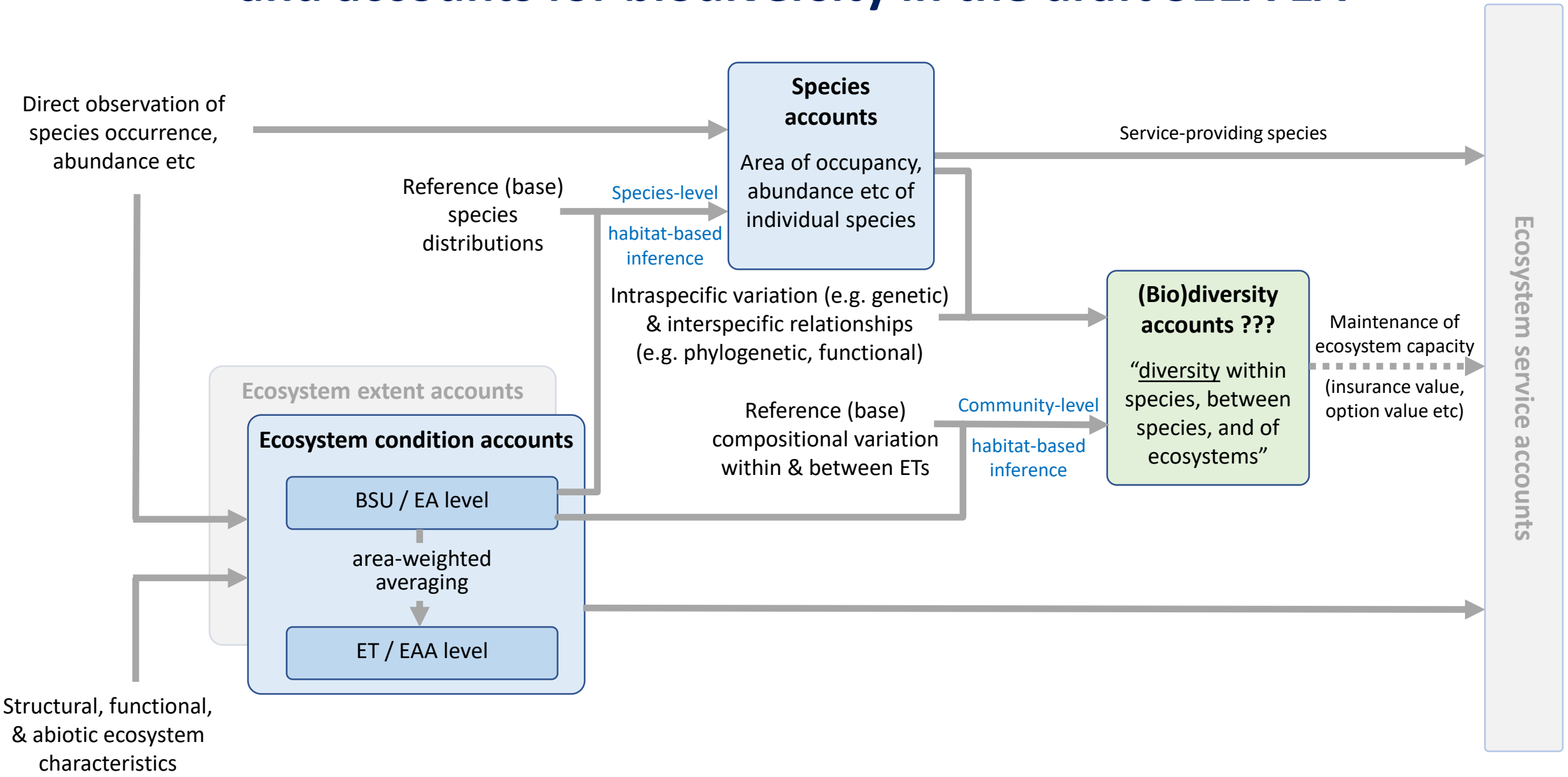
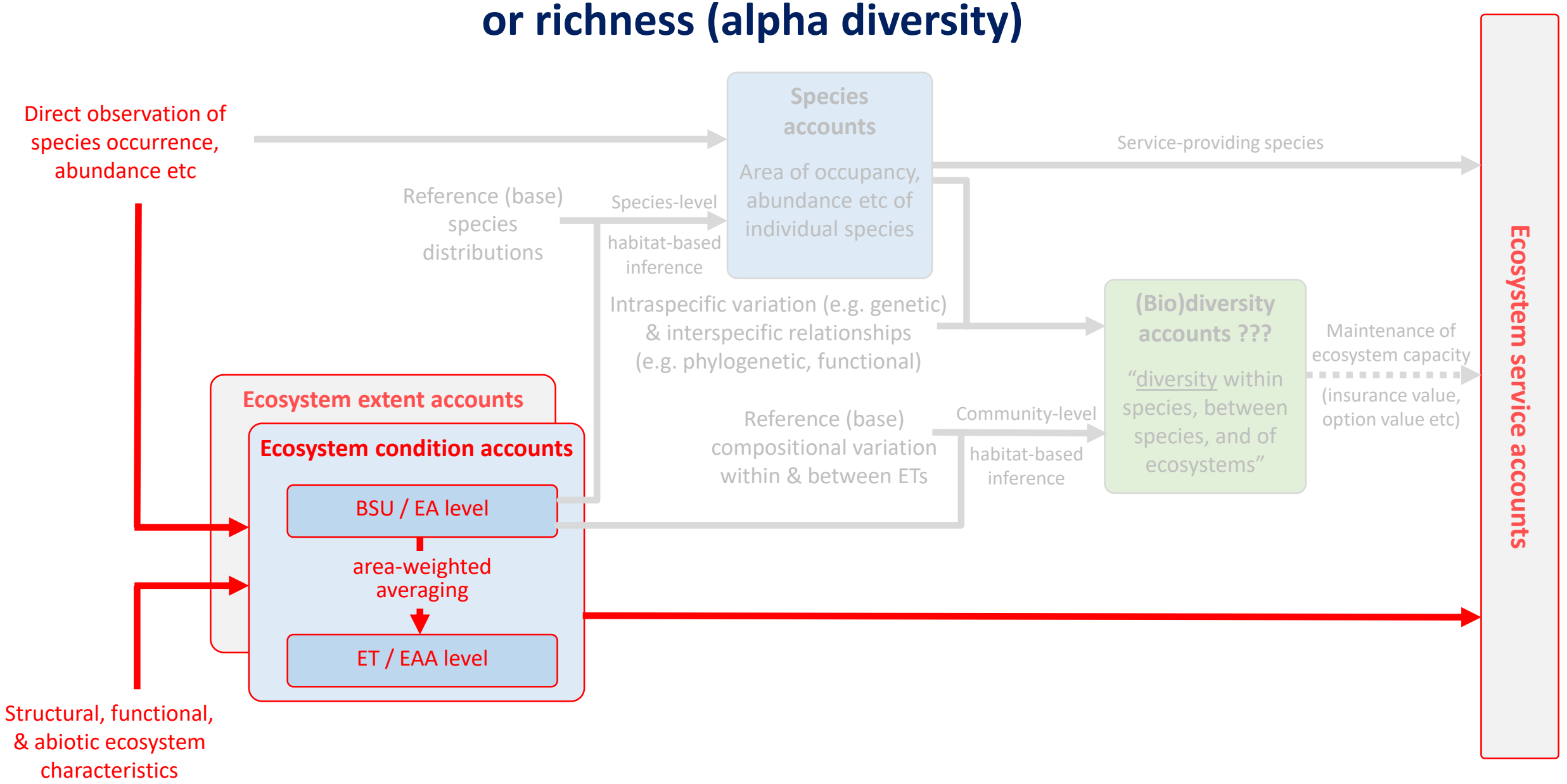
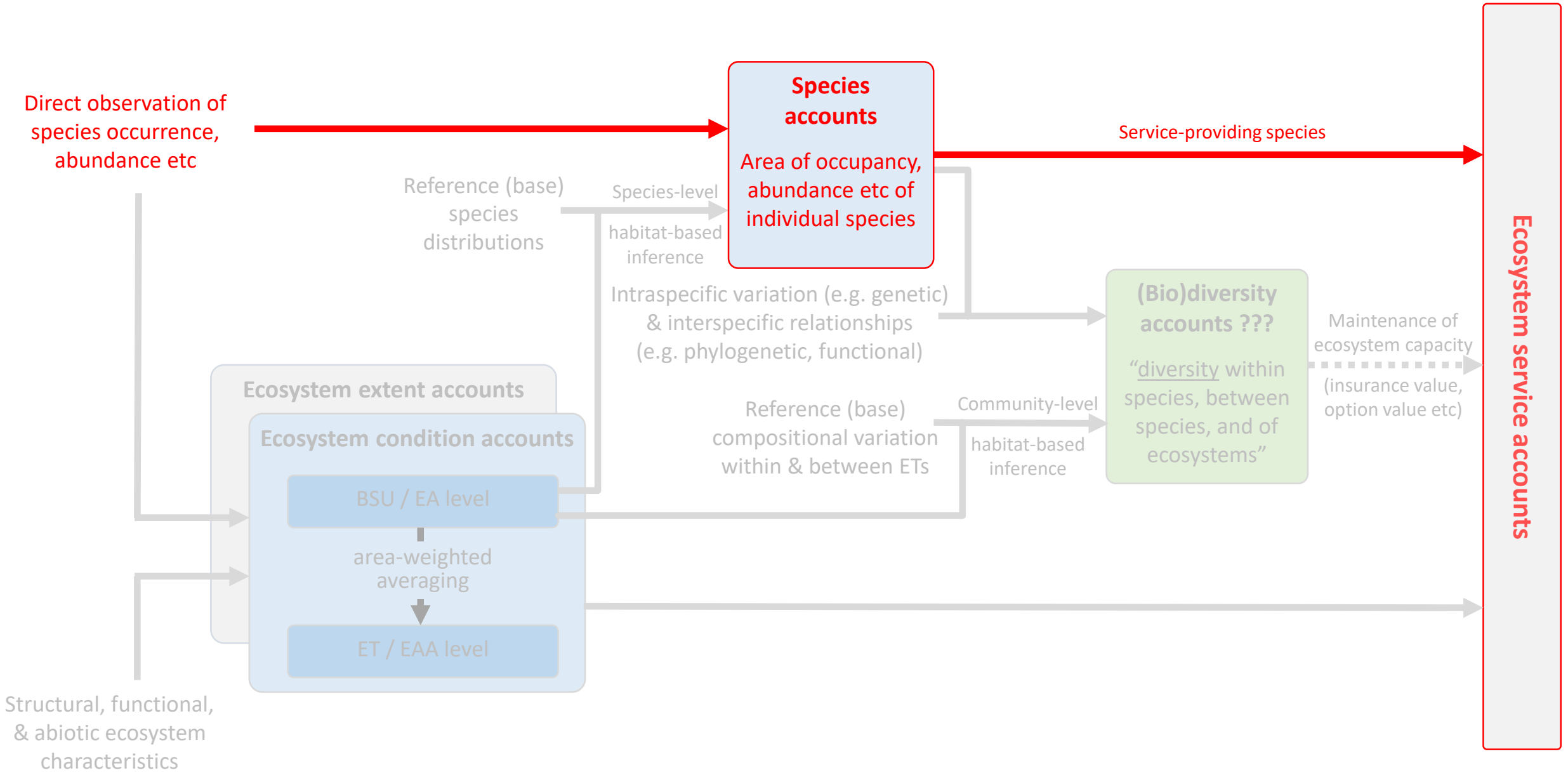
Simon Ferrier (CSIRO): Reflections on the introductory presentation and accounts for biodiversity in the draft SEEA EA



