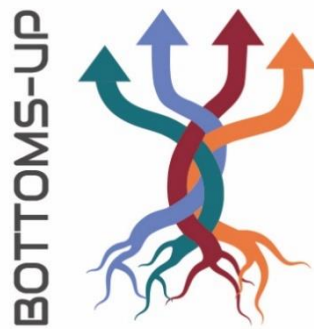


COST ACTION BOTTOMS-UP

BIODIVERSITY OF TEMPERATE FOREST TAXA ORIENTING MANAGEMENT SUSTAINABILITY BY UNIFYING PERSPECTIVES

CA18207



WORKING GROUP 1

TOWARDS COMMON TOOLS FOR FOREST MULTI-TAXON RESEARCH AND MONITORING

DELIVERABLE 1

PLATFORM DESCRIPTION

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with the contribution of all consortium members listed in Annex 2



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INTRODUCTION

Human activities represent an increasing threat to biodiversity and ecosystem functions, which in turn has negative impacts on human wellbeing worldwide (Díaz et al., 2019). Each year €3.5-18.5 trillion in ecosystem services are lost due to the biodiversity decline related to land-cover change, and €5.5-10.5 due to land degradation (OECD, 2019).

Forests provide habitat for about three-quarters of terrestrial plant, fungi and animal species (*Global Forest Resources Assessment, 2020*). At the same time, forests are an essential source of necessary goods and services. The increasing concerns related to forest ecosystem health and biodiversity impose a shift in paradigm from single-objective forest management (e.g., focused productive functions) to embrace the multifunctionality of service and goods provided by forests, while maintaining and enhancing ecosystem functionality and diversity. Therefore, a combined strategy of protected areas (land sparing) and integration of conservation goals in multifunctional forests (land sharing) is needed (Bollman & Braunisch, 2013). In this view, sustainable forest management is globally recognized as a crucial tool for contrasting biodiversity loss, and to promote sustainable development (UN, 2015).

Although about 12% of European forests are protected for biodiversity conservation (Forest Europe, 2015), only a minority of them (8% of protected forests) is not subjected to interventions (Forest Europe, 2015), resulting in only 0.7% of European forests recently mapped as primary (Sabatini et al., 2018). Within this framework, and notwithstanding the call of the 2030 EU Biodiversity Strategy for an increase in the share of strict reserves, the sustainability of forest management is crucial to maintain forest biological diversity in Europe, also in the perspective of increasing the quantity, quality and resilience of European forests.

Nevertheless, indicators for forest management sustainability with special reference to the maintenance of biodiversity either account only for tree species (e.g. stand structural indicators, tree species composition, regeneration, threatened forest species), or are landscape scale indicators (e.g., naturalness, fragmentation, protection) often not definitively tested (Gao et al., 2015).

Stand structural indicators related to tree size and age distribution, gap structures, dead wood amounts and presence of tree microhabitat structures are often used as biodiversity indicators (e.g. Larsson et al., 2001; Müller & Bütler, 2010; Larrieu et al., 2018). In most cases, however, their value is limited to specific taxa and contexts (Burrascano et al., 2018).

Overall, neither information on tree species composition and structure, nor landscape scale parameters represent highly effective indicators of forest biodiversity (Fuller, Ondei, Brook, & Buettel, 2019; Barton et al., 2020; Volenec & Dobson, 2020). Indeed, the richness and complexity of forest biodiversity requires the direct analysis of several taxonomic groups to soundly assess its key drivers and guide sustainable management (Burrascano et al., 2018).

Only recently, it was planned to include common bird species as a direct indicator of forest management sustainability (Forest Europe, 2015). Also in this case most taxonomic groups making up

forest biodiversity remain neglected, although some of them include species of high conservation concern as it is the case for about 20% of saproxylic beetles (Calix et al., 2018), or are essential for forest ecosystem functioning, such as fungi (Brunialti et al., 2020).

Multi-taxonomic biodiversity sampling is usually not included in forest inventories since it requires relevant resources in terms of money, time, and, especially, of a diverse range of expertise and competences. In addition, sampling different taxonomic groups entails different spatial scales and sampling schemes, therefore poses challenges for the spatial integration of multi-taxon information within a forest stand. Recently, several research institutions took up the challenge of multi-taxonomic field sampling. The majority of these research projects are local or regional, with single- to multiple-site sampling that are designed to address specific research questions. The effects of forest structure and management on biodiversity are by far the most common topics in such studies (Van Loy et al., 2003; Király et al., 2013; Sabatini et al., 2018; Elek et al. 2018, Byriel et al. 2020).

Although local, these projects invested considerable resources in collecting data for several biodiversity, structural, environmental and management variables, whose use at the continental scale is hampered by a lack of harmonization and integration.

The COST Action BOTTOMS-UP - *Biodiversity Of Temperate forest Taxa Orienting Management Sustainability by Unifying Perspectives* (CA18207) formed a synergy across the different research groups that collected multi-taxon data at local or national scales. It addresses the challenge of switching forest multi-taxon biodiversity monitoring and study from the local to the continental scale. The first step of the Action was to build the most comprehensive dataset of European forest biodiversity by standardizing and merging the existing information collected by multi-taxon studies associated with forest structural and management information. The aim is to establish a standardized and open platform for sharing data on biodiversity, structure, and management of European forests.

The wide participation in the Action (30 European countries) as well as the high degree of interest overlap between the parties, allowed for a successful collection of relevant information on European forest ecosystems in general, beyond the original Action focus on temperate forests only. This would not have been possible without a trust-building process that was one of the main achievements in the first year of the Action.

The platform will have multiple outcomes and benefits for the knowledge of European forests. Preliminary objectives are to use the platform to: (i) establish a network of forest sites with baseline multi-taxon, structure and management information; (ii) define a shared standard for sampling protocols; (iii) develop a common understanding of the relationships between forest management, structure and biodiversity in European forests; (iv) defining an improved set of indicators of sustainable forest management; (v) coordinate forest manipulation experiments across Europe; and ultimately (vii) define sustainable management guidelines to be applied foremost within forests that are under specific certification schemes and within protected areas.

METHODS

Building the platform included both technical and networking steps (Fig. 1). Merging data was prepared by a survey of the available information, based on which the structure of the platform was built. In parallel, a strong basis for agreement and confidence has to be built to provide the conditions for data contribution and exchange. As highlighted by the two-way arrows of the workflow (Fig. 1), there was (especially in the first phases of data collection and bylaws drafting) a large amount of work of progressive adjustment of the data based on one-to-one or common discussions and meetings.

