

Example of Analyses with **funrar**

Matthias Greni 

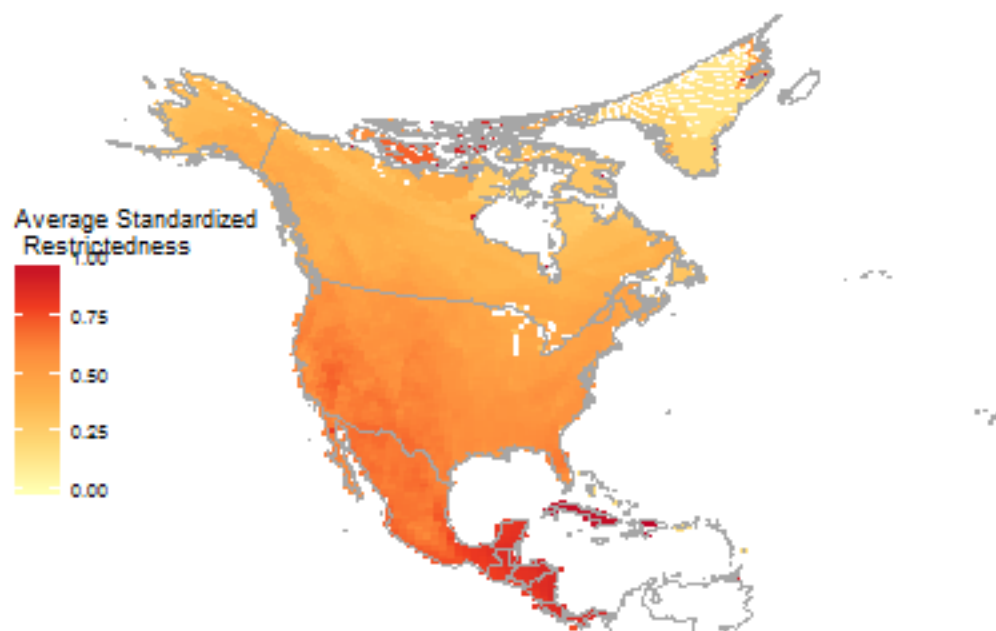
17 f vrier, 2017

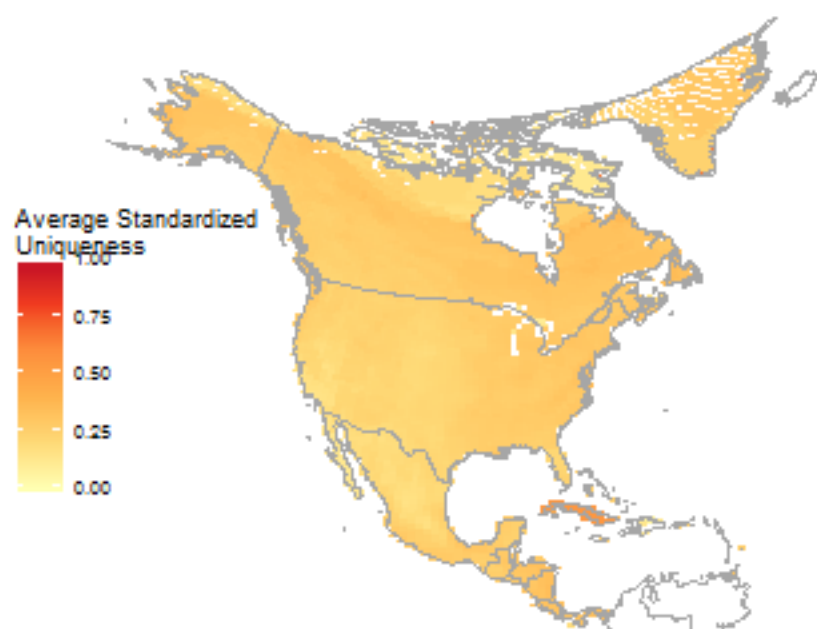
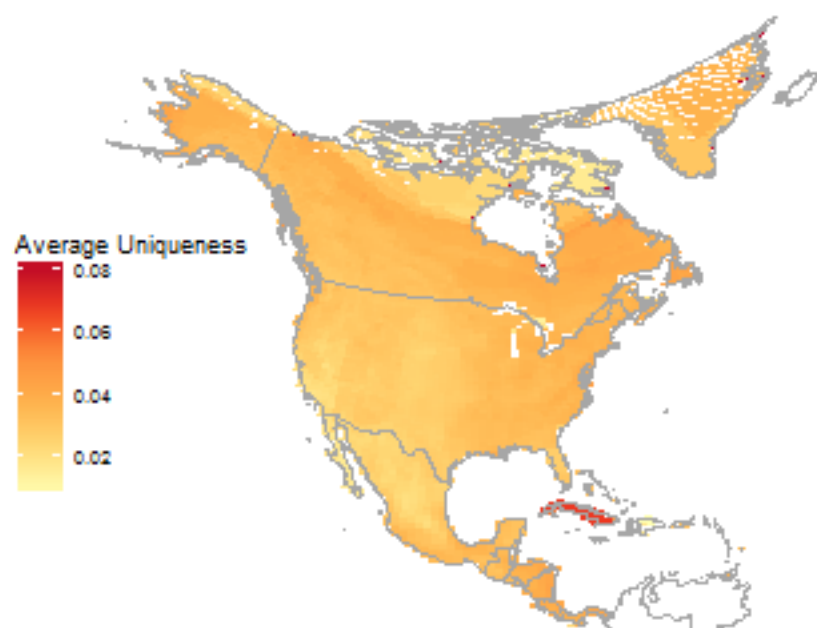
With **funrar** you can compute **F**unctional **R**arity indices. We are using a North American Mammals datasets to show the kind of questions you can come up with.

