Forecasting biodiversity reorganization with climate change

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AIST-16-0052

Additional funding: NSF Macrosystems Biology, NSF EAGER, NSF Community Ecology

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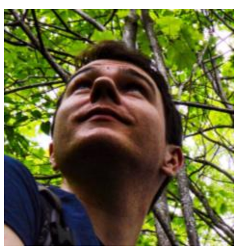
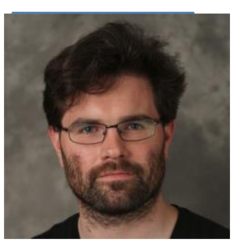
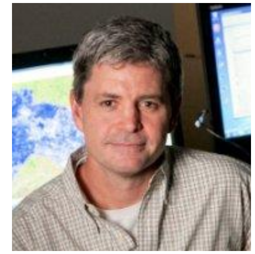


Bradley Tomasek, PhD Student



Christoph Hellmeyr
Post-Doc



John Fay
Geospatial analysist, programmer

Chase Nuñez,

PhD Student

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Master of Environmental Management student

Decision-makers, scientists anticipate biodiversity change

Goals

Expand access to data and effective modeling

Automate real-time prediction

Approach

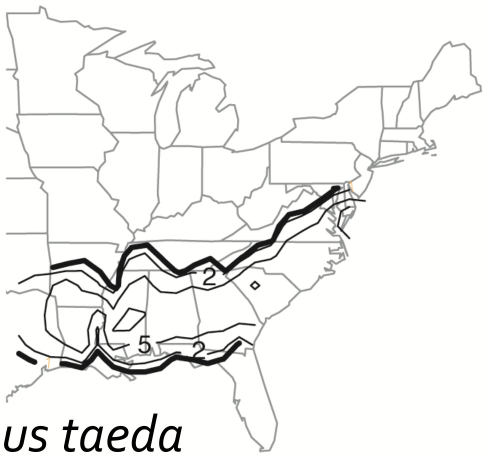
- Cloud-based predictors (climate, soils, remotely sensing), biodiversity responses (plants, birds, mammals, arthropods)
- Interactive interface
- Generalized joint attribute modeling (GJAM) analyzes community at multiple scales combined with food
- Predictive distributions/sensitivity, entire *community response*

Current models provide limited guidance

- Species distribution models (SDMs), species richness models (SRMs):
  - anywhere from 0 to 50% of species at risk (Urban et al. *Science* 2015)
  - recent meta-analysis: 8%

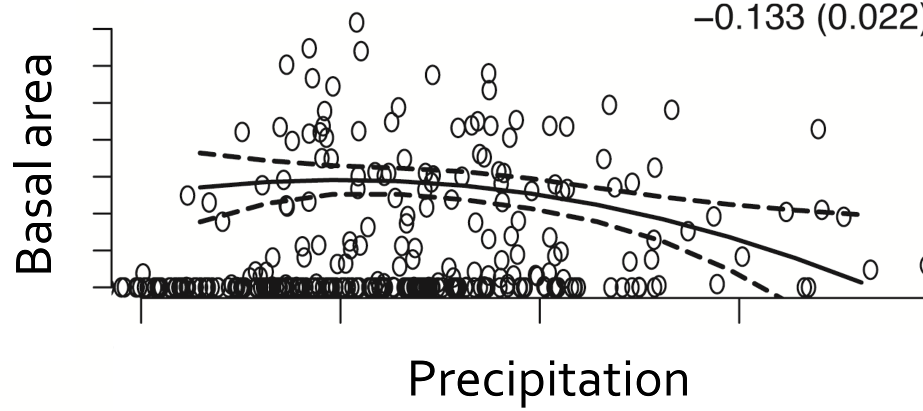
- Scale mismatch: fit at one scale, predict at another
  - SDMs: Independent models for each species
  - SRMs: only the number of species
  - '*Simpson's Paradox*', the '*ecological fallacy*' (Clark et al. 2011)

Scale paradox
SDM: aridity benefits loblolly

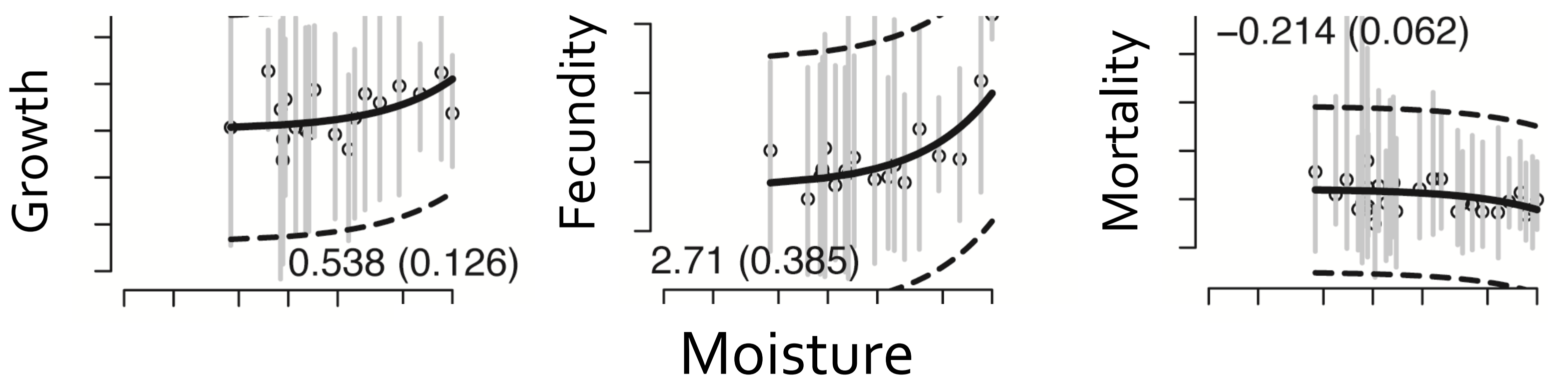


Pinus taeda

Plot scale



Individual scale: moisture benefits loblolly

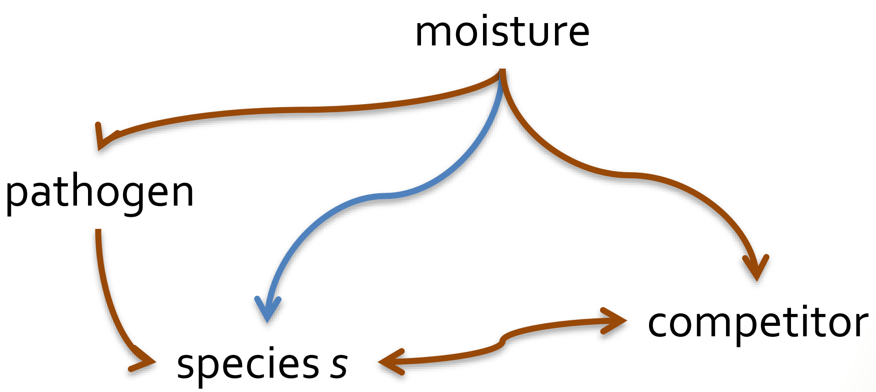


Simpson's Paradox

Clark, et al. ***Global Change Biol*** (2014)

What's hard about community response?

- Data are:
  - Multivariate
  - Multifarious
  - Median-zero



- Models are:
  - Individual species
  - Limited to one species group or to presence-absence
  - Zero-inflated; non-linear link functions

Clark et al. 2014, ***Ecol Appl***

Multifarious observations

Discrete abundance: counts

Continuous abundance: biomass, concentration

Count composition: microbiome, paleoecology

Fractional composition: satellite imagery, photoplots

Ordinal scores: health status, phenological state

Categorical: plot status, traits

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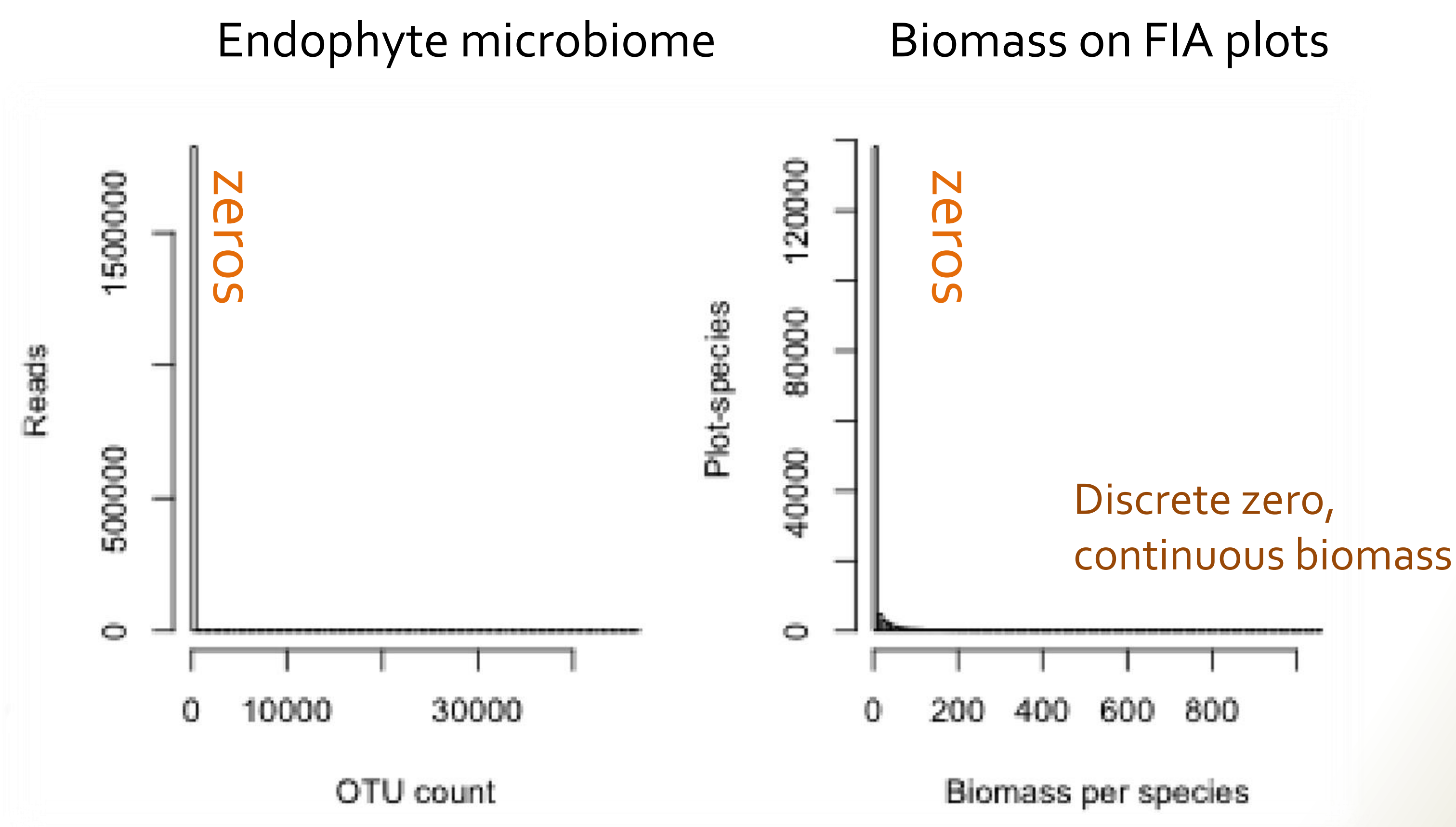
Clark et al. ***Ecol Monogr*** (2017)

