Integration of microbial communities into large-scale ecosystem models

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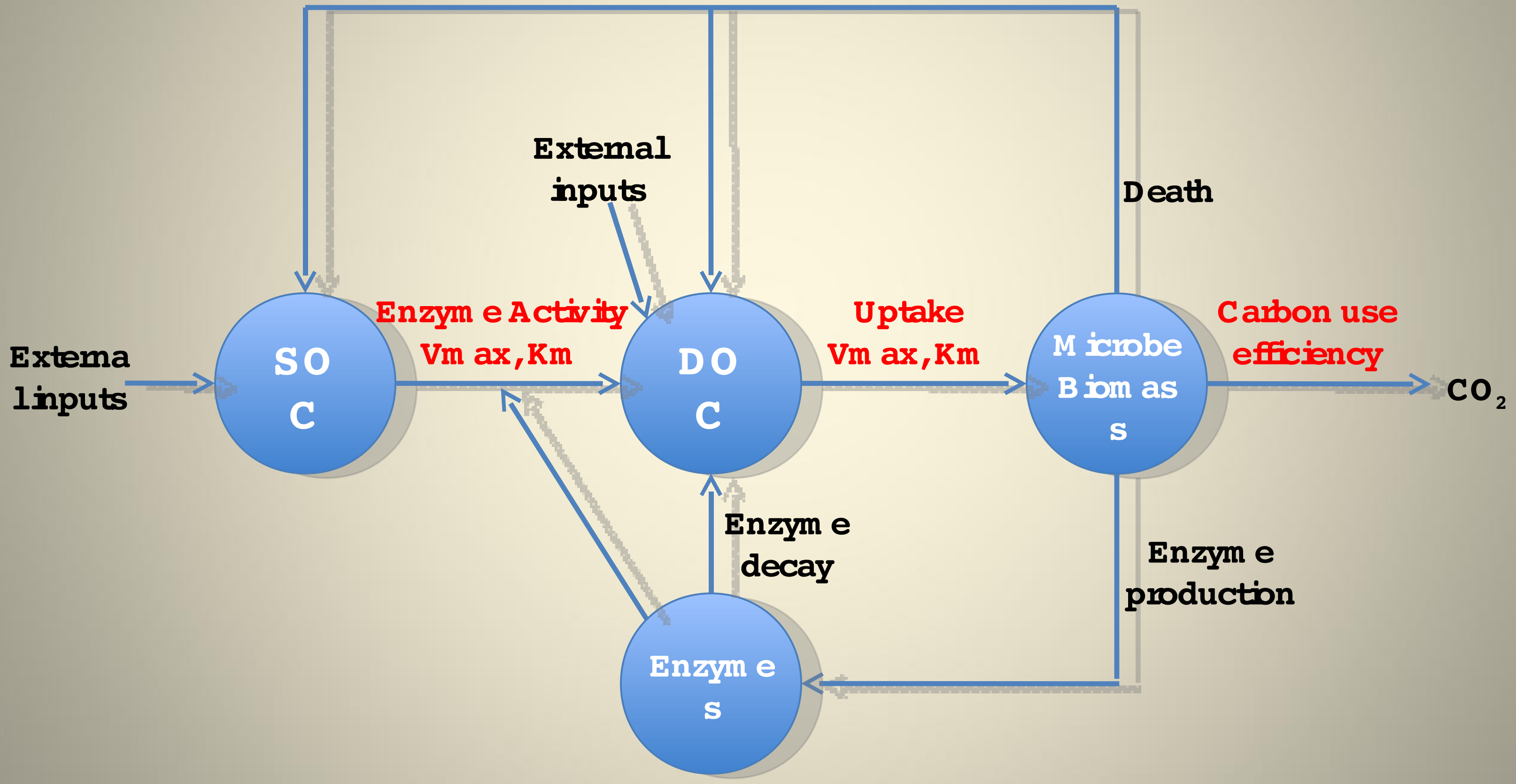
Diverse microbial communities drive biogeochemical processes

- Genetic and metabolic diversity:
  - 10^9 bacteria/fungi per gram soil
  - 10^7 bacteria per ml seawater
- Challenge: integrate microbes into models

Example: Soil warming model



External inputs

SOC

Enzyme Activity
Vmax, Km

External inputs

DOC

Uptake
Vmax, Km

Microbe Biomass

Death

Carbon use efficiency

CO_2

Enzyme decay

Enzyme production

Enzymes

sensu Schimel and Weintraub, 2003

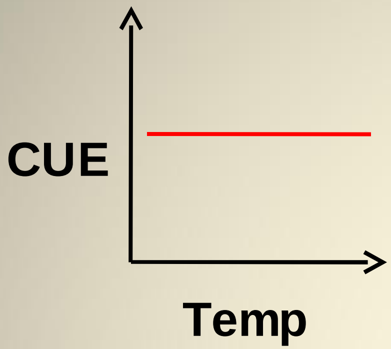
Explaining ephemeral CO_2 response to warming (e.g. Melillo et al. 2002)

