

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

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# ▶ To cite this version:

Sabina Burrascano, Francesco Chianucci, Giovanni Trentanovi, Sebastian Kepfer-Rojas, Tommaso Sitzia, et al.. Where are we now with European forest multi-taxon biodiversity and where can we head to?. Biological Conservation, 2023, 284, pp.110176. 10.1016/j.biocon.2023.110176. hal-04185032

HAL Id: hal-04185032 https://hal.inrae.fr/hal-04185032

Submitted on 22 Aug 2023

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WHERE ARE WE NOW WITH EUROPEAN FOREST MULTI-TAXON BIODIVERSITY AND WHERE CAN WE HEAD TO?

3 ABSTRACT

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- 4 Forestry implementation significantly impacts forest biodiversity. Despite the promotion of
- 5 Sustainable Forest Management (SFM) in Europe, sustainability assessments hardly account for
- 6 direct biodiversity indicators. We aim to i) gather and map the existing information on forest multi-
- 7 taxon biodiversity associated with stand structure and management in Europe; ii) identify knowledge
- 8 gaps for forest biodiversity research; and iii) discuss the research potential associated with multi-
- 9 taxon biodiversity data.
- 10 We established a research network focused on multi-taxon biodiversity, stand structure and
- management data of European forests; and fitted species records, standing trees, lying deadwood,
- and sampling unit metadata from 34 local datasets.
- Suitable information was available for 3,591 sampling units, each surveyed for on average 4.6
- taxonomic groups. Standing tree diameters, tree height deadwood and tree-related microhabitats
- were sampled in respectively 2,889; 2,356; 2,309 and 1,388 sampling units. Sampling unit metadata
- includes spatial coordinates, and compositional and management descriptors.
- 17 Available data cover all the 14 European forest compositional categories but are unevenly distributed
- among them, with European beech forests being over-represented as compared to thermophilous
- 19 and boreal forests.
- 20 Overall, the available information has the potential to inform the development of conservation and
- 21 SFM strategies for European forests by supporting: (i) methodological harmonization and
- coordinated monitoring; (ii) the definition and testing of SFM indicators and thresholds; (iii) data-
- 23 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
- 25 sensed information.

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# **INTRODUCTION**

- 28 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
- 30 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 SFM on the diversity of multiple taxonomic groups, hereafter multi-taxon biodiversity, are not sufficiently known due to the high demands of multi-taxon biodiversity sampling and analysis, which requires significant 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 unmanaged 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). 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.

# **M**ETHODS

## 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 & 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.*, submitted). 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 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).

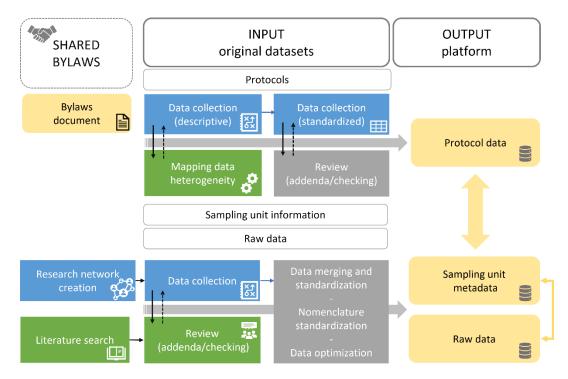


Figure 1. Workflow of the platform building process. Blue boxes identify in-progress products; green boxes identify phases of common decisions, brainstorming and comparison with scientific literature; gray boxes indicate data processing; yellow boxes are the outcomes.

## **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 (Tab. 1).

| 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) |  |  |  |

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

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 & 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 (<a href="https://www.gbif.org/">https://www.gbif.org/</a>). 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: XXX 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 (XXX). 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: XXX. A Shiny Web-App (XXX) was created to smooth the proposal of projects by allowing for data exploration and filtering based on the sampling unit metadata (SI-2).

