Provisioning forest and conservation science with high-resolution maps of potential distribution of major European tree species under climate change

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Abstract
Key message We developed a dataset of the potential distribution of seven ecologically and economically important tree species of Europe in terms of their climatic suitability with an ensemble approach while accounting for uncertainty due to model algorithms. The dataset was documented following the ODMAP protocol to ensure reproducibility. Our maps are input data in a decision support tool “SusSelect” which predicts the vulnerability of forest trees in climate change and recommends adapted planting material. Dataset access is at https://doi.org/10.5281/zenodo.3686918. Associated metadata are available at https://metadata-afs.nancy.inra.fr/geonetwork/srv/fre/catalog.search#/metadata/fe79a36d-6db8-4a87-8a9f-c72a572b87e8.

Keywords biomod2 · Ensemble species distribution model · ODMAP

1 Background

Climate change is likely to cause widespread shifts in the composition and range of plant communities worldwide (Scheffers et al. 2016). For long-living communities such as forests, such change may lead to a drastic decline in their ability to support multiple ecosystem services (Maroschek et al. 2009; Härtl et al. 2016; Mina et al. 2017). In Europe, the effects of climate change on forests may include changes in forest productivity (Reyer et al. 2014), changes in the distribution of tree species (Dyderski et al. 2018; Thurm et al. 2018), the economic value of forests (Hanewinkel et al. 2013), effects of intensifying disturbance regimes (Seidl et al. 2011, 2014), and droughts (Allen et al. 2010).

As such, there has been considerable interest in estimating the potential distribution of tree species under scenarios of climate change. Species distribution models (SDMs), often referred to as ecological niche models (ENMs), are the most widely used tools for this purpose (Sykes et al. 1996; Thuiller et al. 2008; Dyderski et al. 2018), because they predict the potential distribution of species by exploiting the correlation between the known occurrence of a species and corresponding environmental conditions.

In the recent decades, SDMs have evolved and were applied for a wide range of questions such as to predict species range in the future (Sykes et al. 1996; Thuiller et al. 2008; Dyderski et al. 2018), to test hypotheses about species distribution limits (Kreyling et al. 2015), to develop conservation and management strategies in climate change (Guisan et al. 2013; Hamann and Aitken 2013; Mcshea 2014; Schueler et al. 2014), and understand the role of genetic variation in tree species distributions (O’Neill et al. 2017).
Despite the recent improvements and widespread use, the free and unrestricted utilization of SDMs in the applied forest and conservation science is often limited due to inadequate documentation and reporting of the predictions and uncertainties. Therefore, Zurell et al. (2020) proposed a reporting protocol known as ODMAP (Overview, Data, Model, Assessment, and Prediction), which offers a standardized way of communicating the results/outputs from SDMs by describing the objectives, model assumptions, scaling issues, data sources, model workflow, model predictions, and uncertainty.

Here we present a dataset on the potential distribution of seven widely occurring tree species of Europe for current and projected future climate scenarios. To ensure transparent reporting and reproducibility, we described the dataset according to the ODMAP protocol suggested by Zurell et al. (2020). The following sections describe the basic elements of the dataset, while the detailed metadata according to ODMAP (Zurell et al. 2020) is presented in Table 2 in Appendix.

2 Methods

2.1 Species occurrence data

Current occurrence (presence and absence) of seven major stand forming tree species in Europe (Table 1) was obtained from the EU-Forest dataset (Mauri et al. 2017). These species are known to form stands in a wide range of forest types across Europe (European Environmental Agency 2006) and are also economically important (Hanewinkel et al. 2013). The Mauri et al. (2017) dataset is one of the most exhaustive, harmonized European tree species occurrence (presence) data available till date, which combines three existing datasets: the Forest Focus (Hiederer et al. 2011), Biosoil (Houston Durrant et al. 2011), and national forest inventories. In our case, the geographic locations of the target species in the EU-Forest dataset were assumed to be true presences, while the presence locations of other target species were assumed to be the absence locations. To ensure that the absence locations are not only climatically dissimilar but also geographically distant from the observed presence locations, we developed the so-called pseudoabsences according to Senay et al. (2013). This is a three-step approach: (i) specifying a geographical extent outside the observed presences, (ii) environmental profiling of the absences outside this geographic extent, and (iii) k-means clustering of the environmental profiles and selecting random samples within each cluster. In our case, a 2-degree buffer was found to be optimum following Senay et al. (2013). The absence locations outside this geographic extent were classified into 10–15 environmentally dissimilar clusters according to the k-means clustering algorithm. The numbers of absence clusters for each species were determined from the elbow of the plot of total within-cluster sum of square (WSS) and number of clusters. The number of pseudoabsence locations was further reduced by randomly selecting a sample of locations defined by the 95% confidence interval from each of the absence clusters. This approach was used to generate the pseudoabsence data for each species.
to generate pseudo-absence for all seven species. The resultant dataset was used to calibrate the SDMs with the biomod2 platform (Thuiller et al. 2016).

