the Potato yellow vein virus-*Trialurodes vaporariorum*-potato pathosystem

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Virus epidemics cause major crop losses throughout the world. Management of viral diseases can be improved if supported by predictive models that can accurately forecast disease spread. Whereas several different modelling approaches have been described for insect pests, specific models for predicting changes in virus epidemics have to date not been developed. In a first step we developed a temperature-dependent phenology model for the insect vector *Trialeurodes vaporariorum* using ILCYM. Next, the efficiency of virus transmission (by adult whiteflies) was determined through controlled laboratory experiments at different temperature, which showed a narrow temperature range of 15-20 C for efficient transmission by the vector. Non-linear equations were developed to estimate the probability for virus transmission by the insect vector in dependent on temperature and validated by transmissions under fluctuating natural temperatures. To determine the probability of virus transmission under different temperature conditions, the transmission function interacts with the prediction of insects surviving to adulthood produced by the life cycle model of *T. vaporariorum*, thereby generating a fully climate responsive model for virus spread and transmission. GIS maps produced by the model reflect very accurately the current occurrence of the virus but also predict new areas at high risk of invasion that could be targeted for surveillance.

Spatially explicit approaches for studying the influence of landscape on the spread of pests

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GIS-based landscape analysis and remote sensing techniques allow to determine different landscape parameters and analyze the spatio-temporal dynamic of pests in order to gain a better understanding of landscape ecological aspects of spatial occurrence and spread. Examples of analysis tools are given for *D. suzukii* (Briem, Golla et al. 2016) and *Diabrotica virgifera virgifera* (Baufeld and EnzianTHE 2005).

Prioritising the quarantine pests listed on the EU Plant Health Directive for Denmark

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At the request of the relevant Danish authority (Naturerhvevrsstyrelsen), the quarantine pests listed on the EU Plant Health Directive DIR 2000/29 Appendices I & II, and the EPPO Alert list were scored for overall risk considering Danish conditions. A precondition was not to evaluate the probability of arrival, and the arrival pathways were not analysed. It was simply assumed that sufficient number of propagules were available for a pest to establish in Denmark. The probability of establishment and spread, and potential impact was assessed and scored using a semi-quantitative scoring system, leading to a five-level scoring from low to very high. Uncertainty had a measurable impact on the final score, which was leading to a lower score in case of high risk and high uncertainty (because the real risk can only be lower, not higher), while a higher score in case of low risk, high uncertainty (because under that scenario, any error will lead to a higher-then-estimated risk). using this scoring system, 27 species on Annex I/A1, 6 species on I/A2, and 18 species on AnnexII/A1 were scored very high risk for Denmark. Mechanistic modelling of root rot, wind and bark beetle dynamics in Finland The changing climate is most likely increasing the risk of disturbances in forest management in the Nordic countries. Currently, the Norway spruce (*Picea abies*) dominated forests face three major threats: root rot caused by Heterobasidion species complex, wind and European spruce bark beetle (Ips typographus). Norway spruce stands infested with root rot are more prone to the heavy winds. In these stands, the infected trees lack the full support of a root system compared to the healthy, non-infected trees. The windthrown trees are the optimal habitat for bark beetle reproduction and can further lead to serious bark beetle outbreaks. In such areas, the overall economic losses can be significant. However, silvicultural choices can affect the disturbance agent dynamics, and the most suitable forest management practices are therefore of great importance.

The purpose of this research was to develop three separate mechanistic models, each representing single disturbance agent dynamics (Honkaniemi et al. 2014, Honkaniemi et al. manuscript, Honkaniemi et al. manuscript). The models were combined with MOTTI tree stand growth simulator (Salminen et al. 2005) to analyse the effect of different forestry management options on the damage risks as well as to compare the financial justification of various control methods. The new software system can be used to include quantitative risk analysis in forest management simulations and further aid decision support and policy making.

Assessing risks of outbreaks of disease vectors through Bayesian analysis of museum specimen data

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The emergence of new plant diseases has been increasing in recent decades due to a combination of factors including novel introductions, climate change, and changes in vector populations. New diseases pose risks to agricultural sustainability through reduced productivity and increased pesticide use. Since the mid-1990s, potato growers in western United States, Mexico, and Central America have experienced severe yield loss from the novel Zebra Chip disease. In response, growers have greatly increased insecticide use to suppress populations of the insect vector, *Bactericera cockerelli*. Despite the severe nature of Zebra Chip outbreaks, the cause(s) of emergence remain unknown. We hypothesized that—because *B. cockerelli* is native to the region and its distribution is constrained by cold winter temperatures—changes in regional climate have allowed the expansion of *B. cockerelli* distribution and have, in turn, caused outbreaks of Zebra Chip disease. We used a large data set of museum specimen occurrence data and a Bayesian occupancy model to analyze changes in occupancy of *B. cockerelli* across California over the last century, and relate any trends to variation in climate. We corrected for biases in the museum specimen data using list length analysis, which estimates *B. cockerelli* probability of detection from the number of related species collected at the same time. We found strong evidence that *B. cockerelli* occupancy has increased over the last century in California. However, these changes appear to be unrelated to climate change. Nonetheless, our analysis provides the first quantitative support for the hypothesis that changes in *B. cockerelli* populations are responsible for Zebra Chip disease emergence. Beyond Zebra Chip disease, our analysis provides a novel macro-ecological approach to comparative risk assessments of pest and disease vector outbreaks under a changing climate. We outline how our analysis can help identify pest species that pose the greatest risk to agricultural sustainability.

