

# Comparative metagenomic and rRNA microbial diversity characterization using Archaeal and Bacterial synthetic communities

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## Background

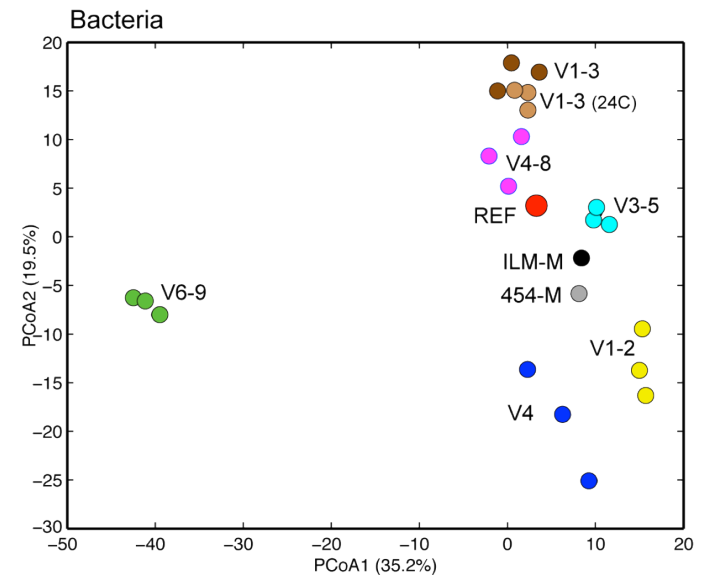
Taxonomic and functional characterization of microbial communities by rRNA gene and metagenomic sequencing have been used extensively. Determining accuracy and performing cross-comparisons between approaches are limited by data incongruences and the lack of knowledge of the true ecological diversity.

## Science

- We used complex mixes of bacterial and archaeal pure genomic DNAs to directly compare inferences from metagenomic and rRNA amplicon sequencing.
- Both Illumina and 454 metagenomic data outperformed amplicon sequencing in quantifying the community composition. The accuracy of public analysis platforms (IMG, MG-RAST) and several widely used software was highly dependent on analysis parameters. Sources of errors were identified and we proposed alternatives to correct them.

## Significance

- A reference community approach is important for calibrating and validating experimental design and data analysis in long term environmental studies.



*Nonmetric multidimensional scaling of Bacteria community composition inferred by metagenomics (454-M and ILM-M) and rDNA amplicon sequencing relative to the known community composition (REF).*

Shakya M, Quince C, Campbell JH, Yang ZK, Schadt CW, Podar M. Comparative metagenomic and rRNA microbial diversity characterization using archaeal and bacterial synthetic communities. *Environ Microbiol.* 2013 Jan 18 (Epub ahead of print).