Global hotspots for soil nature conservation

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Abstract

Soils are the foundation of all terrestrial ecosystems [1]. However, unlike for plants and animals, a global assessment of the hotspots for soil nature conservation is still lacking [2]. This hampers our ability to establish nature conservation priorities for the multiple dimensions supporting the soil system: from soil biodiversity to ecosystem services. Here, we conducted a global field survey including biodiversity (archaea, bacteria, fungi, protists, and invertebrates) and function (critical for six ecosystem services) observations within 615 composite topsoil samples from a standardized survey in all continents, to identify global hotspots for soil nature conservation. We found that each of the different soil ecological dimensions (i.e., soil species richness [alpha diversity, measured as ASVs], community dissimilarity, and ecosystem services) peaked in contrasting regions of the planet, and were associated with different environmental factors. Temperate ecosystems showed the highest species richness, while community dissimilarity peaked in the tropics, and colder high-latitudinal ecosystems were identified as hotspots of ecosystem services. These findings highlight the complexities of simultaneously protecting multiple soil ecological dimensions. We further show that most of these hotspots are not properly covered by protected areas (over 70%), and are vulnerable in the context of multiple global change scenarios. This first global estimation of soil nature conservation priorities, highlights the fundamental importance of accounting for the multidimensionality of soil biodiversity and ecosystem services to conserve soils for future generations.

Main text:

Soils are essential to support terrestrial life on the planet [1]. They are home to diverse assemblages of organisms across all major lineages of life from bacteria to invertebrates, and provide multiple ecosystem services such as soil fertility, carbon (C) storage, waste decomposition, pest control, and water retention [3–5] that are critical for food production and human well-being [6–8]. However, soils are also highly vulnerable to anthropogenic disturbances such as climate change [9,10] and land use intensification (e.g., land-use change, pollution, and erosion [11,12]). For an adequate conservation of soils, it is critical to consider and protect the

multiple ecological dimensions supported by soils, from their biodiversity to the different ecosystem services they support. A first step in this direction is identifying the global ecological hotspots for soil nature conservation [13] to inform and guide policymakers and conservation managers on how to extend nature conservation to the world belowground. Concurrently, establishing and negotiating adequate global nature conservation policies and priorities (e.g., the 2030 biodiversity targets [14]) requires knowledge about the distribution of global biodiversity, including identifying ecological hotspots [2]. While these ecological hotspots were established decades ago for plants and animals, this critical information for soil biodiversity and ecosystem services does not exist and is therefore absent from current biodiversity assessments [15]. Recent developments in ecological modeling and soil macroecology have improved our understanding of the global distribution of multiple soil communities [16–21] and their potential future trends [9,22]. These studies have found potential mismatches between below- and aboveground biodiversity, suggesting that hotspots of plant diversity are poor proxies of belowground diversity [23] and, therefore, are unlikely to provide sufficient protection for life belowground. While this may be true, plant species richness, like the one found in the tropics, is known to increase the diversity in soil organic matter compounds and, therefore, provide resources for a diverse soil microbiological community [24]. This also opens the question to if the hotspots of different soil ecological dimensions (e.g., diversity, community composition, functions) coincide in space and how these are affected by global change, with recent studies pointing to diverging global patterns [22]. Yet, many recent developments are based on merged meta-analytical data, which are rarely measured using the same methods or do not simultaneously consider multiple soil ecological dimensions in the same locations. Unfortunately, we still lack globally standardized field surveys that explicitly consider the ecological multidimensionality of soils that simultaneously capture information on multiple soil taxonomic groups and ecosystem services, across a wide range of global environmental conditions [25]. Closing these knowledge gaps is essential to inform the establishment of nature conservation areas, steer management decisions, and set effective policy targets that address the ecological conservation of soils.

Herein, we combined machine learning models with a standardized global field survey, including 615 composite topsoil samples from all continents and climates (Supplementary Fig.1) to estimate, for the first time, the extent, associated environmental factors, and climate change vulnerabilities of the global hotspots of soil biodiversity and ecosystem services. Our dataset is based on >11,000 individual standardized observations and including information on 16 biodiversity and ecosystem service attributes (Methods; Supplementary Table 1). Our study moved beyond the analysis of alpha diversity (here based on soil DNA amplicon sequence variant, ASVs) and extended its scope to community dissimilarity (i.e., composition

heterogeneity, based on Jaccard distance from presence/absence data) of five soil groups of organisms (archaea, bacteria, fungi, protists and invertebrates). Measuring the hotspots of community dissimilarity and comparing them to the ones of alpha diversity allows us to identify areas with high local diversity that, at the same time, contain unique communities. In addition, to fully grasp the conservation potential of soil systems, soil functional properties related to six key soil ecosystem services were assessed, including soil C storage (total soil organic C), fertility (total nitrogen (N), phosphorus (P), potassium (K), and magnesium (Mg) contents; terrestrial ecosystems in this study were not fertilized, and therefore, total nitrogen represents the stocks of nitrogen in soil organic matter), organic matter decomposition (three enzymes associated with starch and chitin degradation, and P mineralization), water retention (water-holding capacity), pest control (inverse of the proportion of soil-borne fungal phytopathogens), and mutualism (i.e. plant-mycorrhizal mutualism, an ecological relationship between plants and fungi that is beneficial to both partners, assessed as the proportion of mycorrhizal fungi). We acknowledge that our study does not cover the entire environmental spectra found on Earth, but it represents a large portion of the environmental variability found in the planet (Supplementary Fig. 1). Locations showing environmental conditions under-represented in our study were excluded from our spatial analyses (Figs. 1-3).

Our analyses revealed that the assessed soil biodiversity and ecosystem services variables are associated with contrasting environmental factors at the global scale (Extended Data Figs. 1 and 2). For example, while soil pH was the main factor associated with alpha diversity of soil fungi and bacteria, soil organic matter (soil C and N contents) was positively associated with the alpha diversity of protists and invertebrates (Extended Data Figs. 2 and 3), and elevation was positively correlated with the alpha diversity of archaea. In the case of the assessed ecosystem services, soil pH was positively associated with soil C content, water retention and pest control, whereas, temperature was associated with organic matter decomposition and fertility, and precipitation seasonality with mutualism (Extended Data Figs. 2 and 3). Although many of these environmental associations are well-described in the literature (e.g., [26,27]), the fact that different soil ecological dimensions could be predicted by contrasting environmental factors was much less clear due to the lack of standardized global field surveys. These contrasting associations and environmental drivers explain the different global distributions found for each ecological dimension and reveal that important trade-offs may exist when considering nature conservation of multi-faceted soil systems. To further visualize these trade-offs, we used machine learning random forest spatial regression models together with available current data and future projections for both climate and land-use change (2015-2070), to predict the distribution of soil biodiversity and ecosystem services and assess their major drivers according to multiple future scenarios (shared socioeconomic pathways (SSP);

SSP1: global sustainability, SSP3: regional rivalry, SSP4: inequality, and SSP5: fossil-fueled development [28]). We standardized each of these spatial distributions and used a Getis-Ord Gi* spatial clustering algorithm to obtain a representation of the global hotspots (clusters of statistically high values) for the modelled distribution of each single biodiversity and ecosystem service variable. These were then aggregated into each soil ecological dimension (Fig. 1A, B, and C). To further strength our conclusions we performed a comparison across multiple methods (Supplementary Figs. 7 and 10) and an uncertainty assessment for the spatial predictions (Supplementary Figs. 5, 11, 12 and 13). A rationale supporting the spatial analysis from our standardized survey, and explaining the limitations of our approach, is available in the Method section.