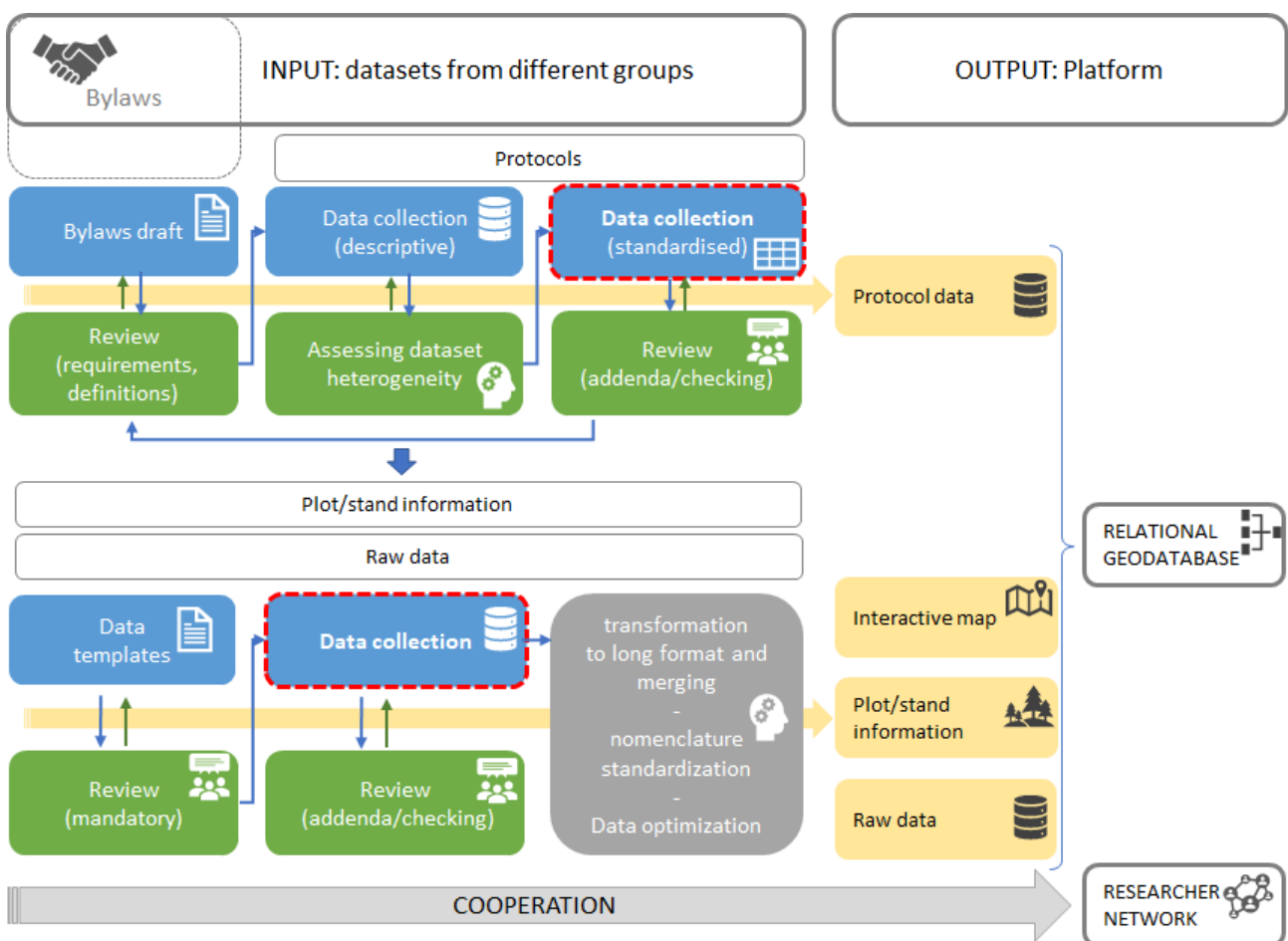


Figure 1. Workflow of platform building. Blue boxes identify milestones; green boxes identify phases of common decisions and brainstorming; the grey box indicates data processing; in yellow are the outcomes of the platform building process.

GOOD AGREEMENTS MAKE GOOD FRIENDS: SHARED BYLAWS AS A BASIS FOR A CONFIDENCE NETWORK

The first step towards the platform was to found a consortium and agree on common bylaws. The founding consortium was identified in those proposers and MC members that were willing to contribute data to the platform. This group of researchers agreed on a set of bylaws (Annex 1).

The bylaws are composed of eight regulation articles partly based on previous experiences of shared datasets. As it is always the case in the beginning of these sharing processes, a give-and-take approach has been chosen. This means that joining the consortium is possible for researchers that provide a dataset complying with specific requirements and provides the right to use the entire set of available data in the platform through specific procedures under the limits and possibilities reported in the bylaws.

The bylaws include the general aim of the platform, agreed definitions of specific terms, details on data requirements, description of the consortium structure and rules for proposing publications that use the platform's data and for the co-authorship to such publications.

Some articles (e.g. those regarding data availability regimes and authorships) of the bylaws were particularly detailed since multi-taxon data are, by definition, the outcome of the work of numerous teams, with interdisciplinary effort involved. Therefore, specific mechanisms were described to allow for a fruitful collaboration between numerous and relatively large research groups. By providing written bylaws, researchers are easily informed on the intentions and procedures of the platform and are therefore more willing to contribute data.

Bylaws also support the communication of the platform with other research groups potentially interested in joining it. This was the case for the Biodiversity Exploratories (<https://www.biodiversity-exploratories.de/en/home>), a database composed by three platforms under the same project funded by the German Science Foundation. In this case, the coordinators of the Biodiversity Exploratories were informed through the bylaws of the aims and intentions of the BOTTOMS-UP platform and based on this an official agreement was established between the two projects. Based on it, the metadata of the forest dataset for the Biodiversity Exploratories were included in BOTTOMS-UP, and data will be provided based on the needs of the different publications that will derive from the platform.

In general, the bylaws rely on one data custodian for each dataset that is responsible for handling the data and that will also manage the relationships between the platform and all the contributors of his/her dataset (see art. 1 of Bylaws). Being included in the consortium means being invited to all the publications deriving from the platform and having the possibility to propose new publications that take advantage from the platform (see art. 2 of Bylaws).

Since some Action participants did not have the possibility to contribute with data fitting the bylaws requirements, a specific call was made for participants who wanted to help in harmonizing and merging data that have been included in the consortium (see art. 2 of Bylaws).

PLATFORM STRUCTURE

The Action participants designed a workflow by agreeing on a specific structure for a multidisciplinary platform such as BOTTOMS-UP.

The first step was to collect methodological metadata for each available dataset to define the amount and heterogeneity of the sampling approaches within the platform. Such metadata included both very general information (e.g., data custodian, country, number of sites and plots) and detailed information on sampling protocols that are being used for the development of the “Handbook for multi-taxon and forest structure sampling” that will represent a further deliverable of the Action.

The structure of the overall platform and of the template tables for collecting the data was discussed in several meetings and call conferences.

The outcome of this process was a database consisting of four groups of data:

1. plot/stand description data;
2. standing trees;
3. lying deadwood;
4. multi-taxon composition.

The platform structure was designed to allow for effective relations across tables based on the dataset ID and on IDs for sites, stands and plots. Contributed data collected in the framework of a single project, therefore sharing sites, aims and methodologies were identified by a univocal dataset ID. It is formed by the acronym of the country where the data were sampled plus the initials of the data custodian.

Table structure aimed at receiving harmonized information from the whole set of data custodians. Therefore, some fields were to be filled mandatorily, others could be filled in only using a predefined set of values. Templates of the tables to contribute data to the platform are available at the Action website.

Plot/stand description table includes several information on the location, general composition, structure, and type of management of the sampled forest stands. Two key variables within this table are forest category and silvicultural system. The former refers to the broader classification into compositional categories defined by the European Environmental Agency (EEA, 2006); while the second refers to a classification of applied silvicultural operations (hereafter silvicultural systems) based on the type of regeneration cut that is performed in each plot/stand according to Matthews (1989). Tables two, three and four are raw data tables (Fig. 1) including information for each plot at the level of species record, standing tree and deadwood element, respectively. Together with these tables the information on data custodians and contributors was collected as a basis for a broad consortium of researchers.

While data custodians proceeded with data entry within the proposed tables, a group of COST Action participants with skills in managing data through R (R Core Team 2020) software discussed the best method to validate, organize and harmonize data in a shared database that could serve the analyses needed for the Action aims. The choice of managing data through R is motivated by two key advantages:

- the development of a code that uploads, checks and merges the data table will allow for future additions to the platform in a semi-automatic way, thus with limited time investment;
- R is an open source software used by most Action participants and widely used by scientific communities.

The R specialist team within the Action organized a specific meeting firstly focusing on a proper online platform to develop a joint code and collaborate managing versioning issues effectively. Finally, a private repository on the platform was created with the name of the Action (<https://github.com/bottoms-up/bottoms-up>).

As soon as the tables relative to a dataset are uploaded in the platform, data check for quality is performed. Data inconsistencies that may have originated from errors in user entries (e.g. typographical errors), data type storage, species nomenclature and adherence of datasets to the table structure (e.g. column names, list of values allowed) are progressively checked by two participants independently (Francesco Chianucci and Sebastian Kepfer-Rojas). Some validation rules have been set for all those inconsistencies that can be checked in an automatic or semi-automatic way based on data range, length, column reference name, list values, null values, blank values, and data types. Examples of data validation rules included data type constraints (e.g. values in a field must meet the desired data type) and range constraints (minimum and maximum values allowed for numerical variables). Nomenclature for all the sampled taxa was checked using the 'gnr_resolve' functionality of taxize package in R (Chamberlain et al. 2013). Higher level taxonomic information was obtained from the National Center for Biotechnology Information, accessed through the taxize and myTAI packages (Drost et al. 2018).

After this validation process, most of the data have been reviewed, checked, and automatically corrected. Many missing or wrong information (e.g., error in reported coordinate reference system EPSG code) requiring back-checking to each data custodian are under processing (Fig. 16).

RESULTS

Up to now 28 datasets out of 39 for which we collected protocol data (Table 1) have been provided in a complete version that could be already included in the platform, i.e., without major inconsistencies.