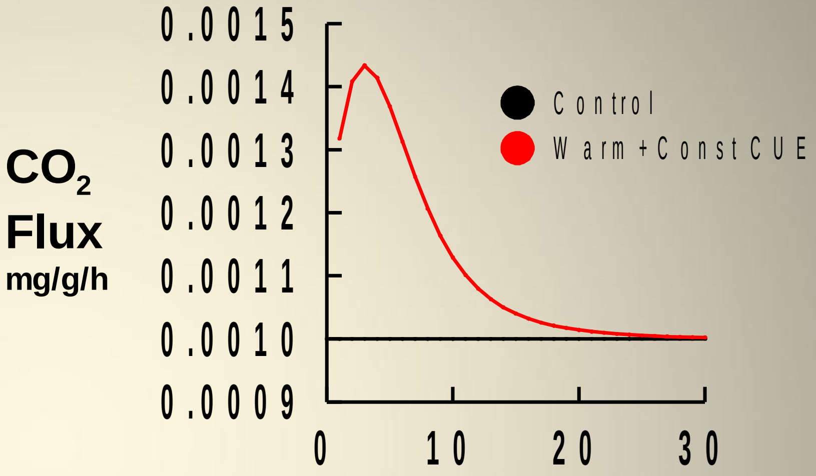
- Substrate depletion: CO_2 respiration returns to control levels because SOC pools are depleted

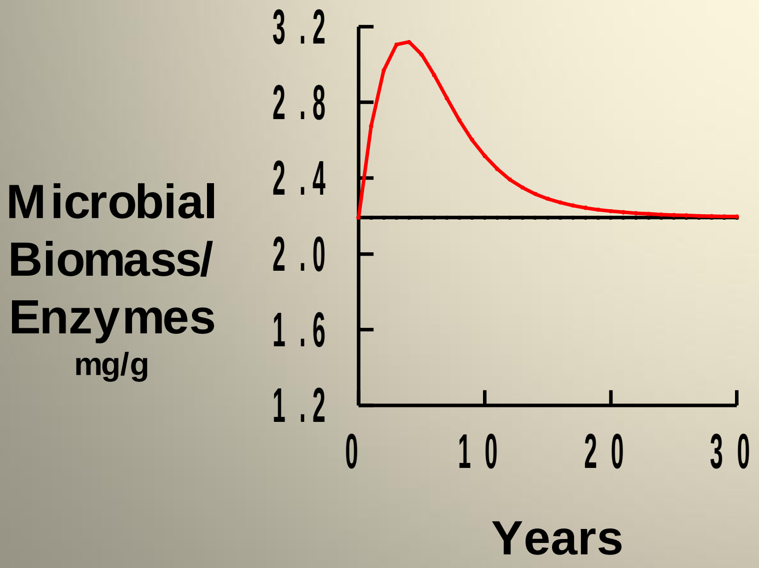
- Thermal adaptation (or acclimation): microbial physiological parameters change in a way that reduces CO_2 respiration

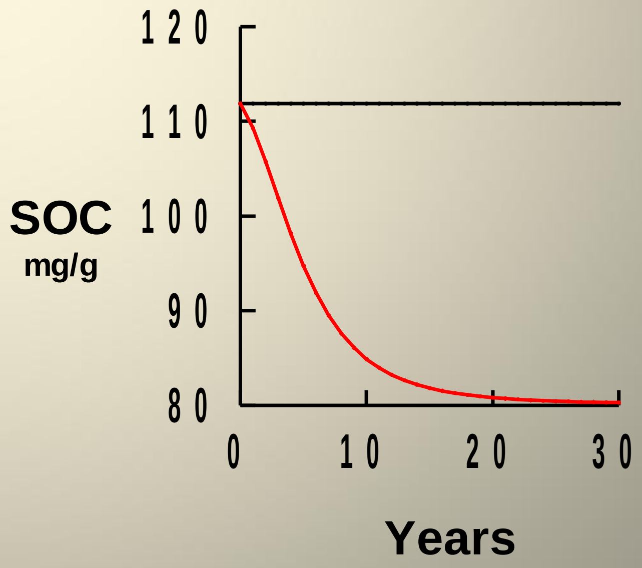
- Focus on Carbon Use Efficiency
  - = C assim / C uptake