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).

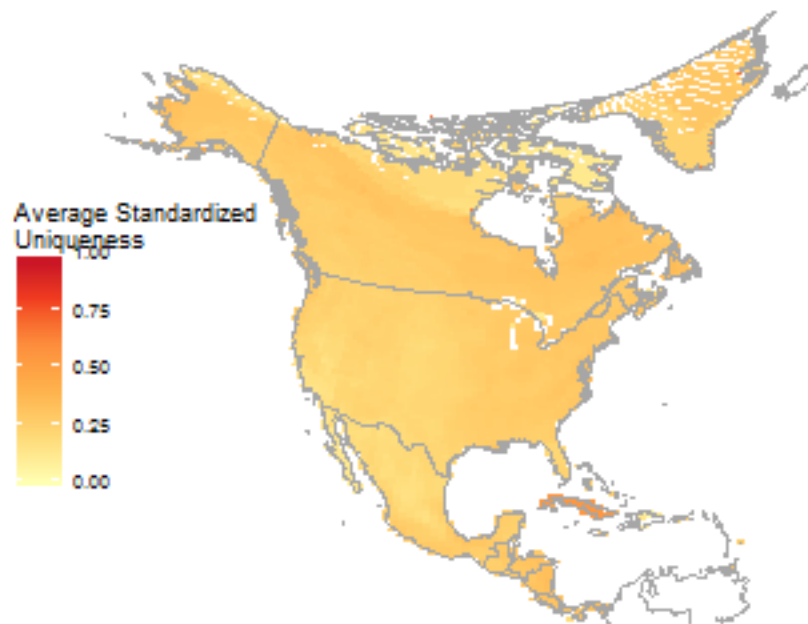
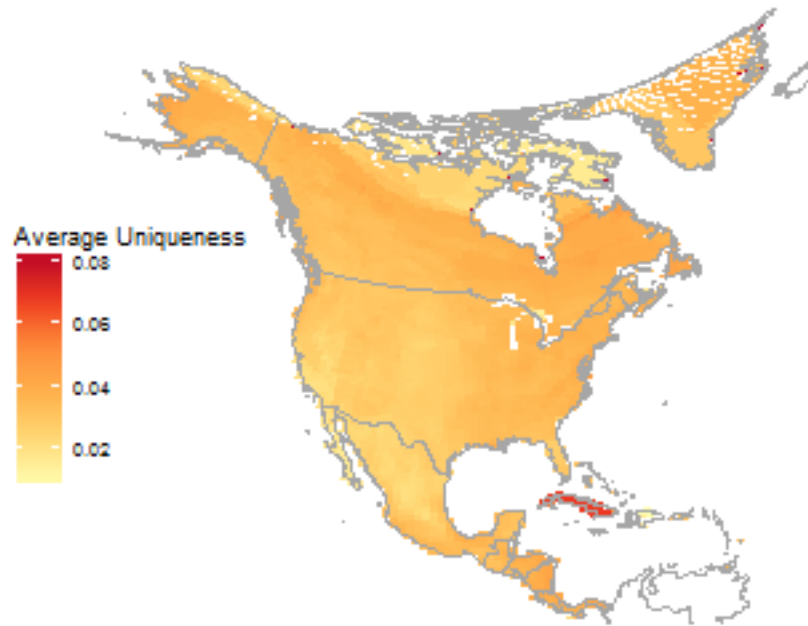
Hotspots

