role of microrefugia in buffering fynbos from global change

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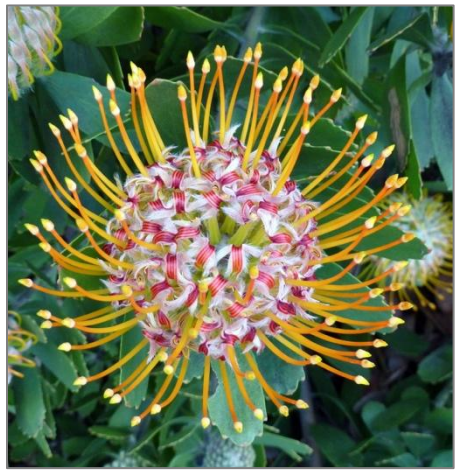
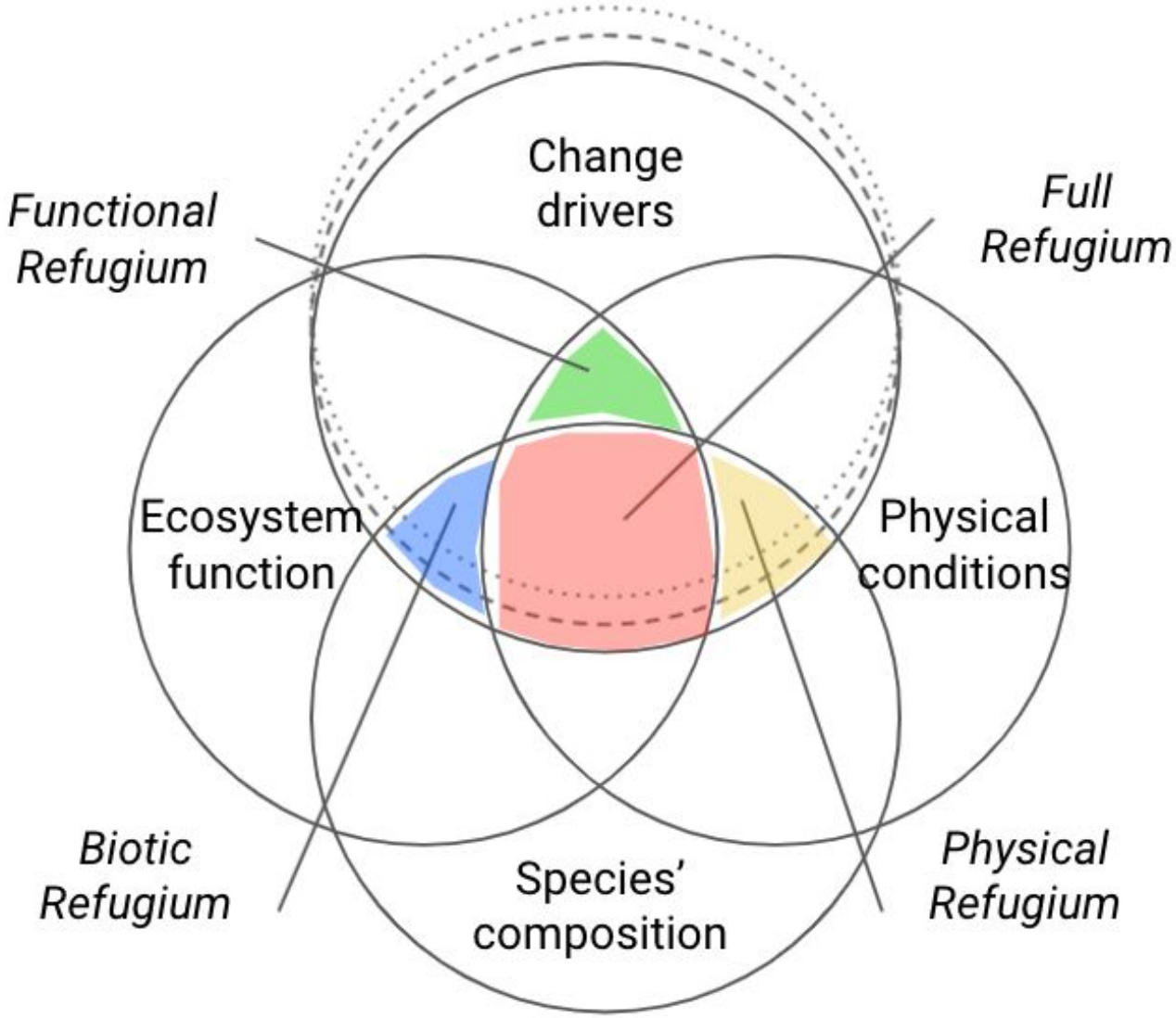
Refugia




Change drivers
Functional Refugium
Full Refugium
Ecosystem function
Physical conditions
Biotic Refugium
Species' composition
Physical Refugium

