

Using meta-omics to unravel biogeochemical changes from cell to planetary scales

Elsa Abs, Christoph Keuschnig, Pierre Amato, Chris Bowler, Eric Capo, Alexander B. Chase, Luciana Chavez Rodriguez, Abraham Dabengwa, Thomas Dussarrat, Thomas Guzman, Linnea K. Honeker, Jenni Hultman, Kirsten Küsel, Zhen Li, Anna Mankowski, William J. Riley, Scott S. Saleska, Lisa Wingate

RESPONSE TO REVIEWERS

General:

The manuscript, No.: egusphere-2025-1716 Elsa Abs et al., “Using meta-omics to unravel biogeochemical changes from cell to planetary scales” presents a thoughtful and robust review of current meta-omics technologies by addressing the applications and limitations of each and the potential for integration in different research scenarios. The authors highlight method-specific details and a diverse collection of use cases. This manuscript will serve as a useful resource for those interested in approaching different omics techniques in their own research. The information collected in Table 1 is a particularly useful summary of current resources for the different omics methods. Overall, this manuscript was informative and enjoyable to read.

My concerns after review are minor and mostly structural. In section 2.3 it is unclear why the examples switch back and forth between being Boxes and Main Text, although this may be more clear in how the authors envision the print version. I would suggest structuring the examples from subsurface systems, air microbiology, global oceans, cryosphere, and plant systems all in the same style (either all as Boxes or all as Main Text). Later on the use of Box 4 and 5 fit better with the structure of section 2.5.

Response 1:

We thank the reviewer for this helpful observation. The alternation between Boxes and main text was intentional but insufficiently signposted: each Box is designed as a standalone, per-system entry point (air, cryosphere, soil, plant, ocean) so that readers can locate the case study relevant to their own system without reading the full article. We have made this rationale explicit in the final paragraph of the Introduction (lines 104–105).

The following specific comments and technical corrections are highlighted by line/section number.

Specific Comments:

54 - 57) Consider focusing these opening statements about relevance more on the aspect of over-exploitation rather than human population dynamics.

Response 2:

We thank the reviewer for this suggestion. We have rephrased the opening of the Introduction so that it now centers on the over-exploitation of natural resources (farming, mining, construction, and other industrial practices) as the driver of pressure on Earth's systems, rather than on human population growth (lines 54–57).

116) this estimate of biomass should have a citation, one suggestion is the Tara oceans report from 2022 that you already cite later on in line 127

Response 3:

Thank you, we added the citation (now line 117).

338) Match the header style between 2.4.2 (Combining meta-omics...) and 2.4.3 (Integrate omics data...). I suggest changing integrate to integrating

Response 4:

Done thank you (now line 294).

Section 3.2) I understand that the metadata curation and data accessibility is not the main point of this manuscript, however, you do nicely highlight metadata standards and frameworks in Table 1 without explaining them or why they are important in the main text. Consider expanding paragraph 3.2 with a few more sentences to define MIxS, ENVO, and the other standards mentioned in Table 1. Or at least include the major citations for each standard (this could also fit within the legend of Table 1).

Response 5:

We thank the reviewer for pointing out this gap between Table 1 and the main text. We have expanded Section 3.2 to define the principal metadata standards and controlled vocabularies referenced in Table 1, including MIxS (with its MIGS/MIMS checklists) and ENVO, and to note the complementary standards used in other domains (ISA-Tab for metabolomics, and ISO 19115 and the CF conventions for geospatial and atmospheric data). The major citations for these standards (Yilmaz et al., 2011; Buttigieg et al., 2013) have been added accordingly (lines 503–512).

Technical corrections:

96) Typo in “metabolomics”

Response 6:

Done thank you.

Glossary: “Binning” is not bold

Response 7:

Done thank you.

243) “Metabolomics are also a tool.” Change to “Metabolomics is also a tool”

Response 8:

Done thank you (now line 245).

456) Remind the reader of what the acronym ESMs stands for again in this new section

Response 9:

Done thank you (now line 460).