



--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 minimum
observed markers &
aligned reads
(2+ markers, 4+ reads)

Reads per filtered
species or taxID
(.txt)

Taxonomy tree
of filtered hits
(.txt)

Summarize alignments per
species (or taxID), no filtering

Reads per
species or taxID
(.txt)

Taxonomy tree
of hits
(.txt)