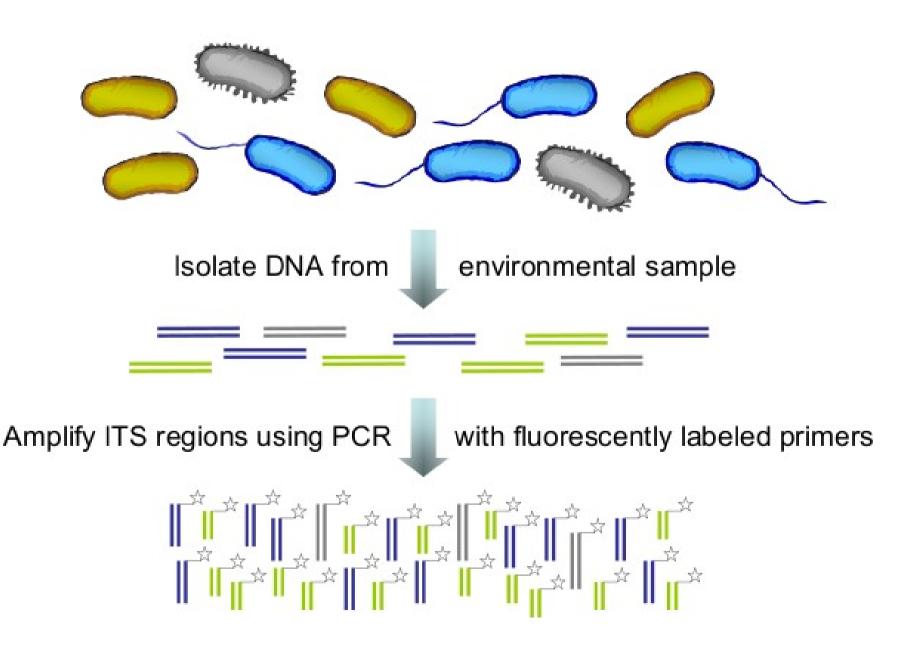
A resource for ARISA

Problems with T-RFLP?

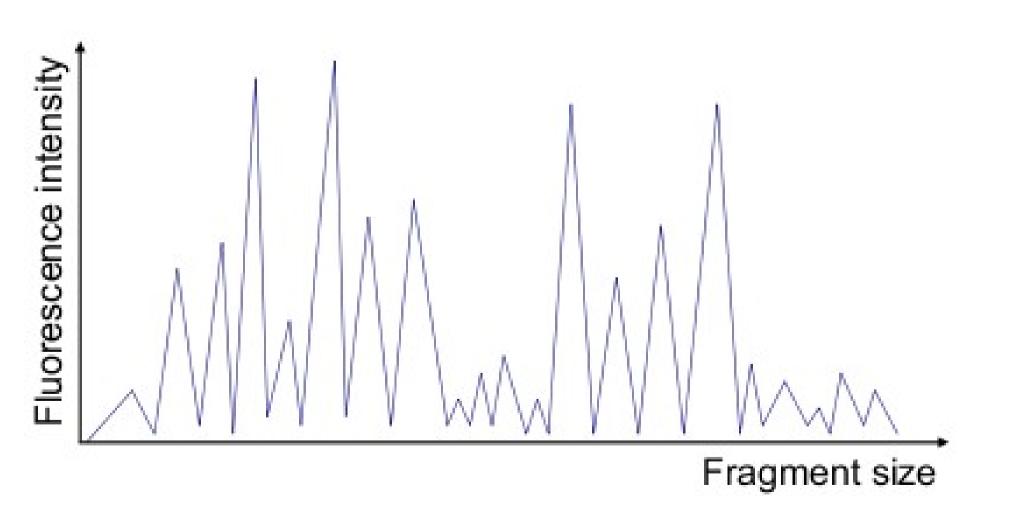
Problems with 16S sequencing?