Median-zero

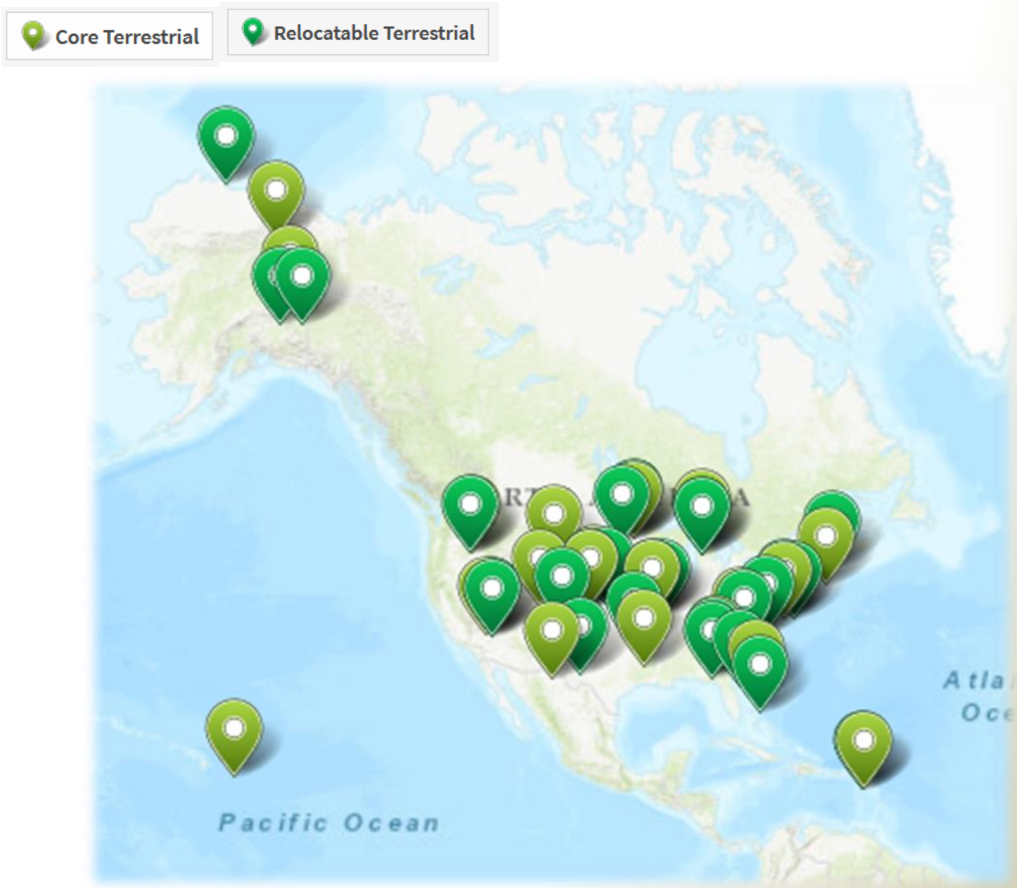


Zero-inflated models don't handle many zeros

Ghosh, Gelfand, Zhu, Clark, ***Biometrika*** 2014

Diverse data: National Ecological Observatory Network (NEON)

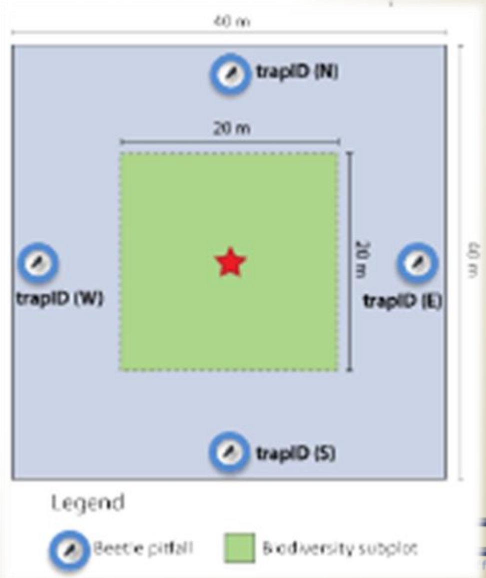
- Thousands of plots
  - Ground beetles
  - Small mammals
  - Mosquitos
  - Ticks
  - Plants
  - Birds
- Hyperspectral and LiDAR data



https://www.neonscience.org/field-sites/field-sites-map

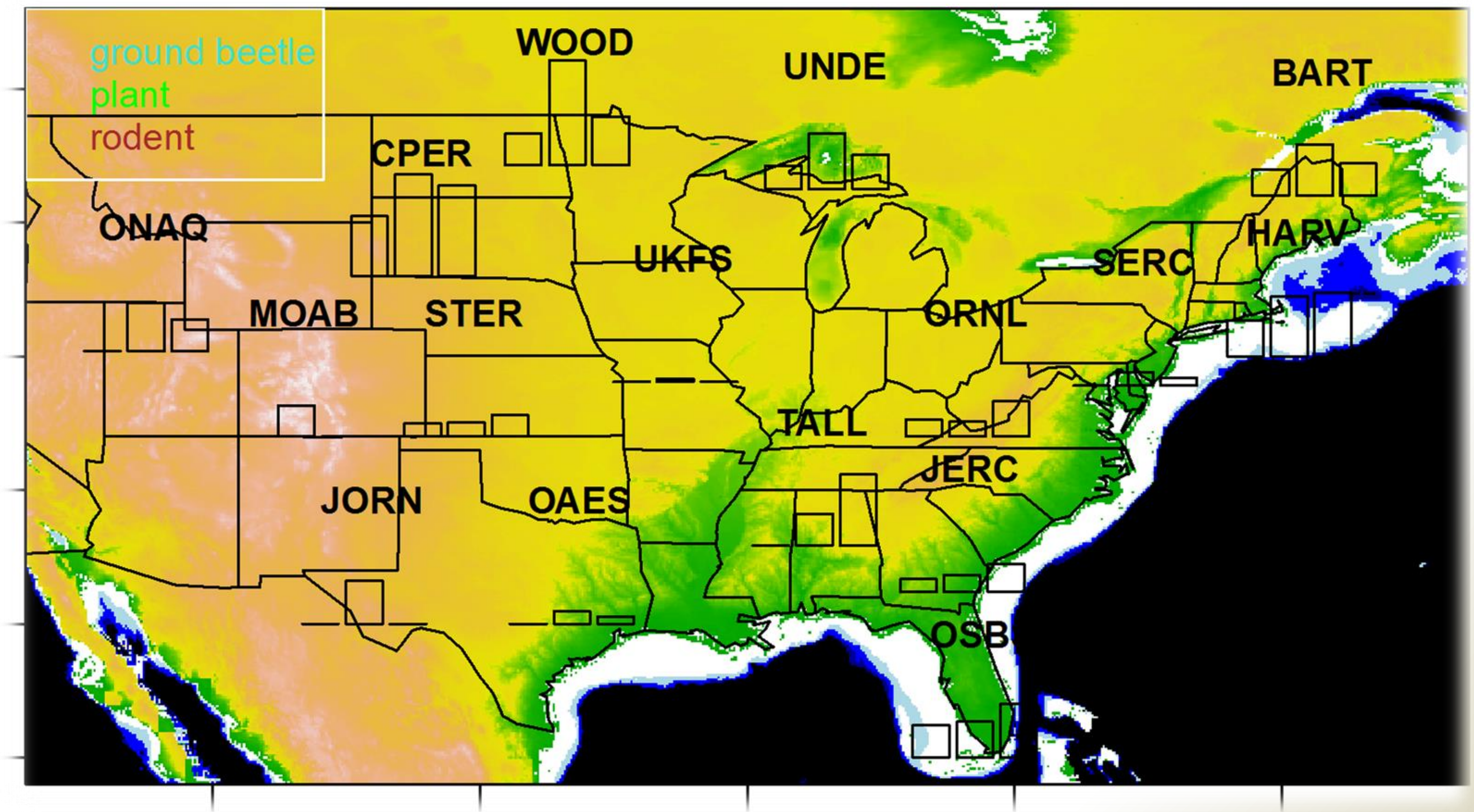
Diverse data: NEON

- **Ground beetles** – pitfall traps; **counts**
- **Plant cover abundance—percent**, censored at 0.5%
- **Small mammals**—live traps; **counts**
- **Birds—**point **counts**



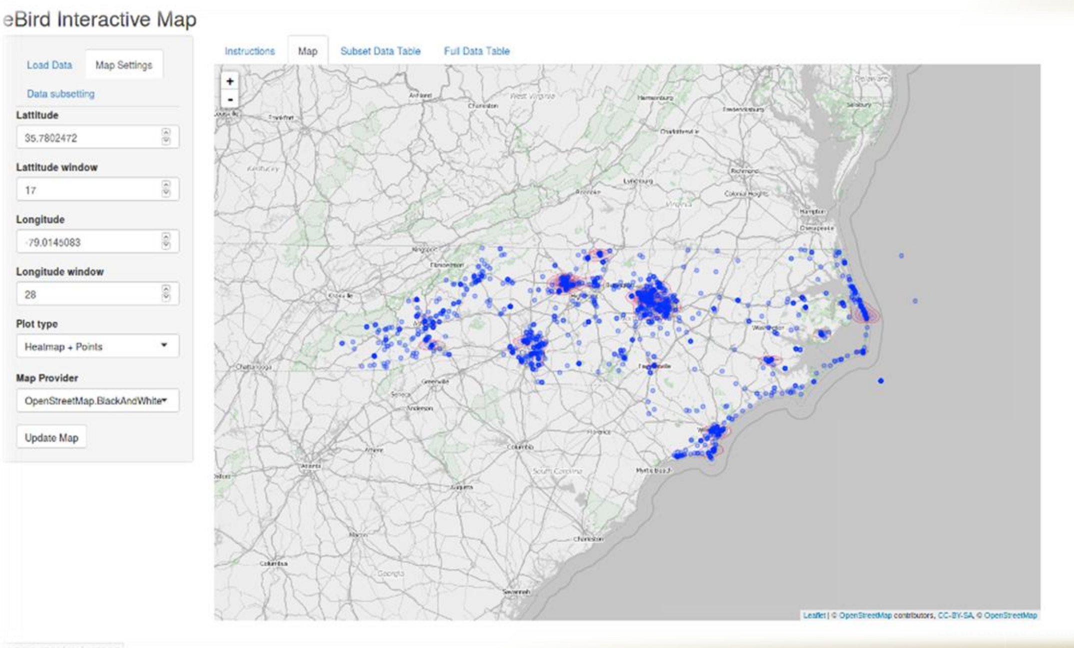
Taxonomically distant species groups in NEON

- Sampling effort/scale varies by group



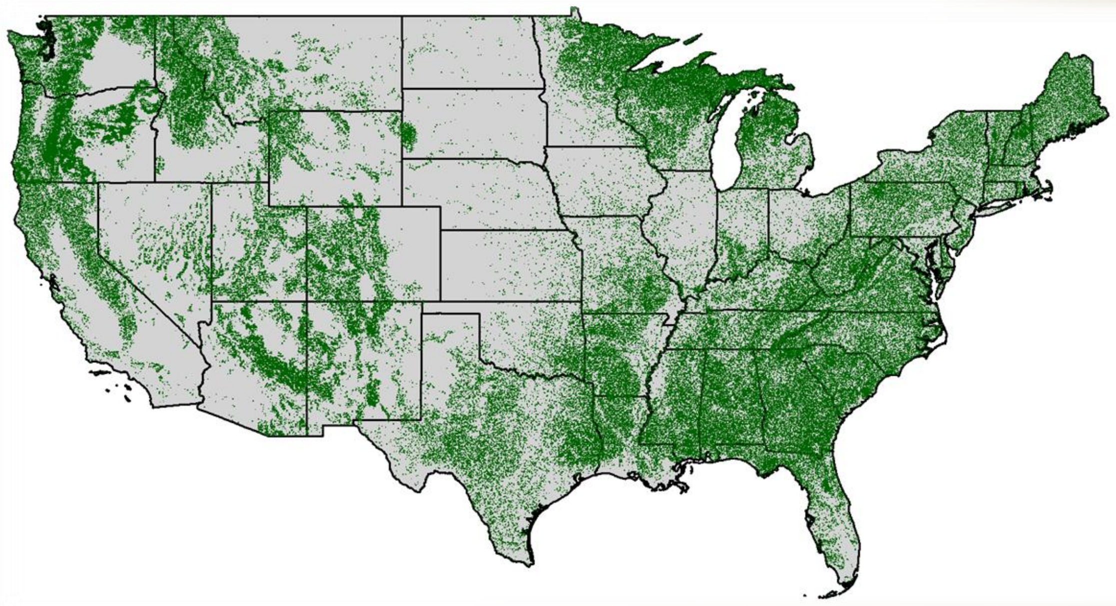
Diverse data: Breeding Bird Survey (BBS) and eBird

- Citizen science data
- Sampling effort available
- Sparse response (99.9% zeros)



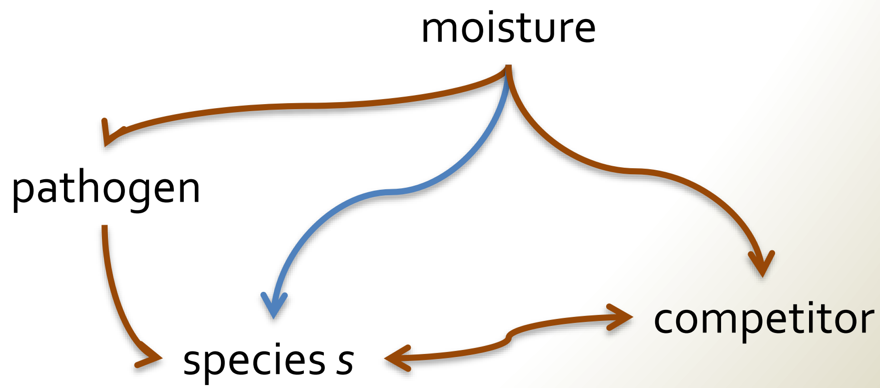
Diverse data: US Forest Inventory Analysis (FIA) Data

- 151,355 locations
- Millions of trees
- Plots re-censused every 5-10 years



Generalized joint attribute modeling—GJAM

- **All species jointly**
  - Direct effects (main effects and interactions)
  - Indirect effects of species on one another
- On the **observation scale** (no non-linear transformations)
- Massive **zeros**
- **Generative**:
  - predict communities given environment
  - inversely, environment given community (i.e. ***fingerprinting***)



Clark et al, ***Ecol Monogr*** 2017

Standard approach (e.g., glm,...)