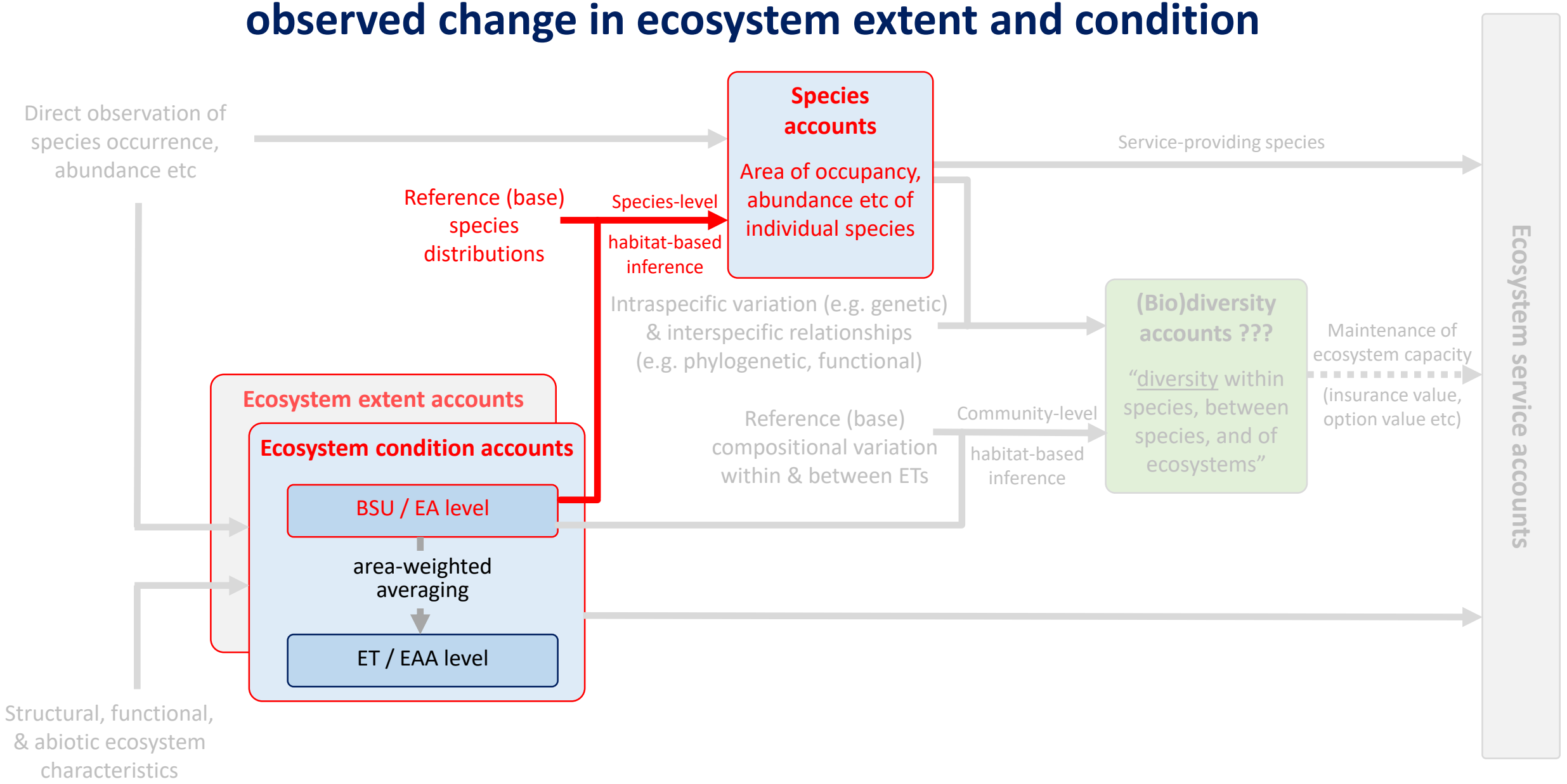
Assessment of Ecosystem Condition at Ecosystem Asset (EA) level can be informed by direct observation of local species occurrence, abundance, or richness (alpha diversity)



