



ForestNavigator

D4.1 Report on the advanced biodiversity modelling framework

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Abstract

This report outlines the modelling framework to assess impacts of forest-based climate change mitigation pathways on forest biodiversity. It describes all included data sources, the data pre-processing, and outlines the individual modelling steps. Furthermore, it introduces the indicators used to quantify biodiversity.

Keywords

Forest biodiversity, species distribution modelling, ecological niche modelling, habitat suitability

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Abbreviations

BREG	Bayesian regularized regression
CHELSA	Climatologies at high resolution for the earth's land surface areas
EBD	eBird basic dataset
EEA	European Environment Agency
EU	European Union
DBH	Diameter at breast height
DEM	Digital elevation model
GARD	Global Assessment of Reptile Distributions
GBIF	Global Biodiversity Information Facility
GDB	Gradient descent boosting
GHS	Global Human Settlement
GISCO	Geographic Information System of the Commission
GLMNET	Regularized elastic net regression
GPP	Gross primary production
IGFS	Improved gridded forest structure data
ISRIC	International Soil Reference and Information Centre
IUCN	International Union for Conservation of Nature
LAI	Leaf area index
NPP	Net primary production
pHiHXO	pH measured in water solution
pHiKCl	pH measured in potassium chloride solution
RCP	Representative concentration pathway
SDM / iSDM	Species distribution model / integrated species distribution model
SEBI	Streamlining European Biodiversity Indicators
SEH	Societas Europaea Herpetologica
SSP	Shared socioeconomic pathways
WP	Work package

I. Introduction

Forest-based climate change mitigation pathways play a crucial role in reducing net greenhouse gas emissions and achieving the climate neutrality goals of the European Union (EU). However, reaching these goals is challenging due to interactions between climate change, natural disturbances, and management strategies. Moreover, conflicts might arise between socio-economic demands, biodiversity conservation, and various other ecosystem services as the aforementioned interactions also influence outcomes of the mitigation pathways. Thus, the *ForestNavigator* project aims to assess the potential and impacts of forest-based mitigation pathways using an integrated modelling framework.

The biodiversity assessment of Work Package 4 (WP4) develops a modelling framework to assess the biodiversity impacts of various climate change scenarios and forest management pathways. Global environmental changes are profoundly affecting forest ecosystems (Hisano et al., 2018; Sala et al., 2000). Among others, this includes direct and indirect effects on biodiversity. Direct effects include that climate change is projected to increase extinction risks for many European plants (Thuiller et al., 2005), alter forest tree species distributions (Dyderski et al., 2018), and enable range expansion of beetle species (Buse et al., 2013). Indirect effects include disturbances due to climate change (Schuldt et al., 2020; Seidl et al., 2017), but also adapted forest management strategies which both can have impacts on forest structure. Forest structure has been shown to be a driver of plant (De Frenne et al., 2013; Gao et al., 2014), beetle (Parisi et al., 2021) and overall (Thom et al., 2017) species diversity. Thus, climate change and the biodiversity crisis are deeply connected (Pettorelli et al., 2021; Pörtner et al., 2023). Furthermore, diversity often increases resilience of ecosystems (Chapin III et al., 2000) and is linked to ecosystem functioning (Ruiz-Benito et al., 2017). Consequently, additionally to carbon stocks and socioeconomic aspects, there is the need for mitigation pathways to consider conservation measures to counteract the biodiversity crisis and its consequences for ecosystem services and society (European Commission, 2020; IPBES, 2019). The modelling framework introduced in this report quantifies impacts of climate change scenarios and forest management pathways on biodiversity. Thus, we are able to identify scenarios and pathways that potentially support or reduce forest biodiversity and identify forest taxa that are extraordinarily resilient or vulnerable to the scenarios and pathways.

To model the response of multiple forest taxa with high conservation relevance to climate change scenarios and forest management pathways, we use integrated species distribution models (*iSDM*). More generally, *SDMs* allow to infer, predict, and project habitat suitability of species in space and time, usually in a raster grid cell context, using statistical relationships between environmental covariates (e.g., climatic conditions or forest characteristics) and species observations (Elith and Leathwick, 2009; Guisan and Thuiller, 2005). *iSDMs* specifically leverage information across various data types (such as multiple biodiversity data sources, priors, offsets, statistical frameworks; Isaac et al., 2020). By balancing and combining strengths across datasets and frameworks, they have the potential to mediate existing spatial and thematic biases present in most openly available biodiversity datasets. Thus, *SDMs* can be used to assess impacts of forestry on biodiversity (e.g., Leitão et al., 2022; Oettel and Lapin, 2021) or identify areas of high conservation value (e.g., Jung et al., 2021).

While *SDMs* have been applied frequently to support forest management (Pecchi et al., 2019), modelled species almost solely include forest tree species (e.g., Bonannella et al., 2022; Chakraborty et al., 2021; Mauri et al., 2022). Furthermore, environmental covariates often do not include information on land use and specifically detailed forest characteristics. Thus, we are

modelling forest biodiversity using multiple forest taxa (e.g., mammals, birds, or arthropods), and including covariates describing environmental conditions as well as forest characteristics affected by forest management practices. Biodiversity indicators are often employed to quantify diversity, typically focusing on the presence of species or species groups that serve as proxies for other species or general habitat characteristics (Gao et al., 2015). The forest taxa included in the biodiversity assessment of WP4 are selected based on their conservation and community relevance and are in line with current biodiversity monitoring frameworks and strategies. Furthermore, they cover a wide range of habitat requirements, dispersal abilities, or general mobility.

This report introduces the modelling workflow in detail. First, we describe how biodiversity data is acquired and which climatic, environmental and forest characteristics covariates are included. Second, we outline all pre-processing steps such as data cleaning and harmonizing applied to both biodiversity data and covariates. Third, we present the *iSDMs* algorithms, and fourth, we present how model outputs are translated into biodiversity indicators.

2. Geographic and temporal extent and resolution

The spatial extent covers all 27 member countries of the EU (Figure 1). We focus on the continental part of the EU, thus excluding all overseas territories and outermost regions (such as French Polynesia or the Canary Islands). Because outcomes of *SDMs* are generally affected by the spatial resolution (e.g., Farashi and Alizadeh-Noughani, 2018; Guisan et al., 2007), this is an important choice. Based on data availability, if possible, we use a spatial resolution of 8×8 km for model parametrization and inference. For future projections we rely on a coarser spatial resolution that is constrained by the resolution of *G4M-X* model outputs, namely ~ 5 arcmins (equals about 10×10 km at the equator).

