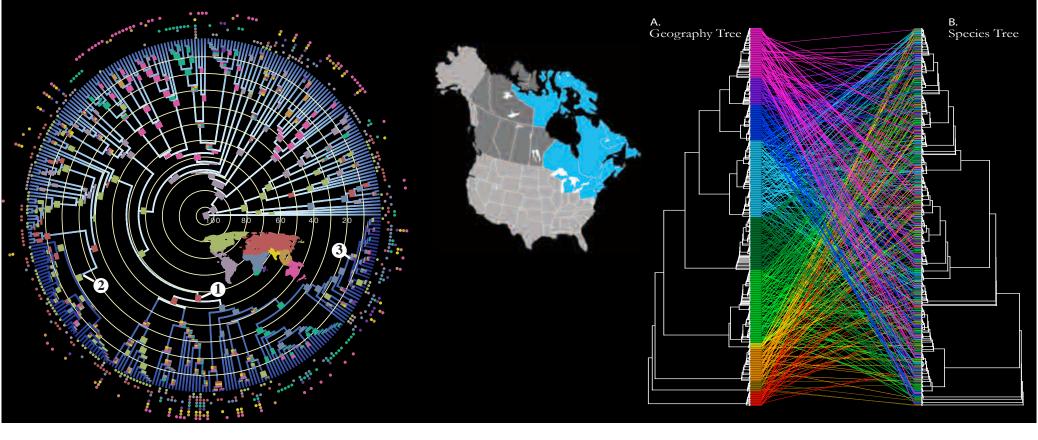


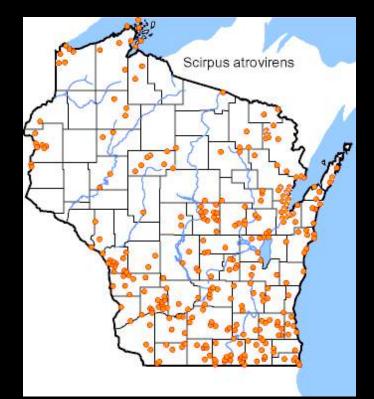
# Harvesting and harnessing data for biogeographical research



inventories and surveys

- natural areas, preserves, state forests, private properties
- development permits
- herbarium/museum specimens
  - collectors often target specific places or taxa
  - records of what, where, when, and by whom

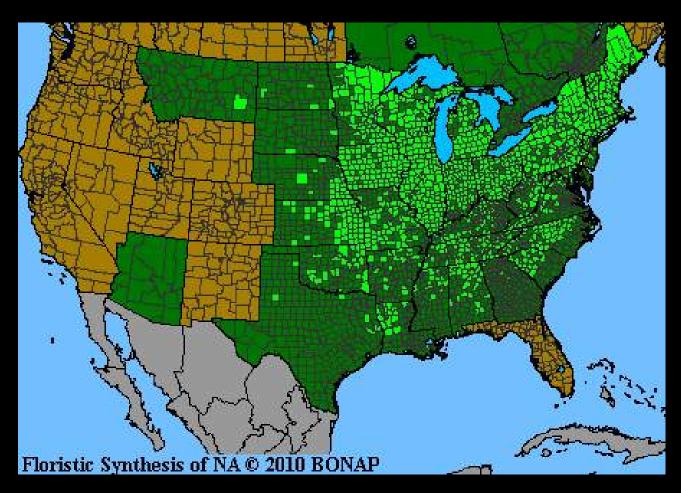
#### $\sum$ Local observations = State Flora





black bulrush

#### ∑ State Floras = National Flora





black bulrush

#### $\sum$ National Floras = Global Flora





black bulrush

# Who manages these data?



# **Benefits of Digitization**

- Preservation of rare/fragile specimens
- Easier to query a database than physical collections (e.g., <u>WISFLORA</u>)
- Efficient data sharing
- Collation yields powerful data repositories

# **Digitization of Distribution Data**





KISCONSIN GREEN County Anemone patens L

ivery common on northeast face and class of the bloff

Noralt Bloff Prairie SNA Hug 39, 4 miles West of Albany (T. 3 N: R. 8 E; Sect. 25) Date: 4-17-91 No. 7

Collector: Rick Horton

MAPPED FOR 1996 FLORA OF WISCONSIN





### Examples of data repositories

- 1. Wisconsin Flora more on this later
- 2. North America Digital Flora
- 3. Biota of North America Project
- 4. Global Biodiversity Information Facility

# North America Digital Flora

- Pros:
  - Great for generating species lists
  - Can query by species, attribute, or geography
  - Incorporates interesting GIS layers
- Cons:
  - Limited to wetland species
  - Geography search lacks precision



- Pros:
  - Comprehensive of NA diversity
  - Great, easy to use distribution maps
- Cons:
  - Can't query the data
  - Can't download data
  - North America only
  - Poor resolution in Canada



