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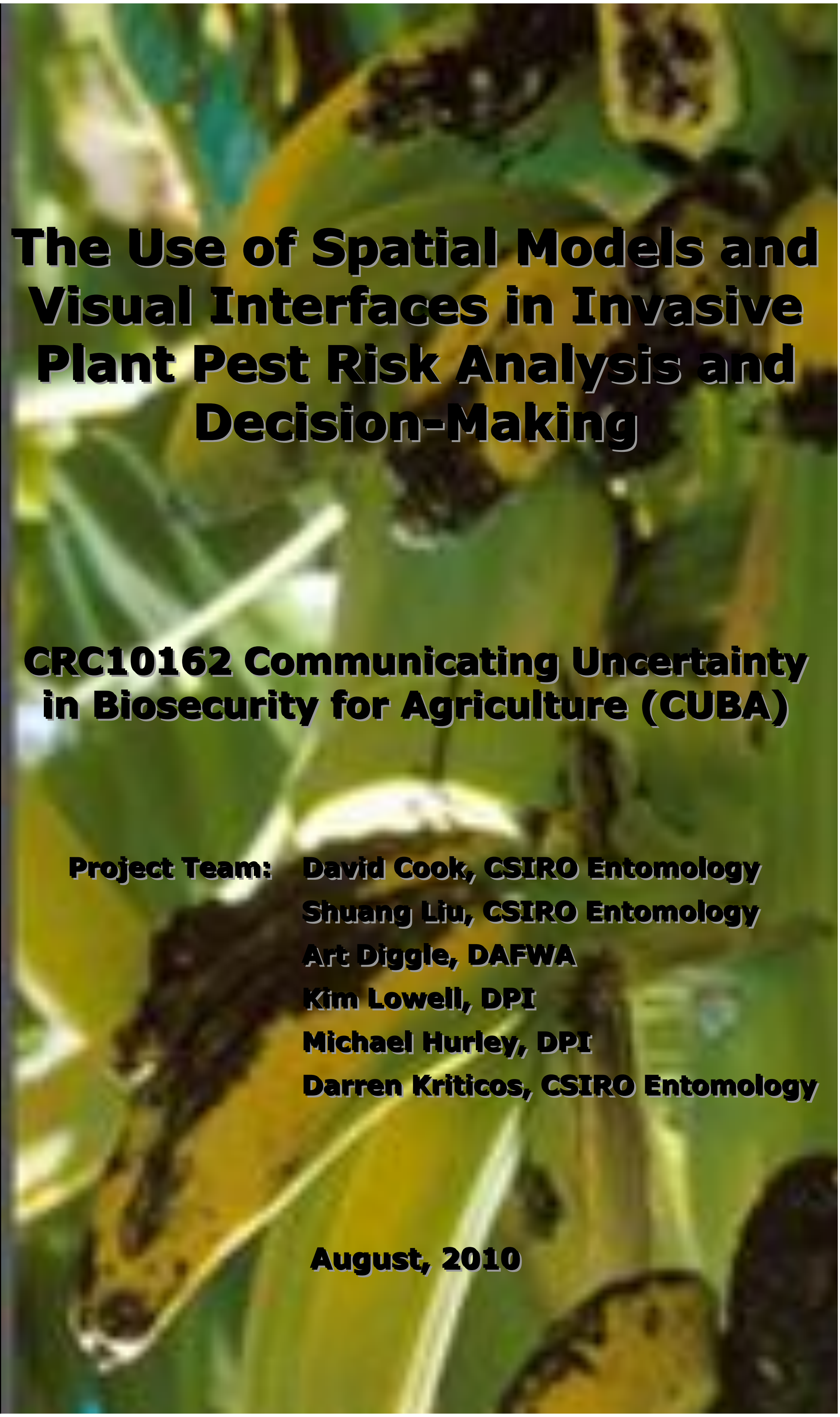

The Use of Spatial Models and Visual Interfaces in Invasive Plant Pest Risk Analysis and Decision-Making

CRC10162 Communicating Uncertainty in Biosecurity for Agriculture (CUBA)

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Table of Contents

Tables

1. Introduction

Recent research and development of decision-support tools to help biosecurity decision makers to make complex investment decisions has relied on the use of Monte Carlo simulation models together with group-based multi-criteria decision analysis (MCDA) (Cook and Proctor, 2007; Cook et al., 2009a; Cook et al., 2009b; Cook et al., 2010; Hurley et al., in press; Liu et al., in press). One of the strengths of the MCDA approach is the transparent communication of uncertainty to decision-making juries through figures and statistics[1]. This is important when, as is often the case in invasive species response policy, decisions are characterised by profound scientific uncertainty and even ignorance about the behaviour of invasive species in environments where they have not been previously observed. In addition to scientific uncertainties, there can also be a great deal of strategic and political uncertainty surrounding risk management decisions. The MDCA approach put forward in Cook et al. (2009a) and Cook et al. (2010) has sufficient flexibility to deal with the changing context of decisions, allowing scientific, economic and social analysts to tailor information to the circumstances of a risk management decision. It can be used to prioritise species by industry or region; to prioritise risk mitigating investments (such as species specific R&D projects or integrated pest management activities); or to determine appropriate management strategies post-invasion (i.e. benefit cost analysis or cost effectiveness analyses).