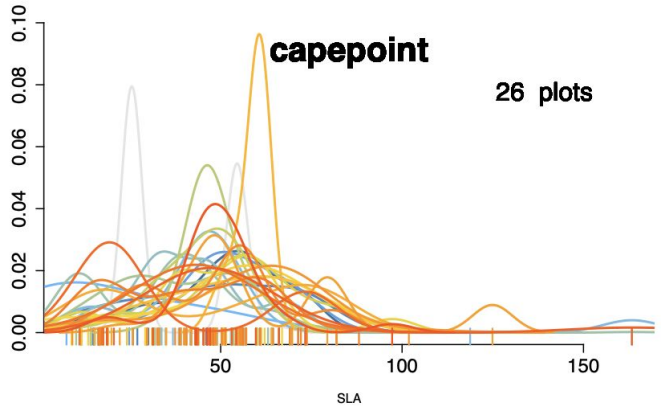
This boils down to prediction

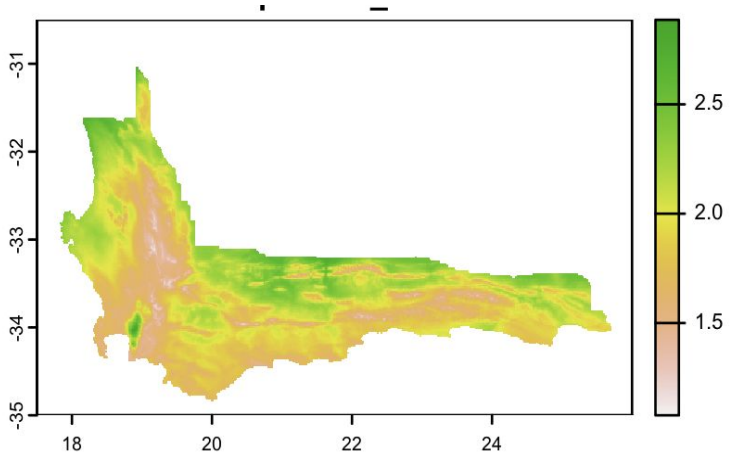
Species	Abun
Erica capensis	.22
Erica ericoides	.13
Cliffortia subsetacea	.05
…	…

Family	Abun
Restionaceae	.22
Proteaceae	.13
Ericaceae	.05
…	…

Functional group	Abun
Overstory shrub	.22
Understory Shurb	.13
Graminoid	.05
…	…

Trait distribution





Borrowing community ecology from genetics

Selection

Immigration

Drift

~~Mutation~~

Vellend 2015

The model

$abundance_{ij}$ ~

Species	Abun	Plot
Erica capensis	.22	1
Erica ericoides	.13	1
Cliffortia subsetacea	.05	1
…	…	1
Protea repens	.34	2
Aspalathus hispida	.13	2
Restio eleocharis	.05	2
…	…	

The model

Immigration

$abundance_{ij} \sim metacommunity\ abundance_i +$

Species	Abun	Plot
Erica capensis	.22	1
Erica ericoides	.13	1
Cliffortia subsetacea	.05	1
…	…	1
Protea repens	.34	2
Aspalathus hispida	.13	2
Restio eleocharis	.05	2
…	…	

The model

Immigration

Selection

$$abundance_{ij} \sim metacommunity\ abundance_i + f(traits_i, env_j) +$$

Species	Abun	Plot
Erica capensis	.22	1
Erica ericoides	.13	1
Cliffortia subsetacea	.05	1
…	…	1
Protea repens	.34	2
Aspalathus hispida	.13	2
Restio eleocharis	.05	2
…	…	

The model

Immigration Selection Drift

$$abundance_{ij} \sim metacommunity\ abundance_i + f(traits_i, env_j) + \varepsilon_{ij}$$

Species	Abun	Plot
Erica capensis	.22	1
Erica ericoides	.13	1
Cliffortia subsetacea	.05	1
…	…	1
Protea repens	.34	2
Aspalathus hispida	.13	2
Restio eleocharis	.05	2
…	…	

Dynamics

state next year = Rules of change * state this year

Dynamics

state next year = Rules of change * state this year

trait distribution (t+1) = Rules of change * trait distribution (t)

Dynamics

state next year = Rules of change * state this year

trait distribution (t+1) = Rules of change * trait distribution (t)

trait distribution (t+1) = Selection / Immigration / Drift distribution (t)

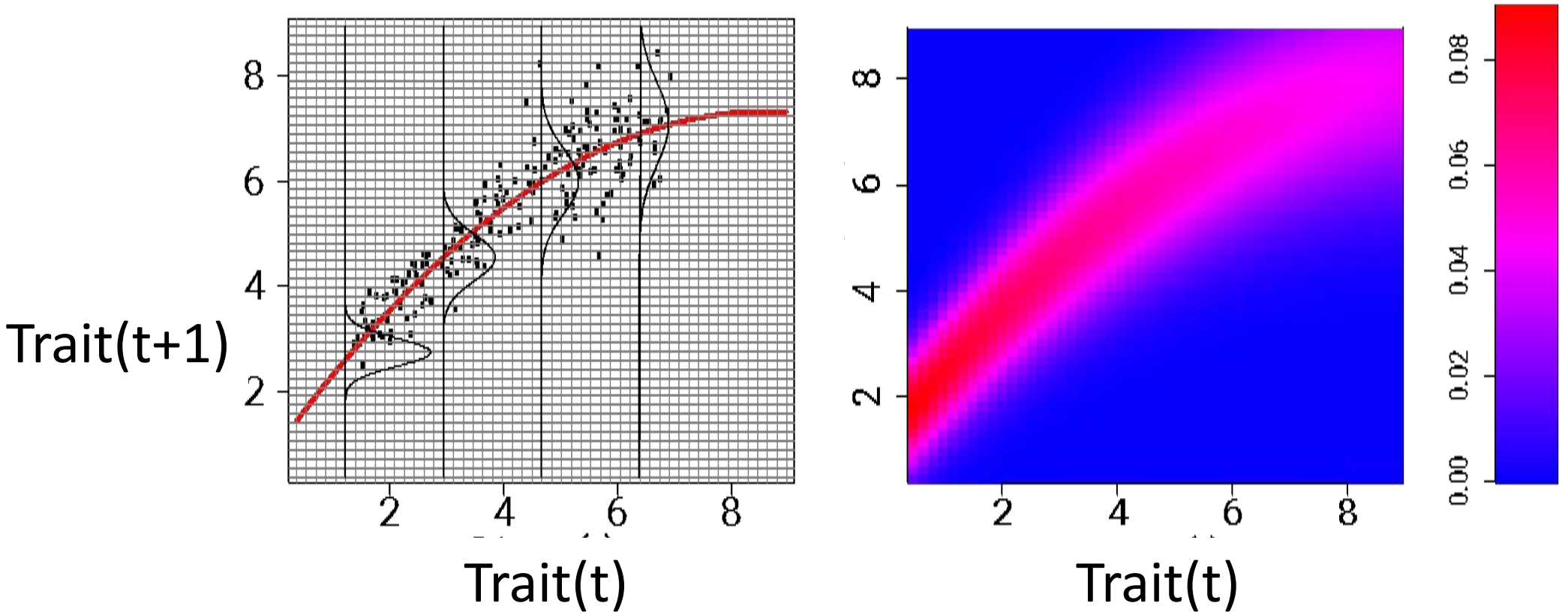
Dynamics

state next year = Rules of change * state this year

trait distribution (t+1) = Rules of change * trait distribution (t)

trait distribution (t+1) = Selection / Immigration / Drift * trait distribution (t)