$X \longrightarrow Y|X$

Predictors

Species data,
Continuous or
non-linear link

gjam idea

No nonlinear link

$$X \longrightarrow W|X \longrightarrow Y|W$$

Predictors

Continuous, joint

Species data, Any data type

Responses and species relationships through covariance

Interpret the data scale

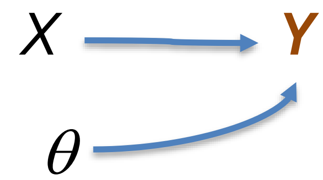
Role of prediction

- Generative model
  - *Predict the fitted data?*

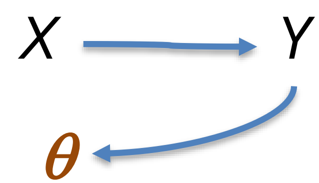
$$\begin{tikzcd} X \arrow[r] & Y \\ \theta \arrow[ur, bend right] & \end{tikzcd}$$

Role of prediction

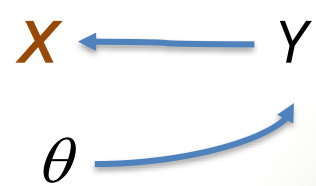
- Generative model
  - *Predict the fitted data?*



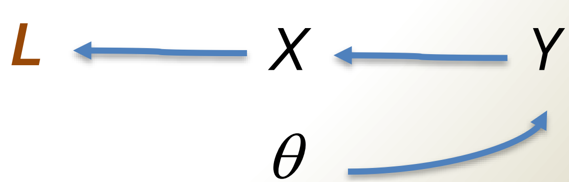
- Parameter estimation
  - *Sensitivity*



- Inverse prediction
  - *Environmental fingerprint*

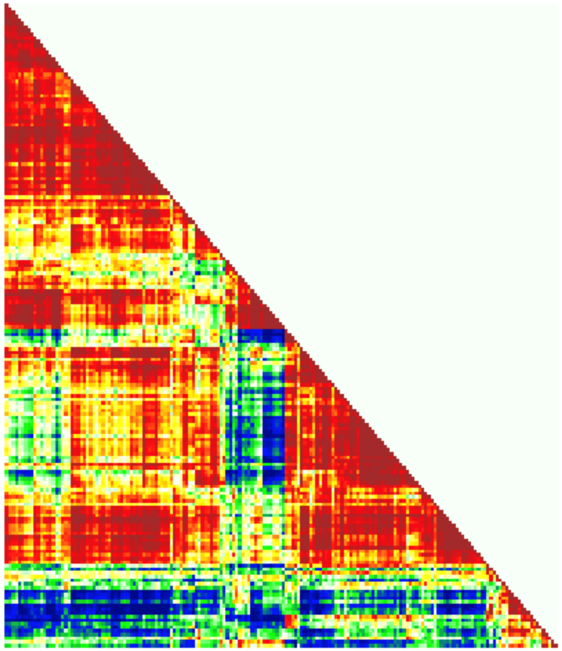


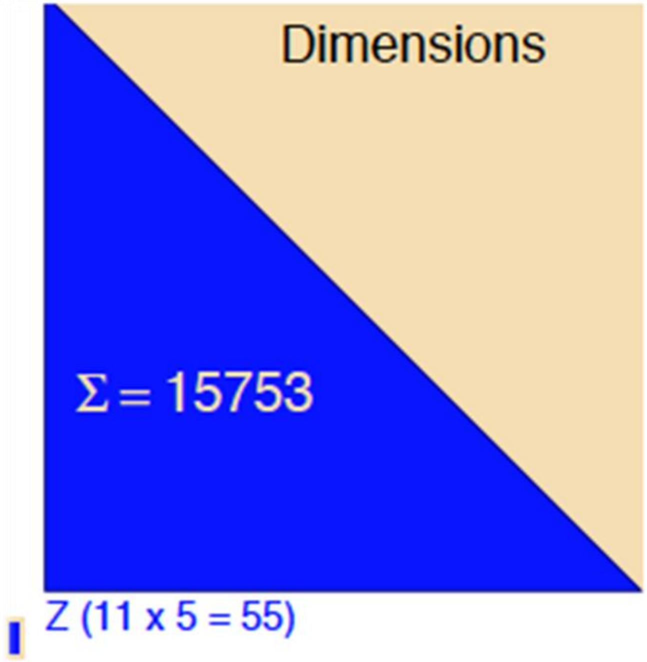
- Location fingerprint
  - Location uniquely determines community?



Dimension reduction

- 10^2 species means 10^4 parameters

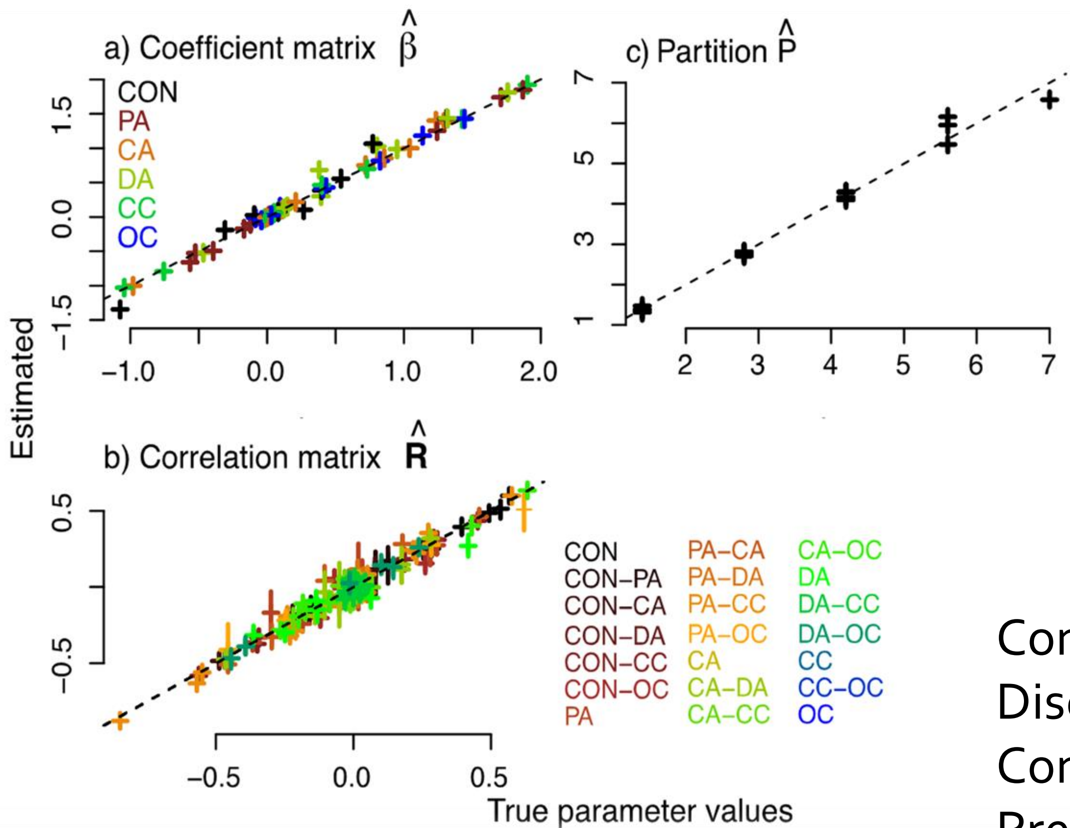




Taylor-Rodriguez, Gelfand, Clark, ***Bayesian Analysis***, 2017

Parameter recovery in simulation

Combine all data types



Continuous (CON)
Discrete abundance (DA)
Continuous abundance (CON)
Presence-absence (PA)
Composition count (CC)
Ordinal count (OC)

Clark et al. *Ecol Monogr* 2017

Why is GJAM model-based?

- **Generative** for community
  - Model-based sensitivity, uncertainty

- **Combine data** types; **uneven effort**

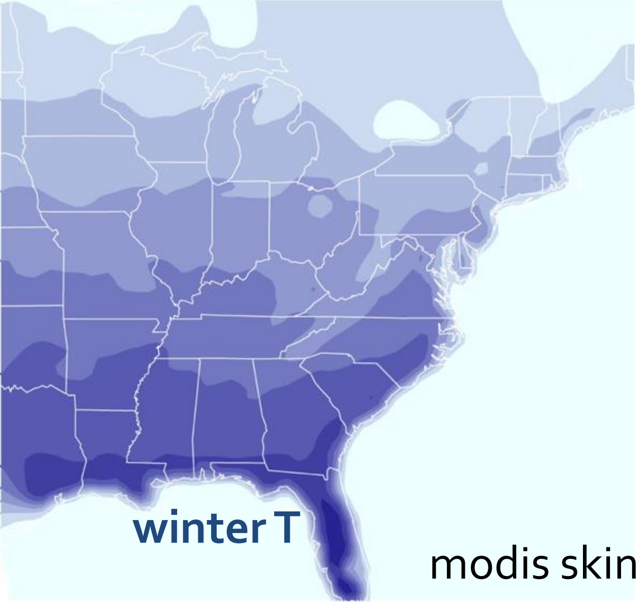
- **High-dimensional** (1000 species/OTUs)
  - Model-based aggregation

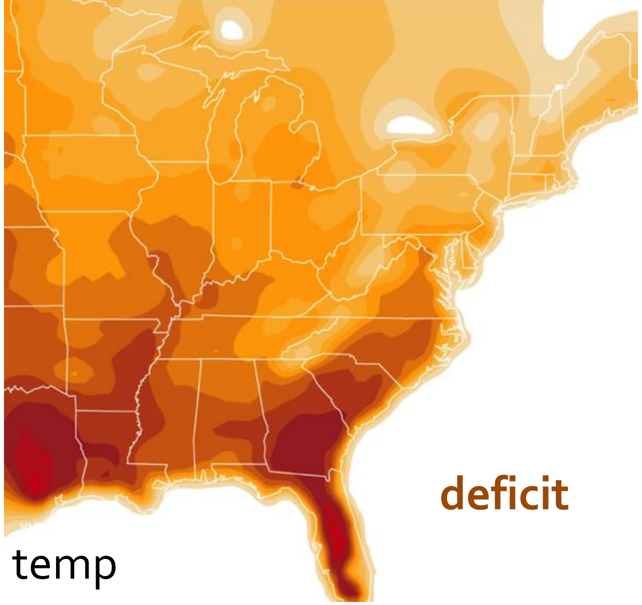
- Estimates on the **observation scale** (no non-linear link)

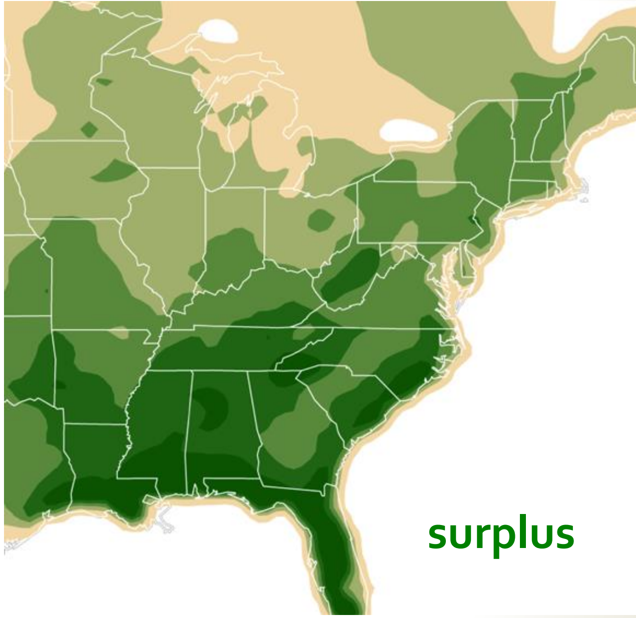
- Accurate **prediction**
  - **Forward**: $X \rightarrow Y$
  - **Inverse**: $X \leftarrow Y$
  - Map **fingerprint**: $L \leftarrow X \leftarrow Y$