Direct observation of species can also be used to generate Species Accounts for individual species of interest, including service-providing species



Species Accounts can alternatively be populated through habitat-based inference, by intersecting reference (base) species distributions with observed change in ecosystem extent and condition



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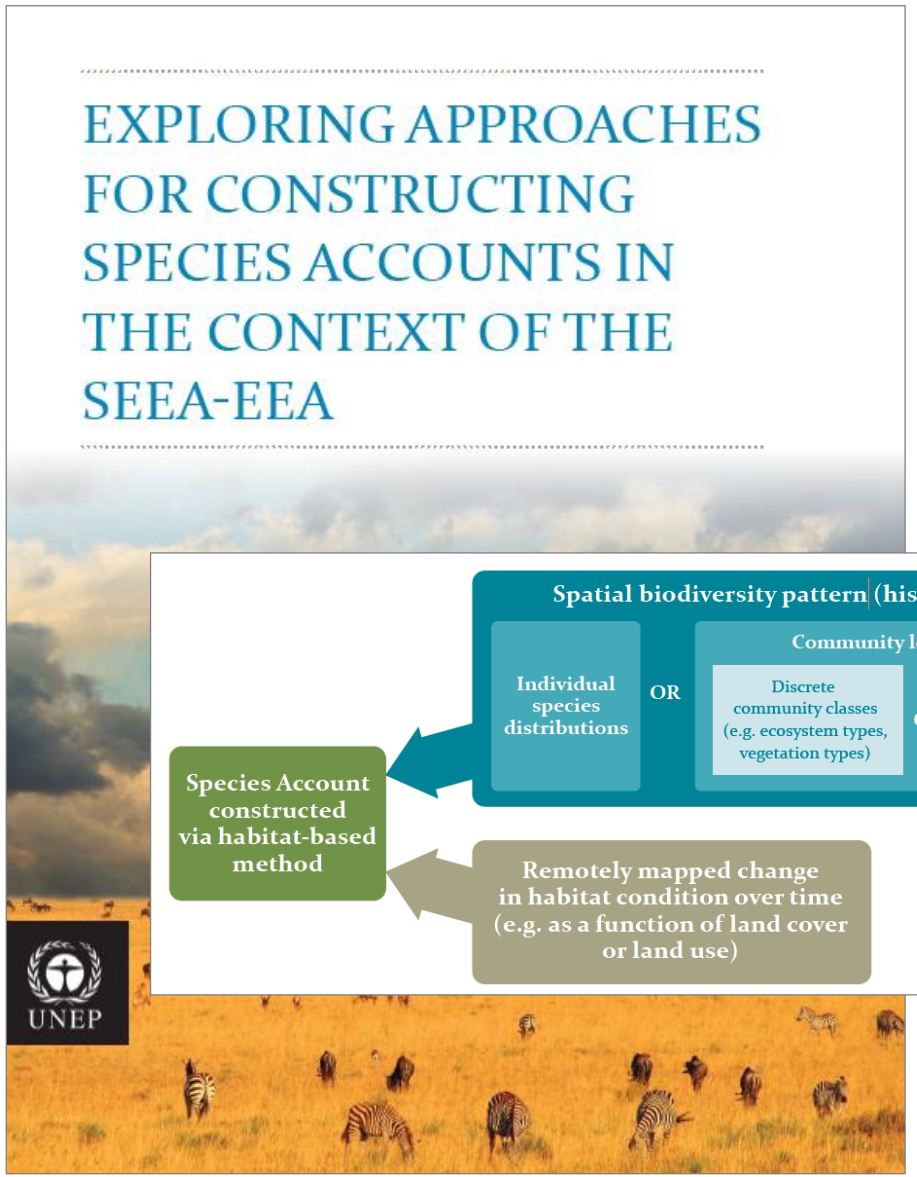
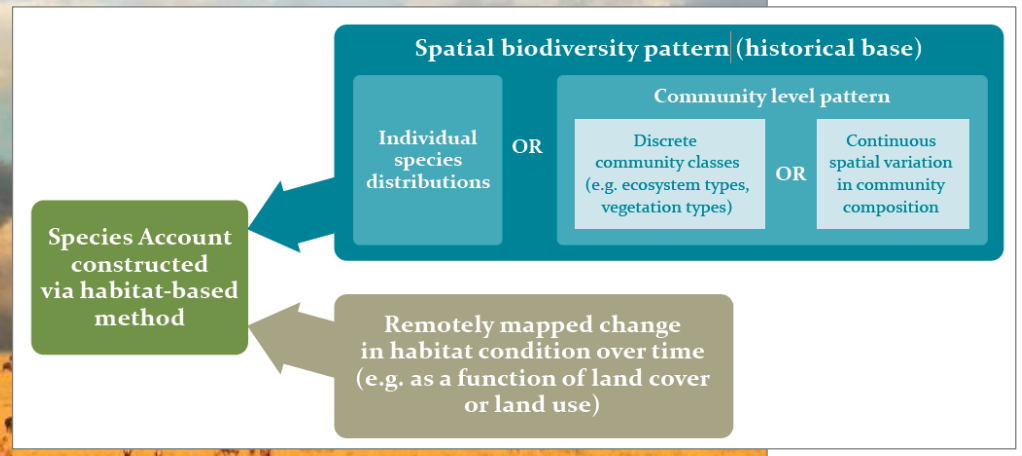
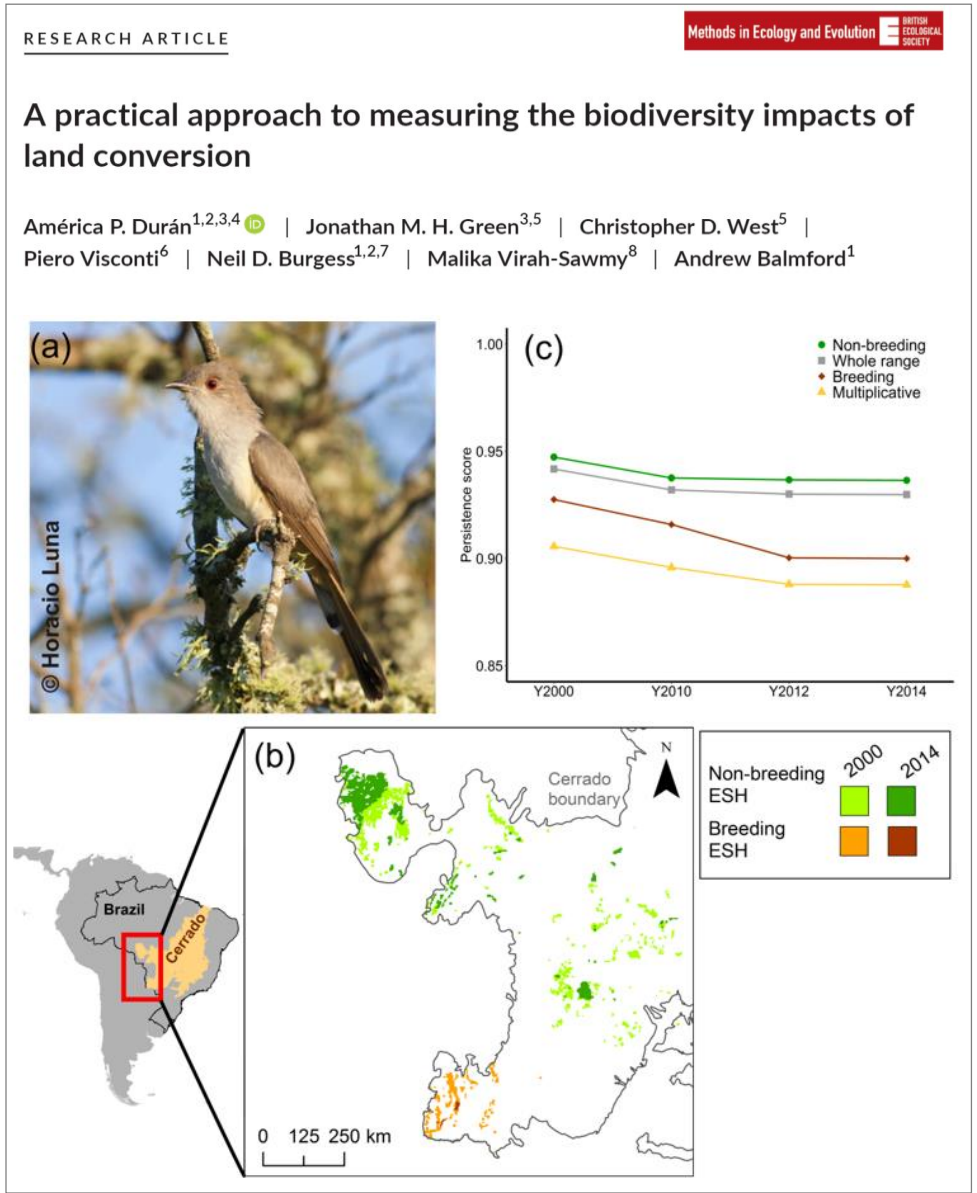
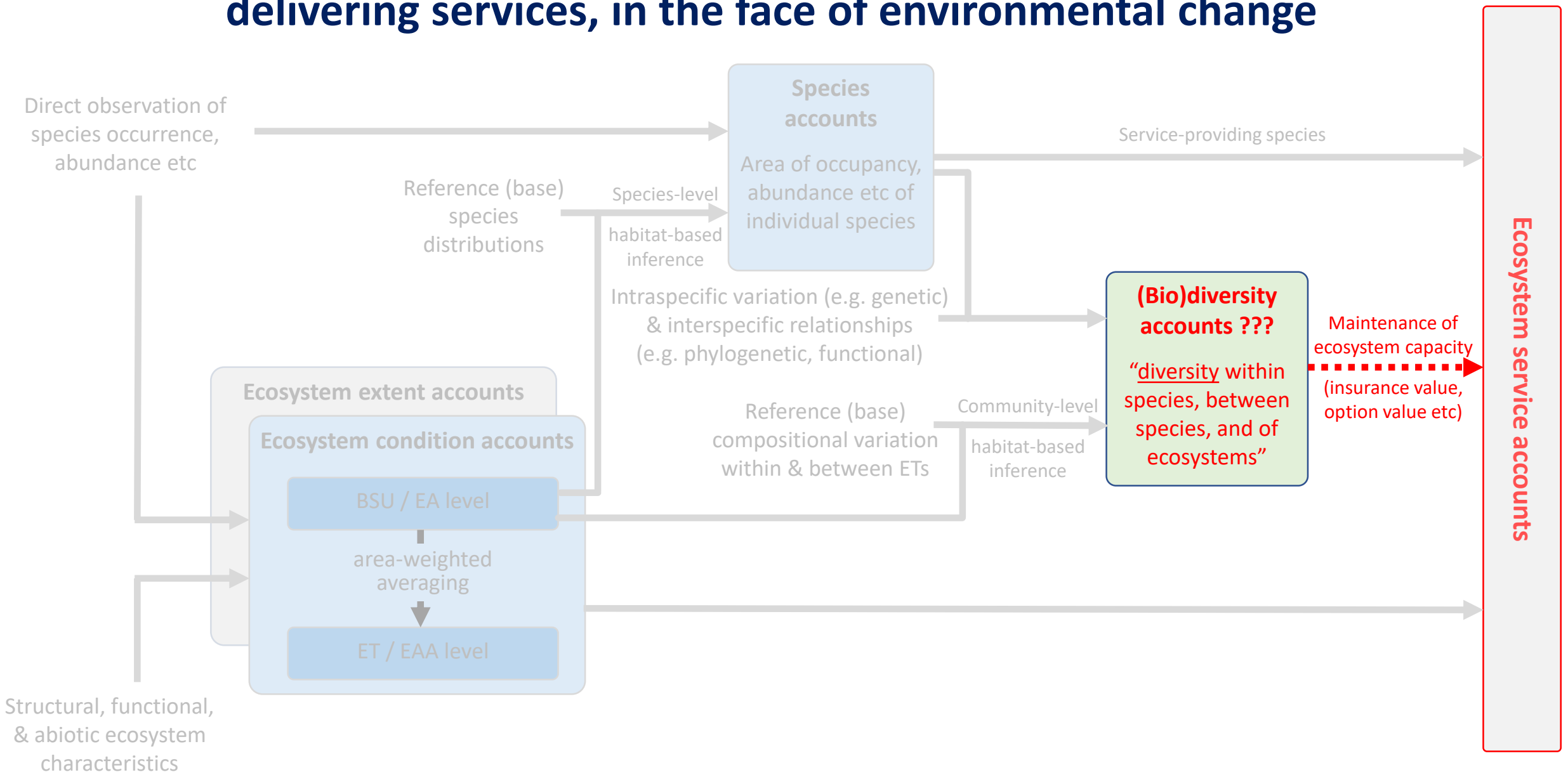