Overall, the temporal extent covers the years 2015 to 2100. For model training, we use data from the year 2015 – 2020 (or as close as possible). For model projections, the trained models are projected up to the year 2100. Range shifts of species due to changing environmental conditions and forest characteristics are rather long-term, even though rates increase (Renwick and Rocca, 2015; Williams and Blois, 2018). Thus, we are using a temporal resolution of 10-year intervals for all projections of species occurrence.



Figure 1: Spatial extent of the biodiversity modelling framework. All included countries colored green.

3. Included data sets

3.1. List of included species

To assess impacts of forest management on diverse forest taxa of conservation and policy relevance, we are using the Annexes I and II of the Article 12 Birds directive and Article 17 Habitats directive, respectively, as well as species listed in the *European Red Lists of Species*. However, only species associated with forests or woodlands are considered as specified in the corresponding habitat descriptions (Table 1). Last, we include species previously modelled by consortium members on national scales. In total, this includes 1,274 species that can be summarized to 13 species groups (Table 2). However, because some species are excluded during data acquisition or pre-processing, this species list only represents the potentially considered species. All species names were cleaned and harmonized using several databases with the help of the *taxize R* package (Chamberlain and Szöcs, 2013).

Table 1: Data sources of potentially included species of the biodiversity modelling workflow.

Data source	Habitat selection criterion	Number of species
Annexes I/II of Article 12/17	Including “preferred” association to “woodlandForest”	510
European Red Lists of Species	Habitat description includes: “forest”, “tree”, “wood”, “coniferous”, “broadleaf”	850
Species previously modelled on national scale (SI S1)	-	42

3.1.1. Species occurrence data

First, we use the *Global Biodiversity Information Facility (GBIF)*, a database collecting biodiversity data from various sources (e.g., surveys, camera traps, remote sensing) and sampling methods (e.g., standardized protocols, opportunistic observations). We download observations for the years 2015 – 2020 including only those that have spatial coordinates and no flagged geospatial issues. Furthermore, we only include observations by humans or machines (e.g., camera traps). The *GBIF* data includes only where a species occurs, but not where the species does not occur, we are using it as presence-only data.

Second, for all bird species we are additionally using the *eBird* basic dataset (*EBD*; Fink et al., 2023; Sullivan et al., 2009). *eBird* is one of the largest citizen science projects and collects data about the presence and abundance of bird species using specified survey protocols. Additionally, the *EBD* includes so-called checklists that describe the corresponding birding activities (Sullivan et al., 2014). We downloaded all observations and checklists for the years 2015 – 2020.

Third, for all plant species we additionally use presence-absence data from the *sPlotOpen* database of vegetation plots. The *sPlotOpen* database consists of numerous regional, national, or continental vegetation-plot datasets that are located in natural or semi-natural vegetation

(Sabatini et al., 2021). We are including only sample plots that are located within forest vegetation as indicated in the database and that were sampled between the years 2015 – 2020.

3.1.2. Range maps and atlas data

Furthermore, we are using expert-derived range maps and atlas data in the modelling workflow. This includes data from the *IUCN Red Lists of Threatened Species* (IUCN, 2022), the *Birds and Habitats directives atlas data*, *BirdLife International* (BirdLife International and Handbook of the Birds of the World, 2022), the *Global Assessment of Reptile Distributions* (GARD; Roll et al., 2017), and the *Societas Europaea Herpetologica atlas data* (SEH Sillero et al., 2014). If several range maps are present for a single species, we summarize them into a single map. However, while for some species groups range maps are available for most species (e.g., Mammals, Birds, Amphibians/Reptiles), for other species groups range maps are less or not available at all (e.g., Butterflies, Bees, Mollusca).

Table 2: Number of forest-associated species separated by species groups.

Species group	EEA Habitats and Birds directives	EU Red List of Species	Previously modelled on national scale
Amphibian	36	19	-
Bees	-	40	-
Beetles	26	181	-
Birds	179	37	-
Butterflies	17	47	-
Ferns	8	23	-
Fungi/Lichens	-	-	11
Mammals	108	14	-
Mollusca	10	97	-
Non-vascular Plants	16	-	21
Vascular Plants	77	160	-
Reptiles	23	17	-
Other Insects	5	102	-

3.2. List of explanatory covariates

To model and project species distributions, we are using several gridded datasets describing diverse aspects of climatic (e.g., precipitation) and environmental conditions (e.g., elevation), as well as forest characteristics (e.g., tree density or basal area). This includes both publicly available data (Figure 2, Table 3, 4) and data produced by other WPs and tasks in the *ForestNavigator* project (Figure 2, Table 4). Some of the data is static (or not projected in the future; e.g., the digital elevation model) and other is dynamic (or projected in the future). Dynamic covariates include climatic conditions and forest characteristics and are assumed to change in the future based on different climate change scenarios and forest management pathways. For all climatic covariates this includes the scenarios *i*) SSP1/RCP2.6, *ii*) SSP2/RCP7.0, and *iii*) SSP5/RCP8.5. For the forest characteristics, we use three forest stewardship storylines, developed by a different WPs and tasks in the *ForestNavigator* project, that reflect different forest management priorities, namely *i*) nature oriented, *ii*) multifunctionality oriented, and *iii*) wood-based economy oriented.

Table 3: Covariates describing climatic and environmental conditions used within the biodiversity modelling framework

Source	Covariate	Unit	Native resolution	Characteristic
CHELSA	Precipitation	kg m ⁻² month ⁻¹	0.0083° (~700 m)	projected
	Temperature	Celsius		
	Temperature min/max	Celsius		
Copernicus DEM	Elevation	Meter	25 m	static
	Slope	Degree		
	Aspect	Degree		
ISRIC	Clay	g/kg	0.0083° (~700 m)	static
	Silt	g/kg		
	Sand	g/kg		
	Soil organic carbon	dg/kg		
	Available water capacity	Percentage		
	pHiHXO/ pHiKCl	pHx10		

We use two main data sources to describe forest characteristics. First, for current forest characteristics, we use the *Improved Gridded Forest Structure* data (IGFS; Pucher et al., 2022) which describes forest characteristics around the year 2015. To describe projected forest characteristics, we additionally use *G4M-X* model outputs created within different WPs and tasks of the *ForestNavigator* project.

