# Example of Analyses with `funrar`

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15 février, 2017

With `funrar` you can compute **Fun**ctional **Rar**ity indices. We are using a North American Mammals datasets to show the kind of questions you can come up with.
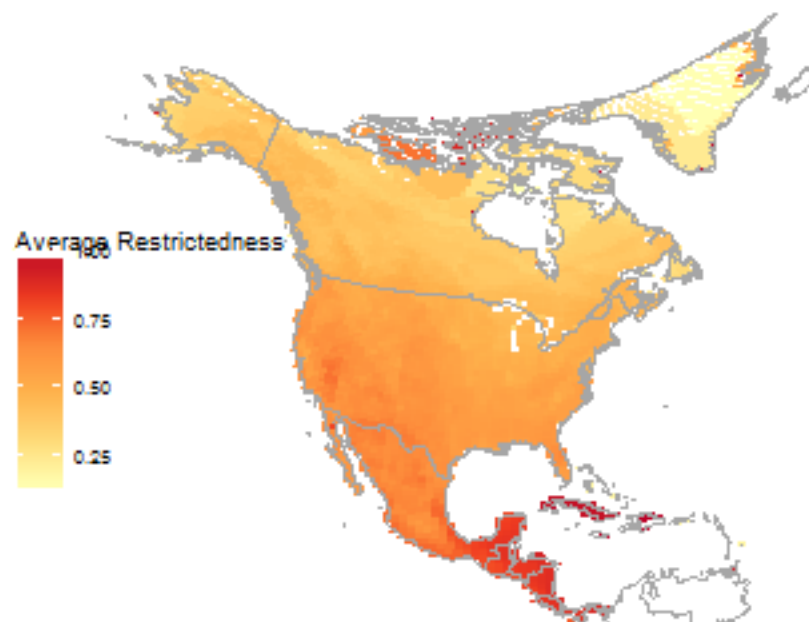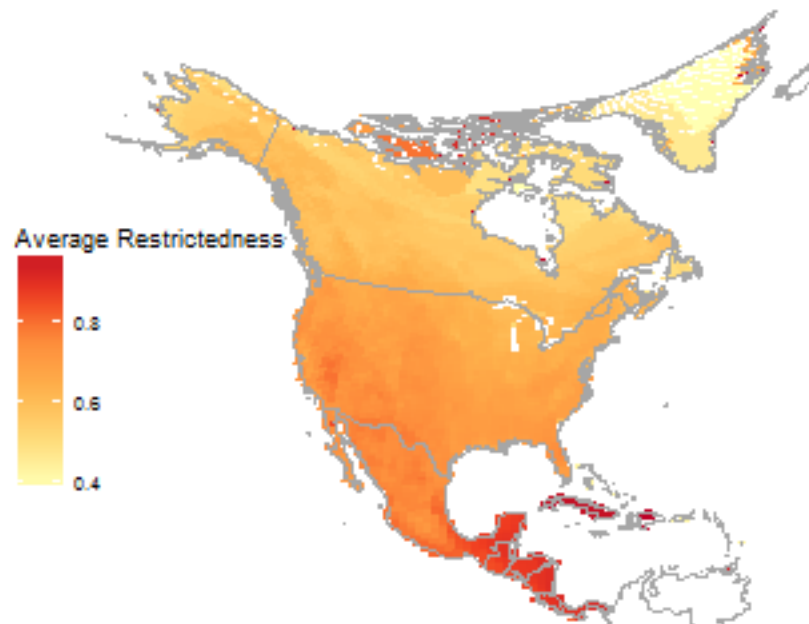
For example, you can try to map the hotspots of Regional Functional Uniqueness, i.e. the communities with highest number of functionally unique species (relatively to the whole species pool).
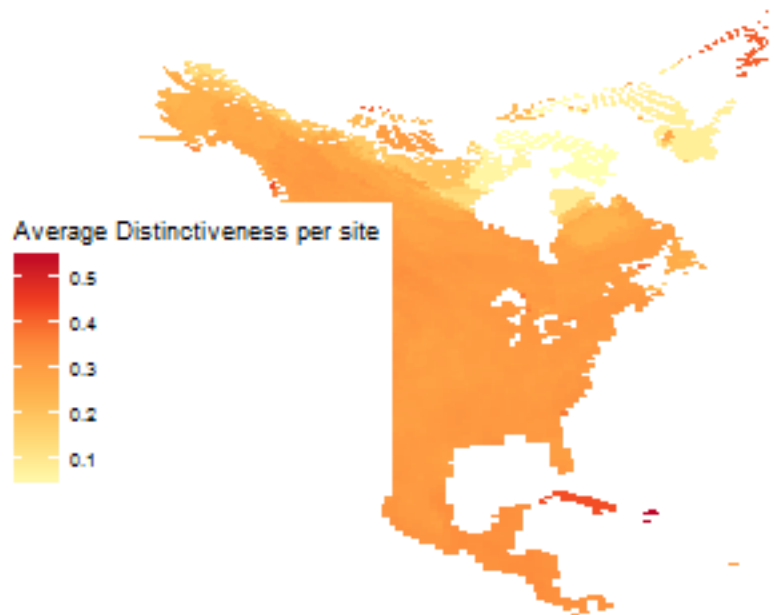
Hotspots

Functional Uniqueness
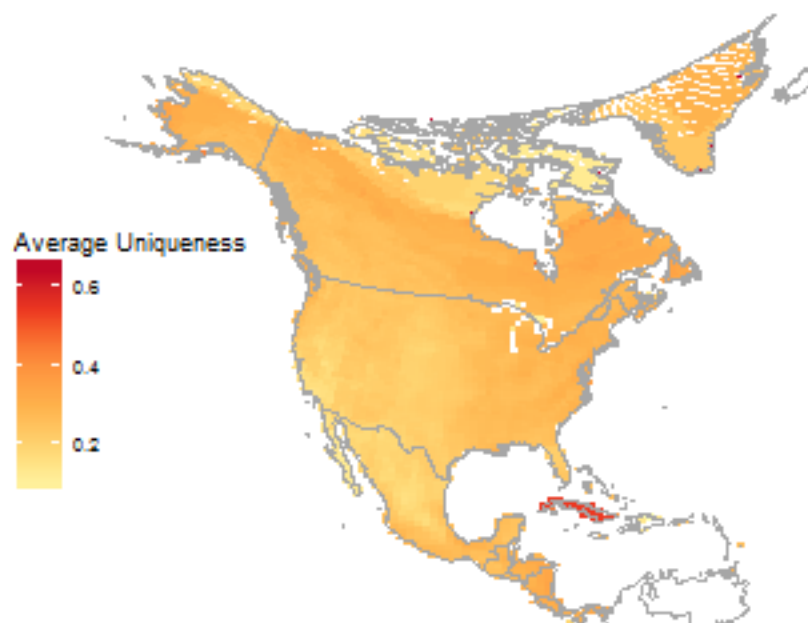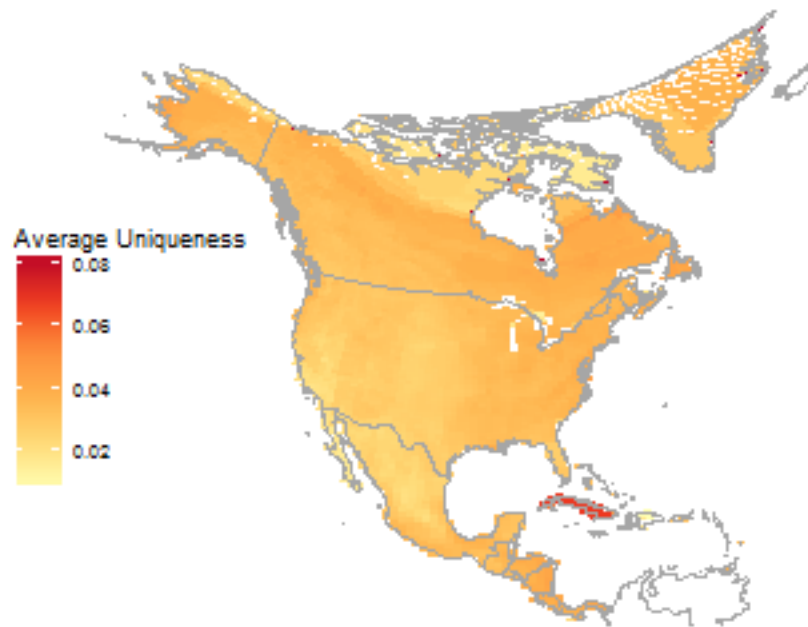
Geographical Restrictedness

