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Response of soil biota to agricultural management practices: A systematic quantitative meta-data-analysis and method selection framework

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ABSTRACT

Soil organisms are vital to soil health, however, their inclusion in monitoring frameworks remains limited. Yet, it is well-known that agricultural management practices distinctively affect soil biota and the functions that they support. In this paper, we systematically evaluated the impact of management practices related to carbon and nutrient, vegetation, pest and disease and soil management, as well as grazing management on soil biota. Using a meta-data analysis approach, we systematically reviewed meta-analyses to quantify management practice(s) effects on soil biological actors, including macrofauna, mesofauna, microfauna, and the microbiome. We identified and screened 698 articles, of which 90 meta-analyses remained eligible after quality control and redundancy analysis, giving rise to a total of 790 pairwise combinations supported by 74′526 observations. In this paper, we demonstrate how specific management practices impact specific soil biota, which in turn may also influence soil processes and functions that these soil biota support. We reveal key knowledge gaps, particularly concerning the soil meso- and macrofauna, but also soil protists. Our study demonstrates which agricultural practices may support or diminish soil biology, providing much needed guidance on the selection of sustainable farming approaches, such as reduced tillage, organic fertilization, cover cropping, and intercropping. Lastly, we introduce a “Utility-Robustness” scoring system for soil actors, using a systematic framework to inform biological indicator selection tailored to specific management contexts. This fully transparent approach is designed to remain adaptable and expandable in the coming years, as new data and insights emerge.

1. Introduction

Soil health is the ability of a soil, at a specified point in time, to function as a vital living system, within natural or managed ecosystem boundaries and land-use boundaries, to sustain plant and animal productivity and health, maintain or enhance water and air quality and to further provide ecosystem services in the long-term without (increased) trade-offs between ecosystem services (van den Elsen et al., 2024). While the role of soil organisms in maintaining soil health has long been recognized, their inclusion in soil monitoring frameworks remains limited (Bünemann et al., 2018), partly because soil science has not yet been able to reach a consensus on standardized biological indicators and a unified minimum dataset. The proposed directive of the European parliament and the council on soil monitoring and resilience, known as the soil monitoring law, aims to create a framework for assessing and monitoring soil health across the European Union (European Commission, 2023). However, as supported by a joint open letter to the European commission, the proposed descriptors for evaluating the biological component of soil health are limited, focusing primarily on soil biodiversity and lacking detailed definitions (Soil Health Law Coalition, 2023). Thus, there is an urgent need for an ambitious and progressive EU Soil Health Law that includes a clear definition of soil health with science-based indicators and a harmonized, legally anchored monitoring system (https://eeb.org/library/open-letter-soil-health-law/). This requires greater contextualization in biological indicator selection and knowledge on the relationships with soil management practices. This is

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particularly important if the proposed directive aims to assess or regulate soil health at the local scale. Creamer et al. (2022) proposed an integrative framework using cognitive models to clarify the "who and how" of biologically mediated soil multifunctionality across four key soil functions: Carbon and climate regulation, water regulation and purification, nutrient cycling, and disease and pest regulation. They argue that soil biology assessments should move beyond the pursuit of a simplistic one-size-fits-all dataset and adopt a more complex context-specific approach. Their framework highlights the connections between soil biota (that they refer to as biological actors) and soil processes, providing a scientific foundation for assessing soil health.

Soil health assessments can fulfill various objectives, making it essential to understand the specific context in which the assessment is conducted (Powlson, 2020). The selection of soil health indicators at the field level should consider environmental context, land use and specific management goals, with different objectives requiring different approaches (Schreefel et al., 2024). For example, different agronomic practices can influence the relative importance of various selection criteria when monitoring agricultural land (Zwetsloot et al., 2022). Additionally, research and monitoring programs often work at different spatial scales, each with a distinct purpose in mind and therefore indicator selection should consider this when selecting appropriate biological methods. Zwetsloot and colleagues (2022) developed a freely accessible online tool (https://biosisplatform.eu/services/method-selection-tool) that relates to the same four soil functions included in Creamer et al. (2022), which are relevant to a wide range of temperate agricultural production systems and provides decision-support for the end user during the selection process of soil biological methods for soil health assessments. The decision support is based on i) the pertinence of the method to assess the respective soil function, ii) the applicability of the method to assess the ecosystem (arable, grassland, and forest), and iii) the more technical aspect regarding e.g. logistics and interpretability of the data. Although the method scoring is very comprehensive in terms of pertinence and technical components, the sensitivity of biological actors to specific agricultural practices that can, in consequence, impact soil health has been less explored and not specifically added to this decision support system.

While environmental factors and pedoclimatic conditions are beyond immediate control, land management practices can be adjusted to influence soil health. Numerous agricultural management practices are employed by land managers, each affecting soil health differently. In long-term experiments across Europe and China, Bai et al. (2018) demonstrated that various management practices affect soil quality indicators such as pH, soil organic matter, earthworm abundance, aggregate stability, and yield. These indicators show clear trends, but the magnitude and direction of change depend on the specific management practice. While the effect of different management practices on soil physicochemical properties is already summarized in meta-data-analyses (Blanchy et al., 2023b; Rietra et al., 2022; Young et al., 2021), a comprehensive review summarizing how the most common arable management practices influence different soil biota groups is still lacking.

Recent studies have systematically examined the effects of certain agricultural management practices on selected soil properties. For example, Blanchy et al. (2023) conducted a meta-data analysis focusing on soil physical properties and demonstrated that practices like incorporating organic soil amendments and promoting "continuous living cover" significantly enhanced soil water regulation by increasing carbon (C) inputs and stimulating biological activity. Likewise, Cozim-melges et al. (2024), in their review of 331 primary articles, found that less intensive practices generally foster greater biodiversity, even though no single management practice benefits all taxa.

In this work, we aim to systematically evaluate the effects of various management practices on soil biota specifically. The management practices we examine fall into the categories of carbon and nutrient management, vegetation management, soil management, pest and disease management, and grazing management. To achieve this, we conducted a meta-data analysis — a systematic and quantitative review of available European and global meta-analyses.

Our study takes a step further by providing a comprehensive review of how management practices affect soil macrofauna, mesofauna, microfauna, and the microbiome. We assess responses not only at the actor level (e.g. nematode, fungi or acari) but at varying levels of detail, such as at property level (abundance, activity, and diversity) or "method" level (e.g. specific methods, distinct (diversity) indices or trophic groups). For the nematodes, we decided to include both the different trophic groups and nematode-based indices, as they provide crucial insights into ecosystem dynamics and health (Du Preez et al., 2022). For the microbiome response group, we opted for a higher level of resolution by accounting for the various methods used to assess microbial properties as techniques have significantly improved sensitivity but also increased complexity and costs (Fierer et al., 2021).

Herewith, we demonstrate how various management practices influence different soil biological actors and thus modulate their effects on soil processes, sub-functions, and functions. This understanding can further guide how management practices impact soil life and which practices yield beneficial outcomes for agroecosystems. Additionally, we highlight gaps in systematically summarized knowledge, indicating the need for future meta-analyses or alternative approaches to address these data/knowledge limitations.

Lastly, we introduce a "Utility-Robustness" scoring system for each soil actor at varying levels of detail, calculated through a harmonized and systematic framework. This scoring system aids in the selection of soil biological indicators by providing transparent, tailored guidance based on the specific context of management practices where sufficient data exists and can be incorporated into a logical sieve for indicator selection, such as that proposed by Zwetsloot et al. (2022) implemented in the BIOSIS platform (https://biosisplatform.eu/services/method-selection-tool). Moreover, this approach is designed to remain adaptable and extendable in the coming years as new data and insights emerge.

2. Methods

2.1. Meta-data-analysis

2.1.1. Literature search

A search string was constructed to systematically identify meta-analyses documenting data concerning management practices and their effects on soil biota. This string was formulated to include a vast majority of agricultural management practices. Additionally, the search string encompassed all actors described in the cognitive models by Creamer et al. (2022). We decided against searching for specific farming systems (e.g., organic farming or conventional farming) due to their utilization of multivariate bundles of management practices. This complexity makes it challenging to disentangle the individual effects of each practice. The following search string "TS=(Soil AND Meta-Analysis NOT Forest NOT Urban AND ((crop AND rotation) OR monocrop* OR (single AND species) OR (crop AND diversification) OR (intermediate AND crop) OR management OR agroforest* OR silvopasture OR (alley AND cropping) OR (mixed AND cropping) OR (multi*cropping) OR undersow* OR intercropping OR (strip AND cropping) OR (cover AND cropping) OR legum* OR (deep AND rooted AND crops) OR (landscape AND elements) OR (vegetative AND strips) OR (flower AND strips) OR (green AND cover) OR *tillage OR subsoiling OR (soil AND (loads OR traffic)) OR liming OR irrigation OR drains OR (organic AND fertili*) OR (recycl* AND fertili*) OR (animal AND manure) OR (green AND manure) OR (liquid AND manure) OR slurry OR compost OR FYM OR (farmyard AND manure) OR (mineral AND fertili*) OR (inorganic AND fertili*) OR biochar OR (crop AND residues) OR (weed AND control) OR pesti*id* OR herbi*id* OR fungi*id* OR bio*id*OR transgenic OR (pest AND control) OR (disease AND control) OR pasture OR (grazing AND intensity)) AND ((microb* OR fungi OR bacteria OR archaea OR nematode* OR protozoa OR protist* OR acari OR collembola OR (soil AND arthropod*) OR microarthropod* OR enchytraeids OR earthworm* OR millipede* OR coleopter* OR spider* OR isopod* OR ant* OR (soil AND biodiversity) OR (soil AND fauna) OR (soil AND invertebrates) OR (soil AND biota) OR (soil AND biolog*)) AND (biomass OR abundance OR activity OR diversity OR richness OR shannon OR ind* OR (functional AND group*) OR communit* OR population* OR (QBC AND index))))" was run in November 2023 and August 2024 using the Web of Science database, yielding a total of 698 articles containing potentially relevant meta-analyses evaluating the impact of management practices on soil biota.

