

amptk ion
amptk illumina
amptk 454
amptk SRA

1. Find barcode (Ion /454), relabel header
2. Merge PE reads (illumina only)
3. Find/Trim Forward and Reverse Primers
4. Trim/Pad read to set length (optional)
5. Combine samples (Illumina only)
6. Create sample mapping file (QIIME-like map file)

amptk cluster
amptk dada2
amptk unoise2

7. Quality filter reads (expected errors filtering)
8. Run "Clustering"
 - UPARSE: 97% clustering into OTUs
 - DADA2: de-noising into inferred sequences
 - UNOISE2: de-noising into inferred sequences
9. Reference chimera filtering (optional)
10. Map reads to OTUs and/or iSeqs
11. Create OTU table

amptk filter

12. Map OTUs/iSeqs to mock community (optional)
13. Calculate index-bleed rate between samples
14. Apply index-bleed filter, remove counts below rate
15. Update FASTA OTUs/iSeqs and OTU table

amptk taxonomy

16. Pre-formatted databases for ITS, 16S, COI, and LSU can be downloaded with 'amptk install'
17. Assign taxonomy using "hybrid" approach
 - Global alignment to reference DB
 - UTAX Classifier based on trained DB
 - SINTAX Classifier based on reference DB
 - parse results and choose best taxonomy
18. Output taxonomy, append to OTU table, create BIOM

amptk SRA-submit

amptk heatmap

amptk summarize

amptk funguild