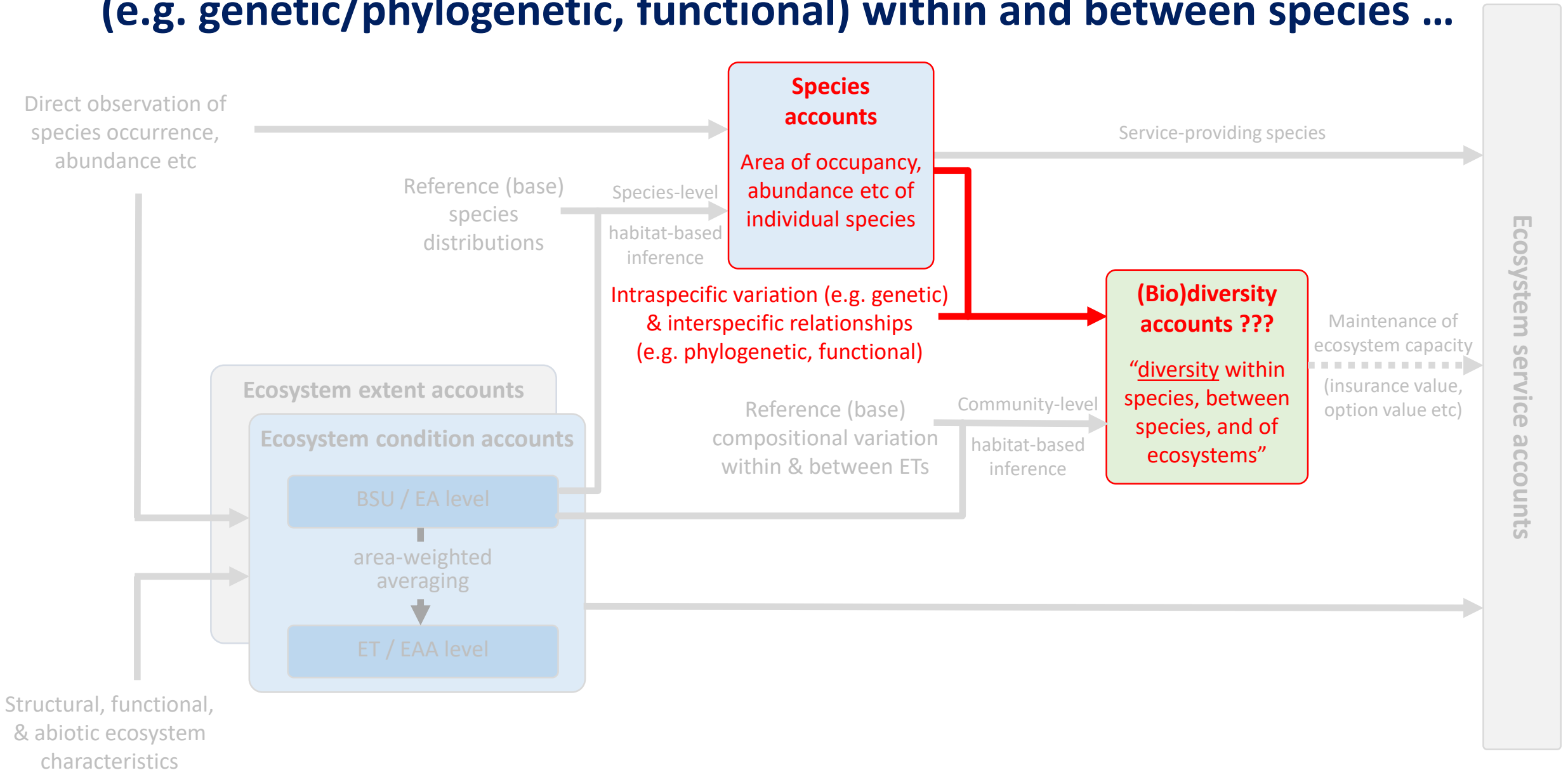




But what about accounting for change in diversity itself (as per CBD definition)? – vital to maintaining the capacity of ecosystems to continue functioning, and delivering services, in the face of environmental change



Two complementary pathways for generating 'diversity accounts' – the first through aggregation of Species Accounts, ideally also accounting for diversity (e.g. genetic/phylogenetic, functional) within and between species …



Two complementary pathways for generating ‘diversity accounts’ – the first through aggregation of Species Accounts, ideally also accounting for diversity (e.g. genetic/phylogenetic, functional) within and between species …

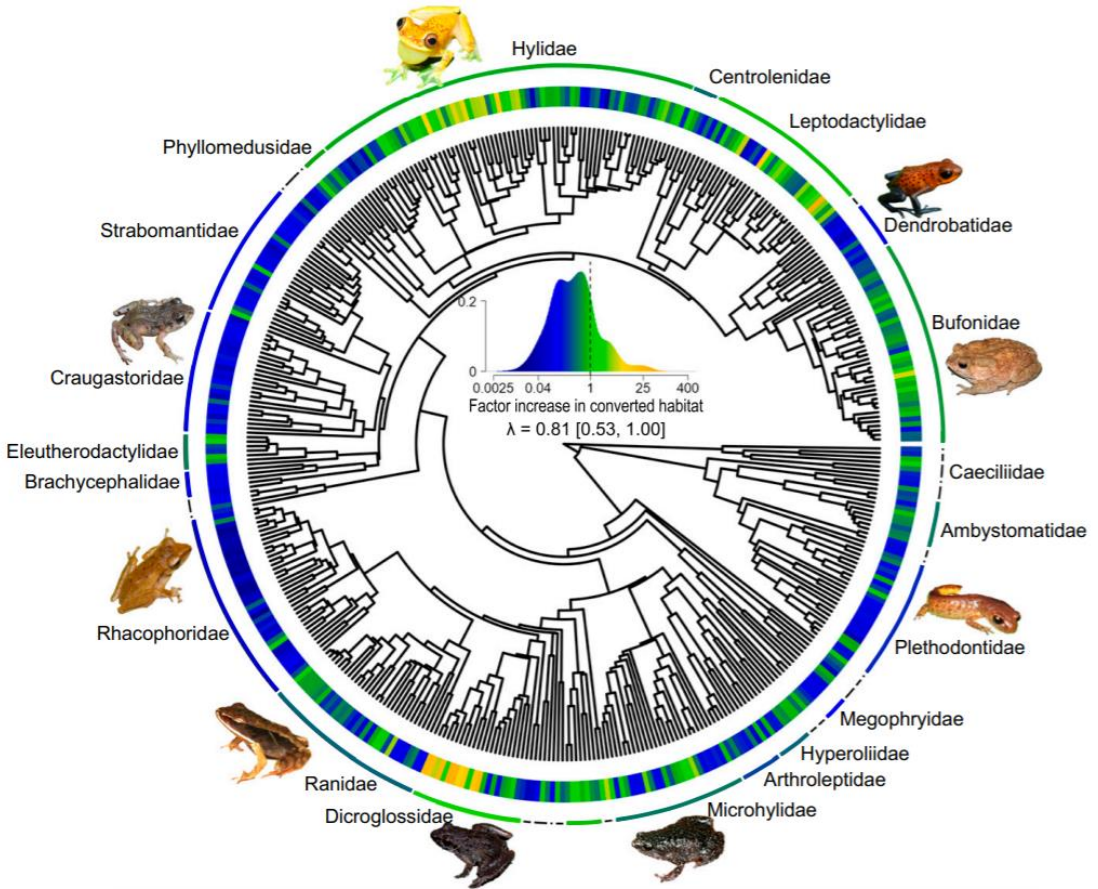
PNAS

Phylogenetic homogenization of amphibian assemblages in human-altered habitats across the globe

