

Example of Analyses with **funrar**

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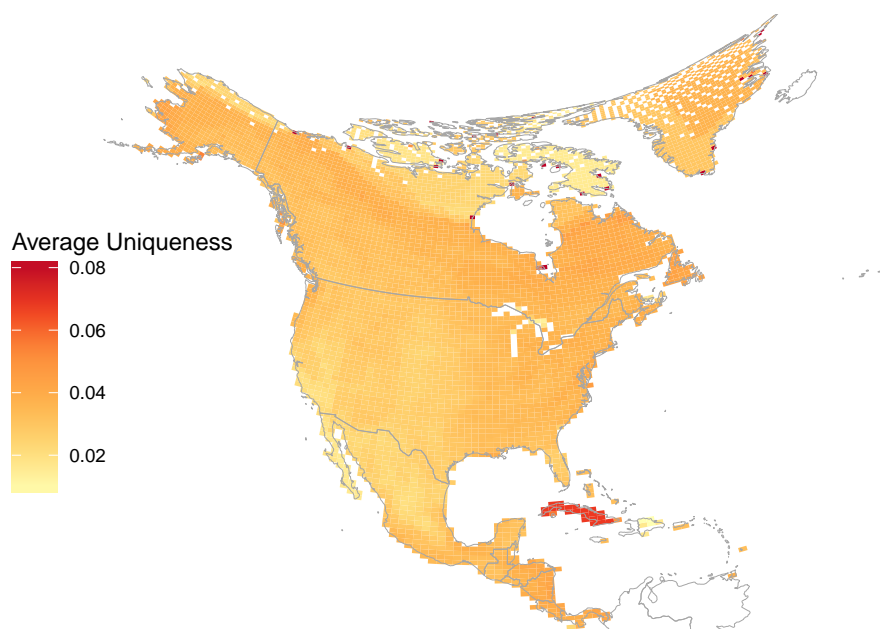
11 janvier, 2017

With **funrar** you can compute **F**unctional **R**arity indices. We are using a North American Mammals datasets to show the kind of questions you can come up with.

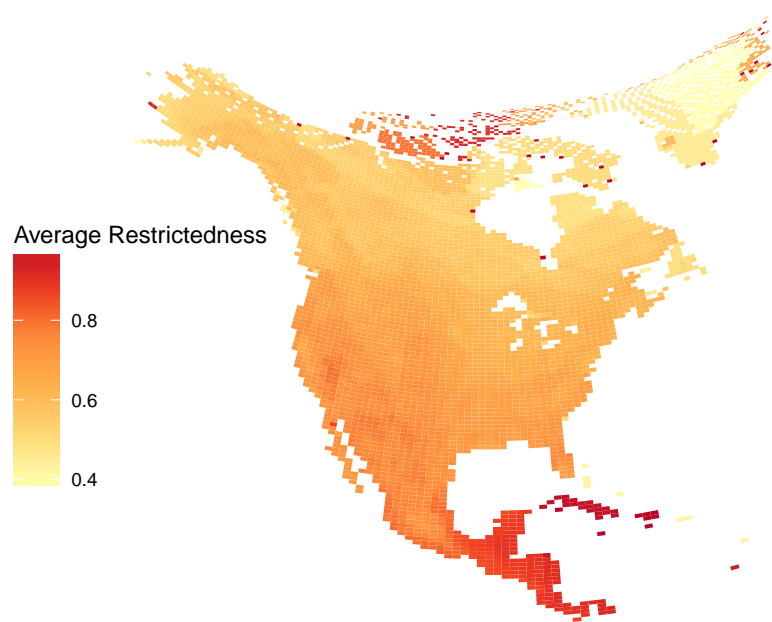
For example, you can try to map the hotspots of Regional Functional Uniqueness, i.e. the communities with highest number of functionally unique species (relatively to the whole species pool).

Hotspots

Functional Uniqueness

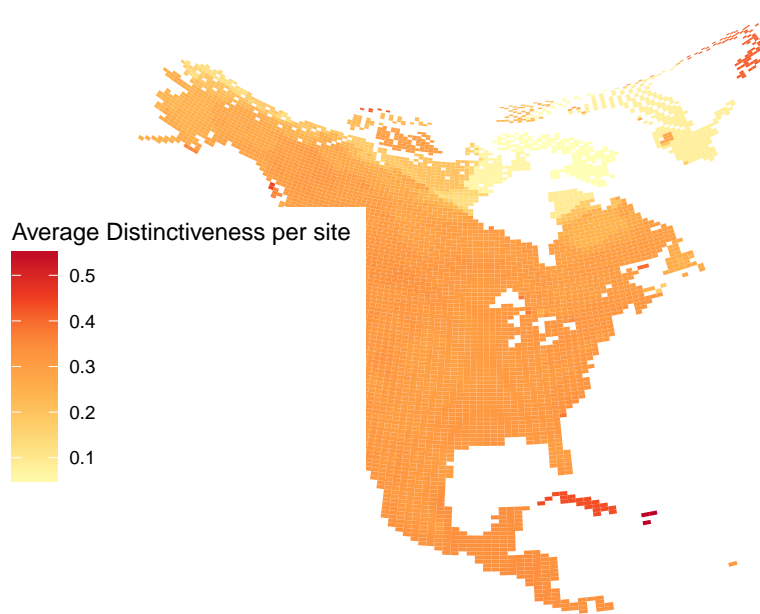


Geographical Restrictedness



Functional Distinctiveness

Warning: Removed 552 rows containing non-finite values (stat_summary2d).