2.1.2. Quality assessment of identified articles

Each of the 698 articles underwent an initial screening process to: i) determine their correct classification as meta-analyses, ii) assess their contextual relevance, iii) ascertain only the inclusion of primary studies with European or from global datasets but no local data outside of Europe, and iv) verify the presence of field data rather than pot or lab data. After applying these initial screening criteria, a total of 142 articles remained as meta-analyses specifically analyzing the effects of management practices on soil biota at a field level across Europe or globally.

The 142 meta-analyses then underwent thorough screening for scope and quality according to the criteria outlined by Beillouin et al. (2019) and Blanchy et al. (2023a and b).

To be able to inform about effect directions and to guarantee good quality data, meta-analyses were excluded if.

- criteria for inclusion and exclusion of primary studies were not described;
- statistics were not sufficiently described or not valid (e.g. t-testing only);
- no statistical significance could be retrieved;
- the number of pairwise comparisons supporting an effect size was not given.

Furthermore, we had to exclude meta-analyses if.

- response variables did not fit our scope (e.g. plant disease);
- data was pooled across several soil biota groups (e.g. pooled micro-, meso- and macrofauna).

This led to a total of 91 meta-analyses (for the complete list of included meta-analyses, seeSI Table 1). Exclusions were mainly due to unclear statistical descriptions, incomplete reporting of effect sizes, and insufficiently detailed descriptions of response variables (pooling across several soil biota or measurements/methods). A PRISMA diagram providing a full overview of the meta-analysis inclusions and exclusions can be found in SI Fig. 1.

2.1.3. Data extraction and harmonization

From each of the 91 meta-analyses, we extracted data on the direction and statistical significance of effects, as well as the number of observations supporting each effect. We categorized the effect as "increasing" when both the average effect size and the entire 95 % confidence interval reported in the meta-analysis were greater than zero. If the confidence interval overlapped with zero, we labelled the effect as "neutral". When both the entire 95 % confidence interval and the average effect size were below zero, we classified the effect as "decreasing". Additionally, we gathered information on driver category (e.g. carbon and nutrient management), driver management practice (e.g. organic fertilization), driver contrast (e.g. unfertilized), response variable (e.g. microbial biomass C), response variable method (e.g. chloroform fumigation extraction), response variable property (e.g. abundance), response variable actor (e.g. microbe), and response variable group (e.g. microbiome). The complete data matrix can be accessed under SI File 1.

We focused exclusively on obtaining the overall effects and did not incorporate data from specific subcategories (such as climate, soil type, or soil properties). Furthermore, we did not include application rates/frequencies or dosages of given management practices in our meta-data analysis, although they can also have an impact. In cases where no overall data was provided but results were available for several management subcategories (e.g., low-intensity grazing, high-intensity grazing), we collected data from these subgroups, as they are aggregated additively in the final dataset. In cases where data for multiple soil layers was provided, we selected the data from the topmost layer. For macro- and mesofauna, we extracted data at the actor level. However, we also extracted taxon or functional group-specific data for the microbiome and nematodes, respectively, as a greater amount of information was reported within the meta-analyses.

Terminology was harmonized to describe drivers, contrasts, and response variables across different meta-analyses to align with the actors described in Creamer et al. (2022) and ensure consistency across all meta-analyses. The following adjustments were made.

- For the drivers (i.e. management practices): All driver management practices were categorized under the driver classes "Soil management", "Vegetation management", "Water management", "Carbon and nutrient management", "Pest management", and "Grazing management". For "Terrain management" and "Pollutant management" no data was available.
- The driver management practices of reduced-tillage and no-till were merged into a single driver management practice labelled as reduced-tillage. This decision derived from the fact that more than half of meta-analyses lacked differentiation between reduced- and no-till *versus* conventional practices, thereby preventing our ability to distinguish between them.
- The two driver management-contrast combinations of organic *versus* mineral fertilizer and organic *versus* unfertilized were merged into a unified category termed organic fertilization *versus* unfertilized/mineral fertilized because only few organic fertilization *versus* unfertilized observations were available.
- The driver management practices intercropping and mixed cropping were merged into intercropping.
- The driver management practice agroforestry is included under crop diversification

For the response variable.

- We kept the actor categories microbe, bacteria, fungi, and archaea (within the actor group microbiome). Any combination of bacteria, fungi, and/or archaea was categorized as microbe.
- If the method for microbial, bacterial, or fungal biomass/abundance determination was not specified, we summarized the findings under abundance categories, such as abundance_microbe, abundance_fungi, or abundance_bacteria. When the method was provided, we included it in our reporting, for example, abundance_bacteria_PLFA (PLFA = phospholipid-derived fatty acids) or abundance_microbe_MBC (MBC = microbial biomass C).
- If both observed richness and richness adjusted for unobserved (Chao) were presented in a meta-analysis, only observed richness was considered. In cases where only Chao was provided (two meta-analyses), it was taken and labelled as richness.
- If multiple alpha-diversity indices were provided per pairwise comparison, only the Shannon index was selected, given its widespread use. If a meta-analysis reported diversity by pooling various alpha-diversity indices, those pairwise comparisons were excluded from our analysis.
- The Biolog technique, employing Eco-plate incubations, was categorized as functional diversity.
- Microbial-derived soil enzymes were categorized into C-cyc (C cycling), N-cyc (nitrogen cycling), and P-cyc (phosphorus cycling),

fluorescein diacetate hydrolysis (FDA) as hydrolase, and catalase, dehydrogenases (DHA), and other enzymes classified as oxidases were grouped under OX. In cases where a meta-analysis did not specify the enzymes measured, the respective pairwise comparison was excluded from our analysis.
- qPCR data was not grouped.
- Acariforms, acari and mite were grouped into Acari.

A similar effort was undertaken for SOC, pH and compaction in order to be able to relate our findings to soil properties commonly measured in soil health assessments (Bünemann et al., 2018; Hoffland et al., 2020). We identified 785 studies using an updated search string potentially assessing management effects on SOC, pH and bulk density, of which 89 remained after the initial scope screening. These 89 meta-analyses then underwent a rigorous quality control screening based on the previously explained criteria, leaving 64 for data extraction, harmonization, and analysis.

2.1.4. Redundancy analysis

To assess the amount of redundancy of primary articles between meta-analyses, we performed a redundancy analysis. If available, primary articles from the 91 meta-analyses were collected, resulting in 5′688 (SI File 1). Meta-analyses sharing more than 40 % of primary articles were examined to determine whether they shared the same response variables. If so, shared response variables only of the most recent meta-analysis were kept.

2.1.5. Data analysis and method selection scoring

Harmonized data was then handled, analysed and visualized in R studio (RStudio team, 2023, version 2023.3.0.386), a development environment for R (Posit, 2023, version 4.3.0) using the tidyverse (Wickham et al., 2019), ggthemr (Tobin, 2020) and ggh4x (van den Brand, 2024) packages. The R script is made available under SI File 2.

To develop a univariate scoring system that informs about the strength of a management effect on a response variable, as well as the responsiveness of a response variable to a given management practice, we calculated Scaled Effect Direction scores (EDS) and Responsiveness scores (RS) for each unique combination of management practice, response variable, and contrast at the actor, property, and method levels as follows:

$$\textbf{EDS} = (\mathrm{Nr}_{\mathrm{ObservationsIncreasing}} - \mathrm{Nr}_{\mathrm{ObservationsDecreasing}}) \,/\, \mathrm{Nr}_{\mathrm{ObservationTotal}}$$

$$\textbf{RS} = (\mathrm{Nr}_{\mathrm{ObservationTotal}} - \mathrm{Nr}_{\mathrm{ObservationsNeutral}}) \,/\, \mathrm{Nr}_{\mathrm{ObservationTotal}}$$

Where $\mathrm{Nr}_{\mathrm{ObservationsIncreasing}}$ represents the number of observations with increasing effects, $\mathrm{Nr}_{\mathrm{ObservationsDecreasing}}$ represents the number of observations with decreasing effects, $\mathrm{Nr}_{\mathrm{ObservationsNeutral}}$ represents the number of observations with neutral effects and $\mathrm{Nr}_{\mathrm{ObservationsNeutral}}$ represents the total number of observations of a given unique combination.

To then integrate the EDS and RS in a univariate scoring system, also taking into account the robustness of the data, described by the number of observations, we calculate the Utility-Robustness Score (URS) as follows:

$$\textbf{URS} = (|\mathrm{EDS}| + \mathrm{RS}) \times \mathrm{Robustness}$$

Where the Robustness coefficient is defined based on the number of observations as:

Robustness = 1.0 for 1–5 observations,

Robustness = 1.1 for 6–10 observations,

Robustness = 1.25 for 11–20 observations,

Robustness = 1.35 for 21–50 observations,

Robustness = 1.425 for 51–100 observations,

Robustness = 1.5 for >100 observations.

The URS index can take values ranging from 0 to 3, where 3 represents the best potential indicator of change for a given practice.

3. Results and discussion

3.1. Data structure

From an initial dataset of 698 meta-analyses, quality control reduced our selection to 91 high-quality meta-analyses published between 2011 and 2024. This significant reduction was due to several factors: many meta-analyses had an incorrect scope, reported only localized data from outside Europe, or included data originating from pot experiments. Additionally, some studies aggregated response variables across multiple actors, failed to report the number of observations per effect size, or did not meet statistical quality control criteria. Ensuring rigorous standards in meta-analyses is essential for valid conclusions and broader generalizations in meta-data analysis. Therefore, we strongly emphasize the importance of quality control measures to uphold scientific integrity and standards, facilitating the use of meta-analyses in meta-data-analysis as described for primary articles by Gerstner et al. (2017).

