

## Review



## Where are we now with European forest multi-taxon biodiversity and where can we head to?

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## ABSTRACT

The European biodiversity and forest strategies rely on forest sustainable management (SFM) to conserve forest biodiversity. However, current sustainability assessments hardly account for direct biodiversity indicators. We focused on forest multi-taxon biodiversity to: i) gather and map the existing information; ii) identify knowledge and research gaps; iii) discuss its research potential. We established a research network to fit data on species, standing trees, lying deadwood and sampling unit description from 34 local datasets across 3591 sampling units. A total of 8724 species were represented, with the share of common and rare species varying across taxonomic classes: some included many species with several rare ones (e.g., *Insecta*); others (e.g., *Bryopsida*) were represented by few common species. Tree-related structural attributes were sampled in a subset of sampling units (2889; 2356; 2309 and 1388 respectively for diameter, height, deadwood and microhabitats). Overall, multi-taxon studies are biased towards mature forests and may underrepresent the species related to other developmental phases. European forest compositional categories were all represented, but beech forests were over-represented as compared to thermophilous and boreal forests. Most sampling units (94%) were referred to a habitat type of conservation concern. Existing information may support European conservation and SFM strategies in: (i) methodological harmonization and coordinated monitoring; (ii) definition and testing of SFM indicators and thresholds; (iii) data-driven assessment of the effects of environmental and management drivers on multi-taxon forest biological and functional diversity, (iv) multi-scale forest monitoring integrating *in-situ* and remotely sensed information.

## 1. Introduction

Forests support about three-quarters of terrestrial plants, fungi and animal species (FAO, 2020), and are at the base of other ecosystem services including the provisioning of raw materials and the regulation of geochemical cycles. These services are threatened by climate change, forest loss and degradation, invasions by non-native species, and over-harvesting (Felipe-Lucia et al., 2020). The increasing concern related to these threats has imposed a paradigm shift from single-objective forest management (i.e., timber production-oriented) to the embracement of forest multifunctionality (Mori et al., 2017).

Sustainable Forest Management (SFM) is defined as the management that concomitantly maintains forest biodiversity, productivity, regeneration capacity, and vitality, as well as forests' potential to fulfill a wide range of functions and services (MCPFE, 1993). As such, SFM is globally recognized as a crucial tool to counteract biodiversity loss, and to promote sustainable development (UN, 2015). Managing forests sustainably is particularly relevant in Europe, where, although about 24 % of forests are formally protected, only a small fraction (2 % of total forest area) is not subject to harvesting interventions (Forest Europe, 2020). Accordingly, the SFM definition reported in the European Union regulation (2020/852) includes a criterion of biodiversity maintenance, reported as the contribution to "enhancing biodiversity, halting or preventing the degradation of ecosystems, deforestation and habitat loss".

Nevertheless, the effects of forest management on the diversity of multiple taxonomic groups, hereafter multi-taxon biodiversity, are not sufficiently known, and the links between indicators of biodiversity and of management sustainability are not always evident and strong (Oettel and Lapin, 2021). As a matter of fact, multi-taxon biodiversity sampling and analysis is highly demanding in terms of funding, time, and a broad range of expertise and competences (Tomppo et al., 2010). For these

reasons, it remains uncertain to which extent, and for which taxonomic groups could forest management for wood supply deteriorate biodiversity compared to unharvested forests, and how SFM can mitigate these effects.

The challenges of multi-taxonomic field sampling are being increasingly addressed at the local or regional scales. In Europe, these efforts often consist of exhaustive species censuses across single- or multiple sites to assess the effects of forest structure and management on the diversity of multiple taxonomic groups (see references in Table 1).

**Table 1**  
Definitions of the silvicultural systems used in the platform.

Silvicultural systems	Treatment description
Unmanaged	No silvicultural interventions applied in the recent past, stands currently under natural development
Selection cutting	Single-tree and group selection cutting are uniformly distributed across the stand.
Shelterwood	Overstorey trees in a forest stand are completely removed through multiple progressive cuts designed to promote regeneration making use of the shelter and seed source of remaining trees
Clearcutting with retention	The forest stand is clear-felled in a single harvesting operation except for solitary trees or tree groups that are deliberately spared
Clearcutting	The forest stand is entirely harvested in a single operation, resulting in a treeless open area mostly artificially regenerated
Coppice with standards	The two vertical strata of the forest stand (even-aged coppice as the understorey, and an overstorey of standards which are trees of seed- rather than sprouting origin) are harvested respectively by a clearcutting and a selection cutting. Standards can be uneven-aged and the two components have quite different rotation periods. This category also includes the combination of coppice and high forest (i.e. compound coppices)

Relatively few examples of such studies can be found in other continents within the temperate and boreal zones (Murray et al., 2017; Bowd et al., 2021; Stokely et al., 2022). The efforts of European researchers to test the effectiveness of SFM reflect the long-lasting and widespread land-sharing approach to forest zoning that characterizes Europe, at least since Möller (1922), as compared to regions where a sparing approach is more common (e.g., Australia, North America). However, compared to continent-wide health forest monitoring networks (e.g., International Co-operative Programme on Assessment and Monitoring of Air Pollution Effects on Forests - ICP Forests), research activities related to European forest biodiversity remain uncoordinated at the continental scale and suffer from a lack of harmonization and integration across local studies.

Here we aim to i) review the existing information on forest multi-taxon biodiversity associated with stand structure and management and ii) identify knowledge gaps in multi-taxon forest biodiversity studies. Starting from this basis, we aim to iii) discuss future research challenges associated with multi-taxon biodiversity in European forests. Ultimately, we intend to encourage new institutional forms of broad-scale forest biodiversity data collection and usage to inform forest conservation and management policies in Europe and elsewhere.

## 2. Methods

### 2.1. Data collection

We aimed at gathering forest biodiversity and stand structural data from many independent research projects and studies on multi-taxon forest biodiversity performed across Europe in the last 20 years. We created a network connecting research groups that collected forest multi-taxon biodiversity data in Europe from local to national scales. The initial network was progressively enlarged by contacting researchers involved in past and ongoing forest multi-taxon biodiversity projects identified through project databases (i.e., LIFE projects'