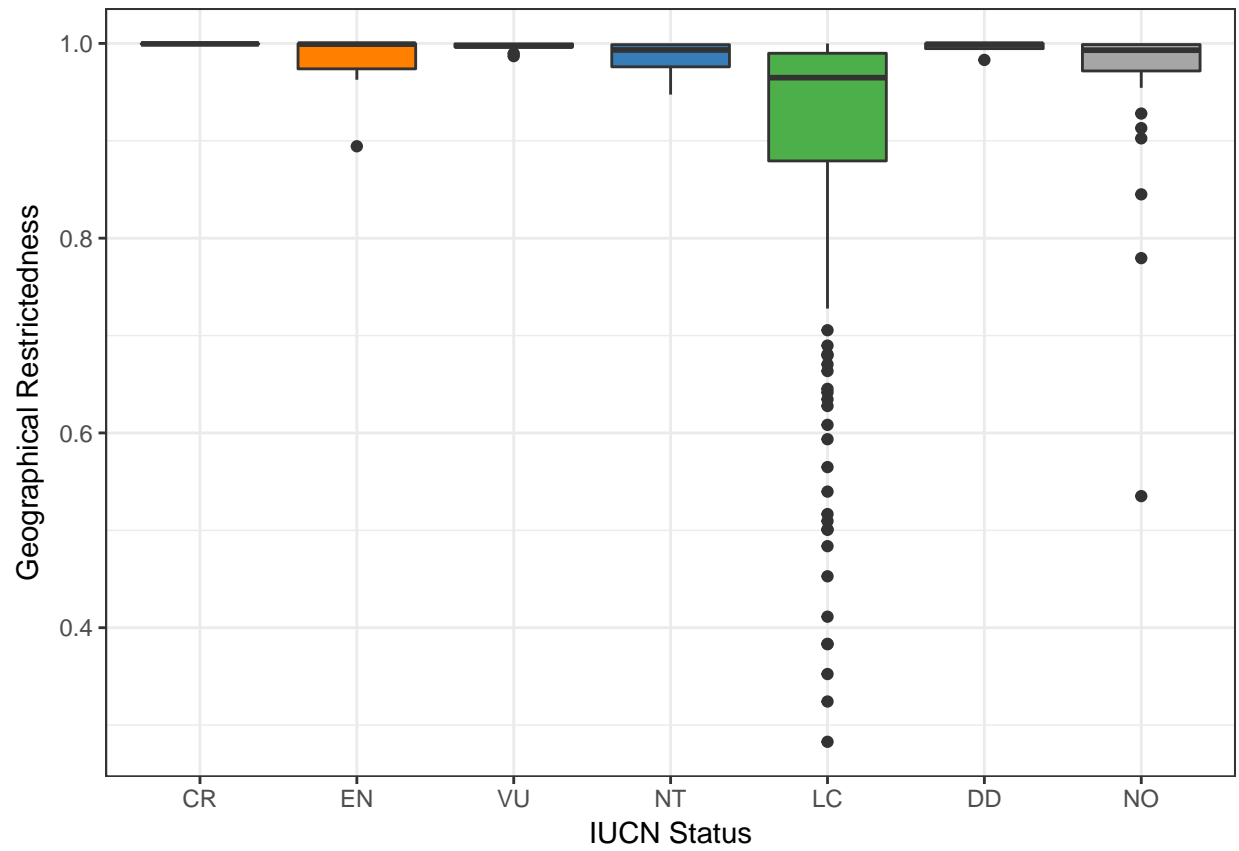
Relation between IUCN status and Functional Rarity Indices

with Geographical Restrictedness

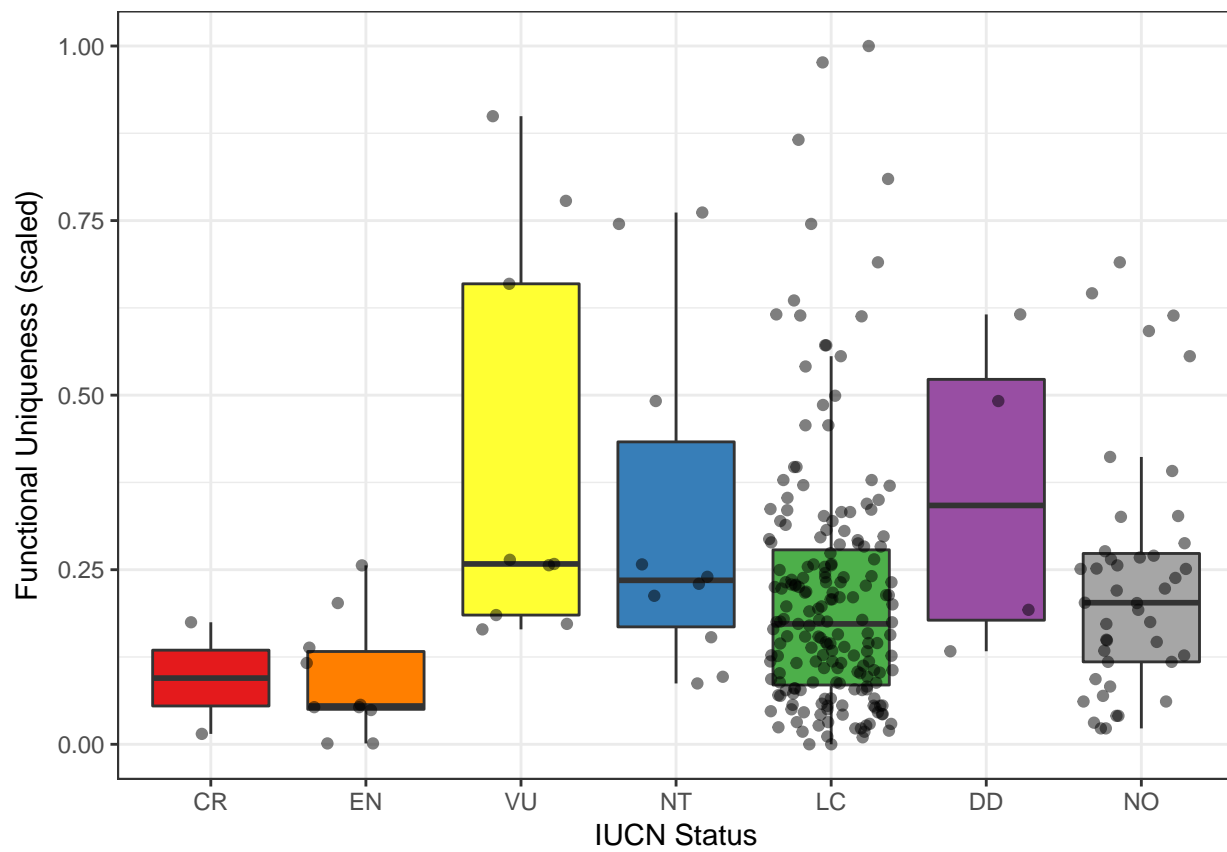
```
## Warning in inner_join_impl(x, y, by$x, by$y, suffix$x, suffix$y): joining
## factor and character vector, coercing into character vector
```

```
## Warning in inner_join_impl(x, y, by$x, by$y, suffix$x, suffix$y): joining
## character vector and factor, coercing into character vector
```

```
##   species           Ui      IUCN_status      Ri
## Length:265      Min.   :0.0006121 CR: 2      Min.   :0.2828
## Class :character 1st Qu.:0.0115721 EN: 10      1st Qu.:0.9242
## Mode :character  Median :0.0223622 VU: 9      Median :0.9787
##                Mean   :0.0281722 NT: 10      Mean   :0.9174
##                3rd Qu.:0.0344888 LC:187     3rd Qu.:0.9966
##                Max.   :0.1243665 DD: 4      Max.   :0.9999
##                NO: 43
##
##      std_Ui
## Min.   :0.00000
## 1st Qu.:0.08856
## Median :0.17575
## Mean   :0.22270
## 3rd Qu.:0.27374
## Max.   :1.00000
##
```