Currently the platform stores a total of 2,868 plots covering 12 European Countries (Fig. 2), and involving a total of 131 researchers among data custodians and contributors (Annex 2).

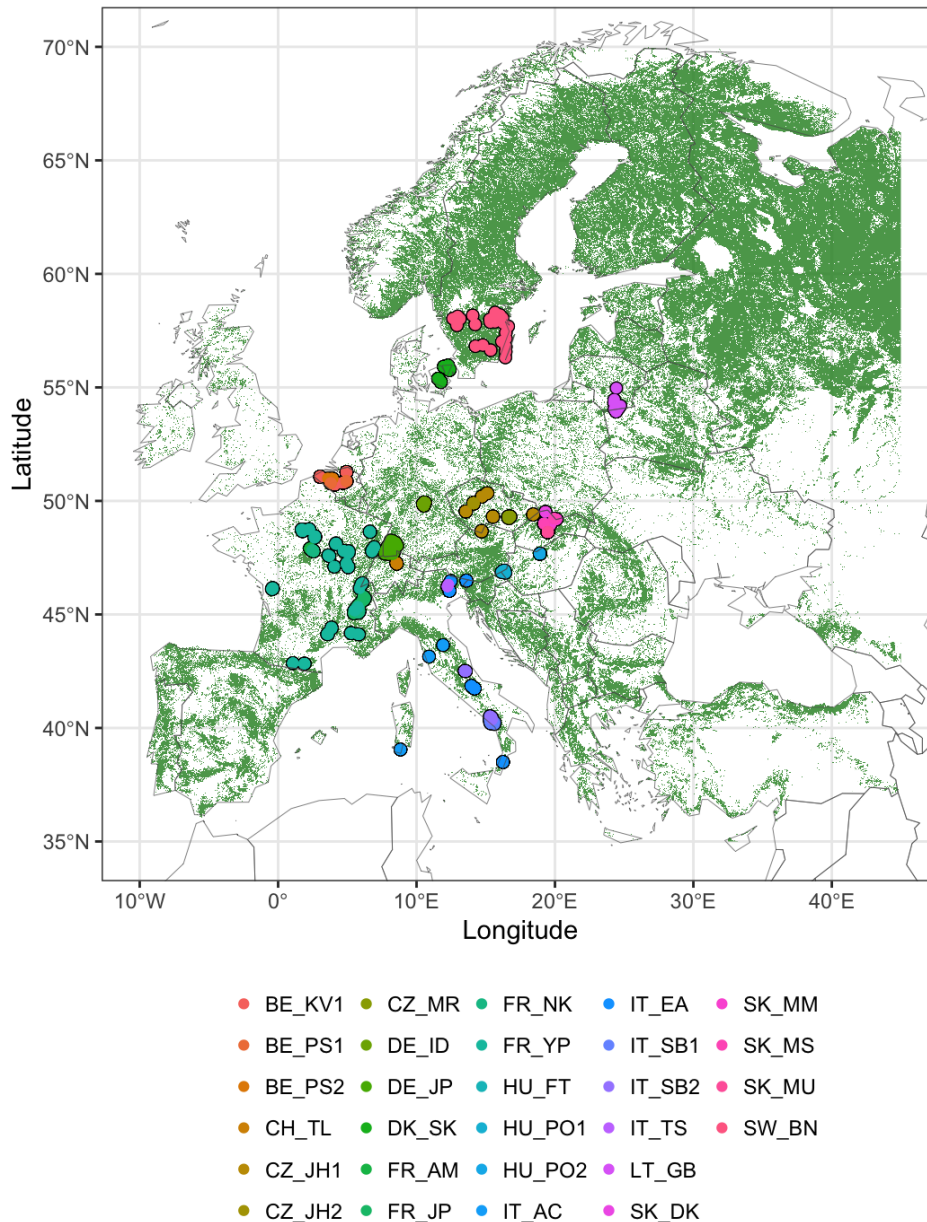


Figure 2. Distribution in Europe of plots/stands included in the platform classified by dataset ID. The first two letters of each dataset indicate the country, the last two are the initials of the dataset custodian. Green areas are those covered by forests by more than 40% according to European Forest Institute (EFI) Forest Map of Europe 2011. Details available at: Kempeneers et al., (2011); Päivinen et al., (2011); Schuck et al., (2002).

According to the bylaws, the datasets we considered for building the platform, should include data on multiple taxonomic groups and forest structure and management. Especially, by multi-taxon, we intended those studies including data on a minimum of three taxonomic groups, representing at least two from each of the following broad groups of organisms: Plantae, Fungi and Animalia, and including at least one taxonomic group of the Animalia kingdom. Taxonomic groups span heterogeneous taxonomic ranks ranging from kingdom to orders and in some cases include only specific morphological or ecological groups commonly used in sampling and identification (e.g. macrofungi, saproxylic coleoptera).

TAXONOMIC COVERAGE AND DISTRIBUTION

The dataset comprises a wide range of taxonomic groups across the kingdoms of animals, plants, and fungi. The taxonomic groups sampled most often in European multi-taxon forest biodiversity studies included are: vascular plants (Tracheophyta), bryophytes (Bryophyta and Marchantiophyta), lichens, beetles (Coleoptera in general or individual families), birds (Aves), fungi (Basidiomycota), bats (Chiroptera) and spiders (Araneae).

Table 1 Broad categories of regeneration type, Forest categories, Taxa represented in each dataset (dataID). N refers to the highest number of plots available in each dataset, i.e., for the taxon/taxa sampled across the highest number of sampling units.

dataID	Regeneration type	Category	Taxa	N
BE_KV1	high forest, coppice	4,5,6,11	ARA, BIR, BRY, COL, FUN, LIC, VAS	625
BE_PS1	high forest	5	ARA, CAR, DIP, FUN, ONI, OPI, VAS	32
BE_PS2	high forest	4,6	ARA, BIR, CAR, DIP, ONI, OPI, VAS	53
CH_TL	high forest	7	BRY, COL, FUN, HET, LIC	69
CZ_JH1	high forest	5,6,7,14	BIR, BRY, COL, FUN, LIC, VAS	482
CZ_JH2	high forest	5,6,14	BRY, CAR, FUN, VAS	227
CZ_MR	high forest	5	ANN, COL, VAS	1845
DE_ID	high forest	6	BAT, BIR, BRY, COL, FUN, HET, LIC, VAS	69
DE_JP	high forest	7	BAT, BIR, BRY, COL, IXO, LEP, LIC, MAM, VAS	135
DK_SK	high forest	6	BRY, CAR, FUN, LIC, STA, TYP, VAS	390

dataID	Regeneration type	Category	Taxa	N
FR_AM	high forest	6	BIR, BRY, CAR, COM, GAM, LIC, MAM, ORI, ROD, VAS	63
FR_JP	high forest	3	COL, LIC, VAS	70
FR_NK	high forest	6	BRY, COM, GAM, ORI	32
FR_YP	high forest	3,4,5,6,7	BAT, BIR, BRY, CAR, COL, FUN, VAS	307
HU_FT	high forest	5	ARA, COL, ENC, VAS	36
HU_PO1	high forest	5	ARA, BIR, BRY, CAR, FUN, LIC, VAS	35
HU_PO2	high forest	5	ARA, COL, ENC, TYP, VAS	30
IT_AC	coppice	7,8,9	BIR, FUN, LIC, VAS	18
IT_EA	high forest, coppice	3,6,7,8	AMP, BAT, BIR, CAR, COL, DIT, REP, VAS	135
IT_SB1	high forest, coppice	7,8,9,13	BIR, BRY, COL, FUN, LIC, VAS	33
IT_SB2	high forest, coppice	7	BIR, COL, FUN, LIC, VAS	33
IT_TS	high forest	3	BIR, CAR, CER, FUN, LIC, SCO, VAS	20
LT_GB	high forest	1,2	BIR, BRY, HYM, LIC, VAS	174
SK_DK	high forest	3	BIR, COL, FUN, LIC	18
SK_MM	high forest	3	BIR, COL, FUN, LIC	22
SK_MS	high forest	3	BIR, COL, FUN, LIC	29
SK_MU	high forest	7,14	FUN, GAS, SOI, VAS	65
SW_BN	high forest	2	BRY, COL, DIT, FUN, GAS, LIC, VAS	60
BE_KV2	high forest	4,5,6,11	ARA, BIR, COL, VAS	204
DE_PS	NA		ARA, BIR, BRY, COL, FUN, HET, HYM, LIC, MAM, OPI, SOI, VAS	150
DK_JC1	NA		BIR, BRY, COL, FUN, LIC, VAS	400
DK_JC2	NA		BIR, BRY, FUN, LIC, VAS	107
DK_JC3	NA		BIR, BRY, COL, FUN, LIC, VAS	50
EE_AL2	NA		BIR, FUN, LIC, VAS	64
EE_AL3	NA		BIR, BRY, COL, DIT, FUN, GAS, LIC, VAS	116
EE_KR	NA		FUN, GAS, LIC	12

dataID	Regeneration type	Category	Taxa	N
EE_MP	NA		BRY, CAR, LIC, VAS	100
ES_RL	NA		BIR, LEP, LIC, MAM	63
HU_RA	NA		BIR, CAR, VAS	16

