

LEAP: Large Experimental Array of Ponds

A new infrastructure for high replication experimental ecology and evolution in complex aquatic (meta)communities.



Plan of presentation

1. Vision and mission of LEAP
2. Construction of LEAP
3. The science we want to do.
4. 2016: Testing, pilot experiments and choice of stressors
5. Points for discussion

Vision:

Large experiments designed to gauge the ability of aquatic systems to adapt to environmental change.

Powerful multi-investigator collaborations to tackle multiple questions within the LEAP infrastructure.

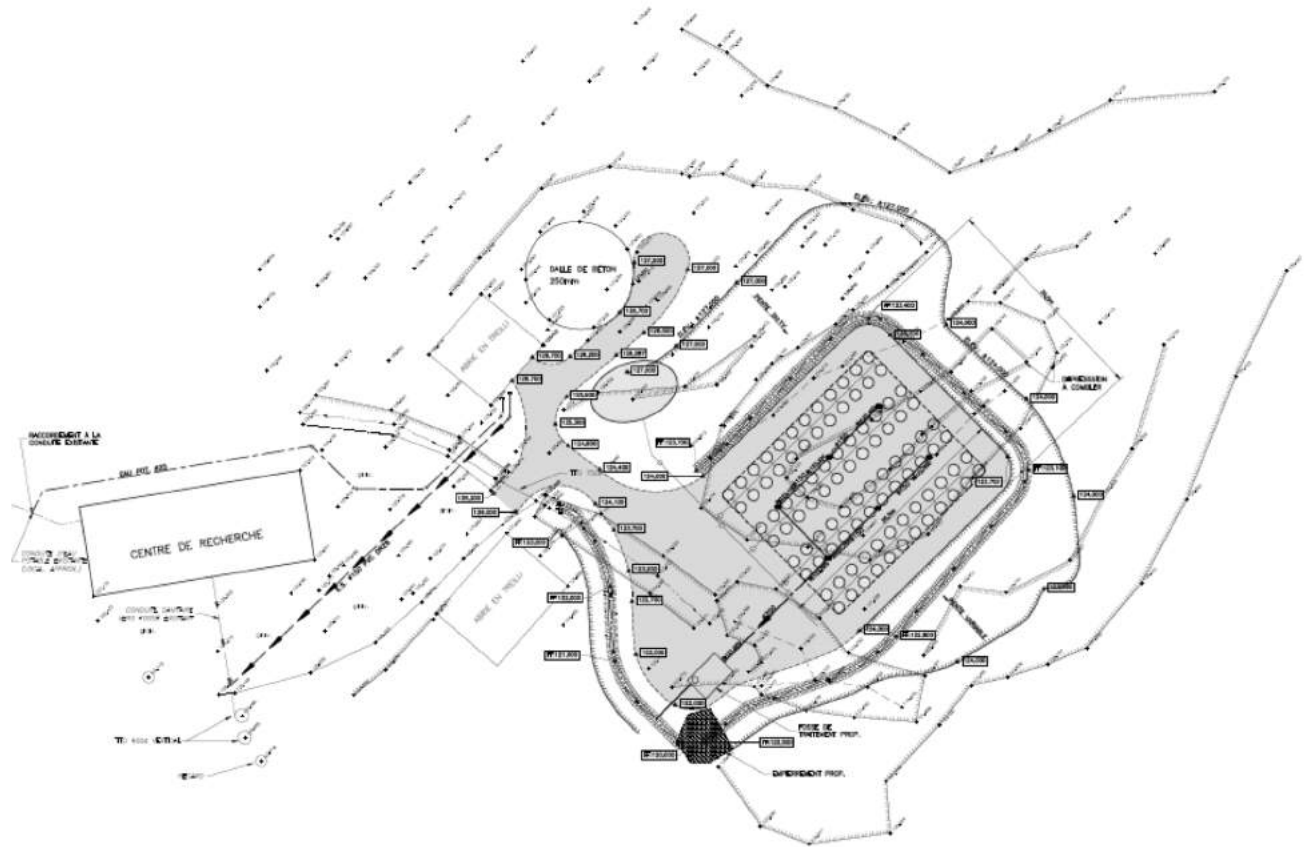
Build an international network of experimental systems (UK, France, Canada, Netherlands, Germany...).