GJAM for the joint community

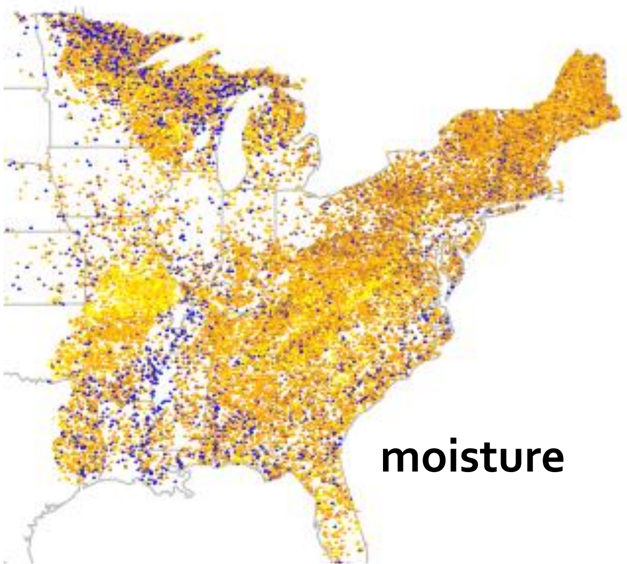
- *Application at NEON*
  - Which species are sensitive?
  - Environment and location fingerprints
  - Community change

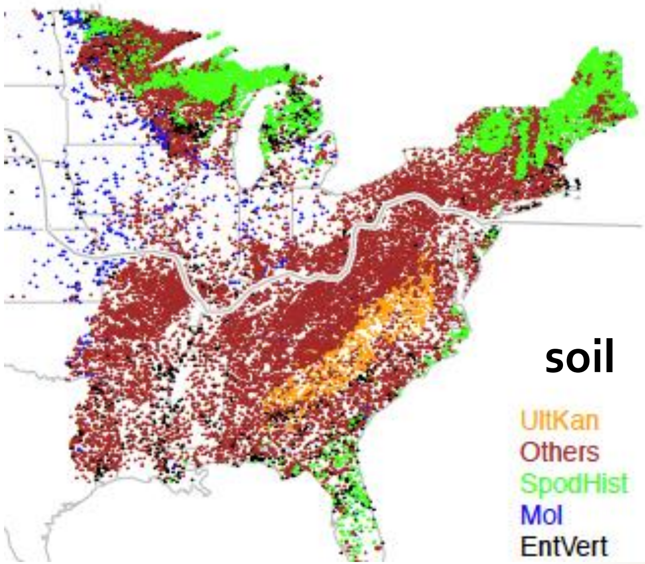






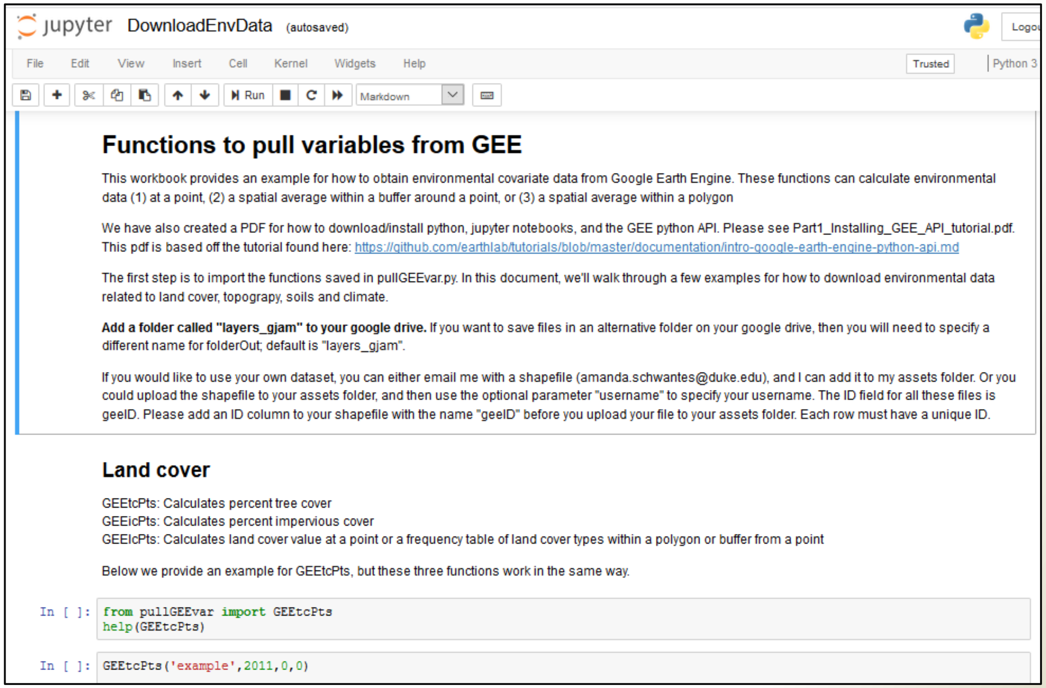
Cloud-based predictors of biodiversity change





Tutorials for data acquisition in GEE

- Environmental and remote sensing data
- Simple inputs:
  - dataset
  - metric of interest
  - temporal/spatial averaging



Automated workflows download/preprocess

- Geospatial climate, landscape variables
  - Climate: precipitation, PET, temperature, water deficit, VPD
  - Topography: slope, elevation, aspect
  - Soils: available water storage, % sand, % clay, …
  - Land cover

- Remote sensing
  - MODIS: LST, ET, GPP, LAI, EVI/NDVI, phenology
  - SMOS: soil moisture
  - Landsat: vegetation and water indices
  - Lidar

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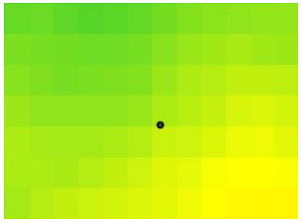
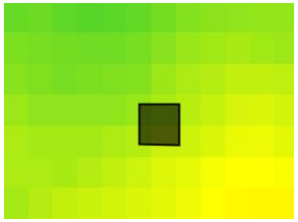
Cloud Computing

- Processing with GEE python API cloud-computing platform
  - Efficient pre-processing (e.g., filtering with QC bands from MODIS, Landsat products)
  - Temporal averaging: months, seasons, years
  - Spatial averaging: points, plots/grids, points with buffers

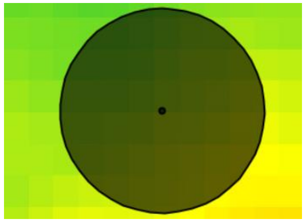
point



plot

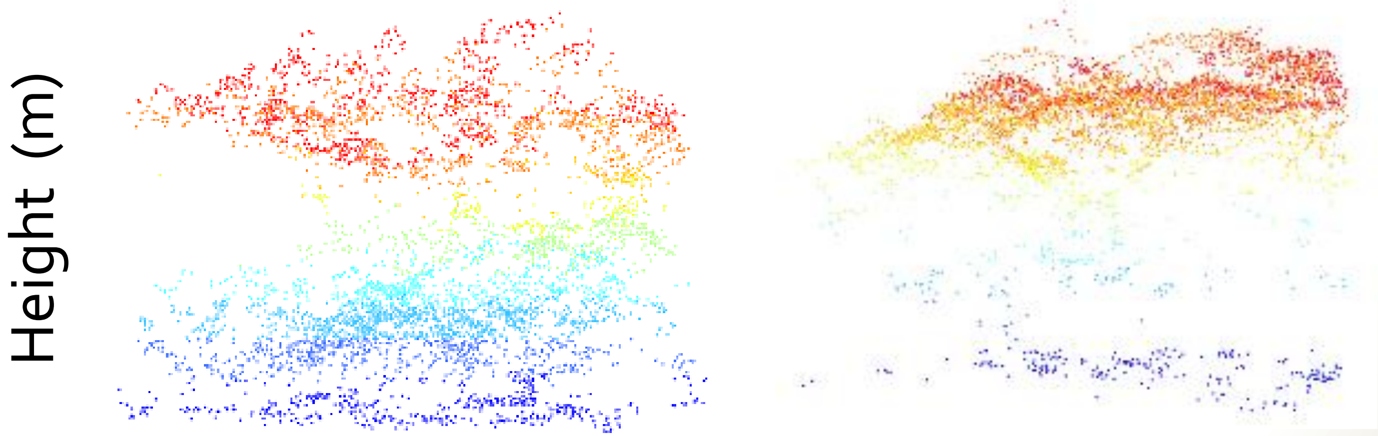


Buffer from point



Lidar: habitat structure

- Data processed for 2017, ~3,000 plots, 39 sites
- Habitat structure metrics



Plot HARV34:	Plot HARV36:
relief ratio: 0.52	0.76
max height: 29.5	29.1
mean height: 15.2 $\pm$ 9.5	22.4 $\pm$ 6.5

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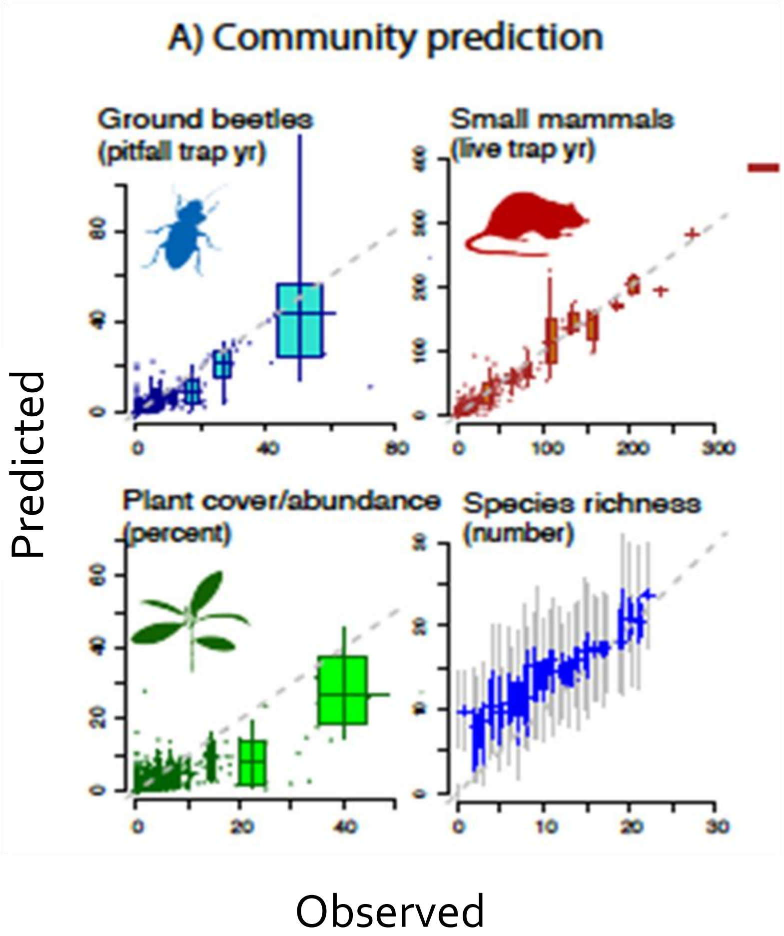
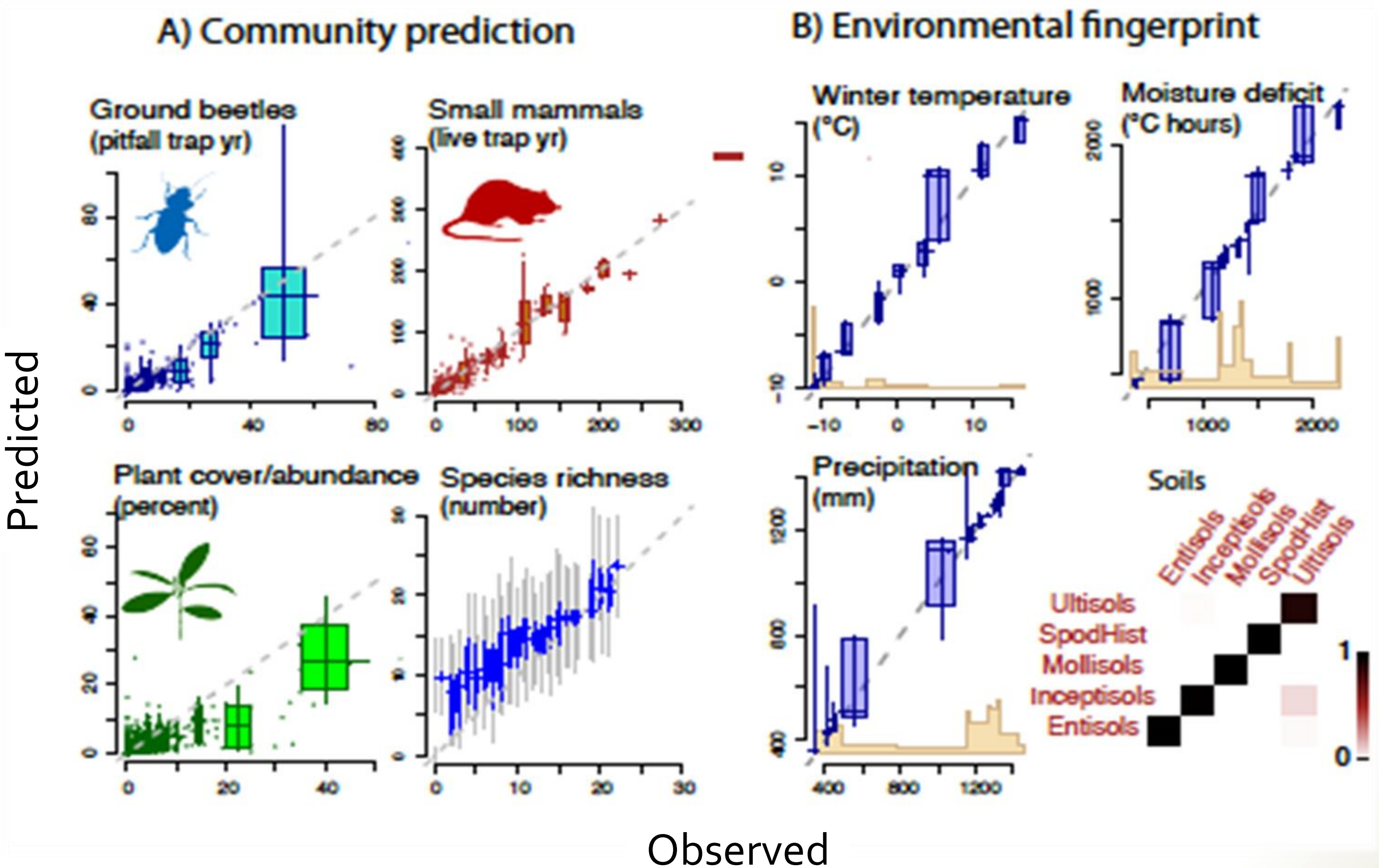
Precision prediction: *one distribution for all species*