Warming with constant CUE

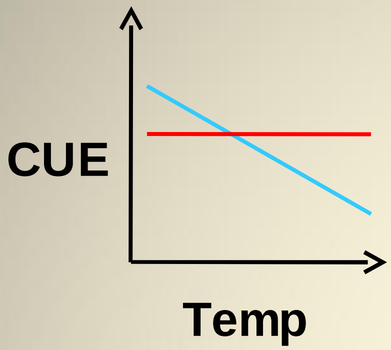


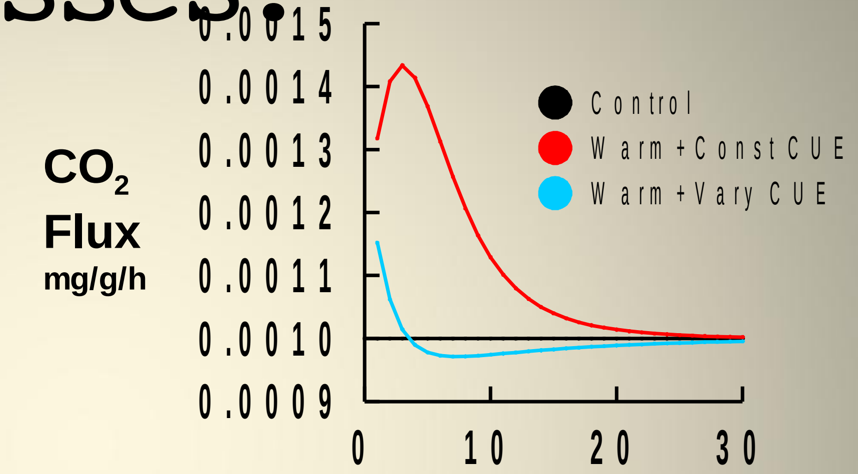


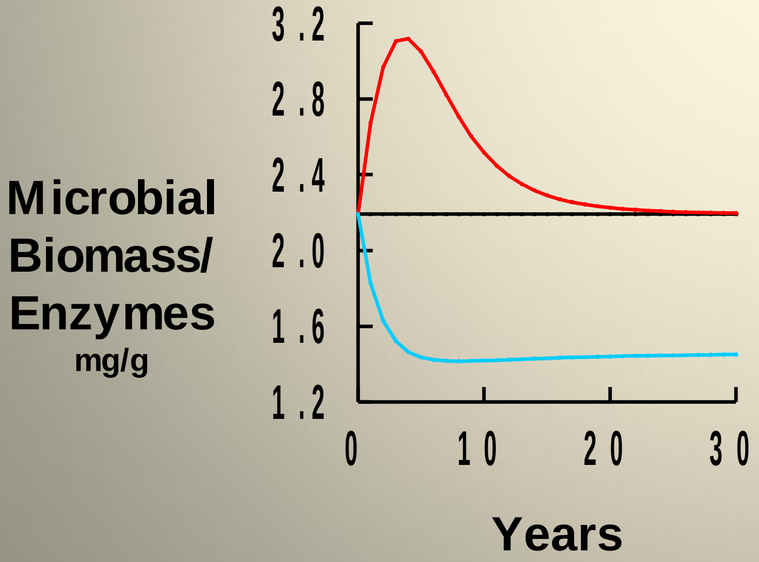


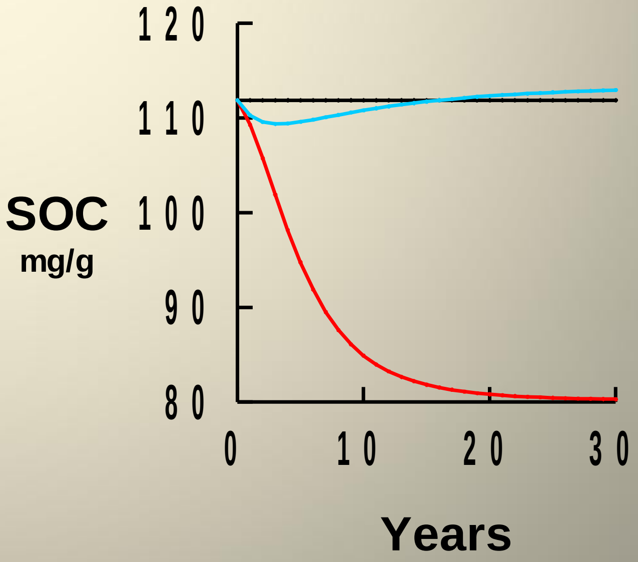


Variable CUE eliminates C losses!