Table 4: Covariates describing forest characteristics used within the biodiversity modelling framework

Covariates	IGFS ^a (static, 8 km)	G4M-X ^b (projected, 5 arcmins)
Tree age	age class	years
Tree height	m	m
Crown width	-	m
Crown length	-	m
Diameter at breast height	cm	cm
Basal area	m ² /ha	m ² /ha
Standing volume	m ³ /ha	m ³ /ha
Stem density	n/ha	n/ha
GPP/NPP	-	tC/ha/year ⁻¹
LAI	-	m ² /m ²
Species composition	Dominant tree species group	Dominant tree species group
Litter	tC/ha (foliage)	tC/ha
Mortality	-	n/ha/year ⁻¹
Deadwood	-	tC/ha

Sources: ^aPucher et al. (2022); ^bForestNavigator project

In general, many of the covariates are available in both data sources (Table 4) and values of the *IGFS* data are reasonably well correlated to the initial timestep of the *G4M-X* model data (Figure 2). Yet, there is also variation between the two data sources which can be explained by various reasons. Even though the *G4M-X* model runs are initialized with the *IGFS* data, some covariates in *G4M-X* are based on internal relationships, such as the tree volume per hectare. Additionally, the *IGFS* includes natural regeneration, which is not included in *G4M-X*. Moreover, the *IGFS* data is based on mixed species and age classes per cell, while *G4M-X* uses a simplified species and age class representation per grid cell.

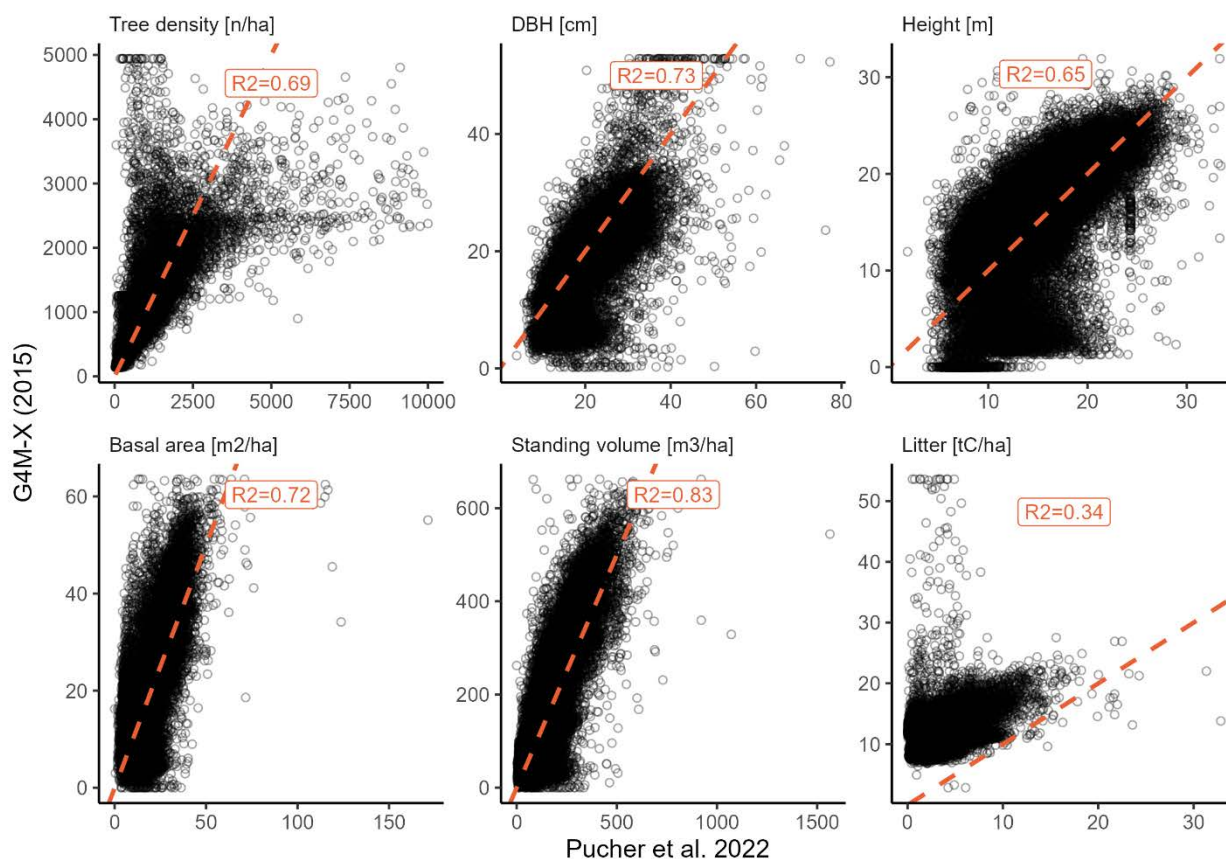


Figure 2: Comparison between continuous covariates describing forest characteristics based on the two used data sources, namely the Improved Gridded Forest Structure data (IGFS; Pucher et al., 2022) and the G4M-X model for the initial time step.

4. Biodiversity modelling workflow

The biodiversity modelling workflow (Figure 3) is implemented in the open-source *R* programming language (R Core Team, 2021). All steps of the workflow are separated into several modular *R* scripts that are hosted and available on the IIASA [GitLab](#) instance and will be updated during the project duration. Key software packages used for general data (pre-)processing include, besides others, *terra* (Hijmans, 2021), *sf* (Pebesma, 2018), and packages from the *tidyverse* (Wickham et al., 2019). To train and project all *iSDMs*, we are using the *ibis.iSDM* software package (Jung, 2023) and landscape metrics are calculated using the *landscapemetrics* software package (Hesselbarth et al., 2019). All packages are openly available on the *Comprehensive R Archive Network* or *GitHub*.

4.1. Pre-processing of data sets

4.1.1. Climatic, environmental and forest covariates

We crop and mask all covariate layers storing climatic and environmental conditions as well as forest characteristics to the same spatial extent using the *NUTS* regions provided by the *GISCO* statistical unit dataset (10 m scale spatial resolution). Within the spatial extent, all covariate layers are aggregated as close as possible to the same spatial resolution using cell arithmetic means or modal values for continuous and discrete layers, respectively, and resampled to the same background layer using bilinear interpolation for continuous values and nearest neighbor values for discrete values. We homogenize all NA cells across layers, remove correlated layers using Pearson's $r \geq 0.7$ as cut-off and scale values using the mean and standard deviation. However in order to guarantee that climate change scenarios are included, specific covariate layers were not removed even if highly correlated, for example temperature and precipitation.

