



BOTTOMS-UP

PAPER PROJECT

Preliminary title: Relationships over time and management types between stand structure and multi-taxon diversity in European forests

Target journals: *Global Change Biology* / *Biological Conservation* / *Forest Ecology and*

Management Outline

Previous research has demonstrated that stand structure is one of the main drivers of biodiversity in forest ecosystems. Stand structure has been described in several ways. Stand parameters have been selected and their values have been related with measures of biodiversity (Sabatini et al. 2016; Bohn & Huth, 2017). Usually, the stand parameters were calculated from easily collectable and monitorable field measures such as standing tree diameter, height, and density (Gao et al. 2014). These have combined with measures of dead trees, standing or fallen. The majority of available studies have used a restricted range of biodiversity metrics, mostly based on species identity of a single or a few numbers of taxa. A meta-analysis made by Paillet et al. (2010) has shown that the taxa more often considered are plants, fungi, bryophytes, lichens, birds and forest invertebrates. The same limitation in the range of biological taxa is evident for management regimes. The majority of the studies have compared clear cuts with other systems of management (Duguid & Ashton, 2013). Even more difficult is finding studies, which treated the stand structure driver from a time perspective. The geographical areas considered in Europe are centered on Northern boreal regions.

The above limitations are considered a barrier for the practical translation of the scientific research into management guidelines. Forester managers need models of stand structure development, particularly of growing stock and productivity, which integrate not just timber or firewood yield but also non-wood forest products, like biodiversity.

Efforts have been made to control the sampling units for their management, development stage, and disturbance regime. This aims to reduce the number of confounding factors that may mask the effect of stand structure as itself. Disturbance history can be considered through long-term experiments, while in observational studies should be retrospectively derived. A functional rather than a species identity approach has also been followed. Several models of forest dynamics integrate the development of forest structure in time and space with changes of other ecosystem components.

Aims

From the first outcomes of the COST database, the dominance of two species, Norway spruce and European beech, is evident. In general, differences in the mean value of some indicators of stand structure, like basal area, are not significant among forest categories. There is also a great deal of variability in basal area in each forest category. This outcome is not surprising, because stands with different densities may well belong to the same forest categories. Basal area, like other stand structure indices, vary more with site conditions, disturbance history, and stages of development than across forest categories. This is particularly true with even aged stands that over time accumulate volume and basal area more than uneven aged stands where stand structure should be more consistent. Moreover, this variability is influenced, to a certain degree, by the size of the sampling unit.

Tree species richness is a very simple index of biodiversity. One of the simplest preliminary analysis correlates this index to silvicultural systems. Like in the previous example, differences in tree species richness among silvicultural systems are not marked. One potential explanation is terminology. Definitions and terms used in silviculture might vary and affected by ambiguity and misunderstandings that might hinder the comparability of data collected by different partners. Assuming that definitions are applied consistently, the selection system is largely the more represented system, followed by simple clearcutting. The distribution of silvicultural systems among forest categories is also unbalanced.

We will explore how interaction effects dictate the stand structure and its effects on multi-taxon biodiversity by focusing on even and uneven-aged stand separately. For even-aged stands, a synchronic sequence of stand structure will be developed. In addition to the variables of the BOTTOMS-UP action, each plot will be assigned to a disturbance intensity level based on Senf & Seidl (2021) and to climate variables based on existing high resolution databases (for example from the CHELSA dataset). In even-aged stands, plot-level multitaxon diversity will be related to stand age. In the uneven-aged stands, structural variables not directly related to age will be calculated and use as explanatory variables. Diversity will be first expressed as number of species. Most represented taxa will be tested separately. Data will be also grouped by forest types. Then, diversity will be expressed including abundance data. Further step will be to express diversity with a multivariate approach, using ordination techniques to test the level of similarity between plots belonging to different stand age or structural classes.

References

- Bohn, F. J., & Huth, A. (2017). The importance of forest structure to biodiversity–productivity relationships. *Royal Society open science*, *4*(1), 160521. <http://doi.org/10.1098/rsos.160521>
- Duguid, M. C., & Ashton, M. S. (2013). A meta-analysis of the effect of forest management for timber on understory plant species diversity in temperate forests. *Forest Ecology and Management*, *303*, 81-90. <https://doi.org/10.1016/j.foreco.2013.04.009>
- Gao, T. et al. (2014). The role of forest stand structure as biodiversity indicator. *Forest Ecology*

and Management, 330, 82-93. <https://doi.org/10.1016/j.foreco.2014.07.007>

Paillet, Y., et al. (2010). Biodiversity differences between managed and unmanaged forests: meta analysis of species richness in Europe. *Conservation biology*, 24(1), 101-112. <https://doi.org/10.1111/j.1523-1739.2009.01399.x>

Sabatini, F.M., et al. (2016) One taxon does not fit all: Herb-layer diversity and stand structural complexity are weak predictors of biodiversity in *Fagus sylvatica* forests. *Ecological Indicators*, 69, 126-137. <https://doi.org/10.1016/j.ecolind.2016.04.012>.

