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Subgroup on accounting for biodiversity in the SEEA EA

Background paper:

Addressing spatial scale in deriving and aggregating biodiversity metrics for ecosystem accounting

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Addressing spatial scale in deriving and aggregating biodiversity metrics for ecosystem accounting

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Context for the Background paper

In 2013 the United Nations Statistical Commission (UNSC) recognised the SEEA Experimental Ecosystem Accounting as providing initial guidance on the development of ecosystem accounting to support the integration of data on ecosystems, including their biodiversity, with standard economic data. A revision process to update and refine the approach described in the SEEA EEA commenced in 2018 and one area of consideration was the appropriate incorporation of concepts and measures concerning biodiversity. To this end, the Subgroup on accounting for biodiversity was formed to consider a range of issues and appropriate material was incorporated into the final SEEA Ecosystem Accounting (SEEA EA) that was adopted by the UNSC in March 2021.

One biodiversity related topic on which it was agreed that detailed guidance would not be incorporated into the final SEEA EA concerned issues of spatial scale relating to the aggregation of biodiversity-focused metrics when compiling ecosystem condition accounts, as well as for deriving habitat-based biodiversity metrics, or indicators, from compiled ecosystem extent and condition accounts. During the revision process this background paper was prepared and it has subsequently been finalised by its authors who are members of the Subgroup on accounting for biodiversity.

The background paper is intended to provide guidance to ecosystem accounts compilers on issues of spatial scale and aggregation in relation to biodiversity by clarifying the different concepts and providing options to address the measurement challenges. The paper is also intended to support compilers in engagement with biodiversity measurement experts.

In addition, it is expected that the background paper, together with material on biodiversity in the SEEA EA itself, will serve as a basis for ongoing discussion on the general topic of accounting for biodiversity. The subgroup of biodiversity experts is continuing to operate beyond the finalisation of the SEEA EA and is developing a research agenda in this area of work that will encompass the issues raised in this background paper.

Introduction

Measurements of biodiversity are an important part of the entire set of ecosystem accounts, but feature most prominently in condition accounts and thematic accounting for biodiversity (Figure 1). One of the main challenges in deriving biodiversity metrics for these accounts relates to spatial scale. Measures of biodiversity at different scales are not neatly "nested", i.e., measures of biodiversity for a large area are not simply the sum of biodiversity measures for smaller areas.

SEEA EA Chapter 5 on ecosystem condition (see section 5.5.4) highlights the need for complementary methods for the spatial aggregation of biodiversity data, which this paper is intended to provide. Condition accounts are compiled at the level of ecosystem assets and, while some measures of biodiversity can be incorporated at that scale to inform the measure of the condition of ecosystem assets, a simple aggregation of condition measures will not encompass all aspects of biodiversity, especially for reporting at the level of ecosystem types and ecosystem accounting areas.

SEEA EA Chapter 13 on accounting for biodiversity (see section 13.3) points to potential for using data compiled for ecosystem extent and condition accounts as a foundation for deriving habitat-based biodiversity metrics. This potential is also raised in section 14.3 on indicator frameworks and the SEEA EA, particularly in relation to the significant role that such metrics could play as indicators for assessing and reporting progress toward the achievement of goals and targets under the post-2020 Global Biodiversity Framework (GBF) currently being finalized by the Convention on Biological Diversity.[1] This background paper proposes technical solutions applicable both to the spatial aggregation of biodiversity data for ecosystem condition accounts, and to deriving habitat-based biodiversity metrics from compiled ecosystem extent and condition accounts.

Habitat-based biodiversity metrics

Unlike approaches based on direct observation of biological change – e.g., field-based monitoring of changes in species occurrence or abundance – habitat-based approaches predict, or infer, change in the state of biodiversity indirectly as a function of observed changes in the extent and condition of habitat on which elements (e.g., species) constituting this biodiversity depend[2]. This is usually achieved by intersecting spatially-complete gridded surfaces of habitat extent and/or condition at different points in time with best-available mapping of natural ('reference' or 'base') patterns in the distribution of biodiversity (e.g. species' ranges prior to human disturbance).