Nonetheless, we compiled a collection of 91 high-quality meta-analyses focusing on the effects of management practices on soil biology. We then performed a redundancy analysis on the 5′688 available primary articles, which revealed ten meta-analyses with more than 40 % shared primary articles (SI Fig. 2). In-depth inspection of the addressed response variables led to the exclusion of one entire meta-analysis and 59 shared response variables across nine meta-analyses (SI File 1). Twenty-two meta-analyses did not report their primary articles; however, they were kept in our dataset as the risk of overinterpreting results due to redundancy is less significant than the risk of excluding high-quality data.

As shown in SI Fig. 3, the publication trend suggests that more meta-analyses will likely be published in the coming years, which should be included in our framework. To facilitate continued research and integration, we have made all data files and R scripts openly accessible, supporting the ongoing advancement of scientific knowledge and the FAIR principles (SI File 1 and 2).

To analyze the effects of management practices comprehensively, we structured the data into *pairwise combinations* as a working unit, representing unique combinations between management practices and actors, properties, or methods. Overall, after removing redundant response values and studies, we collected a total of 790 pairwise combinations across 90 meta-analyses, supported by a total of 74′526 observations. The distribution across response group categories was largely uneven (SI Fig. 4A), with microbial data being the most abundant, followed by microfauna, and relatively few meso- and macrofauna instances. A similar pattern is observed across the response property categories (SI Fig. 4B) and, consequently, also across response actor categories (SI Fig. 4C). This pattern suggests a lack of reviewed or summarized data for meso- and macrofauna in meta-analyses, likely due to a more limited number of available primary articles. The distribution of driver “management classes” also exhibited unevenness, with the highest number of pairwise combinations classified under “Carbon and nutrient management”, followed by “Soil management” and “Vegetation management” (SI Fig. 5A). Conversely, “Pest and grazing management” had the smallest number of pairwise combinations (SI Fig. 5A). Overall, we identified a total of 18 unique pairwise combinations of driver management practices and contrasts (SI Fig. 5B). The underrepresentation of meso- and macrofauna and pest and grazing management practices highlights a need for further primary studies and meta-analyses in these areas to ensure a comprehensive understanding of soil biology responses across management practices.

To ease downstream visualization, we excluded the driver contrast pairs salinization *versus* no salinization; Bt-GMO crops *versus* non-Bt-GMO crops and biocontrol *versus* no biocontrol as they are represented by only a few observations. However, the extracted knowledge remains available for use in the indicator selection framework. This structured dataset provides a robust foundation for analyzing the effects of management practices on soil biology and highlights critical gaps that warrant further research.

3.2. Management practice effects on soil biota

To assess the overall effect of management practices on various soil biological factors, we aggregated the extracted biological data across three levels of detail: actor level (e.g., specific soil taxa such as nematodes or fungi), property level (abundance, activity and diversity), and method level (e.g., specific techniques for microbial property assessment or nematode-based indices/trophic groups, SI Fig. 6). Depending on the focus or scope, the required level of resolution may vary. At a policy level, actor-level information might be more appropriate, as it is easier for stakeholders to understand and communicate. In contrast, scientists monitoring soil health in long-term experiments focusing on specific soil functions often require more fine detailed data, such as method-specific information.

We must note that while aggregated data creates a more complete representation of management practices and soil biota properties to identify trends and gaps, it might also introduce potential biases. For instance, merging results from meta-analyses using multiple methods assessing the same actor-property combination (e.g. microbial abundance via PLFA, CFE and qPCR) may obscure variability. Furthermore, in some cases, such as with nematodes, aggregating data may be illogical - for example combining different nematode trophic groups or nematode-based indices. This can lead to a highly ambiguous response of the respective actor to a given management practice. In the cases where effects are contrasting, a deeper analysis may be essential to identify which specific properties or methods are driving this variability. On the other hand, aggregating data allows us to evaluate management effects on specific actor-property combinations without needing detailed methodological information, thereby enabling the inclusion of more observations, that have not recorded all this information. Thus, it is important to acknowledge that each level of detail has its strengths and limitations.

On the actor level, we present in Fig. 1 the result of 79 management-contrast-response actor combinations with a total of 73′744 observations (60′845 observations in response group “microbiome”, 10′594 observations in “microfauna”, 1′594 observations sizes in “mesofauna” and 711 observations “macrofauna”). This uneven distribution underscores the need for more research on meso- and macrofauna (Geisen et al., 2019). In agreement with Cozim-Melges et al. (2024), we found that no single management practice enhanced all taxonomic groups for which we have available data. At the property level, we focused on variables related to abundance, activity, and diversity, excluding nematode-based indices. Fig. 2 summarizes 129 management-contrast-response actor property combinations, with a total of 69′069 observations (58′237 in the response group “microbiome,” 8′527 in “microfauna,” 1′594 in “mesofauna size,” and 711 in “macrofauna”).

For the microbiome response group, we provide an even higher level of resolution based on the methods used to describe microbial parameters (Fig. 3). Methods for assessing microbial communities have significantly advanced over recent decades. These methods have become more sensitive but also more expensive and complex to analyze and interpret. Consequently, we have decided to incorporate a wide range of microbial methods, spanning from less sensitive methods like colony-forming units (CFU) to highly sensitive approaches such as next-generation sequencing (NGS) data. Furthermore, a distinction between various diversity indices for the property of diversity within the microbiome was also evaluated at this level of resolution. Thus, response variables extracted from meta-analyses that lack a method description were removed beforehand. We present the effects of 295 pairwise combinations supported by 34′367 observations across 65 different microbial response methods. Considering the actor-based methods, the most commonly used method for assessing the property “abundance” in the response group “microbiome” was NGS-derived data (4284 observations) followed by PLFA (3′789 observations) and MBC (2′873 observations). While MBC and PLFA reflect absolute values, NGS can only inform about relative changes. Regarding diversity, the top-ranking metric was the Shannon diversity index with a total of 3′628 observations, followed by richness with 1′873 observations and functional Shannon diversity with 100 observations. In the methods for assessing the property “activity”, C-cyc enzymes were the most frequently assessed (3′835 observations), followed by P-cyc enzymes (2′064) and OX enzymes (1017). In contrast to actor-based methods, which serve as proxies to assess soil processes and are presented in this study, process-based methods, which directly measure rate variables representing soil processes, are not included in this study.

For the response actor nematode, we also present data at a deeper level of resolution (under “methods level” designation), emphasizing their importance as indicators for evaluating changes in soil function and health. Their ubiquitous distribution and capacity to thrive in various environments, coupled with their representation across multiple trophic levels in the soil food web, make them effective for monitoring soil conditions. They also indicate alterations in terrestrial habitats due to their quick response to environmental and human-induced disturbances (Du Preez et al., 2022; Ferris, 2010; Ferris et al., 2001). Nematodes are members of several trophic groups and have been classified according to their strategy as either colonizers or persisters (Bongers, 1990; de Goede et al., 1993; Ferris et al., 2001; Yeates et al., 1993). Consequently, many ecological indicators have been proposed that link the nematode community to soil processes and impacts (Du Preez et al., 2022). For example, the enrichment index reflects food availability and nutrient enrichment by calculating the relative proportion of enrichment opportunists’ nematode species, while the structure index informs about food web structure or complexity by looking at the relative abundance of slow-growing members of higher trophic groups. The Channel Index reflects the predominant pathway of organic matter decomposition. The plant-parasitic index is calculated based on biological features, such as life cycle characteristics and reproduction rates of plant-parasitic nematodes (Ferris et al., 2001). Often, nematode trophic groups are studied independently too. In Fig. 4, the results of 131 management-contrast-nematode-method combinations are presented, supported by a total of 7′168 observations. Due to their specificity, for the fertilization and tillage practices, the response groups nematodes and microbiome will be discussed separately from other groups.

3.2.1. Identified knowledge gaps

One clear outcome of Figs. 1 and 2 is the presence of “gaps”; highlighted in SI Fig. 7. These gaps arise either from a lack of meta-analyses for specific pairwise combinations or from the exclusion of studies that did not meet our inclusion criteria. Four major gaps stand out: (i) the effects of “Vegetation management” on macro- and mesofauna, (ii) the effects of “Pest management” on macro- and mesofauna, (iii) the effects of “Pest management” on the microbiome, and (iv) the effects of “Grazing management” on macro- and mesofauna (SI Fig. 7). Additionally, there are significant gaps in the “Carbon and Nutrient Management” category regarding the effects of biochar and crop residues, as well as in the “Soil Management” category concerning liming effects on soil macro-, meso-, and microfauna. In contrast, certain management practices, such as specific fertilization strategies and reduced tillage, are well represented in our dataset across all four response groups: macrofauna, mesofauna, microfauna, and the microbiome. Lastly, when considering the property level (Fig. 2), the limited information available at the diversity level for the majority of actors (especially meso- and macrofauna), remains a notable gap.