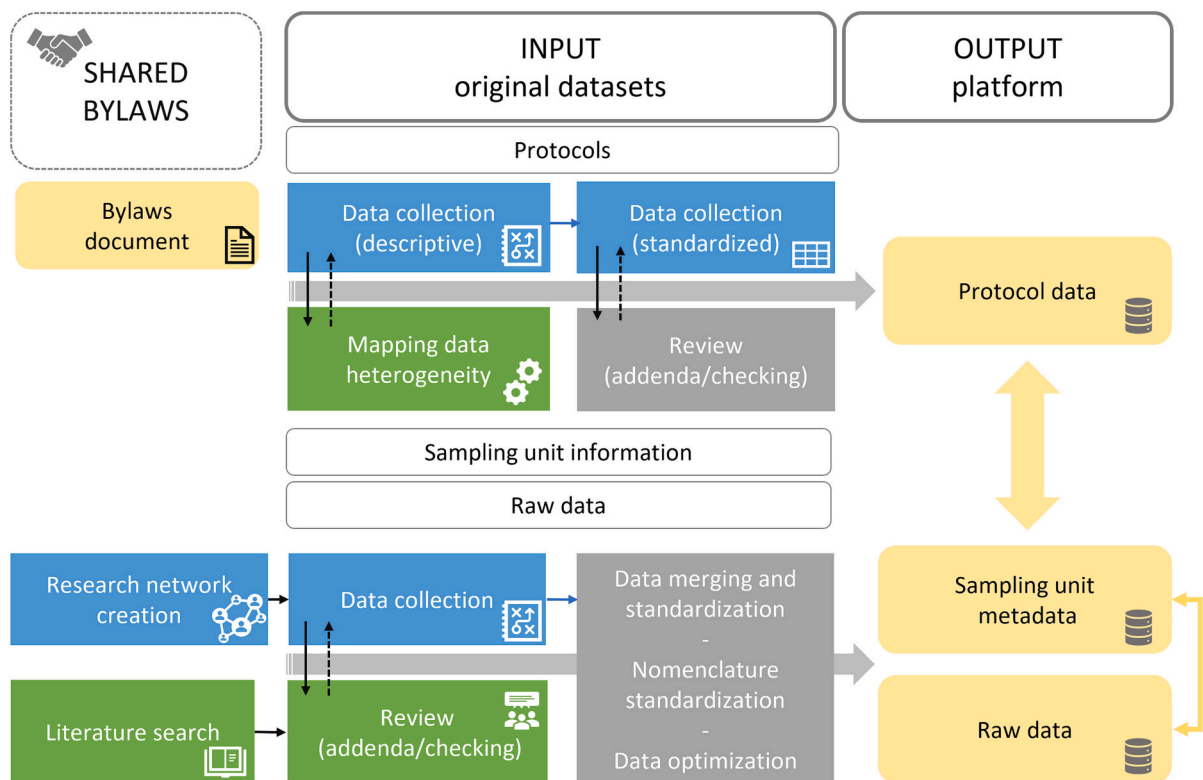
database: <https://webgate.ec.europa.eu/life/publicWebsite/search>), publications and personal information.

We defined a *forest* as an ecosystem in which tree cover was equal or greater than 40 % (Sasaki and Putz, 2009). We intended *multi-taxon* to include simultaneous information on a minimum of three taxonomic groups, representing at least Plantae or Fungi, and Animalia. *Stand structure* data was defined as tree species composition, volume and size distribution of standing trees (both living or dead), and of lying deadwood when available.

To test the comprehensiveness of the platform, we surveyed the research network on relevant literature and gathered 117 published articles (Trentanovi et al., n.d.). We added further articles found through a literature search on ISI Web of Science (accessed on November, 17, 2022 and limited to articles published before 2022) with the formula (TS = (forest AND multi-tax\* AND biodiversity)). This search resulted in 130 additional articles, of which 61 describe studies performed in Europe. Among these, 17 focused on non-forest habitats (e.g., wood pastures, urban or agricultural areas), 17 did not fit the multi-taxon or stand structure requirements, five had a different focus (sampling methods, biotic disturbance). Only 22 articles fitted the platform requirements, among which 11 were already listed in the literature gathered through the research network, and five were relative to datasets already included in the platform. Based on this literature assessment we deemed the platform as significantly representative.

For each dataset in the platform, we firstly gathered and harmonized the information on sampling designs and protocols (see the 'protocols' of Fig. 1) into three ancillary tables that include standardized sampling protocol descriptions of: standing trees, lying deadwood, and biodiversity data. (i.e., 'protocol data' in the output section of Fig. 1).

The spatial hierarchy of the platform encompasses plots (i.e., delimited forest areas of known geographical coordinates) that are nested into stands (i.e., management spatial units), and stands that are nested into sites (i.e., environmentally homogeneous geographical



**Fig. 1.** Workflow of the platform building process. Blue boxes identify in-progress products; green boxes identify phases of common decisions, brainstorming and comparison with scientific literature; gray boxes indicate data processing; yellow boxes are the outcomes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

areas). We generally refer to sampling units to include both plots and stands, since in a minority of cases (about 15 % of the stands do not have plot IDs but stand IDs), data were sampled at the stand scale, without specific sampling plots. It is also relevant to point out that for most of the collected datasets, several ecosystem components, i.e., taxonomic groups and stand structure, were sampled in the same *plots*, but in a minority of cases different components were sampled using various designs across a forest stand, allowing for cross-taxon analysis only at the stand scale (see Burrascano et al., 2021 for a thorough discussion of the pros and cons of the two approaches).

The studies included in the platform were mainly observational but some experimental studies were also included. In both cases, we collected information on stand age and/or development stage, a categorical definition of the silvicultural system adopted, and many other associated quantitative management data (e.g., time since last harvesting).

## 2.2. Data management

Each original dataset was associated with one data custodian, responsible for data preparation and handling within the platform, and for communication with the dataset contributors. The heterogeneity in sampling designs, measurement methods, spatial scales, target variables and taxonomic groups required the definition of standardized procedures to harmonize raw information and produce a common data structure.

We built a relational structure encompassing several tables whose organization and templates derived from an iterative process of proposals and refinements carried out through a wide and open discussion (see connections between boxes in the ‘Input’ section in Fig. 1).

The core of the platform (i.e., ‘Sampling unit metadata’ and ‘Raw data’ in Fig. 1) consists of four tables: one containing sampling unit metadata and the others containing the raw data separately for standing trees, lying deadwood, and multi-taxon species composition.

The sampling unit metadata includes location, ownership, structure, regeneration and management type. Two key variables within this table are the forest compositional category and the silvicultural system. The former refers to the classification into 14 categories of ecologically distinct forest communities in Europe dominated by specific assemblages of tree species (SI-1). These categories were designed to facilitate the interpretation and communication of indicators on the status and trends of forests in Europe (EEA, 2006; updated by Barbati et al., 2014). The classification into broad silvicultural systems was based on the type of regeneration cut according to Matthews (1989) and refined through an extensive discussion within the network (Table 1).

Data were processed in the R programming environment (R Core Team, 2021, R version 4.1.1) using version control to ensure the widest possible hands-on collaboration and data cross-checking. Data inconsistencies that may have originated from data entry errors (e.g., typographical errors), data type storage, species nomenclature, and adherence of datasets to the table structure (e.g., column names, list of possible and plausible values) were qualitatively checked through several validation rules. These (semi)automatic rules were based on data range, length, column reference name, list values, null values, blank values, and data types. After this validation process, data have been corrected or integrated mostly through back-checking to data providers.

