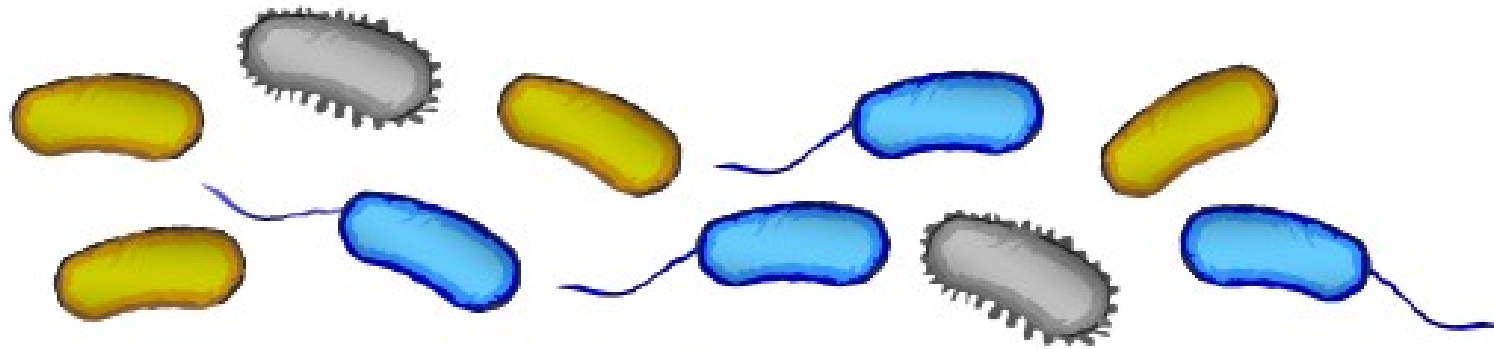# ADAPT/ADAPTdb
A resource for ARISA

- Problems with T-RFLP?