A. Justin Nowakowski[a,1,2], Luke O. Frishkoff[b,1,2], Michelle E. Thompson[c], Tatiana M. Smith[a], and Brian D. Todd[a]

[a]Department of Wildlife, Fish, and Conservation Biology, University of California, Davis, CA 95616; [b]Department of Ecology and Evolutionary Biology, University of Toronto, Toronto, ON M5S 3B2, Canada; and [c]Department of Biological Sciences, Florida International University, Miami, FL 33199

Edited by David B. Wake, University of California, Berkeley, CA, and approved February 16, 2018 (received for review August 22, 2017)

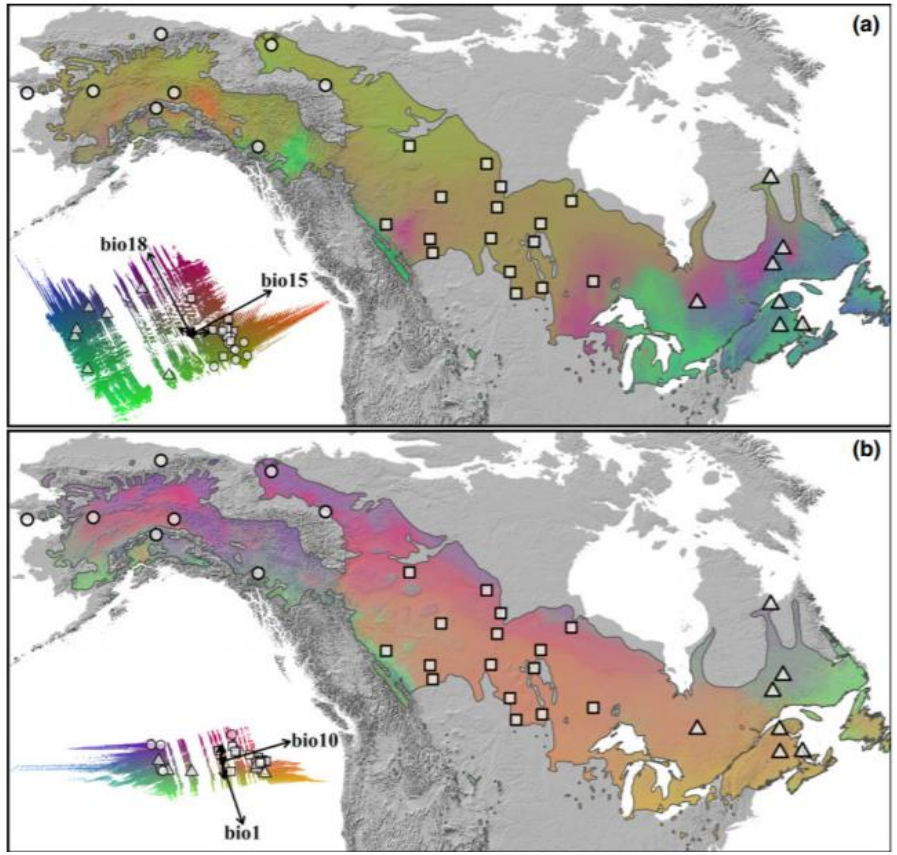


ECOLOGY LETTERS

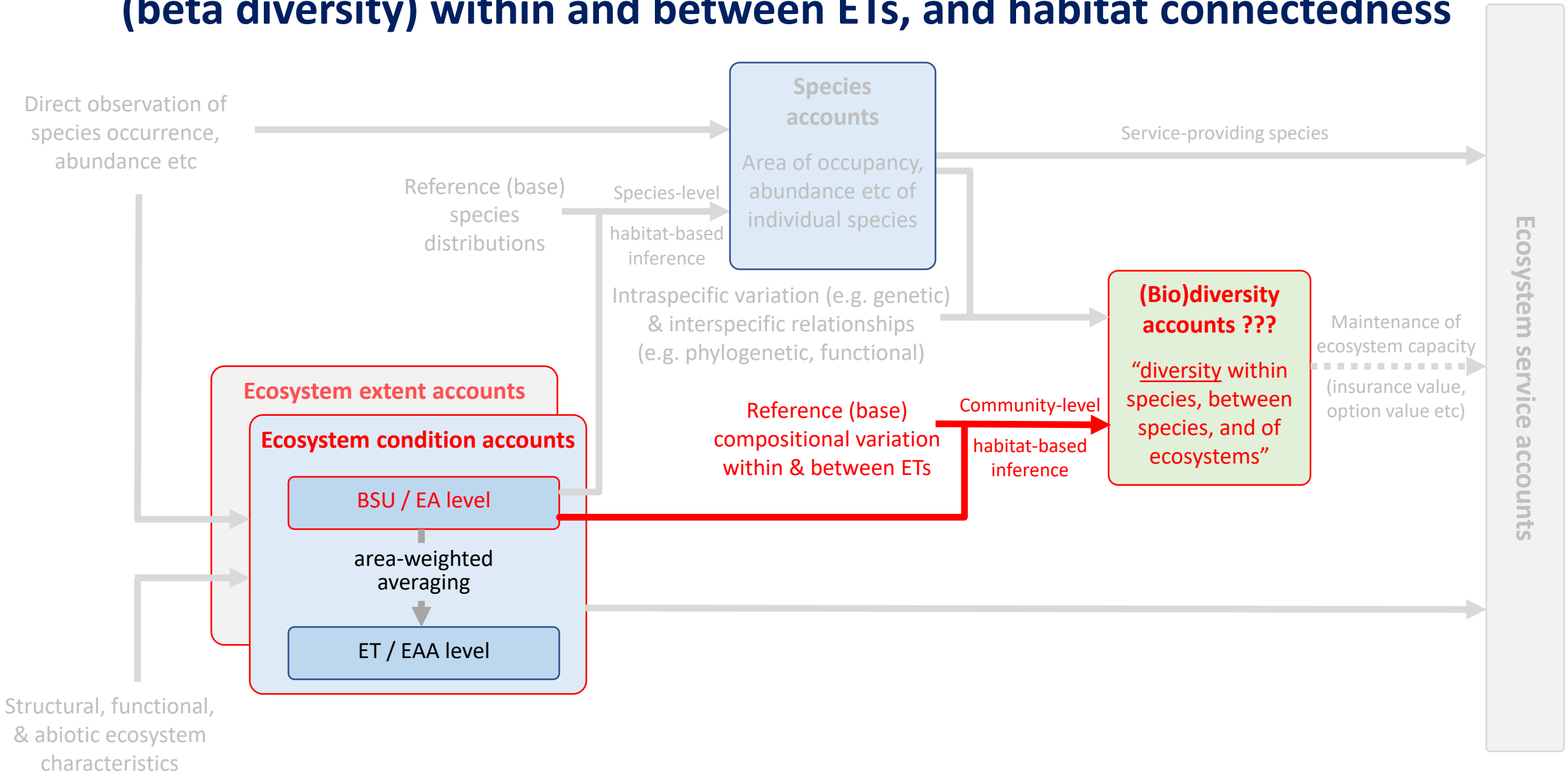
Ecology Letters, (2014) doi: 10.1111/ele.12376

IDEA AND PERSPECTIVE

Ecological genomics meets community-level modelling of biodiversity: mapping the genomic landscape of current and future environmental adaptation