Abbreviations: See Fig. 7 for the key for forest categories. Taxa: AMP=Amphibians, ANN=Annelida, ARA=Araneae, BIR=Birds, FUN=Fungi, BRY=Bryophytes, CAR=Carabidae, CER=Cerambycidae, BAT=Bats, COL=Coleoptera, COM=Collembola, DIP=Diplopoda, DIT=Diptera, ENC=Enchytraeidae, FUN=Fungi, GAM=Gamasida, GAS=Gastropoda, HET=Heteroptera, HYM=Hymenoptera, IXO=Ixodida, LEP=Lepidoptera, LIC=Lichens, MAM=Mammals, ONI=Oniscidea, OPI=Opiliones, ORI=Oribatida, REP=Reptiles, ROD=Rodents, SCO=Scolytinae, SOI=Soil microbes, STA=Staphilinidae, VAS=Vascular plants, TYP=Typulidae

So far, 308,363 observations from 31 higher taxonomic groups across 25 datasets have been revised and reported herein. Among these, 81% of the individual observations have been nomenclature-checked at the species level, amounting to 5,961 unique species from 615 families, 159 orders and 37 classes. The classes more widely represented in this subset include several families of plants, bryophytes and insects which are represented in more than 50 % of the plots (Fig. 3).

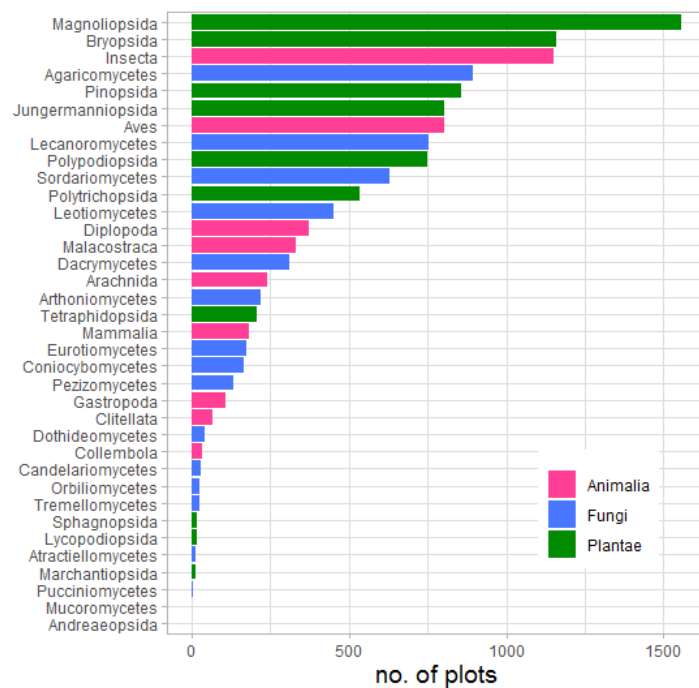


Figure 3. Frequency distribution of different taxonomic classes including only records where species taxonomies have been checked (N = 266,380).

Reflecting the criteria for inclusion of data, individual datasets have sampled several different taxonomic groups ranging from 3 to 10, and on average 5.73 different taxonomic groups have been sampled on each plot (Fig. 4).

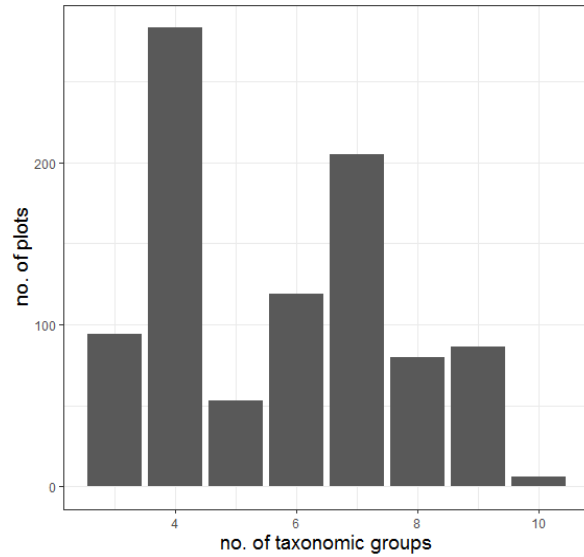


Figure 4. Frequency distribution of the number of taxonomic groups. Bars show the number of plots for each number of taxonomic groups sampled jointly.

The representation of different taxonomic groups reported so far varies widely among forest categories (Fig. 5) and silvicultural systems (Fig. 6), likely reflecting differences in number of plots, datasets, and targeted taxonomic groups. Major taxonomic groups of plants, animals and fungi seem to be balanced within each forest category, except for forest categories 1, 8 and 9, i.e., boreal, thermophilous deciduous and broadleaved evergreen forests, where only a low number of families of animals and fungi were sampled.

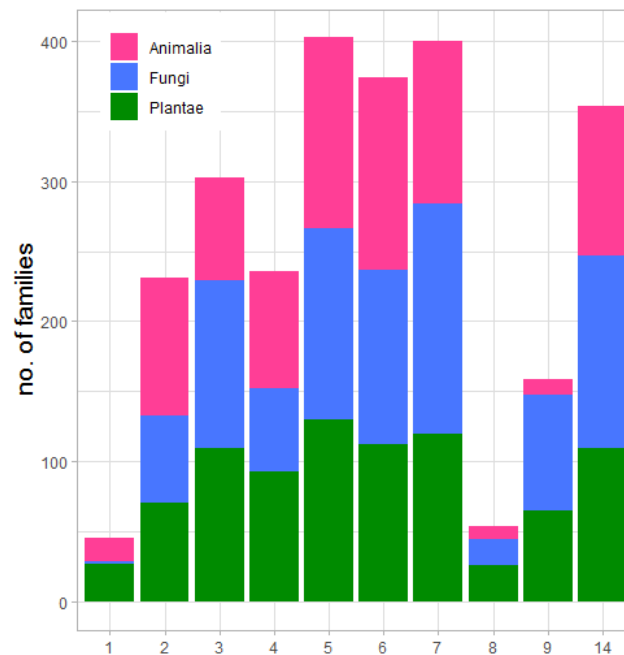


Figure 5. Number of different families reported for each major kingdom in forest categories. The key for forest categories is reported in figure 7.

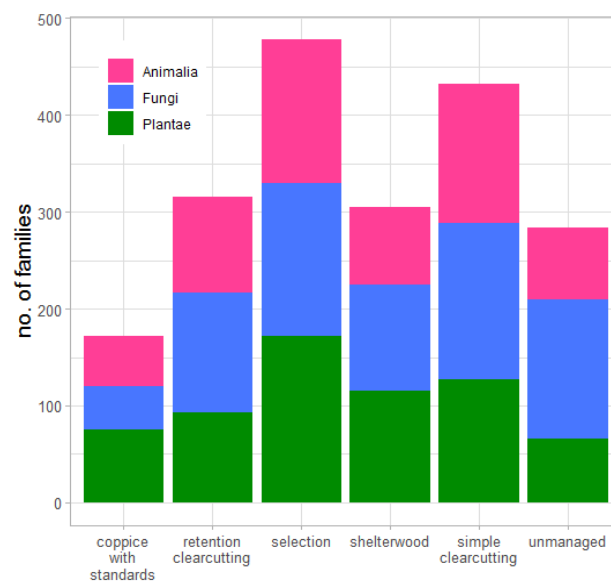


Figure 6. Number of different families reported for each major kingdom across silvicultural systems.