Across the broader domain of biodiversity assessment, habitat-based approaches have long played a vital role in complementing more direct approaches to deriving biodiversity metrics and indicators, especially for the sizeable proportion of the planet's surface inadequately sampled by field-based monitoring efforts. From the perspective of SEEA EA these approaches can enable considerable additional value to be generated from data collected or compiled for producing ecosystem extent and condition accounts. Chapter 5 of SEEA EA addresses the contribution that direct biodiversity

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[1] https://www.cbd.int/conferences/post2020

[2] UNEP-WCMC (2016). Exploring approaches for constructing Species Accounts in the context of the SEEA-EEA http://wcmc.io/Species_Accounting. King S *et al.* (2020) Linking biodiversity into national economic accounting. *Environmental Science & Policy* 116: 20-29.

observations (e.g., of species abundance or richness) can sometimes make to estimating the condition of ecosystem assets (EAs). Habitat-based assessment of biodiversity change complements this perspective by focusing instead on the reverse relationship. Observed changes in ecosystem extent and condition, particularly where these can be mapped across large spatial extents based on remotely-sensed structural and functional attributes, are here used as inputs to inferring change in the compositional dimension of biodiversity (Figure 1).

As shown in Figure 1, habitat-based approaches used to inform Species Accounts also provide an important analytical link between ecosystem extent and condition accounts and the ecosystem services that are underpinned by individual species (e.g., iconic species for ecotourism) or species groups (e.g., pollinators). The (Bio)diversity accounts (Figure 1) supplement this by providing information about variations between and within different species assemblages (or ecosystems) within an Ecosystem Accounting Area (EAA). This can inform the capacity to supply current and future ecosystem services, which is very dependent on the interactions between the different components of biodiversity across scales. As highlighted by the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES), maintaining this biological diversity is of particular relevance to forward looking perspectives on ecosystem services (e.g., with respect to option and insurance values). This focus on maintaining variation across multiple levels of biological organization also aligns strongly with the CBD definition of biodiversity.

Deriving habitat-based metrics and indicators of biodiversity change from data compiled for ecosystem extent and condition accounts also has potential to serve as a key point of interaction between ecosystem accounting under SEEA EA, and CBD post-2020 monitoring. Of particular note is the potential contribution that such indicators can make to better addressing the critical interrelationship between ecosystem-focused and species-focused goals in the GBF.

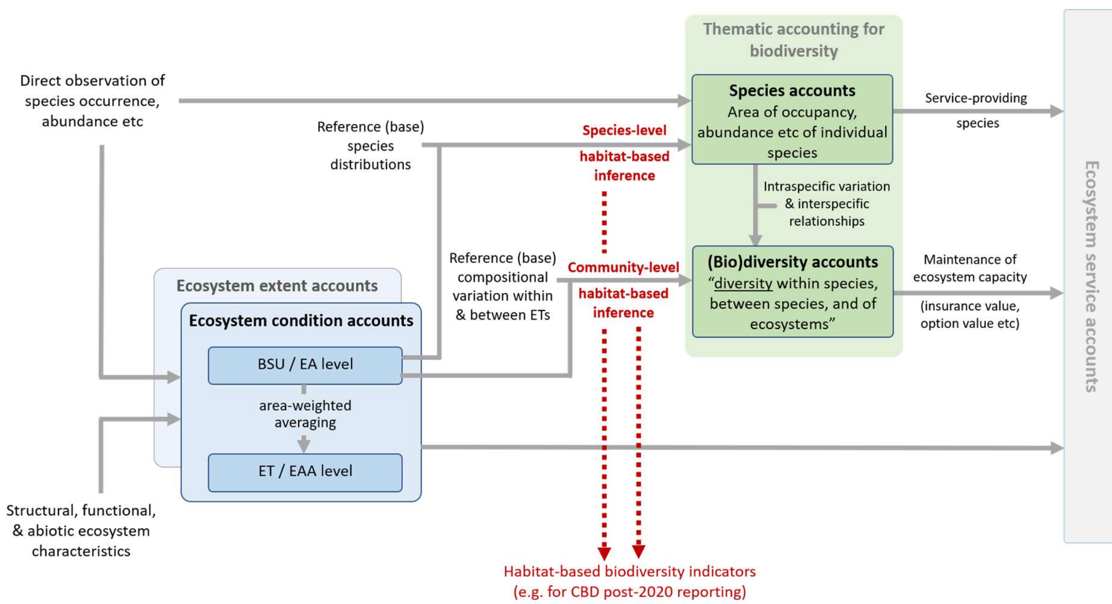

Figure 1: General framework for using habitat-based approaches to link ecosystem extent and condition accounts with thematic accounting for biodiversity, and with the derivation of biodiversity indicators for use in broader assessment processes, including CBD post-2020 monitoring

