



Evaluation of Bayesian networks for modelling habitat suitability and management of a protected area



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ABSTRACT

To be effective, management of protected areas should be based on the best available evidence, including the scientific literature and expert knowledge. However, lack of such evidence in a suitable form to support decision-making may hinder effective management. Here we examine the use of Bayesian networks to support the management of protected areas, through the development of habitat suitability models for eight species of conservation concern. Bayesian networks were constructed on the basis of the scientific literature and expert knowledge, and were then tested using results from a field survey. Models of all species demonstrated very high discrimination between presence and absence sites, as indicated by AUC values >0.8, with values >0.9 obtained for four species, and Kappa values in the range of 0.4–0.9. The Bayesian networks were then used to examine the impact of different management interventions on habitat suitability of each species, including tree cutting, grazing and burning. Species differed in terms of their sensitivity to different management interventions, and model output provided evidence of both negative and positive interactions between types of intervention. These results highlight the trade-offs that must often be made when undertaking conservation management, and demonstrate the value of Bayesian networks in helping to make such trade-offs explicit. The identification of management impacts through analysis of available evidence also demonstrates the value of Bayesian networks for supporting evidence-based approaches to protected area management.

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Introduction

Effective conservation management is dependent on knowledge of where organisms occur and what their specific habitat requirements are, as well as the potential impacts of management interventions on habitat condition. In practice, the distribution of many species is imperfectly known, as resources for field surveys are often lacking and many species are cryptic or difficult to survey (Lomolino, 2004). In these circumstances, it can be useful to identify potential areas of species occurrence based on analysis of habitat suitability. Such analysis can be of value for assessing the potential impacts of climate, land use and other environmental changes on species distributions; increasing the efficiency of field surveys of rare species; and supporting the development of conservation management plans (Cayuela et al., 2009; Guisan & Thuiller, 2005; Lütolf et al., 2006; Rodríguez et al., 2007). Potential areas of species occurrence can be identified using species distribution or habitat suitability models, which relate presence or abundance of species to environmental predictors (Elith et al.,

2006; Guisan & Zimmermann, 2000). The development of modelling techniques and the increasing availability of environmental data has led to rapid growth of research in this area (Brotons et al., 2004; Dormann, 2007; Franklin, 2010; Guisan & Zimmermann, 2000), and its increasing application to conservation problems (Cayuela et al., 2009; Sinclair et al., 2010).

A wide variety of modelling approaches have been used to model species distributions, including generalised linear models, generalised additive models, bioclimatic envelopes, habitat suitability indices, maximum entropy models and the genetic algorithm for rule-set prediction (GARP) (Cayuela et al., 2009; Elith & Burgman, 2003; Elith et al., 2006; Guisan & Zimmermann, 2000; Phillips et al., 2006). While each approach has its particular strengths and weaknesses, different methods can produce very different predictions (Guisan & Thuiller, 2005; Thuiller, 2004). In addition, each method is associated with a number of statistical issues. First among these is the amount and quality of available data, which are often limited and highly biased (Guisan et al., 2007), particularly when systematic surveys of species distributions are lacking (Cayuela et al., 2009). Many species require specific small-scale habitat attributes, such as topographic, geomorphic, or edaphic features, which are generally excluded from species distribution models, because they are unavailable in spatial format (Sinclair et al., 2010). As a result

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of such data deficiencies and errors in model specification, there is a need to examine the impacts of uncertainty when using species distribution models, particularly when they are applied in a conservation context (Elith & Leathwick, 2009). However, relatively few studies employing these techniques explicitly consider uncertainty (Beale & Lennon, 2012; Elith & Leathwick, 2009).

Given such limitations, some form of expert judgement is often required to evaluate the outputs from species distribution models. While expert knowledge is already recognised as an essential source of information for assessing the conservation status of species (Newton & Oldfield, 2008), the effective integration of expert knowledge with species distribution modelling approaches has been identified as a key challenge for the future (Cayuela et al., 2009). A further key issue is one of scale. Most studies employing species distribution models examine large spatial extents, reflecting a widespread focus on analysing species responses to climate change (Elith & Leathwick, 2009; Franklin, 2010). Such investigations tend to ignore local-scale variation, despite the fact that local-scale heterogeneity in variables such as light availability and soil characteristics may be greater than that occurring at the regional scale (Austin & Van Niel, 2011). Relatively few studies employing species distribution models have been undertaken at the local or landscape scales relevant to conservation management (for example, see Fei et al., 2007; Gibson et al., 2004; Podchong et al., 2009; Seoane et al., 2006), despite recognition of the potential value of these methods at such scales (Guisan & Zimmermann, 2000).

