

Biogeography of Chemotaxis in Soils

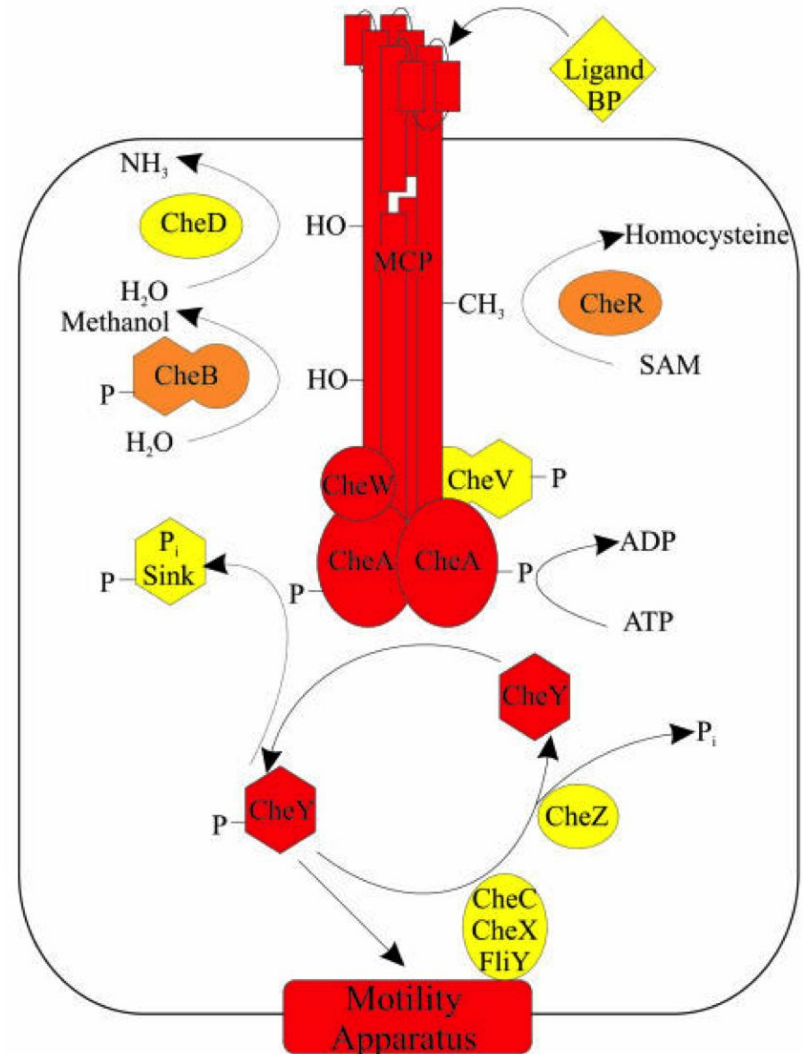
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Background

Chemotaxis

- control system for motility
- bacterial IQ, extroverts VS introverts



Environmental Controls on Chemotaxis

Observation: Microorganisms that inhabit stable ecological niches encode primitive signaling strategies, whereas environmental organisms that have sophisticated systems of environmental sensing and signal transduction encode more complex signaling strategies.

Galperin 2005

Goal: explore key genes for chemotaxis and understand global distribution patterns across ecosystems