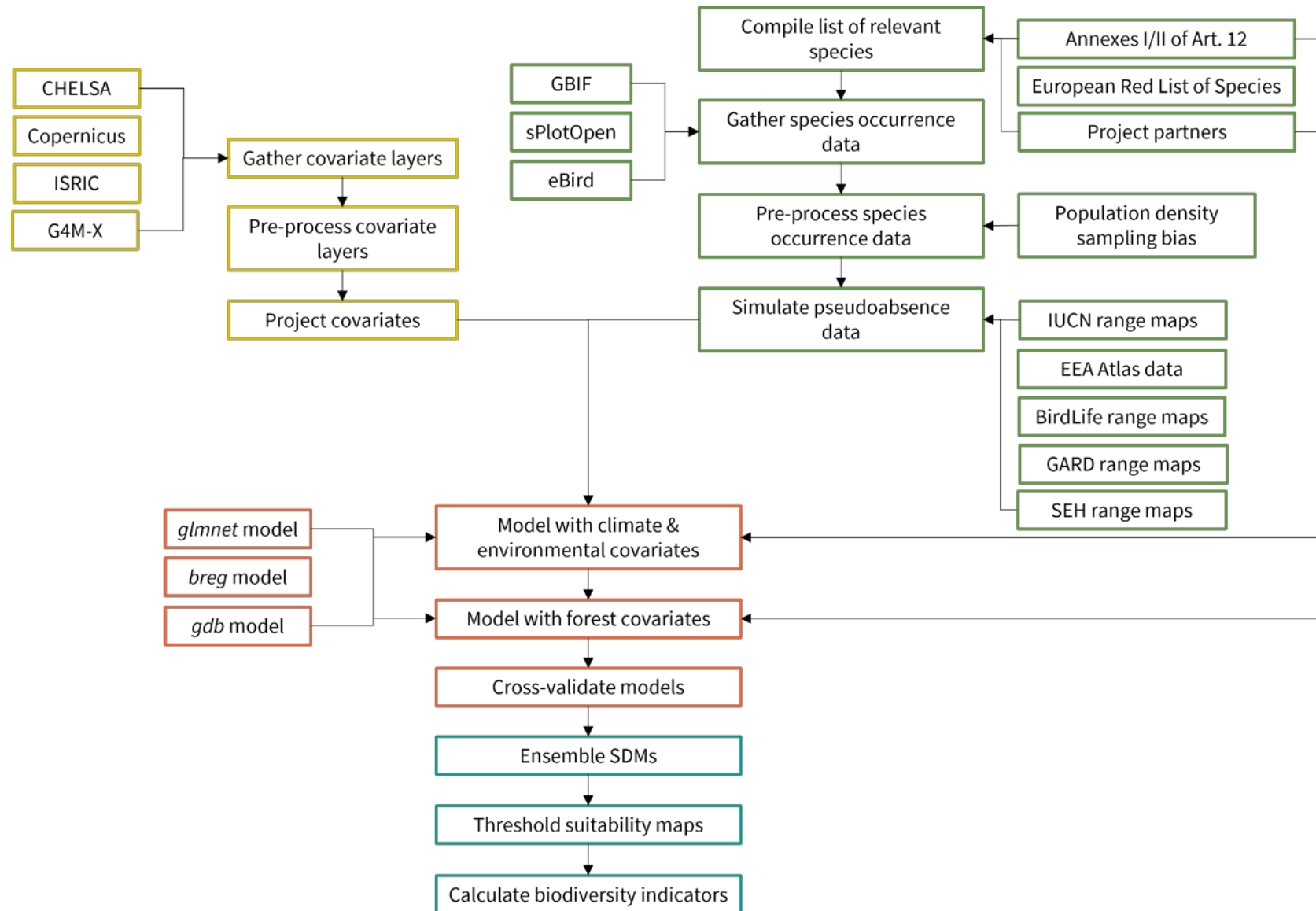


Figure 3: Overview of the biodiversity modelling workflow.

4.1.2. Preparation of species occurrence data

Because model accuracy of *SDMs* decreases with less than about 25 – 30 observations (Hernandez et al., 2006; Wisz et al., 2008), we include only species with at least 35 observations, thus limiting our list of species that can be reliably estimated.

The data quality on *GBIF* is frequently criticized, e.g., due to spatial biases based on sampling accessibility (Beck et al., 2014). Thus, before data can be used reliably, it needs to be pre-processed and cleaned. First, because the individual count value is not always provided or seems problematic (e.g., very high values), we set the individual count information to one for all *GBIF* occurrence data. Second, we remove all records with a coordinate uncertainty larger than 5 km or that do not report any coordinate uncertainty. Third, we use the *CoordinateCleaner R* package (Zizka et al., 2019) to further remove low-quality records from the data. Here we remove all coordinates located in capitals or urban areas, at country centroids, at the *GBIF* headquarters, at known biodiversity institutes, in the ocean, or general outliers and duplicates.

For the *eBird* data, we transform the presence-only to presence-absence data, one of the advantages of *eBird*. This can be done due to the checklists, and specifically including only checklists which reports all observed species. Then, based on the assumption that if a specific species is not listed in a specific checklist, it was truly absence (so-called zero filling). Yet, the effort across checklists differs, which is a potential source of bias (Johnston et al., 2021). Thus, for better homogeneity of observation probabilities following the “Best Practices for Using eBird Data” (Strimas-Mackey et al., 2023), we remove all observations that were collected during birding activities longer than 6 hours, with a travelled distance longer than 10 kilometer, or including more than 10 people.

Because *sPlotOpen* is based on traditional vegetation plots, the data can be used as presence-absence data (Sabatini et al., 2021). Similar to the *eBird* data, for all sample plots at which a specific species was not recorded, we assume that the species is absent.

Geographic sampling bias is a well-known issue for (citizen-generated) species occurrence data (Hijmans, 2012) and occurrence data might not reflect where species are present, but rather where they are observed. This can be quantified by extracting the climatic and environmental conditions at all species occurrences and within expert-derived range maps/atlas data. The overlap between the values can be described by the modified Hellinger metric (Warren et al., 2008). For all species with a small overlap (e.g., < 25%), we assume that the occurrence data does not reflect the true range of a species, i.e., there is a geographic sampling bias (Figure 4). Spatial thinning is an approach to mediate this bias (Aiello-Lammens et al., 2015; Steen et al., 2021) and previous to training *iSDMs* assuming that more observations are made closely to highly populated areas we thin occurrence data for each species using the *GHS*-population grid from the year 2015 as bias layer (Schiavina et al., 2023).