Similarly, when looking at the representation of the different kingdoms across silvicultural systems there is a general balance. Only animalia and fungi are relatively underrepresented in coppiced forests likely in relation to the limited amount of data for this silvicultural system (see following section).

Data distribution across compositional and management categories

Out of 14 European Forest Categories (EEA 2006), 12 are covered by the BOTTOMS-UP platform; among them, about two-thirds are distributed as follow:

- beech forests (36% of the total number of plots);
- mesophytic deciduous forest (19%);
- mountainous beech forests (16%).

We compared these data with the share of forest area covered by different categories across Europe (Barbati, Marchetti, Chirici, & Corona, 2014) and detected some substantial gaps in the current available multi-taxon information (Fig. 7).

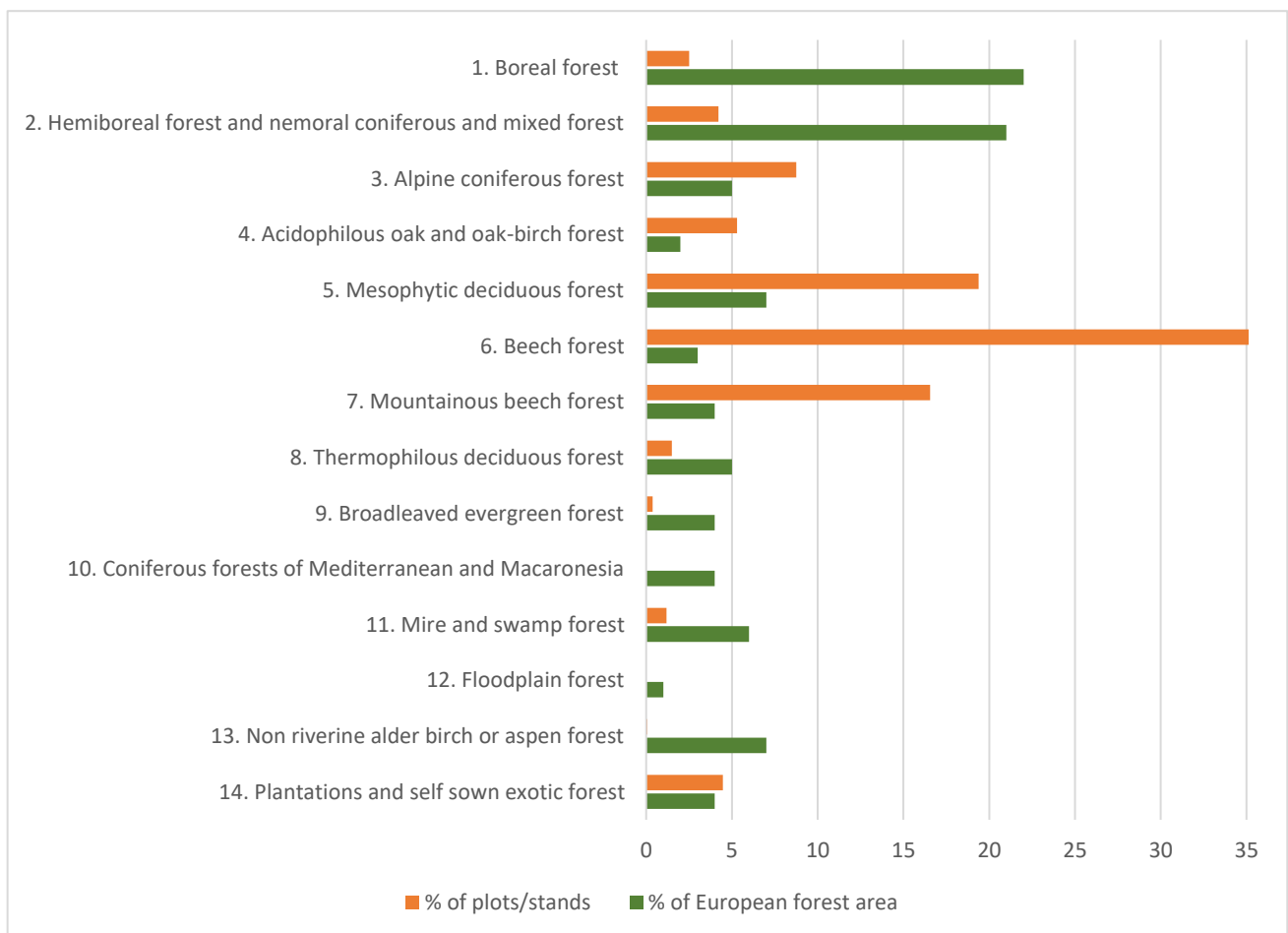


Figure 7. Share of the total number of plots (in orange) and of forest area in EU-28 (in green) based on (Barbati, Marchetti, Chirici, & Corona, 2014) across different Forest Categories (sensu EEA, 2006).

Based on the reconstruction by McGrath et al. (2015), in 2010 about 70% of European forests were high forests, whereas about 15% were coppices and a similar share were unmanaged. We can think these rough estimates are still valid and conclude that our platform covers substantially the most

widespread management strategy, i.e., high forest (Fig. 8). Also unmanaged forests are well covered by our platform (18% of available plots), whereas coppices are under-represented in forest multi-taxon studies, with only 3% of plots focused on this regeneration method.

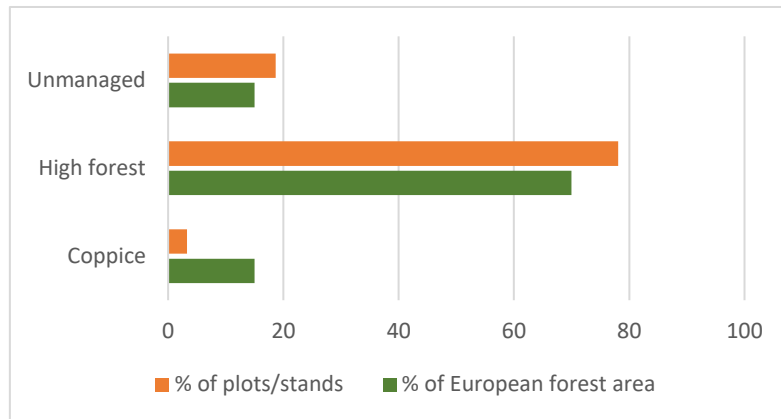


Figure 8. Percentage of plots/stands (in orange) and of the share of forest area in Europe (in green) based on McGrath et al. (2015) across two broad methods of regeneration and the absence of any silvicultural system (unmanaged).

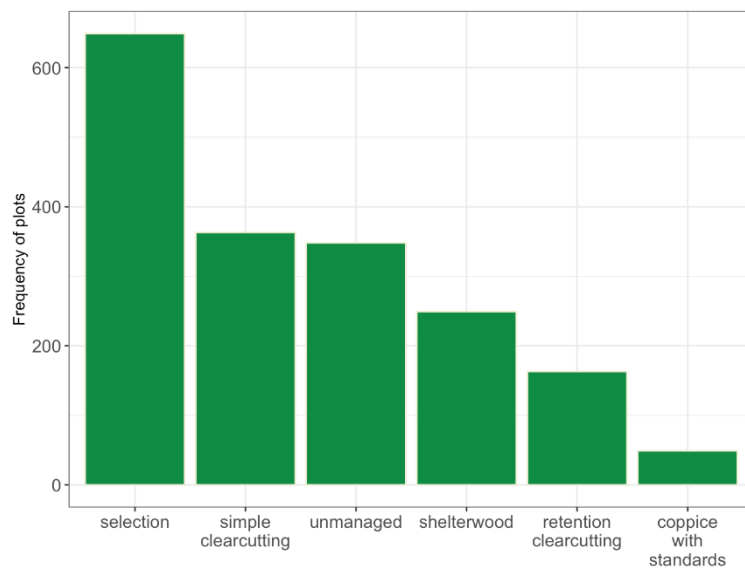


Figure 9. Distribution of the platform plots across silvicultural systems.

Data distribution across silvicultural systems (Fig. 9) shows that the systems most commonly sampled for multi-taxon biodiversity is selection system (30% of plots), followed by shelterwood (24%) and simple clearcutting (18% Figure 9) systems. Unmanaged forests account for about 19% of the sampled plots.