Species names and higher taxonomic information were extracted from databases and corroborated by experts. All species names were firstly checked using the `gnr_resolve()` function in the ‘taxize’ package (Chamberlain and Szöcs, 2013). The species names obtaining scores greater than 0.90 were accepted, while those with lower scores were sent to experts for corroboration. For vascular plants, a further screening was performed through the ‘WorldFlora’ package (Kindt, 2020). Finally, species names that could not be corroborated by experts were checked against the GBIF database (<https://www.gbif.org/>). Complete taxonomic classification was extracted with the `taxonomy()` function in the

‘myTAI’ package (Drost et al., 2018).

Relationships across tables operate at different spatial scales through univocal IDs for sites, stands, and plots. The templates of the tables for contributing data to the platform are available at: <https://www.bottoms-up.eu/en/participants/contribute/contribute-data.html> to promote further implementation of the data.

Data management is coordinated by a governing board elected by the consortium involving all data contributors according to common bylaws that were discussed and accepted by all the consortium participants (downloadable here: <https://www.bottoms-up.eu/en/participants/contribute/propose-a-project.html>). The bylaws are composed of eight regulation articles partly based on previous experiences of shared datasets (e.g., Biurrun et al., 2019). As it is always the case in the beginning of these sharing processes, a give-and-take approach has been chosen (Kattge et al., 2020; Bruelheide et al., 2019); therefore, joining the consortium is possible for researchers that provide a dataset complying with the bylaws requirements. Data usage is open to anyone proposing a research project involving at least one consortium member by following the instructions at: <https://www.bottoms-up.eu/en/participants/contribute/propose-a-project.html>. A Shiny Web-App (<https://www.bottoms-up.eu/en/results/data-explorer.html>) was created to smooth the proposal of projects by allowing for data exploration and filtering based on the sampling unit metadata (SI-2).

## 2.3. Data analysis and visualization

The proportion of sampling units for each compositional category was compared with the share of such categories in the European Union forest area as reported in Barbati et al. (2014). Similarly, sampling unit distribution across broad regeneration strategies (high forest and coppice), and unmanaged areas were compared with the share of forest area under these conditions as reported in McGrath et al. (2015). Sampling unit metadata were visualized through alluvial plots using the ‘ggalluvial’ R-package (Brunson, 2020).

The distribution of species and species records across higher taxonomic ranks (phyla and classes) was represented through a phylogenetic tree, encompassing 7335 out of the 8724 species of the platform. The tree was obtained through PhyloT (<https://phylot.biobyte.de/>) in Newick format and imported in R through the ‘ape’ package (Paradis and Schliep, 2019). To each species in the tree, we associated its higher taxonomic ranks derived through the ‘myTAI’ package (Drost et al., 2018) and the number of occurrences across sampling units (SI-3). The combined information was visualized by using the ‘ggtree’ package (Yu et al., 2017).

In addition to the mentioned check for plausible ranges of values, structural data were subjected to specific integration processes. Heights of standing trees were integrated by means of height-diameter relationships (hypsometric models); whereas deadwood fragments measurements were integrated through data imputation performed using the ‘mice’ package (van Buuren and Groothuis-Oudshoorn, 2011). Data integration was performed individually for each dataset by applying the predictive mean matching (PMM), i.e., assessing imputation uncertainty through the examination of the variation in imputed values when treated as real, and including forest compositional categories and types, and spatial variables (plot and site). Few datasets lacked any measures of height/length and were integrated by using the whole data platform. A total of 42,643 tree heights out of 178,098 were calculated by means of hypsometric models; and 5011 diameters and 9317 lengths were imputed out of 58,824 lying deadwood fragments. Based on these data, the distributions of sampling unit mean of Diameter at Breast Height (DBH) for standing trees and of diameter for lying deadwood were calculated (SI-4, SI-5).

Biodiversity and stand structure indices may be related to environmental conditions by using parameters published in the framework of other research projects. For instance, each sampling unit was spatially associated with data on soil characteristics that were obtained from the



European topsoil physical properties map (Ballabio et al., 2016). Among the multiple soil properties available in this dataset, those currently linked to each forest multi-taxon sampling unit over a 1000 m buffer from the center of the sampling unit are: Available Water Capacity, Bulk density (derived from soil texture datasets), Soil textural classes derived from clay, silt, and sand maps. Similarly, climatic data were obtained from CHELSA v.2.1 (Karger et al., 2017), at 1000 m resolution. Bioclimatic variables were derived as long-term means or sums over the 1981–2010 period, and included mean annual temperature, annual range of air temperature, annual precipitation amount, and precipitation seasonality. Each sampling unit is also associated to a heat load index (HLI) expressing the topographic influence on incident solar radiation (McCune and Keon, 2002).

### 3. Results

#### 3.1. Overview of the existing data

##### 3.1.1. Sampling units

A total of 3591 sampling units across 220 sites in 12 European countries were gathered (SI-2, <https://zenodo.org/record/7886698#.ZFES7HZBxD8>), ranging from Sweden to southern Italy in latitude, and from France to Lithuania in longitude (Fig. 2). The harmonization involved 34 local datasets (Table 2) and 185 researchers.

In general, no clear pattern of association appears between silvicultural systems and forest compositional categories. For instance, shelterwood is applied to almost all compositional categories (Fig. 3); even though coppice with standards were associated mostly with mesophytic

and thermophilous deciduous forests.

Importantly, most sampling units (94 %) were referred to a habitat type of conservation concern according to the European cornerstone of biodiversity conservation, the Habitats Directive (92/43/EEC). The highest representation (82 %) was found for the forests of temperate Europe (group 91). About a quarter (27 %) of the total number of sampling units referred to as priority habitat types, with, in order of decreasing frequency, 91H0\*- Pannonian woods with *Quercus pubescens*, 91G0\*- Pannonic woods with *Quercus petraea* and *Carpinus betulus*, 91E0\*- Alluvial forests with *Alnus glutinosa* and *Fraxinus excelsior* (Alno-Padion, Alnion incanae, Salicion albae).

##### 3.1.2. Taxonomic information

The dataset comprises a wide range of taxonomic groups across the kingdoms of fungi, plants, and animals (SI-3, <https://zenodo.org/record/7886698#.ZFES7HZBxD8>), with 8724 species, 2979 genera, 729 families, 193 orders, 44 classes, and nine different phyla (Fig. 4). The taxonomic groups originally considered in each study include heterogeneous taxonomic ranks, from kingdom to order, and, in some cases, include only specific morphological or ecological groups commonly used in sampling and identification (e.g., macrofungi, epiphytic lichens, saproxylic beetles). Most plots have information on four or more different taxonomic groups, with an average of 4.6 groups per plot. Some plots have information on only one or two taxonomic groups, but on at least three taxonomic groups at the stand level, as required by the platform bylaws.