- Taxonomically diverse species groups

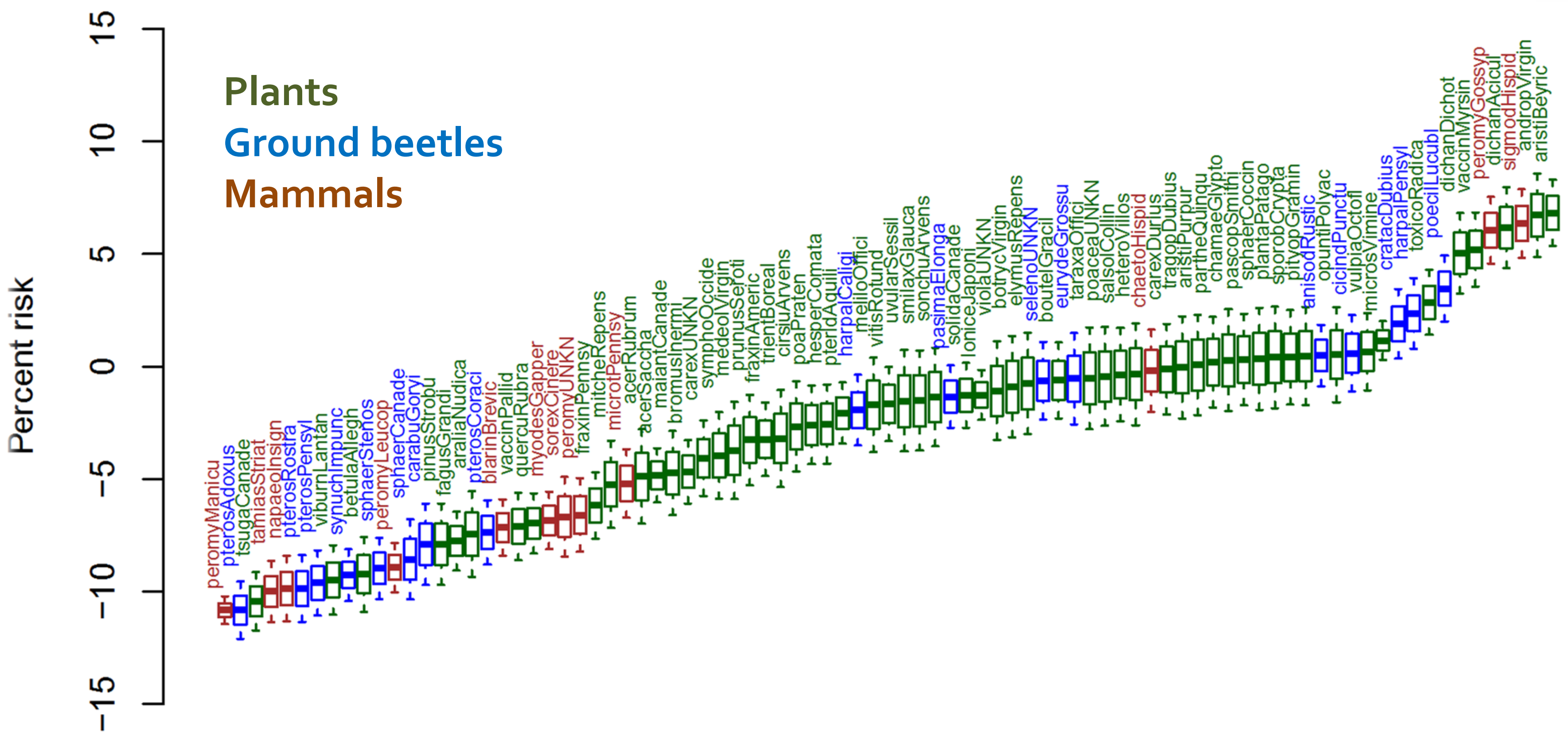
Ground beetle pitfall
Plant cover plot
rodent live trap

The community 'fingerprints' its environment…



Species at risk with +2°C

- The value of a generative model-based



Clark et al. 2017, ***Ecol Monogr***

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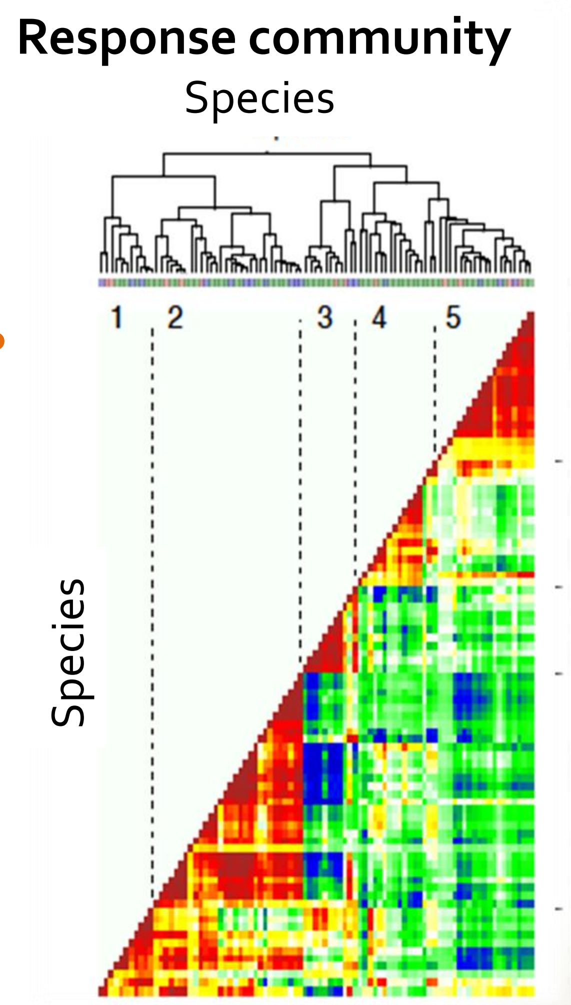
Communities defined by response to the environment

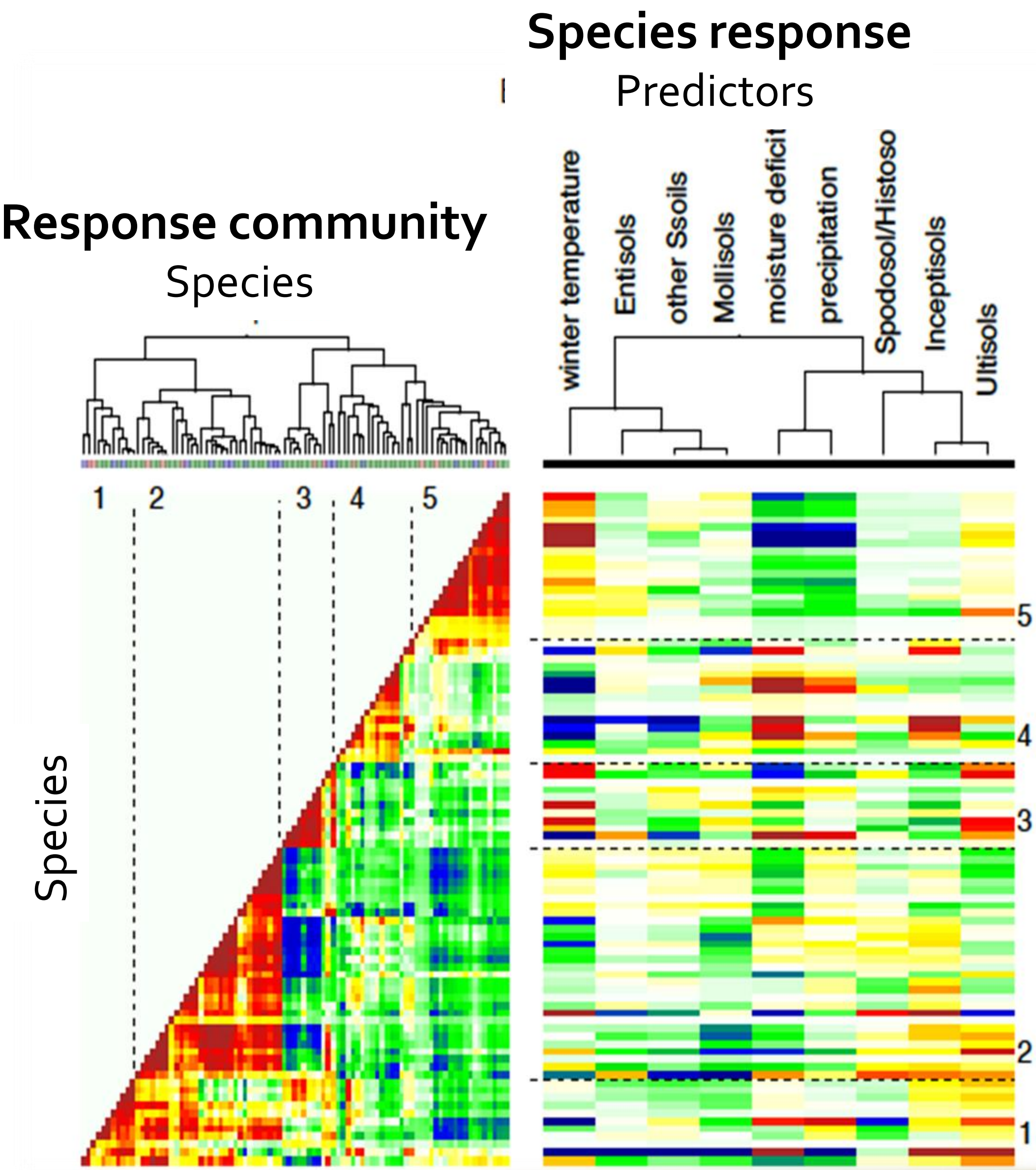
- *left: communities defined by response*