As effective as MCDA approaches are as transfer vehicles for complex invasive species information, to date they have been limited to non-spatial decision contexts due to a lack of specificity in Monte Carlo simulation models. Where host environments are largely homogenous this does not pose a problem, but in agriculturally and environmentally diverse regions the spatial characteristics of invasive species impacts can be highly varied, and important in a risk management context. This is particularly true when considering the intertemporal effects of invasive species across different landscapes. Improving the spatio-temporal element of MCDA techniques used in biosecurity can be achieved through the use of maps to communicate information, in addition to traditional statistical indicators. These may be used as both output devices to express predictions and uncertainties, as well as input devices to capture scientific expert judgement in cases of high uncertainty about a species and its relationship with a host.

When an event occurs in the "here and now" decision-makers tend to have a lot of information about it, and therefore think of it in concrete, low-level (i.e. intricate detail) terms. But, when an event like a pest incursion is further removed from direct experience (i.e. is more distant into the future), decision makers have less available and reliable information about it, leading to the formation of a more abstract and schematic representation of the event (Trope et al., 2007). Moreover, words and statistics carry the essence of the referent event, whereas

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[1] For a thorough review of MCDA methods see Cook et al. (2010).

pictures are concrete representations that carry the properties of an invasion event in full detail (Liberman and Trope, 1998; Liberman et al., 2002). Therefore, when a decision-making group is psychologically 'near' to an event, pictorial representations of it are more effective decision aids than words and statistics (Förster et al., 2004).

In this paper we review the use of visual devices in group-based, interactive decision making settings and suggest tools and methods that can be used to maximise the effectiveness of visual inputs in to MDCA. We look at different applications from the literature, although we concentrate mainly on the invasive species literature. We draw out features and techniques that can improve visual information quality received by decision-making groups with the aim of improving invasive species risk management decisions. In structuring the review, we cite several of the recommendations put forward in Hirzel and Le Lay (2008) for the production of meaningful species habitat suitability maps, and expand them to provide insights into the effective use of maps in group-based MCDA offering support and examples from the literature along the way.

2. Predictive model scale selection

2.1. Population models

In the context of invasive species, projecting the potential spread and impact of newly-introduced species requires the use of a population spread model. Since the seminal work of Fisher (1937) and Skellam (1951) ongoing attention has been devoted to the development of species spread models in ecology as a means of either understanding how organisms spread, developing new modelling techniques or predicting their spread rates (reviewed in Higgins and Richardson, 1996; Hastings et al., 2005). This form of modelling has also identified the role of different spread pathways (Robinet et al., 2009) and valued the adoption of a strategic control zone to slow the spread of IAS (Sharov and Liebhold, 1998; Sharov, 2004; Buckley et al., 2005).

Given this substantial body of work exists, it is somewhat surprising that there appear to be relatively few attempts to build spread models with a view to more effective management of invasive species at a regional scale (but see Higgins et al., 2000; Buckley et al., 2005; Fox et al., 2009). This may be due to several persistent problems plaguing dynamic spread modelling. Firstly, there is a propensity for spread models to occupy inevitably all of the available habitat space. This results from the exponential process that spread models attempt to represent, the reproduction and dispersal of a population distribution within a finite environmental resource, in this case space. In addition, the outcome of each temporal step results in repeating divergence between replications. That is, the species distribution at a particular timestep is based on the stochastic events of every previous timestep. A third problem concerns the lack of proper validation opportunities with which to engender confidence in the approach.

Since there is scarce literature to draw from that explicitly sets out the process decision-makers should follow when attempting to use spatio-temporal risk mapping tools, it is prudent to start with a few of the basic steps before moving into model design and use.

2.2. Scale

To maximise the effectiveness of maps or pictorial representation of invasive species risks, the first essential step is to use the correct spatial dimension (Pitt et al., 2009). The economic, environmental and social risks posed by invasive species are complex with interactions at various scales due to different entry pathways, establishment and spread vectors (Yemshanov et al., 2009). Indeed, Gibson and Austin (1996) assert that since they are so complex, deterministic models may be most appropriate for representing the spread of epidemics over large spatial scales.

Predicting species abundance and distribution at coarser scales can be achieved through habitat suitability modelling. Species niche models can and have been applied to assess species invasion risks (e.g. Sutherst and Maywald, 2005; Kriticos et al., 2007), and climate change impacts on species potential ranges (Stephens et al., 2007) (the latter being transferable in space or time (Randin et al., 2006))[2]. Jarvis and Baker (2001), for example, use a process-based insect phenology model running at a daily time step for 30 years over 1km grid squares to predict the possible effects of the Colorado potato beetle in England and Wales. Sutherst et al. (2007) discuss sources of change in plant pest distributions over time under climate change scenarios, and likely effects over time.

It is also possible to use species assemblage to infer likely future distributions of invasive species over large scales using self organising map analysis, which is a type of artificial neural network. This technique uses worldwide species associations to determine which species have the highest likelihood of establishing in a particular region (Worner and Gevrey, 2006; Paini et al., 2010). Gevrey and Worner (2006) a worldwide species distribution data from CABI/EPPO (2003) to predict the likelihood of two pest species, the Mediterranean fruit fly (*Ceratitis capitata*) and gypsy moth (*Lymantria dispar*), becoming established in New Zealand in any given year. It is important to note that self organising map analysis does not specifically map spread over time, but instead calculates the likelihood that a species will become established in a certain region given its presence or absence in comparable regions around the world.

