Global soil microbiomes under different pH conditions

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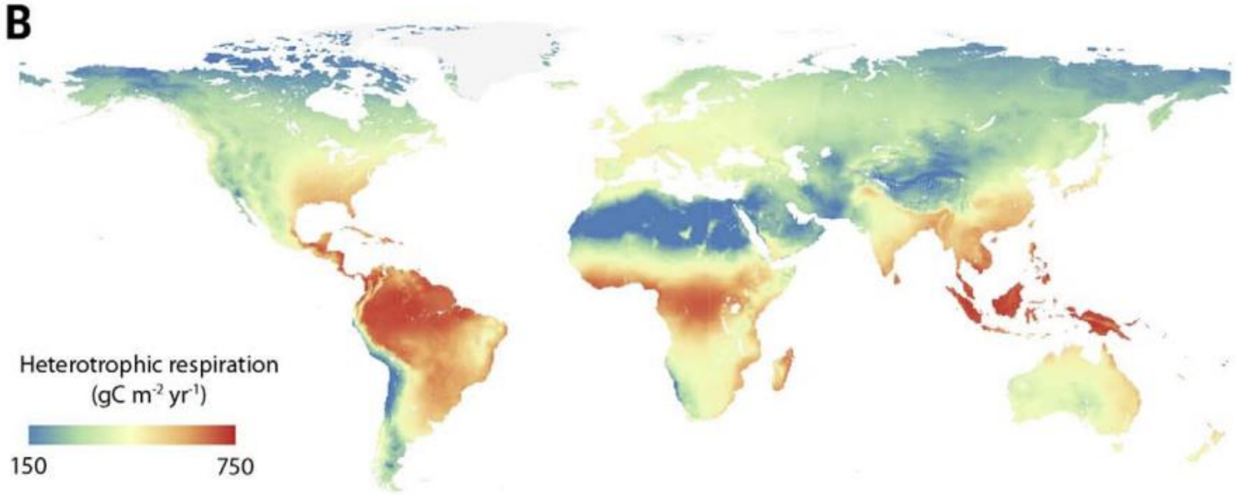
Motivation

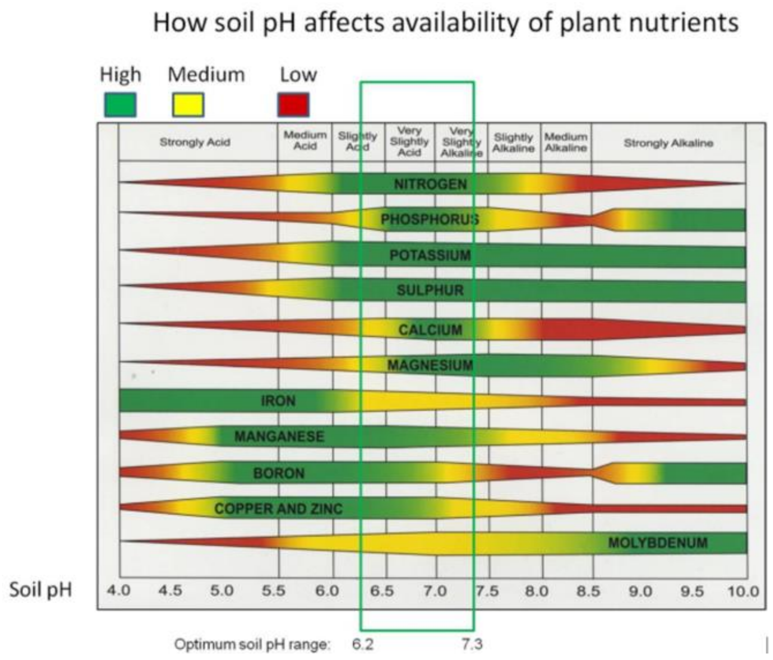
- Soil microbes are critical for the functioning of ecosystems.
  - Control nutrient and carbon cycling
  - Influence plant productivity
  - Key players in the Climate Change