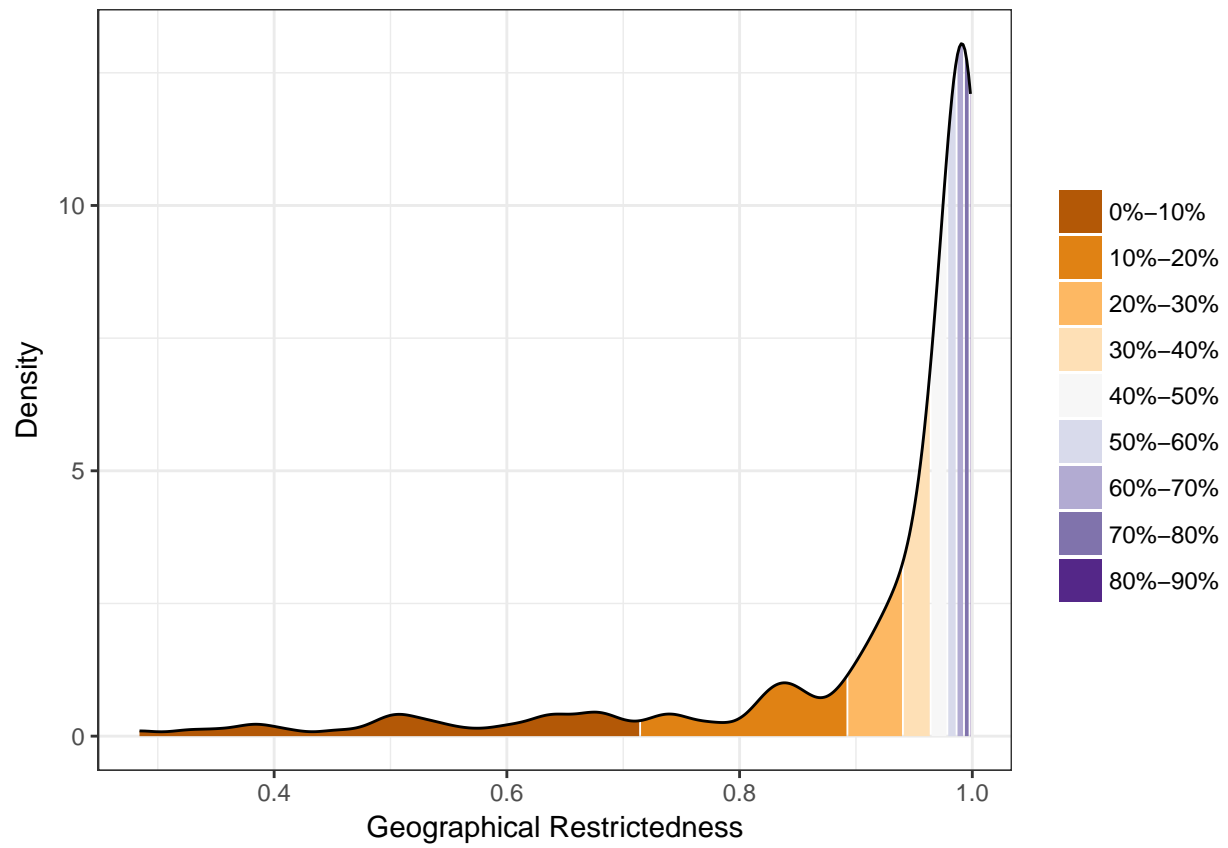


with Functional Uniqueness

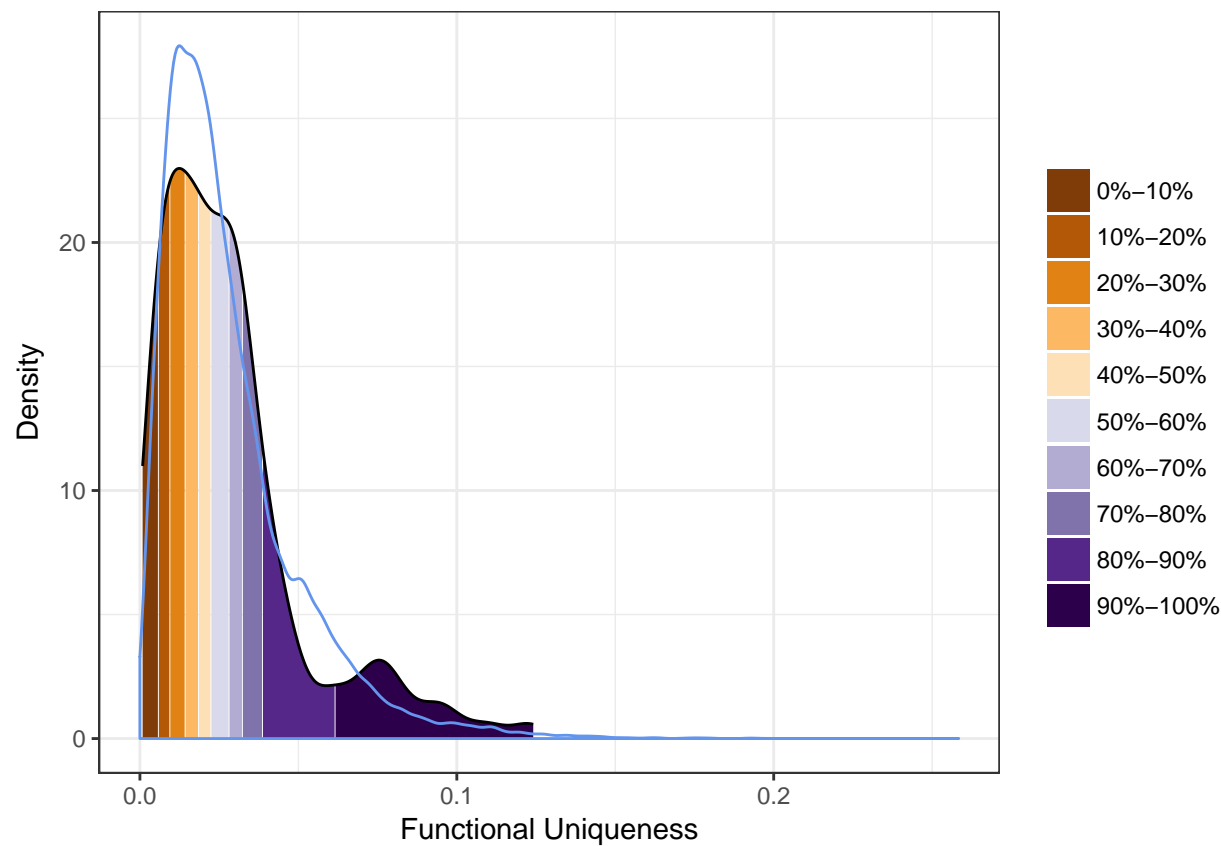


Total distribution of indices

