Integrating microbial community data with ecological theory

Steve Allison
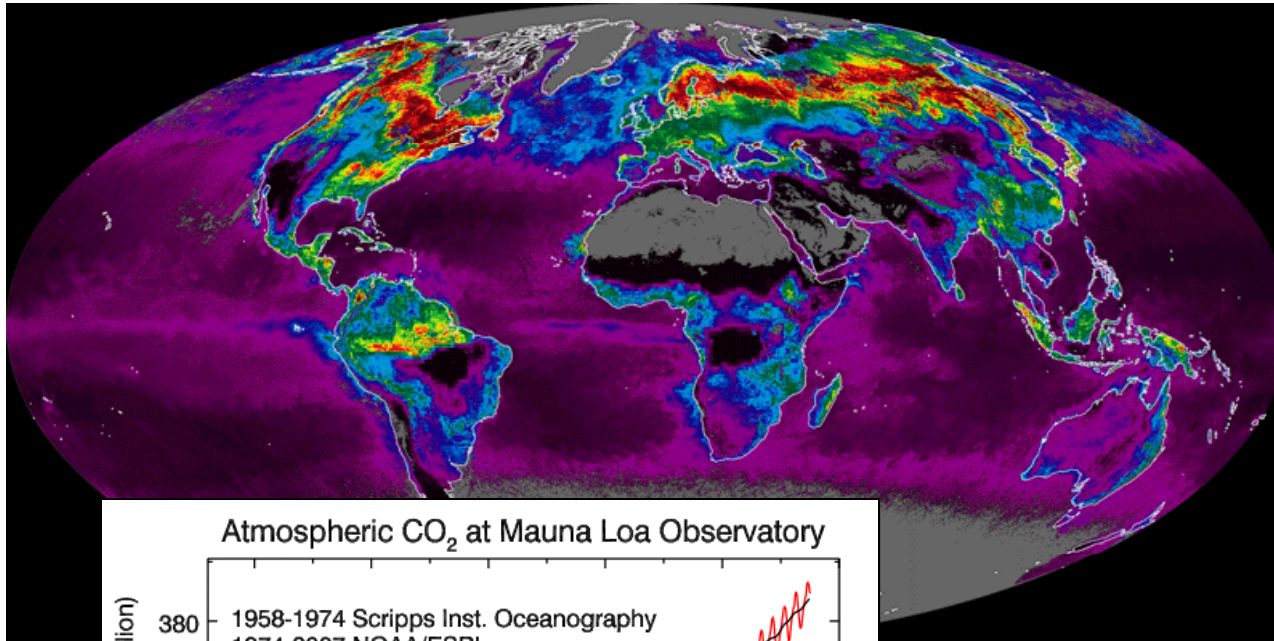**UC Irvine**
Ecology and Evolutionary Biology
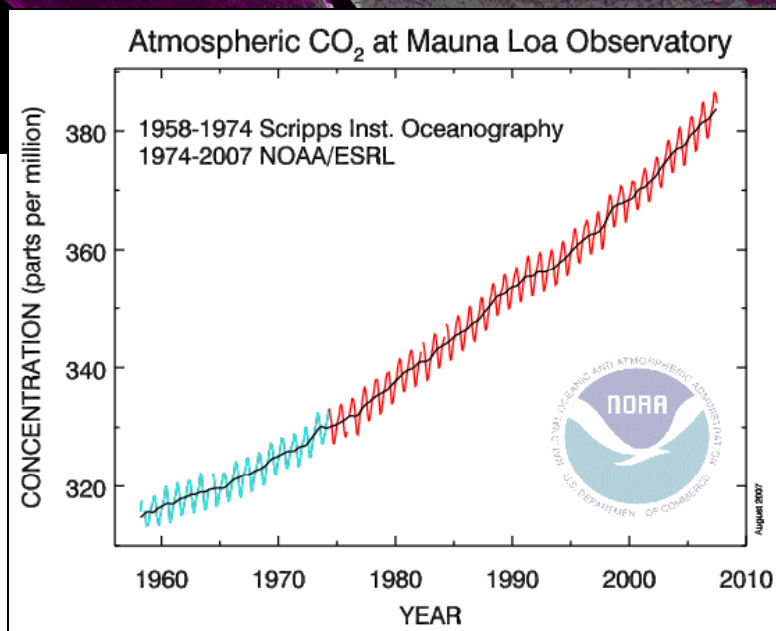**Earth System Science**
allisons@uci.edu

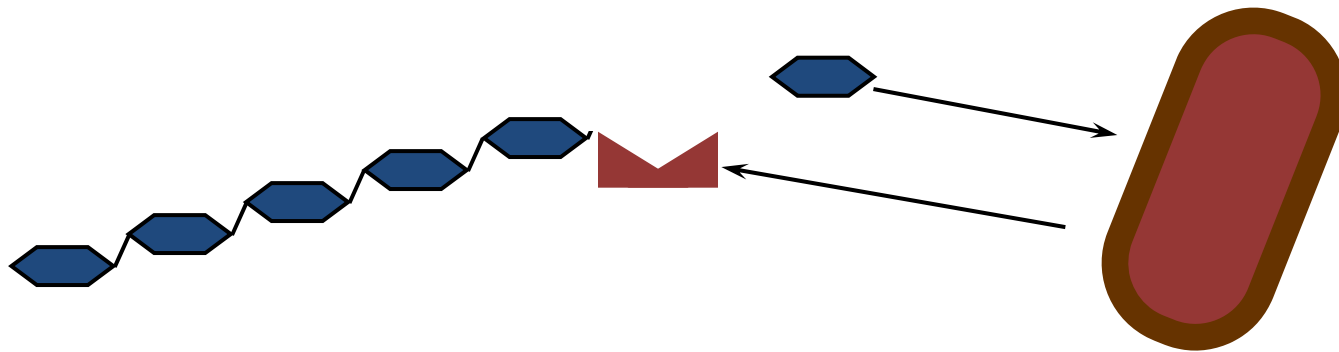# What controls C stability?

