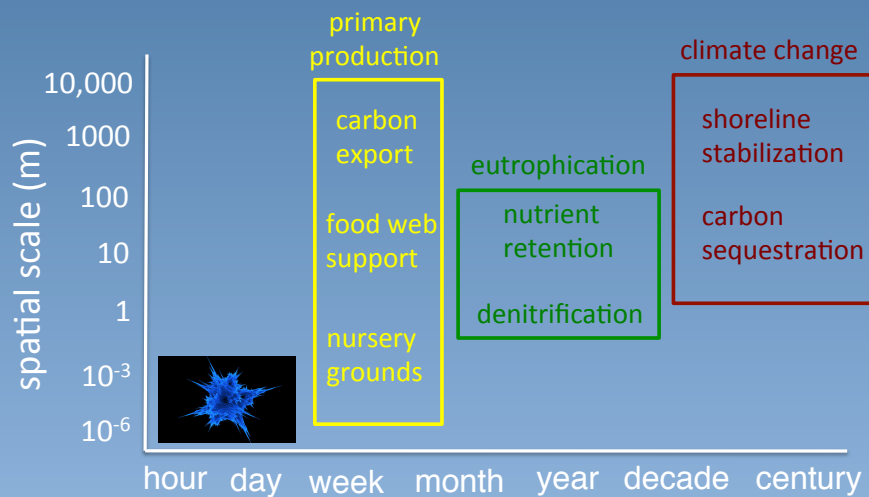


Responses of Microbial Communities to Increases in Nitrogen Loads in Salt Marshes

Jennifer L. Bowen
University of Massachusetts Boston

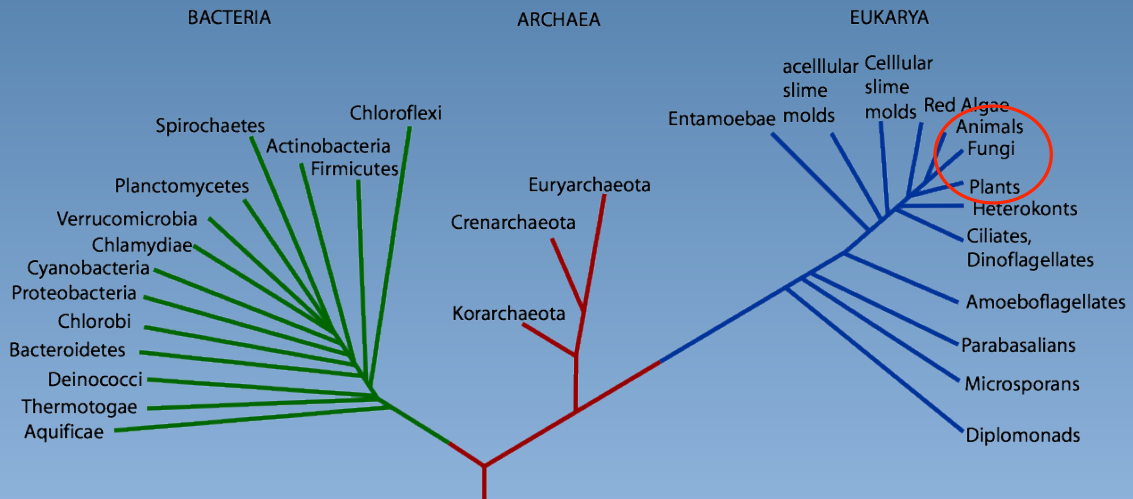
Symposium on C/N Cycling and Ecosystem Valuation of Tidal Wetlands in the Northeast
Waquoit Bay National Estuarine Research Reserve
24 January 2013

Motivating question: *What role does microbial diversity play in the ecosystem services provided by salt marshes*