Functional Distinctiveness

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

## Total distribution of indices

```
##                        species         Ui                Ri
##  Alouatta_palliata        :  1   Min.   :0.0006121   Min.   :0.2828
##  Alouatta_pigra           :  1   1st Qu.:0.0115721   1st Qu.:0.9242
##  Ammospermophilus_interpres:  1   Median :0.0223622   Median :0.9787
##  Ammospermophilus_leucurus :  1   Mean   :0.0281722   Mean   :0.9174
##  Ammospermophilus_nelsoni  :  1   3rd Qu.:0.0344888   3rd Qu.:0.9966
##  Antilocapra_americana     :  1   Max.   :0.1243665   Max.   :0.9999
##  (Other)                   :259
##     std_Ui
##  Min.   :0.00000
##  1st Qu.:0.08856
##  Median :0.17575
##  Mean   :0.22270
##  3rd Qu.:0.27374
##  Max.   :1.00000
##
```
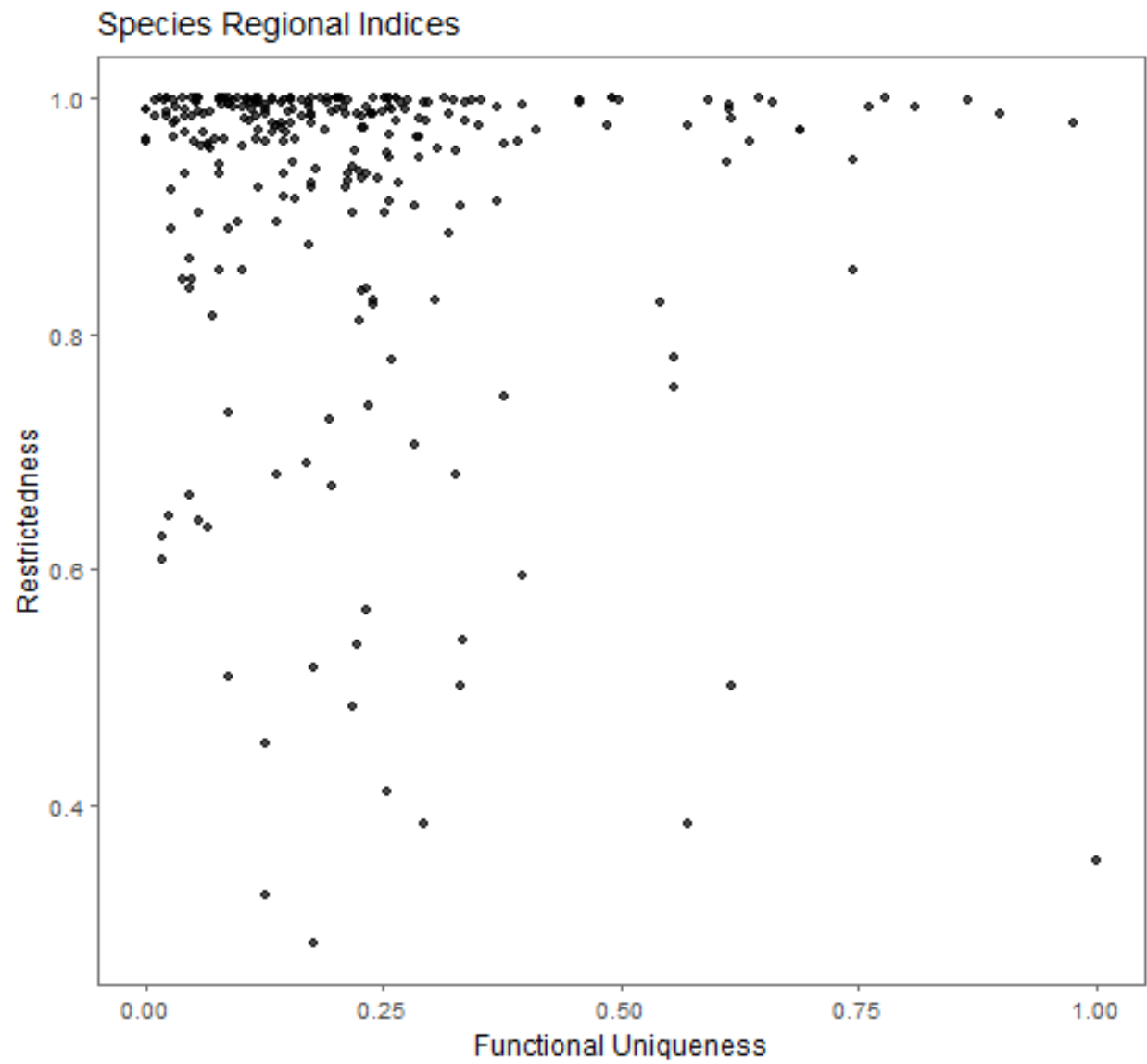
Geographical Restrictedness
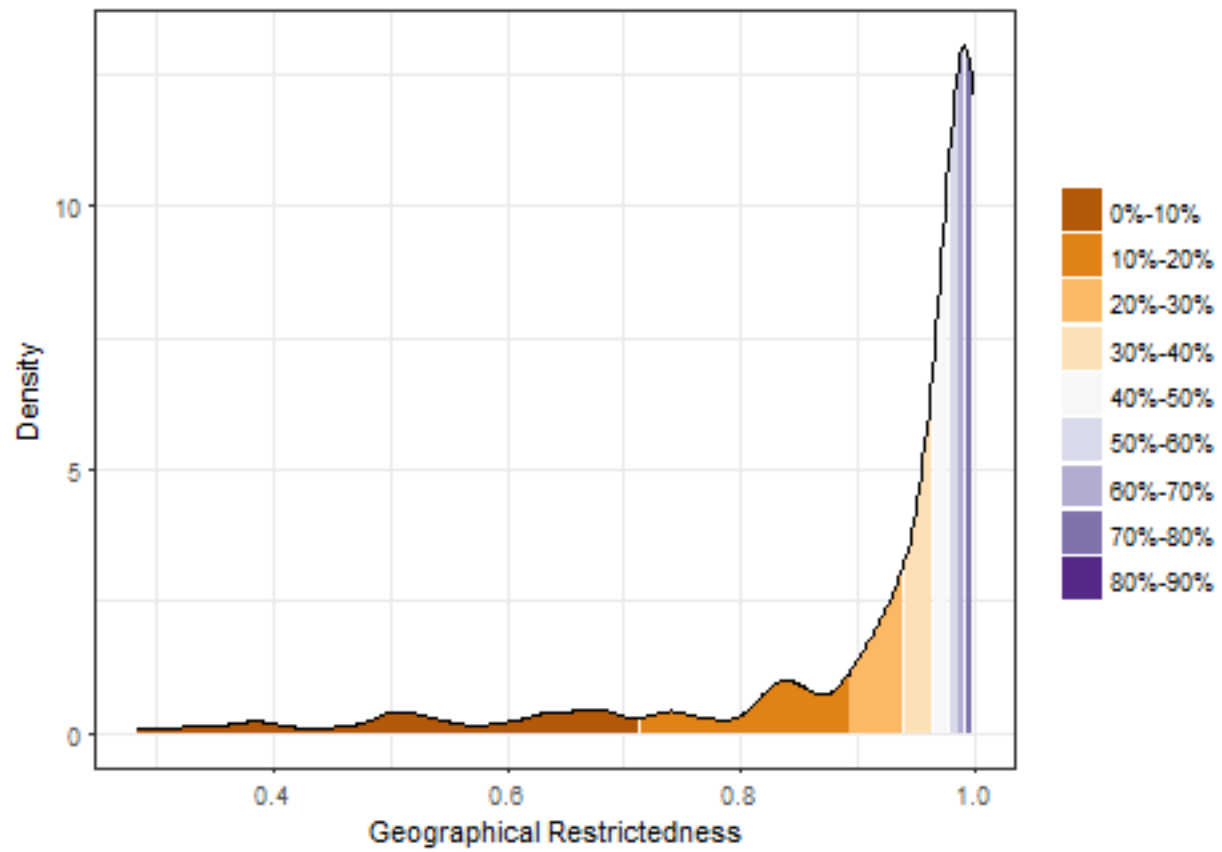
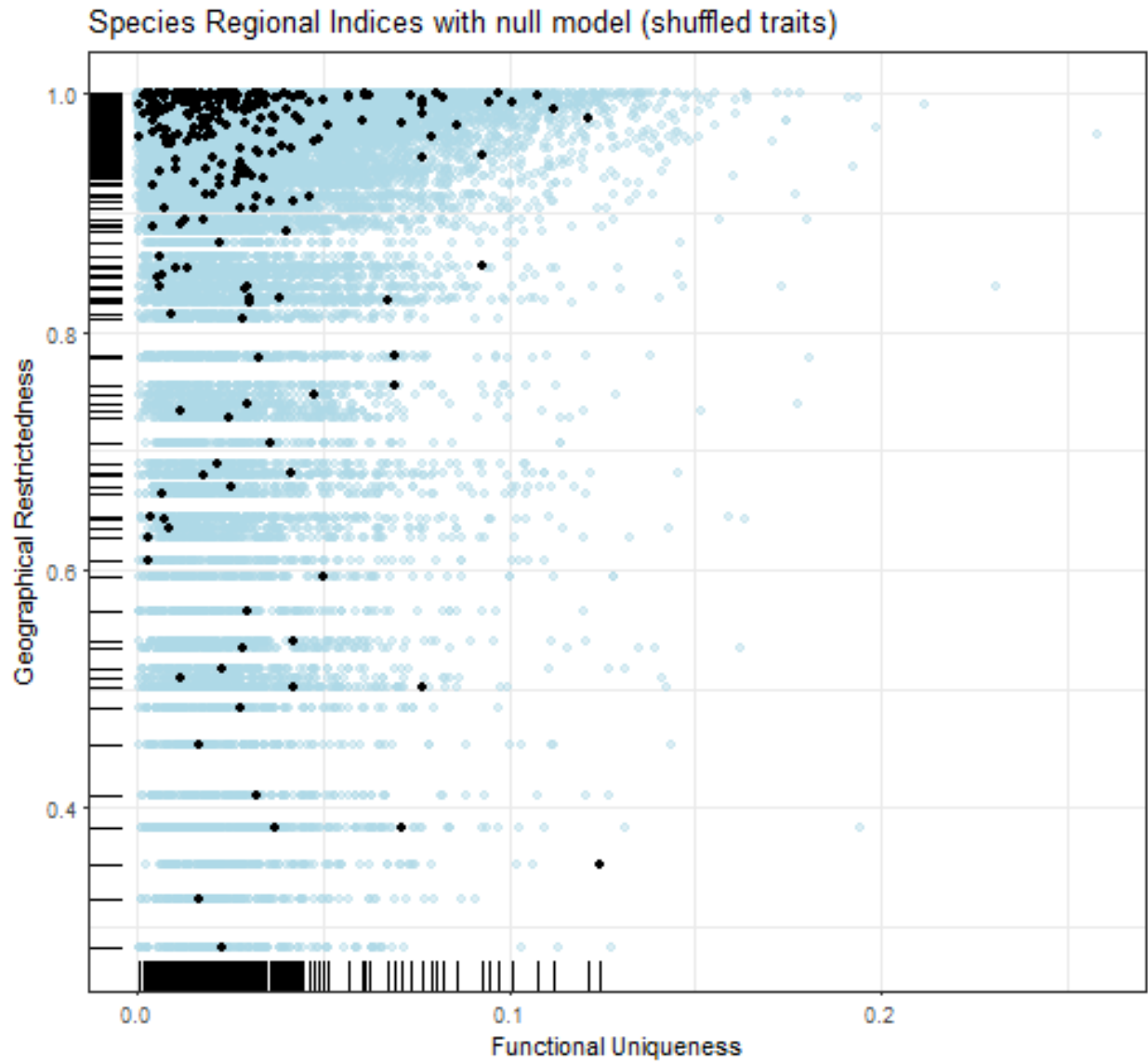**Functional Uniqueness**
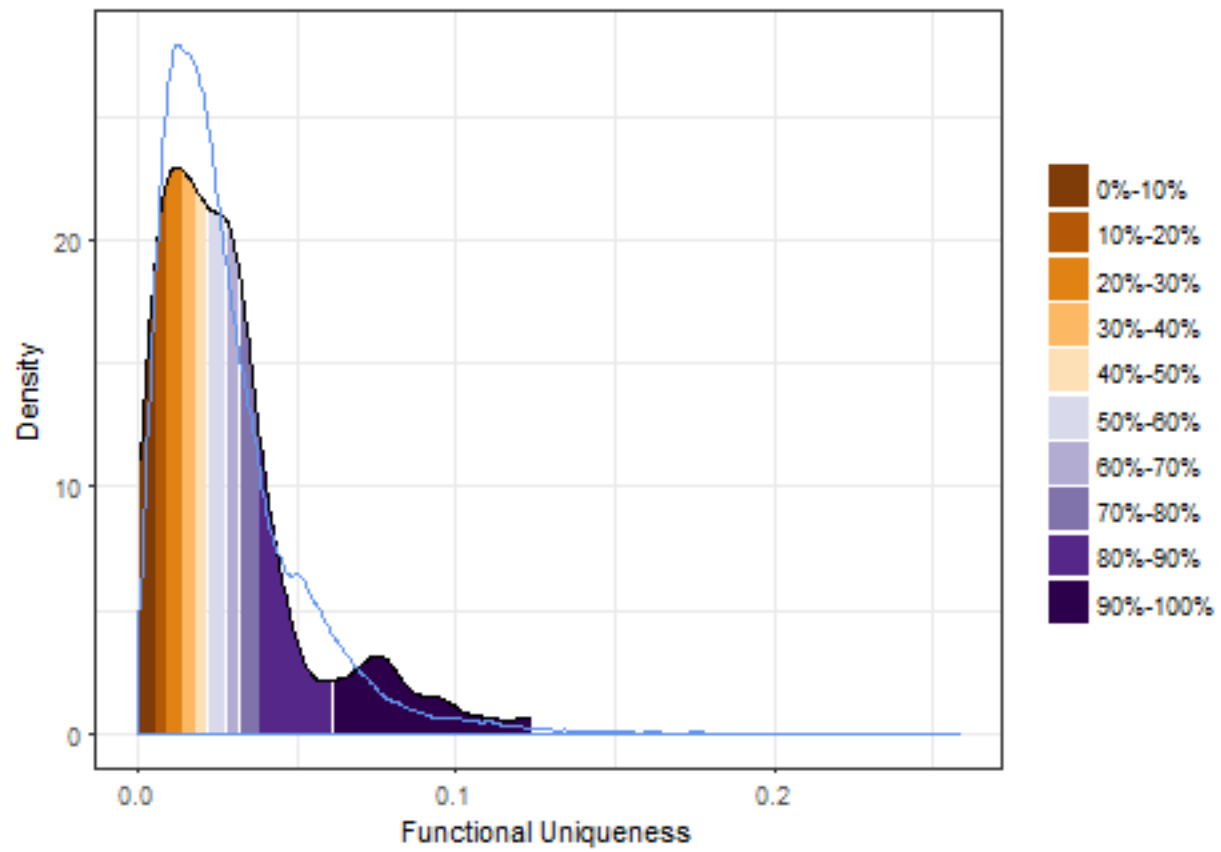
Functional Uniqueness and Geographical Restrictedness Biplot