ILCYM’s Index Interpolator tool for regional pest risk assessments in mountainous regions

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The use of global coarse and monthly sources of climate surfaces is limiting the precision of predictions of the potential distribution and abundance of insect pests in mountainous regions along altitude gradients (e.g., Andean region). To improve the Insect Life Cycle Modeling (ILCYM) software capacity to capture the small-scale distribution of pests, a new module called “The Index Interpolator (II)-tool” was developed for analyzing pest risk indices at finer spatial and temporal resolution. The II-tool inputs daily minimum and maximum temperature data and calculates three risk indices (establishment index, ERI, generation index, GI, and activity index, AI) location by location. We used the thin-plate smoothing spline algorithm for the indices interpolation using latitude, longitude, and elevation as independent variables. The analyses of the indices at high spatial (pixel size of 90 m) and temporal resolution (daily data) enables capturing the potential establishment, distribution and abundance of insects at small regional scales particularly in mountainous areas. The application of the II-tool was tested in the Mantaro valley of Peru. As input daily data temperatures collected from 23 weather stations homogenously distributed across the valley at altitudes ranging from 3,300 to 4,200 masl were used. The II-tool simulated with high precision the existing distribution and abundance of pests and provided detailed index variability that can be partly lost at lower resolutions. Application and use of insect phenology modeling for regional and global pest risk assessments Insects cannot internally regulate their own temperature and depend on the temperature to which they are exposed. The relationship between temperature and the insect life-history (development, survival, reproduction, etc.) can be well described by process-based phenology models. These models can be used to identify environments where pests might persist to predict their risks of establishment and population growth potential. The International Potato Center has developed a novel approach and software, named Insect Life Cycle Modeling (ILCYM), to support the development of process-based temperature-driven and age-stage structured insect phenology models based on temperature-dependent life-table data and to apply these models for insect species distribution and risk mapping. ILCYM is an open-source computer-aided tool built on R and Java codes and linked to uDig platform, which is a basic geographic information system (GIS) to help ILCYM’s users in analyzing and visualizing the risk assessment maps. The software has three main modules: the model builder, the validation and simulation module, and the potential population distribution and risk mapping module. Phenology models and risk maps on global and regional scales have been developed for a wide range of pests. The modeling steps in ILCYM will be explained and examples given to apply this approach for pest risk assessments under current and future climates.

Gathering empirical data for disease spread models. The case of *Monochamus galloprovincialis* as vector of pine wood disease

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Most of Models on pathways, spatial distribution and potential abundance of pests in the risk assessment area are done from existent data in the scientific literature. Obtaining these data to feed the models (presence / absence, spatial abundance, short and long distance dispersal, altitudinal distribution…) is very costly and slow. However, a huge amount of data are collected by public entities of management (public bodies, civil servants, rangers, environmental administration, etc.), but most of these data are not published in impact journals (SCI) so they are frequently unknown by scientists, as there is no channel for their proper use in feeding models for example. The particular case of the modelization of the phenology and dispersal ability of the European vector of Pine Wood Disease (PWD), *Monochamus galloprovincialis*, from management data, represents a clear example of how these management data can be use to contribute to the plant health modelization.

Plant health for human and animal health

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Fungi are worldwide spread organisms with great impact on plant health, with implications in human and animal health. Mycotoxins, secondary metabolites produced by fungi as response to stressor factors, can be detected in many crops and derived products. This pose a serious treat for human and animal health due to possible acute or chronic toxic effects after ingestion. Several efforts have been devoted in the last two decades to mitigate human and animal exposure, also using modelling approach as valuable support. Two mechanistic models developed in Italy, to describe the dynamic of mycotoxin accumulation during crop growing and to predict the risk of mycotoxins contamination at harvest, represent a relevant contribute in decision making for mitigation. AFLA-maize (Battilani et al., 2013) predicts *Aspergillus flavus* growth and aflatoxin B1 (AFB1) contamination of in maize; following a comparable approach, *A. carbonarius* on grapes and ochratoxin A (OTA) production were faced, resulting in OTA-grape model (Battilani and Camardo Leggieri., 2015a). The opportunities offered by using AFLA-maize, so as comparable predictive models, in decision making were widely described by Battilani and Camardo Leggieri (2015b), both in term of possible predictions and of final users. Apart the common application for farmers and technicians, a successfully application was the prediction of AFB1 contamination in maize and wheat in Europe in climate change scenarios (Battilani et al., 2016), crucial support for decision makers.