Clark et al. 2017, ***Ecol Monogr***

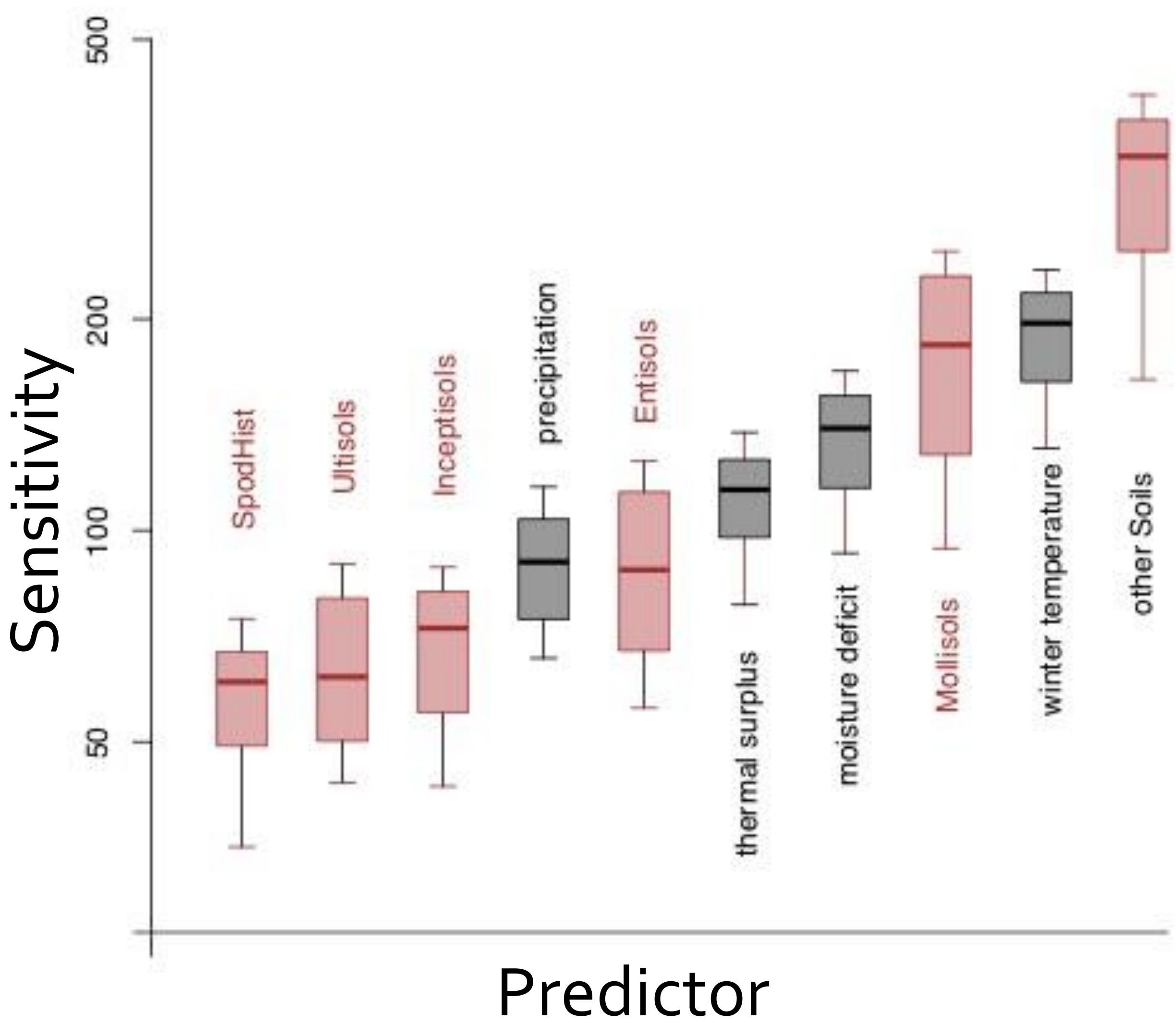
Communities defined by response to the environment

- *left: communities defined by response*
- *right: species by environment responses*



Clark et al. 2017, ***Ecol Monogr***

Community-wide effects



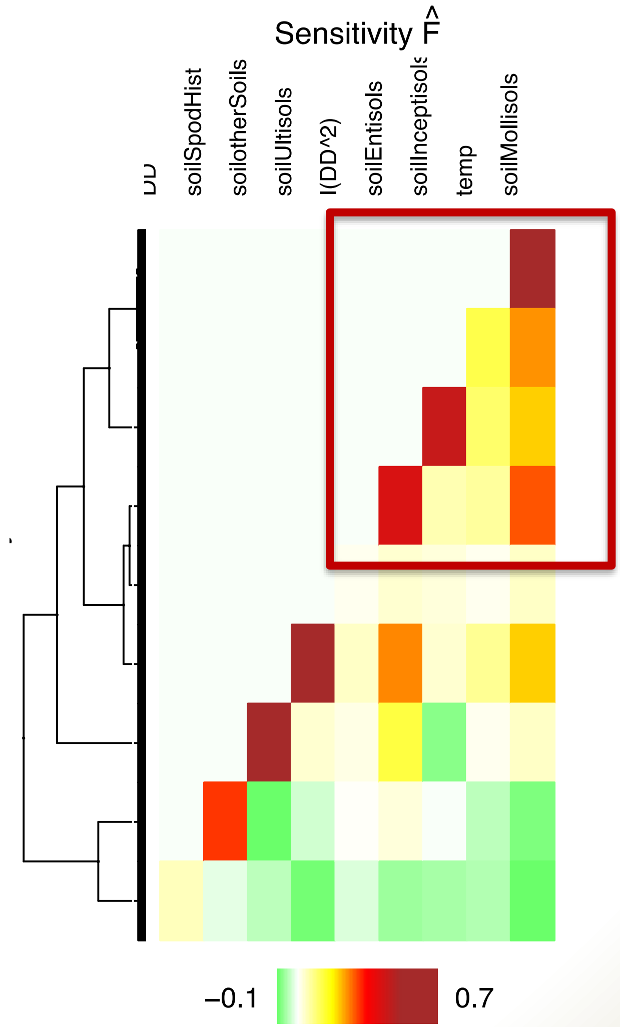
Clark et al. 2017, ***Ecol Monogr***

Environment defined by effect on community

Community effect

Predictors

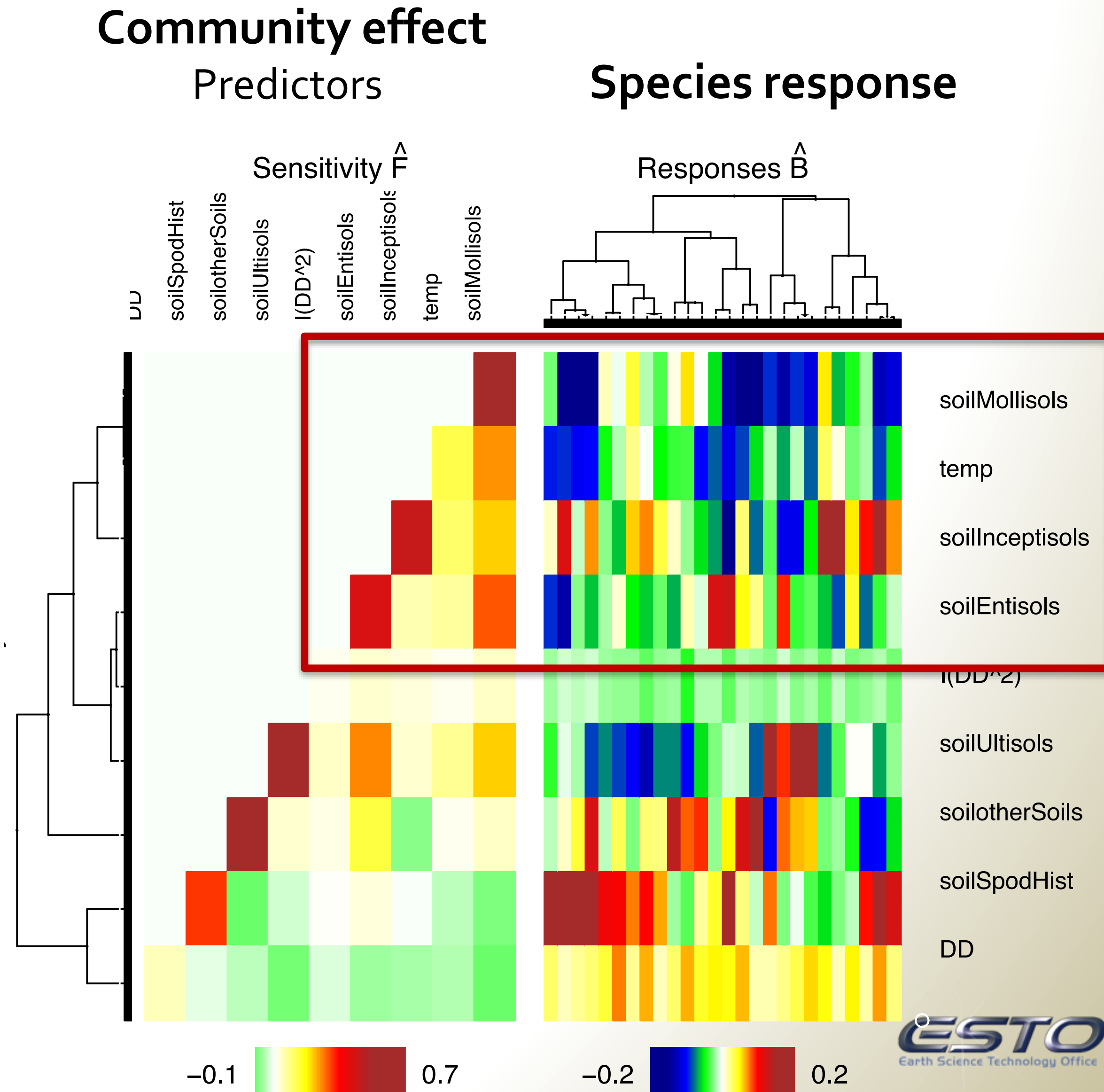
Species response



- *left: predictors defined by effect*

Clark et al. 2017, ***Ecol Monogr***

Environment defined by effect on community

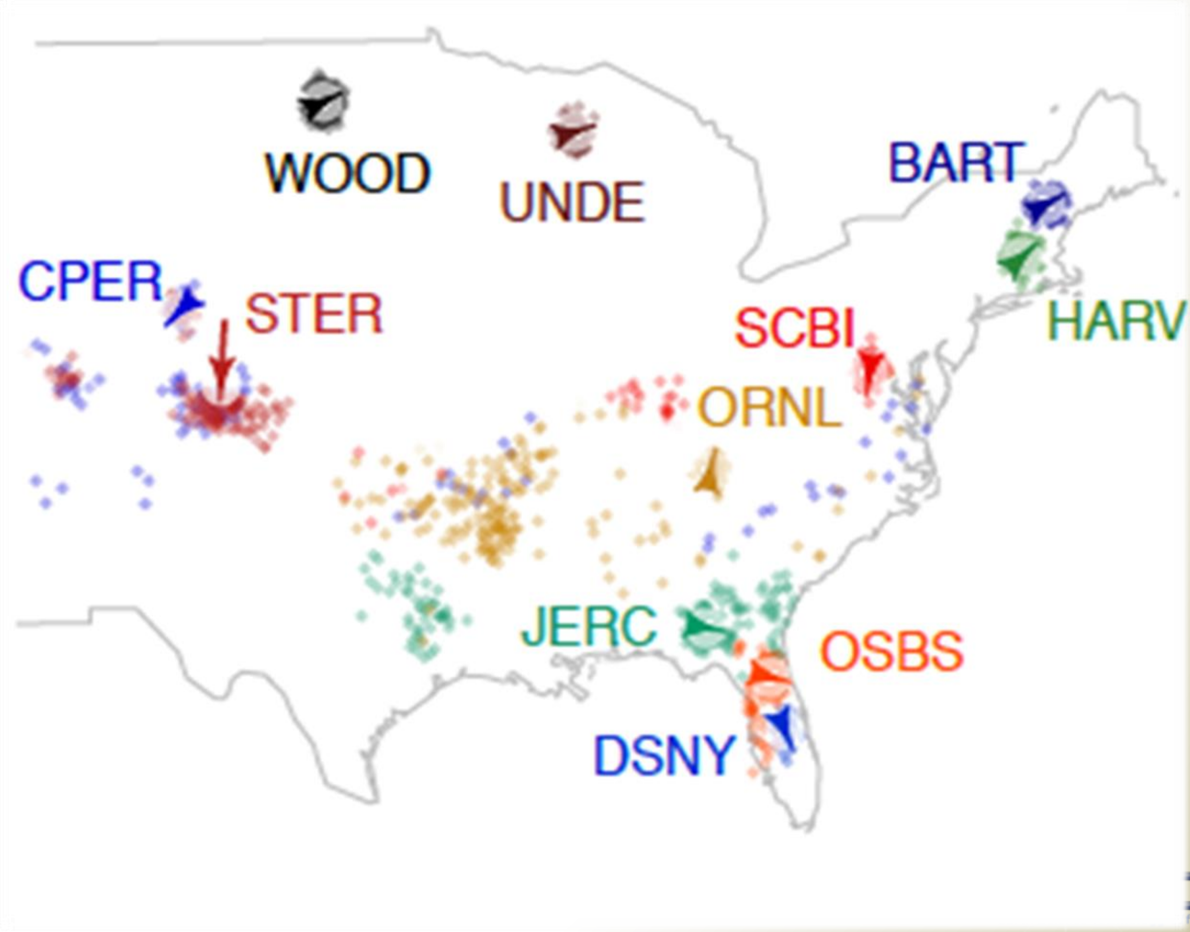


- *left: predictors defined by effect*
- *right: species by environment responses*

