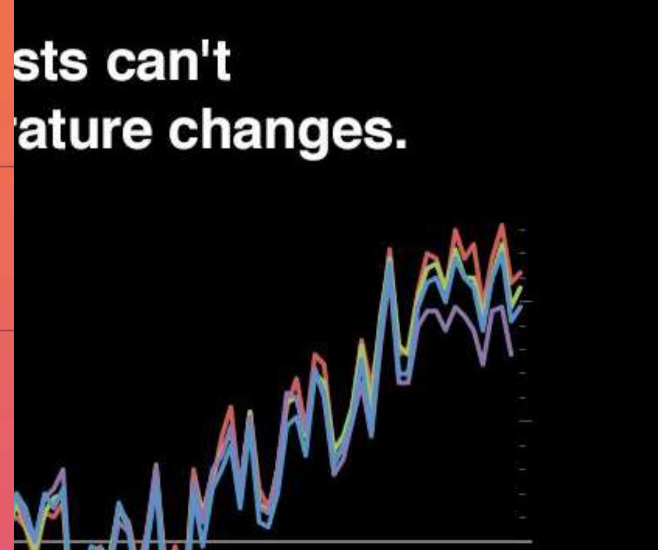
Quantitative Community Ecology in an Era of Global Change:

Integrating Empirical Research, Model Development, and Data Synthesis

Daijiang Li

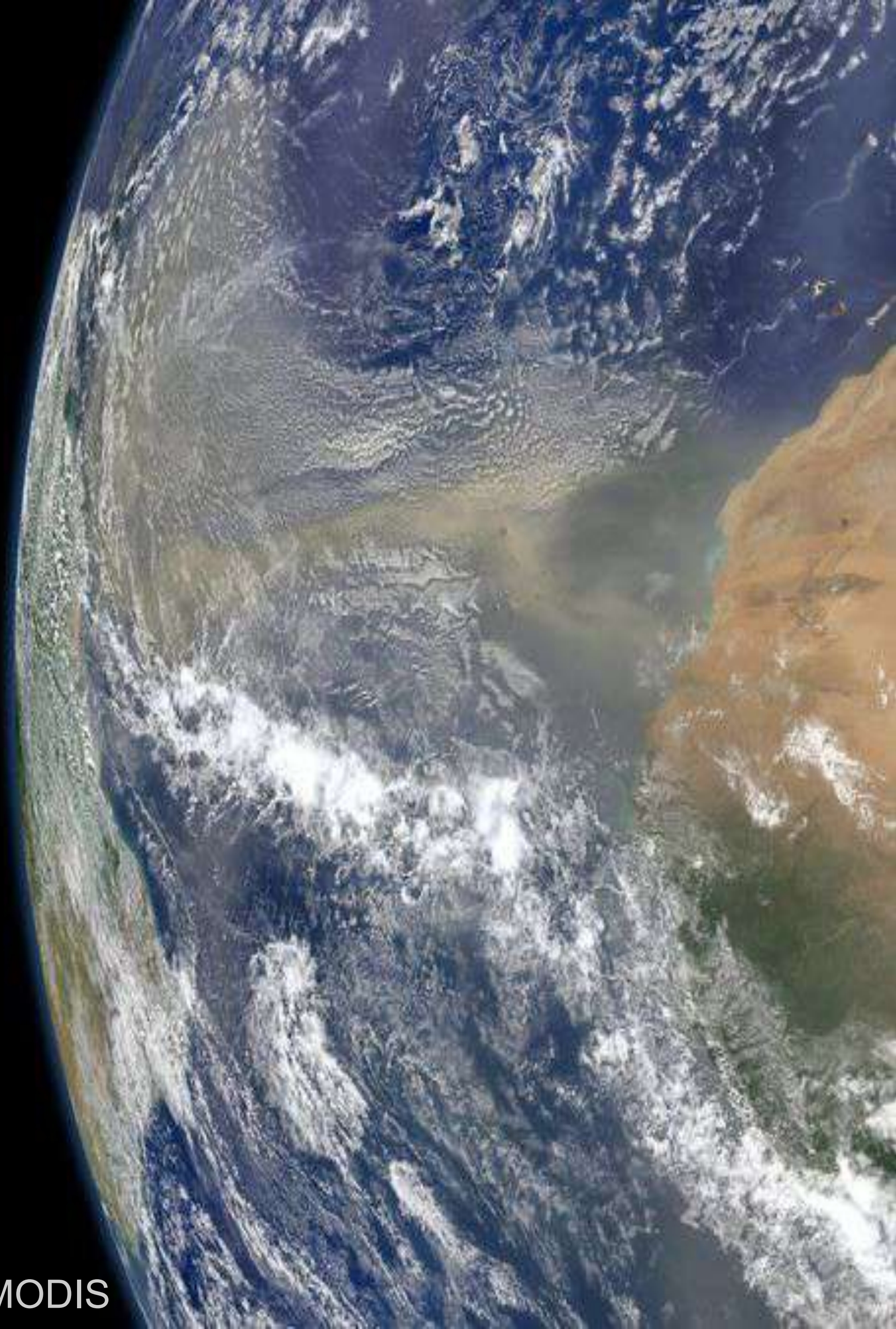
@_djli https://daijiang.name

University of Florida



Global Changes

How have global changes interactively affected plant communities?



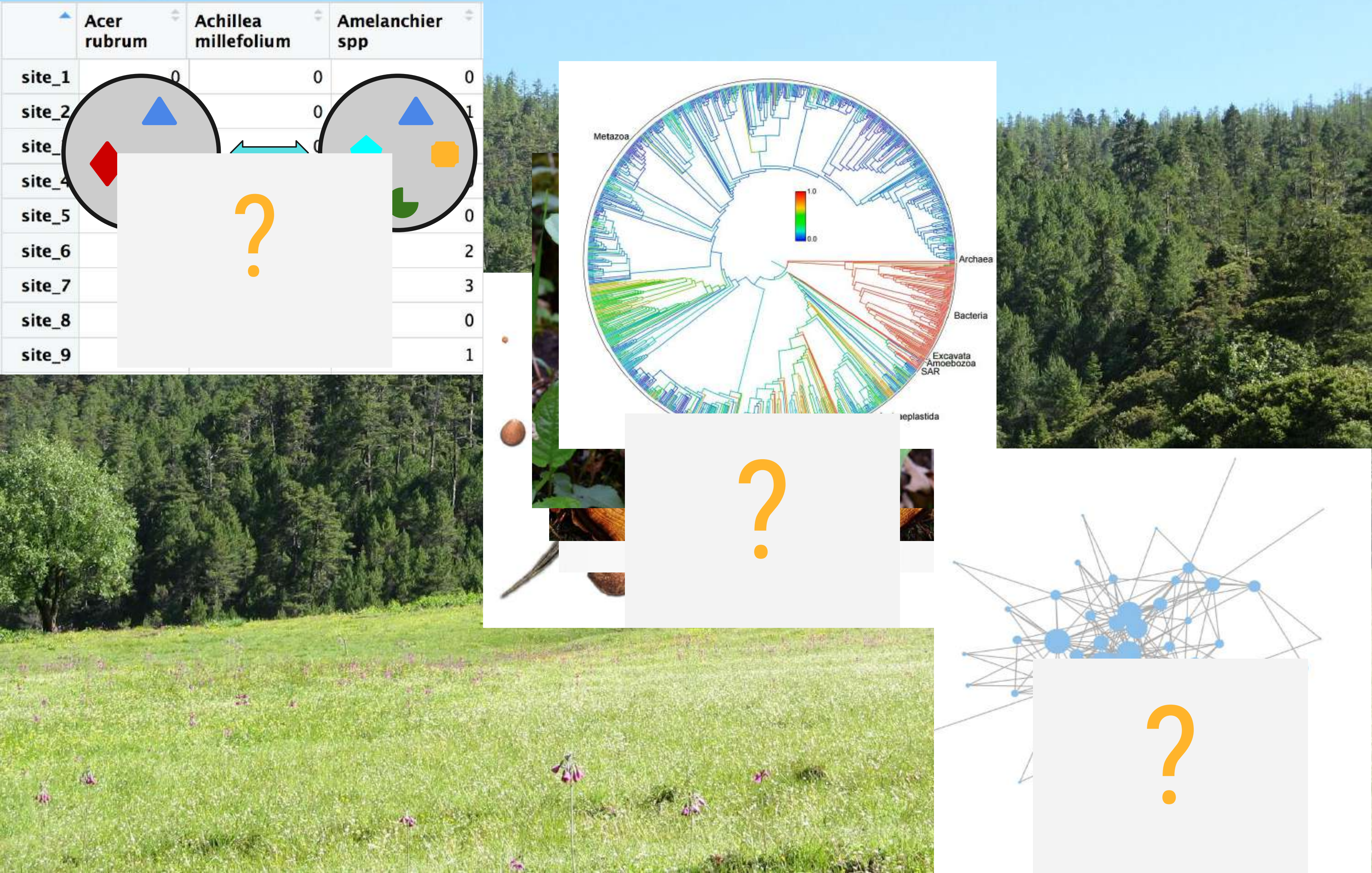
NASA MODIS

Research projects

1. Field research on plant community changes at the regional scale
2. Development of novel statistical models to get more out of field data
3. Analysis of big data to study global changes at the continental scale

Why should we care about plant communities?

Ways to measure a plant community?



Research projects

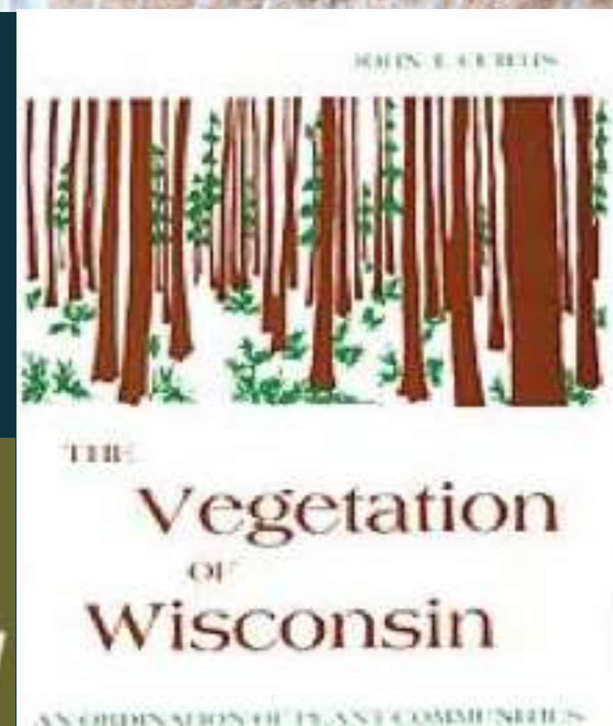
1. Field research on plant community changes at the regional scale
2. Development of novel statistical models to get more out of field data
3. Analysis of big data to study global changes at the continental scale

What do we need?