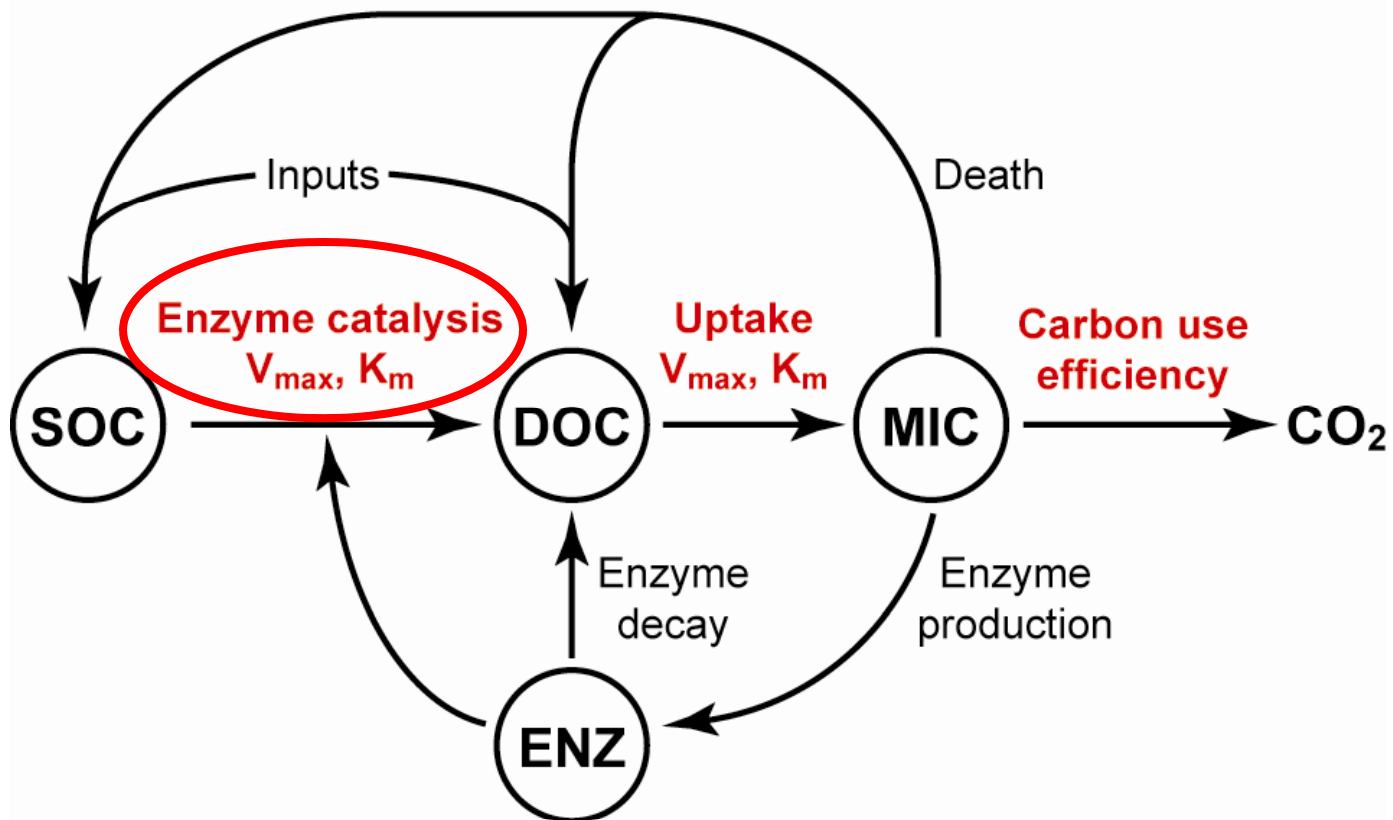Ocean: 1000 Pg

Terrestrial: 2000+ Pg

Extracellular enzymes

- Degrade complex molecules from plants, animals, and other microbes

- Ecosystem consequence: prevent the world from filling with dead bodies

Enzyme-based warming model
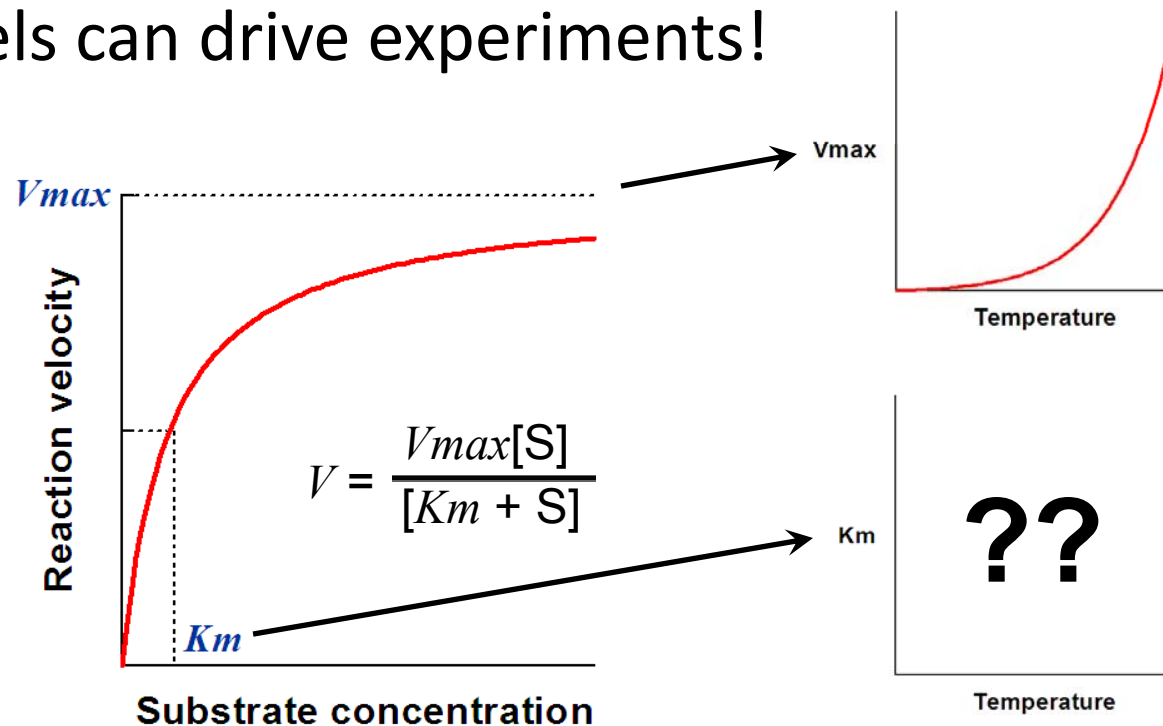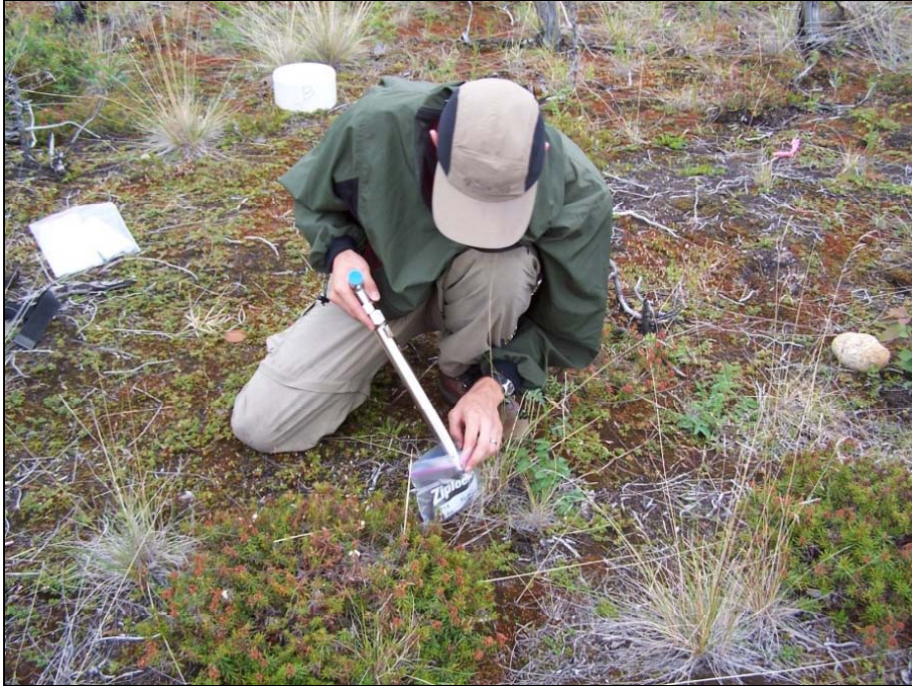
sensu Schimel and Weintraub, 2003

Collaborators:
Mark Bradford
Matt Wallenstein

Allison et al. 2010, Nature Geosci

How do we model enzyme response to warming?

- Michaelis-Menten relationship
- Exponential increase in Vmax (Davidson & Janssens 2006)
- Km response unknown in soil
- Models can drive experiments!

Soil sampling

Enzyme assays:
Maddie Stone
Kathleen Marcelo
Stephany Chacon
Donovan German

Temperature response:
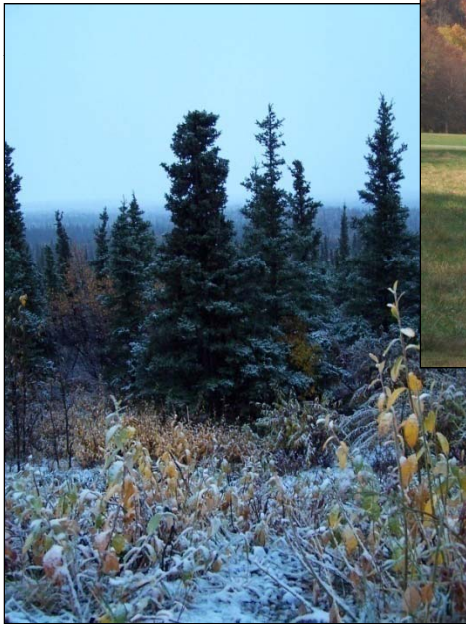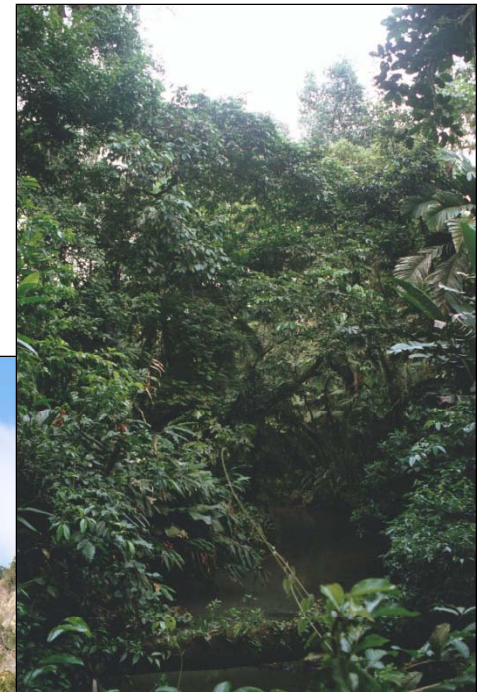Assay activity at 4°C to 40°C

What if microbes adapt to warming?