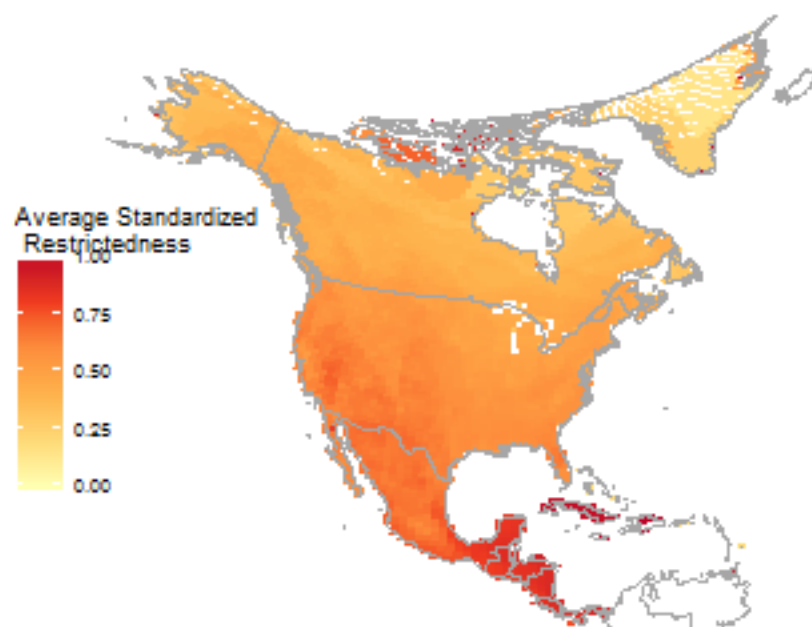
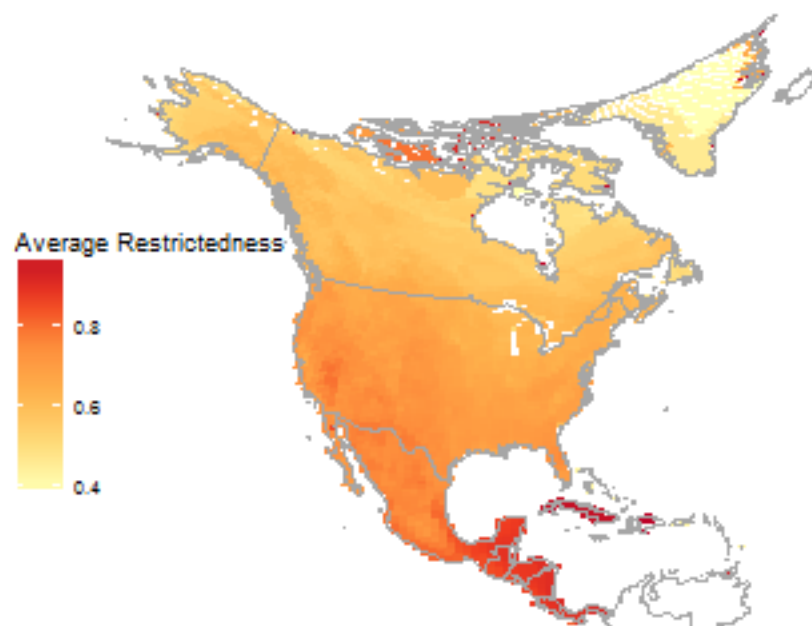
Functional Uniqueness