LEAP was funded via CFI LOF

Award: \$935k

IOF: \$74k over 5years (maintenance, consumables, salary for manage...)

Equipment: Fluoroprobe, multi-meter, microscope + camera, computers



LEAP is a system with through-flow from a pristine ecosystem into a replicated semi-batch array of ponds with season-to-season continuity.

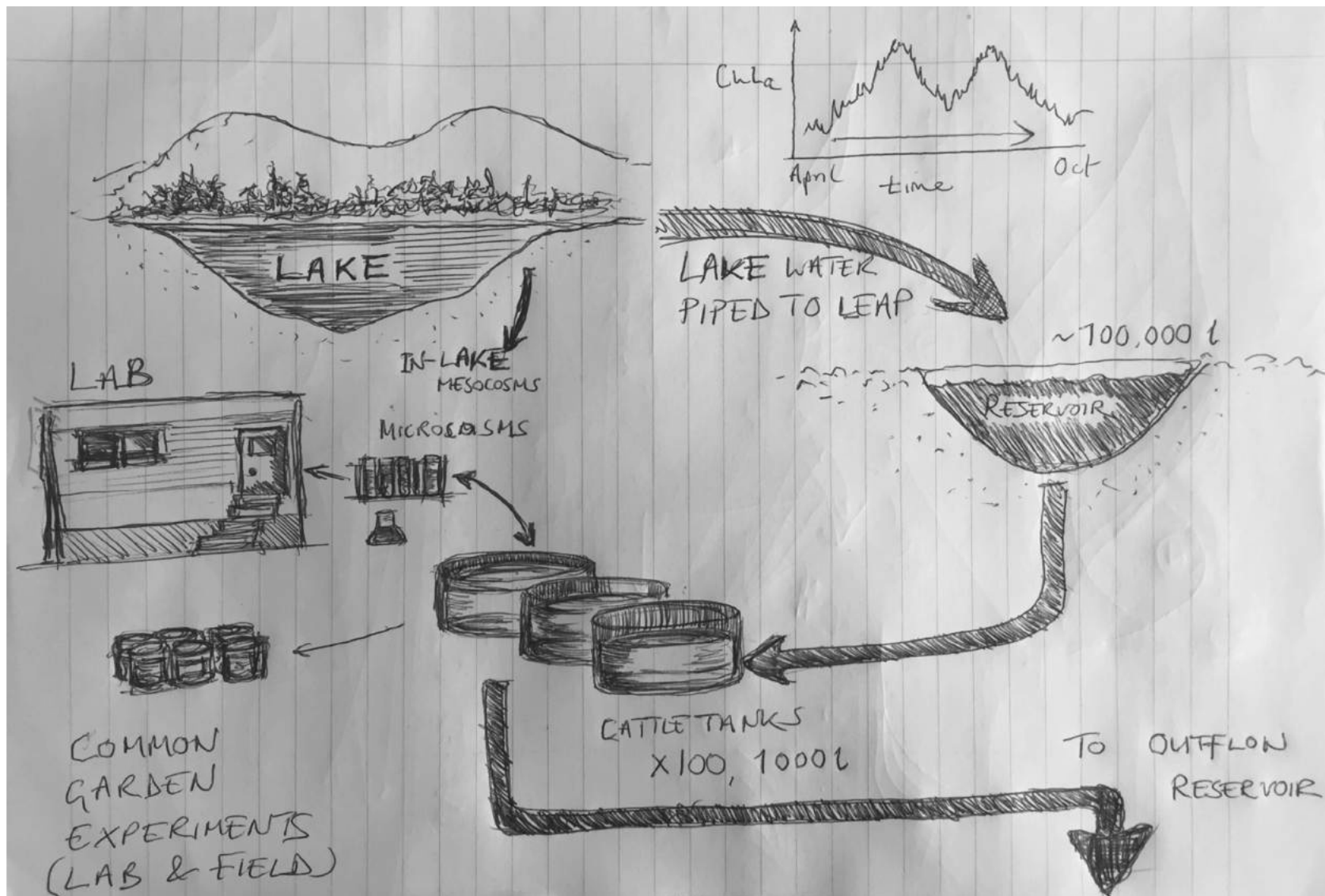
Core foci:

Multiple relevant stressors

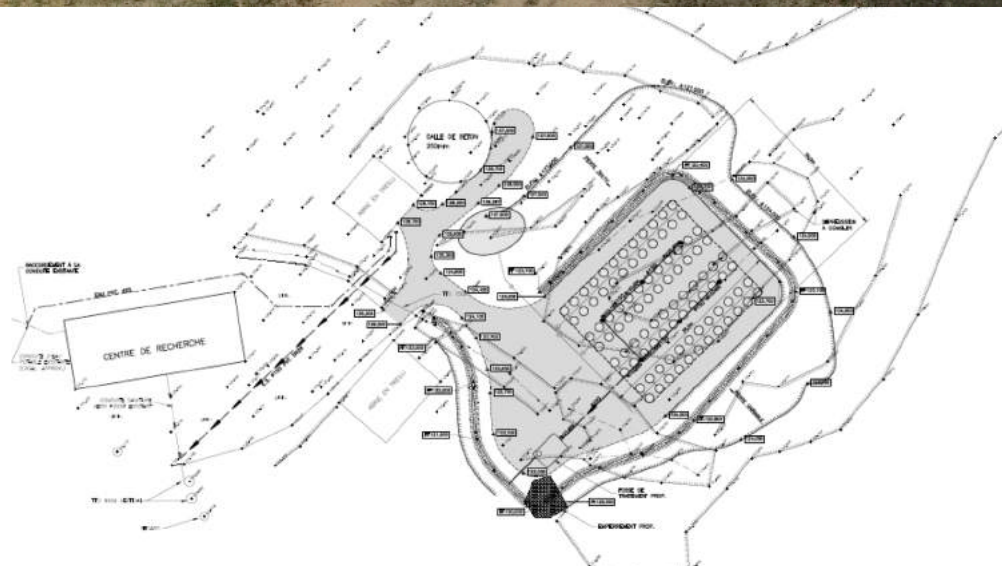
Tracking complex communities and ecosystem functions

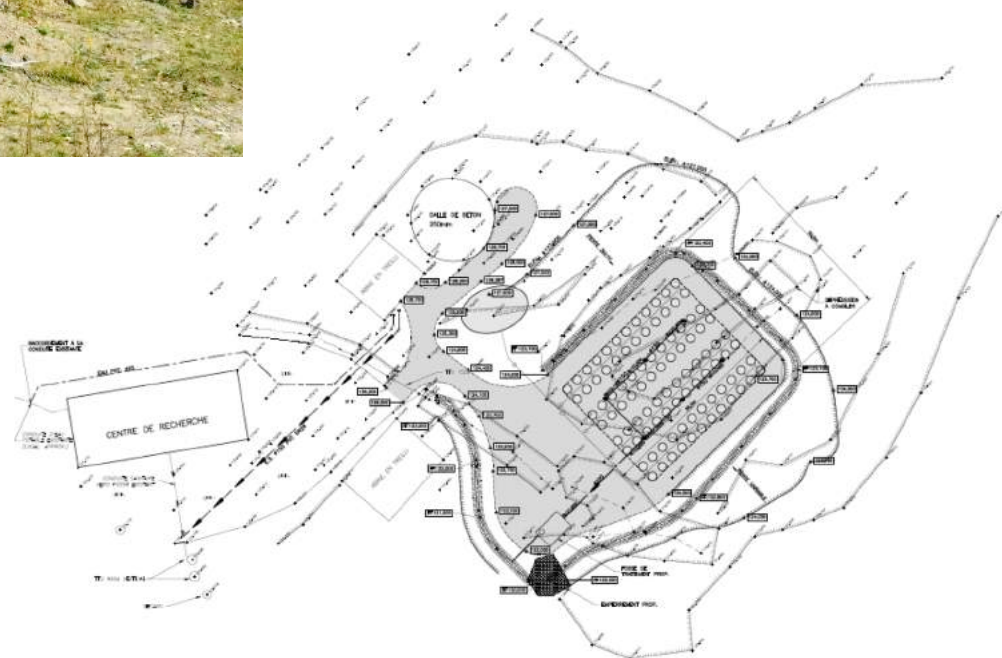
Controlling dispersal via spatial connectivity