- Return toward initial state due to physiology, evolution, community shifts

1) Vmax might increase less than expected with warming -> reduces enzyme activity

2) Km might change less than expected (declines in Km INCREASE activity)

Latitudinal gradient
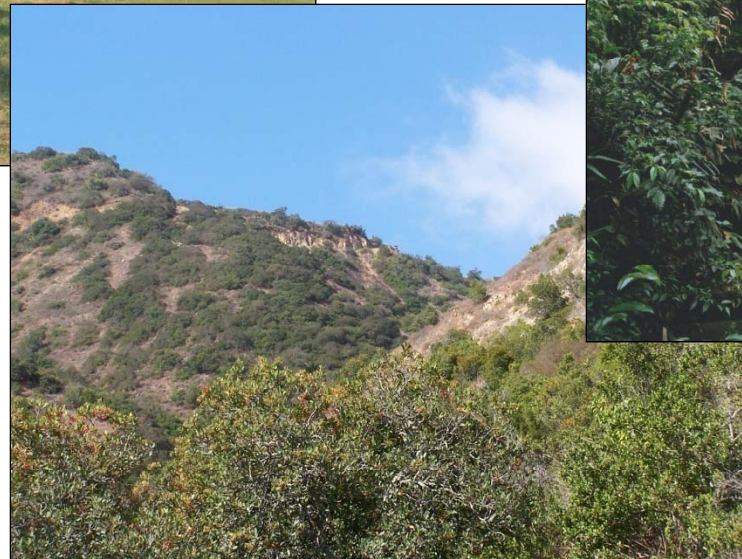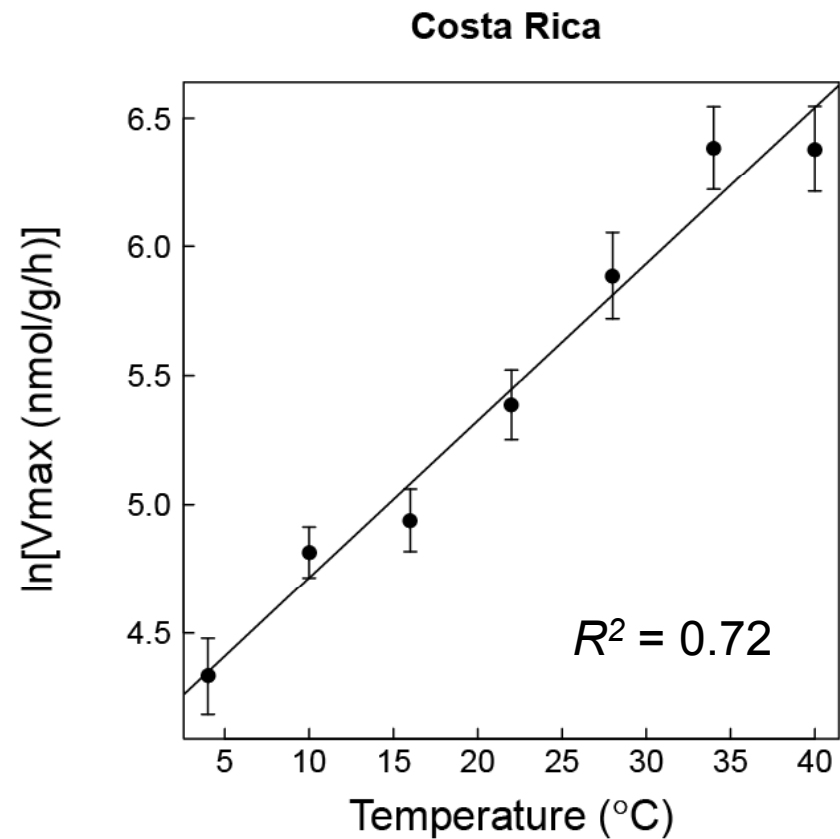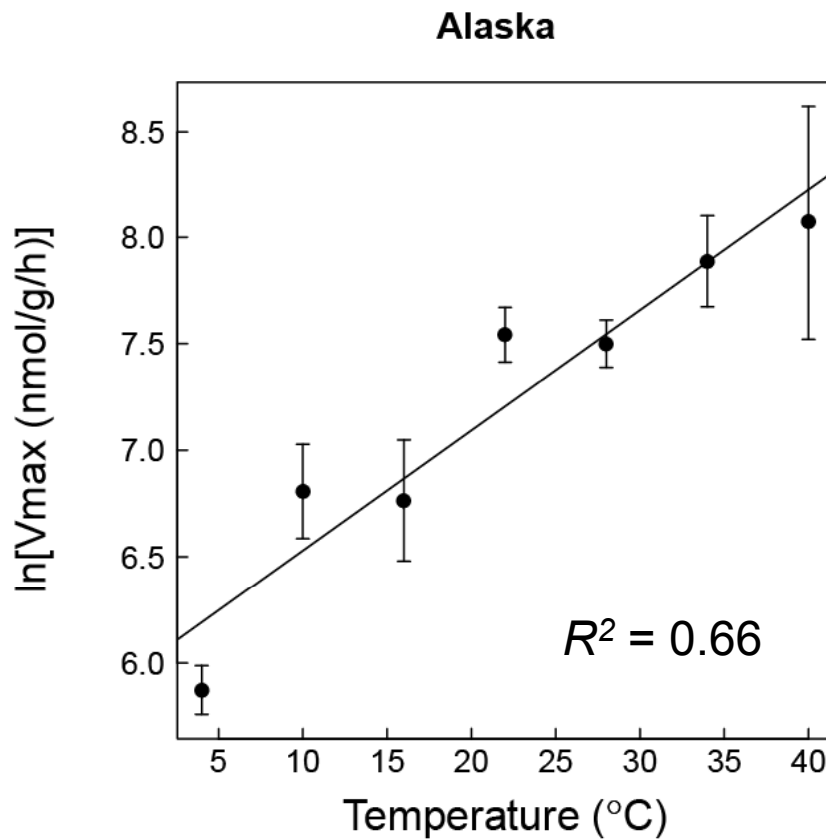
Hardwood forest: Maine, West VA
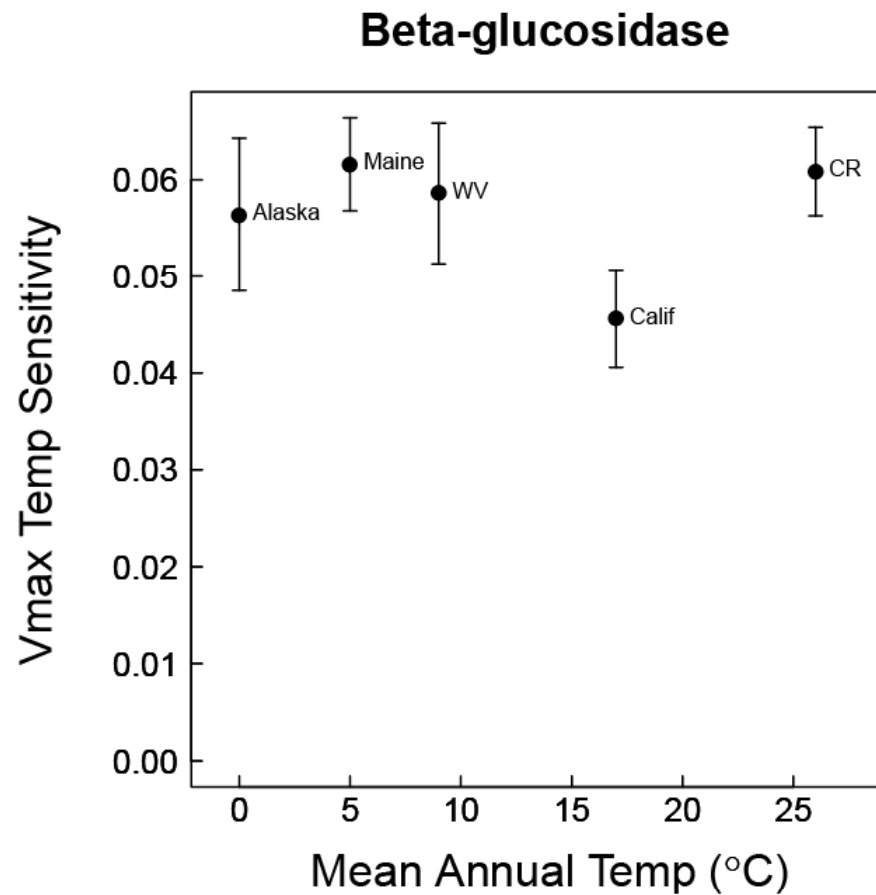
Costa Rica

Boreal Alaska

California grassland

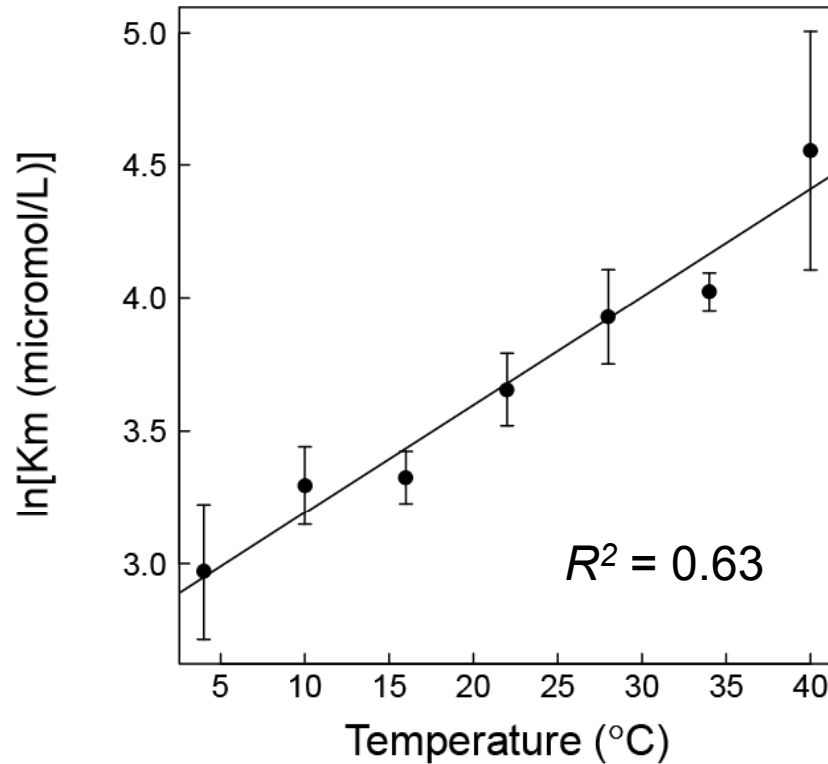# Vmax temp. response within sites: Beta-glucosidase