The classes that are represented by the highest number of species are also those represented by the highest number of records (Fig. 5), i.e.,

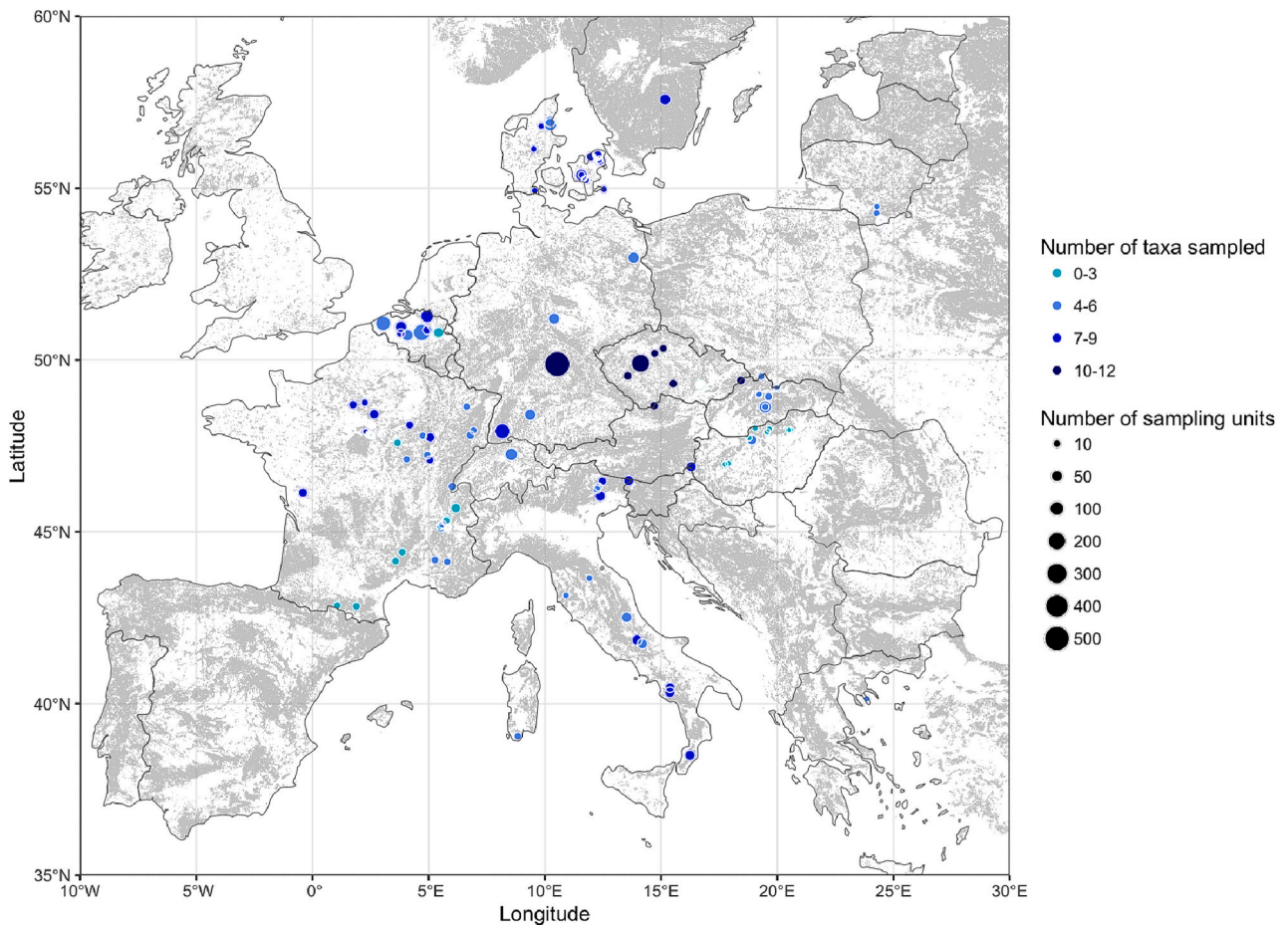


Fig. 2. Distribution of the platform sampling sites in Europe. Gray areas are covered by forests with a tree cover greater than 40 % according to the European Forest Institute Forest Map of Europe (Kempeneers et al., 2011). Number of taxa are represented by color, while number of sampling units by dot size.

**Table 2**

General descriptors of the local datasets. Dataset ID: ID of dataset, Country: country where the study has been made, N sites: number of sampled sites, N units: number of sampling units, Reference: main literature references of the 34 datasets collected for this work.

Dataset ID	Country	N sites	N units	Reference
BE_PS1	BE	2	32	De Smedt et al., 2019
BE_PS2	BE	1	53	de Groot et al., 2017
BE_KV1	BE	5	462	Vandekerckhove et al., 2016
CH_TL	CH	1	69	Haeeler et al., 2021
CZ_JH1	CZ	6	106	Hofmeister et al., 2019
CZ_JH2	CZ	1	230	Hofmeister et al., 2013
CZ_MR	CZ	1	45	Chamagne et al., 2016
DE_ID	DE	1	526	Doerfler et al., 2017
DE_JP	DE	1	135	Storch et al., 2020
DE_PS	DE	3	150	Schall et al., 2018
DK_JC1	DK	6	40	Lelli et al., 2019
DK_JC2	DK	2	107	Mazziotta et al., 2016
DK_JC3	DK	1	30	–
DK_SK	DK	16	386	Byriel et al., 2020
FR_AM	FR	12	33	Cocquelet et al., 2019
FR_JP	FR	3	70	Janssen et al., 2018
FR_NK	FR	35	43	Korboulewsky et al., 2021
FR_YP	FR	24	300	Paillet et al., 2015
GR_FX	GR	1	4	–
HU_FT	HU	1	36	Horváth et al., 2023
HU_PO1	HU	1	35	Tinya et al., 2021
HU_PO2	HU	1	30	Elek et al., 2018
HU_RA	HU	8	22	–
IT_AC	IT	3	18	Cutini et al., 2021
IT_EA	IT	6	199	D'Andrea et al., 2016
IT_SB1	IT	1	36	Blasi et al., 2010
IT_SB2	IT	2	66	Sabatini et al., 2016
IT_TS	IT	2	20	Sitzia et al., 2017
LT_GB	LT	20	143	–
SK_DK	SK	3	18	Kameniar et al., 2021
SK_MM	SK	3	22	Kozák et al., 2021
SK_MS	SK	3	18	Langbehn et al., 2021
SK_MU	SK	1	65	Ujházy et al., 2018
SW_BN	SW	25	50	Götmark, 2013

*Insecta* (3244 species across 88,338 records), *Agaricomycetes* (2077 species across 44,418 records), *Magnoliopsida* (1182 species across 71,458). However, this pattern differs for *Bryopsida*, which are represented by only 280 species in a very high number of records (27,551). This means that some *Bryopsida* species occur in a very high number of sampling units; for instance, *Hypnum cupressiforme* is the species occurring in the highest number of sampling units (5082) among all species in the platform (see also Blasi et al., 2010). On the other hand, *Insecta*, *Magnoliopsida* and *Agaricomycetes* are the most represented classes among species singletons (i.e., species occurring only once in the platform) with respectively 35 %, 29 % and 13 % of singletons vs. less than 3 % for *Bryopsida*.