At finer scales (e.g. regional or sub-regional), species spread models which represent populations as collections of discrete individuals rather than as a continuum may be more appropriate than habitat suitability models or artificial neural network analysis. At these more refined scales, stochastic spatio-temporal epidemiological models enable decision-makers to have the randomness inherent in real biological systems represented to

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[2] At present, climate-based niche modelling techniques typically employ gridded climate datasets of moderate spatial resolution (0.5 degree), although biosecurity decision-makers continually seek greater spatial precision in the risk map products (Kriticos and Leriche, 2010).

them in model form[3]. However, it should be borne in minds that the model design chosen by an analyst informing a risk management decision may be very influential on the choice made by decision makers. For instance, control strategies can be highly sensitive to the particular form of stochastic model selected (Gibson and Austin, 1996).

2.3. Explanatory variables

Having identified an appropriate modelling scale or resolution to represent invasive species risks to a decision-making group, the particular geographical area to be considered by the group must be established. This may be a small sub-set of the area simulated by probability models, or it may involve the entire area. In instances where the study area selection is simply dictated by the resource allocation decision that needs to be made, the choice of what area is considered is relatively straightforward. Where this is not clear, expert testimony and stakeholder knowledge may be required to refine the appropriate or preferred area.

Once the study area has been clearly identified, the relative abundance of available information on that area must be determined. Guisan and Zimmerman (2000) outline four main sources of environmental information that ideal for the purpose of characterising the study area: (1). field surveys or observational studies; (2). printed or digitized maps; (3). remote sensing data (numerical aerial photographs and satellite images), and; (4) maps obtained from GIS-based modelling procedures. In relation to the management of species populations, delineation of the study area depends on the data sampling plan and whether difficult-to-detect individuals or groups are present, be they newly established invasive pests, nearly eradicated pests, or displaced species.

Venette *et al.* (2002) review the literature related to the detection of rare individuals in order to improve management. They suggest that sampling for rare species should follow the biology of that particular organism but also the principles governing the power of a sampling strategy. They recommend the use of the fundamentals of probability theory as a foundation for any sampling or monitoring program, with consideration of the level of inference that can be drawn from these samples, especially when resources are limited. Specific approaches include binomial, beta-binomial, and hypergeometric-based sampling strategies for quarantine inspections for exotic pests.

Since, in most cases, resources devoted to surveys are small relative to the area possibly affected, there are methods that can be employed to maximise the value of the information available about the chosen study area. For instance, Carpenter *et al.* (1993) predict bettong distributions

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[3] The use of individual-based, spatio-temporal stochastic models is not new. Mollison (1977), for instance, uses models scaled at the level of the individual to predict the spatial spread of a population or epidemic. In these models each population member produces offspring according to a Poisson process with the displacement between offspring and parent drawn from a probability distribution, known as the *contact distribution*.

using DOMAIN which is a range-standardized, point-to-point similarity metric that quantifies the similarity between two sites. This method performs well using presence only data and is sufficiently flexible for use in sampling survey design, reserve selection and potential mapping of rare and common species. Guisan and Zimmerman (2000) suggest the use of the Digital Elevation Model (DEM) in species distribution modelling and mapping as it spawns other environmental variables such as aslope and aspect[4].

However, climatic variables are also of central importance and constitute important information that must be garnered about a study area. Sutherst and Bourne (2009) find that regression models are unable to explain different seasonal patterns across latitudes and longitudes due to selective independent variables in their study context. This variable selection issue can be partially overcome by using factors such as annual average temperatures and rainfall or moisture indices, but fall short in considering biologically relevant combinations of suitable temperature and moisture, extreme conditions of different durations or by using different modelling methods (Sutherst and Bourne, 2009). Population distribution range densities are determined by many variables that interact in complex ways through space and time. Recent studies have highlighted influences of heterogeneous temperature, population demographics, community interactions (e.g. keystone species), biogeographic differences and anthropogenic effects (Sagarin et al., 2006). Jarvis and Baker (2001) focused on the assessment phase of pest risk analysis and in particular aspects relating to the likelihood of a pest becoming established in a country after arrival based on the host temperature during its developmental period.

3. Comparison of modelling approaches to ensure relevant selection

3.1. Deterministic models

Invasive species distribution can be modelled using a large variety of deterministic methods. Included in these methods are Generalized Linear Models (GLMs), ordination and classification methods, Bayesian models, locally weighted approaches (e.g. GAM), environmental envelopes or even combinations of these models (Guisan and Zimmermann, 2000). Table 1 (p. 11), adapted from Guisan and Zimmermann (2000), provides a summary of these and other species distribution modelling methods. Barry and Elith (2006) suggest the use of flexible regression techniques such as BIOCLIM, Distance-based models, and various regression techniques. Selection of an appropriate method should not depend solely

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[4] In this paper, Guisan and Zimmerman (2000) clearly distinguish between spatial resolution and map accuracy. Map accuracy can be tested by determining the errors of mapped entities or gradients. For example, a DEM and its basic derivatives – slope, aspect, topographic position and curvature – may be the most accurate maps available, but will not necessarily have the highest predictive potential.

on statistical considerations but should also consider the shape and nature of the species' response. Regression-based techniques such as GAM, Multivariate Adaptive Regression Splines (MARS), Boosted Regression Trees (BRTs) and maximum entropy modelling offer better performance than GLMs due to flexibility in response curves (Barry and Elith, 2006). One advantageous feature of more rarely used models such as BRT, Maximum Entropy (MAXENT), and MARS is that they all share a high level of flexibility in fitting complex responses (Elith et al., 2006).

