



--mode runall

--mode aln

Align to marker database (bowtie2)

Filter by alignment length (>80% read length)

Quality filter (MAPQ > 30)

Raw alignments (.bam)

--mode filter

Low-complexity filtering (Komplexity)

Duplicate read filtering (samtools)

Filtered alignments (.bam)

Count aligned reads, coverage, & percent sequence identity

Reads per marker (.txt)

Filter species & taxIDs by observed markers & aligned reads

Reads per filtered species or taxID (.txt)

Taxonomy tree of filtered hits (.txt)

Summarize alignments per species (or taxID)

Reads per species or taxID (.txt)

Taxonomy tree of hits (.txt)