Questions

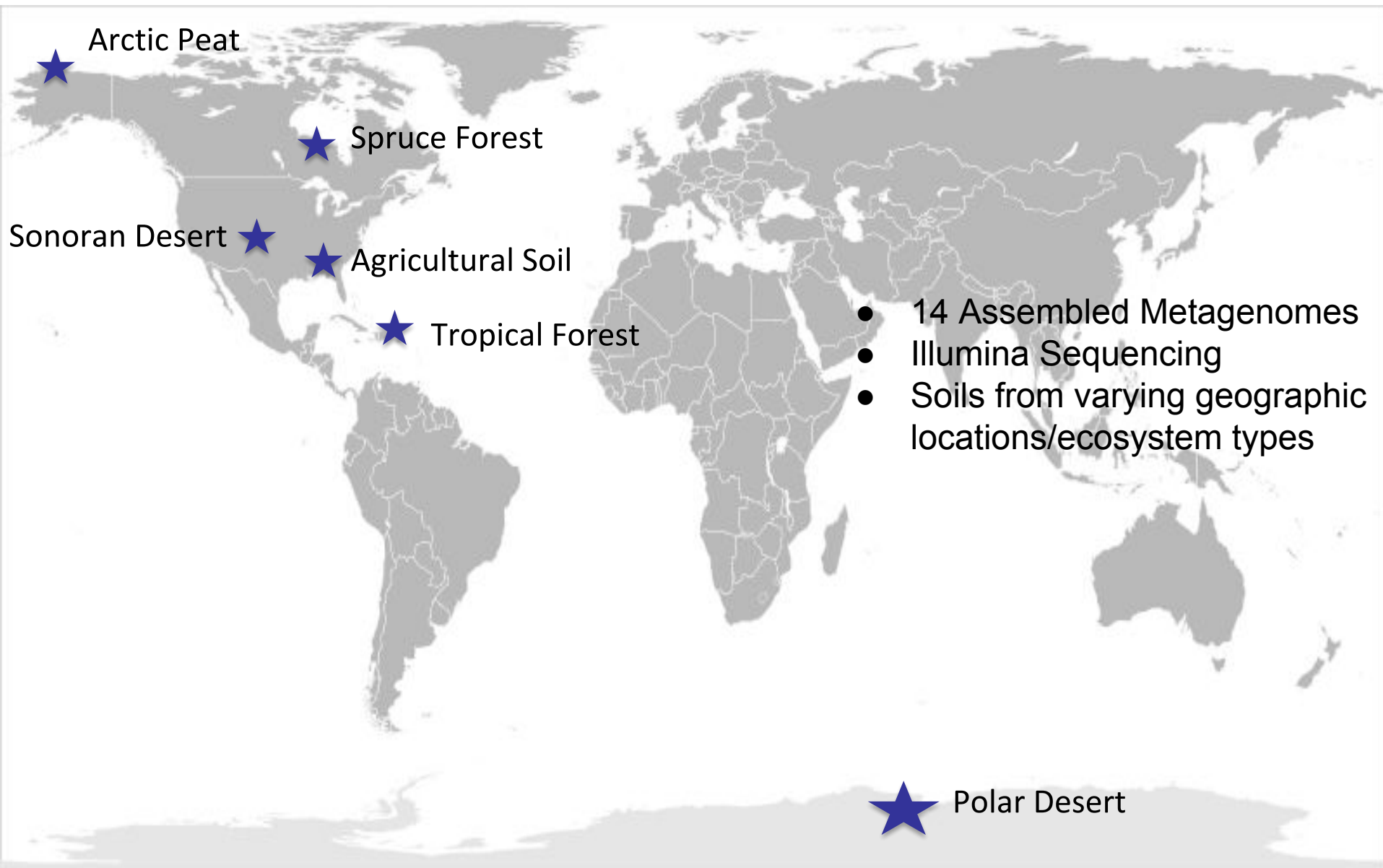
1. Can we use chemotaxis as a proxy to survey chemical complexity of soil?