### 3.1.3. Structural attributes

Being required by the bylaws, diameters of standing trees are available for all sampling units, either at the plot or stand scale, with a total 2889 sampling units, with additional data on tree height, deadwood and tree-related microhabitats in respectively 2356, 2309, and 1388 plots.

The mean diameters of standing trees (both living and dead) and lying deadwood within each sampling unit across the platform vary across silvicultural regimes. The former shows a left-skewed distribution for clearcutting and clearcutting with retention and a bimodal distribution for coppice with standards. The lying deadwood mean diameters have a peak at lower values if compared with standing tree DBH distributions, and often show a wider range, in some cases with a bimodal distribution (Fig. 6).

## 3.2. Gaps in knowledge

### 3.2.1. Sampling units

Sampling units with multi-taxon biodiversity data associated with stand structure and management information (SI-2) are available for all the 14 European forest compositional categories (Barbati et al., 2014) although unevenly distributed among them. European beech forests are over-represented with respect to the area they occupy (Fig. 5A), with lowland and mountainous beech forests representing more than 55 % of the sampling units (Barbati et al., 2014) (Fig. 5A). The distribution of sampling units across management systems, i.e., timber harvesting relying on resprouting (coppice) or seed regeneration (high forest) or no harvesting (unmanaged), differed from their area extent (McGrath et al., 2015) only for coppices (Fig. 5B).

Relevant gaps remain for some crucial management information, for instance type and year of last intervention were not available for about 40 % of sampling units. This indicates that detailed management information is often not available to forest biodiversity researchers. However, the sampling unit metadata allow a close look into the management and composition of the forests included in the platform. Most of the available sampling units are within public forests, naturally regenerated, with shelterwood and selection cutting systems being by far the most represented, and single- and multi-storied forests being similarly frequent (Fig. 3).

### 3.2.2. Taxonomic information

Some taxonomic classes are underrepresented both in terms of species and records, and this is especially true for fungi other than Agaricomycetes. For instance, Eumycetozoa, Mucoromycetes and Pucciniomycetes are represented by only one species that occurs in less than 5 sampling units. The rarity of these classes is even more striking if we account for the fact that fungi were among the most commonly sampled groups of organisms.

### 3.2.3. Structural attributes

Notwithstanding differences in the forest definition adopted and in DBH threshold, the diameter distributions of the data within the platform reflect the distribution of growing stock across diameter classes at the European level (Forest Europe, 2020), with most sampling units having a mean DBH between 20 and 40 cm (Fig. 6). On the other hand, in European multi-taxon studies, the share of trees over 40 cm is higher than the share below 20 cm. This means that multi-taxon studies are partly biased towards mature developmental phases. On the one hand, this may result in an underrepresentation of species related to different phases of the forest succession (Hilmers et al., 2018), especially of the earliest; on the other hand, it may contribute to demonstrate the links between large trees and forest biodiversity (Kozák et al., 2023).

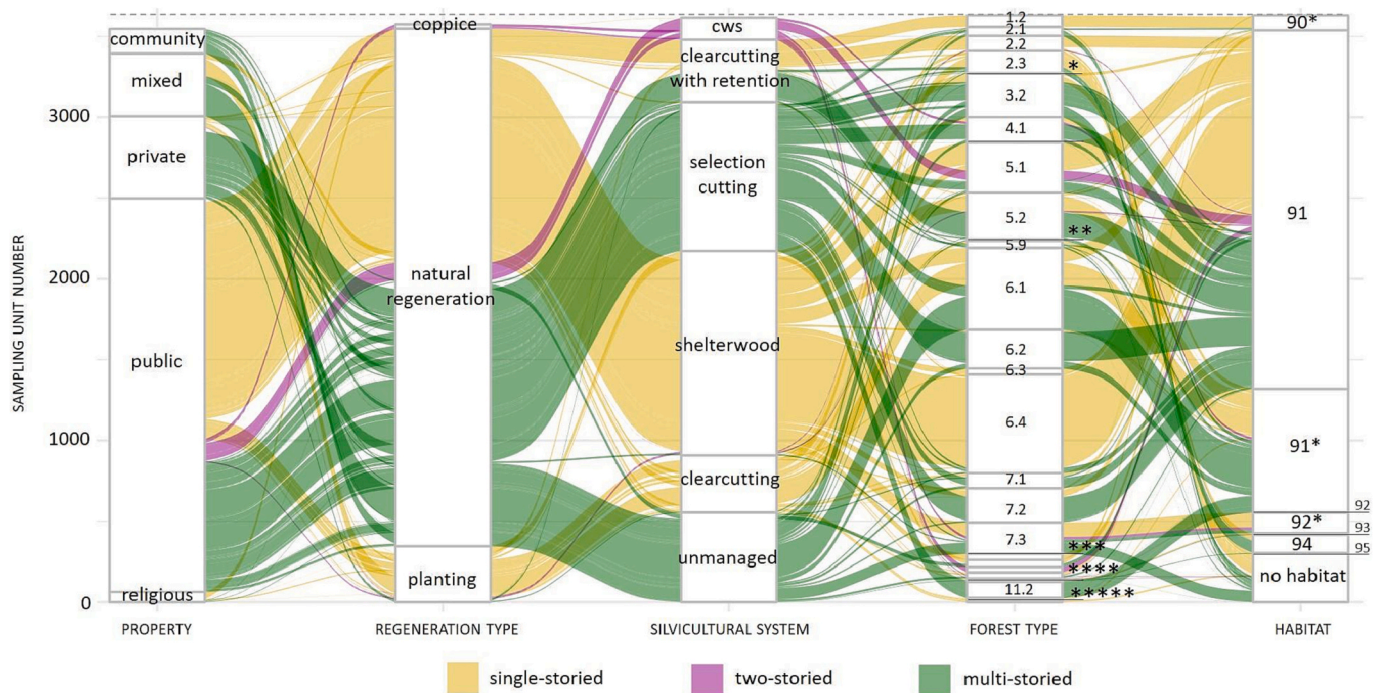
## 4. Discussion

### 4.1. Solids and voids of the existing data

This study is the first attempt, both in Europe and globally, to encompass extensive and comprehensive information on forest management, structural attributes, and multi-taxon biodiversity in a single, harmonized and publicly explorable platform.