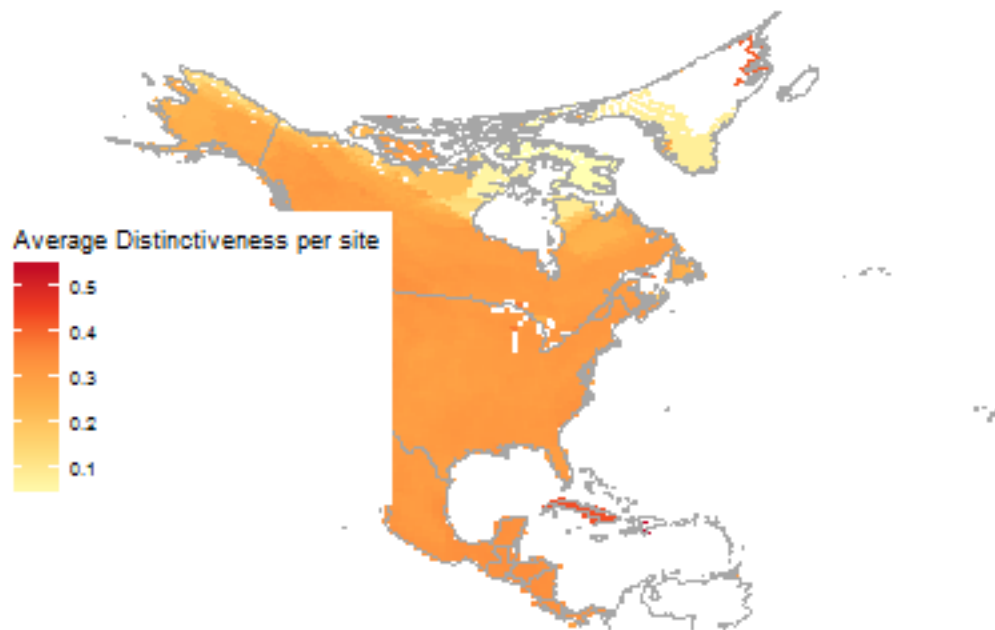
Geographical Restrictedness





Functional Distinctiveness

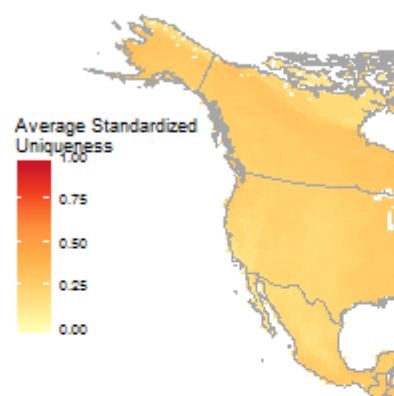
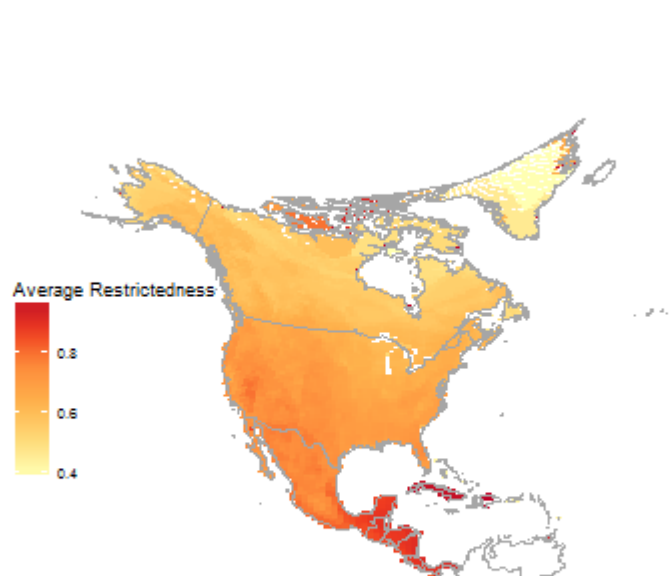
Warning: Removed 552 rows containing non-finite values (stat_summary2d).