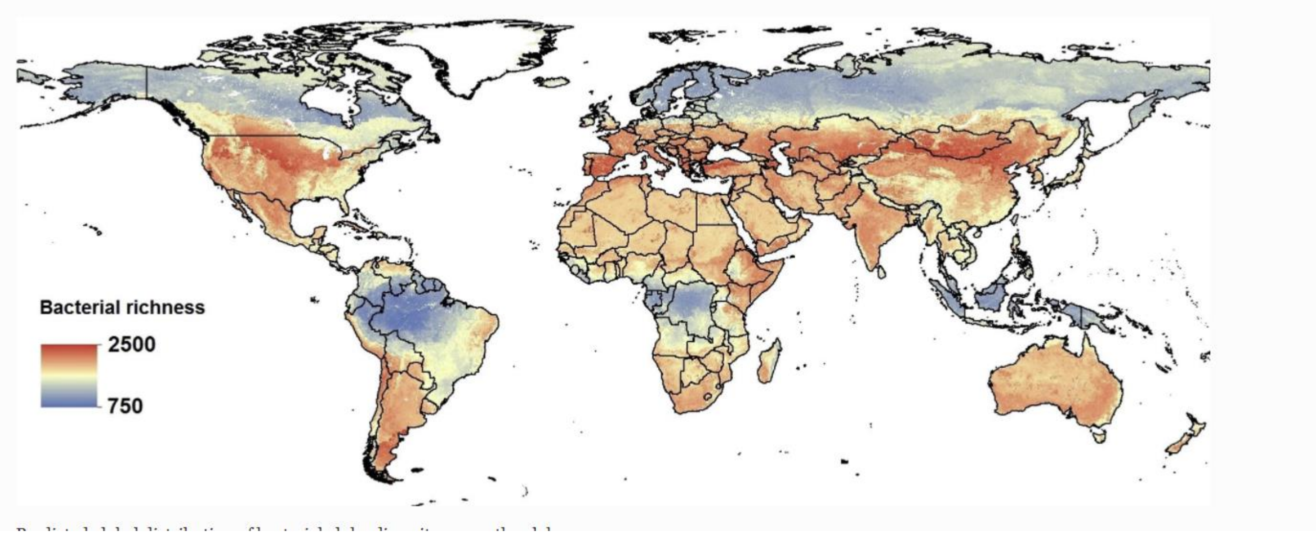


Crowther et al., Science 365, 772 (2019)

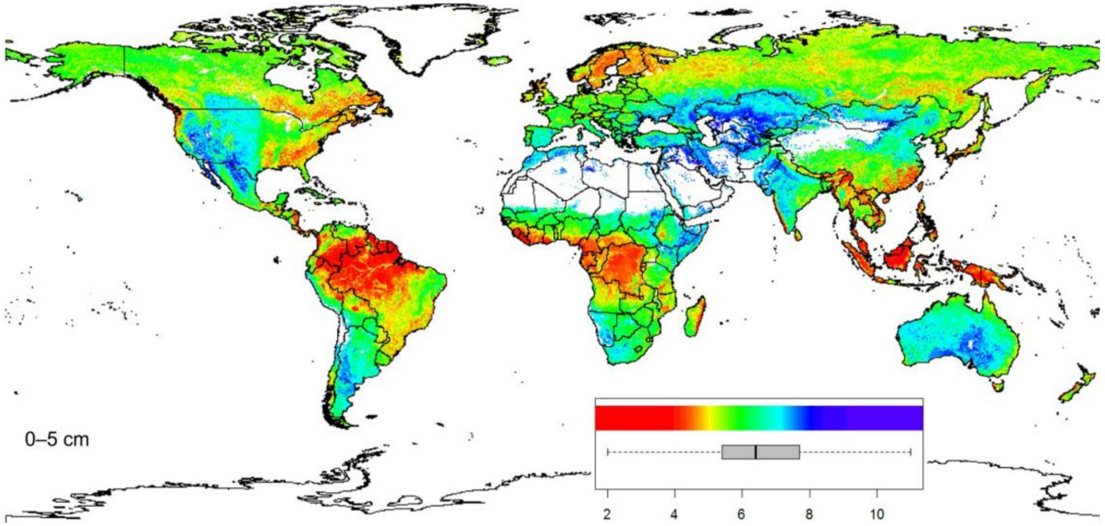
Motivation

- Soil pH affect nutrient availability in soils
    - Change soil biotic diversity


