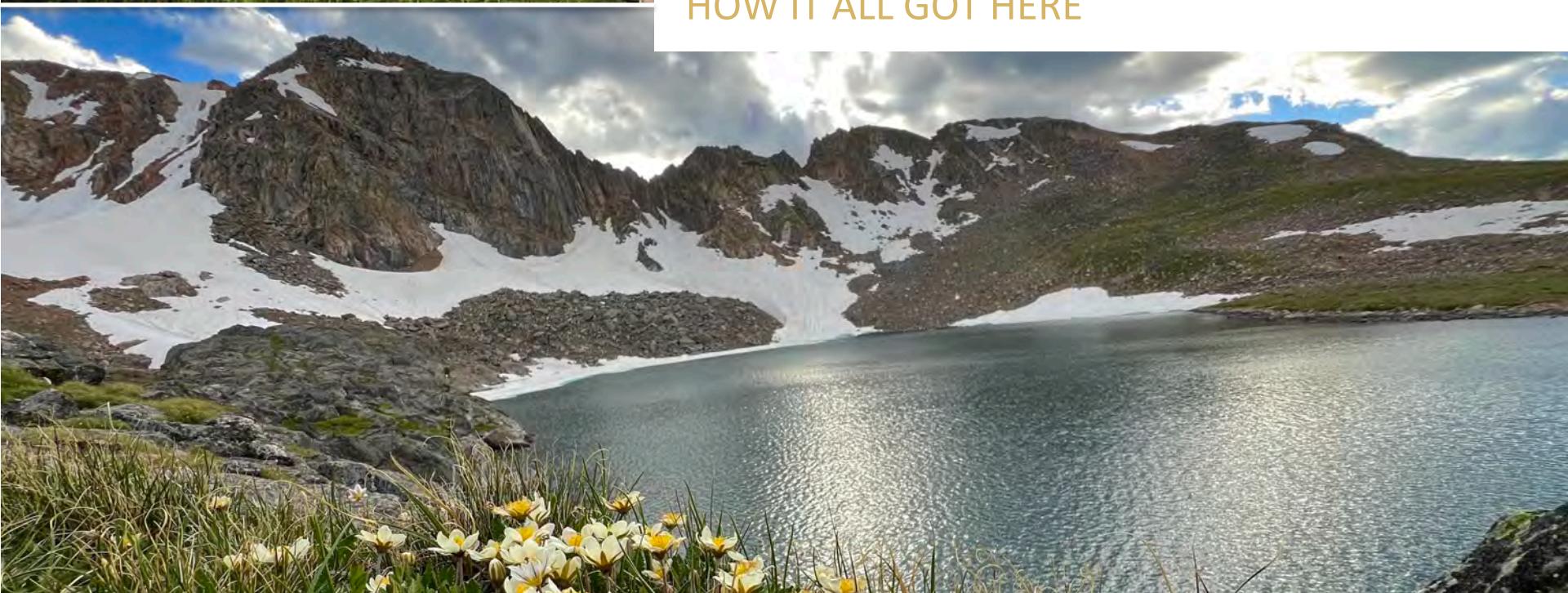


HOW IT ALL GOT HERE



WHAT

TAXONOMY & SYSTEMATICS

WHERE

SPATIAL DATA

WHEN  
(and what)

GENETICS

WHY

ENVIRONMENT

# Baby Bort



nature

## LETTERS

### Phylogenetic biome conservatism on a global scale

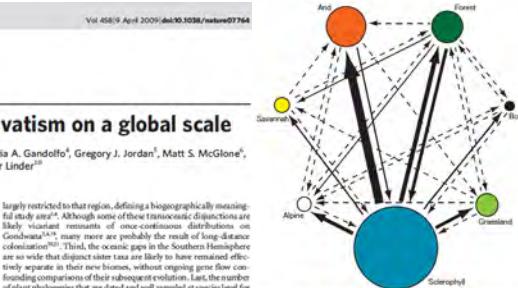
Michael D. Crisp<sup>1</sup>, Mary T. K. Arroyo<sup>2</sup>, Lyn G. Cook<sup>3</sup>, Maria A. Gandolfo<sup>4</sup>, Gregory J. Jordan<sup>5</sup>, Matt S. McGlone<sup>6</sup>, Peter H. Weston<sup>7</sup>, Mark Westoby<sup>8</sup>, Peter Will<sup>9</sup> & H. Peter Linder<sup>10</sup>

How and why regions are distributed as they are has long intrigued evolutionary biologists<sup>1–4</sup>. The tendency for species to retain their ancestral ecology has been demonstrated in distributions on local and regional scales<sup>5–7</sup>, but the extent of ecological conservatism over tens of millions of years and across continents has not been tested. Here we show that the number of species that have outstripped ancestral biomes by a ratio of more than 25:1, by inferring ancestral biomes for an ecologically diverse sample of more than 11,000 plant species from around the Southern Hemisphere, is far greater than that expected from random colonization. Availability of a suitable biome could have substantially influenced which biomes establish on more than one landmass, and this in turn influences the rarity of the dispersal events that ensue. Conversely, the tendency for the distribution of biomes has probably been strongly influenced by the rarity of species transitions between biomes. This study has implications for how species distributions have shifted over time, and how to shift biomes<sup>8</sup>, but their evolutionary potential could be strongly compromised by biome contraction as climate changes.

In recent years, the extent to which species retain ancestral ecological traits has been tested, but the extent of biome conservatism<sup>9</sup> has been debated<sup>10–12</sup>. Whether ecology is evolutionary labile or conserved appears to be scale dependent, but most of the evidence for conservatism has come from smaller (continental) and shorter-scale<sup>10,11</sup>. Larger-scale ecological conservatism is not well studied but there is evidence that ecological tolerances (for example as reflected in latitudinal gradients) are relatively conserved in lineages over long periods of evolutionary time. In this lead, the percentage of lineages that might colonize new biomes<sup>13</sup>, however, the frequency of transitions has not been estimated<sup>10</sup>.

Biomes are broad vegetation types defined by climate, life-form and ecological processes. The extent to which conserving the large-scale pattern of ecological conservatism, biome conservatism might be a major determinant of the global distribution of biodiversity, such as the latitudinal gradient, which is often attributed to biogeographic factors such as climate and plate tectonics<sup>14</sup>. Global comparisons across multiple lineages are needed to investigate the generality of conservatism and how much it has influenced the distribution of biomes. Investigating the frequency of biome changes using a large sample of plant phylogenies distributed across many biomes and landmasses is a challenge.

The widely separated landmasses in the Southern Hemisphere provide an opportunity to test the hypothesis that the relative frequency of phylogenetic biome conservatism on a broad scale and over long time periods (tens of millions of years). First, southern continents contain such a rich array of biomes among which taxa can have moved. Second, many taxa are spread across the southern landmasses and are



**Figure 1** Biome shifts within landmasses. Shifts occurred within 356 of 10,000 speciation events within landmasses. Number of species sampled within each biome is proportional to the area of each circle: scroph, 7250; arid, 1,683; wet arid, 1,065; temperate grassland, 504; savannah, 242; arid/temperate, 159; Alpine, 10; Bog, 1; Greenland, 1. Solid lines with arrows indicate one or more shifts between biomes. Each arrow is labeled with the number of shifts. Dashed lines indicate no shift. Colored arrows indicate shifts in one direction, ranging from 6 to 95 events; dashed lines indicate 1–5 events and lack of an arrow indicates that there was no event.

source biome<sup>14</sup>. An interesting parallel is the niche conservatism observed in many invasive species that are introduced by humans and usually establish in the same biomes as in their regions of origin<sup>15,16</sup>.

We assembled a data set comprising 11,664 species of vascular plants in 43 taxa from extrazonal Africa, Madagascar, Australia–New Guinea, New Caledonia, New Zealand, South America, equatorial South America, and the island arcs of the Southern Hemisphere. We reconstructed ancestral distributions and, by dating divergences, inferred which shifts were likely to be the result of long-distance dispersal events. We found that the frequency of shifts between biomes was structured by biome size and by date of divergence. Each biome had a unique pattern of shifts, with the number of shifts ranging from 1–95 events; dashed lines indicate 1–5 events and lack of an arrow indicates that there was no event.

For example, we found support for the hypothesis of phylogenetic biome conservatism because biome shifts were, being associated with 10,306 (3.6%) of the approximately 11,000 evolutionary diversifications in the data set. More than 90% of these shifts (11,111) and 40 lineages had shifts in the same colonizing biome. The number of shifts in each direction, ranging from 6 to 95 events; dashed lines indicate 1–5 events and lack of an arrow indicates that there was no event.

Investigating biome conservatism, we found a consistent pattern in which lineages that were more ecologically similar than expected by chance (based on the number of shifts) were more likely to colonize the same biome. This was consistent across all landmasses. For example, Goodenowia relic taxa (for example for Anacardiaceae, Casuarinaceae, Nethrophyllaceae<sup>17</sup>) or otherwise (for example eucalypts, graminoids and some legume lineages) had a higher probability of colonizing the same biome than lineages that had no change of biome (sign test:  $n = 226$ ; biome shifts,  $40, P = 0.00001$ ). Moreover, a bias towards biome shifts was consistent across all landmass pairs in both directions (Fig. 2; Wilcoxon matched-pairs signed-rank test:  $n = 10$ ;  $z = 2.23$ ,  $P = 0.027$ ). The number of biome shifts in colonizations was consistent across Nemesia (Table 1), whether conserving some biomes (Wilcoxon matched-pairs signed-rank test:  $n = 7$ ,  $z = -2.197$ ,  $P = 0.014$ ). We found that conservatism on biome shifts following colonization from one landmass to another is a consequence of the dynamics of colonization. The frequency at which a biome shifts following colonization from one landmass to another is likely to be extremely small. For successful colonization, immigrant propagules must germinate and establish reproductively successful populations. Establishment would be easier in a biome to which the species is pre-adapted than in one it is apparently equivalent to in

its native range. The number of shifts in each direction was proportional to the number of colonizations, such as:  $Arctagia$  thickness  $\propto$  number of shifts  $\propto$  number of colonizations (Fig. 1). This is consistent with the hypothesis that conservatism on biome shifts is a consequence of the dynamics of colonization. The frequency at which a biome shifts following colonization from one landmass to another is likely to be extremely small. For successful colonization, immigrant propagules must germinate and establish reproductively successful populations. Establishment would be easier in a biome to which the species is pre-adapted than in one it is apparently equivalent to in its native range. The number of shifts in each direction was proportional to the number of colonizations, such as:  $Arctagia$  thickness  $\propto$  number of shifts  $\propto$  number of colonizations (Fig. 1). This is consistent with the hypothesis that conservatism on biome shifts is a consequence of the dynamics of colonization.

**Figure 2** Biome conservatism in transoceanic plant colonizations around the Southern Hemisphere. Proportion of colonizations that have the same biome as the colonizing biome. Number of shifts in each direction is proportional to the number of colonizations, such as:  $Arctagia$  thickness  $\propto$  number of shifts  $\propto$  number of colonizations (Fig. 1). This is consistent with the hypothesis that conservatism on biome shifts is a consequence of the dynamics of colonization. The frequency at which a biome shifts following colonization from one landmass to another is likely to be extremely small. For successful colonization, immigrant propagules must germinate and establish reproductively successful populations. Establishment would be easier in a biome to which the species is pre-adapted than in one it is apparently equivalent to in its native range. The number of shifts in each direction was proportional to the number of colonizations, such as:  $Arctagia$  thickness  $\propto$  number of shifts  $\propto$  number of colonizations (Fig. 1). This is consistent with the hypothesis that conservatism on biome shifts is a consequence of the dynamics of colonization.

## Crisp Lab



## Cook Lab



*“Using phylogenies to test hypotheses about date, rate and mode of diversification and evolution of Australian plants and animals”*



## ARTICLE

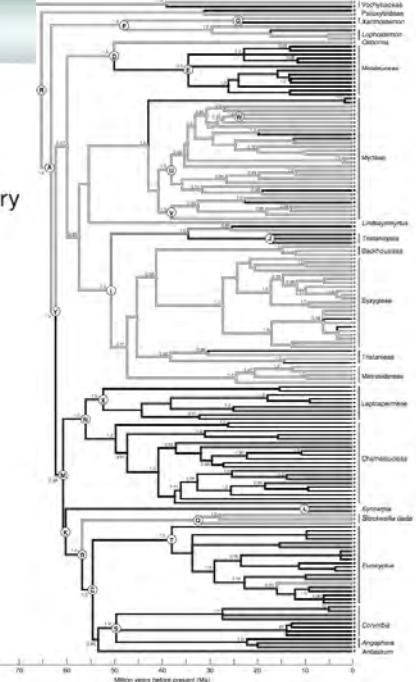
Received 20 May 2010 | Accepted 12 Jan 2011 | Published 15 Feb 2011

DOI: 10.1038/ncomms1191

### Flammable biomes dominated by eucalypts originated at the Cretaceous–Palaeogene boundary

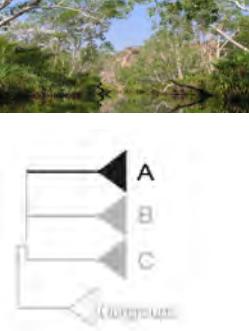
Michael D. Crisp<sup>1</sup>, Geoffrey E. Burrows<sup>2</sup>, Lyn G. Cook<sup>3</sup>, Andrew H. Thorrill<sup>4</sup> & David M. J. S. Bowman<sup>5</sup>

Fire is a major modifier of communities, but the evolutionary origins of its prevalent role in shaping current biomes are uncertain. Australia is among the most fire-prone continents, with most of the landmass occupied by the fire-dependent sclerophyll and savanna biomes. In contrast to biomes with similar climates in other continents, Australia has a tree flora dominated by a single genus, *Eucalyptus*, and related Myrtaceae. A unique mechanism in Myrtaceae for enduring and recovering from fire damage likely resulted in this dominance. Here, we find a conserved phylogenetic relationship between post-fire resprouting (epicormic) anatomy and biome evolution, dating from 60 to 62 Ma, in the earliest Palaeogene. Thus, fire-dependent communities likely existed 50 million years earlier than previously thought. We predict that epicormic resprouting could make eucalypt forests and woodlands an excellent long-term carbon sink for reducing atmospheric CO<sub>2</sub>, compared with biomes with similar fire regimes in other continents.

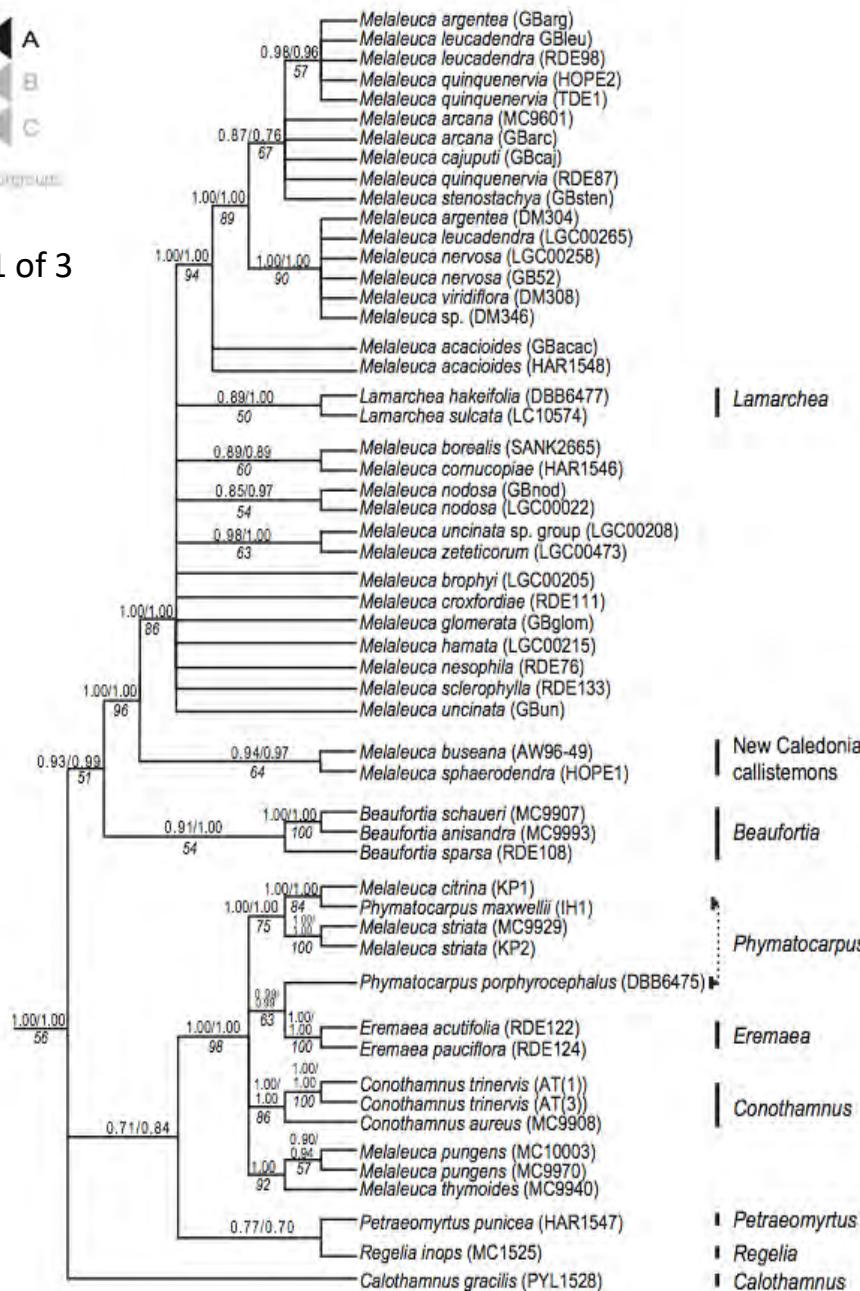


**Figure 2** Inferred evolutionary history of biome flammability mapped onto a Bayesian phylogeny of Myrtaceae. Time scale is millions of years before present (Ma). Labels indicate higher fire monitored in the tree. Shading of boxes at tips and along branches indicates scoring for flammability (black = flammable; black or non-flammable = white). Ancestral states reconstructed by parsimony are shown at internal branches; grey indicates an equivocal reconstruction. Nodes labelled with upper case letters in circles are for reference from the text and tables. Decimal values on branches indicate Bayesian posterior probabilities; integers (in *Cyrtodendron*) indicate parsimony bootstrap values.

# Systematics of *Melaleuca*



Clade 1 of 3



Edwards & al. • *Melaleuca* revisited

TAXON 59 (3) • June 2010: 744–754

## *Melaleuca* revisited: cpDNA and morphological data confirm that *Melaleuca* L. (Myrtaceae) is not monophyletic

Robert D. Edwards,<sup>1,2</sup> Lyn A. Craven,<sup>3</sup> Michael D. Crisp<sup>1</sup> & Lyn G. Cook<sup>1,2</sup>

<sup>1</sup> The Australian National University, Research School of Biology, Canberra ACT 0200, Australia

<sup>2</sup> The University of Queensland, School of Biological Sciences, Brisbane QLD, 4072, Australia

<sup>3</sup> Australian National Herbarium, CSIRO Plant Industry, Canberra ACT 2601, Australia

Author for correspondence: Robert D. Edwards, r.edwards2@uq.edu.au

TAXON 63 (3) • June 2014: 663–670

Craven & al. • Nomenclatural novelties in *Melaleuca*

## New combinations and names in *Melaleuca* (Myrtaceae)

Lyn A. Craven,<sup>1</sup> Robert D. Edwards<sup>2,3</sup> & Kirsten J. Cowley<sup>4</sup>

<sup>1</sup> Australian National Herbarium, CSIRO Plant Industry, Canberra ACT 2601, Australia

<sup>2</sup> Research School of Biology, The Australian National University, Canberra ACT 0200, Australia

<sup>3</sup> School of Biological Sciences, The University of Queensland, Brisbane QLD 4072, Australia

Author for correspondence: Lyn A. Craven, lyn.craven@csiro.au

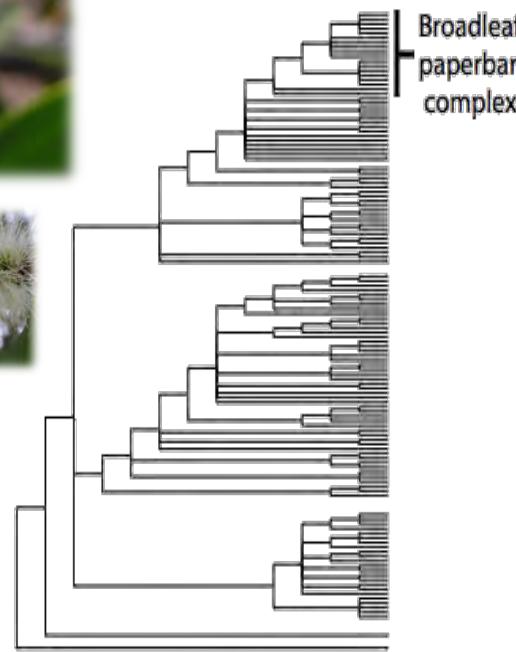
DOI: <http://dx.doi.org/10.12705/633.38>

**Abstract** The taxonomy of Melaleucaeae has been re-assessed in the light of DNA sequence studies and it is concluded that all genera should be placed within *Melaleuca*. *Beaufortia*, *Calothamnus*, *Conothamnus*, *Eremaea*, *Lamarchea*, *Petraeomyrtus*, *Phymatocarpus* and *Regelia* and their constituent species are formally transferred to *Melaleuca*. One hundred and six nomenclatural changes are provided of which 72 are new combinations and 34 are new names.

