Biodiversity across Scales:

Mapping taxonomic, phylogenetic, and functional diversity with eDNA, field surveys, and remote sensing

BIOSCAPE
Biodiversity Survey of the Cape

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Motivation

How do eDNA, field, and remote sensing observations of biodiversity **relate across space and time**?

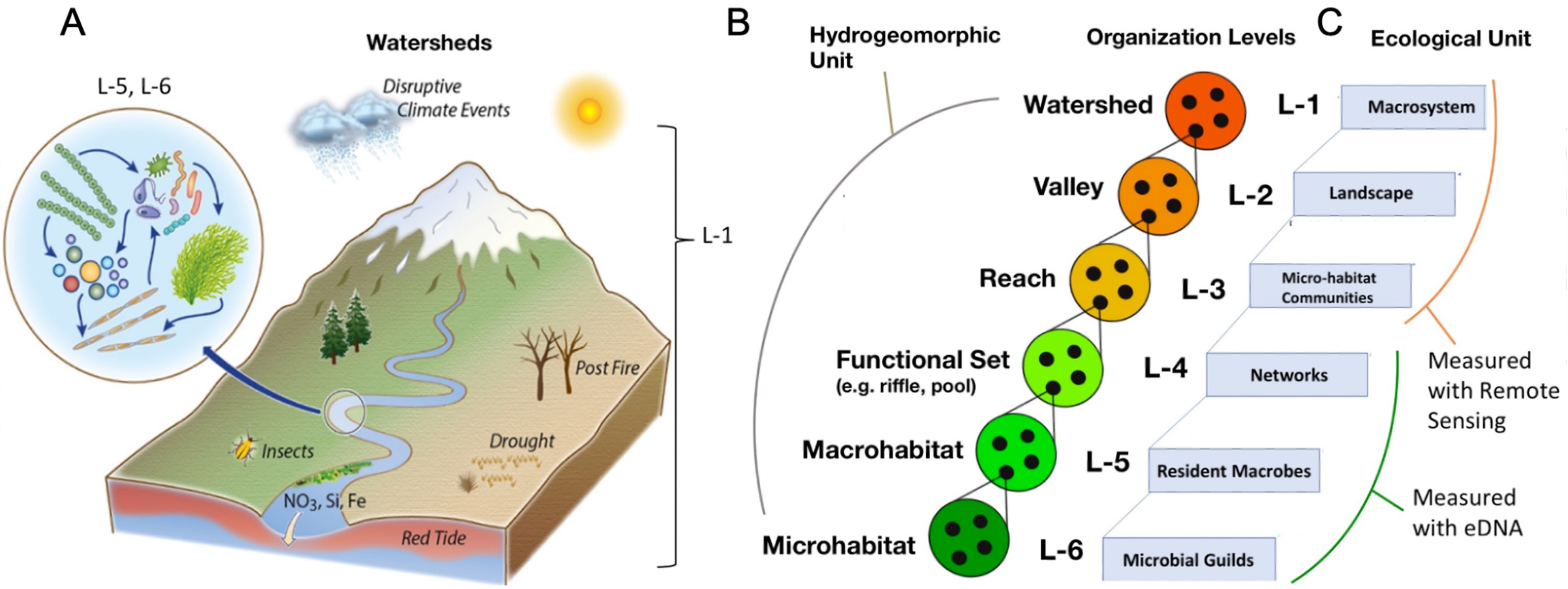


Image credit to M. Newcomer and D. Swantek (LBNL) as part of collaborations for similar work in the Russian River (CA) watershed.