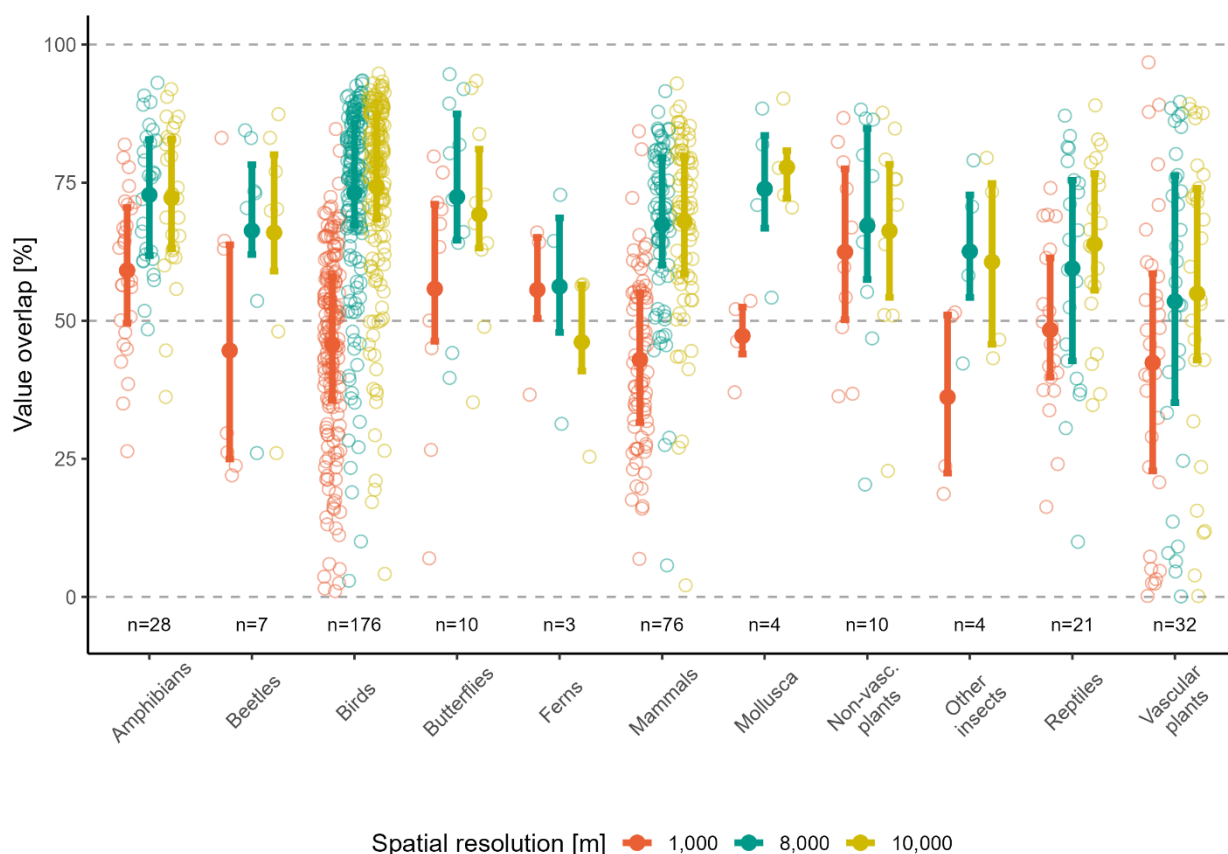


Figure 4: Value overlap of climatic and environmental covariates between species occurrence data and expert-derived range maps. The overlap is calculated for different spatial resolutions indicated by color. The error bars describes the 25 % – 75 % quantiles for each resolution and species group, the solid point the mean value. Additionally, the number of species with an existing range map per group is included.

4.2. Species distribution modelling

4.2.1. Training species distribution models

We use covariates and species occurrence data for the years 2015 – 2020 (or as close as possible) to train the *iSDMs* using current climatic and environmental conditions as well as forest characteristics. For the parametrization, we used modelling approaches that requires presence-absence data (Barbet-Massin et al., 2012). Thus, for the presence-only datasets we simulate pseudo-absence data with a ratio of $r = 2.5$, i.e., creating just over twice as many absence points than presence points for each species. If a range map is available, all absence points are generated outside the species range, thus integrating this information into the prediction. If no range map is present, absence points are generated outside the minimum convex hull of all presence points. Similar, we subsampled all *eBird* and *splotOpen* absence data to the same presence-absence ratio.