Further, we showed that different ecological dimensions for soil conservation peak in different regions of Earth (Fig. 1A, B, C). Model fitness (measured as overall training R^2) varied between 0.855 and 0.914 for alpha diversity and community dissimilarity (Supplementary Table 5) and between 0.801 and 0.936 for ecosystem services (Supplementary Table 6). Hotspots of alpha diversity tend to have a wider distribution across the world, peaking in temperate and Mediterranean regions, as well as in alpine tundra (overall occupying between 30.9%, for archaea, and 42.4%, for bacteria, of the world). However, hotspots of community dissimilarity occur around two contrasting global conditions, tropical systems and drylands (overall occupying between 35.7%, for Archaea, and 43.0%, for Fungi, of the world). For Fungi, our results were further compared and validated with an independent dataset (Supplementary Fig. 6). While higher alpha diversity may intuitively imply a direct decrease in dissimilarity, directly varying in tandem, our results show that at the global scale this is not the case (Supplementary Table 15). Archaea showed the highest proportion of shared hotspot areas with 19%, with all other groups obtaining less than 8% (alpha diversity and community dissimilarity for the same taxa; Supplementary Table 3). Our findings further suggest the existence of important trade-offs in soil nature conservation priorities (Extended Data Fig. 3). For example, locations with higher alpha diversity tend to be less dissimilar, and only a small proportion of locations were found to support both high dissimilarity and alpha diversity (Fig. 1B). This proportion is smaller for fungi (3.9%) and higher for Archaea (19.0%; Supplementary Table 2). Similarly, locations with higher dissimilarity tend to have less soil C content, fertility, and higher proportion of plant pathogens (Extended Data Fig. 3). Moreover, our global maps indicate that alpha diversity (Fig. 1A), community dissimilarity (Fig. 1B), and ecosystem services (Fig. 1C) have their hotspots in mostly contrasting regions of the planet, existing only in a few locations supporting high levels of more than one of these dimensions (0.1% of the evaluated areas in the world; based on Fig. 1). This contrasts with results found for other biodiversity groups like plants and mammals [e.g., 29,30] and supports recent findings of a mismatch between soil biodiversity and

other taxonomic groups (Supplementary Table 13; [23]) While globally, tropical and arid systems were mostly classified as locations with relatively low alpha diversity across taxa, these areas are hotspots for soil community dissimilarity, supporting the most unique soil community assemblies (Fig. 1B). In the case of bacteria, for example, locations with high pH support a higher richness (e.g., in temperate systems); however, these are always similar organisms which thrive in neutral-alkaline soils. This suggests that, while local diversity in tropical systems may be low (e.g., as a consequence of acidic soils), these environmentally contrasting areas of the globe may harbor unique communities, which in turn may result in high gamma (regional) diversity. While this was already suggested in the past [16,22], the present study represents the first robust confirmation of this hypothesis.

Our results highlight the fact that preserving soils from a nature conservation perspective requires a holistic approach that considers multiple soil ecological dimensions such as alpha diversity, community dissimilarity, and ecosystem services in the context of a nature conservation profile (Fig. 1D). Being able to position a given area within this soil nature conservation profile allows to establish adequate conservation goals that effectively target the preservation of soil communities and their effects on ecosystems [31]. For example, an area that falls into a community dissimilarity hotspot may focus on indicators and conservation goals to track and prevent species losses, since these may be unique to its limits, while an area in an ecosystem service hotspot may favor indicators that target ecosystem service supply. This does not imply that conservation areas should not prioritize all soil ecological dimensions, but rather that management strategies and conservation targets should be adjusted to the ecological reality of each region and conservation area [2]. Moreover, while local approaches are still needed to refine the local distribution of these hotspots [32], these results also suggest that no particular region can protect all dimensions of soil conservation, making a further argument for global cooperation and for establishing global soil nature conservation targets.

Given the contrasting regions supporting the highest biodiversity and services, identifying which ecological dimension is the most relevant for the conservation of soil ecological conditions is not a simple task. Some ecosystems depend on a high alpha diversity while others do not need such high levels of alpha diversity to properly function but rely on more dissimilar soil communities (Fig. 1D; [33]). Conversely, while for microbial communities [34], functional redundancy driven by community composition may be more important than alpha diversity per se, in general terms, ecosystems with lower alpha diversity are likely to be more sensitive to ecosystem change [35] and for that, more targeted conservation actions are required. Although it is known that soil organisms play a crucial role in ecosystem service supply [36], it is not clear that it is biodiversity per se that governs this entire process. For example, some specific ecosystem services may depend on the presence of only a few

species, such as specific components of the soil nitrogen cycle [37], while others are the result of the activity of many species with high levels of redundancy, such as soil respiration [38]. Therefore, we defined priority areas for soil nature conservation as areas supporting relatively high levels of either soil biodiversity or ecosystem services. We were then able to identify key regions of the planet surpassing high thresholds of either biodiversity or ecosystem service provision - the hotspots for soil nature conservation - (Fig. 2). Considering the areas with the highest accumulation of soil biodiversity hotspots (top 5% of areas), it is possible to identify tropical systems and substantial areas in North America, in Northern Europe, and in Asia as having high priority for nature conservation (Fig. 2A). These areas maximize different dimensions of soil ecology and may thus require integrative strategies, not only from a nature conservation perspective but also considering the socio-economic appropriation of belowground systems. To this respect, it is striking that ~50% of these global nature conservation priority areas are not under any form of nature conservation, and that only ~10% correspond to areas fully preserved (Fig. 2B). Since these global soil nature conservation priority areas are the areas with the highest nature conservation relevance and given that currently soils do not have any specific nature conservation targets, this is a worrisome state for the conservation of soil biodiversity worldwide [2]. This situation is also observed if we consider other thresholds for the soil nature conservation potential (Fig. 2B). While soil conservation may not be able to maximize all ecological dimensions at the same time, and each region may have different specificities with specific research being required, a number of actions may be considered. These include nature-based solutions in land management for enhancing ecosystem services [39], landscape-level actions like the preservation of permanent forest and natural coverage in the surrounding of managed systems [40], or nature-based solutions focused on restoring or improving soil functional outputs [41]. Our work provides key information for regional and continental decision-makers to develop nature protection goals that specifically target soil systems and biodiversity, including identifying areas with high potential to establish soil-based nature conservation areas.

In the context of climate and land-use change, nature conservation areas and targets will need to adapt to new conditions and also focus on mitigating potential impacts [42–44]. Thus, focusing on the global soil nature conservation priority areas (top 5%), we conducted an additional analysis to predict the future changes in hotspots according to four shared socio-economic pathways (Fig. 3; 2015-2070). Our projections highlight the fact that the soil nature conservation hotspots will change as a result of climate and land-use change linked to substantial declines in both alpha diversity and ecosystem services. Globally, across scenarios, net differences between 2015-2070 range from 1.5% net gains in SSP3 and -12.2% net losses in SSP5. In most cases these net changes actually hide substantial losses of

