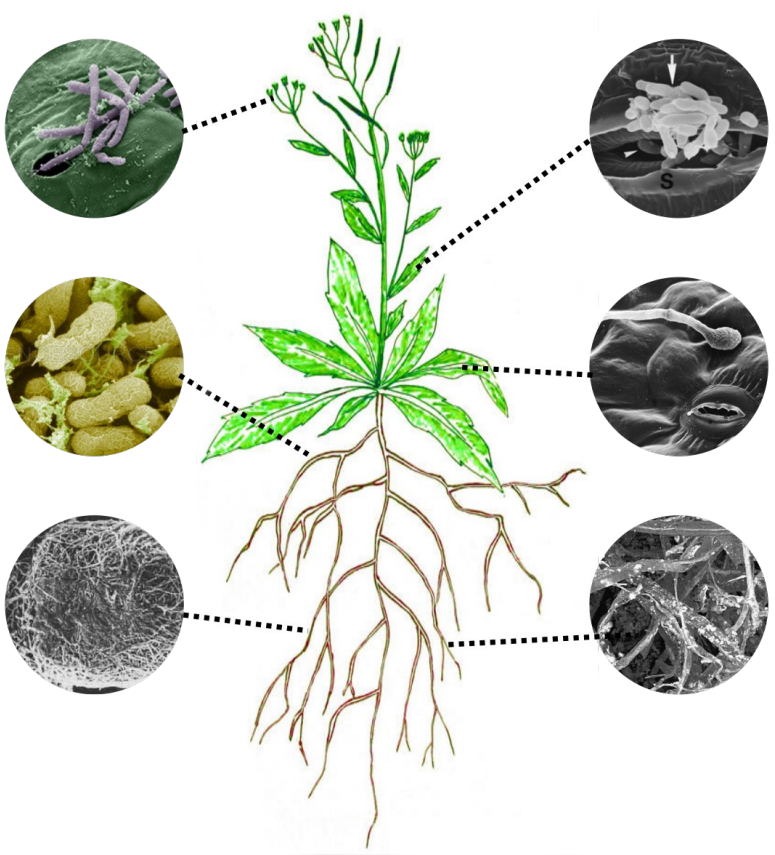
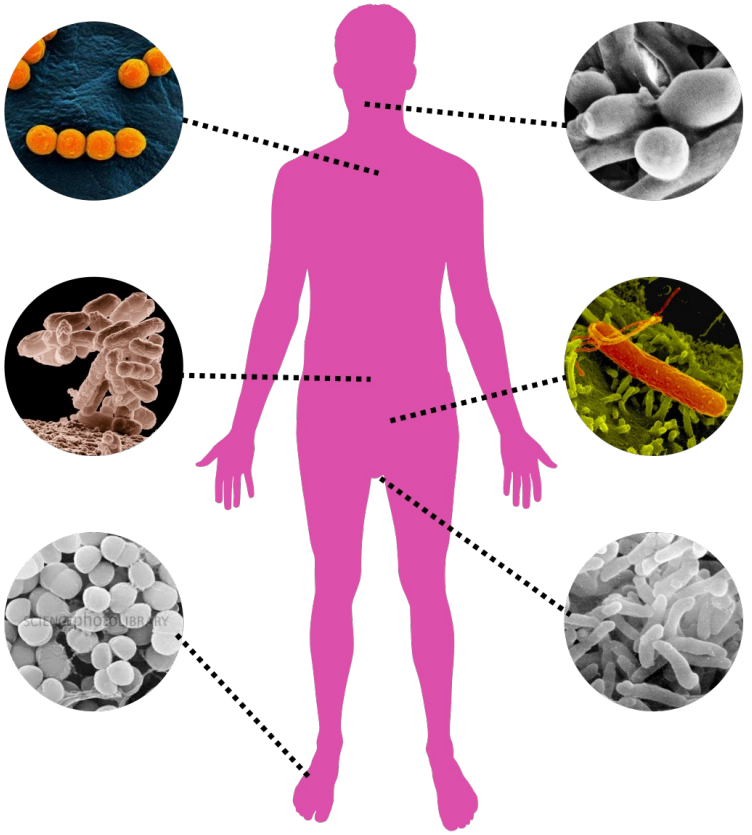