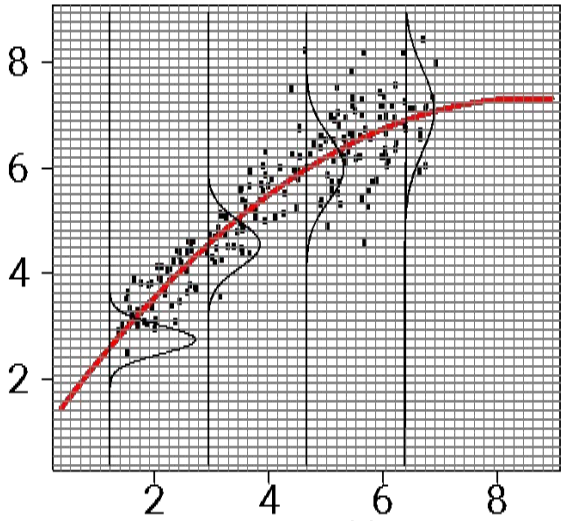
$$N_{t+1}(trait_1, trait_2) = \int_{trait} f(trait, env) N_t(trait_1, trait_2)\, dt1 dt2$$



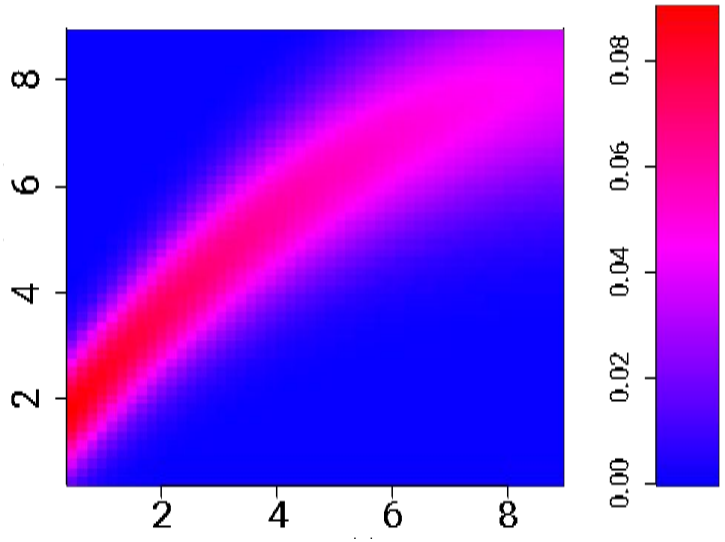
$$N_{t+1}(trait_1, trait_2) = \int_{trait} f(trait, env) N_t(trait_1, trait_2)\, d t1 dt2$$

Ecosystem Predictions

Trait(t+1)



Trait(t)



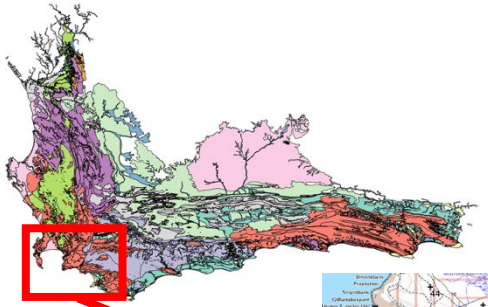
Trait(t)

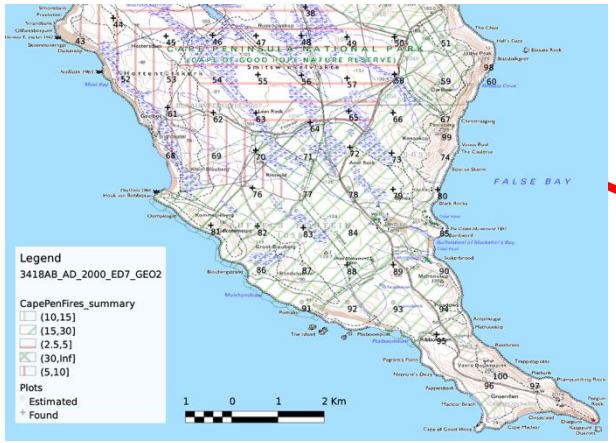
Ecosystem Quantity	Metric
Net Primary Productivity	Dominant right eigenvalue
Trait distributions	Dominant right eigenvector
Resilience	Damping Ratio
Duration of successional stages	Life Expectancy
Sensitivity/Elasticity	Eigenvectors

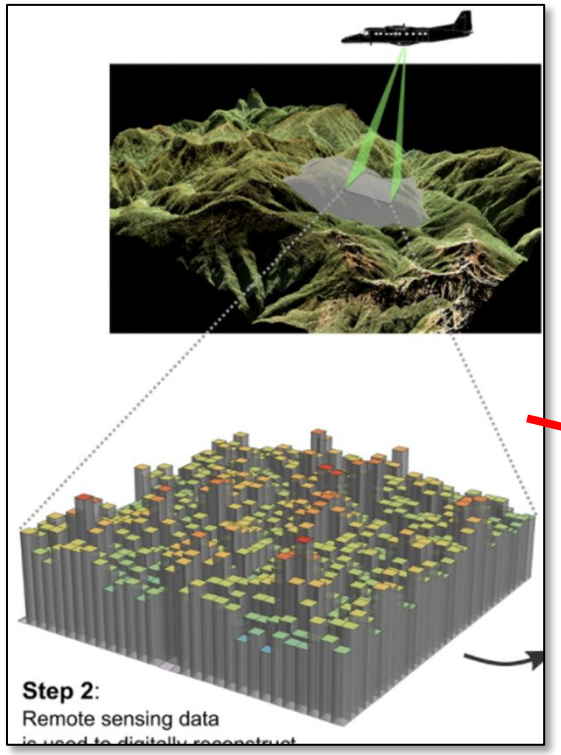
Spatial scaling

Immigration **Selection** **Drift**

$$abundance_{ij} \sim metacommunity\ abundance_i + f(traits_i, env_j) + \varepsilon_{ij}$$