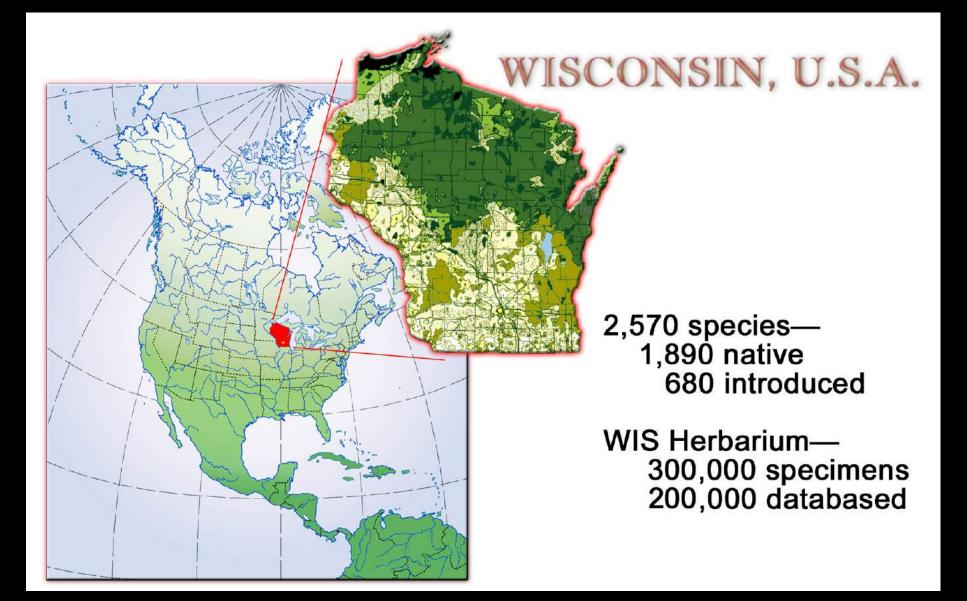
- Pros
  - Global data of plants, animals, fungi
  - Database is fully searchable
  - Data are downloadable
- Cons
  - Data are incomplete (WIS not in yet)
  - Some records are suspect

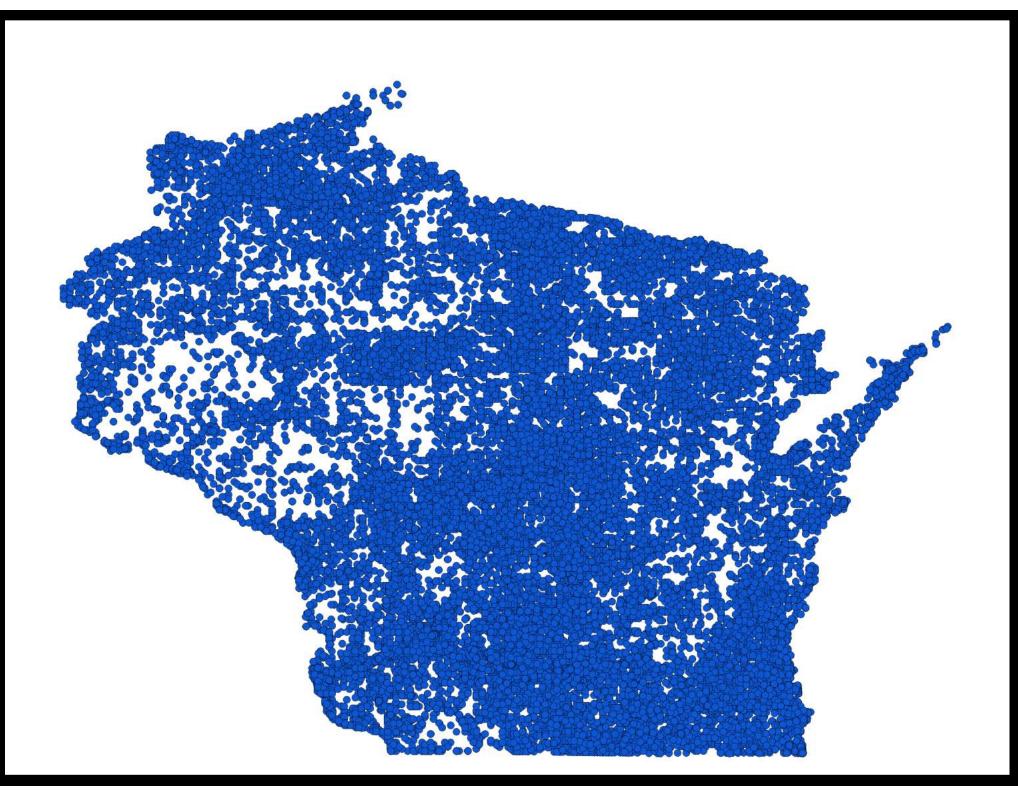
## What can you do with these data?

- Test biogeographic patterns in Wiscosnin
- Historical biogeography
- Characterize species distributions
- Obtain species "climatic envelope"
- Identify areas exhibiting high levels of endemism
- Predict responses to global climate change
- Track and predict spread of invasive species

