Soil bacteria diversity and function is influenced by different environments and soil pH

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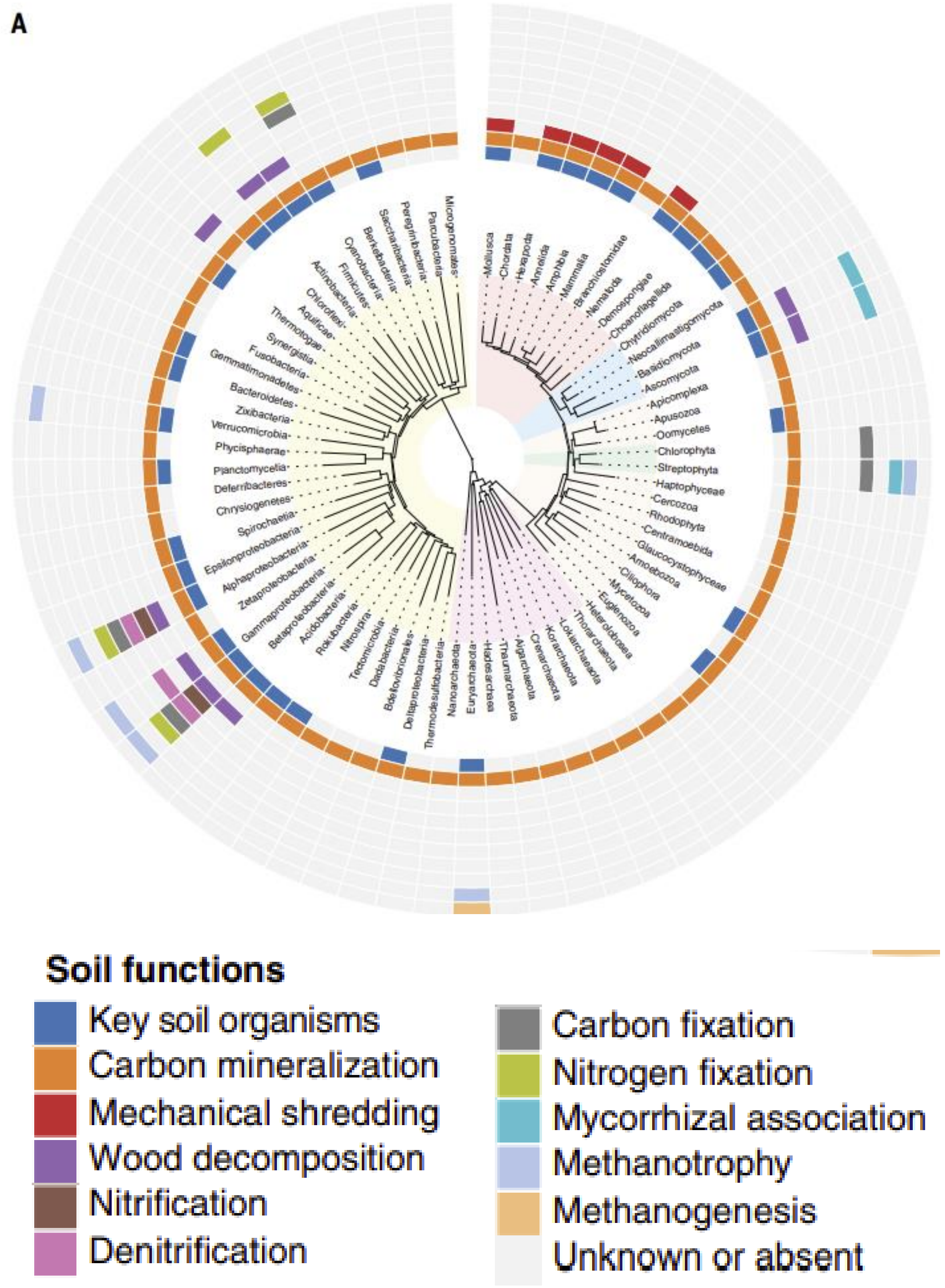
Bacteria role in soils

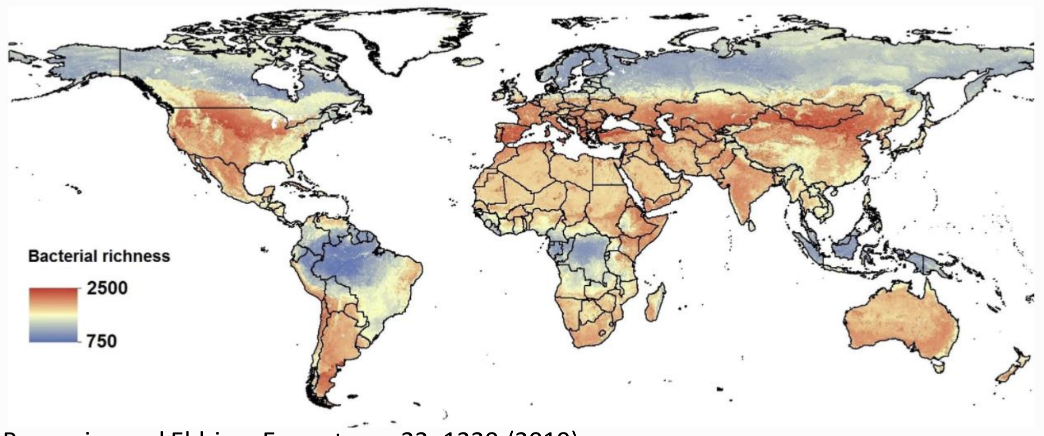
- Soil bacteria are critical for the functioning of ecosystems.
  - Control nutrient and carbon cycling
  - Influence plant productivity