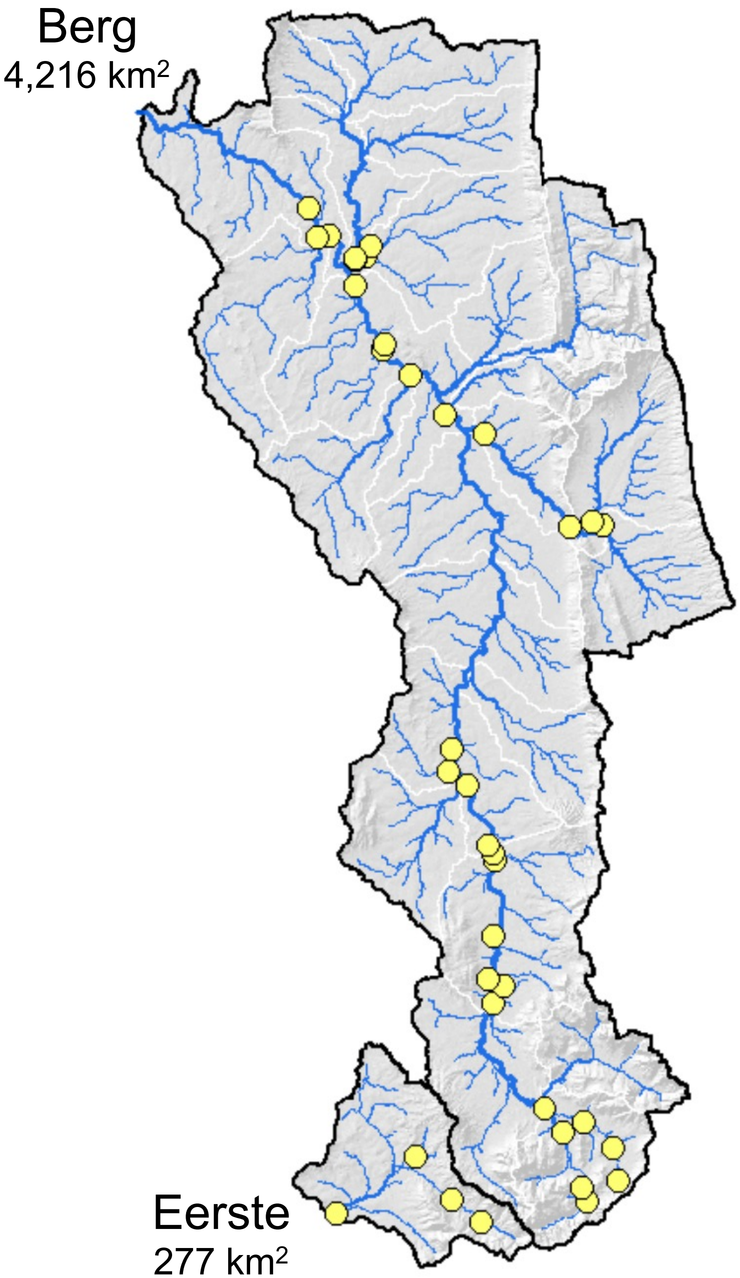
Project Objectives

Question	Hypothesis	Significance
RELATION: How are phylogenetic, taxonomic, and functional diversity related to each other?	(H1): Phylogenetic, taxonomic, and functional diversity **are directly related** to each other along the Berg and Eerste River systems.	Map biodiversity consistently, globally, and at regular intervals using remote sensing
SPACE: How does the hydrologic structure of watersheds organize phylogenetic, taxonomic, and functional diversity spatially?	(H2) Spatial dynamics, flow pathways, and functional process zones **organize** phylogenetic, taxonomic, and functional diversity spatially such that measures of biodiversity are **scale dependent**	As watersheds change and/or are modified, spatial patterns in biodiversity are also expected to change.
TIME: How do hydroclimatic processes influence the temporal signal of phylogenetic, taxonomic, and functional diversity ?	(H3) Stochastic hydrology (seasonality, floods) influence the **temporal signal** of phylogenetic, taxonomic, and functional diversity.	Constrain when and how frequently we need measurements of biodiversity using eDNA and remote sensing

Approach

Nested watershed approach towards sampling.

- Unmix tributary contributions
- Sample across environmental gradients
- Repeat sampling (two field seasons)



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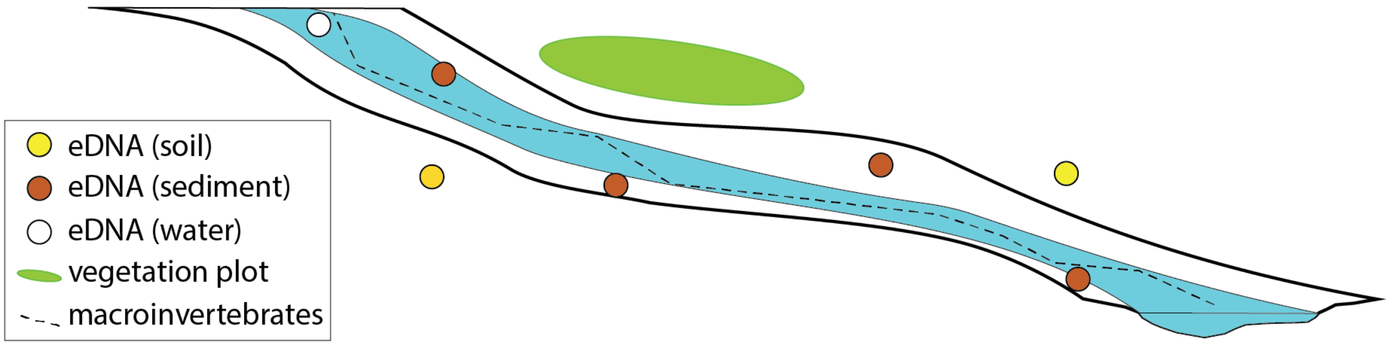
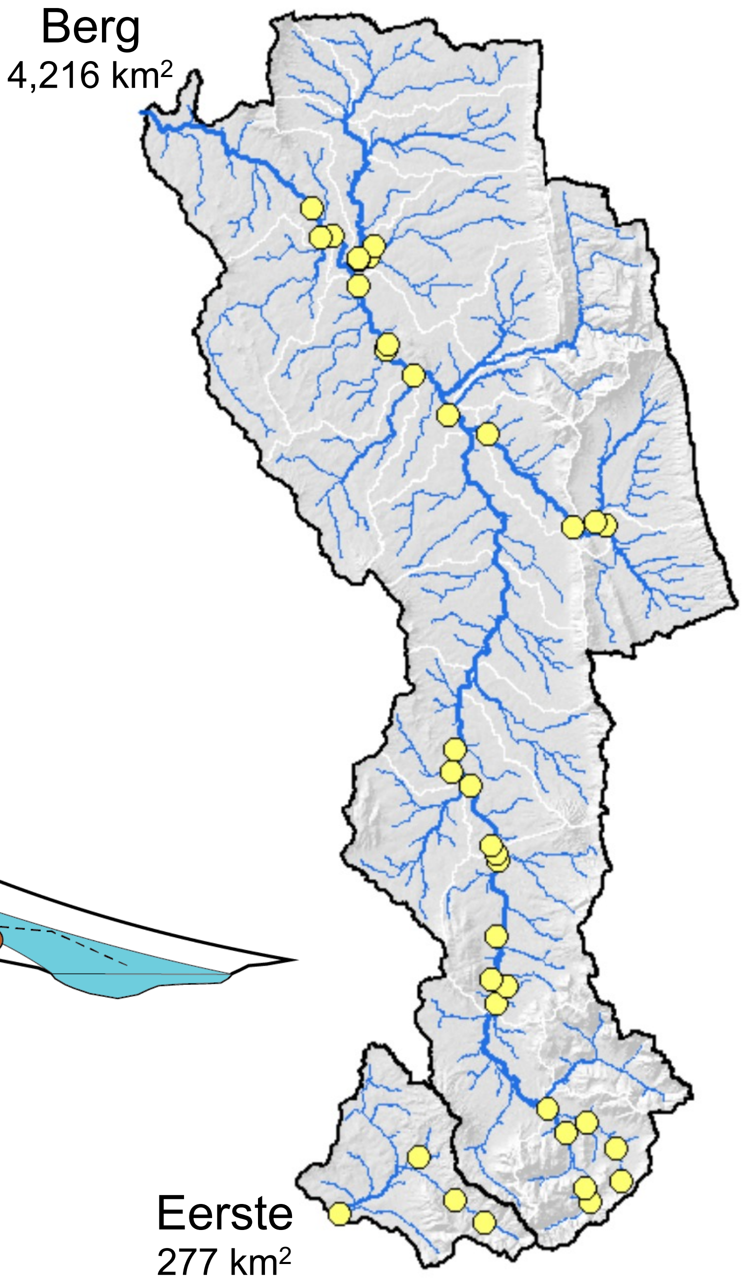