Modelling the expected entry rate of *Grapholita molesta* into Canada using @Risk

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Fruit are generally regarded as poor conveyances of pests (see ISPM 32; IPPC 2009), unless the pest is an internal fruit pest that can be carried with the fruit to new locations. These have generally been regarded as having high entry potential in Canadian risk assessments, and the recent and repeated spread of certain pests, especially fruit flies, suggests that this is correct. A recent re-evaluation of the risk of *Grapholita molesta* (Lep.: Tortricidae, the oriental fruit moth) to Canada allowed an opportunity to apply an @Risk model to estimate the probability of such an event actually occurring. Data collected from the literature: import volumes of the various host fruit, relative rates of attack and damage in orchards subject to economic pest control, sales distribution of the commodity within Canada and survival of life stages within the fruit, were included in the @Risk model. Several assumptions had to be made, and the final likelihood had to ignore the potential for clumped distribution of the pest within a commodity shipment, for lack of data. The final result suggests that several tens of thousands of oriental-fruit-moth-damaged fruit arrive to British Columbia (regulated as a pest-free area for Canada), but that the likelihood of that leading to successful establishment: between one-half and 2 'sales events' (the purchase of infested fruit) per year is very low. So much damaged fruit is expected to be culled at inspection, discarded by purchasers into either landfill or commercial composting, that the chance of fruit leading to an infestation in the uninfested part of Canada is extremely low, even before Allee effects are considered.

Data fusion and expert elicitation for species distribution mapping for Pest Risk Assessment

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Species distribution, vegetation and land use data are crucial for several steps of pest risk assessment (PRA), namely pest establishment, spread and impact. The availability of these data however is often scarce, and the spatial and thematic resolution can represent a constraint. Even in a relatively well investigated area, such as Europe, it is very difficult to find reliable and realistic data on species distribution at the appropriate scale. In some cases data on the potential distribution of plant species are available, but this type of information is not appropriate for conducting PRA.

The *Diaporthe vaccinii* risk assessment required to have an estimate of the distribution of certain Vaccinium species across Europe. The mapping exercise was based on the use of the following datasets: 1) Maps of realized distributions of *Vaccinium myrtillus* and *Vaccinium vitis-idea* (Meusel et al. 1978, recomplied by EW) at 10 x 10 km resolution; 2) Maps of terrestrial Ecoregions (Olson et al.); 3) Corine Land Cover data (EEA 2012); 4) Annual average/minimum air temperature (Worldclim, Hijmans et al. 2005).

Furthermore we requested a group of vegetation experts to provide estimates of the coverage of Vaccinium species within the Terrestrial Ecoregions of Europe. The general, large scale distribution of the two species was obtained using a Species Distribution Model (SDM) based on macroclimatic data at 10 x 10 arc min resolution. The prediction of the realized distribution was based on land cover data and on fine scale resolution climatic data (30 arc sec). The estimate of Vaccinium cover, within the predicted area of realized distribution was based on the Terrestrial Ecoregion map (WWF) and on expert knowledge elicitation.

Eco-climatic assessment of the potential establishment and spread of *Phytophthora ramorum* in Slovenia

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Phytophthora ramorum (Peronosporaceae) is harmful organism which infects among large number of host species also several tree species as: *Quercus spp.*, *Larix spp.*, *Castanea sativa*, *Fagus sylvatica* and others. In Slovenia, a survey of *P. ramorum* has been ongoing since 2003 and since then interceptions of infected ornamental plants in containers were recorded every year. Only in 5 cases infected plants were found in parks or gardens. All necessary measures aiming to eradicate the disease were taken and no infection of potential host trees was noticed at those sites. However, overwintering of *P. ramorum* in soil was confirmed with baiting technique in central part of Slovenia in winter 2006. Due to possible threat of *Phytophthora ramorum*, Slovenian eco-climatic conditions for potential establishment and spread were assessed. For modeling of potential infection development of *P. ramorum* weather dataset in the period 2010 – 2015 of 16 selected weather stations of Slovenian agrometeorological network was used. According to literature reference of minimal time period for sporulation and spore germination we were looking for periods of consecutive 30 hours of leaf wetness, combined with air temperature higher than 9.5°C. An index which combines share of years with possible infection in investigated period and an average number of infections per year was calculated. Two regions, Goriška region with submediterranean climate bordering Italy and South east region with continental climate bordering Croatia exhibit relatively high potential for establishment and eventual spread of *P. ramorum* while the central part of the country has moderate potential. Spatial distribution and quantification of hosts were also presented. Based on climate analyses results and host distributions possible threat exists for establishment and spread of *P. ramorum*.

Dealing with uncertainties when modelling the spread of *Ditylenchus destructor*

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The EFSA Panel on Plant Health performed a pest risk assessment on *Ditylenchus destructor*, the potato rot nematode, for the EU. It focused the assessment of entry, establishment, spread and impact on two crops: potato (*Solanum tuberosum*) and tulip (*Tulipa spp.*). A modelling approach was used to quantitatively estimate entry, spread and impact. For the purpose of this contribution only the spread of this pest will be presented.