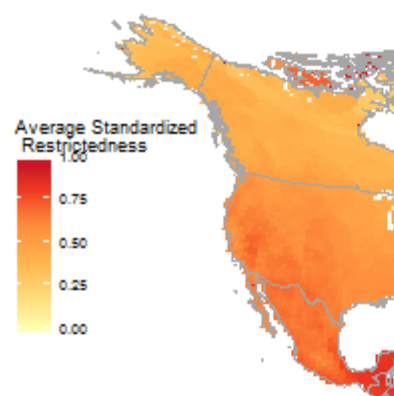
Functional Rarity $(U_i + R_i)/2$

Full comparison

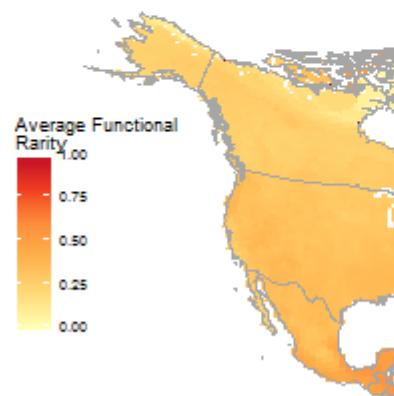
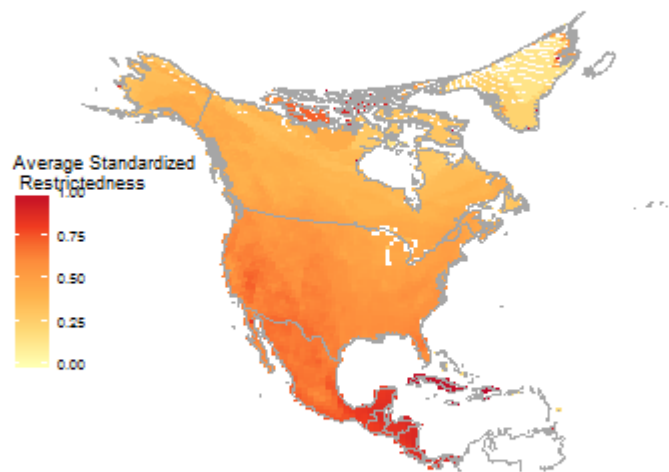
A