Additionally, to the gaps mentioned in SI Fig. 7, no eligible meta-

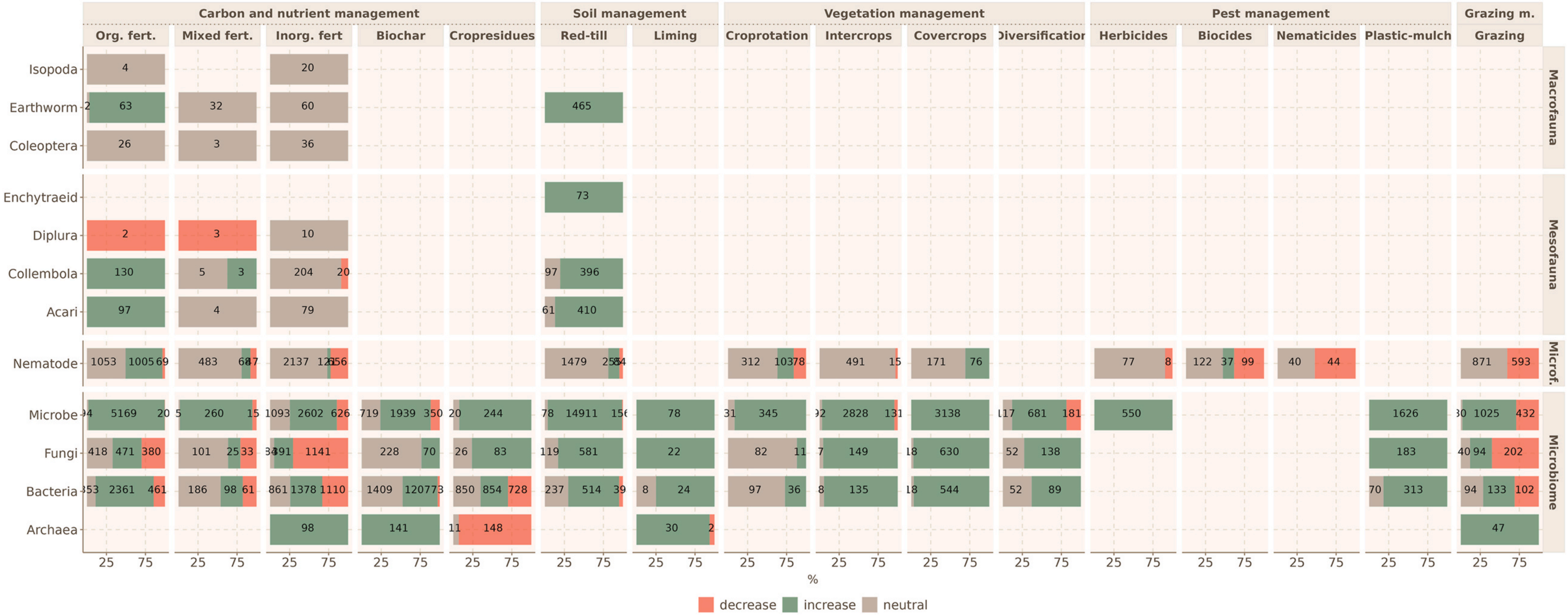

Fig. 1. Overview of management practice effects on soil biota on the actor level. Effect directions are indicated by color (red = significant decrease, green = significant increase, grey = neutral; insignificant results). The absolute number of observations supporting each effect direction is displayed within each bar, whereas the x-axis represents the percentage distribution. Herein presented data is aggregated across several properties, microbial methods and nematode trophic groups; nematode-based indices were excluded from this analysis. The contrasts of management practices were as follows: Organic fertilization (Org. fert) vs. unfertilized or mineral fertilized, mixed fertilization (Mixed fert) and inorganic fertilization (Inorg. fert) vs. unfertilized, reduced tillage (Red-till) vs. conventional tillage, crop rotation vs. no rotation, intercrops vs. monocrops, cover crops vs. bare fallow, diversification vs. monocrops, grazing vs. ungrazed and all pesticide management practices vs. untreated. Microf. = Microfauna. A color-blind-friendly version of this plot is available in SI File 5. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

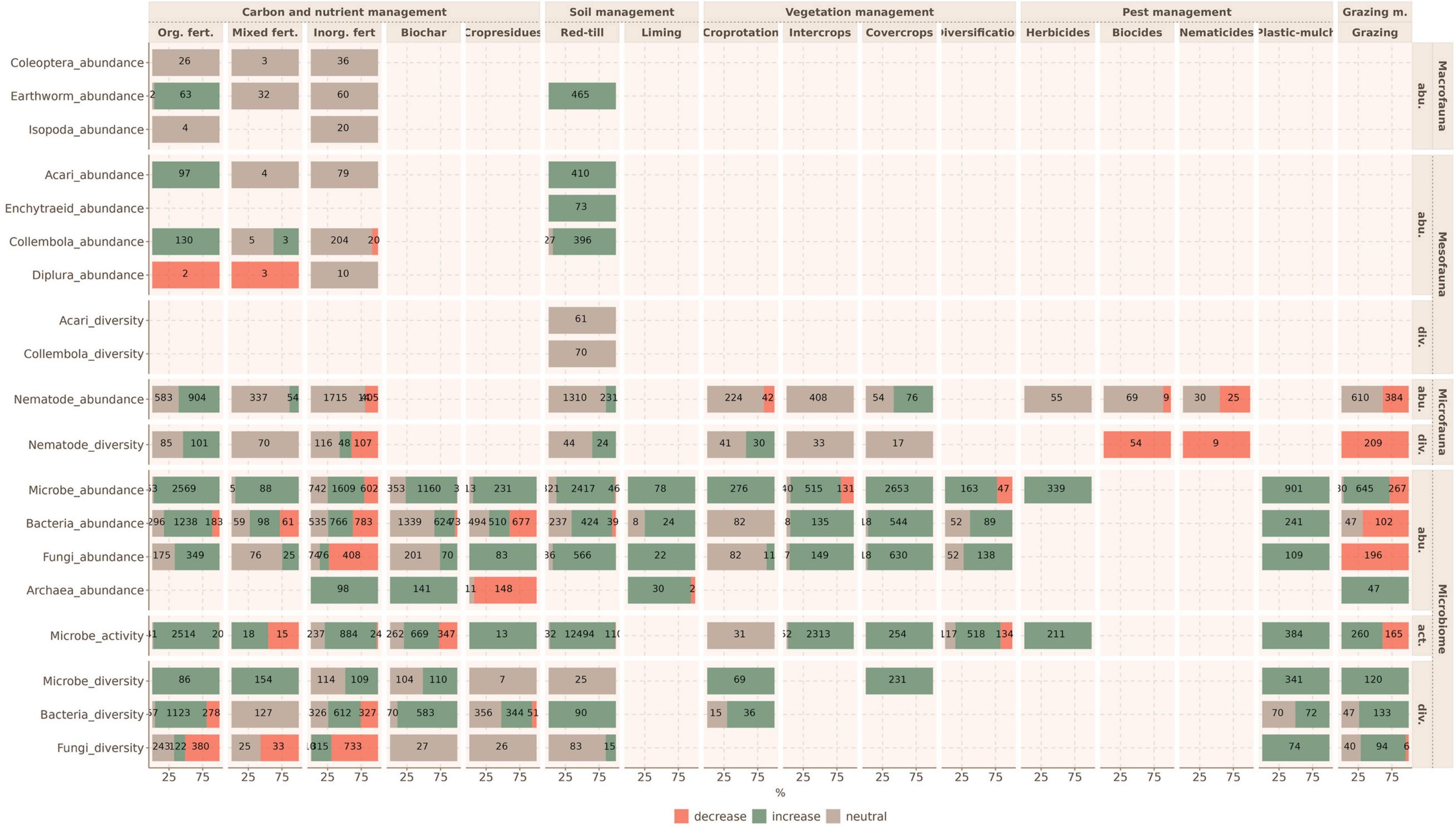

Fig. 2. Overview of management practice effects on soil biota on the property level. Effect directions are indicated by color (red = significant decrease, green = significant increase, grey = neutral; insignificant results). The absolute number of observations supporting each effect direction is displayed within each bar, whereas the x-axis represents the percentage distribution. Herein presented data microbial data is aggregated across several methods and nematode abundance across several trophic groups; nematode-based indices were excluded from this analysis. The contrasts of management practices were as follows: Organic fertilization (Org. fert) vs. unfertilized or mineral fertilized, mixed fertilization (Mixed fert) and inorganic fertilization (Inorg. fert) vs. unfertilized, reduced tillage (Red-till) vs. conventional tillage, crop rotation vs. no rotation, intercrops vs. monocrops, cover crops vs. bare fallow, diversification vs monocrops, grazing vs. ungrazed and all pesticide management practices vs. untreated. Abu. = Abundance, div. = Diversity, and act. = Activity. A color-blind-friendly version of this plot is available in SI File 5. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

Fig. 3. Overview of management practice effects on soil microbiome across the method level. Effect directions are indicated by color (red = significant decrease, green = significant increase, grey = neutral; insignificant results). The absolute number of observations supporting each effect direction is displayed within each bar, whereas the x-axis represents the percentage distribution. The contrasts of management practices were as follows: Organic fertilization (Org. fert) vs. unfertilized or mineral fertilized, mixed fertilization (Mixed fert) and inorganic fertilization (Inorg. fert) vs. unfertilized, reduced tillage (Red-till) vs. conventional tillage, crop rotation vs. no rotation, intercrops vs. monocrops, cover crops vs. bare fallow, diversification versus monocrops, grazing vs. ungrazed and all pesticide management practices vs. untreated. A color-blind-friendly version of this plot is available in SI File 5. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