Selection function

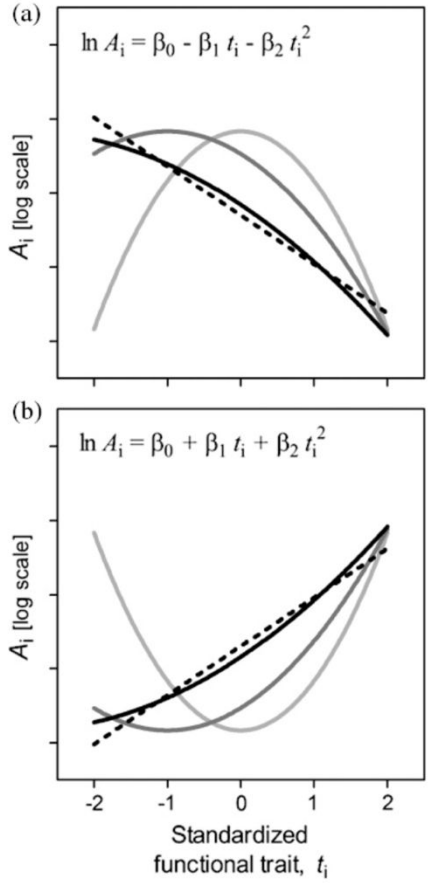
Immigration + Selection + Drift

$abundance_{ij} \sim metacommunity\ abundance_i + f(traits_i, env_j) + \varepsilon_{ij}$

