Monitoring Mediterranean Floodplain Restoration Using Multi-Sensor Fusion And Environmental DNA

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What We Have Learned So Far

1 Floodplain biodiversity is driven by species replacement rather than richness differences

2 Riparian patches increase regional diversity through species turnover

3 Through generalized dissimilarity modeling, remote sensing datasets may be able to model species turnover across floodplains undergoing restoration

Introduction

California's 30 x 30 commitments require significant investment in areas of special interest to biodiversity conservation and restoration, such as lowland floodplains. Despite their relatively small area, these Mediterranean floodplains provide outsized contributions to regional biodiversity, prompting California to invest in their restoration.

Advances in remote sensing, combined with the use of multi-locus metabarcoding to quantify full tree of life taxonomic and functional community composition, may allow for the monitoring of floodplain biodiversity throughout the process of restoration activities.

Objectives

Using a gradient-based transect sampling design coupling multi-locus metabarcoding, remote sensing, and field-based measurements across a floodplain undergoing restoration, we seek to:
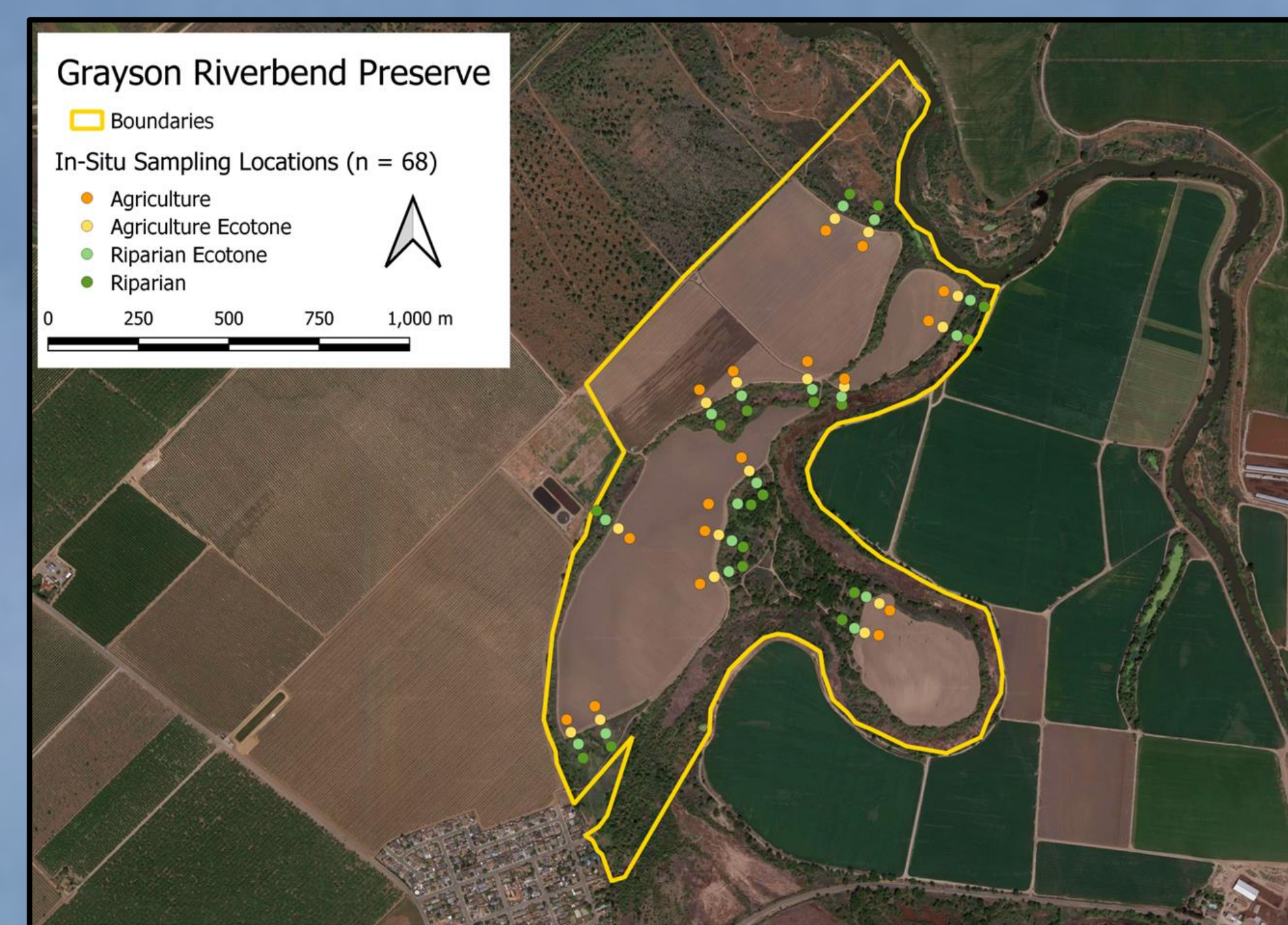
1) Quantify the diversity of species across an agricultural-riparian matrix prior to riparian restoration.
2) Classify organisms into functional groups based on their ecosystem function for assessment of biodiversity and ecosystem function relationships.
3) Test the ability of remote sensing metrics to elucidate biodiversity patterns and processes.