- A system that has experienced global changes

- Baseline data

John
Curtis
(1913-1961)



University of Wisconsin
Plant Ecology Laboratory


Jack pine
(*Pinus banksiana*)
Northern pin oak
(*Quercus ellipsoidalis*)

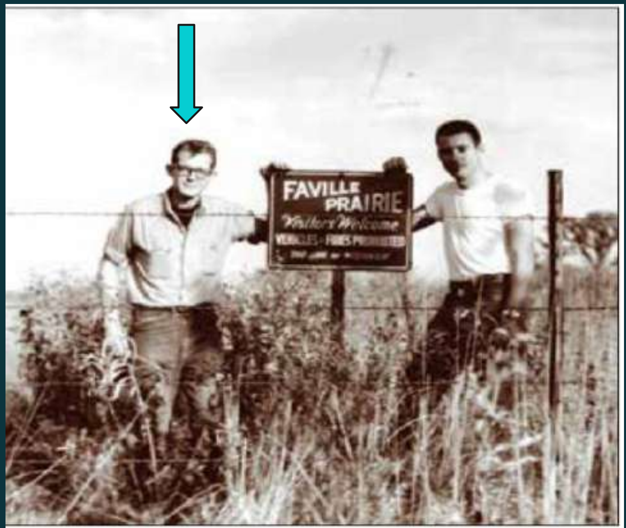
James R. Habeck (1958)

Wisconsin Academy of Science, Arts and Letters

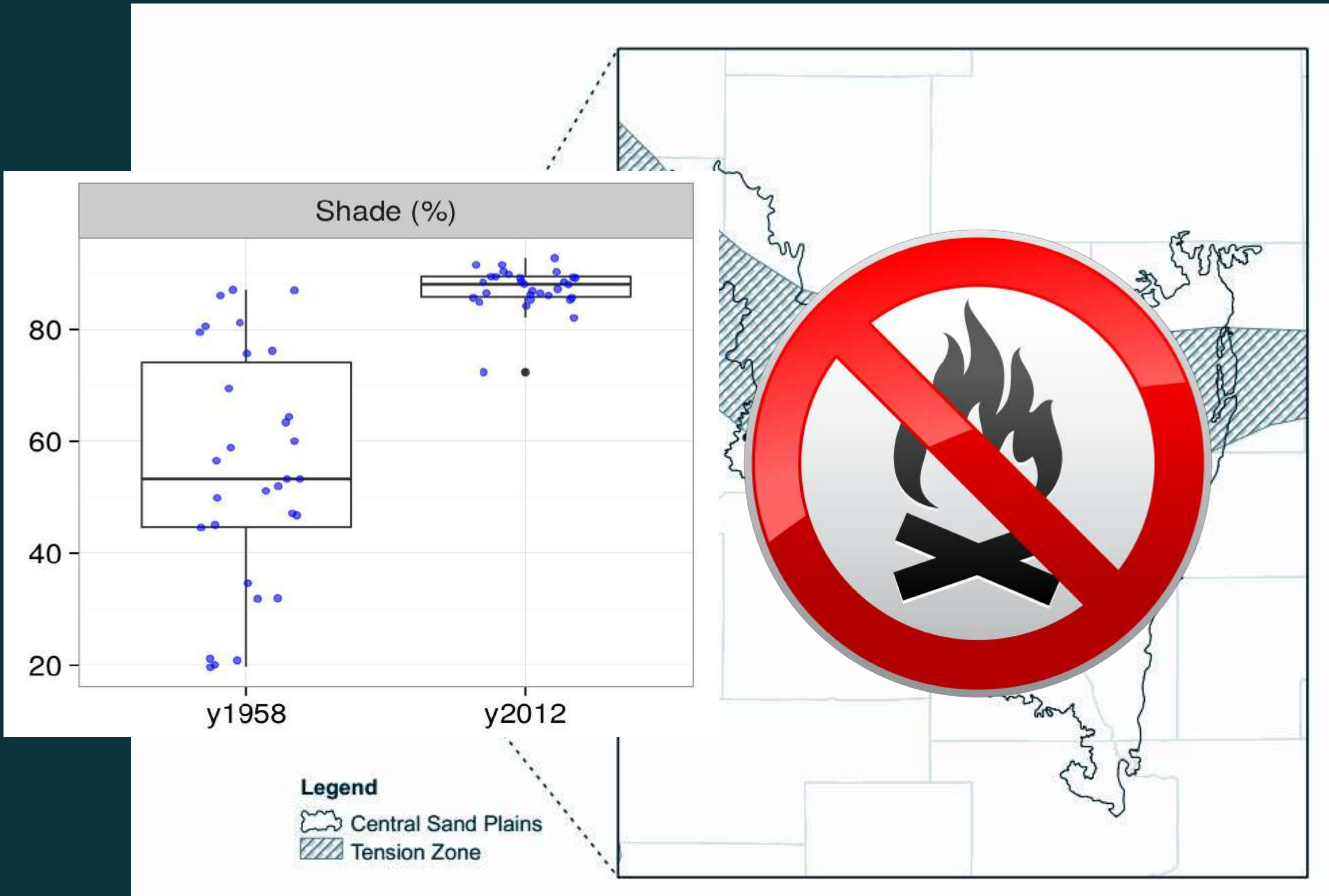
A PHYTOSOCIOLOGICAL STUDY OF THE UPLAND FOREST COMMUNITIES IN THE CENTRAL WISCONSIN SAND PLAIN AREA[1]

JAMES R. HABECK

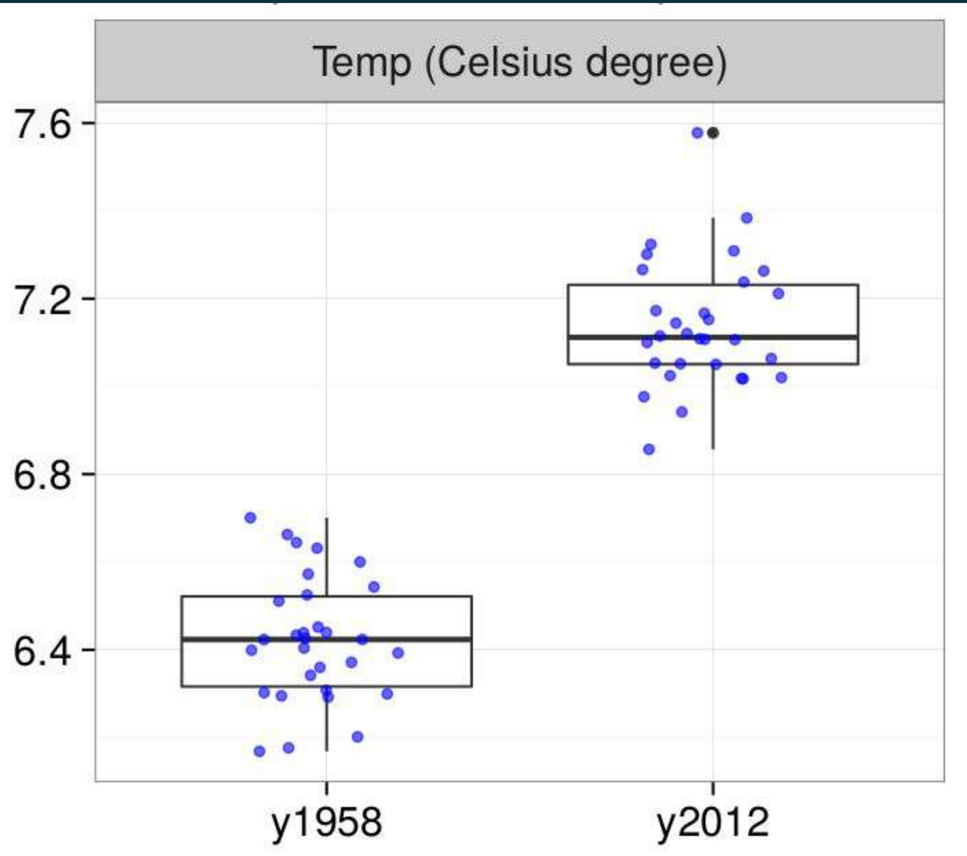
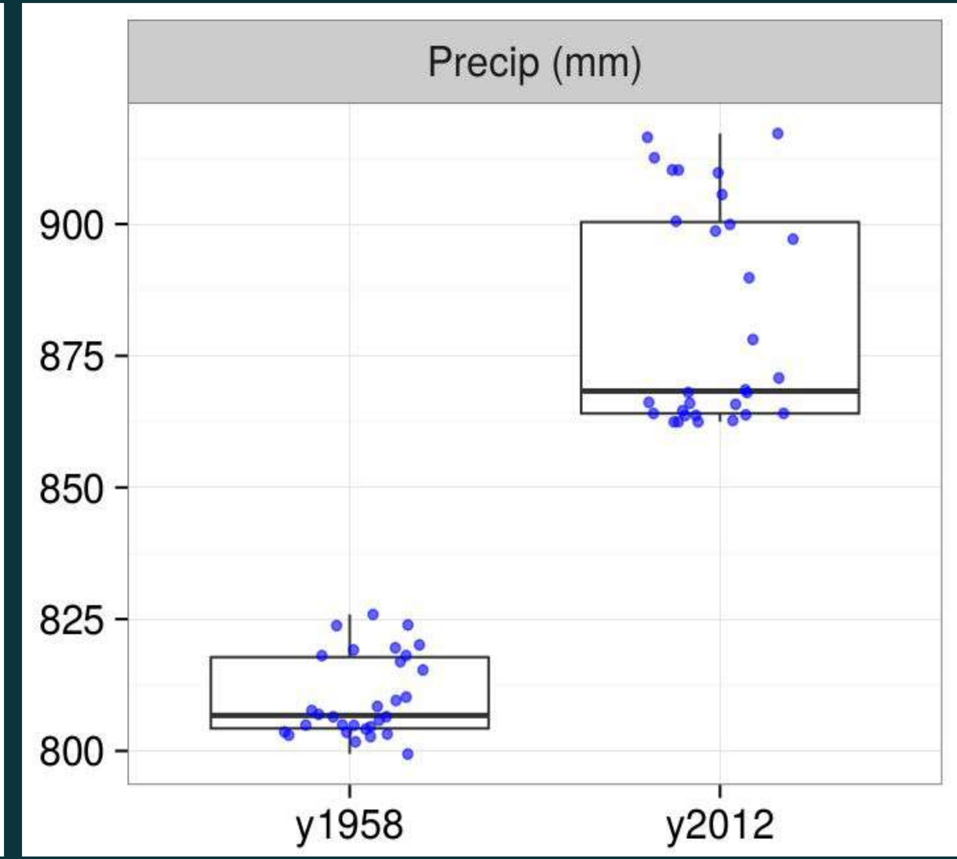
Botany Department, University of Wisconsin, Madison



Jim Habeck (left) in the spring of 1955.