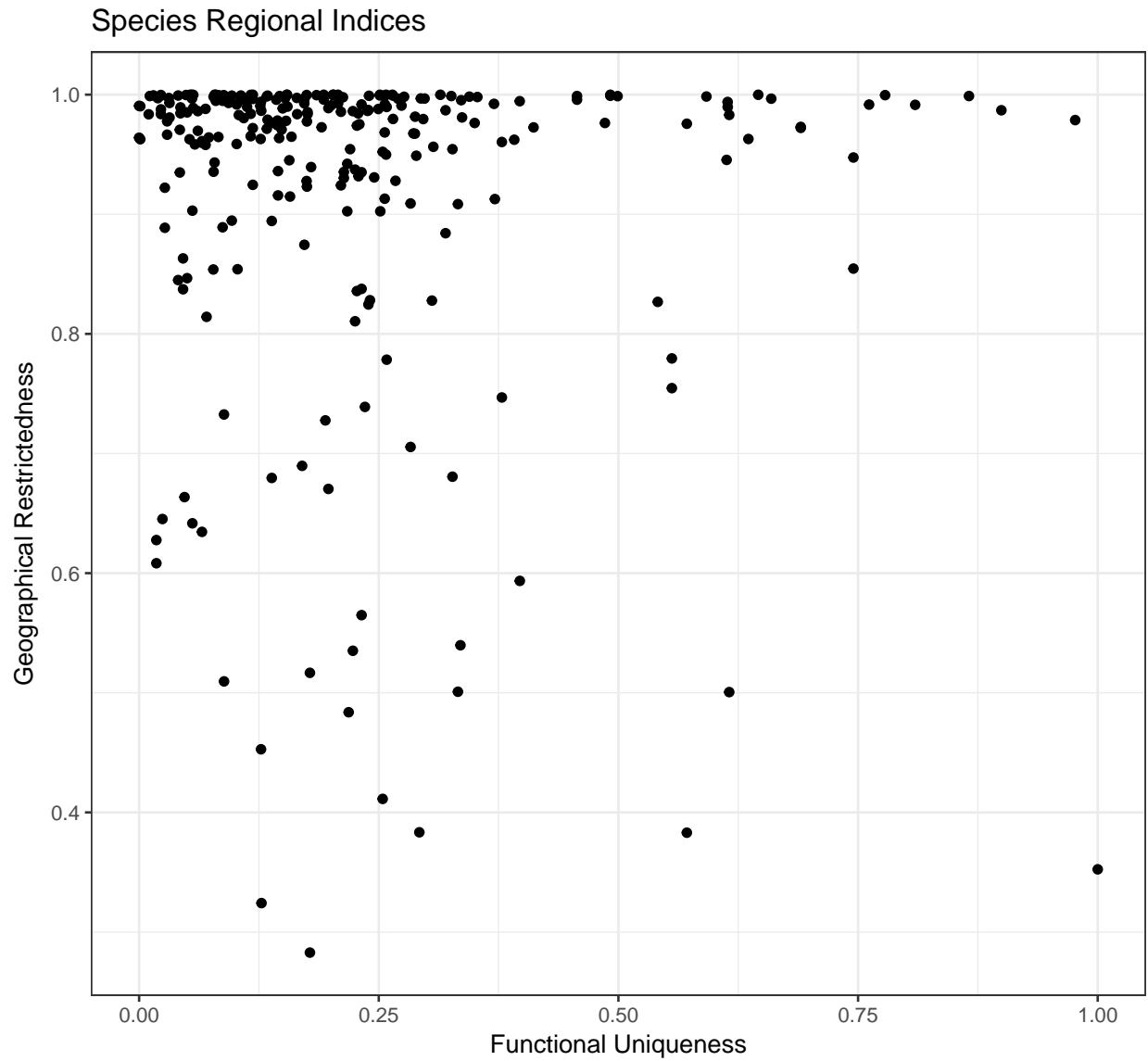
Geographical Restrictedness



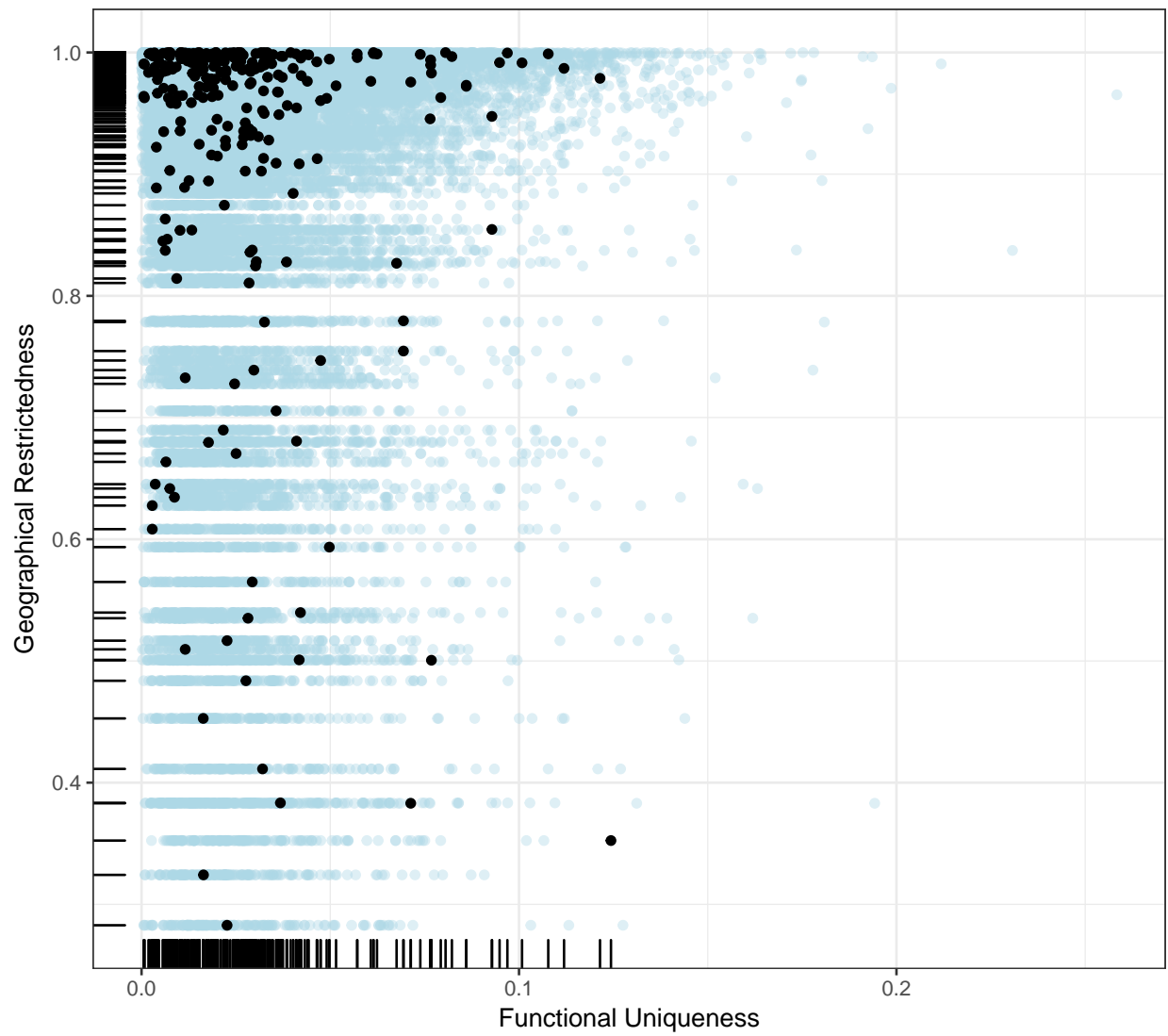