Study Area

The Grayson Riverbend Preserve is a 285-acre riparian restoration site which was previously under agricultural cultivation for silage corn production until November 2021. The land was tilled and fallowed until April 2022, when restoration work began. Our study collected samples between April-May 2022, just as assisted vegetation plantings began on site.

Methods

Grayson Riverbend Preserve

In-Situ Sampling Locations (n = 68)
- Agriculture
- Agriculture Ecotone
- Riparian Ecotone
- Riparian

Boundaries

Sites were sampled along 150m transects using a gradient-directed sampling design to capture the heterogeneity in vegetation, elevation, and soil type across the study area.

The data obtained includes:

- 68 triplicate surface eDNA samples w/ concurrent soil samples to a 15cm depth for total C and N + in-situ soil temperature, moisture, and salinity
- 204 5-min measurements of CO_2 flux from CO_2 chambers
- 13 DJI Phantom 4 flights (photogrammetry)
- 20 Planet SuperDove acquisitions
- 12 Sentinel-2 acquisitions
- 1 AVIRIS acquisition
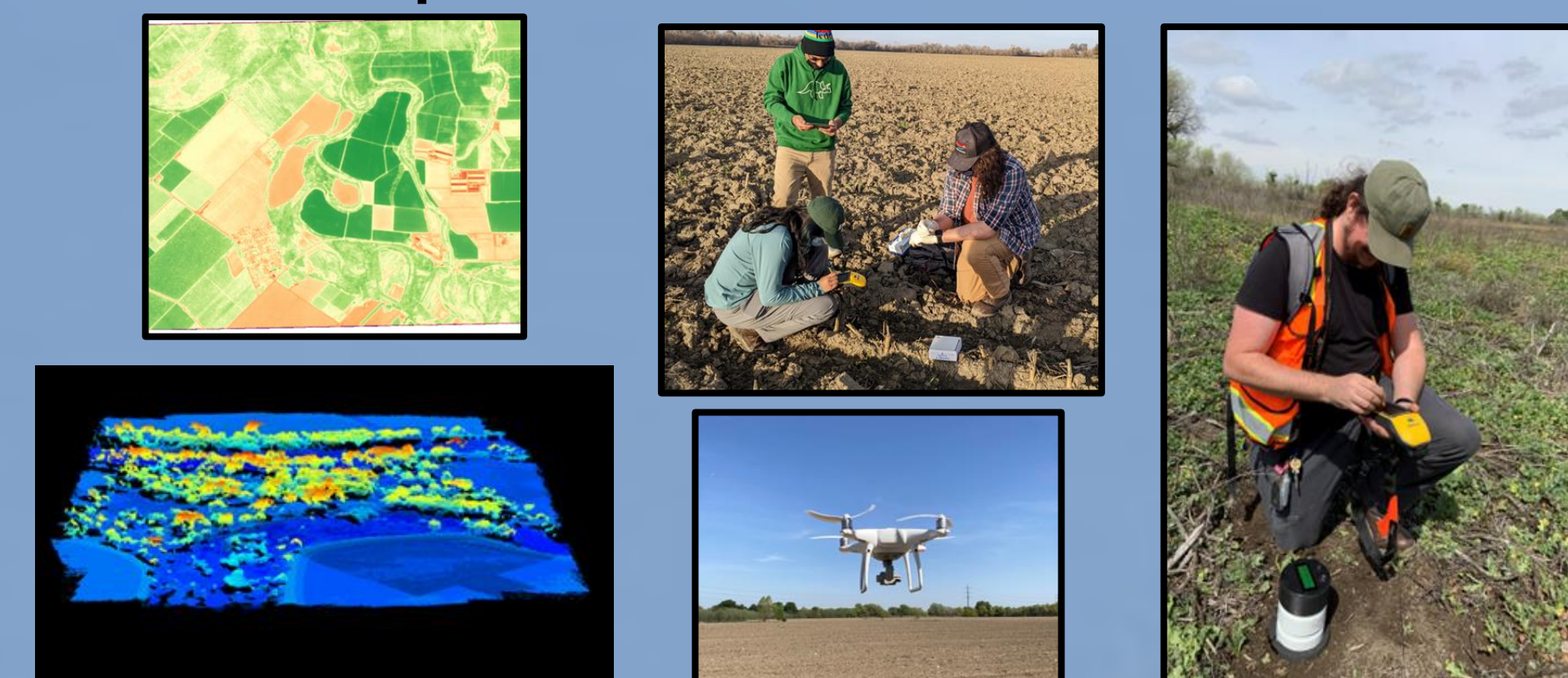
Vegetation indices, PCA and MNF rotations, texture metrics, and spectral diversity metrics from Planet SuperDove, Sentinel-2, and AVIRIS, as well as canopy height models from UAV-based Structure-from-Motion were calculated at 3m, 15.6m, and 20m resolutions. Analysis of total C and N was performed by UC Davis Analytical Lab. Our collaborators with UC Santa Cruz and CALeDNA performed metabarcoding using the 12S, 16S, 18S, CO1, PITS, and FITS primers to capture full tree of life biodiversity.