current soil nature conservation priority areas with 7.1% (SSP4) to 17.5% (SSP5) of current areas being lost globally across different future scenarios (Supplementary Table 7). Our results reveal that most of the net area losses are related to declines in ecosystem services, particularly C stocks (average loss across scenarios = -6.8%) and mutualism (-3.8%) and litter decomposition (-3.6%), and in alpha diversity of specific groups, particularly invertebrates (-2.6%), fungi (-1.3%) and archaea (-1.1%). Our projections also show that new areas will emerge as key areas for soil nature conservation across the world, corresponding to expansions ranging from 5.3% in SSP5 (relative to the current area) to 9.5% in SSP3. Surprisingly, scenarios that consider higher challenges for adaptation to climate change motivated by higher regional income inequality and rivalry (SSP3 and SSP4; [45]), also show the most positive effects for maintaining or expanding current nature conservation priorities for soils, particularly in Africa and South America (Fig. 3). Overall, these positive effects are mostly expected in the global south, with systematic negative effects in the global north across scenarios. In fact, the only scenario where the global north has slight net gains (0.3-2.0%) corresponds to the so-called “sustainability scenario” (SSP1). Nevertheless, in this scenario, most of the rest of the world shows important net losses (-5.7% in Africa and -5.9% in Asia Pacific) or just mild net gains (0.8% in South America) due to expected increases in global economic development (Fig. 3). This is even more worrisome when considering recent reports that show that 30% of the population across tropical countries are highly dependent on nature [46]. Across all regions, the fossil-fueled economy scenario (SSP5) produces the strongest net losses, with regions losing priority areas from -5.9%, for Asia-Pacific, to -31.8%, in the case of North America (with most of these losses being driven by decreases in ecosystem services). Furthermore, our results suggest that the current simplistic view on carbon-based targets provides little protection for all soil ecological dimensions. In fact, the sustainability scenario shows an overall global improvement in ecosystem services, with soil C leading these improvements but with clear losses in alpha diversity. Together, these results indicate that hotspots of soil biodiversity and ecosystem services are highly threatened by future climatic and land-use changes, and stress the need for immediate protection of these locations. Our findings also suggest that these hotspots might move in the future, with current sanctuaries of soil biodiversity being subject to degradation.

In summary, based on the largest global standardized survey, including sixteen biodiversity and ecosystem service variables, our work provides the first estimate of the global hotspots for nature conservation of multiple soil ecological dimensions. Here, we identified critical unique areas for the conservation of soil biodiversity and ecosystem services at the global scale, with soil alpha diversity, dissimilarity, and services peaking in temperate, tropical, and boreal regions, respectively. While recent literature highlights the need for extending nature

conservation to ensure global sustainability and the preservation of biodiversity [47], it also underlines that this increased protection requires context-based solutions [48]. By unveiling important trade-offs in soil biodiversity and ecosystem services, we also highlighted that no particular region of the world could simultaneously protect all soil ecological dimensions. Therefore, the conservation of soil biodiversity and ecosystem services requires an integrated approach that probably should not focus on locally maximizing all ecological dimensions at the same time. Also, the fact that we found that these three ecological dimensions do not necessarily match in terms of their spatial hotspots also showed the complexity of soil ecosystems and highlighted the difficulty that land managers and policymakers face when designing soil conservation measures. Nevertheless, we also showed that these nature conservation priority areas are currently highly unprotected, with less than ~10% of these locations under adequate conservation status. We acknowledge that our study is just a first step towards understanding and mapping the global hotspots of soil nature conservation and that high-resolution monitoring systems and multiple time periods are needed to better guide regional conservation and policy options [2]. Still, our work suggests that current priority areas of soil nature conservation are vulnerable to global change drivers in all future scenarios considered, and stresses the need for immediate nature conservation targeting and protection of these regions. This novel information and indicators should enable governments and decision-makers to set soil nature conservation as a priority in the context of the 2030 Biodiversity Targets negotiations, paving the way for a more integrative view of nature.

Author contributions

C.A.G. and M.D-B. developed the original idea of the analyses presented in the manuscript. M.D.-B. designed the field study and wrote the grant that funded the work. Field data were collected by M.B., S.A., F.D.A., A.R.B., J.L.-B., A.d.l.R., J.D., T.G., J.G.I., Y-R.L., T.P.M., S.M., M.A.M-M., A.M., T.U.N., G.F.P-B., C.P., J.P.V., A.Re., A.R., A.L.T., C.T-D., P.T., L.W., J.W., E.Z., X.Z., X-Q. Z. and M.D-B. Lab analyses were done by M.D-B., H.C., F.B., J.L.M., S.P. and L.T. Statistical analyses, mapping and ecological modelling was done by C.A.G., M.D-B. and M.B.. Bioinformatic analyses were done by B.S. and J-T.W. The manuscript was written by C.A.G. and M.D-B., edited by N.E. and D.E., with contributions from all co-authors.

Data and code availability

All the materials, raw data, and protocols used in the article are available upon request and without restriction, and all data is be made publicly available in: 10.6084/m9.figshare.20221713

Competing financial interests

The authors declare no conflict of interest.

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Fig. 1 Current distribution of global soil ecological hotspots. The proportion of land occupied by hotspots of alpha diversity (A), community dissimilarity (B) and ecosystem services (C) (Supplementary Table 2; Extended Data Fig. 4 and 5). The top row corresponds to the proportion of global area occupied by single taxa (A, B) or ecosystem services (C), and the bottom row to the global representation of accumulated hotspots across taxa (A, B) or ecosystem services (C). Together, these three soil ecological dimensions create a soil nature conservation profile where both areas that maximize a given dimension and areas that allow for preserving a combination of global soil biodiversity hotspots are identified (D). Grey areas correspond to areas that were not assessed during calculation due to high uncertainty and insufficient environmental coverage (corresponding to 38.4% of the terrestrial world; Supplementary Figure 5). A further estimation of spatial uncertainty for each dimension considered is given in Supplementary Figures 12 and 13.

Fig. 2 Current distribution of the global soil nature conservation priority areas. Spatial representation of the top 5%, 10%, 20%, and 30% areas with the highest accumulation of soil biodiversity and ecosystem services hotspots (A), and the proportion of those areas that are under some form of nature conservation regime (B). Grey areas correspond to areas that were not assessed during calculation.

Fig. 3 Expected changes (2015-2070) in the total area of soil nature conservation priorities (top 5%) according to 4 different future shared socio-economic pathways (SSP1, SSP3, SSP4, and SSP5 [28]).

ECA: Europe and Central Asia, NMA: North and MesoAmerica, SA: South America, AP: Asia-Pacific, Af: Africa. Light grey areas correspond to areas that were not assessed during calculation.

Methods

A global standardized survey to investigate topsoil biodiversity and function

We used composite topsoil samples from global field surveys which were conducted between 2016-2019 following standardized field protocols. This global field survey includes 151 locations from all continents and 23 countries, from which 615 composite topsoil samples were collected, providing a large representation of all climatic and vegetation biomes in the planet (Supplementary Fig. 1). The locations of the soil samples was not established following a random protocol but rather were selected taking into account the local representativeness of the vegetation within the ecosystem types sampled. In global terms, the approach aimed to include as much climatic and edaphic variability as possible given the constraints of such a sampling scheme. Between three and five composite soil (top ~0-10cm) samples (from 5-10 soil cores) were collected in these locations (ranging between 0.09-0.25 ha) following the protocol described in Maestre et al. (2012). By including multiple composite samples within each location, we aimed to account for within-location heterogeneity variation in soil properties, biodiversity and services. We focused on the topsoils, because they are known to hold the largest portion of soil biodiversity, and constitute the critical zone supporting key soil processes from OM decomposition to plant-soil interactions. A portion of these soils was frozen (-20 ºC) after sampling for molecular analyses, while another portion was air-dried and used for determining soil properties. We recognize that while our dataset provides a quite complete coverage of global environmental conditions, an increase of sampling locations in less represented regions of the globe would increase the strength of the study. To this respect, we aimed at adequately representing the spatial limitations of our study by eliminating and masking out all the regions that were poorly represented (Supplementary Figure 5). It is also important to mention that reaching this spatial representation is not a trivial endeavor with several logistic limitations (e.g., absence of local resources for sample preservation and consequent material degradation; [25]), and overshadowed by war and current transport embargos. These issues disproportionally affect these underrepresented regions and result in important gaps in Africa and South-East Asia. Dataset available here: figshare.com/s/fb33c5a79f cee29e70dc

Soil biodiversity

The alpha diversity (corresponding to the number of phylotypes) and community dissimilarity (averaged Jaccard distance across samples from presence/absence matrices to account for dissimilarity in phylotypes, measured as ASVs, rather than in their proportions) of archaea, bacteria, fungi, protists and invertebrates was determined using amplicon sequencing technology (Illumina Miseq platform) following the protocol in Delgado-Baquerizo et al. (2019). Both these measurements are critical to understand the nature and conservation potential of specific areas. While alpha diversity refers to the number of species (or ASVs in this case) contained in a particular location, typically seen as priority areas for nature conservation, community dissimilarity refers to the uniqueness of the community, signaling the presence of specific species that are not common elsewhere. The later also represents a critical aspect for the selection of new conservation areas [49]. Soil DNA was extracted using the Powersoil® DNA Isolation Kit (MoBio Laboratories, Carlsbad, CA, USA) according to the manufacturer's instructions. A portion of the bacterial/archaeal 16S and eukaryotic 18S rRNA genes were sequenced using the 515F/806R and Euk1391f/EukBr primer sets [50–52], respectively.