To better enable the use of historic and available occurrence data (presence data alone) Elith *et al.* (2006) compare 16 modelling methods over 226 species from 6 regions of the world. Presence-only data is then used to fit models, and independent presence-absence data to evaluate the predictions. They then make a comparison between common models such as GAMs, Genetic Algorithm for Rule Set Production (GARP) and BIOCLIM, and more rarely applied techniques such as BRT, MAXENT, GDM and MARS, to model species' distributions. Interestingly, they find that the novel methods consistently outperform the more established methods.

Leathwick *et al.* (2005) also incorporates MARS, a technique that uses piece-wise linear segments to describe non-linear relationships between species and environmental variables. Analysis results are imported into a Geographic Information System. Guisan and Harrell (2000) show how models based on ordinal data, which is common in ecology, perform just as well as logistic regression for presence/absence and abundance predictions for plants. Models include the Proportional Odds, the Continuation Ratio and the Stereotype models. Aspinall (1992) used a predictive spatial distribution model for deer in Scotland based on Bayes theorem. The uniqueness of the papers' approach lies in the use of a combination of different data sets to predict a single data set. Guisan *et al.* (1998) analyse and predict correlations between alpine plant species distribution and environmental variables using two types of GLMs in Switzerland. The first model uses a binomial GLM with only the mean annual temperature, while the second uses a logistic model restricted to areas within temperature range so that ordinal abundance data can be adjusted. Both models are mapped using GIS. The stratified modelling approach is concluded to better fit the variability within the optimal altitudinal zone for the species. As the model does not include areas outside of the species range, the prediction of new areas, as required in invasive pest modelling, may not be well adapted to this technique.

Biomapper is a GIS and statistical tool designed to build habitat suitability models and maps for different species of animal or plant (Hirzel et al., 2002). It is based on the Ecological Niche Factor Analysis that computes HS models without absence data and that explain the ecological distribution of the species. The extracted factors are totally uncorrelated but have biological signification. This first factor is the marginality factor, which describes how far the species optimum is from the mean habitat in the study area. The specialisation factors are sorted by decreasing amount of explained variance. They describe how specialised the species is by reference to the available range of habitat in the study area. Therefore, only a few of the first factors explain the major part of the whole information.

Table 1. Modelling techniques/tools used to predict invasive species distributions

Modelling technique	Type of predictions	Description	Type of response variable	Capability for treatment of Uncertainty	Spatial	Reference
BIOCLIM	Probabilistic	Envelope model- Climate pattern-matching with minimum bounding rectangle (MBR)	P	No	Capability to inform GIS	Elith J, *et al.* 2006; Barry S, Elith J. 2006
Classification tree	Class Multinomial	General statistical procedure for defining set membership based upon environmental correlates	PA	Yes	Capability to inform GIS	Guisan A, Zimmermann NE. 2000; Araújo and New 2007
GARP	Probabilistic	rule sets from genetic algorithms - Generates environment-description rules using machine-learning techniques	PA	No	Capability to inform GIS	Guisan A, Zimmermann NE. 2000; Peterson AT, Vieglais DA. 2001; Elith J, *et al.* 2006; Araújo and New 2007
GAM	Probabilistic	regression: generalised additive model	PA	Yes	Capability to inform GIS	Richardson DM, Thuiller W. 2007; Elith J, *et al.* 2006
GLM	Probabilistic	regression; generalised linear model	PA relative abundance, Individual counts, species richness	Yes	Capability to inform GIS	Guisan and Theurillat, 2000; Vincent and Haworth, 1983
MARS	Probabilistic	regression; multivariate adaptive regression splines	PA	Yes	Capability to inform GIS	Leathwick *et al.* 2005
MAXENT	Probabilistic	maximum entropy Probabilistic machine learning technique based on the distribution of maximum entropy	PA	No	Capability to inform GIS	Phillips *et al.* 2006; Araújo and New 2007
maximum-likelihood classification	Probabilistic	based on two principles of normal distribution of cells in the multidimensional space and Bayes' theorem.	Qualitative (categorical, nominal)	considers both the variances and covariances of the class signatures	Capability to inform GIS	Frank, 1988
Bayes formula	Probabilistic Binomial	shows the relation between one conditional probability and its inverse	PA	Uncertainty analysis	Capability to inform GIS	Aspinall, 1992; Brzeziecki *et al.*, 1993
Artificial Neural Networks (ANN)	Classification	General modelling technique based on machine learning	PA	Rare or often only point estimates however Bayesian techniques possible	Capability to inform GIS	Gevrey and Worner 2006
CLIMEX	Probabilistic	Match climates function Climate pattern-matching procedure generates an index of climatic similarity	PA	Sensitivity Analysis	Built-in	Sutherst RW, Bourne AS. 2009
DOMAIN	measure of multivariate distances	Climate pattern-matching using a point-to-point similarity index	P	variable sensitivity	Built-in	Carpenter *et al.* 1993
BIOMAPPER - ENFA (Ecological Niche Factor Analysis)	Probabilistic	Computes suitability functions by comparing the species distributions in ecogeographical variables space with that of the whole set of cells using a multivariate approach	P	No	Built-in	Hirzel *et al.*, 2000
NAPPFAST	Probabilistic	Online templates for phenology, infection, and empirical models and a climate-matching tool	PA	Identifies biases and uncertainty ranges at fixed levels of risk using Percent Absolute Difference (PAD) analysis.	Built-in	Magarey *et al.* 2007