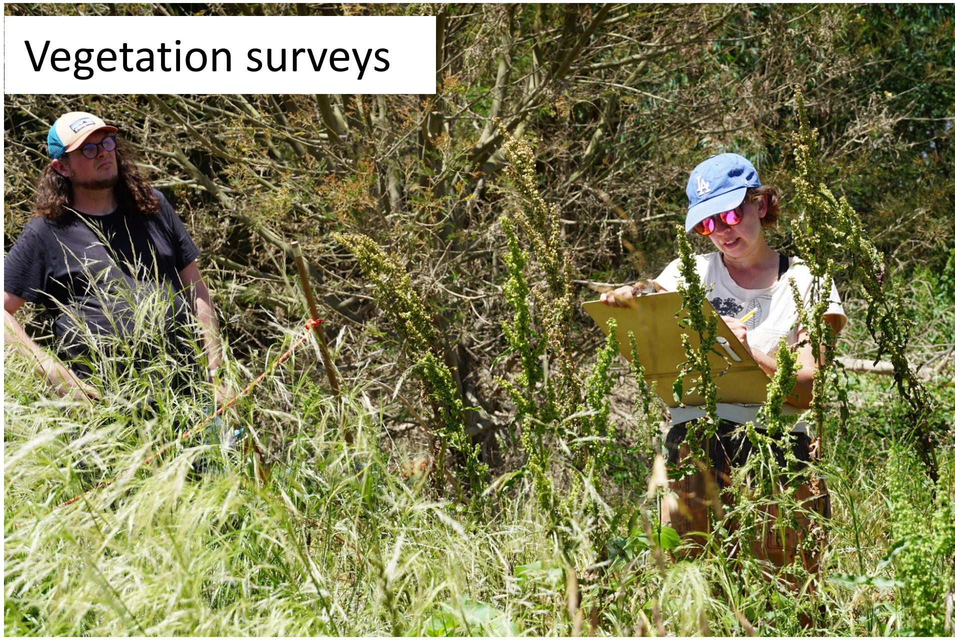


Field Work (2023)

Water samples (eDNA)

Macroinvertebrates

Soil & Sediment samples (eDNA)

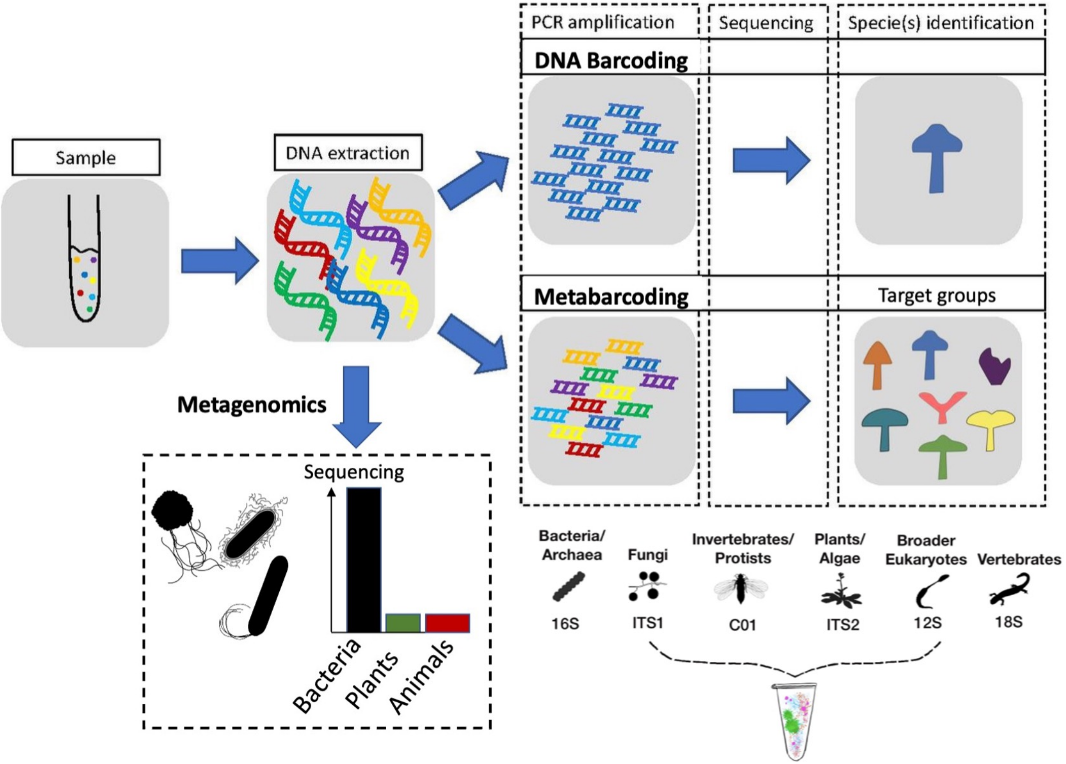


Vegetation surveys

eDNA processing

Each sampling site:

- Sediment @ 4 locations (triplicate)
- Soil @ 1 location (triplicate)
- Water @ some locations
- X2 field seasons



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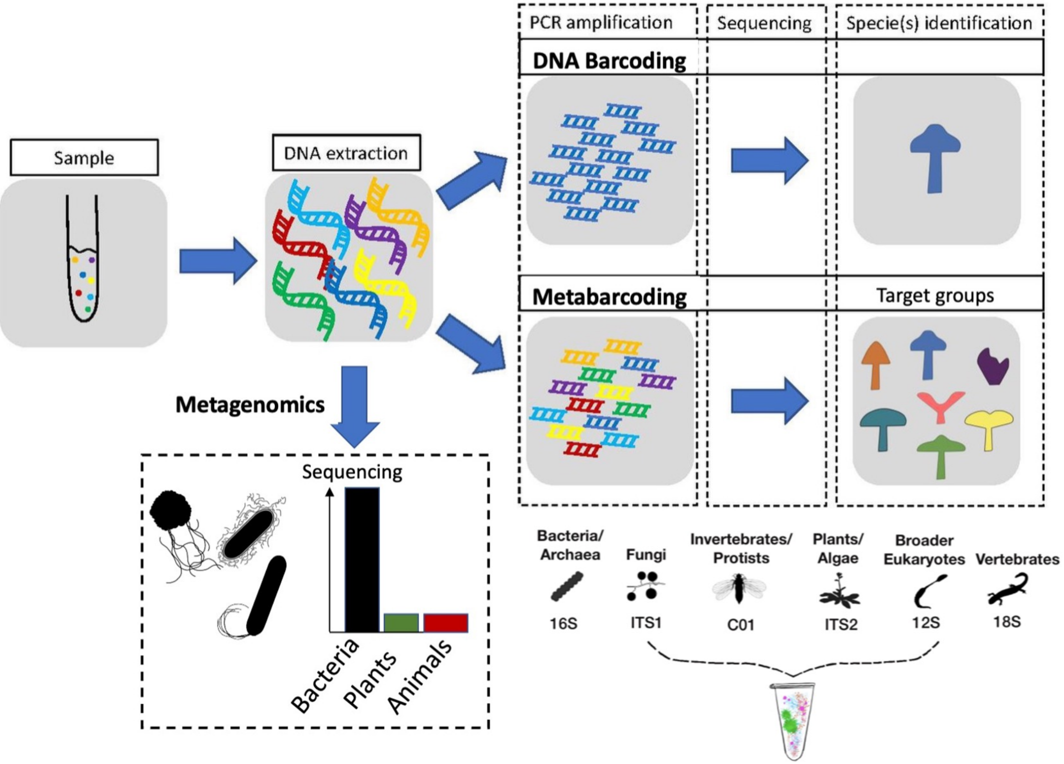
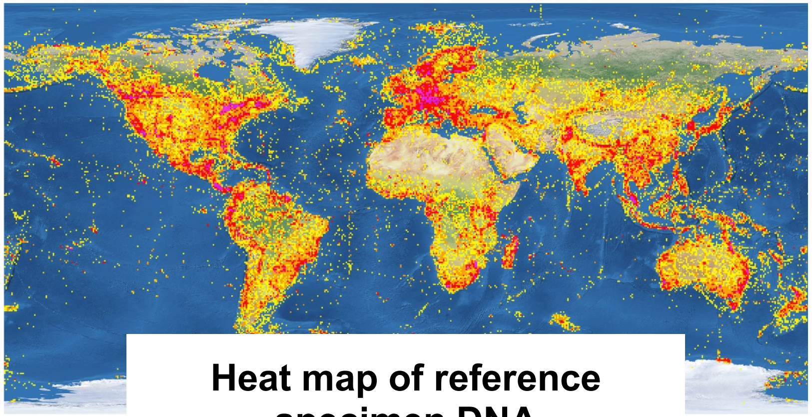


Year 2 focus:

- Processing samples from both field seasons
- First results from metabarcoding **coming this summer**!
- Metabarcoding and metagenomics records 100s-1000s of species per sample
- While libraries are vast, challenge remains that large inventories are needed



Heat map of reference specimen DNA

Remote sensing analysis

	Wavelengths	Spectral resolution	Spatial resolution	Temporal resolution
AVIRIS-NG	380 - 2510 nm	5 nm	0.3-4 m approx.	Single pass
NEON AOP	380 - 2500 nm	10 nm	1-3 m approx.	Single pass

Using NEON to build workflow:

- Quantify how **functional richness** and **functional divergence** vary as a function of scale

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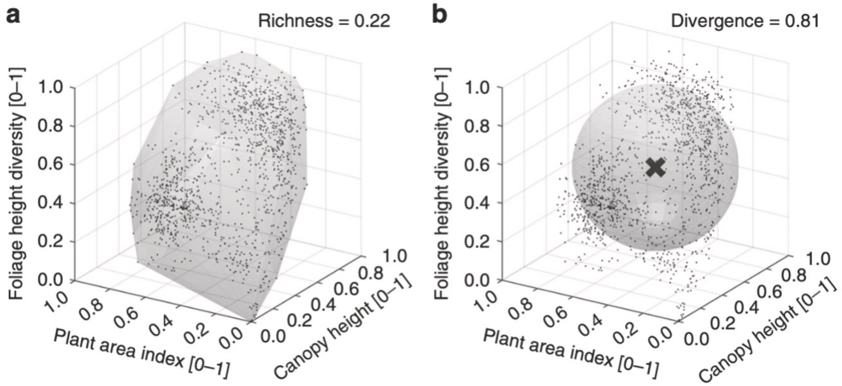
Divergence = spread