$f(traits_i, env_j) =+ env$

$+ trait + trait^2$

$+ trait^3 + trait^4$



Stabilizing Selection

Destabilizing Selection

Rolhauser & Pucheta 2017

Selection function

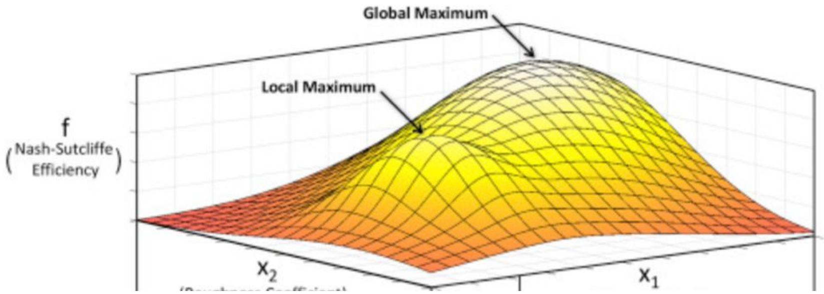
Immigration | Selection | Drift

$abundance_{ij}$ ~ metacommunity $abundance_i$ + f($traits_i$, env_j) + ε_{ij}

f($traits_i$, env_j) =+ env

+ trait + trait^2

+ trait ^3 + trait ^4

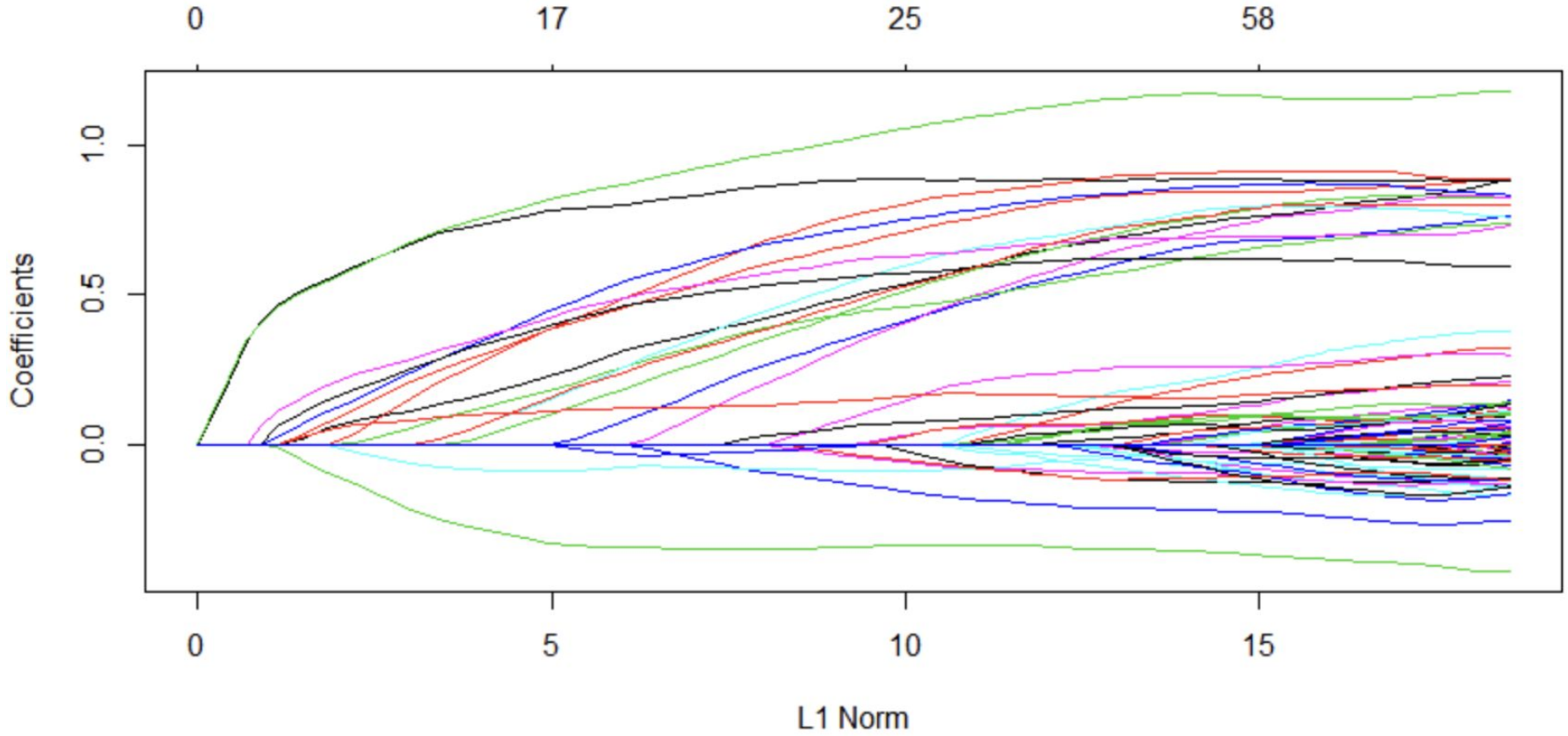


+ env* trait + env* trait^2 + env* trait ^3 +env * trait ^4

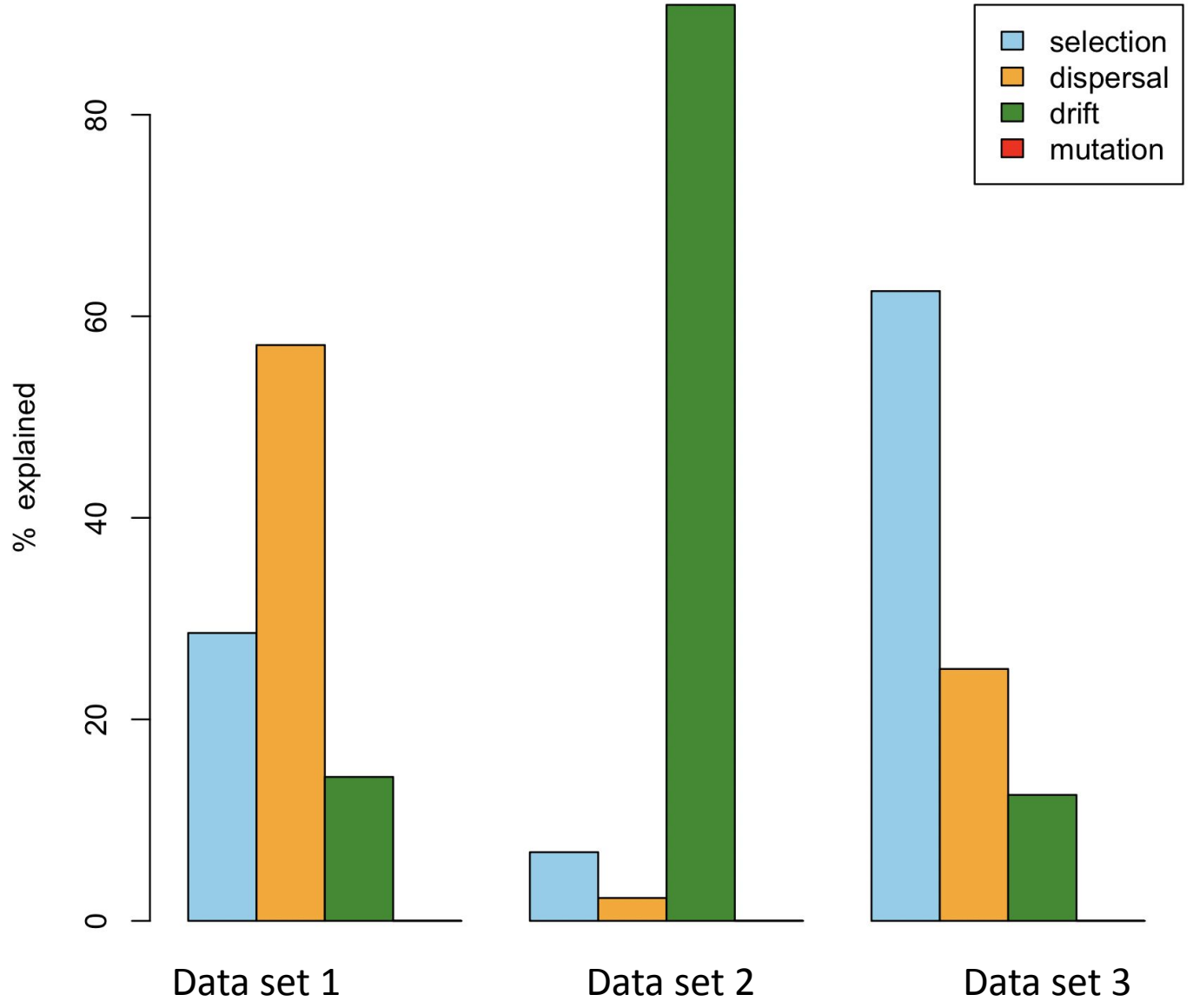
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4
+trait + env + trait * env + trait^2 + trait ^3 + trait ^4 + env* trait^2 + env* trait ^3 +env * trait ^4