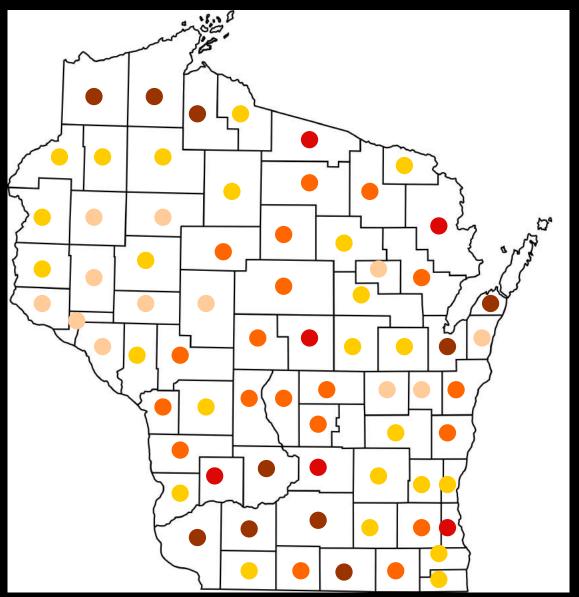
#### All without spending \$1

#### Wisconsin Flora Mapping Project





#### Wisconsin Flora Mapping Project

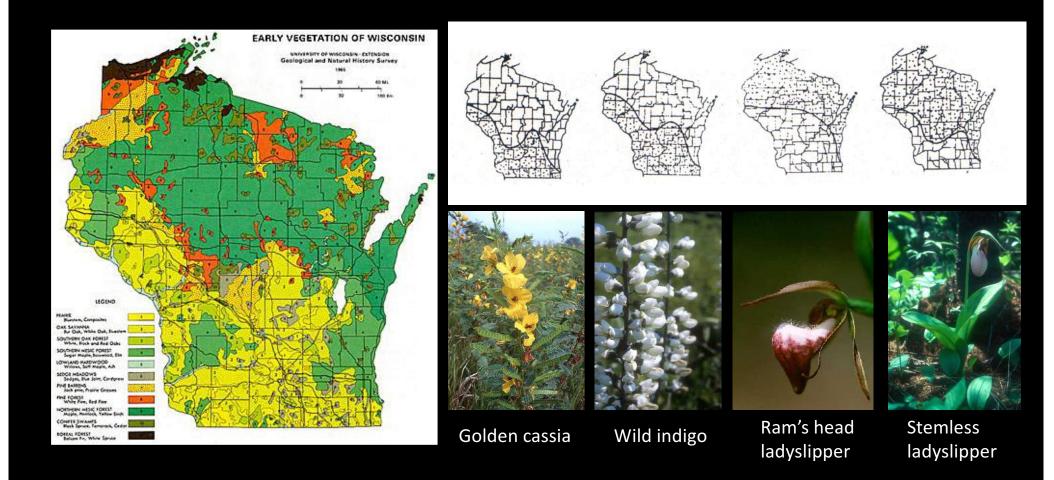


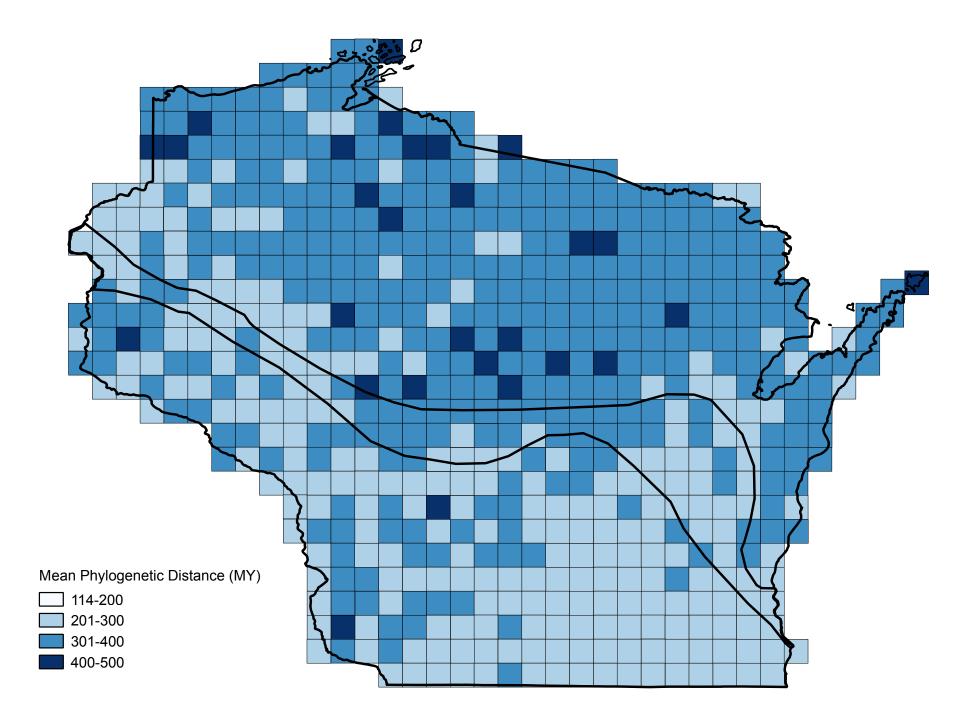
Wisconsin is not equally inventoried

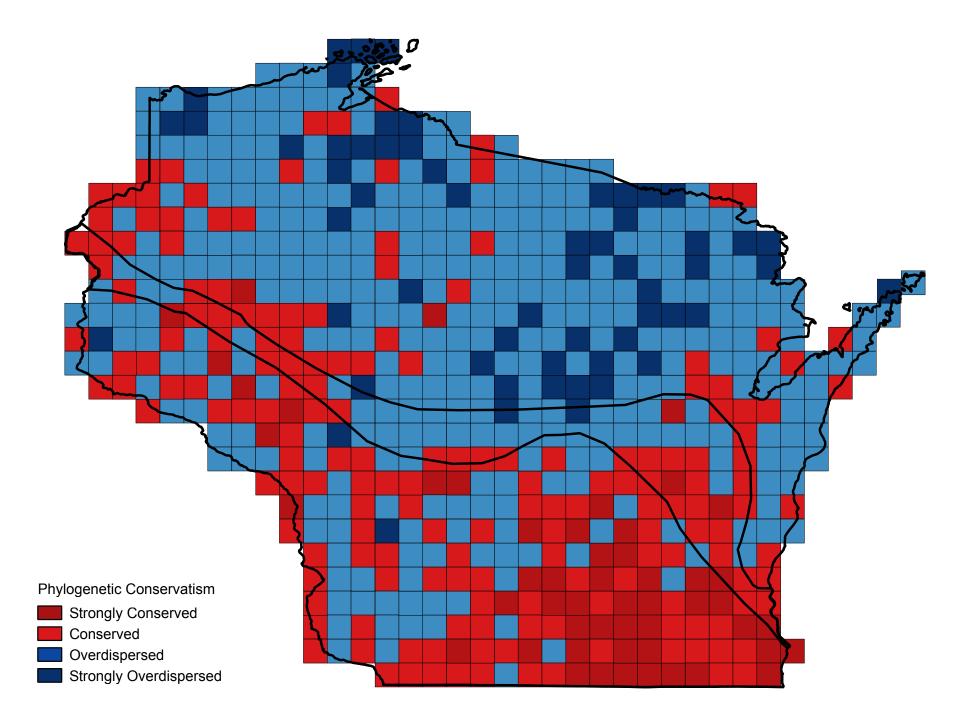
- > 10,000 specimens
- 8,000 6,000
- 6,000 4,000
- 2,000 4,000
- < 2,000

#### Wisconsin Flora Mapping Project

The tension zone separating the two provinces is based on the