Species Regional Indices

Species Regional Indices with null model (shuffled traits)

Functional Distinctiveness

For each site-species combination

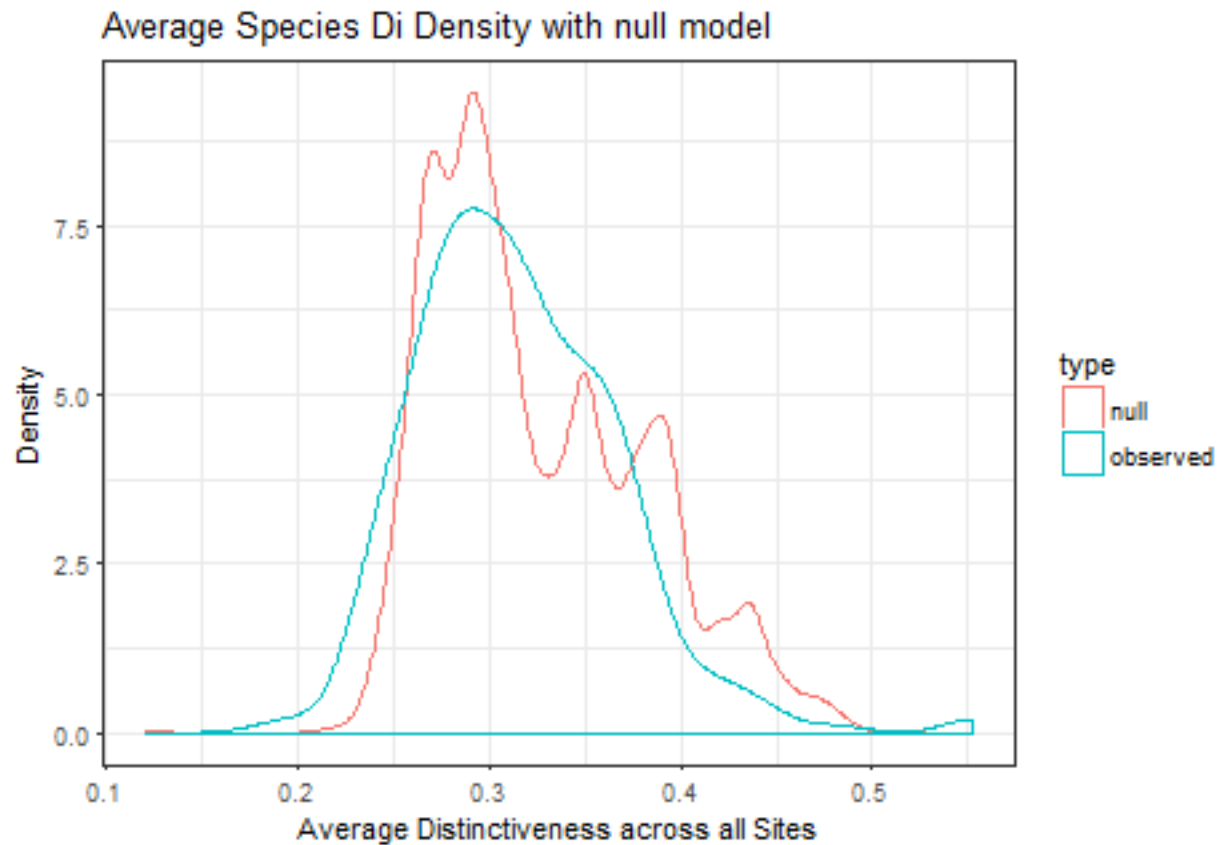## Density of each species-site Distinctiveness value
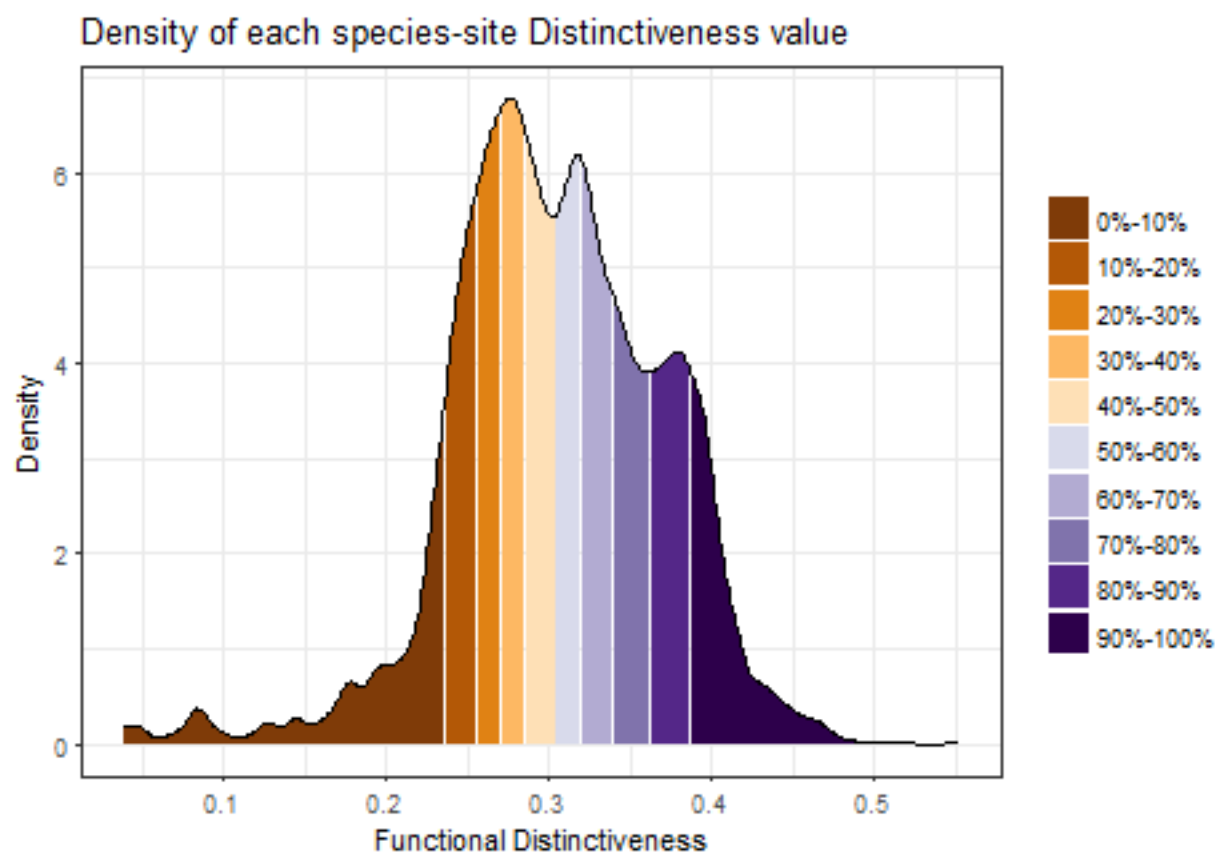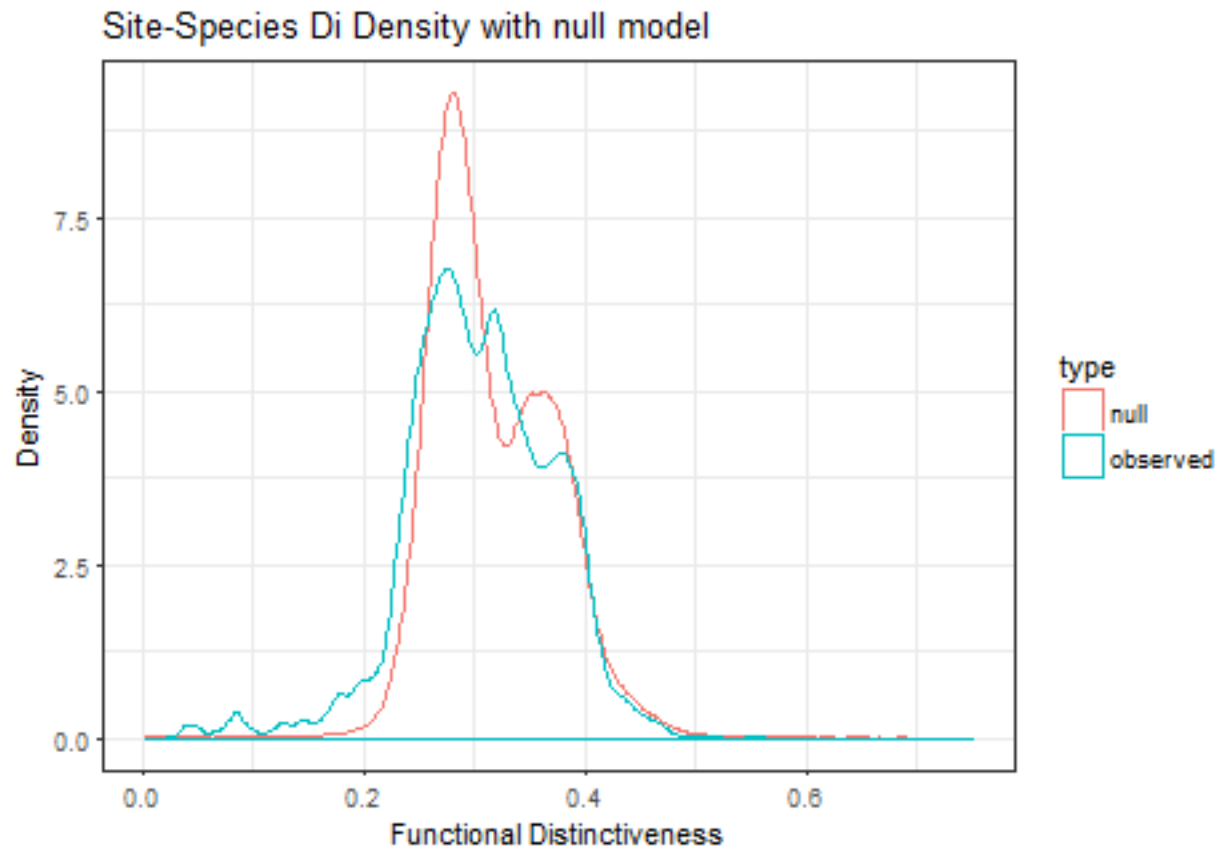