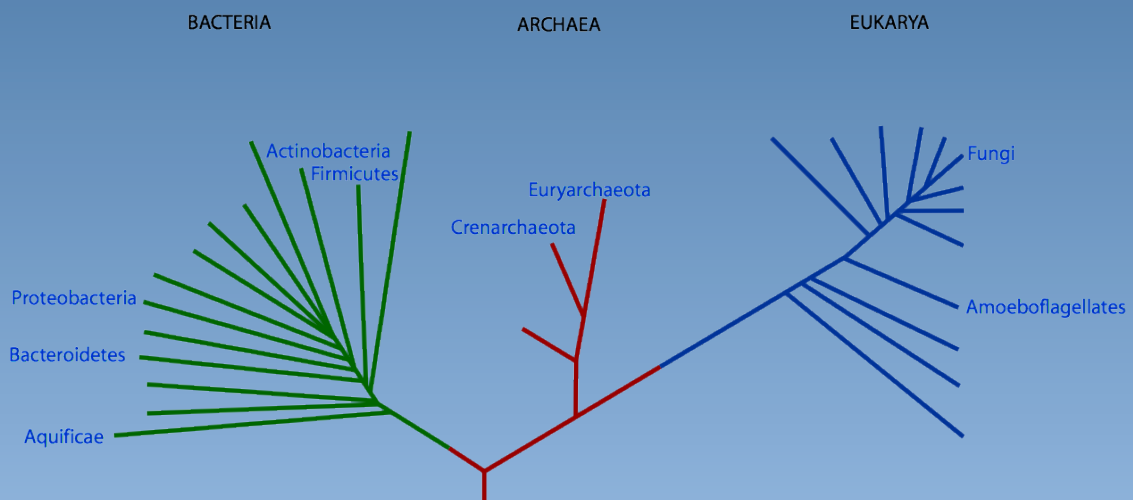
“To scale from the leaf to the ecosystem to the landscape and beyond, we must understand how information is transferred from fine scales to broad scales and vice versa. We must learn how to aggregate and simplify, retaining essential information without getting bogged down in unnecessary details” -Simon Levin (1992)

Introduction: the unseen diversity



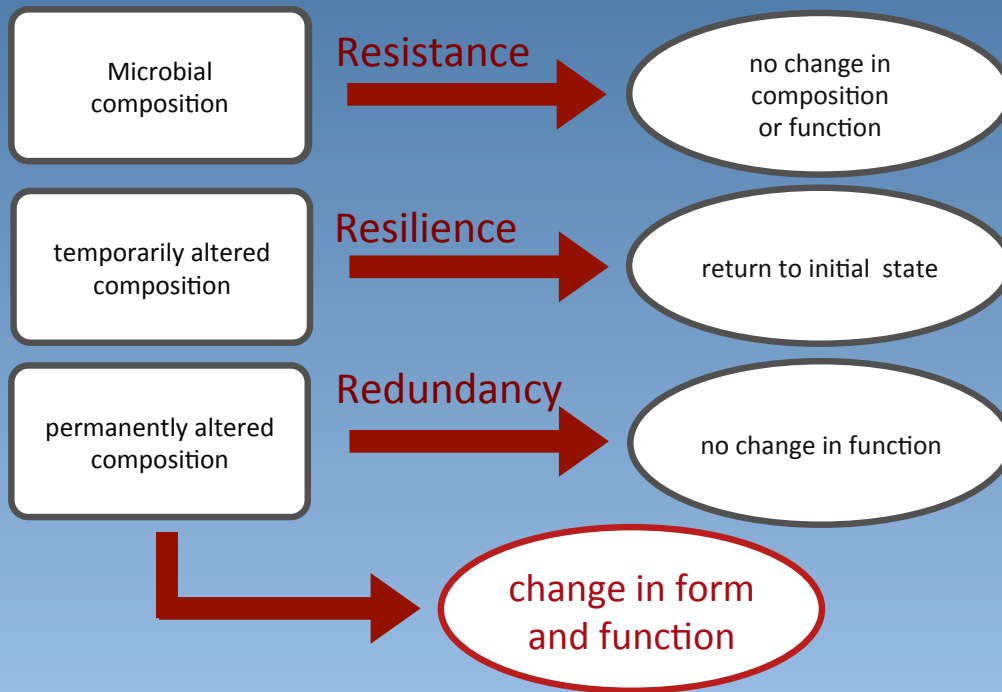
-Woese 1987

Introduction: The REALLY unseen diversity (denitrifying microbes)