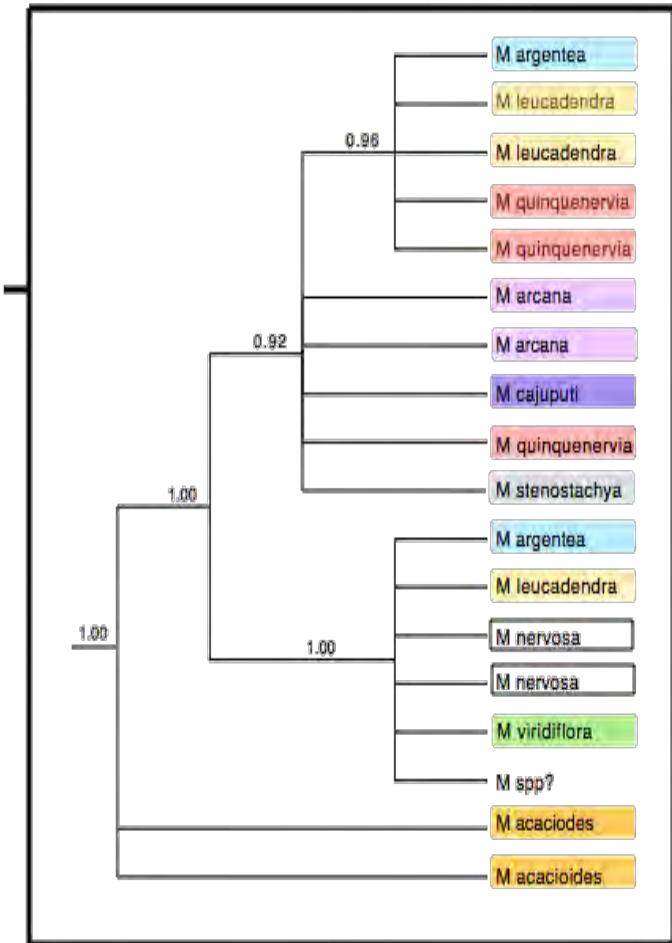
**Keywords** Australia; *Beaufortia*; *Calothamnus*; *Conothamnus*; *Eremaea*; *Lamarchea*; *Melaleuca*; *Petraeomyrtus*; *Phymatocarpus*; *Regelia*



# Systematics of *Melaleuca* - Broadleaved Paperbarks



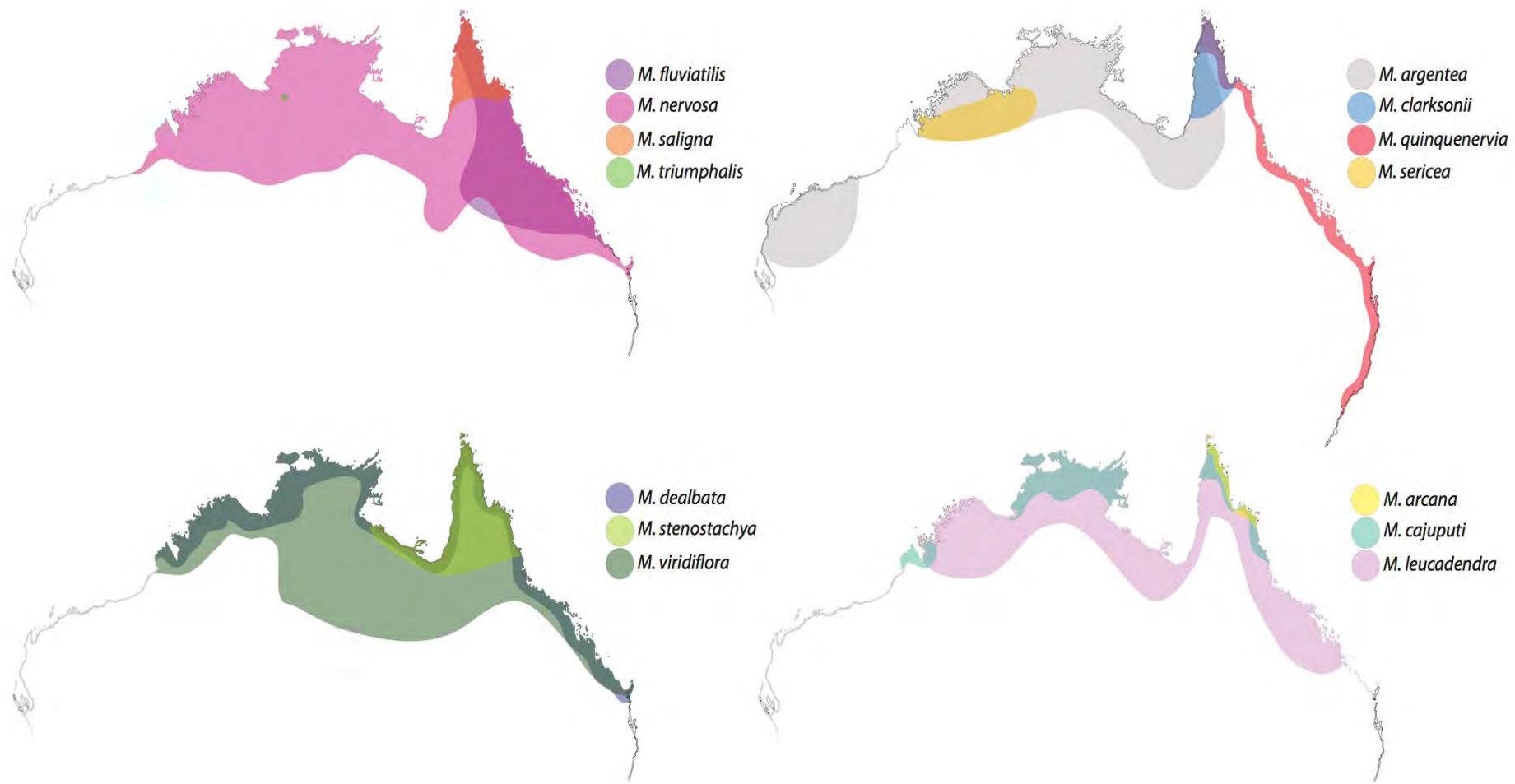
(Edwards et al., 2010)



(Cook et al., 2008)



# Systematics of Melaleuca - Broadleaved Paperbarks





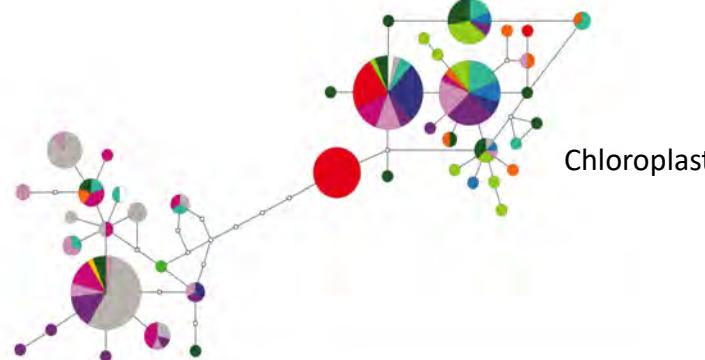
# Systematics of Melaleuca - Broadleaved Paperbarks

CSIRO PUBLISHING

Australian Systematic Botany, 2018, 31, 495–503  
<https://doi.org/10.1071/SB18032>

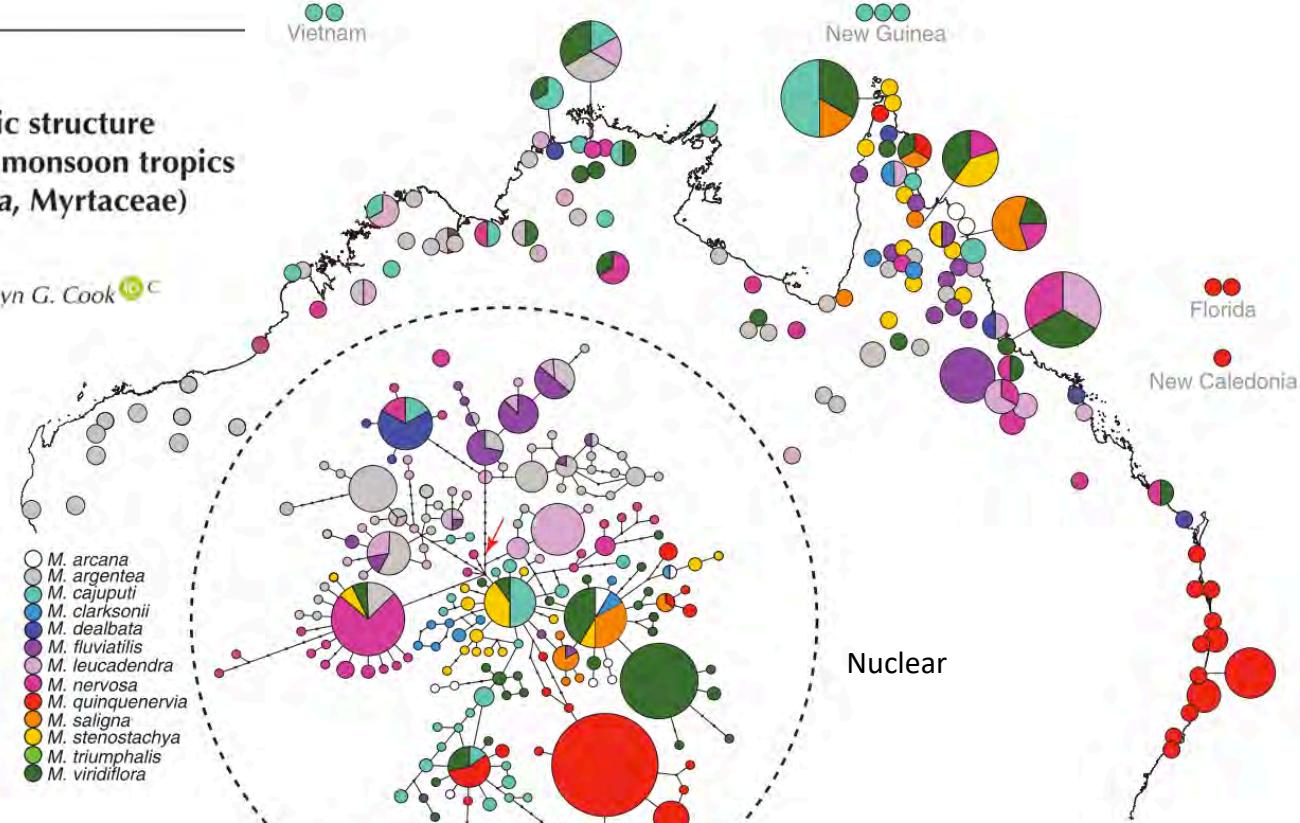
Species limits and cryptic biogeographic structure  
in a widespread complex of Australian monsoon tropics  
trees (broad-leaf paperbarks: *Melaleuca*, Myrtaceae)

Robert D. Edwards <sup>A,D</sup>, Michael D. Crisp <sup>B</sup> and Lyn G. Cook <sup>C</sup>



Chloroplast

- *M. arcana*
- *M. argentea*
- *M. cajuputi*
- *M. clarksonii*
- *M. dealbata*
- *M. fluviatilis*
- *M. leucadendra*
- *M. nervosa*
- *M. quinquenervia*
- *M. saligna*
- *M. sternostachya*
- *M. triumphalis*
- *M. virens*



Nuclear



Florida

New Caledonia



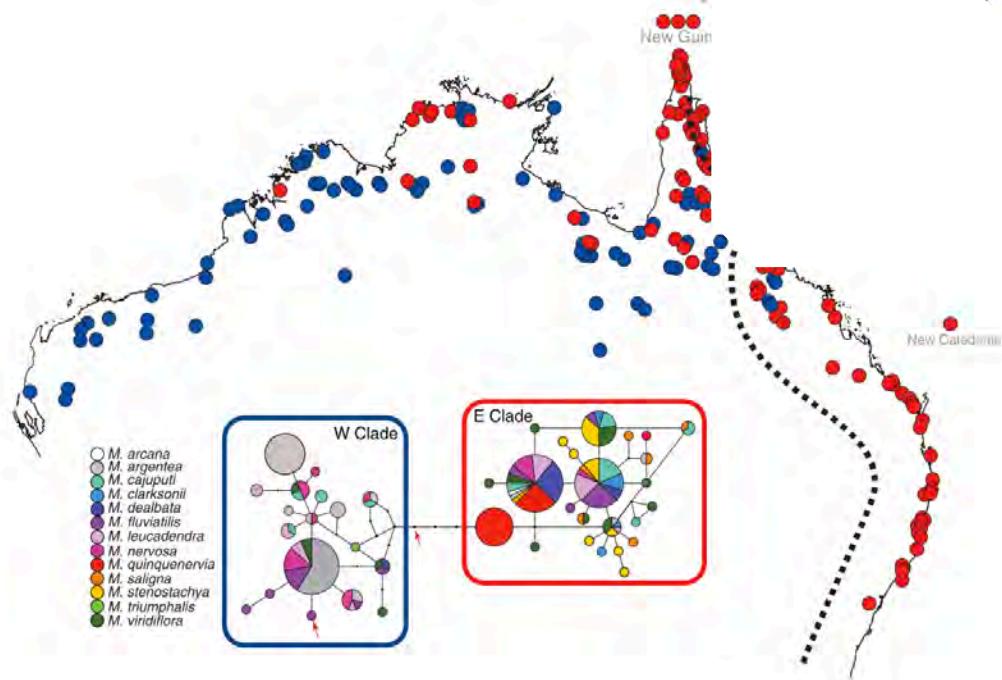
# Systematics of Melaleuca - Broadleaved Paperbarks

CSIRO PUBLISHING

*Australian Systematic Botany*, 2018, **31**, 495–503  
<https://doi.org/10.1071/SB18032>

## Species limits and cryptic biogeographic structure in a widespread complex of Australian monsoon tropics trees (broad-leaf paperbarks: *Melaleuca*, Myrtaceae)

Robert D. Edwards<sup>1,2</sup> A.D., Michael D. Crisp<sup>1,3</sup> B and Lyn G. Cook<sup>1,4</sup> C

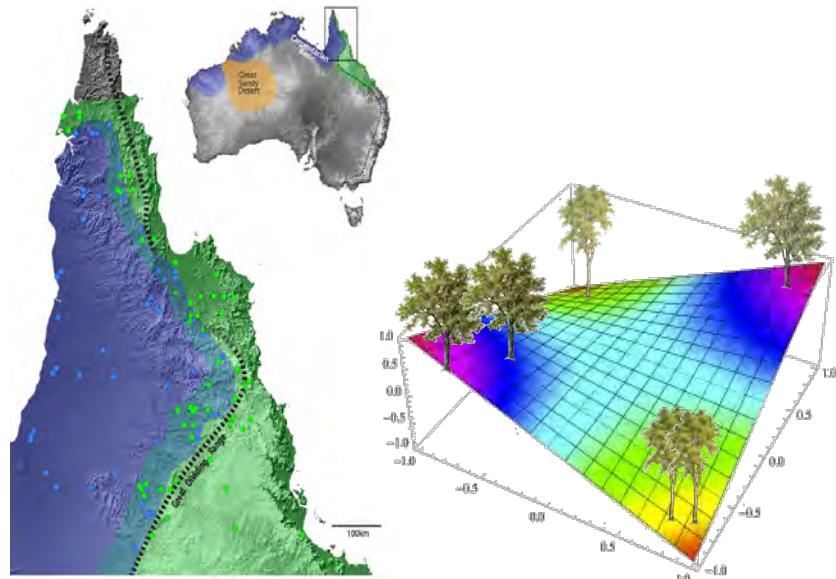


*Journal of Biogeography* (J. Biogeogr.) (2013) **40**, 559–569



## Niche differentiation and spatial partitioning in the evolution of two Australian monsoon tropical tree species

Robert D. Edwards<sup>1\*</sup>, Michael D. Crisp<sup>2</sup> and Lyn G. Cook<sup>1</sup>



- Niche values estimated via MaxEnt (Phillips *et al*, 2006)
- Values within and between species ranges are compared against randomized distributions (ENMtools (Glor & Warren, 2010)



# Biogeography of the Australian Monsoon Flora

PLOS ONE

## RESEARCH ARTICLE

### Congruent biogeographical disjunctions at a continent-wide scale: Quantifying and clarifying the role of biogeographic barriers in the Australian tropics

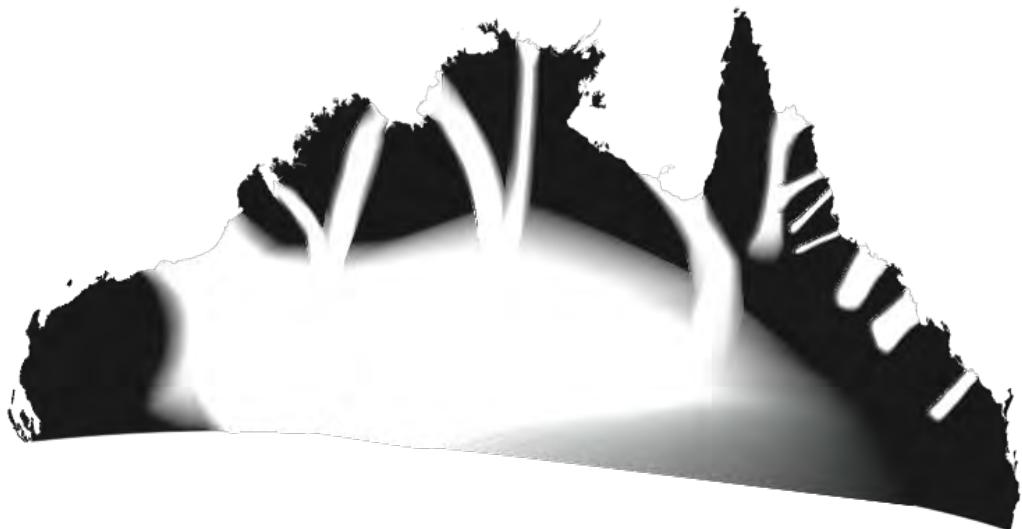
Robert D. Edwards<sup>1\*</sup>, Michael D. Crisp<sup>2</sup>, Dianne H. Cook<sup>3</sup>, Lyn G. Cook<sup>1</sup>

**1** School of Biological Sciences, The University of Queensland, Brisbane, Queensland, Australia.

**2** Research School of Biology, The Australian National University, Acton, Australian Capital Territory, Australia, **3** Department of Econometrics and Business Statistics, Monash University, Clayton, Victoria, Australia

✉ Current address: Department of Botany, National Museum of Natural History, MRC166, Smithsonian Institution, Washington, DC, United States of America

\* [robert.edwards@uq.edu.au](mailto:robert.edwards@uq.edu.au)





# Species-isolation genes in *Drosophila*



# Environmental Drivers of Species Diversity



Vicki Funk



Elisabeth Bui



Chase Mason



Marty Goldhaber



Ian Pearse



Travis Nauman



Jen Cartwright



Pamela Soltis



Brian Anacker



Joe Miller



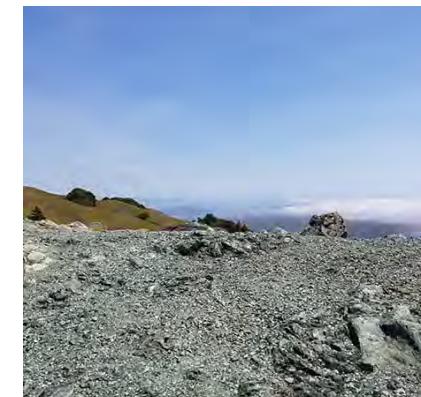
Jim Thompson





## Defining and Delimiting Extremes

Extreme environment: *a habitat where conditions are outside the optimal range for organisms to survive*





## Defining and Delimiting Extremes

Extreme environment: *a habitat where conditions are outside the optimal range for organisms to survive*



Extreme habitats are often identified by a lack of organisms or lack of diversity of organisms



What for one organism is considered intolerable may not be so for another



Multiple factors may be “extreme” and contribute to the inhospitability of an environment



As a result the threshold(s) for “extreme” are often idiosyncratic and determined on a by-species and/or by variable basis

### **Challenge:**

Define extreme environments objectively

Test hypotheses on the response of biotic processes non-circularly and across many species

- eg. trait presence, body size, species diversity



# Defining and Delimiting Extremes

## Challenge:

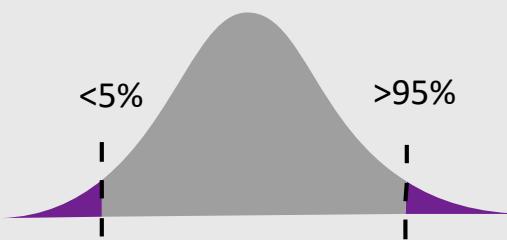
Define extreme environments objectively

Test hypotheses on the response of biotic processes non-circularly and across many species

- eg. trait presence, body size, species diversity

For terrestrial organisms the comfortable envelope for survival typically exists towards the middle of the range of environmental variables

ie. (by definition) the upper and/or lower tail of values for a variable are the extremes





# Defining and Delimiting Extremes

## Climate

Worldclim2 – 19 variables

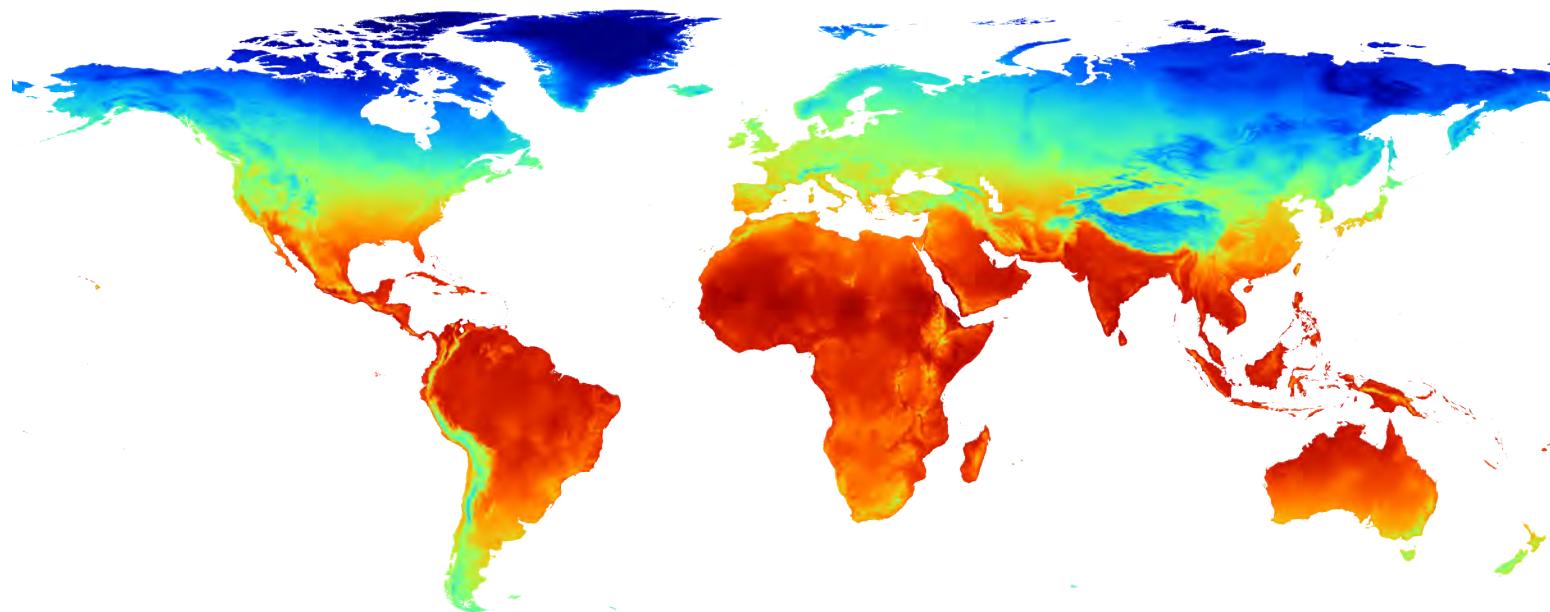
(Fick et al., 2017)

## Soil and Elevation

SoilGrids 1km – 21 variables

(Hengl et al., 2017)

Initial 40 variables reduced to 24 relevant non-colinear set

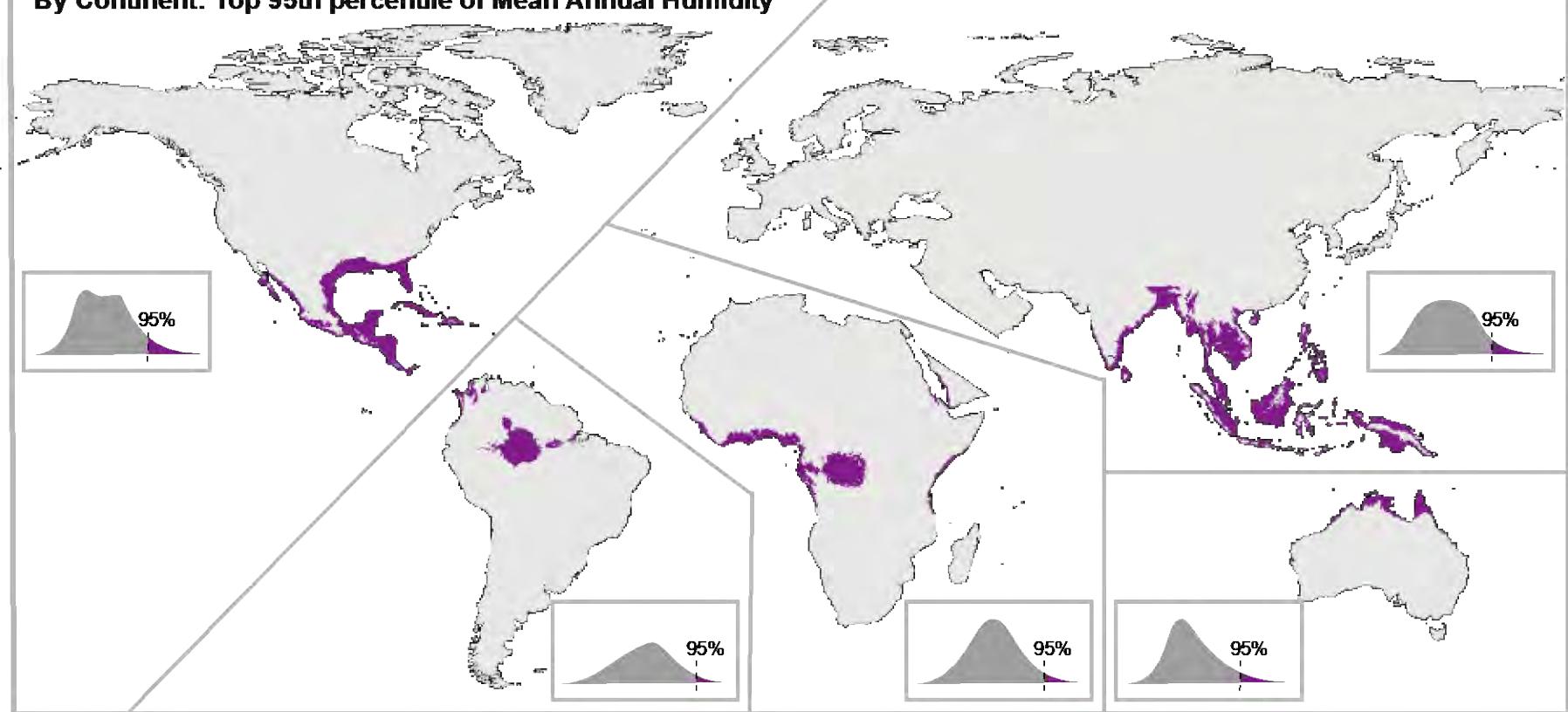




## Defining and Delimiting Extremes

Individual variable

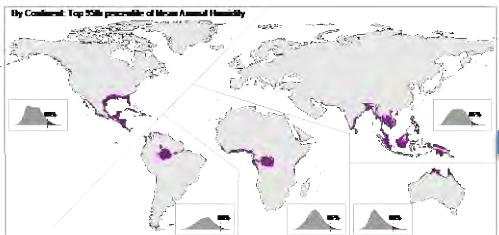
By Continent: Top 95th percentile of Mean Annual Humidity



