## Input Sequences **rRNA** <600 bp LAST fast candidate search hmmalign multiple alignment Taxonomic Summaries >600 bp LAST fast candidate search Infernal multiple alignment Krona plots, Number of reads placed for each marker gene profile HMMs used to align candidates to reference alignment pplacer phylogenetic placement search input against references protein LAST fast candidate search hmmalign Sample Analysis & multiple alignment Comparison parallel option Edge PCoA, Tree visualization, Bayes factor tests AST hmmalign multiple alignment fast candidate search