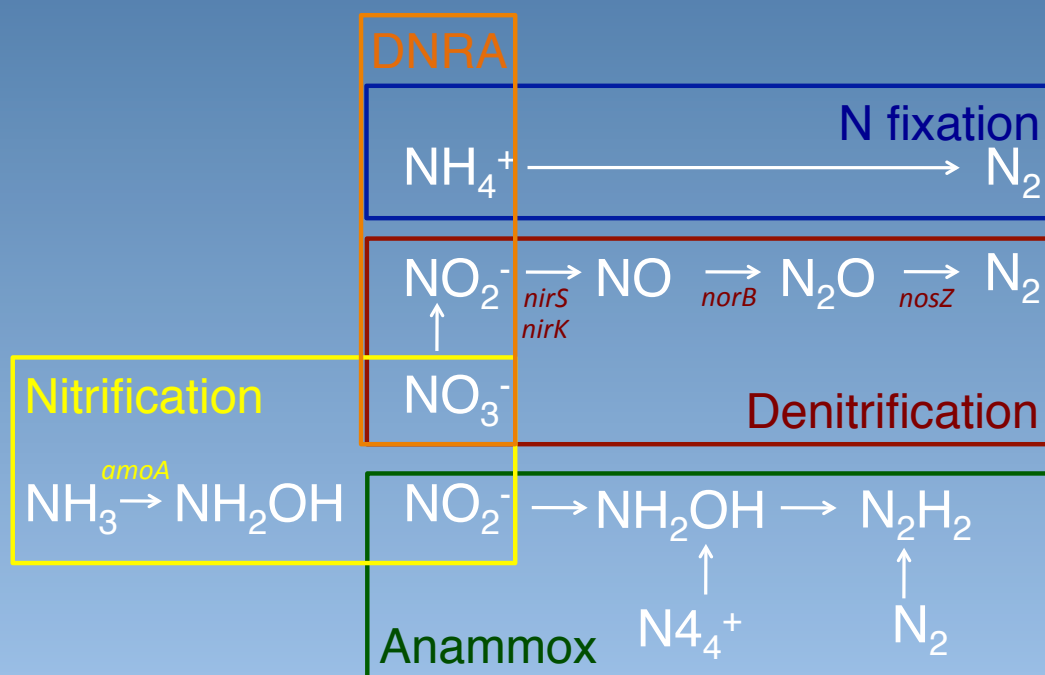
-Woese 1987

Introduction: The 3Rs — essential information or unnecessary detail?



-modified from Allison and Martiny 2008

Methods: We can assess the 3 Rs, and whether they matter to ecosystem services, by looking at microbial genetics