How soil pH affects availability of plant nutrients



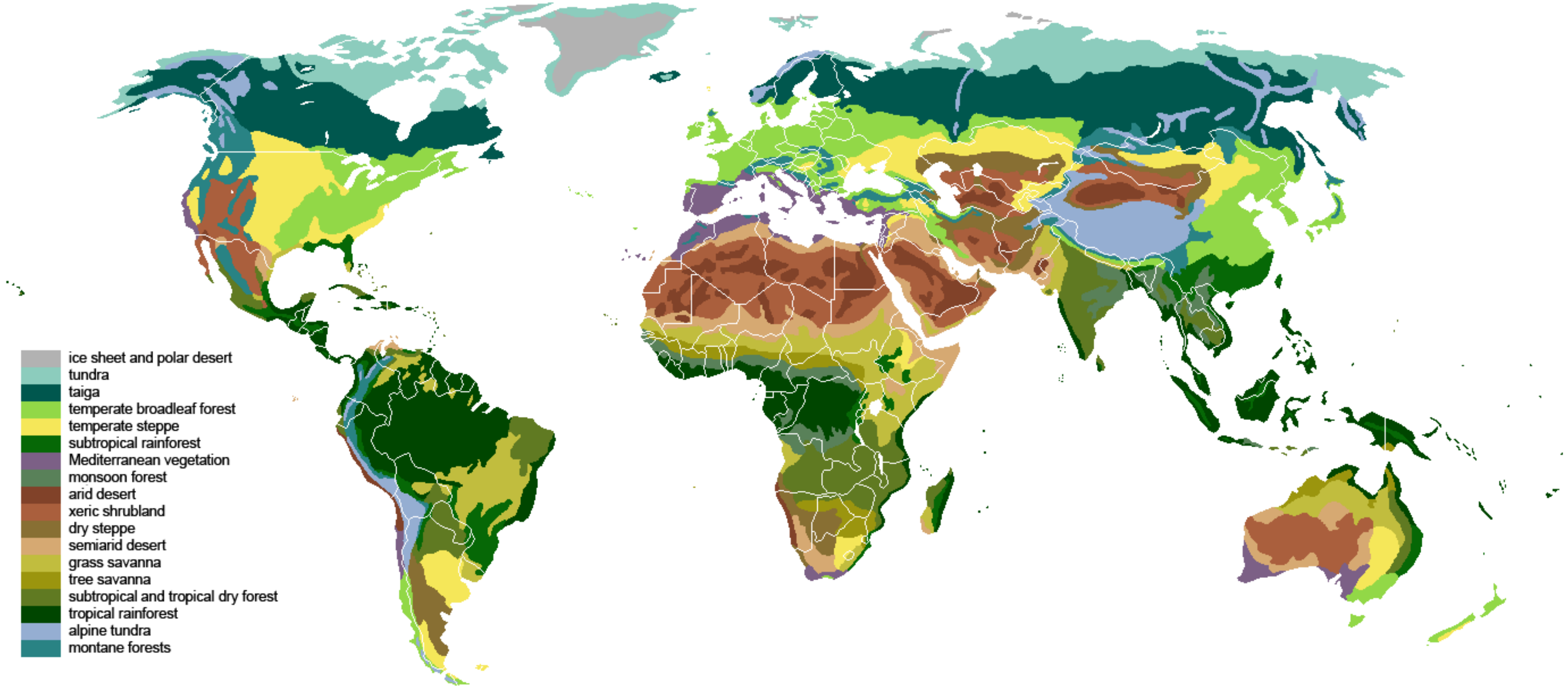
Baquerizo and Eldrige, Ecosystems 22, 1220 (2019)



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

Research question

How do soil microbiomes under different environmental conditions associate with pH globally?