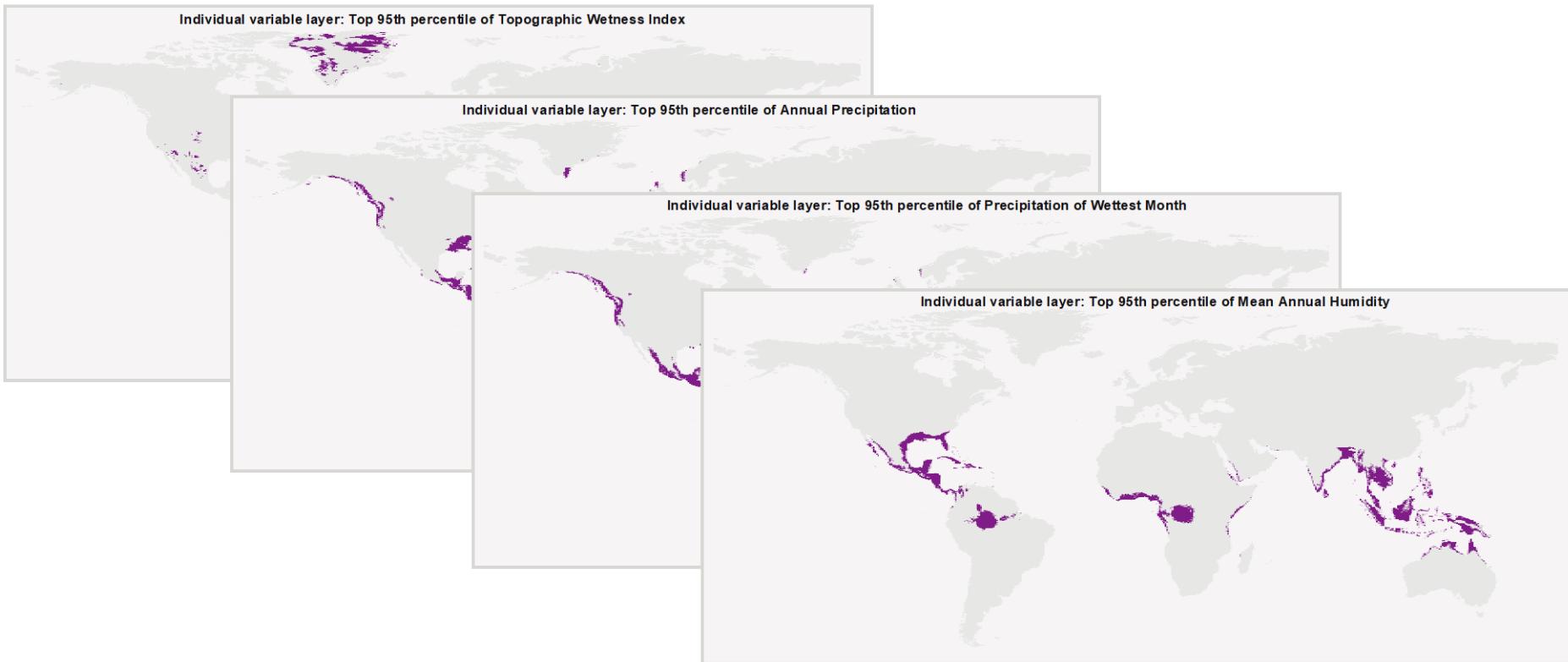
1km<sup>2</sup> pixel resolution



# Defining and Delimiting Extremes



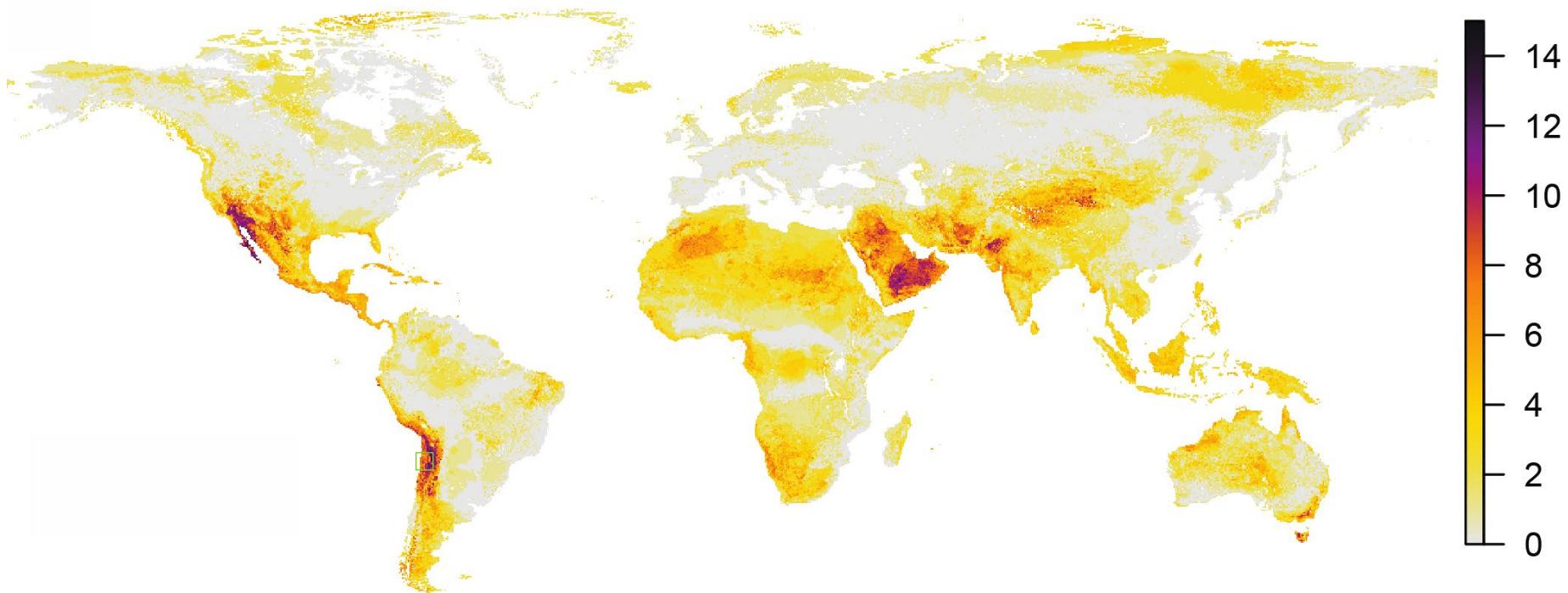
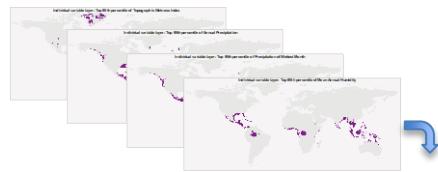
## Stack of variables





# Daisy Diversity Response to Extremes

- Defining and Delimiting Extremes

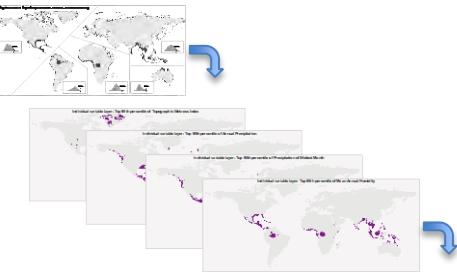


**Number of Overlapping Extremes**

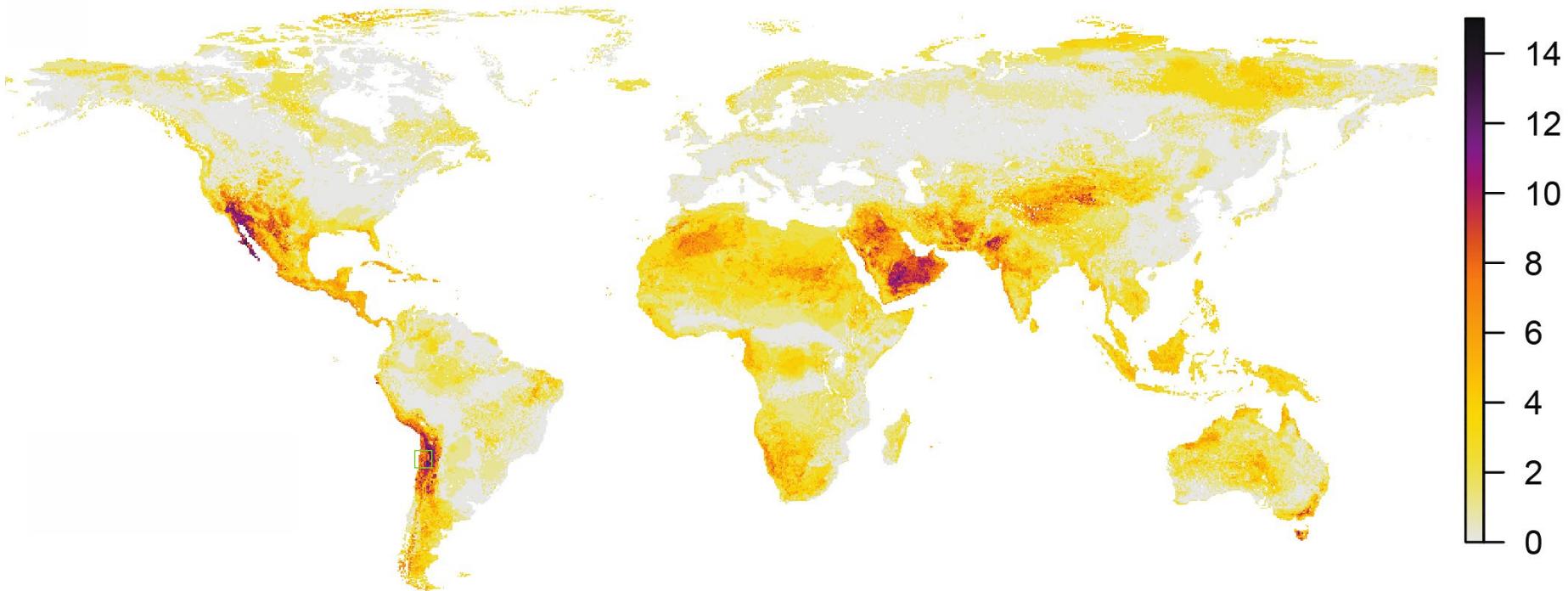


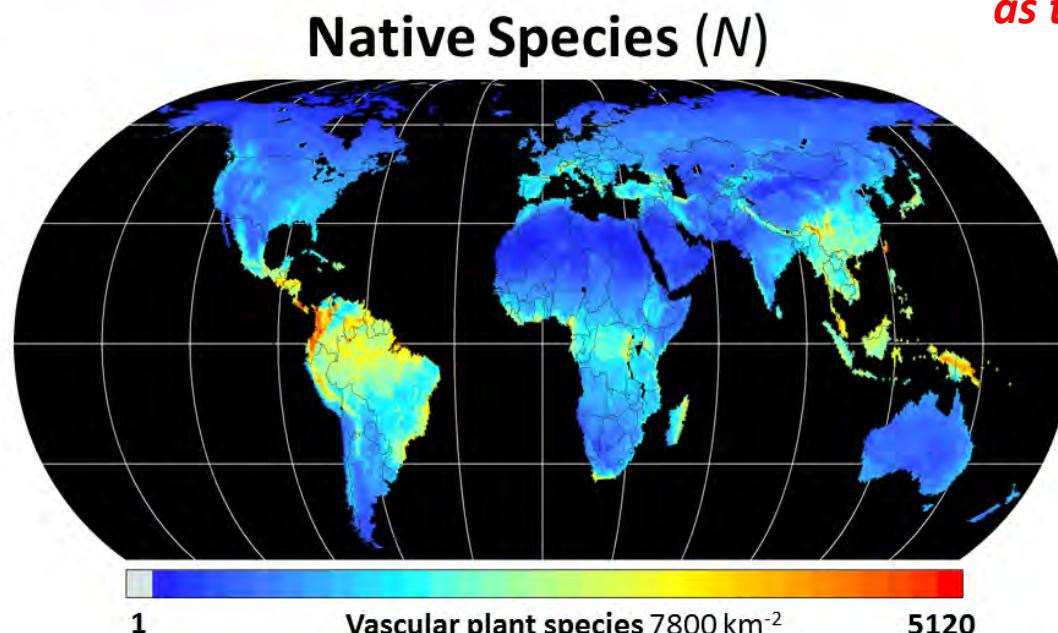
# Daisy Diversity Response to Extremes

- Defining and Delimiting Extremes



**Hypothesis:**  
*Species diversity will decrease as the number of overlapping extremes increases*





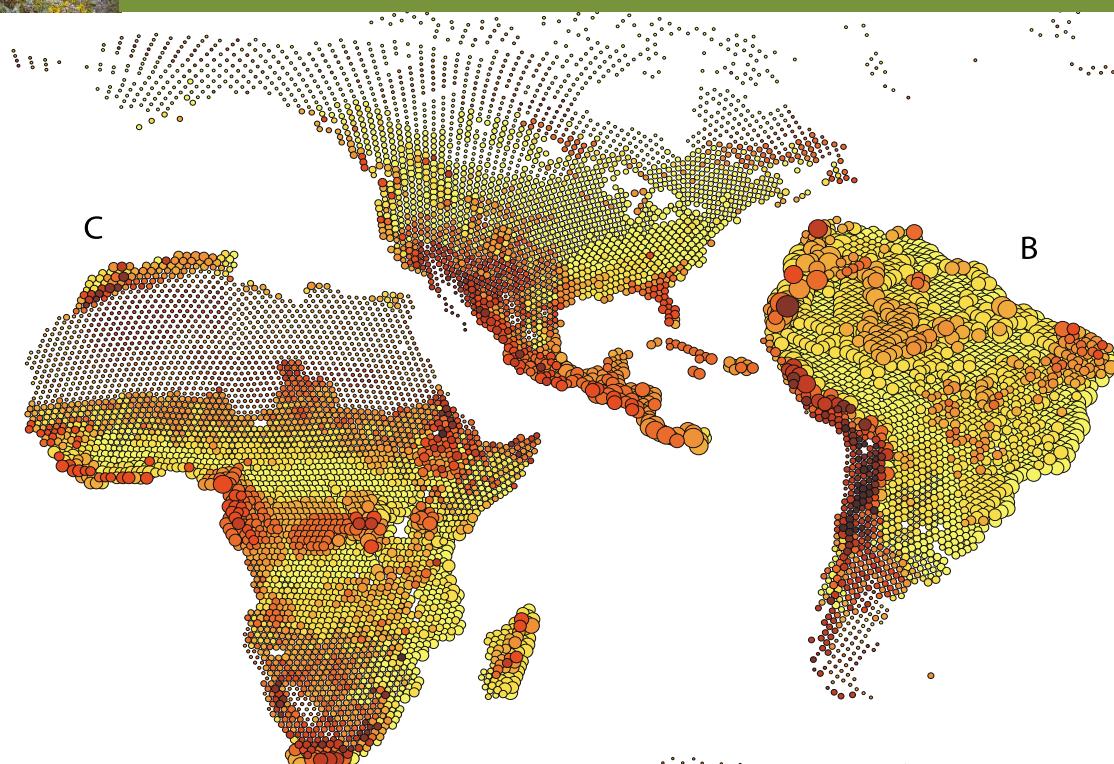
**Hypothesis:**  
*Species diversity will decrease as the number of overlapping extremes increases*

- 16,461 equal area polygons each with a value for flowering plant richness
- Value for the number of extremes also recorded for the centroid of each polygon



# Flowering Plant Diversity Response to Extremes

- Global



## Hypothesis:

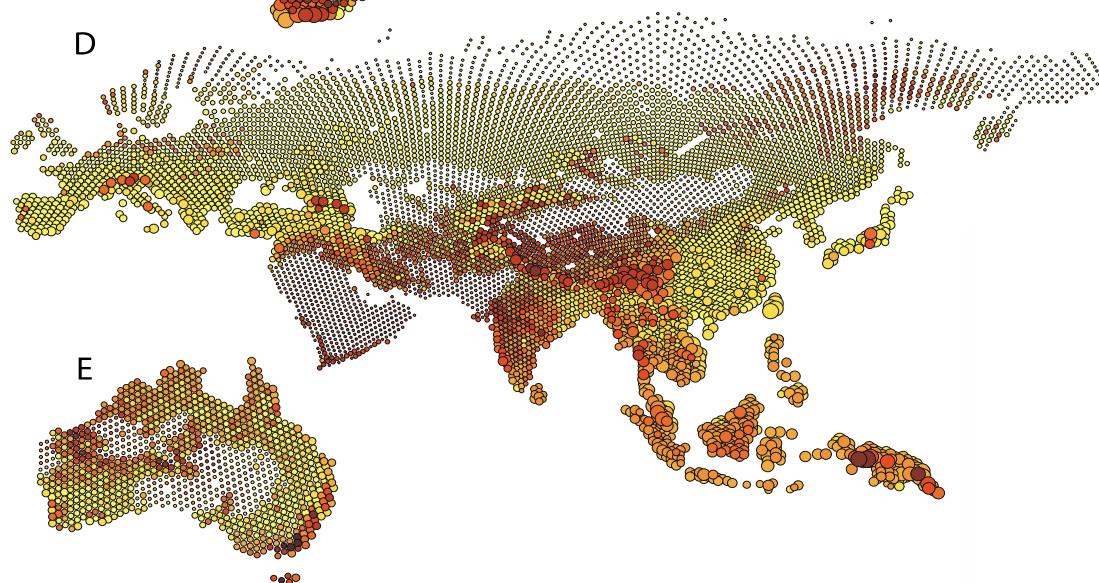
*Species diversity will decrease as the number of overlapping extremes increases*

### Richness

- 0 - 512
- 513 - 1024
- 1025 - 1536
- 1537 - 2048
- 2049 - 2560
- 2561 - 3072
- 3073 - 3584
- 3585 - 4096
- 4097 - 4608
- 4609 - 5121

### Extremeness

- 0
- 1
- 2
- 3
- 4
- 5
- 6
- 7
- 8





# Flowering Plant Diversity Response to Extremes

- Global



**Hypothesis:**  
*Species diversity will decrease as the number of overlapping extremes increases*

Calculate the average species richness for each number of overlapping classes

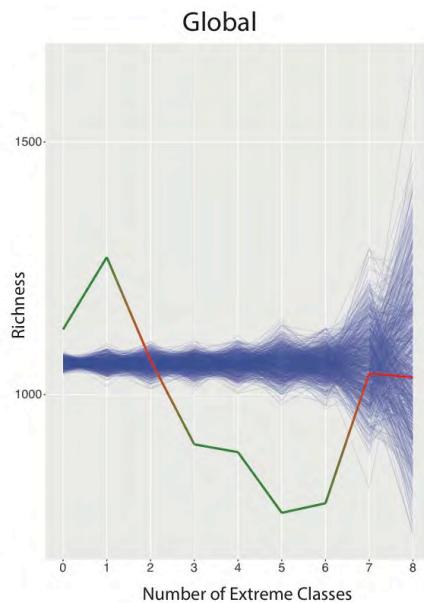
Null distribution generated from 999 Randomizations of richness values for each grid cell while holding number of overlapping classes constant



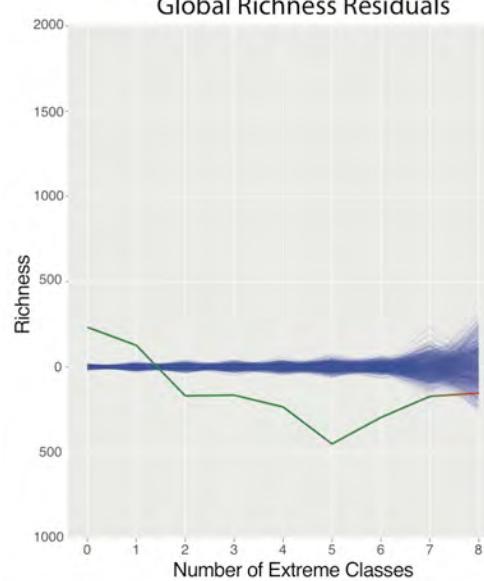
# Global Flowering Plant Diversity Response to Extremes

## Latitudinal Species Gradient?

Global



Global Richness Residuals



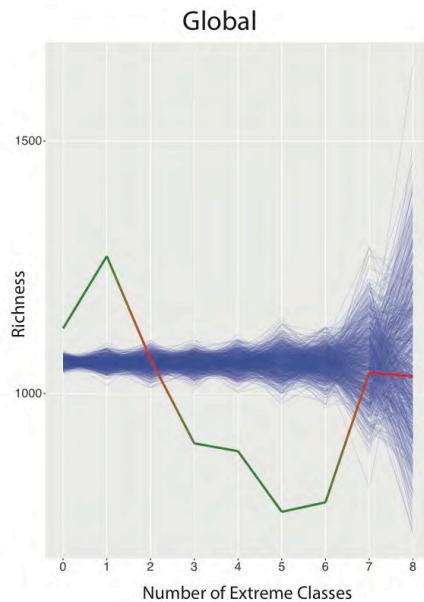
Regression of number  
of extreme classes  
against latitude:  
 $R^2 < 0.145$



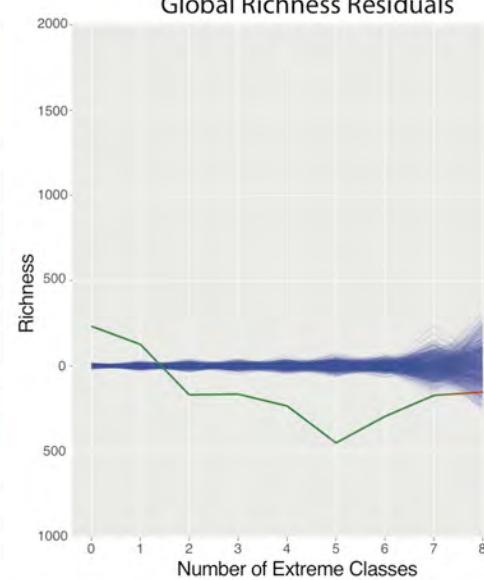
# Global Flowering Plant Diversity Response to Extremes