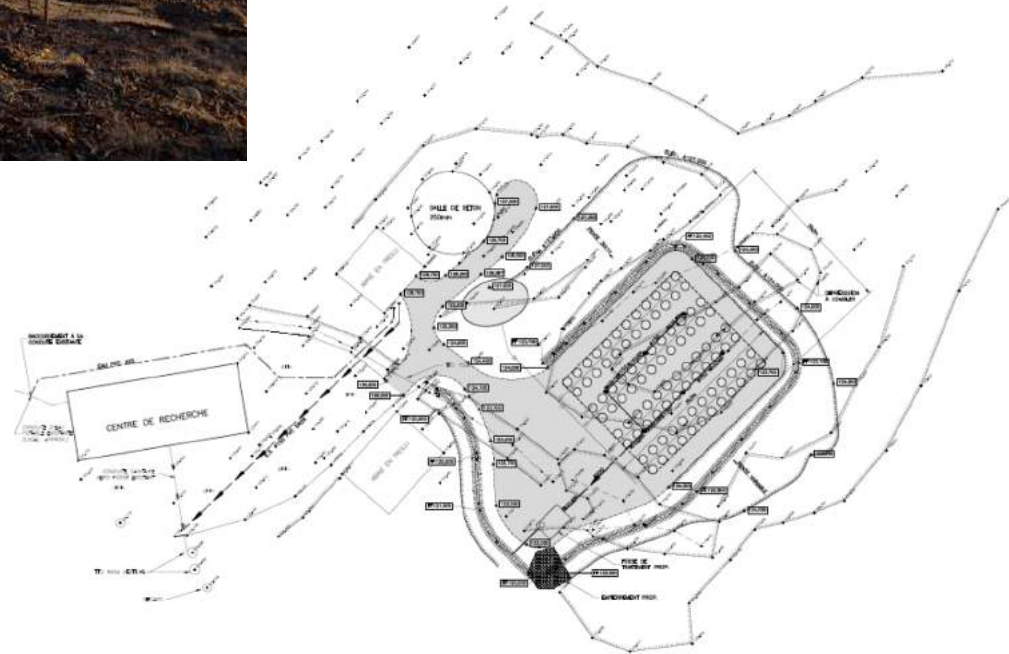
Experimental evolution: cycles of natural and artificial selection





















Why LEAP? What was needed?

- Metacommunity perspective: effects of dispersal on community responses to stressors. Unit of replication = metacommunity of connected ponds. Requires a lot of ponds.
- Highly replicated experimental evolution in the field: effects of rapid evolution on community responses to stressors. Multi-year experiments, combined with experimental evolution, common garden experiments, etc.

Kellogg biological station
(Leibold, Downing, etc.)



Tyson Research Center (Chase)



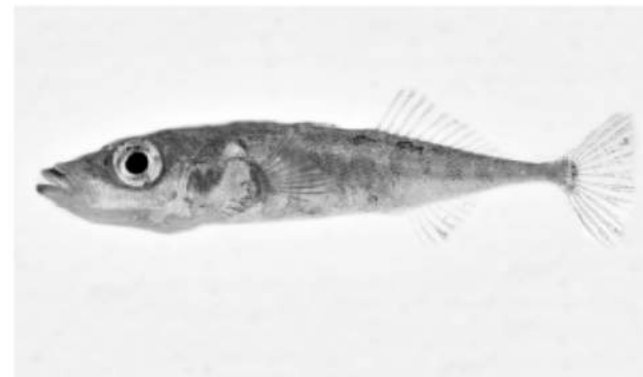
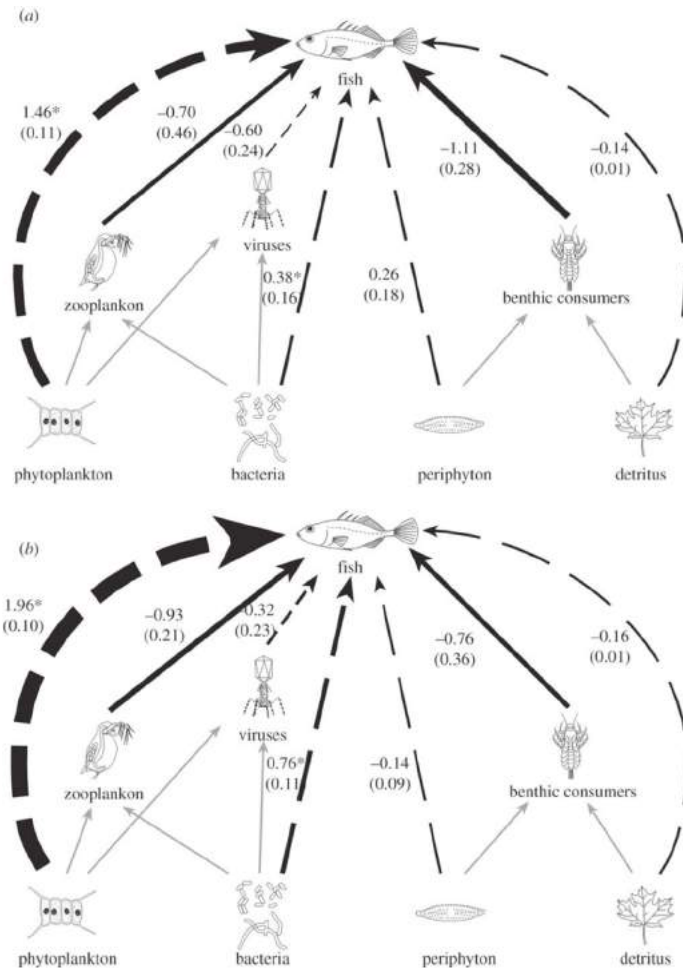
UC Santa Cruz (Palkovacs)