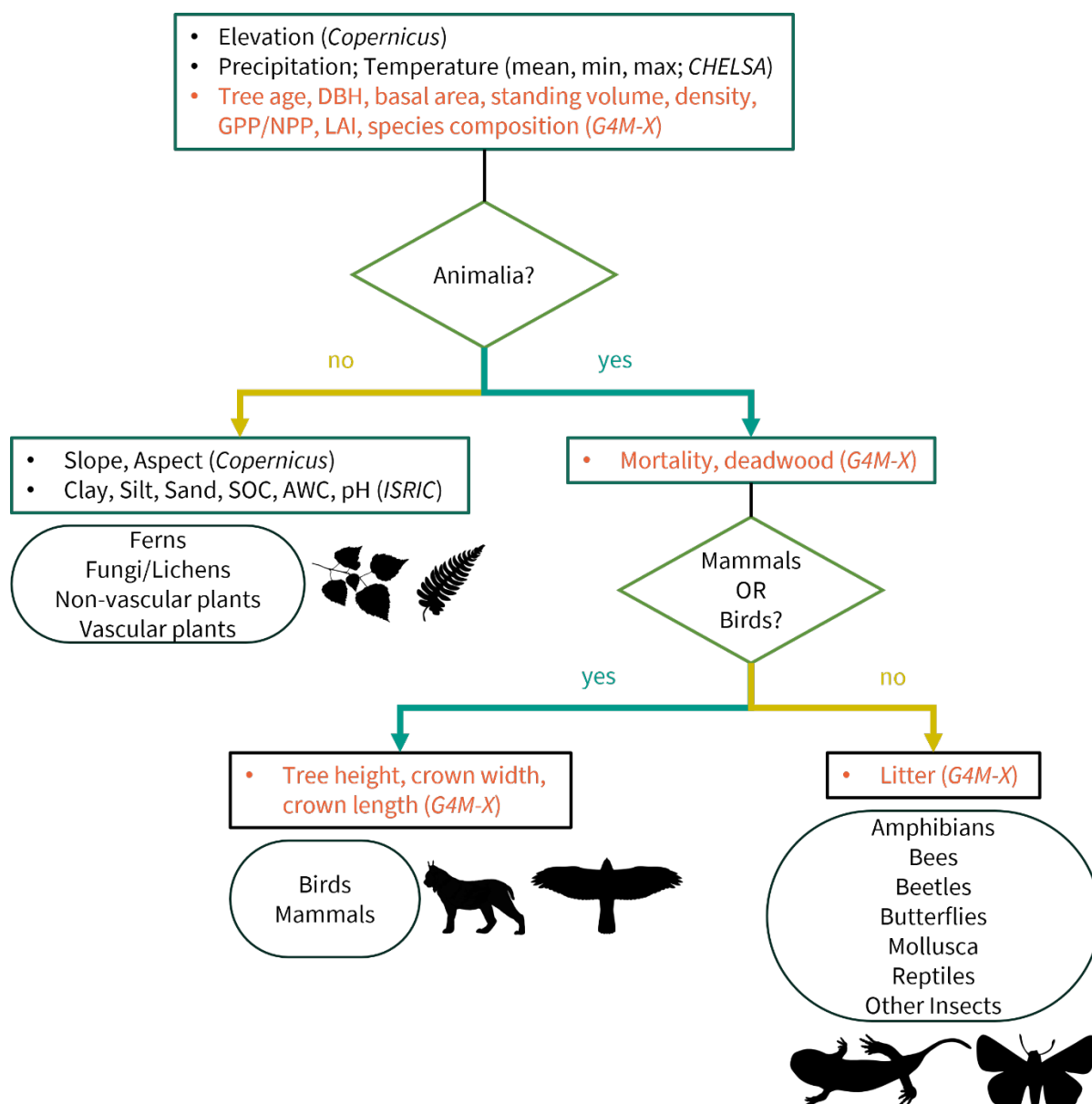
We used a sequential (or step-wise) integration of two models using different sets of covariates. More specifically, the first model uses climatic and environmental covariates and the resulting habitat suitability is used as an additional covariate in the second model including all forest characteristic covariates. Furthermore, in order to keep the models as simple as possible, we include covariates depending on the species group based on assumptions on their typical biology and habitats (Figure 5). For example, we assume that soil conditions are mostly relevant for members of the kingdoms Plantae and Fungi, but not for members of the kingdom Animalia.

Additionally, we use priors for all species and forest characteristic covariates where such information is available. By using priors, we are able to influence the direction and/or magnitude of model parameters based on *a priori* ecological knowledge. We include priors for saproxylic species (i.e., species depending on deadwood) as well as for species that are characteristic of old-growth forests. This is based on published literature and databases (Blasi et al., 2010; Eckelt et al., 2018; Gao et al., 2015; Graf et al., 2022; Lachat et al., 2012; Oettel and Lapin, 2021; Stokland and Meyke, 2008) and certain terms in the “Habitats” column of the *European Red Lists of Species* (namely “deadwood”, “woody debris”, “saproxylic” or “old-growth”, “primary forest”, “primeval forest”). For all saproxylic species we use a prior for mortality and deadwood, for all old-growth forest species, we set a prior for forest age and diameter at breast height (*DBH*).

To model species distributions, we use different statistical frameworks (herein *engines*), such as elastic-net regularized generalized linear models (*glmnet*), Bayesian regularized regression (*breg*), or gradient descent boosting (*gdb*). For each engine, a habitat suitability projection and block validation via cross-validation is made. The output of the engines describe the probability of occurrence or relative habitat suitability in each raster grid cell. The projections of all engines can be combined (or ensembled) through a weighted mean using the cross-validation results. For further analysis of the results, the continuous habitat suitability maps are converted into binary presence-absence maps using threshold methods, such as a percentile threshold (e.g., $p = 15\%$) or the minimum predicted value of a known species occurrence.

4.2.2. Cross validation

We use cross-validation to verify the habitat suitability maps and get insights into the precision and extrapolation errors of the trained models (Roberts et al., 2017). We use the *blockCV R* package (Valavi et al., 2019) to split the species occurrence data in $k = 3$ folds. For each fold, we hold back a test subset of the data during model training. The test subset is then used to evaluate the trained model using appropriate metrics, such as Continuous Boyce Index (Hirzel et al., 2006). The evaluation metrics are used as weights for model ensembling by constructing a weighted average of all candidate models, whereas all with a remarkably low evaluation metric could be removed from the ensemble.



2017). For example, the European Environment Agency (EEA) developed the Streamlining European Biodiversity Indicators (SEBI), however, they are not criticism-free (e.g. Feest, 2013). Generally, the most common species groups used as indicators in forest ecosystem studies are arthropods (including saproxylic species), birds (including woodpeckers), or plants (Oettel and Lapin, 2021). Furthermore, mammals, reptiles, vascular plants, bryophytes, lichens, and fungus can be found in the literature (Gao et al., 2015). To describe and capture biodiversity, usually more than just one indicator is recommended (Santini et al., 2017). Thus, we are applying several indicators simultaneously. Indicators are calculated for all climate change scenarios and forest management pathways. Importantly, this also includes a comparison of the indicator values to a reference values, i.e., before projecting species distributions temporally. This allows us to compare the indicator to the “reference” state and to evaluate impacts of the scenarios and pathway on biodiversity.

Habitat suitability and presence-absence maps: Habitat suitability maps for each species are the most unprocessed indicators that we produce. For each raster grid cell, the maps hold the probability of occurrence or (relative) habitat suitability. The maps allow to spatially highlight areas with biodiversity value. Furthermore, presence-absence maps based on thresholded habitat suitability values are produced for all species. These are closely related to the SEBI 01 indicator (“Abundance and distribution of selected species”).

Area of suitable habitat: The presence-absence maps can be summarized to a single indicator by calculating the total area of all raster grid cells that indicate species presences, or in other words the total area of suitable habitat. While the total area of suitable habitat is an important indicator, also more detailed information about the suitable habitat patches (a patch being defined as connected habitat cells) are of interest. Thus, we are also including more detailed indicators such as the number of patches and the mean patch area.

Configuration of suitable habitat: Besides the area of suitable habitat, also the spatial configuration of the habitat in the landscape is crucial (Lucas et al., 2019). Thus, we are using several landscape metrics (e.g., Gustafson, 2019) to further quantify the presence-absence maps. For example, this includes the mean distance to the nearest patch, or the percentage of like adjacencies. While the first contains information about landscape connectivity, the later describes the fragmentation of the landscape.