Li & Waller, 2015, *Ecology*


Temp (Celsius degree)
7.6
7.2
6.8
6.4
y1958
y2012

Precip (mm)
900
875
850
825
800
y1958
y2012

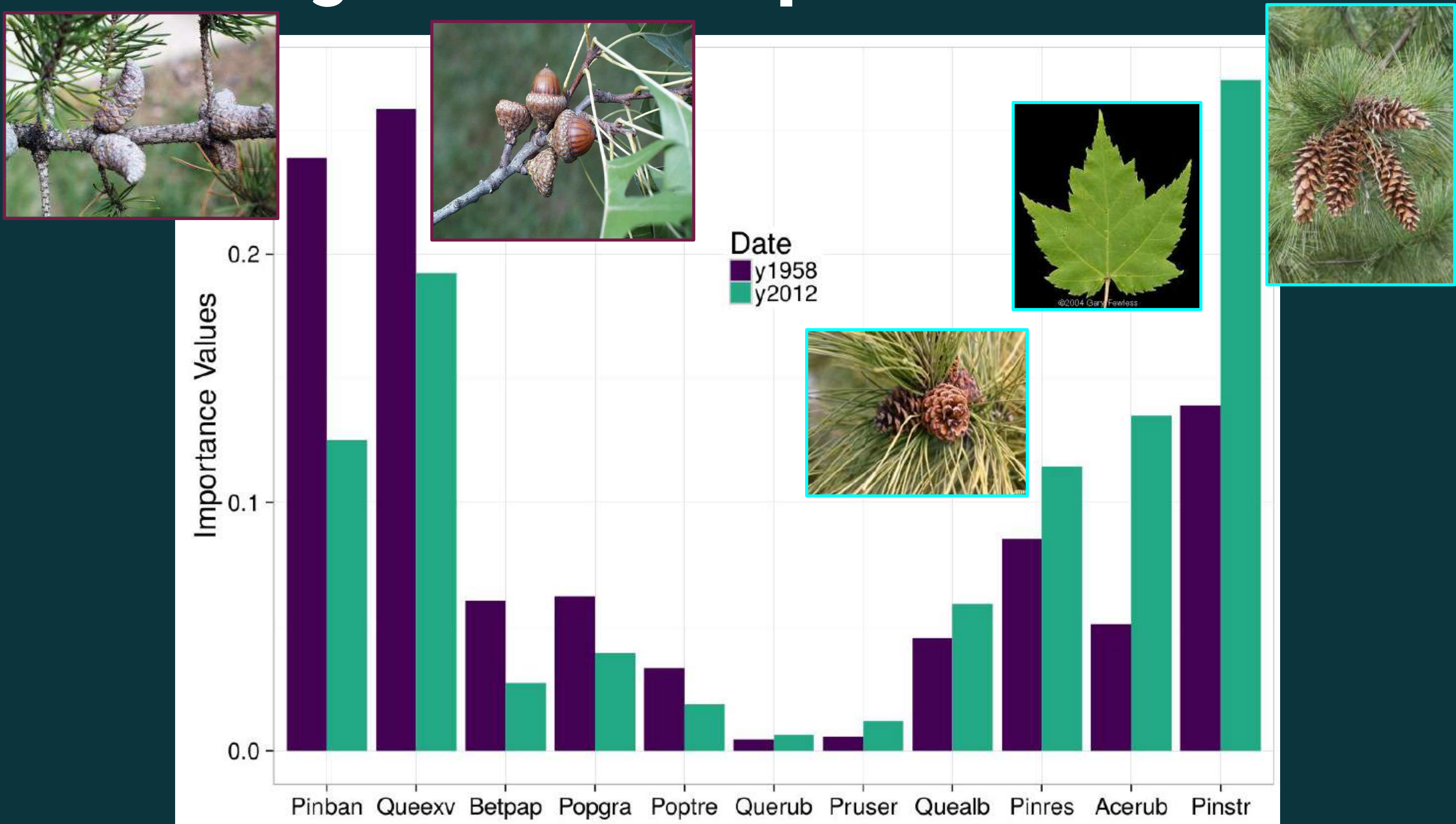
How have fire suppression and climate change affected pine barrens?