upper and lower limits of the southern and northern species, respectively.







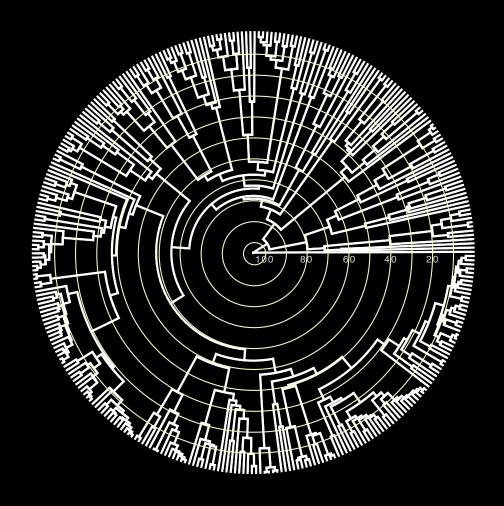
 If you wanted, you could build a phylogeny of 300,000 organisms using 187 billion base pairs from <u>Genbank</u>





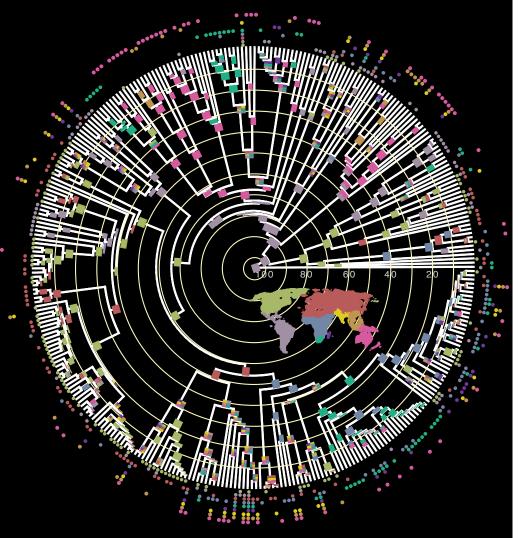
e.g., family Cyperaceae (sedges, bulrushes) – Spalink et al. 2016

- Build a phylogeny
  - Date the phylogeny



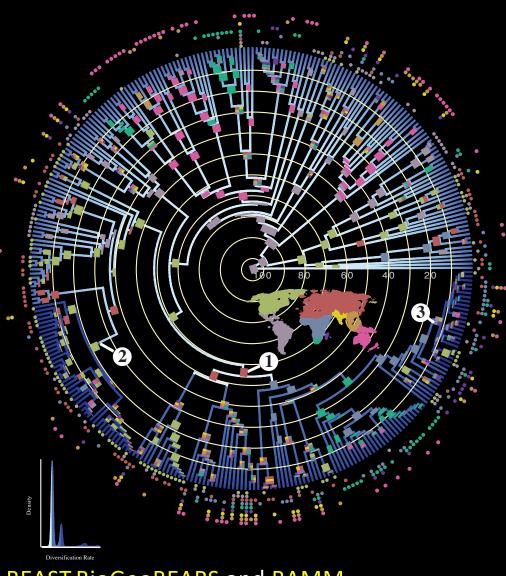
Data from **Genbank**, analyzed using **BEAST** 