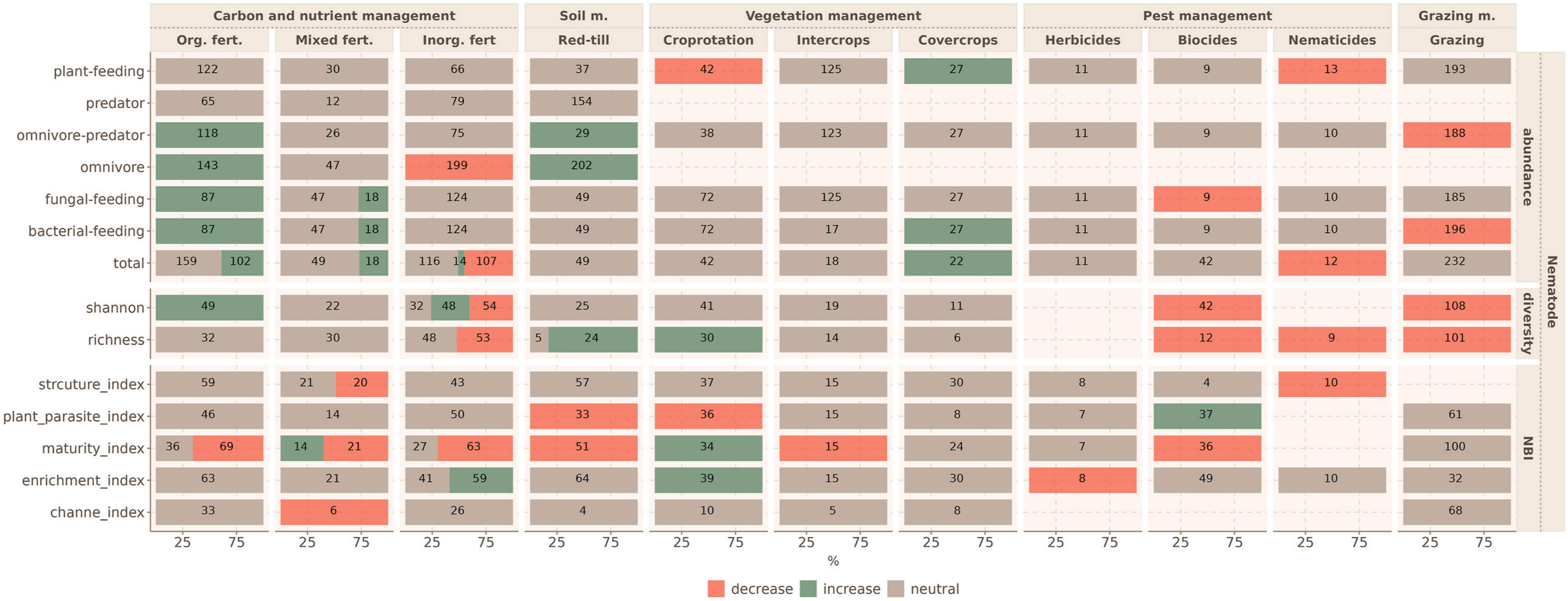

Fig. 4. Overview of management practice effects on nematode trophic groups and nematode-based indices. Effect directions are indicated by color (red = significant decrease, green = significant increase, grey = neutral; insignificant results). The absolute number of observations supporting each effect direction is displayed within each bar, whereas the x-axis represents the percentage distribution. The contrasts of management practices were as follows: Organic fertilization (Org. fert) vs. unfertilized or mineral fertilized, mixed fertilization (Mixed fert) and inorganic fertilization (Inorg. fert) vs. unfertilized, reduced tillage (Red-till) vs. conventional tillage, crop rotation vs. no rotation, intercrops vs. monocrops, cover crops vs. bare fallow, diversification versus monocrops, grazing vs. ungrazed and all pesticide management practices vs. untreated. NBI= Nematode-based index, total = total nematode density. A color-blind-friendly version of this plot is available in SI File 5. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

analysis assessing our management practices of interest was found for the actor protozoa. This should also be considered a major knowledge gap as they are a vital and irreplaceable component of soil biology and play a crucial role in the soil food web (Geisen et al., 2018). No data from eligible meta-analyses could be recorded for the actors' millipedes and spiders, which were also included in our original search string.

Addressing these gaps in future research is crucial for a more holistic understanding of management effects on soil biota. Ideally, this should be achieved through further research on these domains and concurrent meta-analyses. In the interim, leveraging large language models to semi-quantitatively summarize abstracts of the ever-growing body of primary articles was shown to help generate valuable insights and filling knowledge gaps (Blanchy et al., 2023a).

3.2.2. *Carbon and nutrient management effects on soil biota*

3.2.2.1. Fertilization practices. The effects of different fertilization practices on soil biota vary across all response groups, both at the actor and property level (Figs. 1 and 2). At the actor level (Fig. 1), organic fertilization (contrasted with mineral or no fertilization) increased the populations of earthworms, collembola and acari, while decreasing diplura and ambiguously affecting microfauna and the microbiome. The observed decrease in diplura, although supported by only two observations, can be explained by the increased activity of other, more dominant soil fauna, which enhances competition for resources and space (Zhou et al., 2022). Under mixed and inorganic fertilization (compared to unfertilized), most macro- and mesofauna remained unaffected, except diplura under mixed fertilization. Assessing the data from a property perspective provides a more nuanced level of resolution and allows for the disentanglement of whether the observed effects at the actor level are primarily driven by abundance, activity, or diversity. Fig. 2 indicates that observed changes in earthworms, collembola, acari, and diplura in response to fertilization practices can only be attributed to changes in abundance, as no information on diversity or activity is available from the identified meta-analyses.

The effects of fertilization practices on nematodes aggregated at the actor level are supported by a large number of observations (Fig. 1). Nematode abundance and diversity increased or remained unaffected under organic fertilization, were largely unchanged under mixed fertilization, and exhibited a more ambiguous response—often decreasing—under mineral fertilization (Fig. 2). Additionally, total nematode abundance was generally unaffected or increased under mixed and organic fertilization, while it remained neutral or decreased under mineral fertilization. However, interpreting the ambiguity of these effects remains challenging, as the aggregation complicates the biological interpretation of the results. Analyzing at a deeper level of detail, organic fertilization generally exhibited increasing or neutral effects on various trophic groups (Fig. 4). In contrast, mixed fertilization primarily resulted in neutral effects, while mineral fertilization showed neutral effects on the overall abundance and a clear negative effect on omnivore abundance (Fig. 4). Long-lived trophic groups with higher colonizer-persister (c-p) values, such as omnivorous and predatory nematodes, are generally more sensitive to environmental disturbances, including increased nitrogen levels from inorganic fertilization (Zhou et al., 2021). Looking at diversity, we identified that organic fertilization increased Shannon diversity, while richness remained unaffected (Fig. 4). Organic fertilizers can stimulate opportunistic nematodes (e.g., bacterial feeders), redistributing community dynamics without increasing the number of species (Freckman, 1988). A possible explanation could be the identified increase in SOC (SI Fig. 8) favoring higher microbial biomass (Fig. 3), as described by Wardle (1992). In contrast, mineral fertilization partially decreased richness, while Shannon diversity showed ambiguous responses. For mixed fertilization, no effects were detected, likely due to the opposing effects of organic and mineral fertilization counteracting each other. However, the relationships between bacterial-feeding nematodes, bacterial diversity, and community composition under combined fertilization remain unclear (Wang et al., 2023). In terms of nematode-based indices, we observed a partial decrease in the maturity index across all fertilization types, indicating disturbed soil conditions that favor opportunistic, stress-tolerant nematodes (Du Preez et al., 2022; Ferris et al., 2001).

In the microbiome response group, bacteria, fungi, archaea, and microbes are treated as distinct actors with no-overlapping observations. This is because the data comes from meta-analyses, which often do not specify whether their response variable was microbial in general or specifically bacterial, fungal or archaeal. Additionally, when methods were provided, the authors of the meta-analyses did not consistently specify which method was used to assess a property. For example, the CFE method assesses total microbial abundance, while qPCR allows for more specific targeting of bacterial or fungal abundance. At the actor level, a clear increase in microbial abundance was observed with organic fertilization, while responses for fungi and bacteria were more ambiguous (Fig. 1). This is further reflected in the nearly exclusive increase in microbial abundance, activity, and diversity in response to organic fertilization (Fig. 2), supported by a high number and balanced distribution of observations. For mixed and mineral fertilization, at the actor level, we observed a more variable response in bacteria, fungi, and microbes, which also extends to the property level (Fig. 2). One possible reason for this variability is the wide range of mineral fertilizers used in the primary studies. Furthermore, primary studies may also strongly differ in fertilization rates.

When assessing the effect of organic fertilization at the property level, a similar pattern, though with some neutral and decreasing observations, was observed for bacterial abundance and diversity (no data on activity available). Fungal abundance generally increased or remained stable under organic fertilization, while fungal diversity tended to decrease, with some neutral or positive observations (Fig. 2). The increase in fungal abundance in response to organic fertilization is plausible, as a majority of fungi are heterotrophic and rely on organic matter as a C source for growth (Ning et al., 2021). Organic fertilizers might therefore promote the growth of saprotrophic fungi. However, a rich supply of C from organic fertilizers can create niches for specialized fungi, potentially affecting diversity. This effect is particularly notable when diversity is measured using indices such as Shannon diversity, which considers both abundance and evenness (Kim et al., 2017). To validate this assumption, an even higher level of detail differentiating between species richness and Shannon diversity is needed. As shown in Fig. 3, which also presents information on the methods for the microbial actor, under organic fertilization the Shannon index indeed tends to decrease while richness generally increases; a similar pattern is observed for bacteria. While richness reflects the number of distinct taxa, the Shannon index also accounts for the relative abundance of these taxa. Thus, while organic fertilization may increase the abundance of certain saprotrophic groups, it can affect the evenness of species distribution (Hartmann et al., 2015), potentially leading to a decrease in the Shannon index. For microbial activity, we observed a general increase in extracellular enzyme activities under organic fertilization, yet microbial respiration showed a partial decrease (Fig. 3). This unexpected reduction could result from a shift toward oligotrophic, slow-growing microbes that are better adapted to nutrient-poor conditions, reducing overall respiration rates (Ho et al., 2017). For mixed and mineral fertilization there is a clear decrease in bacterial and fungal Shannon diversity and richness, whereas for activity measurements, responses are mainly either increased or neutral (Fig. 3). These contrasting responses in microbial activity metrics further highlight the importance of selecting appropriate methods for soil health assessment, as outcomes can vary depending on the property measured and the applied fertilization context.

At a deeper taxonomic resolution, NGS-derived data revealed less uniform, taxon-specific responses to fertilization practices (as well as to other management practices). For example, *Proteobacteria* and

Bacteroidetes increased under all fertilization types, while *Nitrospirae* and *Gemmatimonadetes* showed a decrease (Fig. 3). *Verrucomicrobia* and *Planctomycetes* responded differently to the various types of fertilization, whereas responses in other phyla were more ambiguous. These variations likely reflect the diverse life strategies of microbial taxa, with some thriving in oligotrophic conditions and others favoring heterotrophic growth, depending on nutrient and C availability (Fierer et al., 2007; Ho et al., 2017; Leff et al., 2015). Such functional and ecological diversity among microbes might shape their prevalence and distribution in response to fertilization.