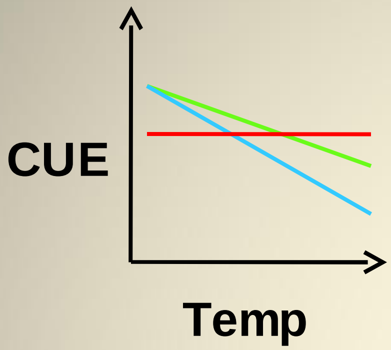


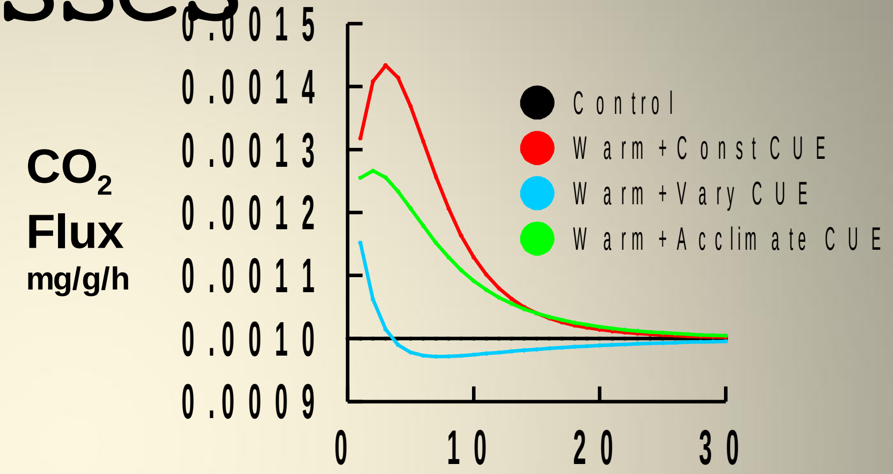


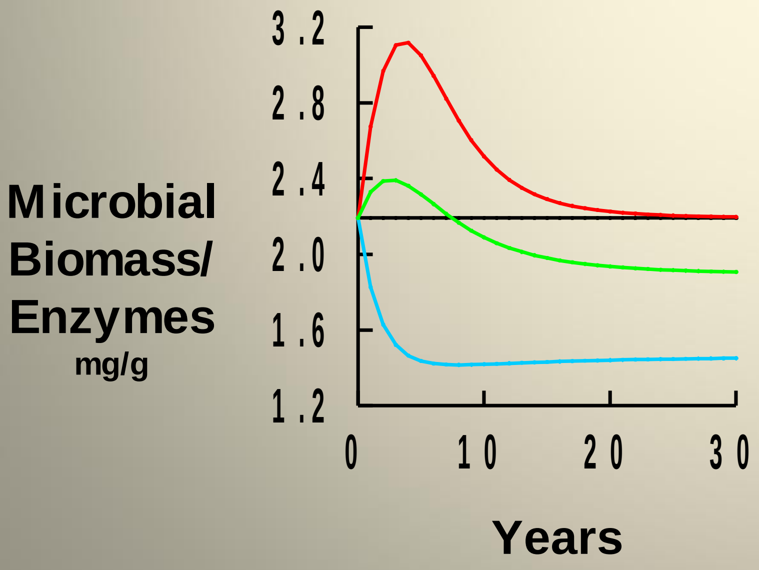


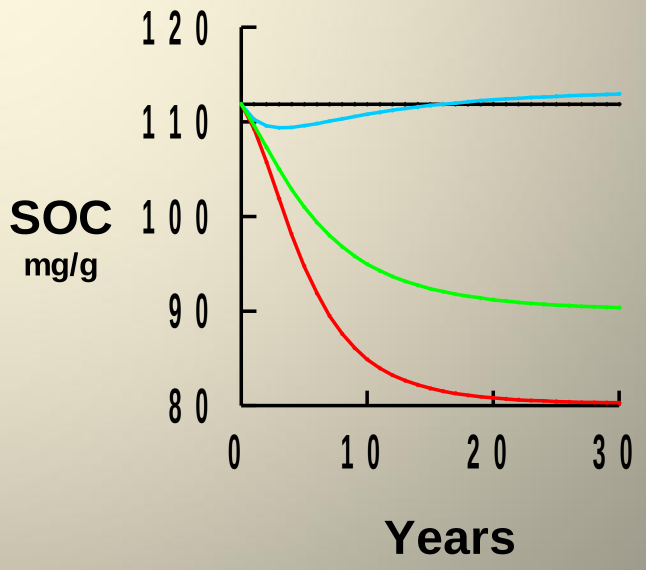


Acclimation of CUE restores losses



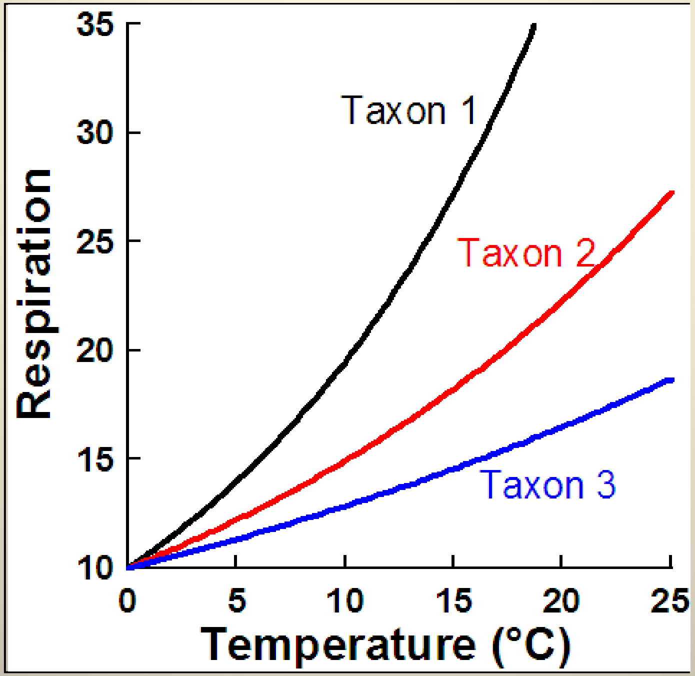






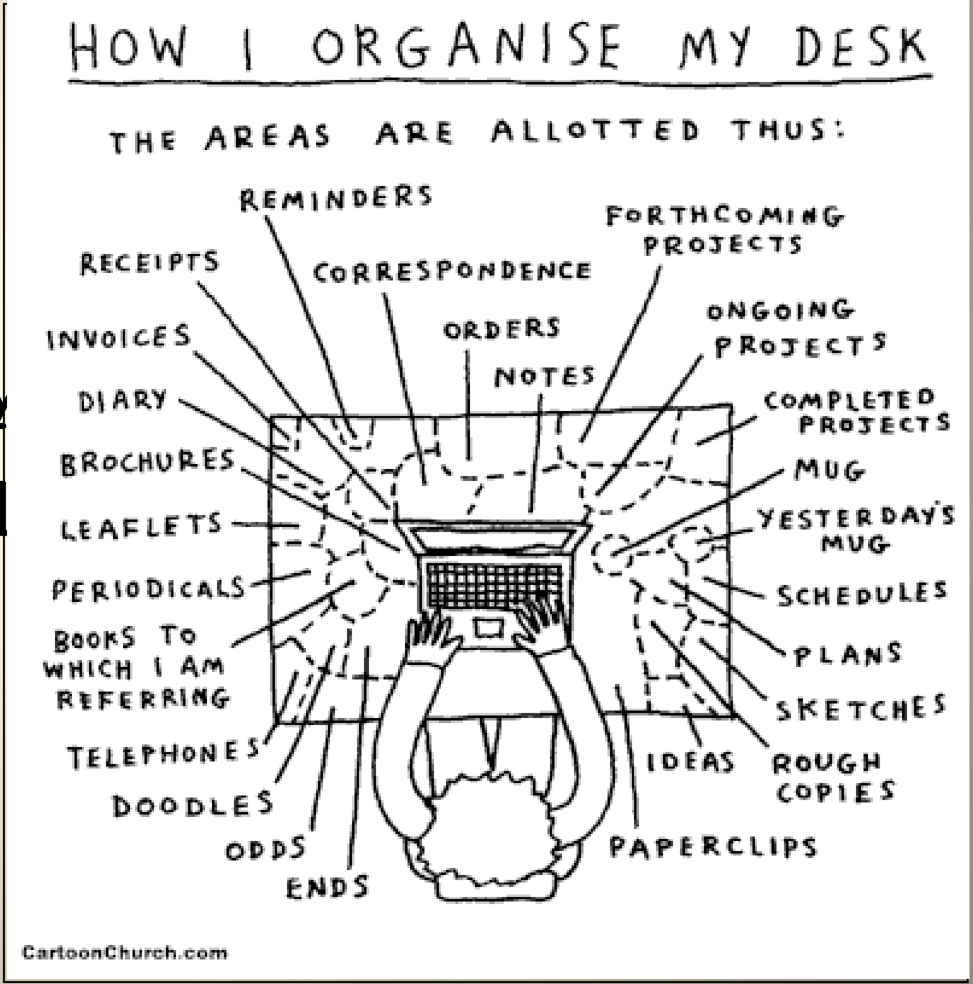
When might we need to model microbial communities explicitly?

Taxon-specific contribution to process rate changes with disturbance



How do we aggregate taxa in microbial communities?

- Total biomass or implicit biomass (e.g. k-values)
- Based on phylogeny
- Based on functional traits