Scale-dependent challenges in spatial aggregation of biodiversity metrics

Ecosystem condition accounts (SEEA EA Chapter 5) report changes in indicators and indices, typically at the level of ecosystem types (ETs) or ecosystem accounting areas (EAAs). In most cases, these ET or EAA-level metrics require aggregation of data from smaller spatial units, usually basic spatial units (BSUs) or ecosystem assets (EAs). For many types of data, this spatial aggregation can be performed through averaging or additive means (Figure 2).

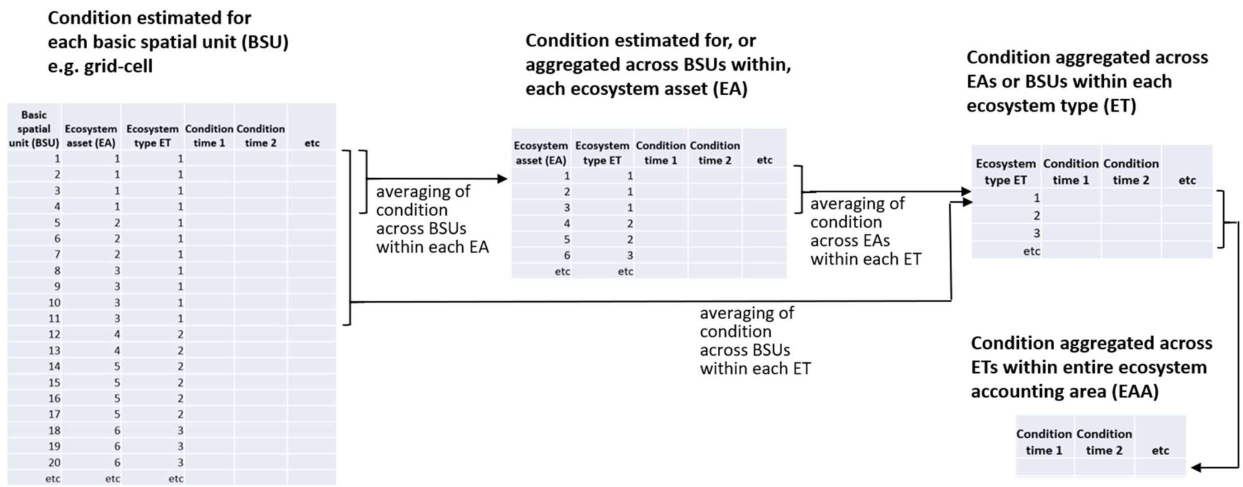

Figure 2: Simple aggregation, through spatial averaging, of condition estimates from basic spatial units (BSUs) or ecosystem assets (EAs) to whole ecosystem types (ETs) or ecosystem accounting areas (EAAs), as described in SEEA EA Chapter 5

However, because of spatial heterogeneity in biodiversity composition as well as spatial relationships and interactions among EAs (or other spatial units), many biodiversity-focused metrics cannot be meaningfully aggregated across broader spatial extents through simple averaging or summation as discussed in the following section.

Similarly, while accounting for biodiversity (Chapter 13) focuses primarily on species accounts, it is also suggested to develop accounts that address diversity *per se*, by describing the variability within species, between species and of ecosystems, as per the CBD definition of biodiversity. Habitat-based approaches can be used to derive metrics for both these broad types of accounts (Figure 1). Application to deriving species accounts is, however, relatively straightforward and this paper therefore directs particular attention to development of metrics for use in (bio)diversity accounts (Figure 1) that quantify spatial variation and complementarity in species composition across regions (i.e., beta and gamma diversity) as well as the effects of spatial configuration of habitat (e.g., connectivity) on biodiversity persistence.

It is important to note that for the sake of simplicity, the text in this paper frequently refers to the aggregation of metrics from EAs to ETs, and sometimes to the level of EAA. However, the same principles apply at all levels of spatial aggregation and to all types of spatial units, including the smallest spatial units (e.g., BSUs).