Undergrad, UW-Madison
Marian Lea

Undergrad, UW-Madison
Amelia Krug


08/13/2012 16:00

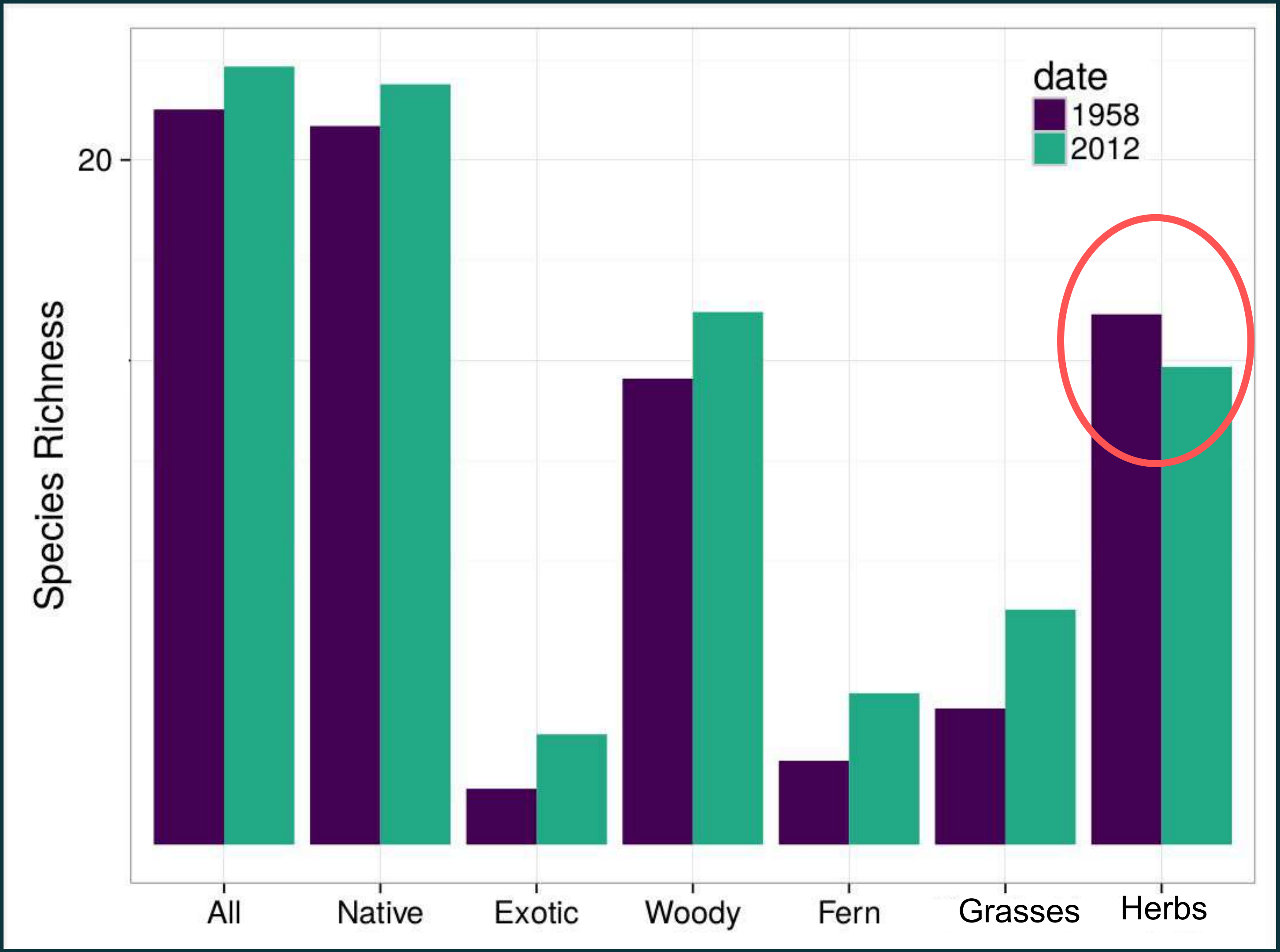
Changes in tree importance values



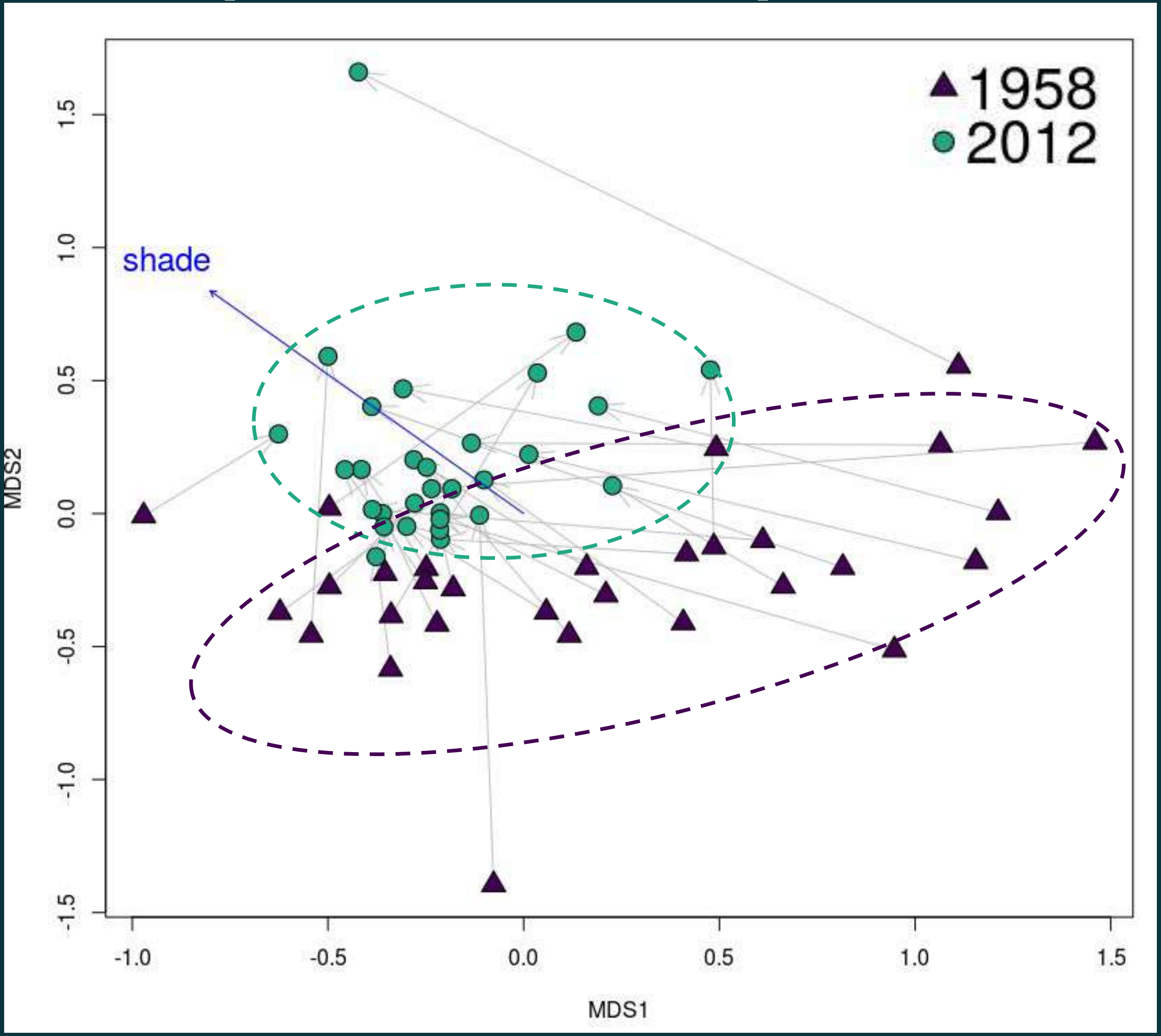
Decreasing the most

Increasing the most

Changes in understory species diversity



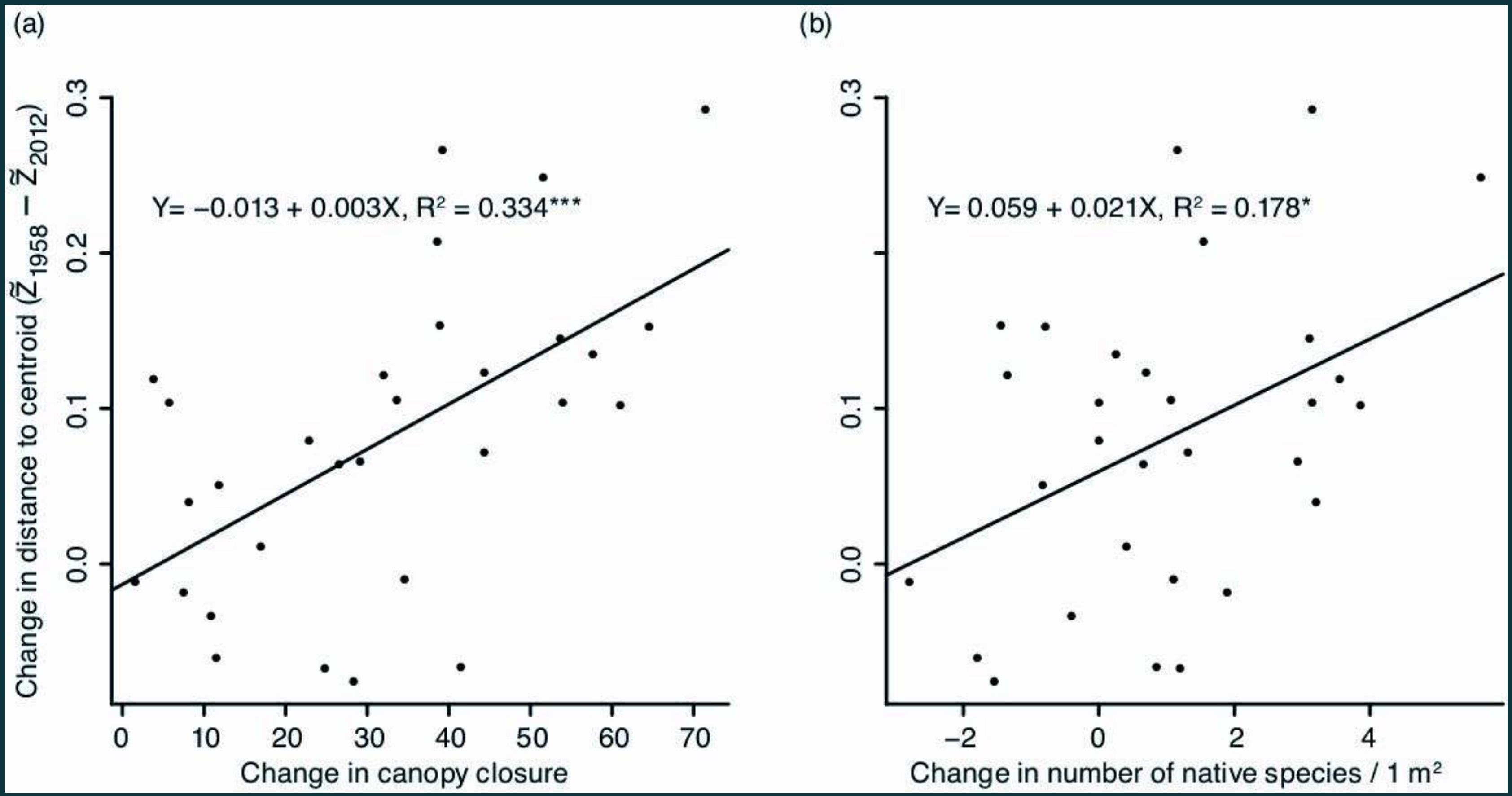
Changes in understory species composition



Li & Waller, 2015, *Ecology*

Drivers of homogenization

High Homogenization



Increasing canopy cover

Increasing native species

No climatic variable is significant; no interactions

Functional traits

Woody

Biotic Pollination

Shade Tolerance

Plant Height

Seed Mass

Specific Leaf Area (SLA, leaf area/dry mass)

Leaf Carbon Content (LCC)

Leaf Nitrogen Content (LNC)

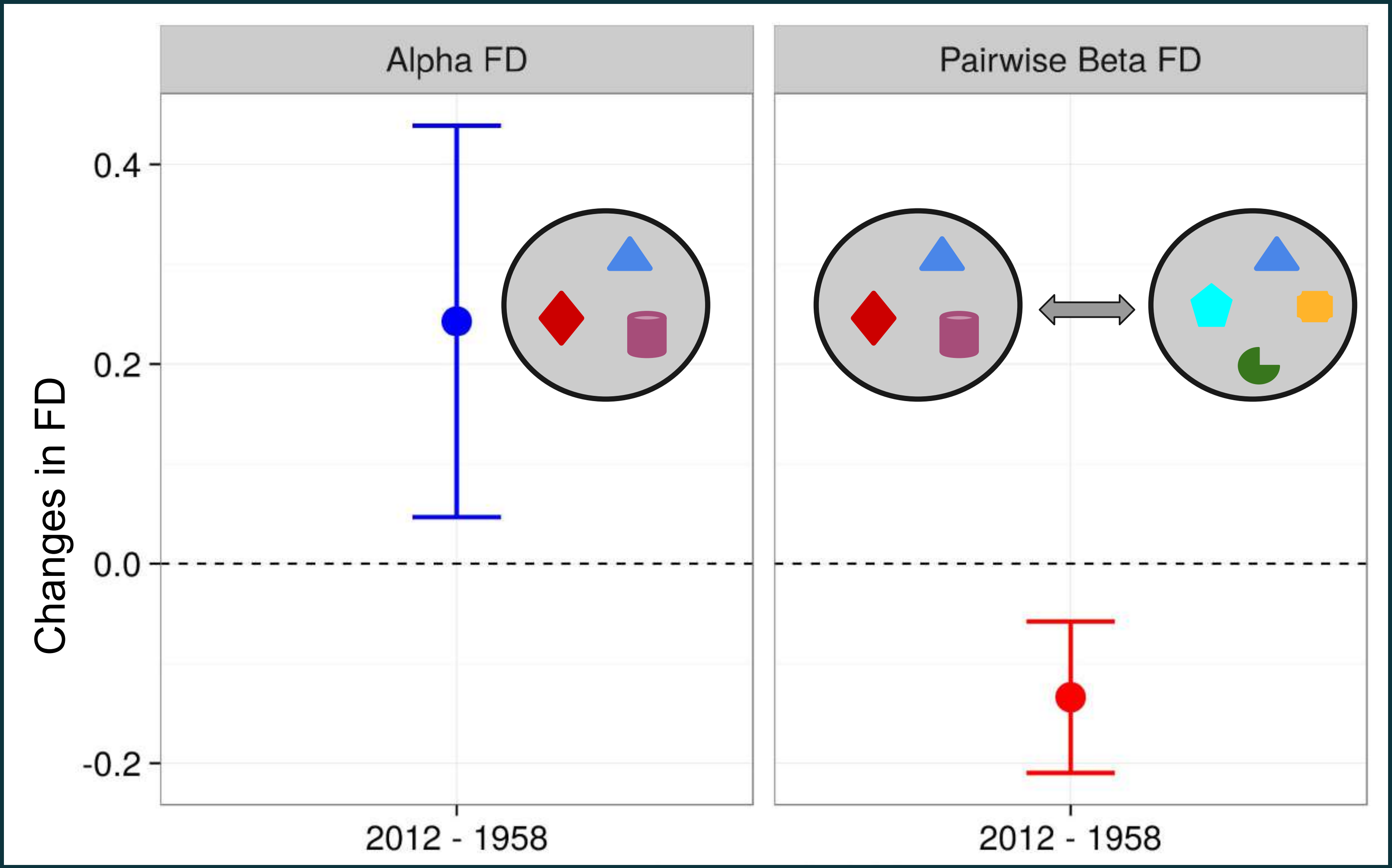
Stem Dry Mass Content (SDMC)

>100 species, including Poison Ivy

Undergraduate students at UW-Madison:

- Alex Arena
- Madeline Grupper
- David Barfknecht
- Kelly Wallin

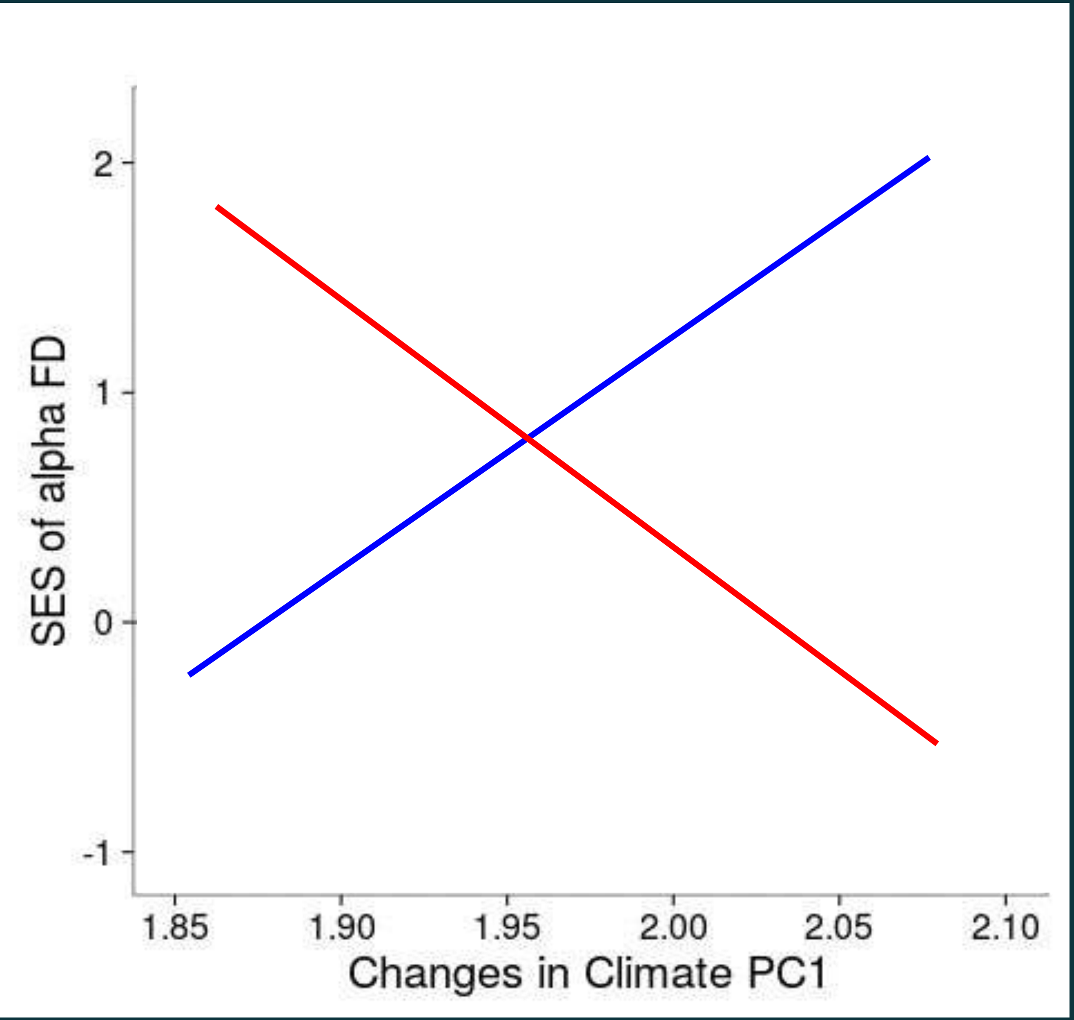
Functional diversity (FD)



Li & Waller, 2017, *Diversity and Distributions*

αFD ~ shade:climate

Higher FD



Warmer and Wetter

Species relationships

	A	B	C	D
site_1	1	0	0	0
site_2	0	1	0	0
site_3	1	1	0	1
site_4	0	0	1	0
site_5	1	0	0	1
site_6	1	0	0	0
site_7	1	0	0	0
site_8	0	1	1	1
site_9	0	1	1	0

	A-B	A-C	B-C	B-D
site_1	0	1	0	0
site_2	0	[illegible]	0	1
site_3	1	[illegible]	1	0
site_4	0	[illegible]	0	1
site_5	[illegible]	[illegible]	[illegible]	[illegible]
site_6	[illegible]	[illegible]	[illegible]	[illegible]
site_7	[illegible]	[illegible]	[illegible]	[illegible]
site_8	1	0	1	0
site_9	1	1	0	0