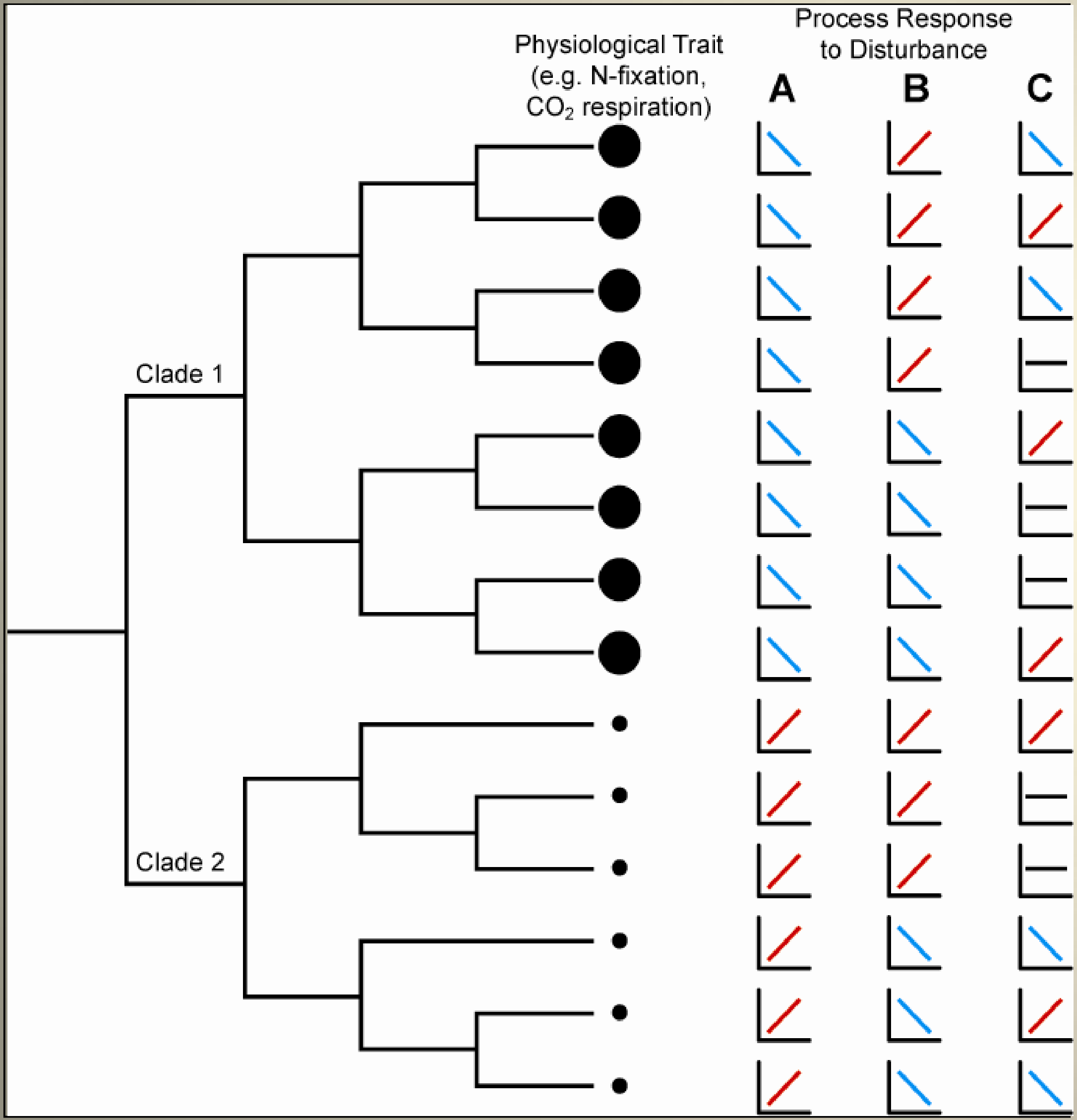


A lesson from dynamic vegetation models

- DGVMs incorporate plant functional types
- Aggregation based on leaf traits, growth form, and phenology
- E.g. “deciduous broadleaf trees”