According to ISPM No. 5, spread is defined as the “expansion of the geographical distribution of a pest within an area”. Spread is therefore usually or ideally assessed on new spatial/geographic units invaded by the pest. In the EU, a system for different spatial units (NUTS-levels - nomenclature des unités territoriales statistiques) can be used. This approach requires knowledge on presence or absences of the pest in the different spatial units through, e.g., surveys. For many pests – including D. destructor - such information is not available. Therefore, spread was assessed at the level of the field.

The main pathways for long and short distance dispersal of *D. destructor* within the EU are plants for planting, including seed potatoes and flower bulbs. Literature and expert judgement were used to estimate model parameters, taking into account uncertainty. A baseline scenario with current pest-specific phytosanitary regulations was compared with alternative scenarios without those specific regulations or with additional risk reduction options.

Simulation of potential natural spread of pine wilt nematode in Slovenia 2000-2100

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We developed a stochastic cellular automata model for potential natural spread of pine wilt nematode (PWN, *Bursaphelenchus xylophilus*) in Slovenia. Spatial resolution of the model was 1 km × 1 km. Several rules were incorporated into the model: (1) spread distance (function of host density); (2) probability of establishment (function of drought stress and mean temperature of July); (3) density of Monochamus populations (rule of +1 year); (4) outbreak and measures (outbreak size is a function of host density; all outbreak locations are recognized and eradicated; probability of eradication was set to 99.5 %); (5) incubation period (parameter was set to three years). We simulated a spread of PWN from three locations. The simulations were repeated for 300 times and calculated for three climate conditions (current and two climate change scenarios). Results showed that the natural spread of PWN was relatively slow process. The spread rate was dependent on the point of introduction. Warmer climate speeded the spread rate of PWN significantly (almost up to twice). Simulation in the case of taking measures lasted up to 30 years' tops. Average speed of spread was 0.65–0.92 km per year in the current climate conditions and 0.84–1.64 km per year in the case of warmer climate. PWN would potentially damage 1.9 Mm3 of wood on 40,324 ha in 25 years.

Network approaches in plant health risk assessment

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Networks are sets of nodes connected by links. Network theory provides a powerful framework that can be used effectively in plant health risk assessment. For example, using EUROPHYT interception data, it is possible to assess the role of various countries/regions as a historical/potential source of emerging plant pests. Moreover, network approaches can be used to model pathways of introduction of quarantine pests. Similarly, the spread of plant pests moving with shipments of plant commodities can be reconstructed or predicted using network theory. Network epidemiological models are increasingly employed to assess and manage the risk posed by plant epidemics, despite the lack of data on the connectivity of plant trade players compared to animal and human health.

Analysing the influence of landscape characteristics on disease spread and management strategies

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Using modelling, many studies have tried to understand disease dynamics to predict epidemics and improve management strategies (Keeling et al., 2008). Spatially explicit models generally represent disease dispersal using epidemiological and management parameters. They are mostly used in a fixed landscape and rarely account for landscapes characteristics. However, the landscape can influence epidemic dynamics; thus, the impact of management strategies is not necessarily transposable from one landscape to another. Here, we present a generic in silico approach which predicts the influence of landscape characteristics on the direct and indirect costs associated with an epidemic. We apply this approach to sharka, the most damaging disease of Prunus trees, caused by Plum pox virus (PPV, family Potyviridae).

PPV epidemics were simulated using a spatiotemporal stochastic model based on an SEIR (susceptible – exposed – infectious – removed) architecture (Rimbaud et al., 2015). This model uses epidemiological and management parameters as inputs, and outputs the number of fully productive trees and the net present value (i.e. an economic criterion balancing the cost of the control measures and the benefit generated by healthy trees).

We simulated various landscapes, differing in plot density and aggregation, by modifying real landscapes and using a T-tessellation algorithm. Then, simulations of PPV dispersal were carried out for the different landscapes, and highlighted that the lower the patch aggregation, the larger the NPV. Sensitivity analyses were undertaken to assess the relative influence of epidemiological and management parameters on each landscape and revealed that 2 parameters related to removals and plantation bans have a strong influence on the NPV. Moreover, we showed that management parameters can be optimized for each landscape but the best management parameter combination differs among landscapes.

This study shows how useful it is to take landscape characteristics into account to predict epidemics. This approach, which is transposable to many epidemics, could thus be used to improve management strategies.