Generally, it is expected that the input of organic matter and thus organic fertilization would trigger a bottom-up effect on the micro-food web (Lavelle, 2000; Wardle et al., 1998). In our study, however, mesofauna was the most clearly affected response group under organic fertilization (Fig. 2; detailed discussion on microbial effects are covered above). Although the bottom-up effect was not strongly evident for organic fertilization, when assessing the overall effects of mixed fertilization, it becomes clear that microbes, and probably also the micro-food web guild, which consists mainly of microfauna that prey on bacteria and fungi, as well as their predators (Lavelle, 1997), are the most impacted. With the introduction of inorganic fertilization, microbes become the most affected trophic level (Fig. 2) indicating a bottom-up effect.

3.2.2.2. Biochar application. Biochar application (contrasted with no biochar application) generally had either a positive or neutral effect on microbes, fungi, bacteria, and archaea (Fig. 1, no data on macro-, meso- and microfauna). At the property level, microbial and archaeal abundance as well as bacterial diversity clearly increased upon biochar application with effects supported by a substantial number of observations. In contrast, fungal diversity remained unaffected, while other pairwise combinations yielded more ambiguous results (Fig. 2). Thus, at the method level, responses are mostly neutral, neutral and increasing, or neutral and decreasing (Fig. 3). The increase in MBC, and partially in MBN may result from the increase in SOC due to biochar (SI Fig. 8). The increase in the fungi to bacteria PLFA ratio and AMF PLFA indicates a dominance of the fungal fraction, which is expected when the C/N increases, as fungi can access C in complex organic compounds that bacteria may not efficiently degrade (Hannula and Morri, 2022). Most of the targeted qPCR genes showed an increase, except for *nifH*, which showed no effect, and *norB*, which decreased. Although based on a limited number of observations, the decrease in *norB* gene abundance may be linked to higher oxygen content in soils with biochar, which is partially supported by the decrease in compaction (SI Fig. 8). Similarly, enzyme activities generally increased, except for C-cycling enzyme activity showing high ambiguity within methods and also possibly driving the decreasing effect in the microbe activity property. The variable effects of biochar on C-cycling enzyme activities may be due to differences in biochar source, production type and dosage and also soil type (Gomez et al., 2014; Gul et al., 2015). Looking at phylum-specific relative abundance NGS data, no dominant effects were observed, except for a decrease effect of *Acidobacteria*, and an increase in *Actinomycetes* and *Firmicutes*. The decrease in *Acidobacteria* is expected and very likely associated with a pH increase (SI Fig. 8, Dai et al., 2021). *Actinomycetes,* as copiotrophic microorganisms, likely thrive in nutrient-rich environments such as those provided by biochar. *Firmicutes* are also known for the copiotrophic lifestyle and several of their members, such as *Bacillus* and *Clostridium*, have been shown to increase their plant-derived C incorporation upon biochar application (Liao et al., 2019). The overall increase in diversity, reflected in the functional Shannon Index for microbes and Shannon index and richness for bacteria, is likely associated with the porous structure and high surface area of biochar, which provides microhabitats offering new niches (Dai et al., 2021).

3.2.2.3. Management of crop residues. Crop residues (contrasted with no crop residues left on the fields) had an increasing effect on microbes and fungi, a neutral effect on bacteria, and a generally decreasing effect on archaea (Fig. 1; no data available for macro-, meso-, and microfauna). At the property level, increasing effects were limited to microbial and fungal abundance and microbial activity, while diversity remained largely unaffected (Fig. 2). In contrast, bacterial abundance showed mixed responses to crop residues, while bacterial diversity was primarily neutral or increased (Fig. 2). The more variable response in bacterial abundance compared to fungal abundance may be due to data aggregation across multiple phyla for bacteria compared to fungi, where often fewer phyla were reported in the meta-analyses. At the method level (Fig. 2), it is clear that a wider range of bacterial phyla is included for microbial abundance compared to fungi. Classical methods, such as microbial biomass C and N, PLFAs, CFUs, and necromass, generally show neutral or positive responses, possibly following the increase in SOC (SI Fig. 8) (Turmel et al., 2015; Wardle, 1992). In contrast, more detailed NGS-based data on relative abundance reveal distinct, phylum-specific increases or decreases in response to crop residue application. *Proteobacteria* and *Bacteroidetes* increased in response to crop residues while *Nitrospirae*, *Gematimonadetes*, *Firmicutes*, *Chloroflexi* and *Cenarchaeota* decreased. The introduction of crop residues and thus more organic matter generally creates a more copiotrophic environment, and an increase in phyla associated with a copiotrophic lifestyle would be expected, while those that thrive under oligotrophic or anaerobic conditions may be at a disadvantage. However, this is only partially supported by our data, highlighting the complexity of the soil microbiome.

3.2.3. Soil management effects on soil biota

3.2.3.1. Reduced tillage. At the actor level, earthworms, acari, enchytraeids, and collembola increased under reduced tillage compared to conventional tillage, while there was no information in meta-analyses available for isopoda, coleoptera, and diplura (Fig. 1). Data at the property level indicated that abundance increases, while mesofauna diversity remains unaffected (Fig. 2). The increased abundance can be attributed to reduced disturbance under reduced tillage, which better preserves soil structure and increases SOC (SI Fig. 8), likely enhancing soil moisture and favoring the proliferation of these organisms. For Collembola and mites, the effect of tillage varies across taxonomic groups (Kladivko, 2001), which may explain the neutral effects observed on mesofauna diversity, as increases in some groups and decreases in others could balance each other out. When considering the macrofauna diversity, no information was available.

The response of nematode diversity and abundance to reduced tillage was primarily characterized by neutral effects, with a few observations of increases (Fig. 2). Given the ecological diversity of nematodes, more in-depth analyses of trophic groups and nematode-based indices might be relevant to catch more nuanced responses to management practices. As shown in Fig. 4, reduced tillage increased the abundance of omnivorous and omnivorous-predatory nematodes, while other trophic groups remained unaffected. The increase in omnivorous and predatory nematodes may be linked to the higher SOC content in topsoil and lower compaction associated with reduced tillage (SI Fig. 8), suggesting a positive effect on the stability of the soil food web (Bongiorno et al., 2019). This is consistent with an increase in nematode richness under reduced tillage (Fig. 4) and can be explained by an increase in the relative abundance of predatory and omnivorous nematodes, which, combined with a rise in microbial biomass, may also drive an increase in bacterial and fungal feeders, ultimately resulting in a lower maturity index (Bongers, 1990). Conversely, the decline in the plant parasitic index suggests a reduction in harmful plant-parasitic nematodes in soils under reduced tillage. This combination of findings illustrates the complexity of nematode responses to reduced tillage.

All microbial actors increased under reduced tillage, except for archaea, for which no information is available in the reviewed meta-analyses (Fig. 1). At the property level, the effects are associated with increases in abundance and activity, while diversity remains unaffected, except for bacteria (Fig. 2). An increase in microbial actors under reduced tillage may be linked to higher SOC concentrations (SI Fig. 8), improved soil structure, and higher soil moisture, all of which favor their proliferation. Interestingly, while bacterial diversity increased, fungal diversity did not exhibit a similar trend (Fig. 3). A higher level of resolution regarding the applied methods is necessary to understand the management effects on microbial actors more clearly. Fig. 3 shows that methods for assessing abundance respond in different directions, however, generally indicating an increasing effect. An increase in enzyme activity under reduced tillage was also observed, while the qCO_2 decreased, suggesting a less stressed environment where microbes divert more energy from growth into maintenance (Killham, 1985). Opposed to the clear increase in microbial biomass C, the ambiguous effects observed in microbial biomass nitrogen under reduced tillage may result from an increase in fungal dominance. While the fungal-to-bacterial ratio remained unchanged, several fungal indicators increased. This likely contributed to the rise in microbial biomass C due to the C-rich nature of fungal biomass. However, the higher C:N ratio of fungi may have led to a reduction in microbial biomass nitrogen, as fungi store less nitrogen compared to bacteria (Sun et al., 2016).

Conventional tillage has a significantly greater negative impact on larger soil organisms compared to smaller ones. As shown in Fig. 2, all macro- and mesofauna showed an increase in abundance under reduced tillage. This effect is primarily driven by the physical disruption of the soil caused by inversion tillage, which buries crop residues, alters soil structure, and modifies soil moisture and temperature dynamics (Kladivko, 2001). Such disturbances create an unstable environment, limiting habitat availability and resource accessibility for larger soil organisms. By reducing or eliminating tillage, litter transformers (e.g., mesofauna) and ecosystem engineers (e.g., earthworms) benefit from improved habitat stability, which supports their role in soil formation and organic matter decomposition (Lavelle, 1997; Wardle, 1995). These groups thrive in environments with minimal soil disturbance, where organic material remains on the surface, and moisture conditions are more stable, fostering favorable conditions for biological activity and overall soil health (Deleon et al., 2020). The retention of crop residues and the preservation of soil aggregates under reduced tillage further enhance these effects, contributing to a more resilient soil ecosystem (Parvisi et al., 2024). Beyond individual taxa, tillage management may also influence trophic interactions within the soil food web, shaping energy transfer and nutrient cycling. Soil food web models (de Ruiter et al., 1995) highlight how shifts in habitat stability can alter predator-prey dynamics, affecting functional guilds across different trophic levels. Under reduced tillage, enhanced habitat conditions support higher detritivore activity, which in turn increases microbial processing and decomposition efficiency (Zhong et al., 2017. This trophic shift is particularly relevant for nematode communities, where bacterivorous nematodes may benefit from increased microbial biomass, while omnivorous and predatory nematodes (more sensitive to disturbances), often decline in conventionally tilled systems (Zhong et al., 2017). The cascading effects of these trophic interactions influence soil ecosystem functions, as enhanced microbial turnover rates under reduced tillage improve nutrient cycling and organic matter stabilization.