Species richness: Species richness is one of the simplest biodiversity that can be computed by overlaying the presence-absence maps for several species or species groups. However, comparing species richness over a large spatial extent can be biased due to biogeographic patterns in biodiversity. Thus, we are also computing relative species richness, which controls for biases by expressing the potential species richness in relation to a local species pool (Vallecillo et al., 2016). We are using a moving window approach to determine the local species pool.

Sørensen similarity index: The Sørensen index is another important biodiversity indicator that describes the similarity (or dissimilarity) between species of two communities in space or time (e.g., Magurran, 2013). Using the species richness maps, we can use the index to describe how biodiversity changes across pathways. To do this, the index is calculated comparing two local communities using a moving window, whereas the communities include the same spatial extent but different scenarios and pathways.

We calculate all indicator values for the entire species pool, as well as for several subsets. This includes indicators separated by taxonomic ranks (e.g., families), different species groups (Table

2), or IUCN Red List status. Furthermore, we calculate all indicators only for species that are categorized as saproxylic species or characteristic of old-growth forest. This is based on the same published literature and databases as the priors of the model training.

4.3. Exemplary trained species distribution model

Figure 6 depicts an exemplary and preliminary trained *iSDM* for *Dendrocopos leucotos* (white-backed woodpecker). The trained model uses the current climatic and environmental conditions as well as current forest characteristics. Thus, the figure does not reflect any “final” results, but rather demonstrates how the reference state for some biodiversity indicators is constructed. The habitat suitability map shows the probability of species occurrence based on a model ensemble using three engines (Figure 6a). The corresponding partial response functions show how the covariates affect the fitted suitability (Figure 6b). The continuous values can be transformed to a presence-absence maps using a threshold approach (Figure 6c). Finally, the presence-absence map can be quantified using several landscape metrics (Figure 6d). The biodiversity indicators and their change will be evaluated in comparison to the reference state under the climate change scenarios and forest management pathways (Figure 7). This allows us to compare and evaluate the different scenario and pathways and their impact on biodiversity.

Dendrocopos leucotos (Birds)

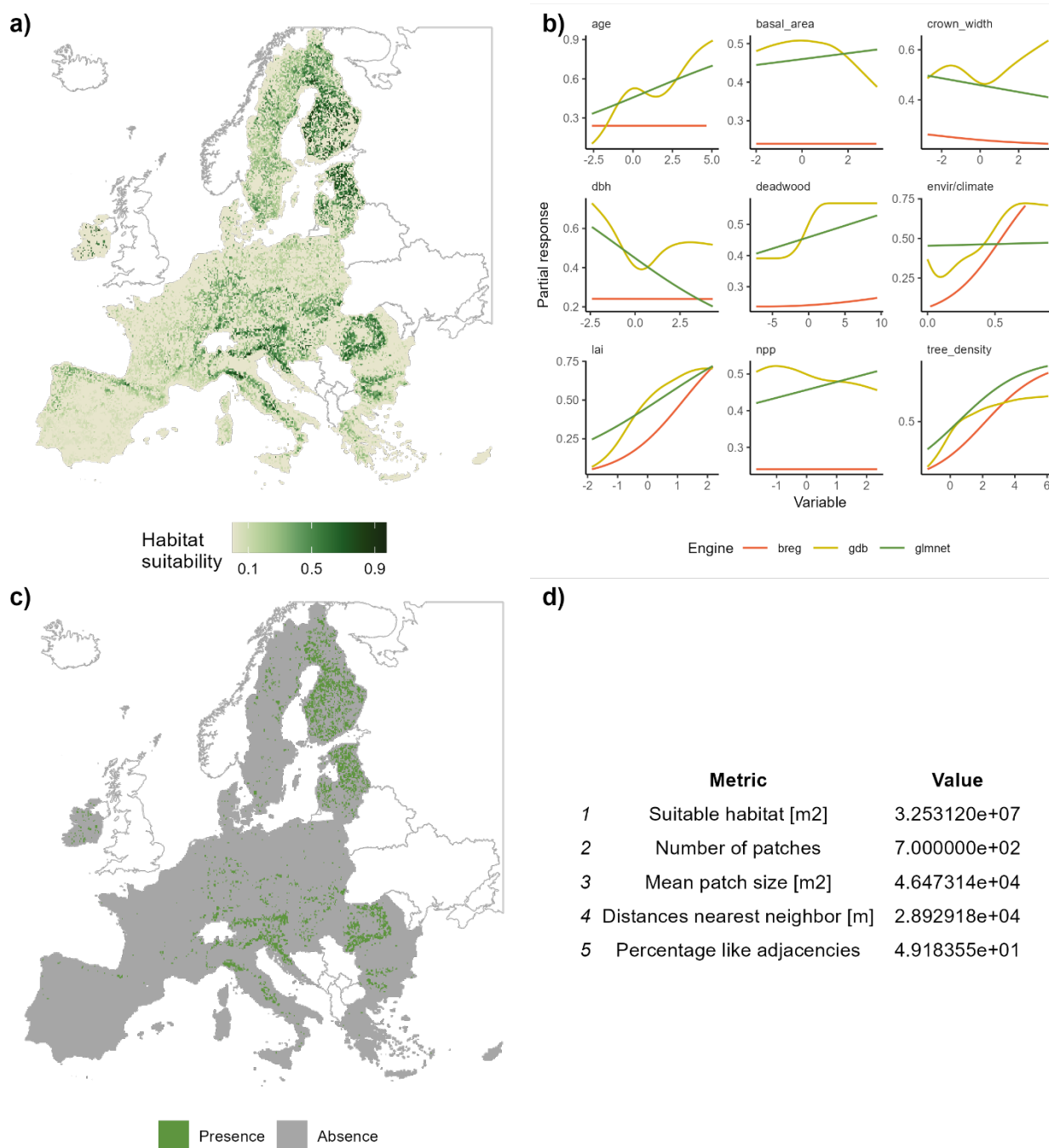


Figure 6: Exemplary trained iSDM using current climatic and environmental conditions and forest characteristics used as reference state. Results include a) the habitat suitability map, b) the partial response functions of the model fit, c) the occurrence of the species based on a threshold, and d) the composition and configuration of the suitable habitat.

