Converting probabilistic tree species range shift projections into meaningful classes for management

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ABSTRACT

The paper deals with the management problem how to decide on tree species suitability under changing environmental conditions. It presents an algorithm that classifies the output of a range shift model for major tree species in Europe into multiple classes that can be linked to qualities characterizing the ecological niche of the species. The classes: i) Core distribution area, ii) Extended distribution area, iii) Occasional occurrence area, and iv) No occurrence area are first theoretically developed and then statistically described. The classes are interpreted from an ecological point of view using criteria like population structure, competitive strength, site spectrum and vulnerability to biotic hazards. The functioning of the algorithm is demonstrated using the example of a generalized linear model that was fitted to a pan-European dataset of presence/absence of major tree species with downscaled climate data from a General Circulation Model (GCM). Applications of the algorithm to tree species suitability classification on a European and regional level are shown. The thresholds that are used by the algorithm are precision-based and include Cohen's Kappa. A validation of the algorithm using an independent dataset of the German National Forest Inventory shows good accordance of the statistically derived classes with ecological traits for Norway spruce, while the differentiation especially between core and extended distribution for European beech that is in the centre of its natural range in this area is less accurate. We hypothesize that for species in the core of their range regional factors like forest history superimpose climatic factors. Problems of uncertainty issued from potentially applying a multitude of modelling approaches and/or climate realizations within the range shift model are discussed and a way to deal with the uncertainty by revealing the underlying attitude towards risk of the decision maker is proposed.

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1. Introduction

A major challenge when managing large-scale ecosystems like forests is to evaluate how climate change may affect the growth and mortality of tree species (Seppälä et al., 2009). A key decision is, which species may still be considered to be suitable for forest management under changing environmental conditions. For this management problem models are often used as decision support (Bolte et al., 2009).

The impact of climate change on the distribution of tree species in Europe is generally evaluated with bioclimatic envelope models (Heikkinen et al., 2006). The interest in applying this technology increases with global change and new methods to model species distribution are discussed (Elith et al., 2006). Beside the major challenges in species distribution modelling under climate change (Thuiller et al., 2008) such as the integration of land cover, CO_2-effects and biotic interactions, progress has been made in the integration of migration speed in biome shift models (Meier et al., 2012). However, shortcomings and uncertainties of the models have to be carefully assessed. One source of uncertainty that has been recently evaluated is the influence of the choice of the threshold to transform probabilities of occurrence produced by the models into binary predictions of presence or absence of the species (Nenzén and Araujo, 2011). There are a multitude of rules for setting thresholds.

Fielding and Bell (1997) cast a critical light on fixed thresholds to transform values as they may lead to exaggerating prediction errors. They state that the modelling method may influence the values of probabilities and consider a single threshold for different models to be unsuitable. In addition, they highlight the importance

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of taking into account the prevalence as it influences the absolute values of the probabilities if a fixed threshold is applied. Nenzén and Araujo (2011: 3346) identified three groups of approaches to set thresholds: (I) fixed (e.g. 0.5); (II) data-driven — using species data and predicted probability values (e.g. prevalence); and (III) accuracy-based — using the threshold that produces the best agreement between the evaluation data and the original data (e.g. Cohen's Kappa). According to them, the goal of accuracy-based thresholds is to minimize prediction errors across the modelled region such as false negatives (modelled absences that are in fact species presences) and false positives (modelled presences that are species absences). Nenzén and Araujo investigate 14 different thresholds for 116 tree species, however their approach is, like in the studies they cite (Thuiller, 2004; Liu et al., 2005; Freeman and Moisen, 2008), restricted to binary predictions, as their main interest is to evaluate extinction risk. Yet, when using bioclimatic envelope models for management decisions, such as the regional choice of tree species (Falk and Mellert, 2011), a binary response of a model, exclusively depicting presence or absence of the species, may be insufficient. Even if a species is outside its ecological optimum and may be classified as "absent" by a binary model (i.e. when it is just below the chosen threshold) it may still be used as an admixture to other more suitable species, e.g. for economic reasons. On the other hand, species distribution models dividing a range of outcomes into a scale of presence (or absence) probabilities without giving any thresholds that are linked to ecological attributes that may be used to classify the suitability may not be looked upon as very useful by decision makers as a probability is per se not a valid decision basis.