Bioinformatics processing was performed using a combination of QIIME [53], USEARCH [54] and UNOISE3 [55,56]. Phylotypes (i.e. Amplicon sequence variant; ASVs) were identified at the 100% identity level. The ASV abundance tables were rarefied at 5000 (bacteria via 16S rRNA gene), 100 (archaea via 16S rRNA gene), 2000 (fungi via 18S rRNA gene), 1000 (protists via 18S rRNA gene), and 250 (invertebrates via 18S rRNA gene) sequences/sample, respectively, to ensure even sampling depth within each belowground group of organisms. Protists are defined as all eukaryotic taxa, except fungi, invertebrates (Metazoa) and vascular plants (Streptophyta). Note that not all samples passed our rarefaction cut-off. The total number of samples included in each soil group is available in Supplementary Table 2.

Library preparation and Sequencing

Triplicate PCR reactions were performed for each of the extracted DNA samples, and we included and sequenced multiple negative controls per plate to check for possible contamination. Each 25µl PCR reaction contained: 12.5µl of Promega GoTaq Hot Start Colorless Master Mix; 0.5 µl of each barcoded primer (bacterial 16S, 515F [5´-GTGCCAGCMGCCGCGGTAA-3´] and 806R [5´-GGACTACHVGGGTWTCTAAT-3´] OR eukaryotic 18S, Euk1391f (5´-GTACACCGCCCGTC-3´) and EukBr (5´-TGATCCTTCTGCAGGTTCACCTAC-3´); 10.5 µl water; 1 µl of template DNA. 'Fusion' primers also included Illumina adapters and 12-bp barcodes to enable multiplexed sequencing. PCR conditions for bacterial 16S rDNA amplifications were 94ºC for 3min; 35 cycles of 94ºC for 45s, 50ºC for 60s, 72ºC for 90s; 72ºC for 5 min. PCR conditions for eukaryotic 18S rDNA amplifications were 94ºC for 3 min; 35 cycles of 94ºC for 45s, 57ºC for 60s, 72ºC for 90s; 72ºC for 10 min. PCR products were cleaned with the MoBio Ultra Clean PCR Clean-Up Kit. Next, we performed PCR-mediated Nextera barcode ligation following the manufacturer's instructions, adding unique barcodes onto amplicons, to allow for multiplexed sequencing. Samples were normalized with the SequalPrep Normalization Plate Kit (Invitrogen) prior to sequencing on the Illumina MiSeq platform.

DNA was first cleaned up using AMPure Xp beads (Beckman Coulter, California, USA) and then quantified using the automated fluorescence-based PicoGreen assay (Invitrogen, Massachusetts, USA). The cleaned DNA was normalized to 1.5 ng/µl and a total of 7 ng of the input DNA was used for each amplicon PCR reaction. Illumina's instruction does not recommend pooled three PCRs (which shouldn't be considered as technical replicates), and one PCR reaction was performed per amplicon. While to minimize the PCR bias in the sequencing, the number of PCR cycles was reduced to 25. In detail, the PCR conditions for bacterial 16S rDNA amplification are: 95 °C for 3 min, 25 cycles of 95 °C for 30 sec, 55 °C for 30 sec, 72 °C for 30 sec, 72 °C for 5 min then hold at 4 °C; and PCR conditions for eukaryotes 18S rDNA amplification is: 94 °C for 5 min, 30 cycles of 94 °C for 30 sec, 55 °C for 30 sec, 72 °C for 30 sec, 72 °C for 5 min then hold at 4 °C. The Illumina forward overhang (5'-TCGTCGGCAGCGTCAGATGTGTATAAGAGACAG-3') and reverse overhang (5'-GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAG-3') adapters were included in the amplicon PCR. Each sample was barcoded with two 8 base indices using the Illumina Nextera XT Index Kit. The 15 ul reaction system was prepared with KAPA HotStart ReadyMix Kit (Merck KGaA, Darmstadt, Germany). A ZymoBIOMICS Microbial Community DNA Standard was used as a positive control together with the samples to assess the bias in PCR. Molecular analysis of the full-length ITS region for fungi was performed using ITS9mun/ITS4ngsUni primer sets and PacBio third-generation sequencing as described in [57].Our sequencing run yielded 3861042 fungal sequences (18s), 534286 invertebrate sequences (18s), 2388020

protist sequences (18s), 8901512 bacterial sequences (16s), and 168749 archaeal sequences (16s).

Bioinformatics

Bioinformatic processing was performed using a combination of QIIME, USEARCH and UNOISE. Briefly, data was demultiplexed and primers were trimmed before further analyses. Default parameters were followed in USEARCH pipeline, except for the bases with a quality score lower than 20 were end-trimmed from the forward/reverse primer reads to minimize the mismatch in merging and to maximize the portion of successful mergers. A maximum of expected error (ee) was set as 1.0 for the merged reads quality filtering using USEARCH (Edgar 2010). zOTUs (or Amplicon Sequence Variant) were gained by denoising (error-correction) the dereplicated merged reads using unoise3 (Edgar 2016). Representative sequences of ASVs were annotated against the Silva database (Quast et al. 2012) in QIIME (Caporaso et al. 2010) using UCLUST [54]. 18S taxonomy annotation used both SILVA and Protist Ribosomal Reference database (PR2, https://pr2-database.org/)[58]. Resultant ASV tables were rarefied at 5000 (bacteria via 16S rRNA gene), 100 (archaea via 16S rRNA gene), 2000 (fungi via 18S rRNA gene), 1000 (protists via 18S rRNA gene), and 250 (invertebrates via 18S rRNA gene) sequences/sample, respectively, to ensure even sampling depth within each belowground group of organisms. They were then imported into QIIME [53]for downstream analysis including diversity and community composition.

Rarefaction resolution and primer set cross-validations

Rarefaction resolution

First, we conducted additional analyses to provide evidence that our choice of rarefaction level did not affect our results or conclusions. Here, using the samples with the highest sequence/sample yield, we tested for the impact of different levels of rarefaction on soil biodiversity. We found highly statistically significant correlations between the diversities of soil archaea (rarefied at 100 vs. 500 sequences/sample; Spearman $\rho = 0.764$; $P < 0.001$; $n = 128$), bacteria (rarefied at 5000 vs. 10000 sequences/sample; Spearman $\rho = 0.992$; $P < 0.001$; $n = 509$), fungi (rarefied at 2000 vs. 10000 sequences/sample; Spearman $\rho = 0.971$; $P < 0.001$; $n = 88$), protists (rarefied at 1000 vs. 5000 sequences/sample; Spearman $\rho = 0.971$; $P < 0.001$; $n = 287$) and invertebrates (rarefied at 250 vs. 1000 sequences/sample; Spearman $\rho = 0.952$; $P < 0.001$; $n = 274$), for a subset of samples wherein high numbers of sequences were available. These results are supported by previous independent global surveys providing evidence that rarefaction options do not influence global patterns in microbial communities [59,60]. See rarefaction curves in Supplementary Figure 3.