Results

Soil analysis across transects reveal gradients in soil temperature, moisture and salinity, as well as stepwise changes in C and N.
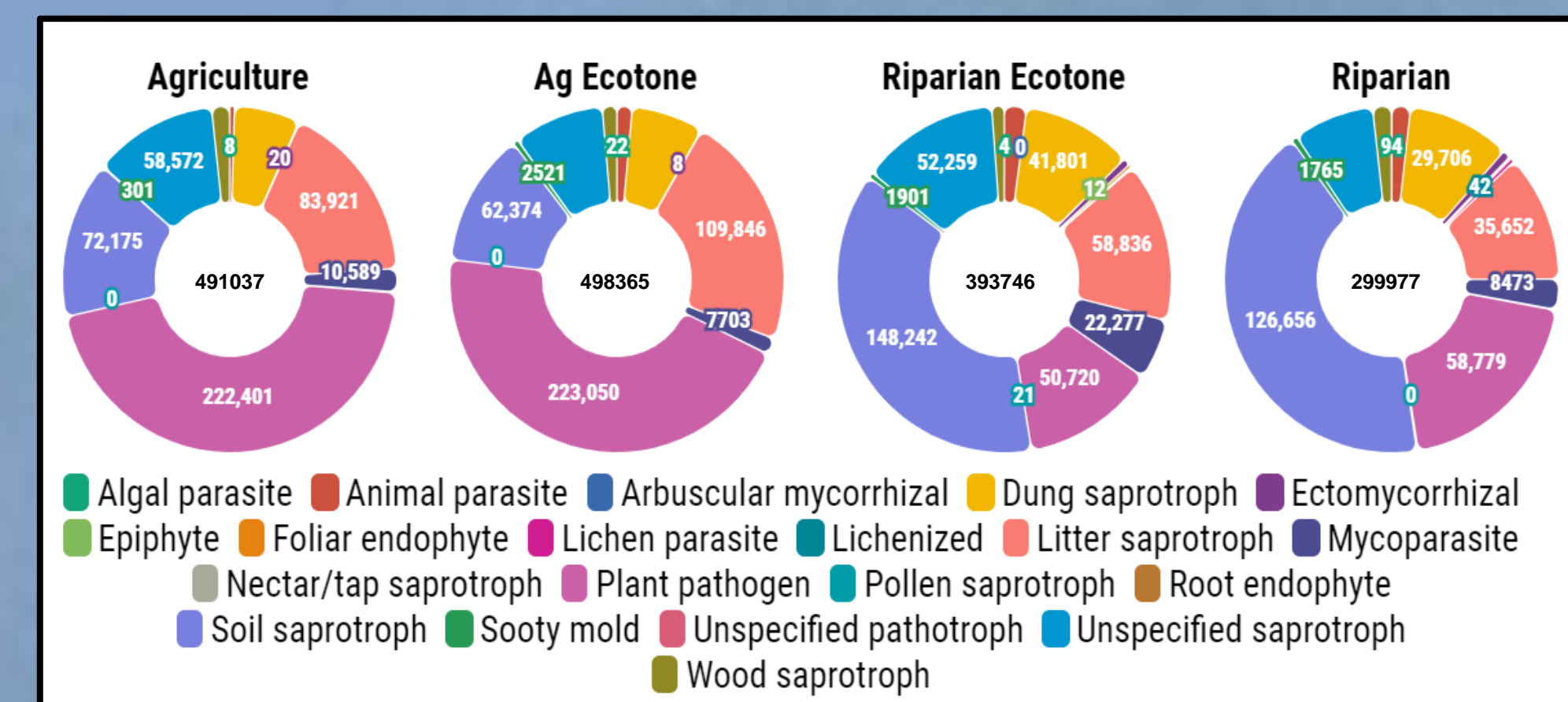
	Agriculture	Ag Ecotone	Riparian Ecotone	Riparian
Total C (Mg/ha)	18.2 (± 3.4)	16.4 (± 5.0)	35.8 (± 14.5)	31.5 (± 9.8)
Total N (Mg/ha)	2.0 (± 0.3)	1.7 (± 0.5)	3.2 (± 1.3)	2.8 (± 0.8)
Soil Temp (°C)	28.5 (± 8.4)	27.1 (± 6.2)	23.7 (± 6.5)	22.1 (± 4.7)
Soil Moisture (m³/m³)	0.079 (± 0.035)	0.115 (± 0.044)	0.168 (± 0.091)	0.239 (± 0.170)
Soil Salinity (dS/m)	0.16 (± 0.024)	0.076 (± 0.067)	0.17 (± 0.21)	0.42 (± 0.81)