The model:
Poisson Point Process fit with **LASSO regression**

Fewer parameters

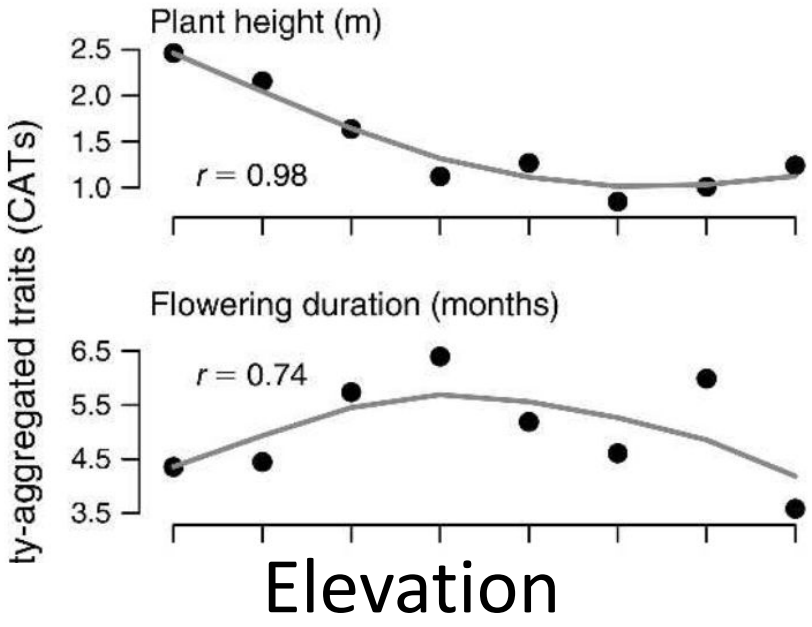


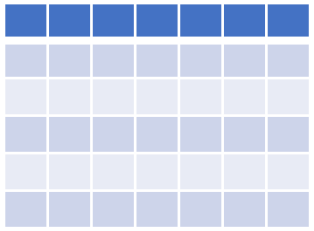
Partitioning contributions



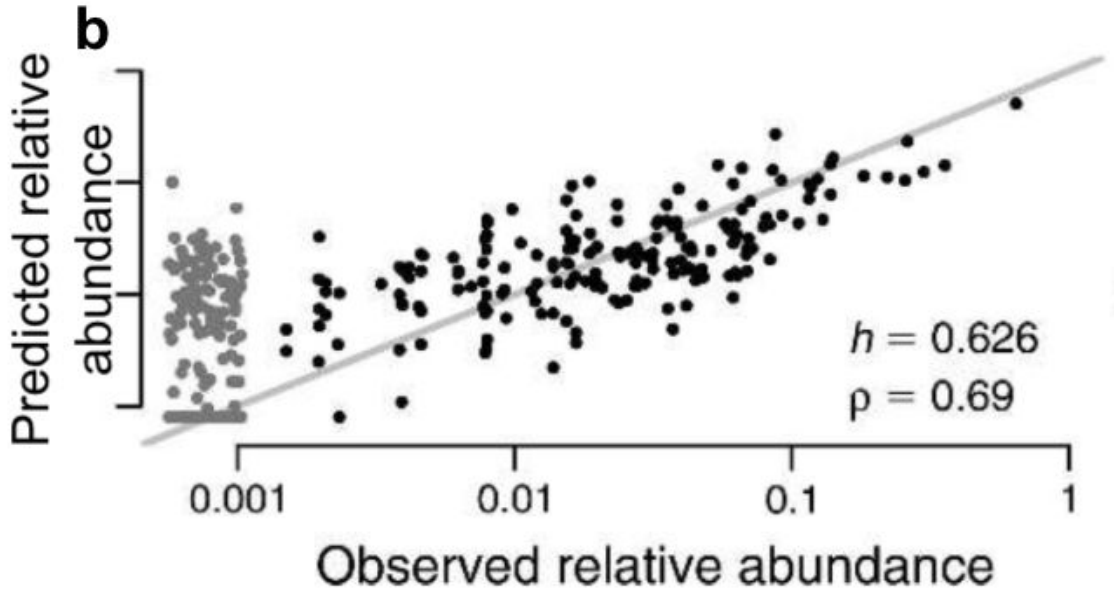
Recovering species composition from trait distributions