Crowther et al., Science 365, 772 (2019)

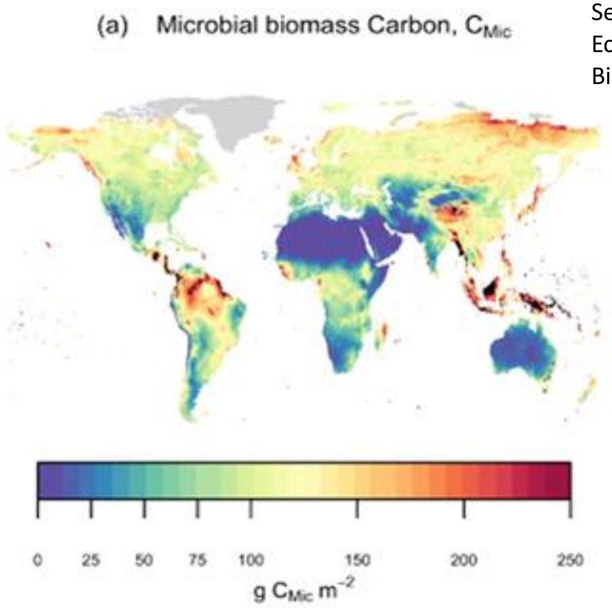
Bacteria is affected by environmental factors

- Global distribution of bacteria diversity (richness) and abundance is affected by:
  - Climate
  - Vegetation
  - Soil resources
  - Soil conditions



Baquerizo and Eldrige, Ecosystems 22, 1220 (2019)

Serna-Chavez et. al., Global Ecology and Biogeography 22.10 (2013)

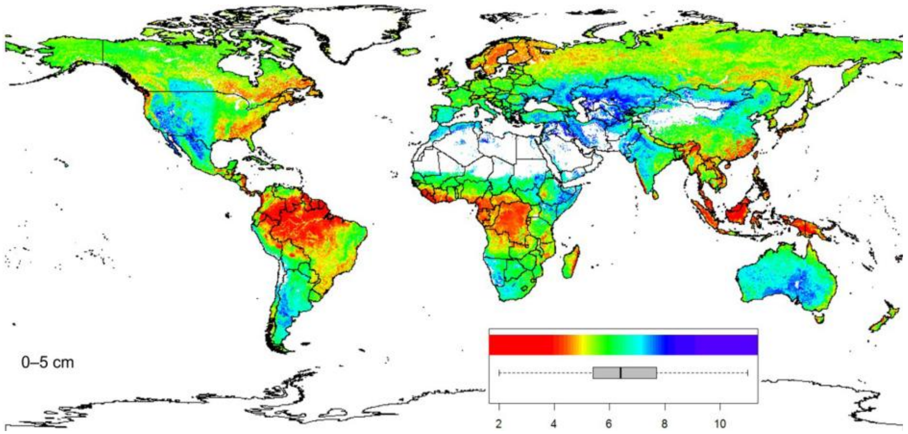


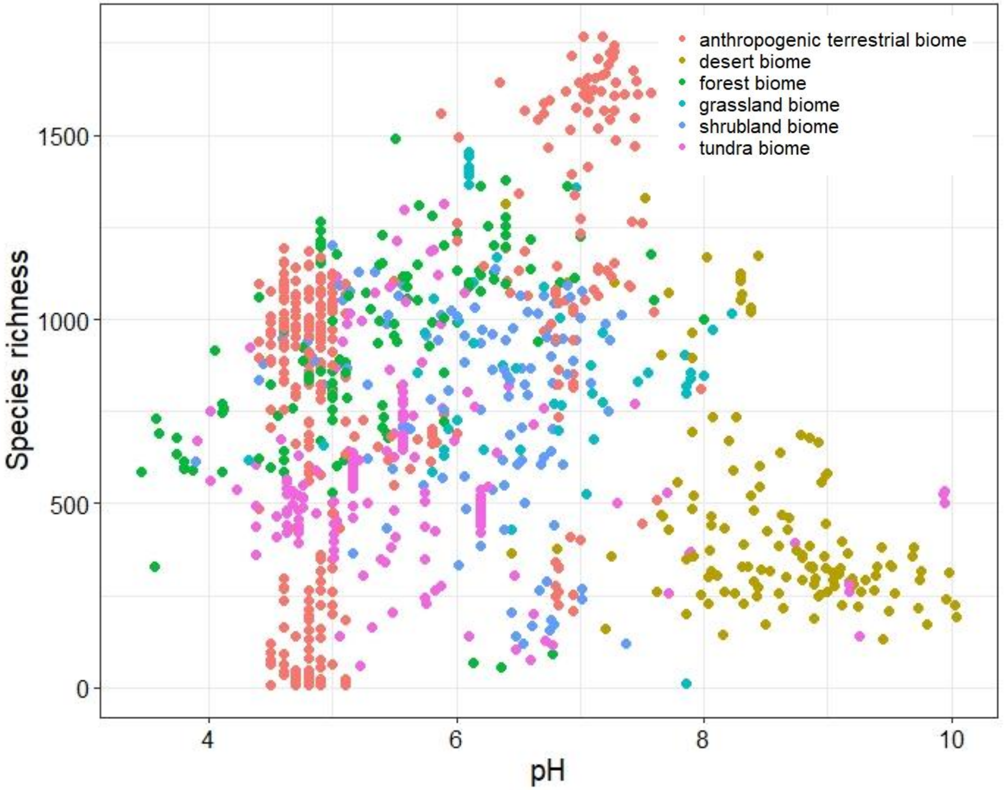
Soil pH as a soil condition

- Soil pH affect nutrient availability in soils influencing
  - Diversity
  - Abundance
  - Function

- Extreme pH conditions create specialize microbiomes.
  - Influences "**who is there**".

