



BOTTOMS-UP

PAPER PROJECT

Preliminary title:

Disentangling the effect of environmental drivers and forest structural heterogeneity multi-taxon biodiversity

Target journals:

Not Defined yet

Outline:

Forest biodiversity has recently gained attention as a key goal of forest management (Aggestam et al. 2020; Simberloff 1999;). Increasing forest biodiversity and structural heterogeneity have become an essential part of sustainable strategies to enhance the resilience of forest ecosystem services such as timber production and carbon sequestration (Ampoorter et al. 2020; Gustaffsson et al. 2020). Most research efforts focused on the effects of forest structural elements on species richness and abundance, such as deadwood and tree size or heterogeneity at the scale of individual sampling units (Cosovic et al. 2020). More recently, the study of forest management/structure/biodiversity relationships has been upscaled to forest sites/landscapes, pointing to the heterogeneity that may derive at this scale from forest management (Schall et al. 2020).

These studies showed how the complex of forest dynamics and species interactions differs at different spatial scales, and how forest multi-taxon biodiversity may show very different patterns depending on the spatial scale of analysis (Burrascano et al 2018). Biodiversity results from a complex network of drivers that operate at different spatial scales, with broad scale environmental conditions that determine community composition, which interact with forestry practices. These elements in turn shapes actively fine scale environmental conditions (Bohn & Hut 2017) that strongly affect forest biodiversity. All the mentioned drivers are linked by causal effects, i.e., environmental conditions affect community's composition with cascading effects on forest biodiversity.

Up to now, broader scales received less attention than fine scale analysis since the former may be based on local or regional studies, within a limited time-lapse, and under specific management policy conditions (Larsson 2001). A broader approach at the landscape level is necessary to understand the effects of forest complexity on biodiversity but was not feasible due to the lack of harmonized biodiversity data at the continental scale.

This research proposes that the sum of the causal effects of environmental conditions such as topography and forest build-in will have both a direct and indirect effects on the abundance and diversity of different groups of birds, fungi, beetles, herb-layer vascular plants, bats and epiphytic lichens and bryophytes (Figure 1).

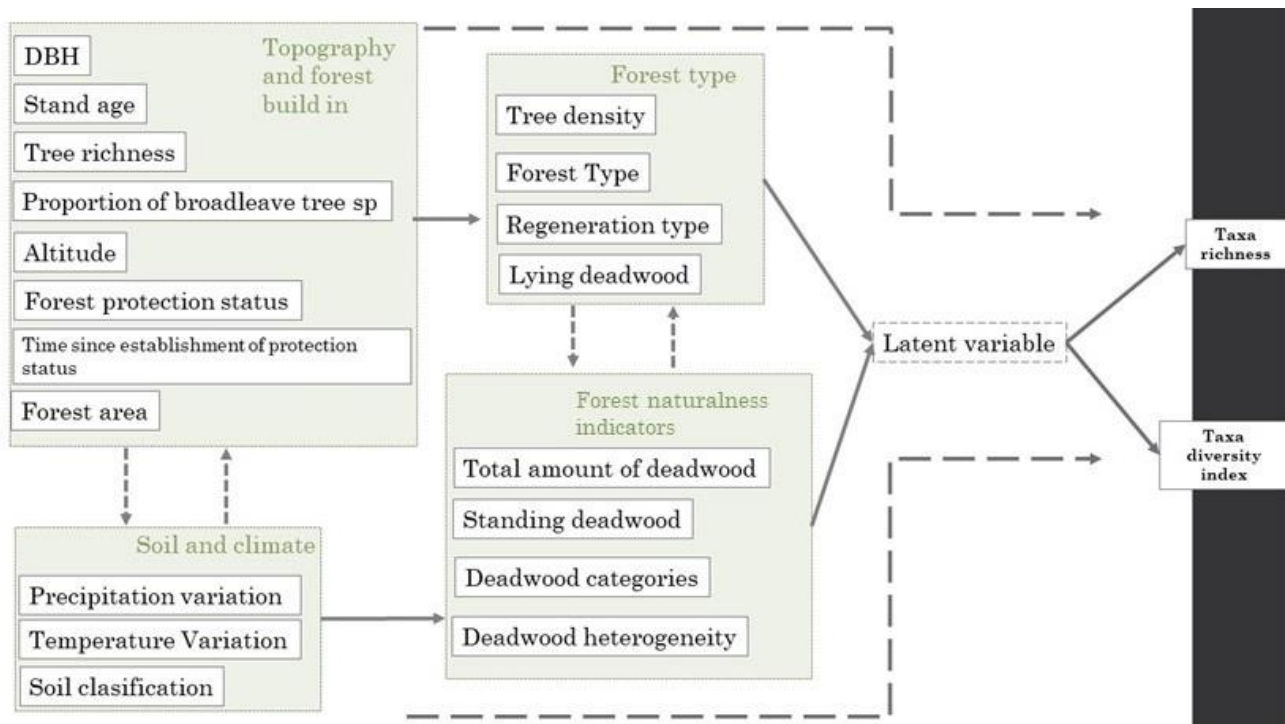


Figure 1: Global conceptual model of causal effect of forest on habitat heterogeneity.