3.2.3.2. Liming. For the amelioration of soil acidity by liming (“liming”, contrasted to “no liming”), only data for the response group of the microbiome was available as current meta-analyses do not report data on macro-, meso-, or microfauna (Fig. 1). Liming generally increased microbial abundance (Fig. 2, no data for activity or diversity was available). The increase in soil pH in acidic soils resulting from liming is primarily beneficial for microbes, as it reduces soil acidity and enhances nutrient availability (Bolan et al., 2003; Holland et al., 2018).

3.2.4. Vegetation management effects on soil biota

Unfortunately, no data from meta-analyses were available regarding the effects of vegetation management practices on soil macro- and mesofauna (Fig. 1). For nematodes, there was high ambiguity, with an overall tendency toward neutral effects (Fig. 1); however, this may be due to the aggregation of several trophic groups. Therefore, more in-depth analyses of nematodes are given in Fig. 4. The abundance of plant-feeding nematodes (often considered agricultural pests) decreased with the inclusion of crop rotations but increased with the introduction of cover crops (Fig. 4). However, it is important to note that an increase in plant-feeding nematodes does not necessarily indicate an increase in known plant pests, and a more thorough analysis of the feeding strategies of these plant parasites or an analysis conducted at the species level would be needed for a more conclusive result regarding effects on pest suppression. The varying impacts of different crop types and strategies on nematodes highlight the need for caution when assessing the effects of vegetation management (Hooks et al., 2010). Furthermore, richness increased under crop rotation, likely due to the more diverse rooting systems and exudates present in crop rotations compared to monoculture (Malik et al., 2024). A decrease in the plant parasitic index under crop rotation, compared to monocrops, suggests a reduction in harmful plant-parasitic nematodes, while an increase in the maturity index indicates a less stressing environment fostered by the diverse plant communities in the rotations. Intercrops did not significantly affect nematodes, except for a decrease in the maturity index. Changes in the maturity index can signal a disturbed environment, such as a decline in c-p 5 specialists, but can also result from increased c-p 1 opportunists (Bongers, 1990), which can be driven by enhanced microbial availability (as shown in Fig. 2). However, cover crops increased the abundance of plant-feeding nematodes, as well as bacterial feeders and total abundance, while other trophic groups and nematode-based indices remained unaffected. The increase in plant-feeding nematodes can be attributed to the extended availability of plant roots from cover crops, which provides a food source for these nematodes. Furthermore, and similar to intercropping, cover cropping also increased microbial abundance (Fig. 2), possibly through an increase in SOC (SI Fig. 8) (Adetunji et al., 2020), providing another food source for bacterial-feeding nematodes.

For the actors in the response group microbiome (and their properties), an overall increasing effect was observed under all vegetation management practices, except for archaea, for which no data is available (Fig. 3). At the property resolution level, bacterial and fungal abundance under crop rotation was unaffected, but diversity generally increased (Fig. 2). Aboveground and belowground diversity are linked (Liu et al., 2020), and thus the more diverse rooting systems and exudates likely foster a more diverse bacterial community (and potentially fungi, although no data is available). For intercrops and cover crops, not only diversity increased, but also abundance. This may be attributed to the multiple crops grown simultaneously, which provide a more continuous biomass input as well as an overall increase in organic matter, subsequently enhancing SOC (SI Fig. 8).

Diversification practices, such as crop rotation, cover cropping, and intercropping, enhance habitat complexity and resource availability, creating conditions that support a broader range of soil organisms, as explained by landscape theory, which states that ecosystem processes and biodiversity are shaped by spatial heterogeneity, where diverse habitats and land uses enhance ecological functions through the creation of varied niches and stable resource flows (Wiersma, 2022). Our findings align with this framework, as increased nematode and microbial abundance and diversity (Fig. 2) suggest that diversified cropping systems provide greater number of ecological niches and organic matter inputs, fostering a more resilient soil system. Furthermore, as described by Dale et al. (2013), landscape ecology provides valuable insights into sustainability by offering theoretical and methodological frameworks to address spatial heterogeneity, scaling, integration, and complexity. Vegetation practices included in our meta-data analysis clearly align with these principles, reinforcing their role as potential promoters of soil health and ecosystem resilience.

3.2.5. Pest management effects on soil biota

In general, the category of pest management shows the biggest gaps in our data, despite the ecological importance of the topic. Only limited data for nematodes and the microbiome have been presented in meta-analyses to date, resulting in an inconclusive picture (Fig. 1). However, plastic film mulch (compared to no mulching) exhibited predominantly positive effects on the microbiome at both the actor and property levels (Figs. 1 and 2). Mulching has proven effective in enhancing soil health by minimizing water loss, improving moisture retention, moderating soil temperature, enhancing nutrient availability and uptake by roots, suppressing weed growth, thus stimulating biological activity, and managing pests and diseases that affect crops (Bo et al., 2024; Kader et al., 2017). It is possible that the benefits of the mulching effect, as reflected by the increasing effect on all microbiome actors included in our analysis, outweigh the potential drawbacks associated with using plastic as a mulching material (Khalid et al., 2023; Steinmetz et al., 2016).

Herbicides (compared to no herbicide) showed a neutral effect on nematode abundance but increased microbial abundance and activity. A possible explanation for this may be the organic input from plants affected by the herbicide as they die. Given that the time since application was not a considered factor in our analysis, we cannot differentiate if these positive effects may diminish over a longer timeframe and are a relic of the sampling framework. Generally, herbicides are known to modulate the soil microbiome (Bueno de Mesquita et al., 2023; Ruuskanen et al., 2023; van Bruggen et al., 2021). However, with the limited data available from the meta-analyses at the actor, property, and method levels, concluding on their impact on soil biota remains challenging. We thus strongly encourage the scientific community to conduct the necessary systematic reviews that are still missing and also consider the factor “time since application” in their analyses.

Both biocide and nematicide applications decreased nematode diversity and, to some extent, overall abundance (Fig. 2). Analysis of distinct trophic groups and nematode-based indices revealed that nematicide application specifically decreased the abundance of plant-feeding nematodes, beyond decreasing overall abundance. The decrease in richness was also accompanied by a decrease in the structure index, suggesting a reduction in the complexity or maturity of the nematode community probably as a result of a non-targeted and wide spectrum effect of classical nematicides (Desaegerand Wram, 2020). For biocide application, a decrease in fungal-feeding nematodes was observed, along with a decrease in Shannon diversity and richness, as well as a decrease in the maturity index and an increase in the plant parasitic index (Fig. 4). This can be explained by the fact that biocides target and reduce the populations of fungi and other microorganisms in the soil, disrupting the balance of the soil food web and leading to a decline in overall soil organism diversity (Gunstone et al., 2021). The observed decrease in the maturity index indicates a shift towards a greater abundance of colonizer or opportunistic nematodes, which are more tolerant of disturbances such as biocide application (Yeates, 2003). In contrast, the plant-parasitic index increases with biocides. This may be explained by the observation that in nutrient-poor natural ecosystems, where plants exhibit lower growth rates, a high proportion of less specialized plant-parasitic nematodes is common. Consequently, the plant-parasitic index shows an inverse relationship to the typical response of the maturity index under enriched agricultural conditions (Bongers, 1990; Bongers et al., 1997).

3.3. Sensitivity of soil biota and methods to management practices – method selection framework

3.3.1. The utility-robustness score

Our meta-data-analysis clearly showed how different management practices distinctively affect various soil biota. We also demonstrated the importance of examining data at specific levels of detail—ranging from actor to property to method level—depending on the context. When it comes to method selection for soil health assessment in grassland and arable systems, the BIOSIS tool, based on the work of Creamer et al. (2022) and Zwetsloot et al. (2022), is available to assist end users in decision-making. However, what is currently lacking is information regarding the sensitivity of soil organisms to management practices. As presented above, the soil biota is differentially affected by management practices, which likely translates into distinct ecosystem functions (Wagg et al., 2014). In addition, the quantity (number of observations) and quality (clear effect direction versus high ambiguity) of information used to derive these effects also differ between pairwise combination(s) of practice and actor. Thus, depending on the management practices applied, and the soil function(s) of interest, biological soil health assessment methods have to be specifically chosen.

To address this challenge, we developed a utility-robustness score (URS) for each pairwise combination at the desired level of detail. The URS integrates: 1) Effect Direction Scores (EDS) informing about the strength and the projected direction of the effect, and 2) Responsiveness Scores (RS) informing about the responsiveness in terms of effect clarity. These scores are multiplied by a factor based on the number of observations available for each effect combination, creating a univariate scoring system that reflects both the effect direction, the responsiveness and robustness of the data, providing standardized and harmonized support for method selection based on specific management contexts. Scores range from 0 to 3, where 3 represents the best potential indicator of change for a given practice.

Applying the URS index introduces a new layer of knowledge, enabling the selection of the most appropriate biological methods for context-specific soil health assessment. A complete list of URS for all pairwise combinations, along with its projected effect directions, is given in SI File 3. In summary, based on URS results at the property level (Fig. 5), collembola abundance emerged as the highest-ranked potential biological indicator for assessing changes under organic fertilization (URS = 3), followed by microbial abundance (URS = 2.94) and microbial activity (URS = 2.93). For mixed fertilization, microbial diversity (URS = 3) was identified as a suitable indicator, closely followed by microbial abundance (URS = 2.7). To assess changes in soil health under biochar and distinct crop residue management practices, archaeal abundance (URS = 3) and fungal abundance (URS = 2.85) were identified as the most suitable indicators, respectively. Regarding soil management, particularly tillage, acari and earthworm abundance received the highest scores (URS = 3), followed by microbial activity (URS = 2.92) and enchytraeid abundance and bacteria diversity, all with a URS of 2.85. For vegetation management practices, the combination of microbial abundance, microbial diversity, and microbial activity yielded the highest URS values (URS = 3 in at least one of the practices included), presenting suitable indicators to detect changes in soil health. For pest management, despite many knowledge gaps, microbial abundance and microbial activity (URS = 3) were identified as the most suitable indicators for assessing changes due to herbicide treatment. For biocides, nematode diversity was the highest-ranked potential indicator (URS = 2.85). In the case of plastic mulch, most microbiome actor/property combinations achieved high scores (URS between 3 and 2.85), except for bacterial diversity. Lastly, for grazing practices, both nematode diversity and microbial diversity were identified as suitable biological indicators to assess changes in soil health, each with a URS score of 3. Additionally, URS scores calculated at the method level can provide more detailed insights to guide the selection of specific microbial methods or nematode trophic groups/nematode-based indices (SI File 3).

