

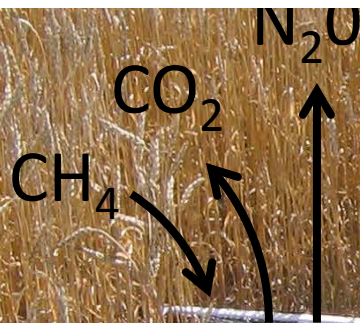
Microbial Community Dynamics and Long-Term Trends in the Flux of Greenhouse Gases

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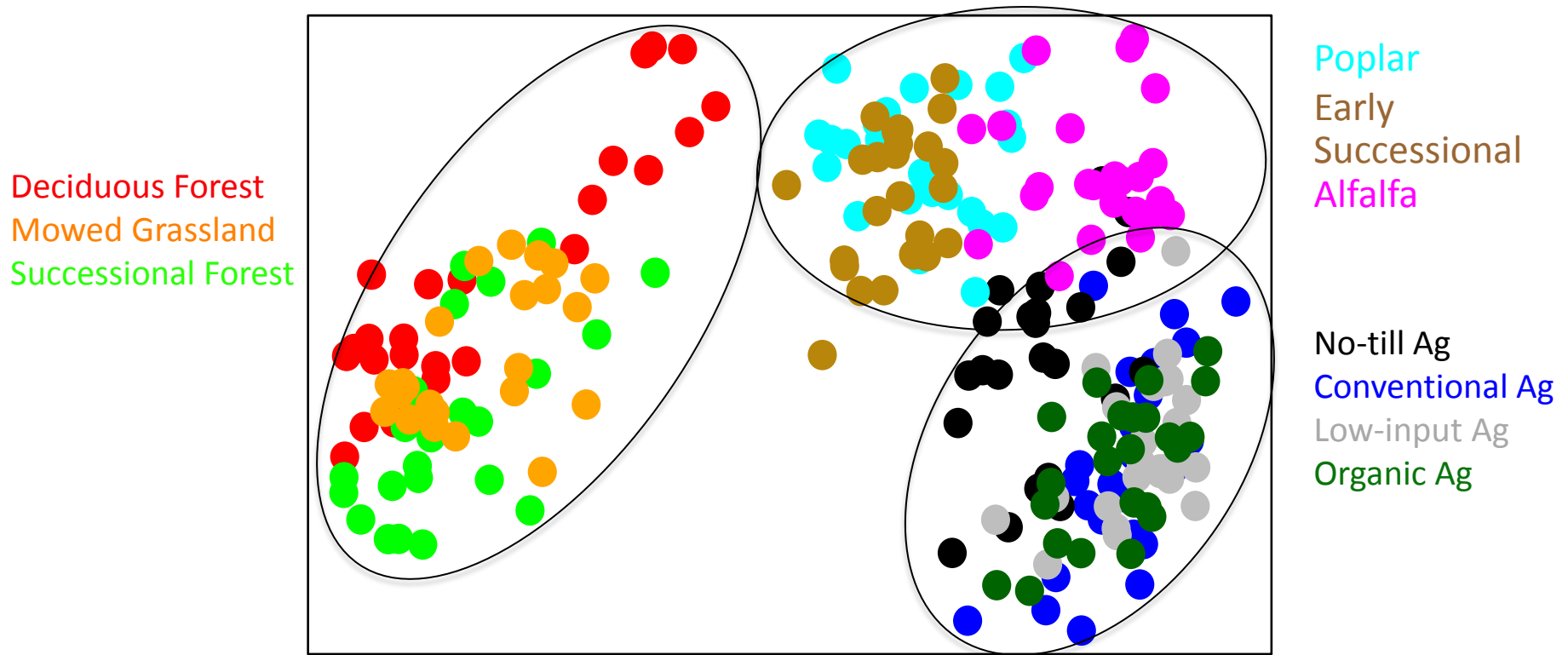
Ultimate goals of research on soil microbiomes:

1. Manage lands to conserve or restore microbial communities that mitigate flux of greenhouse gases.
2. Improve predictive models of biogeochemical cycles in soil, including carbon sequestration.

Outline

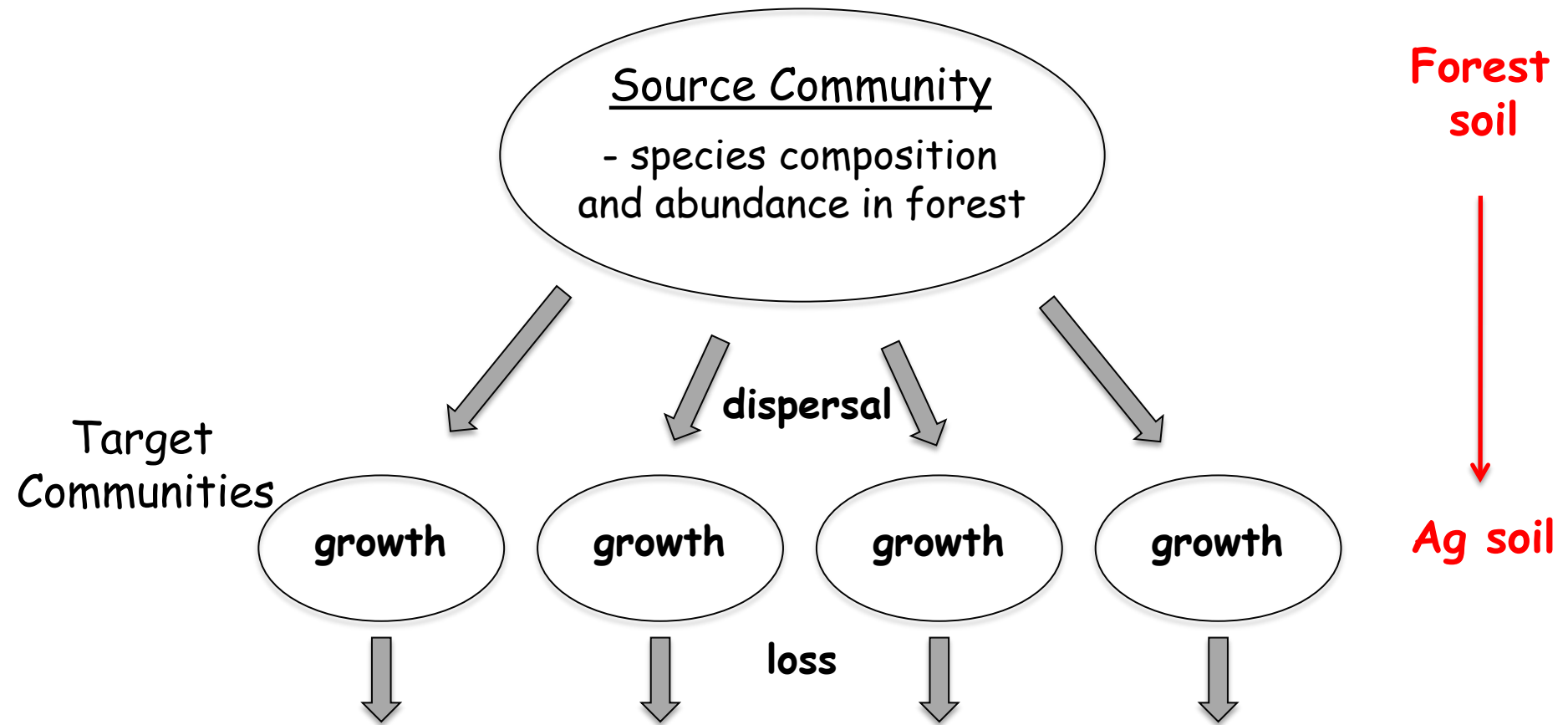
1. Compare structure of microbial communities in soil
 - *contributions of dispersal and selection*
the neutral model
2. Relate N₂O production to microbial communities
 - *comparative metagenomics*
3. Measure CO₂ production vs. biomass generation
 - *tradeoff between growth rate & growth efficiency*