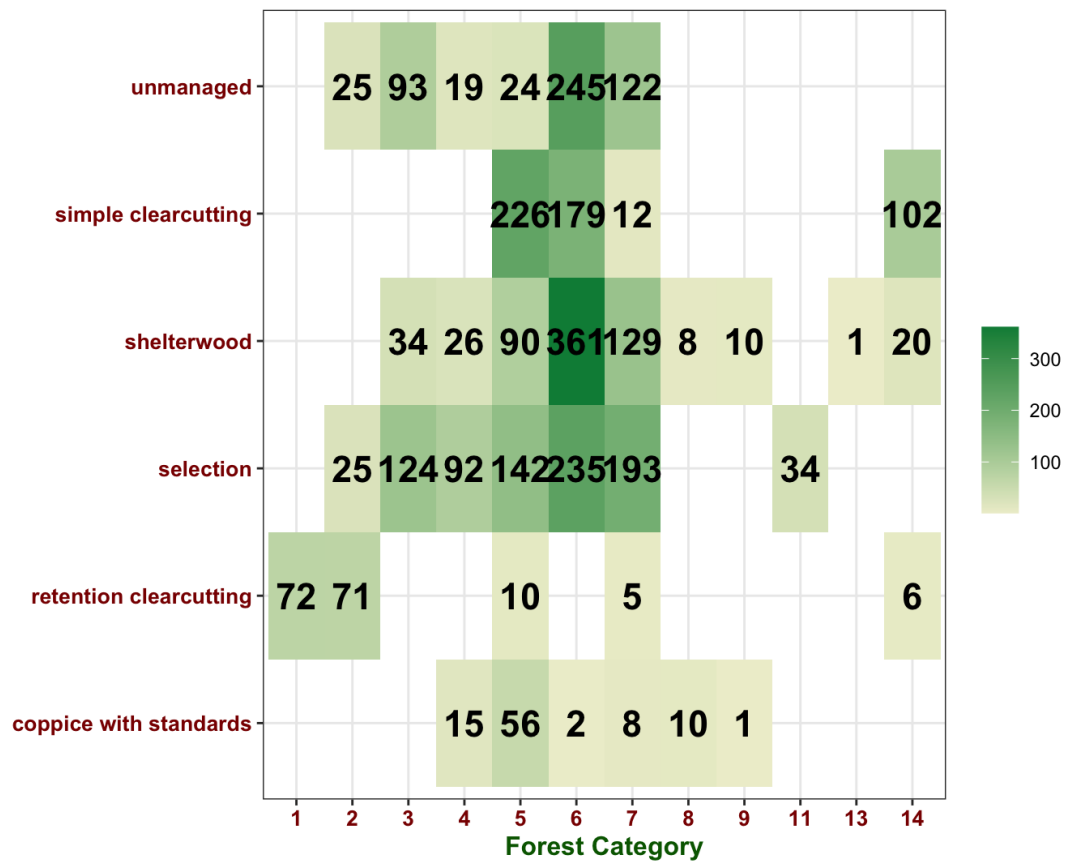


Figure 10. Heatmap of the number of plots in the platform for different combinations of forest categories and silvicultural systems.

Interestingly, when the information on forest compositional and silvicultural systems is combined (Fig. 10), no clear pattern of association appears for some systems, e.g., shelterwood is applied to almost all the compositional categories represented in the platform; while other silvicultural systems show clear patterns of association, e.g., retention clearcutting for boreal and hemiboreal forests, and coppice with standards for thermophilous deciduous forests.

TREE SPECIES COMPOSITION AND STRUCTURAL ATTRIBUTES

TREE SPECIES COMPOSITION

The tree-level data included in our platform allowed us to analyze jointly the tree layer composition and stand structure of the studied forests. Tree-level dataset so far comprises 118,753 records (trees) of which 111,316 are correctly identified at the species level. The trees without correct species identification are a small share (6% of the total) that derives from few plots where trees were identified at the ‘genus’ level, or from rare species observed in individual plots. In fact, about 66% of the total number of plots have 100% tree nomenclature-checking rate, and more than 75% have up to 90% of the tree species nomenclature checked.

Tree-level data confirm the prevalence of beech-dominated forests across multi-taxon studies. European beech (*Fagus sylvatica*) was the most frequent species, about 23% of the total number of sampled trees (Fig. 11). Apart from Norway spruce (*Picea abies*), reaching 17% of the records, Scots pine (*Pinus sylvestris*; 8%), two oak species (*Quercus petraea* and *Quercus robur*; 8% and 5% respectively), and silver fir (*Abies alba*; 5%), the contribution of other species was <5% each in our dataset.

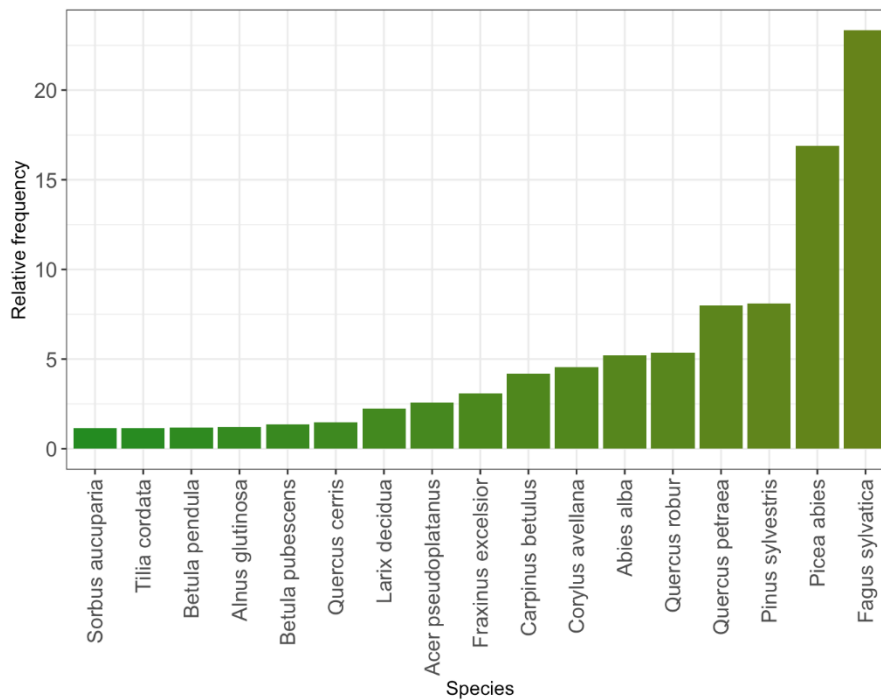


Figure 11. Relative frequency (%) of the most abundant tree species found in the overstorey of the studied plots. Only trees with their nomenclature checked at the species level were considered (111,316 trees).

The structure of our platform allows us to easily combine the information gathered at different scales, as it is the case for plot/stand scale information and tree level information.

For instance, we were able to point out some differences in tree species richness and structure across forest categories and silvicultural systems. We found that the number of tree species was unevenly distributed across forest categories, with high values found in thermophilous deciduous forests (EFC: 8; mean 7.6, s.d. 1.7), while other forest categories have values below 5 (Figure 12). Other categories show a high heterogeneity (2; 5; 8) that does not allow to define a general trend.

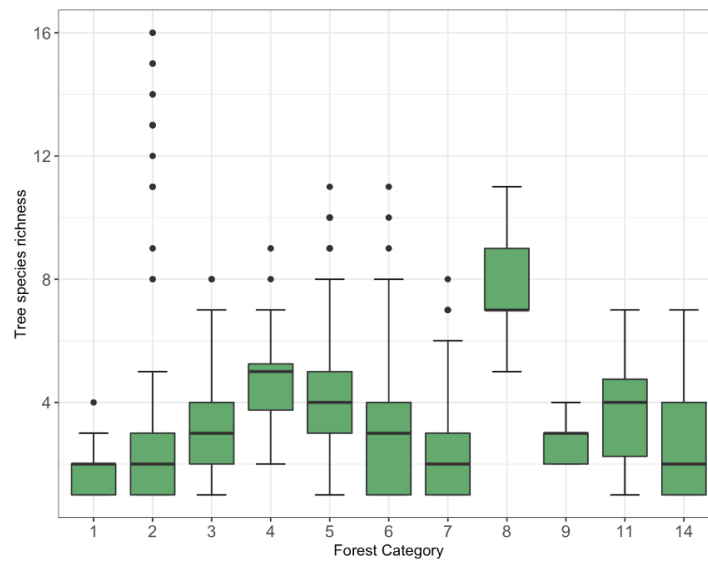


Figure 12. Number of tree species per plot according to the different European Forest Categories. Please note plots included in the platform have different sizes. For this figure only plots with at least 90% of tree taxonomic nomenclature checked at the species level were considered. Forest categories are listed in Fig. 7.

