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Ideas and perspectives: Using meta-omics to unravel biogeochemical changes from cell to planetary scales

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Abstract. Increased human impacts on Earth systems are radically altering biogeochemical cycles. While long-term environmental observatories and Earth System Models (ESMs) provide valuable insights into the mechanisms of nutrient dynamics, their performance is limited at the fine spatial scales controlled by the functional diversity of plant and microbial communities. This gap in our understanding concerning the roles of microbial diversity and plant-microbial interactions in decomposition and nutrient dynamics extends across many global ecosystems. Recent advances in meta-omics technologies, including metagenomics, metatranscriptomics, metaproteomics, and metabolomics, offer a wide array of tools for assessing metabolic to genetic to evolutionary drivers of ecosystem functioning. Here, we explore the integration of meta-omics with traditional ecological approaches to examine responses to global environmental changes. We present case studies from diverse environments—soils, aquatic systems, clouds, and paleoarchives—demonstrating how meta-omics can unravel the roles of microbial diversity, metabolic pathways, and trait distributions critical to understanding greenhouse gas fluxes,

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nutrient cycling, and biogeochemistry. Although meta-omics is still beset with challenges including data heterogeneity arising from wide-ranging methods, omics-derived traits, kinetic parameters, and machine learning tools can be used to enhance ESM predictive capability. For example, emerging applications of meta-omics to ancient environmental DNA are extending our capacity to link historical patterns with future projections, offering a long-term perspective on ecosystem dynamics. This review highlights the potential of integrating omics with experimental manipulations alongside existing monitoring and modelling efforts to refine predictions of ecosystem responses to natural and anthropogenic-driven environmental changes. Because omics approaches cross a range of scientific domains, they could be used to foster collaboration and even integration within existing models, thus laying the foundation for informed conservation and ecosystem management strategies from local to global scales.

1 Introduction

The rapid increase in human populations over the last century has intensified pressure on the biosphere, hydrosphere, and atmosphere (Rockström et al., 2023). Losses of natural habitats and over-exploitation of resources (e.g., farming, mining, construction, and other industrial practices) have led to rapid shifts in the biogeochemical properties of our ecosystems (Lewis and Maslin, 2015; Waters et al., 2016). These human-induced changes in global biogeochemical cycles alter energy fluxes that contribute to our current climate and biodiversity crises. The resulting pollution and environmental degradation that have been measured and communicated for decades by geoscientists and biologists necessitate continued biogeoscience research internationally (reports of the Intergovernmental Panel on Climate Change).

To understand the impacts on biogeochemical processes, long-term observatory studies with large-scale ground-based or ocean-based infrastructures—such as LTER (terrestrial and aquatic systems across the USA), NEON (diverse U.S. ecosystems), ICOS (European forests, wetlands, and grasslands), ITEX (Arctic tundra), BATS and SPOT (Atlantic and Pacific oceanic waters), and HOT (subtropical North Pacific Ocean)—were established to document the dynamic responses of ecosystems to changes in climate, species invasions, and management impacts (Franz et al., 2018; Mollenhauer et al., 2018; Sanclements et al., 2022). These local scale observatories are often equipped with instruments to measure the water, energy and greenhouse gas (GHGs) fluxes (CO_2, CH_4, N_2O) at the interface between surface ecosystems (soil, plant canopies, water bodies) and the atmosphere, providing valuable insights on the response of ecosystem processes, that underpin GHG budgets, to short (extreme and seasonal weather systems) and long term changes in climate and management. When these local scale measurements are coordinated across networks, the spatial and temporal variations in GHG budgets and ecological processes can be assessed over larger scales and used to generate predictive models, which in turn can be confronted at large scale by satellite and atmospheric station observations.

In addition to modern-day monitoring, the information preserved in sedimentary archives provides knowledge about past environmental changes and their potential consequences on biodiversity (Gregory-Eaves and Smol, 2024). The use of organic climate proxies (contained in tree rings, pollen, charcoal, corals, diatoms and foraminifera) and inorganic proxies (contained in varves, stalagmites, sediments and ice cores) provide a direct link to the effects of environmental change on ecosystem properties, such as changes in functional diversity, species abundances, and biogeographic distributions. For example, by identifying traits linked to present-day climate niches, researchers can extrapolate to past and future scenarios, using geological climate parallels to anticipate ecosystem responses (McElwain et al., 2024).

To date, most large-scale and long-term infrastructures have shown that representing a certain level of plant functional diversity can improve the predictive accuracy of Earth System Models (ESMs), particularly in simulating interactions among carbon, water, and nutrient cycles (Anderegg et al., 2022; Wullschleger et al., 2014). However, ESMs still face considerable limitations in capturing the full complexity of biogeochemical processes and energy fluxes, especially those mediated by microbial communities. These models often underrepresent key microbial functions that influence decomposition, nutrient cycling, and GHG fluxes. While primary production by higher plants is relatively well parameterized in many land surface models, the roles of microbial primary producers, heterotrophic decomposers, and organisms involved in secondary metabolism remain poorly understood and largely absent from ESM formulations. This gap includes processes such as microbial biomass growth, litter degradation, and the regulation of carbon use efficiency, which all influence the fate of organic matter and the balance between carbon storage and release (He et al., 2024b). The ecophysiology of these microbial communities has a direct feedback on the chemistry of the atmosphere and consequently climate (Conrad, 1994; Lovelock and Margulis, 1974; Monson and Holland, 2001). Yet, integrating mechanistic representations of microbial abundance, diversity, and function into ESMs remains incomplete, due to uncertainty about which processes are most critical, how to describe them mathematically, and how to scale them appropriately across spatial and temporal dimensions.

Meta-omics data, which encompass the comprehensive analyses of genes, transcripts, proteins, and metabolites of communities, provide powerful insights to bridge this knowledge gap. For example, molecular ecology techniques (e.g., metabarcoding, metagenomics, metatranscriptomics, metaproteomics, and metabonomics) used to study functional microbial ecology provide new ways to quantify and identify GHG production hotspots with novel metrics based on key traits (Frostegård et al., 2022). If implemented across networks that monitor large-scale and long-term changes in ecology and function (e.g., flux measurement sites) or through paleoecological archives, an omics framework could provide an important bridge between disciplines (Fig. 1). For example, microbial ecologists could then help identify ‘keystone’ organisms that disproportionately impact ecosystem functioning, such as regulating GHG flux rates or those responding to climate variations.

In this perspective, we highlight the immense potential of omics data to advance our understanding of global biogeochemical cycles by showcasing key insights gained across diverse systems—from land to ocean to atmosphere—and addressing the remaining challenges and future opportunities.

