

16S rRNA Analysis – A Quick Guide

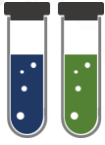
Sampling and Wet Lab

Bioinformatics

Step

Look out for:

Sampling



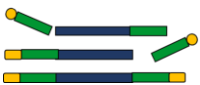
- Preserve samples to maintain original sample community
- Include sampling controls
- Include biological replicates if possible

DNA Extraction



- Select (and test) sample appropriate extraction method
- Work in sterile environment
- Include extraction controls
- Include technical replicates if possible
- Assess DNA quality and quantity

Amplification (PCR)



- Select Primers that target region of interest, e.g. V3/V4 region
- Use barcoded primers when working with more than one sample
- Select correct temperature settings (e.g. primer specific annealing temperature)
- 30 - 35 cycles are commonly used for 16S rRNA PCR
- Include negative and positive controls
- Include technical replicates
- Check PCR product visually (Gel, tape station) and assess quantity

Sequencing

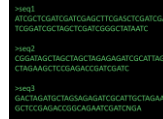


- Clean up and pool (if more than one sample)
- Select correct sequencing platform and chemistry depending on length of PCR product (e.g. Illumina 2x150bp)
- Attach sequencing adapters

Step

What to watch for

QC and pre-processing



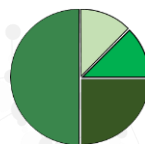
- Remove reads of poor quality or length
- Trim sequencing adapters
- Common tools: FastQC, Cutadapt
- Demultiplex samples based on used barcodes

ASV/OTU picking



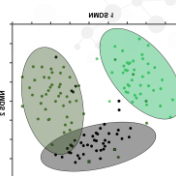
- Merge reads (not necessary when single end sequencing was used)
- Identify amplicon sequence variants (ASVs) or operational taxonomic units (OTUs) to identify which sequences are similar to each other
- Set an appropriate threshold for sequence similarity (OTUs)

Taxonomic assignment



- Assign taxonomic identities to ASVs/OTUs using reference databases such as SILVA or RDP
- Use negative control data to remove contamination ASVs/OTUs

Diversity Analysis



- Calculate alpha diversity metrics (e.g., Shannon) to measure diversity within individual samples.
- Evaluate beta diversity using distance metrics (e.g., Bray-Curtis) to assess differences in community composition between samples.
- Perform statistical tests (e.g., ANOSIM, PERMANOVA) to determine the significance of observed differences.

Visualization

- Visualize data using bar charts, bubble plots, heatmaps, PCoA plots or trees

Need more information?
Contact us at info@greengategenomics.com