Earth Microbiome Project (**EMP)**

- Database of 27,751 samples from 97 studies across different environments and humankind (Thomson et al., 2017)
  - 16S rRNA amplicon sequencing
  - Metagenomes
  - Metabolomics

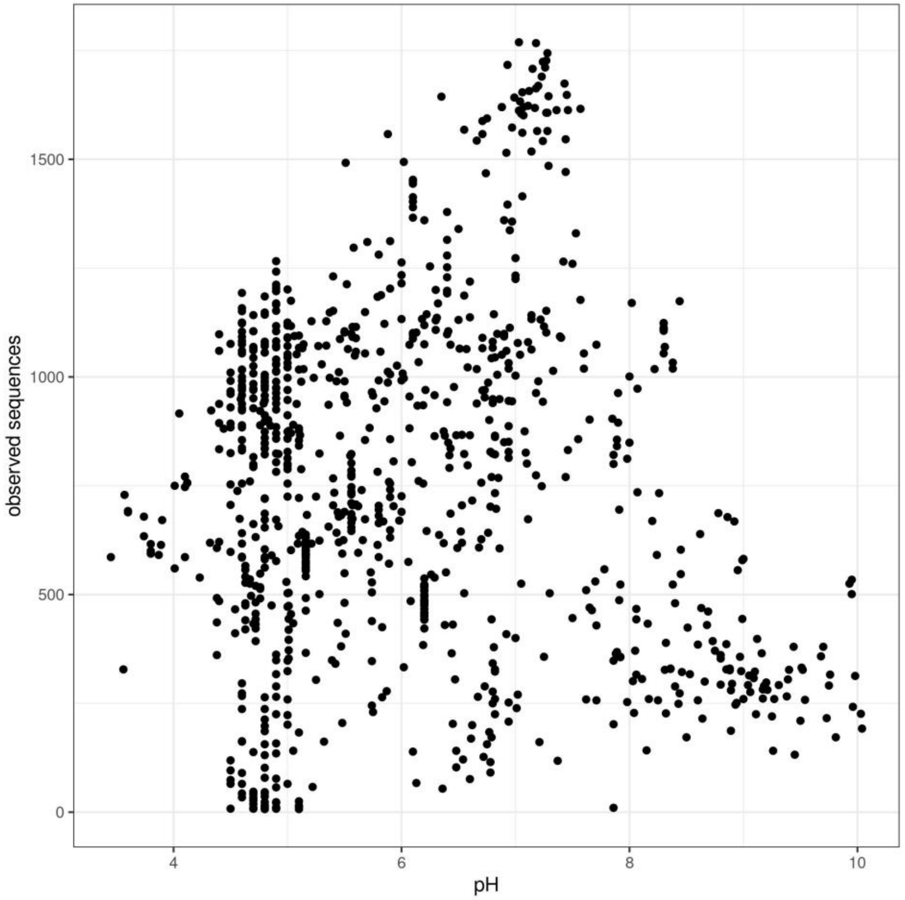
- OTU (Operational Taxonomic Unit) table: ID, Sequence, Kingdom, Phylum, Class, Order, Family, Genus, and Species.
- The sample table contains ID and Sample Name.
- Metadata table: 76 environmental information from each sample.
  - We used Sample ID, pH, Environment Biome, and Environment Feature.