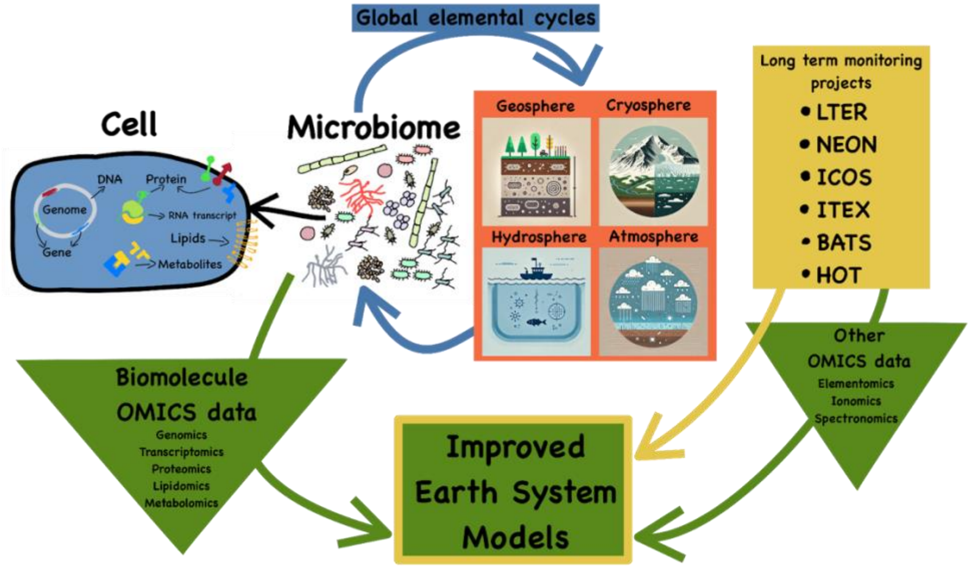

Figure 1: Conceptual framework for advancing our understanding and prediction of Earth's biogeochemical cycles under environmental change. This figure shows the proposed integration of omics data into long-term monitoring and modelling efforts. Orange: earth systems adapting to pressures on ecosystem balances; blue: microbial communities driving the biogeochemical processes critical in global elemental cycles.; yellow: long-term monitoring projects that supply key knowledge and response variables for biogeochemical models; green: proposed integration of omics data into biogeochemical models, and ultimately into Earth system models.

Glossary of omics vocabulary

Microbiome: the collective community of microorganisms (such as bacteria, archaea, fungi, viruses, and sometimes protists) that inhabit a specific environment.

Community: a group of populations found in a shared environment.

Population: a group of cells that have the same genome.

Amplicon sequencing

Amplicon sequencing: PCR amplification and sequencing of a portion of the genome found in multiple populations.

Amplicon Sequence Variant (ASV): similar to OTU - represents amplicon sequences where sequencing error has been taken into account and usually providing higher accuracy for taxonomic annotation.

Internal transcribed spacer (ITS): a sequence region between the small and large rRNA genes mostly used as a phylogenetic marker for fungi.

Metabarcoding: Method based on the high-throughput sequencing of DNA markers, typically specific gene or genomic regions, to simultaneously identify and characterize multiple species within complex environmental samples.

Operational taxonomic unit (OTU): a collection of amplicon sequences that are similar at a specific level of identity (i.e., 97 or 99 %) that is assumed to be phylogenetically closely related.

rRNA genes: ribosomal RNA coding genes - often used as a phylogenetic marker for prokaryotes (16S rRNA) and eukaryotes (18S rRNA).

Whole genome and metagenome sequencing

Assembler: bioinformatic software which creates contigs by various approaches.

Binning: grouping of contigs with similar features in a metagenome following the assumption they originate from the same genome.

Coding region: region of sequence/contig that encodes for a gene.

Contig: overlapping reads that have been assembled to a longer (contiguous) sequence. Resulting contigs are called assembly.

Gene: a segment of the region on a genome of sequence that encodes the information to produce a functional product such as proteins or RNA.

Genome: complete set of DNA from a single organism.

Genome sequencing: sequencing of the entire DNA of an organism.

Metagenome: the collection of genomes across multiple organisms in a given environment/sample.

Metagenome assembled genome (MAG): a genome that is constructed from a metagenome using sequence read assembly and binning.

Operon: cluster of functionally related genes found primarily in prokaryotes that are transcribed together. The encoded proteins often work in the same metabolic or regulatory pathway.

Protein: Amino acid sequence synthesized during translation of the RNA transcript by ribosomes, resulting in a functional molecule.

Read: a single sequence outputted by a DNA sequencer. This is the unit from which downstream analyses create assemblies from.

Transcript: RNA sequence produced from the transcription of a gene's DNA.

Meta-omics

Meta-omics: refer to the analysis of communities, as opposed to single cells or populations.

Metagenomics: method based on the sequencing of all DNA fragments present in a given DNA extract without the use of prior targeted approaches (e.g., PCR, hybridization capture). It is also referred to as shotgun sequencing or shotgun metagenomics.

Metatranscriptomics: method based on the reverse transcription of all RNA fragments and sequencing of complementary DNA (cDNA) from a given RNA extract without the use of prior targeted approaches.

Metaproteomics: method based on the direct interpretation of all proteins present in a sample, providing information on the active functions at the time of sampling.

Metabolomics: method based on the direct interpretation of all metabolites present in a sample, providing information regarding active functions and metabolic pathways at the time of sampling.

Metalipidomics: method based on the direct interpretation of all lipids present in a sample, providing information on i.e., cell membrane compositions, energy storage capacity and metabolic pathways of lipids.

Spectranomics: approach to link plant canopy species and their functional traits to their spectral-optical properties.

Volatilomics: subbranch of metabolomics, which studies the different types of volatile organic compounds that may be present in a certain biological matrix.

2 New insights on ecosystem dynamics and functional diversity

2.1 Global distribution of biodiversity

While around 1.5 million species have formally been catalogued to date, these estimates largely ignore microbes (both prokaryotes and eukaryotes, as well as viruses) that are estimated to encompass as many as a trillion species. The inability to characterize this dark matter of life is highly problematic, given microbes regulate and maintain all of Earth's biogeochemical processes including carbon (primary production in the ocean is performed almost entirely by microbes, and is comparable to all photosynthetic activity by plants on land), and nitrogen (e.g., nitrogen fixation and denitrification). Even viruses, generally not considered living organisms, are now recognized for playing major roles in nutrient recycling, e.g., carbon and iron cycles (Twining and Baines, 2013). Not only does much of the Earth's biodiversity reside in microorganisms, microbes are highly abundant (est. 1030 cells on Earth) and, together, represent the second largest contributor to Earth's biomass despite their microscopic size (Bar-On et al., 2018; Bar-On and Milo, 2019). The immense amount of microbial abundance and diversity reflects billions of years of metabolic innovation and evolution to exploit nearly every resource on Earth. These key contributions of microbes as the engines of Earth's biogeochemical cycles and for assuring the survival of Earth's life are grossly neglected by most people, including by the majority of scientists, although efforts are now afoot to give a voice to this unseen majority (Doumeizel and Dolan, 2024; Falkowski and Knoll, 2007; Tara Ocean Foundation et al., 2022).

Thanks to multiple international efforts, a comprehensive picture of microbial diversity is emerging. Notable examples are the Earth Microbiome Project (Thompson et al., 2017), soil microbiome and fungal projects like SPUN (Sanchez-Tello and Corrales, 2024), and Tara Oceans (Sunagawa et al., 2020). These datasets allow us to build genomic catalogues (e.g., (Ma et al., 2023; Nayfach et al., 2021; Paoli et al., 2022)) to characterize the patterns and processes governing microbial distributions. Gene atlases of these organisms could also be used to infer functions related to biogeochemical cycles and thus start to define who does what, how they interact with their environment, and how they impact ecosystem functioning (e.g., (Guidi et al., 2016)). As illustrated in the next section, such blueprints from multiple microbes provide multiple hypotheses to test the origins, current status, and future of life on Earth.