### 2.2 Climate data

Biologically relevant climate variables were obtained from the ECLIPS 2.0 dataset (Chakraborty et al. 2020a, b). This dataset was developed from dynamically downscaled, and bias-corrected regional climate model results from the EURO-CORDEX with a resolution of 30 arcsec. The EURO-CORDEX (www.eurocordex.net) is an initiative of the World Climate Research Program (Giorgi et al. 2009) for coordinating dynamic regional downscaling of the global climate projections from the CMIP5 (Coupled Model Intercomparison Project Phase 5) (Jacob et al. 2014). All projections were corrected for bias using a distribution scaling method (Yang et al. 2010) to produce 0.11° × 0.11° resolution gridded data for daily mean, minimum, and maximum near-surface air temperature and precipitation. We further refined this 0.11° × 0.11° resolution bias-corrected data to 30 arcsec using the delta algorithm for spatial downscaling (Ramirez-Villegas and Jarvis 2010; Moreno and Hasenauer 2016). With this approach, we developed a gridded dataset for 80 climate variables (Table 3 in Appendix) for historic climate (1961–1990) and three future time frames which include averages of (2041–2060, 2061–2080, and 2081–2100) for two Representative Concentration Pathway (van Vuuren et al. 2011), RCP 4.5 and RCP 8.5. The RCP 4.5 or the moderate scenario assumes a 650 ppm atmospheric CO₂ concentration and a 1.0–2.6°C increase in annual temperature by 2100, whereas in RCP 8.5, a pessimistic scenario assumes a 1350 ppm CO₂ and 2.6–4.8°C increase in annual temperature by 2100 (van Vuuren et al. 2011). The ECLIPS 2.0 dataset is available at https://doi.org/10.5281/zenodo.3952159.

### 2.3 Variable selection

From the list of potential predictor variables (Table 3 in Appendix), the ones which explain most of the variation in the observed presence and absences of each species were selected with a recursive feature elimination approach (RFE) implemented within the Random forest algorithm (Breiman 2001). Within the RFE approach, the variables were eliminated iteratively, starting from the full set of potential predictors and retaining only those variables that reduce the mean square error over random permutations of the same variable. The variables which were linearly correlated with other variables and had a variance inflation factors VIF > 5, a commonly used threshold in detecting multicollinearity (Craney and Surles 2002; Thompson et al. 2017), were identified. The identified collinear variables with the lower value according to the Akaike Information Criteria (AIC) (Akaike 1974) were retained for further model development. This subset of uncorrelated climate variables (Table 4 in Appendix) was used as predictor variables for developing the ensemble species distribution models.

### 2.4 Ensemble species distribution models

To model the potential distribution of the seven European tree species, an ensemble distribution modeling approach, implemented through the R package, biomod2 (Thuiller et al. 2016), was used. biomod2 offers a computational platform for multi-method modeling that generates models of species’ potential distribution for each species. The model algorithms include GLM (Generalized Linear Models), GAM (Generalized Additive Models), GBM (Generalized Boosted regression Models), CTA (Classification Tree Analysis), ANN (Artificial Neural Networks), SRE (Surface Range Envelop or BIOCLIM), FDA (Flexible Discriminant Analysis), MARS (Multivariate Adaptive Regression Spline), RF (Random Forest for classification and regression), and MAXENT. Tsuruoka. Hence, biomod2 combines the strengths of multiple modeling algorithms while accounting for their uncertainties. We used biomod2 default settings for all the modeling algorithms (Thuiller et al. 2016). Each model algorithm predicted the probability of the potential distribution for each species. Such probabilities predicted from the individual models were ensembled into a consensus model by combining the median probability over the selected models with true skill statistics threshold (TSS > 0.7) (Allouche et al. 2006; Coetzee et al. 2009). The median was chosen because it is known to be less sensitive to outliers than the mean. The estimated ensemble model predictions were presented as GeoTIFF rasters. These raster files are available at https://doi.org/10.5281/zenodo.3686918.
2.5 Model evaluation and uncertainty analysis

Model evaluation was carried by splitting the occurrence dataset into 75% for model training and 25% for model testing. Besides, biomod2 allows specifying the number of runs for each combination of training and testing data. Therefore, 10 independent runs, each with a randomly selected set of training and test data, were implemented.

For each such model run as well as the final ensemble models, the model evaluation statistics were recorded. These statistics were true skill statistics (TSS) and area under the relative operating characteristic (ROC), model sensitivity (the ability of the model to predict true presences), and model specificity (the ability of the model to predict the true absences). TSS takes into account both omission and commission errors and ranges also from −1 to + 1, not being affected by prevalence as KAPPA (Allouche et al. 2006). TSS values ranging from 0.2 to 0.5 were considered poor, from 0.6 to 0.8 useful, and values larger than 0.8 were good to excellent (e.g., Coetzee et al. 2009). Prediction accuracy is considered to be similar to random for ROC values lower than 0.5; poor, for values in the range 0.5–0.7; fair in the range 0.7–0.9; and excellent for values greater than 0.9 (Pontius and Parmentier 2014).

Model uncertainty was also estimated in terms of coefficient of variation (CV) among the predictions of the individual models. The estimated CVs are presented as GeoTIFF rasters where each cell corresponds to a CV value, whereby higher and lower CV values indicate higher and lower uncertainties, respectively, in the ensemble model. These raster files are available at https://doi.org/10.5281/zenodo.3686918.

In addition to internal evaluation, the model predictions were also tested against independent data on European Forest Genetic Conservation Units (GCU) (Lefèvre et al. 2013). The geographic locations of the 3354 genetic conservation units (Fig. 3 in Appendix) were used to extract the predicted probability of occurrence from the models for the seven target species for the period 1961–1990. The ensemble models were used to predict the distribution of the seven target species at each GCU location. Predicted probability < 60 were assumed to be, “incorrectly predicted,” whereas those > 60% were treated as “correctly predicted” following Dyderski et al. (2018). For most species, the incorrectly classified GCUs are those located in the southeastern part of their potential distribution (Fig. 3 in Appendix).