Although we collected most data deriving from forest multi-taxon studies performed in Europe, the resulting data is unevenly distributed across compositional categories. Further efforts should thus focus on attaining a good representation for boreal, hemiboreal, thermophilous and Mediterranean compositional categories, as well as for mire, swamp, and floodplain forests. Among these, boreal and hemiboreal forests are widespread in Europe, thus their underrepresentation in the platform is a clear knowledge gap. Other categories, instead, have a limited extent across Europe, with floodplain forests displaying the lowest cover (Barbati et al., 2014). Although floodplain forests are





**Fig. 3.** One-, two-, and multi-storied forest sampling unit distribution across type of ownership, regeneration, silvicultural system (cws: coppice with standards), forest type, and habitat type. Vertical blocks represent clusters of sampling units for which the same condition (e.g., natural regeneration) occurs, with block height depending on the number of sampling units for which that condition occurred across structural types (single-, two- and multi-storied). Flows between the blocks show the combination of values for different structural types (e.g., number of one-storied plots within a public property originated from planting). In the forest type column, left numbers refer to the forest categories as reported in SI 1 and in [EEA \(2006\)](#), while the number after the dot refers to a specific type within that category (please refer to [EEA, 2006](#)). Forest types represented by less than 50 sampling units are identified by stars (\* 3.1; \*\* 4.2; \*\*\* 7.4, 7.5; \*\*\*\* 8.1, 8.2, 8.7, 8.8, 9.1, 10.1, 11.1; \*\*\*\*\* 11.3, 11.4, 12.1, 13.2, 14). In the Habitat column, sampling units are gathered in groups of habitat types divided among those having priority (followed by “\*\*”) or not, and referred to the codes: 90: Forests of Boreal Europe, 91: Forests of Temperate Europe, 92: Mediterranean deciduous forests, 93: Mediterranean sclerophyllous forests, 94: temperate mountainous coniferous forests, 95: Mediterranean and Macaronesian mountainous coniferous forests.

considered as biodiversity hotspots ([Przepióra and Ciach, 2022](#)), these habitats are nowadays not only rare in European landscapes, but occur in settings that have been profoundly altered by humans, thus characterized by high habitat fragmentation and low ecosystem integrity. For these reasons, floodplain forests should be primarily addressed by biodiversity studies, especially in view of restoration actions ([Dufour et al., 2019](#)). On the other hand, the share of sampling units referred to as priority habitat types (27 %) is higher than what is reported in terms of area, i.e., 23 % according to [European Commission \(2019\)](#), showing a great potential of the existing data in the assessment of the conservation status and relation with management of forests of primary conservation concern in Europe.

The distribution of the existing data across silvicultural systems shows a tendency among researchers to perform multi-taxon biodiversity studies in forests that are perceived as less intensively managed, such as those under selection or shelterwood management regimes. Clearcutting is represented mainly in plots related to experimental studies testing novel harvesting practices as this silvicultural system is deemed as strongly threatening forest depending species ([Savilaakso et al., 2021](#)). Unmanaged forests have often been sampled as a relevant reference in comparison to managed forests, especially if strategies that are generally perceived as sustainable are applied ([Paillet et al., 2010](#)). However, it should be noted that the unmanaged sampling units in the platform may not be associated with old-growth condition since they vary widely in terms of time passed since the last management intervention, i.e., from 20 to more than 100 years, and these differences have to be accounted for when contrasting managed and unmanaged forests within the platform.

The distribution across unmanaged, coppiced and high forests confirms that coppicing systems are relatively understudied, particularly for

multi-taxonomic biodiversity. This may be partly related to the perception of these forests as less relevant for biodiversity and related ecosystem services. Nevertheless, some studies suggest the opposite ([Hédli et al., 2010](#)) and demonstrated a certain degree of association of species of conservation concern with actively coppiced stands ([Kosulic et al., 2016](#)). This uneven distribution may also be related to the progressive reduction of coppiced forests in Europe, which are gradually being actively or passively converted into high forests, or simply abandoned ([Burrascano et al., 2017](#)). In general, the lack of multi-taxon biodiversity information from coppices represents a knowledge gap for supporting policy decisions on coppice forest management, which is especially relevant in view of their renewed prominence in climate adaptation policies and forest multifunctionality ([Cutini et al., 2021](#)).

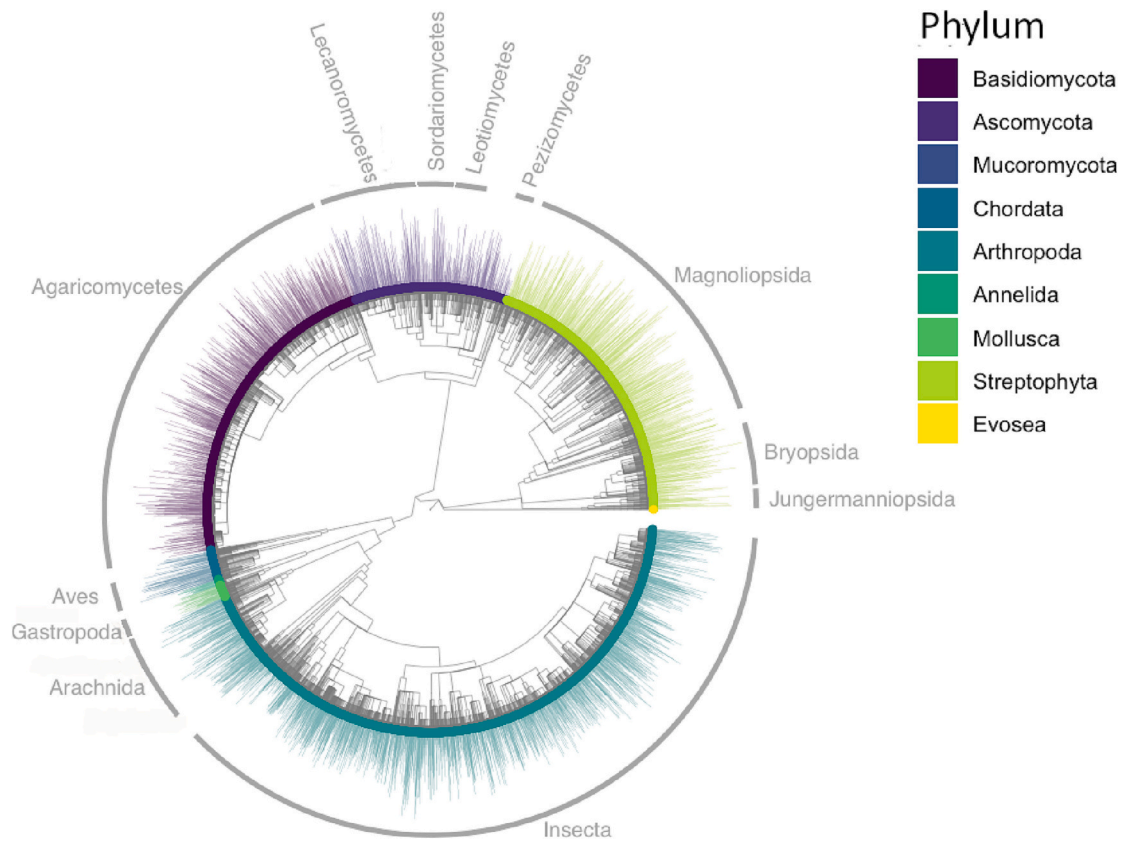
#### 4.2. Research potential and working hypotheses

Conversely to other data sharing platforms focusing on individual aspects of ecosystems, e.g., vegetation ([Bruehlheide et al., 2019](#)), forest multi-taxon studies put in place different expertise and data on the three main components of ecosystems: species composition, structure and function. As such, these data collectively have the potential to promote interdisciplinary studies and to unveil the outcomes of different conservation and management policies on the biodiversity of multiple taxonomic groups as mediated by structural stand features, e.g., the diameter distributions of standing trees and lying deadwood.