The challenges of spatial aggregation for biodiversity metrics fall into two general categories:

1. *Pattern-related issues:* Many species will occupy only parts of each of the ETs in which they are known to occur, especially if ETs are defined at a relatively high (general) level of classification. For example, a species might be limited to a particular subset of the environmental and/or geographical space spanned by an ET (depending on the precise niche requirements, and biogeographical limits, of the species concerned). This means that the amount and quality of habitat available for species associated with an ET is not simply a function of total ecosystem extent and condition, but also of how well remaining occurrences (EAs) of this ET span, or 'represent', gradients of environmental and geographical variation within that ecosystem. Any given ecosystem classification, including the IUCN Global Ecosystem Typology, attempts to partition a highly complex multidimensional world into a simple set of classes, each of which is as biologically homogeneous, and as ecologically self-contained, as possible. Deciding what classification resolution (number of classes) to employ involves an important trade-off between these two criteria. By splitting broad classes to achieve greater within-class homogeneity – e.g., splitting rainforest into different types of rainforest – the resulting classes become less self-contained (from an ecological-process perspective) and exhibit higher levels of overlap in biological composition (e.g., number of species shared) between classes. Regardless of the precise classification employed, any such assessment needs to ideally move beyond treating ecosystem types as internally homogeneous, and mutually exclusive from one another in terms of both biological composition and ecological processes.
2. *Process-related issues:* Persistence of species contributing to the collective biodiversity of an ET or EAA is a function not only of the biodiversity of individual EAs within that ET, but also of spatial relationships and interactions between these EAs, e.g., the significant effect that varying levels of isolation and/or connectedness of EAs has on population and metapopulation dynamics. This is further complicated by the reality that many species will utilise resources from, or will disperse through, more than one ET, and therefore the effect of proximity and connectedness of EAs within a given ET with EAs in other relevant ETs also needs to be considered.

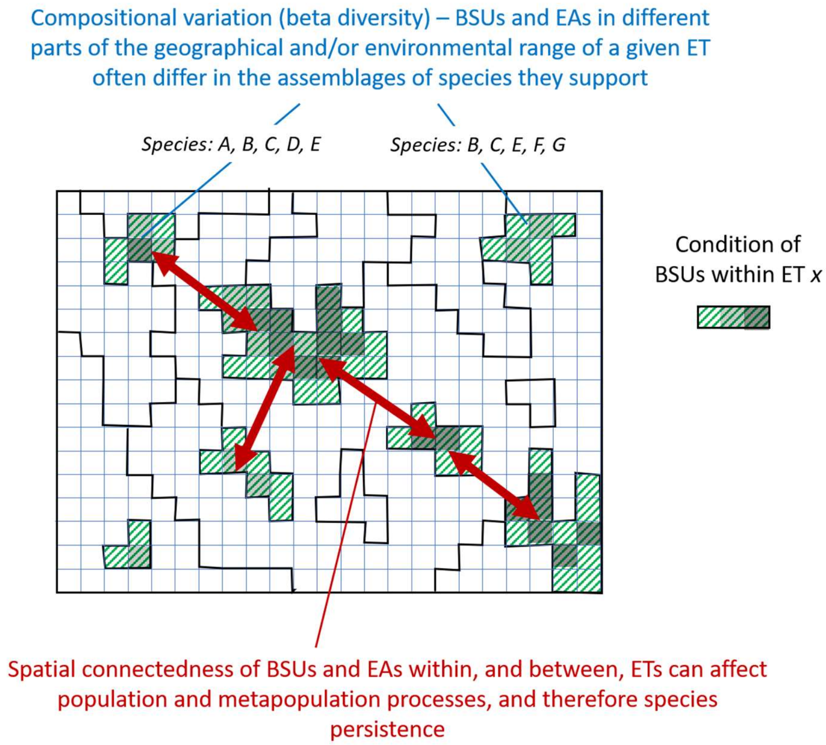

Figure 3: The challenges of aggregating biodiversity data from smaller to larger spatial units are related to pattern (e.g., composition) and process (e.g., dispersal)

Practical solutions

The broader biodiversity-assessment community of practice has already developed, and applied, a variety of approaches to aggregate biodiversity data and derive habitat-based biodiversity metrics which address the issues outlined above. These approaches are targeted across a range of ecological units, but they are also more generally applicable to ecosystem types and ecosystem accounting areas. The following simple typology is proposed to aid understanding and discussion of existing, and potential, approaches of relevance (Figure 4). This typology lays out options in relation to three attributes of any given approach: (1) the type of information used to account for compositional variation (beta diversity) within an ecosystem type; (2) the spatial data structure used to address habitat connectedness; and (3) the level of integration achieved in addressing compositional variation and habitat connectedness.

