

Doctoral Dissertation

Biodiversity assessments with machine learning based on forest inventory data

submitted by

DIⁱⁿ Jana-Sophie ETTE, BSc, MSc

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Supervisor:

Univ.Prof. DI Dr. Dr. Thomas Geburek Institute of Silviculture Department of Forest- and Soil Sciences

Affidavit

I hereby declare that I have authored this dissertation independently, and that I have not used any assistance other than that which is permitted. The work contained herein is my own except where explicitly stated otherwise. All ideas taken in wording or in basic content from unpublished sources or from published literature are duly identified and cited, and the precise references included. Any contribution from colleagues is explicitly stated in the authorship statement of the published papers.

I further declare that this dissertation has not been submitted, in whole or in part, in the same or a similar form, to any other educational institution as part of the requirements for an academic degree.

I hereby confirm that I am familiar with the standards of Scientific Integrity and with the guidelines of Good Scientific Practice, and that this work fully complies with these standards and guidelines.

Vienna, 18/08/2023

Jana-Sophie ETTE

J. He

"Müsset im Naturbetrachten Immer eins wie alles achten; Nichts ist drinnen, nichts ist draußen:

Denn was innen, das ist außen. So ergreifet ohne Säumnis Heilig´ öffentlich Geheimnis.

Freuet euch des wahren Scheins, Euch des ernsten Spieles: Kein Lebendiges ist Eins, Immer ist's ein Vieles."

Goethe (1827)

Supervisory team and reviewers

Supervisory team

Heino Konrad, DI. Dr. Manfred Josef Lexer, Univ.Prof. DI. Dr. Tim Ritter, BSc. MSc. Dr. Sonja Vospernik, Assoc. Profⁱⁿ. Drⁱⁿ.

Reviewers

Emanuele Lingua, Assoc. Prof. Dr. Konstantinos Poirazidis, Assoc. Prof. Dr.



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List of publications

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Ette JS: Conceptualization, Data Curation, Formal analysis, Investigation, Methodology, Project administration, Software, Validation, Writing – Original Draft, Writing- Review & Editing, Visualization

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Abstract

Loss of biodiversity threatens the provision of ecosystem services and erodes the foundation of civilization. As biodiversity monitoring is lacking, extent of global biodiversity crises and thresholds for ecological collapses are largely unknown. Main reasons are severe knowledge gaps in indicator choice and aggregation next to limited availability of resilient long-term data. The aim of the doctoral project is to advance forest biodiversity assessments in Central Europe by applying machine learning. Following research questions are targeted: (1) Is actual European biodiversity monitoring reliable? (2) How can understanding of indicator-indicandum relationships be extended? (3) How can forest biodiversity be assessed reliable in Central Europe? Machine learning ('R randomForest') provides new insights into indicatorindicandum relationships and intercorrelation within indicator sets. The approach demonstrates the forest stand characteristics indicated by forest structural biodiversity indicators and highlights the importance of indicator choice. Negative binary generalized models and generalized linear models prove that national biodiversity monitoring systems fail to report actual biodiversity loss in Europe. Hence, a novel Biodiversity Composite index (BCI) based on forest inventory and forest typing data is tested. BCI delivers high-resolution spatial maps of ecosystem-, species-, genetic-, and biodiversity. Advantages of the BCI approach are easy transferability, cost-efficiency, forest type rankings and a monitoring system in line with the Convention on Biological Diversity. In the case study Tyrol, Central Europe, coniferous forest types display higher potential to maintain biodiversity than deciduous and mixed forests. BCI supports decision-making in forest policy (e.g., cost-benefit analysis), biodiversity conservation (e.g., restoration priorities) and Sustainable Forest Management. Monitoring with BCI can help to halt forest biodiversity loss on the national scale.

Kurzfassung

Biodiversitätsverlust gefährdet die Ökosystemleistungen und somit die Grundlage der Biodiversitätsmonitoring sind Zivilisation. Durch fehlendes Ausmaß der globalen Biodiversitätskrise und Schwellenwerte für den Kollaps von Ökosystemen weitgehend unbekannt. Hauptgründe hierfür sind große Wissenslücken bei der Auswahl und Aggregation von Indikatoren und begrenzte Verfügbarkeit von belastbaren Langzeitdaten. Ziel der Dissertation ist es, Biodiversitätsmonitoring in Zentraleuropa mit Hilfe von künstlicher Intelligenz weiterzuentwickeln. Folgende Forschungsfragen werden bearbeitet: (1) Wie zuverlässig ist Biodiversitätsmonitoring in Europa? (2) Wie kann das Verständnis von Indikator-Indikandum-Beziehungen verbessert werden? (3) Wie kann Waldbiodiversität in Mitteleuropa zuverlässig bewertet werden? Machine learning ('R randomForest') liefert neue Einblicke in Indikator-Indikandum-Beziehungen und Interkorrelation innerhalb von Indikatorensets. Die Ergebnisse verdeutlichen, wie Standortscharakteristika des Waldes durch gängige Strukturdiversitätsindikatoren indiziert werden, und heben die große Bedeutung der Indikatorenwahl für Biodiversitätsbewertungen hervor. 'Negative binary generalized models' und 'Generalized linear models' unterstreichen, dass die nationalen Monitoringsysteme den tatsächlichen Biodiversitätsverlust Europas aktuell nicht erfassen. Daher wird ein neuer Biodiversitätsindex (BCI) auf der Grundlage von Waldinventurdaten und Waldtypisierung getestet. BCI liefert hochauflösende, räumliche Karten von Ökosystem-, Arten-, und genetischer Vielfalt, sowie der Biodiversität. Die Vorteile des BCI-Ansatzes sind einfache Übertragbarkeit, Kosteneffizienz, ein Ranking der vorkommenden Waldtypen und ein Monitoring im Einklang mit der Biodiversitätskonvention. In einer ersten Fallstudie in Tirol, Zentraleuropa, zeigen Nadelwälder höheres Potential zum langfristigen Erhalt der Biodiversität als Laub- und Mischwälder. BCI kann zur Entscheidungsfindung in der Forstpolitik (z. Bsp. Kosten-Nutzen-Analyse), zur Prioritätensetzung im Naturschutz, und für Weiterentwicklung nachhaltige Waldbewirtschaftungskonzepte verwendet werden. Monitoring mit BCI kann dabei helfen, den Verlust der biologischen Vielfalt im Wald auf nationaler Ebene aufzuhalten.

1. Introductory overview & Biodiversity crisis

Nature is within severe biodiversity crisis (Singh 2002, Koh et al. 2004). Climate crisis and biodiversity crisis mutually reinforce each other (IPBES 2019, Pörtner et al. 2021). Real extent of biodiversity crisis is largely unknown, but species extinction rates are about one hundred to one thousand times greater than the natural baselines (Ceballos et al. 2010, 2015). Main drivers of species extinction and biodiversity decline are of anthropogenic origin (Sala et al. 2000, Newbold et al. 2015). Forest degradation, fragmentation, and loss as side effects of human economic activities already caused severe biodiversity losses (Newbold et al. 2015, FAO & UNEP 2020).

The rapid rate of biodiversity loss (Cardinale et al. 2012, Reich et al. 2012) is an emerging public concern. Biodiversity plays a crucial role in biological processes, productivity, forest multifunctionality and stability of forest ecosystems (Hooper et al. 2005, Balvanera et al. 2006, Mace et al. 2012, Gamfeldt et al. 2013, Liang et al. 2016, FAO & UNEP 2020). There is high scientific evidence for a positive relationship between the loss of biodiversity and the decline of forest ecosystem services (Hooper et al. 2005, Balvanera et al. 2006, Isbell et al. 2011, Mace et al. 2012, Gamfeldt et al. 2013). Biodiversity loss threatens the provision of ecosystem services at an accelerating rate and erodes the foundation of civilization (IPBES 2019).

1.1. Challenges in biodiversity policy

"Biological diversity means the variability among living organisms from all sources including, inter alia, terrestrial, marine, and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems."

(Convention on Biological Diversity 1992)

1.1.1. Awareness for biodiversity

The idea of 'biological diversity' was firstly mentioned in a work of J. Arthur Harris (1916). In 1986, the term 'biodiversity' was invented at a scientific conference in 1980 by Walter G. Rosen in Washington D.C. (Wilson 1988), making biodiversity research a young, but rapidly emerging scientific field. Today, biological diversity is the main target of conservation actions (Sutherland et al. 2009).

Extent of the biodiversity crises, magnitude of decline and thresholds for ecosystem, species or genetic collapses are still unknown. However, potential consequences of biodiversity loss for ecosystem services and their immense financial value for macro- and microeconomy can be assessed more easily. Leaving aside potential consequences for societies, individuals, the responsibility towards upcoming generations and ethics, potential economic consequences of are devastating.

Acknowledging the importance of biodiversity for humanity, numerous measures in policy, public and sciences have been taken to halt biodiversity loss. By signing the UN Convention on Biological Diversity (CBD) in 1992, 196 countries committed themselves to halting the loss of biodiversity. From 1992-2003, about 14.4 billion USD have been spent globally to reach this aim (Waldron et al. 2017). These investments and rising public awareness succeeded to slow down the rate of predicted species decline by 29% (Waldron et al. 2017). However, the CBD strategic plans and targets to control biodiversity loss were never met (CBD 2014, Tittensor 2014). In addition to lacking capacities in terms of coordination, science, administration, and legislation, the lack of success in biodiversity policy implementation is related to gaps in biodiversity monitoring (Pareira et al. 2012, CBD 2018).

Furman et al. (2007) identified four types of constraints, (i) Social constraints (e.g., participation, communication, legitimacy, perception), (ii) Policy constraints (e.g., research, data, policy options, integration, coordination), (iii) Economic constraints (capital, labor, natural resources) and (iv) Resource constraints (e.g., rarity of habitat, species, ecosystem characteristics). Consequently, successful biodiversity conservation integrates social, cultural, and economic aspects. This thesis should contribute to overcome social and policy constraints to halt the loss of forest biodiversity.

1.1.2. How much biodiversity is enough?

As part of the 'shifting baseline problem', biodiversity scientists need to balance various stakeholder requirements while being asked to answer this question and evaluate own study outcomes. The doctoral thesis might be relevant for four stakeholder groups: The public, conservationists (Protected Area Management, NGOs), policy makers, and scientists. Scientists might be most interested in methodology (Ette et al. 2023a, 2023b), while other stakeholder groups may benefit from study outcomes, indicator choice, potential contribution to decision-making in forest policy and evaluation of biodiversity policy implementation (Ette and Geburek 2021, Ette et al. 2023a, 2023b).

Whether a biodiversity level is considered being 'high enough' depends on the underlying stakeholder perspective. Stakeholder requirements for biodiversity policy can differ considerably in quantitative, spatial, and temporal aspects. From public point of view, main requirements could be to locally assure sufficient biodiversity levels to live a 'good life' or maintain status quo for this and the upcoming human generation. Contrary, conservationists would like to conserve as much biodiversity as possible, long-term on all spatial scales, following ethical and ecological considerations. Main political requirements could be to maintain a minimum biodiversity level which does not lead to major negative consequences for both, economy, and society, in the short-term on large spatial scales.

As a fact, biodiversity evolves very slowly and is driven by ecological forces (CBD 1992). Species and genotypes are unique products of 3.5 billion years of evolution (Schopf 2006). Losing ecosystem, species or genetic diversity might therefore be an irretrievable loss. This doctoral project focuses on unmanaged reference areas, forest typing, machine learning, and various model approaches to tackle the baseline problem of biodiversity assessments.

1.2. Material & Challenges in biodiversity research

"An attempt to measure global diversity is a mission worthy of the best efforts of science." (Wilson 1988)

1.2.1. Biodiversity indicators and indicator choice

Biodiversity cannot be measured directly. Ecological and environmental indicators play an essential role in assessing biodiversity and were established in large numbers (Lindenmayer et al. 2000, Larsson et al. 2001, Chirici et al. 2011). Indicators should be based on achievable, quantitative data, be policy and ecosystem relevant, assessable to monitoring, sensitive to pressures on biodiversity, have an indicative value and stable properties (CBD 1997). These standards are very difficult to fulfill. Scientists, policy makers, and resource managers are facing knowledge gaps while having to decide which and how to choose and aggregate biodiversity indicators (Yoccoz et al. 2001, Katzner et al. 2007, Jones et al. 2011). Sometimes also value judgments need to be made which makes biodiversity indicator choice neither entirely objective nor easy (CBD 1997).

Some biodiversity indicators are criticized for poor indicator-indicandum relationships (Ferris and Humphrey 1999, Margules et al. 2002, Duelli and Obrist 2003, Gao et al. 2015). Following Heink and Kowarik (2010), an indicator is of major relevance for a given issue, e.g., assessment of a certain impact for conservation policy, while an indicandum is the phenomenon indicated.

Inter alia, forest biodiversity indicators can be classified into indicators of species diversity and indicators of (structural) variety. Due to weak correlations to the indicandum, indicator species concepts have not succeeded as surrogates for biodiversity (Margules et al. 2002, Duelli and Obrist 2003). However, there is broad scientific evidence for positive relationships between measures of forest structural variety and elements of biodiversity (Begon et al. 1991, McNally et al. 2001, Winter et al. 2008). Structural diversity concepts indicate potential habitat quality, niche differentiation, structural complexity (Heym et al. 2021), mating systems of forest trees and other sources of forest biodiversity (McElhinny et al. 2005) e.g., for umbrella species (Müller et al. 2009) and bird species (MacArthur and MacArthur 1961). Hence, assessing forest biodiversity based on forest inventory data, the doctoral project's indicator choice favors indicators of structural variety over indicators of species diversity.

In this dissertation surrogates, indices, and indicators of forest biodiversity are evaluated. Even in scientific publications, distinction between these terminologies is not always straightforward. Indices are metrics of biodiversity, while indicators are metrics of biodiversity of major relevance for a given issue which proved relationship to a certain indicandum (McGeoch 1998, Heink and Kowarik 2010). Although the relationship to the indicandum may not be fully understood yet, we will refer to all metrics of biodiversity as 'biodiversity indicators' in the following. Surrogates characterize biodiversity levels if direct measurement (s.str., metrics) of biological diversity are not feasible (Bredemeier et al. 2007). For all approaches, spatial and temporal assessment scales determine applicability of surrogates (Shmida and Wilson 1985, Rahbek 2005) and indicators (Fleishman et al. 2003, Hess et al. 2006) of biodiversity. Predictive power of biodiversity indicators tends to increase from local to global scales (Bredemeier et al. 2007). The doctoral thesis targets large spatial and temporal scales to support biodiversity conservation. Priority in indicator evaluation was given to the national

beta-diversity which is in line with national biodiversity reporting obligations and the CBD's conservation strategy.

1.2.2. Forest inventory data

On large spatial and temporal scales, the availability of reliable data sets is a limiting factor for biodiversity assessments and monitoring (Purvis and Hector 2000, Heym et al. 2021). Forests, especially in moist tropical regions, host most biodiversity of terrestrial ecosystems (Gibson et al. 2011, FAO & UNEP 2020). Without sound biodiversity monitoring and reporting systems, natural resources get overexploited or marginalized in decision making (Norton 1998, European Commission 2023).

National Forest Inventories (NFIs), which most European countries have long-term experience with, were originally designed to assess wood volume on the national level (Chirici et al. 2011). Under the threat of biodiversity loss, Central European countries could benefit from evaluating these large, statistically robust data sets and timelines with comparably small grid sizes.

Yet, large scale forest inventories have rarely been used for structural diversity assessments (Kändler 2006, Polley 2010). Nonetheless, forest inventories proved potential to overcome data deficits on large spatial and temporal scales (Winter et al. 2008, Müller et al. 2009, Chirici et al. 2011, Corona et al. 2011, Storch et al. 2018). Major advantages of inventory-based biodiversity assessments are the repeated measurements which detect temporal changes (Heym et al. 2021) with low additional costs (Corona et al. 2003, 2011) at a high number of attributes, forest types, sample sizes and scales (Storch et al. 2018, Heym et al. 2021). In long term, changes in forest biodiversity may even be related to forest management activities (Storch et al. 2018) and forest policy measures which makes it highly reasonable to choose diversity indicators based on available forest inventory data.

1.3. Objectives & Research questions

"Biodiversity research starts with the right question."

(Bredemeier et al. 2007)

The aim of the doctoral project is to advance forest biodiversity assessments in Central Europe based on available forest inventory and forest typing data. The dissertation should contribute to closing the knowledge gaps on forest-inventory based indicators, indicator-indicandum relationships, establishment of comprehensive indicator sets by using machine learning and state-of-the art data pre- and post-processing. The outcomes can support biodiversity policy implementation, biodiversity conservation and Sustainable Forest Management to halt the loss of biodiversity establishing reliable, high-resolution forest biodiversity monitoring.

The dissertation aims to maximize the biodiversity-related, informative value of available inventory data, which is a very pragmatic approach to provide long-term scientific policy consulting. Starting with a master thesis in the Vienna woods in 2018, forest biodiversity research has been conducted in two working groups and research institutions simultaneously until 2023 which is the reason for deviating study areas.

The three research questions of the dissertation are:

1. Is actual European biodiversity monitoring and reporting reliable?

Which kind of biodiversity indicators are currently monitored in Europe? What is the actual European conception of biodiversity?

2. How can understanding of indicator-indicandum relationships be extended?

How do well-established biodiversity indicators relate to aspects of forest diversity? How do comprehensive indicator sets relate to aspects of forest diversity?

3. How can forest biodiversity be assessed reliable in Central Europe?

How can inventory grid data be used for area assessments?

Which ecosystem, species and genetic diversity levels can be found in a case study in Central Europe?

How can a novel biodiversity index based on forest inventories support forest biodiversity conservation?

The research questions of the cumulative dissertation are answered by three scientific publications.

Research Question 1: Is actual European biodiversity monitoring and reporting reliable?

Ette JS, Geburek T (2021) Why European biodiversity reporting is not reliable. Ambio 50: 929–941. https://doi.org/10.1007/s13280-020-01415-8

In this publication, biodiversity indicator choice of 42 CBD national reports is systematically reviewed. *Negative binary generalized models* and *generalized linear models* are used to detect significant relationships between national biodiversity indicator choice and geographic and socio-economic country properties. The work determines whether European biodiversity reporting and monitoring is reliable, which kind of biodiversity indicators are currently monitored in Europe, and whether the European conception of biodiversity is in line with the CBD definition.

Currently, there is no internal mechanism in the CBD body established to monitor nationallevel compliance and the implementation of biodiversity policies (Morgera and Tsioumami 2011, Vordermayer-Riemer 2019). Freedom of indicator choice in biodiversity reporting allows for conceptions of biodiversity that differ from the CBD definition, which would be disadvantageous for halting biodiversity loss globally. Our scientific objective is to support the implementation of the CBD by systematically reviewing biodiversity indicator choice and evaluating scientific evidence for the countries' biodiversity status reported.

Considering 42 European national CBD reports, following scientific questions are answered: (1) Which kinds of biodiversity indicators are particularly prevalent? (2) Are ecosystem, species, and genetic diversity considered adequately? (3) Is freedom of indicator choice in

CBD reporting guidelines beneficial for monitoring and reporting quality? The publication is a pre-study for the design of the Biodiversity Composite Index (Ette et al. 2023b).

Research Question 2: How can understanding of indicator-indicandum relationships be extended?

Ette JS, Ritter T, Vospernik S (2023a) Insights in forest structural diversity indicators with machine learning: What is indicated? Biodiversity and Conservation 32: 1019–1046. https://doi.org/10.1007/s10531-022-02536-0

In this publication, a machine learning approach to provide novel insights in indicatorindicandum relationships of biodiversity indicators and comprehensive indicator sets is presented. The indicators tested are parameters of forest spatial and structural heterogeneity. We surveyed a comprehensive indicator set of Clark & Evans-, Shannon, Stand Density, Diameter Differentiation index, and Crown Competition Factor with randomForest and examine their indicative value for twenty explanatory stand variables.

Biodiversity indicators are sometimes criticized for displaying poor indicator-indicandum relationships (Ferris and Humphrey 1999, Margules et al. 2002, Duelli and Obrist 2003, Gao et al. 2015). Machine learning proves to be a useful tool to overcome these knowledge gaps and provides additional insights in indicator-indicandum relationships. This scientific work is the second pre-study for designing the Biodiversity Composite Index and deepens understanding of statistic properties of forest-inventory based biodiversity indicators and comprehensive indicator sets.

Examining 37 unmanaged core areas in the Vienna Woods, following scientific questions are answered: Which levels of structural diversity can be found in the unmanaged core areas of the Biosphere Reserve Vienna Woods? (2) Which stand characteristics are indicated by single structural diversity indicators? (3) Which stand characteristics are indicated or neglected by a comprehensive indicator set? (4) How strong is the intercorrelation in an indicator set?

Research Question 3: How can forest biodiversity be assessed reliable in Central Europe?

Ette JS, Sallmannshofer M, Geburek T (2023b) Assessing Forest Biodiversity: A Novel Index to consider Ecosystem, Species, and Genetic diversity. Forests 14(4): 709. https://doi.org/10.3390/f14040709

From the first pre-study, we learned that current European perception of biodiversity is biased, and that genetic diversity is neglected in European biodiversity monitoring and reporting. The second pre-study highlighted the importance of indicator choice and demonstrated that knowledge about indicator-indicandum relationships is crucial for establishing comprehensive biodiversity indicator sets. With the final publication (Ette et al. 2023b), a novel composite biodiversity index (BCI) is presented.

With BCI, a systematic approach for establishing a comprehensive indicator set out of available forest monitoring data is proposed. Data referencing and spatial modeling is based on forest typing and machine learning. In a case study, forest biodiversity of the Austrian

province of Tyrol is assessed in high resolution on the level of ecosystem, species, and genetic diversity. The new approach is designed to be transferable to neighboring Central European areas with forest-typing and can be repeated cost-efficiently in each inventory period.

Large scale forest inventories have rarely been used for structural diversity assessments (Kändler 2006, Polley 2010). However, forest inventories proved potential to overcome data deficits on large spatial and temporal scales (Winter et al. 2008, Müller et al. 2009, Chirici et al. 2011, Corona et al. 2011, Storch et al. 2018). The intention of BCI is to aggregate ecological information in a surrogate approach, advance forest-inventory based biodiversity assessments, and monitor all levels of forest biodiversity in line with the CBD.

The BCI approach assembles of indicators, which (1) are based on available data sets, (2) are of high scientific evidence relevant to biodiversity, and (3) equally consider ecosystem, species, and genetic diversity. BCI should be seen as a further step towards objective and reliable forest biodiversity assessments to halt the loss of biodiversity on the national level.

1.4. Biodiversity theories

"Biodiversity comprises the expression of life on earth in all its various forms and at all its relevant levels of complexity, in a hierarchy from genes to the biosphere." (Bredemeier et al. 2007)

Biodiversity is the main target of conservation actions (Sutherland et al. 2009). In biodiversity science and conservation, a large variety biodiversity-maintaining mechanisms have been proposed (Palmer 1994). Biodiversity theories are meant to ease biodiversity assessments and conservation. However, biodiversity theory choice should be well considered. From the variety of theories, contrasting conservation measures can be derived and subjectivity is added to conservation activities.