No evidence for Vmax adaptation

Beta-glucosidase

Km temp. response within sites: Beta-glucosidase
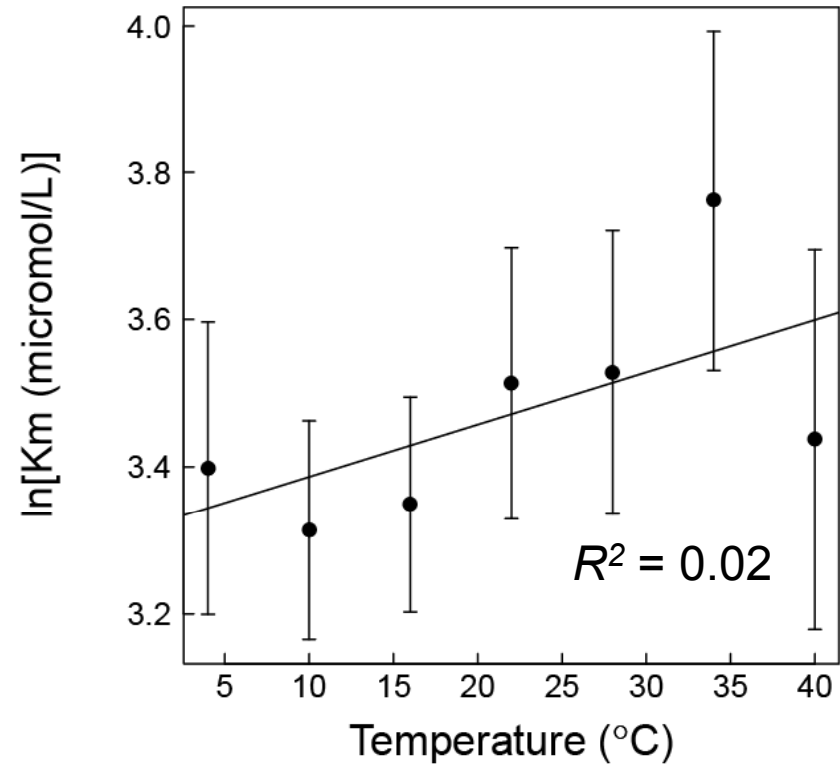
Possible Km adaptation
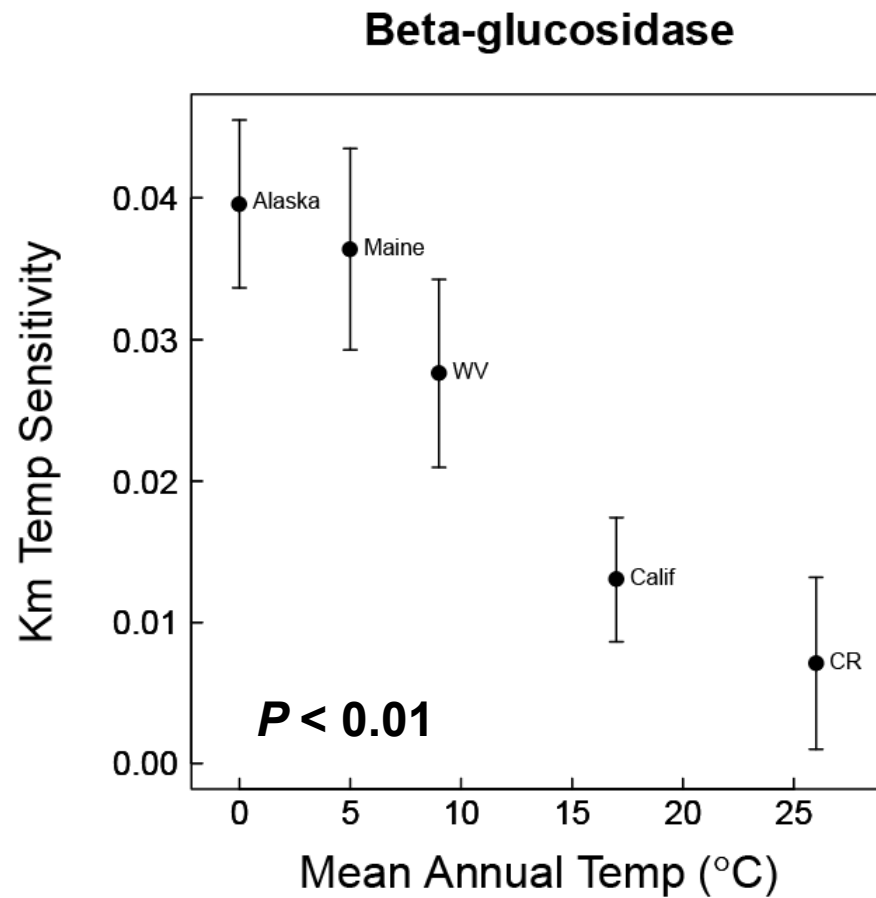
Beta-glucosidase

Integrate theory and data into model

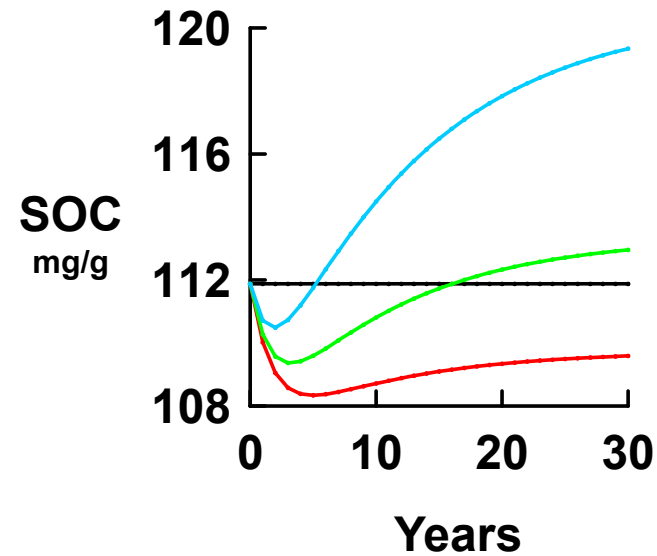**Km adaptation: lose SOC**

Vmax adaptation: gain SOC

Integrate theory and data into model

Km adaptation: lose SOC

Vmax adaptation: gain SOC
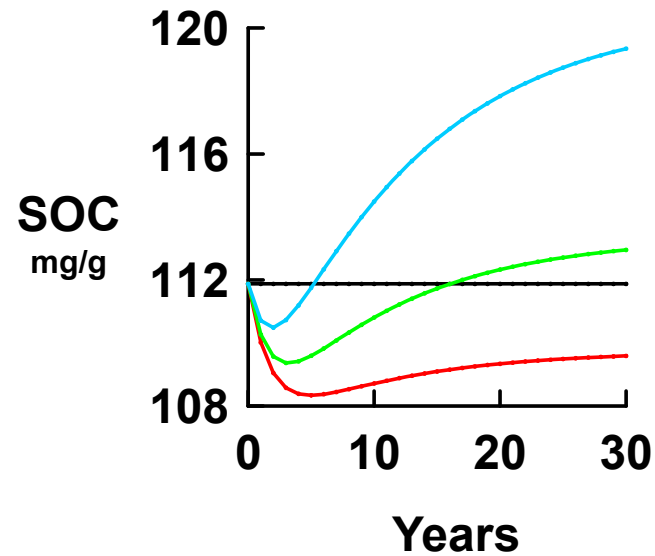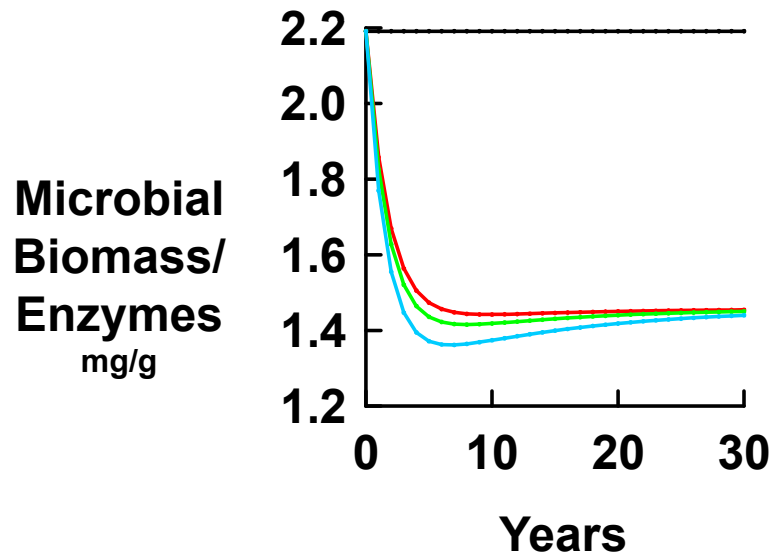
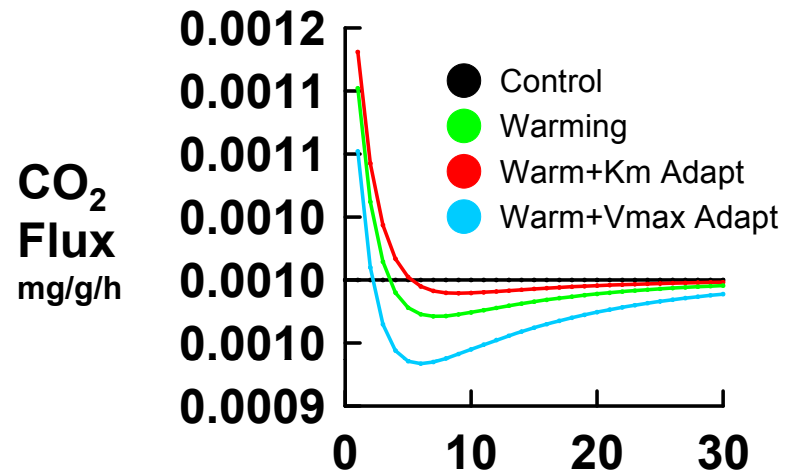# Summary: Temperature responses