Functional Uniqueness



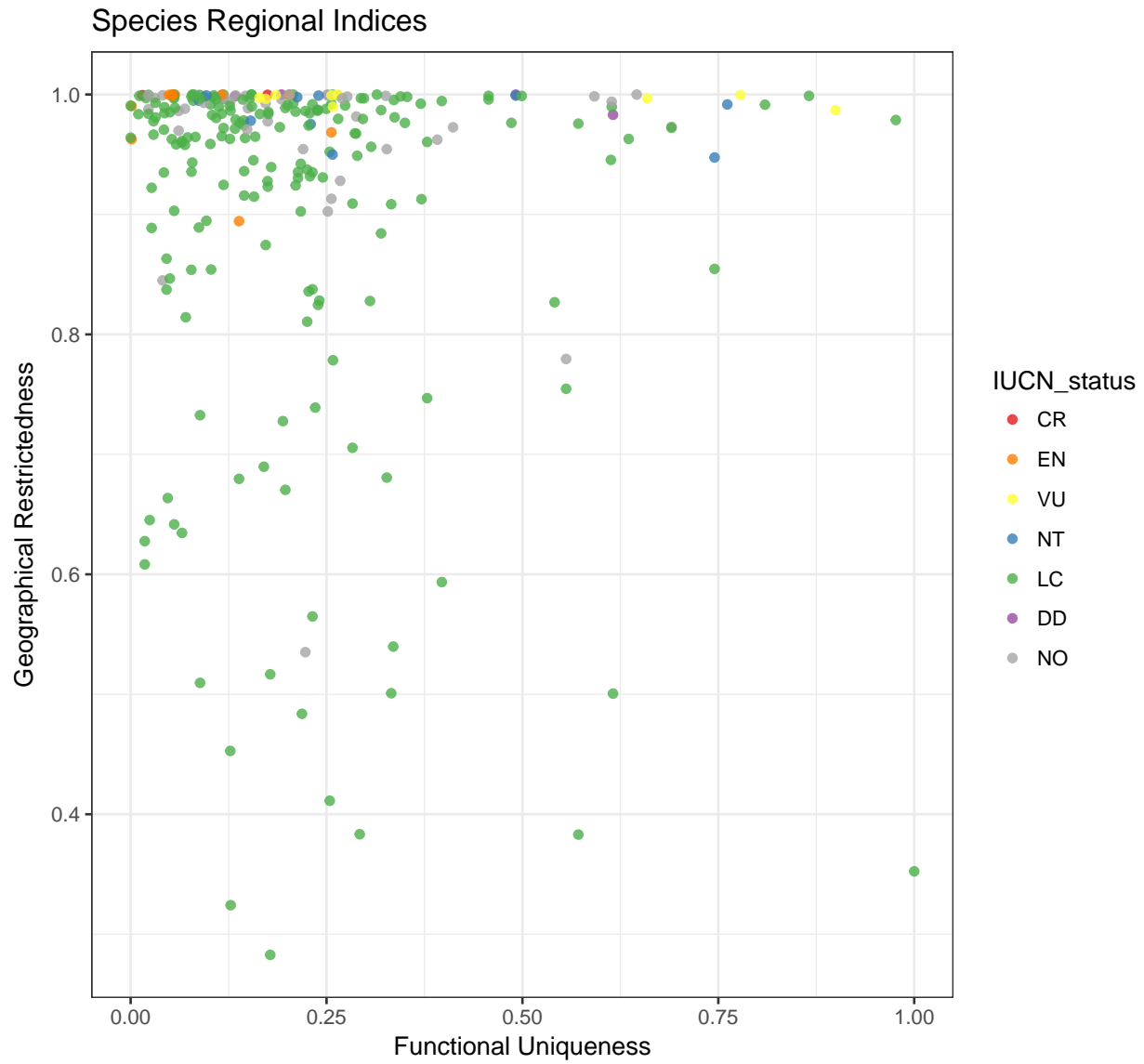
Biplot



Species Regional Indices with null model (shuffled traits)