Six Ecosystem Types

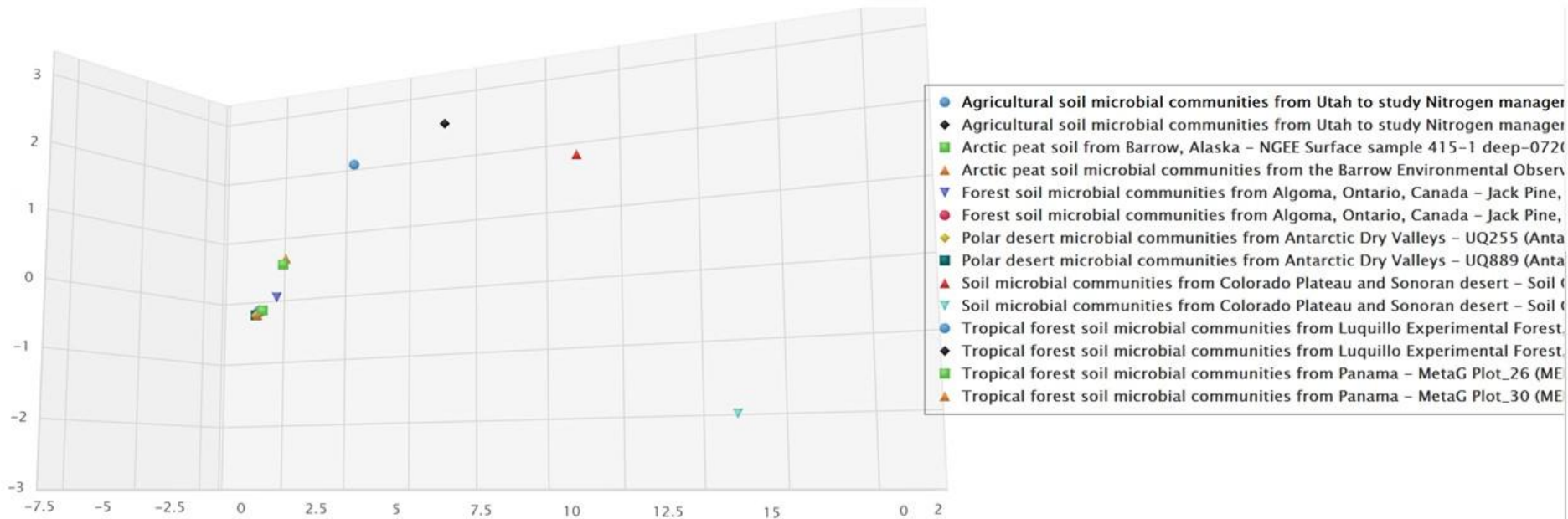


- Tropical Forest - Puerto Rico (USA) (2x) and Panama (2x)
- Desert Soil - Colorado (USA) (2x)
- Polar Desert - Antarctica (2x)
- Arctic Permafrost - Alaska (USA) (2x)
- Boreal Forest - Ontario (Canada) (2x)
- Agricultural soil - Utah (USA) (2x)