- Vmax increases with temperature

- No Vmax adaption: no advantage to reducing enzymatic potential in warm soils

- Km also increases with temperature; substrate binding weakens due to instability

- Km may adapt because lower Km in warmer soil enhances enzyme activity

Enzyme gene (AG, BG, etc.)

Vmax

Temp

Trait vector

Trait distribution

Trait model framework

Randomization

Physiological Trait (e.g. N-fixation, CO₂ respiration)

Process Response to Disturbance
A   B   C

Clade 1

Clade 2
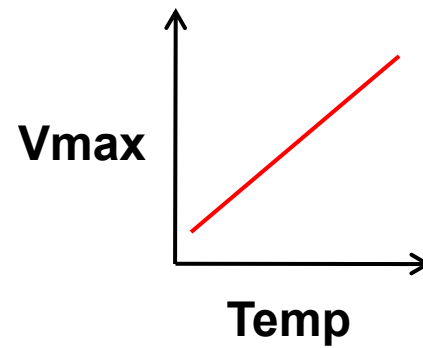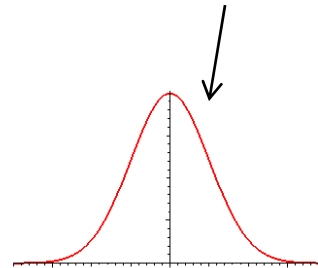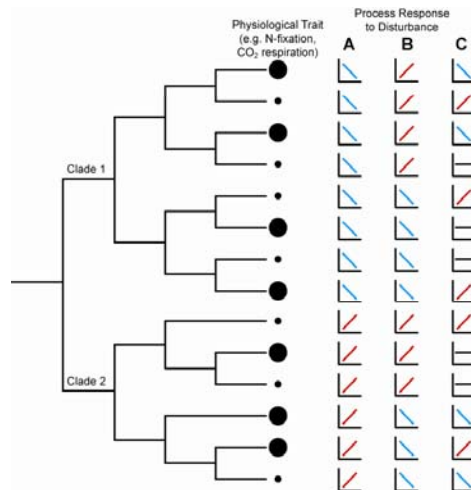
Environment

