

# Reproducibility of Computational Analyses to Understand Microbiome Composition and Functional Profile

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## **Abstract**

Reproducibility remains a critical challenge in computational bioinformatics, particularly in the analysis of 16S rRNA sequencing data. This study systematically analyzes the reproducibility of an existing bioinformatics pipeline for 16S rRNA sequencing by applying established reproducibility metrics from available literature and identifying key trends in computational consistency and output variability. A structured and well-documented code framework is developed to systematically assess the pipeline's reproducibility, ensuring transparency and facilitating future evaluations. The analysis identifies key challenges and best practices for improving computational reproducibility in microbiome research. This work contributes to the ongoing effort to establish reproducibility as a standard practice in bioinformatics.