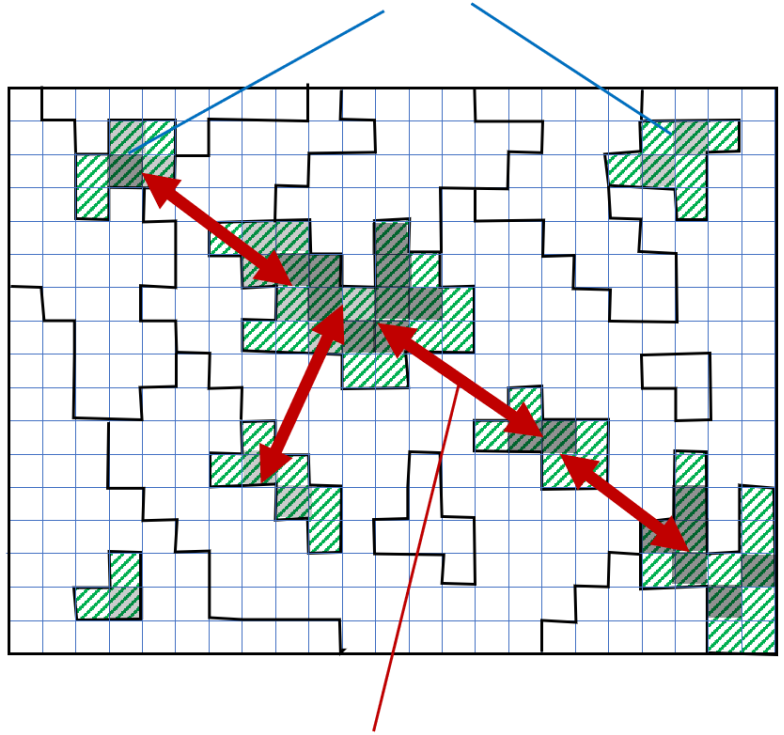


… and the second through aggregation of Ecosystem Condition estimates for all EAs across an EAA, while also accounting for compositional variation (beta diversity) within and between ETs, and habitat connectedness



… and the second through aggregation of Ecosystem Condition estimates for all EAs across an EAA, while also accounting for compositional variation (beta diversity) within and between ETs, and habitat connectedness

Compositional variation (beta diversity) – EAs in different parts of the geographical and/or environmental range of a given ET often differ in the assemblages of species they support



Condition of BSUs within ET *x*

Spatial connectedness of EAs within, and between, ETs can affect population and metapopulation processes, and therefore species persistence

Estimation of condition of individual EAs or BSUs

Spatial aggregation of condition across all EAs or BSUs within an ET or EAA

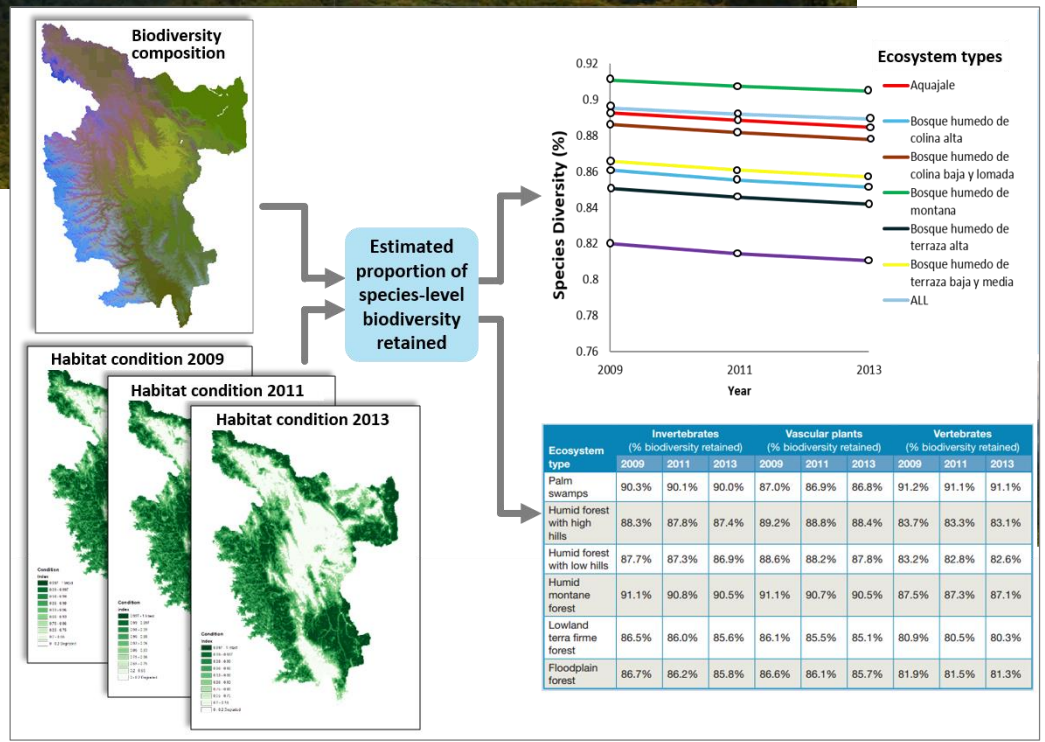
Accounting for compositional variation using one of:
- direct species data;
- species range maps or distribution models;
- modelling of continuous variation in community composition;
- mapped ecosystem sub-types or other discrete subdivisions; or
- non-spatial consideration of compositional variation

Accounting for habitat connectedness using either:
- patch-based approaches; or
- grid-based approaches

