



Comparison of alternative strategies for invasive species distribution modeling

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ABSTRACT

Species distribution models (SDMs) can provide useful information for managing biological invasions, such as identification of priority areas for early detection or for determining containment boundaries. However, prediction of invasive species using SDMs can be challenging because they typically violate the core assumption of being at equilibrium with their environment, which may lead to poorly guided management resulting from high levels of omission. Our goal was to provide a suite of potential decision strategies (DSs) that were not reliant on the equilibrium assumption but rather could be chosen to better match the management application, which in this case was to ensure containment through adequate surveillance. We used presence-only data and expert knowledge for model calibration and presence/absence data to evaluate the potential distribution of an introduced mesquite (*Leguminosae: Prosopis*) invasion located in the Pilbara Region of northwest Western Australia. Five different DSs with varying levels of conservatism/risk were derived from a multi-criteria evaluation model using ordered weighted averaging. The performance of DSs over all possible thresholds was examined using receiver operating characteristic (ROC) analysis. DSs not on the convex hull of the ROC curves were discarded. Two threshold determination methods (TDMs) were compared on the two remaining DSs, one that assumed equilibrium (by maximizing overall prediction success) and another that assumed the invasion was ongoing (using a 95% threshold for true positives). The most conservative DS fitted the validation data most closely but could only predict 75% of the presence data. A more risk-taking DS could predict 95% of the presence data, which identified 8.5 times more area for surveillance, and better highlighted known populations that are still rapidly invading. This DS and TDM coupling was considered to be the most appropriate for our management application. Our results show that predictive niche modeling was highly sensitive to risk levels, but that these can be tailored to match specified management objectives. The methods implemented can be readily adapted to other invasive species or for conservation purposes.

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1. Introduction

Species distribution models generally proceed by first identifying environmental characteristics that are associated with a species occurrence and then extrapolating this information to detect other areas that possess similar characteristics (Underwood et al., 2004). For invasive species, this information can then be used to develop management strategies, determine containment boundaries and identify priority areas for early detection and rapid response (Elith et al., 2006; Morissette et al., 2006; Jiménez-Valverde and Lobo, 2007). However, such predictions can be challenging for introduced invasive species, which frequently have wide ecological niches and may not yet have reached equilibrium within their new environment (Sutherst and Bourne, 2009; van Klinken et al., 2009; Václavík and Meentemeyer, 2009). Hence, the key challenge for predict-

ing the potential ranges of an invasive species is handling the uncertainty inherent in distributional data where it has not yet reached the full extent of habitat that could support it. How this uncertainty is handled will depend on management objectives (e.g. eradication, containment or impact reduction) and on the resources available to implement the management strategy. In this paper we explicitly consider the relationship between uncertainty (considered within a risk framework) and management. In this approach, the model assuming equilibrium becomes just one of a suite of possible scenarios that are assessed to suit management objectives (Underwood et al., 2004; Jiménez-Valverde et al., 2008; Sutherst and Bourne, 2009).

A number of techniques for species distribution modeling have been reviewed in the literature (c.f. Franklin, 1995; Guisan and Zimmermann, 2000). Correlative models, for example, rely on the detection of a correlation between species distribution records and the environmental predictor variables used to make predictions (Beerling et al., 1995; Robertson et al., 2003). However, particularly with introduced species, there may not be an overt cause

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for the correlation (Beerling et al., 1995). In addition, correlative models assume distribution records represent the entire range of sites that can be occupied by the target species (the equilibrium assumption) and thus, when used with accurate presence and absence records, approximates the actual or realized distribution (Jiménez-Valverde et al., 2008). However, the equilibrium assumption is violated by actively expanding invasive species and, therefore, the actual distribution relating to a point in time may be a conservative representation (Franklin, 1995; Beerling et al., 1995; Austin, 2002; Hulme, 2003). While a conservative modeling approach is likely to increase the likelihood of predicting sites where a species exists (few false positives), or may survive, it may severely underestimate areas where a species may potentially exist (Jiménez-Valverde et al., 2008) thereby misdirecting management action and policy development. For example, underestimation may result in invasion going unnoticed until the species is well established (Robertson et al., 2004) and beyond successful eradication (Rejmánek and Pitcairn, 2002). Instead, it can be argued that relaxing the level of conservatism (thereby increasing risk levels) to capture a greater number of known presence sites (potentially at the expense of a greater number of false positives) may be more desirable for providing an early warning for species that are still expanding.