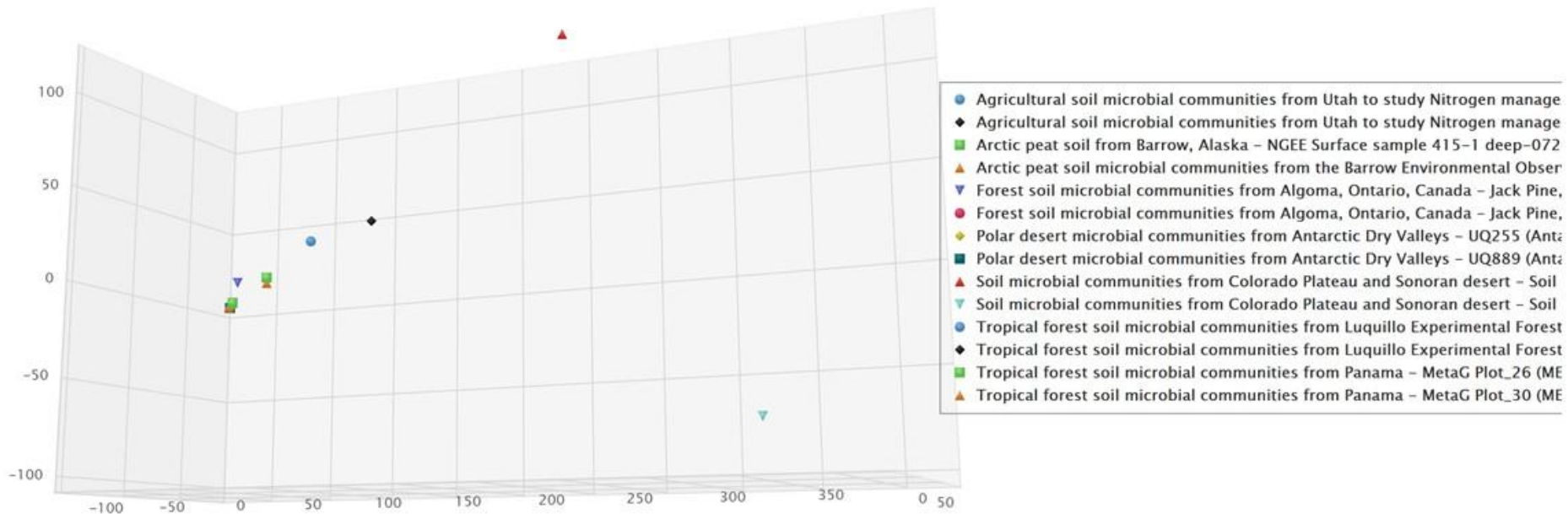




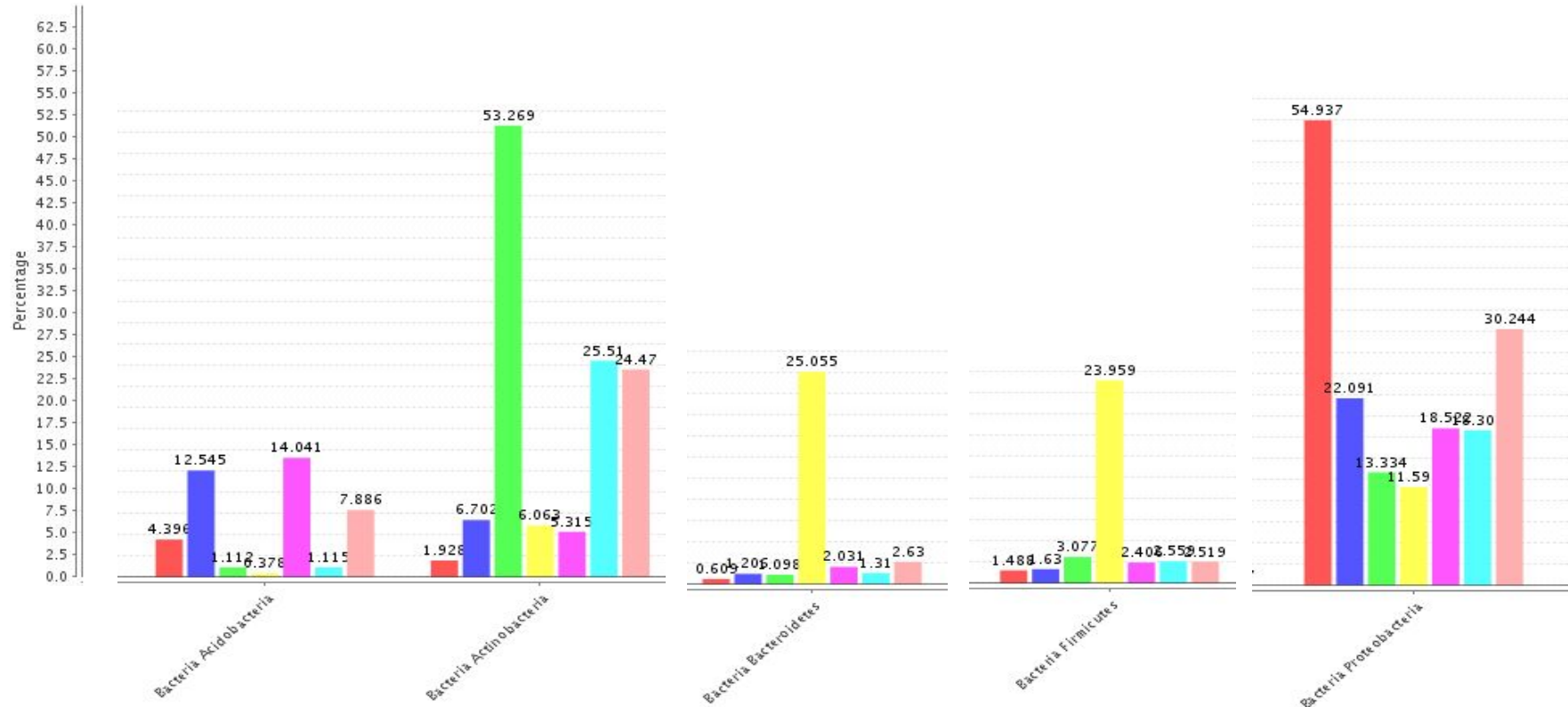
How different are metagenomes based on their KO functions?



and based on taxonomy?