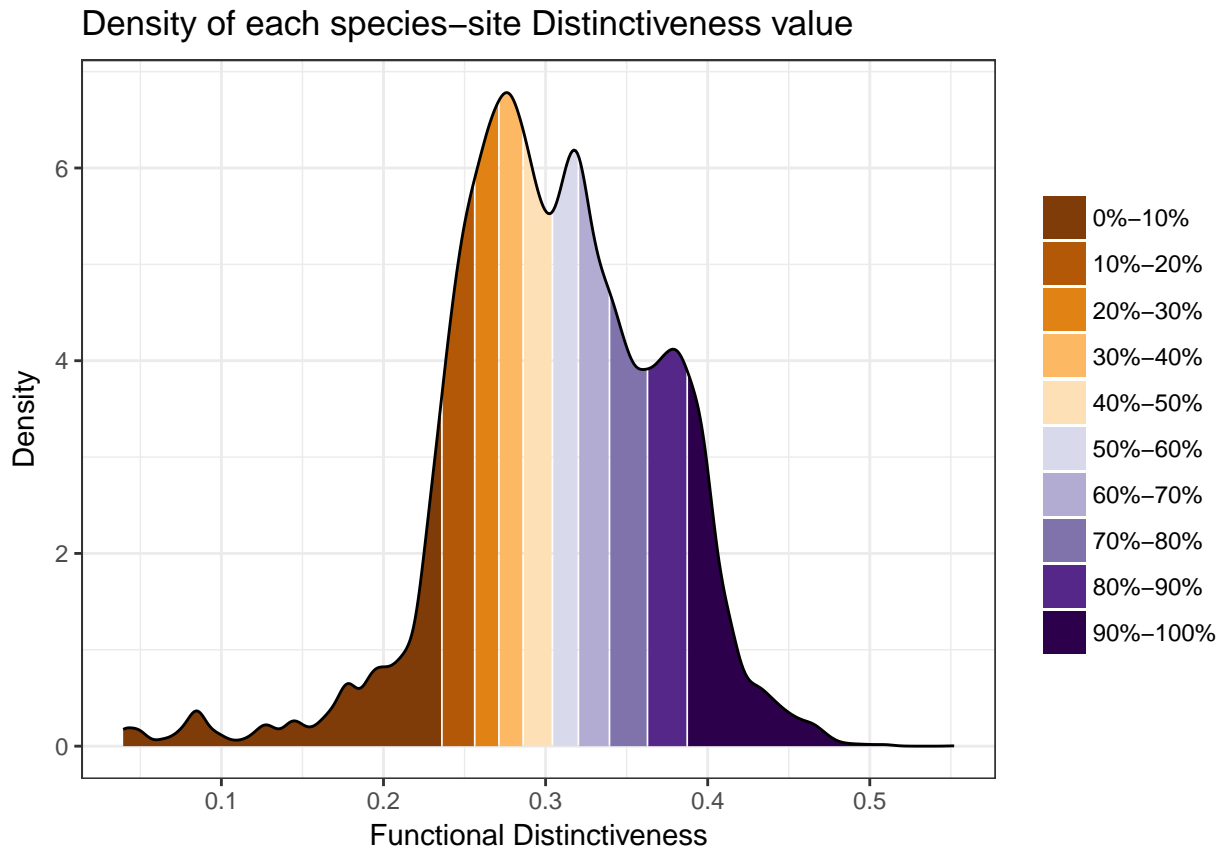


With IUCN status

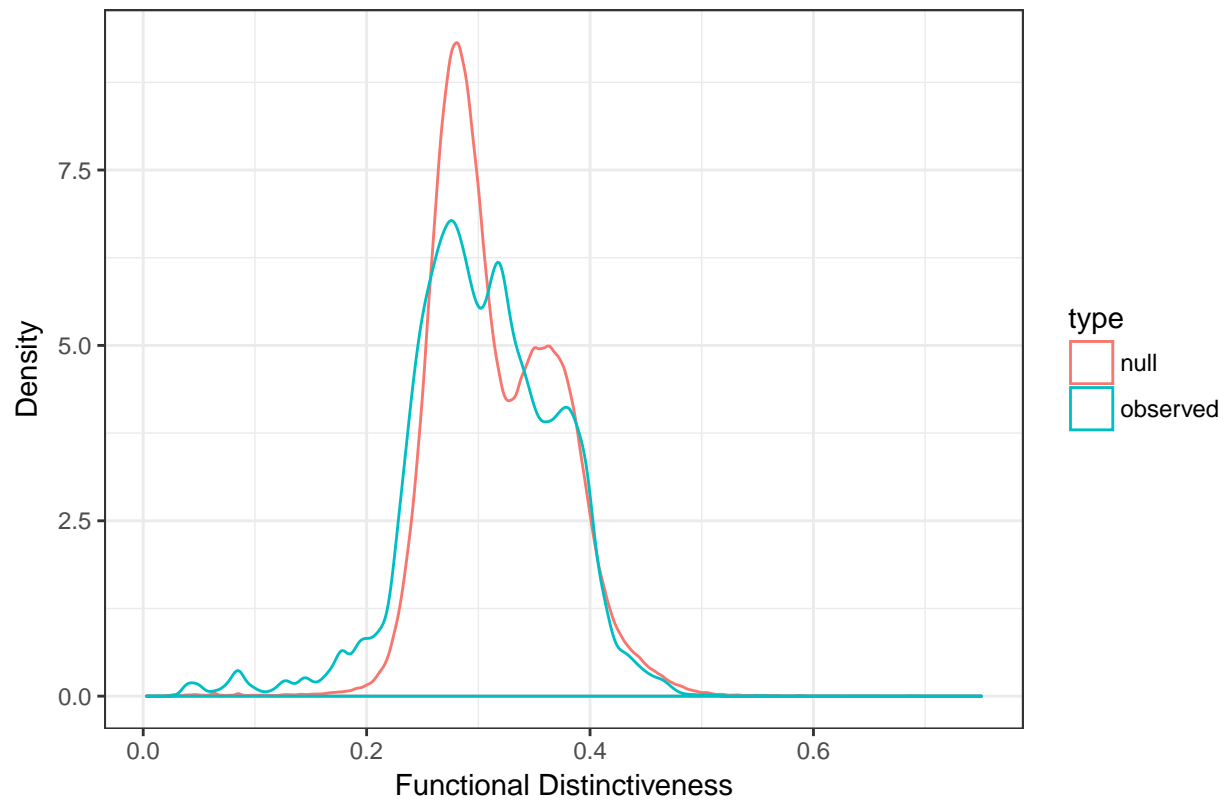


Functional Distinctiveness

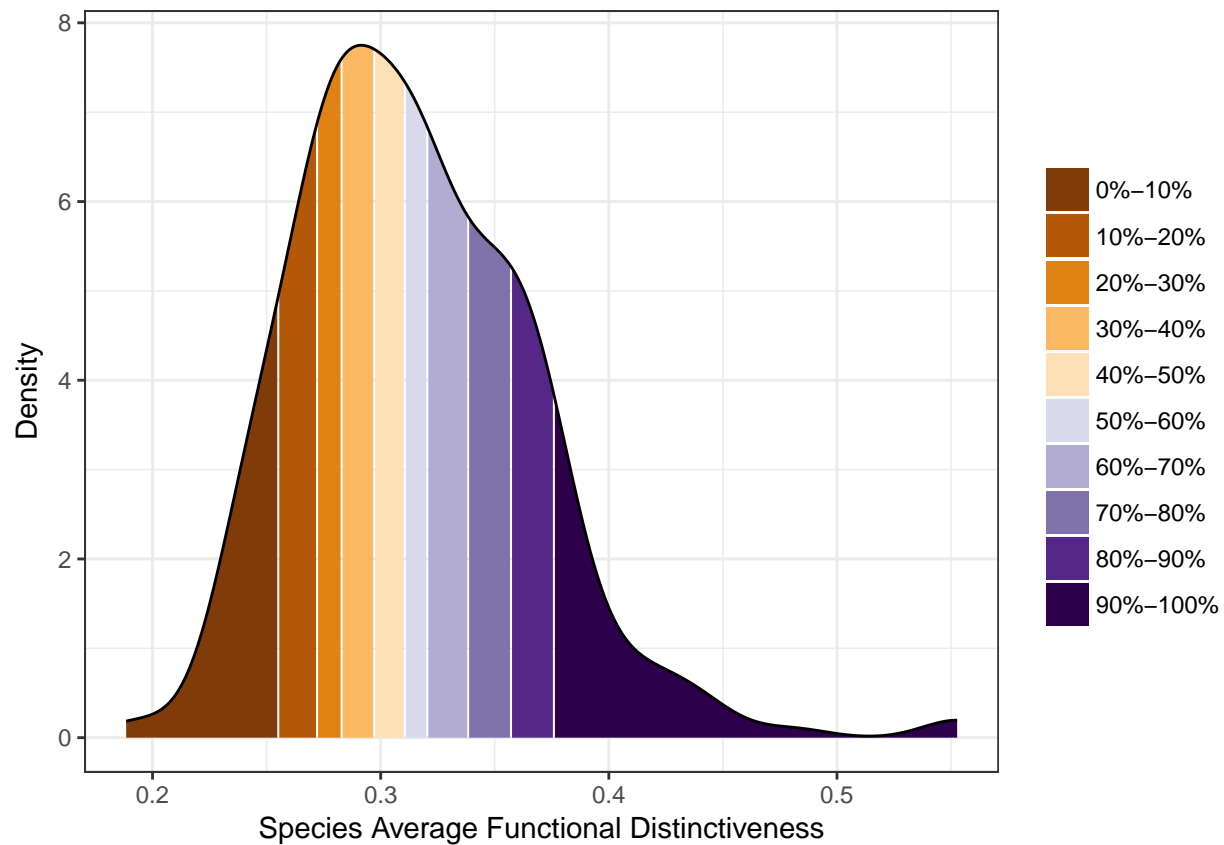
For each site-species combination



Site–Species Di Density with null model