Ordination Analysis Distinguishes Bacterial Communities in Soils Under Different Land Uses



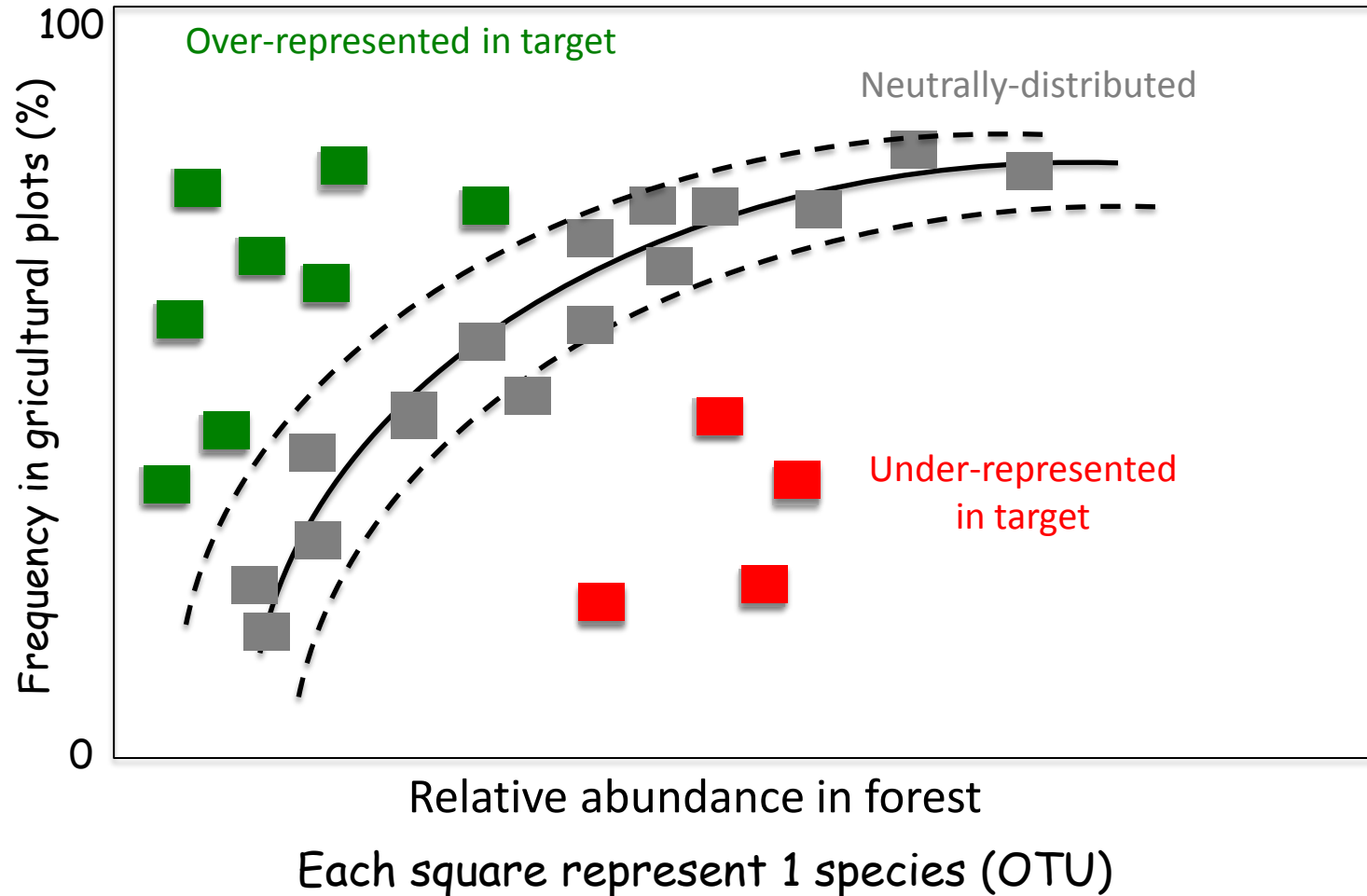
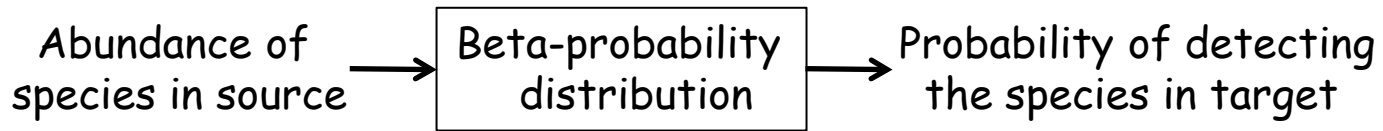
What is the relative impact of selection and stochastic processes on the composition of microbial communities?

Overview of the Neutral Model



Does composition and abundance of species in target communities differ from what could be generated by stochastic processes?

Implementing a Neutral Model

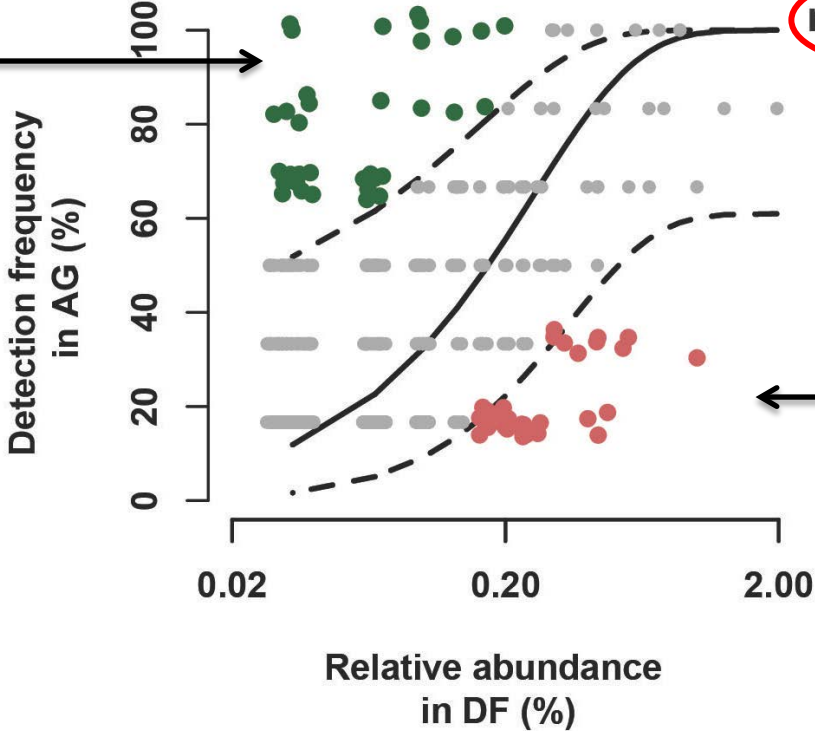


Neutral Model Analysis of Microbial Communities in Forested and Agricultural Plots