- Build a phylogeny
  - Date the phylogeny
  - Reconstruct areas inhabited by ancestors



Data from <u>Genbank + eMonocot</u>, analyzed using <u>BEAST</u> and <u>BioGeoBEARS</u>

- Build a phylogeny
  - Date the phylogeny
  - Reconstruct areas
     inhabited by ancestors
  - Measure rates of diversification
  - Track evolution of morphological traits across time and space



Data from Genbank + eMonocot, analyzed using BEAST, BioGeoBEARS and BAMM

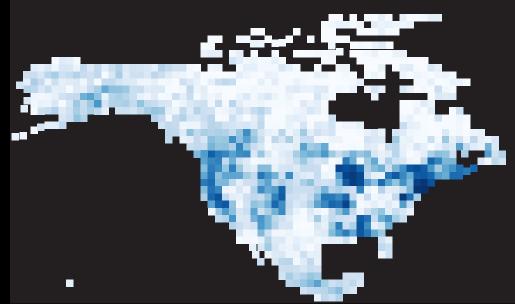
#### **High Resolution Species Distributions**

Characterize distributions

 of species for 1.45 million
 species using 460 million
 geo-referenced
 occurrences

#### **High Resolution Species Distributions**

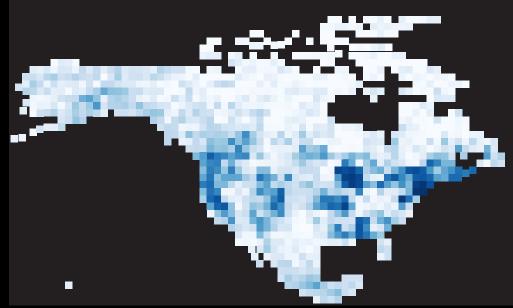
- Characterize distributions of species for 1.45 million species using 460 million geo-referenced occurrences
  - Identify species rich areas

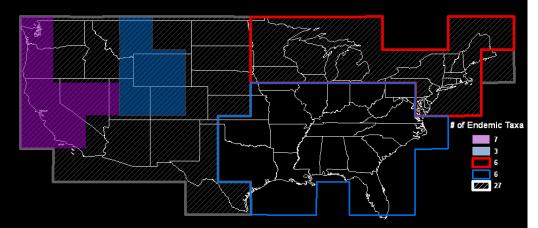


Data from <u>GBIF</u>, analyzed in <u>QGIS</u>

#### **High Resolution Species Distributions**

- Characterize distributions of species for 1.45 million species using 460 million geo-referenced occurrences
  - Identify species rich areas
  - Define regions with high levels of rare or endemic taxa



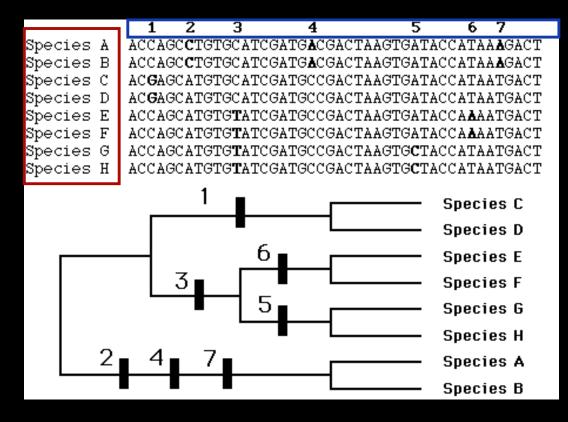


Data from <u>GBIF</u>, analyzed in <u>QGIS</u> and <u>PAUP\*</u> - available in systematics lab

# Parsimony Analysis of Endemicity (PAE)

Parsimony: typically used in phylogenetics...

#### Species Characters

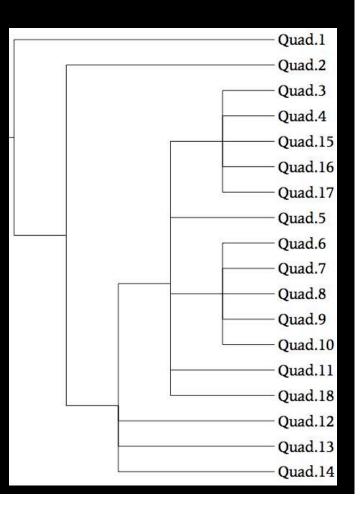


# Parsimony Analysis of Endemicity (PAE)

#### ...but, can be applied to PAE

|         | Species A | Species B | Species C | Species D | Species E | Species F | Species G | Species H |
|---------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|-----------|
| Area 1  | 1         | 0         | 1         | 0         | 0         | 0         | 0         | 0         |
| Area 2  | 1         | 0         | 1         | 0         | 0         | 0         | 0         | 0         |
| Area 3  | 0         | 1         | 0         | 1         | 0         | 0         | 0         | 0         |
| Area 4  | 0         | 1         | 0         | 1         | 0         | 0         | 0         | 0         |
| Area 5  | 0         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |
| Area 6  | 0         | 0         | 0         | 0         | 1         | 1         | 0         | 0         |
| Area 7  | 0         | 0         | 0         | 0         | 1         | 1         | 0         | 0         |
| Area 8  | 0         | 0         | 0         | 0         | 1         | 1         | 0         | 0         |
| Area 9  | 0         | 0         | 0         | 0         | 1         | 1         | 0         | 0         |
| Area 10 | 0         | 0         | 0         | 0         | 1         | 1         | 0         | 0         |
| Area 11 | 0         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |
| Area 12 | 1         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |
| Area 13 | 1         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |
| Area 14 | 1         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |
| Area 15 | 0         | 1         | 0         | 1         | 0         | 0         | 0         | 0         |
| Area 16 | 0         | 1         | 0         | 1         | 0         | 0         | 0         | 0         |
| Area 17 | 0         | 1         | 0         | 1         | 0         | 0         | 0         | 0         |
| Area 18 | 0         | 0         | 0         | 0         | 0         | 0         | 0         | 0         |