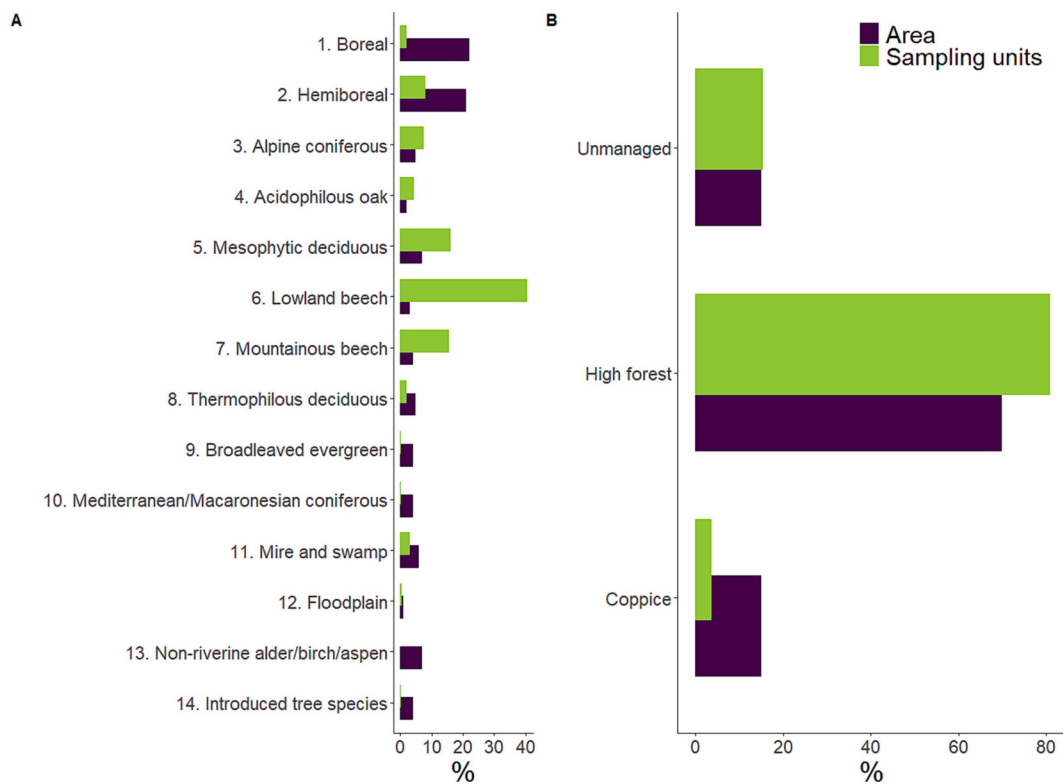
##### 4.2.1. Harmonizing methods and schemes

The joint assessment of existing forest multi-taxon biodiversity data already stimulated a harmonization effort for sampling protocols ([Burrascano et al., 2021](#)). Similarly, a harmonized platform may serve as a

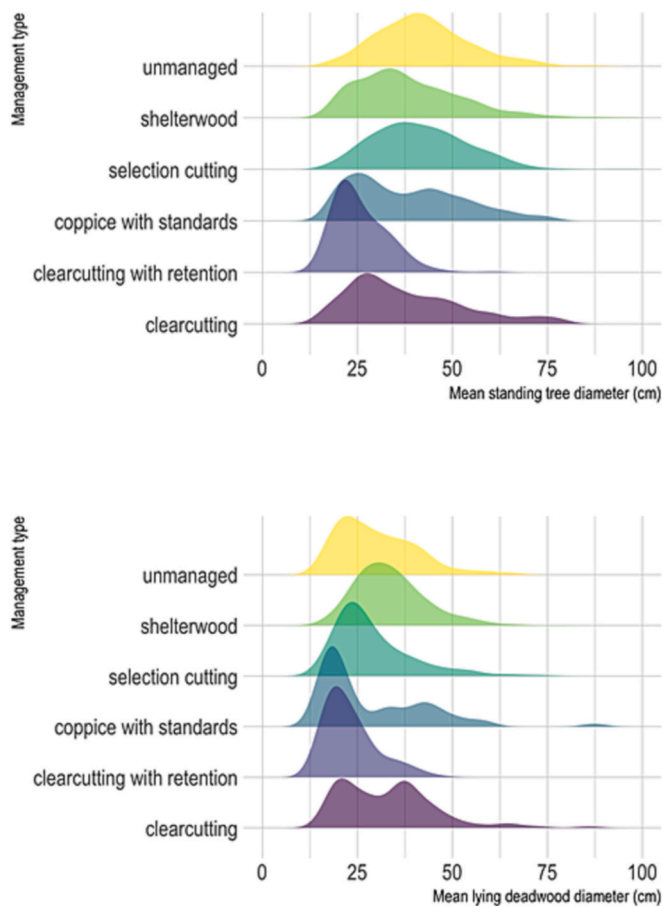




**Fig. 4.** Phylogenetic tree of the species enclosed in the data platform (7335 out of the 8724 could be included). The colored sectors refer to phyla; external bars show the log-transformed number of records for each species; gray circular sectors show the representation of the classes for which more than 50 species occur.



**Fig. 5.** A: Share of the number of sampling units and of forest area across different forest compositional categories (A) in EU-28 based on [Barbati et al. \(2014\)](#); and across two broad methods of regeneration (coppice and high forest) and the absence of silvicultural intervention (B) based on [McGrath et al. \(2015\)](#).



**Fig. 6.** Distribution of sampling unit's mean diameters for living (Diameter at Breast Height – DBH) and dead standing trees (upper portion) and lying deadwood (lower portion) across different silvicultural systems. Mean diameters were calculated after applying a lower threshold of 15 cm to limit the effect of different sampling protocols within the platform.

pilot dataset to assess the effort needed in terms of number of sampling units and sites (Guerra-Castro et al., 2021) to investigate how European forest species richness and composition changes along management and environmental conditions, respectively included in the platform and associated from external datasets. This will inform integrated European projects that could be able to provide useful information for the newborn FISE platform (Forest Information System of Europe - <https://forest.eea.europa.eu/>).

