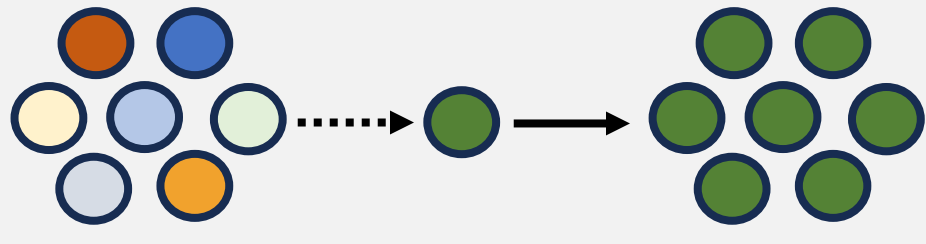


Microbial communities respond to environmental change via various ecological and evolutionary mechanisms

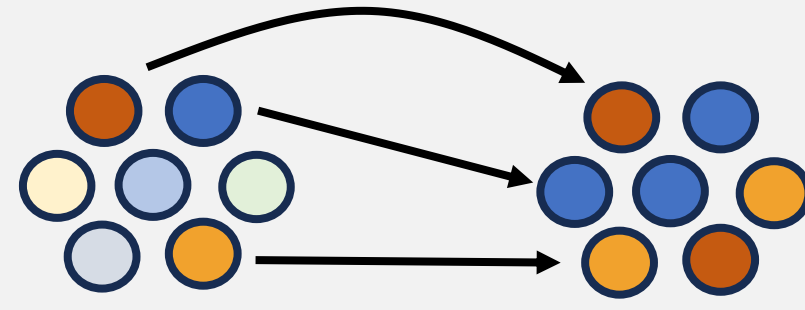
Local effects

Adaptation



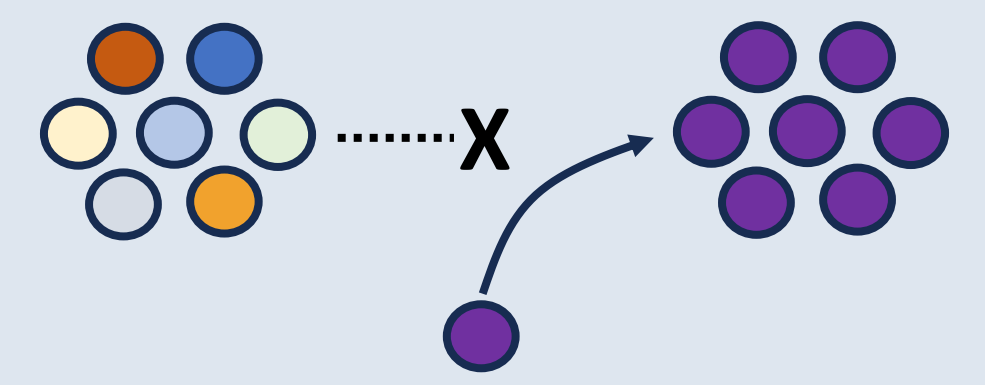
Populations evolve via beneficial mutations; however, this may be constrained in complex communities¹.

Species Sorting



The parent community harbours a diversity of pre-adapted strains which 'switch on' when their preferred environmental conditions are met, without immigration or adaptation².