Major differences from phylogenetic comparison



- Tropical forest (Puerto Rico)
- Forest soil (Ontario)
- Polar desert (Antarctica)
- Arctic peat soil (Alaska)

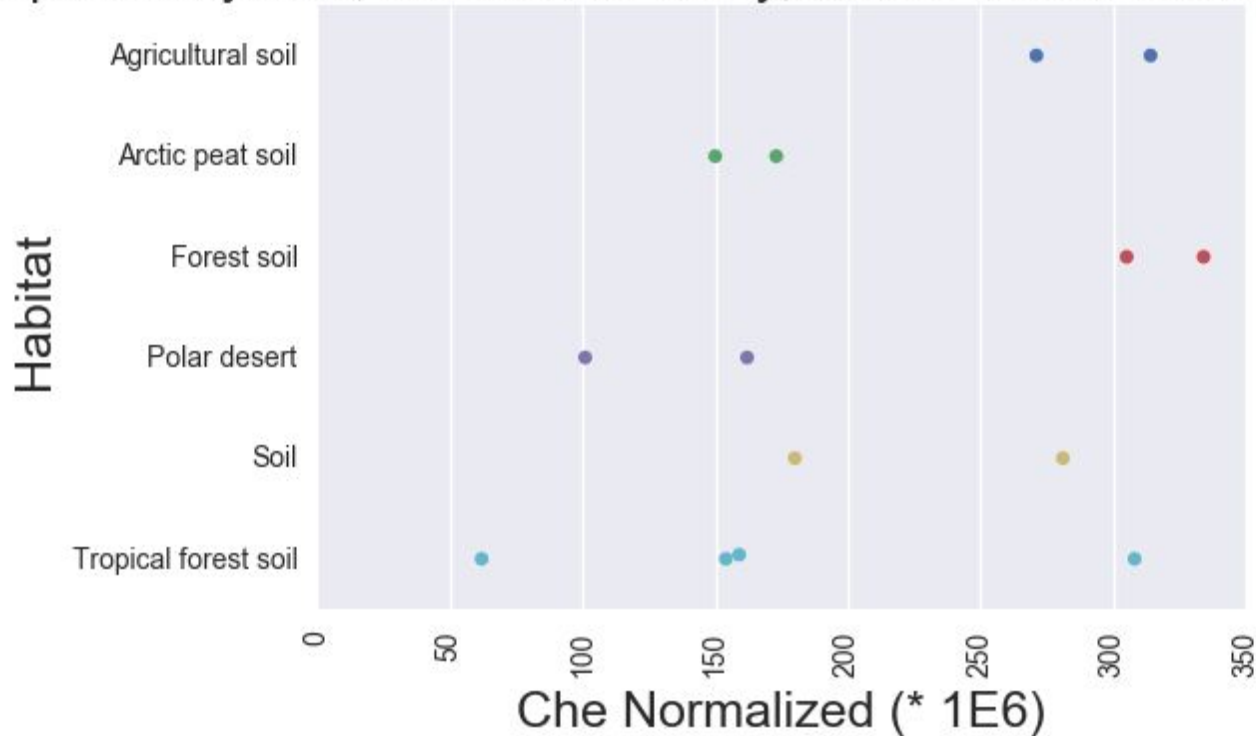
- Forest soil (Massachusetts)
- Desert soil (Colorado)
- Agricultural soil (Georgia)