2.2 Using omics to link diversity to biogeochemical functions: a conceptual foundation

"We can say something about the community by giving a list of its species composition, but a community is poorly described by such a list alone." -Robert Whitaker (1975)

Ecosystem ecology sits at the nexus of understanding the flow of energy and materials through the biosphere and other abiotic pools. Traditionally, ecosystem ecologists have focused on the role of species variation across environmental gradients to predict ecosystem functions; for example, correlating plant species diversity with an ecosystem's measure of productivity. However, for microorganisms, we have limited knowledge of how microbial diversity translates to functional variation. For one, most microorganisms are uncultured and, therefore, remain unknown and uncharacterized (Steen et al., 2019). Second, the equivalent of the biological species concept does not apply to microorganisms, as there are ambiguities in what constitutes a microbial population, or genetic units belonging to the same species (Chase et al., 2019; Shapiro et al., 2016). Therefore, microbiome analyses typically rely on extracting all the genetic information from an environmental sample for microbial classifications, as this circumvents the need to culture and identify individual microbes. Generally, microbiome scientists cluster and collapse the immense genetic diversity and complexity within microbiomes into taxonomic units based on their genetic relatedness, such as the implementation of operational taxonomic units (OTUs) or metagenome assembled genomes (MAGs). These OTUs can be compared to reference databases for taxonomic approximations ranging from phyla to strain level matches. However, it is important to note that these taxonomic groupings are assigned based on computational convenience and do not necessarily reflect biological organization. It is unclear whether these genetic aggregations represent a family, genus, species, a mosaic genome composed from a composite of strains (Tyson et al., 2004), or even the genetic diversity present in natural populations (Meziti et al., 2021). Therefore, microbiome-focused ecosystem assessments are inherently forced to move away from the rich literature and theory developed for species to a broader view centered on community-wide metrics such as alpha- and beta-diversity metrics, community-level traits, or interaction metrics, e.g., with co-occurrence networks (Chase and Martiny, 2018).

This "community-wide" approach has several advantages, such as compiling global catalogs of microbial diversity across geographic scales that reveal biogeographic processes structuring environmental microbiomes (Fierer, 2014) and understanding potential metabolic interactions across various trophic levels encoded within the genetic makeup (Schimel and Schaeffer, 2012). Yet, these broad approaches mask intra-community functional trait variation that inevitably contributes to ecosystem functioning (Larkin and Martiny, 2017), especially in the context of environmental change (Scales et al., 2022). To illustrate this point, a bacterial OTU is assigned by clustering related genetic sequences of the conserved 16S rRNA gene region at varying thresholds. Depending on the genetic resolution used (ranging from amplicon sequence variants (ASVs) or

1-3% genetic divergence), these OTUs are estimated to represent 50-150 MYA of evolutionary time, or roughly equivalent to when all modern bird species evolved from a common ancestor (Martiny et al., 2023). Given knowledge of bird trait and physiological interspecies variation and their contributions to geographic distributions, no ornithologist would argue to collapse all bird species into a single OTU to study their impact on ecosystem dynamics. Likewise, microbial community analyses should understand the degree of trait variation within their taxonomic designations and determine whether that functional variation is relevant to biogeochemical fluxes (Abs et al., 2023; Defrenne et al., 2021).

Given that microbiome assessments rely on genetic material, we can also utilize that genomic information to infer functional traits at multiple biological levels. All functional traits, to some degree, are phylogenetically conserved. Some, such as pH or salinity responses, are broadly conserved at higher taxonomic levels while others, such as the responses to predicted anthropogenic factors (i.e., added nitrogen or drought) (Chase et al., 2017), exhibit fine-scale genetic variation at the genus, species, or even population levels (Martiny et al., 2015). Therefore, microbiome assessments of functional consequences need to prioritize and identify their functional trait of interest and understand the system's diversity accordingly (McLaren and Callahan, 2018). For example, the globally distributed marine phototroph Prochlorococcus (Cyanobacteria) is estimated to produce ~20% of the oxygen generated each year by photosynthesis on the planet and is predicted to be highly sensitive to changes in projected surface sea temperatures (Flombaum et al., 2013). Prochlorococcus is composed of several ecotypes, or highly clustered strains occupying the same ecological niche (Cohan, 2002). Ecotypes are geographically and vertically distributed in the water column through their partitioning of resources, including light, iron, temperature, and other nutrients (Johnson et al., 2006). Therefore, an understanding of how oxygen production may shift under future climate scenarios will be dependent on the individual responses of each ecotype and their functional differences (Ustick et al., 2023). These patterns aren't unique to Prochlorococcus and have been increasingly observed in abundant soil taxa driving leaf litter degradation and carbon turnover (Chase et al., 2018), glacier-fed streams (Fodelianakis et al., 2022), marine sediments (Chase et al., 2021b), and bogs (García-García et al., 2019).

Given the current limitations in relating functional and taxonomic diversity, metagenomic (DNA-based) and/or metatranscriptomic (RNA-based) assessments of microbiomes can provide direct information on the functional genes present in a community. These functional approaches provide crucial insights into how the metabolic potential of communities may be used to predict responses to environmental change (Piton et al., 2023). It is important to note that these data reflect genomic potential, not necessarily the realized production, unless such data are paired with proteomics or metabolomics. However, even with such paired datasets, reference databases are incredibly sparse; for example, metagenomic pipelines fail to characterize 90-99% of environmental microbiomes (Nayfach et al., 2016) at fine taxonomic levels and <5% of metabolites can be identified in marine systems (Bouslimani et al., 2014). This sparsity has the high potential to bias trait interpretations and their relationship to environmental variables (Osburn et al., 2024). Ultimately, scaling from traits to ecosystem processes requires understanding the degree to which variation in microbial traits (and their adaptive strategies) are linked to the environment (Abs et al., 2020, 2024a), as ecosystem ecologists have done for decades with macro-organisms.

2.3 Using omics to predict biogeochemical functions at the site scale

2.3.1 Example from a subsurface system

We define the terrestrial subsurface to begin below the depth of greatest plant root density and extend into deeper aquifers. Life in the subsurface influences the composition of gases and liquids moving through it, acting as an open biogeoreactor driven by surface-derived organic matter, nutrient inputs, and a process known as dark carbon fixation (Küsel et al., 2016). In environments lacking sunlight, dark carbon fixation refers to the ability of chemolithoautotrophic microbes to use energy from reduced compounds (e.g., sulfur, nitrogen, hydrogen) to fix inorganic carbon into organic matter, thereby generating a self-sustaining energy source. This process is particularly significant in groundwater ecosystems, where reduced inorganic electron donors fuel primary production, replacing the role of photosynthesis at the surface.

Omics approaches, such as metagenomics, are invaluable for unravelling the metabolic capacities of these microbial communities, offering insights into the dynamic and complex biogeochemical processes that drive subsurface life. Metagenomic studies have revealed a high abundance of chemolithoautotrophs in groundwater, accounting for 12% to 47% of the microbial community, suggesting that dark carbon fixation is central to subsurface trophic webs (Overholt et al., 2022). This process might also have global significance, as the subsurface and surface biospheres are tightly linked through the exchange of energy and matter. Overholt et al. (2022) estimated that dark carbon fixation in deep subsurface environments could contribute between 1.4 and 2.5 Tg of CO_2 per year to the atmosphere globally.

Box 1: Example from aeromicrobiology

The theory of spontaneous generation was disproved when atmospheric deposits were shown to inoculate environments with living microorganisms (Pasteur, 1861). Since then, it has been established that bacteria can remain suspended in the atmosphere for several days (Burrows et al., 2009) and be transported across continents (Griffin et al., 2017), enduring harsh conditions such as low water and nutrient availability, thermal and osmotic shocks, high UV exposure, and oxidants. Clouds are critical environments for complex multiphase chemical processes driven by light and oxidants, significantly impacting atmospheric composition and elemental cycles (Lelieveld and Crutzen, 1990). Additionally, they serve as relative hotspots of microbial activity, with biological processes contributing to chemical reactivity (Amato et al., 2019; Péguilhan et al., 2024). Clouds are also major components of the hydrological cycle, and play a key role in the deposition of airborne particles, including living microorganisms and genetic material, to surface ecosystems through precipitation (Péguilhan et al., 2021).