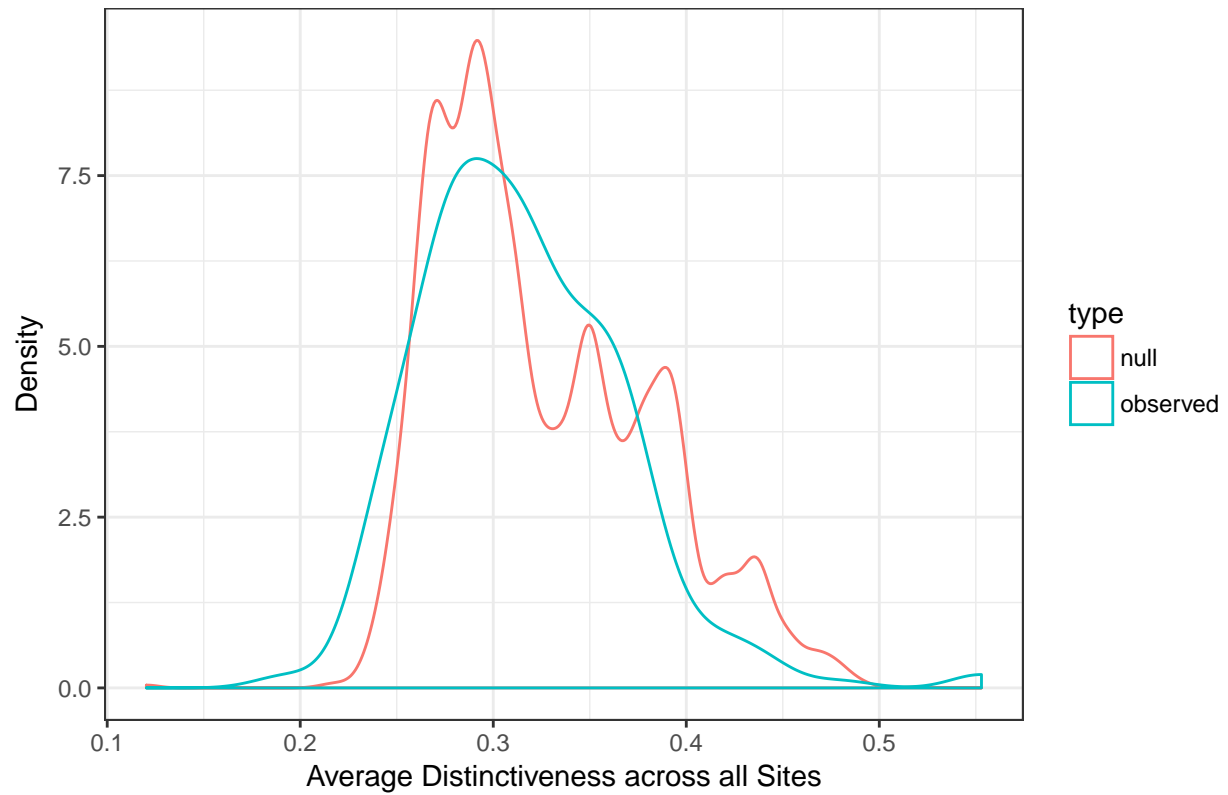


Average Distinctiveness of a species across all sites



```
## Warning in bind_rows(x, .id): binding factor and character vector,
## coercing into character vector
## Warning: Removed 1 rows containing non-finite values (stat_density).
```