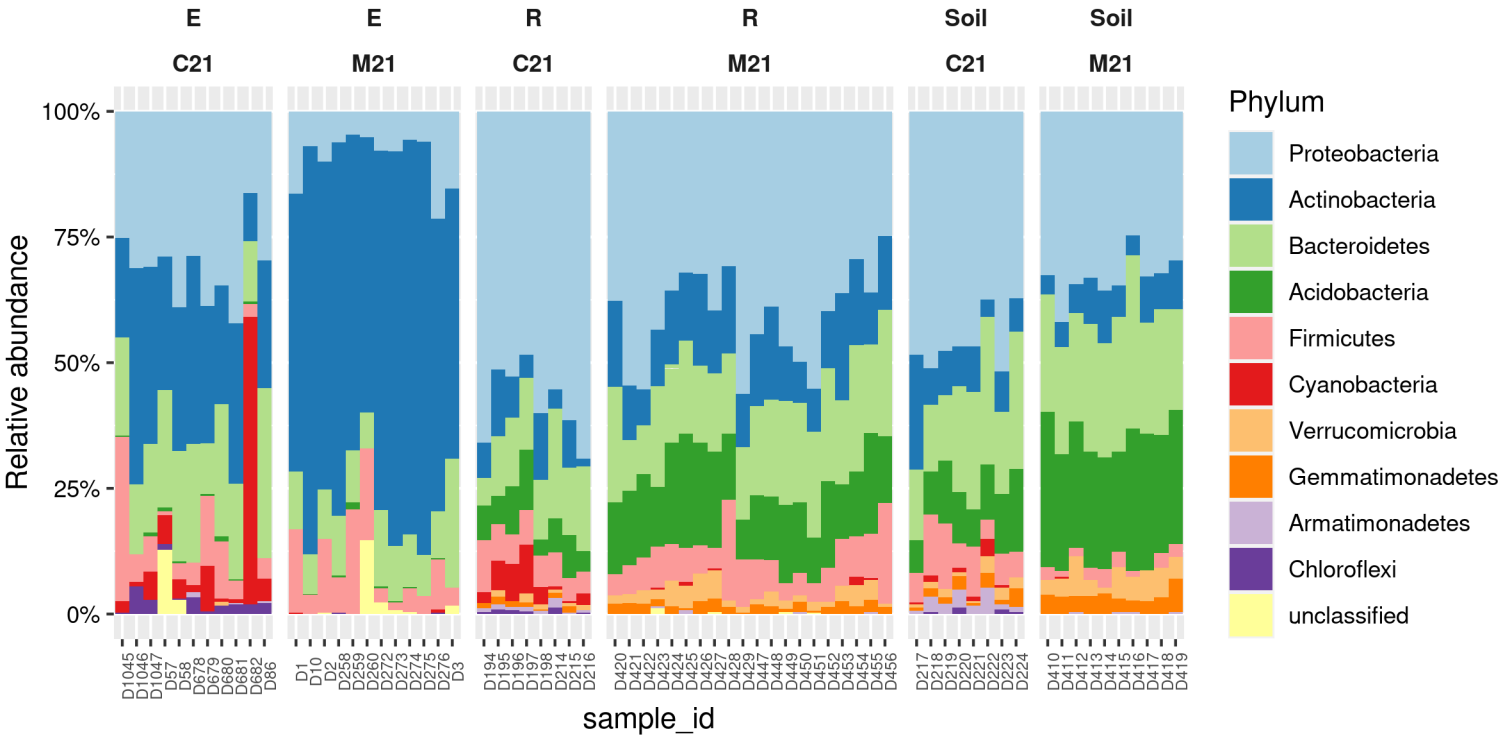
The World is microbial