Community Trait

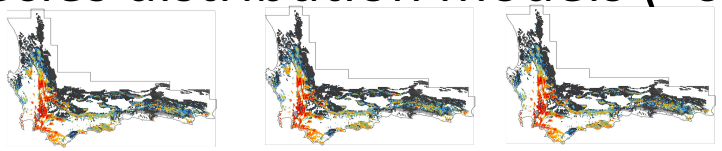




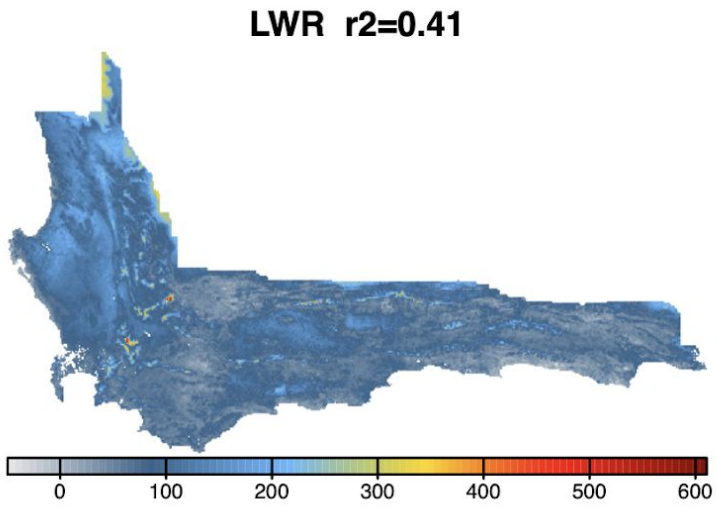
Trait Matrix

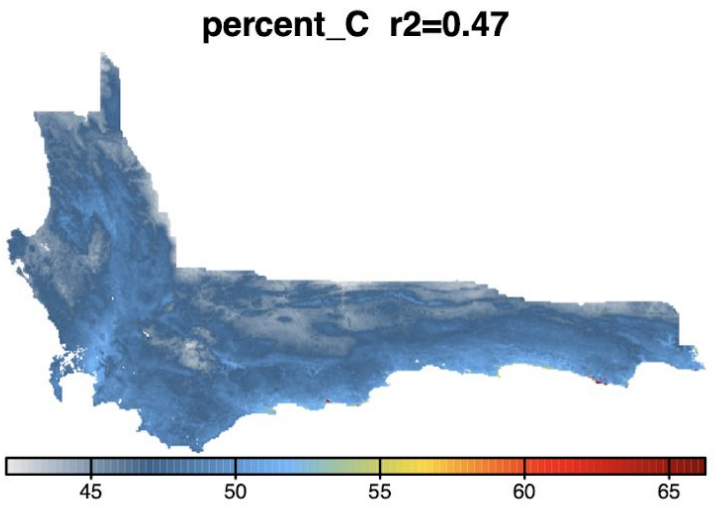


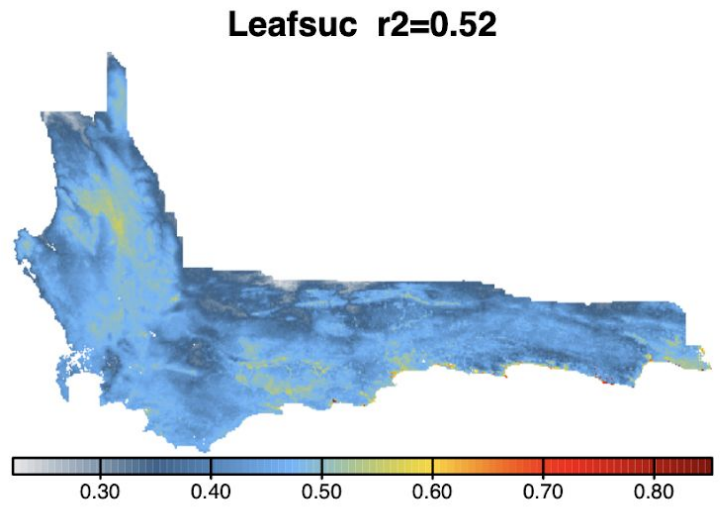
Species distribution models (~6k plants)

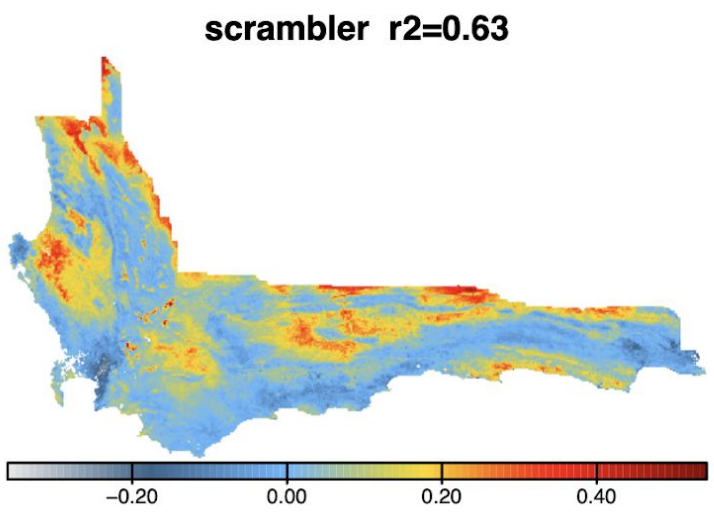


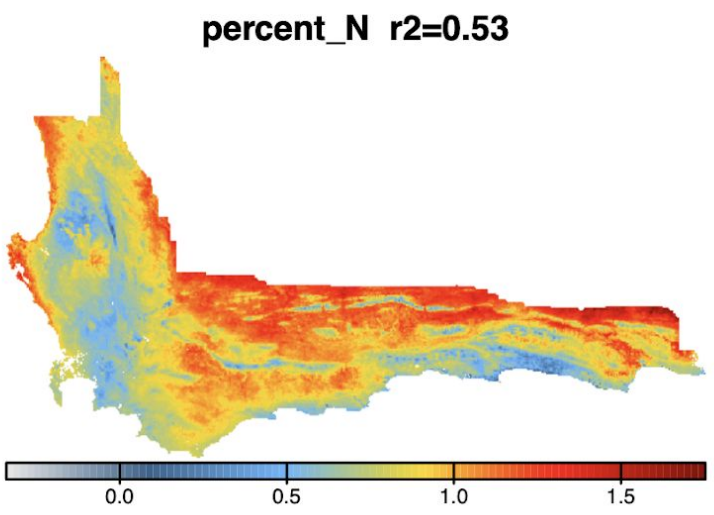
Some community mean traits are predictable