2. Goal of the study

Goal of the present study is to develop an algorithm that classifies the output of a range shift model for major tree species in Europe into multiple classes that can be linked to qualities characterizing the ecological niche of the species. The classes should be used to evaluate tree species suitabilities not only in terms of presence/absence, but also in terms of population structure, competitive strength, site spectrum and vulnerability to biotic hazards. We first define four theoretical classes describing niche areas of tree species. We then define statistical thresholds between these classes and develop an algorithm that calculates these thresholds based on the output of a biome shift model. We interpret these classes from an ecological point of view and use the attributes of the ecological interpretation to validate the results of the classification with an independent dataset.

We demonstrate the functioning of the algorithm using the example of a generalized linear model that we fitted to a pan-European dataset of presence/absence of major tree species with downscaled climate data from a General Circulation Model (GCM). We discuss the problem of uncertainty issued from potentially applying a multitude of modelling approaches and/or climate realizations within the biome shift model and we propose a way to deal with the uncertainty by revealing the attitude towards risk of the decision maker. We show applications of the algorithm to tree species suitability classification on a European and regional level.

3. Material and methods

3.1. Database

We used presence/absence information per species derived from the 'Data on Crown Condition of the systematic grid (16 × 16 km)' (Level I) from the 'International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects on Forests' (ICPF) (Fischer et al., 2010) as response variable. This response was modelled using derivations of precipitation and temperature from the WorldClim − database.

3.1.1. Distribution data

The ICPF, established by the 'Convention on Long-range Transboundary Air Pollution under the United Nations Economic Commission for Europe', has been monitoring forest condition in Europe from 1987 on. The Level I database contains 8393 distinct plots (for most of which the 37 countries participating in the ICPF did not report data every year). There are 135 different species observed, of which 42 species have presence observations for one or more years on at least 42 distinct plots. For 8366 of the Level I plots we could derive temperatures and precipitation from the WorldClim database, the missing 27 plots being mostly located near the Scandinavian coastline.

3.1.2. Climate data

The WorldClim dataset is described in detail by Hijmans et al. (2005). We calculated nineteen bioclimatic variables following Nix (1986) and Houlder et al. (2000), plus an additional set of six bioclimatic variables consisting of the number of days per year with mean temperature above 5° Celsius, the yearly heat sum above 5° Celsius (bio26), mean temperature and precipitation sum in summer (which we defined as the months May to September) and annual and summer drought index following O'Neill et al. (2007).

3.1.2.1. Climate scenarios − spatial resolution. We used the 30-arc-second tiles for precipitation, the minimum and maximum temperatures of the WorldClim data for current conditions to derive the predictors for the model fit. For prediction under future conditions, we used output from the global circulation model HADCM3 (Gordon et al., 2000) driven by the SRES scenarios B2a and A2a, which was calibrated and statistically downscaled to 30-arc-second tiles using the WorldClim data for 'current' conditions. All climatic datasets were obtained from www.worldclim.org.

3.2. Statistical approach: the model − GLM

To analyse the data we opted for a statistical modelling approach (cf. Guisan and Zimmermann, 2000). This implies modelling the realized niche (Austin, 2002) and assuming (at least pseudo-) equilibrium between the response variable and the predictors (Lischke et al., 1998).

3.2.1. Model formulation

For reasons of simplicity and interpretability Austin (2002) recommended using generalized linear models (GLM). Elith et al. (2006) and Guisan et al. (2007) found GLM did not perform markedly worse than other competing statistical methods such as: generalized additive models (GAM, with or without the BRUTO adaptive backfitting algorithm), multiple adaptive regression splines, boosted regression trees, maximum entropy and generalized dissimilarity modelling. Randin et al. (2006) found that GLM could be slightly better transferred in space than GAM, which tended a bit more to overfitting the data. They concluded that the same would hold for projections in time instead of space.

Considering these findings, we chose for this demonstration example of our algorithm to fit GLM with logit link functions, (i.e. logistic regressions), without interactions between the predictors. We used second-order polynomials of the bioclimatic variables described in 3.1.2 on the link scales of the GLM to achieve bell shaped response curves, which match with the common notion of ecological niches.