## 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

177 in McGrath et al. (2015). Sampling unit metadata were visualized through alluvial plots using the 178 'ggalluvial' R-package (Brunson, 2020). 179 The distribution of species and species records across higher taxonomic ranks (phyla and classes) was 180 represented through a phylogenetic tree, encompassing 7,335 out of the 8,724 species of the 181 platform. The tree was obtained through PhyloT (https://phylot.biobyte.de/) in Newick format and 182 imported in R through the 'ape' package (Paradis & Schliep, 2019). To each species in the tree we 183 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 184 185 using the 'ggtree' package (Yu et al., 2017). In addition to the mentioned check for plausible ranges of values, structural data were subjected to 186 187 specific integration processes. Heights of standing trees were integrated by means of heightdiameter relationships (hypsometric models); whereas deadwood fragments measurements were 188 189 integrated through data imputation performed using the 'mice' package (van Buuren & Groothuis-190 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 191 the variation in imputed values when treated as real, and including forest compositional categories 192 193 and types, and spatial variables (plot and site). Few datasets lacked any measures of height/length 194 and were integrated by using the whole data platform. A total of 42,643 tree heights out of 178,098 195 were calculated by means of hypsometric models; and 5,011 diameters and 9,317 lengths were 196 imputed out of 58,824 lying deadwood fragments. Based on these data, the distributions of sampling 197 unit mean of Diameter at Breast Height (DBH) for standing trees and of diameter for lying deadwood were calculated (SI-4, SI-5). 198 199 Biodiversity and stand structure indices may be related to environmental conditions by using 200 parameters published in the framework of other research projects. For instance, each sampling unit 201 was spatially associated with data on soil characteristics that were obtained from the European 202 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 203 204 from the center of the sampling unit are: Available Water Capacity, Bulk density (derived from soil 205 texture datasets), Soil textural classes derived from clay, silt, and sand maps. Similarly, climatic data 206 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).

# **RESULTS**

## OVERVIEW OF THE EXISTING DATA

# Sampling units

A total of 3,591 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 (Tab. 2) and 185 researchers.

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 Groote et al., 2017     |
| BE_KV1     | BE      | 5       | 462     | Vandekerkhove et al., 2016 |
| CH_TL      | СН      | 1       | 69      | Haeler 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., 2017     |
| 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             |

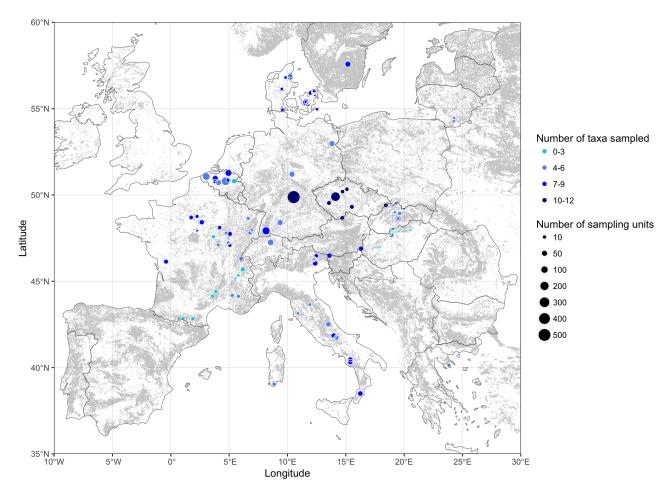


Figure 2. Distribution of the platform sampling sites in Europe. Grey areas are covered by forests with a tree cover greater than 40% according to the European Forest Institute Forest Map of Europe (Kempeneers *et al.*, 2011). Number of taxa are represented by color, while number of sampling units by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

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).



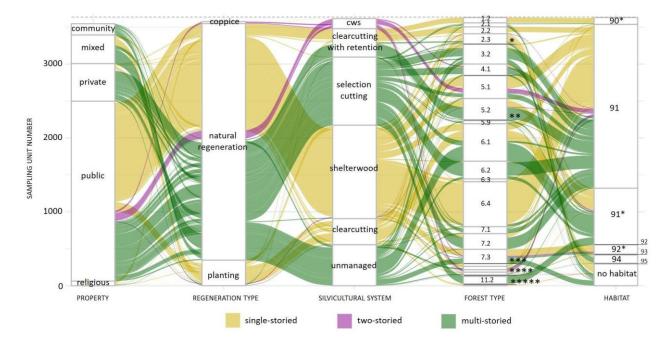


Figure 3. One-, two-, and multi-storied forest sampling unit distribution across type of ownership, regeneration, silvicultural system (cws: coppice with standards), forest type, and habitat type. Vertical blocks represent clusters of sampling units for which the same condition (e.g., natural regeneration) 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.