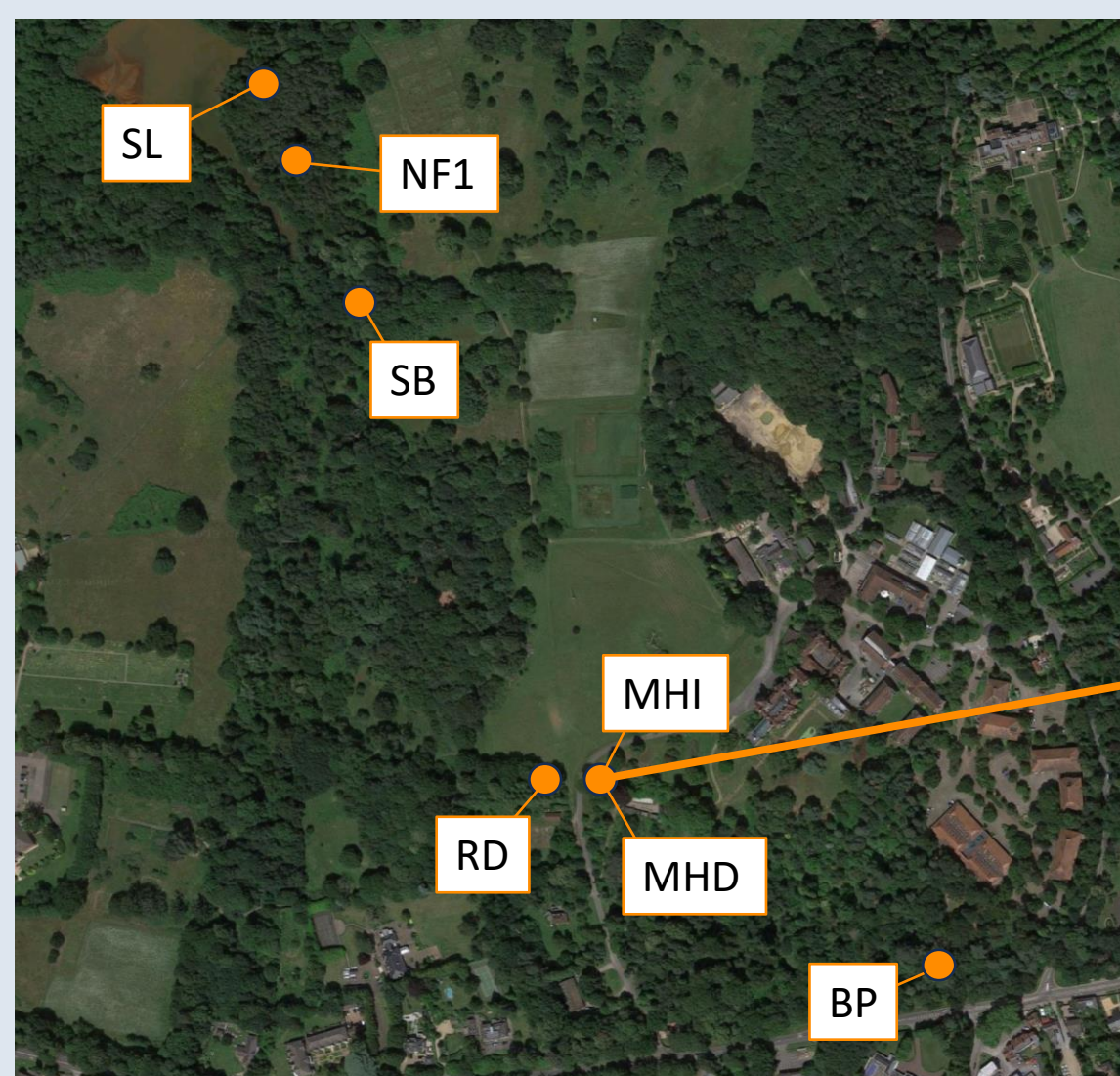
Dispersal and immigration



New species colonise the patch from elsewhere, which may impair or enhance the community response, depending on the environmental context³.

Question: what impact does the influx of new genotypes and species have on the community's capacity to respond to environmental change?

Study System – Beech “Treeholes”



We study the microbes living in temporary pools of water formed between the roots of beech trees.



We extracted all water and sediment from 4 focal treeholes and divided each of these to create replicated microcosms.