## Latitudinal Species Gradient?

Global

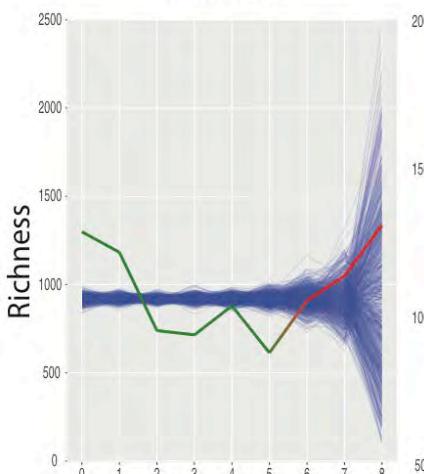


Global Richness Residuals

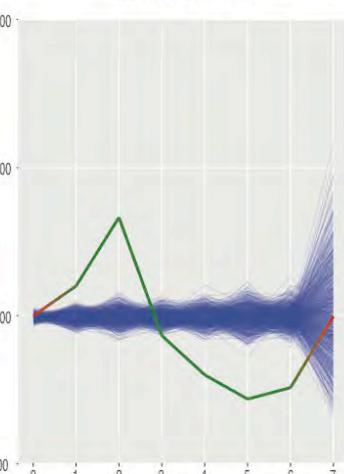


Regression of number  
of extreme classes  
against latitude:  
 $R^2 < 0.145$

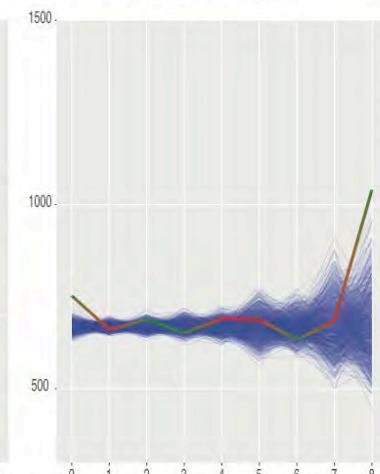
Africa



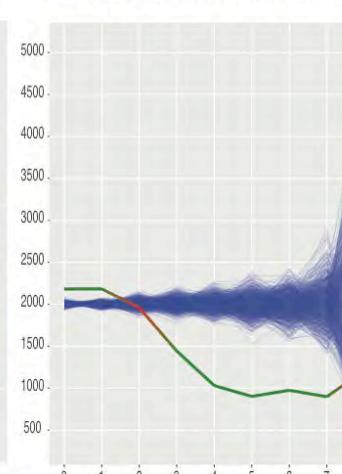
Eurasia



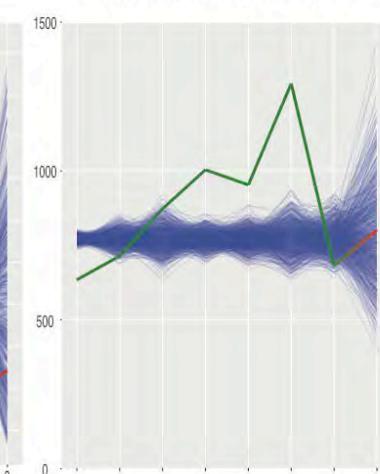
Australia



Sth America



Nth America

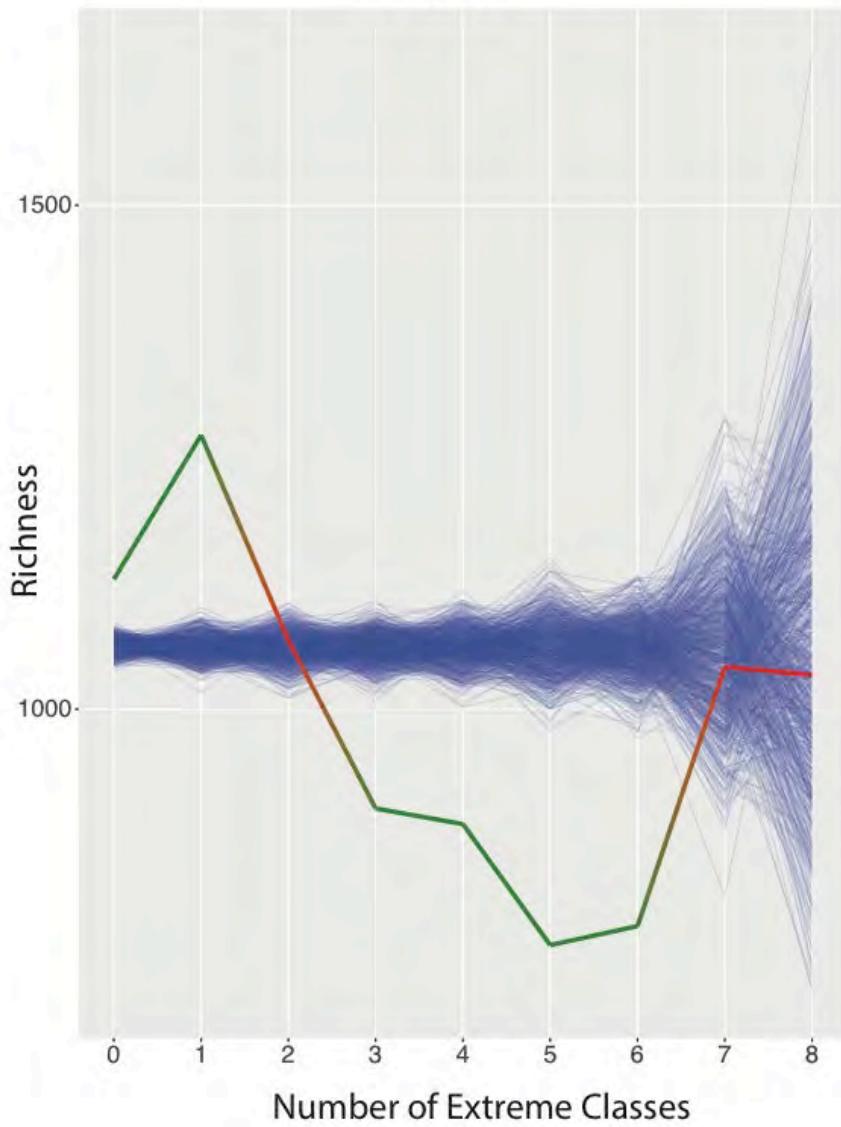


Number of extremes

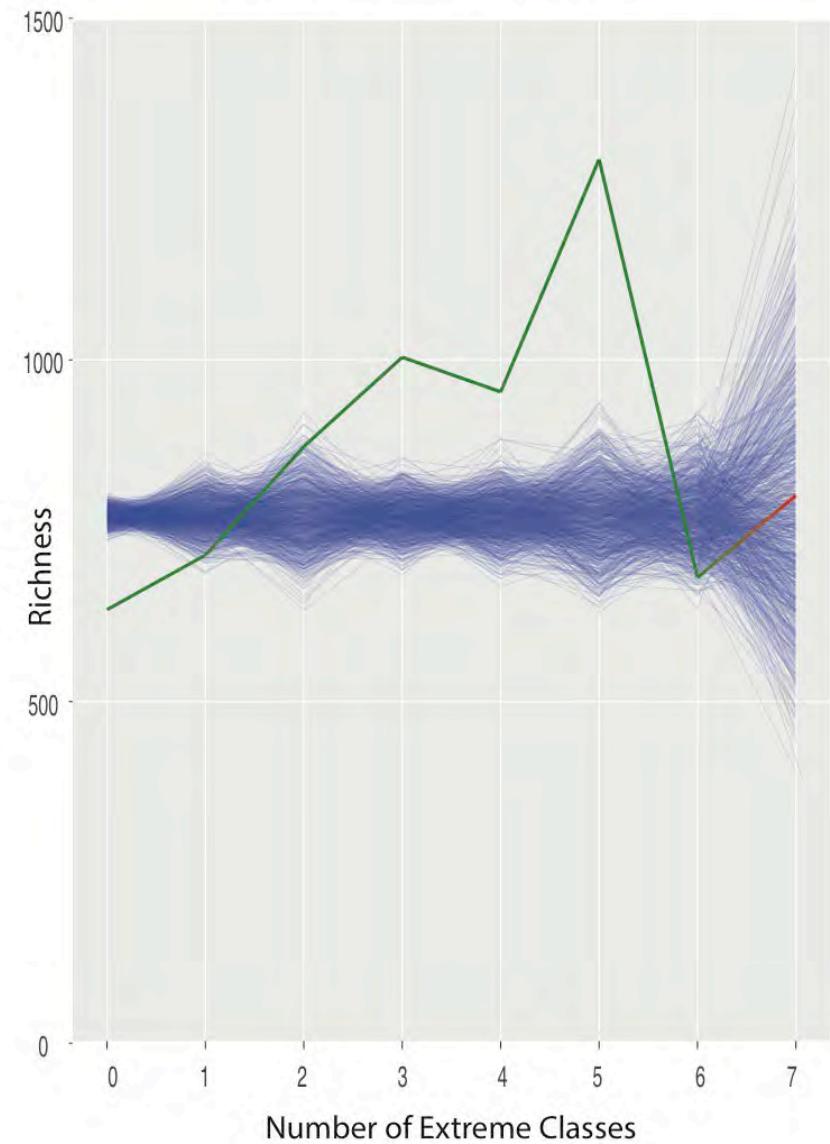


# Flowering Plant Diversity Response to Extremes

Global



Nth America  
All Flowering Plants





# Daisy Diversity Response to Extremes

## North American Compositae (Asteraceae)

Daisies, sunflowers, thistles, tarweeds etc

Massively diverse (~1 in 10 flowering plants)

Known for occupying a wide range of challenging environments





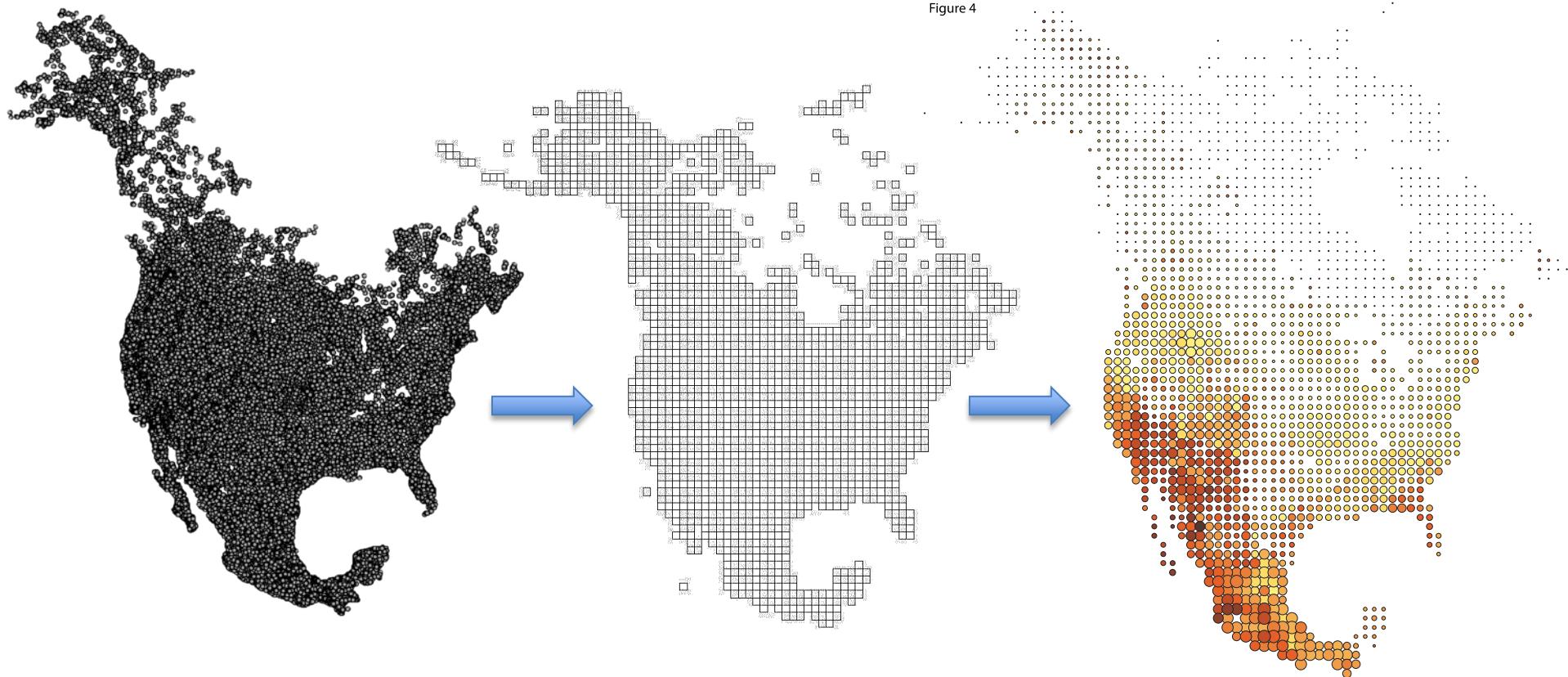
# Daisy Diversity Response to Extremes





# Daisy Diversity Response to Extremes

Figure 4



3,116 species  
~500,000 collection records  
(after cleaning)

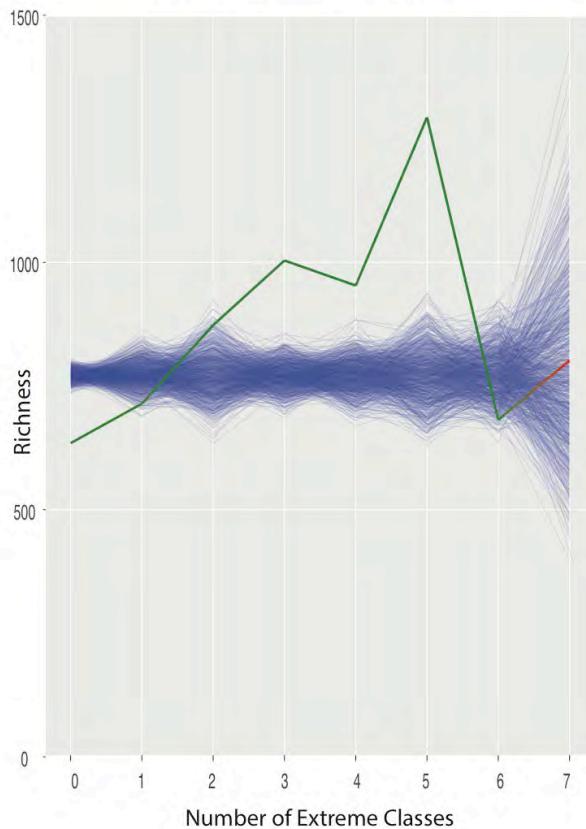
Aggregated to 100km grid cells

Richness calculated



## Daisy Diversity Response to Extremes

Nth America  
All Flowering Plants

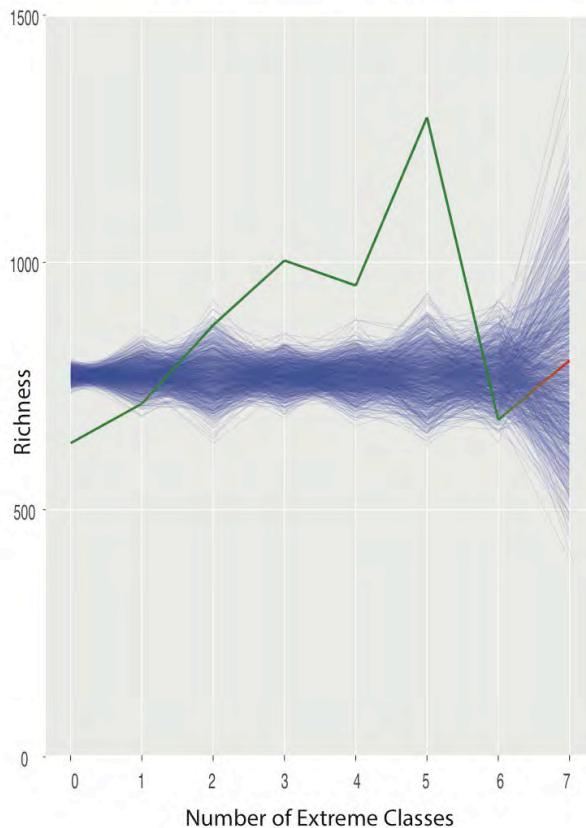


In Nth America species richness increases with extremeness...

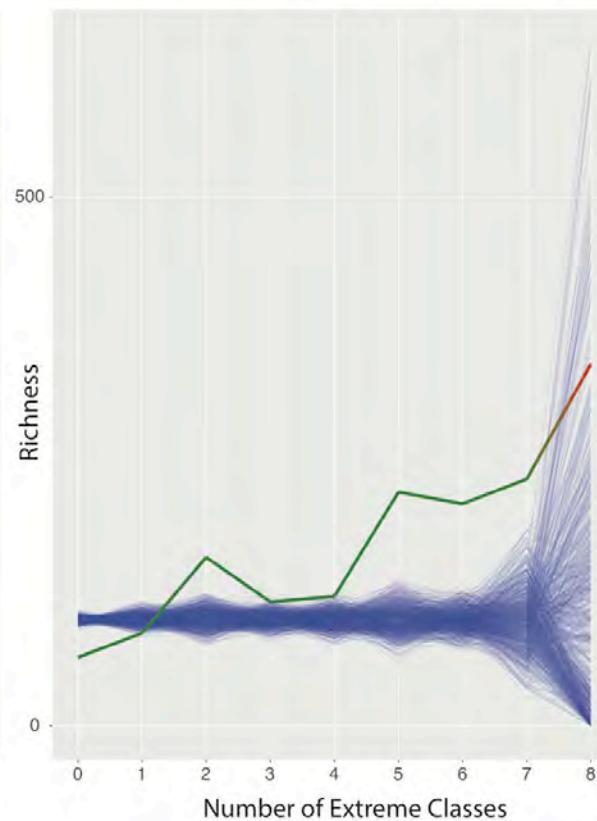


# Daisy Diversity Response to Extremes

Nth America  
All Flowering Plants



Nth American Compositae



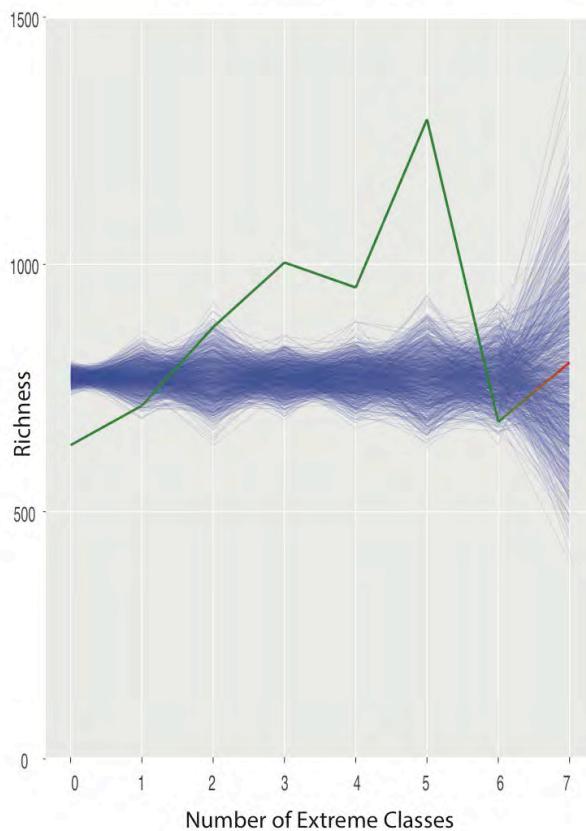
In Nth America species richness increases with extremeness...

...this trend is especially prominent in the daisy family...

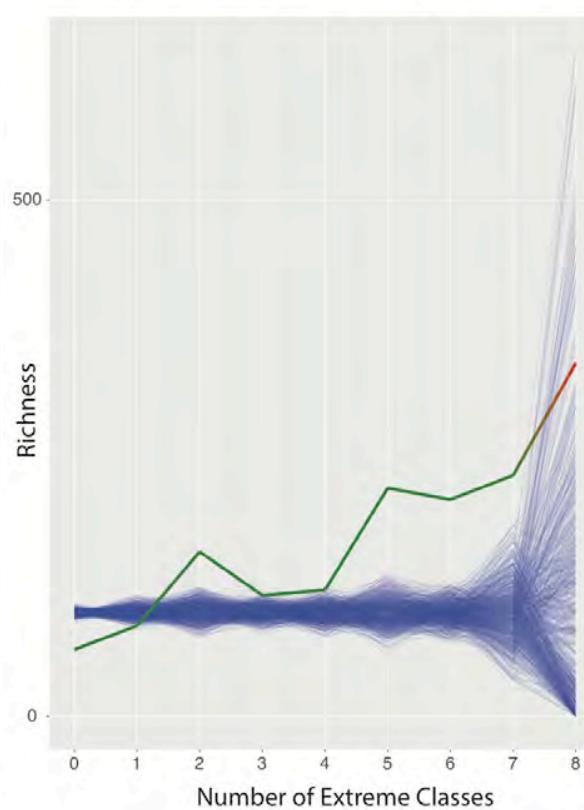


# Daisy Diversity Response to Extremes

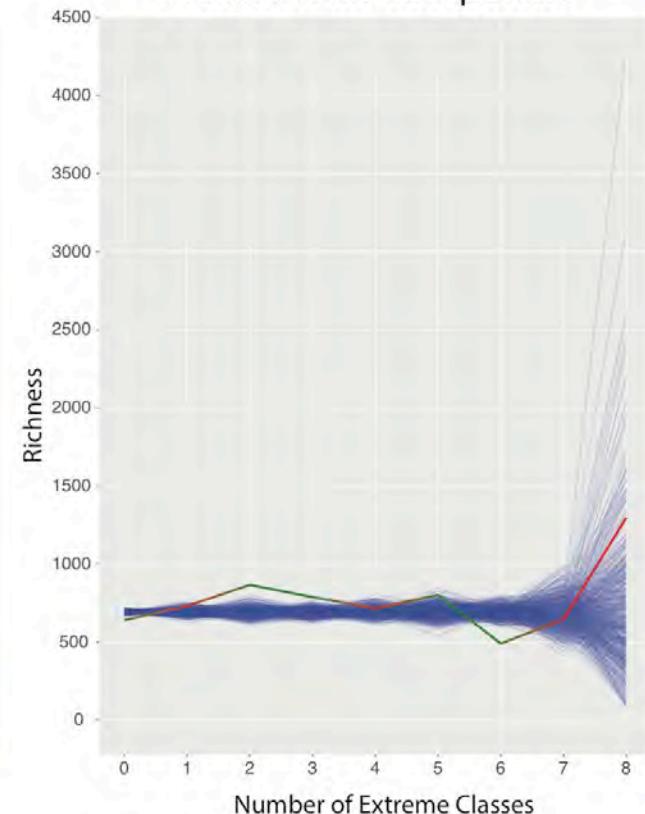
Nth America  
All Flowering Plants



Nth American Compositae



Nth American Flowering  
Plants Minus Compositae



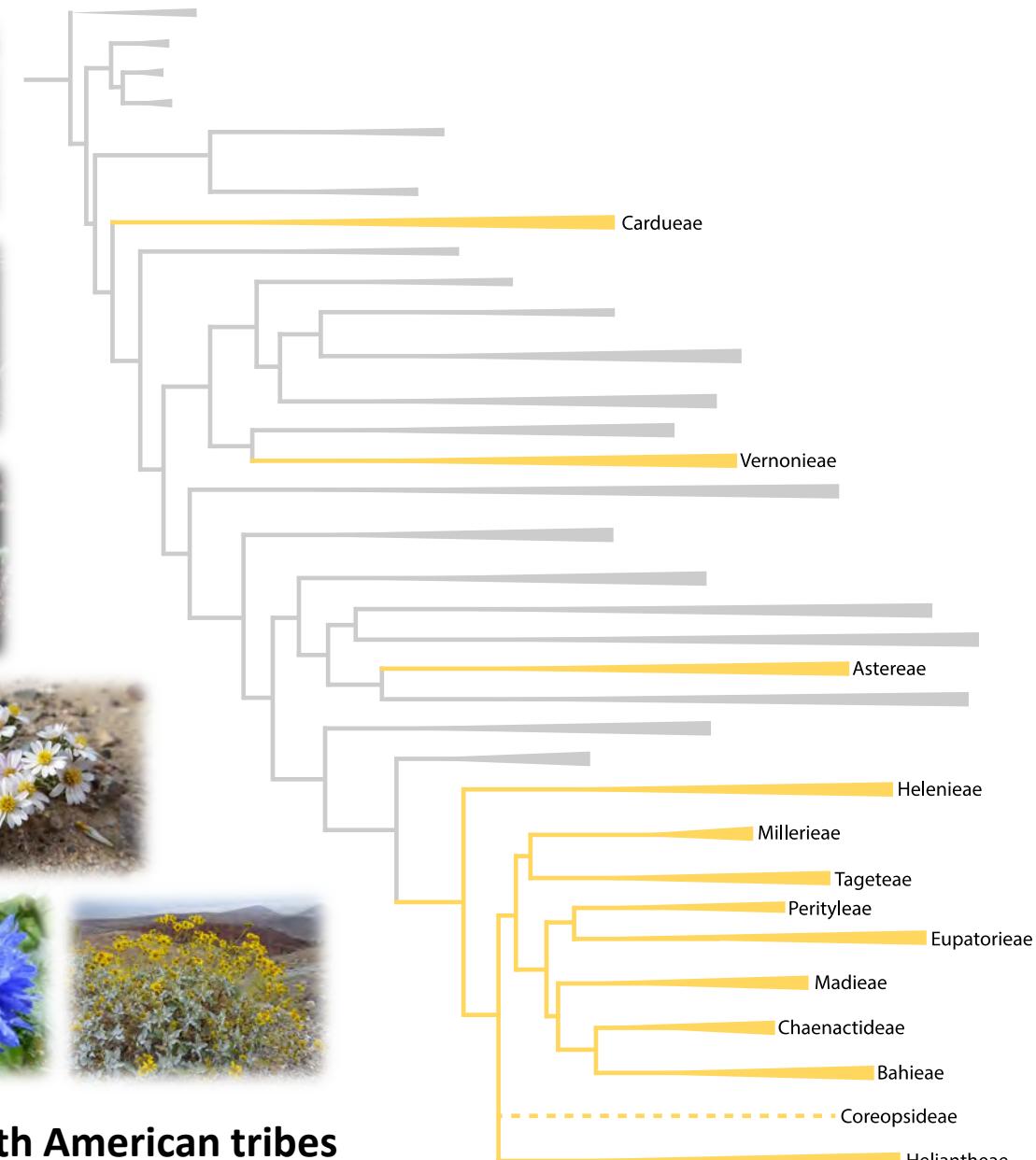
In Nth America species richness increases with extremeness...

...this trend is especially prominent in the daisy family...

...to the point that they account for almost all of it!