Source: forest
Targets: agricultural plots

B

Species enriched in agriculture

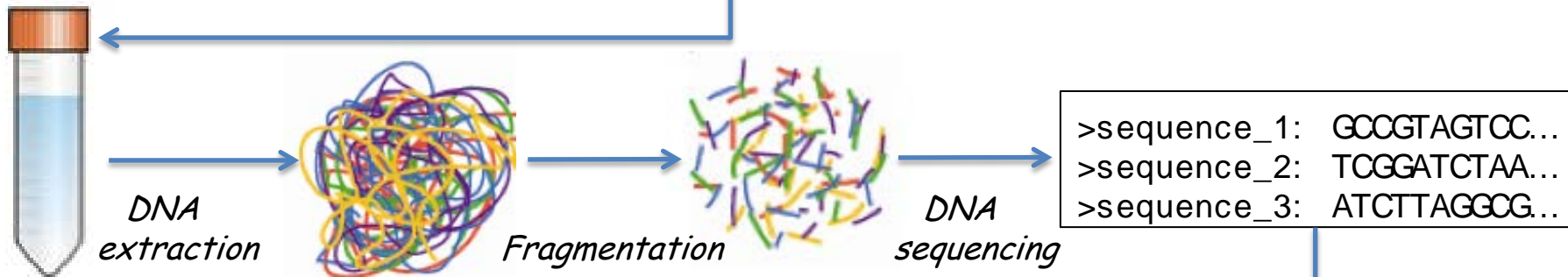


$r_s = 0.32$

Poor fit to neutral model

Species enriched in forest

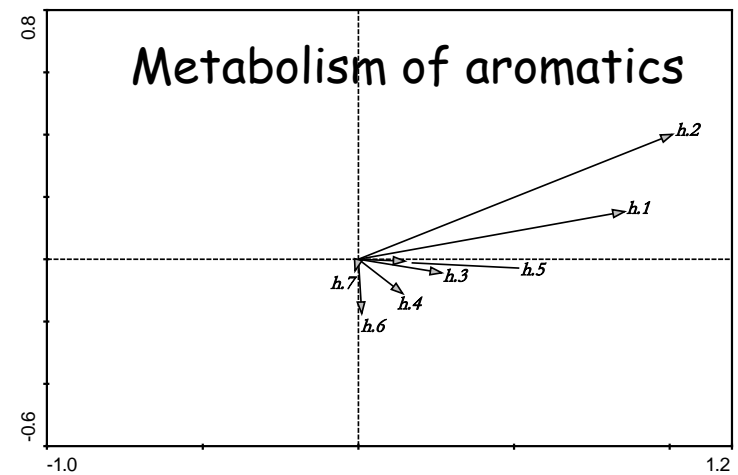
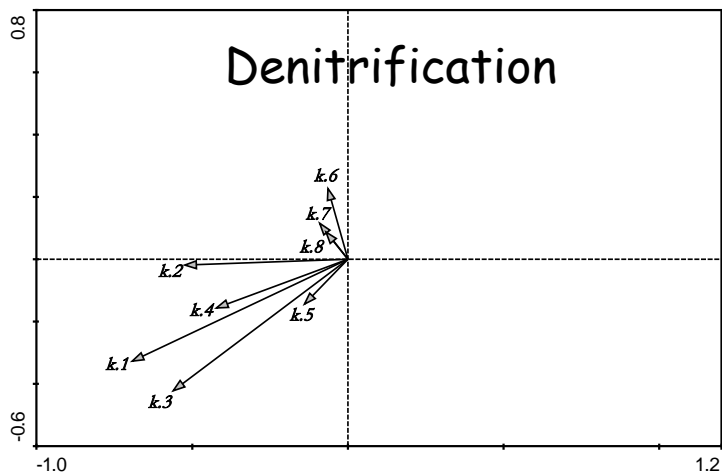
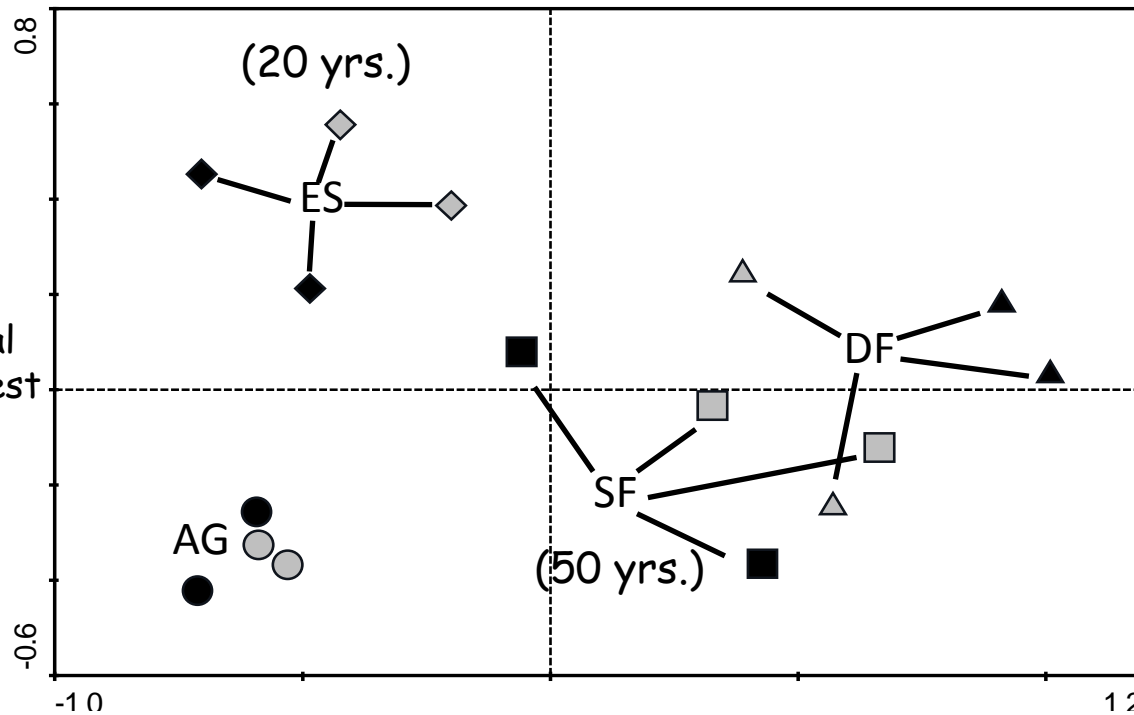
What is driving selection? Compared Metagenomes