Biodiversity theories are based on including or excluding the processes ecological drift, natural selection, speciation, and species dispersal in single species or community approaches (Vellend 2010) to explain biological diversity and its persistence in ecosystems. Following Meyer et al. (2018), biodiversity theories can be grouped into *island biogeography* (e.g., MacArthur and Wilson 1967), *niche* (e.g., MacArthur 1972, Tilman 1982, Gause 2003) and *neutral theories* (e.g., Hubbell 2001). In particular ecosystems, scientific evidence is available for all groups of theories (Meyer et al. 2018). Scientists and conservationists use a particular biodiversity theory or combined approaches (*intermediate theories*) to reduce ecosystem complexity in models and ease decision making in biodiversity conservation.

Island biogeography theory considers ecological drift and species dispersal. Classic niche theories solely involve the processes of natural selection (e.g., Tilman 1982) and seldomly speciation and species dispersal (e.g., Ricklefs 1987). Neural biodiversity theories focus on ecological drift and sometimes consider speciation and species dispersal (e.g., Hubbell 2001). Frequently, biodiversity theories are consulted implicitly in biodiversity conservation and science (Meyer et al. 2018). Nonetheless, theory choice can be decisive and frames study design. Niche theories and island biogeography theories have been very influential for biodiversity conservation concepts (Schulte et al. 2006). This dissertation relies on classic

niche (Ette at al. 2023b) and island biogeography theories (Ette and Geburek 2021, Ette et al. 2023a).

Niche theories

Selection-focused niche theories (MacArthur 1972, Tilman 1982, Gause 2003) explain coexistence of species with unique species traits and ecological niches varying in space and time. Consequently, species cannot be interchanged easily in a community (Meyer et al. 2018), making explanations and assessments of biodiversity with niche theories highly complex (Rosindell et al. 2011). Today, ecological niche theory is well-established for decision-making in nature conservation (Meyer et al. 2018). Following niche theories, conservation of single species can be an important step to maintain overall biodiversity.

In this dissertation, niche theories are used to assess forest biodiversity on fine spatial scale (Ette et al. 2023b). Trees are the foundation species of forest ecosystems. Tree species composition and abundance are the basis for forest structure, crown structure, habitat availability and structural elements. They are also decisive for light, water and nutrient cycles and shape air humidity, light waves, wind turbulences, soil properties and organic decomposition. Deviation of the actual plant communities (Austrian Forest Inventory) from expected plant species and social dominance is affecting BCI species diversity ratings negatively. In a surrogate approach, two BCI indicators award close-to-natural tree and plant species are treated as *flagship species* of the forest type providing habitat, food, and shelter to associated species. Non-native invasive plants effect BCI evaluations negatively and cannot add to the BCI species diversity ratings. Using indicators for intraspecific genetic diversity of Norway spruce manifests the overall importance of niche theories for the Biodiversity Composite Index. Niche theories applied in BCI promote beta-diversity to conserve forest biodiversity.

Island biogeography theories

Drift-focused island biogeography theories use stochastic effects to explain biodiversity maintenance (Rosindell et al. 2012). Conservation actions derived from island biogeography theories support the maintenance of species-rich communities (high alpha diversity) and ecosystem processes (e.g., natural disturbance theories) to guarantee ecosystem function stability (Meyer et al. 2018). Following drift-focused biogeography theories, conservation of single species is of minor importance and species can be interchanged more easily within a community. Those theories have limited applicability to communities of (red listed) species with high habitat-specificity (Meyer et al. 2018). Island biogeography theories support insurance hypotheses (Yachi and Loreau 1999), which are one of the important motivations of policy makers to protect biodiversity.

Island biogeography theories are applied in two out of three scientific publications of the cumulative dissertation (Ette and Geburek 2021, Ette et al. 2023a). They are advantageous for biodiversity studies on large spatial scales and can effectively reduce study complexity for abstract, statistical considerations about indicator-indicandum relationships (Ette et al. 2023a) and biodiversity reporting reliability (Ette and Geburek 2021). Both publications search for statistical significance in large data sets. The pre-studies' objectives are to deepen understanding of indicator choice, composite index design, and machine learning in biodiversity assessments.

1.5. Conception of biodiversity

"Biodiversity means different things to different people." (Noss 1990)

Capturing the complexity of life

Our knowledge about diversity of life on earth is dramatically incomplete (Bredemeier et al. 2007). Global estimations for species richness range between five million (Costello et al. 2013) and one trillion species (Locey and Tennon 2016). Even under conservative estimations, 86% of land and 91% of marine species are undiscovered (Sweetlove 2011). Hence, concerns about ongoing erosion and decline of biodiversity is based on observations of key species loss and increasing ecosystem degradation. Leaving genetic diversity loss aside, a strong line of reasoning in biodiversity conservation is the link between habitat and species loss (Bredemeier et al. 2007).

Biodiversity theory provides evidence for indicator choice and rating, whereas underlying definition of biodiversity (conception of biodiversity) can provide logic structure to a composite index (Ette at al. 2023b) and biodiversity monitoring systems (Ette and Geburek 2021). As real status of biodiversity is unknown, it is fundamental to consider underlying biodiversity conception. The conception of biodiversity should match study objectives, ecological knowledge, data sets, relevant scales, and stakeholders involved.

Many parameters of forest spatial heterogeneity (Reineke 1933, Shannon & Weaver 1949, Clark & Evans 1954, Krajicek et al. 1961) date back before biodiversity emerged as a topic in science. These parameters deal with forest structural diversity as a statistical problem of information theory (Bredemeier et al. 2007). They provide numerical information about spatial distribution of species and objects based on random sampling (e.g., forest inventories). Other ideas e.g., to order species by their ecosystem function, were also formulated earlier (Elton 1927) and later resumed by conservation science to assess *functional diversity*.

Single species focus

Proceedings in biodiversity research are closely linked to international environmental policy. Before the Convention of Biological Diversity (CBD 1992), biodiversity conservation strongly focused on species diversity maintenance (*umbrella, flagship, and target species*) to protect the variety of life (Furman et al. 2007). Until today, species abundances and species counts are perceived a very intuitive way to assess biodiversity and enjoy a high degree of public credibility. The first formal policy recommendation to focus on biological diversity in biological monitoring was given in the *Brundtland Report* (WCED 1987). Early European biodiversity monitoring programs tried to describe effects of human pressure on economic important ecosystems (e.g., effects of increased acidification on forest soil) but rapidly started to surveil particular target species instead (Furman et al. 2007). In short terms, indicator organisms for improvement of soil, water, and air quality measurements became internationally accepted (Spellerberg 1991). Until, in terms of key ecosystem functions (LaRue et al. 2019) and indicator-indicandum relationships (Gao et al. 2015), structural indicators and surrogate approaches began to prove higher scientific evidence than species indicators.

Genetic diversity focus

According to the CBD, biodiversity has three components of equal value: Ecosystem, species, and genetic diversity which can be aggregated to overall biodiversity. With this conception, the CBD body follows a *hierarchical level model*. Biodiversity is regarded as consisting of various, hierarchically nested organizational and spatial scales making assessments highly complex. The key functions of genetic diversity are recognized and anchored in the CBD definition of biodiversity. Genetic diversity is the foundation of all biological diversity and enhances persistence and the evolutionary potential of all species (Allendorf et al. 2012). In certain ecosystems, genetic diversity may provide biological functions similar to that of species diversity (Cook-Patton et al. 2011).

Nonetheless, genetic diversity is frequently neglected in actual biodiversity conservation (Pareira et al. 2012). Monitoring genetic diversity requires complex laboratory analyses whereas assessing ecosystem diversity and species diversity may be less challenging. Consequently, genetic diversity is still not being monitored on the national level and genetic diversity indicators and thresholds are missing (Laikre et al. 2010). CBD policies concerning genetic diversity lag behind implementation for other levels of biodiversity, although knowledge of conservation genetics, molecular genetics and statistical tools is scientifically available (Hunter and Gibbs 2006, Fussi et al. 2016).

Community focus & Complex surrogate approaches

In 1995, biological long-term monitoring was recognized to be an essential tool to assess the extent of biodiversity loss by distinguishing between human-made and natural ecosystem changes (Stork and Samways 1995). Then, scientific proceedings enabled processing of large datasets providing a deeper understanding and advancements towards more complex ecosystem and community approaches. Molecular markers, machine learning and big data (e.g., satellite data) can be seen as milestones in biodiversity assessments (Bredemeier et al. 2007). They paved the way for new discoveries in speciation, adaptation, ecosystem complexity, habitat fragmentation, species migration, and intraspecific diversity. With these novel techniques, the scientific focus in biodiversity research broadened to examine genetic diversity, functional diversity, and large study scales in surrogate and indicator approaches.

The better science understood the relationships and interactions between elements of the ecosphere, the less the severe impact of human activities on ecosystems could be denied. The conviction of mankind being part of the ecosystems brought new perspectives on biodiversity initiatives (Furman et al. 2007). It became broadly recognized that the future of humanity is depending on sustainable development and that biodiversity is the foundation of our civilization (IPBES 2019). Scientists started to include human pressure on biodiversity in *pressure-state-response (PSR-) models*. Some authors refined this approach to additionally consider biodiversity drivers and impact factors (*DPSIR-models*). Congruently, *'composition, structure & function'* (Franklin et al. 1981) is an advancement of the CBD definition. It adds ecological and evolutionary processes (e.g., gene flow, nutrient cycling) to ecosystem, species, and genetic diversity to assess biodiversity (Noss 1990).

Today, there are at least eight biodiversity conceptions widely used to conserve, assess, and manage biodiversity on different scales (Tab. 1). Most of them evolved simultaneously based on ecological findings after the CBD's Earth Summit. However, admiration for rare species and high alpha diversity ('biodiversity hotspots') never vanished from the public mind and is still shaping nature conservation funding, measures, and science on behalf of more complex mathematical approaches (e.g., Ette & Geburek 2021).

	Name	Establishment & Case studies	Possible study objectives	Common stakeholder perspective	Scales
ngle Species Focus	Umbrella, flagship, and target species	Lambeck (1997), Noss (1999), Crosby et al. (2015), Eckelt et al. (2018)	-species diversity: species extinction, red- listed species -nature protection: rare ecosystems, species migration, habitat ranges, protected area & landscape management	Media, NGOs, public	Spatial: medium- small, temporal: small
0	Functional diversity	Elton (1927), Tilman (2001), Van Tienderen et al. (2002), Pla et al. (2012), Laureto et al. (2015)	-ecosystem services: ecosystem stability, ecosystem productivity, natural hazards -soil functioning: agriculture, land use	Science, soil organisms, taxonomy, agriculture	Spatial: medium- small, temporal: large- medium
Diversity	Alpha-, Beta- and Gamma- diversity	Whittaker (1960, 1972), Loreau (2000), Crist and Veech (2006), Walters and Martiny (2020), Kazerani et al. (2021)	-conservation planning: landscape management, land use -landscape ecology: Species coexistence, species communities, soil microbiomes	Policy, protected areas, ecologists	Spatial: large- small, temporal: small
Genetic D	Genetic diversity	Wilcox (1984), Olivieri et al. (2008), Carrasco et al. (2016), DeWoody et al. (2021)	-genetics: conservation genetics, molecular genetics, population genetics, speciation, -agrobiodiversity -rare species	Evolution research, genetics, agriculture, breeding	Spatial: large- medium, temporal: large- small
Surrogate Approaches / Community Focus	Ecosystem, species, and genetic diversity (CBD definition)	Norse and Stout (1986), OTA (1987), CBD (1992), Ette and Geburek (2021), Ette et al. (2023b)	-environmental policy: climate change adaption, biodiversity reporting, sustainable development goals -nature protection: biodiversity conservation, Conservation genetics	NGOs, policy, nature protection	Spatial: large, temporal: large
	Composition, Structure, and Function	Franklin et al. (1981), Noss (1990), Heym et al. (2021), Ette et al. (2023a)	-forestry: quantitative biodiversity indicators, Sustainable Forest Management -decision making -habitat complexity	Forest management, policy, protected areas, NGOs	Spatial: medium, temporal: medium- small
	Pressure- State- Response (PSR)	OECD (2003), Levrel et al. (2009), Geburek et al. (2010), McGeoch et al. (2010), Burgess et al. (2017), Fen et al. (2022)	-environmental policy -land use: urban areas, ecosystem integrity, -bioeconomy: Sustainable Forest Management, carbon management	Landscape planning, Natural resource management, NGOs, policy	Spatial: large, temporal: small

Driver-	Rapport and Friend	-decision making	Environmental	Spatial:
Pressures-	(1979), OECD (1993),	-landscape	policy,	large,
State-Impact	EC (1999), Essayas	management: marine	protected	_
Response	(2010), Patrício et al.	and river management	areas	temporal:
(DPSIR)	(2016), Pagan et al.	-biodiversity policy		small
	(2020)	reporting		

Tab. 1: Eight common conceptions of biodiversity and their establishment over time.

The Convention on Biological Diversity has three main goals: (1) conservation of biological diversity, (2) sustainable use of biodiversity and (3) fair and equitable sharing of benefits arising out of the utilization of genetic resources (CBD 1992). According to the CBD definition of biodiversity, an intergovernmental negotiation process between 195 member states and the European Union, biodiversity has three components of equal value (ecosystem diversity, species diversity and genetic diversity) which can be aggregated to biodiversity (CBD 1992). Globally, the CBD definition of biodiversity is still having a great impact upon biodiversity conservation (Furman et al. 2007).

The dissertation employs the CBD definition of biodiversity for several reasons: (I) Study objectives; (II) forest inventory-based machine learning approaches to assess large scales; (II) target group are policy makers, the CBD secretary, forest companies and protected area management; (III) data sets allow for genetic diversity assessments. It is highly reasonable to stick to the definition of biodiversity on which 195 CBD members states and the European Union have agreed on to support biodiversity policy implementation. Having to choose a spatial scale, priority was given to the national beta-diversity which is in line with reporting obligatoriness and overall CBD strategy. Beta diversity denotes diversity between ecosystems by focusing and comparing taxa that is unique to a country (Whittaker 1960). The European Union's nature protection measures follow this approach e.g., by inventing Natura2000 areas, restoration of degraded ecosystems, environmental impact assessments, and programs for red-listed species and ecosystems.

1.6. Methods & Modeling approaches

"Applying machine learning approaches in monitoring allows to scale projects by an order of magnitude while maintaining conservation costs." (Klein 2015)

1.6.1. Count data regression

In Ette and Geburek (2021) count data derived from the national CBD reports is tested by performing regression analysis following the approach of Naidoo and Adamowicz (2001). Twelve hypotheses about relationships between national geographic or socioeconomic characteristics and national biodiversity indicator choice are tested to determine reliability of European biodiversity reporting. The hypotheses are merged into eight models. Nonlinear regression analysis predicts the value of the dependent variables based on covariates (Naidoo and Adamowicz 2001).

To avoid inconsistent parameter estimation through incorrect distribution expectations, two model types are established: *Negative binary generalized models* (NBGM) and *Generalized linear models with Poisson error structure* (Poisson GLM). The NBGM assumption variable distribution, i.e., variance is a quadratic function of the mean, differs from Poisson GLM assumption, i.e., variance equals the mean (Naidoo and Adamowicz 2001).

The models are built with the R packages 'foreign', 'ggplot2' and 'MASS'. The 'MASS'-package uses an alternating iteration process for the NBGM calculation. The parameter theta and null deviance describe NBGM model fit. Chi squared distribution test compares model fit by likelihood ratio (Venables and Ripley 2002).

Overdispersion i.e., the variance of the response variable exceeds the variance of the mean, may lead to an underestimation of the standard errors and overestimation of the significance of the regression parameters (Cox 1983). Overdispersion occurs frequently building models on count data (Dormann 2016). The Poisson GLMs were tested for overdispersion using the R package 'AER'. For Poisson GLM, model fit is displayed by the deviation and overdispersion value.

1.6.2 Machine learning for classification tasks

'R randomForest' for ensemble problems

The randomForest classifier trains an ensemble of regression trees to predict data splits. In the language R (R Core Team 2020), the packages 'randomForest' (Breiman 2001, 2002), 'VSURF' (Geneuer et al. 2015) and 'randomForest explainer' (Ishwaran et al. 2010) are applied. Every random forest is composed of 500 regression trees. For every regression tree, a training set is drawn using bootstrap aggregating (bagging). The decision tree is built by rule-based splitting of the bagging sample into subsets, maximizing the variance between the subsets (Venables and Ripley 2002). At each split in the learning process, a random subset of explanatory variables is used (Ho 1998). The size of the random subset is determined by the square root of the number of explanatory variables. The splitting process is repeated recursively on each derived subset, until (i) the subset has identical values with the target variable or (ii) the splitting does no longer add value to the prediction (Quinlan 1986). The mean value of the target variable within a final subset (leaf of a decision tree) is used as the conditional prediction of the target variable for a corresponding combination of explanatory variables (Venables and Ripley 2002).

Variable selection

In the publication Ette et al. (2023a), 15 random forest models are trained, three for each of the five structural diversity indicators. One random forest model to consider 15 explanatory stand variables, one to consider 20 explanatory stand variables, and one to characterize the interrelation within the comprehensive indicator set. Models are trained with a set of forest inventory plots. A two-step variable selection procedure is implemented in the R package 'VSURF' (Geneuer et al. 2015). 'VSURF' strengthens the models by preselecting a subset of explanatory variables with sufficient explanatory power and removing variables with little or no explanatory power in advance.

Variable importance

The importance of every explanatory variable j is assessed by two measures, the percentual increase of the mean squared error (%IncMSE) and the average minimal depth (AvgMinDepth). To compute the mean squared error (%IncMSE), the out-of-bag error for every variable j is recorded during the fitting process and averaged over the random forest. Then,

the estimated values of j are randomly permutated in the out-of-bag data and dropped down every fitted tree. Afterwards, the out-of-bag error for each tree is computed again and %IncMSE is calculated (Geneuer et al. 2015, Zhu et al. 2015). To compute the average minimal depth (AvgMinDepth), the level on which variable j is used on average to split the decision tree for the first time is assessed (Ishwaran et al. 2010). The minimal depth for each variable is recorded for every decision tree, while zero is always the initial level. Averaging MinDepth over 500 decision trees yields the average minimal depth (AvgMinDepth) in the case study.

1.6.3 Machine learning for regression tasks

In Ette et al. (2023b), the highly accurate data-mining machine learning algorithm R randomForest (see 1.6.2) is used to spatially predict ecosystem-, species- and genetic and biodiversity in four models based on forest typing. Austrian Forest Inventory plots with BCI ratings are treated as training data set to predict BCI values for forest type centroids. Predictive model performance is improved by adding the variables forest type, forest type group, sea level and geographical coordinates to the data sets. Model fit is controlled by additionally repredicting the training set and compare the deviation of prediction from training data. On the landscape scale, regional BCI outcomes for ecosystem-, species- and genetic and biodiversity can be derived from area weighted means of the forest area objects in QGIS.

1.7. Contributions

"Ko te Kai o te tangata Hei Matauranga Tona Ngahere Ki te Ao."

[The food of the people is knowledge; the world is their forest] (Noku 2022)

1. Is actual European biodiversity monitoring and reporting reliable?

European national reports differ heavily in elaborateness and often are of limited informative value. While information about status and trends of biodiversity in a country remains very vague, overall biodiversity indicator choice is misleading. Biodiversity indicators reported to the CBD are not statistically related to important national geographic and socioeconomic characteristics.

Biodiversity monitoring in Europe fails to report the real status of biodiversity. Freedom of indicator choice in the CBD reporting guidelines is disadvantageous for European biodiversity monitoring and CBD reporting quality.

Which kind of biodiversity indicators are currently monitored in Europe?

Among ecosystem indicators, the categories 'nature protection' and 'human pressure' are mentioned most frequently in national CBD reports. For species indicators, high choice frequency of 'semi aquatic-terrestrial species' is demonstrated. Among genetic indicators,

choice frequency was almost balanced between indicators for plant and animal genetic diversity.

On the level of indicators, ecosystem indicators chosen prevalent are 'protected areas' (97.6% of all CBD national reports) and 'protection activities' (92.9%). For species indicators, vascular plant (92.9%), bird (90.5%) and fish species diversity (90.5%) are commonly monitored. Among genetic indicators, 'ex situ actions for domesticated plants' (69.1%) and 'in situ actions for wild animals' (69.1%) are prevalently reported to the CBD.

What is the actual European conception of biodiversity?

Ecosystem diversity, species diversity, and genetic diversity are reported in an unbalanced manner. Even though our evaluation method was adapted to favor genetic diversity indicator choice, species and ecosystem diversity indicators are still chosen with a disproportionate frequency in comparison to genetic diversity indicators. To treat all indicator categories in the evaluation equally would have been more logical. However, the frequency of genetic indicators would have been close to zero, and de facto, these indicators would have been disregarded.

The study Ette & Geburek (2021) underlines that current biodiversity indicator choice in European CBD reports and national biodiversity monitoring systems favors ecosystem and species diversity conservation while neglecting genetic diversity. The joint European conception of 'biodiversity' and the focus of national conservation policies differs largely from the CBD definition. The evaluations support the finding that some species groups and certain ecosystems seem to be arbitrarily preferred in European nature conservation policies (Zisenis 2009, Cardoso et al. 2011).

For species diversity, the study demonstrates that the way species are currently monitored does not reflect the majority of European taxonomic species richness. Instead, most funding for monitoring and conservation is invested in a small number of species showing comparably low taxonomic diversity (e.g., vascular plants, bird, and fish species diversity). Consequently, major parts of species diversity in Europe (e.g., fungi, protozoa, and invertebrates) are neither monitored nor directly protected. This is an alarming finding indicating that status and trends in European species diversity is largely unknown.

2. How can understanding of indicator-indicandum relationships be extended?

Machine learning as integral part of artificial intelligence may be a novel, effective and entire objective way to gain new insights into indicator-indicandum relationships on variable scales. The prediction outcome is decisively impacted by type and number of explanatory variables tested. The smaller the number of input variables, the more parsimonious is the model. Preselecting variables with regression algorithms (e.g., VSURF) is highly recommended. Random Forest models assumes interval scaled variables. Therefore, the impact of interval-scaled, common features on biodiversity can effectively be evaluated with machine learning. Relevance of qualitative variables and rare events may be underestimated. The methodology described might be more suitable to review quantitative (measurable) than qualitative (observed) variables.

The case study Vienna Woods shows how random forest models can be applied for the indicator validation on large spatial scales, considering intercorrelated data and comprehensive sets of structural diversity indicators. Case study outcomes might not transferable to other parts of Central Europe. Nonetheless, the study highlights that machine learning might be a useful tool to design and test biodiversity indicator sets and close knowledge gaps. The findings support the great potential of randomForest in the context of

forest biodiversity assessments and indicator choice. More ecological studies of this kind are needed to explore indicator-indicandum relationships in detail.

How do well-established biodiversity indicators relate to aspects of forest diversity?

Indicator choice is the most crucial step in biodiversity assessments. In the case study Vienna Woods, the Shannon index is found to be most useful to indicate the variable category 'soil & bedrock' and 'vertical structure'. Variables of 'age & density' are best considered using the Stand Density index which indicates a low number of stand characteristics in high accuracy. The Crown Competition Factor indicates the variables of the category 'forest site' best and overall displays closest relation to all stand characteristics under study. The Diameter Differentiation index is the only indicator to mirror 'game impact' and reflects natural disturbance regimes well. Overall, The Shannon index indicates highest, the Stand Density index lowest number of forest stand characteristics.

How do comprehensive indicator sets relate to aspects of forest diversity?