Primer set cross-validation

Then, we provide additional evidence that primer sets are not influencing the global patterns reported here. For a subset of samples, we generated additional molecular information for fungal (ITS PacBio sequencing; ITS9mun/ITS4ngsUni primer sets) and bacterial (16s rRNA Miseq Sequencing; 341F/805R primer sets) data. We found that the richness soil microbial communities used in this study were highly significantly and positively correlated to those using these alternative primer sets both for bacteria (Spearman $\rho = 0.403$; $P < 0.001$; $n = 128$) and fungi (Spearman $\rho = 0.656$; $P < 0.001$; $n = 228$). Similarly, the community composition of bacteria (Spearman $\rho = 0.479$; $P < 0.001$; $n = 128$) and fungi (Spearman $\rho = 0.414$; $P < 0.001$;

n = 228) were significantly and positively correlated to those using these alternative primer sets. More importantly, we also found that the main predictors of bacterial and fungal richness (soil pH in both cases; Supplementary Fig. 2) in this study followed the same pattern for bacterial and fungal richness using alternative primer sets (Supplementary Fig. 4). We would like to further highlight that the 18s primer sets used here to describe protists and invertebrates are the gold standard for the sequencing of these organisms [52,61] and have been previously cross-validated in the literature [62–64]. We acknowledge that there are multiple alternative primer sets, especially when specifically targeting particular groups of organisms within protists (e.g., mtDNA COI gene). Nevertheless, while specific primers may deliver higher resolution for specific groups, these are known to be inefficient in identifying a wide range of organisms from environmental samples [65].

Mapping the distribution of fungal functional guilds

Finally, to provide further evidence that 18s rRNA Miseq Sequencing can in this case provide a solid representation of the global patterns in soil-borne mycorrhizal fungi and fungal potential plant pathogens, we compared the global patterns (see mapping method below) in the proportion of soil-borne mycorrhizal fungi and fungal potential plant pathogens determined using 18s rRNA Miseq Sequencing with the subset of data including ITS PacBio sequencing (see above). Our results showed that the proportion of soil-borne mycorrhizal fungi and fungal potential plant pathogens determined using two independent methods followed similar patterns and had a strong and positive correlation worldwide (Supplementary Fig. 6 and Table 8 and 9), allowing us to tentatively use the 18S rRNA gene as a proxy for phylotype richness. The number of AMF phylotypes retrieved from ITS PacBio sequencing was not enough to conduct this analysis, so we used Ectomycorrhizal fungi in our mapping comparison.

Soil ecosystem services

Six soil functions directly related to key ecosystem services were determined using highly standardized methods: water retention (water holding capacity), fertility (nitrogen, phosphorus, potassium, and magnesium content), carbon storage (total soil organic carbon content), mutualism (proportion of arbuscular and ectomycorrhizal fungi), pest control (inverse of the proportion of soil-borne potential plant pathogens; as defined here [66]) and OM decomposition (three enzymes associated with C, N and P cycle). Percentage of water holding capacity was determined as in [67]. Soil nitrogen was determined using a CN analyzer. Soil phosphorus, potassium, and magnesium concentrations were determined using ICP (Inductively Coupled Plasma) Spectroscopy after acid digestion [68]. Total soil organic C content was determined from CN analyzer (after removing soil carbonates) and wet-chemistry methods [59]. The proportion of soil-borne fungal potential plant pathogens and fungal plant-soil mutualistic organisms (arbuscular and ectomycorrhizal fungi) were determined as the sum of all taxa classified as such from Funguild [69] using our 18S dataset. We found Funguild information for 297 ASVs of arbuscular mycorrhizal fungi, 217 ASVs of ectomycorrhizal fungi, and 165 ASVs of soil-borne potential fungal plant pathogens. Pest control was calculated as the inverse of the proportion of soil-borne potential plant pathogens (-1 x proportion) as done in [66]. Thus, locations with higher levels of pest control also have lower proportions of plant pathogens. We only focused on those taxa supporting unique trophic life styles. The activity of phosphatase (phosphorus mineralization), beta-glucosidase (starch degradation) and N-acetyl-β-glucosaminidase (chitin degradation) was determined as in [70] using a high-throughput fluorescence microplate method. The exact number of available information might differ for

different ecosystem services (available in Supplementary Table 2). The total number of samples available for each soil attribute is available in Supplementary Table 2. We calculated ecosystem services as the standardized (0-1) average of soil attributes within each ecosystem service (e.g., Fertility: N, P, K and Mg; Mutualism: arbuscular and ectomycorrhizal fungi; OM decomposition: phosphorus mineralization, chitin and starch degradation) using a multifunctionality approach [71]. Furthermore, we acknowledge that the number and type of ecosystem services considered here might be limited to characterize the range of ecological functions driven by soil communities. Therefore, for a subset of the data where other variables are available, we correlated our ecosystem services to additional information on carbon content, enzymes, nutrient availability from IEMS (a proxy of N mineralization; [72]) and metagenomics (see Supplementary Table 10).

Environmental data

Elevation and climatic information for each location was obtained from WorldClim v2 (1 km^2 resolution; https://www.worldclim.org/data/bioclim.html), including information on climatologies and on the seasonality of temperature and precipitation. Soil pH was determined with a soil pH-meter from a soil-water mix [73]. Texture was determined as in Maestre et al. [73] and, in the case of missing information, this was filled using Soilgrid v2 (https://soilgrids.org; as in [16]). Information on dominant vegetation (forest, shrublands or grasslands) was obtained as part of the field survey.

Drivers of soil biodiversity and services

To investigated the environmental factors associated with soil biodiversity and services, we first used machine learning Random Forest modeling [74]. We used the R package "rfpermute" to conduct these analyses. To further strengthen our results, we repeated the same analysis using XGboost algorithms [75,76]. XGboost allows for fine-tuning of the model outcomes, and thus results are interesting for answering not only this comment by the reviewer but also the next four comments. In brief, we used a gbtree booster using as an objective function the RMSE using k-fold cross-validation. We tunned the ETA (learning rate), min_chld_weight, max depth, resample, gamma and nfold [77] using a Bayesian optimization approach with the package "ParBayesianOptimization" in R [78]. This allows for efficient implementation of an optimizing search. The parameter we decided to optimize was the test rmse (rather than the train one), in order to prevent overfitting [79]. The number of trees fitted was also estimated on this criterion using the function xgb.cv from package xgboost in R with 10% of data as validation set. As feature importance, we extracted the gain obtained in predictive, using the function xgb.importance (the results for this second analysis can be found in Supplementary Figure 7; Supplementary Table 11 and 12). Here we chose to train the resulting models using the function xgcv, which fits from 1 to 200 trees to the data and confronts trained models to the cross-validation set. We chose to use the number of trees that minimized the test RMSE. In general, this procedure allows to prevent overfitting (whereas train RMSE might continue being improved, the point where validation RMSE is minimized corresponding to the maximum learning ability without overfitting. In the new analyses, we parameterized 8 important hyperparameters, including the number of trees (nroud) and the number of features (colsample_bytree). A full table of the resulting parameters is reported in Supplementary Table 11). To further strength our analysis, we compared the results obtained with our approach with results obtained using a GAMM model (considering random factors). GAMMs were performed by flooring coordinates (latitude and longitude) and using their combination as a random factor:

("mdl=gamm(data = ddi,formula = y~s(Latitude)+s(Longitude.cosine)+s(Longitude.sine)+s(s_elev)+Forest+Grassland+Shrubland+ s(s_MAT)+s(s_TSEA)+s(s_PSEA)+s(s_MAP)+s(s_SOC)+s(s_Texture)+s(s_pH) random = list(RF=~1))"; being RF the floored combination of latitude and longitude: "dd$RF=as.factor(paste(floor(coords$long),floor(coords$lat)))"). This approach allows to control for spatial autocorrelation, apart from the nested structure of our data. Our results show (Supplementary Fig. 10) that the GAMM model provided highly correlated results (Spearman correlations >0.7) for all variables considered and almost identical (very aligned to 1:1 line) predictions to the machine learning algorithms used in our manuscript, suggesting that the type of modelling (e.g., Random Forest vs. GAMM) does not influence our results and conclusions. We also conducted Spearman correlations to better describe the direction of the relationship between environmental factors and soil biodiversity and services. We also correlated all soil biodiversity and services attributes looking for potential trade-offs using Spearman rank correlations. All the analyses in this section are non-parametric, and are especially recommended when dealing with both linear and non-linear relationships. Analyses were done at the sample level to account for within-location variation in soil properties, biodiversity and services.