Taxonomic aggregation

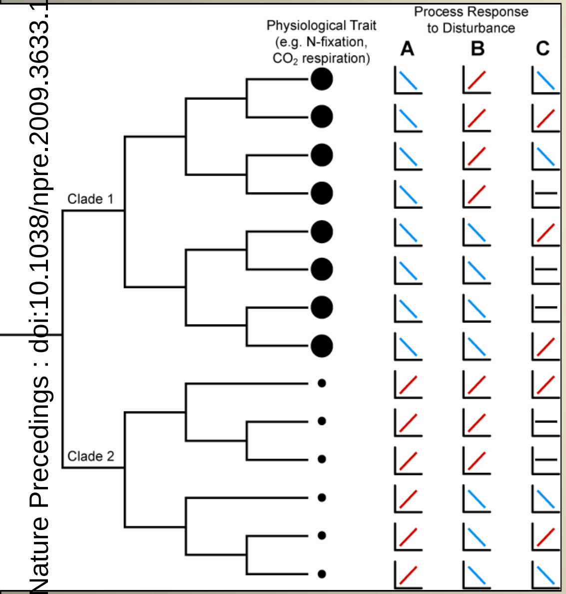


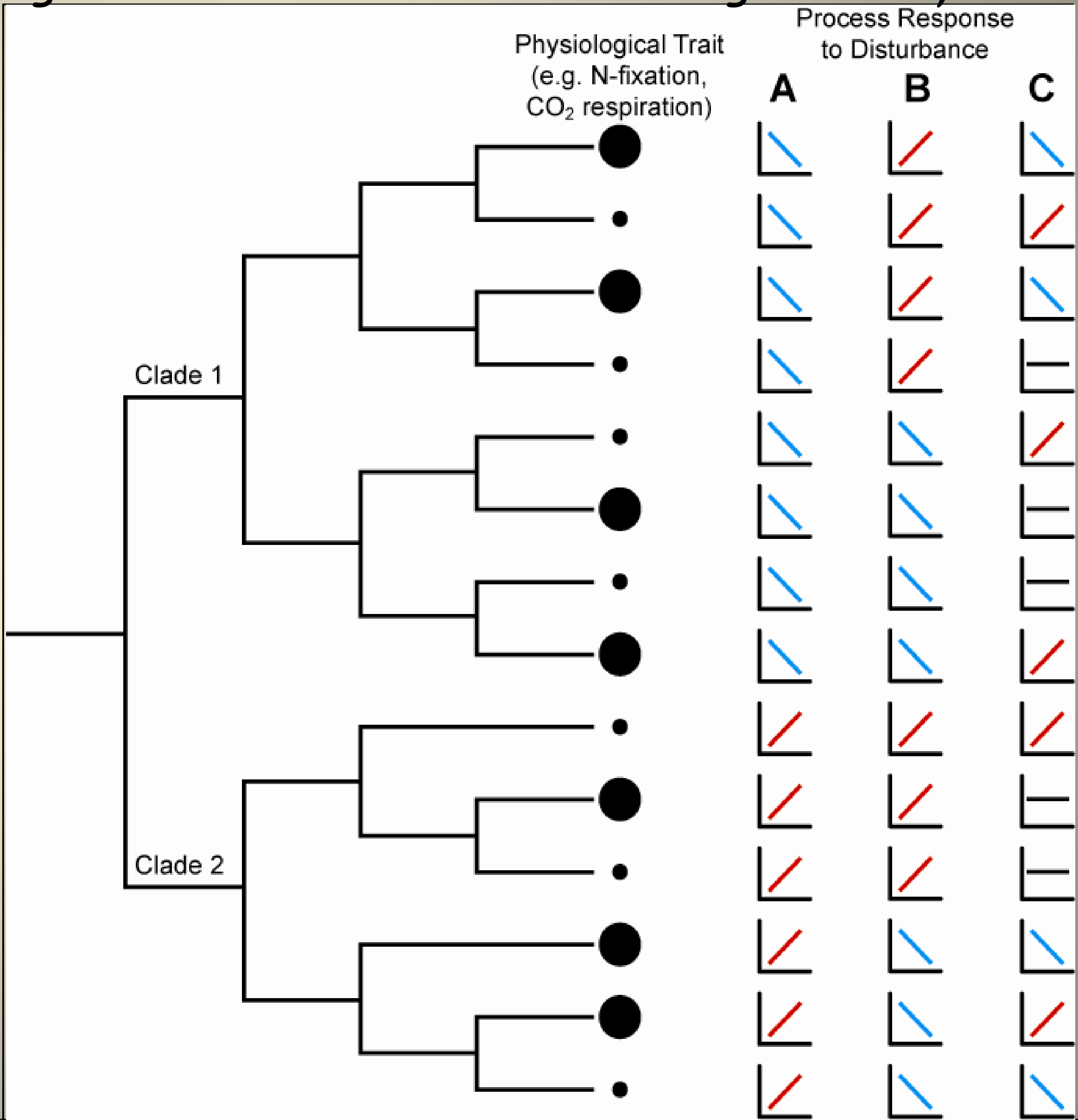
Processes may be **broad** or **narrow** (Schimel, 1995).

Many versus few microbial groups contribute.

Allison and Martiny 2008

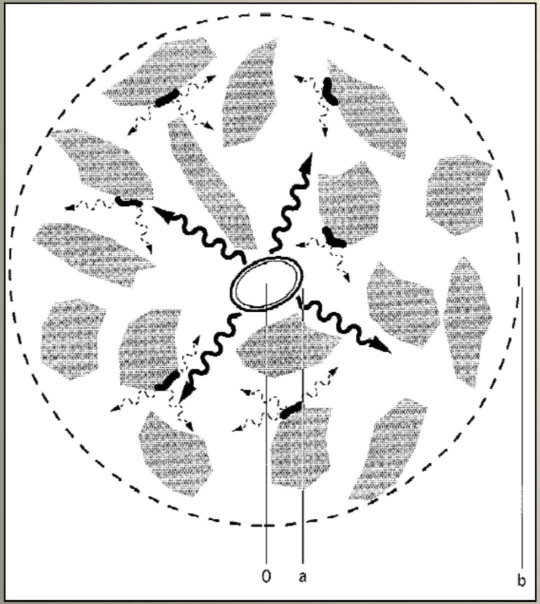
Trait-based aggregation also possible (e.g. Moorhead and Sinsabaugh 2006)