Average Distinctiveness of a species across all sites
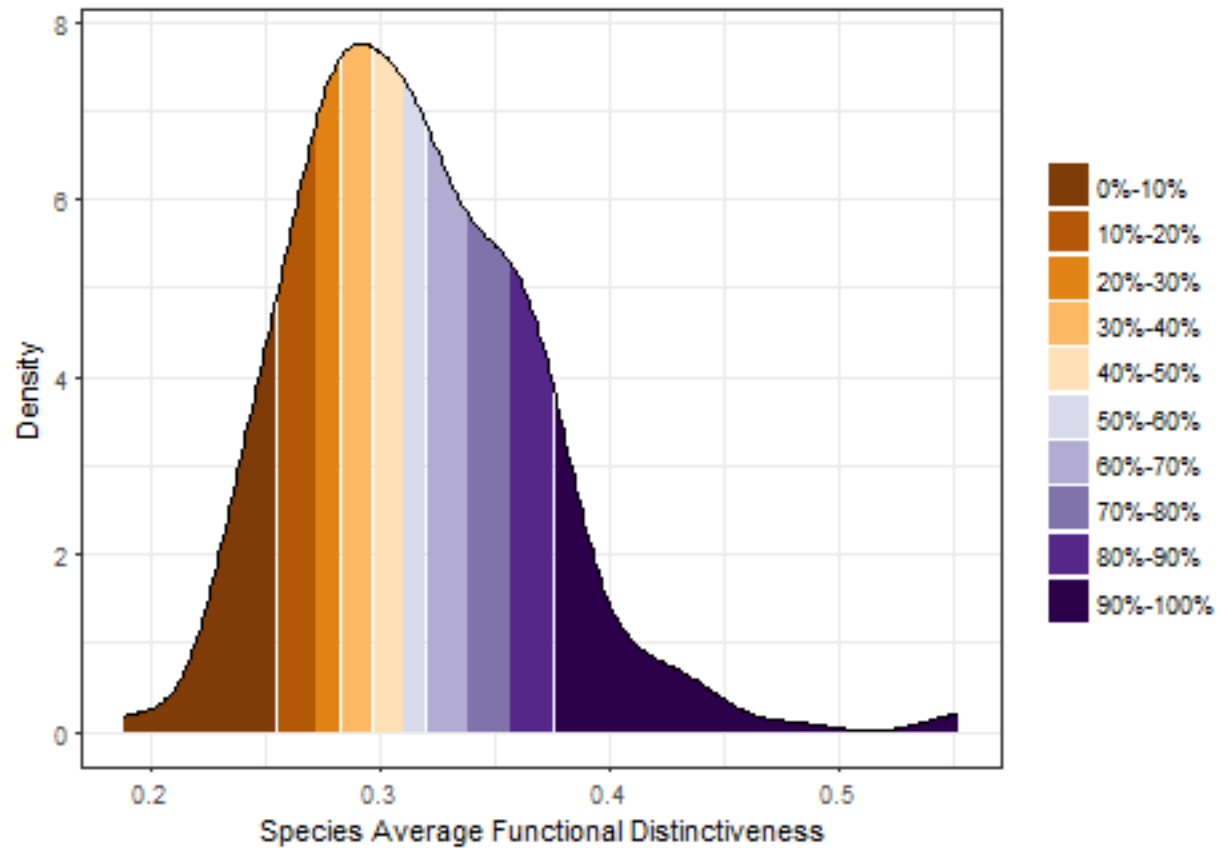
```
## Warning in bind_rows_(x, .id): binding factor and character vector,
## coercing into character vector
```

```
## Warning: Removed 1 rows containing non-finite values (stat_density).
```