3 Access to the data and metadata description

The dataset is accessible through https://doi.org/10.5281/zenodo.3686918. Associated metadata are available at https://metadata-afs.nancy.inra.fr/geonetwork/srv/fre/catalog.search#/metadata/fe79a36d-6db8-4a87-8a9f-c72a572b87e8

4 Technical validation

In general, for all species, a high correlation was observed between the predictive performance of the models calibrated with both training and evaluation data with mean TSS ranging from 0.79 to 0.92 and mean ROC ranging from 0.92 to 0.98 (Table 1). Average sensitivity or the ability of the models to predict true presences across all species and models range from 95 to 98% and average specificity or the ability of the models to predict true absences range 86–96% (Table 1). Detailed performance of individual models can be found in Table 5 in Appendix.

Model evaluation against independent data reveals that out of the total 3354, 80–96% of the species occurrence in the European genetic conservation unit (GCU) dataset was correctly predicted by our ensemble SDMs (Table 6 in Appendix).

The ensemble SDMs predicts a substantial change in the potential distribution of the seven target species (Fig. 1). A general trend of a northward shift in potential climate suitability (probability > 60%) was predicted, as also observed by recent studies such as Dyderski et al. (2018). Median uncertainty represented by the coefficient of variation between individual models varies between 6 and 15% and with Larix decidua and Abies alba having higher prediction uncertainty compared to other species (Fig. 2).

5 Reuse potential and limits

The dataset is currently being used to develop a decision support tool, SusSelect Smartphone app https://play.google.com/store/apps/details?id=com.topolyx.susselect&hl=en, which calculates the vulnerability of tree species under climate change. The dataset is also being used to develop an Integrated Toolbox that combines tools from Interreg CE, Horizon 2020, and EU Life projects. This integrated toolbox (TEACHER-CE) is under development and focuses on climate-proof management of water-related issues such as floods, heavy rain, and drought risk prevention, small water retention measures, and protection of water resources through sustainable land-use management. For details see: https://www.interreg-central.eu/Content.Node/TEACHER-CE.html.
Fig. 1 Potential distribution of seven European tree species under the historical period (1961–1990) and predicted future scenario of 2080–2100 under RCP 4.5 and RCP 8.5
Ecological niche models or SDMs assume that the relation between climatic drivers and the species distribution remains constant also in climate change. This assumption needs to be taken into account while interpreting the results of the paper.

**6 Dataset citation**

Chakraborty D, Móricz N, Rasztovits E, Dobor L, Schueler S (2020). Provisioning forest and conservation science with high-resolution maps of potential distribution of major European tree species under climate change (Version v1) [data set]. Zenodo. http://doi.org/10.5281/zenodo.3686918

**Appendix**

Provisioning forest and conservation science with high-resolution maps of potential distribution of major European tree species under climate change.
Table 2 Description of the dataset according to the ODMAP protocol

| ODMAP elements | Contents |
|----------------|---------|
| **Overview**   |         |
| Authorship     | Authors: Debojyoti Chakraborty, Norbert Móricz, Ervin Rasztovits, Laura Dobor, Silvio Schueler |
|                | Contact email: debojyoti.chakraborty@bfw.gv.at |
|                | Title: |
|                | DOI: |
| Model objective| SDM Objective: forecast/transfer |
| Taxon          | Target output: probability of occurrence of target tree species |
| Location       | Europe |
| Scale of analysis| Spatial extent (Lon/ Lat): |
|                | Longitude: $-32.65000^\circ E, -69.44167^\circ E$ |
|                | Latitude: $30.877982^\circ N, -71.57893^\circ N$ |
|                | Spatial resolution: 30 arcsec |
|                | Temporal resolution: We modeled for historic climate (1961–1990) and three future time frames which include averages of (2041–2060, 2061–2080, and 2081–2100). The predictions were done for two Representative Concentrations RCP 4.5 and RCP 8.5 |
| Biodiversity data overview | Observation type: standardized monitoring |
| Type of predictors | Response data type: presence/absence data |
| Conceptual model/hypotheses | A large body of scientific studies indicate that climate is one of the major drivers of the distribution of tree species at the continental scale. We exploited this correlation between species’ current occurrence and climate to develop SDMs that predict the potential distribution of the target tree species |
| Assumptions | We assumed that species are at pseudo-equilibrium with the environment. The source of the presence/absence data (Mauri et al. 2017) used in this study is largely from national forest inventories where tree individuals below a certain diameter at breast height are not recorded. We assume that this data collection procedure did not bias our occurrence data |
|                | Since our occurrence dataset covers the whole current distribution of the target species, which represents both current and likely future climate of Europe, we safely assumed that the species retain their niches across space and time and the current occurrence–climate correlation remains stable when predicting the models for future climate |
| SDM algorithms | Algorithms: We selected 10 modeling algorithms: GLM (Generalized Linear Models), GAM (Generalized Additive Models), GBM (Generalized Boosted regression Models), CTA (Classification Tree Analysis), ANN (Artificial Neural Networks), SRE (Surface Range Envelop or BIOCLIM), FDA (Flexible Discriminant Analysis), MARS (Multivariate Adaptive Regression Spline), RF (Random Forest for classification and regression), and MAXENT. Tsuruoka. These model algorithms were implemented through an ensemble model platform biomod2 (Thuiller et al. 2016) |
|                | Model complexity: The individual models were run using the standard default settings of biomod2 that are designed to balance model complexity and overfitting |
|                | Ensembles: The prediction of individual model algorithms were ensembled through biomod2 (Thuiller et al. 2016) |
Table 2 (continued)

