

Reproducibility and robustness of metabarcoding

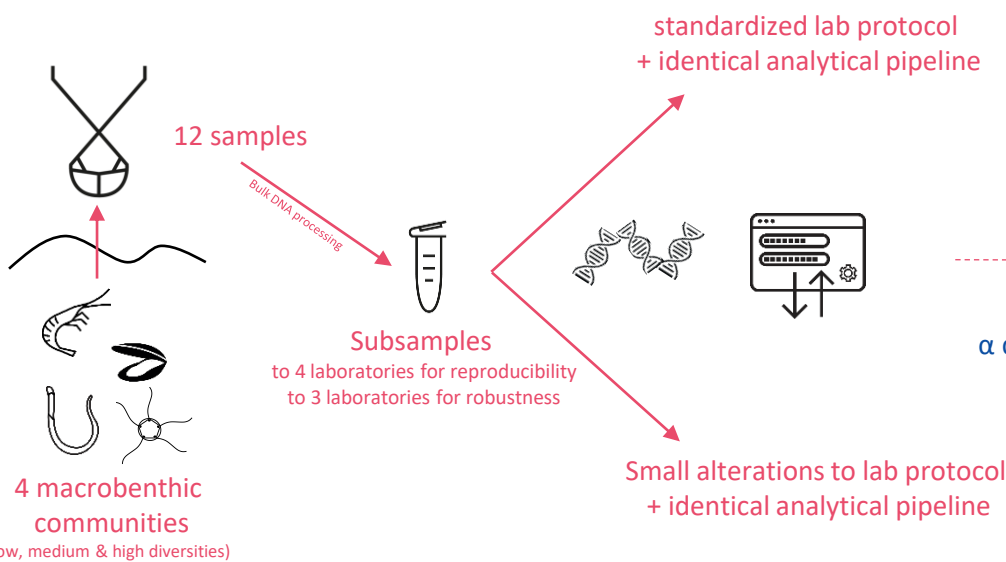
WHY do DNA-based methods need to be reproducible and robust?



Metabarcoding requires a number of processing steps, with each step prone to a variability that can influence the final result. Hence, testing the reproducibility and robustness is a key step in the implementation process. Only robust and reproducible methods will allow comparisons across studies, regions and time series.

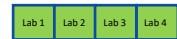
HOW did we test reproducibility and robustness?

(based on GEANS ring test data, 2023)

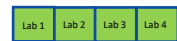


REPRODUCIBILITY

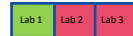
α diversity*: very similar



β diversity*: almost identical



α diversity: significant differences



β diversity: minor differences



ROBUSTNESS

* α diversity: calculated as species richness, Shannon diversity index and inverse Simpson index
 β diversity: community patterns as derived from multivariate analyses



The different alpha diversity measures are affected by changes to the laboratory protocol. Standardization is vital for comparability between studies and regions.



Community patterns are reproducible between labs and robust to small changes to the lab protocol, supporting the suitability of DNA-based methods for studying ecological multivariate patterns.

A standardized protocol allows to compare metabarcoding results from different studies. In the absence of an agreed standardized protocol across countries, we stress the importance of providing a detailed description of the used lab protocol.



Read more: <https://www.sciencedirect.com/science/article/pii/S1470160X23003497?via%3Dihub>