Forest structures given by landscape, soil climate and forest management (left extreme variables) have direct effect on forest structure heterogeneity (defined as forest variables influenced by both, forest structures and specific environmental conditions). The forest structure heterogeneity determines the forest structure (yet to be calculated as a latent variable), and finally this affect richness and abundance of species of different taxa. The indirect effect of forest structure and forest heterogeneity on species richness and abundance is also considered. Potential covariances need to be evaluated and considered in the model

This causal effect on biodiversity might not be equally dominated by the same variables (amount of deadwood, tree size, tree diversity) such as suggested by Cosovic et al. (2020). We hypothesize that for each specific group, different elements will take a key role in their composition. Due to the complexity of forest structures, it seems highly unlikely that a small set of variables (deadwood, tree size, tree density or tree species, etc.) have a dominant effect on a broad range of taxonomic groups. We rather expect a more differentiated result where different elements play different roles, explaining the assemblages observed along a gradient of forest management intensity (Bohn & Huth 2017).

This research aims to describe and analyze the causal effect of forest patterns on different taxonomic groups in the managed temperate forests across central Europe. Using structural equation models, we will fit and test a causal effect model that includes the direct effect, indirect

effect, and the interactions among elements that better explain the model (e.g., Simons et al., 2016). We will also focus in the estimation of latent variables that could define and describe the concept of habitat heterogeneity effect as explanatory variable for each taxa.

This study will provide a causal effect model that will contribute to a better mechanical understanding of biodiversity dynamics within managed forests. Its contribution to the Working Group 2 needs to be complemented by the effect of time and forest management strategies evaluated by Sitzia et al (2021). Therefore, we propose to work in close collaboration with Sitzia et al (2021) during the data analysis and discussion in order to produce a set of 2 research papers. Considering the similarities on the time schedule of both proposals, we aim to deliver our paper around the same time that Sitzia's team.

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Core authors from BOTTOMS-UP: Sebastian Kepfer Rojas, Francesco Chianucci, Yoan Paillet, Johannes Penner

Core authors outside BOTTOMS-UP: Carsten Dormann, Jürgen Bauhaus, Thomas Asbeck, Xiang Liu, Dina Emrich, Jan Helbach, Nolan Rappa, Joao Cordeiro, Marco Basilie, Sebastian Schwegmann, Max Wieners.

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:

1,- I request to use the Raw_data_taxa dataset at plot level for: birds, bats, beetles, lichens, understory vegetation and fungi in all 224 available sites including the forest categories 4, 5, 6, 7, 8, 9. The data will be aggregated at sites level or subsites (depending the results of explorative analysis) before been used in the Structural Equation Modeling.

2,- As environmental variables to describe the forest structure in terms of tree richness, average DBH, proportion of native tree species, amount of deadwood, tree density, total number of TREMs, index of non-native tree species, Shannon index of TREMs, DBH variation, variation in deadwood decay categories, deadwood categories, regeneration type, area, and .I request to use both "Raw_data_structure" and "Plot_Stand_description" data set at plot level in all 224 sites including

the forest categories 4,5,6,7,8, and 9. The data will be aggregated at sites level or subsites (depending the results of explorative analysis) before been used in the Structural Equation Modeling.

- Do you need data for specific regions, forest categories or silvicultural regimes?

If yes please give details through coordinates ranges (Ref. System: 4326) or identifying categories based on the sheet "metadata description" (columns: value range, list values) of the attached table "Template for data contribution".

I need to use all the variables for forest categories: 4,5,6,7,8, and 9 described in the following table:

Variable name	Description
Plot stand description	
datalD	Unique code of the dataset where the same protocol sampling is applied
sitelD	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)
silsl1	Current silvicultural system - Hierarchical level 1
silsl2	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
clastd	Total number of decay classes used for standing deadwood (standing dead tree + snag)
clalyd	Total number of decay classes used for lying deadwood (logs+stump)
clalog	Total number of decay classes used for logs
clastu	Total number of decay classes used for stumps
refdec	Reference paper or study used for the determination of deadwood decay classes
refvit	Reference paper or study used for the determination of tree vitality classification
Data Standing structure	
sitelD	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)
decsta	Decay stage class (just for standing dead trees)
plosiz	Size of the plot where the reference tree is surveyed
weisiz	Plot area ratio per hectare
Data Lying structure	
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
genus	Tree genus Latin name
species	Tree species Latin name
treesp	Full scientific species name
typldw	Type of lying deadwood
oriart	Origin of the element (if detectable)
diam01	Largest diameter measured
diam02	Smallest diameter measured
diam03	Median diameter measured (if different from the previous ones, otherwise NA)
lenhei	Length or height measured
volume	Volume measured
lis	Logs surveyed using LIS (line intercept sampling) method
decsta	Decay stage class
plosiz	Size of the plot where the reference element is surveyed
weisiz	Plot area ratio per hectare
Raw Data Taxa	
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

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

I will use the two

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

I will use the data for the following taxa

Taxa		
Aves	Coleoptera	Lichinales
Basidiomycota	Bryophytes	Chiroptera
Bryophyta	Fungi	Tracheophyta

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

Yes

- Do you need data on lying deadwood?

Yes

Based on the data subset that derives from your answers a group of data providers that should be included in the manuscript with least effort on the analytical and writing part will be identified according to the platform bylaws (providing more than 2% of the data needed).

Please note that always according to the bylaws all the consortium will be invited to participate in your project but in this case only in view of a substantial contribution to the analysis and writing.

Time line:

Deadline for permission of data usage from custodians: October 2021

Extraction of data from BOTTOMS-UP: November 2021

Data preparation and analysis: by the end of December 2021

Raw results to be sent to the wider author team: January 2022

Workshop with the wider author team: February 2022

Writing up of the paper (including preparation/optimization of figures): End of April 2022

Feedback round of co-authors to MS: May-June 2022

Submission: July- August 2022

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