Hengl et. al., Plos One 9(8)e105992 (2014)





Research questions

1. How do microbiomes cluster base on environmental conditions?

2. How pH can influence richness, abundance and function?

Methods

- Sampling
  - Targeted soil microbiomes with soil pH information from Earth Microbiome Project database.
- Clustering
  - Used Vintage Sparse Principal Component Analyses (VSP)
  - Define K = 6
- **Contextualizing**
  - Used biomes as an ecosystem (climate, vegetation) and features as soil type (disturbed, weathered, new) classification.
  - Used taxonomy and function classification.
- **Relating**
  - Related richness, abundance and function to soil pH.

Contextualize by environment

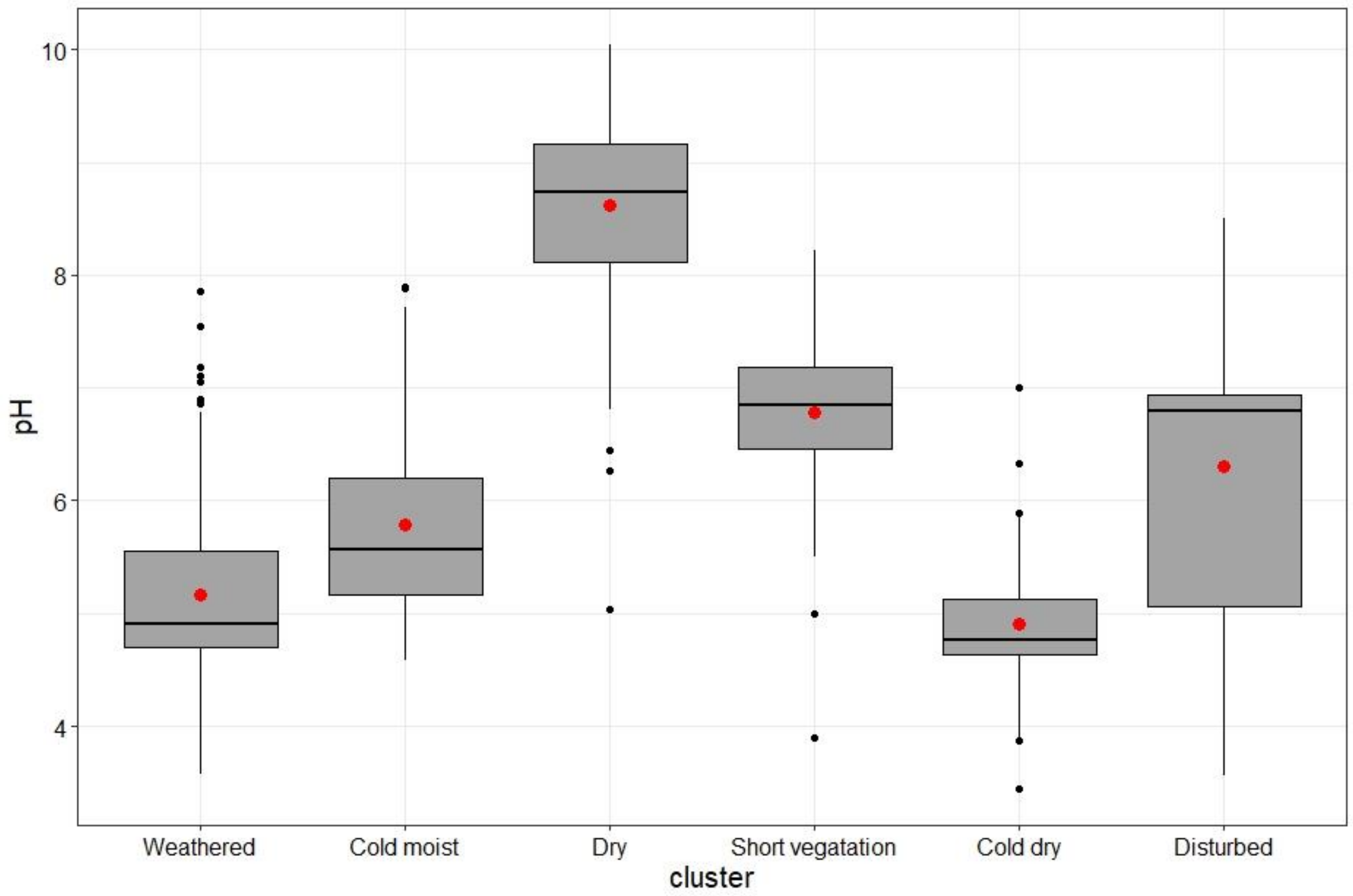
- Many clusters share similar environmental condition.
  - However, the combination of each environmental condition makes each cluster unique.

