

A) The MLTreeMap pipeline

1) identify marker genes in raw nucleotide sequence fragments



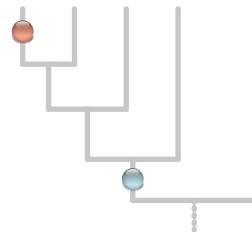
[BLAST, GeneWise]

2) add detected genes to curated reference alignments



[hmmalign, Gblocks]

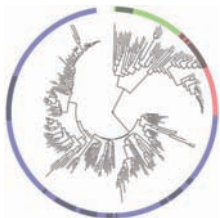
3) Maximum Likelihood placement into annotated reference phylogenies



[RAxML]

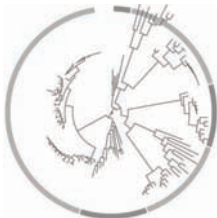
B) Reference phylogenies in MLTreeMap

Tree of life



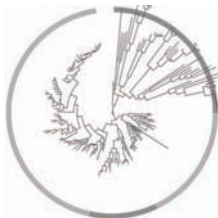
Archaea, Bacteria,
Eukaryota

RuBisCo



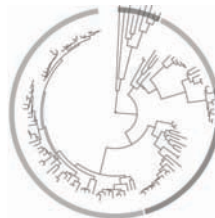
Forms 1, 2, 3, 4a, 4b
and unclassified

nifH



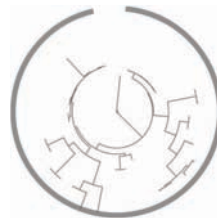
Groups 1, 2, 3, 4

nifD



Groups 1, 2, 3
and unclassified

MMO



Methane Monooxygenase