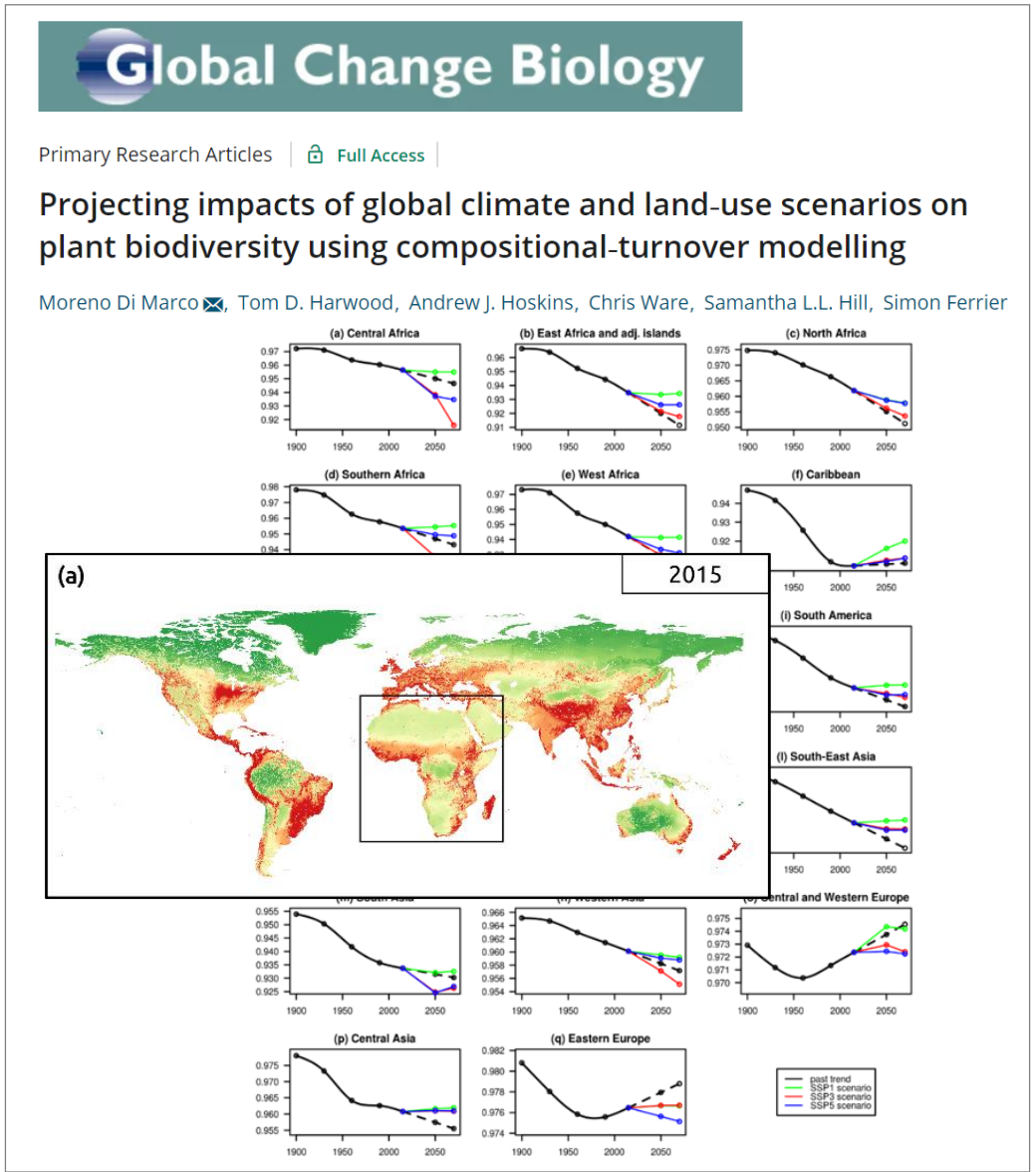
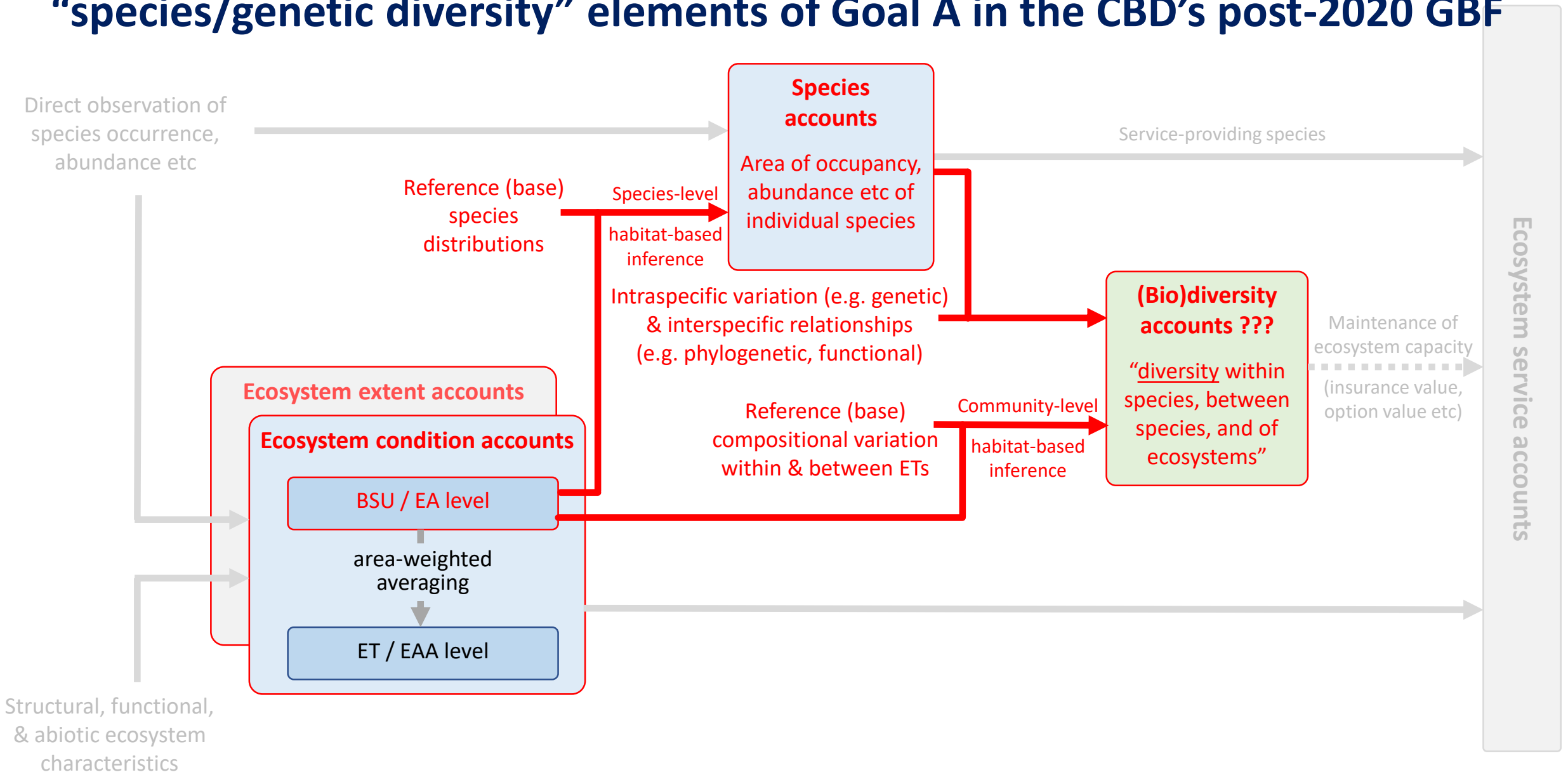
and either:
- neighbourhood-level analysis; or
- system-level analysis

Synthesis through either:
- simple arithmetic combination; or
- integrated analysis

… and the second through aggregation of Ecosystem Condition estimates for all EAs across an EAA, while also accounting for compositional variation (beta diversity) within and between ETs, and habitat connectedness



Ecosystem type	Invertebrates (% biodiversity retained)			Vascular plants (% biodiversity retained)			Vertebrates (% biodiversity retained)		
	2009	2011	2013	2009	2011	2013	2009	2011	2013
Palm swamps	90.3%	90.1%	90.0%	87.0%	86.9%	86.8%	91.2%	91.1%	91.1%
Humid forest with high hills	88.3%	87.8%	87.4%	89.2%	88.8%	88.4%	83.7%	83.3%	83.1%
Humid forest with low hills	87.7%	87.3%	86.9%	88.6%	88.2%	87.8%	83.2%	82.8%	82.6%
Humid montane forest	91.1%	90.8%	90.5%	91.1%	90.7%	90.5%	87.5%	87.3%	87.1%
Lowland terra firme forest	86.5%	86.0%	85.6%	86.1%	85.5%	85.1%	80.9%	80.5%	80.3%
Floodplain forest	86.7%	86.2%	85.8%	86.6%	86.1%	85.7%	81.9%	81.5%	81.3%



In combination, these two pathways of habitat-based inference offer a powerful means of linking the "ecosystem area, connectivity & integrity" and "species/genetic diversity" elements of Goal A in the CBD's post-2020 GBF