...and so are we

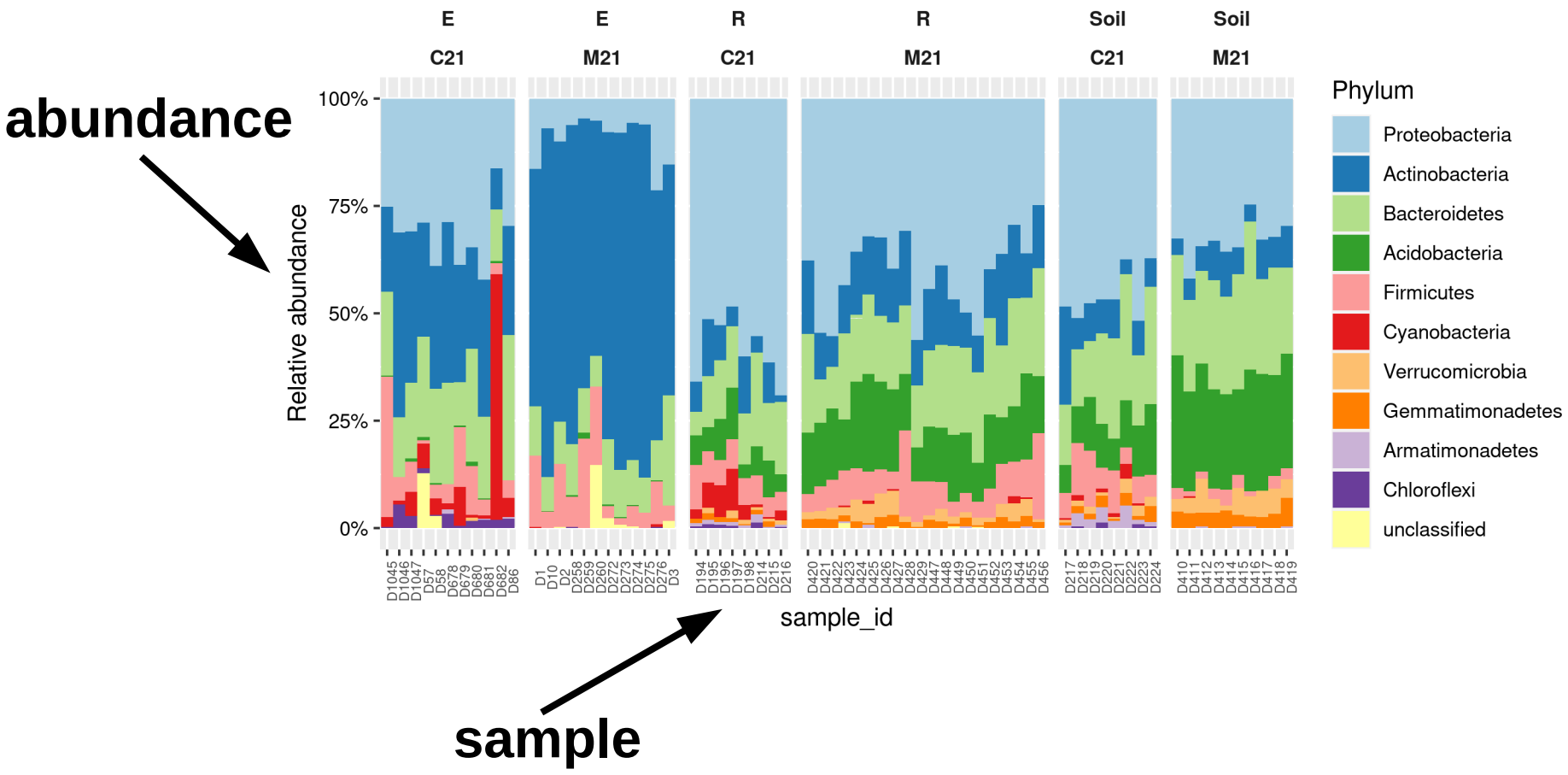


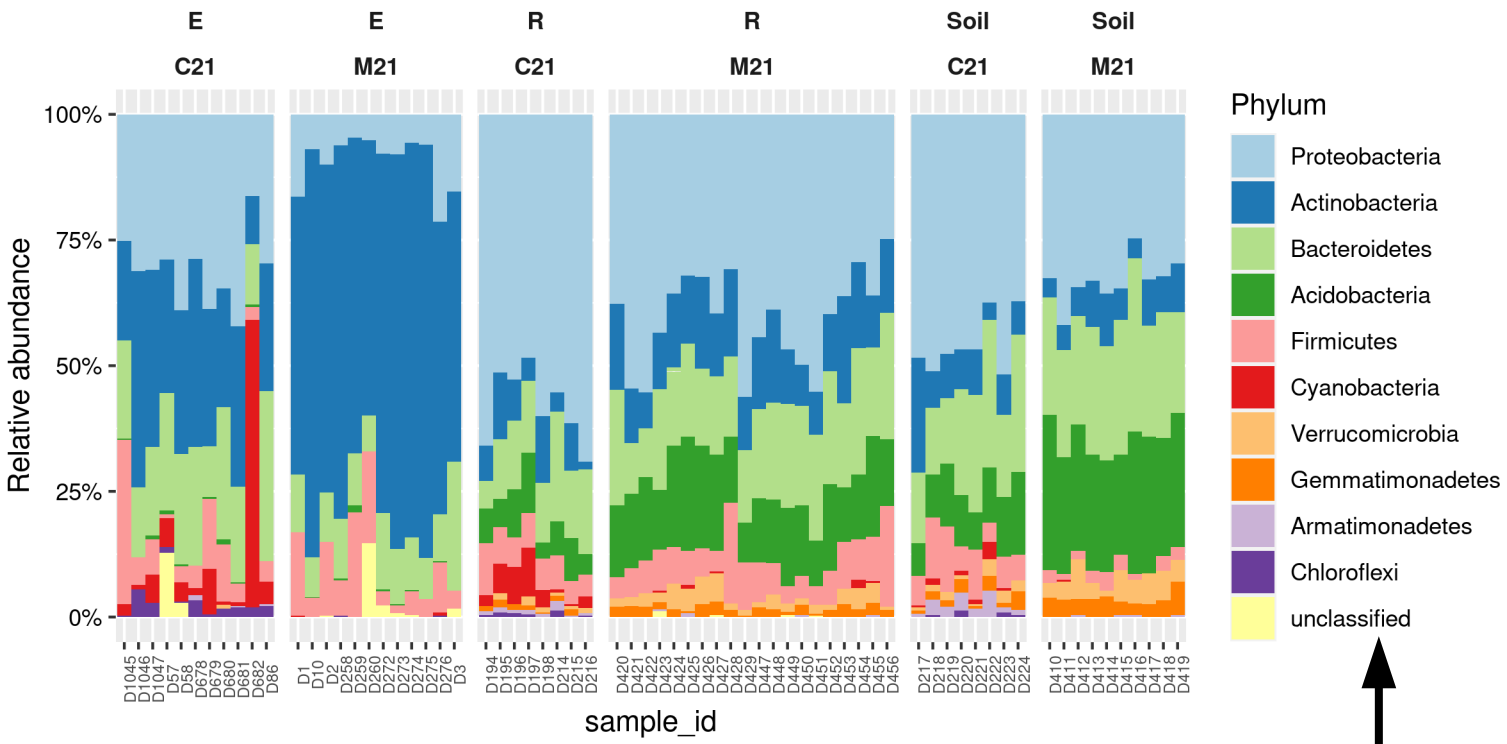



E
C21
E
M21
R
C21
R
M21
Soil
C21
Soil
M21
100%
75%
50%
25%
0%
Relative abundance
sample_id
Phylum
Proteobacteria
Actinobacteria
Bacteroidetes
Acidobacteria
Firmicutes
Cyanobacteria
Verrucomicrobia
Gemmatimonadetes
Armatimonadetes
Chloroflexi
unclassified