Methods

- Sampling
  - Target soil microbiomes with soil pH information from EMP
- Build adjacency matrix
  - OTU-sample bipartite adjacency matrix dim(A)=116,658 × 945
- Clustering
  - Use Vintage Sparse Principal Component Analyses (VSP)
  - Define K (or rank) base on theoretical information and scree plot
- Contextualizing
  - Use bff from VSP R package
  - Use biomes as an ecosystem (climate, vegetation) classification
  - Use features as soil type (disturbed, weathered, new) classification
  - Use pH as soil condition classification

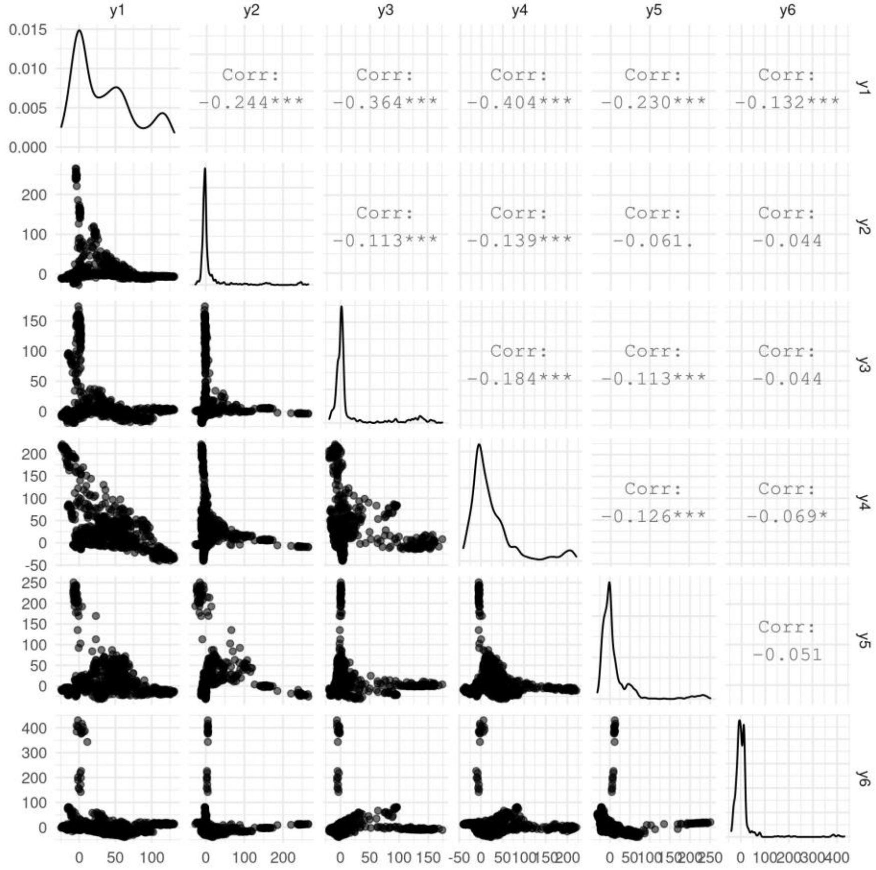
Preliminary results

- Overall trend of pH-Sequence diversity
  - Diversity increases from acidic to neutral and then decreases from neutral to basic
  - Diversity variance in neutral pH is greater