- Problems with 16S sequencing?
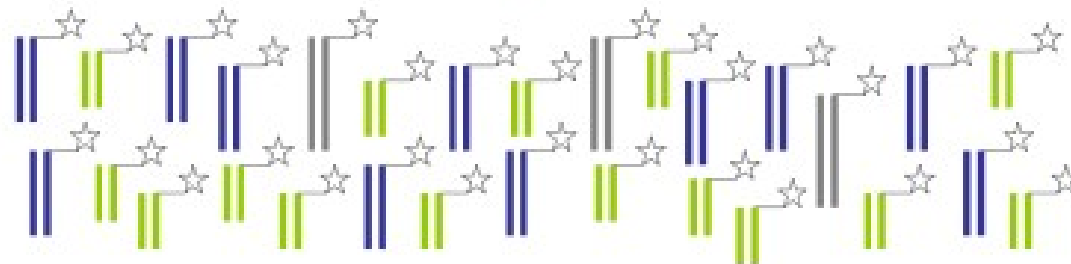
- Problems with metagenomics
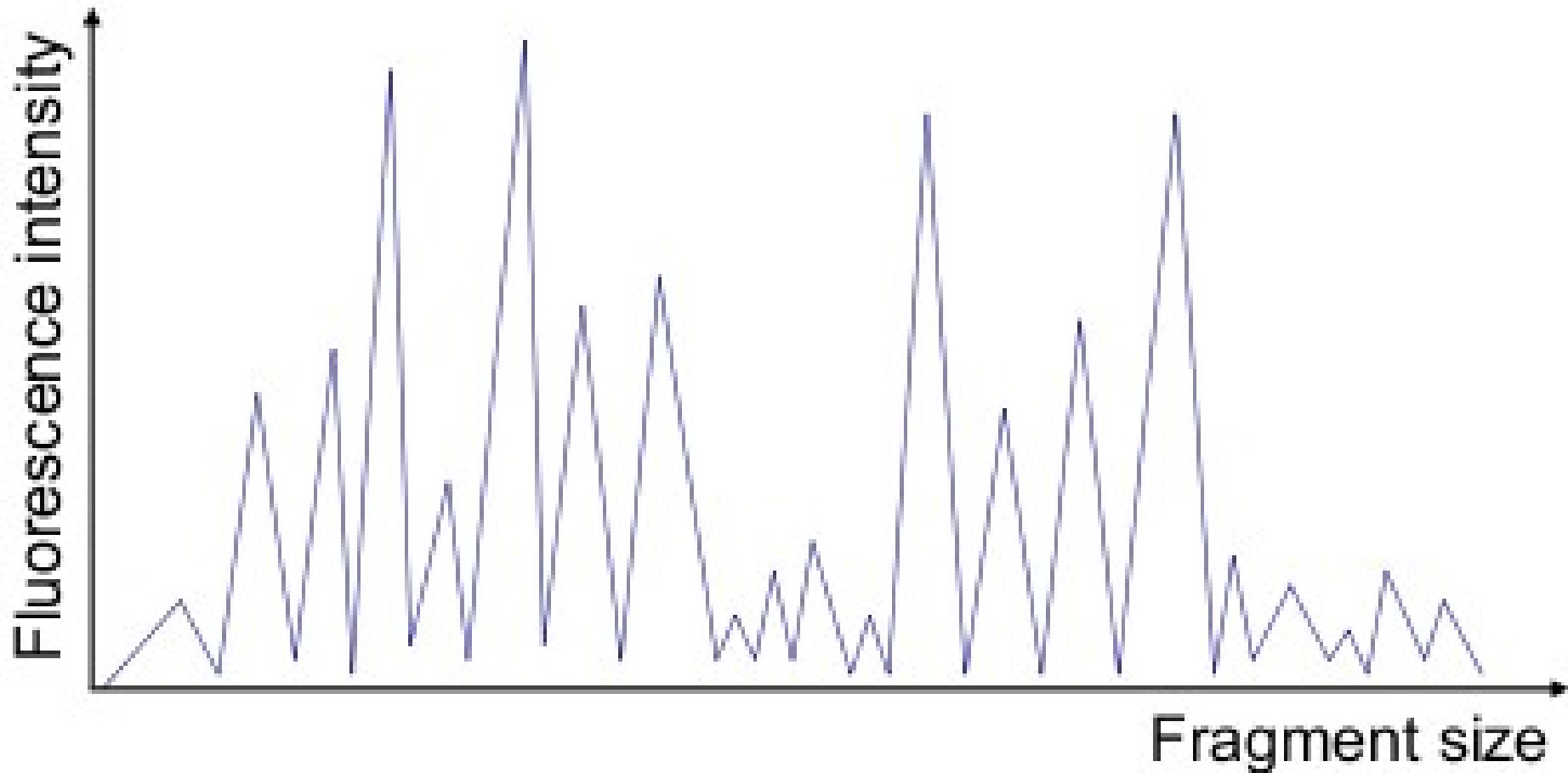
Can ARISA help?

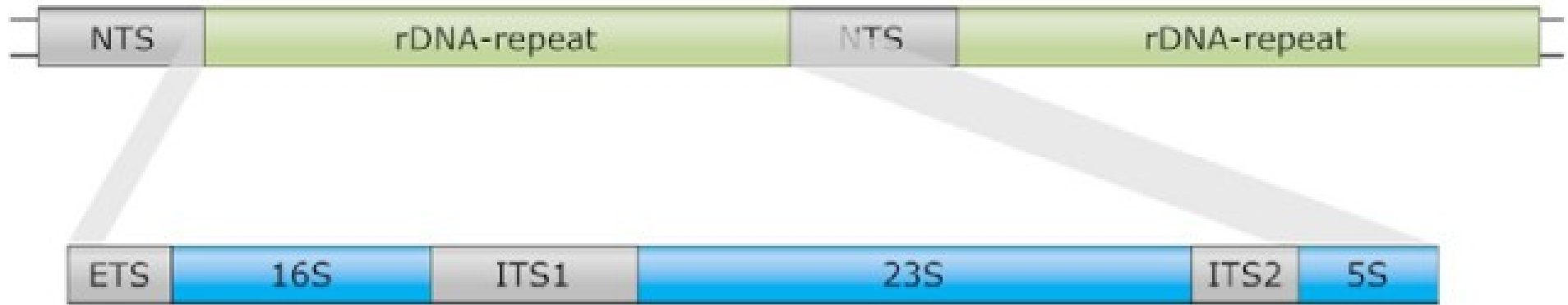Isolate DNA from environmental sample

Amplify ITS regions using PCR with fluorescently labeled primers

Still uses a sequencing machine!