Normalization step

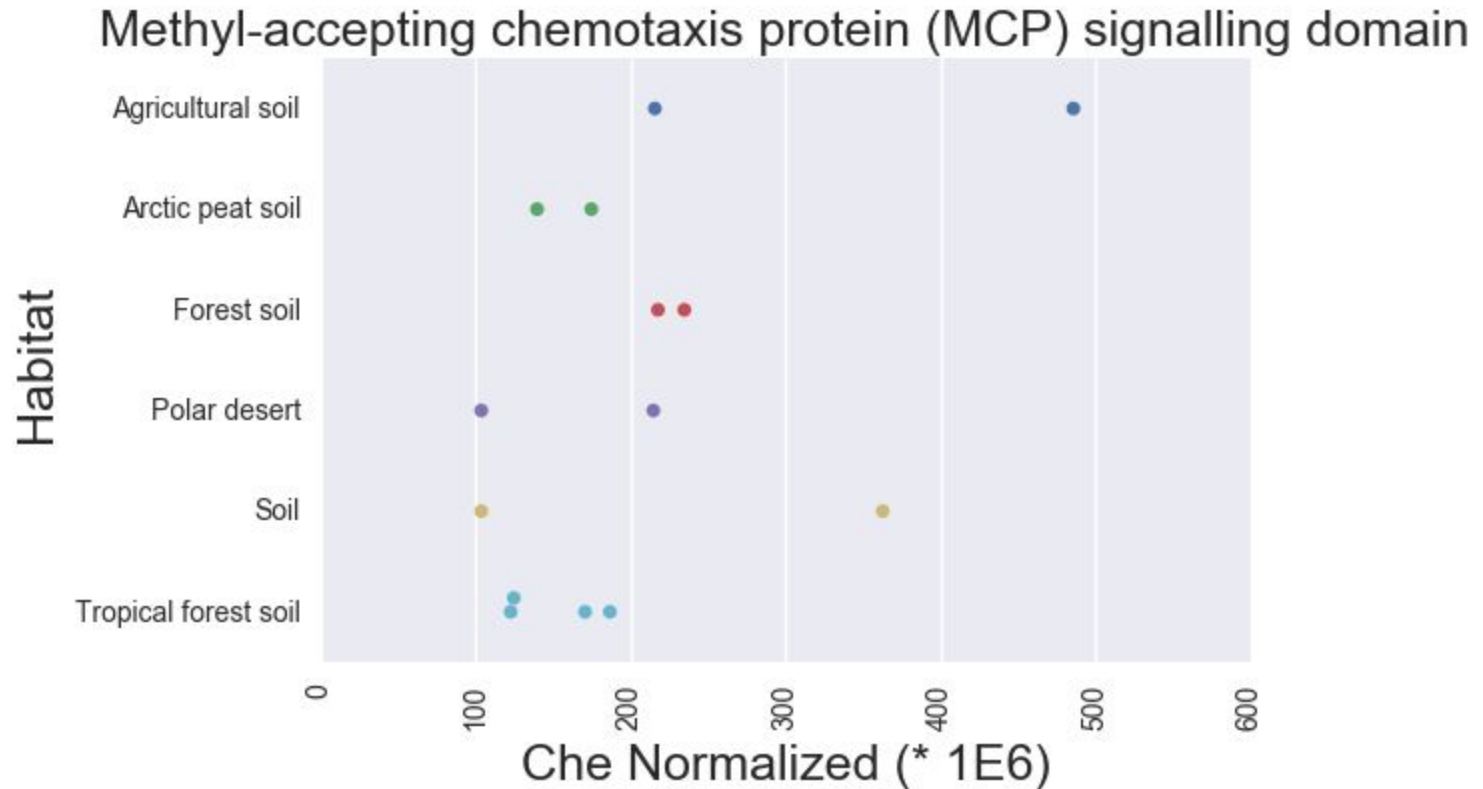
$$\text{Che Normalized} = \text{Che counts} / \# \text{ gene count}$$