Contextualize by environmental biome and feture

Weathered	Cold moist	Dry	Short vegetation	Cold dry	Disturbed
cultivated habitat	tundra	polar desert	vineyard	dry lake	cropland
forest soil	permafrost	cold temperature habitat	tropical shrubland	tundra	plant-associated habitat
tropical shrubland	bog	desert	volcano	tundra	cultivated habitat
volcano	tundra	dry soil	grassland soil	montane shrubland	desert
tropical moist broadleaf forest	montane shrubland	tundra	grassland	mountain	agricultural soil
forest	mountain	shrubland	desert	coniferous forest	dry soil
forest	plant-associated habitat	temperate grassland	forest soil	forest	shrubland
cropland	taiga	basin	dry soil	plant-associated habitat	bog
montane shrubland	peatland	rocky desert	montane shrubland	agricultural soil	dry lake
mountain	pasture	urban	agricultural soil	taiga	temperate grassland

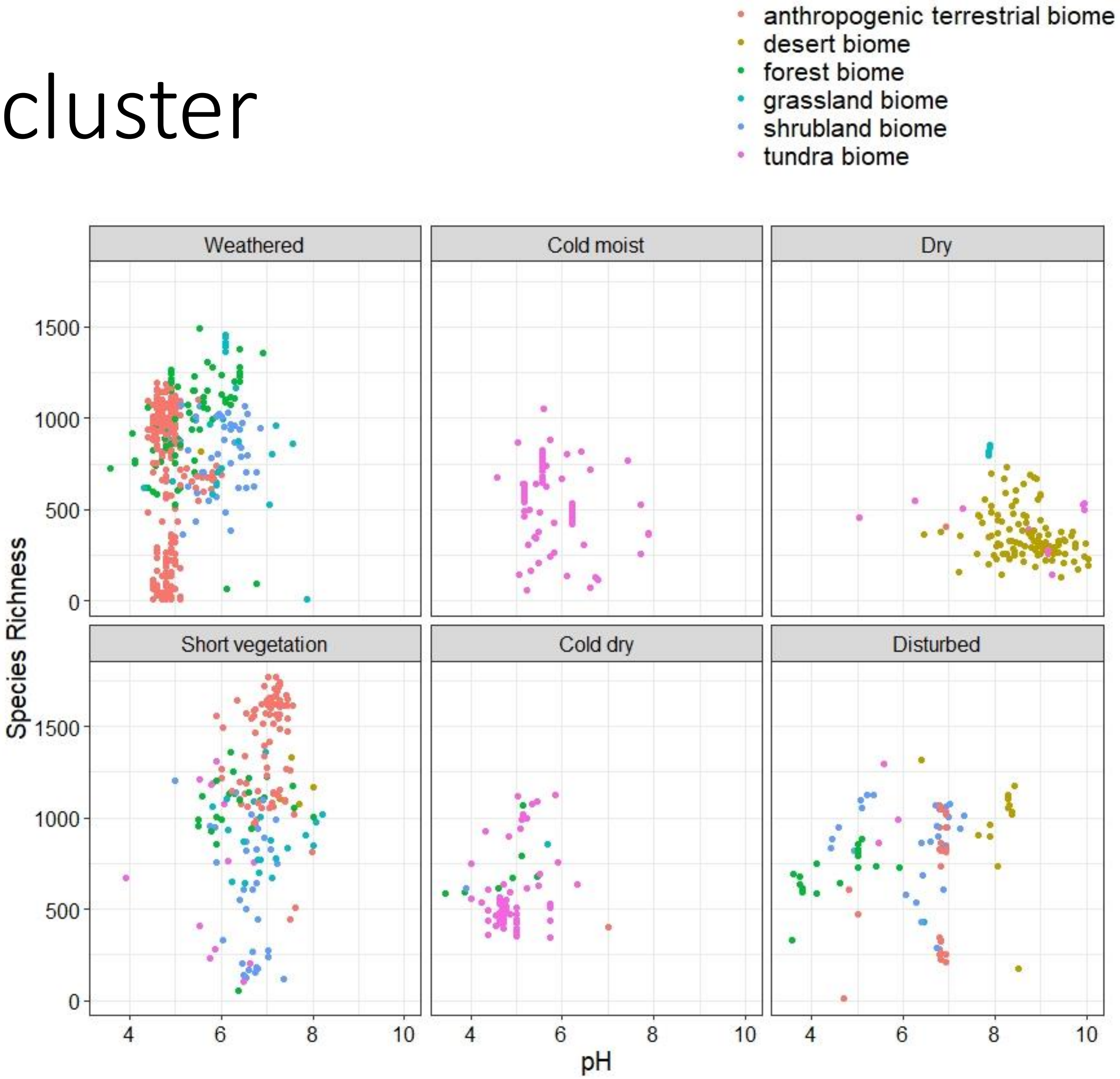
Some clusters can be described by pH

- Dry cluster pH is very alkaline.
- Short vegetation has a neutral pH
- Weathered and Cold dry clusters are acidic.
- The variability of pH in Disturbed is high.