Fragment length depends on ITS

Does everyone have an ITS?

Phylum	# Organisms	# ITS regions	ITS / organism
Crenarchaeota	21 (0.92%)	69 (1.46%)	3.29
Euryarchaeota	43 (1.89%)	46 (0.97%)	1.07
Actinobacteria	452 (19.83%)	628 (13.30%)	1.39
Bacteriodetes	33 (1.45%)	75 (1.59%)	2.27
Chlamydiae	55 (2.41%)	71 (1.50%)	1.29
Cyanobacteria	173 (7.59%)	223 (4.72%)	1.29
Firmicutes	569 (24.97%)	1467 (31.07%)	2.58
Fusobacteria	38 (1.67%)	46 (0.97%)	1.21
Proteobacteria	853 (37.43%)	2020 (42.79%)	2.37
Rare Bacterial spp.	42 (1.84%)	76 (1.63%)	1.81
Total	**2279**	**4721**	**2.07**

http://edwards.sdsu.edu/adapt
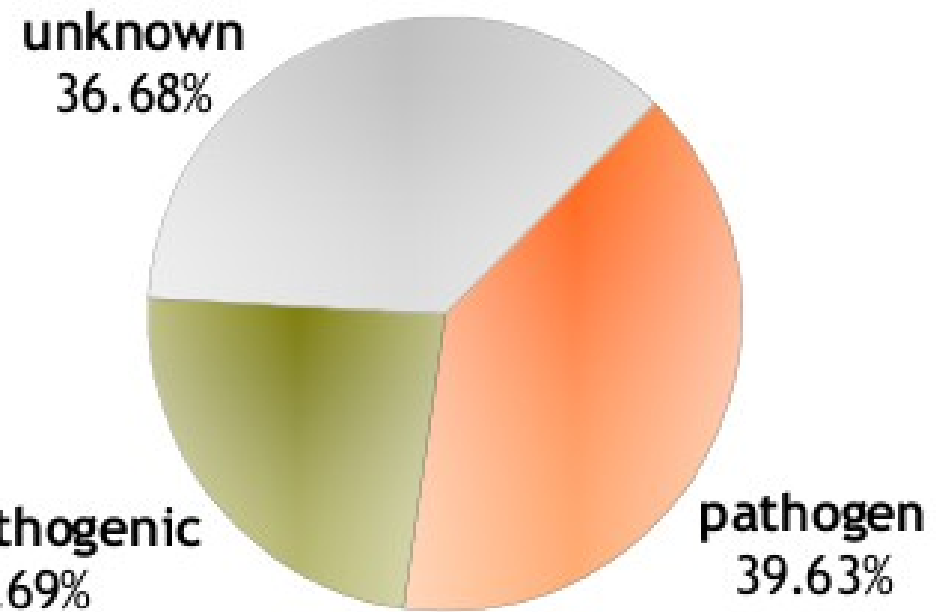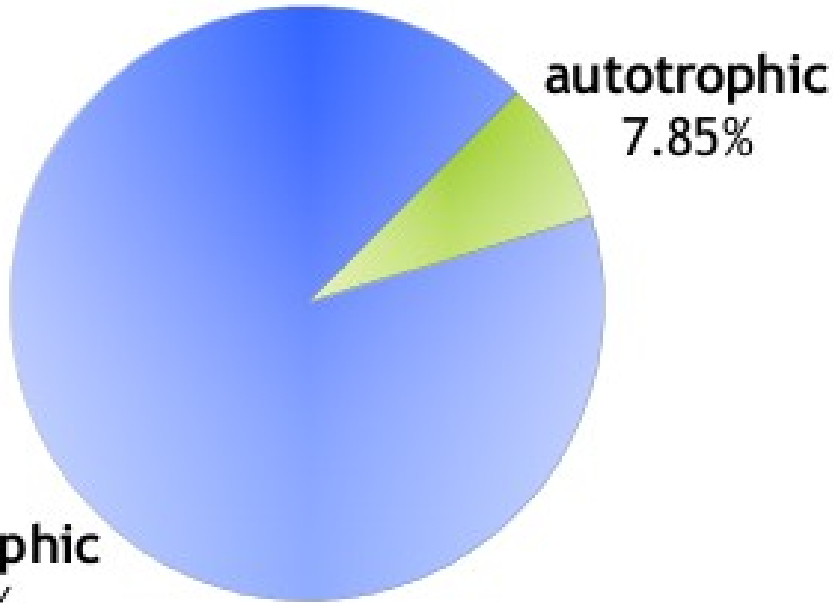
You can remake T-RFLPs *in silico*
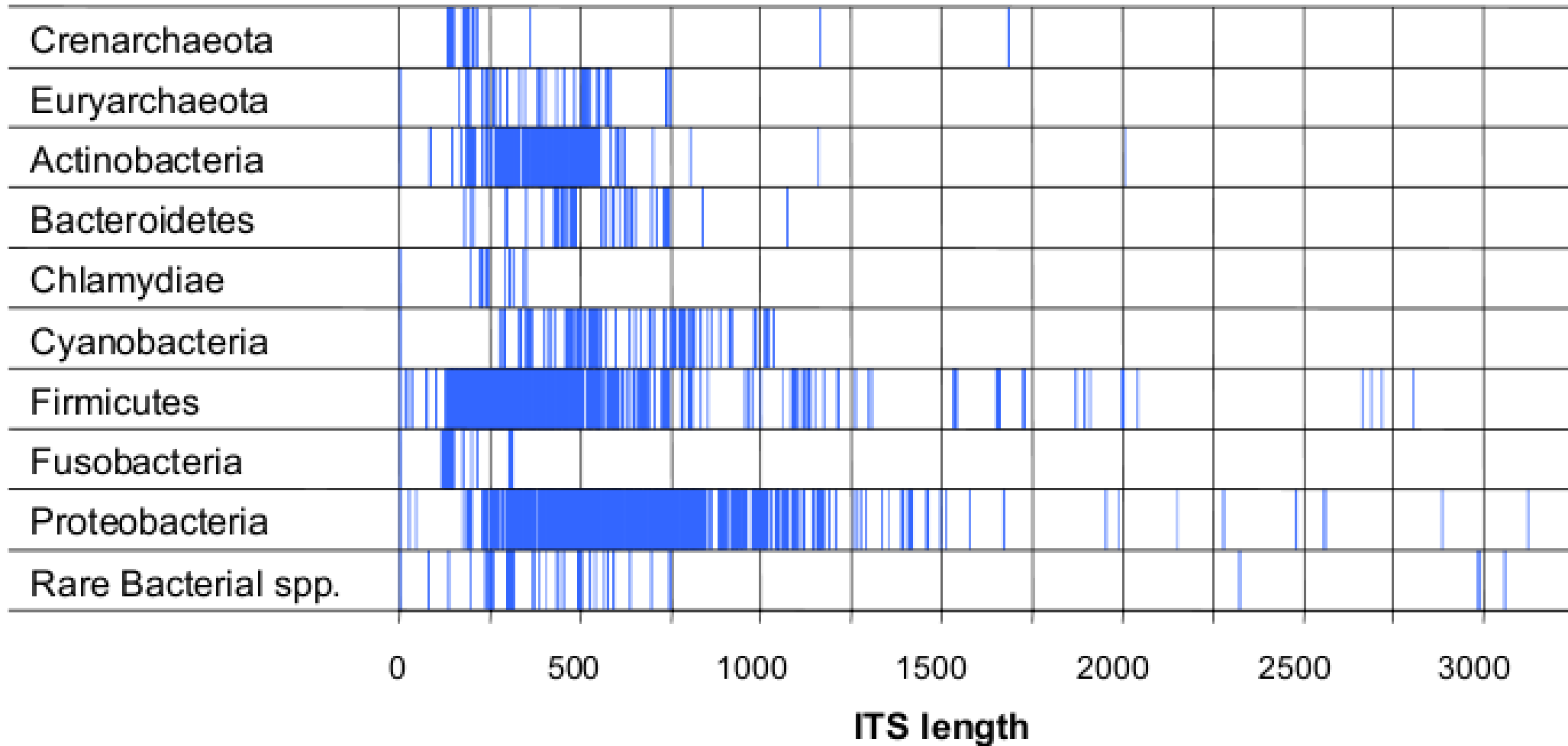
We can categorize organisms

autotrophic
7.85%

heterotrophic
92.15%

unknown
36.68%

non-pathogenic
23.69%

pathogen
39.63%

BACK!