The set of forest structural diversity indicators is established following the classification in Pretzsch (2002). With Clark & Evans-, Shannon-, Stand Density-, Diameter Differentiation index, and Crown Competition Factor, five surrogates for horizontal distribution, tree species diversity, stand density and stand differentiation are considered. By the comprehensive indicator set examined, the variable category 'age & density' is overrepresented. Partially reflected are the categories 'forest site' and 'vertical structure'. Variable categories neglected are 'game impact' and 'soil & bedrock'. Stand characteristics reflected best by the indicator set are 'stem basal area', 'stem density', 'standing stock volume', and 'quadratic mean diameter'. Contrary, the stand characteristics 'coarse woody debris >25 cm', 'tree browsing', and 'humus type' are neglected in all models.

In the comprehensive indicator set some stand characteristics are indicated disproportionally while other important ones known to be important for forest biodiversity are neglected in the case study Vienna Woods, Austria. Strong correlations between indicators may arise due to indication of the same forest structural aspect in the indicator sets and/or by sharing direct elements in the formula. To rise reliability of biodiversity assessments, both should most possibly be avoided.

3. How can forest biodiversity be assessed reliable in Central Europe?

BCI indicators are based on available data sets, are of high scientific evidence relevant to biodiversity, and do considering ecosystem, species, and genetic diversity equally in line with the CBD. The framework follows classic ecological niche theories. The BCI set consists of twelve indicators. Nine of them refer to common, three of them to rare forest traits. On the one hand, rare but ecologically highly valuable traits (*bonus indicators*) may compensate for a lower level of common forest traits (*biodiversity indicators*). On the other hand, missing but rarely occurring forest traits are not rated disadvantageous and BCI does not benchmark against particular scale of temporal variation in forest ecosystems. BCI assessments can be performed on the level of species-, ecosystem-, genetic- and biodiversity. Outcomes are expressed as percentage (0-100%) to ease interpretation. Renouncing indicator weighting and thus rendering them interchangeable, BCI is designed to be transferable to neighboring Central-European regions with forest typing in e.g., Austria, Italy, and Germany.

How can inventory grid data be used for area assessments?

- 1. Assign forest types to grid sampling plots and calculate biodiversity and bonus indicators on the (sub) plot level.
- 2. Reference indicator values with unmanaged forests based on the forest typing.
- 3. Aggregate indicators on the level of ecosystem, species, genetic diversity.
- 4. For biodiversity ratings, add ecosystem, species, genetic diversity ratings without weighing.
- 5. Create centroids of forest typing areas in GIS.
- 6. Add information about sea level, geographical coordinates, and forest type groups to grid sampling plots (training data) and centroids (prediction data).
- 7. Apply machine learning for ecosystem, species, genetic and biodiversity on both data sets.
- 8. Repredicting training data to control model fit.
- 9. Intersect centroids with forest typing areas to assign prediction to forest polygons.
- 10. Compute area weighted mean of forest type polygons for ecosystem, species, genetic and biodiversity on a landscape scale.
- 11. Facultatively, cube spline interpolation may be used in GIS to additionally predict nonforest area.

Which ecosystem, species and genetic diversity levels can be found in a case study in Central Europe?

Case study assessment outcomes are not transferable to other parts of Central Europe. Nonetheless, potential of BCI assessments in Central Europe is exemplary demonstrated. The case study of displays an average biodiversity rating of 57% out of 100% for Tyrol, Austria. Respective rating for ecosystem diversity is 49%, for genetic diversity is 53% and for species diversity is 71%. Coniferous forest types show higher biodiversity ratings than deciduous and mixed forests in our case study. Species diversity displays highest spatial heterogeneity.

BCI models indicate lowest ecosystem diversity in the Tyrolean forest types 'Moist basic (gray alder) maple-ash mixed forest' (40%), 'Colline grey alder riparian forest' (38%) and 'Silicate hardwood spruce-fir forest' (37%). Species diversity conservation in Tyrol should focus on 'Warm carbonate oak-ash-lime forest' (44%), 'Rich loam-deciduous beech forest' (43%) and 'Fresh silicate lime-ash-pedunculate oak forest' (27%). Efforts for genetic diversity conservation should target 'Colline grey alder riparian forest' (49%), 'Fresh clay beech forest with conifers' (49%) and 'Montane grey alder riparian forest' (40%), 'Montane grey alder riparian forest' (46%), 'Montane grey alder riparian forest' (45%) and 'Fresh silicate lime-ash-pedunculate oak forest' (42%).

How can a novel biodiversity index based on forest inventories support forest biodiversity conservation?

BCI focuses on the strategic CBD target to monitor biodiversity on all levels and halting biodiversity loss on the national scale. Quantitative aggregation of ecological information may help policy makers and conservationists to implement biodiversity policies and distribute conservation funding e.g., for ecosystem restoration. Ranking of forest types and high-resolution spatial maps of forest diversity can support decision-making in biodiversity conservation (e.g., target forest types, target regions, ecosystem-, species or genetic restoration, conservation priorities) and retrospectively evaluate effectiveness of financial resources spend on ecosystem restoration and Sustainable Forest Management. Within one

forest inventory period, performing cost-benefit-analysis of e.g., biodiversity conservation efforts, forest management practices, forest road building, regional forest policy funding and Sustainable Forest Management measures will be made available.

The BCI concept could not overcome all weaknesses of forest inventory-based approaches described in Storch et al. (2018), e. g., large-scale forest inventory design may not capture small areas like nature reserves well enough and very rare forest types must be excluded from the analysis. Plot measures may not be representative for the forest stand and most biodiversity aspects can only be addressed through surrogates. Additionally, most genetic diversity indicators focus on the major tree species of Tyrol, Norway spruce, as data for other species is lacking (e.g., eDNA data). It is not possible to directly compare our case study outcomes with other biodiversity assessments due to unavailable indicator values in Tyrol (e.g., bark diversity, hollow trees, litter dry weight, litter decomposition, tree age, vegetation cover), different scales, and different study purposes.

Nevertheless, by using ecological modeling, referencing indicators by forest type, employing GIS data such as orthophotos, and machine learning, we were able to advance reliability and spatial resolution of forest biodiversity assessments. Quantifying forest biodiversity with BCI allows to manage biodiversity on purpose and distribute biodiversity values evenly on the regional scale. BCI can be used as a measurable, objective, and quantitative guidance for regional forest and conservation policy.

PERSPECTIVE



Why European biodiversity reporting is not reliable

Jana-Sophie Ette D, Thomas Geburek

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Abstract The Convention on Biological Diversity (CBD) aims to end the loss of biodiversity, which is one of the greatest ecological challenges of our time. The lack of success in biodiversity policy implementation is partly related to gaps in biodiversity monitoring. Our overall objective is to contribute to the preparation of the upcoming post 2020 period by a review of biodiversity indicator choices in European CBD reports and hence in national monitoring systems. Negative binary generalized models and poisson generalized linear models prove that through free indicator choice in CBD reporting, countries do not choose biodiversity indicators according to their national geographic and socioeconomic characteristics. Moreover, species and ecosystem diversity indicators were chosen with a disproportionate frequency compared to that of genetic diversity indicators. Consequently, trends derived from national CBD reports and monitoring systems in Europe are not reliable, which should be an alarming signal concerning biodiversity policy implementation. Finally, a flow chart to revise national biodiversity monitoring systems is proposed.

Keywords Biodiversity indicators · Biodiversity monitoring · Biodiversity policy implementation · European species diversity

INTRODUCTION

With global extinction rates being one hundred to one thousand times greater than the natural baseline (Ceballos

et al. 2010 and 2015), the loss of biodiversity is one of the greatest and most serious ecological challenges of our time (CBD 2006; Rockström et al. 2009). Biodiversity loss threatens the provision of ecosystem services at an accelerating rate and erodes the foundation of humanity (IPBES 2019). Nonetheless, the main drivers of extinction are of anthropogenic origin (Sala et al. 2000; Newbold et al. 2015).

Convention on biological diversity

Therefore, two hundred countries committed themselves to halt the loss of biodiversity by signing the UN Convention on Biological Diversity (CBD) in 1992. Thus, 14.4 billion USD was spent globally from 1992 to 2003 to slow down biodiversity loss. This effort reduced the expected species decline in that period by 29% (Waldron et al. 2017). Nonetheless, strategic CBD targets were not achieved until 2010 (CBD 2014), and Aichi targets for the successive period 2011 to 2020 will not be accomplished (CBD 2014; Tittensor et al. 2014). Why do the member countries fail to reach the targets even though numerous financial efforts have been made? Actually, there is no internal mechanism in the CBD body established to monitor national-level compliance and the implementation of biodiversity policies (Morgera and Tsioumami 2011; Vordermayer-Riemer 2019). Therefore, scientific evaluations of implementation deficits and the reasons for these deficits may be particularly valuable.

In addition to lacking capacity in terms of coordination, science, administration and legislation, the lack of success in biodiversity policy implementation is related to gaps in biodiversity monitoring (Pareira et al. 2012; CBD 2018). Scanning the Aichi targets (CBD 2012), we believe that establishing effective national biodiversity monitoring

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(target 19) is the basis for reaching eight out of twenty Aichi targets (targets 2, 5, 7, 8, 9, 11, 12, and 14). Improving biodiversity monitoring and reporting may greatly improve the ability to reach future strategic CBD goals.

Therefore, this paper focuses on the biodiversity indicator choice and biodiversity monitoring as important factors in biodiversity policy implementation. Biodiversity cannot be quantified directly, and thus, assessments are highly complex. Indicators are needed that are based on achievable, quantitative data, are policy and ecosystem relevant, assessable to monitoring, sensitive to pressures on biodiversity, have an indicative value and stable properties (CBD 1997). Actually, these ambitious requirements are very difficult to fulfill. Sometimes also value judgments have to be made, which makes biodiversity indicator choice neither entirely objective nor easy (CBD 1997). However, as the CBD reporting guidelines allow for the freedom of indicator choice, European indicator choice in national CBD reports may also display the conception of the complex term of biodiversity.

CBD post-2020 period

According to the definition of biodiversity used by the CBD body, biodiversity has three components of equal value (ecosystem diversity, species diversity and genetic diversity). However, freedom of indicator choice may allow for the use of conceptions of biodiversity that differ from the CBD definition, which would be disadvantageous for halting biodiversity loss. Genetic diversity is frequently neglected (Pareira et al. 2012), although genetic diversity is the foundation of all biological diversity and enhances persistence and the evolutionary potential of all species (Allendorf et al. 2012). In certain ecosystems, genetic diversity may provide biological functions similar to that of species diversity (Cook-Patton et al. 2011). However, monitoring genetic diversity requires complex laboratory analyses, whereas assessing ecosystem diversity and species diversity may be less challenging.

In this paper, we attempt to determine whether European biodiversity reporting and monitoring is reliable and whether the biodiversity conception is in line with the CBD definition. Gaps in biodiversity policy implementation may be closed by adapting institutional CBD reporting requirements and through the efforts of CBD member countries. Considering 42 European national CBD reports, we tried to answer the following questions: (1) Which kinds of biodiversity indicators are particularly prevalent? (2) Are ecosystem diversity, species diversity, and genetic diversity considered adequately? In addition, considering the CBD institutional point of view, we wanted to determine whether (3) the freedom of biodiversity indicator choice in CBD reporting guidelines is beneficial for biodiversity monitoring and reporting quality. Our scientific objective is to support the implementation of the CBD by systematically reviewing national reports and to contribute to preparing for the upcoming post-2020 period.

MATERIALS AND METHODS

Prevalent biodiversity indicators

First, the fifth national reports (strategic period 2011-2020) of all European CBD members (n = 43) were downloaded from the CBD homepage (https://www.cbd.int/countries/). Only 42 of these could be considered for further analysis, as a linguistic barrier impeded the evaluation of Belarus' national report.

Due to the amount of data, analyzing a subset of five randomly chosen CBD reports was necessary to prepare a list of the biodiversity indicators reported most frequently in European national reports. In the following, these biodiversity indicators were grouped into three main categories: (1) ecosystem indicators, (2) species indicators, and (3) genetic indicators. Moreover, these categories were further divided into four subcategories (Table 1). Then, two additional reports not included in the subset were used to pretest the indicator list. Finally, all 42 national reports were systematically evaluated using the approved indicator list.

Biodiversity reporting reliability

To evaluate reporting reliability in a second step, country characteristics (concerning geography and socioeconomy) were obtained from online platforms (Electronic Supplementary Material S1). Additionally, geographic isolation was measures as the ratio of country coastline to total country border length.

Table 1	Biodiversity	indicator	categories	and	subcategories

(1) Ecosystem indicators	(2) Species indicators	(3) Genetic indicators
(1a) land use	(2a) aquatic species	(3a) domesticated plants
(1b) forest structure	(2b) semiaquatic- terrestrial species	(3b) wild plants
(1c) nature protection	(2c) terrestrial flora	(3c) domesticated animals
(1d) human pressure	(2d) species of particular interest	(3d) wild animals

Indicator choice evaluation

Generally, all countries in our analysis prepared their national reports in accordance with the CBD reporting guidelines by answering the predetermined questions. However, the reports differ greatly in terms of elaborateness and information density, which impedes a direct comparison. To tackle this problem, we evaluated the biodiversity indicator choice by using a binary-coded indicator list (valid vs. not valid). For (1) ecosystem indicators and (2) species indicators, one measurable, quantitative value appearing in the national CBD report validated the indicator. For instance, the wording "The population of the bird species Eurasian bittern (Botaurus stellaris) is now 320 breeding pairs" in a national CBD report would be a valid bird species diversity/subcategory 2b count. For (3) genetic indicators, however, qualitative declarations about existing national programs or activities were rated as being sufficient (e.g., "The country established a gene bank for wild crop relatives" would result in a valid wild crop relative ex situ/subcategory 3b count). To treat all indicator categories in the evaluation equally would have been more logical. However, the frequency of genetic indicators would have been close to zero, and de facto, these indicators would have been disregarded. Detailed outcomes of the evaluation of the 42 national CBD reports can be found in Electronic Supplementary Material (S2).

Biodiversity reporting and monitoring reliability

To assess the reliability of national CBD reporting and monitoring, two assumptions had to be made: (1) National CBD reports reflect the indicator choice for national biodiversity monitoring and (2) reliable monitoring accurately reflects the geographic and socioeconomic characteristics of a country.

The first assumption could not be addressed by this study, but it seems very unlikely that member countries put large financial efforts in biodiversity monitoring without reporting to the CBD. The second assumption is a logical conclusion, as natural biodiversity levels are primarily determined by geographic factors (e.g., mean latitude, area size, biogeographic regions). However, the biodiversity present may differ from natural levels, mainly due to an anthropogenic impact (Sala et al. 2000; Newbold et al. 2015). Therefore, the second assumption is in line with the pressure-state-response framework underlying the CBD body, which states that "CBD indicators should monitor and assess status and trends of biodiversity and its components (CBD Articles 7(b) and 25 (2a)) and the causes of biodiversity loss or effects of processes which are likely to have an adverse impact on biodiversity (CBD Articles 7(b),

14(a)) and the effectiveness of measures taken (CBD Articles 25 (b) and 26)" (Vordermayer-Riemer 2019).

To check the reliability of biodiversity reporting, 12 hypotheses were elaborated based on well-established scientific findings. These hypotheses address the relationships between national characteristics (geography and socioeconomy) and their importance for a specific biodiversity indicator category.

For hypotheses 1–6, we chose the geographic variables land area size, coastline length, geographic isolation, mean geographic latitude, and number of biogeographic regions as important factors describing the national biodiversity status. Additionally, for hypotheses 7–9, agricultural area, forest cover, and human population density were used as variables of human pressure reflecting the extent to which landscapes have been modified. For hypotheses 10–11, the gross domestic product was chosen as a proxy for percapita income to reflect the nation's economy. For hypothesis 12, the duration of EU membership was employed as a variable for biodiversity funding and policy.

Countries can benefit from the freedom of indicator choice by adapting their reporting and monitoring according to national state and pressure on biodiversity. We examined this by assessing whether national geographic and socioeconomic characteristics impacted the number of biodiversity indicators chosen from a particular indicator category.

If the majority of the hypotheses are verified, then indicator choice is strongly affected by state and pressure on national biodiversity. In such cases, the freedom of indicator choice would be beneficial for national reporting quality. In contrast, if the hypotheses are not verified, then the CBD reporting guidelines need to be scrutinized.

Negative binary generalized models and poisson generalized linear models

Twelve hypotheses (Table 2) address the statistical association between country characteristics (independent variables with continuous values (x), see Electronic Supplementary Material S1) and the biodiversity indicator choice in the national CBD reports (dependent variables with nonnegative integer values (y), see Electronic Supplementary Material S2).

Following the approach of Naidoo and Adamowicz (2001), the count data derived from the national CBD reports were tested by performing regression analysis; thus, twelve hypotheses were merged into eight models sharing the same dependent variable. Nonlinear regression analysis helps predict the value of the dependent variable based on the covariates (Naidoo and Adamowicz 2001). The distribution of discrete response variables places probability mass at nonnegative integer values only. To avoid

Nr	Hypotheses	Rationale
1	The country's <i>total land area</i> correlates with the total number of biodiversity indicators in the national monitoring systems	Species-area relationship: Rosenzweig (1995) Niche differentiation: Connell (1980)
2	The country's <i>total land area</i> correlates with endemic species as biodiversity indicators	Endemics-area relationship: Storch et al. (2012) Minimum viable population size: Shaffer (1981)
3	The country's <i>total coastline</i> correlates with the number of aquatic species indicators	About 80% of marine species diversity occurs in the coastal zones: Ray (1991)
		In oceans, microbial diversity of coastal waters is about a magnitude higher than in open water: Glöckner et al. (2012)
4	The <i>geographical isolation</i> of a country correlates with endemic species as biodiversity indicators	Island biogeography: McArthur and Wilson (1967)
5	The <i>mean latitude</i> of a country correlates with the number of species indicators	Latitudinal diversity gradient: MacArthur (1972)
6	The number of Biogeographical Regions in a country correlates with	Niche differentiation: Connell (1980)
	the number of species indicators	Biogeographical processes influence local species composition: Ricklefs (1987), Wiens and Donoghue (2004)
7	The country's <i>forest cover</i> correlates with forest structural indicators and indicators of terrestrial flora diversity	Structural diversity is a very important group of indicators to assess forest biodiversity: McElhinny et al. (2005), Dieler (2013)
		Forests provide habitat for 80% of all terrestrial species: FAO (2010)
8	The country's <i>agricultural area</i> correlates with the number of genetic indicators of domesticated plants and animals	Domestication is another important facet of biodiversity. Of 5000 vertebrate species described, 30–40 birds and mammals were domesticated: Dirzo and Raven (2003)
		About 30% of 500 families of flowering plants contain at least one crop species: Hammond (1995)
9	The country's <i>population density</i> correlates with the number of indicators related to human pressure	Biodiversity loss is driven by human socioeconomic pressures: Naidoo and Adamowicz (2001)
		Biodiversity changes can be predicted by human development pressures: Waldron et al. (2017)
10	The country's <i>GDP</i> (gross domestic product) correlates with genetic indicators as well as with the total number of biodiversity indicators	The GDP correlates significantly positively with number of published scientific conservation and ecological articles and research expenditure: Doi and Takahara (2016)
11	The country's <i>GDP</i> correlates with endemic species as biodiversity indicators	Strong, positive correlation between number country-endemic freshwater species and GDP can be found globally: Collen et al. (2004)
12	The duration of EU membership correlates with the total number of biodiversity indicators in the national monitoring systems	European membership requires to adopt international commitments and the expansion of conservation areas: Grodzinska-jurcazak and Cent (2010)
		EU Nature Directives had positive impact on EU's biodiversity: Beresford et al. (2016)

Table 2 Hypotheses established to test the association between country's characteristics (x) and the biodiversity indicator choice (y) and their rationales

inconsistent parameter estimation through incorrect distribution expectations, we developed two types of models: Negative binary generalized models (NBGM) and a generalized linear model with poisson error structure (Poisson GLM). The assumption of NBGM, i.e., variance is a quadratic function of the mean that differs from the assumption of Poisson GLM, i.e., variance equals the mean concerning variable distribution (Naidoo and Adamowicz 2001). Thus, the model fit was rated using null deviance and theta parameter values and was compared using the likelihood ratio Chi squared distribution test (Venables and Ripley 2002). For this purpose, the R packages "foreign", "ggplot2" and "MASS" were used. The "MASS"-package uses a system modification to include the additional parameter theta and an alternating iteration process for the NBGM calculation. Hence, the means are fixed while the parameters are computed by using score and information iterations (Ripley et al. 2019). The model fit of the data is shown by the theta parameter for NBGM and the deviation value and overdispersion parameter for Poisson GLM.

The regressions calculated using the Poisson GLM were checked for overdispersion. Overdispersion frequently

occurs when using count data, i.e., the variance of the response variable exceeds the variance of the mean and may lead to an underestimation of the standard errors and therefore overestimation of the significance of the regression parameters (Cox 1983). The Poisson GLMs were tested using the R package "AER". Approved overdispersion implies that the poisson model assumptions were not met, and the model output is not confidential (Dormann 2016). For theta as well as for the overdispersion parameter, a small parameter outcome is favorable.

RESULTS

To determine whether European biodiversity reporting and monitoring is reliable and biodiversity conception is in line with the CBD definition, we approached the following questions.

Which kinds of biodiversity indicators are particularly prevalent?

Among ecosystem indicators, "nature protection (1c)" and "human pressure (1d)" were mentioned most frequently, whereas subcategory "forest structure (1b)" indicated a low importance (Fig. 1). For species indicators, the high choice frequency of subcategory "semi aquatic-terrestrial species (2b)" was obvious, whereas "aquatic species (2a)" was of lowest importance (Fig. 2). Among genetic indicators, choice frequency was almost balanced between indicators for plant and animal genetic diversity (Fig. 3).

Are ecosystem diversity, species diversity, and genetic diversity considered adequately?

Following the CBD definition, biodiversity has three components of equal value (ecosystem diversity, species diversity, and genetic diversity). Therefore, we expected national CBD reports to mirror a quantitative balance in choice frequency among these three components.

On the level of single indicators (Fig. 4), prevalent ecosystem indicators found were "protected areas" (97.6% of all reports) and "protection activities" (92.9%). In contrast, "old forest stands" (17%) and forest glades (5%) were seldom chosen.

For species indicators, namely, "vascular plant" (92.9%), "bird" (90.5%) and "fish" species diversity (90.5%) were commonly used. However, "benthos" (36%) and "protozoa" (10%) were rarely reported.

Among genetic indicators, "ex situ actions for domesticated plants" (69.1%) and "in situ actions for wild animals" (69.1%) were prevalently mentioned. Scarcely, the reports referred to "genetic reserve forests" (29%) and "game impact" (12%).

Species indicators and ecosystem indicators are generally chosen with a disproportionate frequency in comparison to genetic indicators. Our results underline that the current indicator choice in European CBD reports and national biodiversity monitoring systems consequently favors ecosystem and species diversity conservation.

Is freedom of biodiversity indicator choice in CBD reporting guidelines beneficial for biodiversity monitoring and reporting quality?

Free indicator choice may give flexibility to members to report and monitor biodiversity according to their knowledge, institutional capacities, financial abilities, and geographic and socioeconomic characteristics.