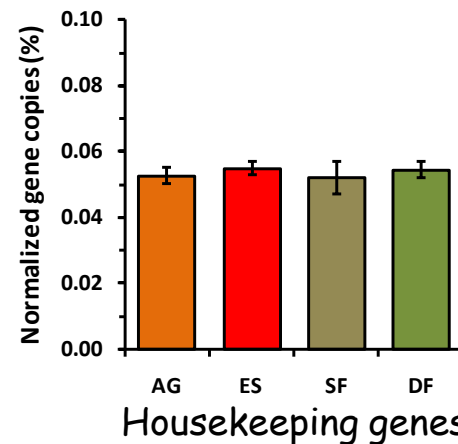
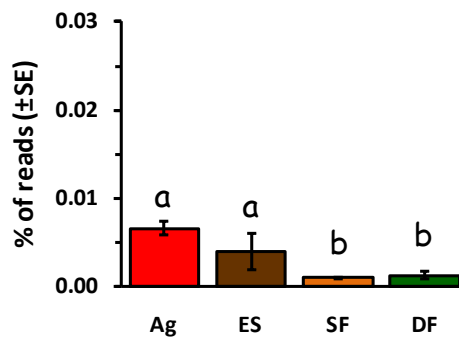
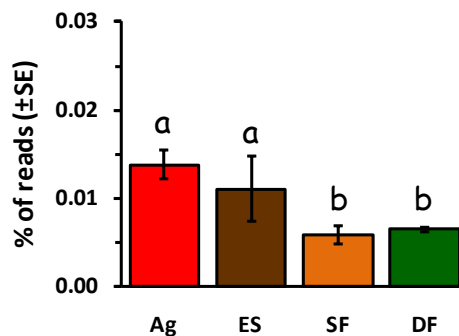
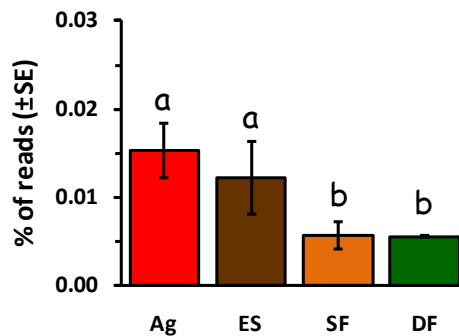
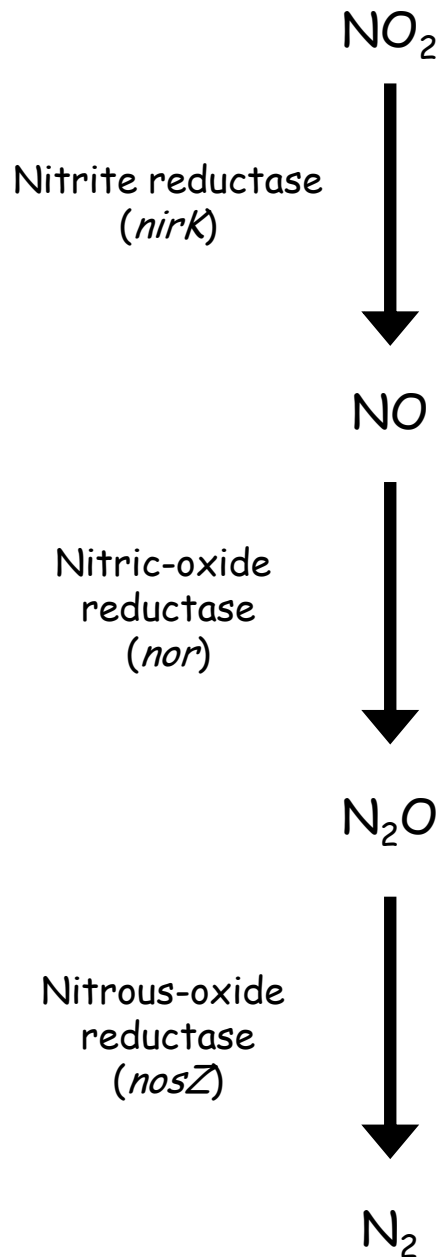
Infer identity by comparison
to sequences of known genes

Ordination Analysis of Annotated Metagenomes

AG = Agriculture
ES = Early Successional
SF = Successional Forest
DF = Deciduous Fores



Denitrification Genes are More abundant in Ag Plots



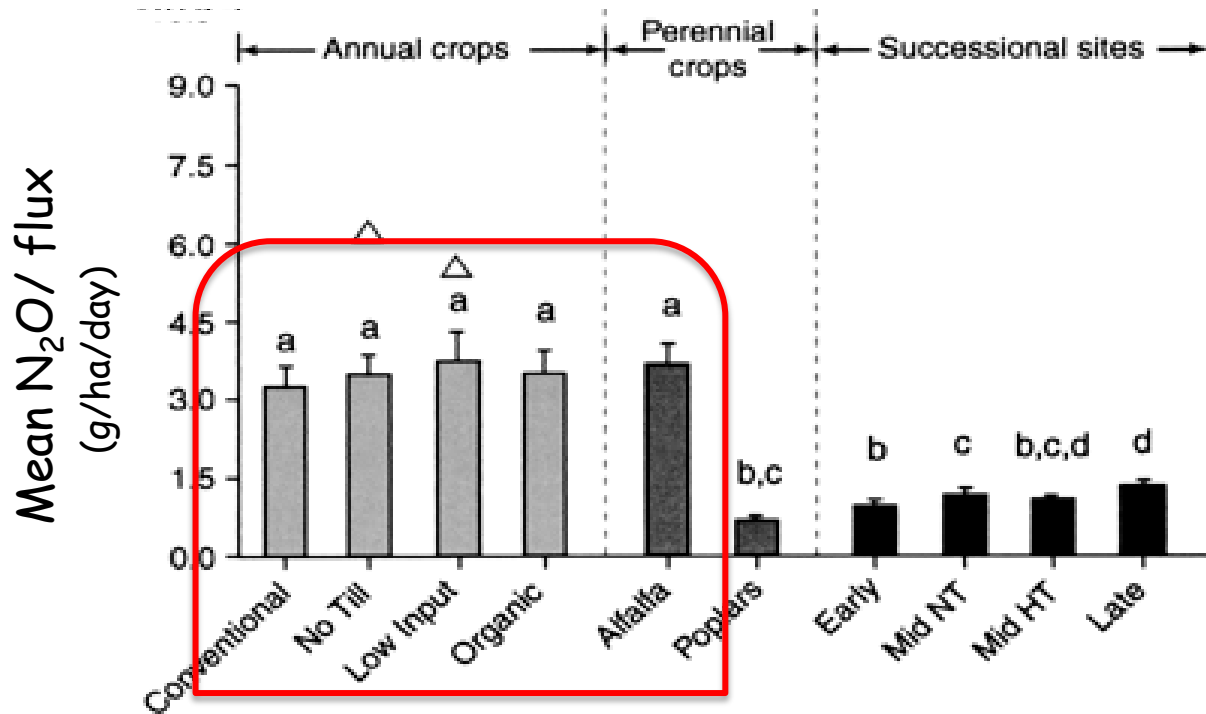
Proportion of bacteria that are denitrifiers

(*nir K* / housekeeping)

Ag 1/3

Forest 1/9

N₂O Production in Agricultural Plots Correlates with Increased Abundance of Denitrifying Bacteria



Denitrification by nitrifying bacteria?
Robertson et al.
Science 289:1922



Carbon Sequestration and Bacterial Growth Efficiency

Proposal: in spatially structured environments, with low concentration resources, selection is for efficient microbes

Bacterial Growth Efficiency (BGE)

Bacterial productivity (BP)

³H-leucine

biomass (# progeny)

(CH₂O)