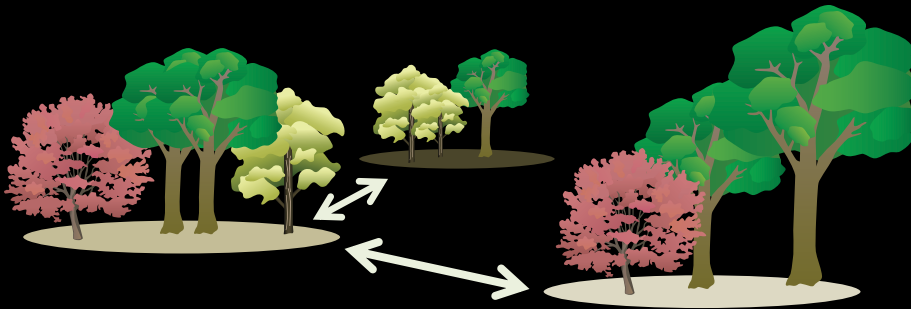
Queen Mary U London
(Woodward, Yvon-Durocher)



UBC Pond site : Experiments (40 cattle tanks) by Jon Shurin, Patrick Thompson, Pavel Kratina & Hamish Greig



Diversity, Evolution & Ecosystem Function in Metacommunities



A trait-based framework for metacommunity function

Species
$$\frac{dN_{ij}(t)}{dt} = [e_{ij}c_{ij}(t)R_j(t) - m_{ij}]N_{ij}(t) + \frac{a}{M-1} \sum_{k \neq j}^M N_{ij}(t) - aN_{ij}(t)$$