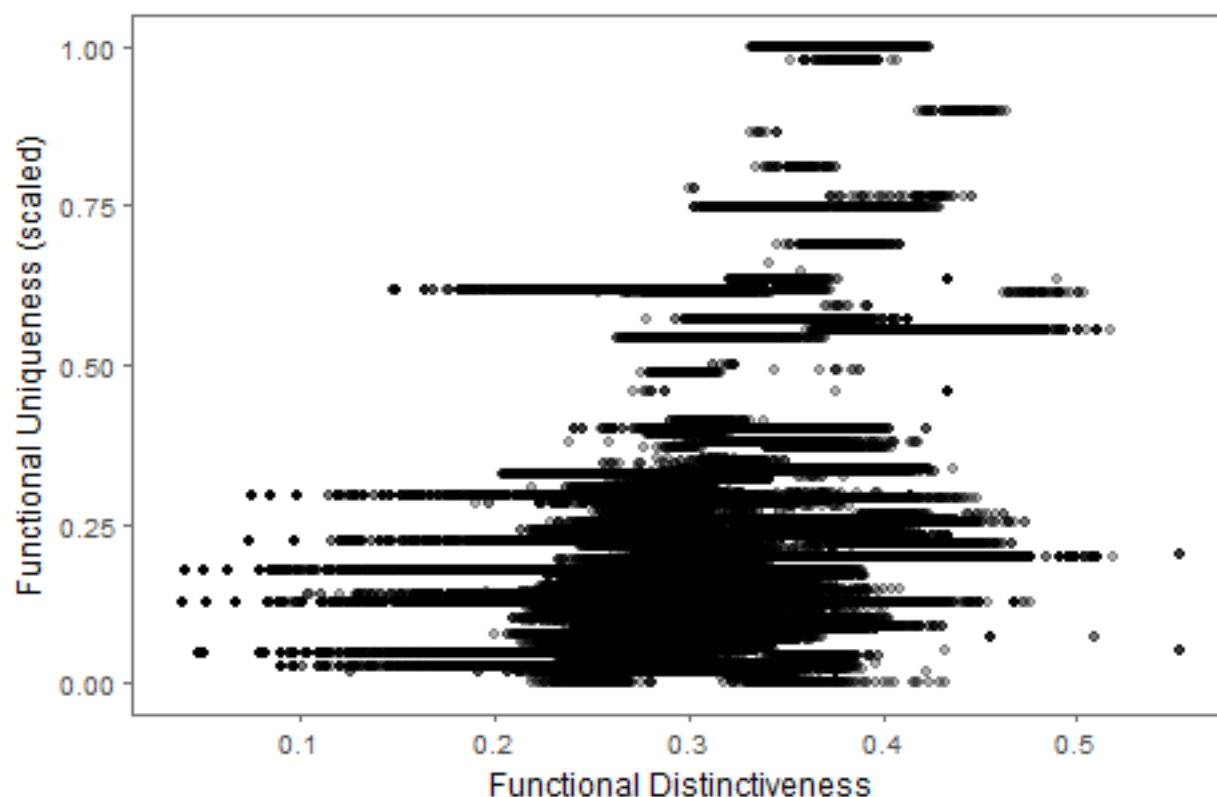Average Species Di Density with null model

Functional Distinctiveness and other indices biplots

```
## Warning in inner_join_impl(x, y, by$x, by$y, suffix$x, suffix$y): joining
## factors with different levels, coercing to character vector
```

