



Goals of the alignment program:

- accurate: because alignment errors confound phylogenetic inference
- scalable to handle up to millions of seqs and fast:

SSU-ALIGN

Includes Infernal CMs for archaeal, bacterial and eukaryotic SSU rRNA

accurate:

- structural alignment of sequences
- probabilistic masking of ambiguous columns

scalable and fast:

- can generate alignment of millions of seqs
- speed is about 1 second/full length sequence
- easily parallelized on clusters

SSU-ALIGN tutorial tomorrow at 10:30