The number of tree species per plot varies substantially also across silvicultural systems, with a marked difference between coppices and selection systems on the one hand and all the other categories on the other hand (Fig. 13). Conversely, the tree species richness of unmanaged plots/stands is comparable with the simple clearcutting systems, and higher than the one found in retention clearcutting and shelterwood systems.

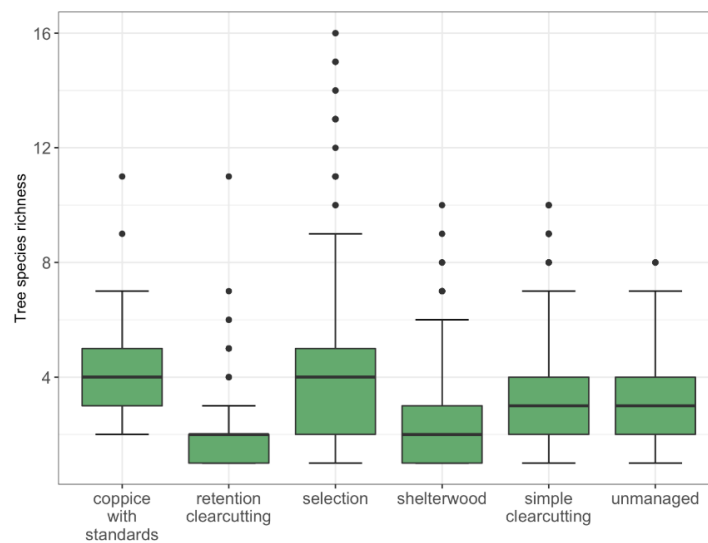


Figure 13. Number of tree species per plot across different silvicultural systems. Please note plots included in the platform have different sizes. For this figure only plots with at least 90% of tree taxonomic nomenclature checked at the species level were considered (about 77% of the total number of plots).

STRUCTURAL ATTRIBUTES

Basal area data for the plots averaged around 30 m² per ha, ranging between average values of 20 to 45, with highly heterogeneous values within and across forest categories (Fig. 14).

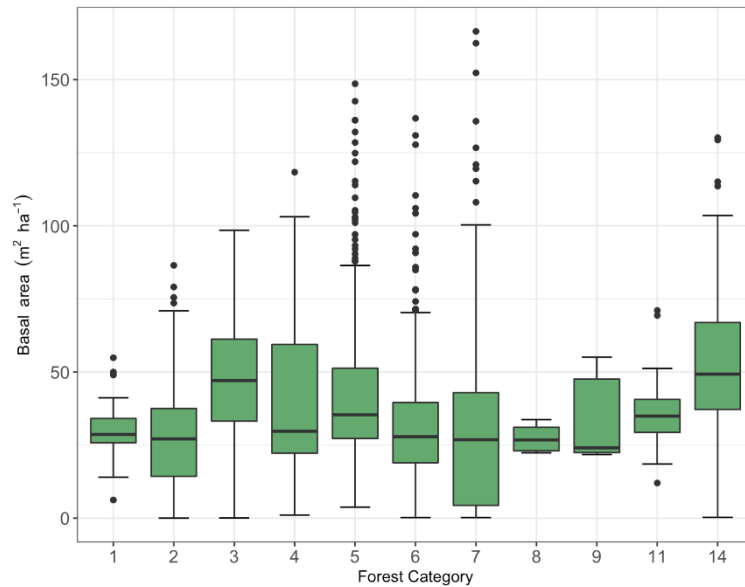


Figure 14. Stand basal area distribution across forest categories.

Conversely, basal area followed an increasing trend when going from coppices over high forests (selection and shelterwood) to unmanaged forests. This trend coarsely reflects the variation of general stock densities among silvicultural systems, notwithstanding the heterogeneity related to developmental stage and intermediate cuttings within each system (Fig. 15).

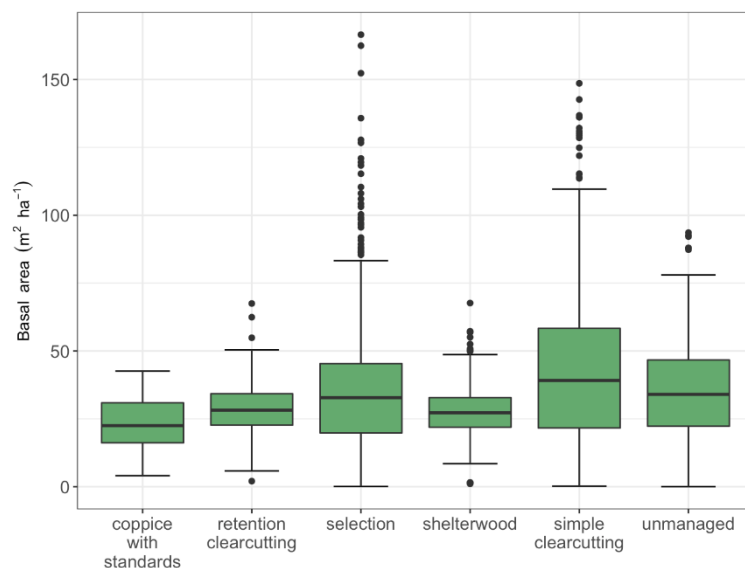


Figure 15. Stand basal area distribution across silvicultural systems.

DISCUSSION

COMPLETENESS AND REPRESENTATIVENESS

The amount of forest biodiversity information collected by the platform is impressive and represents the first attempt to include such comprehensive information in a single, harmonized data platform, both in Europe and globally.

Even with some relevant gaps for certain compositional and management categories in the current dataset, the BOTTOMS-UP platform could effectively serve to provide the data required for the study of the effect of structural stand features and specific management regimes on multi-taxon forest biodiversity.

We noticed that beech forests represent the larger share of the project's multi-taxa samples, whereas certain forest types are still underrepresented or missing in the current version of the platform. This uneven distribution is not surprising since the Action was originally focused on temperate forests only. It is true, however, that the Action participants immediately focused on involving researchers with multi-taxon data across all European forest categories and, as a matter of fact, it was not possible to attain a good representation for boreal and hemiboreal forest categories, thermophilous and Mediterranean categories, and forest categories depending on freshwater resources.

Very few forest categories are completely lacking from the platform (EFC 10 and 12). One of the means of the Action to deal with these gaps is to start filling them through new sampling efforts performed within the context of the Action through cross-country activities of researchers with different expertise (e.g. supporting sampling methods and protocols). For example, for the category "Coniferous forests of the Mediterranean and the Macaronesian regions" (EFC 10), participants from Greece (Dr. Fotios Xystrakis and Dr. Dimitris Fotakis) sampled some plots in summer 2020 in order to contribute their data and start a constructive path on this category. Although useful, these initiatives cannot thoroughly cover the existing gaps in the short term. Therefore, the platform will focus at first on those categories for which a fair amount of information is available, or on generalizations across forest categories when possible.

Another forest category that is not represented in the platform is "Floodplain forests". In this regard, it has to be said that this category is the least represented category in Europe also in terms of forest area. Besides being relatively rare in European landscapes, this category often includes highly fragmented and degraded forests that should be the focus of forest biodiversity studies especially in view of restoration actions.

When looking at data distribution across silvicultural methods, the coverage of our platform shows the tendency to perform multi-taxon biodiversity studies in those forests that are perceived as less intensively managed, such as those under selection or shelterwood management regimes. Clearcut is an exception that is represented mainly in experimental studies that conversely stem from the

perception of clearcutting as threatening for forest biodiversity. Unmanaged forests have been often sampled as a relevant reference in comparison to managed forests in general, especially to those that are managed through strategies that are generally perceived as sustainable.

The comparison with forest areas across coppice, high forest and unmanaged forests confirms the fact that coppicing systems (coppice and coppice with standards) result relatively understudied for multi-taxonomic biodiversity among European forests. This is partly related to the perception of these forests as less relevant for biodiversity and the related recreational value, even if some studies would point in the opposite direction (Hedl et al. 2010). This uneven distribution may also be related to the progressive reduction of coppiced forests in Europe, that are gradually being (actively or passively) converted into high forests. In general, the lack of multi-taxon biodiversity information on coppices may represent a crucial gap for supporting policy decisions on coppice forest management, also in view of their renewed prominence in climate adaptation policies and multiple ecosystem services provisioning (Fabbio 2016).

