Identifying Biases and their Potential Solutions in Human Microbiome Studies

Jacob Thomas Nearing

André M. Comeau

Morgan G. I. Langille

Video Byte

Keywords: Microbiome, methodology, bias, metagenomics, amplicon, contamination, structure, abundance, microbe

Posted Date: October 14th, 2021

DOI: <https://doi.org/10.21203/rs.3.rs-968131/v1>

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Abstract

Recent advances in DNA sequencing technology have made it possible to investigate community-wide changes in microbes that live on and within the human body. Unfortunately, different studies can have different results, often due to systemic biases introduced at various stages of sequence-based microbiome studies. Sample collection can introduce biases depending on the source site and method of collection. Consistent collection methods are essential, and care must be taken when choosing storage methods, times, and reagents. Increasing the usage of benchmark samples and technical replicates may also help to mitigate batch effects during sample collection and processing. Additional bias can arise during DNA extraction due to differing extraction efficiencies, contamination, and the introduction of DNA from non-living organisms. Introducing steps to this process to reduce contamination and measure inter-plate and inter-assay variability will help to reduce these effects. Finally, considering additional biases introduced during PCR amplification, sequencing, and bioinformatic analysis is critical to uncovering the true microbial communities present in a sample. Using consistent protocols, aiming to reduce bias, and clearly reporting techniques used will help researchers to ensure the reproducibility of their results.