Schneider et al. (2017) Nature

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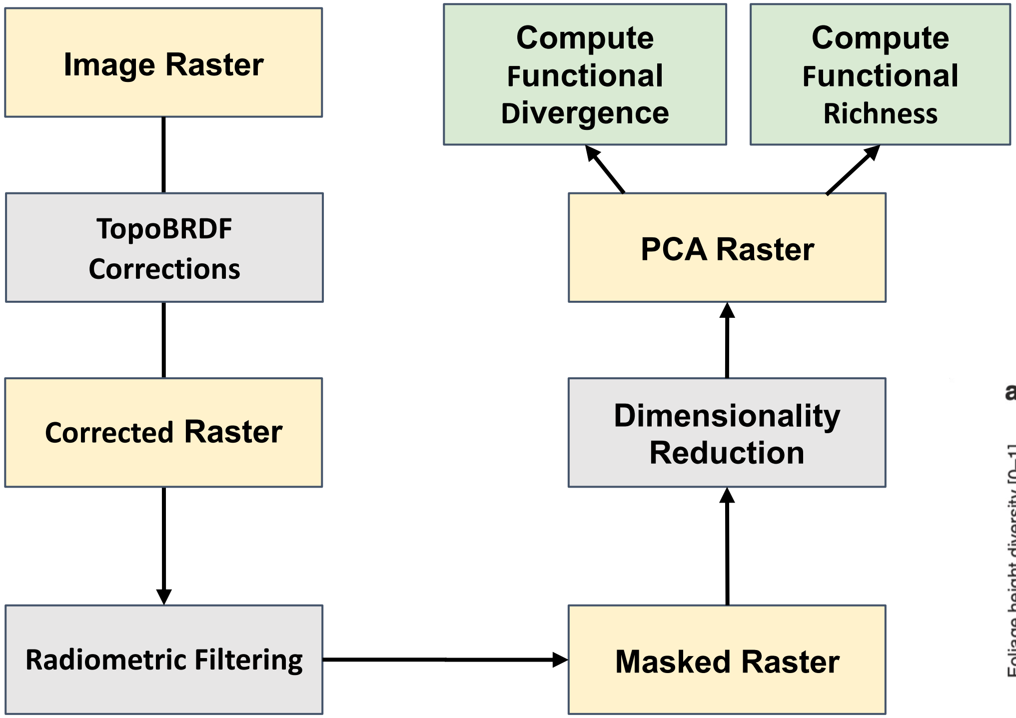

Image Raster

TopoBRDF Corrections

Corrected Raster

Radiometric Filtering

Masked Raster

Dimensionality Reduction

PCA Raster

Compute Functional Divergence

Compute Functional Richness

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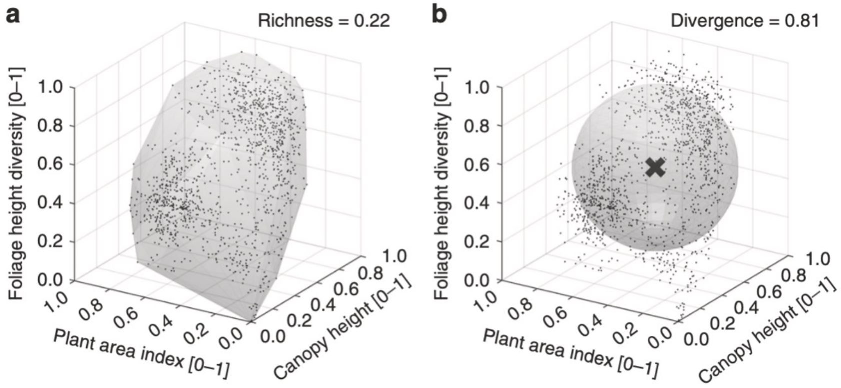

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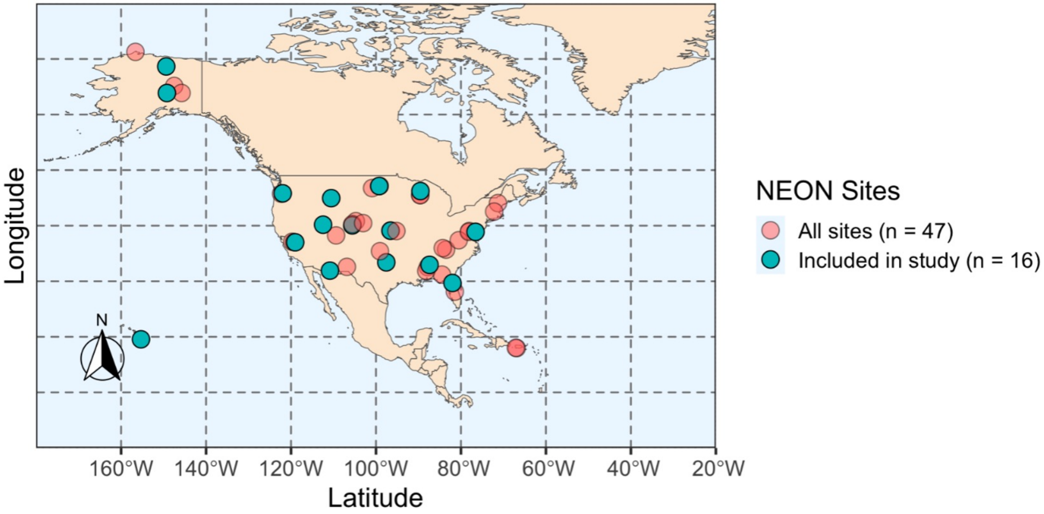
Functional richness



