



## Comment on soil-2021-148

Anonymous Referee #2

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Referee comment on "Lower functional redundancy in "narrow" than "broad" functions in global soil metagenomics" by Huaihai Chen et al., SOIL Discuss., <https://doi.org/10.5194/soil-2021-148-RC2>, 2022

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### General comments:

In this paper, the authors investigated the relationship between taxonomic composition and functional profiles to understand if microbial functional redundancy varies between "broad" and "narrow" functions. Using public metagenomes from a variety of environments, the authors assessed the taxonomic composition, diversity, and co-occurrence of taxa from 5 "broad" and 5 "narrow" functions. Ultimately, their findings supported their hypothesis that functional redundancy does vary significantly depending on the type of function. Although this is likely expected by many, it is a well designed and executed in-depth analysis into this hypothesis that provides concrete evidence of the significant difference in microbial functional redundancy depending on the type of function. Overall, it is a very well written manuscript.

Methods: I highly recommend creating an overview figure highlighting how the data was input, transformed, and analyzed. Although the manuscript lays out a lot of detail in the methods section, I think this will really help the reader keep track of the data analyses.

### Specific Comments:

Line 206 – how did you deal with the differences in taxonomic classification level across datasets? Likely certain datasets had more unclassified than others. Did you take this into account?

Line 437-438 – I think this sentence describing the differences in positive and negative

links between broad and narrow function networks is really interesting and would benefit from some more discussion about the implications and reasoning behind these differences. For example, adding some information about why broad functions like carbon cycling would increase the positive linkages compared to narrow functions like iron cycling.

Lines 358-368 and Supplemental Figure 1 – Something that stood out to me was how distinct the ice cap and sometimes arid desert was from the other environmental samples. I think this is something to be mentioned in your discussion about the relationship between microbial metabolic function coupling to certain environmental factors may be more coupled and less likely to decouple when you are discussing extreme environments that already have significant selective pressure.

Technical Comments:

Line 106 – change “contructed” to “constructed”

Line 156 – change “conductingeach” to “conducting each”

Line 305 – I suggest adding/changing your topic sentence to something that helps transition the reader. Right now, it is rather abrupt.