

You find what you look for: Improving reference-based methods of classifying metagenomic sequences

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Characterizing microbial diversity

Amplicon Sequencing

- Region of genome is amplified
- All reads assigned
- No functional information
- Can't compare between kingdoms

Shotgun Metagenomics

- Comparison of reads to reference library
- Functional and strain information
- Comparison between kingdoms
- Some reads unassigned