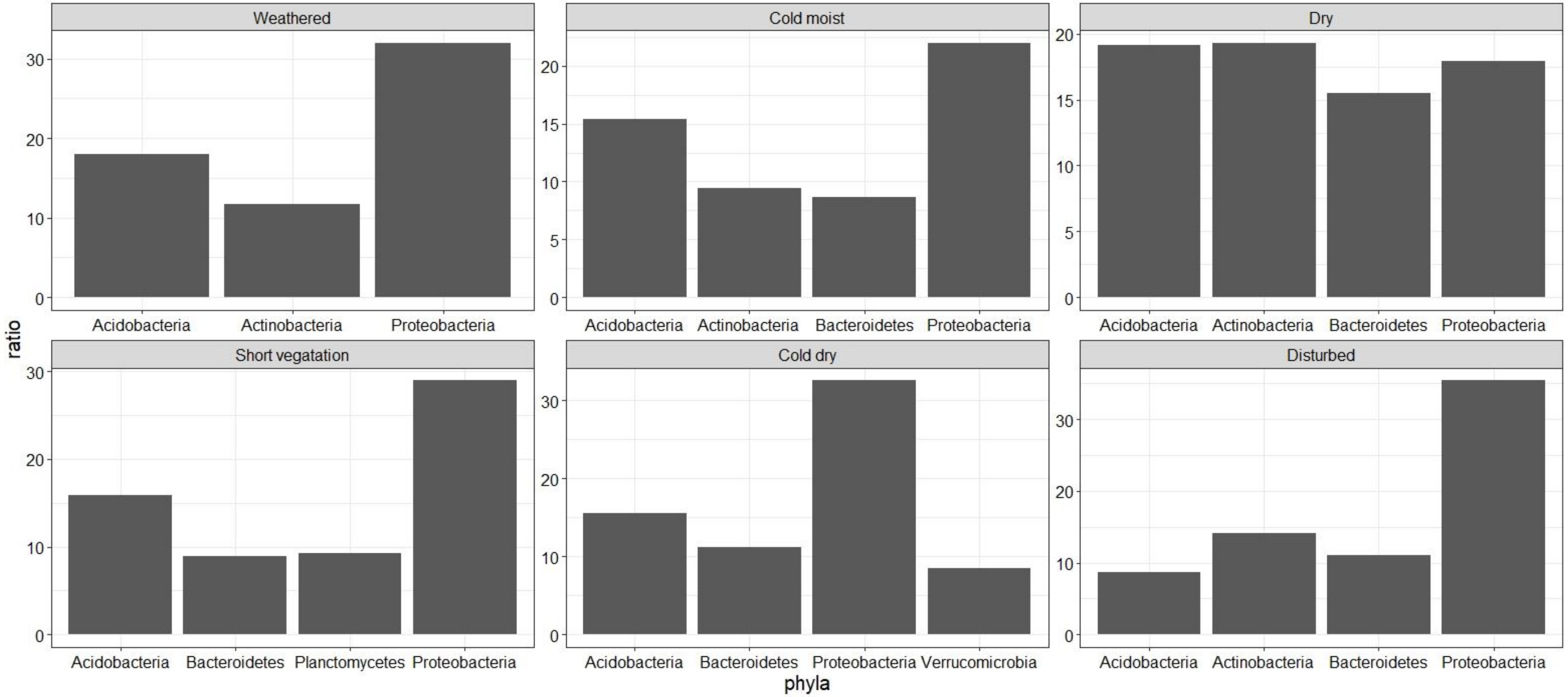
Richness vs pH per cluster

- No obvious linear relation between pH and species richness.
- Under each cluster, species richness can be explained by general global biomes.



Phyla composition within each cluster

- Acidobacteria and proteobacteria are common in all clusters.
- **Short vegetation** has planctomycetes.
- **Cold dry** has verrucomicrobia.