Competition/ evolution

Community structure
Process rates

Approach for model-data integration

- For a process of interest, determine relevant traits and environmental drivers

- Constrain trait distributions with empirical data

- Sample trait distributions or assign functional groups in model

- Let the environment select on community and process

- Thank you: Lab members, NSF, audience

Constant CUE = large SOC losses
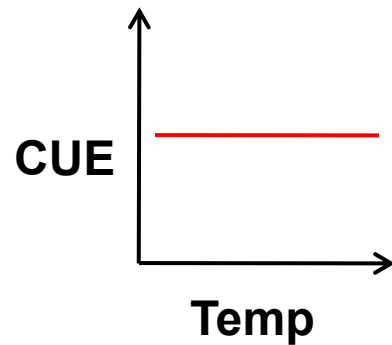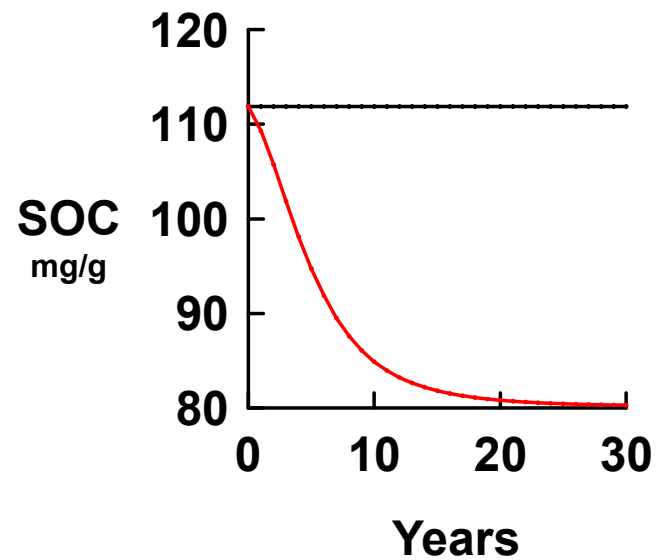
Constant CUE = large SOC losses
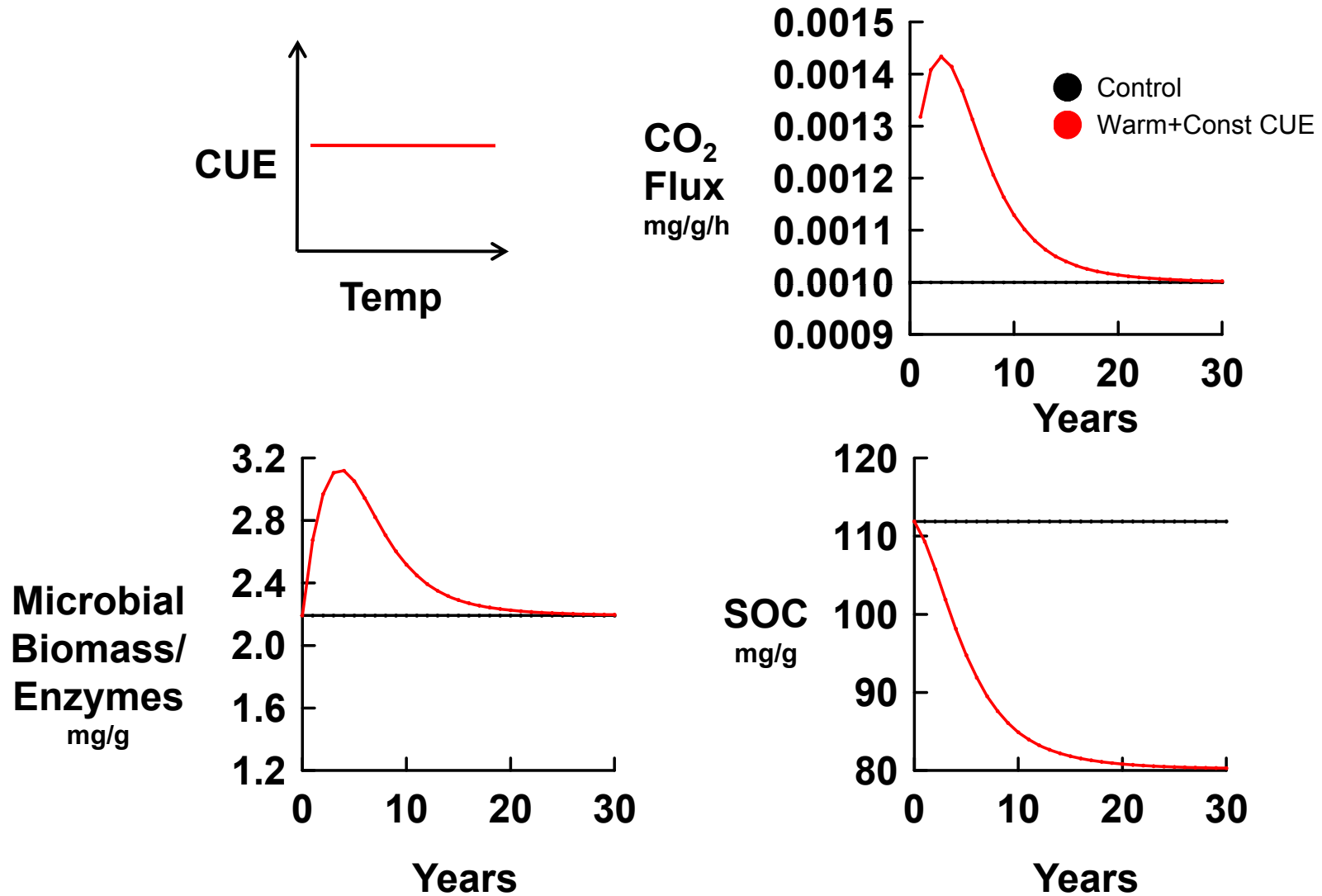
Varying CUE increases C storage
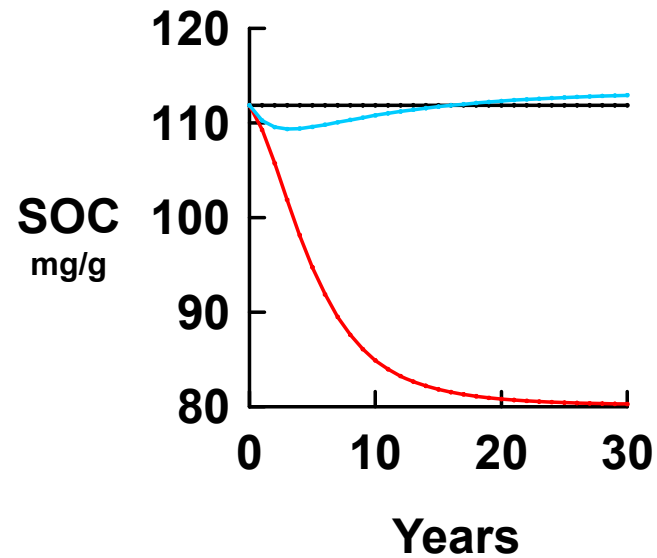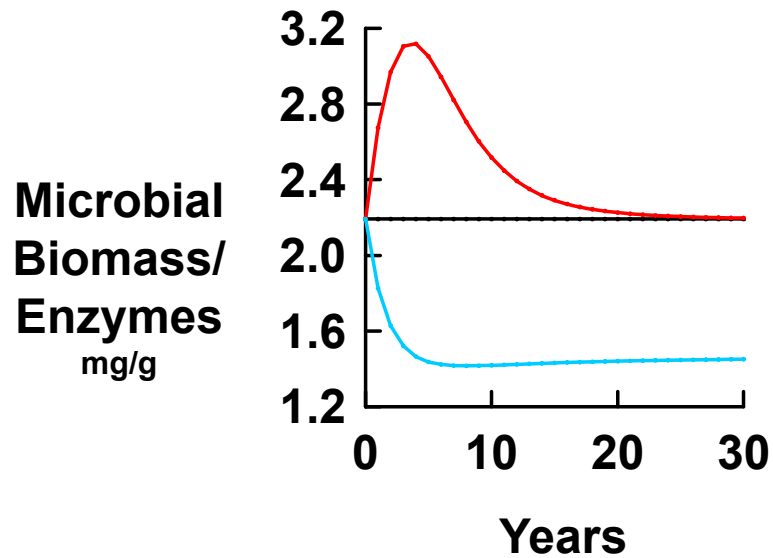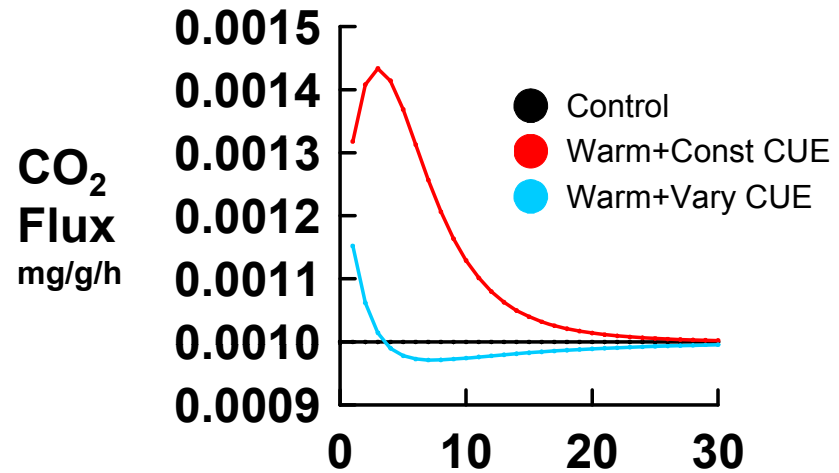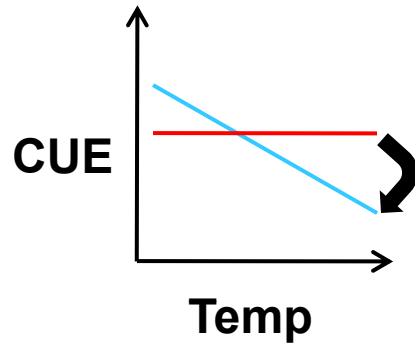
Acclimation of CUE restores losses
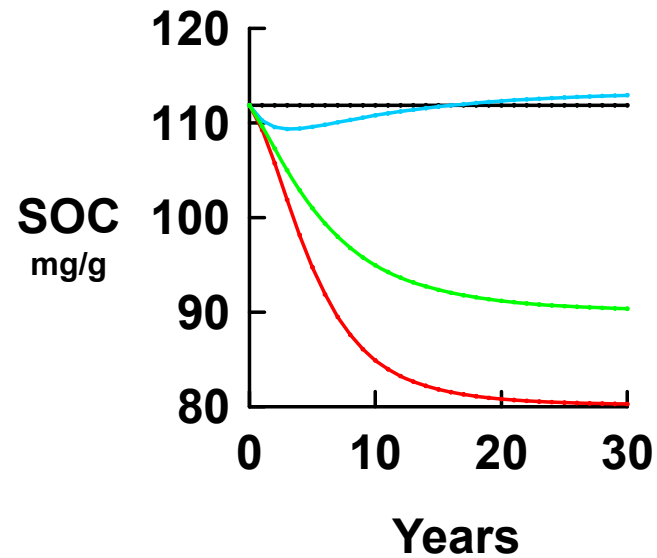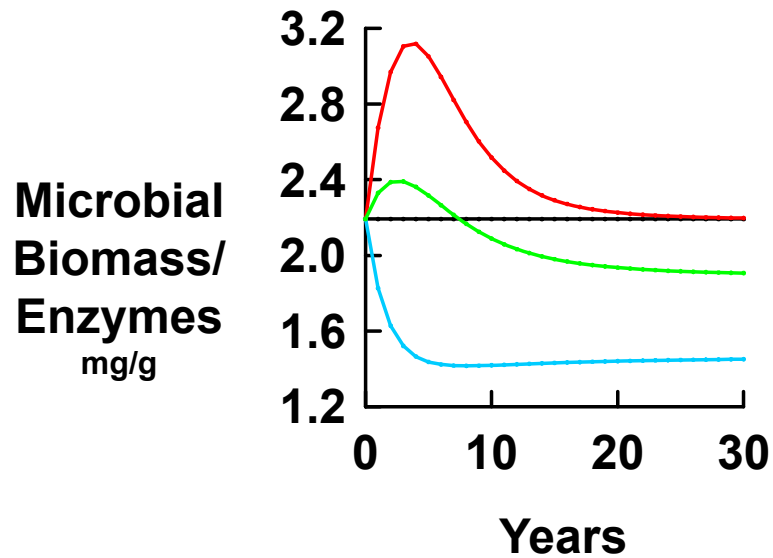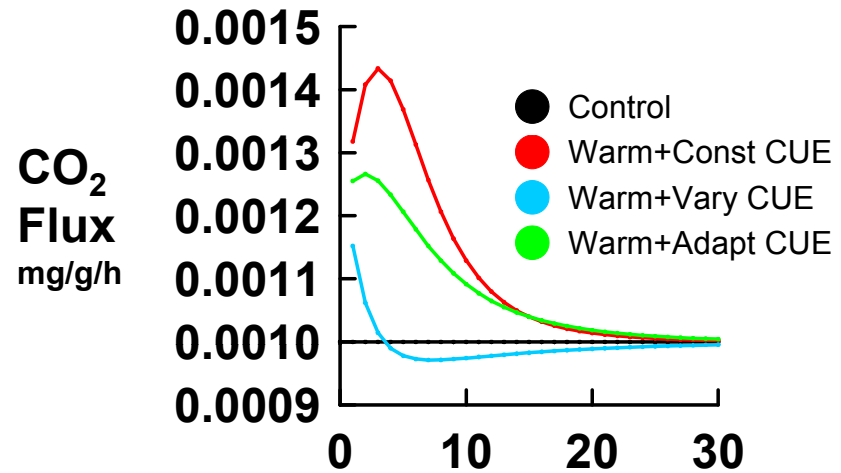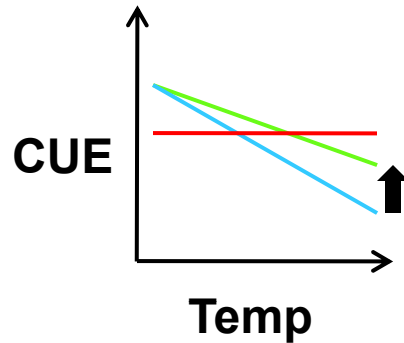
Acclimation of CUE restores losses
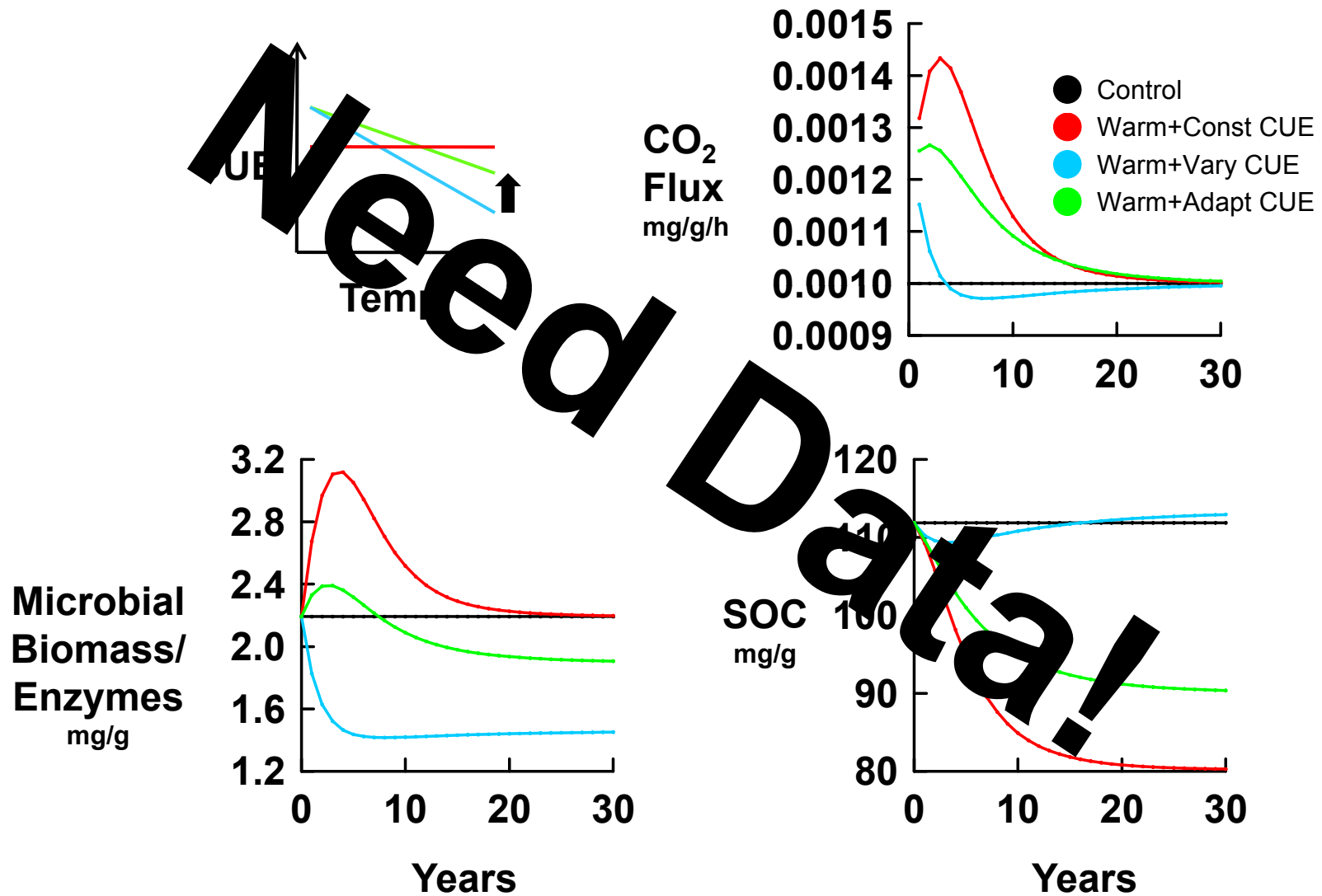
Temperature constraints