The low biomass in the atmosphere (< 104 cell m^{-3}) and its high variability over short timescales pose significant challenges to study, but omics approaches offer decisive insights into a variety of scientific topics, including:

Early detection and surveillance of pathogens

The air contains a variety of potential pathogens affecting plants, animals, and humans, as well as microorganisms of sanitary concern (e.g., those harbouring antibiotic resistance genes). Omics-based methods offer rapid and accurate detection of these microorganisms at early stages, enabling powerful tools for epidemiological surveillance and outbreak prevention (Kuske et al., 2006).

Defining the role of biological processes in atmospheric chemistry

In the 2000s, clouds were identified as environments supporting microbial activity that interacts with atmospheric chemical processes. Laboratory experiments on natural cloud water incubated in bulk demonstrated active biological processes, where microorganisms metabolize dissolved organic compounds, produce biomass, and process dissolved chemicals (Amato et al., 2007). These findings suggested that microorganisms significantly influence atmospheric chemistry, which was further specified by modelling (Khaled et al., 2021; Nuñez López et al., 2024).

Defining the role of the atmosphere in microbial ecology

Microorganisms aerosolized from various surfaces enter the atmospheric environment, where they are exposed to extreme conditions. Some reach clouds and eventually return to ecosystems via precipitation. Certain microorganisms likely survive atmospheric processing better than others, enabling their long-distance dispersal. Investigating the biological functions involved in microbial survival—at the gene, transcript, protein, or metabolite level—can help us understand the selection pressures exerted by the atmosphere and its role as an environmental filter (Šantl-Temkiv et al., 2022).

Capturing environmental DNA (eDNA)

Airborne material from multiple surfaces carries genetic information, allowing the air to serve as a proxy for biodiversity within a given area. Airborne nucleic acids can be analysed through targeted or untargeted metagenomics to assess environmental diversity and track ecological changes (Lynggaard et al., 2022; Métris and Métris, 2023).

2.3.2 Example from a coastal system

Meta-omic data provide powerful tools for understanding how human-induced deoxygenation of coastal water columns is altering microbial metabolisms and their contributions to global biogeochemical cycles. Oxygen levels in marine waters are declining due to global warming and increased anthropogenic nutrient loading (Doney et al., 2012). This deoxygenation is expanding oxygen-minimum zones and creating so-called dead zones in near-shore ecosystems (Breitburg et al., 2018), with profound implications for ecosystem functioning. These changes reduce habitats and resources for organisms like fish and cause significant shifts in carbon, nitrogen, and sulfur fluxes between the sea and atmosphere (Wakeham, 2020).

Microbial metabolisms are particularly affected, as anaerobic respiration processes become dominant in oxygen-depleted environments. These metabolisms include the use of nitrogen, sulfur, carbon compounds, and trace elements as alternative energy sources. Other processes, such as anoxygenic anaerobic photosynthesis (the use of light to produce organic matter in sunlit anoxic environments) and the microbial transformation of mercury into the neurotoxin methylmercury, are also induced (Bravo and Cosio, 2020). Thanks to meta-omic data, we can now study present-day microbial ecology and biogeochemical processes associated with oxygen depletion. For example, Capo et al. (2022b) demonstrated through environmental chemistry, metagenomics, and metatranscriptomics that microbial production of methylmercury is prevalent in oxygen-deficient water layers of two basins in the Baltic Sea. Combining such contemporary meta-omic analyses with historical DNA data from sedimentary archives offers a unique opportunity to explore the links between increasing anoxia in water columns and shifts in microbial metabolisms.

Box 2: Example from the cryosphere

Global warming is more pronounced in the Arctic regions than the rest of the globe, causing fundamental changes in ecosystem structure and functioning (Cavicchioli et al., 2019). Recent calculations showed that the Arctic is actually warming not two times but four times faster than the rest of the globe (Rantanen et al., 2022) and this warming has been observed to be stronger in the winter months (Post et al., 2019). Many omics studies, especially ones focusing on soil microbiomes, have been conducted in the summer period as the sites are accessible and measurements easier to conduct. In addition, safe transport of samples to the laboratory for analysis is simpler than in the winter seasons when sites are covered with up to meters of snow. Snow acts as an insulator and thus the soil may not freeze totally from the surface layers so that microbes may remain active and respire, producing both CO_2 and methane (CH_4) (Poppeliers et al., 2022; Walter Anthony et al., 2024).

Transition seasons with fluctuating conditions for microbes can also be of interest. In the springtime, the melt water brings nutrients for microbial metabolism. Besides, CH_4 and CO_2, produced by microbes, can be trapped in soil during winter and be released after thaw and for this reason these transition seasons should be studied in detail. In autumn, the length of the freeze-thaw events before the frozen season can vary depending on the timing of snowfall, resulting in an insulating snow cover which can fall on frozen or thawed soil—conditions that influence microbial processes during the winter months. With climate warming the autumns have changed in the Scandinavian subarctic while after plants have reduced photosynthesis with limited light sources, the weather stays warmer. Thus, in these seasons there is limited competition with the plants

(Riley et al., 2018, 2021) for the resources and nutrients. Therefore, the need for arctic research is not only in the growing season but also during winter and transition seasons autumn and spring (Riley et al. 2021).

Omic approaches allow focus on metabolic function together with the taxonomic signatures of the microbial communities. Studies from the growing seasons have shown changes in microbial community composition and functions in sites with differing vegetation cover (e.g., Pessi et al., 2022; Woodcroft et al., 2018) and activity of the microbes has also been shown to vary (Viitamäki et al., 2022). Sub snow microbial communities in the arctic have shown diversity similar to summertime (Männistö et al., 2024). Intriguingly, the activity of functional genes has shown differences in CH_4, hydrogen and carbon metabolism between summer and winter (Viitamäki et al. in prep). In addition to soil, focus should also be in the snow as recent studies have demonstrated high microbial diversity and abundance of the same taxa as in soil in snowpacks (Keuschnig et al., 2023). Phospholipid fatty acid composition of tundra soils has shown temporal differences (Björk et al., 2008) and thus the possibilities of omics approaches in creating understanding on microbial processes and role during this long, forgotten season.

2.3.3 Example from a terrestrial plant system

Metabolomics are also a tool to better predict the influence of climate change on ecosystem dynamics. Chemical ecologists recently included phytochemical traits as niche dimensions based on their central functions in plant responses to their environment (Müller and Junker, 2022). For instance, the so-called "predictive metabolomics" approach can be used to predict patterns of phytochemical diversity in Alpine regions independently of plant lineage (Defossez et al., 2021). Similarly, modelling was used to predict the environment of multiple plant species from the Atacama Desert using their metabolism (Dussarrat et al., 2022). Metabolomics was also used to analyse changes in soil microbial function in response to drought (Brown et al., 2021). Overall, predictive metabolomics peaks as an ideal tool to predict and anticipate losses or modifications of chemical and functional diversity in response to climate change (Dussarrat et al., 2022, 2025; Frugone-Álvarez et al., 2023).

2.4 Using omics to predict biogeochemical functions at the global scale

2.4.1 Large-scale metagenomics

The examples in Sect. 2.2 illustrate how omics approaches can help identify the drivers of biogeochemical processes. Large-scale metagenomic analyses offer a powerful tool to extend findings from individual studies to a global scale. A variety of large-scale metagenomic datasets from diverse ecosystems are now available (Bahram et al., 2018; Duarte, 2015; Sunagawa et al., 2020), allowing researchers to screen for the presence of pathways of interest in a large number of MAGs, understand their global distribution, and assess their susceptibility to environmental conditions. This, in turn, helps to predict their potential impact on biogeochemical cycling at a planetary level.