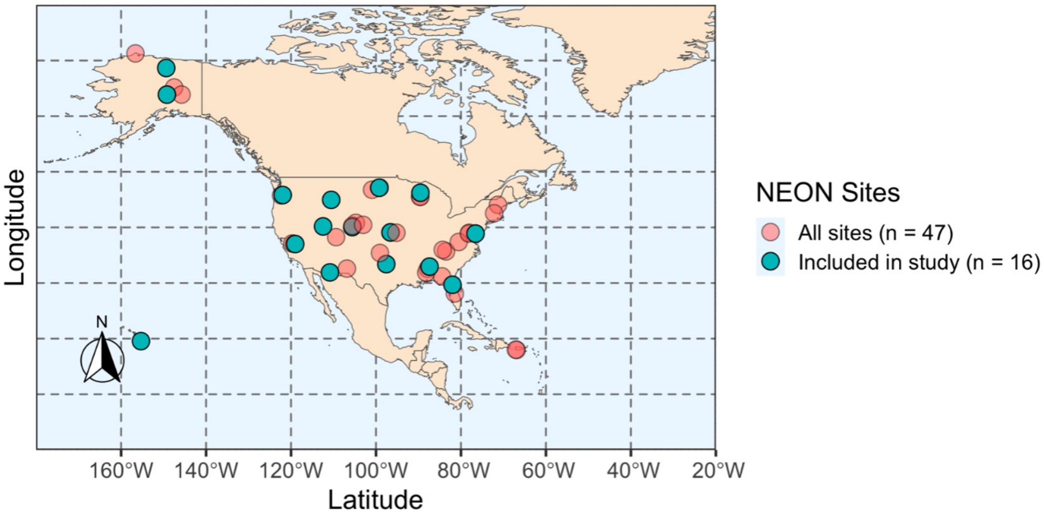
Site selection:

- 16 sites with order 6-12 plots per site

- Inter-plot variations in functional richness are high

- Need for **way to compare** across plots and sites

Functional richness



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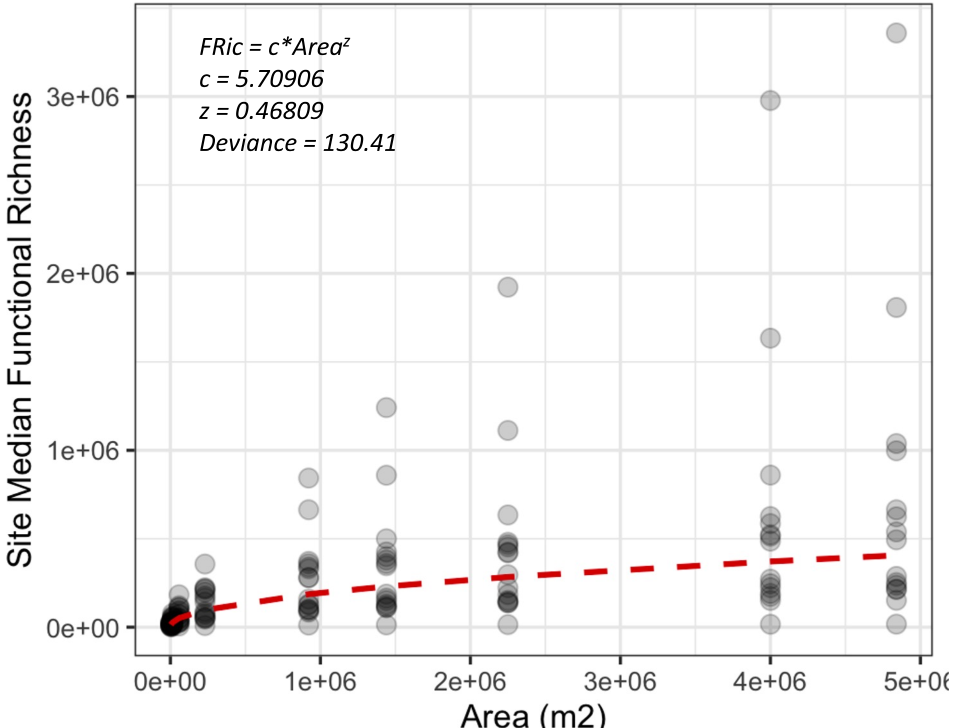


*FRic = c*Area^z*
c = 5.70906
z = 0.46809
Deviance = 130.41

Scaling relationships:

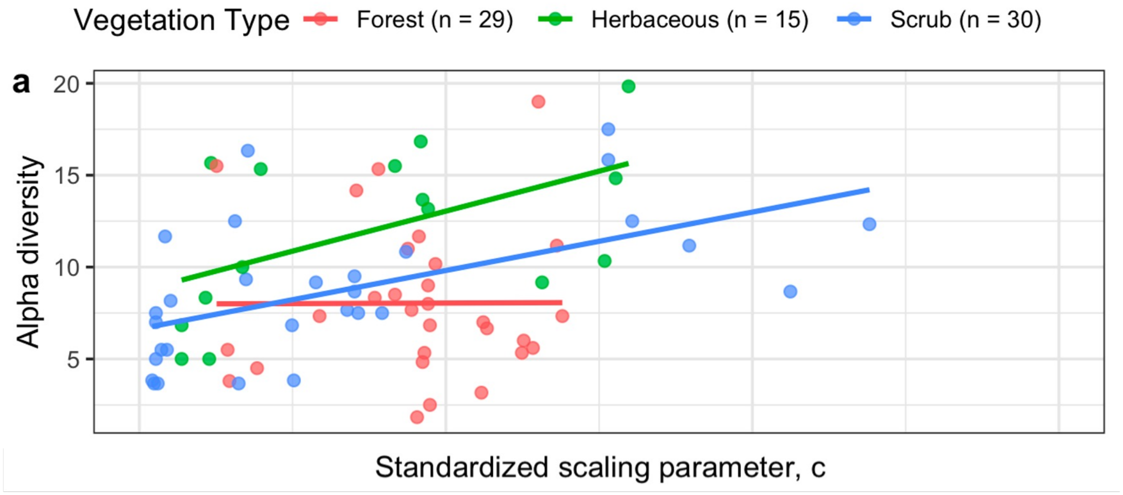
- Sublinear scaling is robust even though it varies a lot
- Median value of z across all plots and sites is ~0.5

$$FuncRich = c_n Area^{z_{ref}}$$

Normalized Coefficient

Functional richness

Functional richness decently correlated with **alpha diversity** for herbaceous and scrub classes (not so much for forested sites)