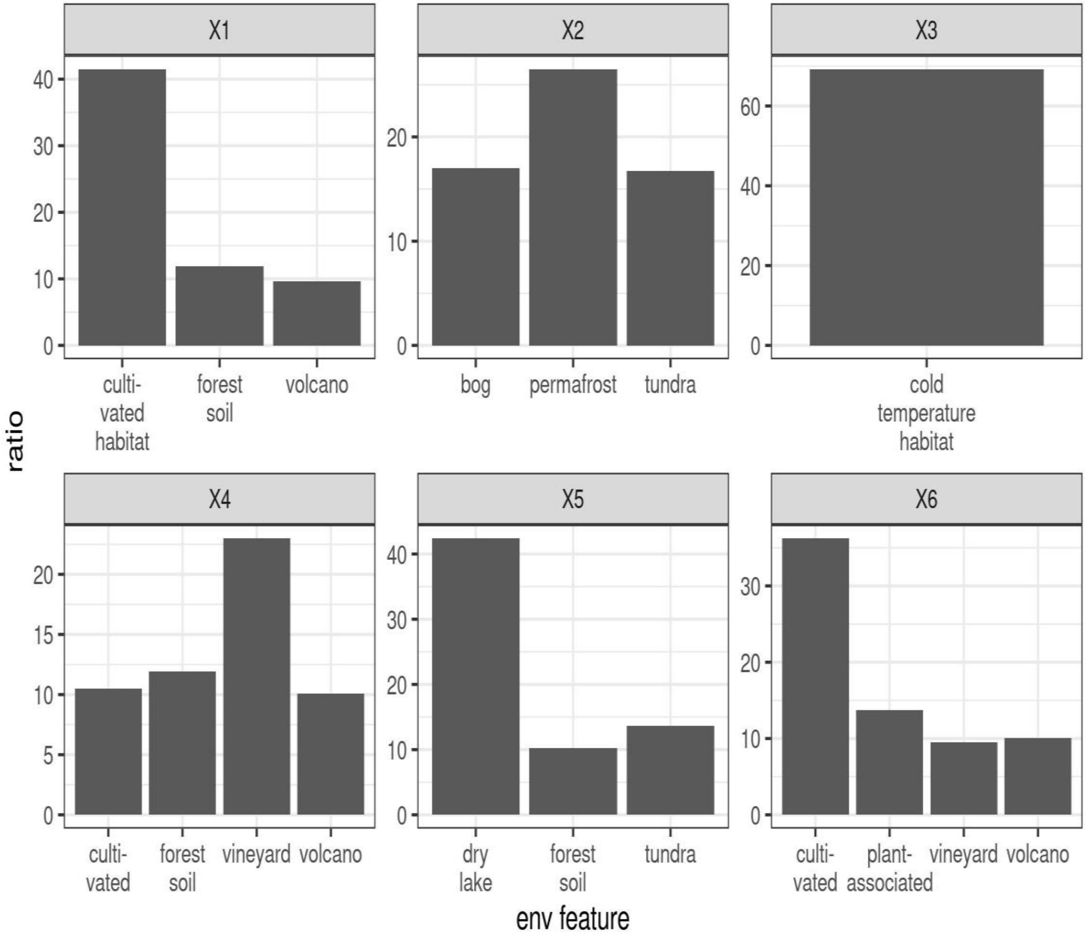


Preliminary results

- Six clusters (k = 6)
  - mixed memberships in some samples
  - cluster: samples with similar OTU composition



- Contextualize with environmental features



Preliminary results

- Contextualization with biome, environment feature and pH
  - Introducing pH provides a clearer classification of clusters

X1 Weathered (acidic)	X2 Cold moist	X3 Dry (basic)	X4 Short vegetation (neutral)	X5 Dry cold	X6 Disturbed
cultivated habitat	tundra biome	polar desert biome	vineyard	dry lake	cropland biome
forest soil	permafrost	cold temperature habitat	tropical shrubland biome	tundra biome	plant-associated habitat
4.8	bog	desert biome	volcano	4.63	6.82
4.6	5.16	dry soil	grassland soil	4.72	6.94
4.9	6.2	tundra	grassland biome	5.01	desert biome
tropical shrubland biome	5.56	shrubland	desert biome	4.76	6.8
volcano	tundra	8.3	7.14	4.38	agricultural soil