B



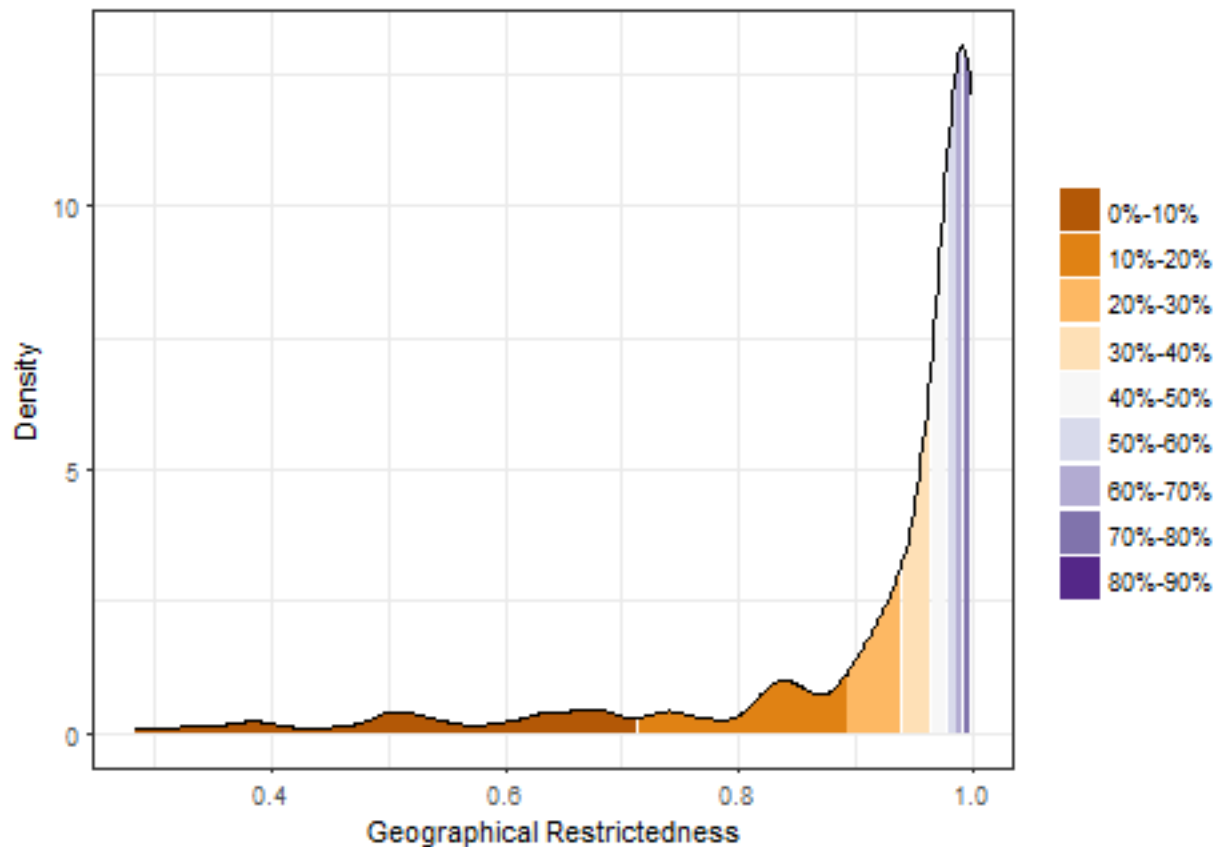
C



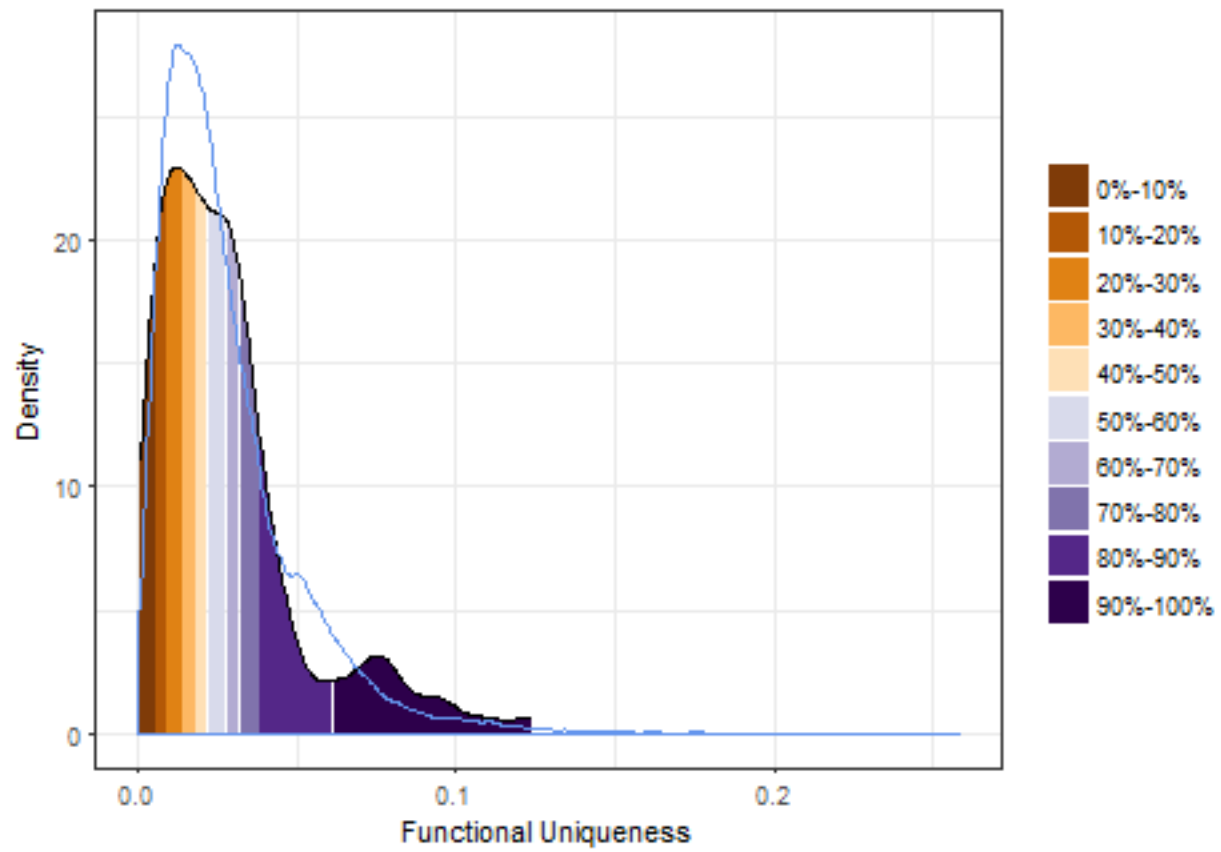
Total distribution of indices

```
##               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      std_Ri
## Min.   :0.00000   Min.   :0.00000
## 1st Qu.:0.08856   1st Qu.:0.8944
## Median :0.17575   Median :0.9705
## Mean    :0.22270   Mean    :0.8850
## 3rd Qu.:0.27374   3rd Qu.:0.9954
## Max.    :1.00000   Max.    :1.00000
##
```