Here we evaluate the use of Bayesian networks to model potential species distributions at the scale of an individual protected area, with the aim of supporting conservation management. A Bayesian network (sometimes referred to as a Bayesian belief network or belief net) is a graphical model that incorporates probabilistic relationships among variables of interest, which are typically presented in the form of a network diagram (Jensen, 2001). Bayesian networks differ from most other approaches to environmental modelling by exclusively using probabilistic, rather than deterministic, expressions to describe the relationships among variables. This feature is particularly useful in the context of risk assessment and for supporting decision making (Borsuk et al., 2004; Bromley et al., 2005; Dorner et al., 2007; Newton, 2009).

Bayesian networks are increasingly being used in environmental modelling and conservation management (Marcot et al., 2006; McCann et al., 2006; Newton et al., 2007; Newton, 2009). This reflects their value for exploring domains characterised by uncertainty, through analysis of the probability distributions associated with the variable states (Jensen, 2001). The visual component of developing a Bayesian network, involving creation of a network diagram, can also provide a useful tool for eliciting, structuring and integrating information from experts (Newton, 2009; Uusitalo et al., 2005). In a conservation management context, Bayesian networks have been used for analyses of ecosystem structure (Milns et al., 2010), site quality (Schapaugh & Tyre, 2012), translocation sites for endangered birds (Laws & Kesler, 2012), and impacts of different land management alternatives on populations of mammals (Lehmkuhl et al., 2001; McNay et al., 2006; Raphael et al., 2001), birds (Howes et al., 2010) and lichens (Nyberg et al., 2006). However, few previous studies have explicitly used Bayesian networks to model habitat suitability (Marcot, 2006; Smith et al., 2007), particularly in the context of protected area management.

The aim of this investigation was to evaluate the use of Bayesian networks to model the habitat suitability of species at the scale of a single protected area, namely the New Forest National Park, UK. To achieve this, networks were constructed using information on the suitability of habitat for selected species of conservation concern, derived from available literature and expert knowledge. The networks were then tested using independent field survey data, and

then used to explore the potential impacts of different management interventions on habitat suitability.

Methods

Study area

The New Forest National Park is situated on the south coast of England in the counties of Hampshire and Wiltshire (Longitude from 1°17'59" to 1°48'8" W, Latitude from 50°42'19" to 51°0'17" N). The Park was designated in 2005 and extends over 57,100 ha (Newton, 2010). Its importance for biodiversity conservation is reflected in its many designations, with some 20 SSSIs, six Natura 2000 sites and two Ramsar Convention sites included at least partly within its boundaries (Newton, 2010). The vegetation is a mosaic of pasture woodland, heathland, grassland, scrub and mire communities. Its present character is strongly dependent on its history as a mediaeval hunting forest, and the long-term survival of a commoning system. As a result, this landscape has developed under the influence of large, free-ranging herbivores, including deer as well as livestock, over a prolonged period (Tubbs, 1968, 2001). In recent years, some 6000–7400 livestock, principally ponies and cattle, have been pastured in the New Forest, which roam freely over a large part of the area. Around 2000 deer are also present in the Park (Newton, 2010, 2011).

Selection of species

To evaluate the value of Bayesian networks in a conservation management context, a range of species of conservation concern were selected with contrasting ecological characteristics. A list of 600 candidate species were extracted from the New Forest Special Area of Conservation (SAC) Management Plan (Wright & Westerhoff, 2001), then filtered to those species that are relatively widespread within the Park (i.e. >100 unique distribution records obtained since 1990), to ensure that enough locations were available for statistically robust model testing. Bird species were excluded as their habitat requirements are relatively well documented. Eight species fulfilled these criteria, including four plant species: wild chamomile (*Chamaemelum nobile* L. (All.)), slender marsh-bedstraw (*Galium constrictum* Chaub.), wild gladiolus (*Gladiolus illyricus* Koch) and pillwort (*Pilularia globulifera* L.); two butterfly species: silver-studded blue (*Plebeius argus* L.), grayling (*Hipparchia semele* L.); one Orthoptera species: wood cricket (*Nemobius sylvestris* Bosc.); and one fungus species: nail fungus (*Poronia punctata* L. (Fr.)).

A literature search was carried out for each species to identify variables important for habitat suitability. Search engines including ISI Web of Knowledge (www.isiknowledge.com) and Google (www.google.com) were used to search (using the species' names as search terms) for information on each species, limiting to studies based in the UK.

Development of network diagrams

In a Bayesian network diagram, variables, data and parameters are represented by different shapes (such as ellipses and rectangles), which are connected by arrows to indicate conditional dependencies. The ellipses representing variables are referred to as *nodes*, whereas the arrows are referred to formally as *directed links* (or alternatively as *edges* or *arcs*). A link between two nodes, from node A (parent node) to node B (child node), indicates that A and B are functionally related, or that A and B are statistically correlated (Fig. 1). Each child node (i.e. a node linked to one or more parents) contains a Conditional Probability Table. This gives the conditional

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