Wilcoxon Tests of alpha diversity were not significant between agricultural and riparian patches. However, PERMANOVA of beta diversity revealed significant differences in the composition of species between agricultural and riparian patches across all six primers.

Primer	Df	SS	R^2	F	Pr(>F)
12S	3	1.6624	0.112	1.469	0.043
16S	3	2.1619	0.177	3.7296	0.001
18S	3	2.4928	0.113	2.5384	0.001
CO1	3	2.7629	0.130	2.8777	0.001
FITS	3	3.4793	0.149	3.5683	0.001
PITS	3	2.8837	0.112	2.2369	0.001

This suggests that it is species turnover, rather than richness differences, that drives biodiversity in mixed agricultural-riparian mosaics.

We are also exploring whether these differences in community composition could result in changes in life history strategies that are linked to ecosystem functions.

Agriculture — Ag Ecotone — Riparian Ecotone — Riparian

Legend:
- Algal parasite
- Animal parasite
- Arbuscular mycorrhizal
- Dung saprotroph
- Ectomycorrhizal
- Epiphyte
- Foliar endophyte
- Lichen parasite
- Lichenized
- Litter saprotroph
- Mycoparasite
- Nectar/tap saprotroph
- Plant pathogen
- Pollen saprotroph
- Root endophyte
- Soil saprotroph
- Sooty mold
- Unspecified pathotroph
- Unspecified saprotroph
- Wood saprotroph

We have had some success linking the FungalTraits database to fungal communities (FITS) at the genus level. By linking other primers to databases capturing primary life strategies, we can gain insight into functional roles of organisms across taxa.

Results (cont.)

Remote sensing may aid in providing a synoptic view of beta diversity through generalized dissimilarity modeling (GDM). By modeling compositional dissimilarity as a function of ecological distances between transformed remote sensing predictors, maps of beta diversity can be produced.

Preliminary GDMs of fungal turnover (FITS) using NDVI and MNF rotation from Planet SuperDove imagery and elevation data from airborne LiDAR explain ~35% of the deviance across the Grayson Riverbend Preserve.

