

input target sequences:



Stage 1:

Align sequence to each model's HMM to find best-matching model and define start/end SSU positions.

archaea HMM

bacteria HMM

eukarya HMM

low HMM score

low HMM score

predicted
SSU start

predicted
SSU end

highest HMM score

Stage 2:

Structurally align (sub)sequence to the best-matching model's CM.

archaea CM

bacteria CM

eukarya CM

output archaeal alignment

output bacterial alignment

output eukaryotic alignment