Recently, there has been a greater emphasis on identifying modeling approaches (e.g. Sutherst and Bourne, 2009), and alternative techniques (e.g. geographically weighted regression) for species that have not yet reached equilibrium (Austin, 2007). A common approach has been to use profile techniques (e.g. Tsoar et al., 2007), which do not take into account data on a species absence and more commonly tend towards approximating areas where a species could live (i.e., the potential distribution) rather than simply where it currently does live (i.e., the actual/realized distribution). These techniques (and others) may also be dichotomized into predicted presence and absence by choosing a suitable threshold that decreases the false negative rate at the expense of an increased false positive rate (e.g. Fielding and Bell, 1997). Our aim is to overcome the limitations of causality and under prediction by using a deductive approach within a geographical information system (GIS) where the rules are derived from a combination of expert knowledge and empirically derived data as described in Eastman et al. (1993), Franklin (1995) and Robertson et al. (2004) and the level of conservatism (or risk) can be adjusted during the process of combining data layers (ecological variables) to suit prediction outcomes. The use of such risk-adjusting techniques to develop a range of scenarios (decision strategies) with varying levels of conservatism (or risk) has received very little attention to date. Here we explore its utility in the context of modeling invasive organisms.

This study adopts a standard, moderate risk-taking, multi-criteria evaluation tool (weighted linear combination (WLC)) (Jiang and Eastman, 2000) and couples it with a risk-adjusting technique known as ordered weighted averaging (OWA) to develop a series of alternative decision strategies. We develop five alternative decision strategies (two more conservative than the WLC model, one equal in risk to the WLC model, and two more risk-taking) for identifying the distribution of an invasive mesquite (Leguminosae: *Prosopis* spp.) population in the Pilbara Region of northwest Western Australia. The population is currently largely restricted to a single property, but is thought to have the potential to invade more widely. The primary focus of management is therefore containment of the core infestation, and eradication and surveillance outside of the core infestation. Mesquite presence and absence data were obtained from a previous airborne survey of the entire known population (ca. 1500 km²), which was in turn used to predict habitat suitability across 112,649 km² of the Pilbara Region (van Klinken et al., 2007). Receiver operating characteristic (ROC) analysis and two threshold determination methods (Liu et al., 2005) were used

to determine which models would best identify suitable habitat assuming that the population was at equilibrium, and assuming the population was still invading, respectively. Comparison of the alternative outputs is examined in the context of our management goal of identifying areas for early warning and surveillance.

2. Methods

2.1. Target species

Several mesquite species (together referred to as “mesquite”) are recognized as being highly invasive, both in their native and introduced ranges (Archer, 1995; van Klinken et al., 2006). They are leguminous shrubs or trees that can form dense thorn-forests, resulting in serious economic, environmental and social costs (Hennessy et al., 1983; Gibbens et al., 1992; Goslee et al., 2003). Mesquite reproduces from seeds and typically has a high fecundity, producing one main crop per year. In Australia, it is ranked nationally as 1 of the 20 most significant weeds (Thorp and Lynch, 2000).

The studied mesquite population is located in the north-west Pilbara Region of Western Australia (centred on 21°11'18"S, 115°56'67"E) and is the result of an intentional introduction to the Mardie Pastoral Station in the 1930s to serve as a drought and fodder plant as well as for shade for livestock (Meadly, 1962). It has since invaded over 150,000 ha, principally on the delta of the Fortescue River where it was first introduced and where most of the approximately 32,500 ha of dense mesquite occurs. However, it is also spreading and increasing in density on adjacent catchments, especially in the Robe River delta to the southwest (van Klinken et al., 2007). The population is described as a hybrid swarm of *P. pallida*, *P. velutina* and *P. glandulosa* var *glandulosa* (van Klinken and Campbell, 2009). *P. pallida* belongs to the *P. juliflora*–*P. pallida* complex, which is native to southern Central America, while *P. velutina* and *P. glandulosa* are a complex native to the USA and Mexico (Pasicznik et al., 2001). The hybridization of these species obtained from diverse geographical areas in the northern hemisphere makes it difficult to extrapolate species-specific observations derived from native range populations to novel environments as has been done in other studies (e.g. De Meyer et al., 2007; Mgidi et al., 2007; Beaumont et al., 2009).

2.2. Validation and calibration data

The entire known mesquite infestation was mapped as an 18.5 ha grid-matrix during a visual aerial survey in 2004 (van Klinken et al., 2007). Mesquite was mapped as absent, isolated, moderate or dense, which we converted to categorical presence/absence data. To minimize the effects of spatial dependency we randomly sampled 500 presence data and 500 absence data for model validation. This also avoided the potential bias caused by different levels of prevalence in presence/absence datasets (Manel et al., 2001). An additional randomly sampled partition of 500 presence data was also used as calibration data for standardizing the compound topographic index (see Section 2.3.3). Calibration of the other criteria used in the model from this data was not possible as the aerial survey did not record data for some of the classes that were located beyond the boundary of the current infestation. These criteria were standardized using expert opinion.

2.3. Criteria selection

Criteria (environmental variables) were selected based on previous ground-based and remote sensing-based studies (van Klinken et al., 2006, 2007; Robinson et al., 2008) designed to determine the habitat preferences of the mesquite population under study. Three

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