A case study presenting a possible scenario of using the URS for context-specific indicator selection is described in SI File 4. When assessing systems with multiple practices, it is important to select actor/property associations that are relevant to more than one practice, as

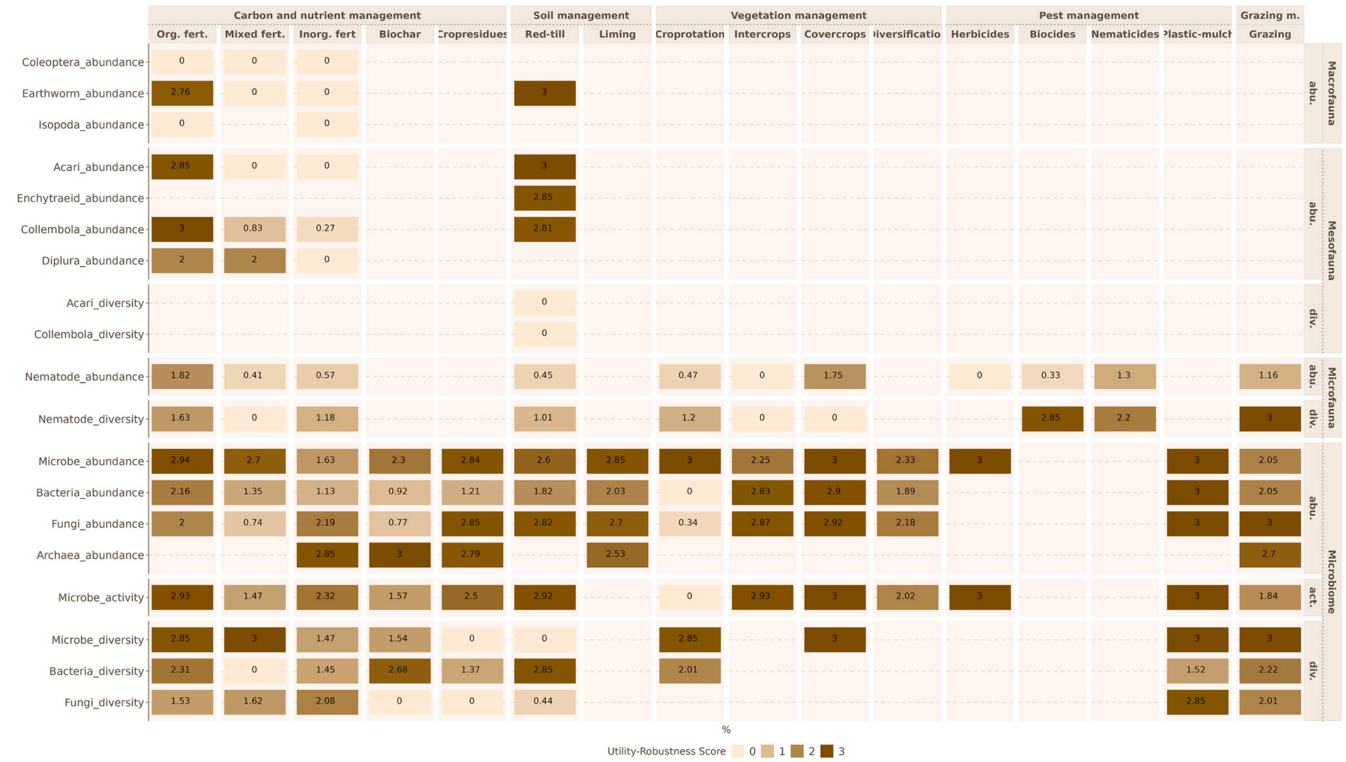

Fig. 5. Overview of Utility-Robustness scores (URS) per pairwise combination. The contrasts of management practices were as follows: Organic fertilization (Org. fert) vs. unfertilized or mineral fertilized, mixed fertilization (Mixed fert) and inorganic fertilization (Inorg. fert) vs. unfertilized, reduced tillage (Red-till) vs. conventional tillage, crop rotation vs. no rotation, intercrops vs. monocrops, cover crops vs. bare fallow, diversification vs monocrops, grazing vs. ungrazed and all pesticide management practices vs. untreated. Abu. = Abundance, div. = Diversity, and act. = Activity. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

demonstrated in the applied case study. Lastly, it should be noted that this dataset is as comprehensive as possible as of the date of this analysis. Therefore, we highly encourage regular updates to the data matrix and the resulting URS scores to enhance their completeness and applicability in the future.

4. Conclusion

In general, meta-data analysis is a powerful tool for summarizing and simultaneously comparing the effects of multiple drivers (management practices) and response variables (biological actors), providing robust, comparable and integrative insights. However, limitations persist, including the absence of meta-analyses in certain knowledge domains. Furthermore, some meta-analyses lack sufficient methodological information used to evaluate effects on actors. This review presents the first systematic overview of a broad range of soil biota and their associated properties. However, its reliability inherently depends on the underlying meta-analyses' quality and comprehensiveness. To further advance this field, a more refined aggregation of data would be needed, incorporating climatic zones, soil textural classes and management subgroup analyses. This approach could help clarify the effects of specific management practices on targeted biological factors, particularly when results are ambiguous. For example, Zuber and Villamil (2016) showed that tillage with a chisel plough had a neutral effect on microbial biomass carbon (MBC), whereas tillage with a disk had a positive effect. Similarly, soil texture can modulate the effects of tillage on biological communities. Liu et al. (2023a, b, c) found that in sandy soils, reduced tillage increased microarthropod abundance, while in clay soils, its effect was neutral. Beyond these observed effects, broader environmental factors such as latitude help explain variations. For example, SOC, a key driver of soil biological activity, is influenced by latitude. Govaerts et al. (2009) highlighted that soil organic matter decomposition, aggregate formation after tillage changes, and carbon input from new cropping practices tend to occur at a more favorable rate in tropical regions, where higher temperatures and moisture accelerate biological processes. Nonetheless, while meta-data analyses do have constraints related to "context", they offer a comprehensive synthesis of available meta-analyses, integrating diverse findings across contexts. This approach allows for insights that transcend the perspective of individual meta-analyses, providing a broader understanding of patterns and overall effect of drivers in soil biological responses.

Despite the limitations, our data highlights the lack of meta-analyses and thus likely upstream scarcity of primary studies, particularly concerning soil meso- and macrofauna but also soil protists. Addressing these gaps through targeted research and meta-analysis is essential to enhance soil health assessments and support the development of more comprehensive frameworks. Our study also demonstrates that agricultural practices beneficial to soil biology are closely aligned with sustainable farming approaches. Ideal farm management sustaining an active, abundant and diverse soil life should incorporate practices such as reduced tillage, organic fertilization, cover cropping, and intercropping.

Furthermore, our analysis underscores the importance of incorporating actor-to-property level analyses (and property-to-methods if applicable) when evaluating management practices in specific contexts. Notably, this approach raises a critical question: do different properties of a single actor exert varying impacts on the soil processes they mediate? Addressing this important question requires further research on soil processes that integrate both actor- and process-based methods. Ideally, a meta-data analysis focusing on the effects of management practices on soil biological processes would provide valuable insights for the soil science community.

The data presented here demonstrates that method selection is a pivotal step in assessing soil health. Biological indicators have often been selected based on the expertise of scientists involved in the research, rather than an independent assessment of which soil biological actors or properties are pertinent to the context under consideration (Creamer et al., 2022). Tailoring method selection to specific management practices when analyzing soil biota could significantly improve the utility of decision-support tools. The herein-introduced URS framework provides a quantifiable measure to rank actors and their properties based on the quantity of information (number of observations) and quality (clear effect direction versus high ambiguity). This approach allows for the identification of the most relevant biological indicators and properties across different contexts, from scientific research to management and monitoring programs. By tailoring indicator selection to specific needs, our results can support a wide range of stakeholders, including farmers, scientists, and policymakers, in making more informed and context-specific decisions. For a broader and more holistic perspective, these findings should be complemented with the BIOSIS tool for a more comprehensive perspective.

CRediT authorship contribution statement

Martina Lori: Writing – review & editing, Writing – original draft, Visualization, Validation, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Ricardo Leitao:** Writing – review & editing, Writing – original draft, Validation, Methodology, Investigation, Formal analysis, Data curation, Conceptualization. **Felix David:** Writing – review & editing, Data curation. **Camille Imbert:** Writing – review & editing, Data curation. **Alessio Corti:** Conceptualization, Data curation, Formal analysis, Investigation, Visualization, Writing – review & editing. **Luis Cunha:** Writing – review & editing, Project administration, Funding acquisition. **Sarah Symanczik:** Writing – review & editing, Conceptualization. **Else K. Bünemann:** Writing – review & editing, Project administration, Funding acquisition. **Rachel Creamer:** Writing – review & editing, Project administration, Funding acquisition, Conceptualization. **Carmen Vazquez:** Writing – review & editing, Project administration, Funding acquisition, Conceptualization.

Data availability

All data and the R script are available as supplementary files.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.soilbio.2025.109815.

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