Araújo and New (2007) advocate the use of multiple models within an ensemble forecasting framework and described alternative approaches to the analysis of bioclimatic ensembles, including bounding box, consensus and probabilistic techniques. An ensemble is an idealization consisting of system copies, considered all at once, each of which represents a possible state that the real system might assume at some specified time. Multiple copies are simulated across more than one set of initial conditions, model classes, parameters and boundary conditions (predictors in a statistical model e.g. climate variables). Each combination is one possible state of the system being forecasted. Multiple simulations using different parameter values enable parameter uncertainty to be assessed. Araújo and New (2007) use different model classes including polynomials and smoothing splines of different orders in general linear or additive models, nodes in classification and regression trees, hidden layers in neural nets, and various forms of process-based models. Model types included Artificial neural networks, Bagging trees, Boosted additive trees, GARP, and MAXENT.

3.2. Climate matching and envelopes

Climate matching is a common technique used to predict where exotic species could occur if establishment in a new region is successful. Richardson and Thuiller (2007), for example, use nonparametric niche-based modelling (i.e. a generalized additive model - GAM) calibrated on the current distribution of each South African biome to map regions of the world that are climatically similar to South African biomes. They determine climate matched countries and biomes in order to evaluate potential invasive plant distributions in South Africa. GAM is used to relate the biome distributions to the four selected bioclimatic variables. The model is calibrated using a random sample of the data and using Akaike Information Criterion (AIC).

Matched climatic conditions do not, however, perfectly explain where a species could occur. The extent and distribution of invasive species are influenced by interactions between environmental conditions such as climate and anthropogenic factors. Hence, when using an approach like GAM exceptions occur in fragments of other biomes, riparian zones, and areas that were planted by humans (Richardson and Thuiller, 2007).

Nevertheless, climate matching still serves an important role in providing screening information that can act as a starting point in the modelling procedure and make the decision-making process more objective. Additional factors need to be considered alongside climate such as the roles of competition or mutual symbiosis in defining actual invasive potential (Richardson and Thuiller, 2007). This is evident in Hartley *et al.* (2006) who note that Argentine ant (*Linepithema humile*) is often competitively dominant against other ant species, and can adapt to wide variety of novel hosts, despite a lack of co-evolutionary history. Climate can alter the state of these interactions, and therefore still exerts a sizeable influence on invasive ant abundance and distribution.

3.3. Stochastic modelling

To capture and characterise the uncertainty inherent in invasive species spread over time, a stochastic simulation model may be appropriate. This approach has not been as widely employed as deterministic approaches, but several important studies focusing on invasive species issues can be cited. Yemshanov *et al.* (2009) use a spatial stochastic simulation to quantify pest risks and uncertainties. Rafoss (2003) develop a method to predict the establishment and spread of a bacterial disease of potato. The study uses a stochastic simulation in GIS to combine environmental variables and simulate dissemination behaviour of the pest. This paper attempts to define the size of an area affected by an introduction of the disease to a given new region. The stochastic model specifies specific land types (e.g., potato cropping areas) and treated entry as a random event.

The method put forward in Pitt *et al.* (2009) is deserved of special mention in this review. The study models *L. humile* spread using a spatially explicit stochastic simulation model of dispersal within a GIS framework to recreate the historical spread of the insect in New Zealand. Probabilistic maps are used to simulate local and human-assisted spread to identify areas at risk of infestation. These model predictions are compared to a uniform radial spread model in terms of its ability to explain the historical data. Their results indicate that the uniform spread model performs optimally early in the invasion process, but the simulation model is more successful in the latter stages of the simulation. This finding is used to highlight the potential for different search strategies to be effective at different stages in an invasion when attempting to optimize detection.

The Pitt *et al.* (2009) study uses raster maps to represent population distributions and open source software - Python and C, within the open-source GIS GRASS. The model is based on a raster map for each year to represent either the presence or absence of the species in a raster cell. The software developed by the author is titled MDiG and presents an open and standardized platform for species dispersal simulation. The results display probability distributions of possible future spread scenarios for the species. Rather than making specific conclusions about where the species will have established and at what time, the results indicate a relative likelihood of establishment across the landscape.

There are several distinct advantages of the MDiG modelling approach put forward in Pitt *et al.* (2009). Firstly, it allows replicates of model runs, keeps track of all the maps, and can merge into an average map for each time step. Secondly, MDiG captures different means of spread including long distance, shaped neighbourhoods and local contiguous. Local spread via budding and jump dispersal facilitated by human transport can be simulated using the model. Potential spread rates are influenced by dispersal kernel shapes that describe the distance that propagules travel and Allee effects that can limit spread rates and constrain population fronts that otherwise are predicted to accelerate indefinitely. A budding spread rate of 150 m/yr for regions where habitat and climate are not limiting (raster resolution of 150 m). The dispersal model links to the habitat suitability layer to dictate survival and controls the probability that an occupied cell might become extinct. The suitability layer is created by expert knowledge about the suitability of various land cover types for persistence of populations of this species.