Functional Distinctiveness vs. Functional Uniqueness

Species Functional Indices (local vs. regional)


```
## Warning in cor.test.default(species_all_ind$Di, species_all_ind$std_Ui, :
## Cannot compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  species_all_ind$Di and species_all_ind$std_Ui
## S = 9.3433e+14, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##       rho
## 0.3700527

##
## Call:
## lm(formula = std_Ui ~ Di, data = species_all_ind)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.48486 -0.13026 -0.03203  0.06274  0.71942
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept) -0.105925   0.002047  -51.74   <2e-16 ***
## Di           1.164589   0.006568  177.31   <2e-16 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
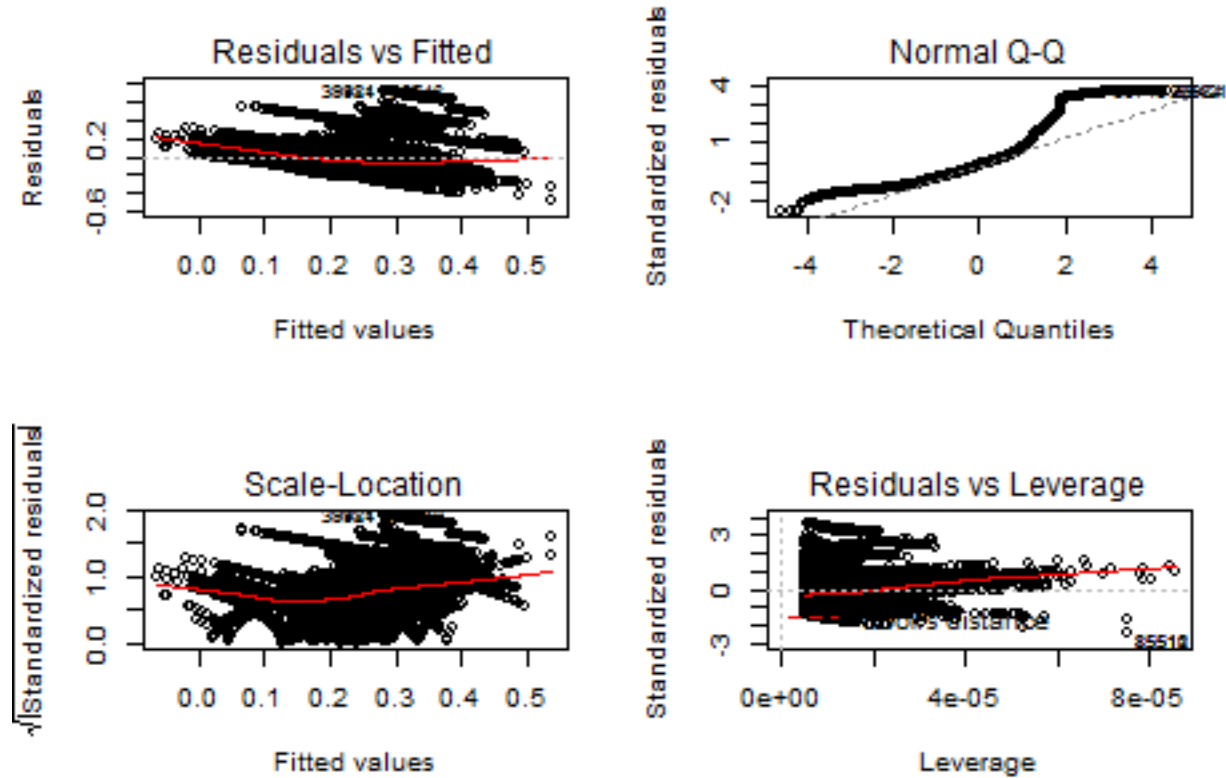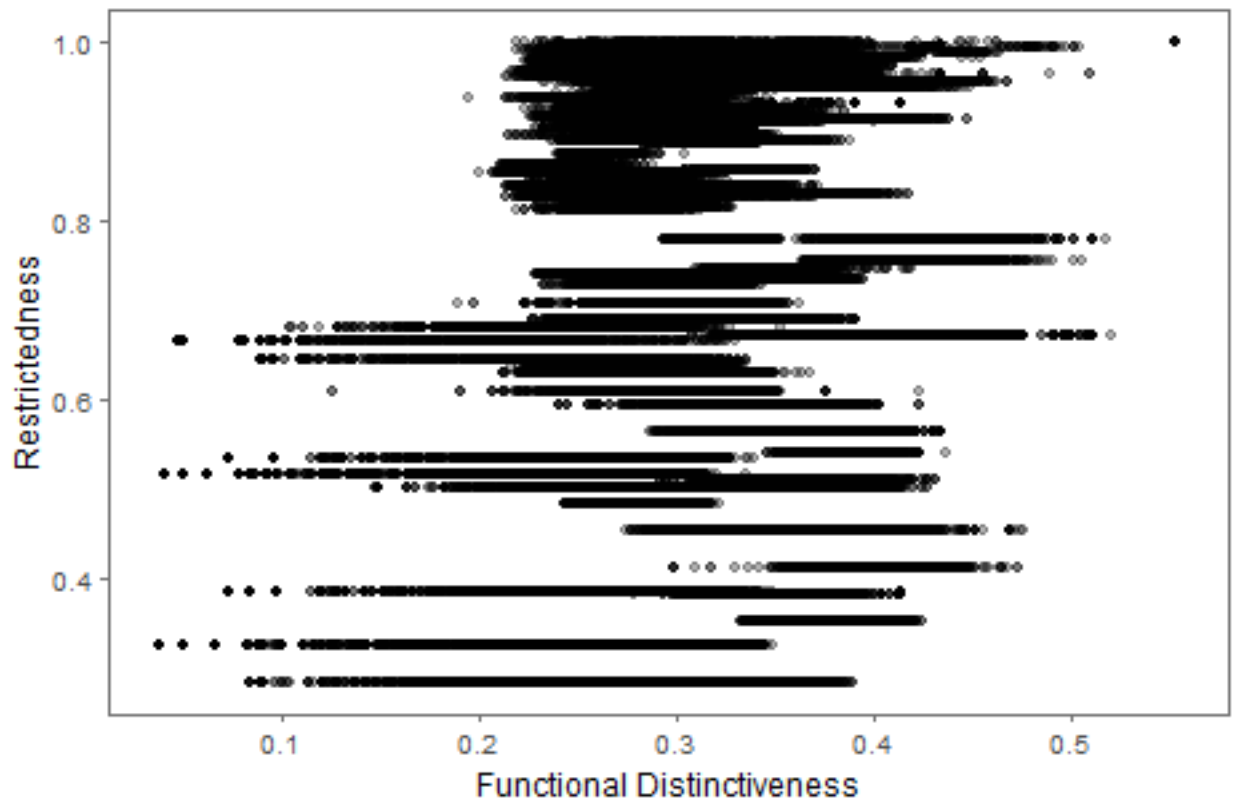
```
##
## Residual standard error: 0.194 on 207226 degrees of freedom
## Multiple R-squared:  0.1317, Adjusted R-squared:  0.1317
## F-statistic: 3.144e+04 on 1 and 207226 DF,  p-value: < 2.2e-16
```
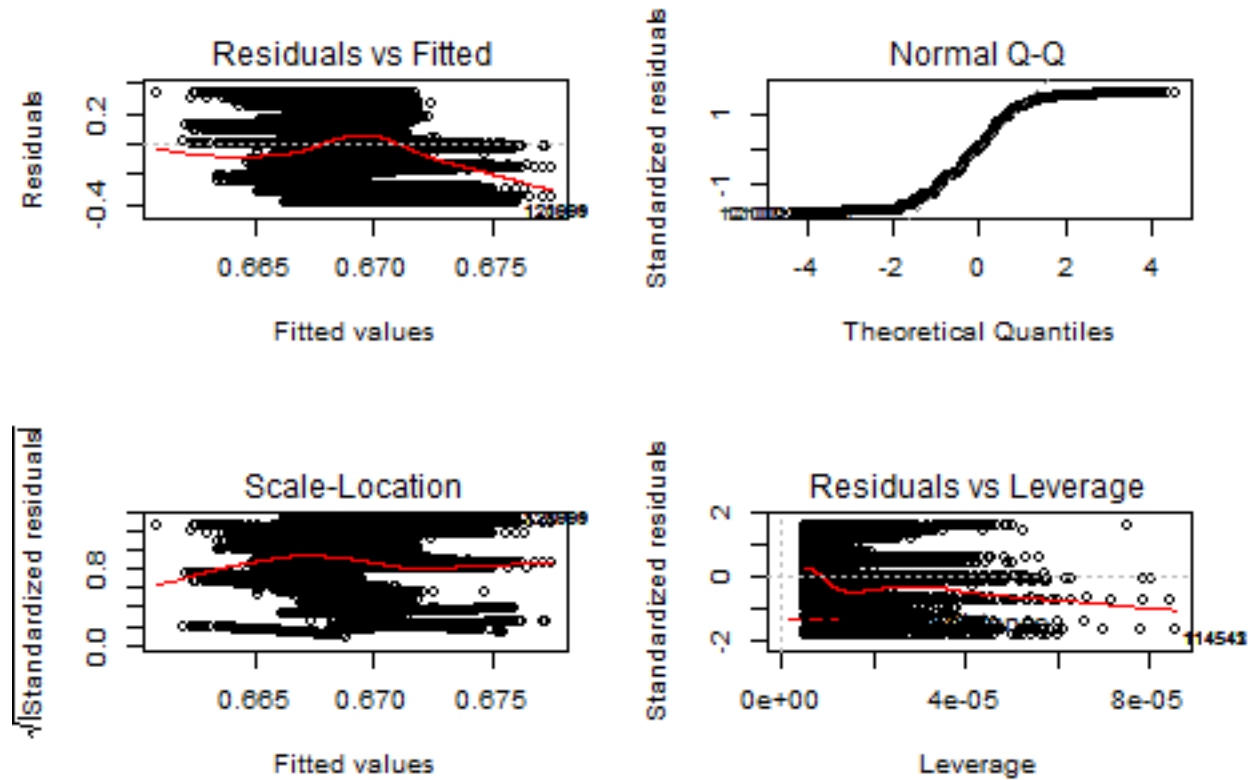

Functional Distinctiveness vs. Geographical Restrictedness

```
## Warning in cor.test.default(species_all_ind$Di, species_all_ind$Ri, method
## = "spearman"): Cannot compute exact p-value with ties

##
##  Spearman's rank correlation rho
##
## data:  species_all_ind$Di and species_all_ind$Ri
## S = 1.5708e+15, p-value < 2.2e-16
## alternative hypothesis: true rho is not equal to 0
## sample estimates:
##         rho
## -0.05904381