# 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 8,724 species, 2,979 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. The plots with information on only one or two taxonomic groups have information on at least three taxonomic groups at the stand level, as required by the platform bylaws.

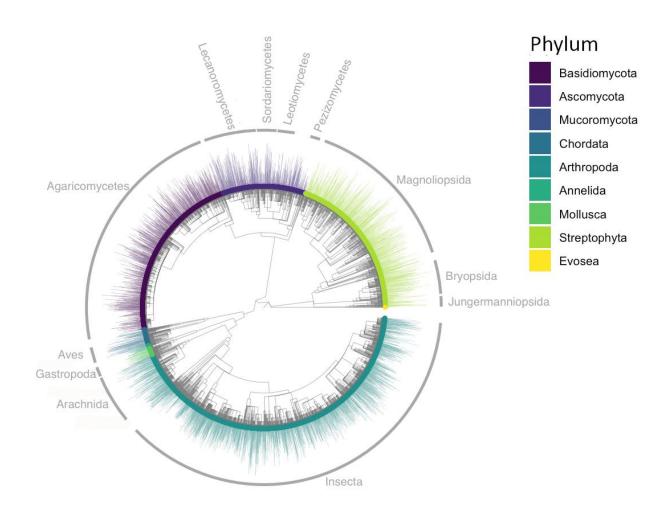


Figure 4. Phylogenetic tree of the species enclosed in the data platform (7,335 out of the 8,724 could be included). The colored sectors refer to phyla; external bars show the log-transformed

number of records for each species; gray circular sectors show the representation of the classes for which more than 50 species occur.

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., *Insecta* (3,244 species across 88,338 records), *Agaricomycetes* (2,077 species across 44,418 records), *Magnoliopsida* (1,182 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 (5,082) among all species in the platform (see also Blasi et al., 2010). On the other hand, *Insecta*, *Magnolipsida* 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 sinlgetons vs. less than 3% for *Bryopsida*.

#### 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 2,889 sampling units, with additional data on tree height, deadwood and tree-related microhabitats in respectively 2,356, 2,309, and 1,388 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).

## **G**APS IN KNOWLEDGE

298 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).

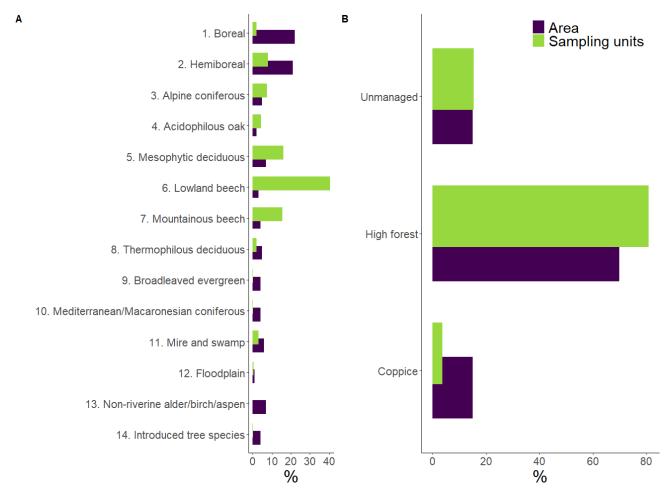


Figure 5. A: Share of the number of sampling units and of forest area across different forest compositional categories (A) in EU-28 based on Barbati *et al.* (2014); and across two broad methods of regeneration (coppice and high forest) and the absence of silvicultural intervention (B) based on McGrath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