- Can we explain ephemeral CO_2 response to warming (e.g. Melillo et al. 2002)

% increase in respiration with warming
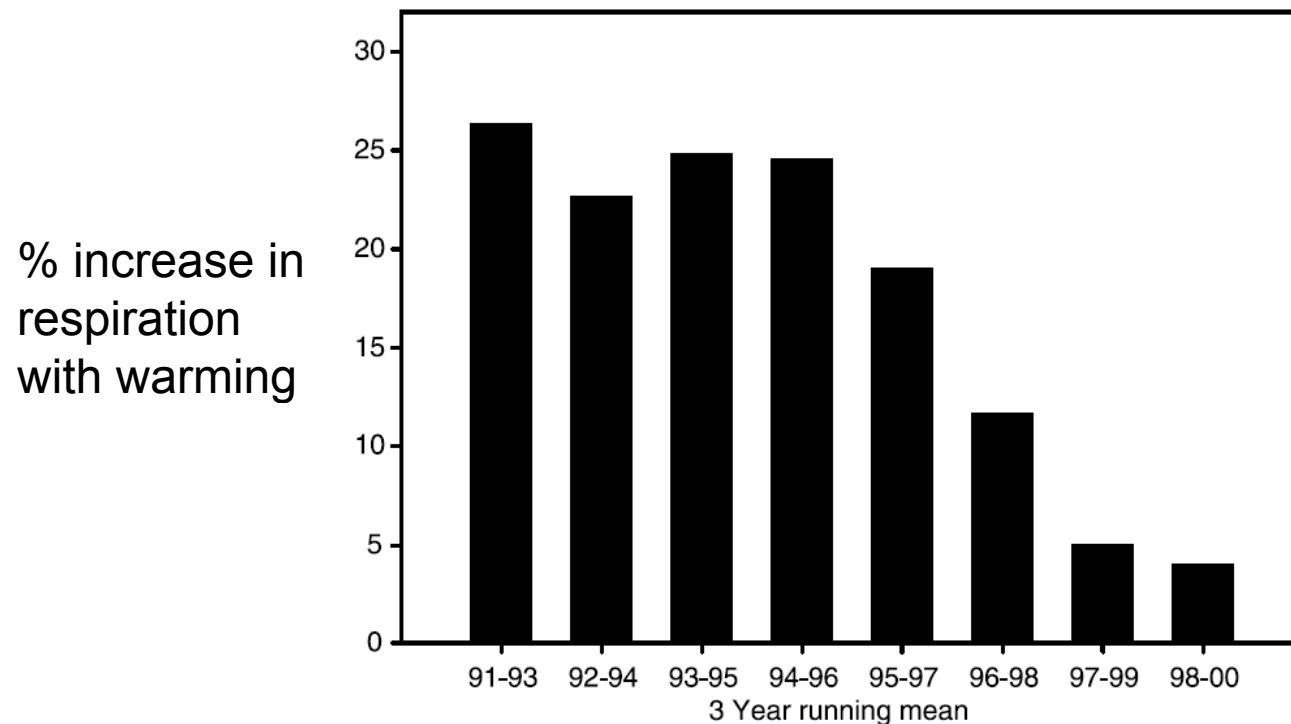
Hypotheses

- Substrate depletion: CO_2 respiration returns to control levels because SOC pools are depleted

- Thermal adaptation (or acclimation): microbial physiological parameters change in a way that reduces CO_2 respiration

