

# Amplicon Processing Overview

Raw data  
fastQC

■ fastqc/multiqc



Primer  
removal

■ cutadapt



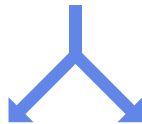
Quality  
filter/trim

● dada2 ▲ bbdut



Filtered data  
fastQC

■ fastqc/multiqc



Resolve  
ASVs

● dada2

Generate  
OTUs

▲ vsearch



Differential  
abundance

● DESeq2



Assign  
taxonomy

■ DECIPHER

- SILVA DB for 16S
- UNITE DB for ITS
- PR2 DB for 18S

■ All

● Illumina data

▲ 454/Ion-Torrent data

## Primary outputs:

- Recovered ASV/OTU sequences (fasta) ■
- Counts of sequences per sample ■
- Taxonomic classifications of sequences ■
- Beta and alpha diversity plots ●
- Taxonomic bar plots ●
- Differential abundance analysis and visualizations ●