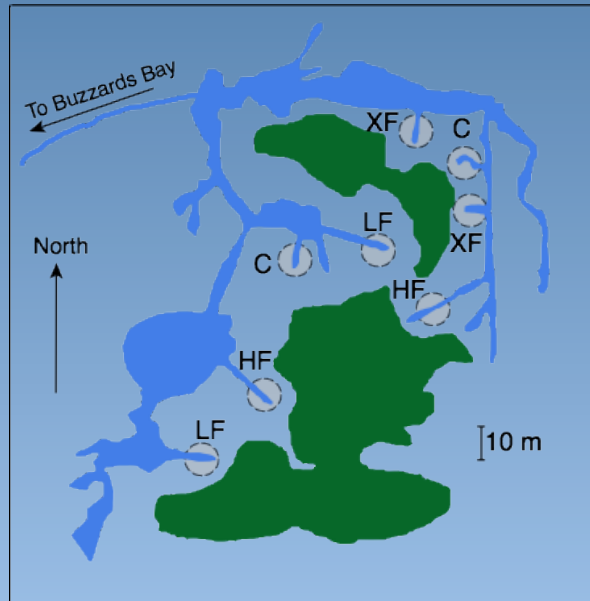
Modified from Philippot et al. 2007

Methods: Sippewissett Salt Marsh plots

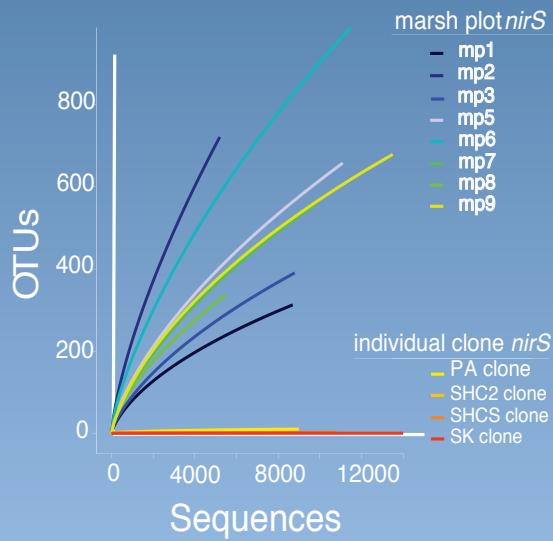
Fertilization began in 1971

4 treatments

1. CONTROL
2. LOW (LF)
~ 0.86 g N/m²/wk
3. HIGH (HF)
~2.52 g N/m²/wk
4. XHIGH (FX)
~7.56 g N/m²/wk



Methods: deep sequencing of functional gene diversity



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FunFrame: Functional Gene Ecological Analysis Pipeline

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Received on XXXXX; revised on XXXXX; accepted on XXXXX

Associate Editor: XXXXXXXX

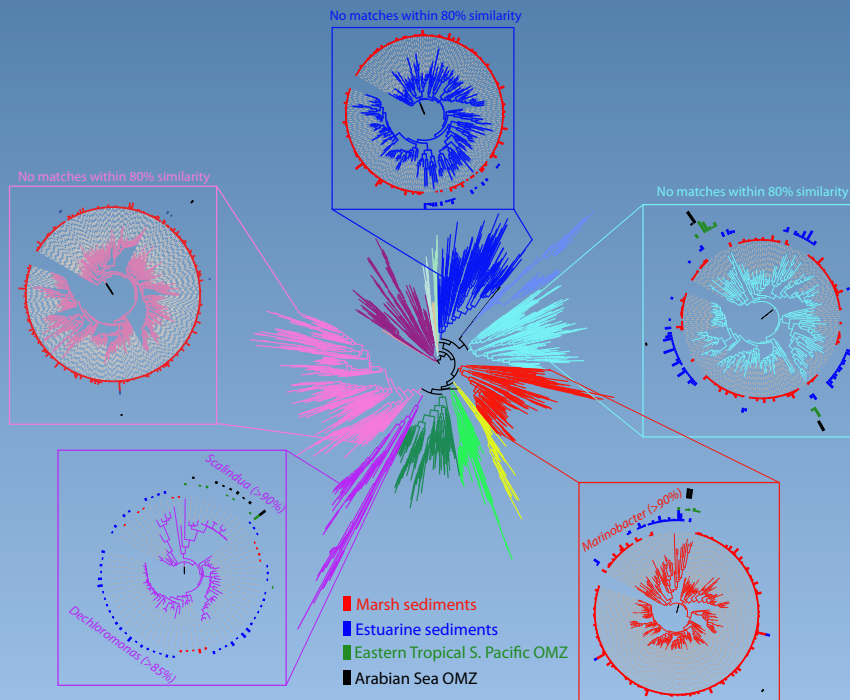
ABSTRACT

Summary: Pyrosequencing of 16S rDNA is widely used to study microbial communities, and a rich set of software tools supports