Global hotspots of soil biodiversity and services

We used spatially explicit random forest models to predict the distribution of each soil biodiversity and ecosystem service variable. We were able to do these spatial analyses for three main reasons: (1) the high-quality standardized biodiversity and ecosystem service dataset wherein biodiversity and services are measured for the same samples, and analyzed using the same protocols; (2) biodiversity and ecosystem services were highly correlated with key environmental factors at the global scale (Extended Data Figs. 2-3); and (3) the large gradient of environmental conditions in our global dataset covers a large portion (61.6% based on a Mahalanobis analysis) of the large scale environmental variability of the planet. Note that we further spatially constrained our analyses to exclude all environmental outliers [22,80].

To map each soil biodiversity and ecosystem service variable we used spatially explicit random forest models. For that, we used ArcGIS Pro that estimates random forest models by using an adaptation of the random forest algorithm (a supervised machine learning regression approach) proposed by Breiman et al. [74,81,82]. Forest-based regressions were trained based on 90% of the dataset, the remaining 10% of the dataset were used for validation purposes. Regression training and validation parameters are given in Supplementary Tables 5 (for Alpha diversity and Community dissimilarity) and 6 (for Ecosystem services). The fitted prediction model was then used to predict the unknown space using a prediction dataset that included all environmental explanatory factors i.e., elevation, carbon, pH, fine texture, mean annual temperature and precipitation, temperature and precipitation seasonality, forest, grassland, shrubland. In the case of the analyses related to the ecosystem services, carbon was excluded from all the models. All models were fitted using 1000 runs for validation and fitting. Prior to prediction all variables included in the dataset and the predictors were resampled to 0.25 degrees using an average estimator and scaled. All predictions were made using a 0.25x0.25 deg. pixel size. All environmental variables used for spatial projection are listed in Supplementary Table 14.

Global hotspots were then calculated using a Getis-Ord Gi* spatial clustering method [83–85]. The Getis-Ord Gi* statistic was calculated for each location (0.25x0.25 deg. pixel) in the

dataset. The resulting z-scores were used to estimate if a given location has statistically high or low values and if these values are spatially clustered. This is done by assessing each location within the context of neighboring locations. Statistically significant positive z-scores indicate clustering of high values (hot spot) and statistically significant negative z-scores the clustering of low values (cold spot). Values for classifying hotspots (positive z-scores) for each variable were taken from the 99% confidence interval. Getis-Ord allows the use of the False Discovery Rate (FDR) correction, which was also applied here, and adjusts the statistical significance of a hot-spot detection to account for multiple testing (with a confidence level of 0.95) and spatial dependency [86]. This analysis resulted in a hotspot map for each combination, i.e., five hotspot maps for alpha diversity, five for community dissimilarity, and six for ecosystem services (Extended Data Figs. 4 and 5). We then overlayed the maps for each ecological dimension (i.e., by summing the hotspot maps for each variable in each ecological dimension: alpha diversity, community dissimilarity, and ecosystem services) to obtain a global representation of soil biodiversity hotspots, where a high value corresponds to a concentration of hotspots across multiple taxa or ecosystem services (Fig. 1A, B, and C)

Spatial uncertainty estimations

One of the difficulties of performing prediction of response variables using a new input dataset is the fact that the new input environmental values might differ substantially from values used to estimate the models. Therefore, estimating uncertainties on the environmental coverage of the datasets as well as the estimations of both biodiversity and ecosystem services is a complex but necessary requirement in such scenario modelling approaches [87]. For this, we have implemented a two-stage approach to tackle both the assessment of the environmental representation of the soil biodiversity and ecosystem services dataset used and the uncertainty related to the estimation of each variable or group of variables. Regarding the first, we calculated the Mahalanobis distance in multidimensional space (here considering the twelve dimensions given by the environmental variables used for modelling (i.e., elevation, carbon, nitrogen, pH, fine texture, mean annual temperature and precipitation, temperature and precipitation seasonality, forest, grassland, shrubland) and centered on the known distribution given by the characteristics, for the same environmental variables, of the soil biodiversity and ecosystem service dataset. This analysis calculates the distance of any point in space to the statistical center, given by the multivariate mean (considering all environmental variables used) of the known distribution. It is often used to detect outliers in point cloud distributions that are assumed to follow a multivariate Normal distribution [80,88]. The Mahalanobis distance follows a Chi-squared distribution with d degrees of freedom, where d is the dimension of the multidimensional space (d = 12 in our case). Environmental outliers were estimated for a Chi-square of 0.9 (areas in grey in Supplementary Fig. 5).

Although this distance is an informative measure of how close a new data point is to the distribution of points in space used to estimate each model, we used a second measure to assess the spatial uncertainty of the estimated values for each model. In order to do this analysis, for each soil biodiversity and ecosystem service variable, we calculated 1000 random iterations of each random forest model and estimated the upper and lower 25% quantile of the distribution of values. We then evaluated uncertainty as the difference between the upper and the lower level of the iteration space for each individual variable. An average representation for each dimension is given in Supplementary Fig. 5.

Projections of soil biodiversity and ecosystem services under global change scenarios

For the projections of soil biodiversity and ecosystem services, we used the available datasets from the Inter-Sectoral Impact Model Intercomparison Project (ISIMIP) [89] and from the land-use Model Intercomparison Project (LUMIP)[90] both activities from the Intergovernmental Panel for Climate Change (IPCC). The selection of scenarios followed the protocol laid out by [91].

In terms of climate change projections, we used a bias-corrected future projections dataset for both precipitation and temperature related variables [89]. We considered three Representative Concentration Pathways RCP2.6, RCP6.0, and RCP8.5 [89] with forcing data from three different general circulation models, the IPSL-cm5a-lr, gfdl-esm2m, and noresm1-m [92]. For land-use projections, we used the dataset provided by the land-use Harmonized v2.0 project (http://luh.umd.edu/) [28,93,94]. This dataset was produced in the context of the World Climate Research Program Coupled Model Intercomparison Project 6 (CMIP6) [28,45,95,96] and contains a harmonized set of land-use scenarios that are consistent between historical reconstructions and future projections. These modeled projections reproduce annual land-use reconstructions for different integrated assessment models (IAMs) and shared socioeconomic pathways (SSP, from 2015 to 2100) at 0.25 degrees resolution, which was developed and widely used to support future biodiversity projections [97,98]. These shared socioeconomic pathways represent a range of plausible futures based on different socioeconomic challenges for climate change mitigation (low in SSP1 and SSP 4; high in SSP3 and SSP5), and potential challenges for adaptation (low in SSP1 and SSP5; high in SSP3 and SSP4). While full descriptions of these pathways and scenarios are given in [28] we provide here a summary of the main characteristics (based on [45]):

SSP1: in SSP1 the world shifts gradually, but pervasively, toward a more sustainable path, with its focus on achieving the global development goals, increasing environmental awareness, and a gradual move toward less resource intensive societies. Currently, emerging economies have followed the resource-intensive development model of industrialized countries, but in SSP1, with the focus on equity, and the de-emphasis of economic growth as a goal in high-income countries, leads industrialized countries to support developing countries in their development goals, including green growth strategies, by providing access to human and financial resources and new technologies.