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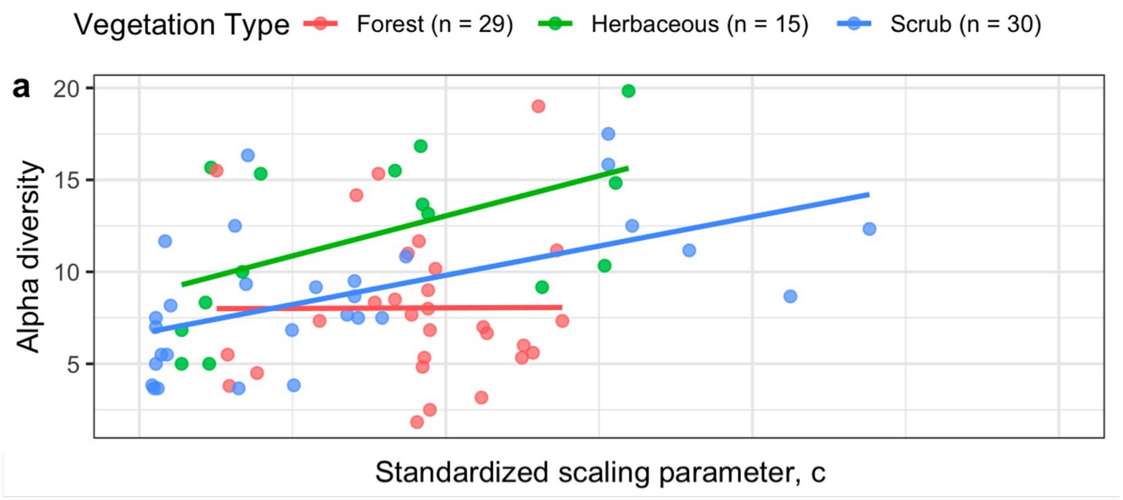