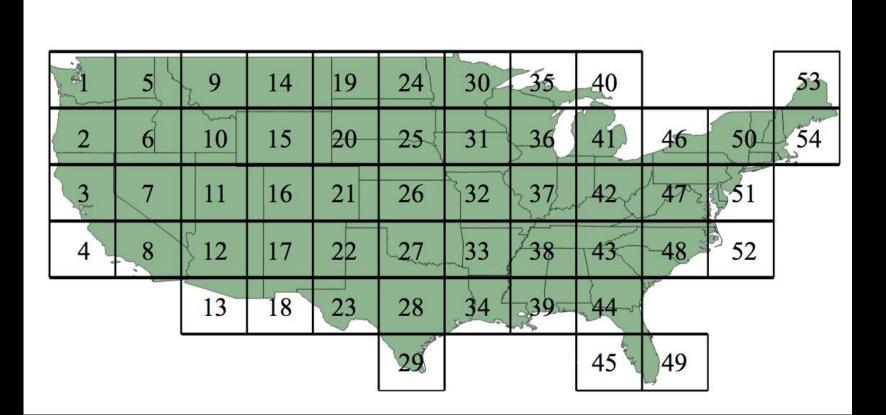
where geographic Areas are treated as taxa, and the presence/absence of the species serve as Characters



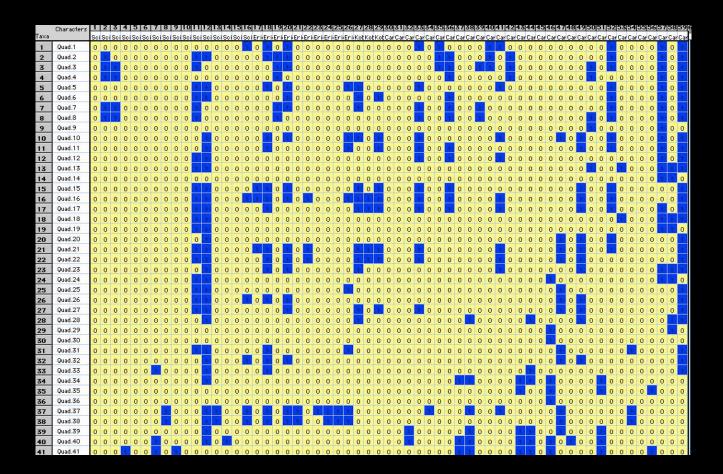
#### Step 1: Get distributional data of all species in N Am



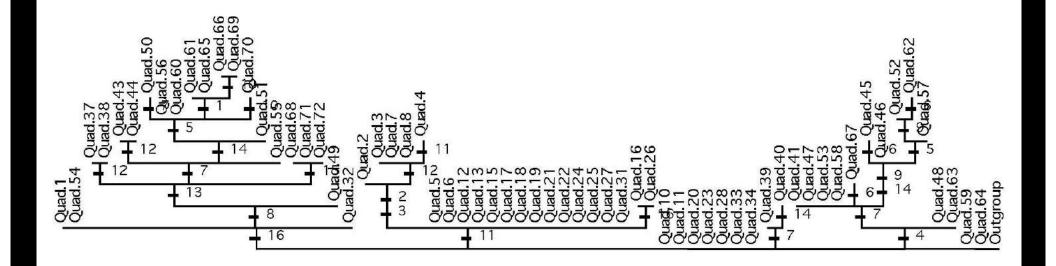
#### Step 2: Define geographic region and divide into quadrats



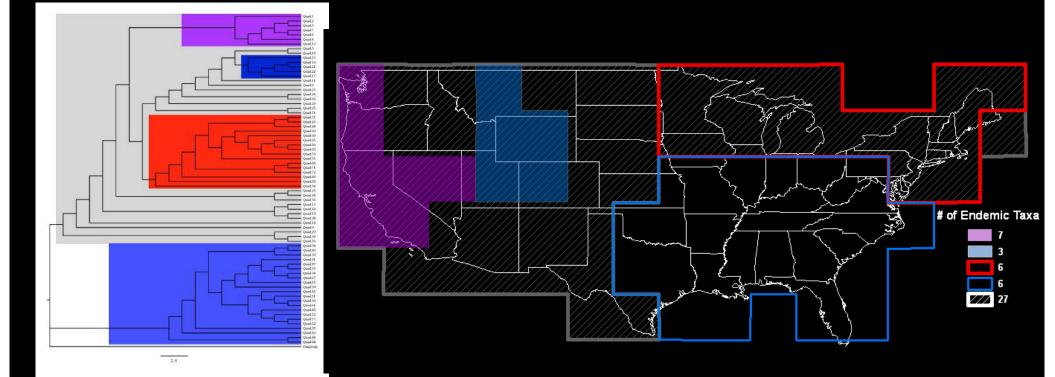
#### Step 3: Construct data matrix: absence = 0, presence = 1



#### Step 4: Conduct parsimony analysis



Step 5: Find clades consisting of 2+ endemic taxa with congruent distributions.