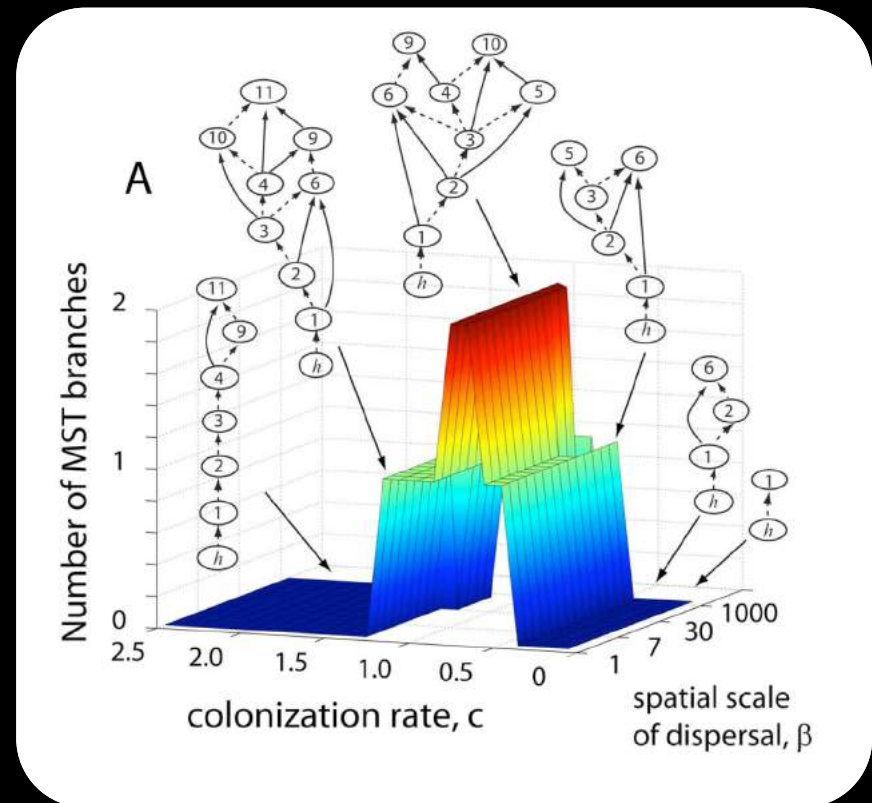
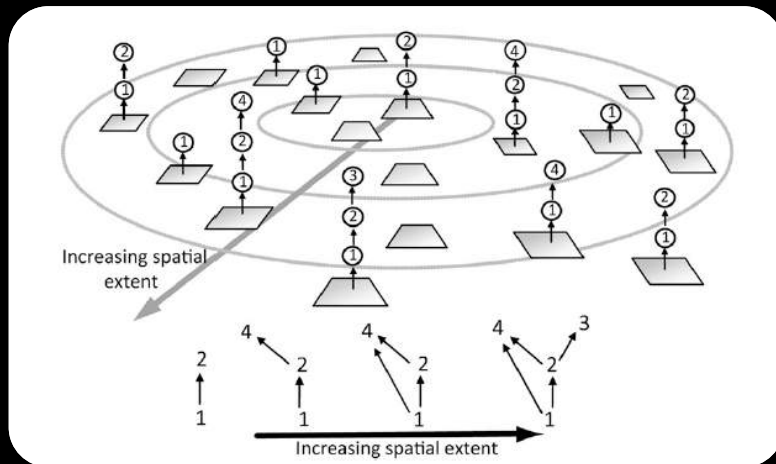
Resources
$$\frac{dR_j(t)}{dt} = I_j - l_j R_j(t) - R_j(t) \sum_i^s c_{ij}(t) N_{ij}(t)$$

Loreau, Mouquet & Gonzalez (2003) *PNAS*

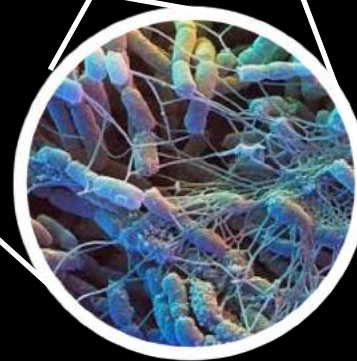
Pillai, Gonzalez & Loreau (2011) *PNAS*

Metacommunity theory of food webs: Networks of networks

Connectivity mediates the emergence of trophic complexity and species richness.