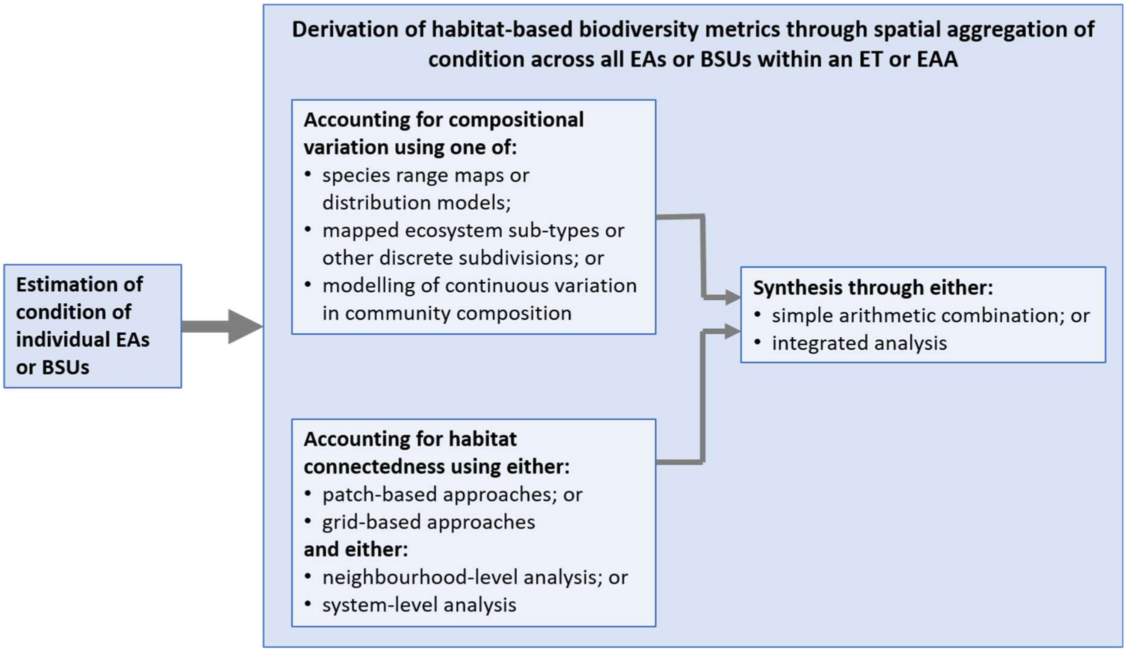

Figure 4: Typology of methodological components and options for aggregating condition estimates from individual EAs or BSUs to derive biodiversity metrics for whole ETs or EAAs

Type of information used to account for compositional variation

The UNEP-WCMC (2016) report on species accounting[3] has already addressed this component of the typology in considerable depth. It is important to remember here that, unlike monitoring based on direct observation of biodiversity change, the information on compositional variation employed in habitat-based approaches is purely spatial - i.e., this information simply describes spatial patterns in the distribution of biodiversity expected in the absence of anthropogenic transformation of natural ecosystems. Temporal change in biodiversity is then inferred by intersecting these spatial patterns with mapping of observed/estimated changes in ecosystem condition.[4] The main types of information which habitat-based approaches can use to account for compositional variation (beta diversity) across spatial scales, are listed below:

- ***Species range maps or distribution models***. For better studied groups, such as vertebrates, digital range maps provide a coarse approximation of the distribution of individual species within that group.[5] These distributions can often be further refined through deductive modelling, in which expert knowledge is used to implement rules that exclude areas within

[3] UNEP-WCMC (2016). Exploring approaches for constructing Species Accounts in the context of the SEEA-EEA. http://wcmc.io/Species_Accounting