An updated EPPO prioritization process to select high priority plant species for risk assessment following the criteria of the Regulation (EU) No. 1143/2014

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When faced with a large pool of invasive alien plants, species prioritization is an essential prerequisite to focus limited resources on species which inflict high impacts, have a high rate of spread and can be cost-effectively managed within the European Union. Under the LIFE project ‘Mitigating the threat of invasive alien plants in the EU through pest risk analysis to support the EU Regulation 1143/2014’, the EPPO prioritization process was amended to meet the requirements of the Regulation with the purpose of determining which alien plant species have the highest priority to perform a risk assessment at the EU level. Specifically, amendments included a focus on impacts on biodiversity and ecosystem services along with a risk management section that evaluates the effectiveness of prevention and management options.

BiOR² : a database/software process dedicated to plant pests ranking

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Recently, the French Agency for Food, Environment and Occupational Health and Safety (ANSES) was entrusted by the French Ministry for Agriculture to rank a list of plant pathogens in order to achieve pests' categorization. The objective is to prioritize the deployment of resources based on risk and impact of a pest. A new methodology was thus developed: BiOR², which stands for "Biological Organisms data Retrieval and Ranking system". BiOR² associates a database to softwares for multi-criteria analysis. First, the database runs under the database management system (DBMS) PostgreSQL. Its content was collected in a semi-automated manner and consists of 55 tables containing information relative to plants' trade, land use, legislation, pest interceptions and climate classification. The database is linked to a graphic user interface that allows, besides the display of previously entered data, to fill in new data on both host plants and pathogens through a questionnaire. Next, 2800 lines of code enable the link between the available data according to specific criteria and provide a multi-criteria matrix, whose uncertainty can be also quantified by BiOR². A base of 24 criteria, defined according to FAO ISPM N°11 document, covers risk of entry, establishment, spread as well as economic, social and environmental impacts. The ranking is finally achieved through Visual PROMETHEE with the possibility of conducting several scenarios where criteria are assigned different weights. The process was applied to metropolitan France and the French Oversea Departments on respectively 278 and 110 plant pests and pathogens. Results were validated by comparison against results of other models and by a panel evaluation. Overall, BiOR² is intended to be objective, generic, based on sound science, highly adaptable to meet various kinds of questions about the management and impact of pests.

Application of different evapotranspiration models to calculate the agricultural water demand in a tropical region

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Today, water in the Long Xuyen Quadrangle-An Giang (LXQAG) (Mekong River delta, Vietnam) is becoming scarce in some seasons and some districts in the region, especially when the scenarios of climate change will affect water resources in the future. Therefore, it is necessary to make decisions about water conservation and distribution to ensure compatibility with the social objectives such as economic efficiency, sustainability and fairness. The mathematical models used for water distribution and balance calculations are the prominent themes nowadays. To perform this task, it needs to calculate the water needs for all economic sectors. In this article we are particularly concerned about water demand calculation methods for crops and aquaculture. Because these are the two main commodities accounting for the highest water usage in the region. Water demand for crops is calculated through potential evaporation using the methods of Hargreaves & Samani; Priestley and Taylor, Penman-Monteith. The results show that the ET0 error in all three methods is not significantly different and so we chose the Penman-Monteith method to calculate water demand for crops and the method of Penman to calculate expansion evaporation for aquaculture. The result shows that the total water demand in 2015 is 6,594 million m3/year. Of this, the agricultural sector accounts for 97%, other sector is 3%. It is estimated that in 2020, water demand will be 22,769 million m3/year of which 99% will be for agriculture and rise by 71% compared to 2015. The reason is that the local managers expect the catfish farming area to increase by 80%, if people apply the “VietGAP standards”.

The risk assessment of introduction of citrus canker in the Mediterranean basin through Citrus rutaceous relatives: ORPRAMed project

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"Citrus Bacterial Canker (CBC) is a severe disease affecting citrus worldwide. Mediterranean area is free of CBC. ORPRAMed project aims at assessing the introduction risk of the pathogen through citrus rutaceous relatives (CRR), especially those not covered by 2000/29EC Directive. Although the relevance of the disease, there are not recent and in depth studies about the interaction between CRR and *Xanthomonas citri* subsp. citri (Xcc), the pathogen agent of the disease.

For the EPPO standards (2016/09) Xcc is currently classified for EU in the A1 list (quarantine pest not present in the area) of “pests recommended for regulation as quarantine pest”. Moreover, EFSA reported that Xcc can be introduced in the Mediterranean Basin by rutaceous ornamental plants through commercial flows, considering that these species are extensively grown in Mediterranean countries, especially in nurseries.

At this early stage, we are collecting datasets about the size of the trade flows in Rutaceous plants / parts of plants using UN Comtrade Database, to evaluate the import dependence of Mediterranean countries for these products. In particular, we are now considering the commercial flows from countries where Xcc is classified as widespread. Then we will attempt to estimate the trade flow in Rutaceous plants in order to assess the risk of a potential introduction and, finally, the economic impact that it could produce in Mediterranean Basin.

The project consortium includes Italian, Spanish, French and Turkish Research centres and Universities with expertise from agriculture economics to plant pathology and genomics.

The project results will contribute to update information on the trade of rutaceae, acquire new data on the behaviour of ornamental rutaceae regarding Xcc, expand the knowledge about the epi-endophytic colonization of the pathogen and update the European import/export regulation on plant protection.