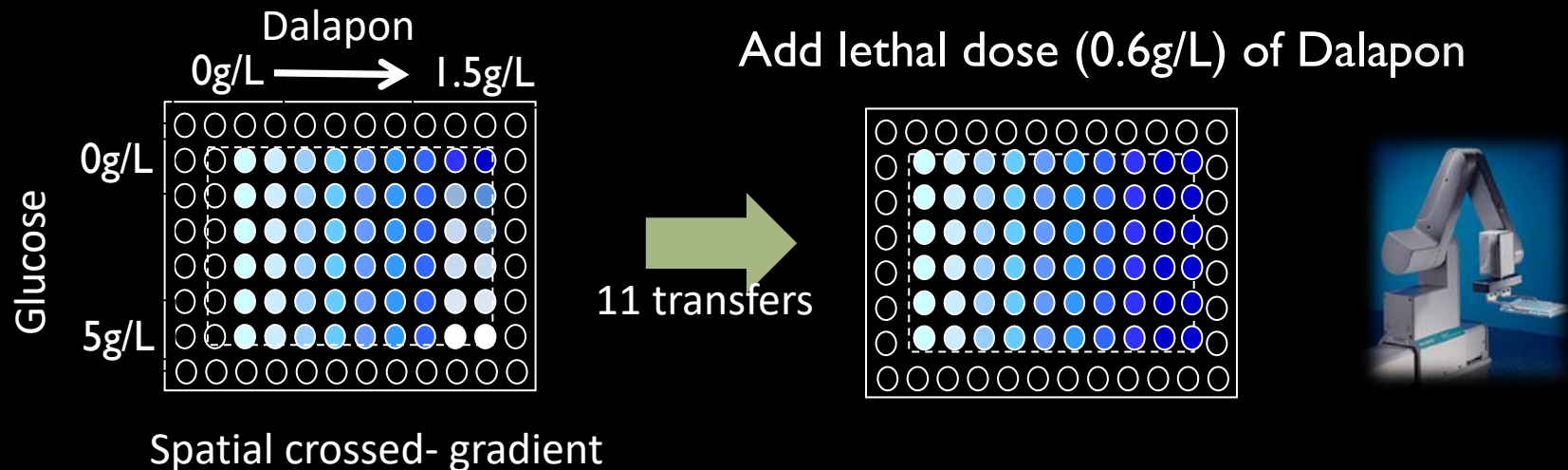
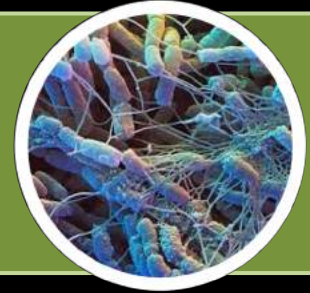


Experimental Metacommunity Evolution



Community composition identified by amplicon metagenomics sequencing (16S and 18S, SSU, ITS1-4) conducted by Research and Testing (Texas USA).

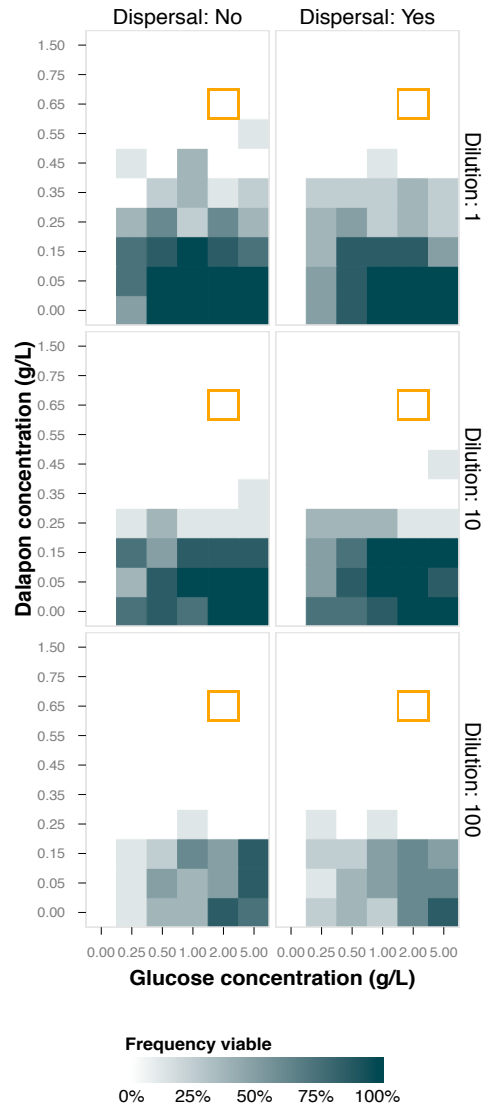
Experimental microbial metacommunity evolution:



Phase 1 Adaptation: 11 transfers (33 days). With or without global dispersal and 3 levels of dilution. Cell yield was scored at each transfer.

Phase 2 Test Rescue: 3 transfers (11 days) at 0.65g/L Dalapon, dispersal stopped.

a. At start of selection
(Phase 1)



Points for discussion

- Distinct research groups tackle different model organisms/groups across the food web as evolutionary 'meters' responding to stress (e.g microbes, phytoplankton, zooplankton, duckweed etc.).
- Combining molecular, isotopic, and ecosystem methods
- Address spatial scales head-on by link lab microcosms, in-pond microcosms and in-lake mesocosms.