The results of NBGM and Poisson GLM are shown in Table 3. Although all hypotheses were scientifically backstopped, the variables poorly explained indicator choice. Of all models, only the Poisson GLM screening for statistical association between country size and total number of biodiversity indicators, was significant (p < 0.01). Moreover, the overdispersion parameter value of the two models could potentially have led to an overestimation of significance. As no Poisson GLM showed both significant association and overdispersion at the same time, this was of least concern.

Based on these results, the reporting and monitoring are biased. Assessing the magnitude of bias for overall biodiversity was impossible in our study. Solely species diversity could be considered to roughly estimate the deviation between reporting and European species richness (Compare Fig. 2 excluding subcategory "species of particular interest" and Fig. 5). Apparently, the bulk of European species richness is not well represented through the free indicator choice. In fact, "protozoa species diversity" was the indicator chosen most rarely in our analysis (4.8%), although protozoa are the most diverse taxonomic group, with approximately 200 000 species in Europe. Concerning species of particular interest, there are 10 810 species red listed in Europe (IUCN 2019) as well as 12 221 nonnative species (Daisie 2009). The number of endemic species can be estimated to be at least 6300 species in Europe, i.e., approximately 5600 endemic vascular plant species, 436 freshwater fish, 142 butterfly, 59 mammal, 46 amphibian, and 18 dragonfly species (Bise 2019). However, the most endangered taxonomic groups are cycads (63% of species globally threatened) and amphibians (41%), whereas birds (13%) are the taxonomic group least threatened (Pareira et al. 2012).

Overall, biodiversity indicators reported in Europe are not statistically related to important geographic and



Fig. 1 Indicators choice frequency for (1) ecosystem diversity indicators in European national CBD reports. Subcategories are (1a) land use, (1b) forest structure, (1c) nature protection, and (1d) human pressures



Fig. 2 Indicators choice frequency for (2) species diversity indicators in European national CBD reports. Subcategories are (2a) aquatic species, (2b) semiaquatic-terrestrial species, (2c) terrestrial flora, and (2d) species of particular interest



Fig. 3 Indicators choice frequency for (3) genetic diversity in European national CBD reports. Subcategories are (3a) domesticated plants, (3b) wild plants, (3c) domesticated animals, and (3d) wild animals



Fig. 4 Indicator choice frequency between (1) species indicators, (2) ecosystem indicators, and (3) genetic indicators in European CBD reports

Dependent variable	Independent variable	NBGM		Poisson GLM	
		Significant variable	Model fit (θ)	Significant variable	Overdispersion
Total number of biodiversity indicators	Country size, gdp, access to EU	Country size $(p < 0.1)$	20.9	Country size $(p < 0.01)$	
Endemic species indicators	Country size, land vs. coast line border lenght, gdp		22 441		1
Nr. species indicators	Mean country latitude, nr. biogeographical regions		61 361		0.5
Nr. aquatic species indicators	Coast line border length		86 722		0
Nr. flora diversity plus forest structural indicators	Land use forest	Land use forest $(p < 0.1)$	41 749	Land use forest $(p < 0.1)$	0.74
Genetics indicators of domesticated plants and animals	Land use agriculture	Land use agriculture (p < 0.1)	33 321	Land use agriculture (p < 0.1)	0.75
Nr. genetics indicators	Gdp		6.9		
Nr. indicators of human pressure on ecosystem	Population density		27 367		0.6

Table 3 Results of the negative binary generalized models (NBGM) and poisson generalized linear models (Poisson GLM)



Fig. 5 Taxonomic species richness of Europe
socioeconomic characteristics. Hence, biodiversity monitoring fails to report the real status of European biodiversity. Freedom of biodiversity indicator choice in the CBD reporting guidelines is disadvantageous for European monitoring and reporting quality.

DISCUSSION

We found the following key findings: Ecosystem diversity, species diversity, and genetic diversity are reported in an unbalanced manner. Freedom of indicator choice negatively affects the quality of biodiversity monitoring and reporting. Species diversity reporting deviates from European species richness. These results point to major gaps in CBD implementation.

Deficits in biodiversity policy implementation

International agreements and policies can only have a positive impact on combating biodiversity loss if implemented (Williams et al. 2012). Lacking robust evaluation of international conservation policies has been heavily criticized (Ferraro and Pattanayak 2006; Morgera and Tsioumani 2011). Actually, there is no internal mechanism established to monitor national-level compliance and implementation of biodiversity policies in the CBD body (Morgera and Tsioumani 2011; Vordermayer-Riemer 2019). On the one hand, missing supervisory mechanisms are a well-known problem of international legal systems, especially concerning multilateral environmental agreements (Morgera and Tsioumani 2011). On the other hand, the evaluation of biodiversity policy implementation is valuable to improve policy design and raise conservation impacts (Siebenhüner 2007).

Zisenis (2009) claimed that there are still serious CBD implementation deficits on the global, European, and national levels. For instance, national CBD reports were delivered increasingly with delay and were even not revised in the last period (CBD 2018) due to unwillingness or lacking resources (Raustiala 2000). However, steps towards further harmonization of national reports in the past were not successful (CBD 1997). On this account, the CBD now works as a pilot project on voluntary individual peer-review processes of national CBD reports in an informal working group (Ulloa et al. 2018).

Our paper contributes to the CBD post-2020 period by analyzing biodiversity indicator choices in European CBD reports and national biodiversity monitoring systems. The most prevalent biodiversity indicators were "protected areas", "protection activities" and species diversity in vascular plants, birds, and fish. The diversity of ecosystems and species is overrepresented, whereas genetic diversity tends to be neglected.

Key functions of genetic diversity are recognized and anchored in the CBD definition of biodiversity. Our findings are in line with Laikre et al. (2010), who stated that genetic diversity on the national level is still not being monitored and indicators and thresholds are missing. CBD policies concerning genetic diversity lag behind implementation for other levels of biodiversity, although knowledge of conservation genetics, molecular genetics and statistical tools is available (Fussi et al. 2016; Hunter et al. 2018).

Reasons for this discrepancy between ecosystem and species diversity vs. genetic diversity could be easier data access (data already compiled, e.g., Natura 2000, European Environmental Agency), higher public and media interest (flagship species, lighthouse projects) or higher economic interest in specific data (national forest inventory, species relevant to hunting and fishery, exotic species). Lower public, governmental and media interest may also explain why monitoring systems for genetic diversity are not yet established in most countries. Additionally, for the genetic level of biodiversity, reporting obligations of the European Union and public funding are probably lower while at the same time demanding scientific expertise for developing and supervising such programs are needed. Overall, the joint European conception of the term biodiversity and even the focus of national conservation policies may differ from the CBD definition.

Our evaluation supports the finding that some species groups and certain ecosystems seem to be arbitrarily preferred in European nature conservation policies (Zisenis 2009; Cardoso et al. 2011). For species diversity, we demonstrate that the way species are actually monitored does not reflect the majority of European taxonomic species richness. This is an alarming finding indicating that the status and trends in European species diversity reported are not reliable. Instead, the majority of the funding for monitoring and conservation actions is probably invested in gaining knowledge about a small number of species showing comparably low taxonomic diversity (vascular plants, bird, and fish species diversity). In contrast, major parts of species diversity in Europe (fungi, protozoa, and invertebrates) are neither monitored nor directly protected. In fact, protozoan species diversity was the indicator chosen most rarely in our analysis, even if it is the most diverse taxonomic group in Europe. This may not only be a European issue. Merely 20-30% of global soil protozoa diversity has been scientifically described (Foissner 1997). Limited knowledge about species hinders adequate management to halt the ongoing loss of this level of biodiversity.



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Revise National Biodiversity Monitoring Systems

Fig. 6 Flow chart guiding to the revision of national biodiversity monitoring systems according to the CBD. Step I and step II should mandatory be fulfilled by all countries, whereas step III could be applied facultatively to further enhance quality of biodiversity monitoring and reporting

Towards closing the gap between science and policy

A need for a clear framework containing a limited number of criteria to assess biodiversity has often been claimed (e.g., Newton and Kapos 2002), as indicators are essential for effective management (CBD 1997). Countries differ strongly in geography, size, natural landscapes, and climate, which impedes a common indicator set. Nevertheless, as a first step, we would like to propose a comprehensive flow chart to revise national biodiversity monitoring systems in accordance with the CBD guidelines (Fig. 6). Step I and Step II are the minimum requirements, which should be fulfilled mandatorily by all CBD signatory countries. To further enhance the comparability and quality of the national monitoring systems, Step III could be used in a facultative manner.

Clearly defined aims are the most elemental attribute of biodiversity monitoring (Pocock et al. 2015). Next, the first preliminary step includes identifying biodiversity indicators in line with CBD requirements (CBD 1997). Suitable indicators need scientific evidence for their indicative value, stable properties, and ecosystem and policy relevance; (2), are quantitatively provided by reliable data sources (3) and are sensitive, achievable, and assessable based on their field sampling methodology (4).

Step II ensures that, according to the CBD definition, (5) all levels of biodiversity (ecosystem, species, and genetic diversity) are considered in the national monitoring.

Step III reveals options of harmonization of national monitoring systems to effectively halt the loss of biodiversity. The number of indicators per level of biodiversity should be statistically large enough (6), so random deviation of one indicator may not lead to major misinterpretations. The monitoring system should be transferable to comparable ecoregions, e.g., whole biogeographic regions (7). Applying an aggregation scheme for indicators used (8), decision makers would gain an ideal biodiversity index as a reliable basis for biodiversity policy implementation.

CONCLUSION

European national reports differ heavily in elaborateness and are often of limited informative value. While information about status and trends in biodiversity in a country remains very vague, overall biodiversity indicator choice is misleading. For the international community, it is impossible to compare country performance and advancements towards the CBD based on national reports. Resources spent on CBD reporting and monitoring could be used more efficiently. Originating from the analysis of all European CBD reports, we would like to recommend harmonization of national reports through a core set of indictors per biogeographical region. They may be reported long term in a table format to easily detect trends in biodiversity based on high scientific evidence. Species indicators should align to domestic taxonomic richness, whereas ecosystem indicators should reflect major landscape elements and determinants for biodiversity. Moreover, applicable quantitative genetic indicators for all member states need to be defined.

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AUTHOR BIOGRAPHIES

Jana-Sophie Ette (\square) is doctoral candidate at the Austrian Federal Research Centre for Forests, Natural Hazards and Landscape. Her research interest includes biodiversity assessment, biodiversity indicators, and biodiversity management.

Address: Department for Forest Genetics, Austrian Federal Research Centre for Forests (BFW), Seckendorff-Gudent Weg 8, 1131 Vienna, Austria.

e-mail: sophie.ette@bfw.gv.at

Thomas Geburek is head of the Department of Forest Genetics at the Austrian Federal Research Centre for Forests, Natural Hazards and Landscape and professor at the University of Natural Resources and Life Sciences Vienna. His research interest includes applied genetic research and genetic diversity management in forest ecosystems.

Address: Department for Forest Genetics, Austrian Federal Research Centre for Forests (BFW), Seckendorff-Gudent Weg 8, 1131 Vienna, Austria.

e-mail: thomas.geburek@bfw.gv.at

ORIGINAL RESEARCH



Insights in forest structural diversity indicators with machine learning: what is indicated?

J. S. Ette¹ · T. Ritter² · S. Vospernik²

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Abstract

Indicator choice is a crucial step in biodiversity assessments. Forest inventories have the potential to overcome data deficits for biodiversity monitoring on large spatial scales which is fundamental to reach biodiversity policy targets. Structural diversity indicators were taken from information theory to describe forest spatial heterogeneity. Their indicative value for forest stand variables is largely unknown. This case study explores these indicator-indicandum relationships in a lowland, European beech (Fagus sylvatica) dominated forest in Austria, Central Europe. We employed five indicators as surrogates for structural diversity which is an important part of forest biodiversity i.e., Clark & Evans-, Shannon, Stand Density, Diameter Differentiation Index, and Crown Competition factor. The indicators are evaluated by machine learning, to detect statistic inter-correlation in an indicator set and the relationship to twenty explanatory stand variables and five variable groups on a landscape scale. Using the R packages randomForest, VSURF, and randomForest *Explainer*, 1555 sample plots are considered in fifteen models. The model outcome is decisively impacted by the type and number of explanatory variables tested. Relationships to interval-scaled, common stand characteristics can be assessed most effectively. Variables of 'stand age & density' are disproportionally indicated by our indicator set while other forest stand characteristics relevant to biodiversity are neglected. Within the indicator set, pronounced inter-correlation is detected. The Shannon Index indicates the overall highest, the Stand Density Index the lowest number of stand characteristics. Machine learning proves to be a useful tool to overcome knowledge gaps and provides additional insights in indicator-indicandum relationships of structural diversity indicators.

Keywords Biodiversity assessments · Biodiversity indicator choice · European beech forests · Forest inventories · Indicator–indicandum relationships · R randomForest

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S. Vospernik Sonja.Vospernik@boku.ac.at

¹ Department of Forest Growth, Silviculture & Genetics, Austrian Federal Research Centre for Forests, Vienna, Austria

² Department of Forest and Soil Sciences, Institute of Forest Growth, University of Natural Resources and Life Sciences, Peter-Jordan-Straße 82, 1190 Vienna, Austria

Introduction

The rapid rate of biodiversity loss is an emerging public concern. There is high scientific evidence for a positive relationship between the loss of biodiversity and the decline of forest ecosystem services (Hooper et al. 2005; Balvanera et al. 2006; Isbell et al. 2011; Mace et al. 2012; Gamfeldt et al. 2013). Biodiversity loss threatens the provision of ecosystem services at an accelerating rate and erodes the foundation of humanity (IPBES 2019).

The main drivers of extinction and decline are of anthropogenic origin (Sala et al. 2000; Newbold et al. 2015). Forest degradation, fragmentation, and loss as side effects of human economic activities already caused severe biodiversity losses (Newbold et al. 2015; FAO 2020). Globally, extinction rates are being one hundred to one thousand times greater than the natural baselines (Ceballos et al. 2010, 2015). This trend is expected to continue globally (Keenan et al. 2015; Newbold et al. 2015).

Acknowledging the importance of biodiversity, numerous measures in policy, public, and sciences have been taken to halt biodiversity loss. Major global initiatives are the Convention on Biological Diversity (est. 1992), the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (est. 2012), and the Sustainable Development Goals (est. 2016). At the European level, the Ministerial Conference on the Protection of Forests in Europe (est. 1990), the Streamlining European Biodiversity Indicators Initiative (est. 2005), the EU Biodiversity Strategy (est. 2011), and the European Green Deal (est. 2019) were initiated. About 14.4 billion USD was spent globally from 1992 to 2003 to halt biodiversity loss (Waldron et al. 2017). Although, the rate of biodiversity decline was below the expected decline, strategic aims to control biodiversity loss are never met (CBD 2014; Tittensor et al. 2014).

One of the reasons for environmental policy implementation gaps may be the lack of effective biodiversity monitoring systems (Pereira et al. 2012; CBD 2018; Ette and Geburek 2021). Biodiversity indicators play a crucial role in assessing biodiversity and were established in large numbers (Lindenmayer et al. 2000; Larsson et al. 2001; Chirici et al. 2011). Nonetheless, biodiversity indicators are still criticized for poor indicator–indicandum relationships (Ferris and Humphrey 1999; Margules et al. 2002; Duelli and Obrist 2003; Gao et al. 2015). Following the definition of Heink and Kowarik (2010) an indicator is of major relevance for a given issue, e.g., assessment of a certain impact on conservation policy, while an indicandum is the phenomenon indicated.

Indicators for biodiversity are considered to be more useful the more precise the correlation between indicator and indicandum is known (Heink and Kowarik 2010). Scientists, policymakers, and forest managers are facing severe knowledge gaps while having to decide which and how to choose and aggregate biodiversity indicators (Yoccoz et al. 2001; McElhinny et al. 2005; Katzner et al. 2007; Jones et al. 2011). On large spatial and temporal scales, the availability of reliable data sets is another limiting factor for biodiversity monitoring (Purvis and Hector 2000; Heym et al. 2021). Therefore, there is no forest biodiversity monitoring approach internationally established or accepted yet (CBD 2018).

Due to a lack of consistent correlations, indicator species concepts have not been successful (Margules et al. 2002; Duelli and Obrist 2003). Structural diversity indicators reflect potential habitat variability, niche differentiation, structural complexity (Heym et al. 2021), and sources of forest biodiversity (McElhinny et al. 2005) e.g., for umbrella species (Müller et al. 2009) and bird species (MacArthur and MacArthur 1961). There

is broad scientific evidence for positive relationships between measures of forest structural variety and elements of biodiversity (Begon et al. 1996; McNally et al. 2001; Winter et al. 2008; Motz et al. 2010).

Forest inventories have a potential to overcome data deficits on large scales (Chirici et al. 2011; Corona et al. 2011; Storch et al. 2018). Major advantages of inventory-based biodiversity assessments are the repeated measurements which reflect temporal changes (Heym et al. 2021) with low additional costs (Corona et al. 2003, 2011) for a high number of attributes, forest types, sample sizes, and scales (Storch et al. 2018; Heym et al. 2021). In the long term, changes in biodiversity can even be related to forest management practices (Storch et al. 2018) which makes it highly reasonable to choose indicators based on forest inventory data. Handling knowledge gaps in choice and aggregation of biodiversity indicators by machine learning approaches has already been explored in permanent grassland and freshwater ecosystems (Gallardo et al. 2011; Plantureux et al. 2011).

Our case study examines the potential of this approach for forest ecosystems. In line with Noss (1990), and McElhinny et al. (2005), it focusses on tree species composition and forest structure in a surrogate approach (Olsgard et al. 2003). Scientifically well-established metrics of structural diversity relevant to forest biodiversity are applied. Although the relationship to the indicandum may not be fully understood yet, we will refer to these metrics as 'indicators' in the following.

Our goal is to promote the applicability of forest inventory-based diversity indicators by precising indicator–indicandum relationships through machine learning. Following Pretzsch (2002), the comprehensive indicator set considers horizontal distribution, tree species diversity, Stand Density and stand differentiation. Machine learning is applied to forest inventory data on a landscape scale in an unmanaged, lowland, European beech (*Fagus sylvatica* L.) dominated forest in Austria to answer the following research questions: (1) Which levels of structural diversity can be found in the unmanaged core areas of the Biosphere Reserve Vienna Woods (BR)? (2) Which stand characteristics are indicated by single structural diversity indicators? (3) Which stand characteristics are indicated or neglected by a comprehensive indicator set? (4) How strong is the intercorrelation in an indicator set?

The hypotheses of this study are that (1) machine learning as an integral part of artificial intelligence is an effective way to gain new insights in indicator–indicandum relationships in forests and (2) some stand characteristics relevant to forest biodiversity are indicated disproportionally in comprehensive indicator sets (in sense of Pretzsch 2002), while others are neglected.

Material

Study area

The case study focuses on the core areas of the Biosphere Reserve Vienna Woods in East Austria, Central Europe (48° 5′ N, 15° 54′ E). The BR Vienna Woods has an area size of 105.000 ha and was established in 2005. The study area is located in the transition zone between the Vienna Basin and the Northern Limestone Alps. The 37 core areas (5.400 ha) under strict nature protection and without forest management are scattered across the Biosphere Reserve (Fig. 1, ESM1). The dominant tree species are European beech (*Fagus sylvatica*) 57%, oak (*Quercus* spp.; *Q. robur*, *Q. petrea*, *Q. cerris*) 22%,



The Biosphere Reserve Vienna Woods

Fig. 1 Map of study area (BFW 2011) & study climate. The study is conducted in the scattered core areas of the Biosphere Reserve Vienna Woods, located in East Austria, Central Europe. Mean monthly precipitation of the climate station "Brunn im Gebirge" ranges between 41 and 99 mm. Mean monthly temperatures are between -0.1 °C and +20.8 °C (EHYD 2021)

hornbeam (*Carpinus betulus*) 11%, ash (*Fraxinus excelsior*) 2%, birch (*Betula pendula*) 2%, larch (*Larix decidua*) 2%, and pine (*Pinus sylvestris*) 2% (BR Vienna Woods Management 2011).

Due to beneficial climatic conditions along the Vienna Thermal Line, the landscape was intensely used for centuries for transportation, settlement, agriculture, and forest management (Schachinger 1934). Historical forest management was favoring oak, black pine, and wild fruit tree species targeting firewood, game, resin, wild fruits, and acorns (Schachinger 1934). The centrally located climate station in "Brunn im Gebirge" shows the highest average monthly precipitation in July (99 mm) and the lowest in February (41 mm). Mean monthly temperatures range between -0.1 °C in January and +20.8 °C in July (Fig. 1). Hydrographic examinations in the Biosphere Reserve show, that annual precipitation amount can diverge up to three times on small spatial scales (EHYD 2021). The Eastern parts of the BR are under Pannonian climate, while the North-Western parts are dominated by Atlantic climate. From a geological point of view, the area under survey can decisively be distinguished in flysch and limestone bedrock. Due to heterogeneity in terms of soil, bedrock, precipitation, and topography, the BR Vienna Woods is ecologically highly diverse. About a quarter of the 125 forest types of Austria (Mucina et al. 1993) occur in the BR.

Core area monitoring

The core area monitoring of the BR Vienna Woods consists of 1555 permanent sample plots in the 37 unmanaged core areas. Since 2007, updated field data is available in a 10 year interval. Depending on the core area size, variable grid spacing guarantees a recording accuracy of $\pm 10\%$ of the living standing volume. For more details, please see the field work manual (Posch et al. 2008), the monitoring results published (BR Vienna Woods

Management 2011), and the core area overview (ESM1). Our study considers data from the first inventory period (2008–2010).

Tree species and growing stock volume

Sample trees were collected using angle count sampling (synonym: relascope sampling, Bitterlich sampling) with basal area factor $z = 4m^2 ha^{-1}$ (Bitterlich 1984). Angle count sampling, which is commonly used in large scale forest inventories (e.g., Gabler and Schadauer 2007), is a variable radius sampling technique, with inclusion probabilities proportional to the trees' basal area. Trees are recorded according to the relation of stem diameter and distance to a central inventory point (Heym et al. 2021). Tree diameter at breast height (dbh) at 1.3 m above ground was measured for all trees in the angle count sample using a caliper. Additionally, tree height of every basal area median tree was measured per tree species and sample plot. In any case of tree top break, tree heights were additionally measured. Heights of all other trees in the sample were estimated using the basal area median tree heights and unified height curves of the Austrian National Forest Inventory (Gabler and Schadauer 2007).

Nearest neighboring tree and forest spatial structure

For each tree in the angle count sample, horizontal distance to the nearest neighboring tree was measured and recorded together with tree species and dbh of the nearest neighbor. A diameter threshold of ≥ 10 cm was applied.

Standing and lying dead wood

To estimate standing dead wood volumes, tree height and dbh of all standing dead wood within the angle count sampling (Bitterlich 1984) was measured. In addition, lying dead-wood was recorded using fixed radius circular sample plots (horizontal radius r=8 m) with 20 cm diameter threshold. Depending on diameter at the midpoint (dm), two different cubing tables were used to calculate the individual wood volume for objects of (i) 20 cm < dm \leq 50 cm ($vol_{20-50 \text{ cm dm}}$) and (ii) dm > 50 cm ($vol_{>50 \text{ cm dm}}$). These single cubations were added up per sample point in both categories, yielding the total volume of lying deadwood with dm > 20 cm ($vol_{>20 \text{ cm dm}}$). The total volume of lying dead wood with dm > 5 cm ($vol_{>5 \text{ cm dm}}$) was deviated from this value by applying a bridging function (Eq. 1) for natural, beech dominated forests following Christensen et al. (2005):

$$vol_{>5 \,\mathrm{cm}\,\mathrm{dm}} = vol_{>20 \,\mathrm{cm}\,\mathrm{dm}} \times (0.0279 \times threshold \,dm \,[20 \,\mathrm{cm}] + 0.8301) = 1.3881 \times vol_{>20 \,\mathrm{cm}\,\mathrm{dm}}$$
(1)

Natural regeneration

At each sample point, young trees between 10 and 130 cm height were recorded on an area of 12.5 m^2 . The last year's browsing damage on leading shoots by ungulates was documented binary (browsed/not browsed).