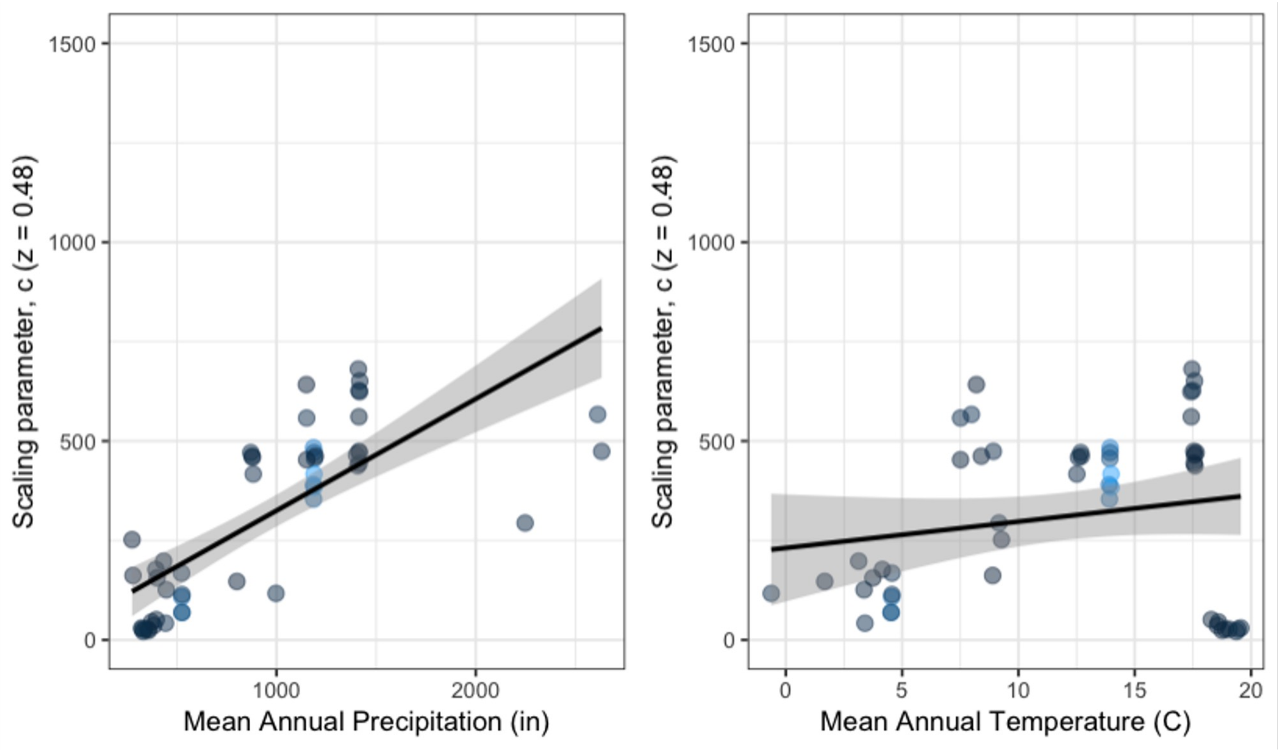

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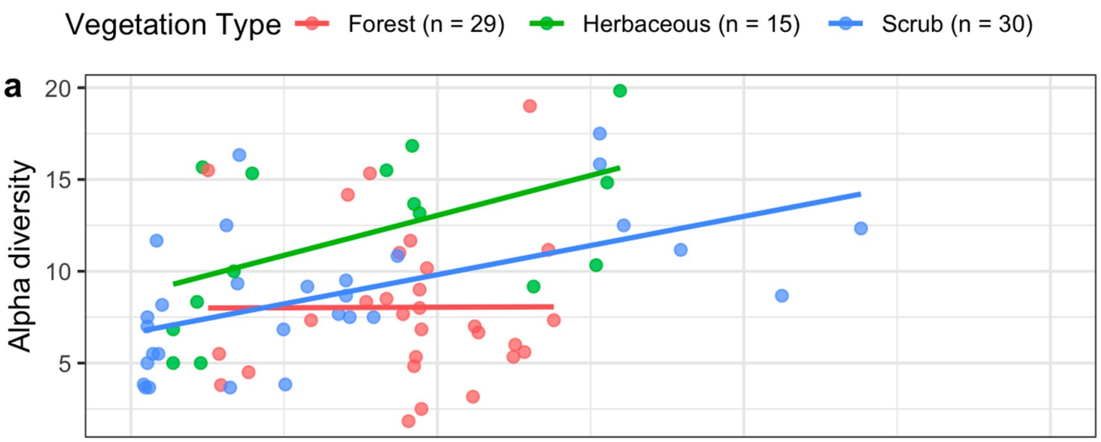
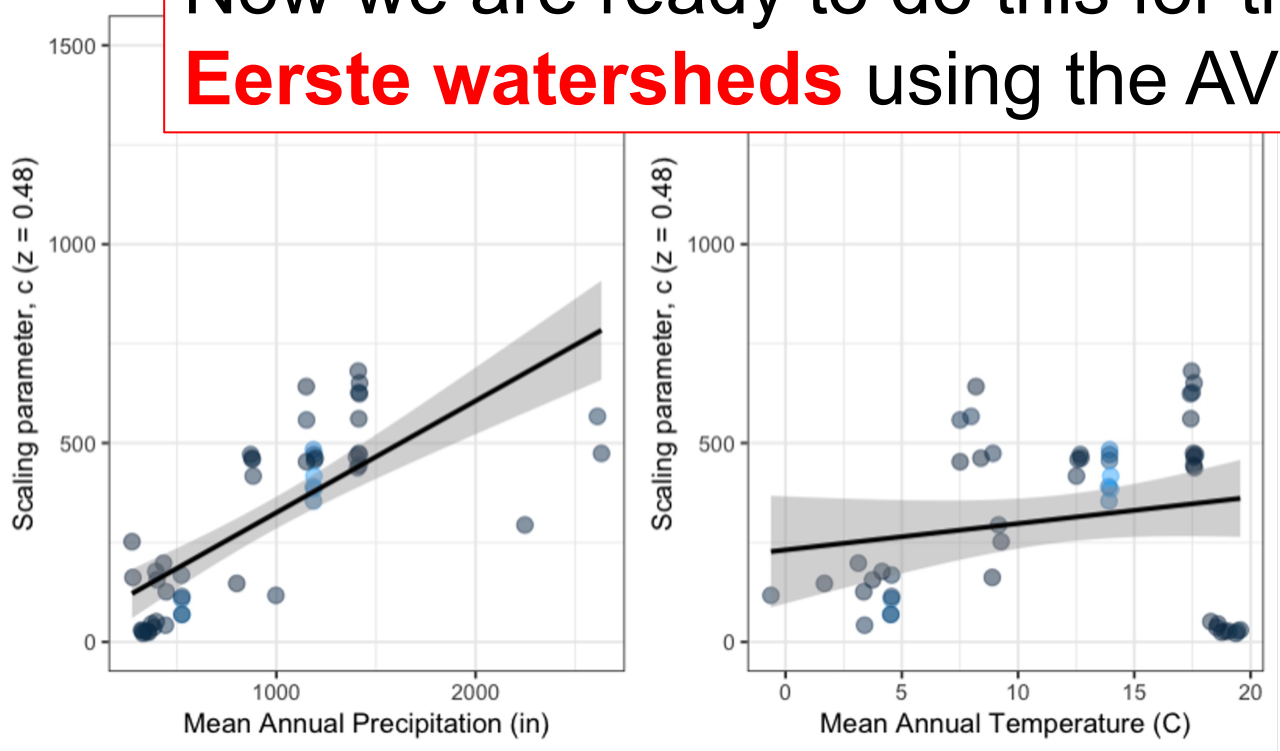


Now we are ready to do this for the **Berg** and **Eerste watersheds** using the AVIRIS-NG data



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Project Status

Year 1	Year 2	Year 3
Field surveys/collections #1	Field surveys/collections #2	Manuscript #3: Berge / Eerste River eDNA
Make new contacts with South African partners	Maintain and make new contacts with South African partners	Work with South African partners to co-produce useful artifacts
Build inventory of expected genera at sampling sites and revise field protocols	eDNA processing (DNA extraction and metabar coding)	Remote sensing package release
Begin to develop remote sensing pipeline in Python	Remote sensing workflow finalized (begin building package)	Develop new ideas for using these data when interrogating disturbance dynamics
Manuscript #1: eDNA analysis of relate work in the Santa Monica Mountains (in revision now)	Manuscript #2: Functional richness across NEON sites (in prep now)	Manuscript #4: Berg / Eerste spatio-temporal analysis of functional traits
	Collaborator Update / Meet-up at end of month	

Much thanks to our sponsors and collaborators