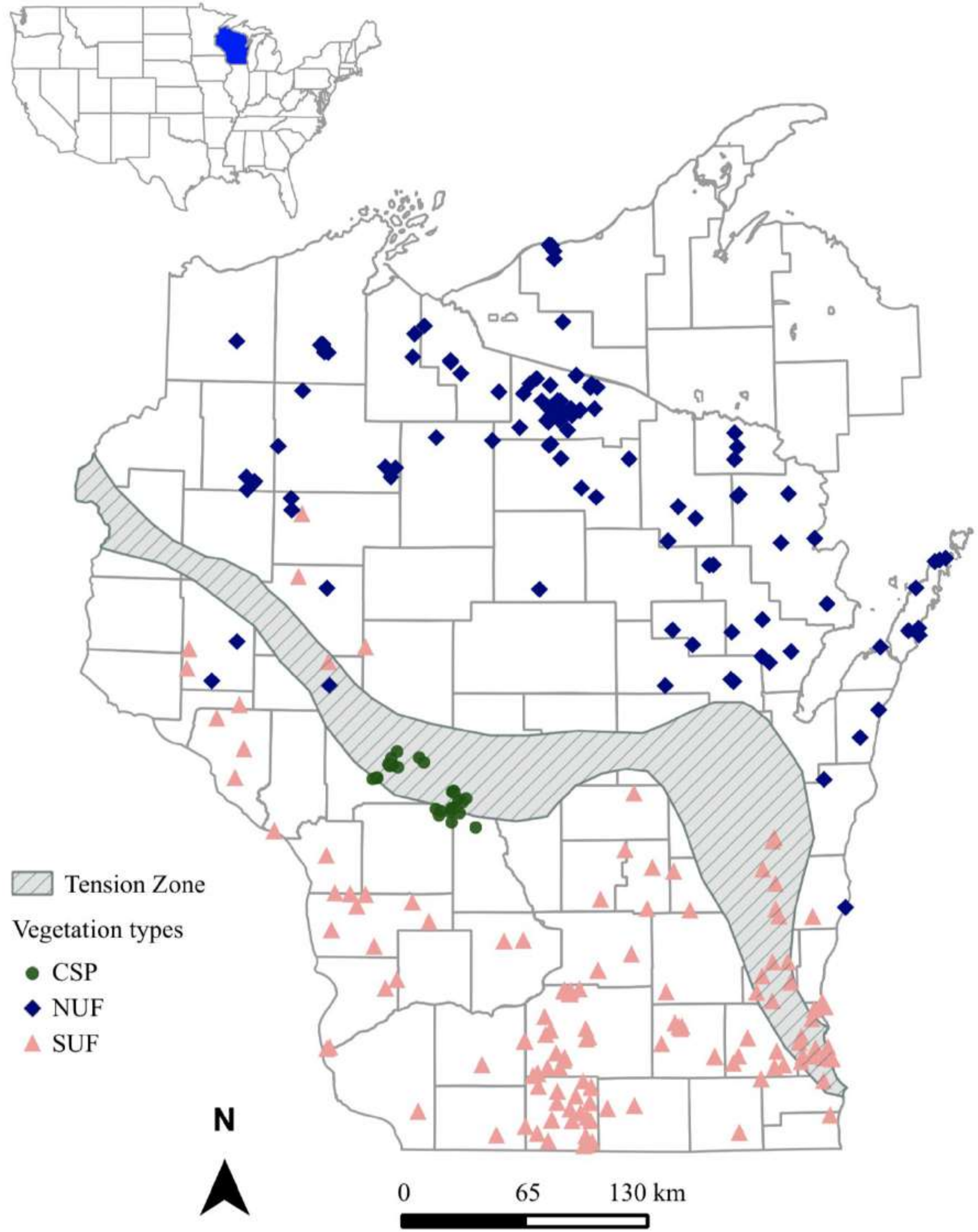
Species composition

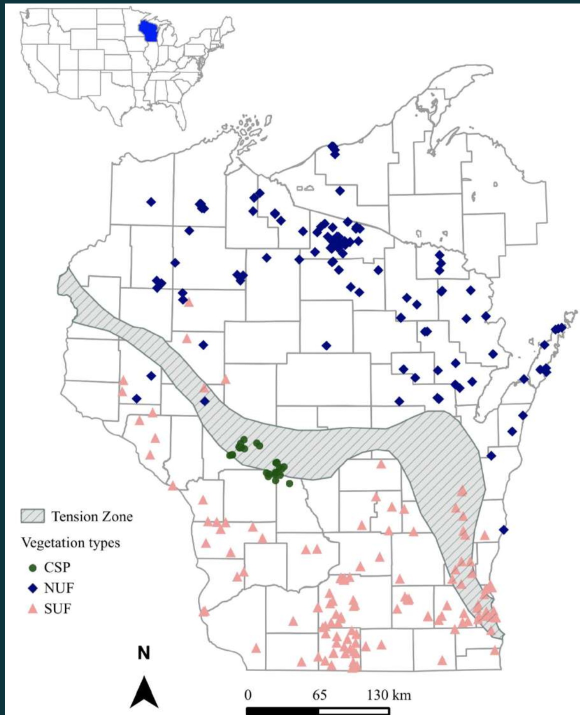
Species association

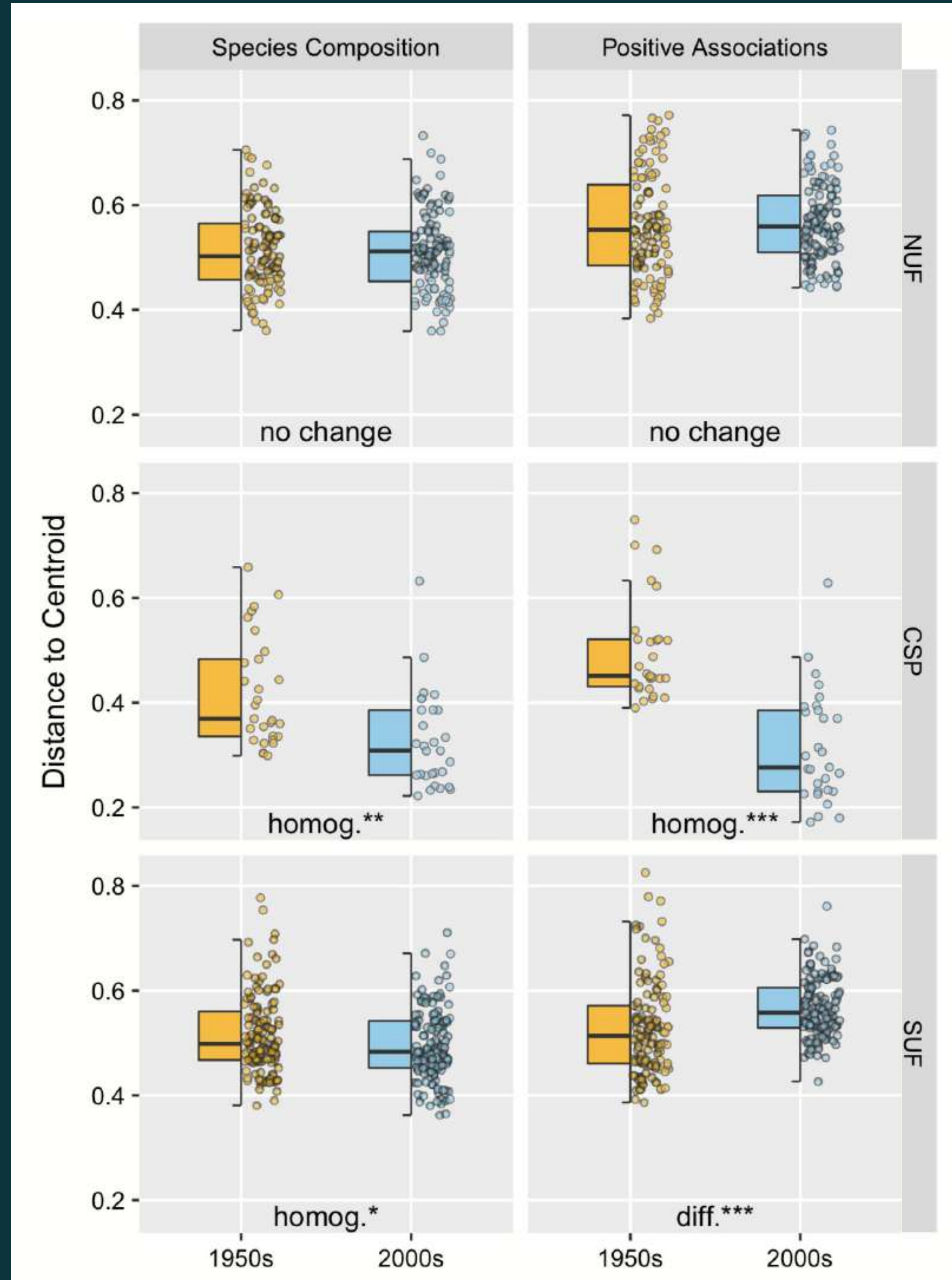
Does homogenization in species composition lead to homogenization in species associations?

266 sites

Li & Waller, 2016, *Global Ecology and Biogeography*







Decoupled!

Li et al., 2018, *Global Ecology and Biogeography*

Summary

- Increasing local species and functional diversity
- Decreasing regional species and functional diversity (biotic homogenization)
- Long-term dynamics of species composition and association are decoupled

With continuous fire suppression and climate change, future diversity may decrease; novel interactions may be more common

Conservation implications

Research projects

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Example of traditional community analysis

Species composition

Environmental variables for each site (e.g. soil pH, climate, etc.)

m sites

	Acer rubrum	Achillea millefolium	Amelanchier spp	Andropogon gerardii
site_1	0	0	0	0
site_2	3	0	1	0
site_3	8	0	0	0
site_4	0	1	0	5
site_5	0	1	0	0
site_6	15	0	2	0
site_7	14	0	3	0
site_8	0	0	0	0
site_9	2	0	1	0

n species

Functional traits for each species (e.g. height, leaf C %, etc.)

Diversity (per site)

Multivariate analysis (e.g. ordination)

Algorithmic!