| ODMAP elements     | Contents                                                                                                                                 |
|--------------------|-------------------------------------------------------------------------------------------------------------------------------------------|
| Model workflow     | The model workflow includes the following:                                                                                               |
|                    | 1. Data cleaning and generation of pseudo absences                                                                                       |
|                    | 2. Finding the best climate variables to fit the models                                                                                 |
|                    | 3. Model running through biomod2 platform                                                                                               |
|                    | 4. Generation of the maps as gridded 30 arcsec rasters                                                                               |
| Software           | Software: All analyses were conducted using R version 3.3.2 (R Core Team 2016). Packages used: biomod2 (Thuiller et al. 2016), Random Forest (Breiman 2001). Data availability: **Presence absence data are available from Mauri et al. (2017)** Climate data is available from Chakraborty D, Dobor L, A, Hlásny T, Schueler S (2020) High-resolution grided climate data for Europe based on bias-corrected EURO-CORDEX: the ECLIPS-2.0 dataset [Zenodo: https://doi.org/10.5281/zenodo.3952159] |
| Data               | Biodiversity data                                                                                                                        |
|                    | Taxon names: Abies alba, Fagus sylvatica, Larix decidua, Picea abies, Pinus sylvestris, Quercus petraea, Quercus robur |
|                    | Ecological level: Species-level                                                                                                          |
|                    | Data source: Species presence-absence data was obtained from the EU-Forest dataset (Mauri et al. 2017). The dataset harmonizes European tree occurrence from National Forest inventories (NFI), Forest Focus (Hiederer et al. 2011), and Biosoil datasets (Houston Durrant et al. 2011). A major part of the data arises from the NFI data (96%) while 4% contributed by Forest Focus (Hiederer et al. 2011), Biosoil datasets (Houston Durrant et al. 2011) |
|                    | Sampling design: The background data included in the EU-Forest (Mauri et al. 2017) varied in their sampling intensity and design. This data was harmonized and aggregated to a spatial resolution of 1 square kilometer, in line with an INSPIRE compliant 1-km × 1-km grid |
|                    | Sample size The dataset includes a total of 1,000,525 occurrence records at a spatial resolution of 1 × 1 km (Mauri et al. 2017) |
|                    | Data filtering: Form the EU-Forest dataset we obtained 412,288 occurrence records about the seven target species Presence-absence data: In our case the geographic locations of the target species in the EU-Forest dataset was assumed to be true presences, while the remaining locations of occurrence of other species were assumed to be the absence locations |
|                    | To ensure that the absence locations are not only climatically dissimilar but also geographically distant from the observed presence locations, we developed the so-called pseudo absences according to Senay et al. (2013). This is a three-step approach: (i) specifying a geographical extent outside the observed presences, (ii) environmental profiling of the absences outside this geographic extent, and (iii) k-means clustering of the environmental profiles and selecting random samples within each cluster. In our case, a 2-degree buffer was found to be optimum following Senay et al. (2013). The absence locations outside this geographic extent were classified into 10–15 (depending on species) environmentally dissimilar clusters according to the k-means clustering algorithm. The number of clusters for each species were determined with a plot of total within-cluster sum of square (WSS) and number of clusters |
|                    | The number of pseudoabsence locations was further reduced by randomly selecting a sample of locations defined by the 95% confidence interval from each of the clusters. This approach was used to generate pseudoabsence for all the seven species |
| Data partitioning  | The occurrence dataset for each target species was partitioned by splitting into 75% for model training and 25% for model evaluation |
| Environmental predictors | Predictor variables Environmental predictors were 80 biologically relevant climate variables comprising of annual, seasonal, and monthly variables From this list of 80 variables, a small subset of potential predictor variables was selected for each target species during the variable selection process Data sources: The spatial resolution of predictor data: 30 arcsec which is roughly equivalent to 1 × 1 km or lower depending on latitude The temporal resolution of predictor variable: Historic climate (1961–1990) and three future time frames which include averages of (2041–2060, 2061–2080, and 2081–2100) for two Representative Concentration RCP 4.5 and RCP 8.5 were used for the SDM predictions Geographic projection: WGS 84 (EPSG: 4326) |
| ODMAP elements | Contents |
|----------------|---------|
| **Variable selection and multicollinearity** | From the list of potential predictor variables (Table 2 in Appendix), the ones which explain most of the variation in the observed presence and absences of each species were selected with a recursive feature elimination approach (RFE) implemented within the Random forest algorithm (Breiman 2001). Within the RFE approach, the variables were eliminated iteratively, starting from the full set of potential predictors (Table 2 in Appendix), and retaining only those variables that reduce the mean square error over random permutations of the same variable. The variables which were linearly correlated with other variables and had a variance inflation factors VIF > 5 as suggested by Booth et al. (1994) were identified, and the ones with the lower value according to the Akaike Information Criteria (AIC) (Akaike 1974) were retained for further model development. This subset of uncorrelated climate variables (Table 3 in Appendix) was used as predictor variables for developing the ensemble species distribution models. |
| **Model settings** | The models were run with the default settings of biomod2 (Thuiller et al. 2016). |
| **Model estimates** | The models estimated median ensemble probability of species occurrence and associated model uncertainty represented by the coefficient of variation. |
| **Model ensemble** | Predicted probabilities from the individual models for each target species were ensembled as a consensus model which combined the median probability over the selected models with true skill statistics threshold (TSS > 0.7) (Allouche et al. 2006; Coetzee et al. 2009). |
| **Threshold selection** | True skill statistics threshold (TSS > 0.7), a commonly used threshold for SDMS (Allouche et al. 2006; Coetzee et al. 2009), was used. |
| **Assessment** | For each such model run as well as the final ensemble models for each target species, the model evaluation statistics were recorded. These statistics were true skill statistics (TSS) and area under the relative operating characteristic (ROC), model sensitivity (the ability of the model to predict true presences), and model specificity (the ability of the model to predict the true absences). TSS takes into account both omission and commission errors and ranges also from −1 to +1, not being affected by prevalence as KAPPA (Allouche et al. 2006). TSS values ranging from 0.2 to 0.5 were considered poor, from 0.6 to 0.8 useful, and values larger than 0.8 were good to excellent (e.g. Coetzee et al. 2009). Prediction accuracy is considered to be similar to random for ROC values lower than 0.5; poor, for values in the range 0.5–0.7; fair in the range 0.7–0.9; and excellent for values greater than 0.9 (Pontius and Parmentier 2014). |
| **Prediction** | Predicted probabilities from the individual models and target species were ensembled as a consensus model which combined the median probability over the selected models with true skill statistics threshold (TSS > 0.7) (Allouche et al. 2006; Coetzee et al. 2009). The median was chosen because it is known to be less sensitive to outliers than the mean. The estimated ensemble model predictions were presented as GeoTIFF rasters. |
| **Uncertainty quantification** | Model uncertainty was estimated in terms of the coefficient of variation (CV) among the predictions of the individual models. The estimated CVs are also presented as GeoTIFF rasters where each cell corresponds to a CV value whereby higher and lower CV values indicate higher and lower uncertainty respectively in the ensemble model. |
Table 3  Potential climate variables from the ECLIPS 2.0 dataset (Chakraborty et al. 2020a, b) used to calibrate the ensemble SDMs