While stochastic modelling is preferable in group-decision making requiring the full extent of uncertainty to be made known to decision-makers, it is noted that it is also possible to use a simpler deterministic modelling approach to minimise complexity. However, there are dangers associated with this approach. For instance, Mayer *et al.* (1993) compare deterministic and stochastic models of screwworm fly (*Cochliomyia hominivorax*) incursion into Australia. They conclude that the main discrepancies between the models occur at the fringes of the expanding infestation, with the deterministic model under-predicting population densities. Essentially, the deterministic model fails to detect the small proportion of the population at the front line of the incursion, while the stochastic model does not. Modellers of systems that encompass extreme events and distributions should consider this difference in model selection.

4. Evaluate the predictions – power and variance

Simulating invasive species impacts over time and projecting them on to maps is invariably a complex exercise involving a lot of biological and ecological uncertainty. It is therefore very important that controls are put in place to avoid the misinterpretations of spread and impact that have the potential to mislead stakeholders. For this reason, independent evaluation of invasive species risk models is needed to avoid flawed results being used to inform decisions, or model results being extrapolated inappropriately.

Several studies highlight the need to evaluate model predictions. Sutherst and Bourne (2009), for instance, compare logistic regression and CLIMEX models in predicting range extensions of the non-equilibrium distribution of the livestock tick in Africa. They find that logistic regression better describes the spatial data but displays inferior performance to CLIMEX in predicting range extensions. They therefore question the effectiveness of descriptive, statistical models (i.e. logistic regression) alone to predict changes in species ranges. Peterson and Vieglais (2001) use the GARP modelling method for ex post (i.e. after the invasion event) projection of models onto new landscapes. Peterson *et al.* (2008) advise that absence data should not be employed in evaluating model quality in niche model applications. This is because ecological niche models are often based on species presence information alone due to a lack of absence information. Even if absence data is available, it is often restricted to current distributional area (Peterson et al., 2008). Hence, for an invasive species niche model prior to introduction into a region, one would have counted its future adventive distributional area as absence even though this area was within its niche extent as shown by the later invasion.

The Receiver Operating Characteristic (ROC) curve provides one option for model evaluation when employing invasive pest risk models as decision-support tools. The ROC curve, is a commonly applied approach to evaluating predictive distribution models that avoids subjectivity in the threshold selection for evaluated probabilities by summarizing model performance over all possible thresholds. However, Lobo *et al.* (2008) questions the reliability of the ROC curve and cautions against its use for several reasons, including: (a) ROC ignores the predicted probability and the goodness-of-fit of the model; (b) it considers model performance in probability levels across the ROC curve which could be irrelevant to the evaluation; (c) it weights false positive and the false negative errors equally; and (d) it does not give information about the spatial distribution of model errors. Lobo *et al.* (2008) make these criticisms based on comparison among models of different species. Of course, species differ in home range sizes and therefore extent, and these problems may not be relevant for model comparison for single species. For example, in regards to criticism (c) a modified ROC can be used that substitutes absence data for proportion of area considered to be presence (Phillips et al., 2006; Peterson et al., 2008). Petersen *et al.* (2008) recommend a modified ROC procedure that disposes of absence data, instead using x-axis values as the proportion of the overall area predicted as present, rather than using commission errors based on the aforementioned issues of absences.

5. Provide a map of prediction confidence with levels of uncertainty

5.1. Indicate where the model is applied, interpolated and extrapolated

It is important when using visual devices like maps and figures in group-based MCDA to be as open and transparent as possible in regards to the uncertainty inherent within it. Venette *et al.* (2010) highlight the need for substantial improvement in visual decision-support model documentation, communication of uncertainty, data accessibility, human behaviour (i.e. agriculture interactions) and improved training. It is important not to portray a false sense of accuracy to decision-makers by concealing what may or may not be captured by a species impact map, or the model behind this map.

With this in mind, Sutherst and Bourne (2009) recommend statistical models combined with GIS for interpolating sample data to fill in missing values. However, for extrapolating beyond the data sets, as is necessary with species invasions or climate change scenarios, a different approach is called for using a tool like CLIMEX. Rather than trying to achieve a precise description of the distribution (i.e. using regression), CLIMEX interrogates the data understand critical climatic conditions for a species (Sutherst and Bourne, 2009). Barry and Elith (2006) consider the sources of errors in species habitat models. They divided them into two main classes: (i) error resulting from data deficiencies, and (ii) error introduced by the specification of the model. Common data errors include missing covariates and samples of species’ occurrences that are small, biased or that lack absences. Almost all models examined in Barry and Elith (2006) contain missing covariates, which introduces significant spatial correlation in the errors of the analysis. Aspinall (1992) create error bounds by using random subsets of the data in a bootstrapping type method. Errors are modified within the GIS by changing from 50m pixel to 1km grid square resolution. The key message of the paper is that by analysing the errors, the model results can be interpreted more appropriately.