Gene Counts : CheA

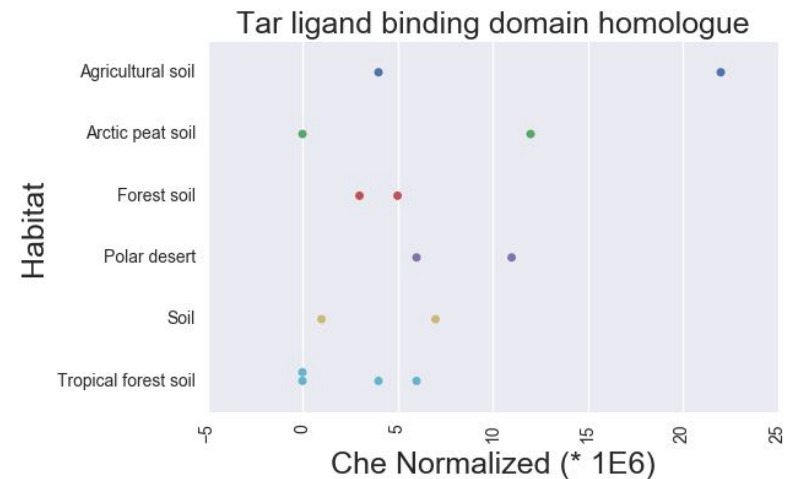
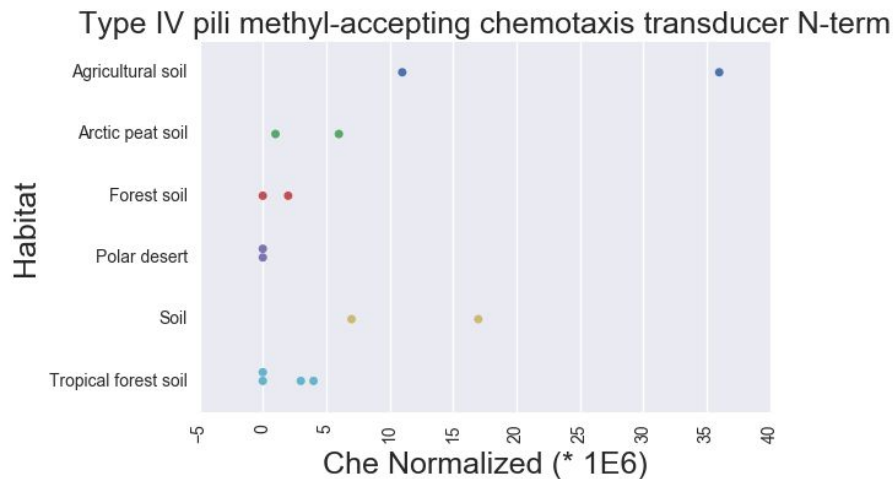
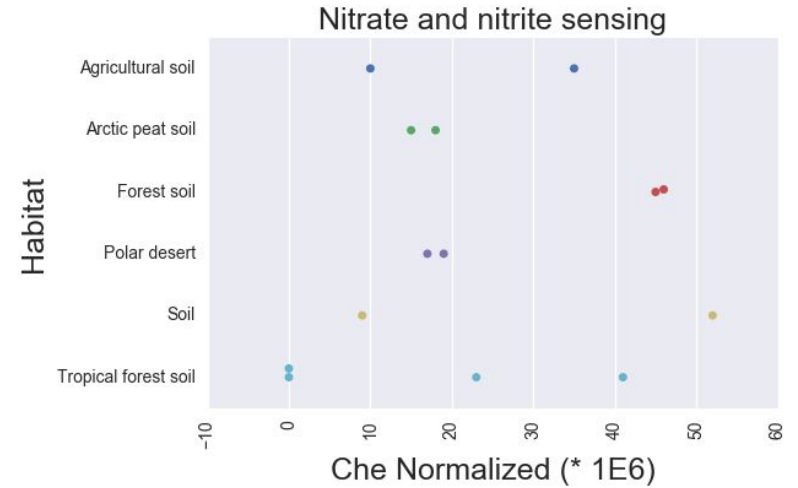
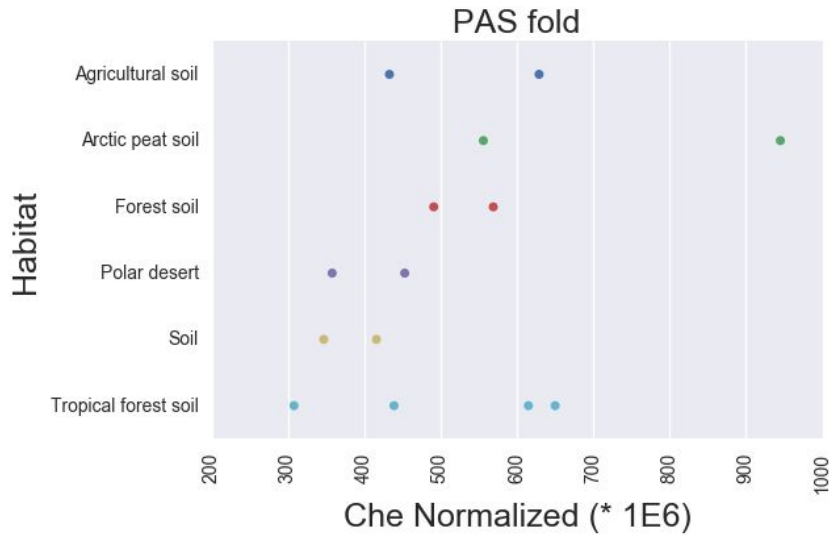
two-component system, chemotaxis family, sensor kinase CheA [EC:2.7.13.3] (cheA)