| Climate variable | Variables | Unit |
|------------------|-----------|------|
| AHM              | Annual heat: moisture index (MAT + 10)/(MAP/1000)) |      |
| bFFP             | The Julian date on which FFP begins |      |
| DDabove18        | Degree-days below 18 °C, heating degree-days |      |
| DDabove5         | Degree-days above 5 °C, growing degree-days |      |
| DDbelow0         | Degree-days below 0 °C, chilling degree-days |      |
| DDbelow18        | Degree-days below 18 °C, heating degree-days |      |
| eFFP             | The Julian date on which FFP ends |      |
| EMT              | Extreme minimum temperature over 30 years | °C    |
| FFP              | Frost-free period | Days  |
| MAP              | Mean annual precipitation (mm) | °C    |
| MAT              | Mean annual temperature (°C) | °C    |
| MCMT             | Mean coldest month temperature (°C) | °C    |
| MSP              | Mean summer (May to Sept.) precipitation (mm) | °C    |
| MWMT             | Mean warmest month temperature (°C) | °C    |
| NFFD             | The number of frost-free days | days  |
| PPT_at           | Autumn precipitation (mm) | mm    |
| PPT_sm           | Summer precipitation (mm) | mm    |
| PPT_sp           | Spring precipitation (mm) | mm    |
| PPT_wt           | Winter precipitation (mm) | mm    |
| PPT01            | Precipitation month 01 | mm    |
| PPT02            | Precipitation month 02 | mm    |
| PPT03            | Precipitation month 03 | mm    |
| PPT04            | Precipitation month 04 | mm    |
| PPT05            | Precipitation month 05 | mm    |
| PPT06            | Precipitation month 06 | mm    |
| PPT07            | Precipitation month 07 | mm    |
| PPT08            | Precipitation month 08 | mm    |
| PPT09            | Precipitation month 09 | mm    |
| PPT10            | Precipitation month 10 | mm    |
| PPT11            | Precipitation month 11 | mm    |
| PPT12            | Precipitation month 12 | mm    |
| SHM              | Summer heat: moisture index ((MWMT)/(MSP/1000)) |      |
| Tave_at          | Autumn (Sep.–Nov.) mean temperature (°C) | °C    |
| Tave_sm          | Summer (Jun.–Aug.) mean temperature (°C) | °C    |
| Tave_sp          | Spring (Mar.–May) mean temperature (°C) | °C    |
| Tave_wt          | Winter (Dec. (prev. yr)–Feb.) mean temperature (°C) | °C    |
| Tave01           | Average temperature month 01 | °C    |
| Tave02           | Average temperature month 02 | °C    |
| Tave03           | Average temperature month 03 | °C    |
| Tave04           | Average temperature month 04 | °C    |
| Tave05           | Average temperature month 05 | °C    |
| Tave06           | Average temperature month 06 | °C    |
| Tave07           | Average temperature month 07 | °C    |
| Tave08           | Average temperature month 08 | °C    |
| Tave09           | Average temperature month 09 | °C    |
| Tave10           | Average temperature month 10 | °C    |
| Tave11           | Average temperature month 11 | °C    |
| Tave12           | Average temperature month 12 | °C    |
| TD               | Temperature difference between MWMT and MCMT(°C) | °C    |
| Tmax_an          | Maximum yearly temperature | °C    |
| Tmax_at          | Maximum autumn temperature | °C    |
### Table 3 (continued)