Soil monitoring

Information about soils in the core areas is available from the BR Vienna Woods soil monitoring which was completed in 2012. Soil samples were analyzed in the laboratory by the Austrian Federal Research Centre for Forests. Every fourth sample plot of the core area monitoring was inventoried. At those 422 sample plots, bedrock, geological unit (flysch and limestone forest), soil type, humus type, and soil water balance were surveyed.

Structural diversity indicators

For a reliable assessment of structural diversity and biodiversity, it is necessary to consider comprehensive indicator sets (Pretzsch 2002; LaRue et al. 2019). This case study uses a surrogate approach (Olsgard et al. 2003). In order to assess structural forest diversity, five structural diversity indicators (Table 1) are evaluated in a comprehensive indicator set following Pretzsch (2002). Two indicators of Stand Density are chosen with the purpose to study the effect of indicator choice on indicator correlation and indicative values of comprehensive indicator sets.

The Clark & Evans-Index (C & E) describes the aggregation of horizontal tree distribution which is calculated by the quotient of the observed to the expected distance between neighboring trees assuming Poisson distribution (Clark and Evans 1954). The Shannon Index (H') indicates the diversity of tree species and their relative abundances in a species mixture (Shannon and Weaver 1949). The Stand Density Index (SDI) displays the allometric relationship between quadratic mean diameter and stem density (Reineke 1933; Pretzsch 2002). The Crown Competition factor (CCF) as a second Stand Density indication is a relative measure of competitive pressure in crown space describing the ratio of area size and crown canopy area (Krajicek et al. 1961). The Diameter Differentiation Index (Diff) reveals distance-dependent structural diversity and quantifies the heterogeneity of plant stands (Füldner 1995). The choice of indicators relevant to biodiversity needs to be legitimated (Heink and Kowarik 2010). Scientific evidence for the expected relation between the structural diversity metric (indicator) and certain aspects of forest biodiversity (indicandum) in order to establish a comprehensive biodiversity indicator set is provided in Table 2.

Methods

Explanatory variables

We apply machine learning on forest inventory data to gain new insights in indicator-indicandum relationships. Twenty stand characteristics are reviewed as potential explanatory variables in ten random forests models. These variables can be grouped into five categories: (i) 'age & density', (ii) 'vertical structure', (iii) 'forest site', (iv) 'game impact', and (v) 'soil & bedrock' (Table 3). The explanatory variables tested were chosen from monitoring data available and based on literature reviews (e.g., McElhinny et al. 2005; Gao et al. 2015; Storch et al. 2018). In this case study, species distribution maps (bats, birds, amphibians, snails, insects, higher plants, mosses, lichens, and fungi)

Table 1 Structural diversity indica	tor set		
Structural aspect	Structural diversity indicator	Formula	References
Horizontal distribution	Clark & Evans-Index	$\mathrm{C\&E} = rac{\left(rac{\Sigma_{i=1}^{2-1} w_{ipp,i_{a}}}{\Sigma_{i=1}^{2} w_{ipp}} ight)}{0.5 \cdot \sqrt{rac{1000 \mathrm{km}^2}{M_{obs}}}}$	Clark and Evans (1954)
Species diversity Stand Density	Shannon Index Stand Density Index	$\mathbf{H}' = -\sum_{i=1}^{S} P_{spec} \cdot \ln(p_{spec})$ SDI = $N_{obs} \cdot \left(\frac{25}{qmd}\right)^{-1.605}$	Shannon and Weaver (1949) Reineke (1933)
	Crown Competition factor	$ ext{CCF} = rac{1}{a} \cdot \sum_{j=1}^{z} \left(rac{cd^2 \cdot \pi}{4} ight) \cdot n_{rep} \cdot 100$	Krajicek et al. (1961)
Stand differentiation	Diameter Differentiation Index	Diff = $1 - \frac{1}{N_{Obs}} \cdot \sum_{i=1}^{n} n_{rep_i} \cdot \frac{\min(dbh_i, dbh_{neone(ghour)})}{\max(dbh_i, dbh_{neone(ghour)})}$	Füldner (1995)
The indicator set considers horizo following Hasenauer (1997).	ntal distribution, tree species diversity, Stand	Density and stand differentiation. To assess the Crown Competi	tion factor, cd was computed
n_{rep} : Represented stem number in a	ugle count sample		
r_a : Distance to nearest tree			
N_{obs} : Stem number per hectare			
qmd: Quadratic mean diameter			
z: Number of trees in an angle cour	nt sample		
S: Number of tree species			
<i>p_{spec}</i> : Proportion of the <i>i</i> th tree spe-	cies		

A: Area

 a_o, a_1 : Tree species specific coefficients

dbh: Diameter at breast height

cd: Crown diameter of open grown tree

in the BR core areas, as well as forest age classes, tree species browsed, fraying & bark peeling effects, and tree structural foursome were not considered.

Machine learning approach

Random forest models

Random forest models are composed from regression trees and are trained to predict the values of five structural diversity indicators. We are using the statistical language R (R Core Team 2020) with the packages *randomForest* (Breiman 2001, 2002), *VSURF* (Geneuer

Structural diversity indicators	Scientific evidence
Clark & Evans-Index	Greater <i>structural spatial diversity</i> increases resource partitioning among species (Kohyama 1993; Yachi and Loreau 2007; Álvarez-Yépiz et al. 2017; Atkins et al. 2018) The <i>variation of tree spacing</i> provides an indication of the size and distribution of gaps (Neumann and Starlinger 2001) and thus indirectly on processes such as mortality, ingrowth, and competition (Svensson and Jeglum 2001)
Shannon Index	 Tree species abundance can be used as a proxy for habitat quality or biotope trees (Heym et al. 2021) and related microhabitats (Larrieu et al. 2014) or habitat types (Kovac et al. 2020); e.g., saproxylic beetles, bryophytes, lichens, fungi, and arthropods (Uliczka and Angelstam 1999; Brändle and Brandl 2001; Berglund et al. 2009; Ulyshen 2011) There is high scientific evidence for a positive relation between <i>tree species diversity</i> and the number of bird (Baguette et al. 1994; Fisher and Goldney 1998), ground beetle (Fahy and Gormally 1998; Davis et al. 2000; Magura et al. 2000), arthropod (Chey et al. 1997) and ground vegetation species (Fahy and Gormally 1998; Humphrey et al. 2002) Tree species richness is a proxy for the number of niche spaces filled by different tree species (Turnbull et al. 2016)
Stand Density Index	The <i>SDI</i> can be used as a proxy for spatial distribution of resource avail- ability in biodiversity assessments (Heym et al. 2021) <i>Gap fraction</i> indicates the availability of open niche space (McElhinny et al. 2005; LaRue et al. 2019) Compared with CCF, <i>SDI</i> is also applicable in mixed forest stands & pure European beech stands (Sdino 1996)
Crown Competition factor	 Greater overlap of crowns indicates a greater use of niche space for light in the canopy (Williams et al. 2017; Zheng et al. 2015) and can therefore be an indirect measure of ecological niche space (LaRue et al. 2019) In a meta-study, <i>tree canopy cover</i> could be related negatively to spider species richness in Europe (Gao et al. 2015) Contrary to the SDI, the CCF can delivers reliable outcomes in uneven aged stands (Sterba 1987)
Diameter Differentiation Index	 Variation of tree dimension can be used as a proxy for habitat quality or biotope trees (Heym et al. 2021) and related macro- and microhabitats (Larrieu et al. 2014), e.g., saproxylic beetles, and lichens (Berglund et al. 2009; Uliczka and Angelstam 1999) Large tree diameters indicate high potential for tree related habitats (Hilmo et al. 2009; Nascimbene et al. 2008)

Table 2 Scientific evidence for a comprehensive indicator set in a surrogate approach

Category	Explanatory variables
Age and density	Stem density (N), stem basal area (BA), standing stock volume (V), and quadratic mean diameter (qmd)
Vertical structure	Dominant tree species (dom spec), coarse woody debris > 5 cm dm (cwd > 5 cm), coarse woody debris > 25 cm dm (cwd > 25 cm), standing dead wood (sdw), and natural regeneration (regen)
Forest site	Mesorelief (MesoR), microrelief (MicroR), aspect (asp), and altitude (alt)
Game impact	Percentage of regeneration with browsing damage (bd) and amount of young trees with- out browsing damage (wbd)
Soil and bedrock	Flysch- or limestone forests (flysch), bedrock (bedrock), soil type (soil t), soil moisture (soil m) and humus type (humus)

 Table 3 Explanatory variables tested

et al. 2015) and *randomForest explainer* (Ishwaran et al. 2010). In total, 15 random forest models are trained, three for each diversity indicator.

The first random forest models consider 15 explanatory variables (Table 2) of the categories 1–4 (i.e., age & density, vertical structure, forest site, and game impact) per diversity indicator. These models are trained based on data of 1555 permanent sample plots. The second random forest models consider 20 explanatory variables (Table 2) of the categories 1–5 per diversity indicator. These models are trained based on 1555 permanent sample plots. The third random forest models characterize the interrelation between the five structural diversity indicators within the comprehensive indicator set. These models are trained based on data of 422 permanent sample plots including soil monitoring information.

Every random forest is composed of 500 regression trees. For every regression tree, a training set is drawn using bootstrap aggregating (bagging). The decision tree is built by rule-based splitting of the bagging sample into subsets, maximizing the variance between the subsets (Venables and Ripley 2002). At each split in the learning process, a random subset of explanatory variables is used (Ho 1998). The splitting process is repeated recursively on each derived subset, until (i) the subset has identical values with the target variable or (ii) the splitting does no longer add value to the prediction (Quinlan 1986). The mean value of the target variable within a final subset (leaf of a decision tree) is used as the conditional prediction of the target variable for a corresponding combination of explanatory variables (Venables and Ripley 2002).

Variable importance

The importance of every explanatory variable *j* is assessed by two measures, the percentual increase of the mean squared error (Geneuer et al. 2015; Zhu et al. 2015) and the average minimal depth (Ishwaran et al. 2010). To compute the mean squared error (%IncMSE), the out-of-bag error for every variable *j* is recorded during the fitting process and averaged over the random forest. Then, the estimated values of *j* are randomly permutated in the out-of-bag data and dropped down every fitted tree. A higher mean squared error (%IncMSE) indicates higher variable importance and higher explanatory power of the variable. Slightly negatively %IncMSE values may arise in case the mean squared error of the original predictor variable exceeds %IncMSE of permuted values.

To compute the average minimal depth (AvgMinDepth), the level on which variable *j* is used on average to split the decision tree for the first time is assessed. Averaging MinDepth over 500 decision trees yields the average minimal depth (AvgMinDepth) in our case study. Lower AvgMinDepth values indicate higher variable importance and higher explanatory power of the variable.

Variable selection

A two-step variable selection procedure implemented in the R package *VSURF* (Geneuer et al. 2015) is used. VSURF strengthens the models by preselecting a subset of explanatory variables with sufficient explanatory power and removing variables with little or no explanatory power in advance. For details, please see Geneuer et al. (2015).

Results

Levels of structural diversity in the unmanaged core areas

In line with Bitterlich (1984), Lappi and Bailey (1987), Sterba (2008) we aggregated indicator scores on the core area level (Table 4) which is particularly important using angle count method data (Storch et al. 2018).

Indicator-indicandum relationships of forest structural diversity indicators in lowland, European beech forests

Variable importance of explanatory variables is measured by two metrics, %IncMSE and AvgMinDepth. In the text, variables are ordered by the %IncMSE values because differences are more pronounced with this indication. Figures 2, 3, 4, 5, and 6 additionally display AvgMinDepth to gain insights in variable importance distribution among the 500 decision trees. For stand variable abbreviations, please refer to Table 3.

The Clark & Evans-Index (C & E)

In the *first random forest model*, variables indicated best are 'stem density' (%Inc-MSE=37.05; AvgMinDepth=1.73), 'quadratic mean diameter' (%IncMSE=29.32; Avg-MinDepth=1.92) and 'standing stock volume' (%IncMSE=28.06; AvgMinDepth=1.90). In the *second random forest model*, 'stock volume' (%IncMSE=22.94; AvgMinDepth=1.42), 'stem basal area' (%IncMSE=19.33; AvgMinDepth=2.26), and 'stem density' (%IncMSE=16.77; AvgMinDepth=2.28) prove to be most relevant. All variables predicted well by C & E belong to the 'age & density' category. The *third random forest model* detects intercorrelation with the Crown Competition factor (%IncMSE=13.12; Avg-MinDepth=1.19) and Stand Density Index (%IncMSE=11.15; AvgMinDepth=1.4).

The Shannon Index (H')

In the *first random forest model*, H' predicts 'dominant tree species' (%IncMSE = 50.45; AvgMinDepth = 1.36) best which belongs to variable category 'vertical structure'

Table 4 Struct	ural diversity levels in	the core a	reas													
Nr. core area	Name	Clark <i>§</i>	t Evans l	Index	Shannoi	n Index		Stand D	ensity Inc	dex	Crown C	ompetitio	n factor	Diamete	r Differe	entia-
		Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max
1	Altenberg	0.97	0.27	1.66	0.47	0	1.39	570.6	185.1	1180.1	20.46	1.07	53.47	0.51	0.04	0.98
2	Anninger Tieftal	0.80	0.18	1.64	0.78	0	1.28	696.7	117.1	1433.5	10.02	0.94	34.55	0.48	0.07	0.97
3	Baunzen	1.02	0.15	1.65	0.48	0	1.49	638.1	84.2	1548.2	9.42	0.08	23.27	0.51	0.05	0.98
4	Deutschwald I	1.18	0.55	1.95	0.31	0	1.33	748.8	333.6	1245.0	35.78	10.88	85.59	0.48	0.04	0.98
5	Deutschwald II	1.19	0.84	1.69	0.62	0	1.24	702.3	267.7	1256.8	88.78	22.94	137.76	0.53	0.07	0.98
9	Dombachgraben	0.99	0.49	1.63	0.27	0	1.09	678.1	242.1	1197.0	22.37	0.69	66.28	0.51	0.05	0.97
7	Dorotheerwald	1.04	0.52	2.42	0.63	0	1.27	8.669	216.6	1408.7	10.00	0.25	31.78	0.53	0.10	0.98
8	Festenberg	1.06	0.38	2.29	0.45	0	1.31	586.0	204.9	1088.8	21.19	0.44	70.47	0.32	0.08	0.81
6	Finsterer Gang	1.15	0.68	1.79	0.79	0	1.68	671.4	356.4	1179.3	18.58	3.78	43.91	0.29	0.05	0.71
10	Gießhübl-Eichberg	1.00	0.27	2.15	0.52	0	1.41	521.6	58.8	1063.8	12.65	0.14	29.61	0.71	0.11	0.98
11	Hainbach	1.06	0.44	2.02	0.41	0	1.50	666.3	65.2	1352.0	7.83	0.16	26.67	0.65	0.07	0.98
12	Helenental	1.01	0.14	2.25	0.61	0	1.61	599.4	61.5	1309.0	6.66	0.46	17.19	0.66	0.19	0.97
13	Hengstlberg	1.15	0.59	2.55	0.24	0	1.28	653.4	90.8	1022.5	13.64	0.15	32.77	0.60	0.09	0.98
14	Hirschenstein	1.03	0.38	1.62	0.67	0	1.43	703.1	87.3	1371.0	7.48	0.19	18.04	0.79	0.21	0.98
15	Hoher Lindkogel	0.98	0.14	2.54	0.40	0	1.31	645.7	76.8	1761.0	2.08	0.02	10.62	0.64	0.01	0.98
16	Höherberg	1.05	0.22	1.64	0.67	0	1.44	736.5	291.7	1689.4	15.09	1.91	36.88	0.29	0.10	0.57
17	Hollergraben	1.15	0.50	2.27	0.65	0	1.32	711.0	365.6	1120.2	122.72	37.52	295.81	0.75	0.14	0.98
18	Johannser Kogl I	0.93	0.54	1.56	0.71	0	1.35	475.7	196.2	1009.0	161.79	11.00	527.82	0.63	0.06	0.98
19	Johannserkogl II	0.99	0.43	1.97	0.65	0	1.15	553.9	146.5	1191.7	151.49	3.94	438.27	0.38	0.11	0.78
20 & 21	Kiental I/II	1.05	0.45	1.90	0.51	0	1.39	683.5	187.6	1337.0	13.61	1.77	41.35	0.33	0.08	0.65
22	Kolbeterberg	1.09	0.55	1.92	0.32	0	1.08	541.0	117.0	1228.3	36.80	0.38	144.63	0.44	0.08	0.88
23	Latisberg	1.28	0.68	2.80	0.49	0	1.09	596.7	185.7	901.5	58.81	1.42	166.34	0.55	0.07	0.98
24	Leopoldsberg I	0.95	0.25	1.73	0.57	0	1.56	478.0	157.4	1235.5	15.06	1.15	45.69	0.83	0.58	0.96
25	Leopoldsberg II	0.96	0.47	1.35	0.60	0	1.56	626.6	50.3	1372.8	50.62	7.43	116.96	0.86	0.34	0.98
26	Mauerbach	1.10	0.46	1.72	0.22	0	1.31	657.0	61.0	1078.1	16.91	0.31	32.34	0.44	0.09	0.99

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Nr. core area	Name	Clark &	Evans I	ndex	Shannor	Index		Stand D	ensity Ind	ex	Crown Co	ompetitio	n factor	Diamete	ır Differe	ntia-
		Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max	Mean	Min	Max
27	Mitterschöpfl	1.08	0.49	1.57	0.35	0	1.28	667.6	112.7	1793.1	9.47	0.09	25.28	0.54	0.08	0.98
28	Moosgraben	1.19	0.50	2.42	0.37	0	1.38	617.4	289.9	6.666	77.88	2.22	200.76	0.80	0.32	0.99
29	Pfaffenberg	1.10	0.43	1.63	0.64	0	1.14	801.5	367.3	1195.5	82.27	17.70	219.36	0.47	0.09	0.87
30	Rauchbuchberg	0.97	0.28	1.74	0.55	0	1.45	567.1	69.8	985.8	53.64	0.35	153.91	0.50	0.06	0.98
31	Sattel	1.03	0.38	1.54	0.43	0	1.24	582.4	97.2	1525.9	21.17	0.28	52.38	0.28	0.00	0.66
32	Schwarzlacken	1.08	0.48	1.63	0.53	0	1.61	678.5	336.5	1390.4	14.50	0.66	32.43	0.36	0.06	0.75
33	Troppberg	1.10	0.20	1.89	0.37	0	1.63	682.6	65.8	1505.4	8.06	0.16	26.29	0.43	0.12	0.98
34	Übelaugraben	1.03	0.51	1.79	0.04	0	0.96	824.1	67.7	1380.1	226.82	14.92	451.33	0.65	0.10	0.98
35	Waldandacht	1.11	0.36	2.09	0.43	0	0.98	747.9	90.8	1350.9	55.02	1.08	159.99	0.56	0.11	0.98
36	Wassergspreng	1.11	0.35	2.17	0.65	0	1.37	644.0	63.0	1558.5	29.19	1.03	84.21	0.26	0.05	0.77
37	Weinberg	1.06	0.20	2.05	0.72	0	1.59	606.4	79.0	994.9	40.49	1.74	92.00	0.25	0.14	0.51
	BR Vienna Woods	1.05	0.14	2.80	0.48	0	1.68	645.3	50.3	1793.1	34.64	0.02	527.82	0.52	0.00	0.99



Fig.2 Indicator–indicandum relationship of the Clark & Evans Index. Minimum depth plots are created by applying the 'R random Forest explainer' package for the *Clark & Evans-Index (C & E)*. The different colors indicate the distribution of the variables' minimal depth (MinDepth) over the 500 decision trees of a random forest. The average minimal depth (AvgMinDepth) of the variables is denoted by the numbers in the white boxes, please note the different scaling. The first random forest model (left panel) considers 1555 permanent sample plots and fifteen explanatory variables, the second random forest model (center panel) considers 422 sample plots and 20 explanatory variables. The third random forest (right panel) considers statistic intercorrelation between the indicators on 1555 permanent sample plots with four explanatory variables.



Fig. 3 Indicator–indicandum relationship of the Shannon Index. Minimum depth plots are created by applying the 'R random Forest explainer' package for the *Shannon Index* (H'). The different colors indicate the distribution of the variables' minimal depth (MinDepth) over the 500 decision trees of a random forest. The average minimal depth (AvgMinDepth) of the variables is denoted by the numbers in the white boxes, please note the different scaling. The first random forest model (left panel) considers 1555 permanent sample plots and fifteen explanatory variables, the second random forest model (center panel) considers 422 sample plots and 20 explanatory variables. The third random forest (right panel) considers statistic intercorrelation between the indicators on 1555 permanent sample plots with four explanatory variables

(Fig. 3). This variable is followed by 'standing stock volume' (%IncMSE=29.94; AvgMinDepth=1.59) and 'stem density' (%IncMSE=23.44; AvgMinDepth=1.77) out of the 'age & density' category. The *second random forest model* indicates highest variable importance for 'dominant tree species' (%IncMSE=25.63; AvgMinDepth=1.76), 'standing stock volume' (%IncMSE=14.74; AvgMinDepth=1.70) and 'soil type' (%IncMSE=14.44; AvgMinDepth=2.05). In the *third random forest model*, H' reveals closest statistical relation to the Stand Density Index (%IncMSE=22.95; AvgMinDepth=1.32) and the Crown Competition factor (%IncMSE=21.49; AvgMinDepth=1.38) within the indicator set.



Fig. 4 Indicator–indicandum relationship of the Stand Density Index. Minimum depth plots are created by applying the 'R random Forest explainer' package for the *Stand Density Index (SDI)*. The different colors indicate the distribution of the variables' minimal depth (MinDepth) over the 500 decision trees of a random forest. The average minimal depth (AvgMinDepth) of the variables is denoted by the numbers in the white boxes, please note the different scaling. The first random forest model (left panel) considers 1555 permanent sample plots and fifteen explanatory variables, the second random forest model (center panel) considers 422 sample plots and 20 explanatory variables. The third random forest (right panel) considers statistic intercorrelation between the indicators on 1555 permanent sample plots with four explanatory variables.



