Synthesis before vacations

Life cycle assessment (LCA) is a tool to quantify potential environmental impacts of systems and products involved in with value chains. [@ISO2006\_ISO14040]. Loss of biodiversity due to human activities, mostly activities associated to material consumption, is a growing concern for society. Protection of biodiversity is an objective in itself but also for the associated potential loss of ecosystem function and contribution to humans [@IPBES2019\_GlobalAssessment;@MEA2005\_EcosystemsHuman].

@IPBES2019\_GlobalAssessment defines the main drivers of biodiversity loss, which is land use change for terrestrial ecosystems. Land use change means loss of habitat from the perspective of the ecological community. The potential impacts of land use on biodiversity has been the focus of methodological developments for more than two decades in the LCA community [@Curran2016\_HowWell]. Methods have been refined over time, increasing the geographical coverage and regionalisation, increasing the taxonomical coverage, accounting for specific limitations such as land use-taxon affinity and habitat fragmentation [@Scherer2023\_BiodiversityImpact].

Among the diversity of methods found in the litterature [@Damiani2023\_CriticalReview], one class of approach is to 1/ focus on changes in community composition [@Pereira2013\_EssentialBiodiversity], in particular by measuring the relative loss of native species, also known as potential diseappeared fraction of species (PDF), and 2/ link regional species richness and land use change using derivates of the species-area relationships (SAR) [@MacArthur2001\_TheoryIsland;@Kuipers2021\_ConsideringHabitat]. Regional biodiversity loss can also be used to derive global biodiversity loss, i.e. extinction of species by introducing regional species extinction risks [@Chaudhary2015\_QuantifyingLand]. Among this class of methods, @Scherer2023\_BiodiversityImpact is currently the most advanced method for assessing the life cycle impacts of land use on biodiversity loss, and is recommended by UNEP SETAC through the GLAM project.

One limitation of this method remains a limited taxonomical coverage. Application at global scale involves important data requirements, especially for species geographical coverage, extinction risks [@IUCN2025\_IUCNRed] and affinity with habitats modified by human activity [@Hudson2017\_DatabasePREDICTS]. However, global soils host most of global species [@Anthony2023\_EnumeratingSoil]. Taxa with highest species count are bacteria (and archae), arthropods, nematodes and fungi. All these taxa are not covered[1] in @IUCN2025\_IUCNRed, leading to a distorded representation of species biodiversity.

Because of this taxonomic gap, results obtained with this method should not be extrapolated to a more complete "idea" of species biodiversity. Global patterns of above below ground biodiversity do not always follow patterns of above ground biodiversity [@Cameron2019\_GlobalMismatches]. The response of microorganisms to land use is not aligned with response of plants and vertebrates [@Labouyrie2023\_PatternsSoil;@Newbold2016\_GlobalPatterns]. Compared to macrobial communities, microbial communities change little across space. This challenges the use of a SAR-based approach for microbes to estimate regional species loss. Microbial taxons show much smaller z-values, leading to reduced (if any) richness loss per unit of area loss [@Storch2012\_UniversalSpecies;@Green2006\_SpatialScaling].

Beyond local or regional changes in species richness, microbes tend to show little endemism [@Doolittle1999\_PhylogeneticClassification] and species extinction risk is not a social concern [@Weinbauer2007\_ExtinctionMicrobes].

The native microbial community can be difficult to define, in order to estimate loss of native species. Many microbial species can be present in ecosytems in inactive forms (dormancy), sometimes undetected [@Sorensen2020\_DormancyDynamics]. Any ecological community is dynamic, speciation and extinction is part of natural evolutionary processes. For macrobes, this process is slow and allows the use of fixist models [@Robert2017\_FixismConservation] such as in [@Scherer2023\_BiodiversityImpact]. For microbes, horizontal gene transfer [@Smillie2011\_EcologyDrives] and reduced reproduction periods increase speciation rates, inducing the need for biodiversity metrics beyond native communities.

It also questions how a species-centric paradigm is inclusive of all life forms when monitoring biodiversity. One ethical basis of biodiversity conservation programs have been to consider existence value to individual species[2] [@Sandler2010\_ValueSpecies;@Himes2024\_WhyNature;@FAO2025\_HowConserve], motivating actions to protect species populations [@IUCN2025\_IUCNRed]. Soil microrganisms are difficult to observe and identify and it is unlikely that we will ever identify all species found in the soil. The existence value of soil microorganisms is limited for the average citizen, habitat or ecosystem function centric approaches are envisaged [@FAO2025\_HowConserve].

Still, there is interest for the description and conservation of soil ecological communities. Modern molecular techniques such as the metabarcoding of environmental DNA (eDNA) are promising to do so [@Orgiazzi2015\_SoilBiodiversity]. However, it is difficult to obtain reliable species diversity metrics (richness, abundance) using these techniques [@Calderon-Sanou2020\_EnvironmentalDNA;@Edgar2025\_InterpretingCounts]. @Labouyrie2023\_PatternsSoil provides patterns in soil microbial diversity across Europe, identifying drivers of bacterial and fungal richness and composition, using the LUCAS Soil eDNA barcodes dataset [@Orgiazzi2018\_LUCASSoil].

@Labouyrie2023\_PatternsSoil quantifies microbial richness using zero distance operational taxonomic units (zOTUs). This highlights the difficulties in the definition of species for bacteria [@Gevers2005\_ReevaluatingProkaryotic;@Edgar2025\_DefiningInterpreting], and it is in fact possible to avoid this issue by classifying species based on functional characteristics. This is the basis of the multi-trophic classification used in @Calderon-Sanou2022\_EnergyPhysiological. We can use this classification build abundance based metrics representing microbial communities, with better correlation to ecosystem function. It abandons a species-centric approach to biodiversity, but the latter is not the only dimension of biodiversity. Abundance in multi-trophic classification would capture additional dimensions of biodiversity, namely species population, species traits and ecosystem function [@Pereira2013\_EssentialBiodiversity].

eDNA based sampling methods are cost efficient to describe soil communities, but are expensive to scale at global level. Also, soil ecological communities are sensitive to variables such as climate, topology, land cover, soil physical and chemical properties, soil parent material and land use. These variables can have fine variations at regional scale. Si Moussi et al. (in prep.) uses deep species distribution models [@Hu2025\_IntroductionDeep] to expand the geographical coverage of multi-trophic biodiversity indicators to Europe by calibrating a model on the LUCAS Soil dataset [@Orgiazzi2022\_LUCASSoil], at a 100m resolution, capturing community variance at local level. The output of this research will be used to derive country level soil biodiversity characterisation factors.

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1. With the exception of a few mushroom forming fungi. The red list has 1300 species over millions estimated to exist.

1. Considering existence value for species beyond individual organisms constituting the species population, and beyond ecosytem functions filled by the population.