Example of model-based community analysis

Abundance of species among sites

Species as random effect

Site as random effect

Average effect of env1

Effects of env1 to sp as random effect

$$\log(Y_i + 1) = \alpha + a_{\mathrm{spp}[i]} + b_{\mathrm{site}[i]} + (\beta_1 + c_{\mathrm{spp}[i]})\mathrm{env1}_{\mathrm{site}[i]} +$$

Overall species abund.

$$\beta_2 \mathrm{trait1}_{\mathrm{spp}[i]} + \beta_3 \mathrm{env1}_{\mathrm{site}[i]} \times \mathrm{trait1}_{\mathrm{spp}[i]} + e_i$$

Average effect of trait1

Interaction between env1 and trait1

i: 1, 2, …, nm

α, β: fixed terms

a, b, c: random terms

e: error term

$a \sim \mathrm{Gaussian}(\mathbf{0}, \sigma^2_{\mathrm{a}}\mathbf{I}_n)$

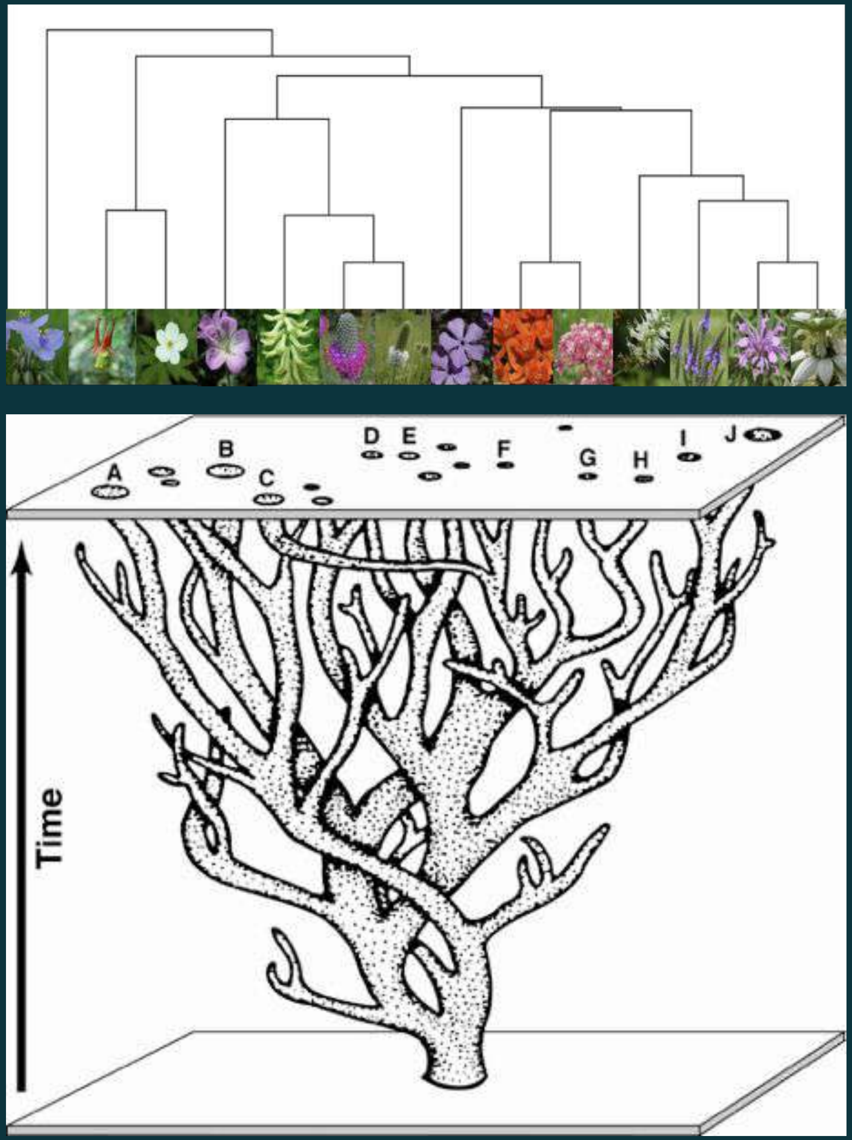
$b \sim \mathrm{Gaussian}(\mathbf{0}, \sigma^2_{\mathrm{b}}\mathbf{I}_m)$

$c \sim \mathrm{Gaussian}(\mathbf{0}, \sigma^2_{\mathrm{a}}\mathbf{I}_n)$

$e \sim \mathrm{Gaussian}(\mathbf{0}, \sigma^2_{\mathrm{e}}\mathbf{I}_{mn})$

Why model-based methods?

- No aggregation to one value/site
- Integrate multiple source of information (and their interactions)
- Model validation/selection/prediction …
- Deeper understanding of community dynamics



Problem

Species are
not independent
samples from the
same statistical
distribution

- Inflated type I error (false positive)
- Well-known problem from comparative analyses
  (Felsenstein 1985; Harvey & Pagel 1991; Garland et al. 1999; Paradis 2012; Garamszegi 2014)
- Same problem for community analyses?

Model-based community analysis

Phylogenetic Linear Mixed Models (PLMM)

$$\log(Y_i + 1) = \alpha + a_{\text{spp}[i]} + \boldsymbol{a}^{\mathbf{p}}_{\text{spp}[i]} + b_{\text{site}[i]} + (\beta_1 + c_{\text{spp}[i]} + \boldsymbol{c}^{\mathbf{p}}_{\text{spp}[i]})\text{env1}_{\text{site}[i]} +$$

$$\beta_2 \text{trait1}_{\text{spp}[i]} + \beta_3 \text{env1}_{\text{site}[i]} \times \text{trait1}_{\text{spp}[i]} + e_i$$

i: 1, 2, …, nm

α, β: fixed terms

a, b, c: random terms

e: error term

$a \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{a}} \mathbf{I}_n)$

$a^p \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{ap}} \boldsymbol{\Sigma}_{\text{spp}})$

$b \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{b}} \mathbf{I}_m)$

$c \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{a}} \mathbf{I}_n)$

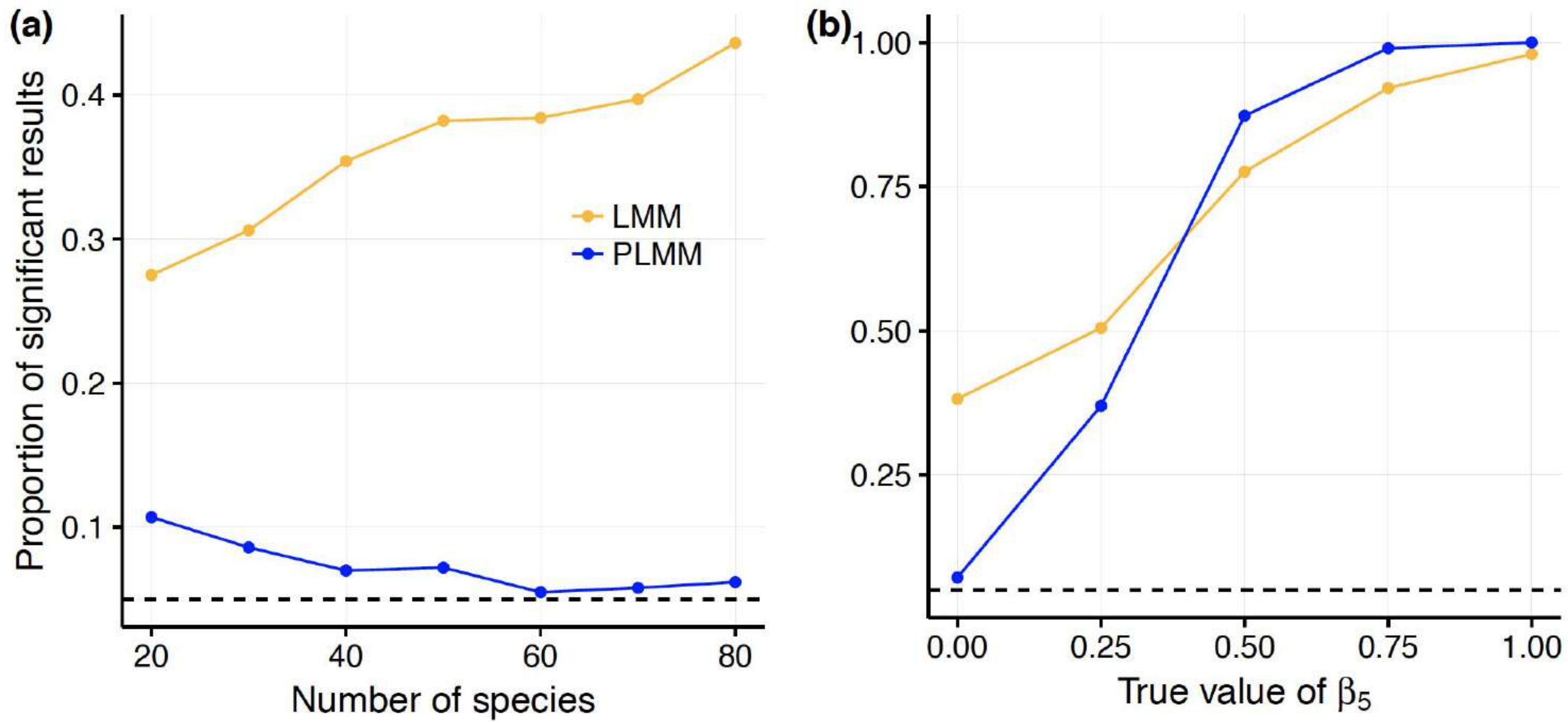
$c^p \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{cp}} \boldsymbol{\Sigma}_{\text{spp}})$

$e \sim \text{Gaussian}(\mathbf{0}, \sigma^2_{\text{e}} \mathbf{I}_{mn})$

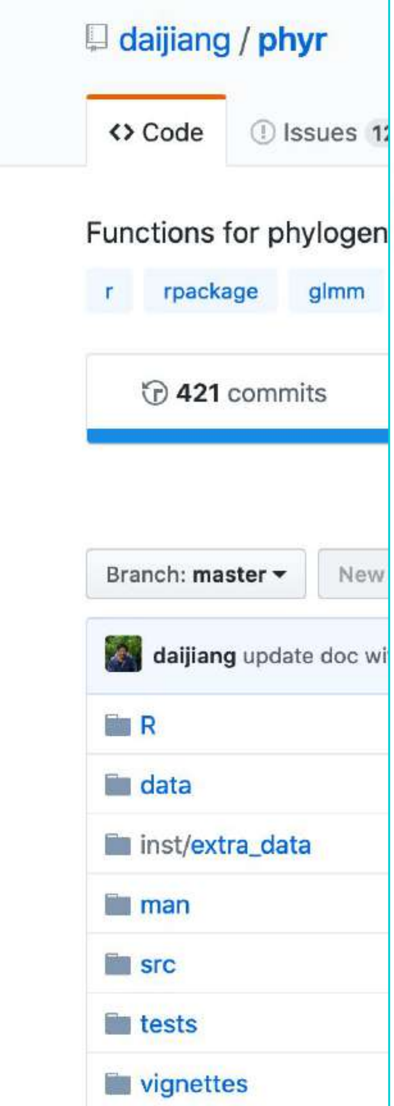
Phylo. Var-Covar matrix

Type I error

Statistical power



Li & Ives, 2017, *Methods in Ecology and Evolution*



phyr: Model Based Phylogenetic Analysis

A collection of functions to do model-based phylogenetic analysis. It includes functions to calculate community phylogenetic diversity, to estimate correlations among functional traits while accounting for phylogenetic relationships, and to fit phylogenetic generalized linear mixed models. The Bayesian phylogenetic generalized linear mixed models are fitted with the 'INLA' package (<http://www.r-inla.org>).