Fig. 5 Indicator-indicandum relationship of the Crown Competition factor. Minimum depth plots are created by applying the 'R random Forest explainer' package for the Crown Competition factor (CCF). The different colors indicate the distribution of the variables' minimal depth (MinDepth) over the 500 decision trees of a random forest. The average minimal depth (AvgMinDepth) of the variables is denoted by the numbers in the white boxes, please note the different scaling. The first random forest model (left panel) considers 1555 permanent sample plots and fifteen explanatory variables, the second random forest model (center panel) considers 422 sample plots and 20 explanatory variables. The third random forest (right panel) considers statistic intercorrelation between the indicators on 1555 permanent sample plots with four explanatory variables

The Stand Density Index (SDI)

All variables indicated well by SDI in the *first random forest model* i.e., 'stem basal area' (%IncMSE=82.79; AvgMinDepth=1.07), 'stem density' (%IncMSE=36.44; AvgMinDepth=0.95), and 'quadratic mean diameter' (%IncMSE=31.75%; AvgMinDepth=1.01) belong to the 'age & density' category. In the *second SDI model*, 'stem density' (%IncMSE=53.16; AvgMinDepth=1.03), 'stem basal area' (%IncMSE=42.02; AvgMinDepth=1.05), and 'standing stock volume' (%IncMSE=29.95; AvgMinDepth=0.97) can be very well predicted. SDI shows closest interrelations to other structural diversity indicators.



Fig. 6 Indicator–indicandum relationship of the Diameter Differentiation Index. Minimum depth plots are created by applying the 'R random Forest explainer' package for the Diameter Differentiation Index (Diff). The different colors indicate the distribution of the variables' minimal depth (MinDepth) over the 500 decision trees of a random forest. The average minimal depth (AvgMinDepth) of the variables is denoted by the numbers in the white boxes, please note the different scaling. The first random forest model (left panel) considers 1555 permanent sample plots and fifteen explanatory variables, the second random forest model (center panel) considers 422 sample plots and 20 explanatory variables. The third random forest (right panel) considers statistic intercorrelation between the indicators on 1555 permanent sample plots with four explanatory variables

Adding any of the remaining indicators to the *third random forest model* yields %IncMSE between 13 and 35%.

The Crown Competition factor (CCF)

Variables indicated best in the *first CCF random forest model* are 'stem basal area' (%IncMSE=62.10; AvgMinDepth=1.57), 'dominant tree species' (%IncMSE=61.22; AvgMinDepth=1.64) and 'quadratic mean diameter' (%IncMSE=47.69; AvgMinDepth=1.61). In *the second model*, four variables prove high explanatory power, namely 'stem density' (%IncMSE=28.99; AvgMinDepth=1.67), 'stem basal area' (%IncMSE=27.35; AvgMinDepth=1.55), 'quadratic mean diameter' (%IncMSE=27.04; AvgMinDepth=1.59), and 'standing stock volume' (%IncMSE=25.77; AvgMinDepth=1.68). The *third random forest model* detects closest intercorrelation between CCF and SDI (%IncMSE=33.18; AvgMinDepth=1.29).

The Diameter Differentiation Index (diff)

Three explanatory variables, all belonging to the category 'age & density', are indicated best by Diff in the *first random forest model:* 'Stem density' (%IncMSE=25.46; Avg-MinDepth=1.28), 'standing stock volume' (%IncMSE=19.53; AvgMinDepth=2.02), and 'stem basal area' (%IncMSE=18.39; AvgMinDepth=2.11). In the *second random forest model*, variables predicted well are 'quadratic mean diameter' (%IncMSE=16.36; AvgMinDepth=1.92) and 'stem density' (%IncMSE=15.43; AvgMinDepth=1.87). The *third random forest model* displays closest intercorrelation to the SDI (%IncMSE=15.13; AvgMinDepth=1.39) and the Crown Competition factor (%IncMSE=14.87; AvgMinDepth=1.54).

Indicator–Indicandum relationships of aa comprehensive forest biodiversity indicator set

The variable category neglected by the indicator set are 'game impact' and 'soil & bedrock' (Fig. 7). Partially reflected are the categories 'forest site' and 'vertical structure'. Variables of the category 'age & density' are overrepresented. There are no major differences between first and second model results. However, variable importance decreases on average about -23% in the second models compared to the first ones which consider a lower number of explanatory variables. Testing fifteen instead of twenty explanatory variables affects the sum of explanatory power between +9%IncMSE (SDI) and +33%IncMSE (H'). Using randomForest to gain insight in indicandum–indicator relationships, a pronounced sensitivity to the number of explanatory variables tested could be found.

Explanatory variables indicated best by the indicator set in the first and second models are stem basal area (BA=154.43%IncMSE), stem density (N=117.61%IncMSE), standing stock volume (V=101.34%IncMSE), quadratic mean diameter (qmd=81.02%IncMSE),



Fig. 7 Indicator–indicandum relationships of a comprehensive indicator set. Overview of the mean squared error (%IncMSE) created with R random Forest to indicate explanatory variable importance for the indicator set, consisting of Clark & Evans-Index (C & E), Shannon Index (H'), Stand Density Index (SDI), Crown Competition factor (CCF) and Diameter Differentiation Index (Diff). Upper panel: First random forest models (1555 sample plots, 15 explanatory variables). Lower panel: Second random forest models (422 sample plots, 20 explanatory variables)

and dominant tree species (dom spec=71.22). 17 of 20 explanatory variables under study are at least once indicated in the ten models. The three stand variables overall neglected by the indicators set are coarse woody debris <25 mm MDM (cwd <25 mm), proportion of regeneration with browsing damage (bd), and humus type (humus).

Intercorrelation within a comprehensive indicator set

The five structural indicators are highly interrelated (Fig. 8). Overall, SDI shows highest statistical relation to other diversity indicators and can also be well predicted by them. Moreover, Adding CCF to a model considerably raises it's explanatory power. Contrary, C & E displays very low statistic relation to other structural diversity indicators. Overall highest correlation can be found between SDI and CCF (33.2–34.8%IncMSE). Strong correlations within indicator sets may arise due to description of the same structural aspect (e.g., Stand Density) and by sharing direct elements (e.g., tree diameter and stem density) in the formula.

Discussion

Model approach

Comparing the use of a machine learning approach (*random Forests*) to gain additional insights into indicator-indicandum relationships and intercorrelation within indicator sets in comparison to e.g., linear regression with forward selection, we see following main advantage for ecological science: (i) no assumptions about linear relationships are needed, (ii) a possible collinearity of variables does not affect model predictions negatively and (iii) stable prediction results in terms of the Out-Of-Bag error. The disadvantages of *random Forests* are that (i) outcomes are more challenging to interpret, (ii) direction of statistic relation is unknown, and (iii) collinearity might affect %IncMSE, are clearly outweighed in our case study. The package *random Forest explainer* proved to be a useful tool to interpret the model outcomes.

Validity of most indicators used is weakly scientifically supported (Gao et al. 2015). A biodiversity indicator is found to be more useful the more precise the correlation with the indicandum is known (Heink and Kowarik 2010). Yet, indicator–indicandum relationships

Fig. 8 Overview of intercorrelation within the comprehensive indicators set. Overview of the mean squared error (%IncMSE) created with R random Forest to characterize the interrelation between Clark & Evans-Index (C & E), Shannon Index (H[']), Stand Density Index (SDI), Crown Competition factor (CCF) and Diameter Differentiation (Diff)



are poorly understood and tested across habitat and scales (Gao et al. 2015). Our case study shows, how *random Forest* can be applied for the indicator validation urgently needed on large spatial scales (Ferris and Humphrey 1999; Gao et al. 2015) considering intercorrelated data and indicators sets.

Indicator-indicandum relationships

The Clark & Evans-Index (C & E)

Actual C & E levels in the unmanaged core areas of the BR Vienna Woods range between 0.76 ('Anninger') and 1.25 ('Latisberg'). In the core area 'Anninger', trees are evenly arranged, while stem distribution in 'Latisberg' already evolved towards a more clustered spatial structure. Comparable C&E levels to 'Latisberg' were found in a 53-year-old pure European beech stand in Germany (Pommerening 2002). Older stands tend to have lower stem numbers and clumped structure, while young stands are often found to be evenly arranged (Pretzsch 2002; Dieler 2013). Even if mean stand age only differs about 20 years between two core areas, 'Latisberg' displays twice the amount of living stock volume and half the number of trees per hectare. In line with Pretzsch (2002) and Dieler (2013), this points towards a more mature successional state of 'Latisberg' which is indicated by C & E.

In unmanaged forests, structural complexity, and diversity significantly increase with stand age, denoted by enhanced levels of lying and standing deadwood and natural regeneration (Pretzsch 2002). In line with the findings of Pretzsch (2002) all these variables (cwd, swd, regen) are very well indicated by C & E in our case study. C & E indicates the variable category 'vertical structure' very well. Moreover, our results underline a profonde indication of the category 'age & density'.

C & E was found to indicate horizontal distribution as a proxy for resource partitioning of light use among species (Kohyama 1993; Yachi and Loreau 2007; Álvarez-Yépiz et al. 2017; Atkins et al. 2018), the size and distribution of gaps (Neumann and Starlinger 2001) and processes such as mortality, ingrowth, and competition (Svensson and Jeglum 2001). Therefore, it is highly plausible that the variable indicated best by C& E in our case study is 'stem density'. C & E shows particularly low statistical relation to other structural diversity indicators.

The Shannon Index (H')

Shannon Index levels varies between 0.04 ('Übelaugraben') and 0.79 ('Finsterer Gang'). Comparable Index levels were described for pure European beech forest (H'=0.09) and oak-beech mixed forest (H'=0.62) in Germany (Pommerening 2002). Rare species increase H' disproportionately, while common species affect it under proportionately (Pretzsch 2002). Overall, the Shannon Index indicates the highest number of variables. Moreover, the category 'vertical structure' and the variable 'dominant tree species' are predicted best by the Shannon Index. This is supported by scientific literature in which the Shannon Index is expected to indicate tree species abundance and diversity and is considered as a proxy for the number of niche spaces filled by different tree species (Turnbull et al. 2016), habitat quality or biotope trees (Heym et al. 2021), diversity of microhabitats (Larrieu et al. 2014), and habitat types (Kovac et al. 2020) for a variegation of taxonomic groups.

Of the five diversity indicators surveyed in this study, H' indicates variables of 'soil & bedrock' best (s. s., soil type, flysch or limestone Vienna Woods, and soil moisture). These variables are interdependent, have major impact on plant communities, and underline the geological peculiarity of the study area. The distinction between flysch and limestone Vienna Woods has crucial implications for the soil types, their chemical composition and water balance, as well as the diversity of occurring animal and plant species (BFW 2011). In the flysch parts of the Vienna Woods, heavy, nutrient-rich, deep soils have developed. These soils are characterized by advantageous water supply and high specific water storage capacity (Leitgeb et al. 2012). Species diversity monitoring in the BR Vienna Woods detects few vascular plant species in high abundances in those areas (BR Vienna Woods Management 2021a). In the limestone parts of the study area, dry, nutrient-poor, and shallow soils are common (BFW 2011). Specific water storage capacity and water supply of these soils is much lower and promote drought tolerance species (Leitgeb et al. 2012). Species diversity monitoring indicates species-rich herbaceous vegetation in low abundances (BR Vienna Woods Management 2021a) making the model outcomes highly reasonable.

The Stand Density Index (SDI)

Of all indicators, the variables 'basal area', 'living wood volume', 'quadratic mean diameter', and 'Stand Density' are indicated best by SDI. The Stand Density Index reflects the lowest number of explanatory variables, all belonging to the category 'age & density', in very high accuracy. In our study, pronounced correlations with other indicators, especially with CCF, are found. Besides directly sharing the element 'Stand Density' in their formula, CCF and SDI describe the same forest structural aspect. The SDI is a proxy for spatial distribution of resource availability (Heym et al. 2021) and indicates the availability of open niche space (McElhinny et al. 2005; LaRue et al. 2019). Actual SDI levels in the core areas of the BR Vienna Woods range between 524.69 ('Leopoldsberg I') and 877.51 ('Rauchbuchberg'). Our findings line up with Vospernik and Sterba (2016) who demonstrated maximum stand densities stands of tree species in Austria. Pure coniferous and mixed stands show comparably higher Stand Density levels than broadleaved stands.

No correlation between SDI and 'dominant tree species' is detected in the case study, even if e.g., tree mortality with increasing Stand Density was found to be strongly tree species dependent (Liang et al. 2007). This indicates that (1) the broad-leaved species observed have similar maximum densities in terms of stem numbers and basal areas or (2) species dependent mortality does not yet play a major role in the core areas of the BR Vienna Woods.

Additionally, occurrence of 'clastic bedrock', on which nutrient-poor soils establish (NW-FVA 2008), is indicated by SDI. Our study shows how canopy competition in the BR Vienna Woods could be a proxy for soil nutrient supply. These findings are in line with Schmidt et al. (2002) and Podrázský et al. (2014), who proved that soil base supply is the most important factor explaining herbaceous species diversity in temperate beech and Douglas fir forests. Greater overlap of crowns indicates a greater use of niche space for light in the canopy (Williams et al. 2017), and limits light transmission to the ground. In future studies, it would hence be interesting to test if ground vegetation diversity or quantity can be indicated by SDI in European beech dominated forests.

The Crown Competition factor (CCF)

The ranking of the core areas deviates between Stand Density assessment with SDI and CCF. Actual CCF levels in the core areas of the BR Vienna Woods range between 225.60 ('Johannserkogel II') and 471.75 ('Übelaugraben'). CCF can be applied to uneven-aged mixed forests (Sterba 2008). Difficulties with CCF can arise with the assessment of pure stands of the very shade-tolerant and large-crowned European beech, for which Sdino (1996) described maximum CCF levels of > 2000. Variables well indicated by CCF are 'stem basal area', 'quadratic mean diameter', and 'dominant tree species'. The indication of 'dominant tree species' by the CCF is in line with Sdino (1996) and Liang et al. (2007) and may occur due to the species-wise crown diameter being considered in the CCF formula.

Moreover, CCF indicates the variables 'altitude' and 'aspect' well. The Vienna Woods contains both, hall-shaped, low understory beech stands and south-exposed hilltops, where European beech (*Fagus sylvatica*) is already water-limited. On those sites, red pine and oak forest communities with rich understory occur (BR Vienna Woods Management 2021b), making this result highly plausible.

The Diameter Differentiation Index (Diff)

The Diameter Differentiation Index is the only indicator to mirror game impact and an overall high number of variables. Closest intercorrelation of Diff is found with CCF and SDI, both of which Diff shares one element (qmd) in the formula with, respectively. Actual Diameter Differentiation Index levels in the core areas of the BR Vienna Woods range between 0.22 ('Hengstlberg') and 0.40 ('Johannserkogel I'). Diameter heterogeneity in unmanaged stands is created by natural disturbance regimes which are decisive for most forest structural legacies. Natural disturbance regimes of European beech forests contain frequent, small-scale, low intensity as well as rare, large-scale, high intensity disturbance events (Leibundgut 1982; Mayer 1984; Tabaku 1999; Meyer et al. 2003).

Species diversity monitoring in the BR Vienna Woods shows that occurrence probabilities for bat, snail, relict beetle, and old-growth forest bird species increase in the core areas compared to the managed parts. The Diameter Differentiation Index seems to mirror plenty of the crucial habitat structures and quality for those guilds best (e.g., altitude, aspect, micro- and meso-relief, natural regeneration and standing dead wood). Deadwood input often relates with the natural disturbance regimes (Christensen et al. 2005). The outcomes line up with findings of Winter and Möller (2008) who showed that the Diff can be an important indicator of microhabitats in forest stands.

Indicative value of a comprehensive biodiversity indicator set

The variable category 'age & density' is overrepresented by the comprehensive indicator set. Partially reflected are the categories 'forest site' and 'vertical structure'. The categories neglected are 'game impact' and 'soil & bedrock'. Using random Forest to gain new insights in indicandum–indicator relationships, pronounced sensitivity to the number of explanatory variables tested could be found. Variables reflected best by the indicator set are 'stem basal area', 'stem density', 'standing stock volume', and 'quadratic mean diameter'. Contrary, stand characteristics like 'coarse woody debris > 25 MDM', 'tree browsing', and 'humus type' are neglected in all models. Scientifically, there is broad consensus for the

relevance of humus type (e.g., Schäfer and Schauermann 1990; Hooper et al. 2000; Ponge 2003; Salmon et al. 2006, 2008), tree browsing (e.g., Gill 1992; Pastor et al. 1997; Reimoser et al. 2003) and large coarse woody debris (Kappes & Topp 2004; Müller et al. 2007; Rondeux and Sanchez 2010; Brin et al. 2011; Lassauce et al. 2011) for forest biodiversity.

In line with LaRue et al. (2019), our study shows that aspects of forest structure indeed are intercorrelated and neither ecologically nor statistically independent. Furthermore, we agree with these authors that structural niche space or ecosystem structure and function cannot be understood by one metric. Indicators which measure either more or less than they are supposed to, i.e., construct-irrelevant variance or construct underrepresentation may bias the qualitative connection between evidence and interpretation (Heink and Kowarik 2010).

Due to unavailable indicator values (e.g., bark diversity, hollow trees, forest communities, litter dry weight, litter decomposition, perennial species richness, tree age, and undisturbed reference areas) or different scales it was not possible to compare our indicator set with the performance of other aggregated biodiversity indicators (Parkes et al. 2003; McElhinny et al. 2006; Geburek et al. 2010; Storch et al. 2018; Heym et al. 2021). However, there is partial agreement in choice of elements of biodiversity studied in McElhinny et al. (2006) and Storch et al. (2018) like quadratic mean diameter, natural regeneration, standing and lying deadwood, stem basal area. Compared to Heym et al. (2021) partly identical structural diversity indicators are chosen (e.g., Shannon Index, SDI).

Handling knowledge gaps in biodiversity monitoring by machine learning approaches has already been explored in permanent grassland and freshwater ecosystems (Gallardo et al. 2011; Plantureux et al. 2011). In line with these authors, our case study underlines the large potential of machine learning for testing indicative value of single indicators and comprehensive forest biodiversity indicator sets. Moreover, machine learning could advance biodiversity indicator choice.

Summary and conclusion

In this publication, a machine learning approach to provide novel insights in indicator-indicandum relationships of biodiversity indicators and comprehensive indicator sets is presented. The indicators tested are parameters of forest spatial and structural heterogeneity. We surveyed a comprehensive indicator set of Clark & Evans-, Shannon, Stand Density, Diameter Differentiation Index, and Crown Competition factor with randomForest and examine their indicative value for twenty explanatory stand variables.

Biodiversity indicators are sometimes criticized for displaying poor indicator-indicandum relationships (Ferris and Humphrey 1999; Margules et al. 2002; Duelli and Obrist 2003; Gao et al. 2015). Machine learning proves to be a useful tool to overcome these knowledge gaps and provides additional insights in indicator-indicandum relationships. This scientific work deepens understanding of statistic properties of forest-inventory based biodiversity indicators and comprehensive indicator sets.

Examining 37 unmanaged core areas in the Vienna Woods, following scientific questions are answered: Which levels of structural diversity can be found in the unmanaged core areas of the Biosphere Reserve Vienna Woods? (2) Which stand characteristics are indicated by single structural diversity indicators? (3) Which stand characteristics are indicated or neglected by a comprehensive indicator set? (4) How strong is the intercorrelation in an indicator set? Indicator choice is the most crucial step in biodiversity assessments. In our study, the Shannon Index is found to be most useful to indicate the variable category 'soil & bedrock' and 'vertical structure'. Variables of 'age & density' are best considered using the Stand Density Index which indicates a low number of stand variables in very high accuracy. CCF indicates the variables of 'forest site' best and altogether displays closest relation to all variables studied. The Diameter Differentiation Index is the only indicator to mirror 'game impact' and might reflect natural disturbance regimes well. Overall, the Shannon Index indicates highest, the Stand Density Index lowest number of forest stand characteristics.

Strong correlations between indicators may arise due to indication of the same forest structural aspect in indicator sets and/or by sharing direct elements in the formula. To rise reliability of biodiversity assessments, both should most possibly be avoided. Some stand characteristics (e.g., variable category 'age & density') relevant to biodiversity are indicated disproportionally in the comprehensive indicator set, while other important ones (e.g., 'coarse woody debris < 25 MDM', 'tree browsing', and 'humus type') are neglected.

More ecological studies are needed to explore indicator-indicandum relationships in detail. Machine learning as integral part of artificial intelligence may be a novel, effective and entire objective way to gain new insights into indicator-indicandum relationships on variable scales. The prediction outcome is decisively impacted by type and number of explanatory variables tested. The smaller the number of input variables, the more parsimonious is the model. Preselecting variables with regression algorithms is highly recommended. Random Forest models assumes interval scaled variables. Therefore, the impact of interval-scaled, common features on biodiversity can effectively be evaluated with machine learning. Nonetheless, relevance of qualitative variables and rare events may be underestimated. The methodology described in this study might be more suitable to review quantitative (measurable) than qualitative (observed) variables.

Our goal was to contribute to the use of inventory-based structural diversity indicators in forests by precising indicator-indicandum relationships through machine learning. This case study shows, how random forest models can be applied for the indicator validation on large spatial scales, considering intercorrelated data and comprehensive sets of structural diversity indicators. It might be a useful tool to create novel biodiversity indicator sets. Our findings support the great potential of random Forest in the context of forest biodiversity assessments and indicator choice.

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Declarations

Conflict of interest The authors declare that they have no conflict of interest.

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Article Assessing Forest Biodiversity: A Novel Index to Consider Ecosystem, Species, and Genetic Diversity

Jana-Sophie Ette *^(D), Markus Sallmannshofer and Thomas Geburek

Austrian Research Centre for Forests, Department for Forest Growth, Silviculture, and Genetics, Seckendorff-Gudent Weg 8, 1130 Vienna, Austria

* Correspondence: sophie.ette@yahoo.de

Abstract: Rates of biodiversity loss remain high, threatening the life support system upon which all human life depends. In a case study, a novel biodiversity composite index (BCI) in line with the Convention on Biological Diversity is established in Tyrol, Austria, based on available national forest inventory and forest typing data. Indicators are referenced by ecological modeling, protected areas, and unmanaged forests using a machine learning approach. Our case study displays an average biodiversity rating of 57% out of 100% for Tyrolean forests. The respective rating for ecosystem diversity is 49%; for genetic diversity, 53%; and for species diversity, 71%. Coniferous forest types are in a more favorable state of preservation than deciduous and mixed forests. The BCI approach is transferable to Central European areas with forest typing. Our objective is to support the conservation of biodiversity and provide guidance to regional forest policy. BCI is useful to set restoration priorities, reach conservation targets, raise effectiveness of financial resources spent on biodiversity conservation, and enhance Sustainable Forest Management.

Keywords: convention on biological diversity; national forest inventory; dynamic forest typing; machine learning; sustainable forest management; temperate forests

1. Introduction

Biodiversity loss is one of the greatest ecological challenges of our time [1] Biodiversity plays a crucial role in biological processes, provision of ecosystem services, and stability of forest ecosystems [2–5]. With current rates of biodiversity loss [6,7], forest multifunctionality and productivity are decreasing at an accelerating rate [8].

Evaluating biodiversity is a highly complex task [9,10]. Additionally, biodiversity indicators are still criticized for poor indicator–indicandum relationships [11–14]. Following Heink and Kowarik [15], an *indicator* is of major relevance for a given issue, e.g., assessment of a specific impact for conservation policy (tree diameter and age classes), while an *indicandum* is the indicated phenomenon (old-growth forests). Although the relationship to the indicandum may not be fully understood yet, we will refer to these metrics as "indicators" in the following.

Due to weak correlations with the indicandum, *indicator species concepts* have not been successful [12,13], while concepts for forest genetic monitoring are missing in Europe [16]. Policymakers, forest managers, and scientists are facing severe knowledge gaps while having to decide which and how to choose and aggregate biodiversity indicators [17–20] as well as defining baselines.