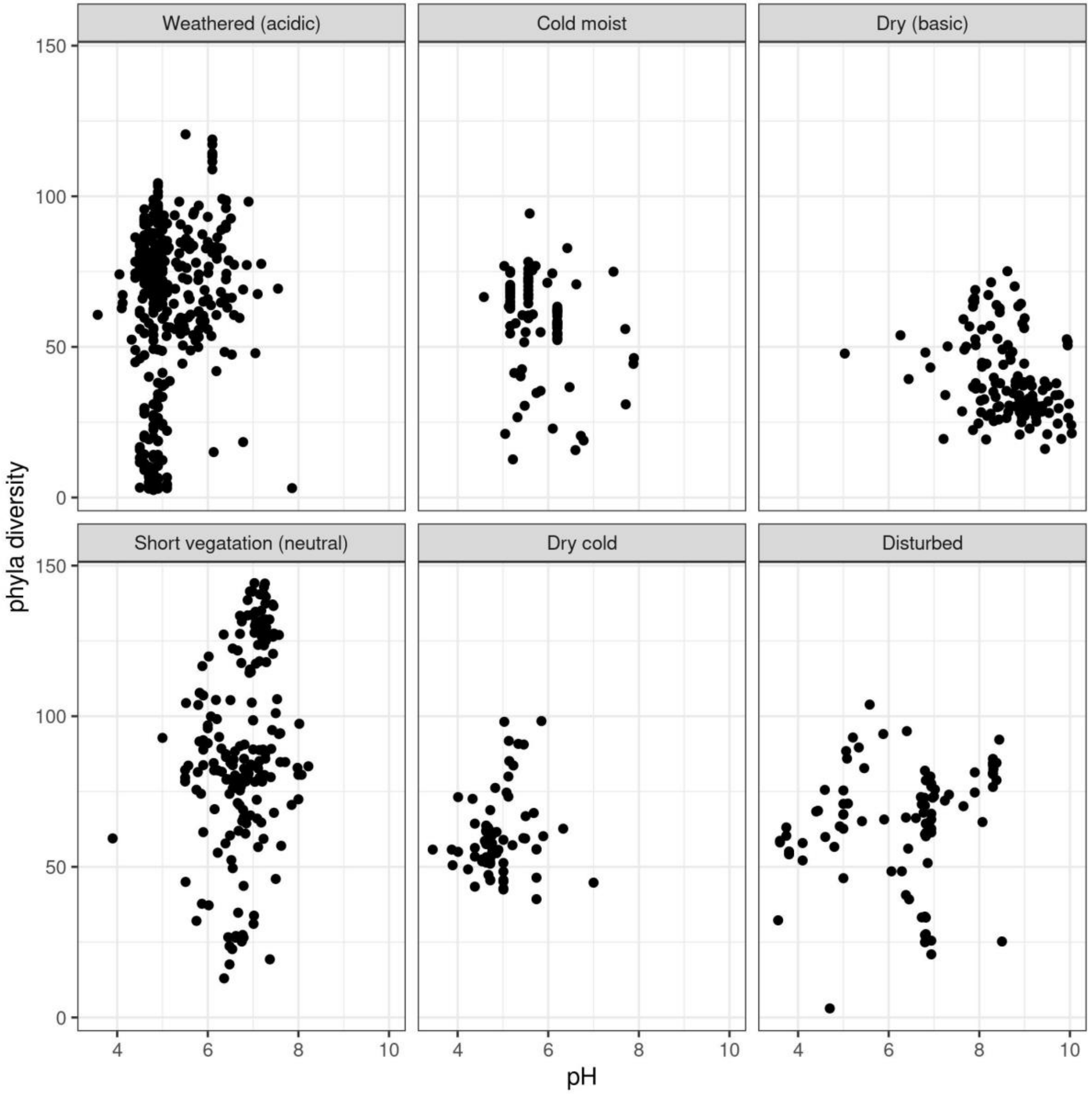
Preliminary results

- pH-phyla diversity trend within each cluster

- Weathered: positive correlation

- Short vegetation: narrow pH range but wide diversity

- More precise pH-phyla composition analysis is necessary to understand pH influence