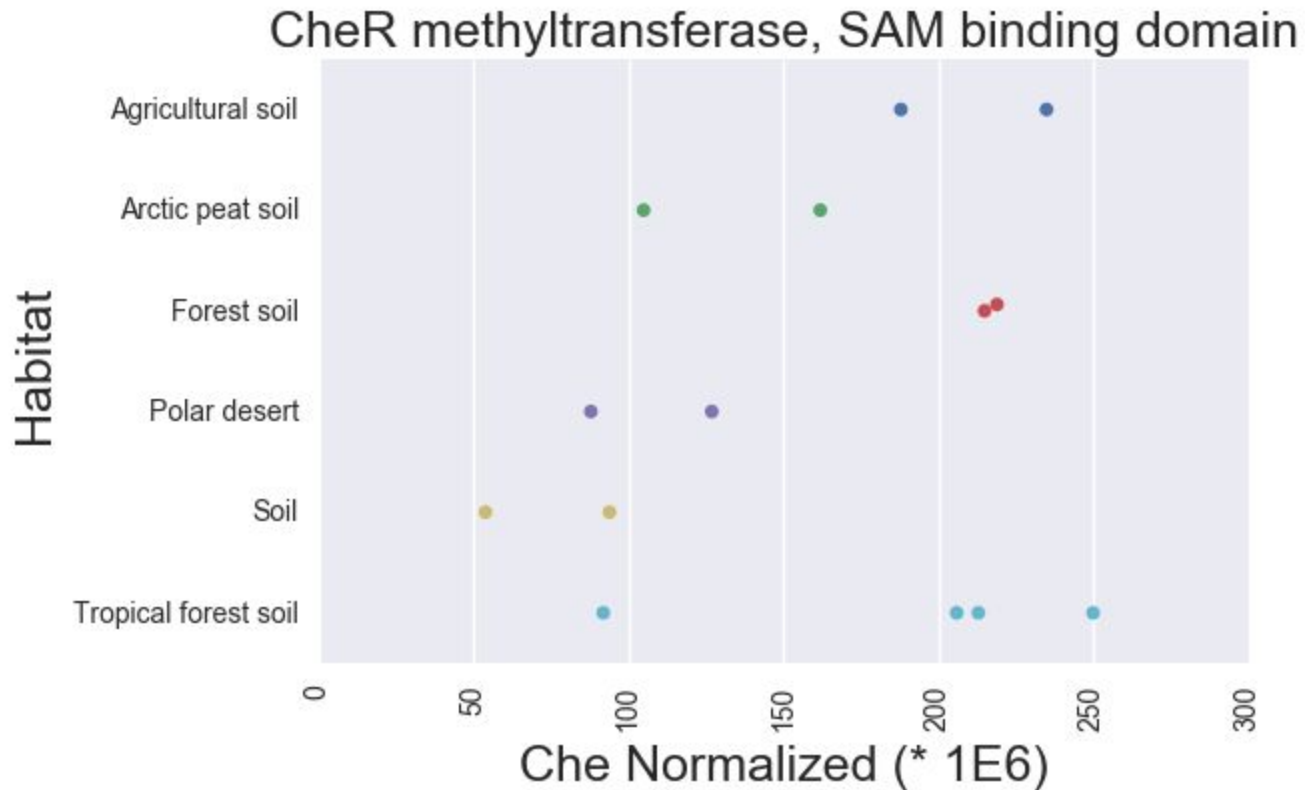
Gene Counts : Receptors



Gene Counts : Sensors



Gene Counts : Adaptation



Conclusions

- Database very diverse -> care pick datasets
- Agriculture/Forest seems to have more chemotaxis genes
- Actinobacteria were dominated in Antarctic soil (specialists normally found in a poor nutrient environment), whereas Proteobacteria were dominated in Tropic soil (generalists normally found in a rich nutrient environment, *Yergeau et al. 2012 ISME*)

Thanks

Conclusions

- Our data was biased due to differences in sequencing techniques
- Agricultural soils had the most genes for chemo-receptors but also the sequencing depth was magnitudes higher than the rest of the metagenomes
- PCA clustering was also affected by sequencing depth
- Actinobacteria were dominated in Antarctic soil (specialists normally found in a poor nutrient environment), whereas Proteobacteria were dominated in Tropic soil (generalists normally found in a rich nutrient environment, *Yergeau et al. 2012 ISME*)

Protein domain models gene abundance in metagenomes