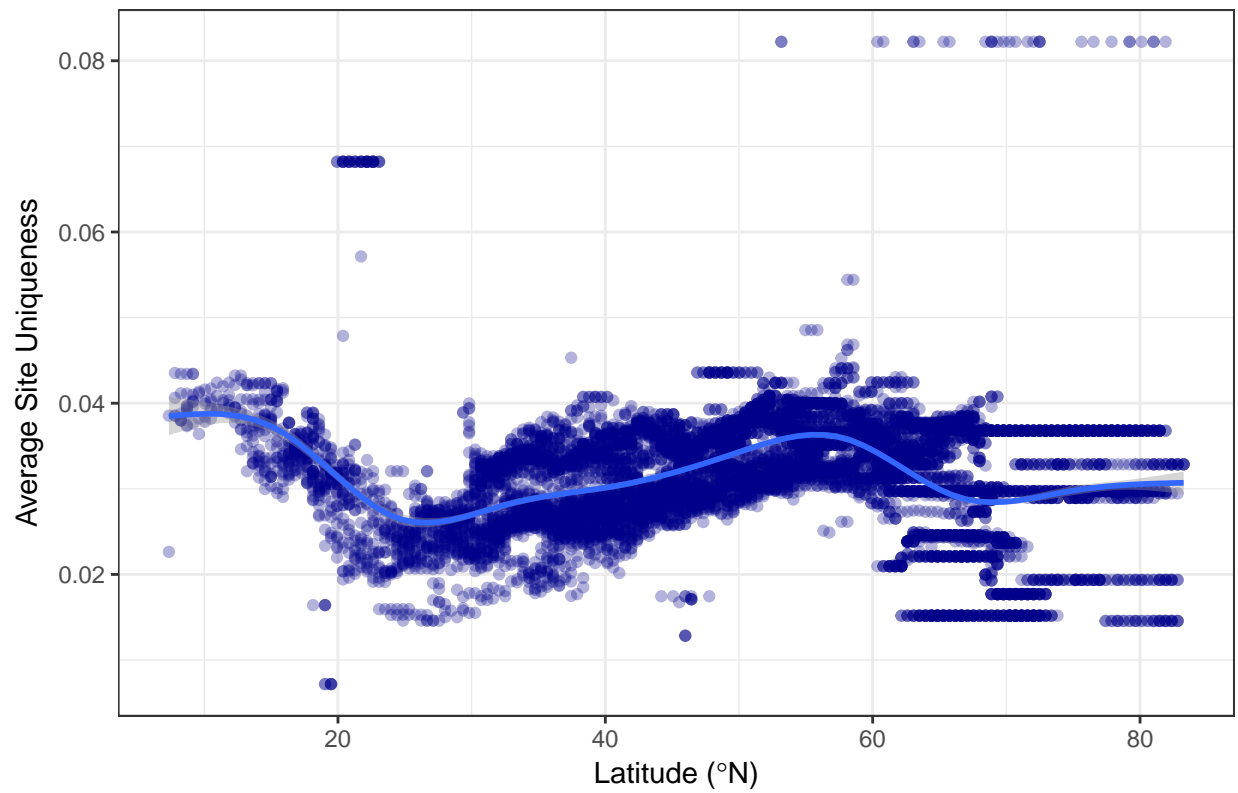
Average Species Di Density with null model



Functional Uniqueness

```
## `geom_smooth()` using method = 'gam'
```

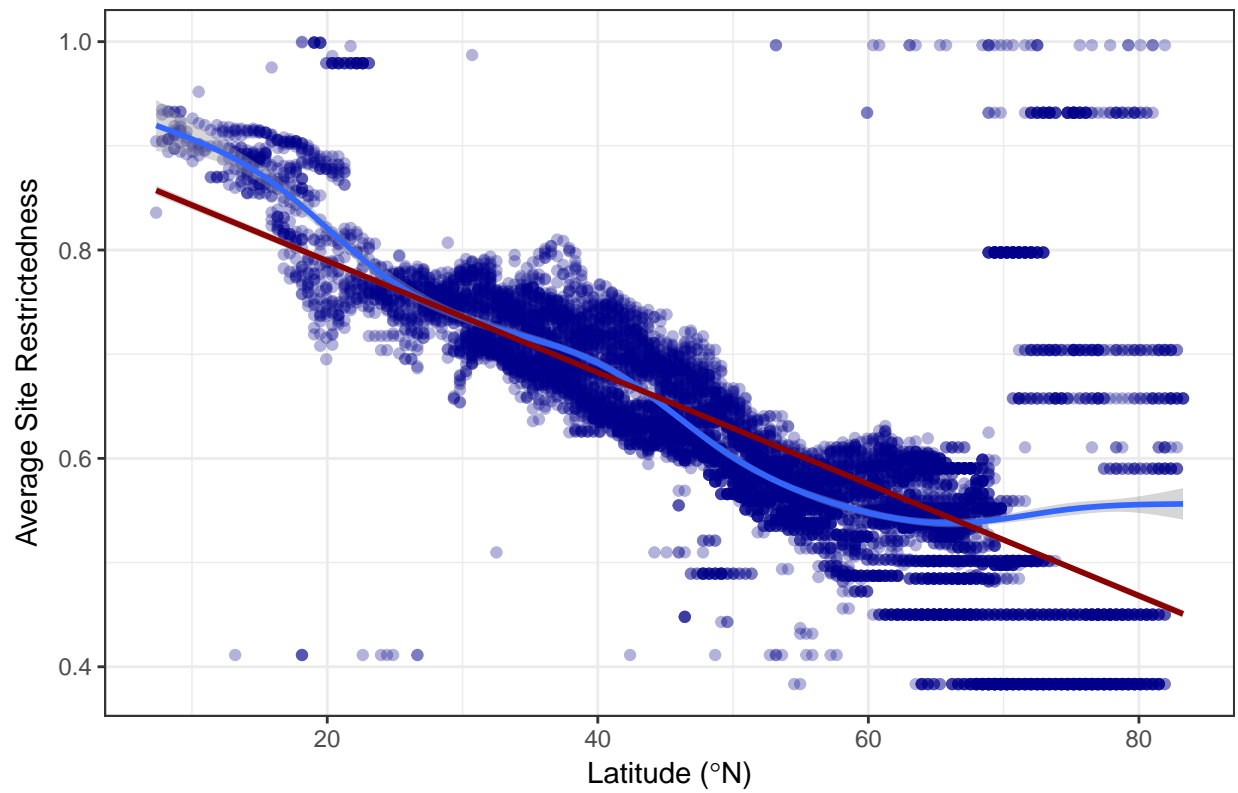
Latitudinal Gradient of Uniqueness (n=9497)



Geographical Restrictedness

```
## `geom_smooth()` using method = 'gam'
```

Latitudinal Gradient of Restrictedness (n=9497)



Functional Distinctiveness

```
## `geom_smooth()` using method = 'gam'  
## Warning: Removed 552 rows containing non-finite values (stat_smooth).  
## Warning: Removed 552 rows containing missing values (geom_point).
```


Latitudinal Gradient of Distinctiveness (n=9055)