SSP3: in SSP3 a resurgent nationalism, concerns about competitiveness and security, and regional conflicts push countries to increasingly focus on domestic or, at most, regional issues. International fragmentation and a world characterized by regional rivalry can already be seen in some of the current regional rivalries and conflicts, but contrasts with globalization trends in other areas. Regional conflict over territorial or national issues produces larger conflicts between major countries, giving rise to increasing antagonism between and within regional blocs, reducing support for international institutions and weakening progress toward the global development goals, particularly in some middle-income countries.

SSP4: in SSP4 highly unequal investments in human capital, combined with increasing disparities in economic opportunity and political power, lead to increasing inequalities and stratification both across and within countries. Both across- and within-country inequality is assumed to arise from biased technology development, generally low and highly unequal investments in education resulting in increased restricted access, and reinforced wealth inequality. This pathway assumes that growth is substantially smaller than it is today, but does not assume that it is halted entirely. It also assumes an increased conflict over energy

resources between consuming countries and producing countries, particularly if resources are further constrained.

SSP5: in SSP5 there is a foreseen acceleration in globalization and rapid development of developing countries. The digital revolution enables an enhanced global discourse which may lead to a rapid rise in global institutions and promote the ability for global coordination. This pathway is driven by the economic success of industrialized and emerging economies to produce rapid technological progress and development of human capital as the path to sustainable development. Global markets are increasingly integrated, with the push for economic and social development coupled with the exploitation of abundant fossil fuel resources and the adoption of resource and energy intensive lifestyles around the world. All these factors lead to rapid growth of the global economy. There is the ability to effectively manage social and ecological systems, including by geo-engineering if necessary. While local environmental impacts are addressed effectively by technological solutions, there is relatively little effort to avoid potential global environmental impacts due to a perceived tradeoff with progress on economic development.

All temporal changes (2070 minus 2015, using forecasting predictions) were calculated using 2015 as a baseline to which all future predictions were compared.

Methods References

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Extended Data Figures

Extended data Fig. 1 Results of Random Forest analysis to identify the main environmental factors associated with soil biodiversity and ecosystem services. Random Forest analyses were done using the rfPermute function of the R package with the same name. MSE = Mean Square Error.

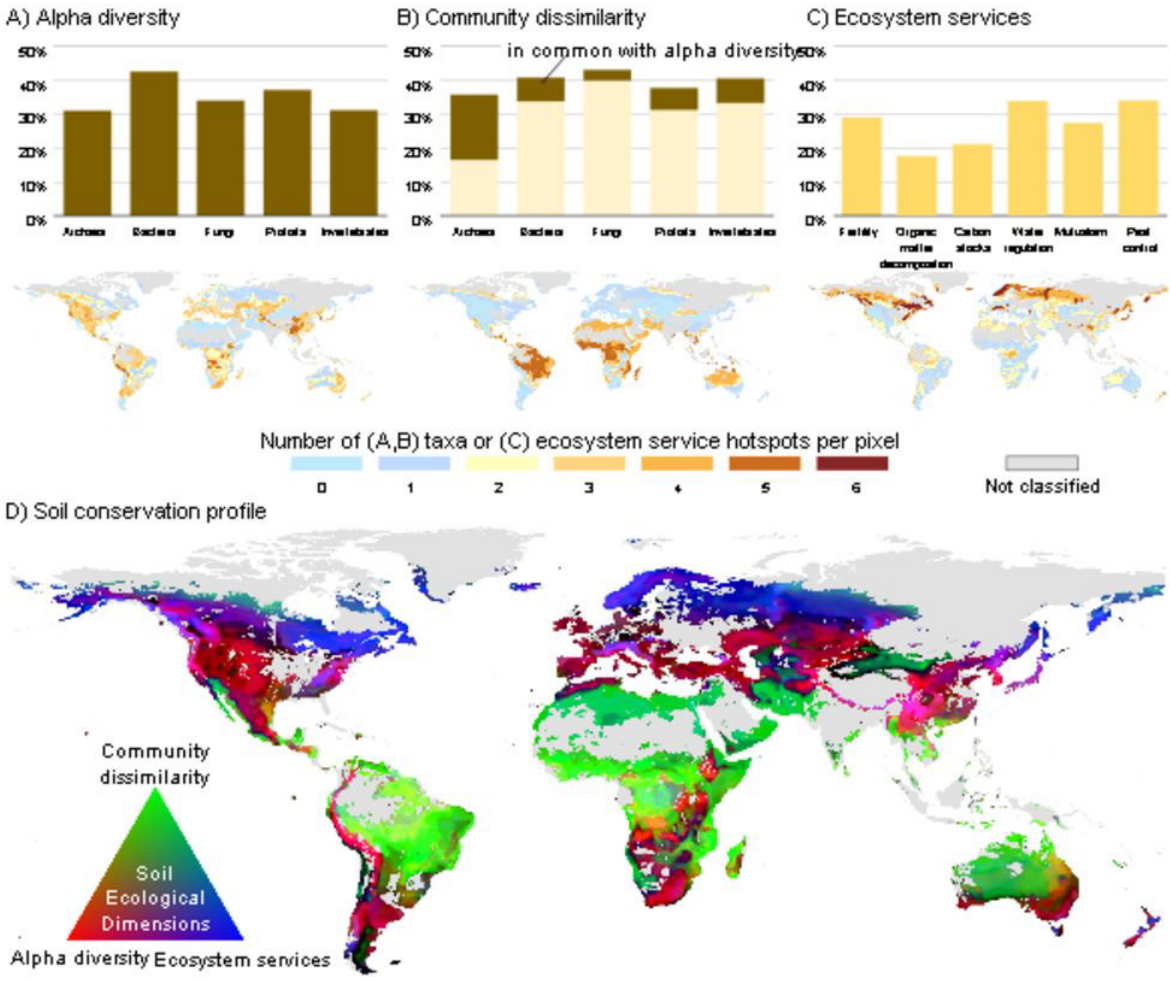
Extended data Fig. 2 Spearman correlations between environmental factors and soil biodiversity and ecosystem services. N in Supplementary Table S1.

Extended data Fig. 3 Spearman correlations between soil biodiversity and ecosystem services. Total n-values in Supplementary Table S1.

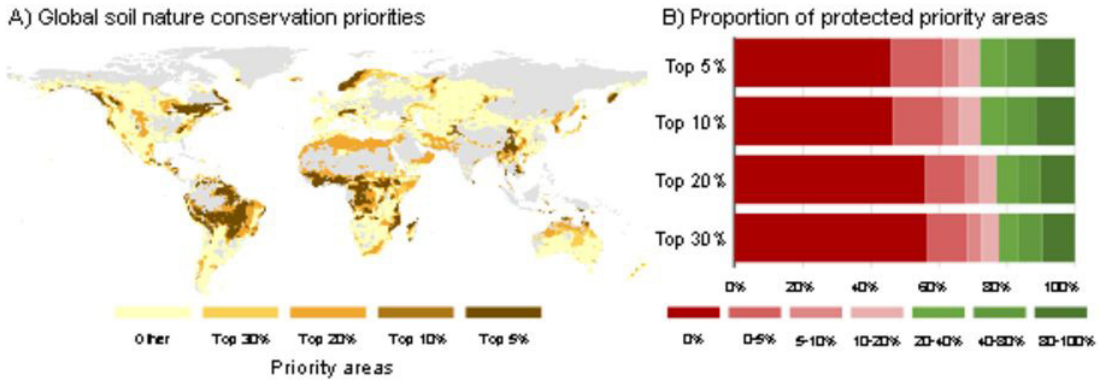
Extended data Fig. 4 Hotspot and coldspot maps for alpha diversity (left) and community dissimilarity (right). The Getis-Ord Gi* statistic was calculated for each location (0.25x0.25 deg pixel size) in the dataset 1–3. The resulting z-scores were used to estimate if a given location has statistically high or low values and if these values are spatially clustered. This is done by assessing each location within the context of neighboring locations. Statistically significant positive z-scores indicate clustering of high values (hotspot) and statistically significant negative z-scores the clustering of low values (coldspot). Values are plotted for both positive (hotspots) and negative (coldspots) 99%, 95%, and 90% confidence levels.