Several papers have reviewed uncertainty methods available for spatial distribution modelling. Elith et al. (2002) review the aspects of uncertainty and methods that are relevant to habitat maps developed with logistic regression. They address the problems of user, model, and random and systematic errors and suggest methods for developing realistic confidence intervals in relation to decision-making. Regan *et al.* (2003) analyse treatments of uncertainty in a variety of population models. The authors define uncertainty as ignorance about parameter values (e.g. measurement error and systematic error). Risk models include an analysis of variability and parameter uncertainty to give the most comprehensive and flexible endpoint. The paper looks at different risk assessment models at the population level and the relevant sources of uncertainty, and identifies *which* modelling techniques have *what* level of uncertainty treatment (see Table 1, "Capability for treatment of Uncertainty" column, p. 10).

Pitt *et al*. (2009) attempt to tackle uncertainty in stochastic models by random sampling from the spread kernel and survival module probability distributions. Hartley *et al.* (2006) develop a novel method to test for uncertainty in spatial predictions specifically for invasive pest distribution models. Their approach uses a multi-model inference to generate confidence intervals that incorporate both the uncertainty involved in model selection as well as the error associated with model fitting. Using *L. humile* as a case-study, the uncertainty analysis is used to determine that not only is the ant most likely to occur at a 7-14°C mean daily temperature in midwinter, but also an important extreme value at the maximum daily temperatures during the hottest month averages 19–30°C. The approach quantifies the costs of making false negatives vs. false positives in order to connect modelling to decision-making[5].

Methods also exist that aim to make the best decision in the face of extreme uncertainty. Moilanen *et al.* (2006) apply information-gap decision theory to develop uncertainty analysis methods for reserve selection in order to seek a solution that is robust in achieving a given conservation target, despite uncertainty in the data. Information-gap theory uses "distribution discounting," in which the conservation value is penalized by an error measure termed *accuracy of statistical prediction*. Information-gap theory can accommodate non-statistical uncertainties such as the subjective choice of candidate variables and the structural assumptions embedded in spatial analysis to account for unknown levels of potentially-extreme uncertainty. The trade-off between predicted probability (i.e. in the case of Moilanen *et al.* (2006), conservation priority value) and the certainty of the prediction may lead to different decisions

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[5] Hartley *et al.* (2006) quantify false negatives by evaluating the unnecessary effort that is expended in border surveillance and response to an incursion against a species that could never establish. This ignores the possibility of a single surveillance procedure designed for one species detecting multiple species. Social and ecological costs that would be incurred in the event of a successful invasion also need to be considered.

that reflect the planner's attitude towards risk. Choosing sites that have lower conservation values with more certainty reflects aversion to risk.

5.2. Consider species habitat and home range

Ecological habitat and species home range are essential in distribution modelling, be it deterministic or stochastic, and can serve as a practical sensibility test for risk maps derived from probability mofdels. As mentioned previously, climatic considerations are a large component of habitat suitability. However, additional ecological variables also garner consideration, and in some cases there may be a great deal of uncertainty as to how these variables will impact distribution patterns.

Peterson and Vieglais (2001) provide an example of predicting invasions by projecting the ecological model onto landscapes that are likely to be invaded. They use a web interface to apply the derived rule set manually to a parallel set of coverages specifically for the test region of special interest. An alternative and more practical approach is to develop the ecological model on a set of coverages that extend across both the native and the potentially invaded regions.

In some instances homogenous habitats can be assumed. For large, broad-acre agricultural regions this may be appropriate, but for more diverse landscapes into which an invasive species may be introduced the spatial heterogeneity must be considered. For complex spatial environments, metapopulation models (e.g. Hanski et al., 2000) or stochastic patch occupancy models (e.g. Moilanen, 2004) may be appropriate.

6. Reclassify predictions into robust, meaningful, and honest values for policy makers and the public

Pest risk maps can be powerful visual communication tools to describe aspects of an incursion (Venette et al., 2010). They enable decision-makers to receive a wealth of information relatively quickly, and to visualise the threat posed by invasive species. Numerous spatial decision support tools for workshop environments have been developed and applied with success. A summary of these applications is contained in Table 2, p. 18. The decision problems to which they are applied are varied, but illustrate the general applicability of mapping techniques group-based decisions. We outline some of the techniques and applications in more detail below.

The Multi-Criteria Analysis Shell for Spatial Decision Support (MCAS-S) is a software tool produced by the Australian Department of Agriculture, Forestry and Fisheries' Bureau of Rural Sciences. MCAS-S is a spatial decision-support tool designed for application in real-time stakeholder workshops, where it helps participants visually link mapped information to a Multi-Criteria Decision Analysis (MCDA) decision making framework (Lesslie et al., 2008). MCAS-S can be used with issues of various scales and resolutions, and does not require GIS programming knowledge by the user. User-friendly features of MCAS-S include the capability for a decision-making group to view, classify and combine different types of mapped information in an interactive, real-time setting. MCAS-S can also produce statistical reports for specific regions quickly and simply.

Table 2. Multi-criteria decision analysis spatial tools: a selected list of GIS-based and standalone software-based applications for natural resource management issues (Lesslie *et al*. 2008).