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Core authors outside BOTTOMS-UP: to be confirmed

Please note that if the outline changes substantially (more than 1 aim is revised substantially), or co author(s) are added to the above lists the governing board should re-vote on the project.

Further opt-in authors:

According to the BOTTOMS-UP Bylaws any member of the BOTTOMS-UP Consortium can declare his/her interest to become opt-in author. The first author is required to preliminarily accept one such offer from each dataset that represents at least 2% of the data in the analysis.

It is upon the

discretion of the first author whether to accept any opt-in offer beyond this requirement. Persons interested in opt-in authorship can be nominated until with e-mail to the first author (and cc: to the BOTTOMS-UP Governing Board), explaining which dataset(s) they represent and preferentially also how they could contribute. Note however that such a nomination only means the option to become co-author. In the end only those persons will be retained as actual co-authors who have made a significant intellectual contribution to the paper during the course of its preparation (in accordance with BOTTOMS-UP Bylaws and compliance to ethics in academy).

Data to be used:

- Do you need data for specific regions, forest categories or silvicultural regimes? No

- Will you use both datasets allowing for stand and plot-level aggregation of multi-taxon data or only one of these two?

Both

- For which taxonomic group do you need data? Please refer to the attached list of taxonomic groups TAXA.xlsx

Yes, see below

- Do you need data on standing trees (including snags, standing dead trees and stumps)? Yes

- Do you need data on lying deadwood?

Yes

Variable name	Description
dataID	Unique code of the dataset where the same protocol sampling is applied
siteID	Unique code of the site (consistent with metadata protocol table)
standID	Original (given by each researcher during field work) unique stand identifier
plotID	Original (given by each researcher during field work) unique plot identifier
cussur	Surname of the data custodian
catego	Forest category (according to EEA 2006)
fortyp	Forest type (according to EEA 2006)
habtyp	Habitat Natura2000 code (According to CE/42/93)
sils1	Current silvicultural system - Hierarchical level 1
sils2	Current silvicultural system - Hierarchical level 2
regtyp	Regeneration type most applied to the plot

manarea Area managed through planned silvicultural practices

noint	Forest stand with no interventions since more than 100 years
lastint	Time since last silvicultural intervention at the time of sampling
typint	Type of last silvicultural intervention
yeasam	Year of the sampling
staage	Stand age (for even-aged forests)
stovol	Stand volume per hectare
stdwvo	Standing deadwood volume per hectare
lydwvo	Lying deadwood and stump volume per hectare
stuvol	Stump volume per hectare
logvol	Log volume per hectare
siteID	Unique code of the site (consistent with metadata protocol table)
standID	Original (given by each researcher during field work) unique stand identifier
plotID	Original (given by each researcher during field work) unique plot identifier
treeID	Original (given by each researcher during field work) unique tree identifier
genus	Tree genus Latin name
species	Tree species Latin name
treesp	Full scientific species name
treedb	Tree diameter at breast height

treeht	Tree top height
treevol	Tree volume
alive	Tree status (dead or alive)
plosiz	Size of the plot where the reference tree is surveyed
weisiz	Plot area ratio per hectare
TreMn1	Unique code or name of Tree-related microhabitat surveyed (according to the reference reported in metadata)
TreMn2	Unique code or name of Tree-related microhabitat surveyed (according to the reference reported in metadata)
TreMn3	Unique code or name of Tree-related microhabitat surveyed (according to the reference reported in metadata)
siteID	Unique code of the site (consistent with metadata protocol table)
standID	Original (given by each researcher during field work) unique stand identifier
plotID	Original (given by each researcher during field work) unique plot identifier
lydwID	Original (given by each researcher during field work) unique dead wood element
typldw	Type of lying deadwood
volume	Volume measured
lis	Logs surveyed using LIS (line intercept sampling) method
plosiz	Size of the plot where the reference element is surveyed
weisiz	Plot area ratio per hectare
siteID	Unique code of the site consistent with metadata protocol table
standID	Original (given by each researcher during field work) unique stand id
plotID	Original (given by each researcher during field work) unique plot id
elemID	ID of the element (tree/subplot/trap) sampled within the plot, enter NA if data were not recorded by element
genus	Genus Latin name
species	Species Latin name
genspe	Full scientific species name
taxon	Taxonomic group
layer	For vascular plants enter the layer occupied
abucov	Abundance (cover or frequency) expressed as percentage cover
abuind	Abundance expressed as number of individuals

Taxa
Aves
Basidiomycota
Bryophyta

Carabidae
Cerambycidae
Chiroptera
Coleoptera
Fungi
Lichinales
Scolytinae
Tracheophyta

Time line:

Deadline for permission of data usage from custodians: September 2021

Extraction of data from BOTTOMS-UP: October 2021

Data preparation and analysis: December 2021

Raw results to be sent to the wider author team: December 2021

Workshop with the wider author team: Early February 2021

Writing up of the paper (including preparation/optimization of figures): End of March 2021

Feedback round of co-authors to MS: April 2021

Submission: April 2021

Confirmation:

I confirm that I will adhere to the BOTTOMS-UP Bylaws.

Date 23/09/2021

Tommaso Sitzia