new SSU sequences

SSU-ALIGN

existing, known reference SSU alignment and tree

new sequences aligned

tree building program

known tree plus new sequences

SSU-ALIGN

A software package for identifying, aligning, masking and visualizing archaeal 16S, bacterial 16S and eukaryotic 18S SSU rRNA sequences.

accurate:
- structural alignment of sequences
- probabilistic masking of ambiguous columns

scalable and fast:
- can generate alignments of millions of seqs
- speed is about 1 second/full length sequence
- easily parallelized on clusters