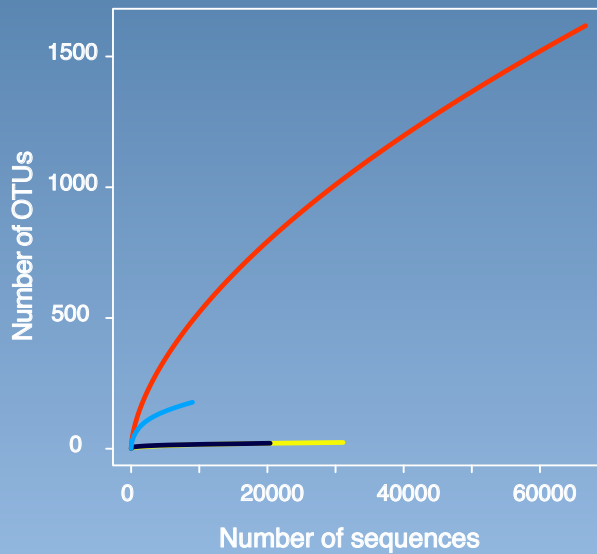
pyrosequencing, as the technology is prone to miscall the lengths of long homopolymers, thereby creating the appearance of false-shift mutations. To reduce the inflated diversity bias with reverse-coding

--Weisman et al. (In press)

Results: There is a LOT of unseen diversity, especially in marshes



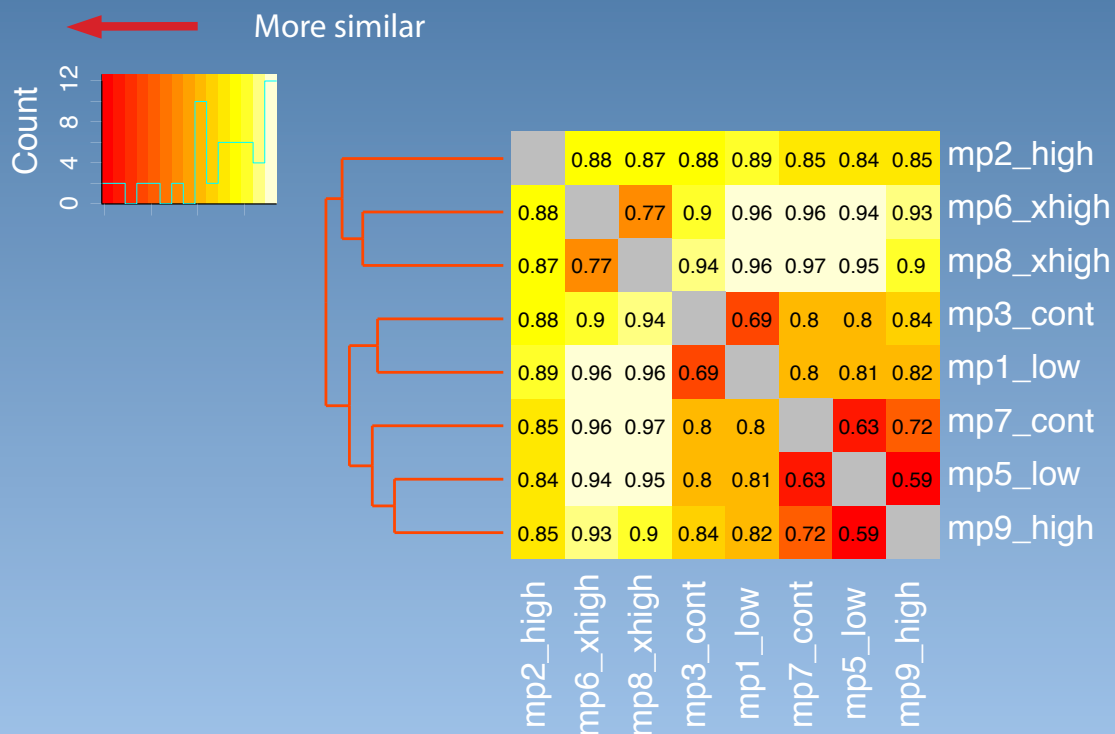
Results: diversity and richness of *nirS* genes vary tremendously