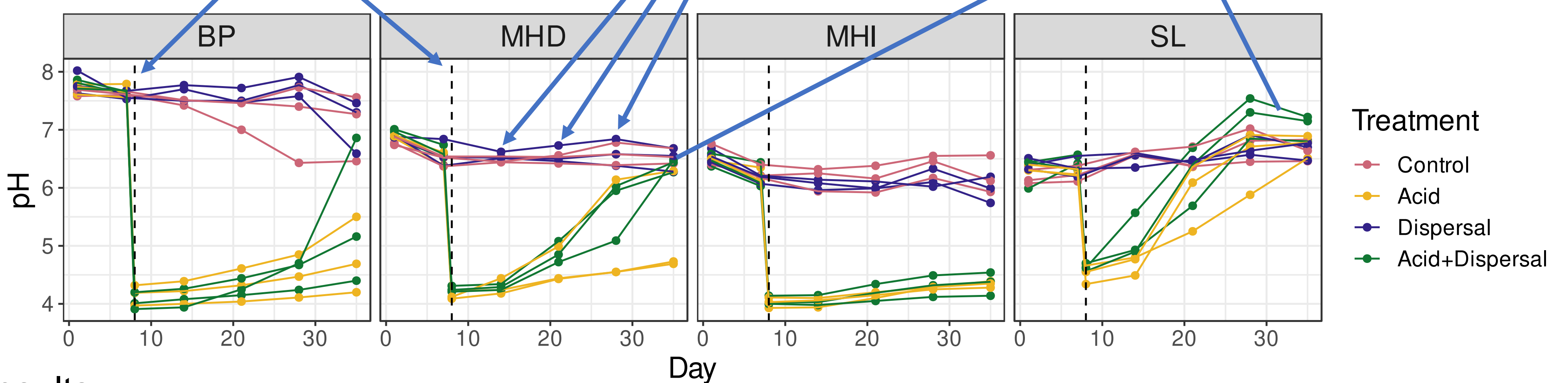
Acidification Experiment

After allowing the microcosms a week to assemble and acclimate to lab conditions, **acetic acid** was applied. pH was tracked through time.

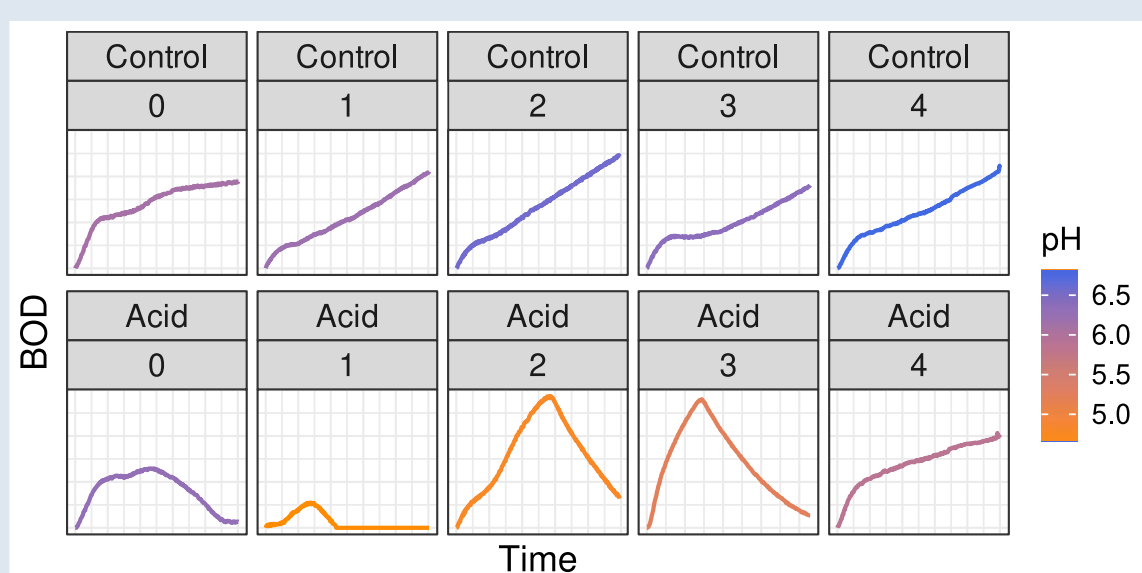
We created a **dispersal treatment** by combining samples from all treeholes from the sampling site. This was applied together with the acid treatment, and at each subsequent timepoint.

Some microcosms buffered themselves against the acidification, and this effect was amplified by the dispersal treatment.

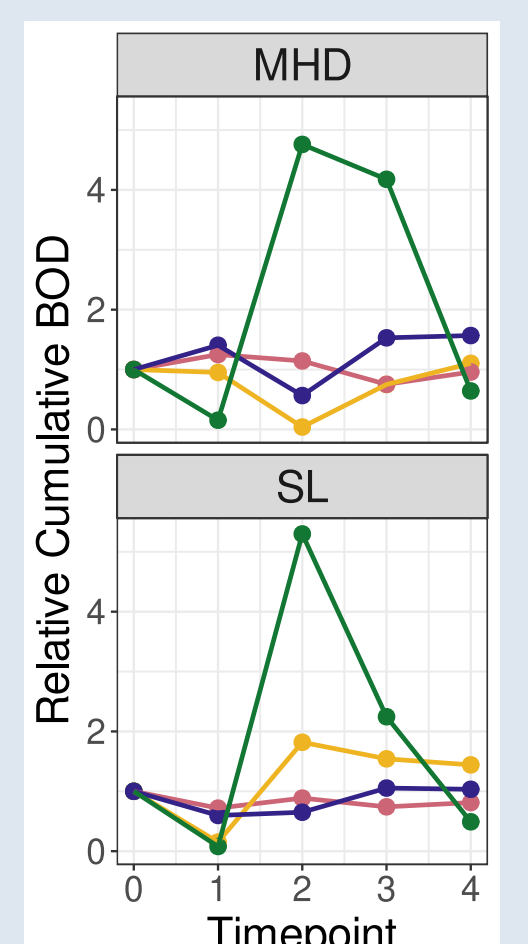
Acetoclastic methanogenesis?
 $\text{CH}_3\text{COOH} \rightarrow \text{CH}_4 + \text{CO}_2$