O₂

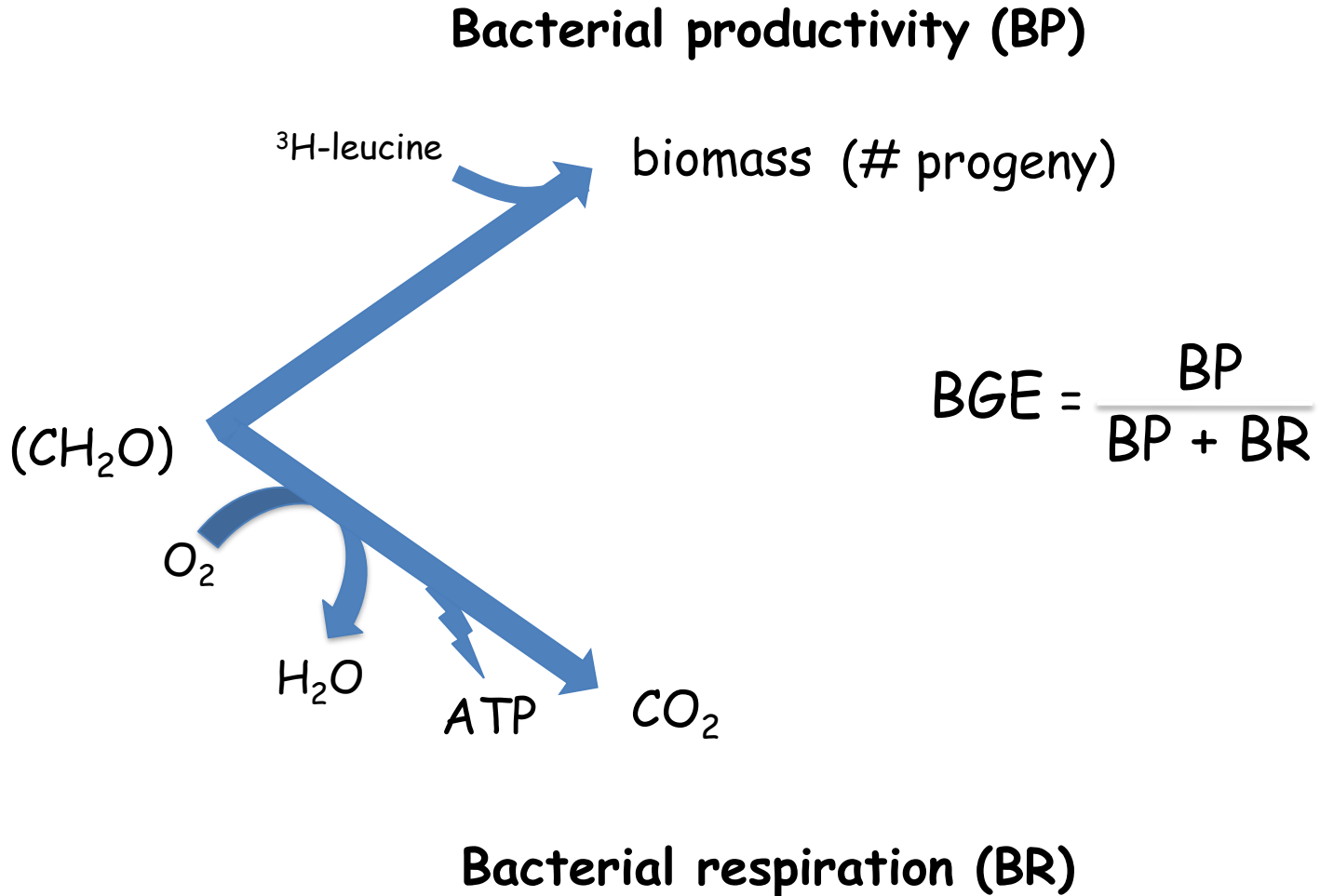
H₂O

ATP

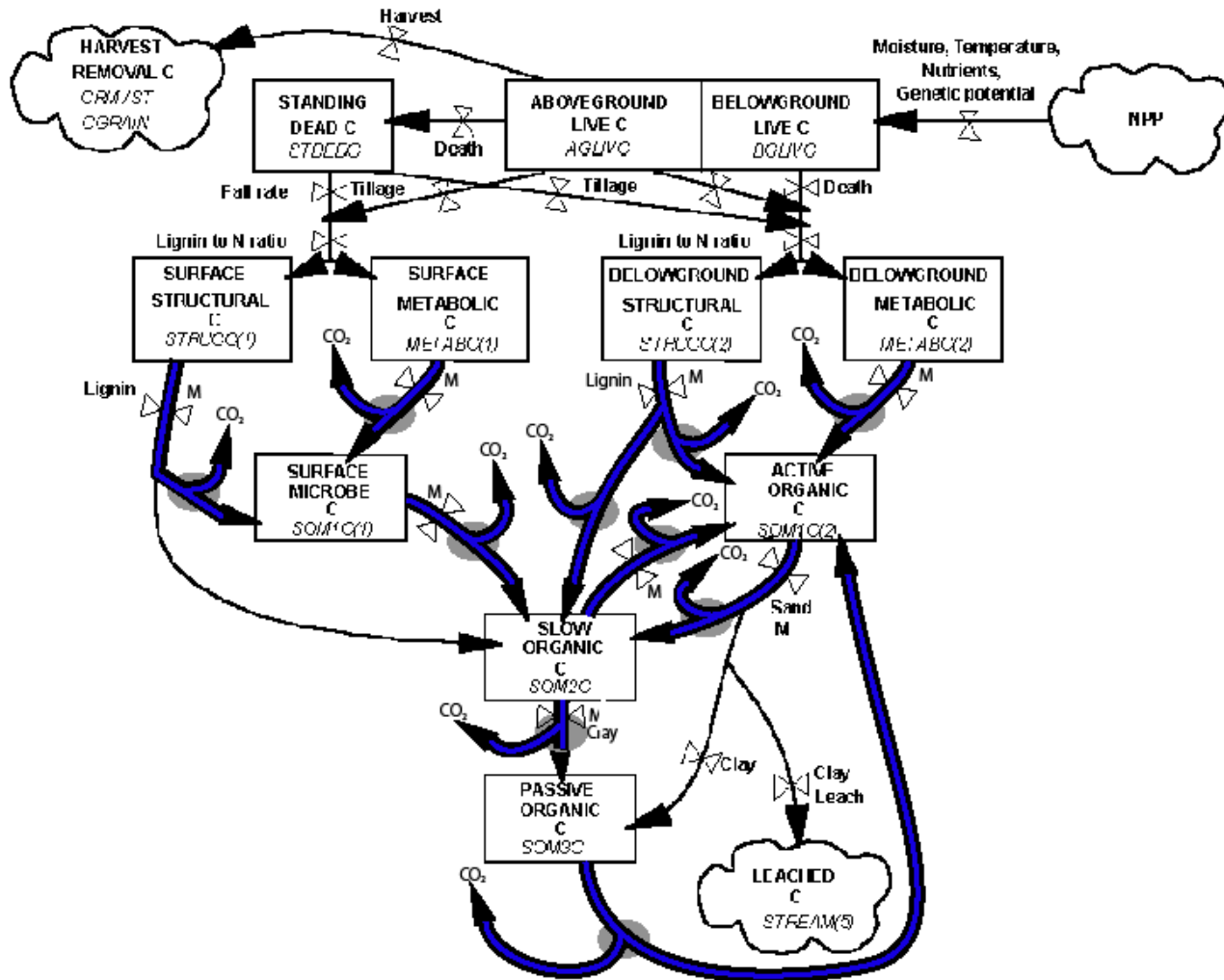
CO₂

$$BGE = \frac{BP}{BP + BR}$$

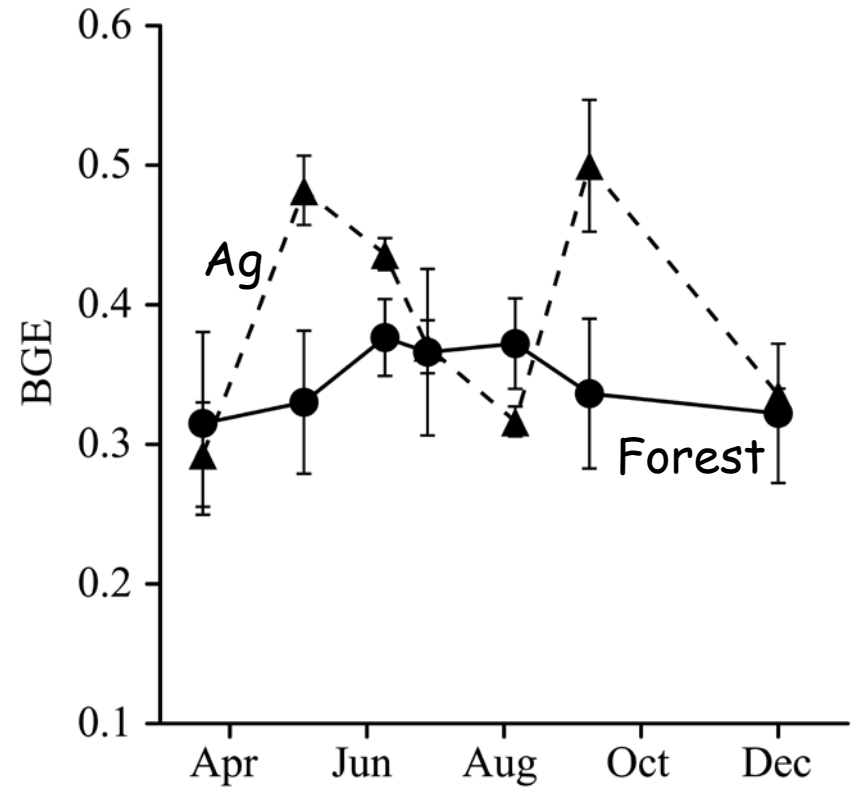
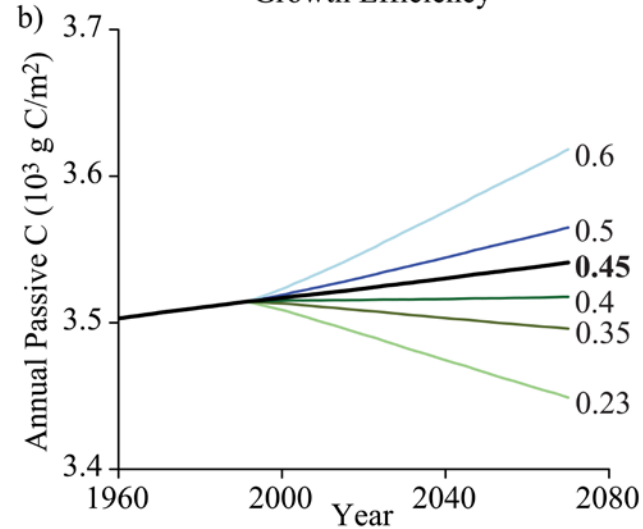
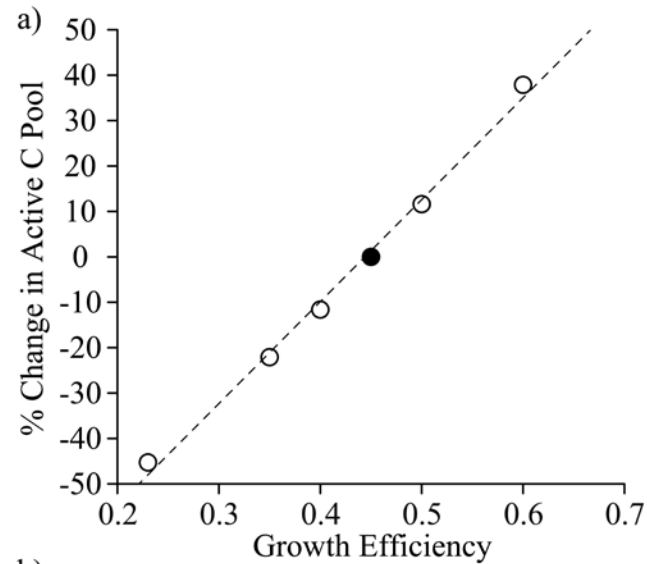
Bacterial respiration (BR)



Century Soil Organic Matter Model