Version:	1.0.2
Depends:	R (≥ 3.1)
Imports:	stats, ape, Rcpp, Matrix, methods, graphics, dplyr, lme4, nloptr, gridExtra, mvtnorm, latticeExtra
LinkingTo:	Rcpp, RcppArmadillo
Suggests:	testthat, pez, tidyr, knitr, rmarkdown, covr, picante, rbenchmark, INLA, MCMCglmm, logistf, phylolm
Published:	2019-11-13
Author:	Anthony Ives [aut], Russell Dinnage [aut], Lucas A. Nell [aut], Matthew Helmus [aut], Daijiang Li [aut, cre]
Maintainer:	Daijiang Li <daijianglee at gmail.com>
BugReports:	https://github.com/daijiang/phyr/issues
License:	GPL-3
URL:	https://github.com/daijiang/phyr/
NeedsCompilation:	yes
Materials:	README
CRAN checks:	phyr results

```
pglmm(formula = freq ~ 1 + shade + (1|sp__) + (1|site__) + (1|sp__@site),
         data = dat,
     cov_ranef = list(sp = phylotree, site = Vspace),
        family = 'poisson', # 'binomial','gaussian', 'zeroinflated.binomial', etc.
         bayes = FALSE)
```

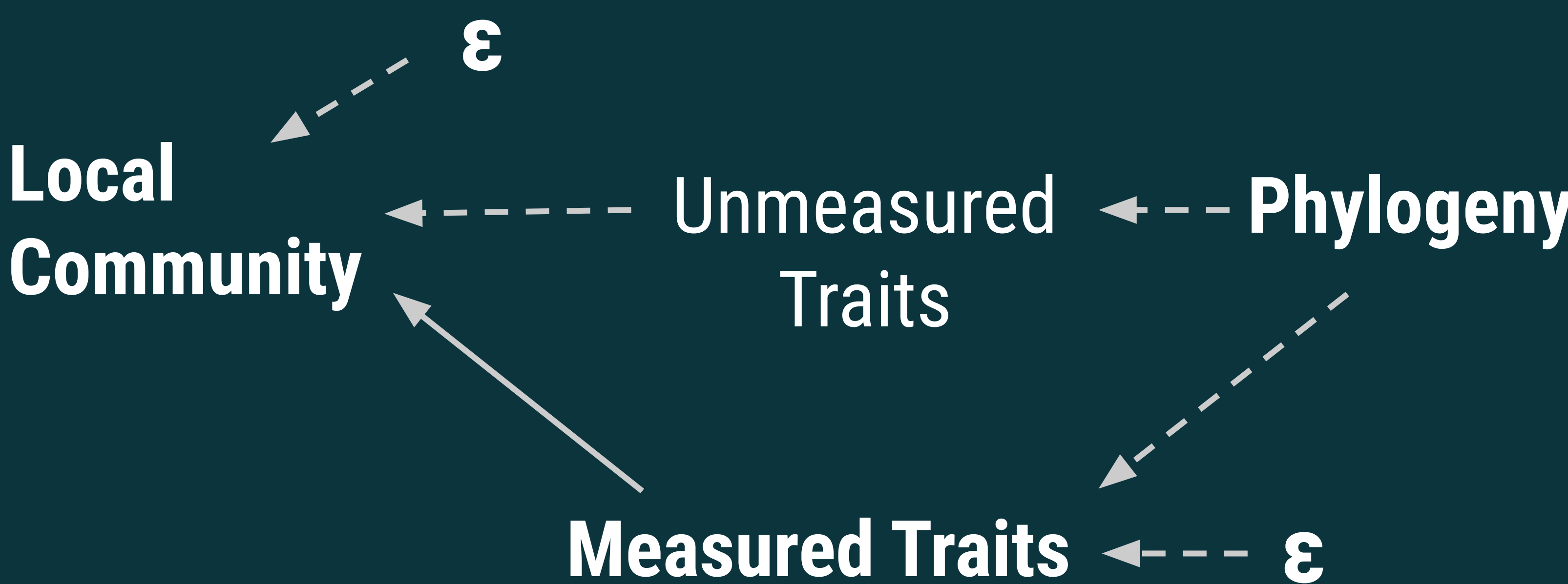
Applications of phylogenetic generalized linear mixed models

- Trait - Environment relationships
- Phylogenetic community structure
- Bipartite questions:
  - plant-pollinator
  - host-parasite

Do we miss important functional traits that can explain phylogenetic signal of species composition?

Li, Ives, & Waller, 2017, *New Phytologist*

Heuristic diagram



$$\text{Gaussian}(\mathbf{0},\ \text{kron}(\mathbf{I}_{site},\ \sigma^2\boldsymbol{\Sigma}_{spp}))$$

$$Y = X\beta + Zu_{\text{phy-full\{Unmeasured traits\}}} + \varepsilon$$

$$Y = (X + \text{measured traits})\beta + Zu_{\text{phy-reduced\{Unmeasured traits\}}} + \varepsilon$$

$$\sigma^2 \approx 0$$

- Random terms
- Fixed terms

Li, Ives, & Waller, 2017, *New Phytologist*

Traits vs. Phylogeny

Pine barrens, WI
10 traits

~100%

Dune meadows, Netherlands
5 traits

~28%

Li, Ives, & Waller, 2017, *New Phytologist*

Summary

- P(G)LMMs: better type I error control & higher statistical power
- Integrating multiple source of data
- Wide range of applications
- Get more out of community data (terrestrial or aquatic)

Research projects

1. Field research on plant community changes at the regional scale
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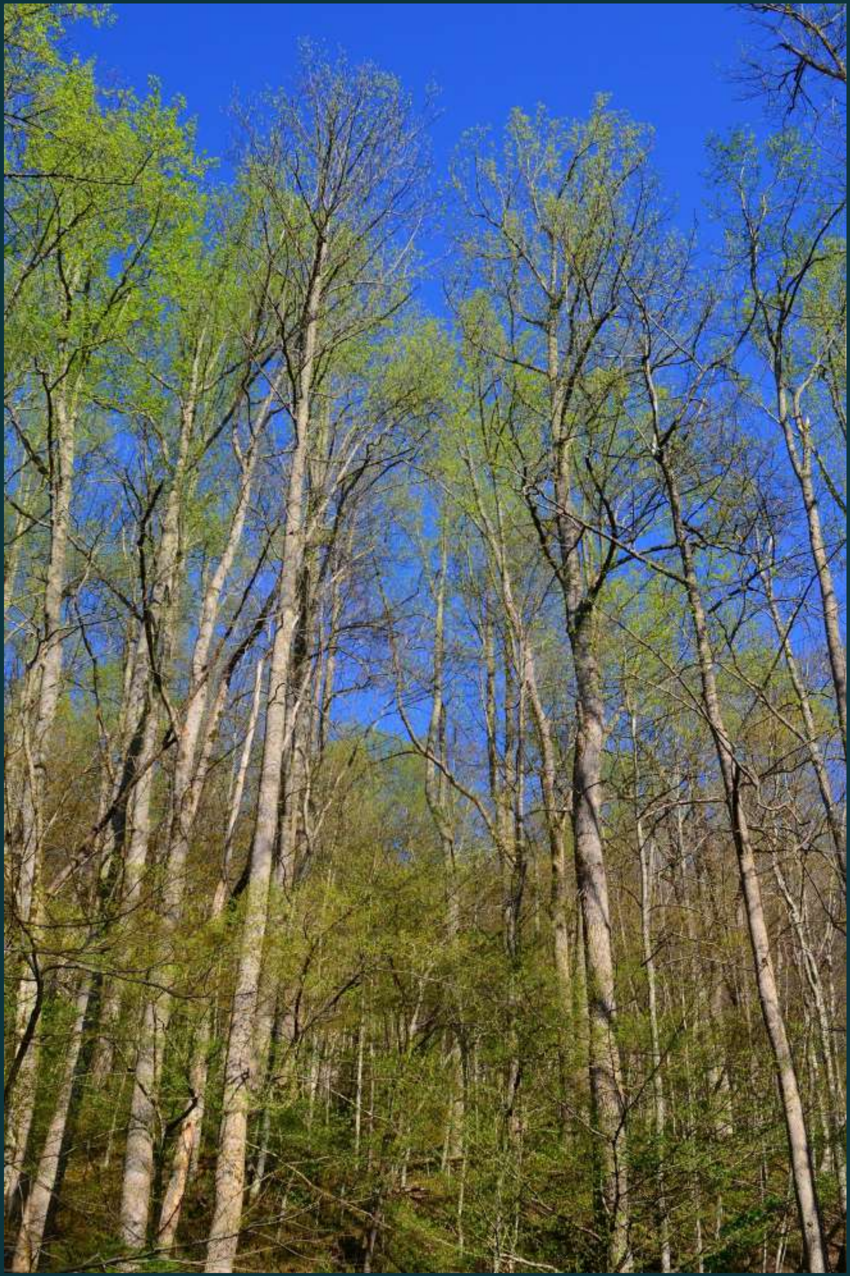
3. Analysis of big data to study global changes at the continental scale

How have global changes (climate change, land-use change, etc.) affected functional traits at large scale?



Plant phenology

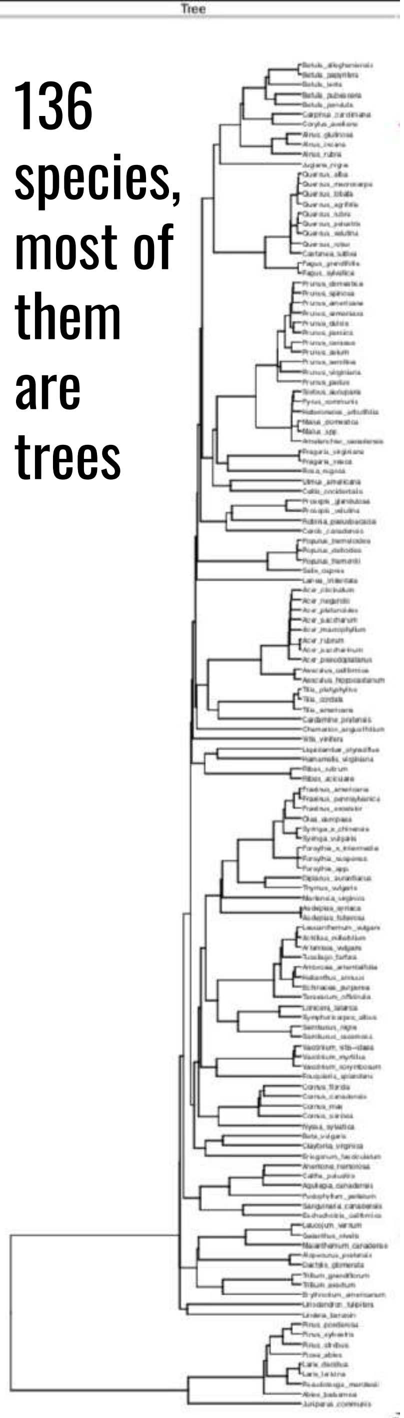
Does the effect of urbanization on plant phenology vary across regions with different climate?