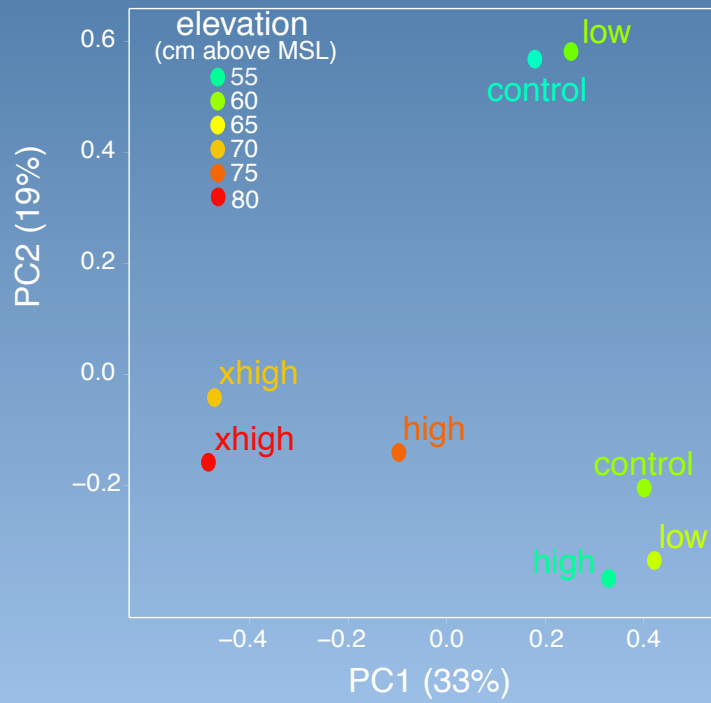
Aggregate score

	Shannon	Chao
<u>Arabian Sea</u>	1.89	20
<u>ETSP</u>	1.40	18
<u>Chesapeake Bay</u>	4.07	238
<u>Sipp. salt marsh</u>	4.94	862

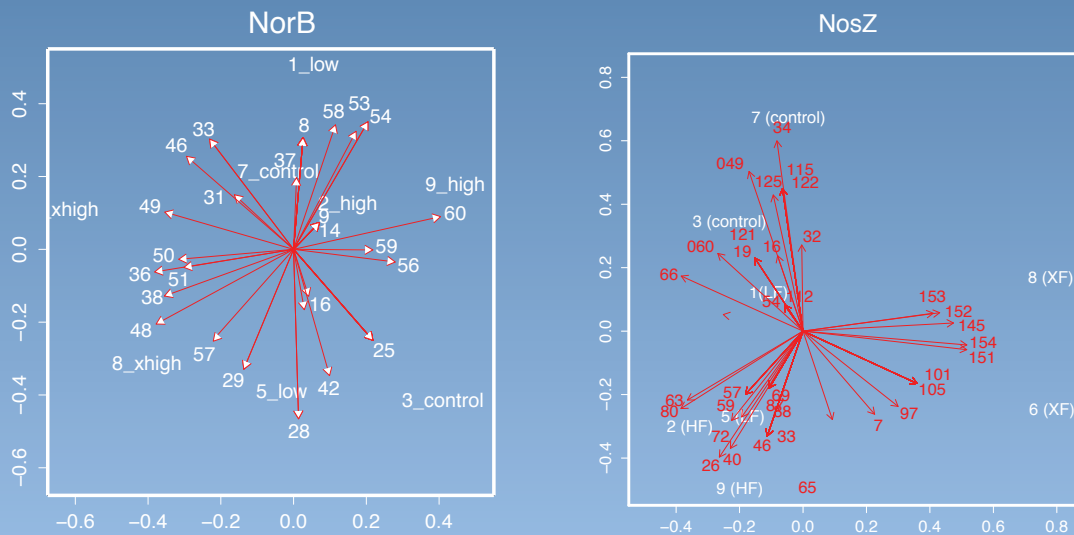
Results: Some effect of fertilization on denitrifiers



Results: But also a strong elevation effect



Introduction: DNF in marine systems accounts for 60% of fixed N loss



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2. Princeton University Council on Science and Technology (to JLB)

3. UMass Boston Startup Fund (to JLB)



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