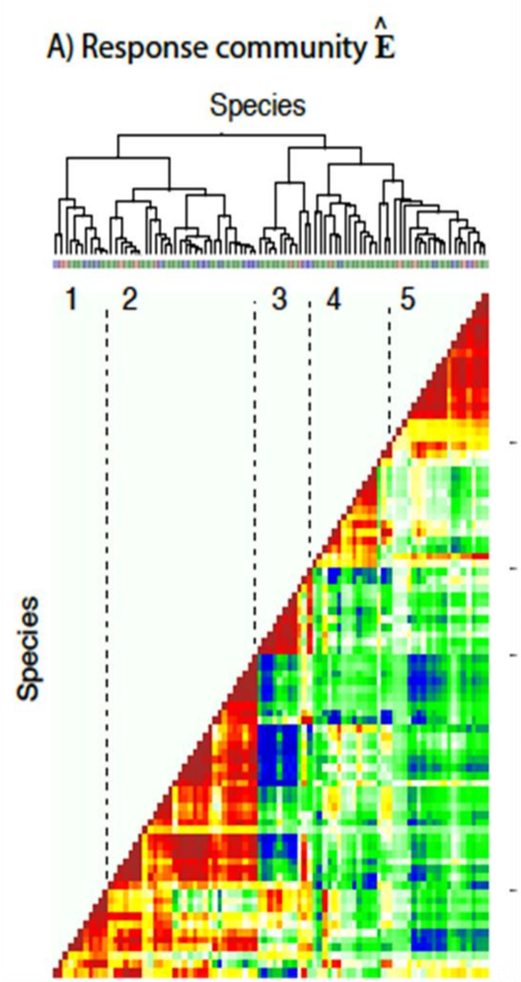
Clark et al. 2017, ***Ecol Monogr***

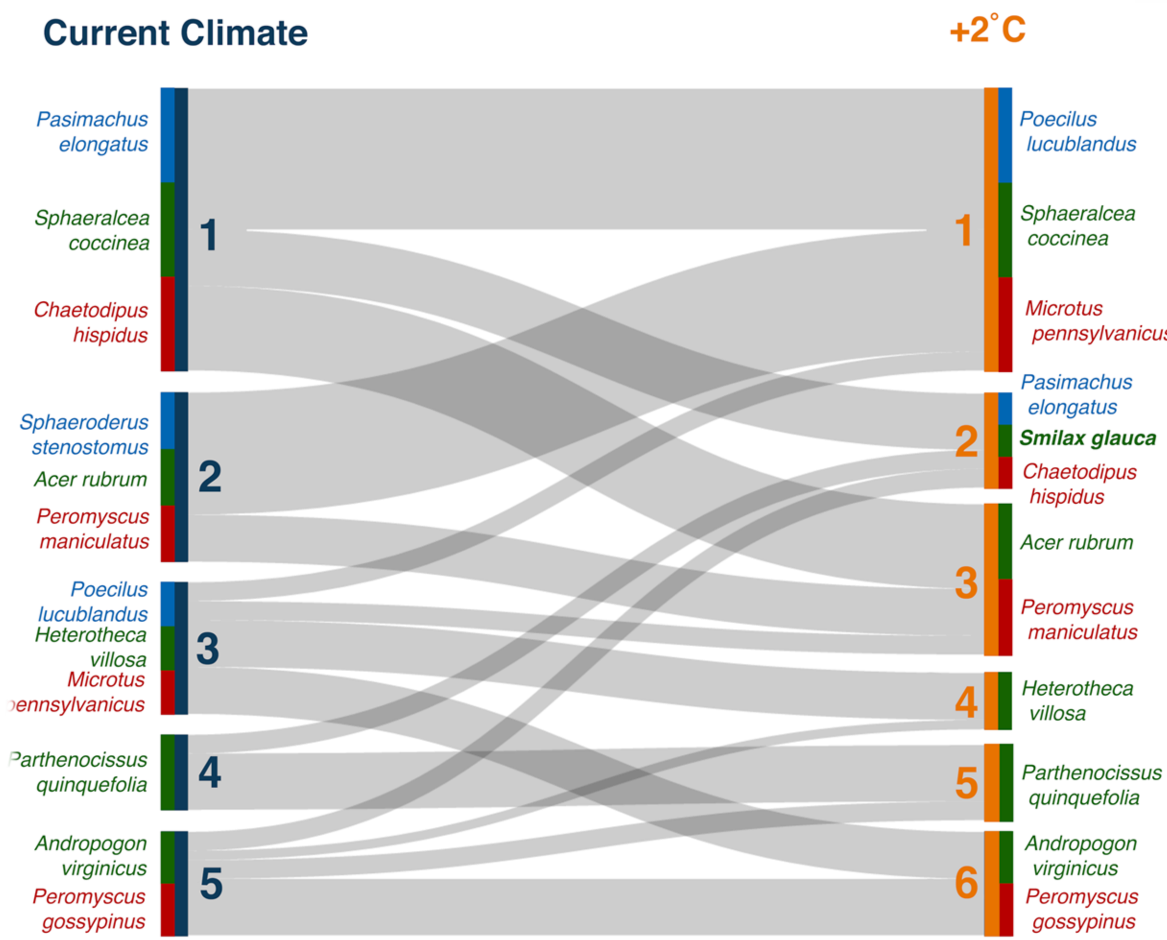
Location fingerprint
the community knows its location

Arrows point from true sample location to predicted sample location



+2°C: Community reorganization

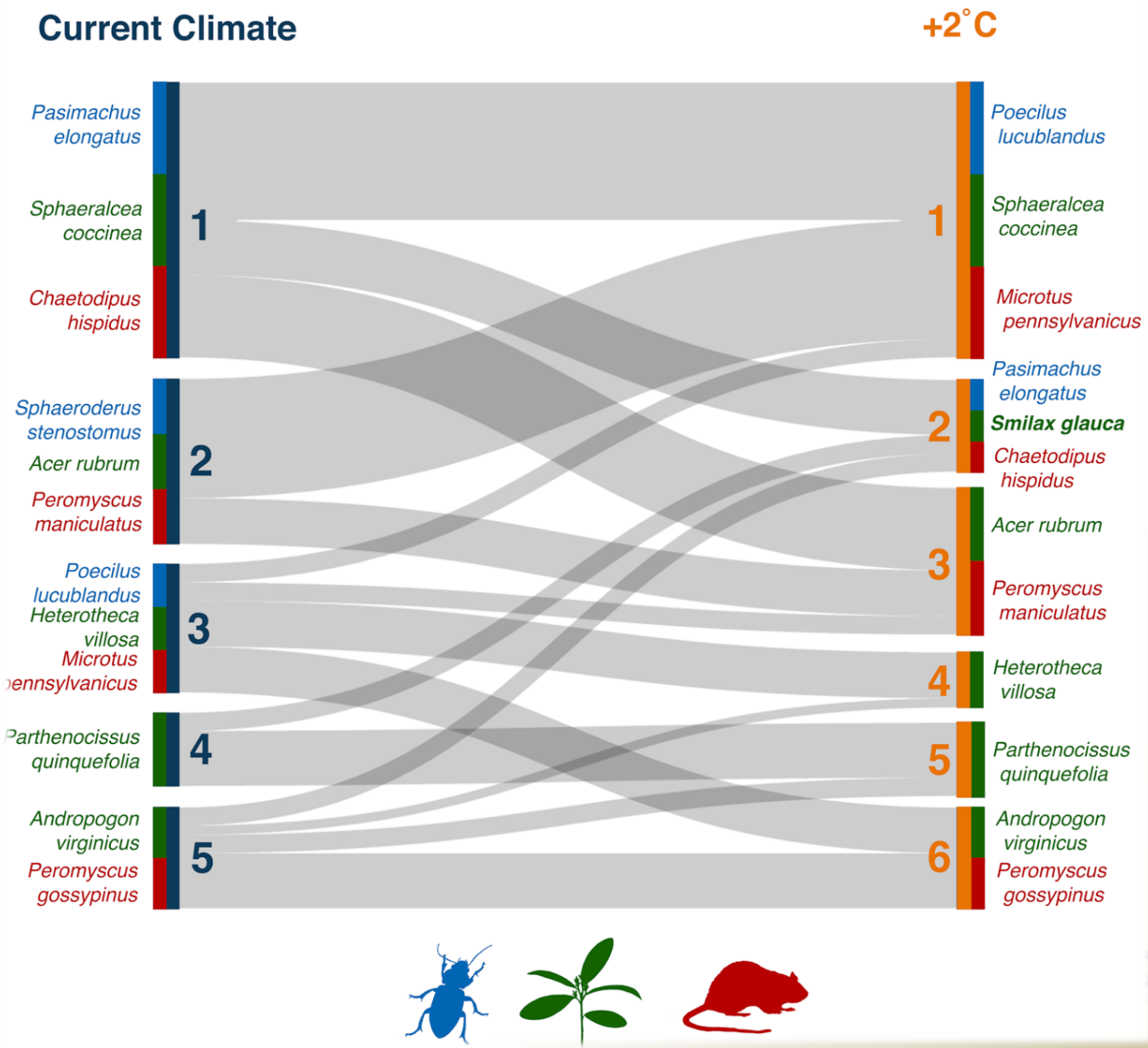




- Current climate

+2°C: Community reorganization

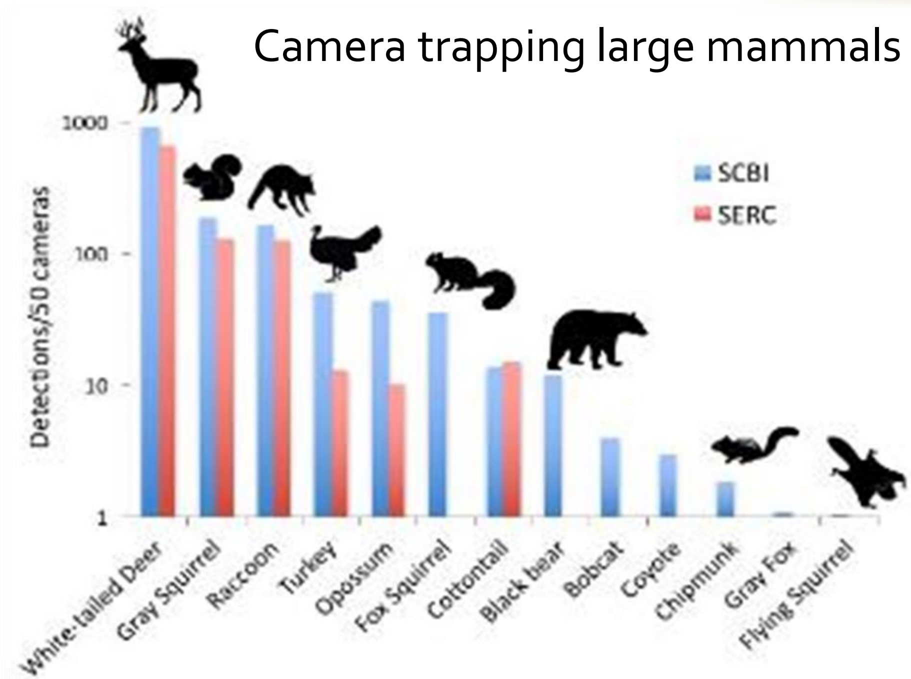
- Change mean and variance of all climate variables, mediated by habitat