[4] Ferrier S. et al. (2017). Biodiversity modelling as part of an observation system. Pp 239-257 in M Walters and RJ Scholes, eds. *The GEO Handbook on Biodiversity Observation Networks*. Springer International Publishing. https://link.springer.com/chapter/10.1007/978-3-319-27288-7_10

[5] e.g., http://www.birdlife.org and http://www.iucnredlist.org.

the broad range of a given species expected to be unsuitable for that species[6] – e.g., "species *x* occurs only above 500m elevation, and only in forest". Alternatively, distributions of individual species can be estimated from correlative species distribution models (SDMs). This involves using statistical or machine-learning techniques to fit an inductive model relating point observations of presence, presence-absence or abundance of a given species to multiple mapped environmental variables, thereby allowing potential occurrence to be extrapolated across an entire study region of interest.[7] Regardless of the precise technique used to map species distributions across a region (e.g. EAA) of interest, these can then provide a foundation for factoring compositional variation into the derivation of habitat-based biodiversity metrics for that region, from data compiled for ecosystem extent and condition accounts. The most straightforward strategy for achieving this is to simply estimate the aggregate value of an ET as the grand mean of average values for all EAs (or BSUs) falling within the distribution of each species - i.e., first average values for each species, then average these individual averages across all species.

- ***Mapped ecosystem sub-types or other discrete subdivisions of ETs***. If sub-types have been mapped within ETs, or if ETs can be intersected with mapping of some other more finely-resolved ecological classification – e.g., of vegetation communities – then such classes can serve as surrogates or proxies for compositional variation within each ET. As for the "species range maps or distribution models" option (above) the most straightforward strategy here is to simply estimate the aggregate value of an ET as the grand mean of average values for all EAs (or BSUs) falling within the distribution of each mapped sub-type (or other finely-resolved ecological class) - i.e., first average values for each sub-type, then average these individual averages across all sub-types within the ET. If information is also available on levels of similarity in species composition between sub-types, then techniques exist for weighting the contribution of sub-types in this final step.[8] Furthermore, this type of data will also allow the computation of beta and gamma ecosystem diversity at two spatial scales and levels of ecosystem classification: the diversity of main ETs within the EAA (or multiple EAAs), and the diversity of sub-types within each ET (possibly stratified per EAA). If average-condition values derived using this approach are expressed as a proportion of the maximum value obtainable if all BSUs or EAs were in perfect condition, then the species-area relationship (SAR)[9] can be used to translate this proportion into the predicted proportion of associated species expected to persist over the long term.
- ***Modelling of continuous variation in community composition***. Compositional variation within an ET typically correlates strongly with abiotic environmental gradients relating to attributes of climate, terrain and soils, and with geographical separation of instances of the ET.

[6] e.g., https://mol.org/ Jetz, W. et al (2012) Integrating biodiversity distribution knowledge: toward a global map of life. *Trends in Ecology & Evolution,* **27,** 151-159.

[7] Elith, J. & Leathwick, J. R. (2009) Species distribution models: ecological explanation and prediction across space and time. *Annual Review of Ecology Evolution and Systematics,* **40,** 677-697.

[8] e.g., Leathwick, J. et al (2010) Complementarity-based conservation prioritization using a community classification, and its application to riverine ecosystems. *Biological Conservation* 143: 984-991.

[9] e.g., Proenca, V. & Pereira, H. M. (2013) Species-area models to assess biodiversity change in multi-habitat landscapes: The importance of species habitat affinity. *Basic and Applied Ecology,* **14,** 102-114.

Environmental variation, and geographical spread, across the distribution of an ET can therefore be used directly as proxies for compositional variation or, alternatively, the relationship between these variables and compositional variation can be modelled more explicitly using best-available species occurrence data. Commonly used approaches to such modelling include generalised dissimilarity modelling (GDM)[10] and gradient forest.[11] GDM, for example, employs occurrence records for all species in a given biological group (e.g., all plants) to fit a non-linear statistical model relating the dissimilarity in species composition observed between two locations to abiotic environmental differences. Once a GDM model has been fitted for the region (e.g., EAA) of interest then this can be used to incorporate consideration of compositional variation into the aggregation of condition estimates across individual locations (e.g., EAs or BSUs) through a special form of weighted averaging, based on predicted levels of dissimilarity in species composition between these locations.[12] As was the case for discrete ecological classes (see previous point) the species-area relationship can again be used to translate this weighted-average condition value into the predicted proportion of species expected to persist over the long term.