Reported: Phyla with higher ratios

Phyla Abundance vs pH per cluster

- **Disturbed**

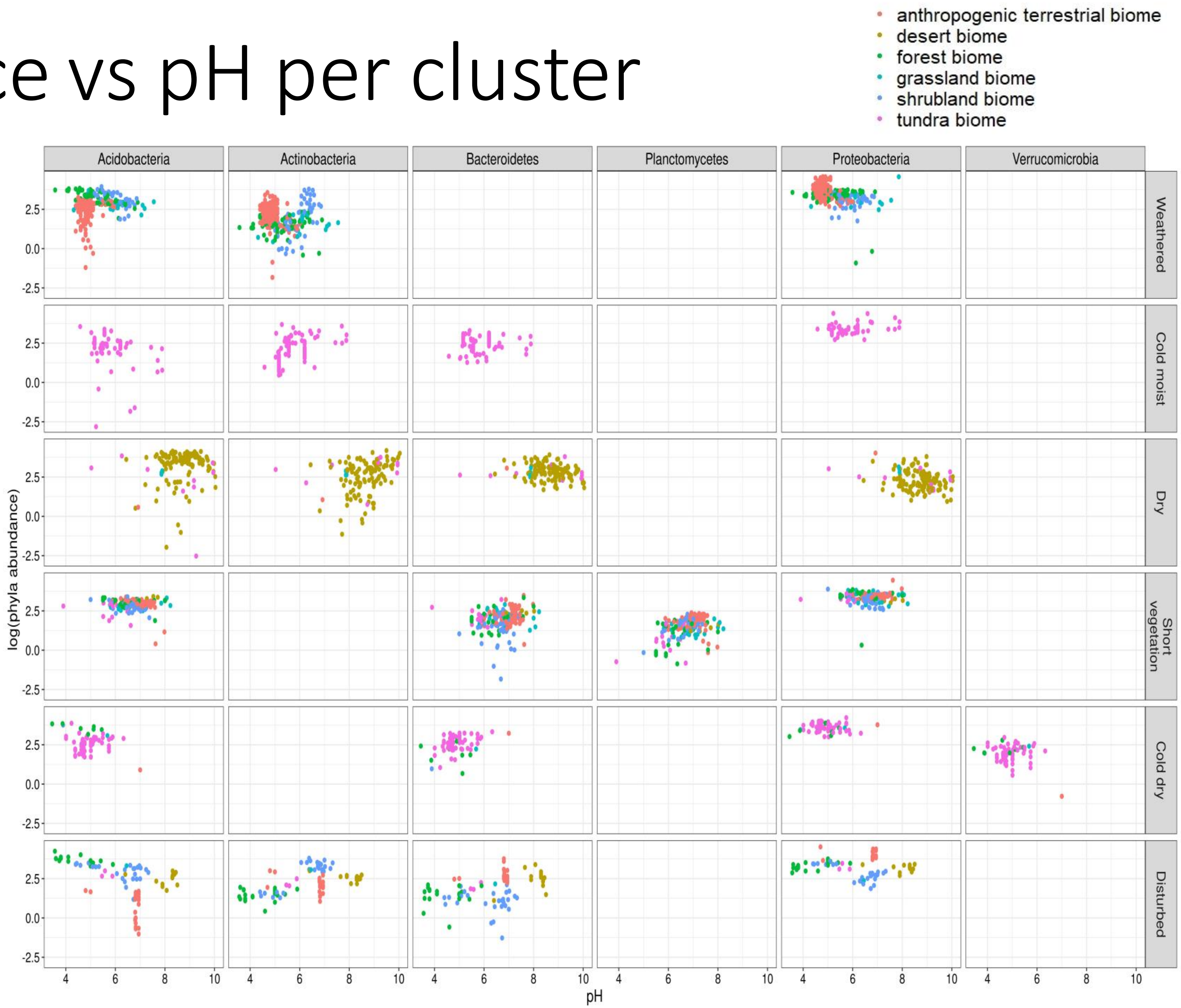
- Acidobacteria – pH (negative corr.)

- Bacteroidetes – pH (positive corr.)

- **Across environment**

- Actinobacteria-pH (positive corr.)

- Acidobactera, Actinobacteria Bacteroidetes thrive across pH & environment (high diversity)



Cluster contextualize by who is there - function

- Common function: decompose organic molecules, e.g., aerobic chemo-
- Some clusters have unique specializations.
  - **Cold moist:** bacteria involve in anoxic carbon decomposition, e.g., methano, Fermentation
  - **Dry:** bacteria that are dependent on sunlight for energy, e.g., photo-
  - **Cold dry:** bacteria that hosts in plants as parasites or symbionts
- Weathered, short vegetation and disturbed influence nutrient cycling and decomposition of carbon to CO_2.

Contextualized by Function

Weathered	Cold moist	Dry	Short vegetation	Cold dry	Disturbed
nitrate denitrification	nitrate denitrification	aerobic chemoheterotrophy	nitrate denitrification	iron respiration	aerobic chemoheterotrophy
aerobic chemoheterotrophy	nitrogen fixation	chitinolysis	aerobic ammonia oxidation	fermentation	aerobic ammonia oxidation
nitrogen fixation	iron respiration	aerobic ammonia oxidation	aerobic chemoheterotrophy	nitrate denitrification	nitrate denitrification
aerobic ammonia oxidation	methanotrophy	photosynthetic cyanobacteria	aerobic nitrite oxidation	nitrogen fixation	methanol oxidation
xylanolysis	methanogenesis	manganese oxidation	chitinolysis	aerobic chemoheterotrophy	xylanolysis
chitinolysis	fermentation	nitrogen fixation	nitrogen fixation	methanotrophy	chitinolysis
aerobic nitrite oxidation	methanol oxidation	photoheterotrophy	iron respiration	methanogenesis	ureolysis
invertebrate parasites	methanogenesis	xylanolysis	manganese oxidation	animal parasites/symbionts	manganese oxidation