| Climate variable | Variables                             | Unit |
|------------------|---------------------------------------|------|
| Tmax_sm          | Maximum summer temperature            | °C   |
| Tmax_sp          | Maximum spring temperature            | °C   |
| Tmax_wt          | Maximum winter temperature            | °C   |
| Tmax01           | Maximum temperature 01                | °C   |
| Tmax02           | Maximum temperature 02                | °C   |
| Tmax03           | Maximum temperature 03                | °C   |
| Tmax04           | Maximum temperature 04                | °C   |
| Tmax05           | Maximum temperature 05                | °C   |
| Tmax06           | Maximum temperature 06                | °C   |
| Tmax07           | Maximum temperature 07                | °C   |
| Tmax08           | Maximum temperature 08                | °C   |
| Tmax09           | Maximum temperature 09                | °C   |
| Tmax10           | Maximum temperature 10                | °C   |
| Tmax11           | Maximum temperature 11                | °C   |
| Tmax12           | Maximum temperature 12                | °C   |
| Tmin_an          | Minimum annual temperature            | °C   |
| Tmin_at          | Minimum autumn temperature            | °C   |
| Tmin_sm          | Minimum summer temperature            | °C   |
| Tmin_sp          | Minimum spring temperature            | °C   |
| Tmin_wt          | Minimum winter temperature            | °C   |
| Tmin01           | Minimum temperature 01                | °C   |
| Tmin02           | Minimum temperature 02                | °C   |
| Tmin03           | Minimum temperature 03                | °C   |
| Tmin04           | Minimum temperature 04                | °C   |
| Tmin05           | Minimum temperature 05                | °C   |
| Tmin06           | Minimum temperature 06                | °C   |
| Tmin07           | Minimum temperature 07                | °C   |
| Tmin08           | Minimum temperature 08                | °C   |
| Tmin09           | Minimum temperature 09                | °C   |
| Tmin10           | Minimum temperature 10                | °C   |
| Tmin11           | Minimum temperature 11                | °C   |
| Tmin12           | Minimum temperature 12                | °C   |
Table 4 Climate variables used to calibrate the ensemble SDMs