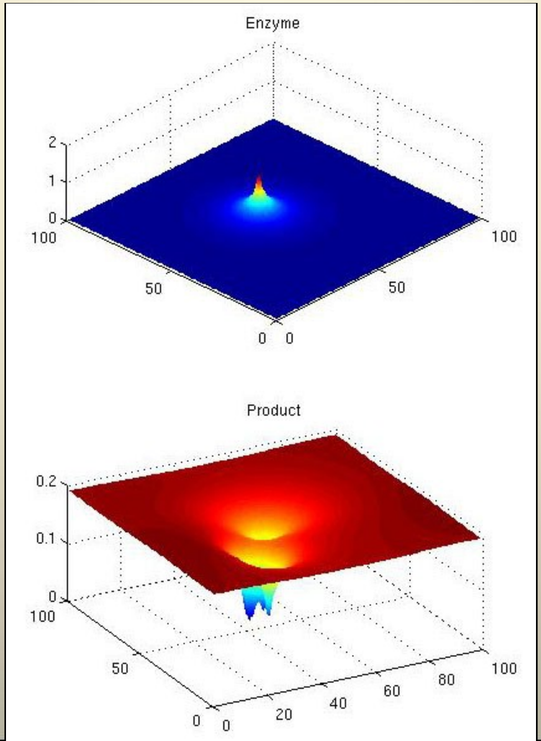




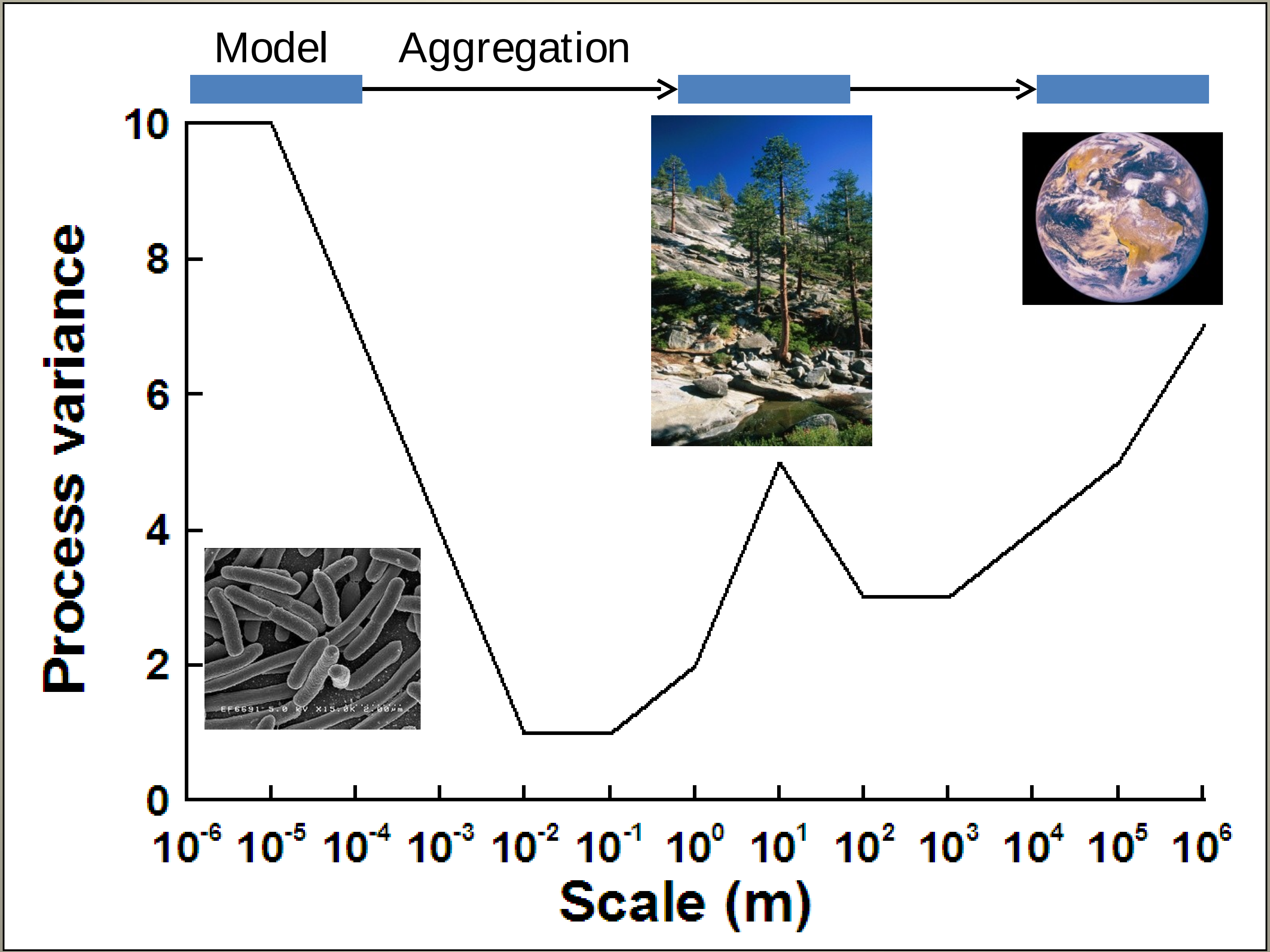
Models of microbial processes across scales

- Single-cell enzyme foraging and uptake: Vetter et al. 1998
- Population/simple community at ~100 micron scale: Allison 2005
- Ecosystem to global scale: CENTURY





Spatial aggregation hypothesis



Research needs

- Explicit modeling of microbial communities
- Data on microbial physiological parameters and distribution across taxa
  - Isolation and manipulation
  - Functional gene distributions
- Measurements of processes across scales

- Questions?