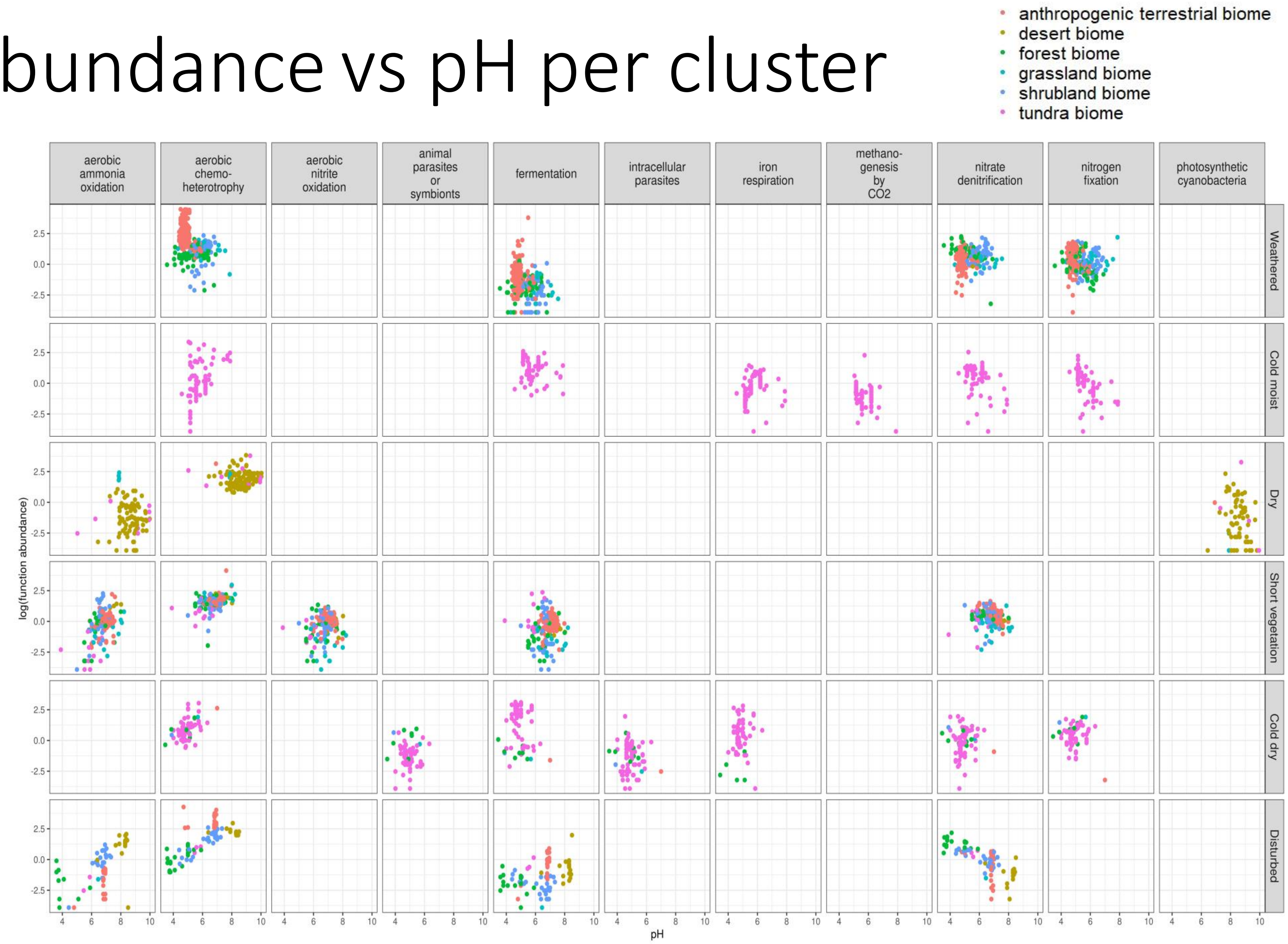
Function Abundance vs pH per cluster

- Aerobic ammonia oxidation
- Short Veg. / Disturbed: higher in alkaline soil (due to available ammonia amount)
- Dry: volatization of ammonia may cancel out

- Aerobic chemoheterorophy
- Disturbed / Cold dry / Cold moist: positive correlation

- Nitrate denitrification
- Disturbed: negative correlation

- Overall, under disturbed, pH can be a key driver for multiple functions



Conclusion

- Different environments and soil pH can influence microbial community functions.
- This is important because microbial functions can influence ecosystem dynamics, including plant productivity and nutrient cycling.
- By understanding microbial diversity and functional changes in different environments and soil pH, we can better understand changes in carbon cycling that could be influencing global climate changes.

Appendix

Linear model summary (log(abundance)~pH, by phyla-cluster)

cluster	PHYLUM	pval	estimate
Weath.	Acidobacteria	0.034	0.046
Weath.	Actinobacteria	0.029	-0.056
Weath.	Proteobacteria	0.000	-0.129
Cold M.	Acidobacteria	0.001	-0.215
Cold M.	Actinobacteria	0.000	0.239
Cold M.	Bacteroidetes	0.803	-0.008
Cold M.	Proteobacteria	0.000	0.069
Dry	Acidobacteria	0.346	0.053
Dry	Actinobacteria	0.001	0.161
Dry	Bacteroidetes	0.058	-0.043
Dry	Proteobacteria	0.001	-0.102

cluster	PHYLUM	pval	estimate
Short V.	Acidobacteria	0.426	-0.015
Short V.	Bacteroidetes	0.023	0.082
Short V.	Planctomycetes	0.000	0.213
Short V.	Proteobacteria	0.573	0.010
Cold D.	Acidobacteria	0.123	-0.083
Cold D.	Bacteroidetes	0.001	0.159
Cold D.	Proteobacteria	0.844	0.005
Cold D.	Verrucomicrobia	0.060	-0.097
Disturb.	Acidobacteria	0.000	-0.175
Disturb.	Actinobacteria	0.000	0.124
Disturb.	Bacteroidetes	0.000	0.119
Disturb.	Proteobacteria	0.622	-0.009