Getting the data

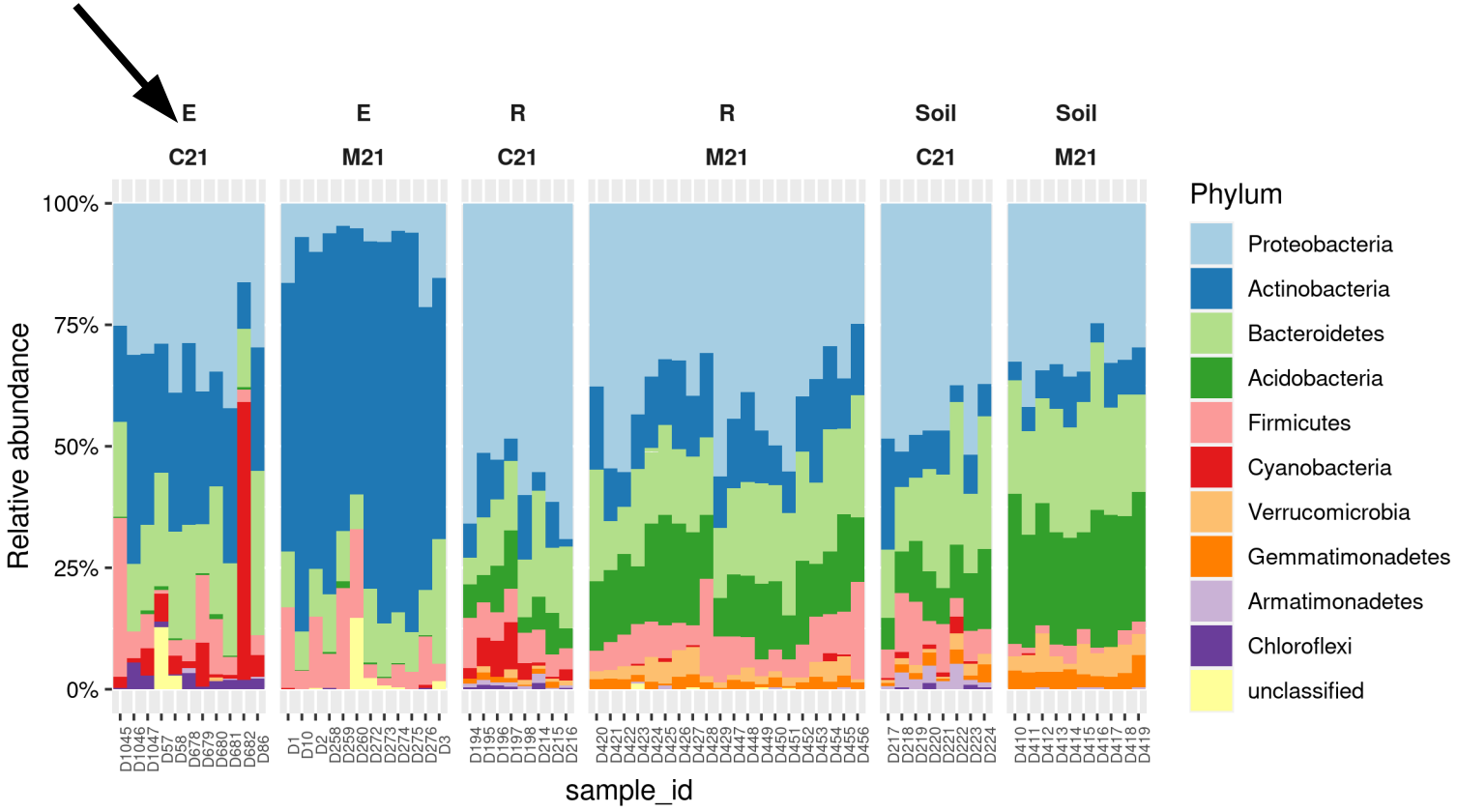
https://github.com/surh/scip_barplot


abundance
E
C21
E
M21
R
C21
R
M21
Soil
C21
Soil
M21
100%
75%
50%
25%
0%
Relative abundance
sample_id
Phylum
Proteobacteria
Actinobacteria
Bacteroidetes
Acidobacteria
Firmicutes
Cyanobacteria
Verrucomicrobia
Gemmatimonadetes
Armatimonadetes
Chloroflexi
unclassified
sample



OTU taxonomy

Sample metadata



Phylum	mean abundance
Proteobacteria	35.40%
Actinobacteria	23.20%
Bacteroidetes	17.90%
Acidobacteria	10.10%
Firmicutes	7.07%
Cyanobacteria	1.97%
Verrucomicrobia	1.72%
Gemmatimonadetes	1.30%
unclassified	0.55%
Armatimonadetes	0.44%
Chloroflexi	0.42%

Summary

1)Create data table with each axis as a colum

2)Add OTU taxonomy

3)Add sample metadata to data table

4)Order taxonomic groups

5)Plot with ggplot2

Extended example & excercises

https://github.com/surh/scip_barplot

¡Gracias!