Microbial carbon use efficiency and fate of carbon



Spectrum of Bacterial Lifestyles

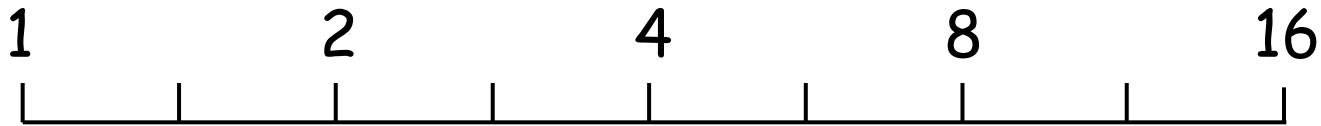
Oligotrophs

Copiotrophs

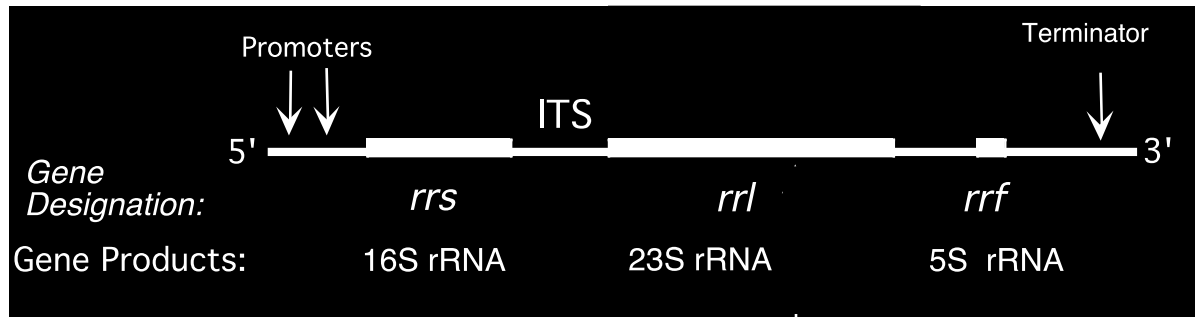


- K-selected
- Efficient growth
- Low K_s

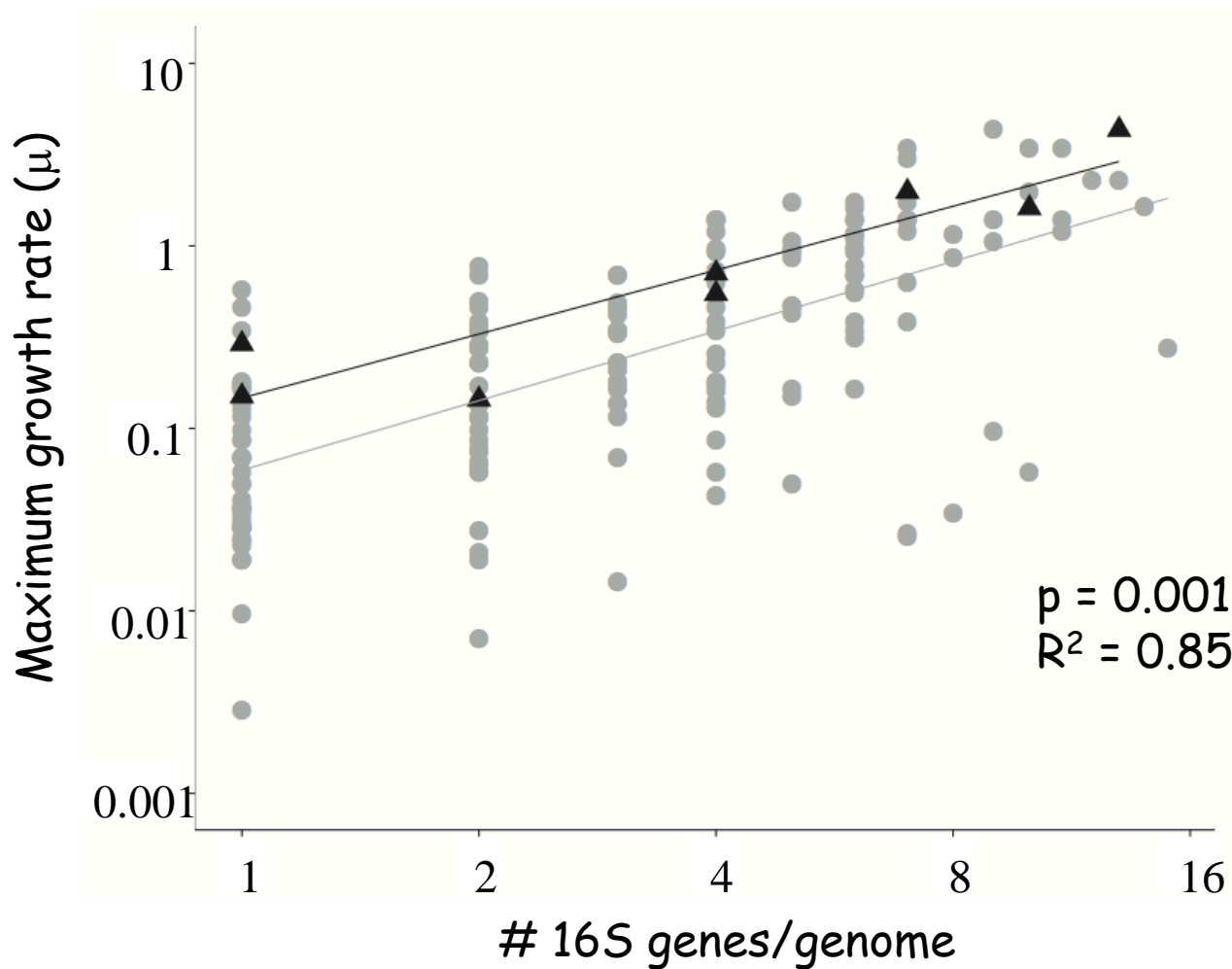
- r-selected
- Rapid response
- High μ_{max}