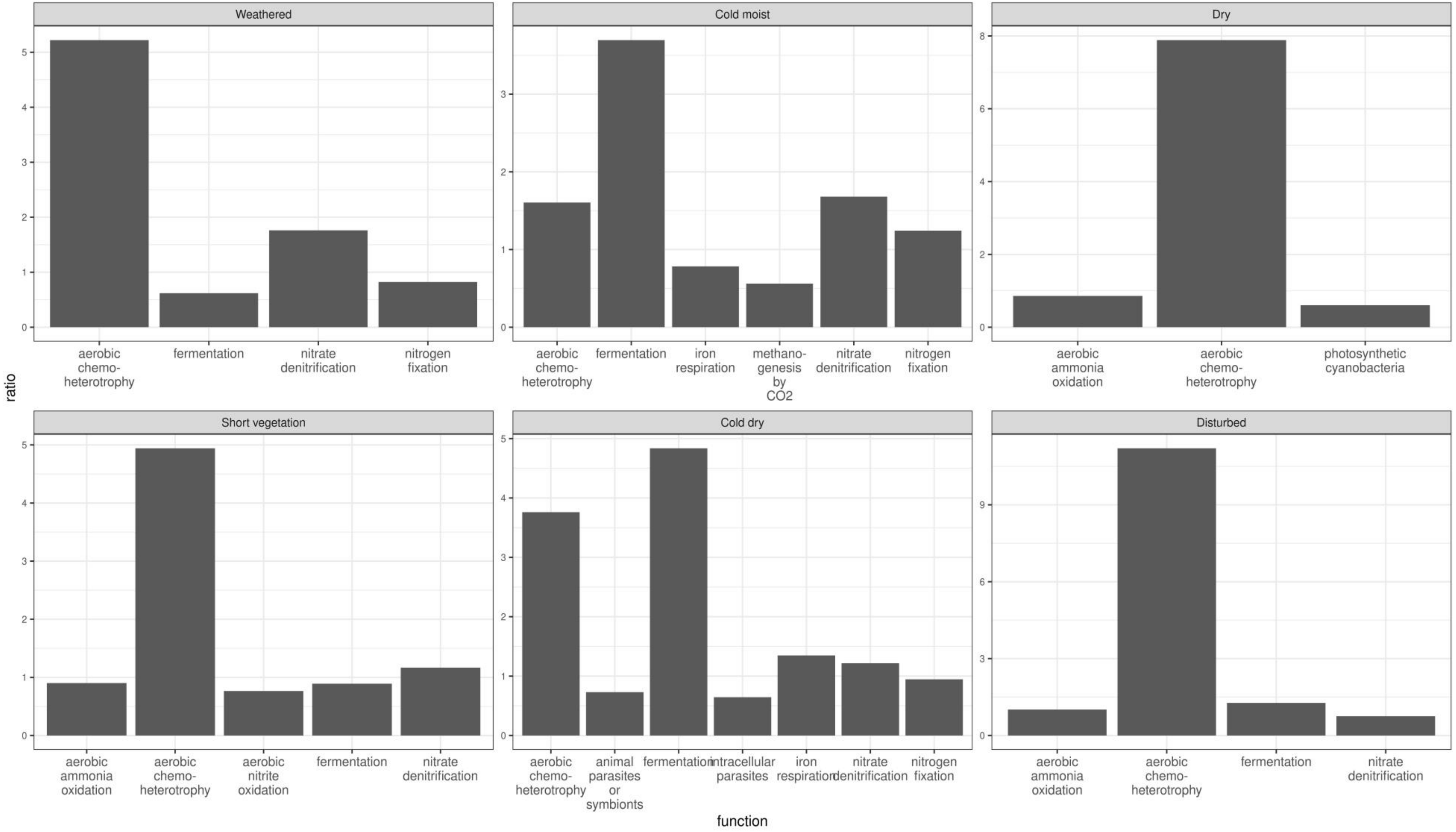
Linear model summary (log(abandance)~logpH, by function-cluster)

cluster	func	pval	estim.
Weath.	aerobic chemo- heterotrophy	0.000	-0.310
Weath.	fermentation	0.000	-0.211
Weath.	nitrate denitrification	0.511	-0.016
Weath.	nitrogen fixation	0.000	-0.149
Cold M.	aerobic chemo- heterotrophy	0.000	0.542
Cold M.	fermentation	0.004	-0.152
Cold M.	iron respiration	0.007	0.186
Cold M.	methano- genesis by CO2	0.000	-0.273
Cold M.	nitrate denitrification	0.000	-0.275
Cold M.	nitrogen fixation	0.000	-0.394
Dry	aerobic ammonia oxidation	0.530	-0.049
Dry	aerobic chemo- heterotrophy	0.989	0.000
Dry	photosynthetic cyanobacteria	0.087	-0.239

cluster	func	pval	estimate
Short V.	aerobic ammonia oxidation	0.000	0.478
Short V.	aerobic chemo- heterotrophy	0.000	0.163
Short V.	aerobic nitrite oxidation	0.007	0.147
Short V.	fermentation	0.199	0.075
Short V.	nitrate denitrification	0.291	-0.036
Cold D.	aerobic chemo- heterotrophy	0.000	0.312
Cold D.	animal parasites or symbionts	0.901	-0.013
Cold D.	fermentation	0.129	-0.218
Cold D.	intracellular parasites	0.620	-0.054
Cold D.	iron respiration	0.171	0.238
Cold D.	nitrate denitrification	0.706	0.038
Cold D.	nitrogen fixation	0.442	-0.062
Disturb.	aerobic ammonia oxidation	0.000	0.317
Disturb.	aerobic chemo- heterotrophy	0.000	0.271
Disturb.	fermentation	0.001	0.127
Disturb.	nitrate denitrification	0.000	-0.264

Function abundance within each cluster

- In all clusters the most abundant functions are related to decomposition processes.



Reported: Function with higher ratios