However, large-scale metagenomics presents several challenges, foremost among them being the accuracy of pathway annotations. Standard workflows rely on automated annotation pipelines, followed by manual curation to correct issues like spurious annotations. As data volume increases, however, manual curation becomes impractical. To overcome this, we propose several steps to enhance the accuracy of pathway predictions from large-scale metagenomic data. These steps include defining marker genes uniquely associated with specific pathways to serve as reliable indicators of their presence. Annotation of these genes should utilize methods sensitive to remote homology and be validated through phylogenetic approaches. Furthermore, pathway completeness should be assessed by identifying other related genes within the MAG of interest. In some cases, the operon-like organization of the genes involved in a pathway can also indicate its functionality, increasing annotation reliability (Bratlie et al., 2010). This property has been used to explore the biosynthetic potential of MAGs generated from Tara Oceans, leading to the discovery of a particularly talented group of formerly unknown bacteria able to generate multiple compounds of interest in biotechnology (Paoli et al., 2022).

Large-scale metagenomic screenings provide a comprehensive view of microbial processes across diverse ecosystems and under varying environmental conditions, thus enhancing our understanding of the phylogenetic and ecological distribution of biogeochemical cycles. Combining these with contextual data (i.e., physical, chemical and biological parameters) can help to predict the link between environmental conditions and a respective biogeochemical pathway. Furthermore, understanding the link between pathways and the environmental conditions in which they occur allows predicting the sensitivity of biogeochemical cycles in a changing environment.

In summary, we can leverage large-scale metagenomics to study the distribution of biogeochemical pathways in diverse environments and make predictions of how their distribution might change under changing environmental conditions. The results from such analyses provide the foundation for new hypotheses and experimental research (e.g., isolation of organisms or studying pathway activity in different conditions).

2.4.2 Combining meta-omics to infer large scale biogeochemistry

In most Land Surface Models (LSMs), vegetation and soil attributes are often prescribed in parameter lists and used to describe how biogeochemical processes vary over the land surface. For example, the representation of vegetation is distilled in a variety of plant functional types (PFTs), with each representing a prescribed range of anatomical and physiological parameter values such as leaf mass area, carboxylation rates, or leaf respiration (Duckworth et al., 2000; Woodward and Cramer, 1996). These PFTs can co-vary with certain soil chemical and physical characteristics that are often prescribed, assimilated and/or predicted after some model initialisation and predetermined spin up procedure that drives the vegetation, soil, and atmosphere into some quasi-steady-state to explore feedbacks on biogeochemical cycles (Friend et al., 2014; Matthaeus et al., 2021; Taylor et al., 2011).

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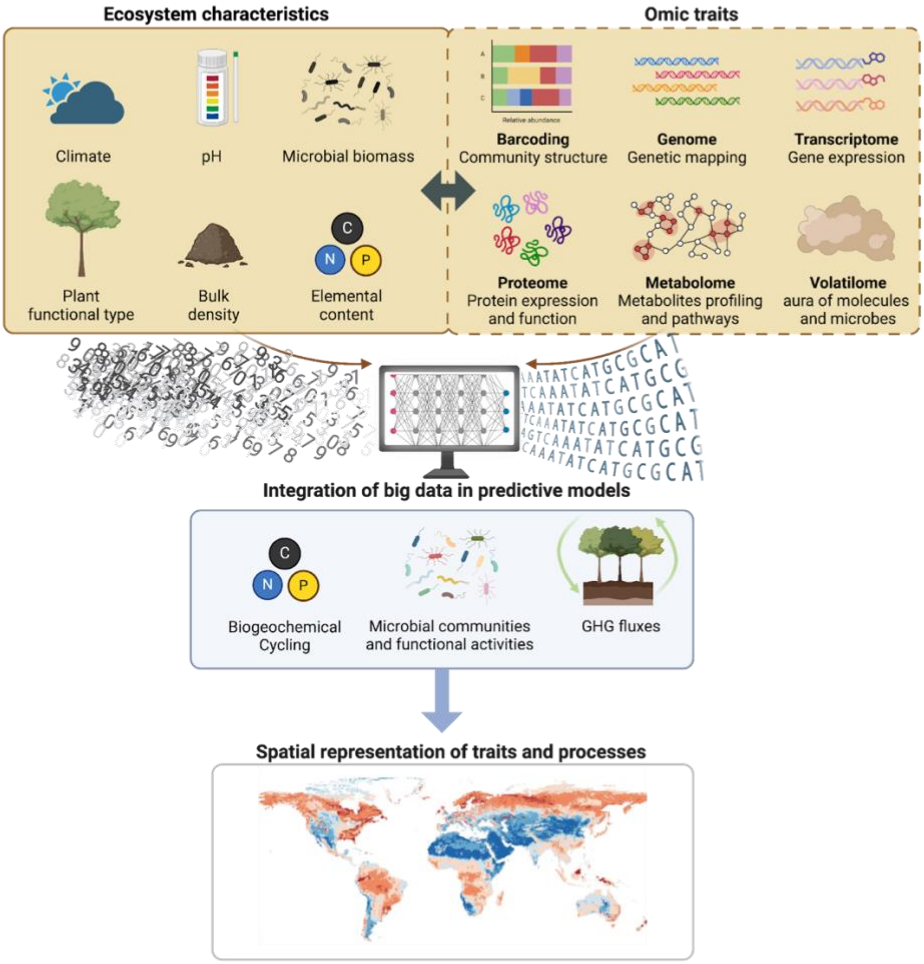

Figure 2: Conceptual figure of bottom-up system approach using meta-omics.

A growing number of databases and maps detailing key soil characteristics—such as soil bulk density, pH, carbon (C), nitrogen (N) and phosphorus (P) content—combined with climate forcing, are now openly available. These resources can support LSM numerical simulations, machine learning models, or hybrid approaches, to predict how soil properties, such as microbial C, N and P biomass, vary across the land surface. These soil characteristics are increasingly being linked to variations in soil microbial community structure and diversity. For example, Delgado et al. (2016) found that certain microbial groups thrive in high-pH soils, itself shaped by vegetation and climate. Similarly, fungal communities can be mapped to how soil mycorrhizal fungal guilds will vary across the land surface, with implications for soil C storage and nutrient acquisition by vegetation (Kivlin, 2020).

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More recently, these databases have been extended to include metagenomic data to show how genes linked to C storage vary across the global land surface (Piton et al., 2023). Linking metagenomic data with measurements of soil GHG fluxes or profiles of soil volatilomes could provide mechanistic insight into the metabolic characteristics of soil communities that control GHG and VOC fluxes with the atmosphere. These, in turn, could offer predictive tools for understanding how GHG and VOC fluxes might change with climate or disturbance (Fig. 2). Likewise, other omic datasets, such as soil proteomes or metabolomes, may provide additional insights into the realized and functional activity of soil microbial communities. For example, examining how soil GHG fluxes and gridded soil characteristics vary with soil metabolomes, proteomes, and community structure could pave the way for predicting soil C storage and GHG variability across large scales and over time, even from discrete soil samples.

2.4.3 Parameterizing ecosystem-level models with omics

Traditional ecosystem models often apply simplified representation of microbial processes, relying on parameters derived from cultivated microorganisms, which may not accurately capture the complexity and diversity of natural ecosystems (Steen, 2019). The increasing availability of metagenomics data presents an opportunity to integrate those microbial traits from genomes into mechanistic ecosystem models, potentially enhancing their predictive capabilities (Bahram et al., 2018; Woodcroft et al., 2018). By inferring microbial traits from genomes obtained in-situ, the metabolic potential of the microbial communities would be better represented, thereby providing more accurate and robust prediction of ecosystem functioning.