A lesson from dynamic vegetation models

- DGVMs incorporate plant functional types
- Mechanistic representation of ecosystem processes like photosynthesis
- Aggregation based on leaf traits, growth form, and phenology e.g. "deciduous broadleaf trees"
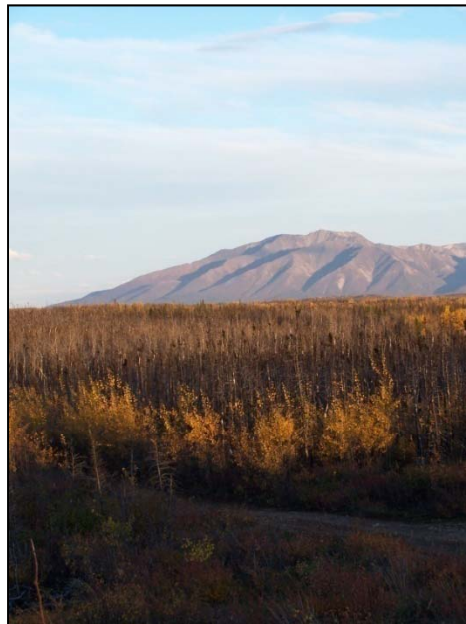
Taxonomic aggregation
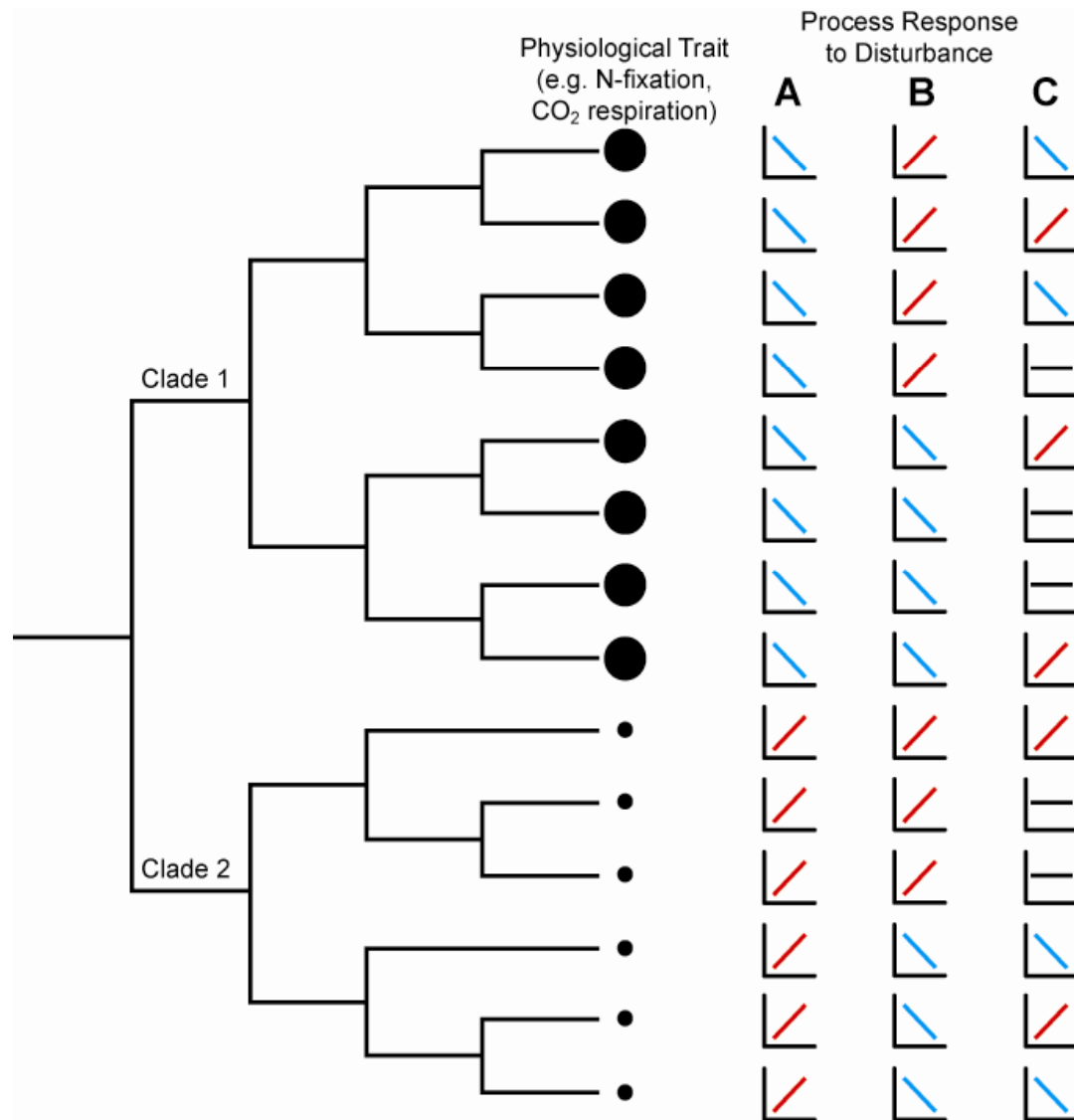
Processes may be **broad** or **narrow** (Schimel, 1995).

Many versus few microbial groups contribute.

Trait-based aggregation also possible
(e.g. Moorhead and Sinsabaugh 2006)
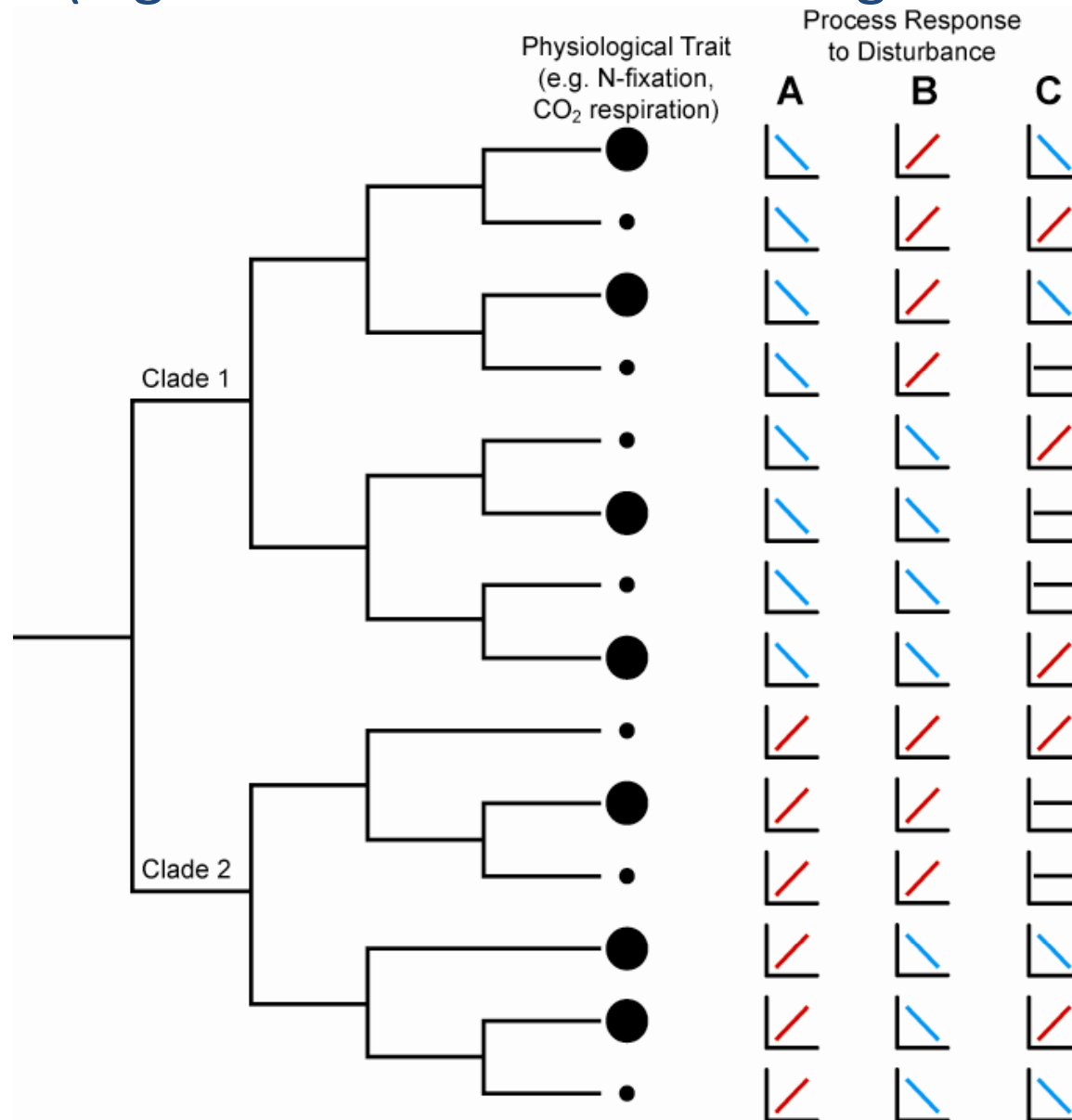
Wednesday, August 4, 2010 - 4:05 PM

SYMP 13-8: Integrating microbial community data with ecological theory

Steven D. Allison, University of California, Irvine

Background/Question/Methods

Molecular and bioinformatics techniques are revealing the rich diversity of microbial communities. These approaches generate valuable data that ecologists could use to develop and test theories that apply to a large fraction of living organisms. However, the complexity of microbial community data is a challenge to achieving this integration. A fundamental question in microbial ecology is how to aggregate microbial communities so that their taxa may be represented in theoretical models. Recently, models based on microbial traits have been developed to tackle this question. Such models may represent microbial taxa as functional groups or stochastic assemblages with a distribution of trait values. Here, I define these two model types and show how they can be used to make predictions about the function of complex microbial communities. I focus on organic matter decomposition and nutrient mineralization because this function is typically driven by complex microbial communities.

Results/Conclusions

When applying ecological theory to predict rates of organic matter turnover, complex communities can be aggregated based on relevant traits, such as the ability to produce extracellular enzymes. Ecological and evolutionary theories provide a framework for predicting the distribution of these traits across time and space. For example, theories on ecological succession may predict the temporal progression of enzyme traits that occur in association with a decomposing substrate. Dispersal parameters from island biogeography theory may determine the movement of enzyme traits across the microbial landscape. Evolutionary theory can be used to predict the appearance and loss of enzyme traits due to selective pressures in microbial ecosystems. All of these theories then determine the abundance of particular functional groups, or the means and variances of trait distributions that directly affect ecological function. Functional group models may be useful in simple systems, but stochastic models based on distributions may be more relevant for complex communities with a diversity of continuous traits and many unidentified members.