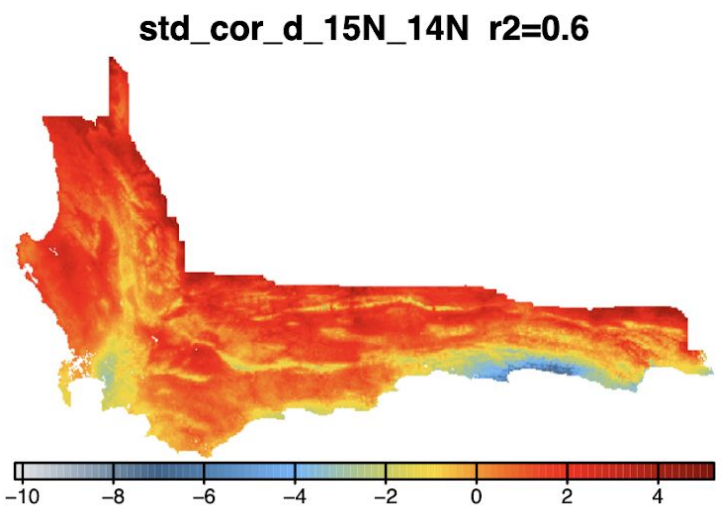




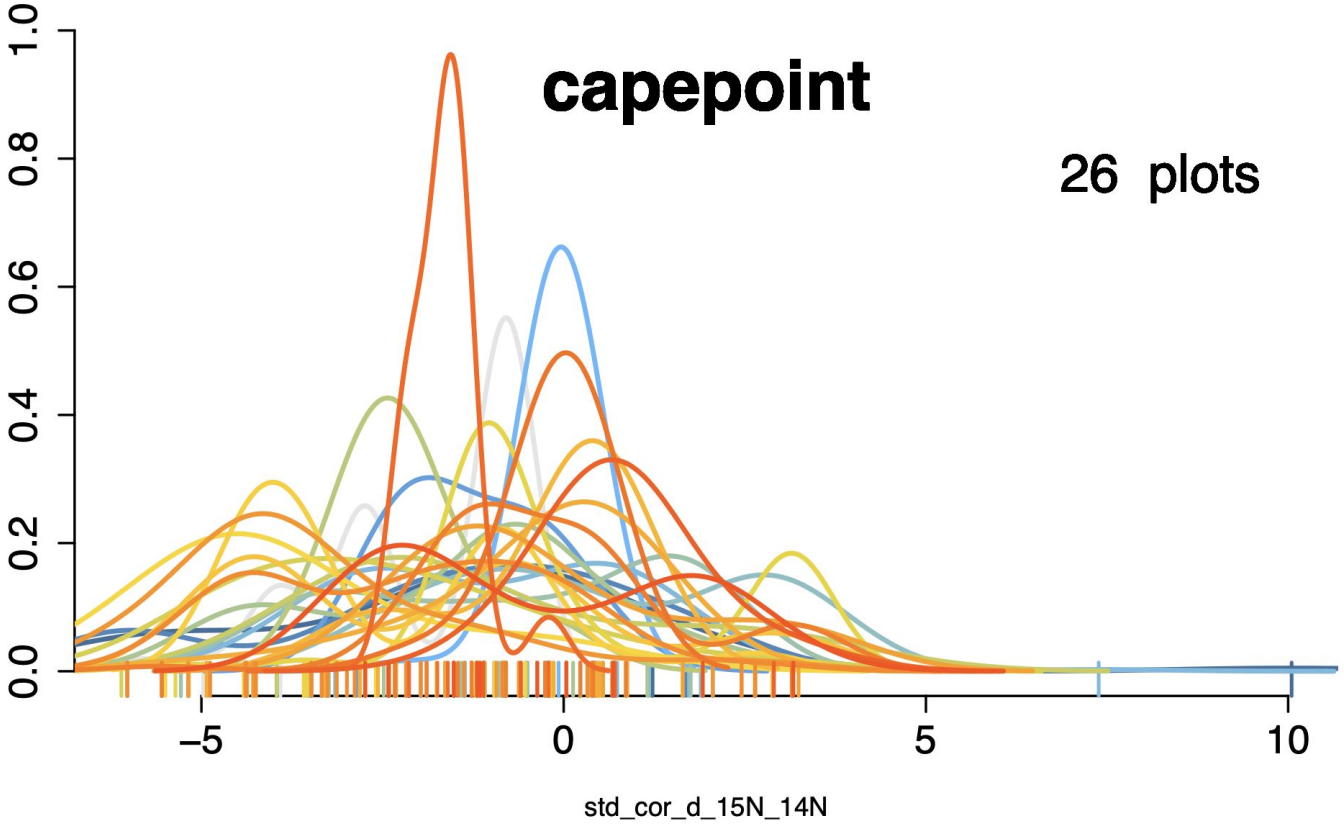


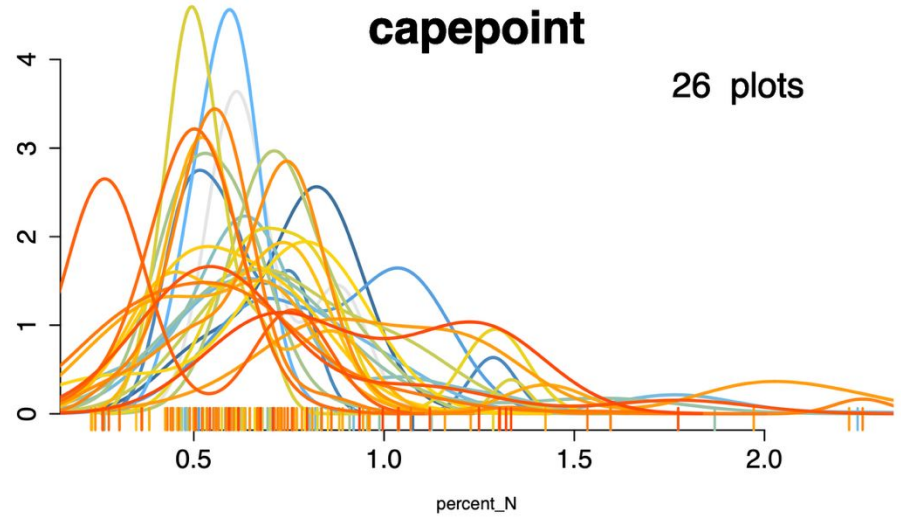


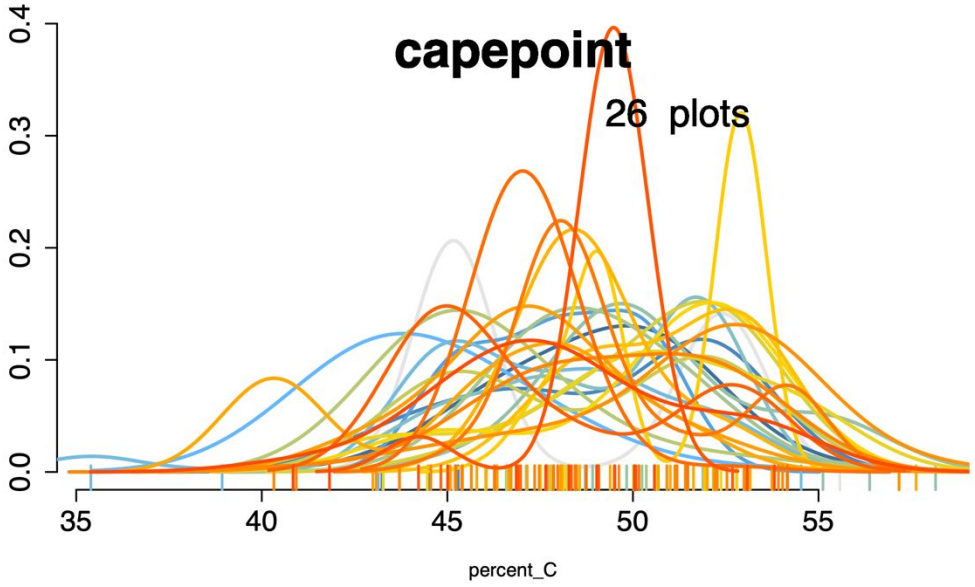




Modal trait distributions







Thanks!

Pep Serra-Diaz

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Nicola van Wilgen

Brian Enquist

Manos Anagnostou

Adam Wilson

Questions?