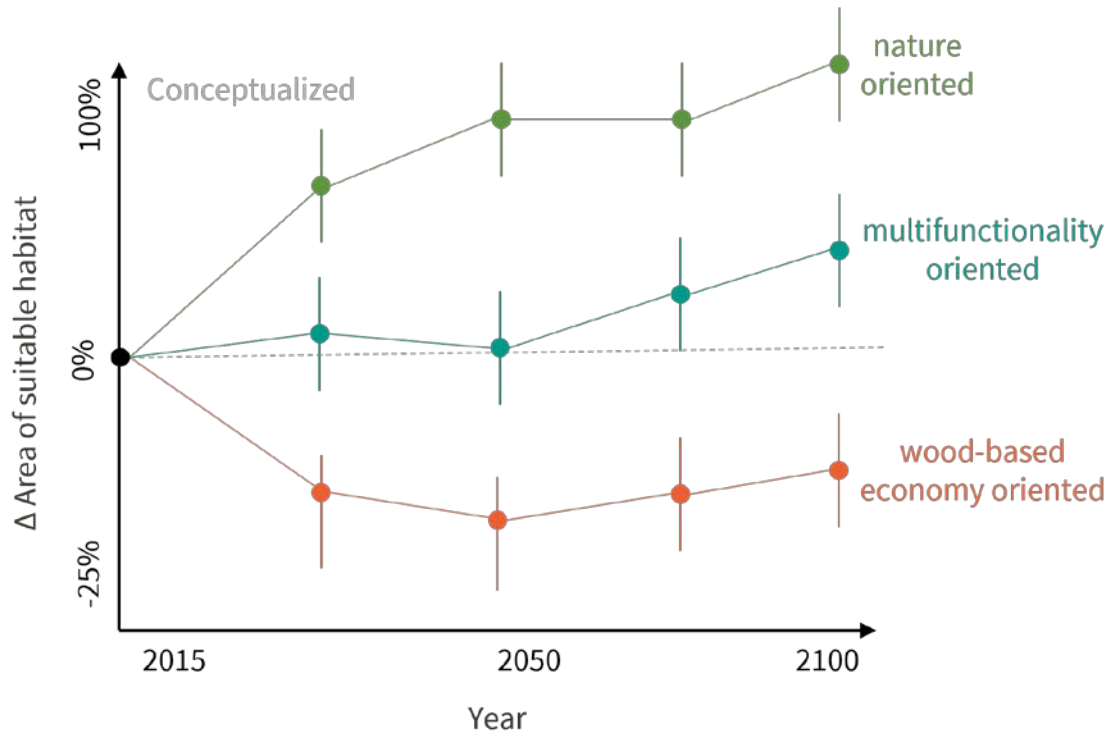


Figure 7: Conceptual figure of the projected area of suitable habitat. The figure shows a hypothesized reference state of the indicator and the relative changes under the three forest management pathways.

5. Summary of next steps

So far, the focus has been on conceptualizing the modelling framework to assess impacts of climate change scenarios and forest-based mitigation pathways on biodiversity using *iSDMs* and biodiversity indicators. Additionally, covariates regarding climatic and environmental conditions as well as forest characteristics and species occurrence data were gathered and pre-processed.

The next steps include gathering and pre-processing of currently missing data, most importantly projected forest characteristics provided by other *WPs* and tasks of the *ForestNavigator* project. Once the data is fully available, the *iSDMs* can be trained, projected on the EU scale, and finally the biodiversity indicators can be calculated. This comprises the following tasks:

Training *iSDMs* based on current climatic/environmental conditions and forest characteristics: Once all covariates describing climatic and environmental conditions and forest characteristics are available and pre-processed, the *iSDMs* can be trained. This also includes the cross-validation of the models.

Project future species habitat suitability: Using the projected climatic and environmental conditions, as well as forest characteristics, species habitat suitabilities can be projected on an EU scale.

Compute biodiversity indicators: We will use the current and projected species habitat suitabilities to compute several biodiversity indicators and more importantly their change under the different climate change scenarios and forest management pathways. This will allow us to assess the impacts of different climate change scenarios and forest management pathways on biodiversity and contribute to informed decision-making in conservation and sustainable forest management.

6. References

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Supporting information

SI: Species previously modelled on national scale

The following species were previously modelled on a national scale by consortium members of the *ForestNavigator* project. Thus, we are also included these species in our biodiversity modelling workflow to compare results across the EU scale modelling and the national scale modelling.

Species	Species group
<i>Trichaptum abietinum</i>	Fungus
<i>Fomitopsis pinicola</i>	Fungus
<i>Gloeophyllum sepiarium</i>	Fungus
<i>Antrodia serialis</i>	Fungus
<i>Phellinus viticola</i>	Fungus
<i>Phellinus ferrugineofuscus</i>	Fungus
<i>Phellinus nigrolimitatus</i>	Fungus
<i>Phlebia centrifuga</i>	Fungus
<i>Fomitopsis rosea</i>	Fungus
<i>Amylocystis lapponica</i>	Fungus
<i>Tetrastes bonasia</i>	Birds
<i>Perisoreus infaustus</i>	Birds
<i>Poecile cinctus</i>	Birds
<i>Aegithalos caudatus</i>	Birds
<i>Ficedula parva</i>	Birds
<i>Picus canus</i>	Birds
<i>Dendrocopos minor</i>	Birds
<i>Picoides tridactylus</i>	Birds
<i>Lobaria pulmonaria</i>	Lichens
<i>Anastrophyllum hellerianum</i>	Non-vascular plants
<i>Anastrophyllum michauxii</i>	Non-vascular plants

<i>Buxbaumia viridis</i>	Non-vascular plants
<i>Callicladium haldanianum</i>	Non-vascular plants
<i>Calyptogeia suecica</i>	Non-vascular plants
<i>Campylophyllum sommerfeltii</i>	Non-vascular plants
<i>Cephalozia catenulata</i>	Non-vascular plants
<i>Dicranodontium denudatum</i>	Non-vascular plants
<i>Dicranum flagellare</i>	Non-vascular plants
<i>Dicranum fragilifolium</i>	Non-vascular plants
<i>Geocalyx graveolens</i>	Non-vascular plants
<i>Herzogiella seligeri</i>	Non-vascular plants
<i>Herzogiella turfacea</i>	Non-vascular plants
<i>Jamesoniella autumnalis</i>	Non-vascular plants
<i>Jungermannia leiantha</i>	Non-vascular plants
<i>Lophozia ascendens</i>	Non-vascular plants
<i>Lophozia ciliata</i>	Non-vascular plants
<i>Lophozia longiflora</i>	Non-vascular plants
<i>Mylia taylorii</i>	Non-vascular plants
<i>Nowellia curvifolia</i>	Non-vascular plants
<i>Odontoschisma denudatum</i>	Non-vascular plants
<i>Scapania apiculata</i>	Non-vascular plants
<i>Scapania carinthiaca</i>	Non-vascular plants