## Drivers of Diversification

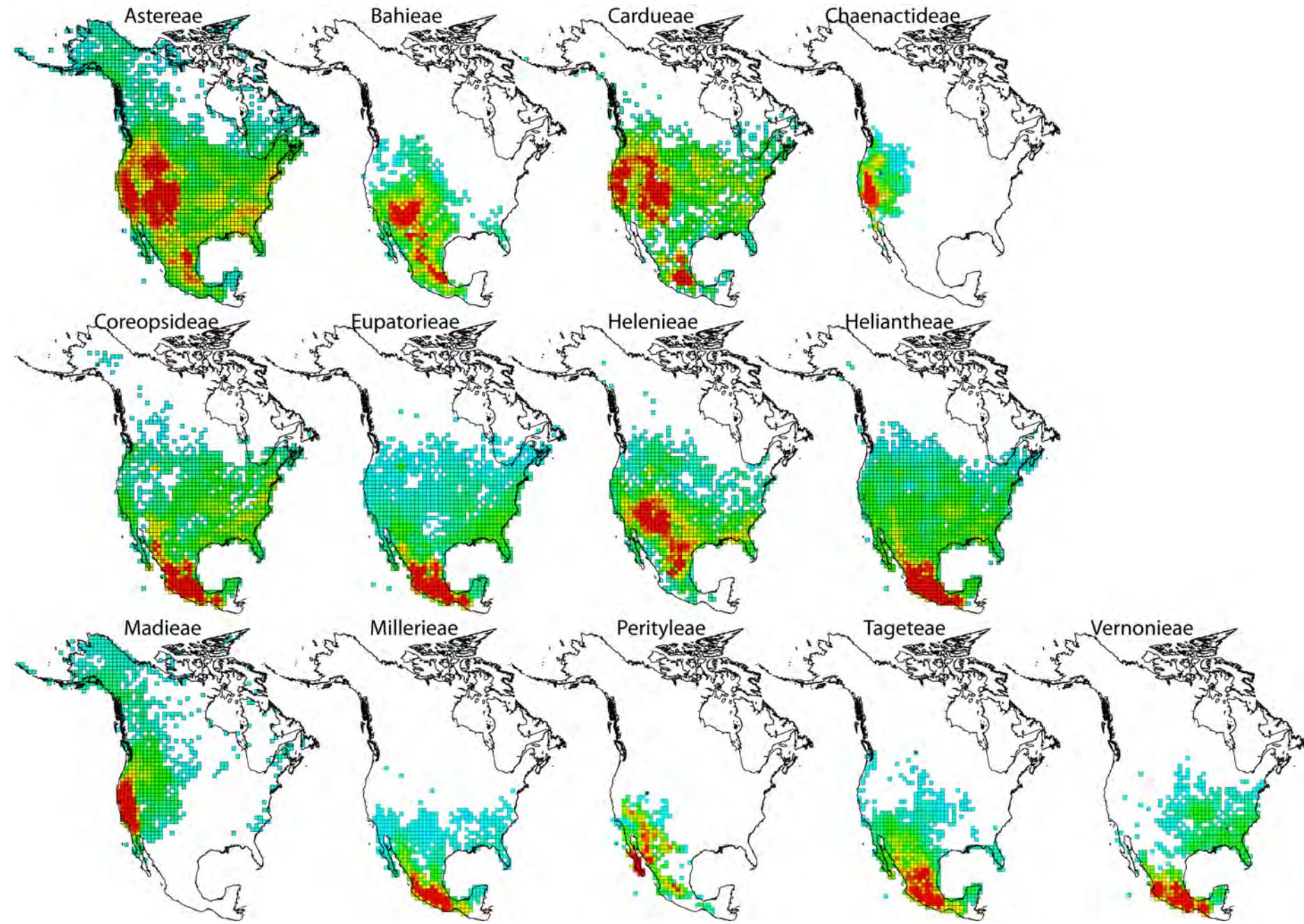


**13 majority endemic Nth American tribes**  
**4 ~independent radiations**

Modified from Mandel et al., 2019



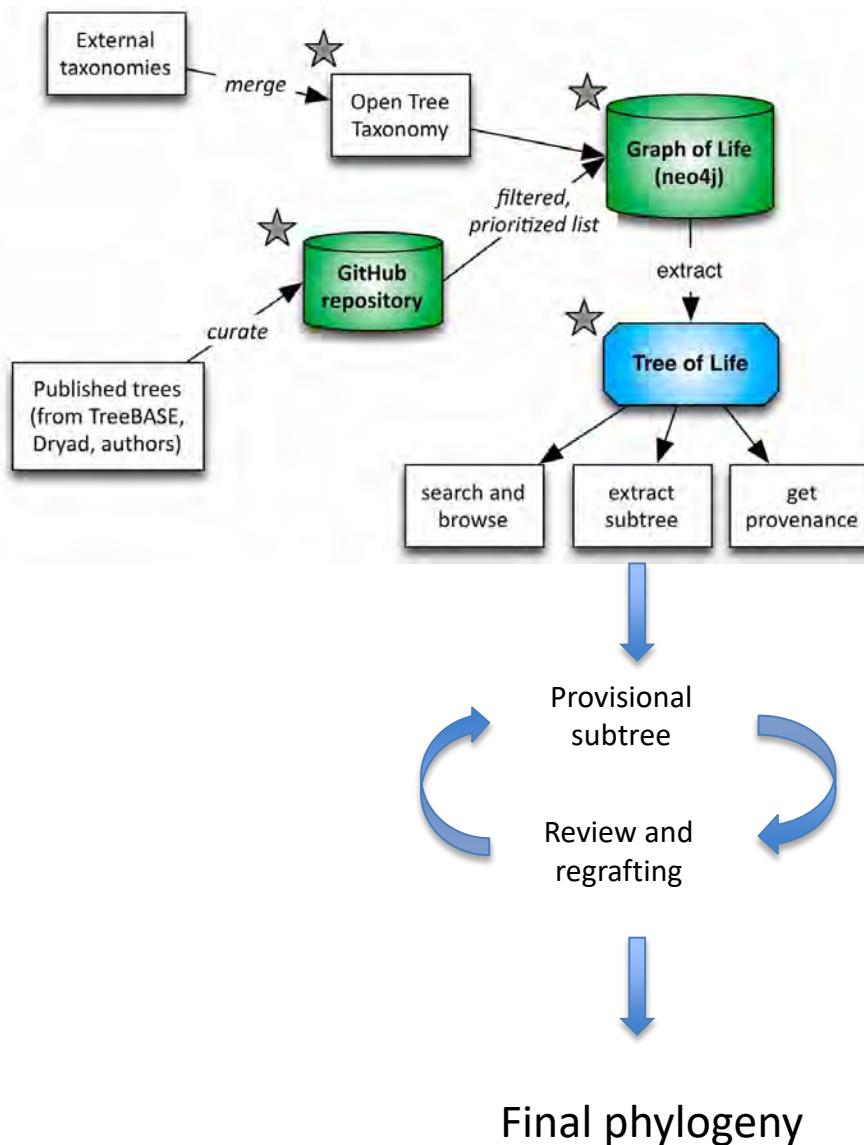
# Daisy Diversity Response to Extremes





# Drivers of Diversification

## Generating a species-level meta-phylogeny



Open Tree of Life

+

GenBank

+

Expert assessment and  
regrafting

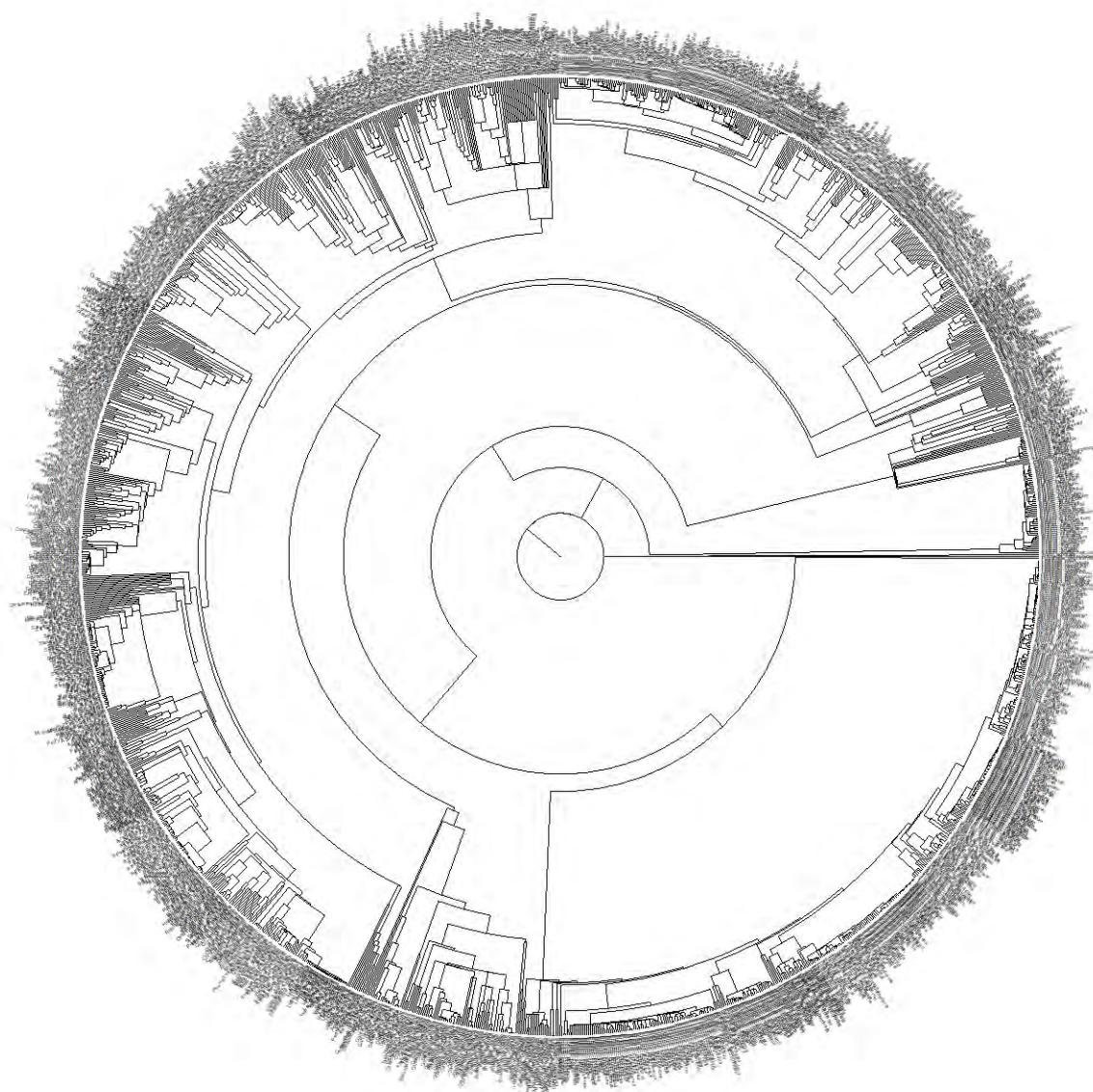
- Polytomies
- Misclassifications
- Missing taxa



Stephen Smith



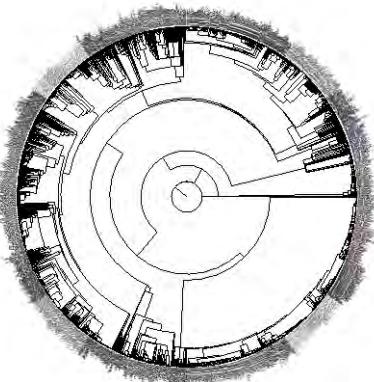
# Drivers of Diversification



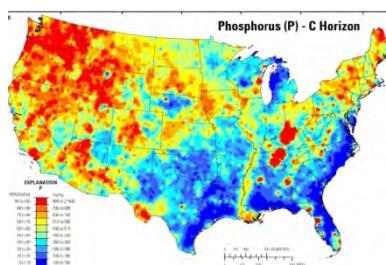
1642 taxa



# Drivers of Diversification



Which environmental variables are associated with increased/decreased diversification?



**Climate** – AdaptWest 1km (ClimateNA v5.10)<sup>1</sup>

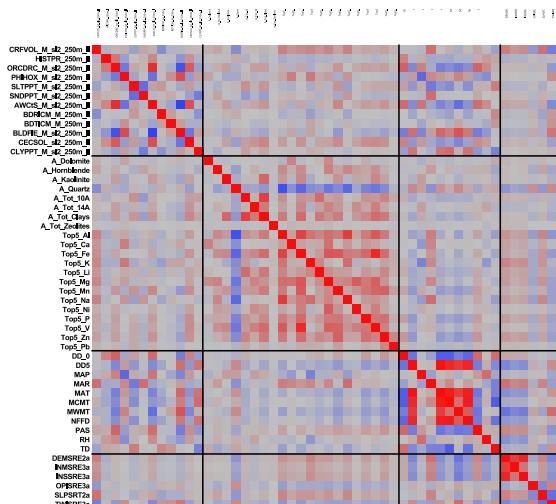
**Soil Profile/Texture** – SoilGrids 250m v0.5<sup>2</sup>

**Topography** – DEM-derived, via SoilGrids<sup>2</sup>

**Soil Geochemical/Mineralogical Data**

– USGS (OFR 2014-1082)<sup>3</sup> [interpolated from 4800 sites]

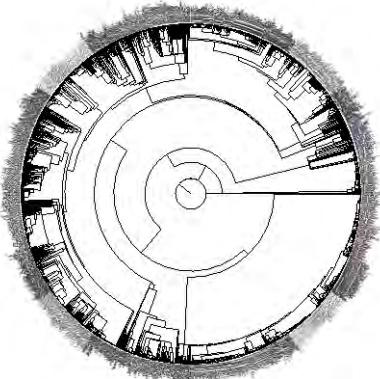
- 182 variables reduced to 50 non-colinear



“Variable reduction is a truly dark art” – Voldemort (probably)



## Drivers of Diversification



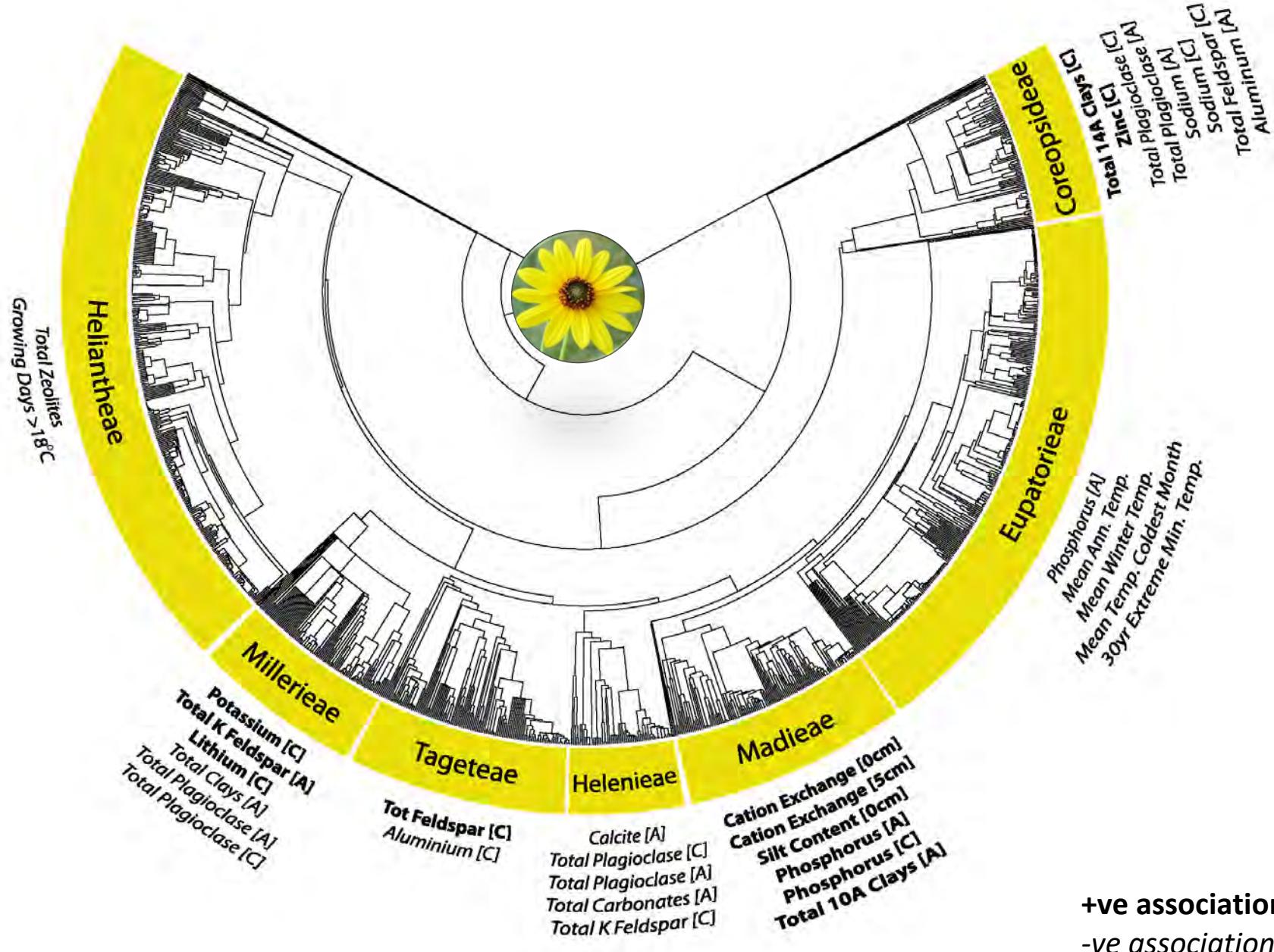
- Tip-rate correlation tests using the Diversification Rate metric (Jetz et al., 2012)
- Ordinary Least Squares regression (to meet assumptions and proven better performance over PGLS - Revell, 2010)
- First regressed diversification rate against single environmental variables
- Then multiple regression with all pairwise combinations of environmental variables that were not autocorrelated ( $r > 0.75$ ), including additive ( $A + B$ ) and multiplicative ( $A^*B$ ).
- To control for false positives, we replaced our environmental data with randomly generated data ( $\times 1000$ ) and repeated the analysis process for each simulated dataset.
- $R^2$  values were pooled across runs, and the 95<sup>th</sup> percentile was used as a cutoff value for interpreting the reliability of results with real data.



Chase Mason & Eric Goolsby



# Drivers of Diversification



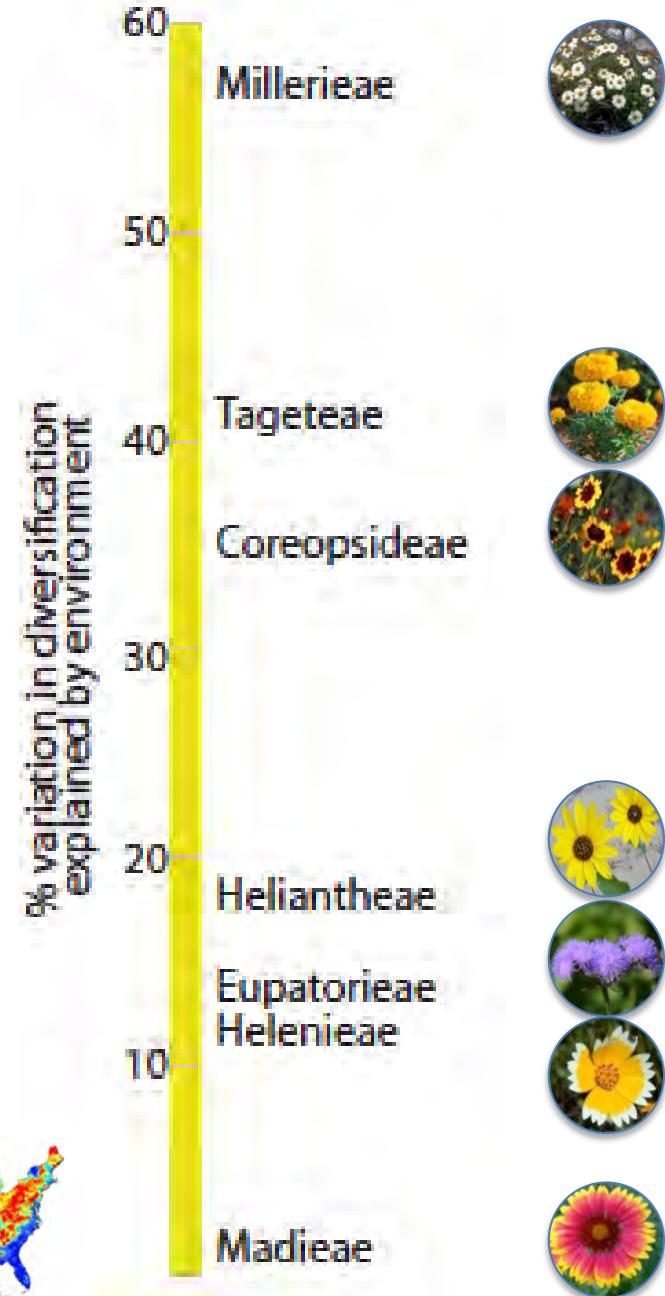
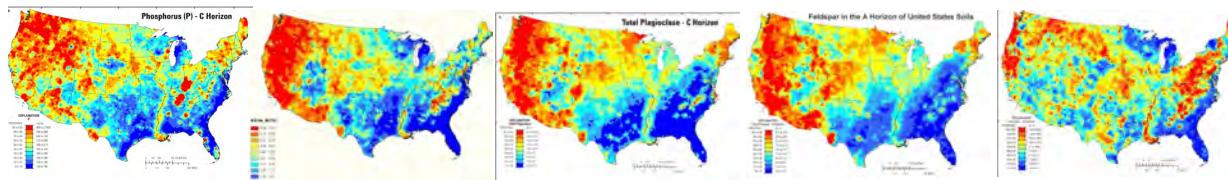
+ve association  
-ve association



# What factors drive diversification across North American Asteraceae?

- Abiotic environmental factors can explain >50% of variation in diversification rate, and up to 30% above randomly simulated data.
- This varies substantially among tribes.
- As a variable class, geochemical and mineralogical factors are consistently more correlated with diversification rate than climate, topography, or soil profile/texture:

*Phosphorus, Potassium, Aluminum  
Plagioclases, Feldspars, Clays*





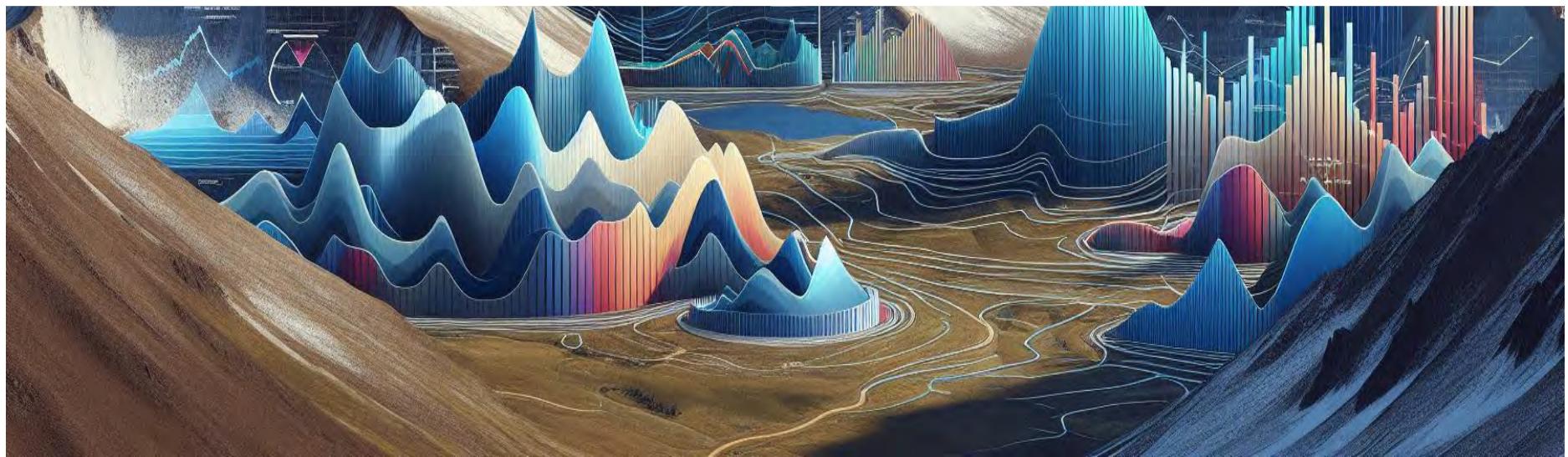
# Global **V**ascular **P**lant **M**aster **T**axonomy

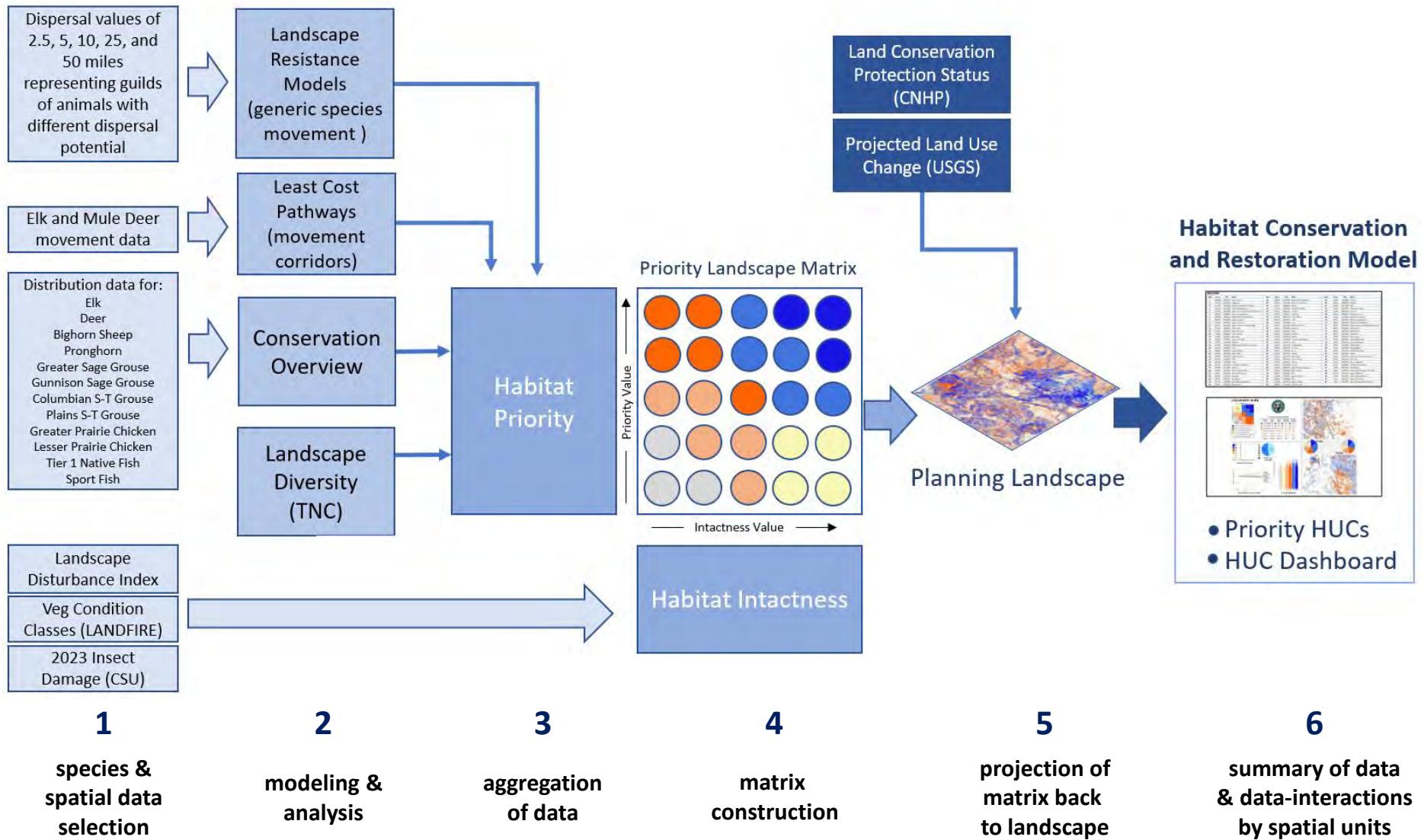
1 831 687 vascular plant names and name variants