### **Ecological Niche Modeling**

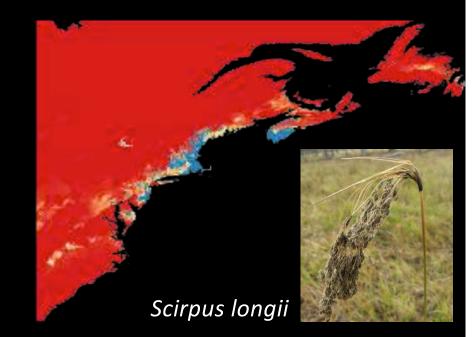
 Develop ecological niche models using waypoint and climate data (<u>BioClim</u>)



Scirpus longii

### **Ecological Niche Modeling**

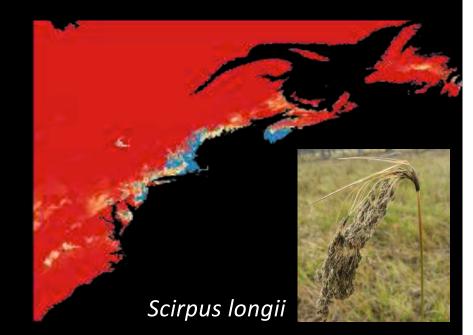
- Develop ecological niche models using waypoint and climate data
  - Identify suitable areas
     for endangered species



Data from **GBIF** and **BioClim**, analyzed with **Maxent** 

# **Ecological Niche Modeling**

- Develop ecological niche models using waypoint and climate data
  - Identify suitable areas
     for endangered species
  - Reconstruct
     distributions during Last
     Glacial Maximum



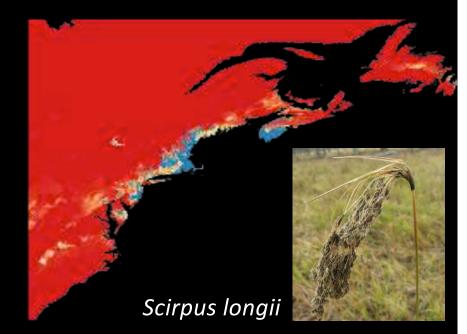


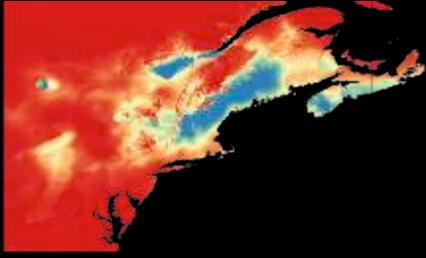
Data from <u>GBIF</u> and <u>BioClim</u>, analyzed with <u>Maxent</u>

## Without spending \$1, you can:

- Develop ecological niche models using waypoint and climate data
  - Identify suitable areas
     for endangered species
  - Reconstruct
     distributions during Last
     Glacial Maximum
  - Predict species
     distributions in 50 years

Data from GBIF and BioClim, analyzed with Maxent





#### Track spread of invasive species

• Where did they originate?

• When did they get here?

• Where are they going?