Incorporating genomic information into ecosystem models requires a structured approach, such as the genome-to-ecosystem (G2E) framework proposed in Riley et al. (2024), which we describe next. The G2E framework is a three-step process: (1) genomic trait prediction from genomes, 2) translation of genomic traits to kinetic traits, and 3) incorporation of kinetic traits into ecosystem models. The first step involves predicting traits from metagenome-assembled genomes which are obtained from environmental samples. For this step, microTrait, which extracts fitness traits from genomic sequences (Karaoz and Brodie, 2022), was applied, but analogous tools are available (Shaffer et al., 2020). In the second step, the predicted fitness traits are translated to microbial kinetic trait parameters commonly used in ecosystem models. DEBmicroTrait, a model based on dynamic energy budget (DEB) theory, for this step (Marschmann, 2024), was applied, but other approaches have also been used (Kumar et al., 2019). DEBmicroTrait translates fitness traits to kinetic parameters, e.g., maximum specific respiration rate (Rmax) and half-saturation constant (Km), which are key parameters in Michaelis-Menten kinetics. In the third step, ecosys, a mechanistic ecosystem model, is used to compute microbial respiration rates based on the Michaelis-Menten rate law, while accounting for dynamic environmental constraints (water, temperature, oxygen, nutrients) (Grant, 1998).

The G2E framework was applied to study the methane (CH_4) emissions from a thawing permafrost system (Li et al., 2025). The study found that variations in genome-inferred microbial traits lead to large differences in CH_4 emissions, demonstrating the critical role of genome-inferred microbial traits in regulating ecosystem functioning. In addition, the findings highlight the importance of including relative abundance of genomes in trait inference and integration with ecosystem models. While the study successfully linked genomic data to ecosystem processes and demonstrated the value of incorporating microbial relative abundance for improved model predictions, several caveats and needed future work are identified. For example, although supported by past research at the site, using relative abundance is a simplification of microbial activity (McCalley et al., 2014). Future work could enhance the trait-inference approach by including absolute abundance or other microbial activity indices. In addition, the current ecosys structure allows for 11 microbial functional groups but does not account for microbial diversity within each functional group, which could impact emergent carbon cycling rates. Future work that expands the current ecosys structure to allow microbial diversity could potentially reduce model uncertainty. Furthermore, the study focused on two sub-habitats within an arctic wetland. Applying the G2E framework to other locations and ecosystems could extend the use of genomic data across larger landscapes, enhancing our understanding and prediction of carbon-climate feedback.

2.5 Using omics to reconstruct past and forecast future environments

2.5.1 Past

Omics methodologies in paleo-ecological reconstructions have advanced from mere novelty to producing new ways of understanding ecosystem functions. Compared with traditional palynology techniques, such as pollen, fungal spores, and bacteria microfossils, metagenomics for instance captures changing trophic relationships among primary producers, consumers, and decomposers albeit at limited spatial scales (Jia et al., 2022). Still, omics and conventional proxies can be successfully combined despite the variations in spatial scale of processes and taxonomic resolution. For example, omics have been utilized to differentiate past ecosystem drivers and expand assessments of vegetation changes in rangeland ecosystems (Box 3). However, combining traditional and omics evidence in palaeo-ecology is still in its infancy because there are few epistemically independent models (Edwards, 2020; Jones and Bösl, 2021).

Molecular paleomicrobiology is an emerging field that leverages ancient and/or historical DNA (aDNA) technologies to uncover how microbial genomes and communities have evolved over time in response to environmental changes (Grasso et al., 2024). By studying ancient microbial remains preserved in dental calculus, paleofeces, archaeological sediments, and even environmental samples like permafrost, aquatic sediments and ice cores, scientists gain insights into historical human-microbe interactions and environmental adaptations (Capo et al., 2022a; Warinner, 2022; Warinner et al., 2014, 2017). Remarkably well-preserved microbial aDNA from stable environments, such as permafrost, allows us to track the evolutionary history of microbial taxa and understand ecosystem responses to past climate shifts. For instance, DNA from two-million-year-old Greenland permafrost has revealed how plant and animal communities from the Middle Pleistocene adapted to environmental changes. However, the complex mixture of DNA from ancient and more recent microbial populations still complicates efforts to disentangle the signals from pioneering microbes and those deposited at a later time (Fernandez-Guerra et al., 2023; Kjær et al., 2022).

While post-mortem DNA degradation complicates the analysis, predictable damage patterns, such as fragmentation and specific base modifications, offer clues to the age of the samples (Briggs et al., 2007). This information is crucial as we work to reconstruct microbial genomes from diverse environments, which might contain amounts of aDNA that may reflect past ecosystems. Recently, DNA could be even extracted from low-biomass containing carbonate rocks with distinct DNA fragmentation patterns allowing us to separate ancient from modern communities (Wegner et al., 2023). Thus, these rock formations might act as potential archives of ancient microbial records. However, MAGs have to be reconstructed from these challenging environments to deepen our understanding of subsurface microbial life and its long-term changes, ultimately refining estimates of microbial populations in the Earth's crust.

Long-term records of aquatic biota are still scarce as monitoring using DNA approaches started about two decades ago. Fortunately, the extraction and sequencing of environmental DNA preserved in sedimentary archives has shown its potential to reconstruct past environmental changes and their impact on aquatic microbial diversity (Capo et al., 2024; Nguyen et al., 2023). In a recent review, Barouillet et al. (2022) highlighted how molecular paleoecology research augments knowledge about the effects of anthropogenic stressors on past aquatic biota. On a longer time scale, Armbrecht et al. (2022) show that photosynthetic genes dated back to 540,000 thousand years ago can be detected from Southern Ocean sedimentary archives. Overall, past DNA data is foreseen to be a valuable proxy for projecting the impacts of near-future environmental changes on microbial diversity across both aquatic and terrestrial systems.

Box 3: Sedimentary ancient DNA in Rangelands

Rangelands provide a habitat for various native and domestic herbivores which interact with and impact these ecosystems throughout history. Wetland sedimentary environments, where pollen accumulates are important areas for herbivores by providing essential resources such as food and water. Herbivores deposit dung in these areas after feeding on various plants like grasses, forbs, shrubs, and trees from parts of landscapes.

Tabares et al (2020) demonstrated that sedimentary aDNA provided a more detailed taxonomic resolution of grasses and forbs, revealing shifts in edible plant species due to fire management. Furthermore, Giguet-Covex (2014) discovered that aDNA was able to trace the functional differences among herbivores, such as equids and bovids, which have varying feeding habits and effects on landscapes. aDNA from sedimentary sources not only enhances traditional pollen -based (palynology) techniques, but metagenomics—analysing all DNA in environments simultaneously—could be a stronger method for assessing trophic shifts in ecosystems thereby improving rangeland conservation (Fig. 3).

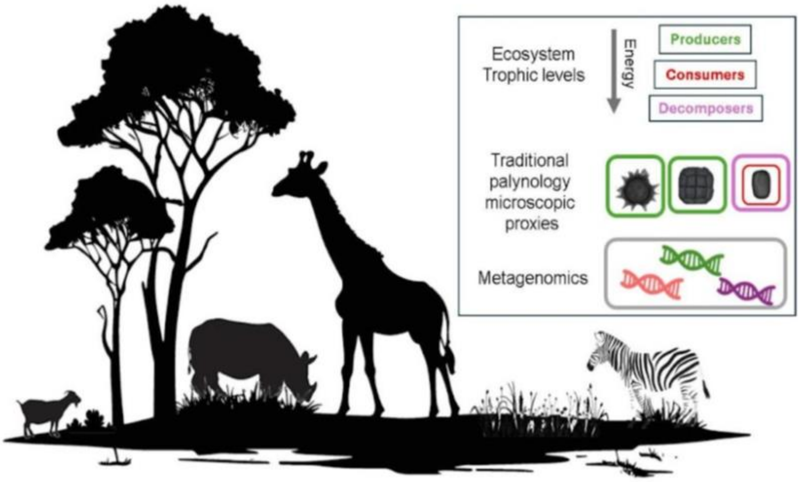

Figure 3: Integration of traditional palynology and new omics tools for tracing trophic relationships in rangelands.