| Acronym | Climate variable                          | Species          |
|---------|-------------------------------------------|------------------|
| SHM     | Summer heat-moisture index                | *Picea abies*    |
| PPT_at  | Mean autumn precipitation                  | *Picea abies*    |
| FFP     | Longest frost-free period                  | *Picea abies*    |
| TD      | Continentality                            | *Picea abies*    |
| MCMT    | Mean coldest month temperature            | *Picea abies*    |
| SHM     | Summer heat-moisture index                | *Abies alba*     |
| EMT     | Extreme minimum temperature               | *Abies alba*     |
| TD      | Continentality                            | *Abies alba*     |
| SHM     | Summer heat-moisture index                | *Larix decidua*  |
| Tave_sm | Average summer temperature                | *Larix decidua*  |
| MWMT    | Mean warmest month temperature            | *Larix decidua*  |
| SHM     | Summer heat-moisture index                | *Pinus sylvestris*|
| DDabove18| Days with mean temperature above 18 °C    | *Pinus sylvestris*|
| Tmax_sp | Maximum spring temperature                | *Pinus sylvestris*|
| Tave_wt | Average winter temperature                | *Pinus sylvestris*|
| SHM     | Summer heat-moisture index                | *Fagus sylvatica*|
| DDabove5| Days with mean temperature above 5 °C     | *Fagus sylvatica*|
| PPT_sp  | Mean spring precipitation                  | *Fagus sylvatica*|
| EMT     | Extreme minimum temperature               | *Fagus sylvatica*|
| Tave_sp | Average spring temperature                | *Fagus sylvatica*|
| DDbelow18| Days with mean temperature below 18 °C    | *Quercus petraea*|
| PPT_sm  | Mean summer temperature                   | *Quercus petraea*|
| MAT     | Mean annual temperature                   | *Quercus petraea*|
| DDabove5| Days with mean temperature above 5 °C     | *Quercus robur*  |
| PPT_sm  | Mean summer temperature                   | *Quercus robur*  |
| FFP     | Longest frost-free period                  | *Quercus robur*  |
| Tmin_sp | Minimum spring temperature                | *Quercus robur*  |
| MCMT    | Mean coldest month temperature            | *Quercus robur*  |
Fig. 3 Locations of the genetic conservation units (Lefèvre et al. 2013) plotted against the predictions of the ensemble SDMs for the period 1961–1990 for the seven target species of Europe. The prediction range 0–1000 refers to 0–100%
The summary of this model evaluation is presented in Table 1.
| Criteria | Testing data | Evaluating data | Sensitivity | Specificity | Model | Species |
|----------|--------------|-----------------|-------------|-------------|-------|---------|
| ROC      | 0.828        | 0.825           | 77.153      | 87.914      | SRE   | Larix decidua |
| TSS      | 0.863        | 0.871           | 95.548      | 91.52       | FDA   | Larix decidua |
| ROC      | 0.974        | 0.974           | 95.303      | 92.251      | FDA   | Larix decidua |
| TSS      | 0.878        | 0.888           | 96.526      | 92.3        | MARS  | Larix decidua |
| ROC      | 0.981        | 0.98            | 96.575      | 92.3        | MARS  | Larix decidua |
| TSS      | 0.997        | 0.96            | 98.386      | 97.661      | RF    | Larix decidua |
| ROC      | 1            | 0.996           | 98.337      | 97.758      | RF    | Larix decidua |
| TSS      | 0.735        | 0.754           | 95.01       | 80.361      | MAXENT* | Larix decidua |
| ROC      | 0.917        | 0.924           | 95.01       | 80.409      | MAXENT* | Larix decidua |
| TSS      | 0.834        | 0.834           | 91.633      | 81.827      | GLM   | Pice abies |
| ROC      | 0.975        | 0.975           | 91.93       | 91.58       | GLM   | Pice abies |
| TSS      | 0.895        | 0.898           | 96.673      | 93.09       | GBM   | Pice abies |
| ROC      | 0.986        | 0.987           | 96.615      | 93.192      | GBM   | Pice abies |
| TSS      | 0.893        | 0.897           | 95.143      | 94.591      | GAM   | Pice abies |
| ROC      | 0.987        | 0.987           | 94.692      | 95.171      | GAM   | Pice abies |
| TSS      | 0.921        | 0.917           | 97.631      | 94.028      | CTA   | Pice abies |
| ROC      | 0.979        | 0.978           | 97.631      | 94.028      | CTA   | Pice abies |
| TSS      | 0.875        | 0.873           | 96.393      | 90.915      | ANN   | Pice abies |
| ROC      | 0.965        | 0.965           | 96.484      | 90.889      | ANN   | Pice abies |
| TSS      | 0.643        | 0.643           | 75.589      | 88.662      | SRE   | Pice abies |
| ROC      | 0.821        | 0.821           | 75.589      | 88.662      | SRE   | Pice abies |
| TSS      | 0.829        | 0.832           | 91.553      | 91.648      | FDA   | Pice abies |
| ROC      | 0.974        | 0.975           | 93.334      | 90.104      | FDA   | Pice abies |
| TSS      | 0.861        | 0.865           | 93.419      | 90.073      | MARS  | Pice abies |
| ROC      | 0.979        | 0.98            | 94.35       | 92.228      | MARS  | Pice abies |
| TSS      | 0.998        | 0.985           | 99.515      | 98.968      | RF    | Pice abies |
| ROC      | 1            | 0.998           | 99.538      | 98.968      | RF    | Pice abies |
| TSS      | 0.606        | 0.604           | 94.019      | 66.362      | MAXENT* | Pice abies |
| ROC      | 0.88         | 0.88            | 94.492      | 65.953      | MAXENT* | Pice abies |
| TSS      | 0.787        | 0.789           | 91.278      | 87.63       | GLM   | Pinus sylvestris |
| ROC      | 0.958        | 0.958           | 91.74       | 87.281      | GLM   | Pinus sylvestris |
| TSS      | 0.872        | 0.864           | 96.999      | 89.344      | GBM   | Pinus sylvestris |
| ROC      | 0.976        | 0.974           | 94.859      | 91.808      | GBM   | Pinus sylvestris |
| TSS      | 0.857        | 0.859           | 94.526      | 91.366      | GAM   | Pinus sylvestris |
| ROC      | 0.976        | 0.976           | 93.778      | 92.26       | GAM   | Pinus sylvestris |
| TSS      | 0.91         | 0.9             | 97.731      | 92.249      | CTA   | Pinus sylvestris |
| ROC      | 0.968        | 0.964           | 97.682      | 92.362      | CTA   | Pinus sylvestris |
| TSS      | 0.886        | 0.886           | 96.08       | 92.537      | ANN   | Pinus sylvestris |
| ROC      | 0.966        | 0.964           | 95.789      | 92.875      | ANN   | Pinus sylvestris |
| TSS      | 0.572        | 0.579           | 76.21       | 81.686      | SRE   | Pinus sylvestris |
| ROC      | 0.786        | 0.789           | 76.21       | 81.686      | SRE   | Pinus sylvestris |
| TSS      | 0.803        | 0.802           | 91.638      | 88.533      | FDA   | Pinus sylvestris |
| ROC      | 0.961        | 0.96            | 93.009      | 87.517      | FDA   | Pinus sylvestris |
| TSS      | 0.829        | 0.831           | 95.176      | 87.917      | MARS  | Pinus sylvestris |
| ROC      | 0.966        | 0.966           | 94.628      | 88.584      | MARS  | Pinus sylvestris |
| TSS      | 0.998        | 0.975           | 99.048      | 98.47       | RF    | Pinus sylvestris |
| ROC      | 1            | 0.997           | 99.145      | 98.44       | RF    | Pinus sylvestris |
| TSS      | 0.503        | 0.506           | 93.101      | 57.479      | MAXENT* | Pinus sylvestris |
| ROC      | 0.819        | 0.816           | 93.413      | 57.243      | MAXENT* | Pinus sylvestris |
| TSS      | 0.849        | 0.851           | 91.782      | 93.277      | GLM   | Quercus robur |
| ROC      | 0.976        | 0.977           | 91.73       | 93.418      | GLM   | Quercus robur |
Table 5 (continued)