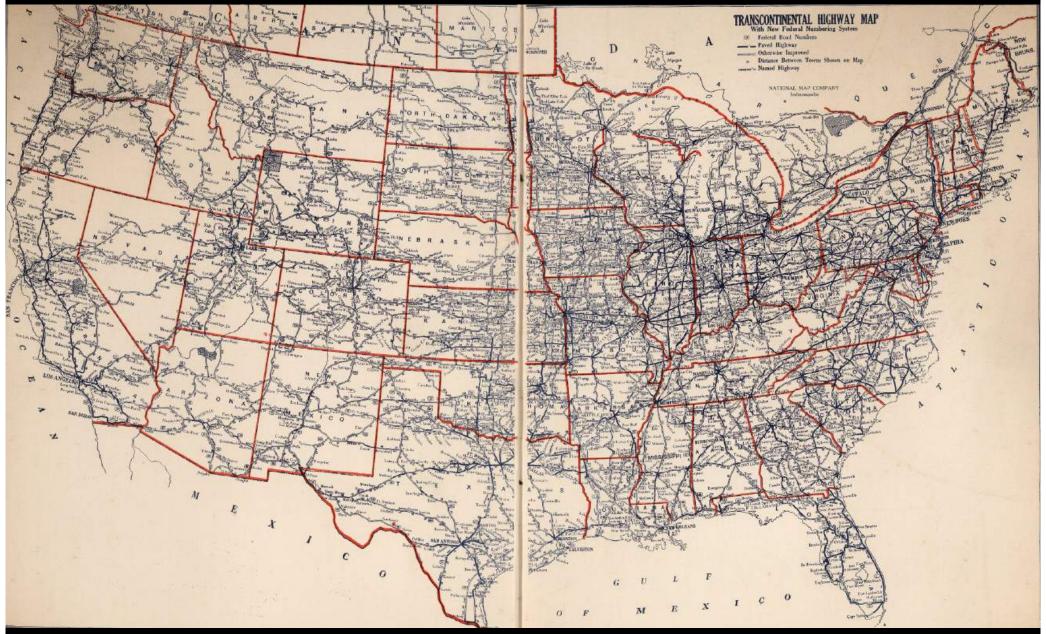








#### 1927 Roadmap



Copyright ©2010 Cartography Associates













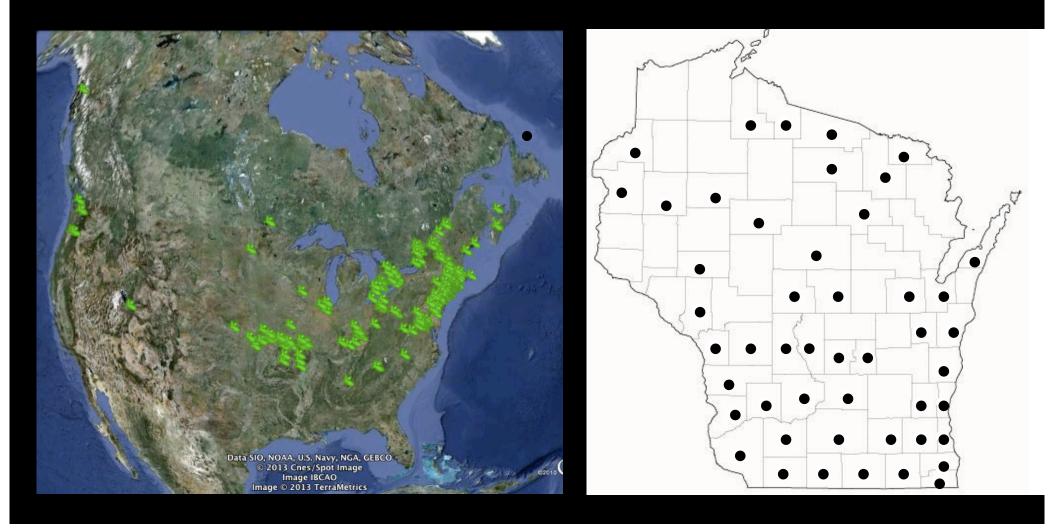
Today

Using ecological niche modeling, you could predict which regions might be under threat of invasion.

#### Some Cautions: Distribution of *Alliaria petiolata* according to:

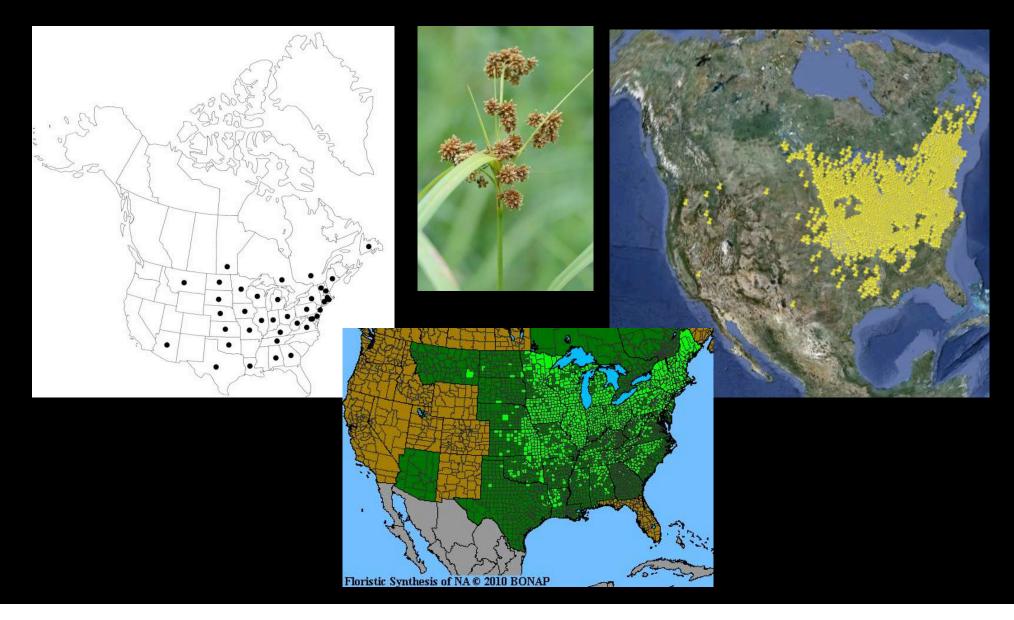
GBIF

WIS Flora



#### Some Cautions:

# How do these maps of the distribution of *Scirpus atrovirens* differ? Why do they differ?



#### **Additional Resources**

- panbiogeography analysis (<u>martitracks</u>)
- simulate origin and spread of species (biogeosim)
- forecast species distributions (biomod)
- spatial analysis of diversity (<u>biodiverse</u>)
- list of free phylogenetic software <u>here</u>
- simulate historical island biogeography (<u>shiba</u>)
- spatial analysis in macroecology (<u>SAM</u>)
- predict and analyze distributions (<u>GARP</u>)