Globa

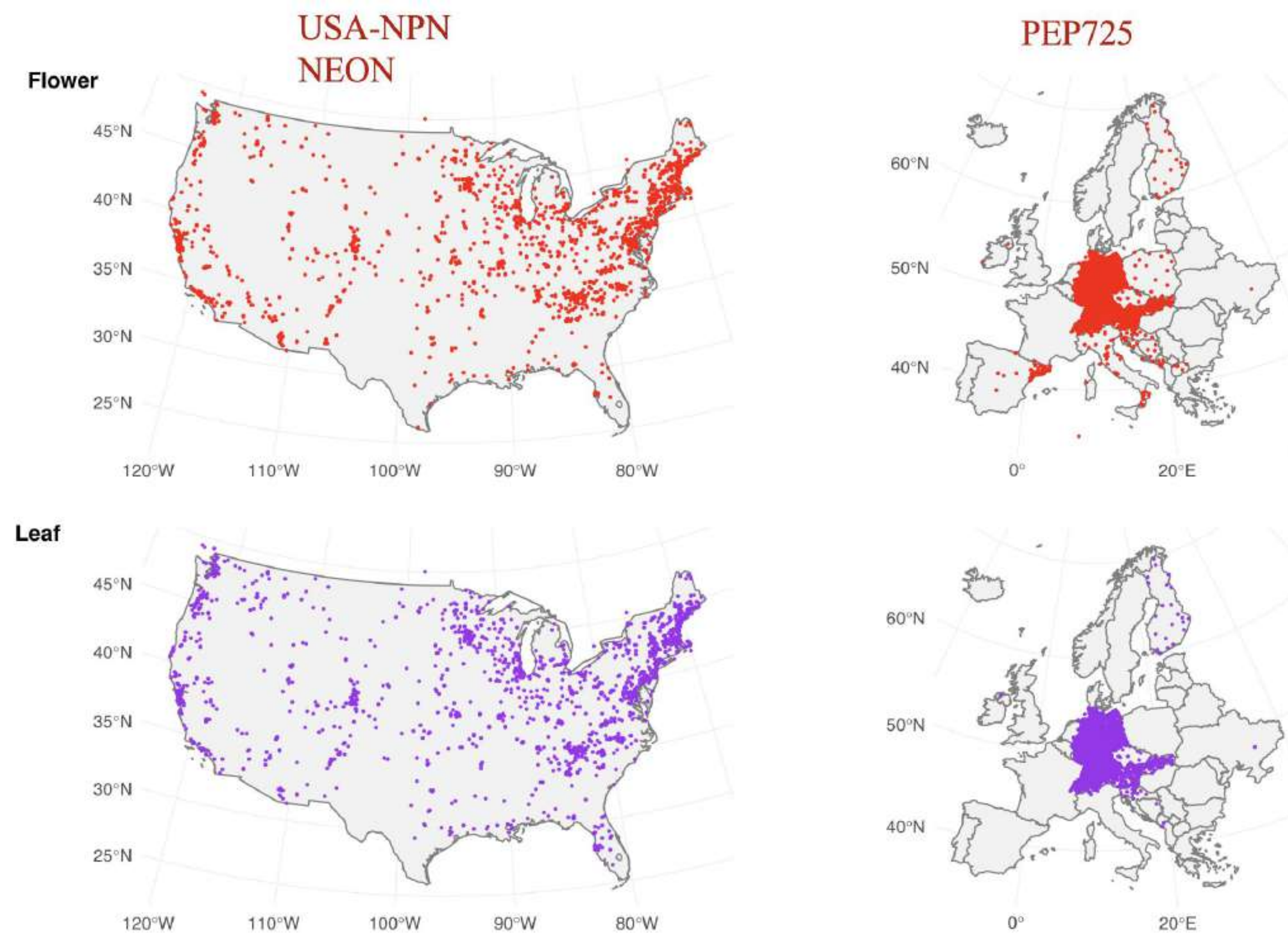
Data

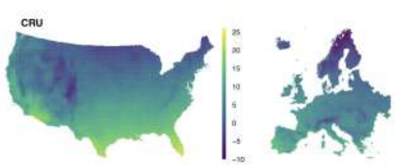
(>22

https://

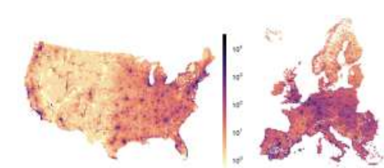


136 species, most of them are trees



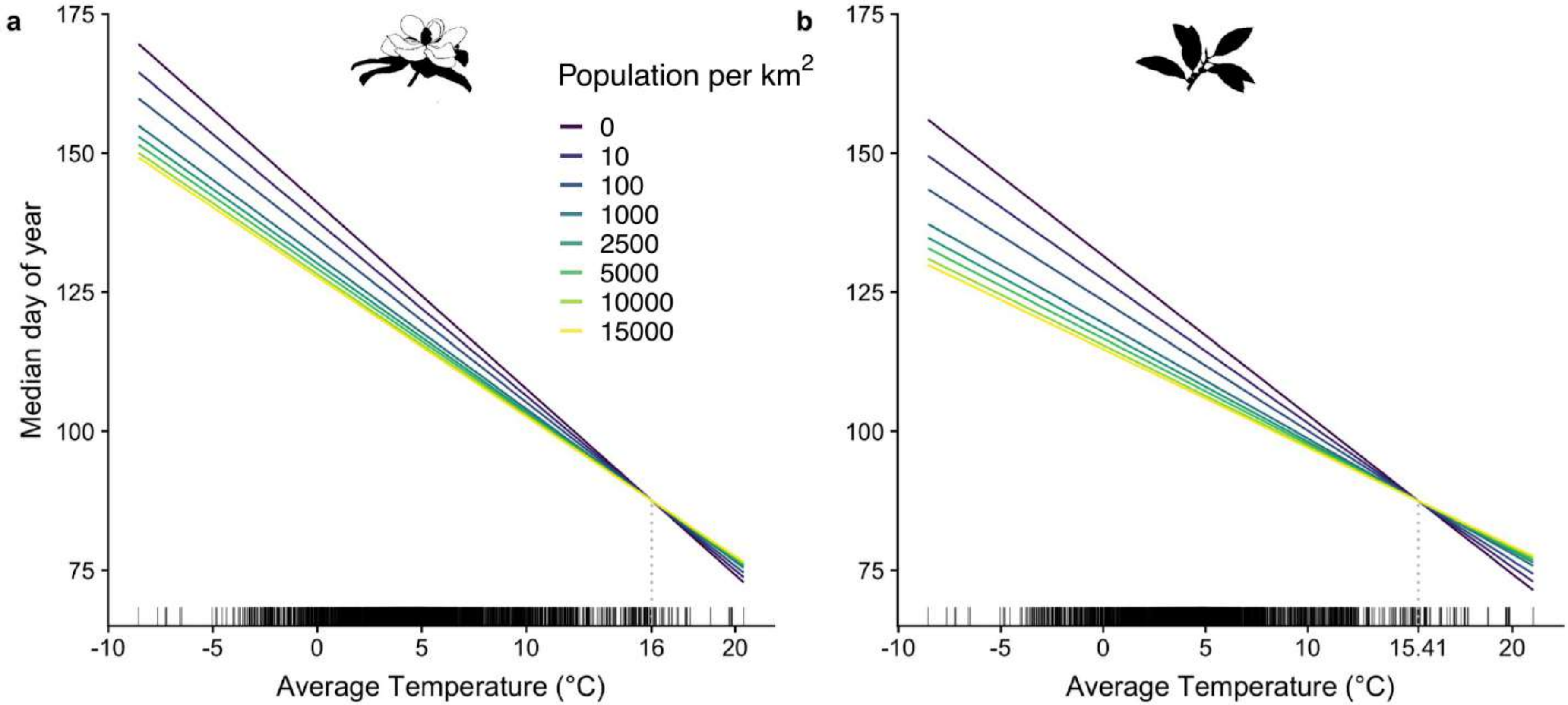


10 km by 10 km grid cells



Linear Mixed Models

Median DOY of Each species (2009-2017) ~ Background Average Temperature (Nov.–May, 1980-2010) × Human Population Density (the 2010s, as a measure of urbanization)




nature ecology & evolution
ARTICLES
https://doi.org/10.1038/s41559-019-1004-1

The effect of urbanization on plant phenology depends on regional temperature

Daijiang Li[1,2*], Brian J. Stucky[2], John Deck[3], Benjamin Baiser[1] and Robert P. Guralnick[2]

Li et al. 2019, *Nature Ecology & Evolution*

Summary

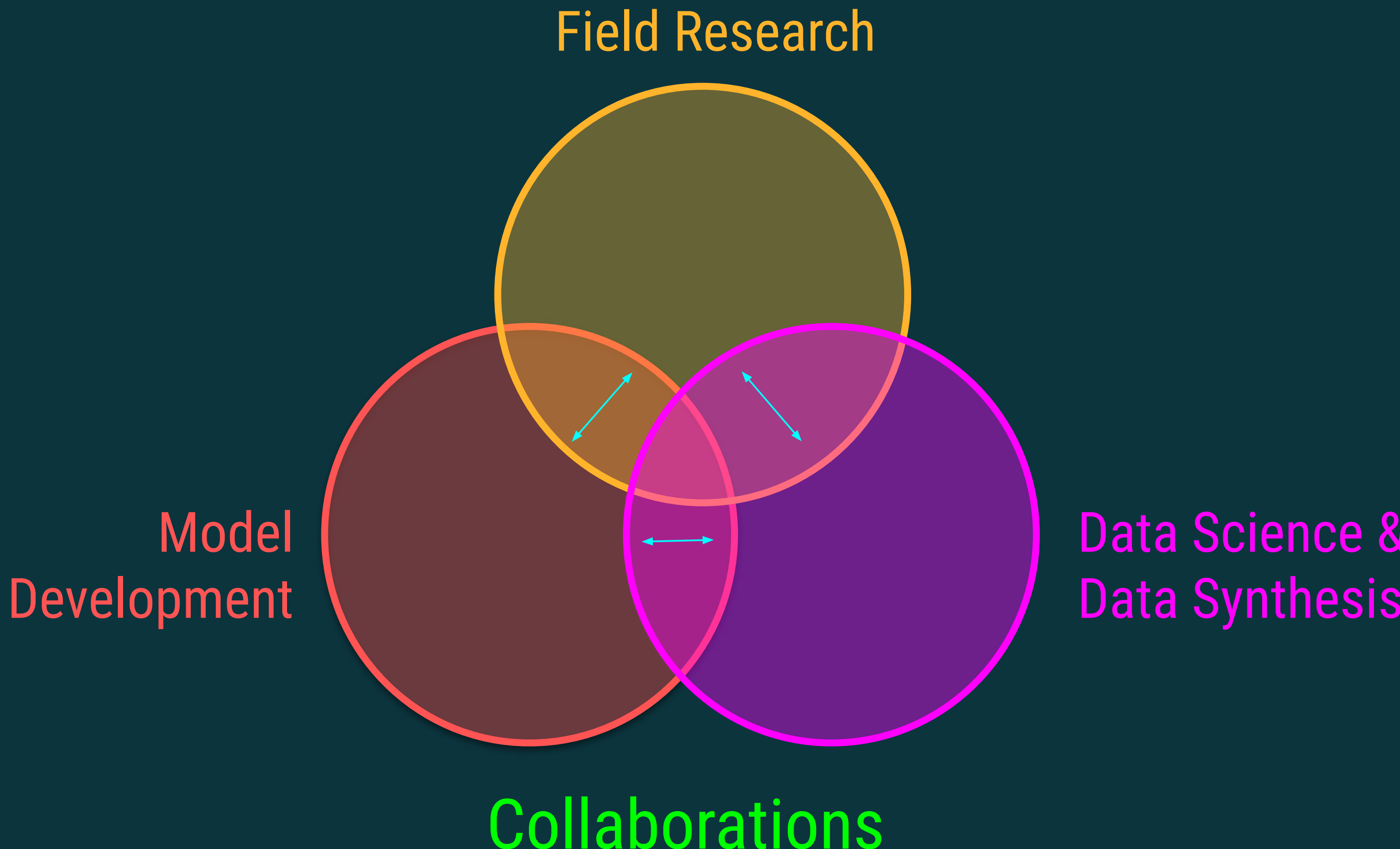
- The influence of urbanization on plant phenology varies with regional temperature
- Mechanisms?
- Including such interaction is necessary for robust understanding and accurate prediction of phenological changes (other traits?)

Contribution and motivation

- Investigate patterns and drivers of **long-term changes** in ecological communities
    - And other systems (e.g. Li et al. *PNAS*, 2019)
- Study **large-scale effects** of global changes on plant phenology, biological invasions, and biodiversity
    - Phylogenetic diversity (Li et al. *Proc. B* In revision); Diversity-area relationships (e.g. Li et al. *Div. Distri.* 2018)
- Develop and disseminate **novel statistical methods** (e.g. R packages)
    - Evaluate and compare existing methods (e.g. Li et al. *Ecology*, 2019)

How multiple aspects of global change have and will affect communities?

Quantitative Community Ecology Lab



Graduate School

Advancing Knowledge through Education and Research

Department of Botany

UF

FLORIDA MUSEUM OF NATURAL HISTORY

NSF

Tony Ives

Don Waller

Ben Baiser

Rob Guralnick

Collaborators:

Susan Harrison

Julian Olden

Julie Lockwood

Pamela Soltis

etc.

Undergraduate students, data contributors, etc.


Thank you