Harmonized sampling protocols and designs are relevant in view of the monitoring and conservation status assessment of forest habitat types for the implementation of the EU Habitats Directive. Important assessment criteria include the actual status and the prospects of structures and functions and typical species (Campagnaro et al., 2019). Up to date, the interpretation manual of European habitats as only a limited descriptions of typical species that mainly include vascular plants, also due to the lack of datasets and methodological frameworks for the consideration of additional taxonomic groups. Nevertheless, the need for a multi-taxon approach to habitat types' typical species has already been indicated (Tsiripidis et al., 2018) and this platform steps towards this direction.

#### 4.2.2. Implementing indicators and thresholds of forest management sustainability for biodiversity conservation

The existing knowledge paves the way to directly test biodiversity indicators of SFM and their thresholds, and to overcome the current approach of assessing forest management sustainability through proxies that mostly showed weak correlation with the *indicandum* (Gao et al.,

2015). For biodiversity sustainability, these proxies include tree composition, size and age distribution, gap structure, deadwood amount and tree-related microhabitats (Müller and Büttler, 2010; Larrieu et al., 2018). Their indirect indication is intrinsically limited (Barton et al., 2020; Zeller et al., 2022) and would need to be complemented with a direct analysis of several taxonomic groups (Burrascano et al., 2018). Recently, in addition to the usual set of indicators of forest management impact on biodiversity (MCPFE, 1993), 34 bird species were accounted for (Forest Europe, 2020), but still, most taxonomic groups contributing to forest biodiversity remain neglected. This is the case for extremely species rich groups including species of high conservation concern, such as fungi (Halme et al., 2017), and saproxylic beetles (Calix et al., 2018). The broad-scale tree level dendrometric information included in the platform may be linked to environmental factors, i.e., climate and soil, and thus contribute to the calibration of habitat-based indicators of forest ecosystem condition (Jucker et al., 2022).

#### 4.2.3. Forest functioning and resilience

Forest functions depend not only on tree species characteristics, but also on the ecological roles of several species across multiple taxonomic groups. For instance, understorey vegetation and saproxylic organisms play a key role in nutrient cycling (Landuyt et al., 2019; Seibold et al., 2021). To maintain forest functions in the face of major environmental changes, these specific functions have to be accounted for in management plans and forest policies. The recent advances in functional traits measurement and harmonization, and their increasing availability for multiple taxonomic groups (e.g., Bernhardt-Römermann et al., 2018; Moretti et al., 2017) allow to trace back the effects of different management approaches and environmental scenarios on different guilds and taxonomic groups and on their role for ecosystem functioning. Accounting for species interactions, also when studying the effect of environmental or management drivers on ecosystem biodiversity and functioning, is emphasized in recent approaches on joint species distribution modelling that could be applied to the platform data (Ovaskainen and Abrego, 2020).

#### 4.2.4. Integration with remote sensing approaches

The continent-wide information on important components of forest biodiversity that are not directly visible by means of remote sensing devices is highly valuable to test and integrate information acquired through remote sensing techniques, such as Airborne Laser Scanning. For instance, the 3591 points of the platform may serve to discriminate the probability of occurrence of different forest types that currently represents the most detailed information in Europe (Mücher and Henekens, 2019). The platform information may be used to integrate and improve multi-scale ecosystem assessment by fine-tuning the links between structural diversity measured by means of Airborne Laser Scanning and multi-taxon biodiversity (Moeslund et al., 2019). Furthermore, specific habitat variables that could be derived from Airborne Laser Scanning were recently identified to improve species distribution models (Moudry et al., 2023), and to model dark diversity (Moeslund et al., 2022), and such advancements would highly benefit from broad-scale harmonized multi-taxon information.

#### 4.3. Conservation implications

The European Union Biodiversity Strategy for 2030 is focused on protected areas and its main objectives are to legally protect a minimum of 30 % of land area, which should be effectively managed and appropriately monitored, and to strictly protect at least a third of such protected areas. In this view, gathering and harmonizing the available information on forest multi-taxon biodiversity can promote the widespread collection of forest biodiversity data through shared approaches and methodologies, with a special emphasis on understudied forest types, which are often also particularly relevant for biodiversity conservation, e.g., floodplain or thermophilous forests.

The availability of widespread forest multi-taxon biodiversity and stand structure information at the continental scale will allow to prioritize forest areas to be protected, or strictly protected, and will set the basis for their appropriate monitoring, in line with the current Biodiversity Strategy.

On the other hand, the European Union Forest Strategy for 2030 is focused on the sustainability of forest management, within and outside protected forests. This would start from the identification of additional indicators, as compared to those assessed by Forest Europe, with thresholds or ranges for SFM concerning forest ecosystem conditions, including biodiversity.

The availability of extensive multi-taxon biodiversity data would allow to define such indicators of management sustainability, as well as their thresholds and ranges, based on their direct links with the diversity of multiple taxonomic groups with different functions in forest ecosystems. This would represent a crucial step forward from the current criteria and indicators whose effectiveness for biodiversity is questionable.

The EU Forest Strategy also stresses how management sustainability indicators, and their thresholds and ranges, should be built on existing work and take into account forest variability, biogeographic regions and forest typology. Our work is perfectly in line with this statement, since we reviewed and valued existing data on forest biodiversity by accounting for different forest habitats, compositional and management categories. Refining indicators of SFM will feed guidelines on closer-to-nature forestry that will be translated into voluntary certification scheme, so that the most biodiversity friendly management practices could benefit from an EU quality label.

Europe has a leading role in the improvement of forest protection and management standards globally. By supporting the objectives of the EU biodiversity and forest strategy, we think that, in the long-term, our work may lead to the improvement of indicator schemes across multiple regions and support an increased sustainability of forest management globally.

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.biocon.2023.110176>.

#### Author contribution

SB, PO, FC, GT, SKR, JHC, TS, FT, YP and ID developed the idea for this manuscript. SB, FC, GT, TC, SKR, TS, LB, EA, RBA and FN collected and harmonized the data. FC, SKR, SB, GT, LB, EA ran the analyses. DM, CP, JN, PG, NR, TL, CB, PO, JHC and FN revised the taxonomic nomenclature and substrate association. All the authors but EA, RBA, DM, CP, NR and FN contributed data. All the authors contributed to the text.

#### Declaration of competing interest

Neither I nor any co-authors have any conflict of interest related to this manuscript, i.e., we exclude any financial and personal relationships with other people or organizations that could inappropriately influence (bias) their work.

#### Data availability statement

All the data used in this manuscript are provided in the supplementary material available at this link <https://zenodo.org/record/7886698>.

An interactive tool for their exploration and filtering, as well as instructions for proposing a project with the data here presented are available at: <https://www.bottoms-up.eu/en/participants/contribute/propose-a-project.html>. Data may be requested for specific projects as described at this link: <https://www.bottoms-up.eu/en/participants/contribute/propose-a-project.html>.

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