The missing component: food

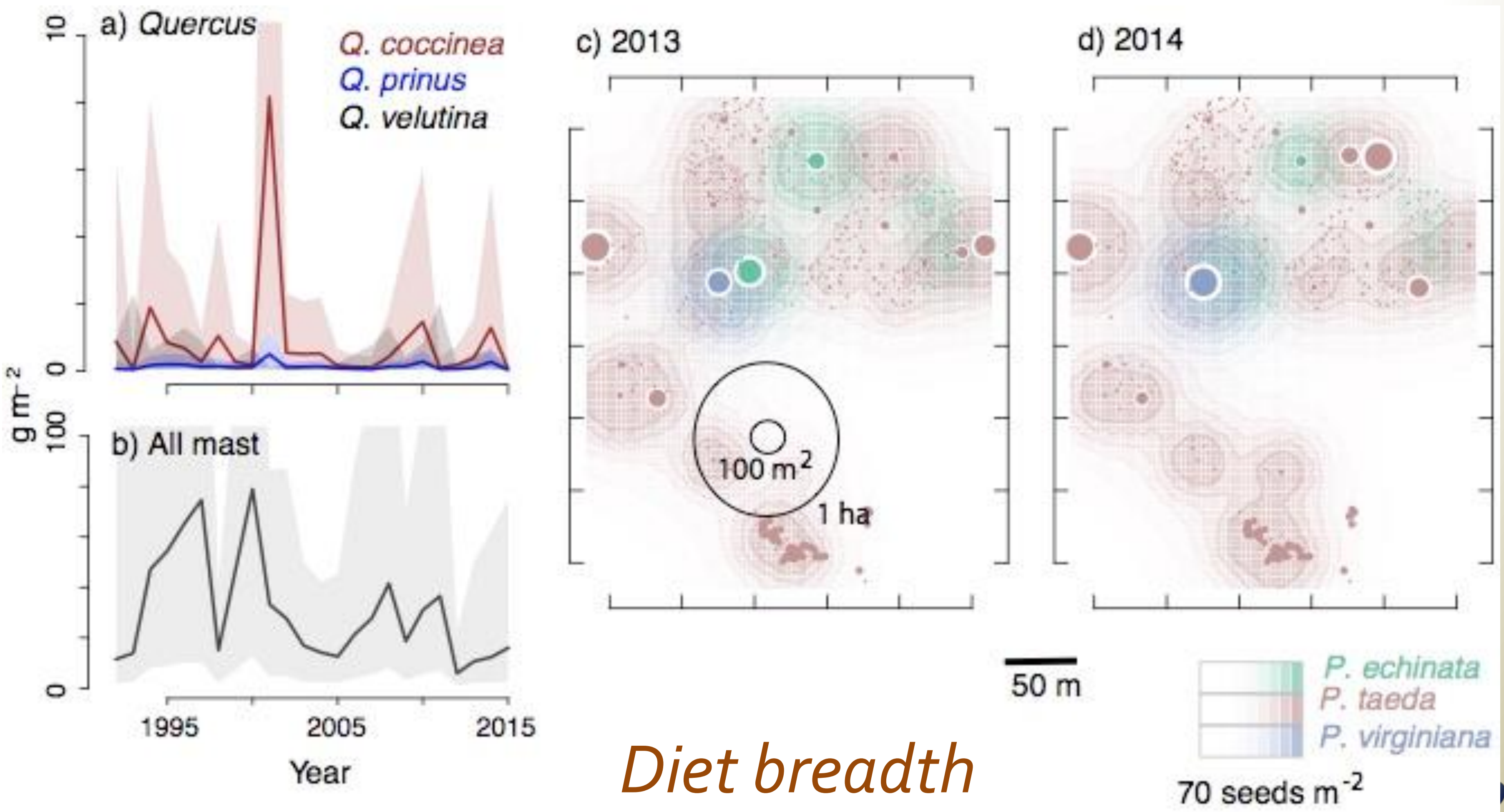
- Biodiversity predictions emphasize climate/edaphic
- Challenge:

  - Mean benefit/variance cost
  - Scale-dependence: each consumer in its own way



Scale-dependent variance in resources

In time *In space*



Diet breadth

Mean benefit vs. variance cost of resources: scale-dependence, diet breadth

Google Earth Engine

Climate variables

Habitat

Long-Term Plots

Tree Characteristics

Seed Rain

Source detection: fecundity of each tree:

Seed Rain = Effort x Fecundity x Dispersal

Habitat-specific mean vs variance at all scales:

Resource Score = Mean Seed Rain x Nutritional Quality / Variance

MASTIF: translate individual fecundity to habitat resource value

Resource Score = Mean Seed Rain x Nutritional Quality / Variance

- Nutritional database of consumer, site-specific resource scores

- Use estimates of fecundity and dispersal to expand inference to FIA

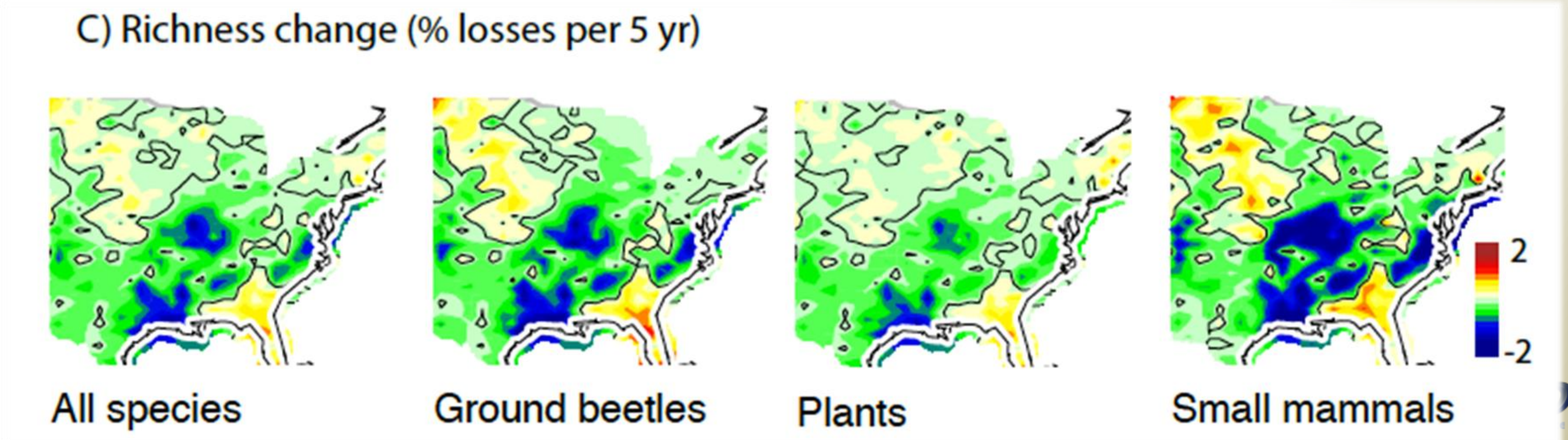
Efficient to add new datasets

- **Biodiversity data**
  - NEON: bird counts, pathogen status of ticks, mammals
  - NSF funding: mast availability and large vertebrates
  - FIA
  - eBird/BBS
  - Scripts/tutorials on GitHub/CRAN for user data
- **Environmental, habitat, remote sensing**
  - Incorporating Lidar from NEON
  - Integrating additional datasets with GEE
  - Download/pre-process from NASA's DAACs for remote sensing data not available on GEE

Web-based predictions

http://www.pbgjam.org/

- Location-based
- Species or species group
- Question-driven
- Explanation-the important variables contributing to change



Fully open-source, algorithm documentation

- Fully open-source on CRAN
- Distribution theory in primary literature
- Algorithm documentation Rmarkdown vignettes, R help pages
- GJAM on cran: http://rpubs.com/jimclark/234762
  - Installed > 16,000 times

- MASTIF built, ready for cran: http://rpubs.com/jimclark/281413

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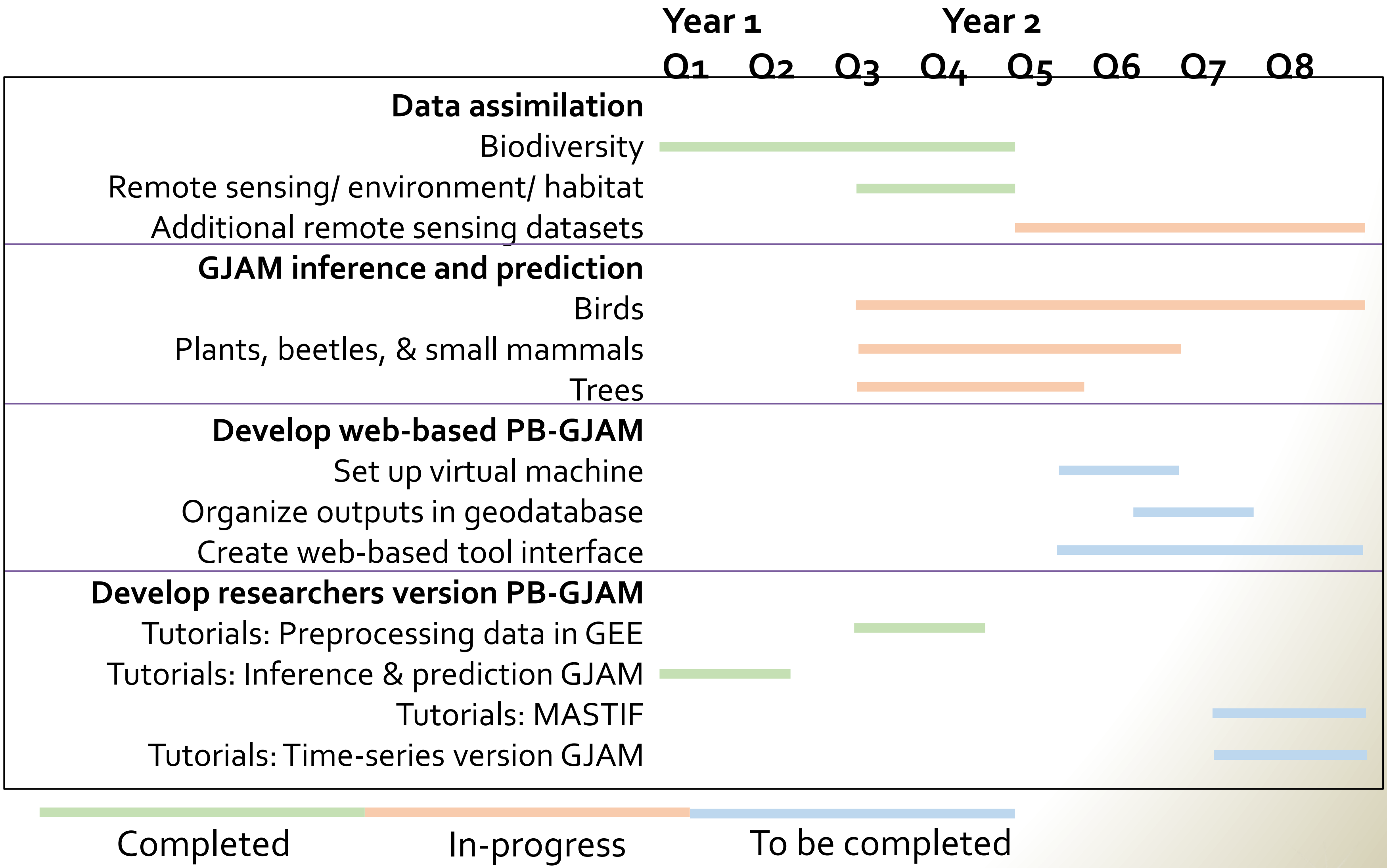
Project Schedule



Additional info

- Bachelot B., Uriarte M., Muscarella R., Forero-Montana J., Thompson J., McGuire K., Zimmerman J.K., Swenson N.G. and J.S. Clark. 2018. *Associations among arbuscular mycorrhizal fungi and seedlings are predicted to change with tree successional status*. ***Ecology***.

- Clark. J.S. 2016. *Why species tell us more about traits than traits tell us about species: predictive analysis*. ***Ecology***.

- Clark. J.S. 2016. **gjam: Generalized Joint Attribute Modeling,** https://cran.r-project.org/web/packages/gjam/index.html

- Clark, J.S., D. Nemergut, B. Seyednasrollah, P. Turner, and S. Zhang. 2017. *Generalized joint attribute modeling for biodiversity analysis: Median-zero, multivariate, multifarious data*. ***Ecological Monographs***.

- Taylor-Rodriquez, D., Kaufeld, K.A., E. M. Schliep, J.S. Clark, and A.E. Gelfand. 2017. *Joint species distribution modeling: dimension reduction using Dirichlet processes*. ***Bayesian Analysis***.