Spatial data structure used to address habitat connectedness

Habitat connectedness is vital to ensuring the persistence of species and their metapopulations. A vast array of analytical approaches to assessing habitat connectedness (and related properties such as fragmentation) have been developed across various ecological disciplines (landscape ecology, metapopulation ecology, conservation biology etc.).[13] These approaches generally work with one of two major data structures (see Figure 5):

- ***Patch-based approaches,*** in which the fundamental spatial units of analysis are discrete patches of vegetation or habitat – equivalent to EAs in the SEEA-EEA framework – and the analysis of connectedness and related properties therefore focuses on attributes of, and spatial relationships between, these patches (e.g., size and proximity, respectively).

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[10] https://cran.r-project.org/web/packages/gdm/ Ferrier, S. et al (2007) Using generalized dissimilarity modelling to analyse and predict patterns of beta diversity in regional biodiversity assessment. *Diversity and Distributions,* **13,** 252-264.

[11] http://gradientforest.r-forge.r-project.org/ Ellis, N. et al (2012) Gradient forests: calculating importance gradients on physical predictors. *Ecology* 93: 156-168.

[12] Allnutt, T. et al (2008) A method for quantifying biodiversity loss and its application to a 50-year record of deforestation across Madagascar. *Conservation Letters* 1: 173-181.

[13] see reviews in: Kindlmann P and Burel F (2008) Connectivity measures: a review. *Landscape Ecology* 23: 879-890; Correa-Ayram CA et al (2016) Habitat connectivity in biodiversity conservation: A review of recent studies and applications. *Progress in Physical Geography* 40: 7-37.