| Criteria | Testing data | Evaluating data | Sensitivity | Specificity | Model | Species               |
|----------|--------------|-----------------|-------------|-------------|-------|-----------------------|
| TSS      | 0.889        | 0.892           | 96.048      | 93.175      | GBM   | *Quercus robur*       |
| ROC      | 0.985        | 0.986           | 94.818      | 94.517      | GBM   | *Quercus robur*       |
| TSS      | 0.88         | 0.882           | 94.87       | 93.328      | GAM   | *Quercus robur*       |
| ROC      | 0.983        | 0.984           | 95.342      | 92.97       | GAM   | *Quercus robur*       |
| TSS      | 0.91         | 0.909           | 96.218      | 94.696      | CTA   | *Quercus robur*       |
| ROC      | 0.977        | 0.978           | 96.218      | 94.696      | CTA   | *Quercus robur*       |
| TSS      | 0.915        | 0.917           | 96.794      | 94.875      | ANN   | *Quercus robur*       |
| ROC      | 0.984        | 0.984           | 96.336      | 95.386      | ANN   | *Quercus robur*       |
| TSS      | 0.718        | 0.72            | 76.93       | 95.066      | SRE   | *Quercus robur*       |
| ROC      | 0.859        | 0.86            | 76.93       | 95.066      | SRE   | *Quercus robur*       |
| TSS      | 0.844        | 0.844           | 92.423      | 92.037      | FDA   | *Quercus robur*       |
| ROC      | 0.974        | 0.977           | 92.044      | 92.523      | FDA   | *Quercus robur*       |
| TSS      | 0.859        | 0.857           | 92.58       | 93.175      | MARS  | *Quercus robur*       |
| ROC      | 0.977        | 0.979           | 92.306      | 93.494      | MARS  | *Quercus robur*       |
| TSS      | 0.996        | 0.965           | 98.574      | 97.968      | RF    | *Quercus robur*       |
| ROC      | 1            | 0.998           | 98.09       | 98.556      | RF    | *Quercus robur*       |
| TSS      | 0.778        | 0.787           | 95.878      | 82.848      | MAXENT* | *Quercus robur*     |
| ROC      | 0.943        | 0.946           | 95.773      | 82.975      | MAXENT* | *Quercus robur*     |
| TSS      | 0.754        | 0.747           | 94.685      | 80.019      | GLM   | *Quercus petraea*     |
| ROC      | 0.942        | 0.945           | 93.45       | 81.709      | GLM   | *Quercus petraea*     |
| TSS      | 0.789        | 0.788           | 89.93       | 88.988      | GBM   | *Quercus petraea*     |
| ROC      | 0.962        | 0.962           | 90.629      | 88.401      | GBM   | *Quercus petraea*     |
| TSS      | 0.806        | 0.805           | 91.865      | 88.565      | GAM   | *Quercus petraea*     |
| ROC      | 0.962        | 0.962           | 91.072      | 89.739      | GAM   | *Quercus petraea*     |
| TSS      | 0.856        | 0.834           | 93.986      | 89.458      | CTA   | *Quercus petraea*     |
| ROC      | 0.957        | 0.953           | 93.986      | 89.458      | CTA   | *Quercus petraea*     |
| TSS      | 0.831        | 0.835           | 92.96       | 90.514      | ANN   | *Quercus petraea*     |
| ROC      | 0.961        | 0.963           | 92.821      | 90.679      | ANN   | *Quercus petraea*     |
| TSS      | 0.643        | 0.658           | 79.674      | 86.124      | SRE   | *Quercus petraea*     |
| ROC      | 0.821        | 0.829           | 79.674      | 86.124      | SRE   | *Quercus petraea*     |
| TSS      | 0.766        | 0.764           | 92.051      | 84.269      | FDA   | *Quercus petraea*     |
| ROC      | 0.949        | 0.951           | 90.49       | 86.194      | FDA   | *Quercus petraea*     |
| TSS      | 0.782        | 0.783           | 95.455      | 82.883      | MARS  | *Quercus petraea*     |
| ROC      | 0.952        | 0.953           | 95.618      | 82.789      | MARS  | *Quercus petraea*     |
| TSS      | 0.992        | 0.901           | 95.431      | 94.811      | RF    | *Quercus petraea*     |
| ROC      | 1            | 0.989           | 95.501      | 94.811      | RF    | *Quercus petraea*     |
| TSS      | 0.702        | 0.685           | 92.238      | 76.286      | MAXENT* | *Quercus petraea* |
| ROC      | 0.9          | 0.898           | 94.126      | 74.618      | MAXENT* | *Quercus petraea* |

MAXENT Tsuruoka

Table 6 Predicted probability of occurrence of the seven target species predicted for independent data of European genetic conservation units from Lefèvre et al. (2013). Probability class of 0–40, and 40–60 were assumed to be incorrectly predicted and > 60% as correctly predicted by the SDMs

| Probability class | A alba | P abies | P sylvestris | L decidua | F sylvatica | Q petraea | Q robur |
|-------------------|--------|---------|-------------|-----------|-------------|-----------|---------|
| 0–40              | 4      | 1       | 17          | 2         | 5           | 26        | 23      |
| 40–60             | 9      | 16      | 24          | 9         | 38          | 18        | 6       |
| 60–80             | 32     | 34      | 18          | 6         | 96          | 95        | 62      |
| 80–100            | 182    | 318     | 152         | 108       | 208         | 86        | 82      |
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