Problems with metagenomics

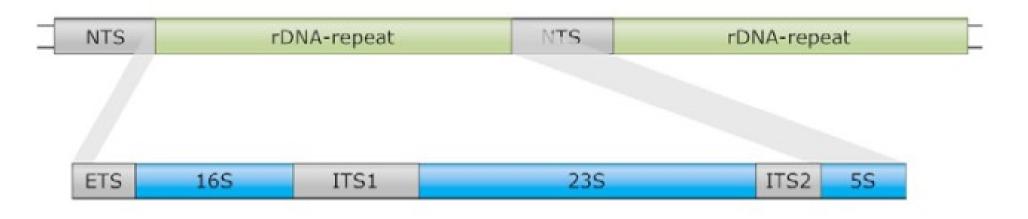
### Can ARISA help?



# Still uses a sequencing machine!



# Fragment length depends on ITS

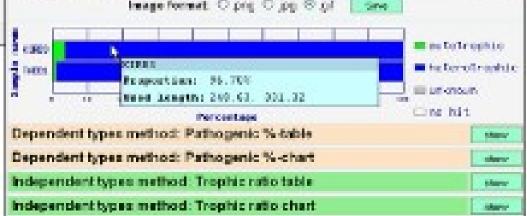


#### Does everyone have an ITS?

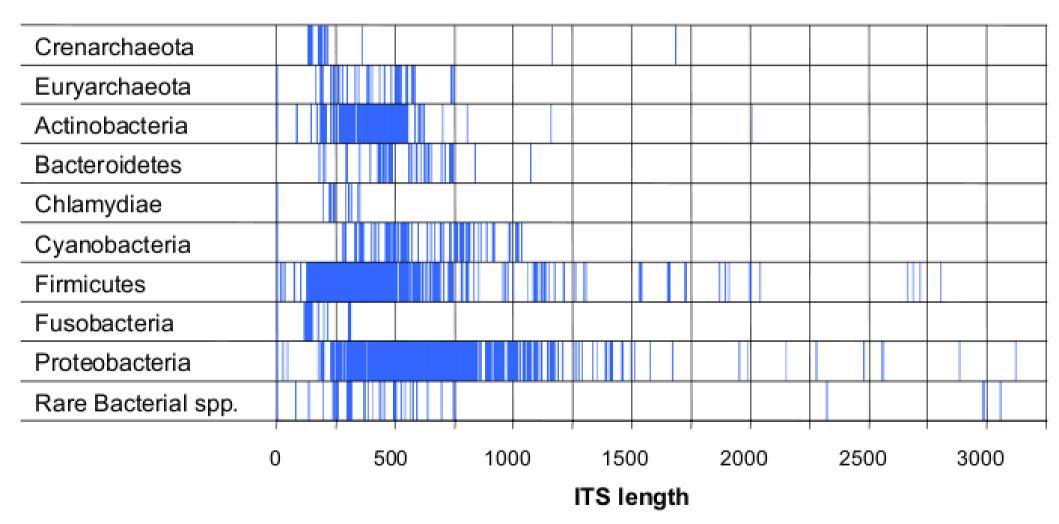
Phylum	# Organisms	# ITS regions	ITS / organism
Crenarchaeota	21 (0.92%)	69 (1.46%)	3.29
Euryarchaeota	43 (1.89%)	46 (0.97%)	1.07
Actinobacteria	452 (19.83%)	628 (13.30%)	1.39
Bacteriodetes	33 (1.45%)	75 (1.59%)	2.27
Chlamydiae	55 (2.41%)	71 (1.50%)	1.29
Cyanobacteria	173 (7.59%)	223 (4.72%)	1.29
Firmicutes	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

ADAPT v1.0 Pros	gram				
ARISA Data Analysis program for Robustanis and Trach	ielesmperilien				
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overage (quadratic heights) O overage (quadratic heights)		Dependent types method: Trophic %-chart Inage format: O pro O pp O pt O pro			
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#### http://edwards.sdsu.edu/adapt



## You can remake T-RFLPs in silico



### We can categorize organisms