2.5.2 Future

Experimental approaches to studying microbial evolution and its role in biogeochemistry

Geological and paleoclimate records provide environmental analogs to how ecosystems may respond to future climate scenarios. However, such studies are typically limited in their scope by generalizing at the ecosystem-level without insights into the processes and mechanisms driving individual species responses. One such response is local adaptation to changing environmental conditions, where species may disperse to new favourable conditions and expand their geographic ranges or evolve adaptive traits over evolutionary time through gene flow with neighbouring populations and/or emergence of advantageous de novo mutations. Given the long timescales to observe adaptive traits, reciprocal transplant experiments have provided direct insights into the ecological and evolutionary responses to predicted climate conditions. For example, plant communities, given their importance in terrestrial ecosystems, have long been studied demonstrating plant species are locally adapted to current environmental conditions. Such studies highlight differential survival and fecundity (i.e., flowering time) to changing conditions, highlighting phenological traits that may contribute to adaptive differentiation and possible evolutionary responses (Ågren et al., 2012). In other words, past evolutionary divergence caused by local adaptation can restrict and influence contemporary ecological patterns and processes (Urban et al., 2020).

Numerous microbial studies have demonstrated, through reciprocal transplant experiments or experimentally manipulating environmental conditions (e.g., drought or temperature), that microbial communities can rapidly respond through the ecological process of species sorting, or the differential survival and reproduction of locally adapted taxa (e.g., DeAngelis et al., 2015; Finks et al., 2021). Furthermore, these taxonomic shifts can have implications for ecosystem functions, such as influencing the rate of decomposition in the leaf litter layer (Glassman et al., 2018) or a reduction in carbon use efficiency from long-term soil warming (Li et al., 2019). Furthermore, other ecological processes, such as dispersal can play a significant role in the recovery or successional dynamics of a microbiome after large-scale disturbances (i.e., wildfires; Barbour et al., 2023) that are only expected to increase in their rate and intensity under future climate scenarios.

However, microbes are distinct in that their generation times, and thus capacity for adaptation, operate on much faster timelines. Combined with large population sizes and their capacity to exchange DNA within and across lineages, microbes are exposed to a vast reservoir of genetic diversity within microbial communities that may contribute to rapid adaptive responses to environmental change. Certainly, lab-based experimental evolutionary studies that manipulate a selective pressure (e.g., heat) have repeatedly demonstrated that microbes can rapidly evolve and adapt over weeks to months (Kent et al., 2018; Tenaillon et al., 2012), although it's unclear how these artificial laboratory conditions translate to natural populations. Recently, natural experiments using a reciprocal transplant approach across a regional climate gradient demonstrated that microbes, as observed in lab-based experiments, can rapidly adapt through de novo mutations in response to predicted climate scenarios (Chase et al., 2021a). However, such adaptive responses under natural conditions are likely operating under reduced selective pressures on monthly and annual timescales and, thus, may have a reduced role compared to rapid ecological responses (Chase et al., 2021a). Nonetheless, a shift in the microbiome under changing climate conditions is dependent on the continuum of ecological and evolutionary processes that operate at the same time. It is the consideration of the relative influence of ecological and evolutionary processes that contribute to a microbiome's response to changing environmental conditions and the timescales in which these changes interact and amplify ecosystem functioning (Abs et al., 2024b, c; Martiny et al., 2023).

Predicting long-term ecosystem responses using omics-parameterized models

Using microbial kinetic traits inferred from multi-year omics data, ecosys can be used to predict future ecosystem dynamics. Specifically, ecosys was employed to predict ecosystem dynamics in an Arctic wetland under the RCP8.5 scenario (RCP: Representative Concentration Pathway) through the year 2100 (Li et al., 2025). That ecosys simulation incorporated genome-inferred microbial traits (i.e., community-aggregated traits weighted by genome relative abundance) and baseline microbial traits. The model results show reasonable seasonal cycles of methane and net ecosystem exchange (NEE) during the late 21st century, and have about 18% and 21% difference in annual methane emissions and NEE, respectively. The differences were mediated by shifts in the overall carbon cycle, largely due to microbial activity, belowground nutrient transformations, and vegetation dynamics (Bouskill et al., 2020). We highlight some caveats to these results. First, the microbial traits inferred from omics that we applied are constants based on current life-history traits (e.g., growth rate, resources utilization, and stress tolerance); however, those traits may adapt to changing environmental conditions (Sokol et al., 2022). Work is underway to develop models of how adaptation may occur, and to integrate those approaches with ecosystem models (Abs et al., 2022, 2024b; Abs and Ferrière, 2020). Second, the genome-inferred microbial traits we determined span ranges within each microbial functional group, reflecting the multiple genomes that perform the same metabolic functions (Li et al., 2025). However, our application of these traits described here considered only a single value for each trait in each microbial group. Ongoing work in ecosys will allow for trait diversity within microbial functional groups, thereby allowing prediction of dynamic community assembly under dynamic and competitive environmental conditions.

Box 4: Predicting future ocean biogeochemistry

Predicting the fate of marine ecosystems in an ocean impacted by dramatic change is not possible without a base line. However, global surveys are rare because of the requisite commitment to standardize sampling and analysis methods on a huge scale. Most attempts to predict future ocean biogeochemistry therefore tend to focus on one parameter, such as how concentrations of a critical nutrient may change as a function of altered temperature or ocean mixing (Shaked et al., 2021), or how the features of one specific region may change in the future (Tagliabue et al., 2017). Alternatively, efforts have been made to combine datasets from different sources, with the inherent problem of ensuring data consistency to avoid comparing apples with oranges. This generally means that only the most rudimentary data types can be combined from different sampling programs. A prominent example of a single global survey that has generated an internally consistent dataset is Tara Oceans (Bork et al., 2015). From 2009-2013, an international team of scientists onboard the research schooner Tara performed a comprehensive sampling program at more than 200 sites worldwide, aimed at exploring the entire size range of organisms within plankton communities in the sunlit upper layer of the ocean, from the smallest viruses of a few tens of nanometres to zooplankton several millimetres in size. The initiative generated tens of thousands of high quality samples, and their subsequent analysis using highly standardized protocols based on omics and microscopy has generated the first ever baseline of life in the ocean at global scale. As a consequence of the highly contextualized, comprehensive open access datasets that have been generated by Tara Oceans scientists that cover the entire community of organisms residing in the plankton (summarized in Sunagawa et al., 2020), many thousands of primary research papers have been generated by the international scientific community. These address multiple fundamental research questions that, in general, have been used for improving our understanding of: 1) Basic molecular and cellular processes in all domains of life, and beyond canonical model organisms, 2) Ecological and evolutionary principles, and 3) The interface between marine ecosystems and functioning of the Earth System, and the feedbacks between them. The Tara Oceans base line can also be used as the starting point to address how marine ecosystems and the geochemical pathways they manage may change in the future. There are now several examples of how this has been done (Frémont et al., 2022, 2023; Ibarbalz et al., 2019), with a typical approach being to project changes in the future ocean simulated in the IPCC climate models. An example is shown in Fig. 4, where anomalies in the biodiversity of major planktonic groups by end-century are predicted based on current patterns of latitudinal diversity gradients. The results predict major changes throughout the global ocean, and especially in high latitude regions that are of particular importance for carbon capture by the biological carbon pump and for the fishing industry. These regions also coincide with high densities of marine protected areas, highlighting the need to take heed of these results in future conservation efforts.