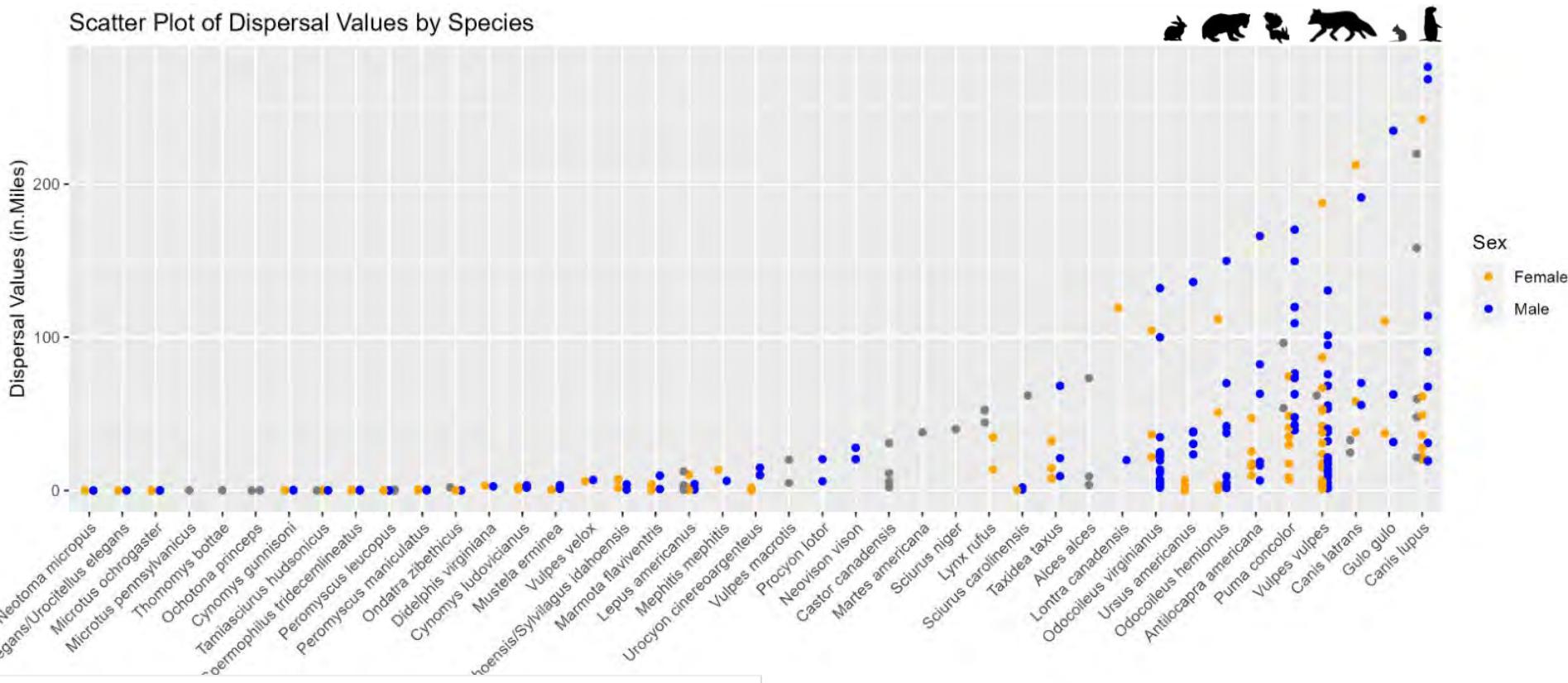
# COLORADO HABITAT CONSERVATION AND CONNECTIVITY PLAN DASHBOARD



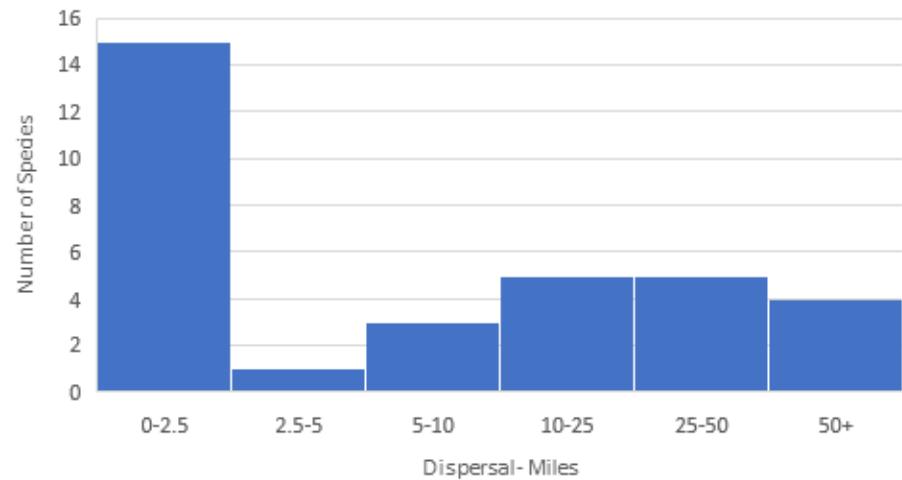


# Ominscape is agnostic of individual species traits and represents generalized movement potential

Scatter Plot of Dispersal Values by Species



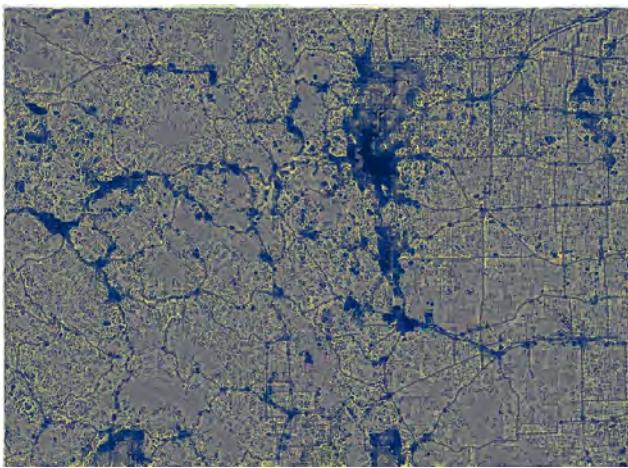
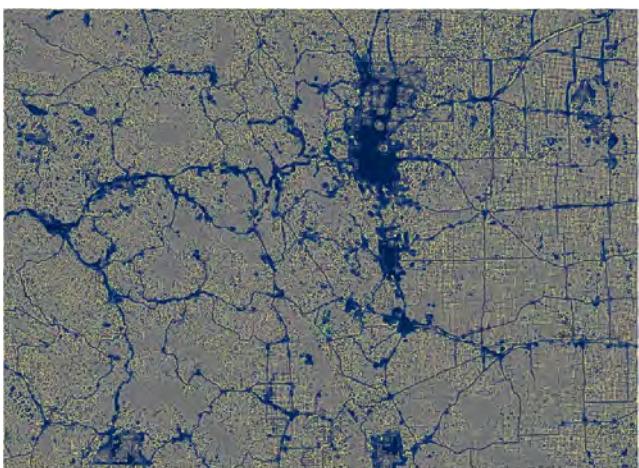
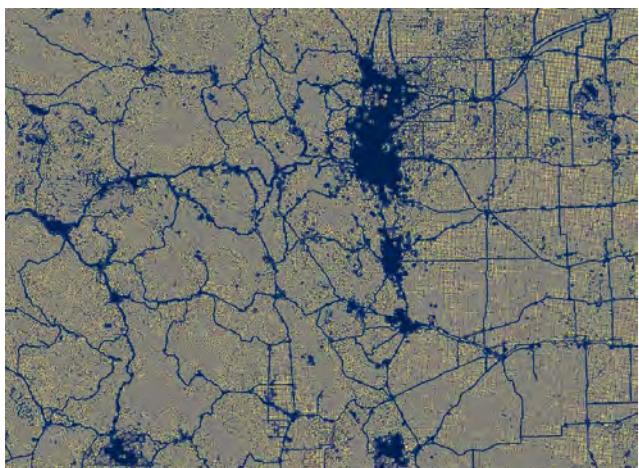
Average Dispersal Distances of Colorado Mammals By Window



**Movement for Colorado mammals skews local**

0.25, 5, 10, 25, and 50 mile radii were used in this study

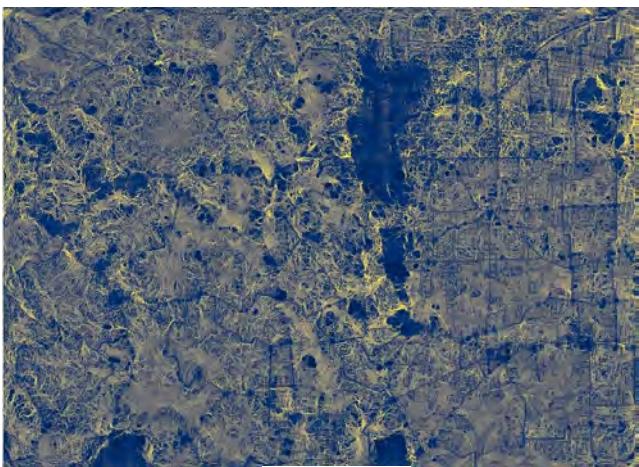
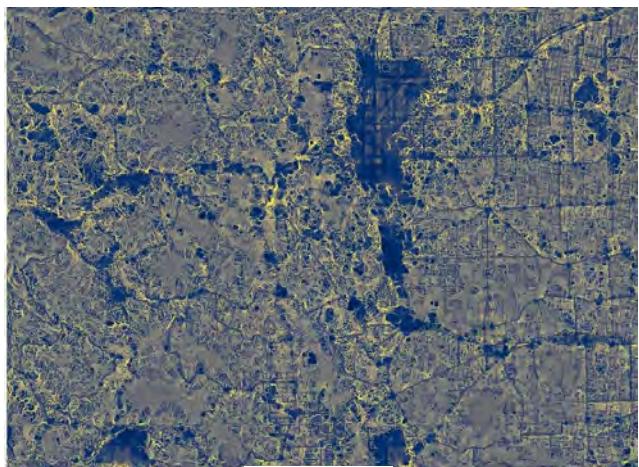
2.5 miles



2.5 miles

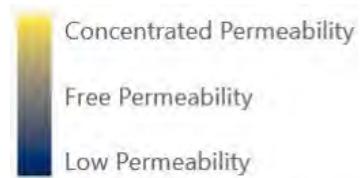
5 miles

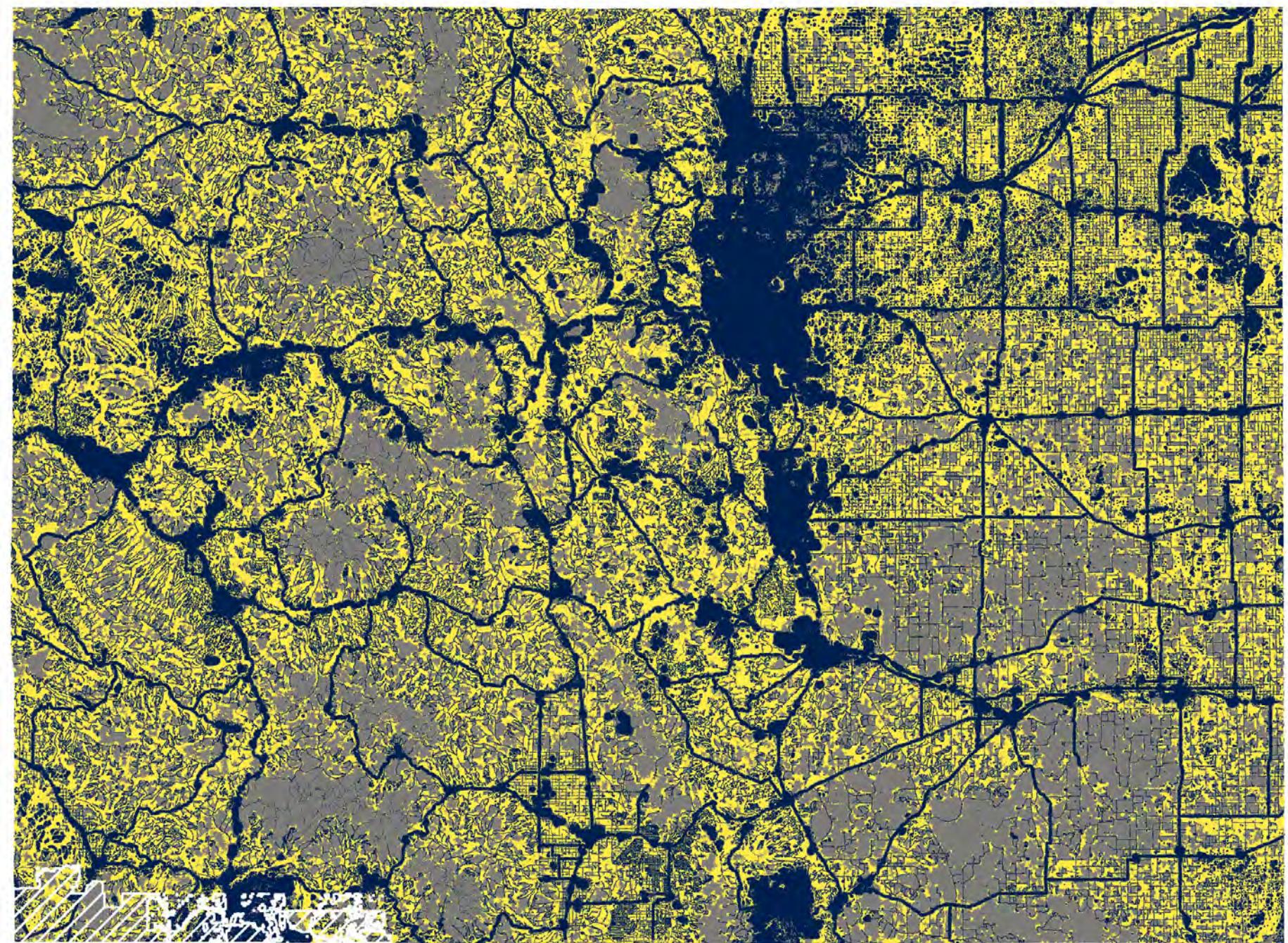
10 miles

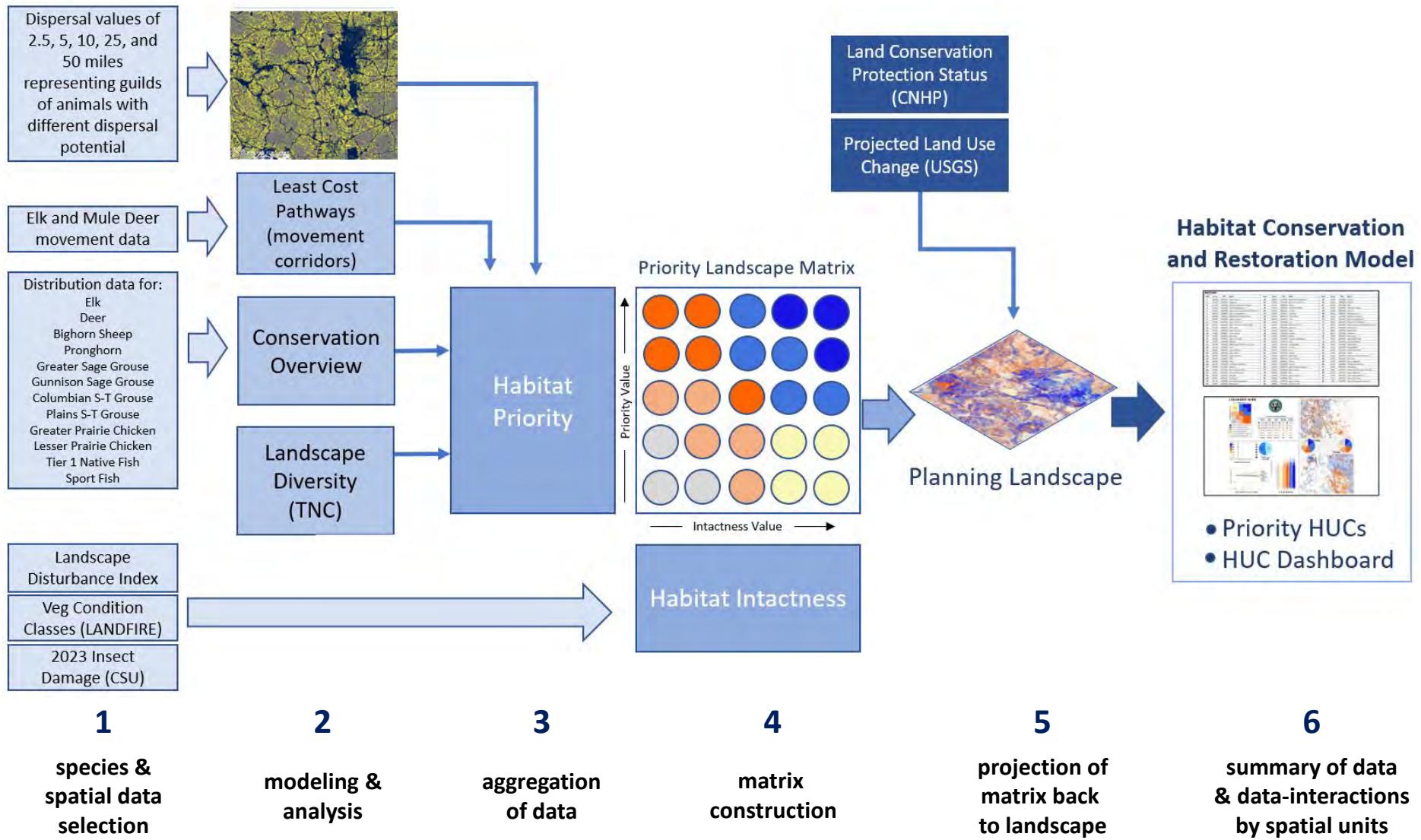


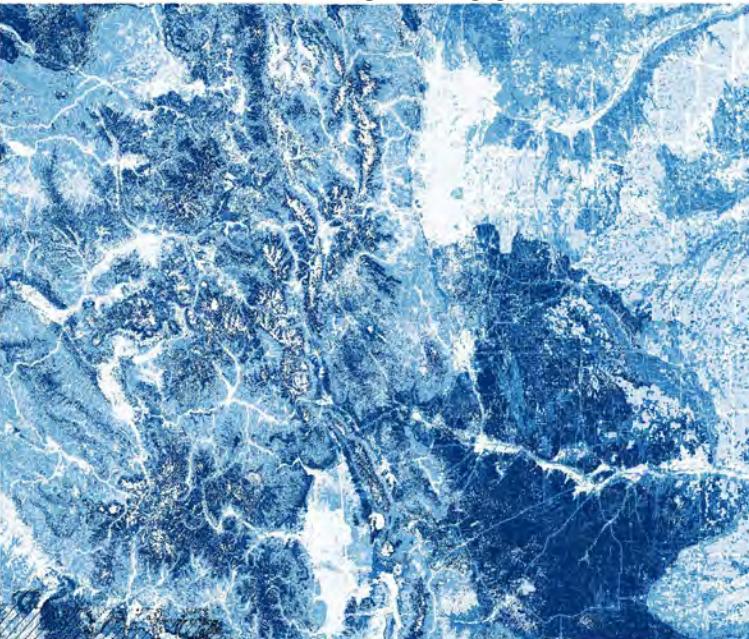
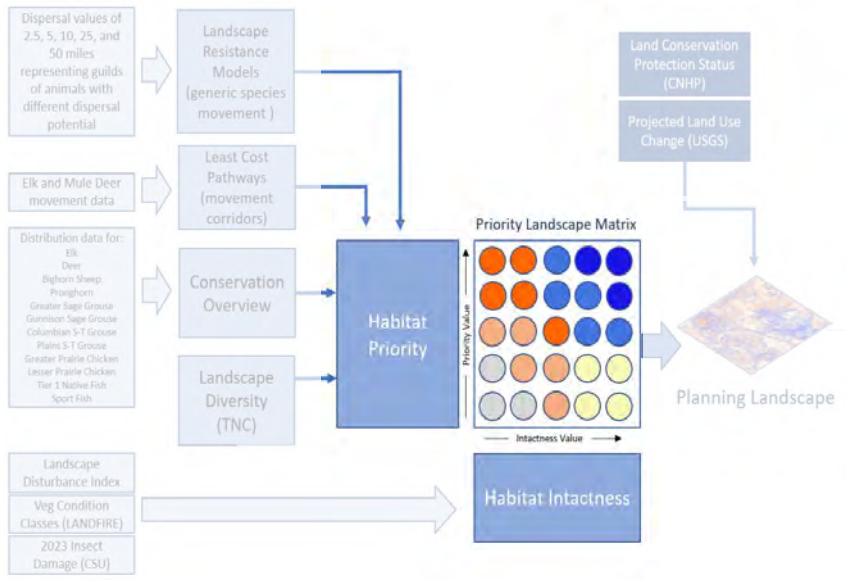
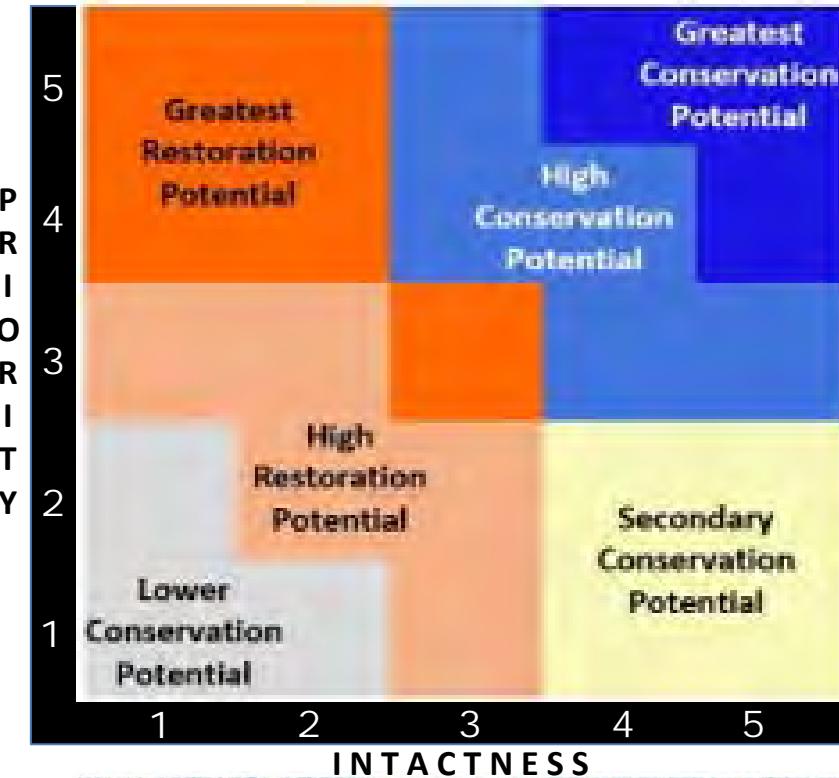
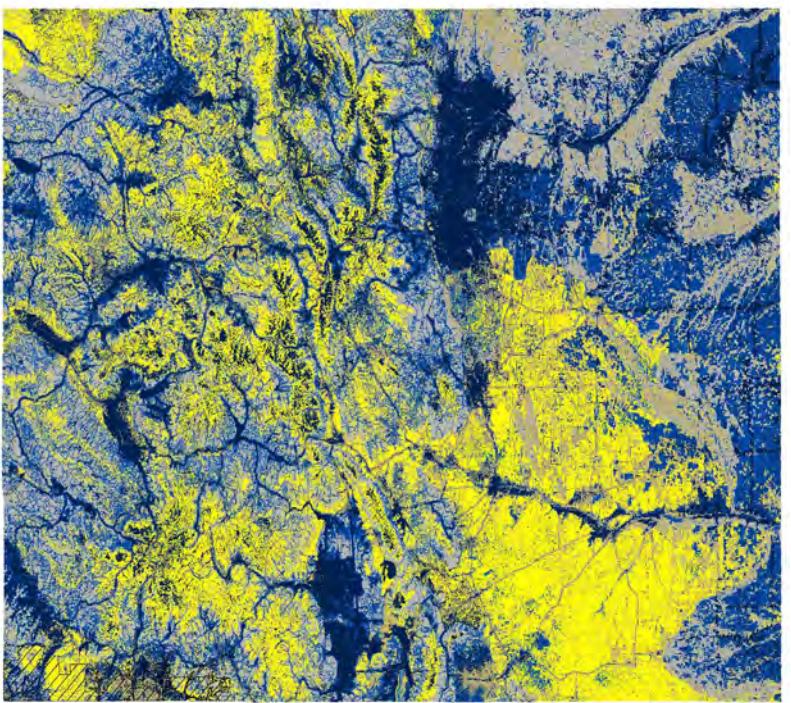
25 miles

