new SSU sequences

alignment program

existing, known reference SSU alignment and tree

new sequences aligned

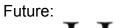tree building program

known tree plus new sequences

Goals of the alignment program:

accurate: because alignment errors confound phylogenetic inference

fast: to handle up to millions of seqs

Sampling of recent SSU studies			
environment	domain(s)	#seqs	year
soil, many others	bacteria	21,752	2007
cecal microbiota of mice	bacteria	5,088	2005
		4,157	2006
Sargasso sea	all 3	1,164	2004
hydrothermal vents	eukarya	374	2002
endolithic environment (pore space of rocks)	archaea, bacteria	342	2005
		588	2007
oxidized iron deposits, marine tidal mat, microbial steamers	bacteria	308	2004
soil & burrow casts of earthworms	archaea, bacteria	204	2002
tidal flat sediment	archaea	90	2005
salt marsh	eukarya	79	2003
dipteran hindgut	bacteria	59	2007

Future:

Human Microbiome Project