Software/analysis	**Application**	**Reference**
1. GIS-based applications		
IDRISI (®Clark University) GIS-based MCA	Earthquake hazards; crop suitability; soil erosion in Ethiopia	Ceballos-Silva and Lopez-Blanco (2003); Dragan *et al*. (2003)
ASSESS (A System for SElecting Suitable Sites) written in *ArcInfo* AML (®ESRI)	Radioactive waste repository; soil conditions; catchment condition	Veitch and Bowyer (1996); Bui, (1999); Walker *et al*. (2002)
ArcView (®ESRI) GIS-based MCA Planning tool	Urban land use	Pettit and Pullar (1999); Dai *et al.* (2001)
ILWIS GIS	Nature conservation value of agricultural land	Geneletti (2007)
MapInfo (®) GIS-based DSS	Urban transport policies	Arampatzis *et al.* (2004)
Spatially-explicit sensitivity analysis framework for decision making	Invasive plant pest management	Roura-Pascual *et al.* (2010)
2. Hybrid applications		
SIMLAND – cellular automata, MCA and GIS written in C and using *ArcInfo* GIS	Land use change	Wu (1998)
HERO (Heuristic multi-objective optimisation) combined with GIS, AHP and Bayesian analysis	Forest planning; habitat suitability	Kangas *et al.* (2000); Store and Kangas (2003); Store and Jokimaki (2001)
3. Stand-alone software		
LMAS – Land Management Advice System	Spatial expert system	Cuddy *et al*. (1990)
MULINO-DSS (MULti-sectoral, INtegrated and Operational DSS) combines simulation models, mapping and MCA	Water resources	Giupponi *et al.* (2004)
IWM – decision support system for Management of Industrial Wastes	Industrial waste	Manniezzo *et al.* (1998)
GSA (Global Sensitivity Analysis) in *SimLab* (Software for Uncertainty and Sensitivity Analysis)	Hazardous waste disposal	Gomez-Delgado and Tarantola (2006)
MCAS-S - Multi-Criteria Analysis Shell for Spatial Decision Support	biodiversity and salinity mitigation trade-offs in revegetation	Lesslie *et al.* (2008)
CommunityViz planning software and the Placeways suite of GIS offerings provide a real-time interactive environment of 3-D visuals, intelligent maps and dynamic analysis tools.	Economic options for rural areas, urban planning, conservation planning	Placeways, LLC Ltd.

CommunityViz® (Placeways LLC, Boulder, Colorado) is another software package that facilitates decisions in a workshop environment and can bring in pest risk maps in a user-friendly manner. The software serves as an extension to ArcGIS (ESRI) in order to create an interactive decision-making platform. The software is designed to inform decisions concerning alternative futures (scenarios) by analysing decision effects, and can create three-dimensional (3D) map outputs. CommunityViz is designed for real-time workshop communication. Some aspects of using this software package are user-friendly so that an inexperienced operator can utilise them, while others are more sophisticated and require knowledge of GIS.

A framework for deciding among options, in the form of static priority maps is developed for the management of woody invasive alien plants in South Africa in Roura-Pascual *et al*. (2010). The framework features a spatially-explicit sensitivity analysis. The authors use a combination of analytical hierarchy process, Earth mover's distance, Shannon Diversity index and Akaike's Information Criteria to determine the best management option based on sensitivities among methods. Unlike MCAS-S and CommunityViz, the majority of the analysis in Roura-Pascual *et al*. (2010) is completed "behind the scenes" by an analyst. However, the models are linked to the decision problem and can therefore be used as part of a decision-making group workshop by presenting clear, meaningful maps. Roura-Pascual *et al*. (2010) includes criteria related to management history, fire risk, and the age, identity, density and spread of invasive plants. Each factor has a weight associated with it that reflected its relative importance in prioritizing areas for management. The authors change the weights using three types of sensitivity analysis and assess the effect of these changes on the spatial structure of the resulting priority maps in three different management regions. Model outcomes are not considered as discrete elements by evaluating rank order when changing the decision criteria, but instead spatial configuration is evaluated spatially explicitly using distance measures. By determining the importance of criteria in shaping priority maps, the sensitivity analysis framework enables the identification of necessary criteria to produce outcomes matching pre-selected management objectives. This is crucial for cost-effective management, as acquisition and curation of data is expensive.

7. Conclusions

This paper has reviewed a cross section of the modelling and ecology literature and described methods and techniques that may be useful in developing visual information tools for use in group-based MCDA for invasive species risk management decisions. These decisions might involve the prioritisation of species by industry or region, the prioritisation of pest and disease entry pathways, or choosing the most desirable pest management strategies post-invasion. In all of these decisions, an invasive species population, spread and distribution model is useful in helping the decision-making group to appreciate the idiosyncrasies of individual invasive species, and to respond to these threats more effectively. Projecting this population and impact information on to maps familiar to the group will enhance the uptake of this information by placing decision-makers psychologically closer to incursion events, but the process of doing so is complex. In this review, we have discussed some of the basic steps that should be followed, including choosing model scale, clarifying the area of interest for the MCDA and choosing the form of population model to use to project population distribution and abundance on to maps. We have also highlighted methods that can be used to evaluate the strength of model predictions and communicate this to decision-makers through maps. We have also discussed a range of group decision-making applications of map-based approaches, and identified some of the tools used. This background knowledge will be extremely beneficial in the design and use of state-of-the-art map-based tools to help Australian plant industries to better manage the biosecurity threats facing their industries.

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