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

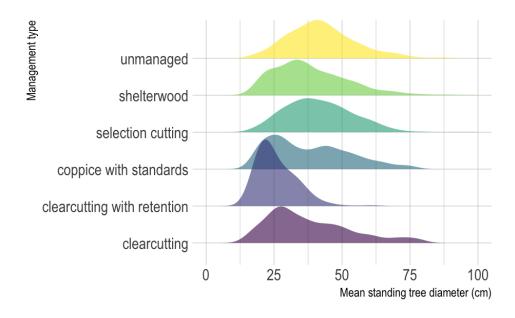
regenerated, with shelterwood and selection cutting systems being by far the most represented, and single- and multi-storied forests being similarly frequent (Fig. 3).

## 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.

## 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, with consequences on the representation of species related to different phases of the forest succession (Hilmers *et al.*, 2018), especially of the earliest.



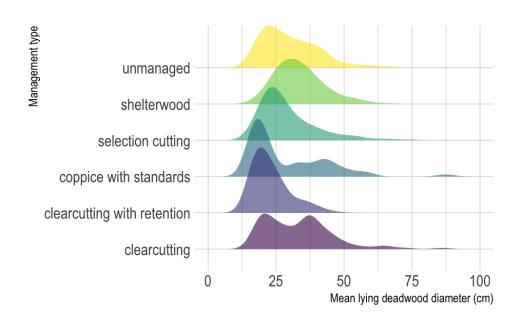


Figure 6. Distribution of sampling unit's mean diameters for living (Diameter at Breast Height – DBH) and dead standing trees (upper portion) and lying deadwood (lower portion) across different silvicultural systems. Mean diameters were calculated after applying a lower threshold of 15 cm to limit the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

# DISCUSSION

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# 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 considered as biodiversity hotspots (Przepióra & 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 perceived 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 (Hédl *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).

#### RESEARCH POTENTIAL AND WORKING HYPOTHESES

Conversely to other data sharing platforms focusing on individual aspects of ecosystems, e.g., vegetation (Bruelheide 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.

#### 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 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 - <a href="https://forest.eea.europa.eu/">https://forest.eea.europa.eu/</a>).

Harmonized sampling protocols and design 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.

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 & Bütler, 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).

## 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 & Abrego, 2020).

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 3,591 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 & Hennekens, 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 (Moudrý *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.

## **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.

464 The availability of widespread forest multi-taxon biodiversity and stand structure information at the 465 continental scale will allow to prioritize forest areas to be protected, or strictly protected, and will 466 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 467 forest management, within and outside protected forests. This would start from the identification of 468 469 additional indicators, as compared to those assessed by Forest Europe, with thresholds or ranges for 470 SFM concerning forest ecosystem conditions, including biodiversity. The availability of extensive multi-taxon biodiversity data would allow to define such indicators of 471 472 management sustainability, as well as their thresholds and ranges, based on their direct links with 473 the diversity of multiple taxonomic groups with different functions in forest ecosystems. This would 474 represent a crucial step forward from the current criteria and indicators whose effectiveness for biodiversity is questionable. 475 476 The EU Forest Strategy also stresses how management sustainability indicators, and their 477 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 478 479 we reviewed and valued existing data on forest biodiversity by accounting for different forest 480 habitats, compositional and management categories. Refining indicators of SFM will feed guidelines 481 on closer-to-nature forestry that will be translated into voluntary certification scheme, so that the 482 most biodiversity friendly management practices could benefit from an EU quality label. 483 Europe has a leading role in the improvement of forest protection and management standards 484 globally. By supporting the objectives of the EU biodiversity and forest strategy, we think that, in the 485 long-term, our work may lead to the improvement of indicator schemes across multiple regions and 486 support an increased sustainability of forest management globally. 487 DATA AVAILABILITY STATEMENT 488 All the data used in this manuscript are provided in the supplementary material available at this link 489

An interactive tool for their exploration and filtering, as well as instructions for proposing a project with

the data here used are available at: XXX. Additional data may be requested for specific projects as

https://zenodo.org/record/7886698.

described at this link: XXX.

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