Statistical modeling of Alfalfa mosaic virus detection in alfalfa seed

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Alfalfa mosaic virus (AMV, Alfamovirus, Bromoviridae) is economically very important in Serbia causing a disease of alfalfa and many other field and vegetable crops. Alfalfa is the most important forage crop in Serbia, grown on 110.000 ha, while seed is a significant export commodity. Epidemiology of seed-borne and vector transmitted AMV requires improvement of alfalfa seed production system using virus-free or seeds of low-level AMV infection. Additionally, there was a need to define 'threshold' levels for AMV infection in seed stocks in order to reevaluate the current Serbian law which allow up to 5% of infected plants in seed crops and 0% of alfalfa seed infection. The main goal was to find suitable and reliable laboratory and statistical methods for determination of AMV seed infection level. The presence of AMV in infected seed stocks was detected using RT- PCR, and for data processing a Graphical User Interface (GUI) application was developed, exploiting statistical method of multiple transfer.

Increasing the number of tested and lowering the number of analyzed samples enabled AMV detection at very low seed infection rates. The samples consisted of 10, 20 and 50 seeds, depending on the expected infection level determined by preliminary tests. The samples were further tested in groups of 25, 50 and 100. Low seed infection rate, such as 0.1%, was successfully determined in compound samples thus significantly lowering the costs without losing the sensitivity.

This protocol and development of GUI application based on multiple transfer method will be applied in standard phytosanitary diagnostic laboratories in Serbia in detecting the rates of seed infection and will be tested as model in reducing disease risk.

The risks assessment of *Aceria kuko* (Kishida) and *Halyomorpha halys* (Stal) pests for the Romanian goji growers

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The present study aims to identify the phytosanitary risk and the dissemination pathways of two new pests, *Aceria kuko* (the goji gall mite) and *Halyomorpha halys* (the brown marmorated stink bug), which both destroyed the goji production in the experimental field of University of Agronomic Science and Veterinary Medicine from Bucharest in 2016. The *A. kuko* mite was mentioned for the first time in Romania in 2013, while the *H. halys* stink bug in 2015. Both pests were first time recorded in Europe in 2007, the goji gall mite being illegally imported in UK, via Netherlands from China by orders by mail, while the marmorated stink bug was first time identified around the city of Zürich in Switzerland. Although the import from third countries into the European Union of Solanaceae intended for planting is prohibited according to Dir. 2000/29/EC, the parcels ordered by mail and the packaging used for different products escape the pest and disease control services. Our field observations regarding the attack frequency, attack intensity and the losses indicate that the non-native pests are a potential threat for Romania, although no attention has been given to them until the present moment. We consider that monitoring the presence of the goji gall mite in the Romanian Goji plantations and research concerning the changes in the *A. kuko*`s and *H. halys* biology has a strategic importance and should be regarded as a biosafety measure not only for Romania, but for entire Europe, as the Goji fruits produced in Romania are mainly exported to the European countries. In the same time, in 2015 and 2016, *H. halys* produced major damages not only to goji, but also to corn, vegetables and some fruit species and also become a nuisance pest in the residential area of Bucharest. Special control measures are demanded by the citizens.

Measuring the economic impact of *flavescence dorée* to Austrian viticulture and related economic sectors

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The aim of the economic impact analysis is to evaluate different intervention and abatement strategies regarding the spread of GFD. There are various quantitative methods available for assessing the economic impact of plant diseases. The most important techniques described in the literature are partial budgeting, partial equilibrium analysis, computable general equilibrium analysis and input-output analysis. These techniques differ from each other particularly with respect to available data, time, experience, skills, funding etc. For a macroeconomic impact analysis the most appropriate method is input-output analysis (IOA). In the project we used a multi-regional IOA to determine the economic impact of GFD in South-East Styria based on a multiregional input-output table. For tow domains the spread model evaluated different initiation scenarios considering the intensity of the initial disease outbreak (severe/limited) and the size of the initial leafhopper population (large/small). Based on the existing data eight scenarios of potential economic impact were calculated depending on the selected intervention scenarios as reaction to given outbreak scenarios. The potential losses calculated vary from zero to more than 5 Mio Euro. In addition we see a positive economic impact in terms of value added based on the control costs for each of the scenarios.

Modelling landscape level impacts of western corn rootworm adaptation to crop rotation in Europe

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The larvae of the invasive western corn rootworm (*Diabrotica virgifera virgifera*, WCR) can cause severe yield and quality loss in maize by feeding of larvae on the root system. As the biology of this pest is strongly linked to its host plant, rotation of maize can break the population build up; and this is an efficient and widely used control measure in Europe. However, adaptation of WCR to crop rotation (also called rotation resistance), i.e. egg-laying into non-maize fields and subsequent larval damage in maize the following season, was reported from the USA since late eighties. In Europe, either an accidental introduction of adapted variant from the USA or adaptation of European population to the rotation may result in a situation where present primary non-chemical control (rotation) may not deliver satisfactory control level. Therefore, we developed a simulation model to estimate scenarios at which adaptation level the recent European rotational strategies would be still efficient.

