

MB590-012
Microbiome Analysis
Exploratory Analysis Practicum

Dr. Christine Hawkes

NC STATE UNIVERSITY

Today's goal: practice exploratory analysis

- Alpha diversity
 - Calculate metrics, plot curves
- Beta diversity
 - Unconstrained/constrained ordination, core microbiome
- New skills (optional)
 - Partition variance in beta-diversity due to environmental vs. spatial variables
 - Partition beta-diversity into turnover and nestedness components
 - Compare ordination outcomes


The data

MOLECULAR ECOLOGY

SPECIAL ISSUE: THE HOST - ASSOCIATED MICROBIOME: PATTERN, PROCESS AND FUNCTION

 Full
Access

Soil abiotic variables are more important than Salicaceae phylogeny or habitat specialization in determining soil microbial community structure

Sonya Erlandson , Xiaojing Wei, Jessica Savage, Jeannine Cavender-Bares, Kabir Peay

First published: 30 March 2018 | <https://doi.org/10.1111/mec.14576> | Citations: 27

- Dryad data archive:

<https://datadryad.org/stash/dataset/doi:10.5061/dryad.5f24ks4>

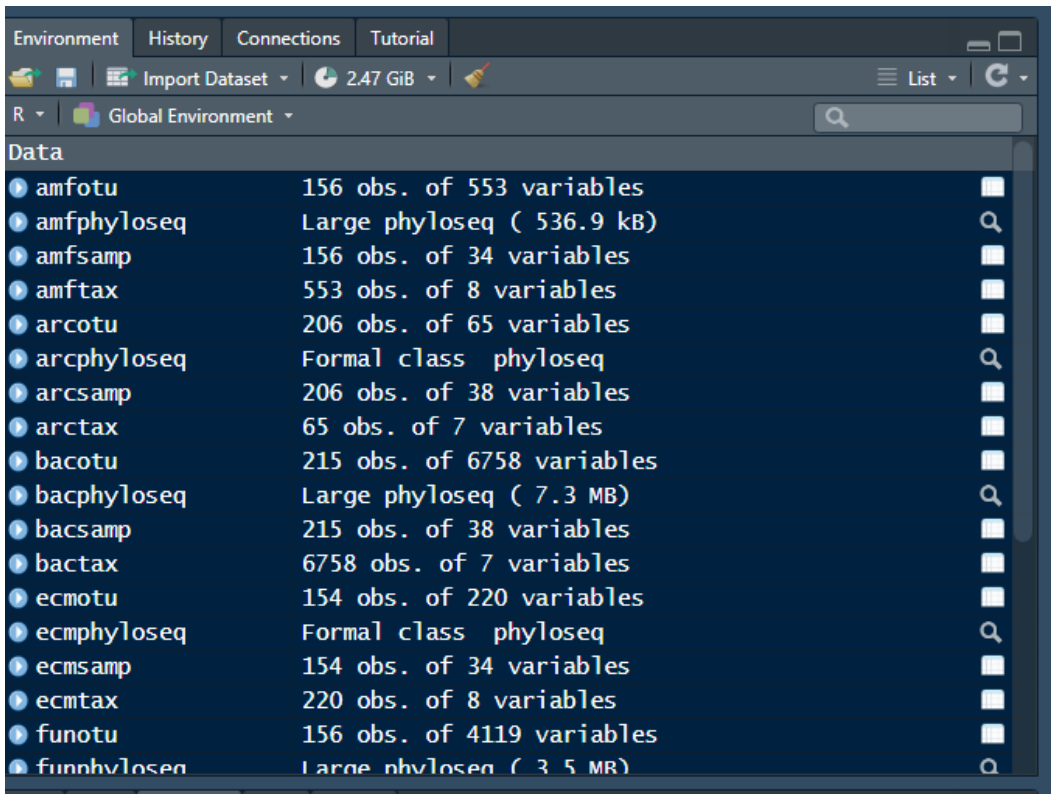
The data

- Factors
 - Treatment → common garden sites
 - D = upland, W=wetland
 - Ecology → habitat specialization of willow species
 - u = upland specialist, w= wetland specialist, i = generalist
 - Plant species (willows) and genotypes
- Environmental variables
 - Soil properties (water table depth, Nmin, NO₃, NH₄, pH)
 - Plant properties (height plus many traits)
- Spatial variables (lat, lon)

The data

```
The taxonomic group and fungal guilds included in this RData are:  
Fungi (ITS)  
Archaea (16S)  
Bacteria (16S)  
#as subsets of the fungal otu table, determined by FUNGuild:  
Arbuscular mycorrhizal fungi (ITS)  
Ectomycorrhizal fungi (ITS)  
Saprotrophic fungi (ITS)  
Pathogenic fungi (ITS)
```

Each group/guild has 4 datasets:
a RAREFIED OTU table,
a taxonomy table,
sample metadata,
and a phyloseq object combining the three separate datasets.



Switch to html

HPC notes (Rachel)

- Login Node
 - Transferring files between local machine + HPC or to working directory (e.g., scp, sftp, cp)
 - Downloading files (e.g., from GitHub)
 - Submit a job
 - Use batch script with job details (e.g., “submit.csh” from tutorial)
 - Allows access to proper node type for computationally intense processes → **compute node**
- Interactive Node
 - Debugging
 - Sections of script (e.g., testing file paths, redirecting plot outputs)
 - Use subset of full data
- Compute Node
 - Accessed through submission of batch script for your application/R script