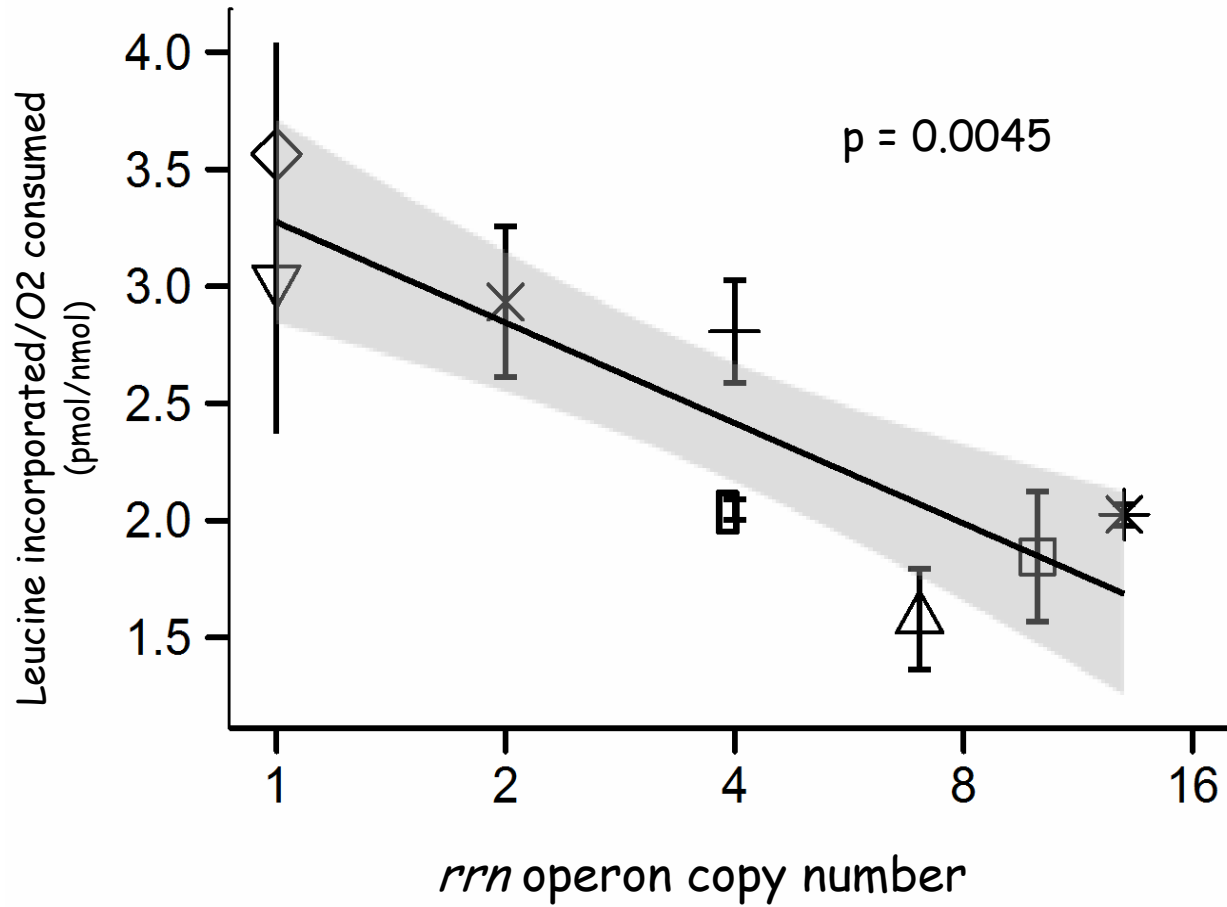
rRNA operon copy number



Growth rate increases with number of 16S genes



Growth efficiency declines with increasing # 16S genes



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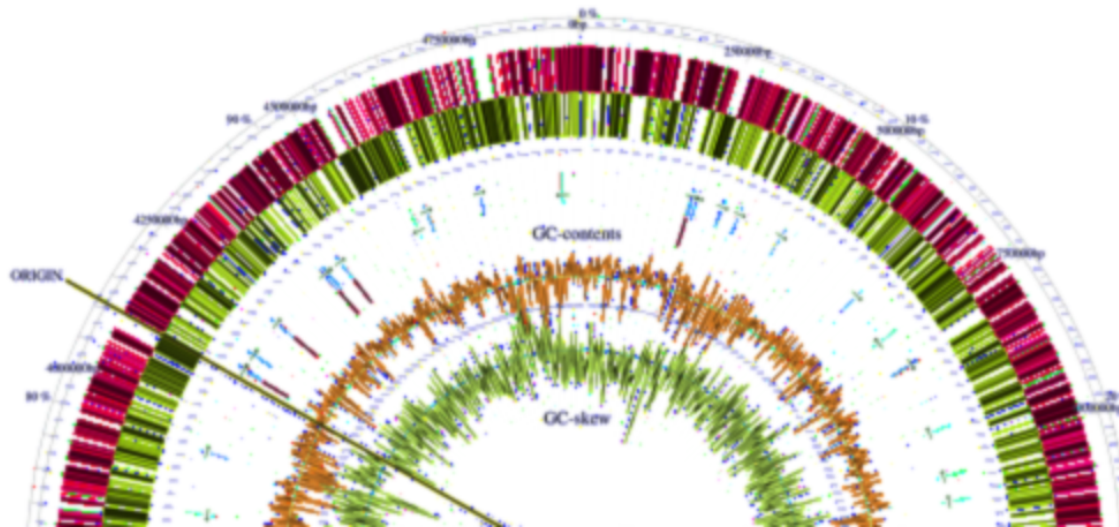
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Latest release:

*rrn*DB
version 4.3.3

November 06, 2014

(see [About *rrn*DB Versions](#)
for changes)