The WCR population dynamics was simulated on landscape level, on a cellular automaton like lattice of fields. The cell updates were performed according to the rotation strategies (e.g. % of rotation and the possible recommendations for rotating maize after 3, 4 or 5 years of continuous cultivation). In our model, WCR adults emerged in maize fields and then dispersed for egg-laying in nearby fields. Moreover, WCR adaptation to rotation was also modelled as a proportion females released from their strict egg-laying behaviour into maize, and laid eggs also in non-maize fields. The model output was the proportion of maize fields with WCR population level above a defined threshold.

Model evaluations showed that introduction of low frequency (<1%) of adaptation to rotation resulted in similar risk levels to the runs without such adaptation, however, higher frequencies (above 10%) increased the risk of larval damage in subsequent year maize on landscape level. These results can contribute to the risk assessment of the WCR adapted to crop rotation.

The JRC MARS Bulletin – Crop monitoring for Europe

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Stipulated by Article 22 on "Monitoring of Agricultural Resources" of the horizontal regulation 1306/2013 of the EU Common Agricultural Policy, the Joint Research Centre of the European Commission produces monthly bulletins on the state crop growing conditions in Europe and its neighbourhood, and publishes quantitative crop yield forecasts along the growing season for the main crops in Europe such as soft and durum wheat, winter and spring barley, grain maize, rye, triticale, rice, rapeseed, potato, sugar beet, and sunflower as well as pasture.

The JRC MARS Bulletin is currently published in its 24th edition and appreciated for its timely and independent information. The crop yield forecasts of the JRC are used by DG Agriculture and Rural Development to produce crop balance sheets and to support market decisions implementing the Common Agricultural Policy. While the primary addressee of the JRC MARS Bulletin is within the European Commission, the bulletin is published on the internet and reaches out to more than 2'000 users within the first days of publication, ranging from national and regional authorities, extension services, and agro-business worldwide.

Information on timely crop yields and crop growing conditions also fed into the Agricultural Market Information System (AMIS), hosted by FAO and founded by a G-20 initiative in 2011 to increase market transparency of agricultural commodities worldwide.

The MARS Crop Yield Forecasting System

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The Joint Research Centre of the European Commission has established the MARS Crop Yield Forecasting System (MCYFS) as the backbone of its regular crop monitoring and yield forecasting activities for EU28 and the European Neighbourhood. The system serves to access, process, and analyse various spatio-temporal datasets that support the monthly in-house expert analysis to evaluate crop growing conditions in Europe and to derive monthly quantitative yield forecasts along the growing season. The following crops are currently considered: soft and durum wheat, winter and spring barley, grain maize, rye, triticale, rice, rapeseed, potato, sugar beet, and sunflower as well as pasture.

The system consists of four main components: 1) a meteorological infrastructure that collects weather observations and forecasts and produces agro-weather related indicators, 2) a crop modelling infrastructure that enables simulation runs of crop growth models, driven by weather observations, to gain insight in the state of crop development and yield formation, 3) a remote sensing infrastructure to access satellite data and to derive information on the state of vegetation at the land surface independent from the previous two components, and 4) a statistical infrastructure to bring together qualitative and quantitative indicators from the three components, confront them with national yield statistics, and derive quantitative yield forecasts by using statistical methods such as regression, trend, and similarity analysis.

The system, developed over the past two decades, receives daily updates of near-real time data and is constantly being reviewed and improved to incorporate latest scientific findings and to increase accuracy and reliability of the yield forecasts.

A framework for simulating maize kernels mycotoxin contamination in Europe

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Mycotoxin contamination in grain maize is the result of a complex pathosystem formed by maize plants, toxigenic fungi and insect borers. Variability of the climate system could have an important impact on the pathosystem, and potential effects are difficult to estimate. The project MIMYCS (Maize Infection and MYcotoxin Contamination Simulator) aims at the development of a modelling system to simulate this complex pathosystem.

MIMYCS has developed a framework of models to simulate at EU scale mycotoxin contamination in grain maize in different climatic, environmental, and agro-management situations. In this context, the development of MIMYCS allows an easy re-use of components developed for performing scenario simulations to (i) inform European policy makers involved in food and feed safety of the effects of European mycotoxin policies by estimating feasible contamination limits, (ii) derive information on climate change effects to the pathosystem and for future maize-based food and feed products safety, (iii) assist maize producers in controlling mycotoxin contamination through agro-management.

Potential distribution and phenological development of the Mediterranean Corn Borer (*Sesamia nonagrioides*) under warming climate in Europe

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A warming climate has the potential to significantly modify the actual distribution and development of agricultural insect pests. We analyzed the case of the Mediterranean Corn Borer (MCB), one of the most important maize borers in Europe. Its distribution and population levels are primarily determined by its sensitivity to sub-zero winter temperatures. In Europe, it has been mainly reported from the coastal regions of the Mediterranean basin and of the Atlantic coasts up to the western Loire region of France. The objective was to analyze the role of temperature in the potential distribution of the MCB in Europe under warming climate.