Structures, processes, and taxonomic groups are currently used as *ecological indicators* [15]. Our study applies metrics of structural diversity relevant to forest biodiversity based on scientific evidence. *Structural diversity concepts* indicate potential habitat quality, niche differentiation, structural complexity [7], and other sources of forest biodiversity [18], e.g., for umbrella species [21] and bird species [22]. There is broad scientific evidence for positive relationships between measures of forest structural variety and elements of biodiversity [23–25].



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Copyright: © 2023 by the authors. Licensee MDPI, Basel, Switzerland. This article is an open access article distributed under the terms and conditions of the Creative Commons Attribution (CC BY) license (https:// creativecommons.org/licenses/by/ 4.0/). On large spatial and temporal scales, the availability of reliable data sets is a limiting factor for biodiversity assessments and monitoring [9,10]. Without sound biodiversity monitoring and reporting systems, natural resources get overexploited or marginalized in decision-making [26]. Gaps in biodiversity monitoring may contribute to the lack of success in biodiversity policy implementation [16]. This may be one of the main reasons why, despite international conventions and large financial efforts [27], current rates of biodiversity loss remain high, threatening the life support system upon which all human life depends [28].

There are three biodiversity indicator sets internationally accepted, developed by the European Environment Agency, Biodiversity Indicators Partnership, and Ministerial Conference on the Protection of Forests in Europe. All of them cannot be used to judge, compare, or predict consequences of forest management for forest biodiversity at the regional level.

Understanding ecological impacts of forest management practices on biodiversity and associated ecosystem processes is essential for developing Sustainable Forest Management approaches [29,30]. Some forest ecosystem services can work in synergy whereas others, such as biodiversity and intensive timber production, are hardly compatible [31]. This policy–policy conflict is one of the most acknowledged trade-offs related to forest management [32–34]. Sustainable Forest Management is characterized by taking consequences of operational decisions for biodiversity into consideration [35], which is very difficult to achieve for forest enterprises. Unambiguous and practical concepts to define and measure forest biodiversity relevant to scale and purpose are needed [36,37].

Selecting appropriate indicators is particularly challenging using forest inventory data which originally were designed for forest resource management purposes [18]. Main impacts of forest management on forest biodiversity are changes in forest structure, species composition [38,39], and forest genetic resources. It is therefore reasonable to monitor changes in these determinants [40,41].

Large-scale forest inventories have rarely been used for biodiversity assessments [42,43]. However, forest inventories proved their potential to overcome data deficits on large spatial and temporal scales [21,25,41,44,45]. Major advantages of inventory-based biodiversity assessments are the repeated measurements which detect temporal changes [10] at low additional costs [45,46] for a high number of attributes, forest types, sample sizes, and scales [10,41]. In the long term, changes in biodiversity may even be related to forest management [41] and forest policy measures, which makes it highly reasonable to choose biodiversity indicators based on existing forest inventory data. Forest typing models cannot solely be used for tree species selection under various climate warming scenarios. An Austrian case study demonstrates the great potential of forest typing models and machine learning for conservation planning and policy guidance.

In this study, a novel biodiversity composite index (BCI) to assess forest biodiversity of the federal autonomous province of Tyrol, Austria, is presented. BCI was created in the Interreg-project "Bio $\Delta 4$ " and was designed to be transferable to neighboring Central European regions in, e.g., Austria, Italy, and Germany. The basic assumption of BCI is that forests of high naturalness can maintain biodiversity best on large temporal and spatial scales. BCI targets heterogeneity and levels of diversity evolving naturally (or nature identical) at a forest stand to conserve overall forest biodiversity on a landscape scale. BCI logic structure is in line with the Convention on Biological Diversity (CBD). It follows the Convention's internationally accepted definition of biodiversity, stating that "biodiversity is the variability among living organisms from all sources including, inter alia, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species, and of ecosystems" (CBD, 1992). In line with the CBD, we define ecosystems as "a dynamic complex of plant, animal and microorganism communities and their non-living environment interacting as a functional unit." In our case study, BCI "ecosystem diversity" indicates the variations in forest ecosystems within the geographical location Tyrol.

Our objective was to create a stand-scale biodiversity index assembled from indicators which (1) are based on available data sets, (2) are based on high scientific evidence relevant to biodiversity, and (3) equally consider ecosystem, species, and genetic diversity. The new approach can be repeated cost-efficiently in each forest inventory period.

BCI provides quantitative aggregation and simplification of ecological information which can help policy makers to implement biodiversity policies and distribute conservation funding, e.g., for ecosystem restoration. Ranking of forest types on four levels and high-resolution spatial maps of forest diversity with BCI can support decision-making in biodiversity conservation (e.g., target forest types, target regions, ecosystems, species or genetic restoration, conservation priorities, etc.) and evaluate effectiveness of financial resources spent on ecosystem restoration and Sustainable Forest Management (e.g., costbenefit-analysis). As a minimum requirement, we recommend a future positive BCI trend on all levels as a quantitative goal for regional to national forest policy in order to halt the loss of biological diversity and meet strategic CBD targets.

2. Material

2.1. Forests of Tyrol

Tyrol has a size of 12,684 km² and is located in the Eastern Alps. The territory is separated into two parts, namely North Tyrol and East Tyrol (Figure 1). It ranges from 500 to 3800 m above sea level and shows an inner alpine mountainous climate with subcontinental traits. The 520,000 ha of alpine coniferous forests are characterized by dense vegetation in combination with cold climate leading to acidic, thick organic soil horizons [47]. Total stock levels are about 114 M. m³ (328 m³/ha) with annual growth rates of 2.2 M. m³ [48]. With 57.6% tree species abundance, Norway spruce (*Picea abies*) is predominant [48].



Figure 1. Study area. Maps of the study area Tyrol, which is located in Austria (47°41′47.30″ N, 13°20′44.64″ E), Central Europe. The map was taken from https://geology.com/world/austria-satellite-image.shtml (accessed 6 March 2023).

Designated protective forests (e.g., forests protecting infrastructure and settlements from natural hazards) can be found on 48% of the total forest area [48]. Forest regeneration deficits in Tyrolean protective forests have repeatedly been reported [48,49]. Severe game impact on forest regeneration can be found on 57% of the forest area [48]. Dead wood levels account for 10.8% of the living stand volume [48].
2.2. Data Sets

This case study combines field-based measures and lidar-derived approaches using data sets provided by the Austrian Research Centre for Forests (AFI (Austrian Forest Inventory), AUPICMAP study (Geographic-genetic map of the Austrian Norway spruce population), Austrian Planting Statistics, and Nature Forest Reserves), and by the Tyrolean Regional Government (Forest typing project, vegetation surveys, TIRIS (Tyrolean Spatial Information System)). Data processing is done in R, QGIS, and python (Table 1). Reference values for the dead wood levels are supplied by protected areas, e.g., the National parks "Hohe Tauern" and "Berchtesgaden". For other biodiversity indicators, reference values can be found in earlier scientific studies [48,50–53].

Table 1. Data provision and processing. Twelve biodiversity indicators are established based on data sets provided by the Austrian Research Centre for Forests, the Tyrolean Regional Government, and national park managements.

Indicator	Method	Data Set	Reference Data	Processing
Tree species diversity	Grabherr et al. (1998) [50]	AFI	Forest typing	R
Ground vegetation	Grabherr et al. (1998) [50]	Vegetation surveys	Grabherr et al. (1998) [50]	R
Surface soil quality	case study Tyrol	AFI	Hotter et al. (2013) [53]	R
Game impact	case study Tyrol	AFI	-	R
Tree layer structure	Grabherr et al. (1998) [50]	AFI	Grabherr et al. (1998) [50]	R
Developmental level	case study Tyrol	AFI	Grabherr et al. (1998) [50]	R
Dead wood	case study Tyrol, Grabherr et al. (1998) [50]	AFI	AFI, protected area management	R, QGIS
Structural features	case study Tyrol, Grabherr et al. (1998) [50]	AFI	Grabherr et al. (1998) [50]	R
Forest gap structure	case study Tyrol	TIRIS	Grabherr et al. (1998) [50]	QGIS
Autochthony	Geburek and Schweinzer (2012) [52]	AFI	AUPICMAP	Python, QGIS
Management constraints	case study Tyrol	TIRIS	Raab et al. (2002) [51]	QGIS
Genetic features	case study Tyrol	AFI, Austrian Planting Statistics	-	R

AFI = Austrian Forest Inventory. TIRIS = Tyrolean Spatial Information System. AUPICMAP = Geographic-genetic map of the Austrian Norway spruce population.

Biodiversity assessment is performed on 1162 Austrian Forest Inventory subplots. The AFI uses a permanent foursome grid sampling with a grid size of 3.89 km (1 AFI plot = 4 AFI sub plots). Biodiversity indicators are assessed on the AFI subplot level. A detailed AFI field sampling manual, calculation methods, and theoretical background can be found in Hauk and Schadauer [54]. High-resolution forest typing of Tyrol based on ecological modeling was performed in 2019. Considering terrain models, geological models, climate models, expert knowledge, and field data [53], ecological modeling demarcates forest types on small scales (Figure 2A).

2.3. Assignment of AFI Plots to Forest Typing

Firstly, forest typing data is spatially overlaid with TIRIS, AFI, AUPICMAP, and reference area data in QGIS version 3.16 LTR (Figure 2B). Secondly, all AFI subplots outside the forest typing objects are excluded from analysis. Thirdly, if AFI subplots lay outside of the forest typing objects but contain field data; they are assigned manually to the forest type with the closest air-line distance by photo referencing (Figure 3). Biodiversity assessment of Tyrol is based on 1162 AFI subplots and 1521 vegetation survey plots. Forest inventory data and vegetation surveys are assigned to 82 forest types [53] and 223,628 QGIS objects. A total of 347 AFI subplots were excluded in the case study.





Figure 2. Processing inventory data with QGIS (47°24′59.99″ N, 11°27′59.99″ E). (**A**) Excerpt of the QGIS forest typing [53]. Different colors and abbreviations indicate the forest types. (**B**) Forest typing data (e.g., beige and green objects) is overlaid with TIRIS (e.g., orthophoto), AFI (orange dots), and reference area (red polygon) data.



Figure 3. Assigning AFI plots to forest types (47°24′59.99″ N, 1°27′59.99″ E). AFI plots (orange dots, numerical codes) are assigned to forest types (colored areas, alpha-numerical codes) in QGIS by position (e.g., 04303108 to Fi3) or photo referencing (e.g., 04303124 to Fi19). AFI subplots without AFI data located outside of forest type objects are excluded from analysis (e.g., 04303100).

3. Methods

Following McElhinny et al. [55], we collected all data sets available for Tyrol and the neighboring countries, quantified all stand attributes, identified a logical structure, defined a set of indicators according to the CBD definition of biodiversity, and combined these attributes into an additive biodiversity index.

Assessments of BCI can be done using one out of four levels, namely species, ecosystem, genetic, and biodiversity. In line with Grabherr et al. [50], indicators can assume

ratings between zero (lowest) and 9.0 (highest) points. Following McElhinny et al. [55], outcomes are expressed as percentage (0%–100%) to ease interpretation.

On the one hand, rare but ecologically highly valuable traits (*bonus indicators*) may compensate for a lower level of common forest traits (*biodiversity indicators*). On the other hand, missing but rarely occurring forest traits are not rated disadvantageous and BCI does not benchmark against a particular scale of temporal variation [56]. Among available data sets, we favored quantitative and high-resolution measurements of high scientific value and large temporal scales in the choice between biodiversity and bonus indicators (e.g., "management constraints" is a biodiversity indicator, "planting intensity" is a bonus indicator).

3.1. Ecosystem Diversity

Ecosystem, species, and genetic diversity assessment considers three biodiversity indicators and one bonus indicator, respectively. If at least two out of four (>50%) indicators are rated, AFI subplots are included. The indication of 100% is always adapted to the maximum number of points possible under the current number of indicators at the AFI subplot (e.g., 100% = 27.0 points if *three biodiversity indicators* could be rated with up to 9.0 points; or 100% = 18.0 points, if *two biodiversity indicators* could be rated with up to 9.0 points).

$ecosystem diversity = BI_{layer} + BI_{devel. level} + BI_{deadwood} + Bonus_{structure}$

 BI_{layer} assesses the deviation of the actual tree layer structure (AFI) from an expected, site-specific layer structure (forest typing). $BI_{devel.level}$ rewards differentiation of successional stages on small scales and late forest successional phases. $BI_{deadwood}$ considers dead wood quantity ($DW_{quantity}$) and quality ($DW_{quality}$). Dead wood quantity is assessed by comparing actual quantities (AFI) to reference values in protected areas and within the AFI data set (Figure 4A,B). *Bonus_{structure}* rewards shrub layers established naturally in certain forest types, late stand ages, and large tree diameter breast heights.



Figure 4. Dead wood reference levels in protected areas $(47^{\circ}15'13.468'' \text{ N}, 11^{\circ}36'5.353'' \text{ E})$. (**A**) AFI plots (orange dots) within protected areas (green, beige, and salmon-colored polygons) and protected area inventories are used as reference levels for dead wood quantity $(DW_{quantity})$. (**B**) In addition, nature forest reserves and protected area inventories are surveyed. Within a forest type, the respectively highest dead wood quantity out of all inventory data sets is compared to the actual subplot level.

3.2. Species Diversity

 $BI_{treespecies}$ is based on a target-performance comparison between actual (AFI) and potential (forest typing data) tree species composition. $BI_{vegetation}$ evaluates the naturalness of species composition of the ground vegetation and their ecosystem disturbance indicating value. BI_{soil} assesses if the actual humus form (AFI) deviates from the expected ones (forest typing). $Bonus_{game}$ rewards extensive game impact on forest regeneration.

$$species diversity = BI_{trees vecies} + BI_{vegetation} + BI_{soil} + Bonus_{game}$$

3.3. Genetic Diversity

 BI_{gap} characterizes forest gap structure by calculating a surface balance between forest and non-forest area (Figure 5). $BI_{autochthony}$ evaluates genetic diversity of the predominant tree species, Norway spruce, by computing intraspecific haplotype distance to reference populations. $BI_{management}$ considers inclination and distance to forest road systems of a forest site to estimate probability of extensive forest management. $Bonus_{regeneration}$ evaluates the probability of tree species to contain a native gene pool by examining their planting intensity. $Bonus_{phenology}$ uses varying branching types of Norway spruce as a proxy for detecting genetically allochthonous plant material.

 $genetic diversit = BI_{gap} + BI_{autochthony} + BI_{management} + Bonus_{genetic}$



Figure 5. Assessment of surface balance (47°15′34.7724″ N, 11°24′1.3500″ E). Squares with side length 150 m are used to compute surface balance around AFI subplots (e.g., plot nr. 03904308) between forest (light orange polygons) and non-forest area (grey polygons) in QGIS.

3.4. Biodiversity

BCI considers nine biodiversity indicators and three bonus indicators (Figure 6). Indicator ratings (0–9.0 points) are aggregated on the AFI subplot level. BCI is computed by addition of indicators and levels of diversity without weighting, which makes the concept transferable and easy to adapt. If at least six out of twelve (>50%) indicators are rated, the AFI subplots are included. Rare forest types containing less than three AFI subplots (n = 14) are not considered in BCI assessment.



Figure 6. BCI index structure. The modular structure equally considers ecosystem, species, and genetic diversity with three biodiversity indicators (black font color) and one bonus indicator (gray font color), respectively. Indicators are aggregated without weighting. Abbreviations are listed in the Appendix A (Table A1).

From a methodological point of view, BCI can be seen as an enhancement of the studies of Grabherr et al. [50] and Geburek et al. [57]. The framework follows classic niche theories [58–60] which explain co-existence of species with unique species traits and ecological niches varying in space and time. Consequently, species cannot be interchanged easily in a community. In the sense of Whittaker [61], BCI targets high beta-diversity levels to conserve overall forest biodiversity.

The choice of indicators relevant to biodiversity needs to be legitimated [15]. Scientific evidence for the relation between the diversity metric (indicator) and indicandum is provided in the Appendix A (Table A2), and detailed description of indicator evaluation can be found in the Electronic Supplementary Material. Following Virkkala [62], Brin et al. [63], and Gao et al. [14], indicators are selected from data sets available according to logical inference and by referring to other studies of high statistical validity.

3.5. Predictive Modeling with R Randomforest

In line with Bitterlich [64], Lappi and Bailey [65], and Sterba [66], evaluation outcomes are aggregated on the stratum level. With the help of the training data set (AFI subplots; n = 1162 data points with BCI ratings) and machine learning, R randomForest predicts biodiversity levels of 223,628 forest patches (QGIS polygons).

We applied the bagging classification algorithm randomForest in R, which is a group of regression trees made from random selection of samples of the training data [67]. Every random forest in this study is composed of 500 regression trees. For every regression tree in the forest, a training set is drawn from the sample plots, using bootstrap aggregating (bagging). The decision tree is built by rule-based splitting of the bagging sample into subsets, maximizing the variance between the subsets [68]. At each split in the learning process, a random subset of impact variables is used [69]. The splitting process is repeated recursively on each derived subset until (i) the subset has identical values with the target variable or (ii) the splitting no longer adds value to the prediction [70]. The mean value of the target variable within a final subset (leaf of the decision tree) is used as the conditional prediction of the target variable for a corresponding combination of impact variables [68]. For the application of a high-precision data-mining machine learning algorithm, we created polygon centroids of all forest type areas in QGIS as a prediction data set (Figure 7A). Predictive model performance is improved by adding the variables forest type (forest typing), altitude (Copernicus V1.1 DEM), geographical coordinates (TIRIS), and forest type groups (Appendix A Table A3) to the training and prediction data set. Model fit is controlled by additionally repredicting the training set and comparing prediction with R randomForest training data. The standard deviance between training and prediction data is 0%–19%. High deviances of 19% occur seldom in case extraordinary low values in the training set are repredicted.



Figure 7. The training and prediction data set in R randomForest (47°15′34.7724″ N, 11°24′1.3500″ E). (A) The training set of AFI subplots. (B) The prediction set of forest typing polygon centroids for modeling ecosystem, species, genetic diversity, and biodiversity with R randomForest.

In the next step, we assigned centroid values of the prediction set to the polygons to create maps of Tyrol (Figure 7B). Overall, we applied four prediction models, as BCI indicators can be aggregated on the level of species, ecosystem, genetic, and biodiversity. For our case study, we considered the area-weighted mean of the forest area objects in QGIS in high resolution.

To illustrate the prediction outcomes, forest area coloring was done in five classes (0%–20%, 20%–40%, 40%–60%, 60%–80%, 80%–100%) in QGIS. For the additional creation of spatial. jpg maps of Tyrolean forest diversity for the Tyrolean Regional Government, we applied cube spline interpolation in SAGA GIS. Before running the final models, we tested the model approach several times, performing probability checks using solely data of the smallest political district of Tyrol ('Innsbruck', forest area 37 km²).

4. Results

BCI spatial area assessments can be interpreted on the level of diversity of species and ecosystem, genetic diversity, and biodiversity. Our study displays an average biodiversity rating of 57% (area-weighted mean of forest area) for Tyrol. The respective rating of ecosystem diversity is 49%; of genetic diversity, 53%; and of species, 71% (Figure 8).



Figure 8. Maps of forest ecosystem, species, genetics, and biodiversity (47°15′13.468″ N, 11°36′5.353″ E). High-resolution maps of forest ecosystem, species, genetics, and biodiversity of Tyrolean forests. Outcomes are displayed in five classes (0%–20%, 21%–40%, 41%–60%, 61%–80%, 81%–100%).

BCI outcomes display high spatial heterogeneity on small scale. The divergence between valleys (e.g., "Inntal") and higher alpine areas in all models is evident through their darker coloring (i.e., lower BCI ratings). This effect is most pronounced for species diversity (Figure 8, left side).

Indicators with high average ratings in the biodiversity assessment are "autochthony" (94%), "tree layer structure" (94%), and "game impact" (91%). Indicators with low average ratings are "structural features" (19%), "management constraints" (36%), and "tree species diversity" (46%).

Indicators available most frequently at the 1507 AFI subplots studied are "forest gap structure" (1507 AFI sub plots), "forest vegetation" (1454 plots), and "structural features" (1004 plots). Indicators with low availability are "autochthony" (520 plots), "surface soil quality" (836 plots), and "tree layer structure" (943 plots).

High-altitude areas received higher BCI ratings than low elevation areas, which is in line with forest type evaluation. Surveying model outcomes on the level of the forest type (Table 2), it can be concluded that coniferous forests in Tyrol are in a more favorable state of preservation and can maintain biodiversity with higher probability than broad-leaved and mixed forests.

Table 2. BCI evaluation outcomes on the forest type level.

Forest Type		Species Diversity [%]	Ecosystem Diversity [%]	Genetic Diversity [%]	Biodiversity (BCI) [%]
Subalpine dry silicate larch-spruce forest	Fs4	77	65	69	70
Overlying humus-carbonate larch-stone pine forest	Zi2	66		87	69

Table 2. Cont.