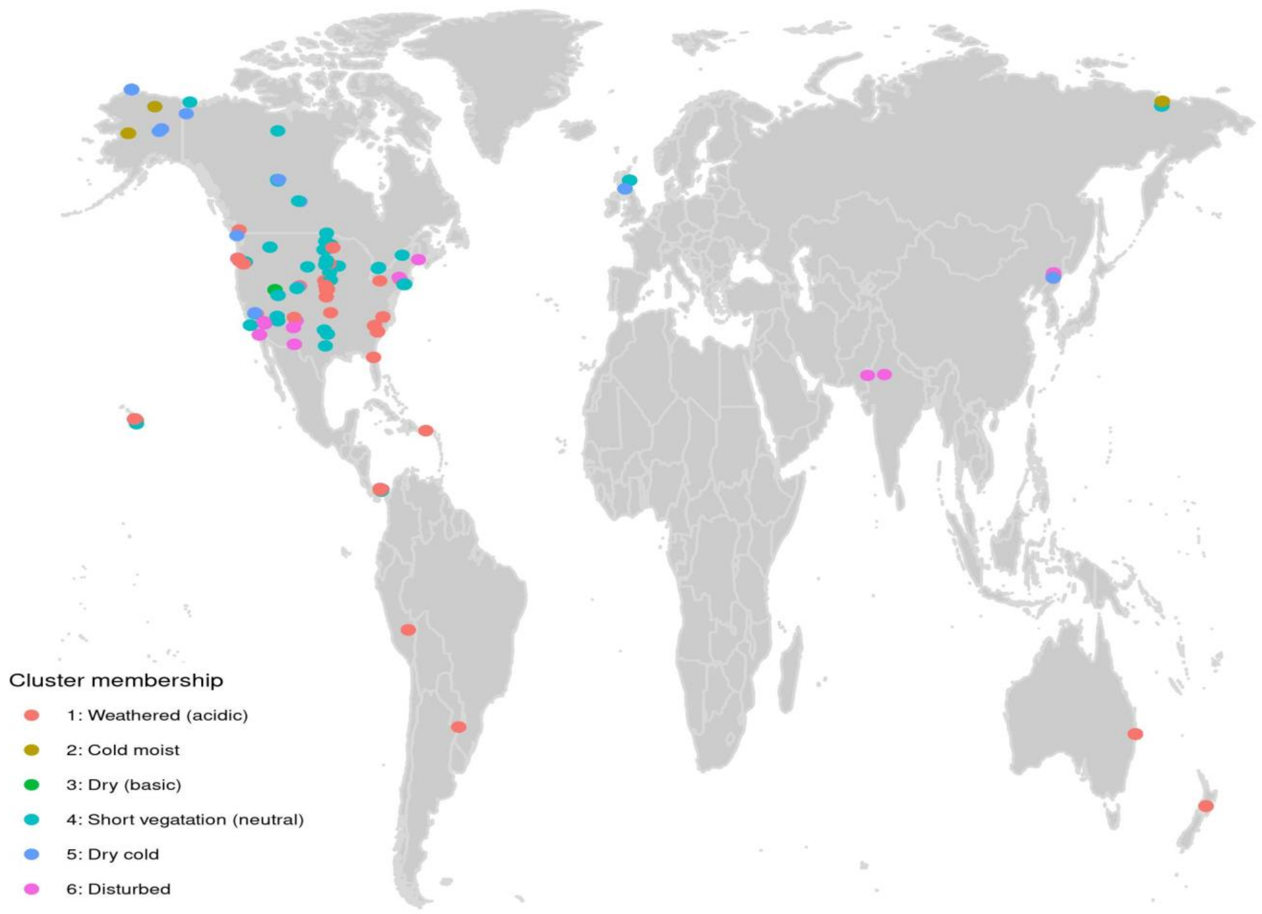


Preliminary results

- Global cluster membership

- Similar community composition can be found across different continents

- Potentially builds the gap between local-scale soil microbial community study and global phenomena



Next steps

- Contextualized the clusters using taxonomical information
  - See who is there
- Identify taxa with more abundance in each cluster
  - Who is more dominant in each cluster
- Relate dominant taxa of each group to pH
  - See if dominant taxa are dominant due to pH or if there are other factors influencing the high abundance