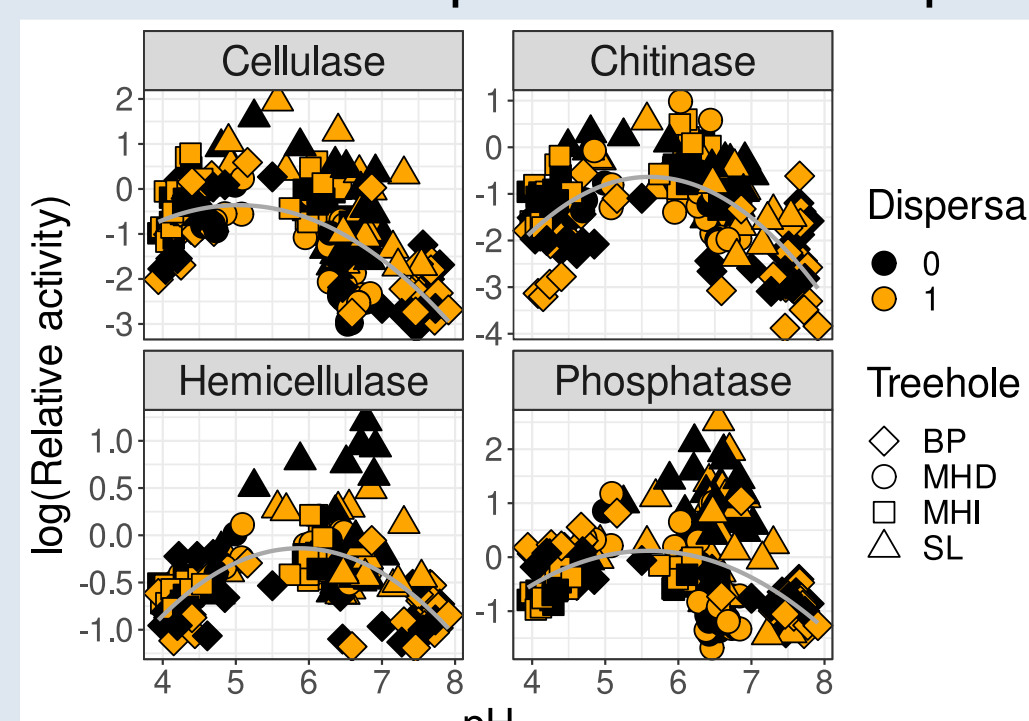
Results



In microcosms with pH recovery, respiration decreased upon acidification and then increased as pH recovered. This was amplified by dispersal.



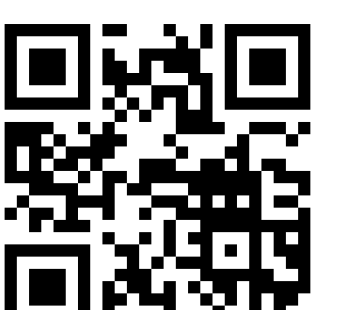
Metabolic enzyme activity dropped upon acidification, but increased as pH recovered. Dispersal had no impact.



We expect changes in broad metabolic function (e.g. BOD) to be driven by changes in the most abundant taxa, and changes in narrow function (e.g. enzyme activity) to be driven by rare taxa⁴.

Sequencing will reveal more...

Check my website for updates and to download this poster!



1. Scheuerl, T. et al. Bacterial Adaptation is Constrained in Complex Communities. *Nature Communications* (2020).

2. Smith, T. et al. Latent Functional Diversity may Accelerate Microbial Community Responses to Temperature Fluctuations. *eLife* (2022).

3. Lawrence, D. et al. The Effect of Immigration on the Adaptation of Microbial Communities to Warming. *The American Naturalist* (2016).

4. Rivett, D. et al. Abundance determines the functional role of bacterial phylotypes in complex communities. *Nature Microbiology* (2018).