Using the AirSoilMS model, the simulated potential distribution is spread in areas where the MCB has never been reported. Other factors linked to overwintering temperature might have an important impact on MCB distribution (e.g. parasitoids, viruses like Baculovirus, effect of consecutive cold years). A modest increase in potential development was simulated in those areas where MCB has already been reported.

This approach can be easily applied to other insect pests. Thanks to the BioMA implementation technology based on framework-independent software components this approach can be easily improved adding new components taking into account other factors that were not considered in this work.

CURRENT EU RESEARCH INITIATIVES ON XYLELLA FASTIDIOSA

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The large outbreak of *Xylella fastidiosa* (*Xf*) affecting olive groves in the Salento peninsula of the Apulia region (southern Italy) and the numerous *Xf* outbreaks reported by the French Authorities in the French island of Corsica, and later on in the mainland, pose major risks to the EU agriculture and plant biosecurity. Because of the complexity of the *Xf*-associated diseases, the management and the control of the infections rely on deep knowledge of the susceptible hosts, of the biology and genetics of the isolate(s), and on their interactions with the insect vector population(s), the climatic conditions and the agricultural practices. As such, the EU Commission mobilized resources within the EU framework programme for research and innovation Horizon 2020. The first research program started at the end of 2015 with the project "Pest Organisms Threatening Europe" (POnTE) dealing with *X. fastidiosa* and other relevant emerging pathogens, indeed at the end of 2016 an H2020 project "*Xylella Fastidiosa* Active Containment Through a multidisciplinary-Oriented Research Strategy" (XF-ACTORS) targeting exclusively *Xf* that has been funded with the aim of fulfilling the research gaps on *Xf* and the development of tools and strategies for prevention and containment of the impact of the disease spread under different agriculture management regimes. Both projects include specific workpackages dealing with the development of effective tools and models for regional pest risk assessment, prevention and eradication. These actions involve very large Consortia with ambitious work-plans covering from basic to applied research on prevention, detection, surveillance and innovative control strategies for *Xf* and its vector(s). The multi-actor approach ensured by these large Consortia will facilitate interactions among research groups, share previous experiences, establish new and strengthen current collaborations among European and non-European research organizations, and increase awareness about the scientific work previously done. Best practices to manage the EU resources are put in place in order to maximize the efforts while avoiding research duplications.

Quantifying an Example Systems Approach Used to Mitigate the Risk of Establishment of Fruit Flies

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Abstract: We investigated how an example systems approach may mitigate the risk of establishment of fruit flies via imported fruit for consumption. We considered an import scenario with the following mitigations: 1) fruit is from an area of low prevalence (5 adult fruit flies per 10,000 fruit), and 2) fruit get a 99.9 percent effective treatment.). Treatment survival was a binomial process with the probability of survival = 0.001. Using a uniform distribution of imported fruit with a mean of 100,000 fruit per container, we simulated the risk of getting at least one mating pair (i.e., a male and female adult) per container. We compared results to a formulaic estimate of treatment efficacy using the means of the above distributions. The probability of a mating pair being present was 0.00066, or about 0.07 percent. That compared to a formula estimate of 0.00061, or close agreement. The probabilistic model further informs that the proportion of shipments with more than one surviving adult was only 0.00132, or 0.13 percent. The estimated mean number of containers to the first mating pair is 1515 (= 1/0.00066), with a five percent chance that the first pair would arrive in the first 78 containers. Using the probabilistic model can help managers decide if the proposed mitigations meet their phytosanitary requirements or if additional measures should be required. We are using this and other models to help define standard systems approaches for exporting nations.

Quantitative Uncertainty Analysis for a Weed Risk Assessment Model

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We developed a quantitative uncertainty model for our weed risk assessment tool for the United States, utilizing the information obtained when assessors rate their uncertainty for each answer given. For each uncertainty rating (negligible, low, medium, and high) we specified a distribution for the likelihood of an answer changing. The simulation model first determines how many answers changed, and then calculates the resulting scores and overall risk rating. We evaluated model sensitivity and behavior, and how often uncertainty results differed from baseline risk ratings. We confirmed that the uncertainty analysis produced a reasonable amount of variation in risk scores and responded to varying levels of uncertainty in the assessments. For over 85 percent of our 204 test species, baseline and uncertainty analysis ratings did not differ. Species assessments with ratings that differed tended to either have risk potential scores near a threshold or greater overall uncertainty. If they differed, the risk rating indicated by uncertainty analysis was almost always greater, but rarely changed all the way from Low to High risk. Uncertainty analysis provides a responsive and informative addition to the baseline weed risk assessment, and provides useful information for analysts, reviewers and decision makers.