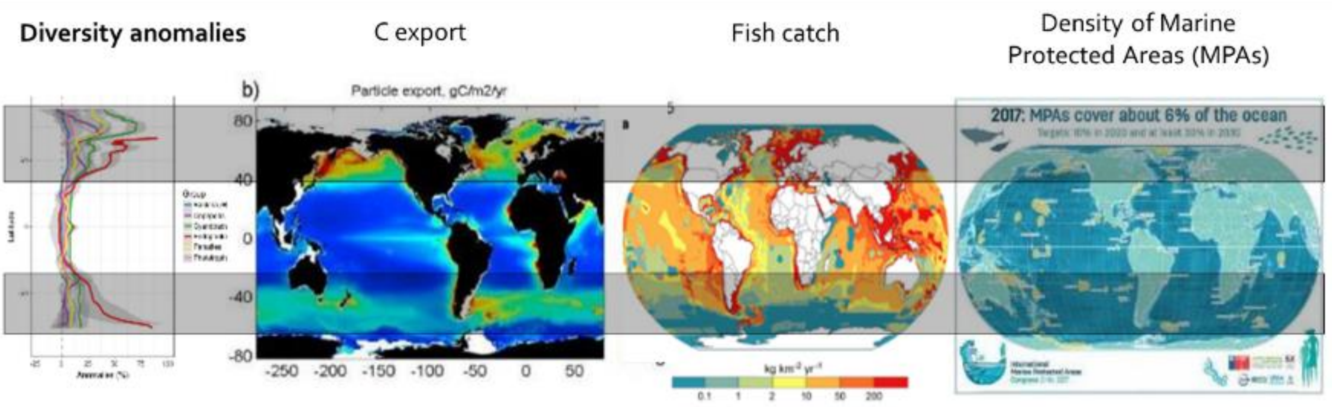

Figure 4: Projected effects of diversity changes within plankton communities on marine ecosystems, fisheries, and biogeochemical cycles (adapted from Ibarbalz et al., 2019).

While exercises such as these provide valuable information about how the ocean's biogeochemical cycles may be impacted by climate change in the future, a major caveat is that they do not include any information about how organisms may adapt to future conditions. Most likely, some organisms will migrate to new environments, others will go extinct, and yet others will adapt or evolve. Our lack of understanding about such processes is a major impediment to understanding what the future landscape of life on our planet will look like. Extensive studies in powerful experimental systems such as mouse, Drosophila and Arabidopsis have revealed much about the importance of both genetic and epigenetic drivers in evolution (Chatterjee, 2024; Feinberg and Irizarry, 2010; Schmid et al., 2018), but much remains to be done to understand adaptation in the natural world.

3 Challenges and perspectives

Long-term Earth system monitoring programs, along with preserved sample archives, present a valuable opportunity to enhance ESMs by providing insights into climate-driven ecosystem transformations. The recent surge in omics-based technologies has catalysed untargeted measurements across diverse environments, as highlighted in this paper with examples from deep-sea sediments, plant canopies, the atmosphere, cryospheric regions and marine ecosystems. However, the proposed implementation of omics driven data into modelling efforts faces challenges outlined in the following:

3.1 Data integration and interpretation

Integration of omics data into ESMs is complex due to the sheer diversity, scale, and volume of data these approaches generate. Multi-omics datasets capture different biological layers, often involving vast amounts of heterogeneous data. This heterogeneity arises because each of these layers represents different types of biological information, from genetic sequences to metabolite profiles and often vary in data structure, format, and the presence of missing information due to limitations inherent in omics technologies (Ramirez Flores et al., 2023).

Connecting these diverse datasets to critical ESM response variables—such as GHG emissions, soil carbon stocks, or other processes relevant to predicting human-induced climate change—is challenging. For instance, microbial-driven methane production is well characterized: its defined enzymatic pathways and environmental controls might enable more straightforward integration of omics data. In contrast, turnover of soil organic carbon is driven by a highly diverse array of microbes operating under variable conditions. This complexity might make it much harder to translate omics-based measurements into accurate process rates for ESM incorporation (He et al., 2024a).

Recent advances in deducing microbial traits from metagenomic data show great promise for integrating omics information into biogeochemical models by linking these data with kinetic parameters (Karaoz and Brodie, 2022). By identifying functional traits from metagenomes, researchers can begin to quantify the roles of various microbes in processes like nutrient cycling or carbon turnover, which holds the potential to enhance the predictive power of ESMs. Extending this approach to other types of omics data could lead to more comprehensive ESMs that incorporate detailed biotransformation kinetics, ultimately resulting in more accurate climate-related predictions.

3.2 Data accessibility and standardization

Ensuring accessibility to omics data and establishing robust community standards constitute essential steps to advance the integration of omics data into ESMs. Initiatives like the National Microbiome Data Collaborative (NMDC) (Eloe-Fadrosh et al., 2022) and Integrated Microbial Genomes & Microbiomes (IMG/M) (Chen et al., 2023) created frameworks that promote data sharing and enforce metadata standardization. These frameworks provide structured approaches for documenting and sharing omics data, ensuring that researchers follow uniform guidelines when collecting, annotating, and storing data. However, the adoption of these standards across the global scientific community has been limited so far. Such a globally implemented and executed framework would help address questions on large scales, as it would enable the aggregation and cross-referencing of omics data from diverse ecosystems worldwide. Additionally, standardized data formats would also facilitate data access to emerging AI-driven tools which hold the potential to play a key role in identifying yet unseen barriers in improvements of ESMs and might also help to overcome those.

3.3 Emerging technologies

Technological advances, particularly in ancient/historical DNA (aDNA) analysis, have opened new pathways for studying long-term ecological responses to environmental changes. aDNA analysis enables scientists to retrieve genetic information from organisms preserved in ancient samples, such as ice cores (Zhong et al., 2021) and sediment layers (Nguyen et al., 2023). By integrating biological data with chemical signatures found in these preserved samples, we can reconstruct ecosystem dynamics over extended historical periods, offering valuable insights into how biomes have responded to past climate variations. Such and other omics data will become increasingly available now as ongoing advancements in omics technology have gradually reduced the amount of analyte required for analysis, making it feasible to use small or degraded samples from ancient archives.

Incorporating these ancient biological signatures into ESMs has the potential to enhance model accuracy significantly. By cross-validating current ESM data with insights from historical records, scientists can better understand the relationships between abiotic factors and biotic responses over time. This integrative approach could improve the models' capacity to predict ecological responses to future climate changes by anchoring them in real historical data, providing a long-term perspective that modern data alone cannot offer.

3.4 The necessity of interdisciplinary collaboration

Unsurprisingly, integrating omics data into ESMs demands collaboration across disciplines like ecology, geochemistry, bioinformatics, modelling, and data science. Each field brings crucial expertise: ecologists and geochemists link biological and chemical processes, bioinformaticians manage complex omics data, modelers translate findings into model parameters, and data scientists develop frameworks to address challenges in data integration and accessibility. Environmental scientists play a key role in identifying biochemical pathways and traits essential for model parameterization, thereby improving the accuracy of ESMs in simulating ecosystem functions.

Collaborative efforts like these would produce enhanced ESMs that incorporate omics data, rooted in comprehensive, relevant datasets and overcoming the barriers of data integration and accessibility. We believe that the EGU community offers an ideal platform for such interdisciplinary initiatives. Leveraging existing long-term ecological monitoring projects through collaborative projects generating omics data aimed for model integration, would be a logical first step in these efforts, and we encourage all stakeholders to use this opportunity and actively participate.

Code/data/sample availability

No code, data or sample were used for this perspective.

Author contribution

E.A. led the writing, E.A., C.K. and L.W. initiated the design and writing of the article. All co-authors wrote at least one subsection and provided input on the manuscript text, figures and discussion of scientific content.

Competing interests

The authors declare that they have no conflict of interest.

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