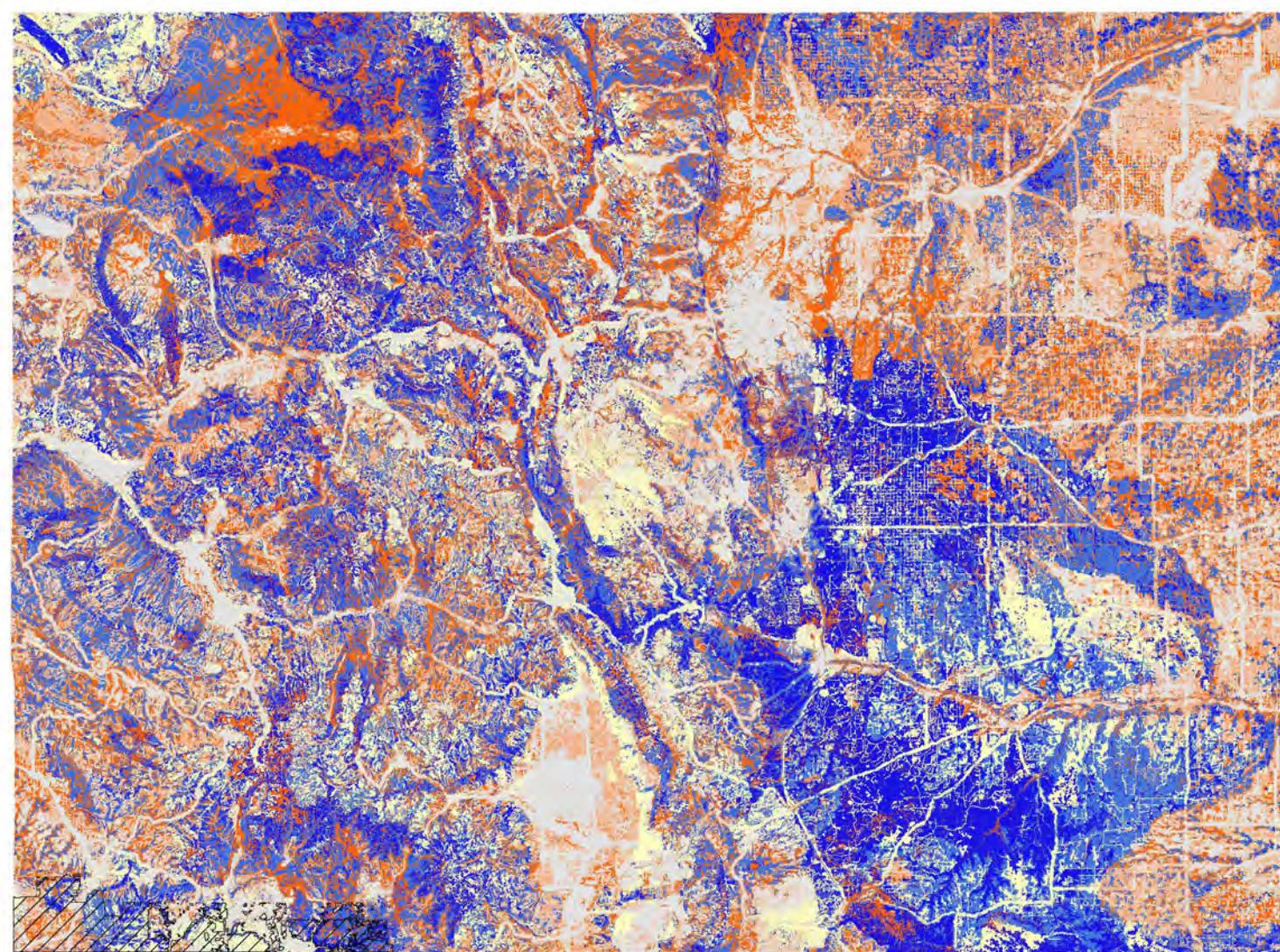
50 miles



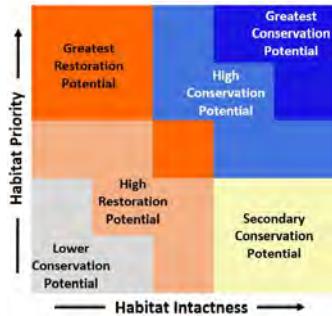






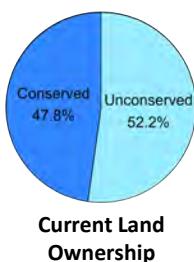


# COLORADO

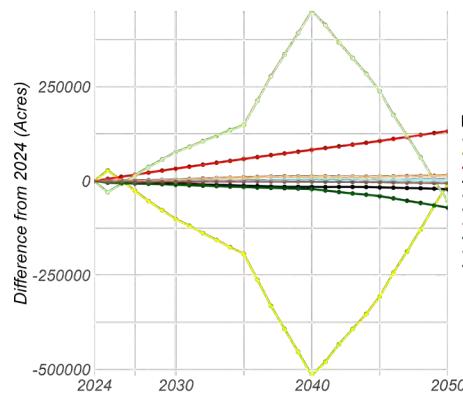


## Landscape Summary Statistics

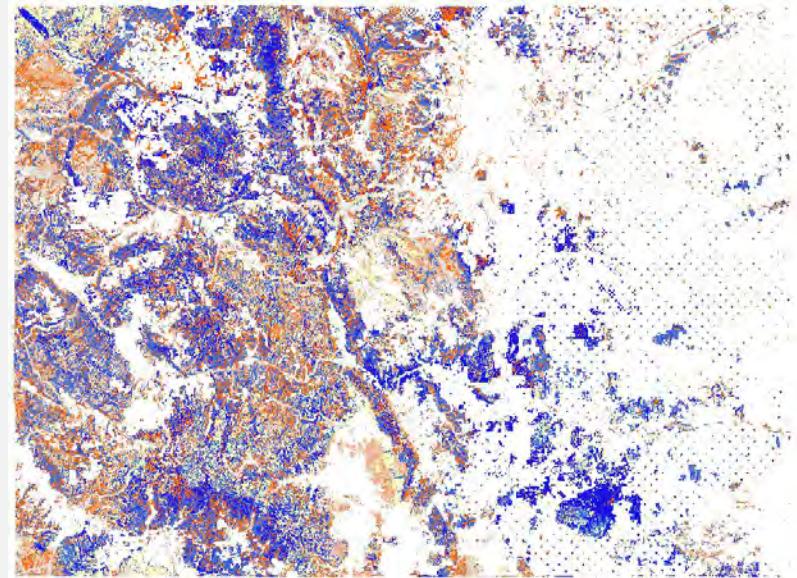
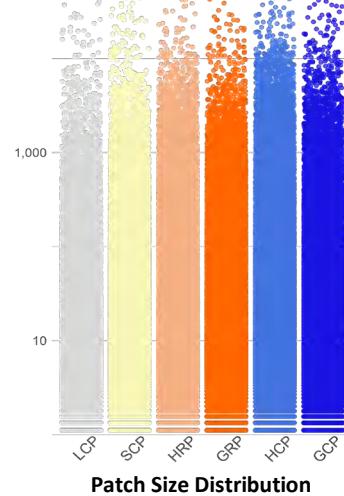
Total Area (acres)	Conserved (acres)	Unconserved (acres)	Aggregation (out of 100)	Cohesion (out of 100)
8,898,313	4,766,693	4,021,916	84.56	98.70
15,827,261	8,933,664	6,696,712	84.45	98.65
11,081,396	5,189,446	5,717,744	82.21	99.05
11,592,918	5,044,816	6,393,939	83.42	98.33
7,467,712	3,960,664	3,407,847	82.65	98.80
11,751,269	3,408,508	8,138,105	89.41	99.91
66,618,872	31,303,794	34,376,266	84.45	98.91



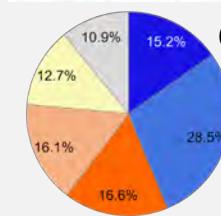
## Current Land Protection



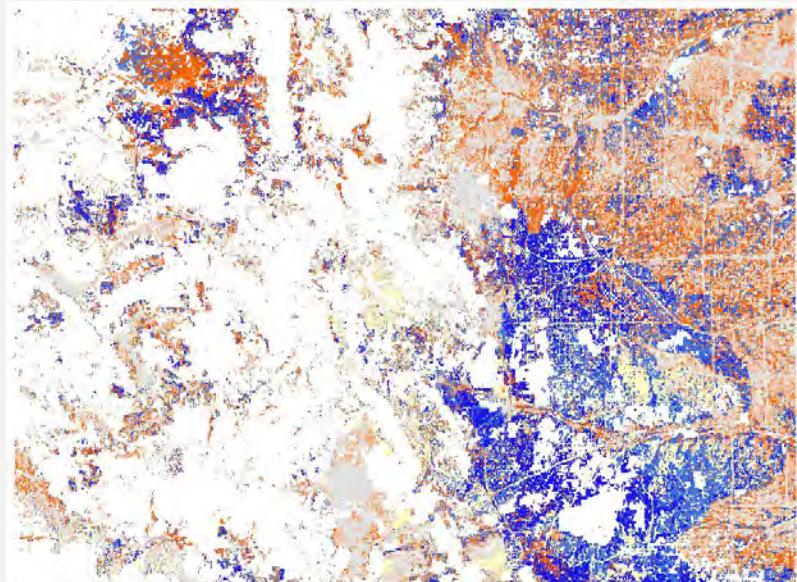
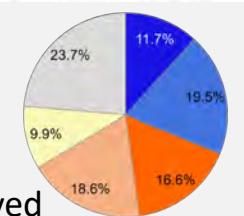
## Patch Size Distribution



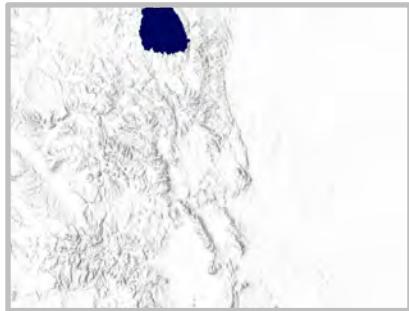
## Conserved



## Unconserved



# NORTH PLATTE HEADWATERS 10180001

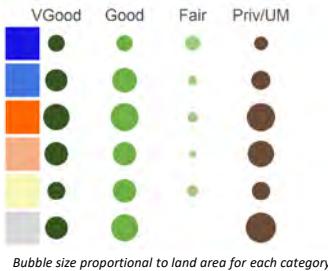
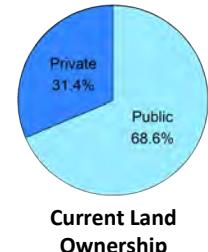


**Protect (Potential Land Conservation) rank:** 43/92  
**Defend (Maintain Land Conservation) rank:** 28/92  
**Restore (Habitat Restoration) rank:** 32/92  
**Combined Rank:** 30/92 (tied)

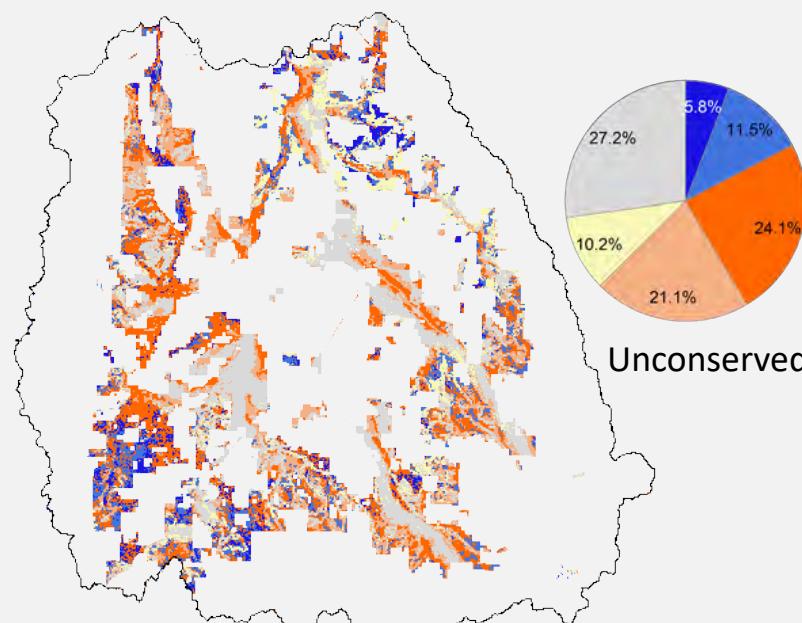
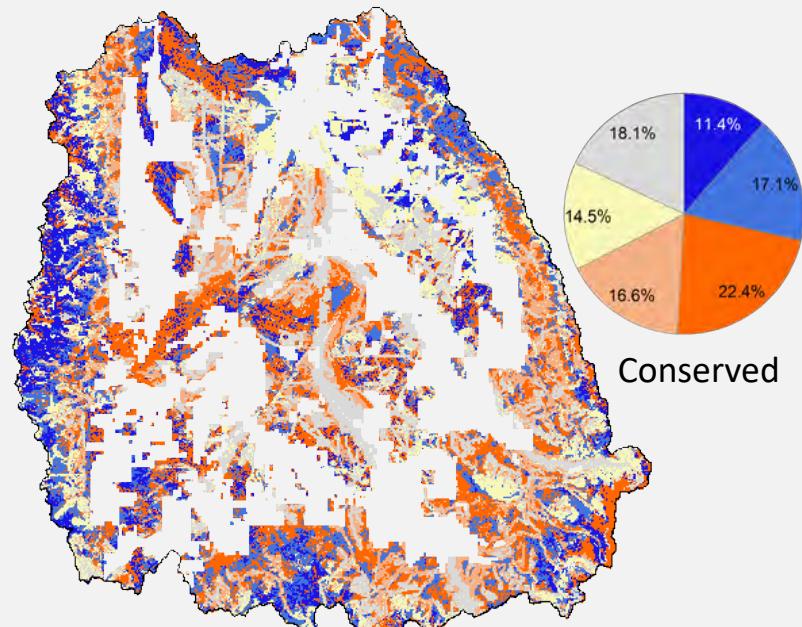
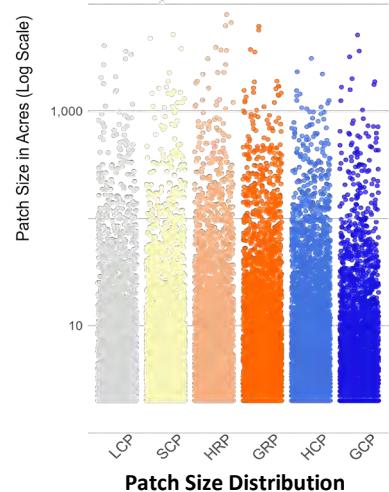
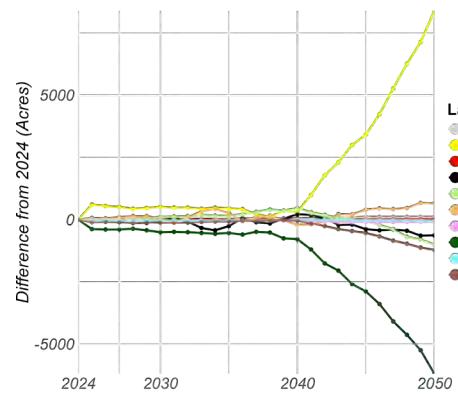
## Landscape Summary Statistics

Total Area (acres)	Conserved (acres)	Unconserved (acres)	Aggregation (out of 100)	Cohesion (out of 100)
88,117	70,189	16,317	75.58	96.84
139,820	105,314	32,076	74.12	95.71
209,852	137,993	67,396	81.70	98.96
163,930	102,233	59,048	78.29	97.82
119,921	89,073	28,627	76.54	97.15
191,075	111,282	75,832	85.07	99.26
912,718	616,086	279,298	78.55	97.62

- █ Greatest Conservation Potential
- █ High Conservation Potential
- █ Greatest Restoration Potential
- █ High Restoration Potential
- █ Secondary Conservation Potential
- █ Lower Conservation Potential



## Current Land Protection



# RIO GRANDE HEADWATERS 13010001

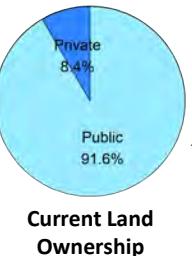
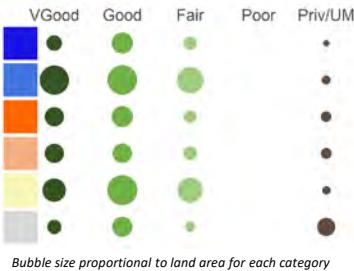


- █ Greatest Conservation Potential
- █ High Conservation Potential
- █ Greatest Restoration Potential
- █ High Restoration Potential
- █ Secondary Conservation Potential
- █ Lower Conservation Potential

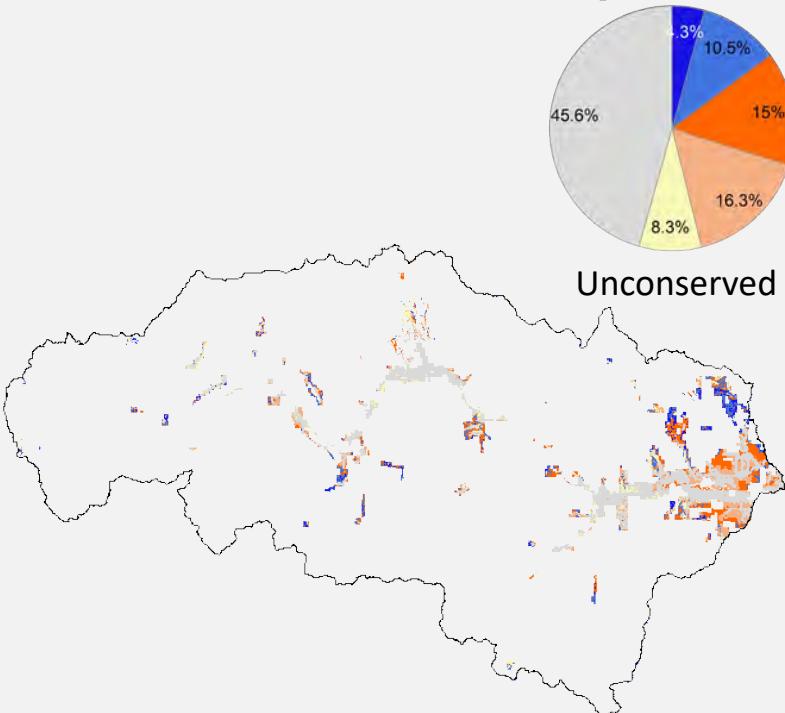
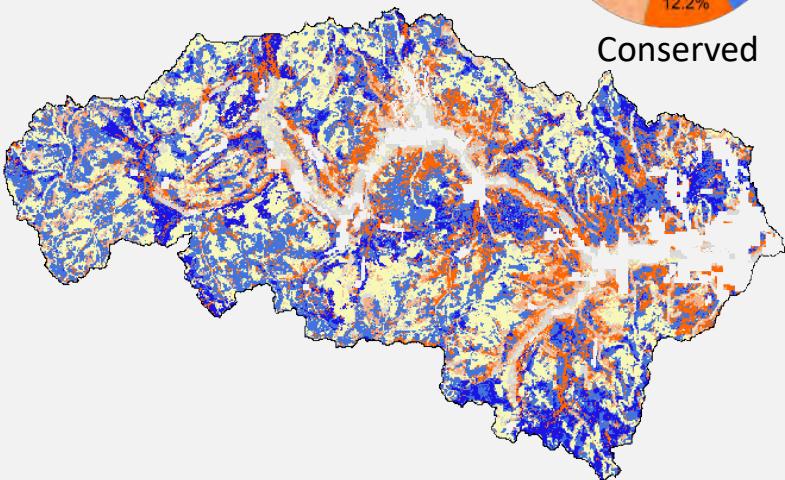
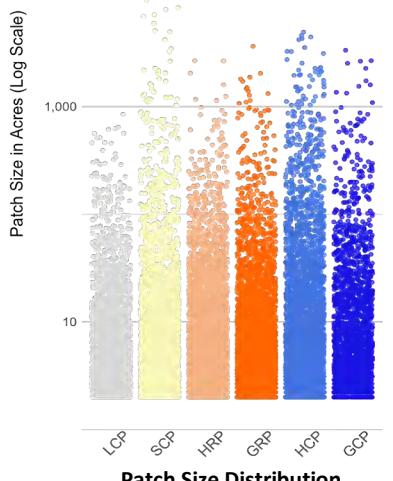
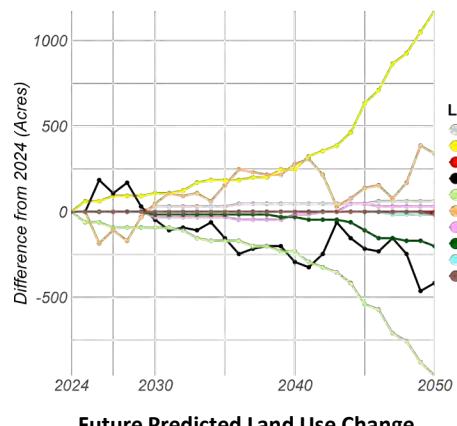
**Protect (Potential Land Conservation) rank:** 72/92  
**Defend (Maintain Land Conservation) rank:** 13/92  
**Restore (Habitat Restoration) rank:** 30/92  
**Combined Rank:** 40/92

## Landscape Summary Statistics

Total Area (acres)	Conserved (acres)	Unconserved (acres)	Aggregation (out of 100)	Cohesion (out of 100)
89,520	85,630	3,000	79.03	96.78
255,789	246,599	7,431	80.15	98.10
110,610	98,494	10,591	73.21	95.94
107,535	94,490	11,495	71.45	94.59
217,402	210,041	5,822	84.94	98.54
104,411	69,465	32,186	81.18	99.01
885,269	804,722	70,528	78.33	97.16

