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Meta-analysis of positive controls and laboratory metainformation in microbiome data

Recent advances in next-generation deep sequencing technologies have revolutionized our understanding of the microbiota's contribution to human health and disease. However, there are as many microbiome-disease associations as there are different protocols for generating microbiome data. This heterogeneity in laboratory data generation methods leads to protocol-specific biases in microbiome data and limits the comparability of microbiome studies. The biases can potentially be quantified by evaluating positive controls, i.e. microbiome mock communities with known sample composition that are processed along with biological samples.

We aim to build a database of published microbiome studies that used standardized, commercially available positive controls, and collect the studies'laboratory metadata to quantify the impact of different laboratory methods on microbiome data.

Therefore, we performed a systematic literature search of scientific papers using commercially available positive controls, and performed an initial meta-analysis for one mock community.

The pilot mock for meta-analysis, MSA-2002, was mentioned in 32 articles, of which seven remained for collection of lab metadata after applying exclusion criteria. On average, these seven studies provided 12 (median) out of 22 required laboratory metainformation factors. Combining the mock sequencing data of a subset of five studies revealed the substantial impact of study-specific biases on microbiome results.

Further analysis of the remaining mock communities is needed to assess whether positive controls can be used to quantify the biases introduced by laboratory methods. Our pilot project has shown that many scientific articles do not provide the necessary laboratory information to understand and reproduce their data. Moreover, the relevant pieces of information are often inconsistently described or scattered across the methods section, requiring automated paper scraping methods to extract them. The field of microbiome research needs to advance its reporting standards for laboratory metainformation to ensure reproducibility and comparability of microbiome data.

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Standards

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Meta-analysis, laboratory metadata, reporting standards

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