Interestingly, the platform includes very different management systems that are found also within the same forest compositional category. This derives from different, independent, forestry regulations across European countries that hence offer different ranges of silvicultural options for the same forest category. It is also true, however, that several data custodians found it difficult to opt for one of the proposed silvicultural systems since these did not include many local or national traditional forest management approaches. In fact, by performing a management synthesis across several different countries, our platform faced the challenge represented by several language and technical barriers in the definition of silvicultural systems. We believe that our effort will progressively improve the database options as well as the ability of data custodians to comply with them.

EXPECTED IMPACT AND LIMITATIONS

The current platform could have a wide impact thanks to its interdisciplinarity. In fact, differently from other data sharing platforms focusing on individual aspects of ecosystems (e.g., vegetation or functional traits), here we made the effort to put together different expertise and data on the three main components of ecosystems: composition, structure and functions.

This will allow us to soundly define the mechanistic relationships that exist between silvicultural systems, structural attributes and the richness and composition of several taxonomic groups that have key roles in forest ecosystem functioning and biodiversity value.

It has to be said that the attribution of a plot/stand to a specific silvicultural system was not always straightforward due to the various local silvicultural approaches that are often hard to translate and standardize into a shared scientific language. However, we believe that our standardization effort will help to improve the communication among researchers across different countries, and in the long-term support finer management classifications that could be finally translated into practice.

Notwithstanding this process, our platform will likely be able to answer several questions related to the management of beech, mesophytic and Alpine forests subjected to shelterwood and selection systems can be soundly investigated through the large amount of data gathered and made available by the platform.

As a first step towards biodiversity-based assessment, we were able to compare the number of tree species across forest categories and silvicultural systems. Oak forests (EFC 4, 8) resulted as the richest in tree species reflecting the highest tendency of oak forests towards mixed canopies. Silvicultural systems did not differ substantially, apart from the greater tree species diversity related to coppice stands and forests managed through selection systems. As a matter of fact, selection systems appear to have achieved a greater tree species diversity as compared to shelterwood, validating the use of these systems to enhance tree species diversity and forest resilience in high forests. Surprisingly, unmanaged forests have a number of tree species per plot similar to those managed through simple clearcutting. However, this can be easily explained by the fact that unmanaged forests are more often found in beech-dominated forests, where very few species tend to attain and maintain canopy dominance, e.g., mountainous beech forests. Overall, our figures on the number of tree species per plot should be taken with caution since they derive from sampling units with different sizes to which our data have not been normalized yet.

Our partial results, encompassing the number of tree species per plot, further stress an underrepresentation of studies in specific forest types, such as alluvial forests and thermophilous oak forests that may be relevant reservoir of tree species biodiversity especially in view of the ongoing changes in climate (Mölder et al. 2019).

A strength of the platform is the high number of taxa sampled in each plot/stand. Such multi-taxonomic information will allow linking fine-scale plot level structural attributes of the forest and multiple species groups simultaneously collected, as well as investigating a wide range of cross-taxon relations to study mechanistic links between specific taxonomic groups within and across forest categories.

Currently, the process of nomenclature standardization was finished only on tree species. By performing the same process on the whole multi-taxonomic species records, we will be able to test the for effects of tree species diversity on multi-taxon forest biodiversity as well as for cross-taxon relationships.

By combining information on forest categories and silvicultural systems, our platform will be able to account for different environmental contexts when evaluating different silvicultural systems. In fact, while patterns exist for some silvicultural systems, e.g., retention clearcutting is applied to boreal and hemiboreal forests, and to plantations of exotic forests; no clear patterns appear for some other systems, such as unmanaged, shelterwood and selection systems. As a matter of fact, these systems are being adopted broadly across very different forest categories, as coppices are being converted into high forests and many forests are being abandoned or included into strictly protected areas.

Surprisingly, also simple clearcutting is applied to a broad range of forest categories regardless of differences in life-history traits among groups of tree species. This may depend on the fact that regulations and restrictions are applied differently across European countries. Therefore, in some countries this silvicultural system may be applied also to forest categories for which it is forbidden or limited in some other European countries.

A means of overcoming the mentioned issues relative to different applications of management categories across different European countries is to analyze stand structural attributes. This is possible because the platform collected tree level data for diameter at breast height and tree height, as well as a series of other information relative to both living trees and deadwood. Our preliminary analyses of basal area show great heterogeneity within individual forest categories likely deriving from differences in forest management approaches within the same category. Conversely, a relatively clear pattern of basal area across silvicultural systems may be identified, even if these figures are strongly influenced by developmental stage: in clearfelling systems, the average will depend strongly on the age classes and share of recent clearcut in the set of samples. This is particularly evident looking at the differences between retention clearcutting and simple clearcutting, clearly deriving from differences in the proportion of different age and developmental phases across the two categories.

Although impressive, the data platform jointly built in the framework of the Action still needs a fair amount of work before being complete and representative of the great diversity of European forests.

The first steps to complete the collection and harmonization of the existing forest multi-taxon data are certainly to be taken together with data custodians. They will be asked to correct and integrate their data based on the quality check that was performed. Further effort is also needed for the check and standardization of multi-taxonomic nomenclature that will be assigned to Action participants with different taxonomic competencies.

Currently, the use of some specific fields is hampered by a fair amount of missing data (Fig. 16), this is particularly worrying for some detailed information on management (e.g., date and type of the last harvesting operation, stand age). An additional effort will be asked to the data custodians to provide this information by contacting local stakeholders or retrieving specific documents.

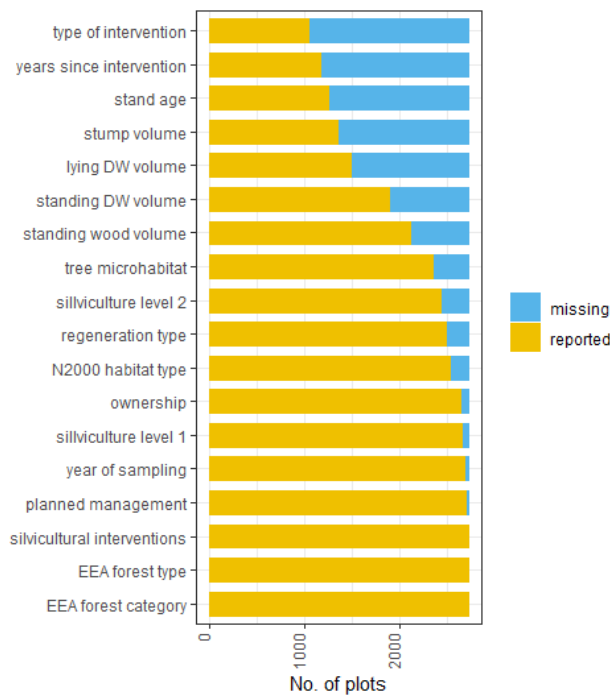


Figure 16. Frequency of missed observations from selected aggregated data.

WAY FORWARD

The platform represents the starting point for several research and monitoring activities related to forest biodiversity conservation.

Among the first mid-term objectives is the use of the data in the platform as a pilot to design a monitoring network for European forest biodiversity. The species diversity data, including both species richness values and species composition will be used to define the effort needed in terms of number of plots and sites to have a thorough monitoring of forest alpha and beta diversity in Europe. This aim will be pursued through e.g. accumulation curves for species richness and simulation based estimates of sampling effort based on pseudo-multivariate standard error for species composition (Guerra-Castro, Cajas, Simões, Cruz-Motta, & Mascaró, 2020).

After defining the necessary sampling effort for a European forest biodiversity monitoring network, this will be shared and discussed with the European Environmental Agency that is taking part to the Action, especially in the view of activating integrated European projects that could be able to provide useful information for the newborn FISE platform (<https://forest.eea.europa.eu/>).

In this view the Action and the related platform will act as promoters of sampling underrepresented areas through shared approaches and methodologies to finally provide the information needed for reliable forest biodiversity indicators of management sustainability.

Through these common steps, we will be able to provide the information for a more evidence-based discussion on forest biodiversity and forest management sustainability in Europe.

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