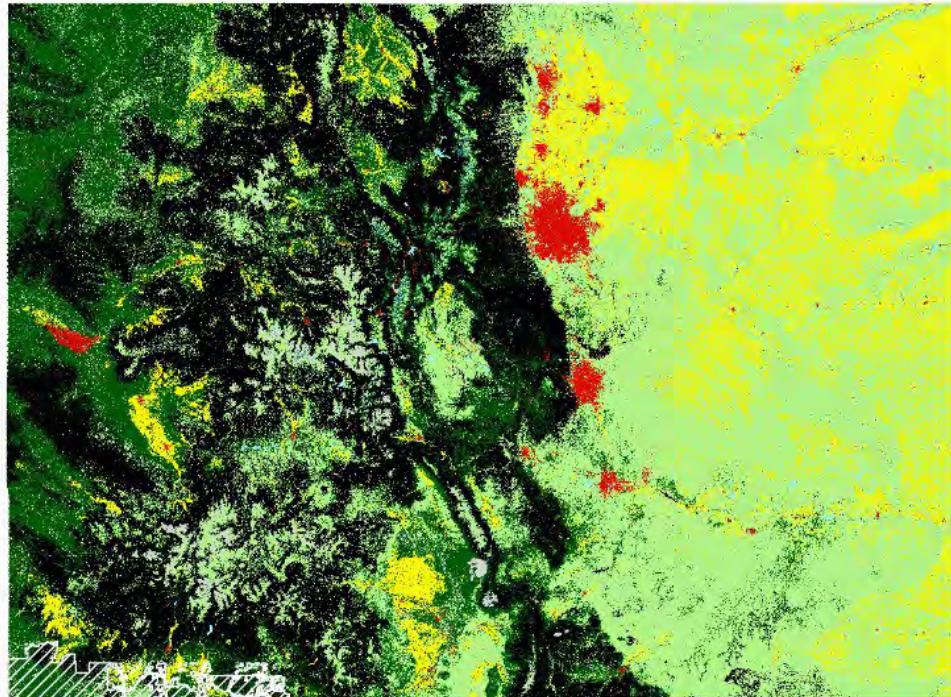


## Current Land Protection

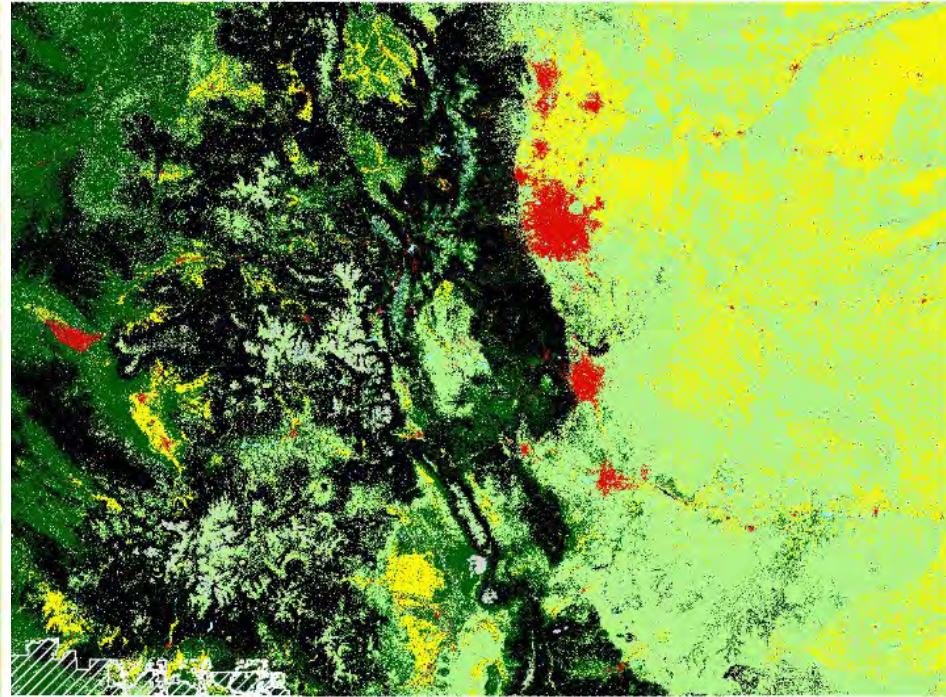


# BASE DATA PROJECTED LANDUSE CHANGE

2024



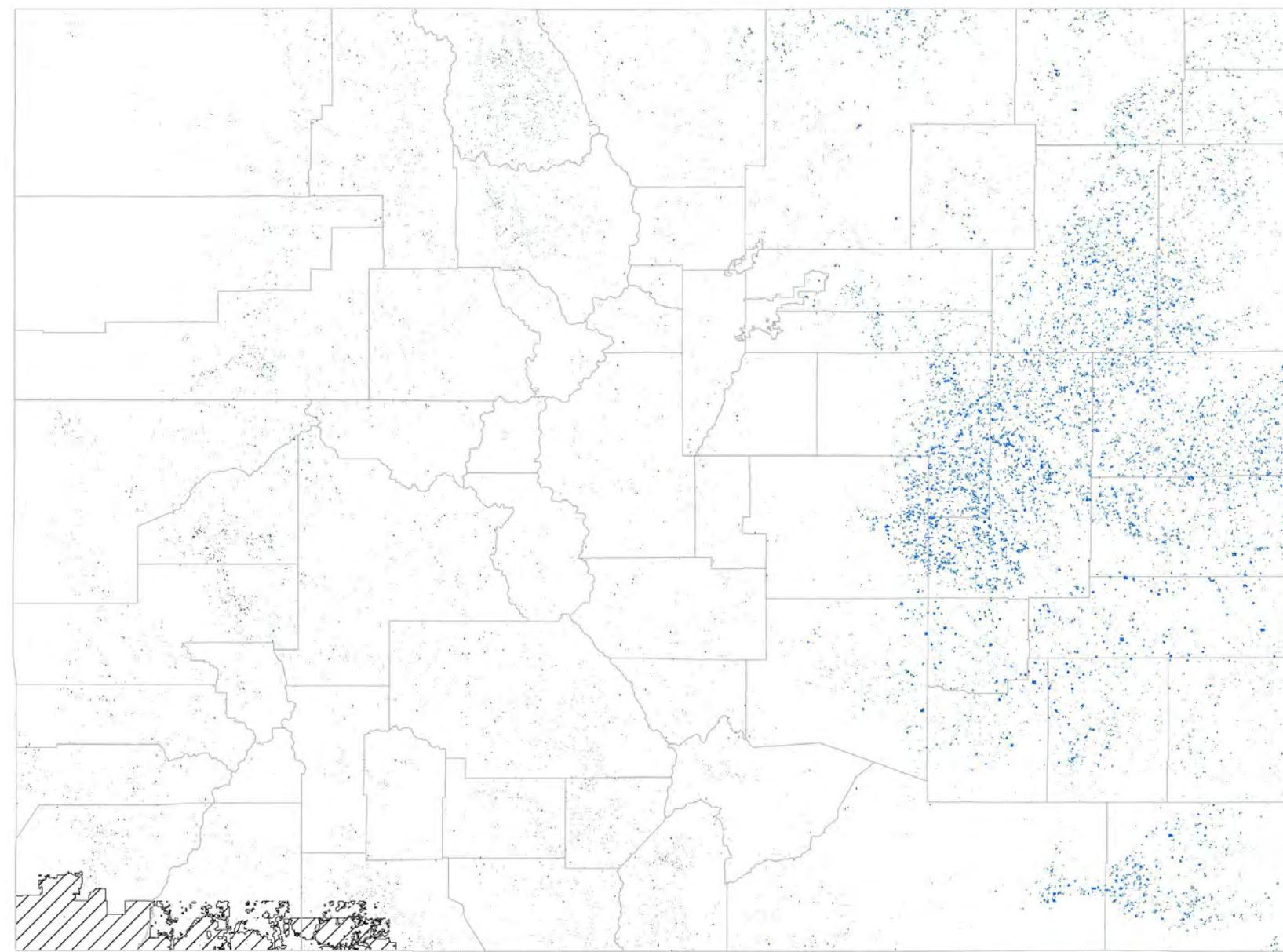
2050



## USGS FORE-SCE Model

- Uses the **IPCC SRES “A2”** scenario (socioeconomic impacts on anthropogenic land use incorporating demographics, energy use, agricultural economics, and other socioeconomic considerations).
- A2 is the “worst case” scenario, with continued economic development and temperature increases 2.0-5.4 degrees C.
- The FORE-SCE model “known” landscape data from 1992-2005 using the A2 scenario, then projects 2006-2100.
- Predicts future land use and land cover.





**Projected Land Use Change 2024 vs 2050  
Under USGS A2 Model**

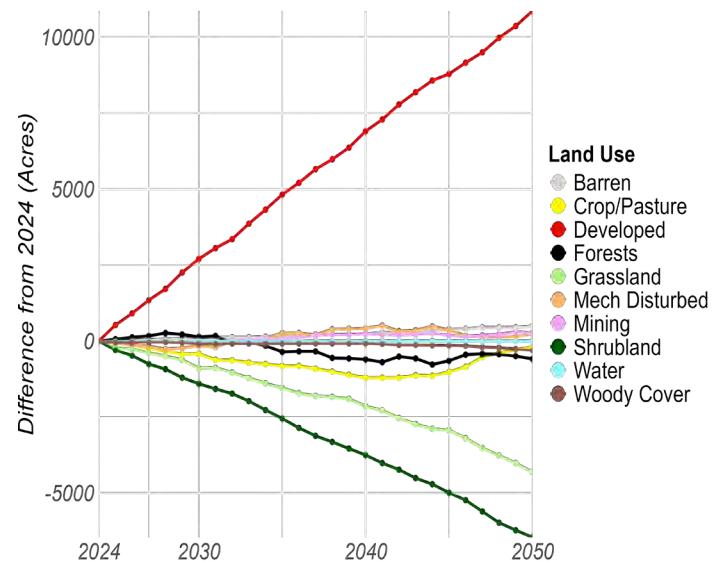
Land Use Change

Tribal Land

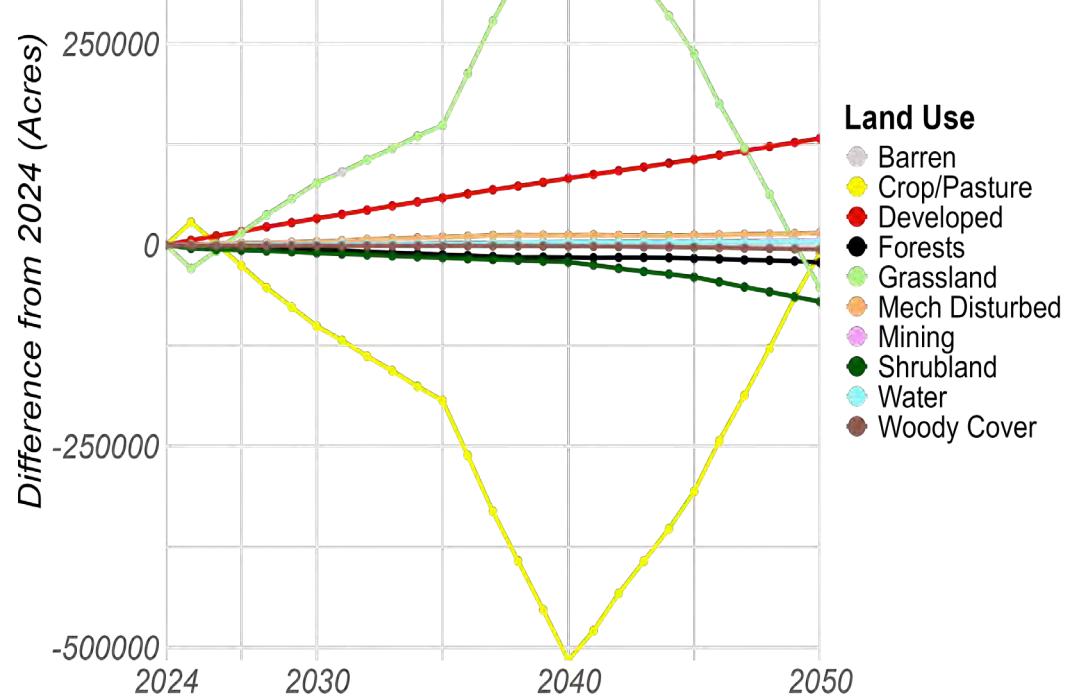
Colorado County Boundaries

## PROJECTED LAND USE CHANGE

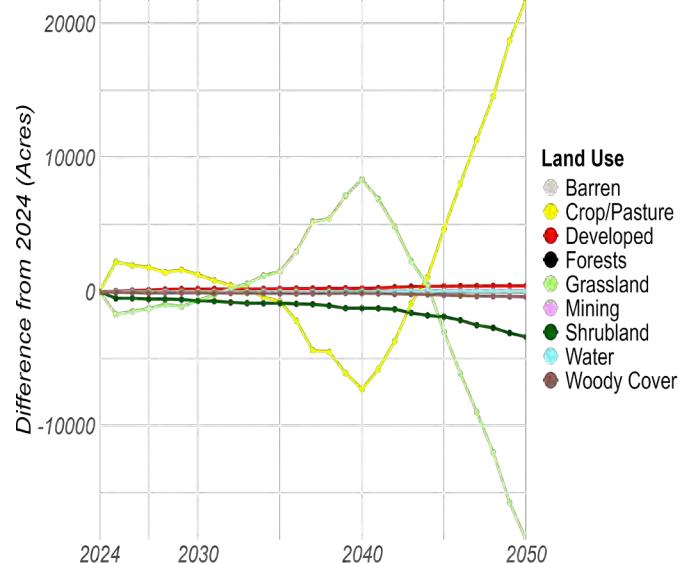
### UPPER ARKANSAS



### ALL COLORADO

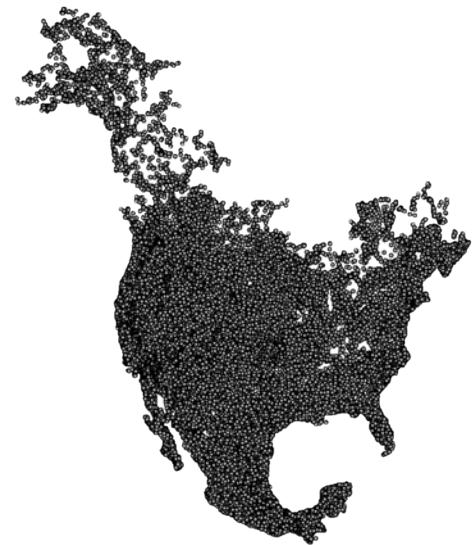


### UPPER ARKANSAS-JOHN MARTIN RESERVOIR

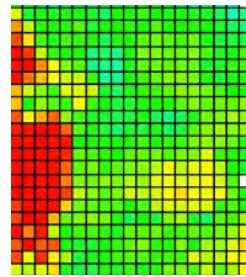




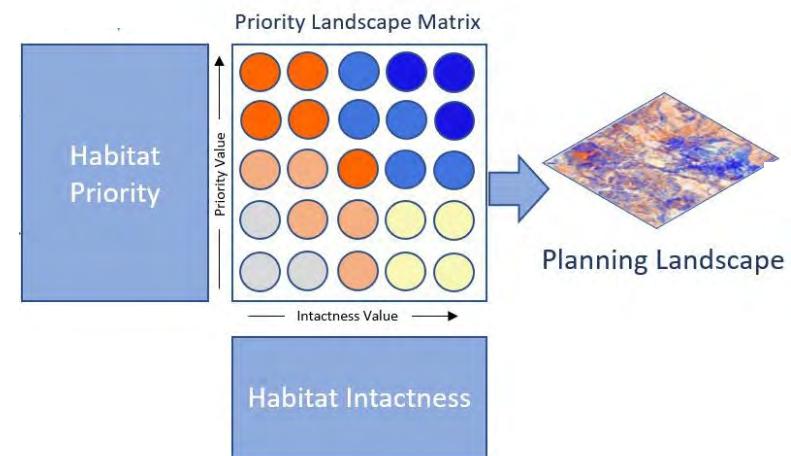
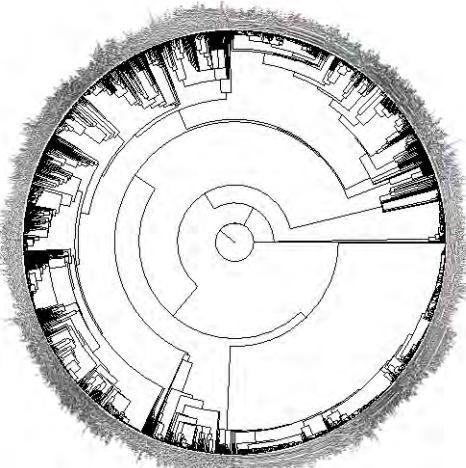
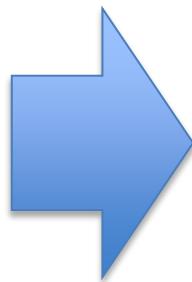
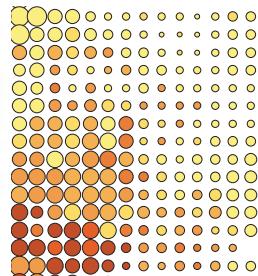
# Future Hopes & Dreams



Colorado  
Species  
Diversity



Colorado  
Genetic  
Diversity



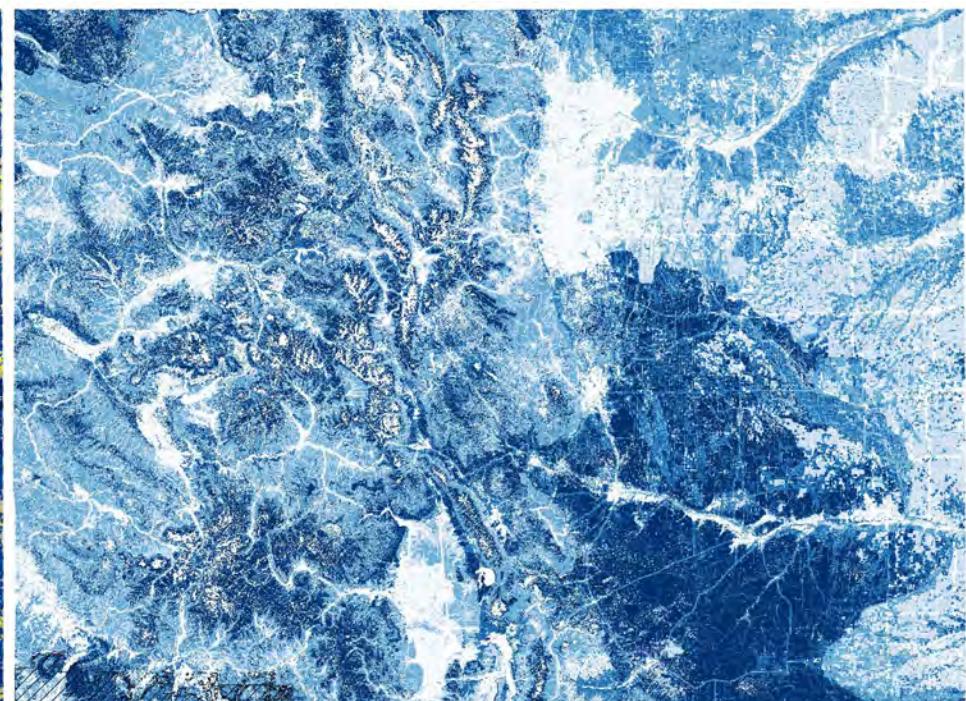
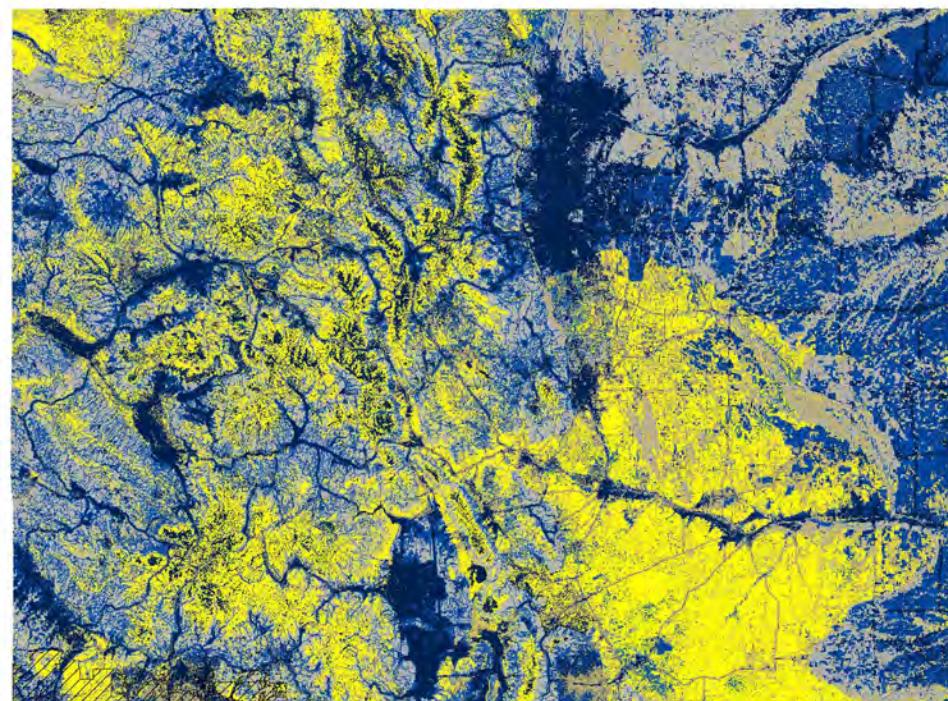


# CNHP- Applying Spatial Data

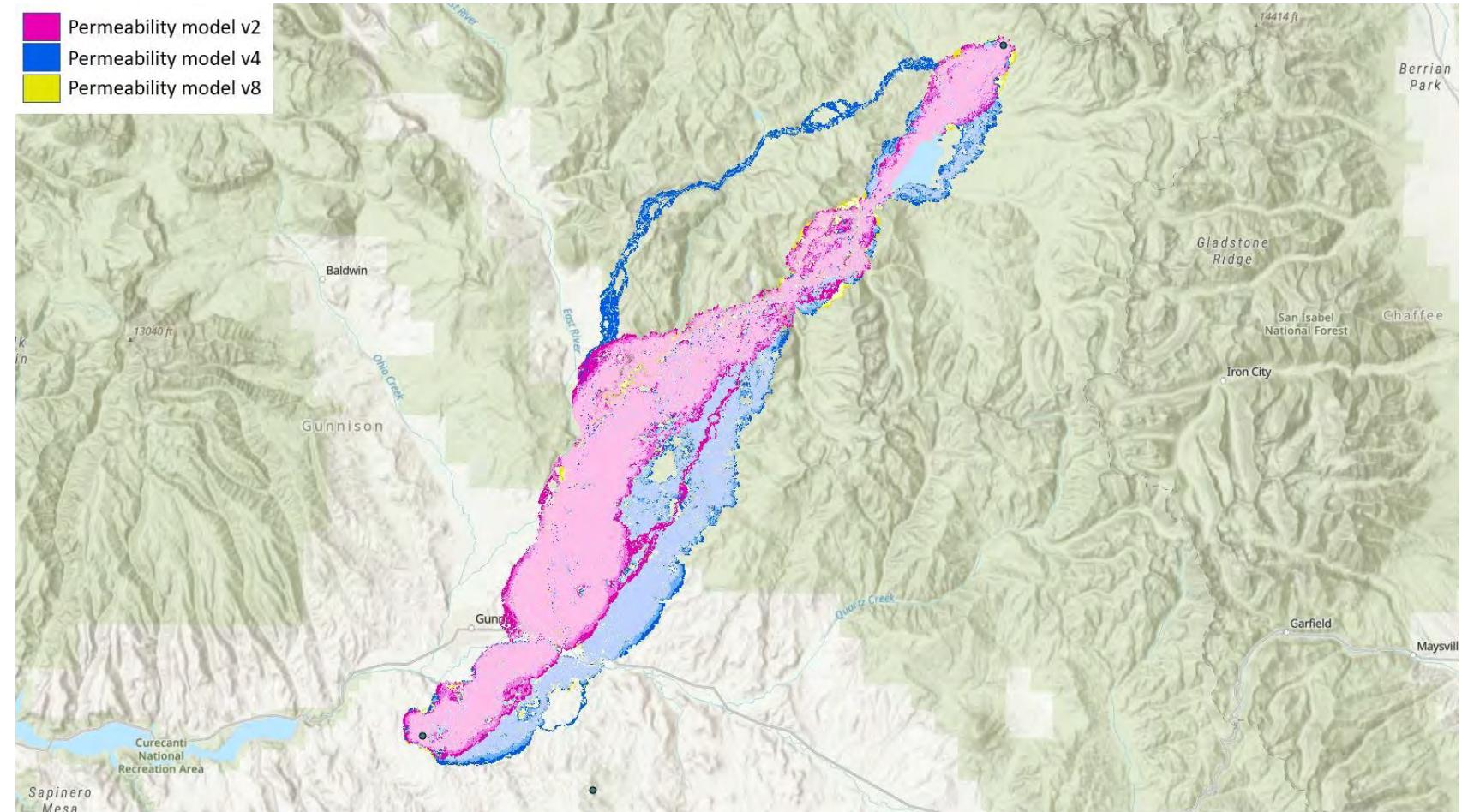


# CNHP- Applying Spatial Data

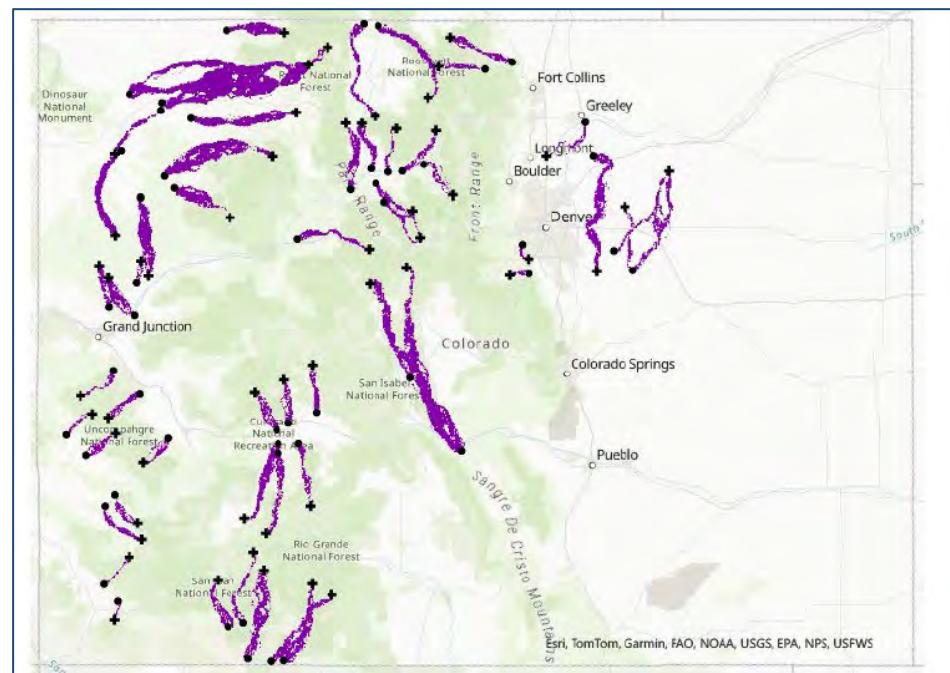




- Ran a set of “known” corridor paths using a subset of the candidate models
- Tested the overlap of those models with the know movement paths



The final model was then used to extrapolate between “unknown” start and end points



Mule Deer



Elk