Extended data Fig. 5 Hotspot and coldspot maps for ecosystem services: soil carbon, fertility, OM decomposition, pest control, mutualism, water retention. The Getis-Ord Gi* statistic was calculated for each location (0.25x0.25 deg pixel size) in the dataset 1–3. The resulting z-scores were used to estimate if a given location has statistically high or low values and if these values are spatially clustered. This is done by assessing each location within the context of neighboring locations. Statistically significant positive z-scores indicate clustering of high values (hotspot) and statistically significant negative z-scores the clustering of low values

(coldspot). Values are plotted for both positive (hotspots) and negative (coldspots) 99%, 95%, and 90% confidence levels.

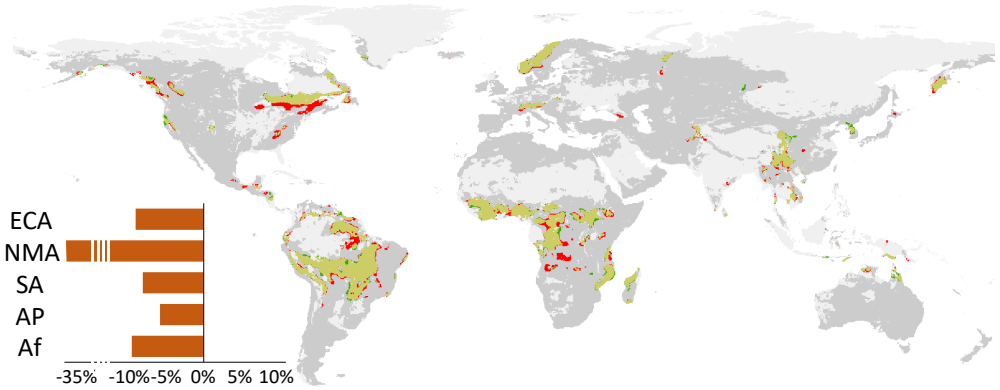

A) Alpha diversity
B) Community dissimilarity
in common with alpha diversity
C) Ecosystem services
50%
40%
30%
20%
10%
0%
Archaea
Bacteria
Fungi
Protists
Invertebrates
Fertility
Organic matter decomposition
Carbon stocks
Water regulation
Mutualism
Pest control
Number of (A,B) taxa or (C) ecosystem service hotspots per pixel
0
1
2
3
4
5
6
Not classified

D) Soil conservation profile
Community dissimilarity
Soil Ecological Dimensions
Alpha diversity
Ecosystem services

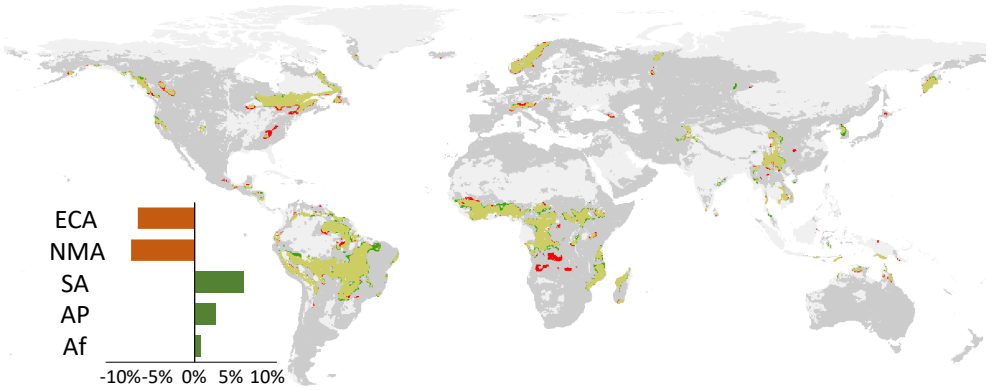

A) Global soil nature conservation priorities
Other
Top 30%
Top 20%
Top 10%
Top 5%
Priority areas
B) Proportion of protected priority areas
Top 5 %
Top 10 %
Top 20 %
Top 30 %
0%
20%
40%
60%
80%
100%
0%
0-5%
5-10%
10-20%
20-40%
40-80%
80-100%

higher challenges for mitigation of impacts

SSP5: Fossil-fueled development

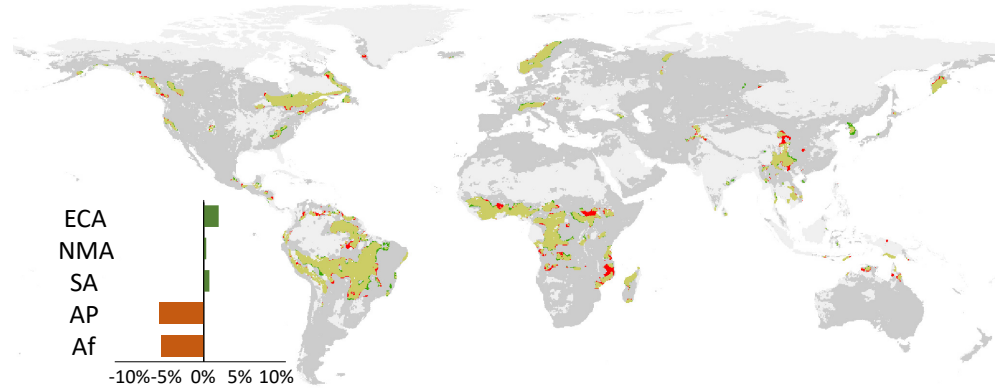


SSP3: Regional rivalry

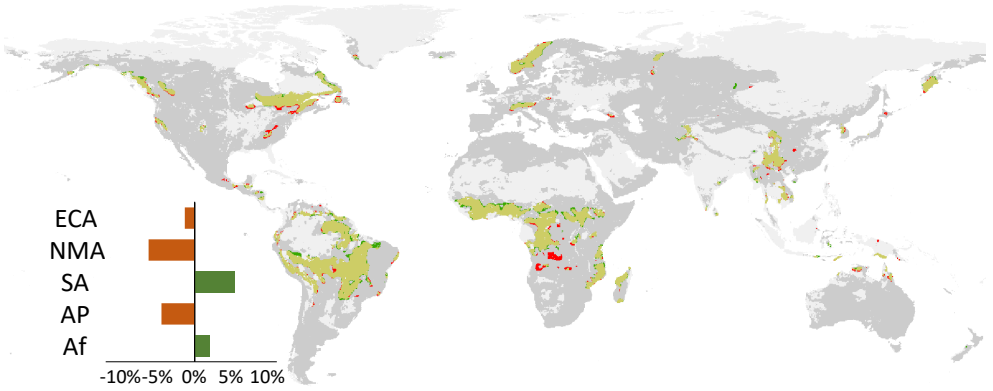


lower challenges for mitigation of impacts

SSP1: Global sustainability



SSP4: Inequality

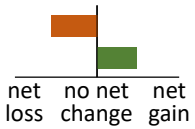


lower challenges for adaptation to changes in climate

higher challenges for adaptation to changes in climate

gains (2015-2070) in priority areas
top 5% priority areas
losses (2015-2070) in priority areas
non-priority areas

Regions:



ECA: Europe and Central Asia
NMA: North and Meso America
SA: South America
AP: Asia-Pacific
Af: Africa