##
## Call:
## lm(formula = Ri ~ Di, data = species_all_ind)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.39324 -0.16682  0.00461  0.18681  0.33873
##
## Coefficients:
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)  0.678825   0.002245 302.407  < 2e-16 ***
## Di          -0.032512   0.007202  -4.514 6.35e-06 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```
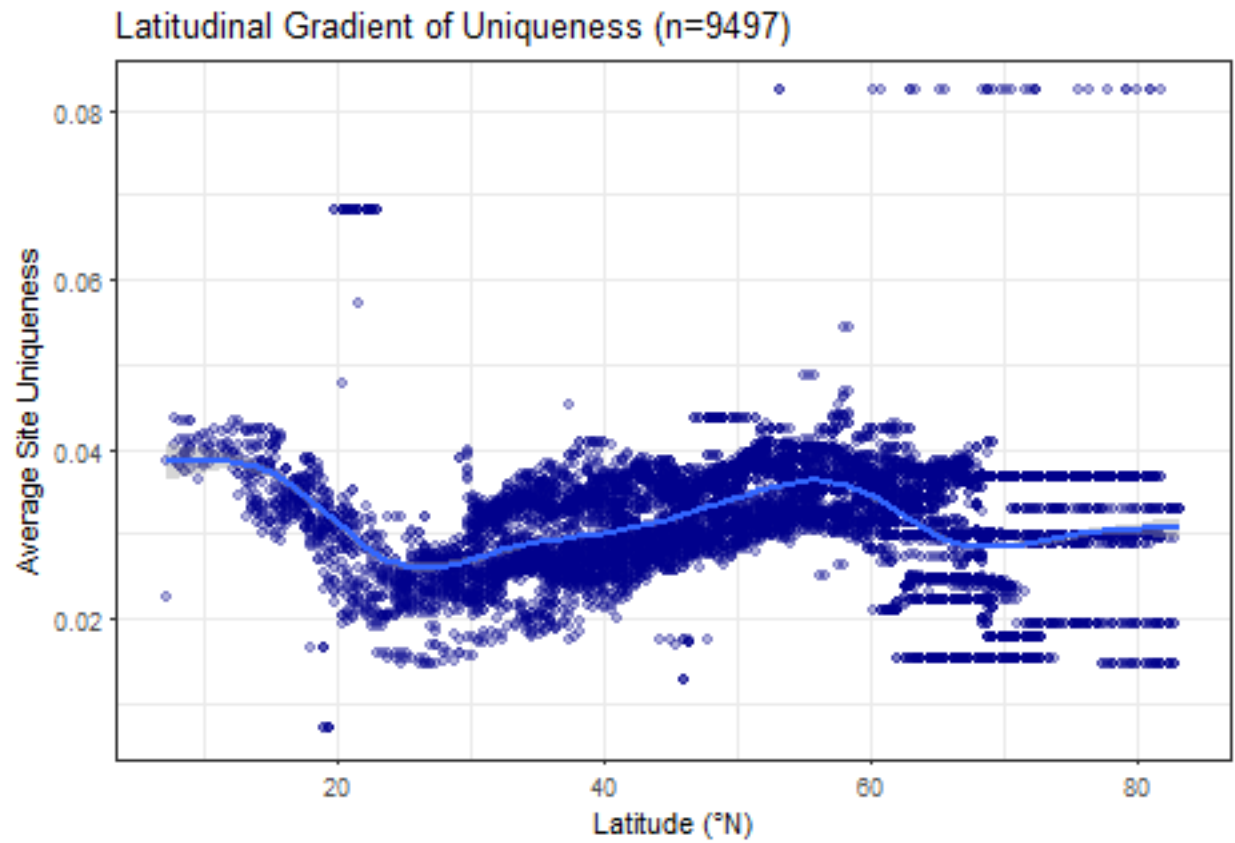
```
##
## Residual standard error: 0.2128 on 207226 degrees of freedom
## Multiple R-squared:  9.834e-05,  Adjusted R-squared:  9.351e-05
## F-statistic: 20.38 on 1 and 207226 DF,  p-value: 6.352e-06
```
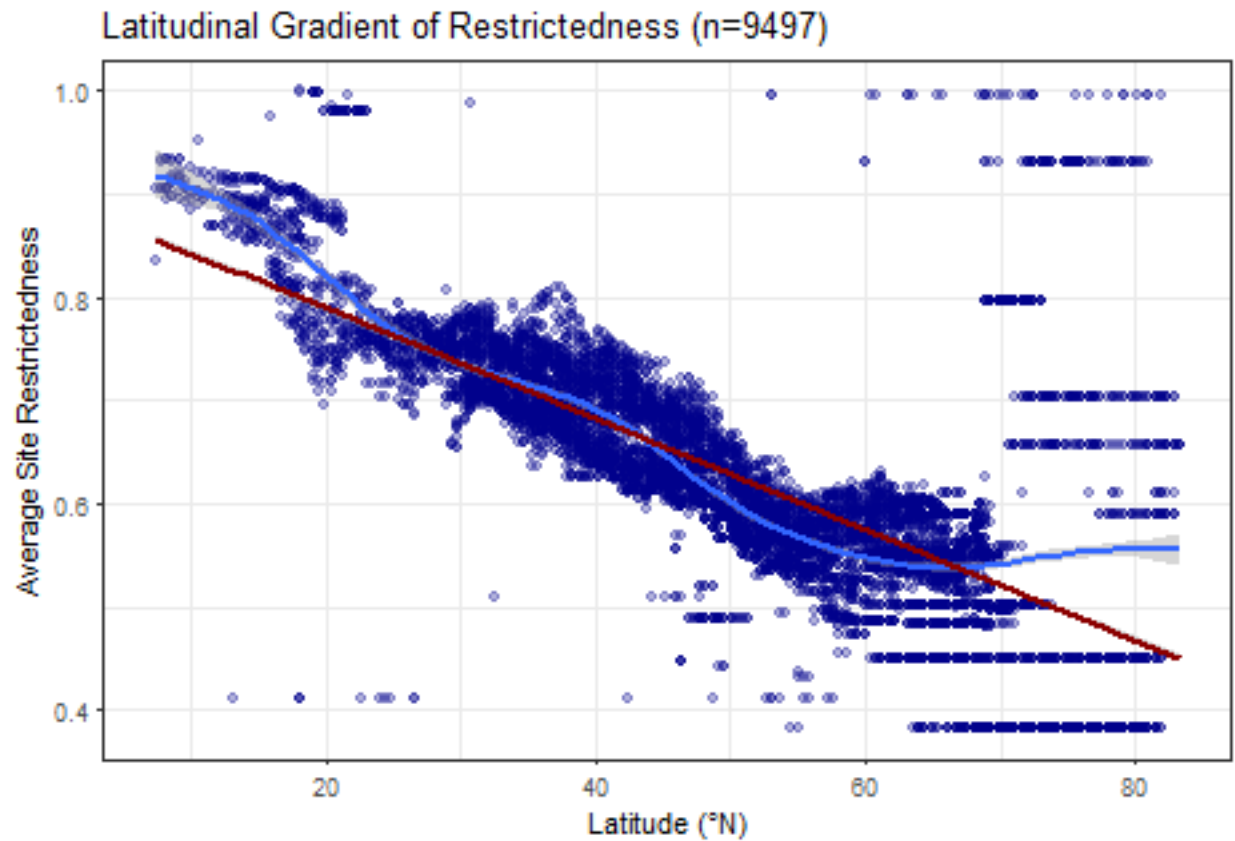

Latitudinal Gradients

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)