*rrn*DB

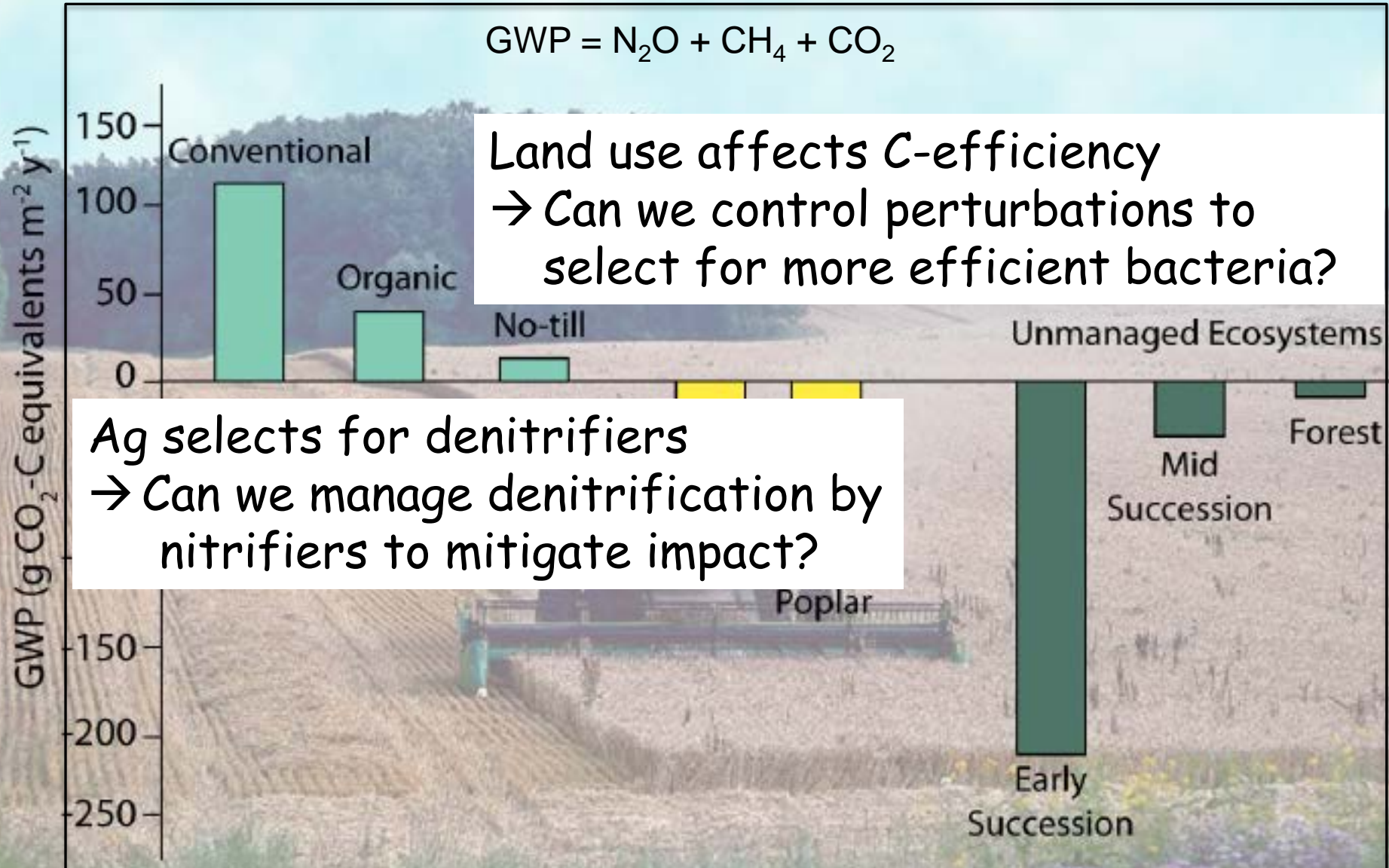
A searchable database documenting variation in ribosomal RNA operons (*rrn*) in Bacteria and Archaea. Find information such as the 16S gene copy number of an organism by looking up its name under the NCBI or RDP taxonomy or by full-text search of *rrn*DB's records.

Please cite the use of *rrn*DB in the following way:

Stoddard S.F, Smith B.J., Hein R., Roller B.R.K. and Schmidt T.M. (2015) *rrn*DB: improved tools for interpreting rRNA gene abundance in bacteria and archaea and a new foundation for future development. *Nucleic Acids Research* 2014; doi: 10.1093/nar/gku1201

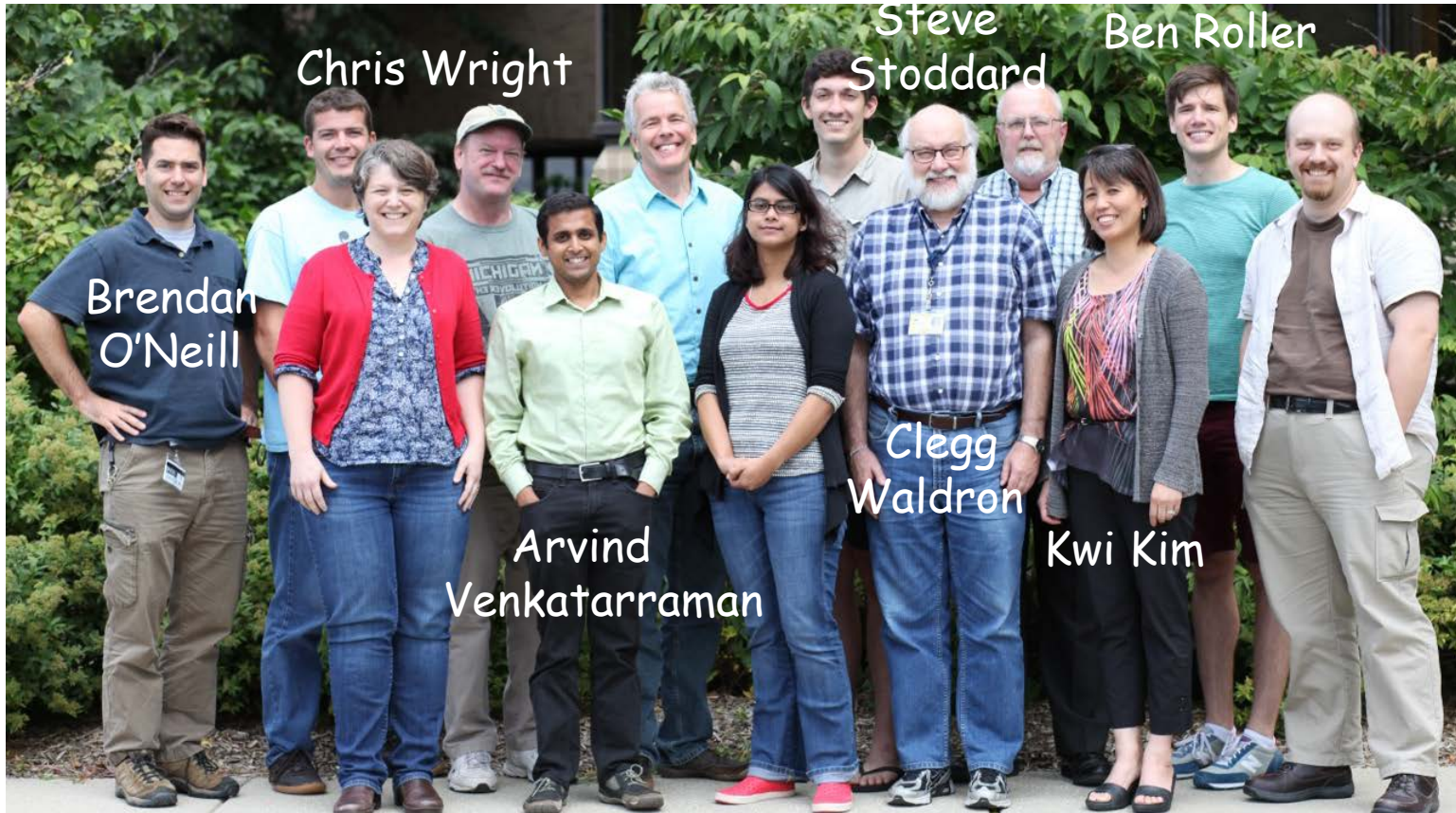
[\[PMID:25414355\]](#)

Conclusions and Questions



Kellogg Biological Station, Michigan State University

Schmidt Lab, 2014



<http://microbiomes.msu.edu>