Geographic — Environmental
- 2.65%
- 34.78%
- 32.13%
- Unexplained 65.22%
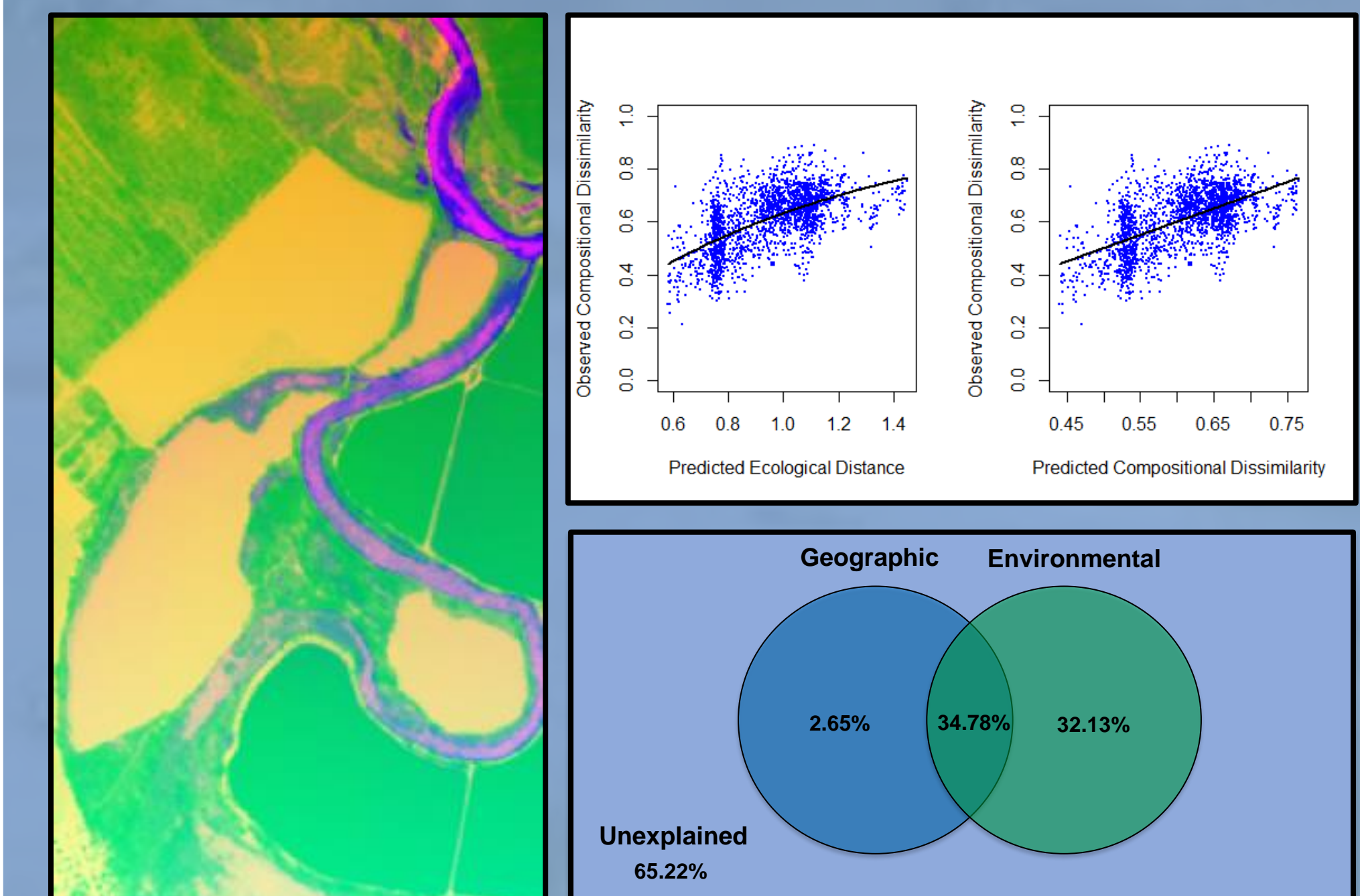
We will continue exploring these modeling approaches to test the relationship between multi-scale remote sensing variables, eDNA, species turnover, and functional turnover.

Acknowledgements