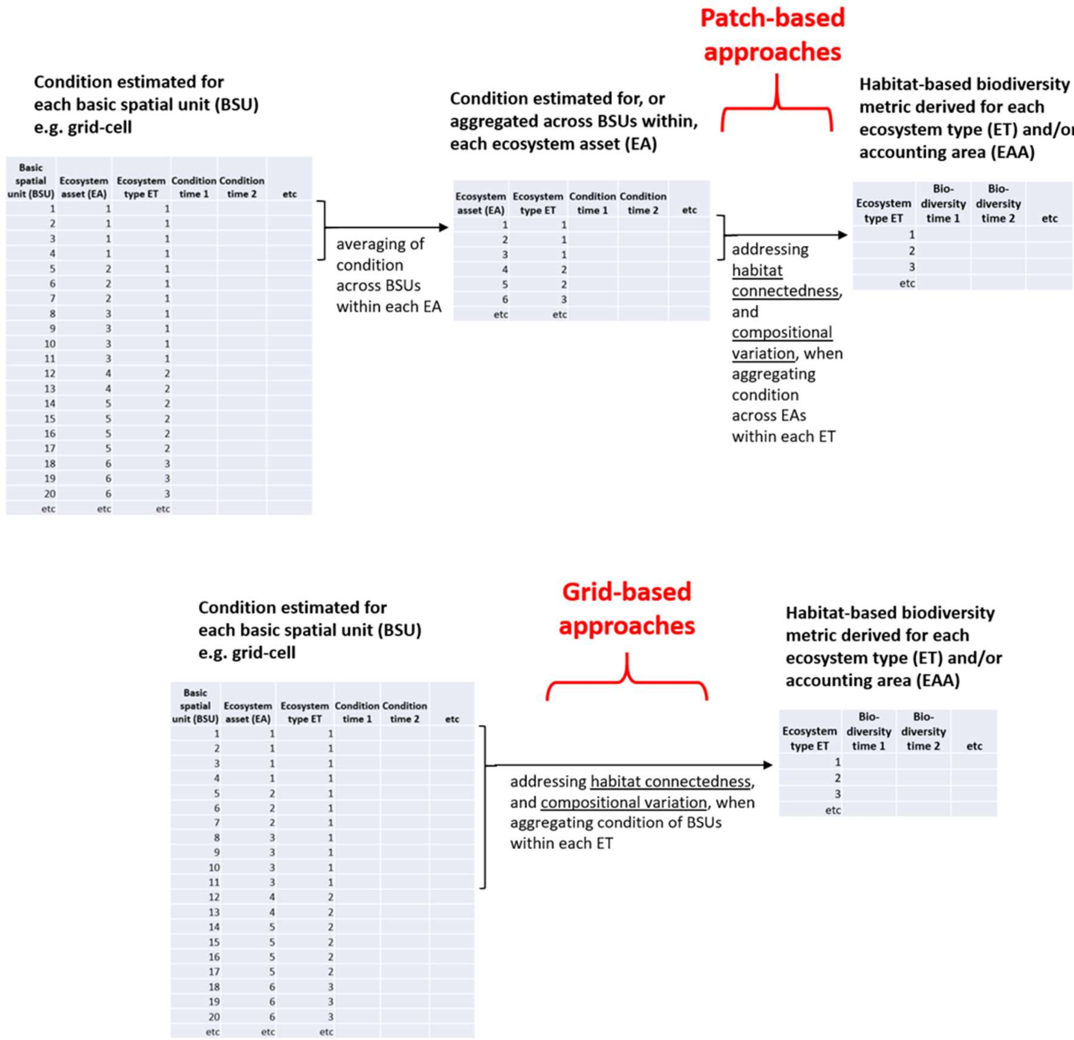

Figure 5: Patch-based versus grid-based approaches to addressing habitat connectedness (and compositional variation) when deriving biodiversity metrics

- ***Grid-based approaches,*** which side-step the delineation of discrete habitat patches and instead work directly with a regular grid of fine-resolution cells – equivalent to BSUs in the SEEA EA framework. These approaches are well suited to the analysis of landscapes in which ETs form complex mosaics, exhibiting intricate patterns of spatial variation in biodiversity and/or condition. Their application within the context of SEEA EA would, however, mean that estimates of the aggregate value/condition of whole ETs within an EAA would now be derived directly from the analysis of BSU-level data, effectively bypassing the delineation and analysis of EAs as discrete sets of BSUs.

Both patched-based and grid-based approaches offer two possible strategies for factoring consideration of connectedness into the aggregation of values from individual EA or BSU level to whole-ET, or whole-EAA, level:

- **Neighbourhood-level analysis**, in which a measure of connectedness is derived independently for each spatial unit (either each EA for patch-based approaches, or each BSU for grid-based approaches), through an analysis of spatial configuration of habitat in the local neighbourhood around that unit - e.g., a distance-decay weighted average of the values of all EAs or BSUs falling within a specified radius of the unit. Subsequent averaging of these connectedness-adjusted scores across all EAs or BSUs within the ET and/or EAA of interest then provides a simple means of factoring connectedness into the spatial aggregation of condition or other biodiversity-related values.
- **System-level analysis**, in which connections between all spatial units (EAs or BSUs) within an ET, or an entire EAA, are analysed simultaneously as a network - e.g., using techniques based on graph theory, metapopulation ecology, or gravity modelling. While somewhat more challenging to implement, this strategy addresses some very important aspects of connectedness which are largely ignored by the neighbourhood-level strategy - e.g., the contribution made by landscape-scale habitat corridors and stepping-stones.

Level of integration in addressing compositional variation and habitat connectedness

While approaches to addressing compositional variation have generally been developed separately from those addressing habitat connectedness, two main options exist for combining consideration of both issues in aggregating biodiversity values for individual EAs or BSUs across an ET:

- ***Simple arithmetic combination,*** of separately derived ET-level measures addressing compositional variation versus habitat connectedness.
- ***Integrated analysis,*** accounting for potential interactions between the effects of compositional variation and habitat connectedness[14] – e.g., the less intact, more fragmented, areas of an ET might be biased towards a particular subset of the compositional variation of that ET, rendering the species associated with those areas particularly vulnerable to extinction. A reasonably straightforward strategy for achieving such integration is to first adjust the biodiversity or condition scores of EAs or BSUs to account for their connectedness, using the neighbourhood-level analysis option (see above), and then to employ these adjusted scores, in place of raw scores, as input to one of the habitat-based approaches for addressing compositional variation within an ET - i.e. intersecting with best-available species range maps or distributions models, modelling of continuous variation in community composition, or mapped ecosystem sub-types.

[14] Ferrier, S. & Drielsma, M. (2010) Synthesis of pattern and process in biodiversity conservation assessment: a flexible whole-landscape modelling framework. *Diversity and Distributions* 16: 386-402.