Forest Type		Species Diversity [%]	Ecosystem Diversity [%]	Genetic Diversity [%]	Biodiversity (BCI) [%]
Subalpine coniferous avalanche sites	FL3	100	48	62	69
Subalpine cool silicate steep slope (green alder-larch) spruce forest	Fs3	79	57	74	68
Cool silicate steep slope spruce-larch fir forest	FT12	77	54	70	67
Montane sunny rock sites on carbonate	FK2	100	63	67	65
Montane dry silicate (pine) spruce forest	Fi4	65	59	73	65
Warm silicate larch-stone pine forest	Zi4	81		56	65
Poor silicate larch stone pine forest	Zi1	80		57	64
Subalpine basic larch-spruce forest	Fs5	84	55	57	64
Dry carbonate pine forest	Ki1	86	48	62	64
Subalpine poor silicate (larch) spruce forest	Fs1	82	48	61	63
Marl steep slope spruce-fir-beech forest	Ftb20	81	52	59	63
Montane poor silicate (larch) spruce forest	Fi2	79	52	59	63
Mountain pine, green alder, hardwood scrub, scrubby areas	k	100	38	54	63
Montane poor carbonate larch-spruce forest	Fi6	81	50	57	61
Lawinar silicate (green alder) larch-spruce forest	Fs10	83	50	51	61
Moderately dry carbonate pine-spruce-beech forest	Fkb1	71	48	67	61
Cool carbonate steep slope larch-pine forest	Ki18	72	43	68	61
Floodplain sites of the montane level	Er12	93	40	49	61
Fresh silicate fir-spruce forest of the intermediate Alps	F110	79	46	55	60
Subalpine fresh silicate spruce forest	FS17	82	47	51	60
Fresh alkaline spruce-fir forest	F19	84	44	49	60
Moderately fresh silicate fir-spruce forest	F122	65	60	50	59
Subalpine warm silicate larch-spruce forest	FSZ	82	45	53	58
Poor silicate spruce-fif forest	F12	<u> </u>	<u>44</u> E1	63	58
Montane warm carbonate spruce forest	F10 E;5	58	50	<u> </u>	58
Montane fresh silicate (larch) spruce forest	F13 Fi1	<u> </u>	47	53	58
Montane mesh shicate (larch) spruce forest		72	52	50	58
Subalning fresh carbonate spruce forest	 	12	53	68	57
Moderately fresh silicate spruce-fir-beech forest	Eth4	68	52	55	57
Moderately fresh carbonate spruce-fir-beech forest	Etb7	68	49	57	57
Subalpine dry carbonate (larch) spruce forest	Fs7	26	64	59	57
Fresh carbonate spruce-fir-beech forest	Etb6	75	45	53	56
Warm carbonate beech forest	B113	66	48	55	56
Fresh silicate spruce-fir forest	FT1	69	47	54	56
High montane carbonate spruce-fir beech forest	Ftb13	66	50	61	56
Rich basic spruce-fir forest	FT6	55	57	47	56
Rich silicate spruce-fir forest	FT5	63	49	55	56
Overlying humus carbonate spruce-fir forest	FT20	45	58	58	56
Fresh silicate beech forest with conifers	TB2	78		44	55
Rich loam-deciduous beech forest	LhB1	72		48	55
Fresh basic spruce-fir beech forest	Ftb8	76	50	52	55
Moderately fresh carbonate spruce-fir forest	FT15	35	54	64	55
Moist acid spruce-fir forest	FT8	68	47	48	55
Warm basic (larch) spruce forest	Fi7	66	50	41	54
Montane poor carbonate spruce-fir forest	Fi23	63	49	48	53
High montane carbonate spruce-fir forest	FT19	39	46	67	53
Fresh loam (beech) spruce-fir forest	FT16	63	51	54	53
Overlying humus carbonate spruce-fir -beech forest	Ftb16	63	48	61	53
Rich clay spruce-fir-beech forest	Ftb10	74	51	43	53
Rich silicate ash-lime mixed forest	Lh3	61		56	52
Fresh basic deciduous beech forest	Bu1	58	51	47	52
Fresh clay spruce-fir-beech forest	Ftb1	62	43	49	52
Moderately fresh carbonate and clay beech forest	Bu17	55	51	44	50

Forest Type	Code	Species Diversity [%]	Ecosystem Diversity [%]	Genetic Diversity [%]	Biodiversity (BCI) [%]
Rich silicate spruce-fir beech forest	Ftb11	40	55	51	50
Montane rich silicate spruce forest	Fi19	60	47	43	50
Fresh silicate spruce-fir-beech forest of the Northern Alps	Ftb2	49	49	49	49
Fresh clay beech forests with conifers	TB1	66		43	49
Warm carbonate oak-ash-lime forest	Lh2	52		48	48
Moist basic (gray alder) maple-ash mixed forest	Lh5	54		41	47
Silicate hardwood spruce-fir forest	LhT1	66		35	46
Colline grey alder riparian forest	Er3	49	38	42	45
Montane grey alder riparian forest	Er2	53	53	21	42
Fresh silicate lime-ash-pedunculate oak forest	Ei1	24	46	44	38

Table 2. Cont.

Deciduous Mixed Coniferous Shrub

High ratings indicate that the forest type is in a more favorable state of preservation and can maintain a certain aspect of biodiversity with higher probability. On the contrary, low ratings display a less favorable state of preservation. They may indicate the need for active management to conserve certain aspects of forest biodiversity.

High ecosystem diversity ratings are displayed by the forest types of "Overlay humuscarbonate larch-stone pine forest" (68%), "Subalpine dry silicate larch-spruce forest" (65%), and "Subalpine dry carbonate (larch) spruce forest" (64%). In contrast, models indicate low ecosystem diversity ratings in "Moist basic (gray alder) maple-ash mixed forest" (40%), "Colline grey alder riparian forest" (38%), and "Silicate hardwood spruce-fir forest" (37%).

In the case study, forest types of high species diversity ratings are "Subalpine coniferous avalanche sites" (100%), "Mountain pine, green alder, hardwood scrub, scrubby areas" (98%), and "Subalpine basic larch-spruce forest" (89%). Low species diversity ratings are assigned to "Warm carbonate oak-ash-lime forest" (44%), "Rich loam-deciduous beech forest" (43%), and "Fresh silicate lime-ash-pedunculate oak forest" (27%).

Our models indicate high genetic diversity ratings for "Subalpine dry silicate larchspruce forest" (82%), "Cool carbonate steep slope larch-pine forest" (82%), and "Overlay humus-carbonate larch-stone pine forest" (78%). Low genetic diversity ratings are found in "Colline grey alder riparian forest" (49%), "Fresh clay beech forest with conifers" (49%), and "Montane grey alder riparian forest" (40%). Highest probability for autochthony of the Norway spruce populations is detected in the Central and Eastern parts of Northern Tyrol. For detailed outcomes, please consider the Supplementary Material.

Overall, high biodiversity ratings can be found in "Subalpine dry silicate larch-spruce forest" (74%), "Subalpine coniferous avalanche sites" (72%), and "Overlay humus-carbonate larch-stone pine forest" (72%). On the contrary, low biodiversity ratings are in "Colline grey alder riparian forest" (46%), "Montane grey alder riparian forest" (45%), and "Fresh silicate lime-ash-pedunculate oak forest" (42%).

5. Discussion

5.1. Approach and Biodiversity Indicator Choice

The BCI approach differs substantially from the way other authors identified, weighted, and scored indicators. As we chose indicators based on inventory data availability and scientific literature, we forwent performing a principal component analysis to test for redundancy, such as in McElhinny et al. [55] and Storch et al. [41]. In line with LaRue et al. [71] and Ette et al. [72], we expect the BCI indicators to be intercorrelated and neither ecologically nor statistically independent.

Some indicators can be a proxy for more than one level of biodiversity which, based on scientific knowledge, might seem difficult to assign, e.g., on the one hand, the availability of about 25 m³/ha of dead wood is an important quantitative threshold value for many endangered species [73,74]. On the other hand, general positive correlations between dead

wood volume and wood-living fungi species, dead wood volume, and saproxylic species diversity, and between dead wood diversity and saproxylic species diversity are found for Europe in a meta-study [14]. However, this does not endanger assessment quality. In our case study, dead wood quantity is an ecological diversity indicator. Ratings are rising linearly with the share of reference levels (see Supplementary Material). If species diversity were targeted instead, ratings other than linear ones might be more appropriate.

Weighting as a final step in aggregation would have a major impact on the results. Nevertheless, respecting the limited knowledge about ecological communities, biological interactions, and genetic diversity in forests, putting weights to biodiversity indicators reveals more about the study authors and scientific community than substantially reaching an assessment that is closer to the true status of biological diversity. We agree with Okland [75] and Storch et al. [41] that indicator weighting is only reasonable for monitoring certain taxonomic groups with known correlations to specific habitat quality requirements. In line with McElhinny et al. [55], we expected weighting to probably subjoin more subjectivity to the BCI without providing additional insights.

5.2. Compare Study Outcomes

Spatial comparison within Tyrol shows that forest areas of high elevation tend to have higher BCI ratings compared to valleys in all models. Coniferous forests are in a more favorable state of preservation and can maintain biodiversity with higher probability than broad-leaved and mixed forests. In Austria, natural or semi-natural forests are mainly stocked in the subalpine, inner parts of the Alps and are characterized by a dominance of coniferous tree species [50]. In Tyrol, only 13% of the area is suitable for permanent settlement [76], which puts high pressure on ecosystems of low elevations such as broadleaved and mixed forests. This effect is most pronounced in a species diversity model which also shows highest assessment heterogeneity on small spatial scales. BCI can be used to regionally define conservation targets, e.g., ecosystem restoration of forest types ('Silicate hardwood spruce-fir forest") in regions with below-average BCI performance (e.g., low elevation sites), or to regionally promote a particular level of biodiversity in a specific area (e.g., measures for ecosystem diversity such as retention trees).

It is not possible for us to directly compare our case study outcomes with other biodiversity assessments [10,41,55,77], due to unavailable indicator values in Tyrol (e.g., bark diversity, hollow trees, litter dry weight, litter decomposition, tree age, vegetation cover), different scales [57], and different study purposes [77]. However, there is partial agreement in the choice of indicators such as perennial species richness [55,77], natural regeneration [41,57,77], standing and lying dead wood [41,55,57,77], old growth trees [10,41,55,57,77], genetic diversity of Norway spruce [57], forest fragmentation [57,77], and tree species frequency [10]. Benchmarking based on vegetation types can also be found in Parkes et al. [77]. The choice of indicators in this study largely corresponds to a meta-study of Gao et al. [14], who demonstrated that the biodiversity indicators chosen most frequently in 142 European ecological studies are dead wood volume, age of canopy trees, vascular plant species, tree canopy cover, decay classes, and dead wood diversity.

5.3. Advantages and Disadvantages

Major advantages of the BCI approach are easy transferability, cost-efficient long-term monitoring of forest policy measures, and the logical indicator structure in line with the CBD. BCI can be used as a conservation planning tool to halt biodiversity loss on the national scale. With our state-of-the-art data pre- and postprocessing, BCI sticks very close to the policy-relevant definition of biodiversity in the CBD, which 183 member countries agreed on in 1992. We provide a new option to assess biodiversity based on available national forest inventory and forest typing data. Outcomes can be interpreted on three levels (diversity of ecosystem, species diversity, and genetic diversity) and aggregated to assess forest biodiversity in high resolution on varying spatial scales. By not weighting indicators, the framework remains easy to adapt to neighboring regions in Central Europe.

Quantitative aggregation and simplification of ecological spatial information may help policy makers and conservationists to implement biodiversity policies and assign conservation funding, e.g., for ecosystem restoration. The ranking of forest types and highresolution spatial maps of forest diversity can support decision-making in biodiversity conservation (e.g., target forest types, target regions, conservation priorities, and ecosystem-, species-, or genetic restoration measures) and retrospectively evaluate effectiveness of financial resources spent on ecosystem restoration and nature conservation. Additionally, effects of different forest management measures on biodiversity can be assessed per forest type and used to advance Sustainable Forest Management. Within one forest inventory period, performing cost-benefit analyses of, e.g., biodiversity conservation efforts, forest management practices, forest road building, regional forest policy funding, and Sustainable Forest Management measures will be made available. Quantifying forest biodiversity with BCI allows targeted management of a landscape's biodiversity and distributed biodiversity values. BCI can be used as a measurable, objective, and quantitative guidance for regional forest and conservation policy using the first BCI assessment as a baseline minimum.

However, the BCI concept could not overcome all weaknesses of forest inventorybased approaches described in Storch et al. [41], e. g., large-scale forest inventory design may not capture small areas like nature reserves well enough and very rare forest types must be excluded from the analysis. Plot measures may not be representative for the forest stand and most biodiversity aspects can only be addressed through surrogates. Additionally, most genetic diversity indicators focus on the major tree species of Tyrol, Norway spruce, as data for other species are not available. The indicators "autochthony", "tree layer structure", and "game impact" display high ratings in the BCI assessment. For upcoming BCI assessments, these indicator evaluations should be revised based on experience gained from the Tyrolean case study. Applying BCI, error propagation of forest typing models can possibly occur. Nevertheless, by using ecological modeling, referencing indicators by forest type, employing GIS data such as orthophotos, and machine learning, we were able to advance reliability and spatial resolution of forest biodiversity assessments.

6. Conclusions

Assessing biodiversity is highly complex. The intention of BCI is to aggregate and simplify ecological information in a surrogate approach, advance forest-inventory based assessments, and monitor all levels of forest biodiversity in line with the CBD.

In the case study, average ecosystem diversity is 49%, species diversity is 71%, genetic diversity is 53%, and biodiversity is 57%. In Tyrol, coniferous forests are in a better state of preservation and can maintain biodiversity with higher probability than broad-leaved and mixed forests. These findings, next to rankings of forest types and high-resolution spatial maps of forest biodiversity, can be used to advance land use policies, forest management, nature conservation, and landscape planning in Austria, e.g., by cost-benefit analysis. The approach is transferable to neighboring regions with forest-typing, e.g., in Germany, Italy, and Austria.

For Tyrol, we highly recommend a second BCI assessment within six years to solve the baseline problem, monitor temporal and spatial changes, detect trends in forest biodiversity, and evaluate effects of forest management and biodiversity conservation. BCI can give objective guidance and feedback to forest policy to counteract the biodiversity crisis. We recommend a future positive BCI trend on all levels as a quantitative goal for regional forest policy to meet strategic CBD targets.

Supplementary Materials: The following supporting information can be downloaded at: https://www.mdpi.com/article/10.3390/f14040709/s1.

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List of Acronyms

been received.

AFI	Austrian Forest Inventory
AUPICMAP	Geographic-genetic map of the Austrian Norway spruce population
BCI	Biodiversity composite index
BI	Biodiversity Indicator
BONUS	Bonus Indicator
CBD	Convention on Biological Diversity
TIRIS	Tyrolean Spatial Information System
QGIS	Quantum-Geographic Information System

Appendix A

Table A1. Abbreviations of indicators.

Ecosystem Diversity	
BI _{layer}	Biodiversity indicator: Tree layer structure
BI _{devel.level}	Biodiversity indicator: Developmental level
BI _{deadwood}	Biodiversity indicator: Dead wood
$DW_{quantity}$	Biodiversity indicator: Dead wood I: Quantity
$DW_{quality}$	Biodiversity indicator: Dead wood II: Quality
Bonus _{structure}	Bonus indicator: Structural features
Bonus _{shrub}	Bonus indicator: Structural features I: Shrub cover
Bonus _{standage}	Bonus indicator: Structural features II: Stand age
Bonus _{dbh}	Bonus indicator: Structural features III: Diameter breast height
Species diversity	
$BI_{treespecies}$	Biodiversity indicator: Tree species diversity
BIvegetation	Biodiversity indicator: Ground vegetation
BI _{soil}	Biodiversity indicator: Surface soil quality
Bonus _{game}	Bonus indicator: Game impact
Genetic diversity	
BI_{gap}	Biodiversity indicator: Forest gap structure
BI _{autochthony}	Biodiversity indicator: Autochthony
BI _{management}	Biodiversity indicator: Management constraints
$m.constraint_{inclination}$	Biodiversity indicator: Management constraints I: Inclination
m.constraint _{distance}	Biodiversity indicator: Management constraints II: Distance to forest road
Bonus _{genetic}	Bonus indicator: Genetic features
$Bonus_{regeneration}$	Bonus indicator: Genetic features I: Natural Regeneration
Bonus _{phenology}	Bonus indicator: Genetic features II: Phenology

Indicators Scientific Evidence Ecosystem diversity indication Structural spatial diversity increases resource partitioning of light use among species [78-80] and indicates tree layer structure the number of niches occurring vertically and horizontally within the canopy [22]. Greater overlap of (s. s., naturalness of tree crowns indicates a greater use of niche space for light in the canopy [37,81] and is a measure of ecological niche space size [71]. Tree layer structure is a proxy for forest management intensity [50]. Heterogenous layer composition) vegetation heights are associated with greater ecosystem function [71]. Variation of tree dimension can be used as a proxy for habitat quality or biotope trees [10] and related developmental level macro- and microhabitats [82]. Forest age differentiation indicates high niche supply and affects community (s. s., diversity of the developmental composition [83]. Late successional stages are proxies for ecosystem productivity [84], biotic resistance to stages) invasion [85], and light absorption [80]. The developmental level can be a hint towards management intensity [50]. The indicator approach is based on mosaic cycle concepts [86,87] and niche theory [88,89]. Dead wood promotes forest biodiversity [74,90–96]. It provides habitat, shelter, growth substratum, and dead wood nutrition for various organisms, e.g., bryophytes, saproxylic insects, and fungi [96–99]. Coarse woody (s. s., dead wood quantity debris supports numerous forest ecosystem functions [100], e.g., nutrient cycling [101,102]. Occurrence of and quality) coarse woody debris may indicate forest ecosystem processes such as mortality, ingrowth, competition [103], and ecosystem disturbance [104]. Structural diversity is a proxy for structural complexity, potential habitat variability, and niche structural features differentiation for umbrella species [21,105]. The occurrence of shrub species can be an important (s. s., shrub cover contribution to maintain forest biodiversity [106]. Shrub and tree height is a proxy for vertical stratification stand age, and of niche space [71], e.g., for birds [22]. Mean canopy height indicates the number of niches filled within the diameter breast height) ecosystem volume [107]. Canopy tree age was found to correlate positively with epiphytic lichen diversity [14]. Large tree diameters indicate high potential for tree-related habitats [108]. Species diversity indication There is high scientific evidence for a positive correlation between tree species diversity and the number of tree species diversity bird [109], ground beetle [110,111], arthropod [112], and ground vegetation species [110,113]. Tree species (s. s., naturalness of tree abundance can be used as a proxy for species diversity of, e.g., saproxylic beetles, bryophytes, lichens, species composition) fungi, and arthropods [114–117]. ground vegetation Plant species diversity indicates partitioning of resource use between species [118]. Native plant species (s. s., naturalness of plant species diversity is a proxy for the number of different niche spaces filled by native plant species [119]. composition, disturbance indication) Most species diversity of Europe can be found in the soil ecosystems [16]. Humus form is one of the surface soil quality regulating factors for the composition of species communities [120–123]. The diversity of zoological groups (s. s., divergence from the expected linearly correlates to soil pH value and humus type [124]. There is high evidence for the relevance of humus humus form) type for forest biodiversity and overall species diversity [2,120,124-126]. Slight changes in physico-chemical components can lead to great changes in soil biota communities [127]. Game impact There is broad consensus on the relevance of tree browsing for forest biodiversity [128–130]. Severe (s. s., extensive game impact on herbivore impact leads to tree species segregation, lacking regeneration, and disturbed forest succession forest regeneration) [131]. Genetic diversity indication Forest fragmentation is a serious threat to genetic diversity [132–135]. Fragmentation subdivides populations into small units and imposes barriers to migration, which is an important driver for extinction [136]. Fragmentation can erode neutral and adaptive genetic diversity and lowers effective population sizes and genetic variability [137,138]. It promotes genetic drift and inbreeding depression [139]. Habitat forest gap structure (s. s., surface balance forest-non fragmentation may affect adaptive potential of populations and their fitness level negatively [135,140]. forest area) Susceptibility to habitat fragmentation and habitat split is highly species-specific [138]. Dispersal ability, migration, habitat availability, and range of environmental tolerance is decisive for genetic consequences for species, populations, and individuals [138,141,142]. Allelic richness is most vulnerable to habitat fragmentation with rare gene expressions preferentially being eliminated [135,139]. Autochthonous populations show small-scale genetic differentiation and local adaption of tree species [143,144], promoting tree population differentiation [145,146]. Negative effects of allochthonous seed sources are maladaptation to the local environment, intraspecific hybridization (introgression), cryptic autochthony (s. s., genetic distance between invasion, and other unintended effects on associated species which can be seen as environmental risks populations of Norway spruce) [144,147]. Genetic variability of introduced forest reproductive material tends to be considerably lower compared to local populations [148]. Artificial transfer of genetic information, e.g., by using forest reproductive material, tends to degrade forest genetic structures [149]. Main drivers of extinction are of anthropogenic origin [150,151]. Forest management may affect forest genetic resources through changes in genetic drift, mating systems, fertility, and species migration [147,152]. Management constraints It can lead to the loss of rare and localized alleles [153,154]. Silviculture influences the major evolutionary (s. s., inclination, and distance to forces of selection, genetic drift, and gene flow [136,155–157]. Forest management can affect mating forest road) systems, genetic variation and population structure of forest trees [158,159], lowers effective population sizes [155,160], and impacts the adaptive potential of forests [159].

Table A2. Indicative value of diversity indicators. Surrogates for forest biodiversity and scientific

evidence for their indicative value.

Table A2. Cont.

Indicators	Scientific Evidence
Genetic features (s. s., tree planting intensity, phenology of Norway spruce, and crown structure)	Choice of reproductive forest material has probably the most significant impact on the genetic diversity of forest trees in Europe [161]. Possible negative effects of long-distance seed transfer on genetic diversity are described in Kremer [147] and Carnus et al. [162]. Hybridization of local and non-local genotypes may affect genetic population structure negatively through outbreeding depression, introgression, demographic invasion, introduction of diseases, and genetic erosion [144,147]. Branching types of Norway spruce may be used as a hint to detect genetically allochthonous plant material [163]. Lower stand density affects pollen and seed dispersal positively and promotes pollen dispersal [164] and pollen densities [165,166]. Decreasing tree density is likely to increase wind turbulences, and pollen and seed long-distance dispersal [164,167,168].

Table A3. Assignment to forest type groups. Assignment of forest types [53] to forest type groups [50].

Forest Type Groups [50]	Forest Types Assigned [53]		
Mountain pine and scrub forest communities	Bu10, Ge1, Ge8, Ge9, Lat2, Lat3, Lat4, Lh8, k		
Carbonate-rich subalpine pine and larch forests	Fs5, Ki20, La1, La2, La4, La6, Lat1, Zi2, Zi3, Zi6		
Carbonate-rich montane mixed spruce-coniferous forests	Fi5, Fi6, Fi7, Fi8, Fi10, Fi13, Fi14, Fi18, Fi20, Fi23, Fi25, Fs13, FT3, FT9, FT13, FT15, FT18, FT19, FT20, LhT2		
Silicate-rich spruce-fir forests	Fi2, Fi3, Fi4, Fi9, Fi11, Fi19, Fi22, FT1, FT2, FT5, FT8, FT10, FT12		
Moist coniferous and birch forests (including bog edge forests)	Fi16, Fi17, FT7, FT22, Ki21, Fs11, Fs14, Fs18		
Mixed pine forests on carbonate	Ki1, Ki2, Ki3, Ki17, Ki18, Ki19, LhK3		
Silicate (spruce-fir) beech forests	Bu5, FT17, Ftb2, Ftb4, Ftb11, Ftb12, LhT1, TB2		
Mixed maple and ash forests	Bu4, Ei1, Lh4, Lh6, Lh9, Lh16, Lh17, Lh18		
Lime and mixed lime forests	Ei3, Ei4, Lh1, Lh2, Lh3, Lh11, Lh13, LhB2		
Base-rich dry beech forests	Bu3, Bu7, Fkb1, Ftb20		
Brown soil (spruce-fir) beech forests	Ftb3		
Downy oak forests	MH2		
Oak and oak-pine forests	Ei2, Ei7, Ei12, Ki4, Ki15		
Willow communities	Er4, Er11, Er12		
Hard riparian forests	Fi21, Ki9, Lh12, Lh14		
Stream-accompanying alder-ash forests	Er2, Er3, Er7, Er8		
Fresh carbonate (spruce-fir) beech forests	Bu1, Bu17, FT16, Ftb1, Ftb6, Ftb7, Ftb10, Ftb13, Ftb 14, Ftb16, LhB1, LhB3, TB1		
High-altitude beech forests with maple	Bu11, Bu20, Ftb8		
Subalpine coniferous forests on silicate	Fi12, Fs1, Fs2, Fs3, Fs4, Fs10, Fs12, Fs17, La5, La7, Zi1, Zi4, Zi5		
Gray alder forests	Er1, Er5, Lh5, Lh21, Er13		
Pine forests on silicate	FT21, Ki6, Ki7, Ki16, La3		
Carbonate-rich subalpine coniferous mixed spruce forests	Fi1, Fs6, Fs7, Fs8, Fs9, FT6		
Block forest, rubble, and rock sites on carbonate (newly established)	FK1, FK2, Fkb2, FL2, Lh10, Klf2, LhK2, Ki23, Zlf4		
Block forest, rubble, and rock sites on silicate (newly established)	FK3, Fkb3, FL1, Klf1, LhK1, Zlf3, Ki5, Lh7, FL3		

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