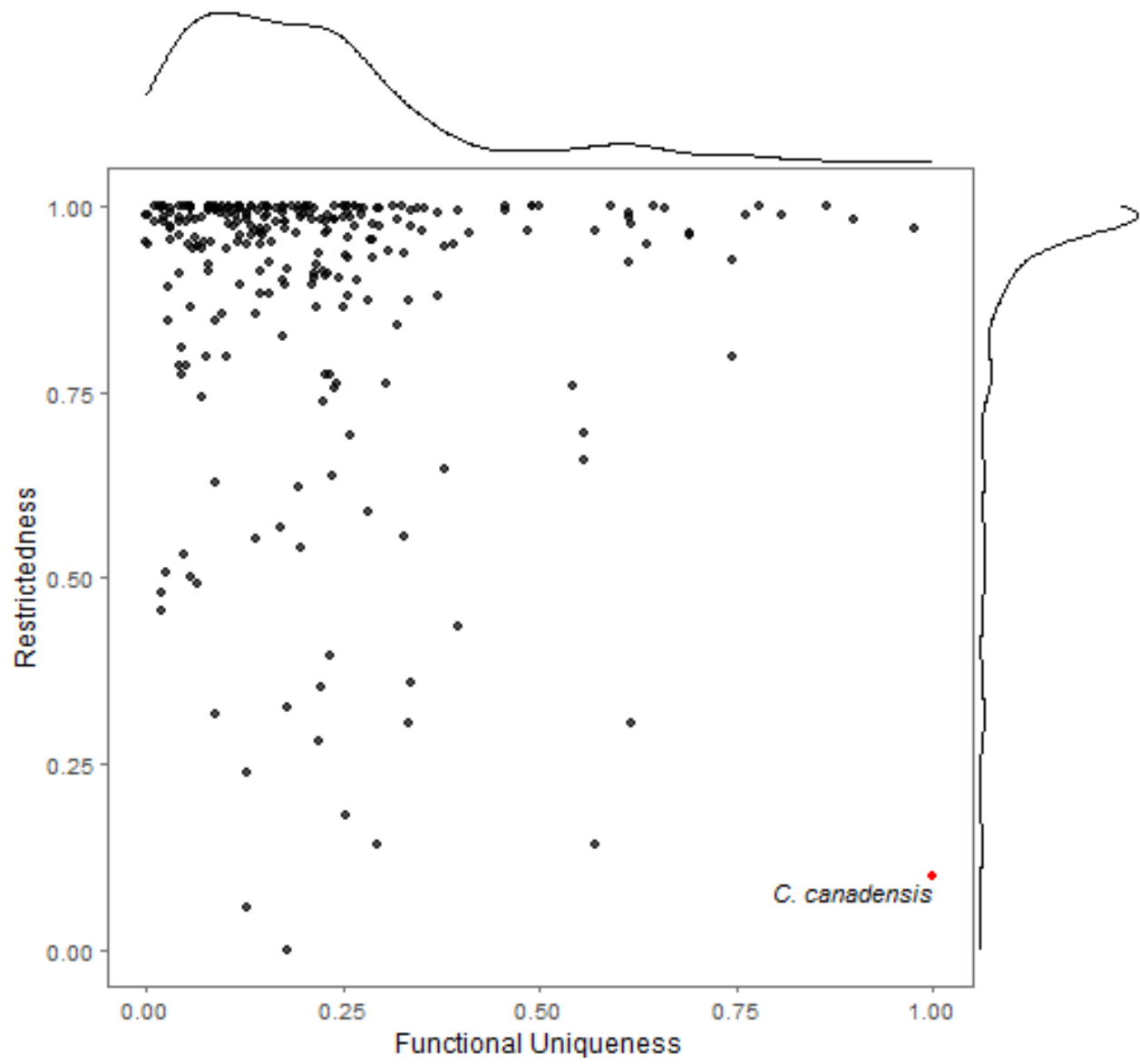
Geographical Restrictedness

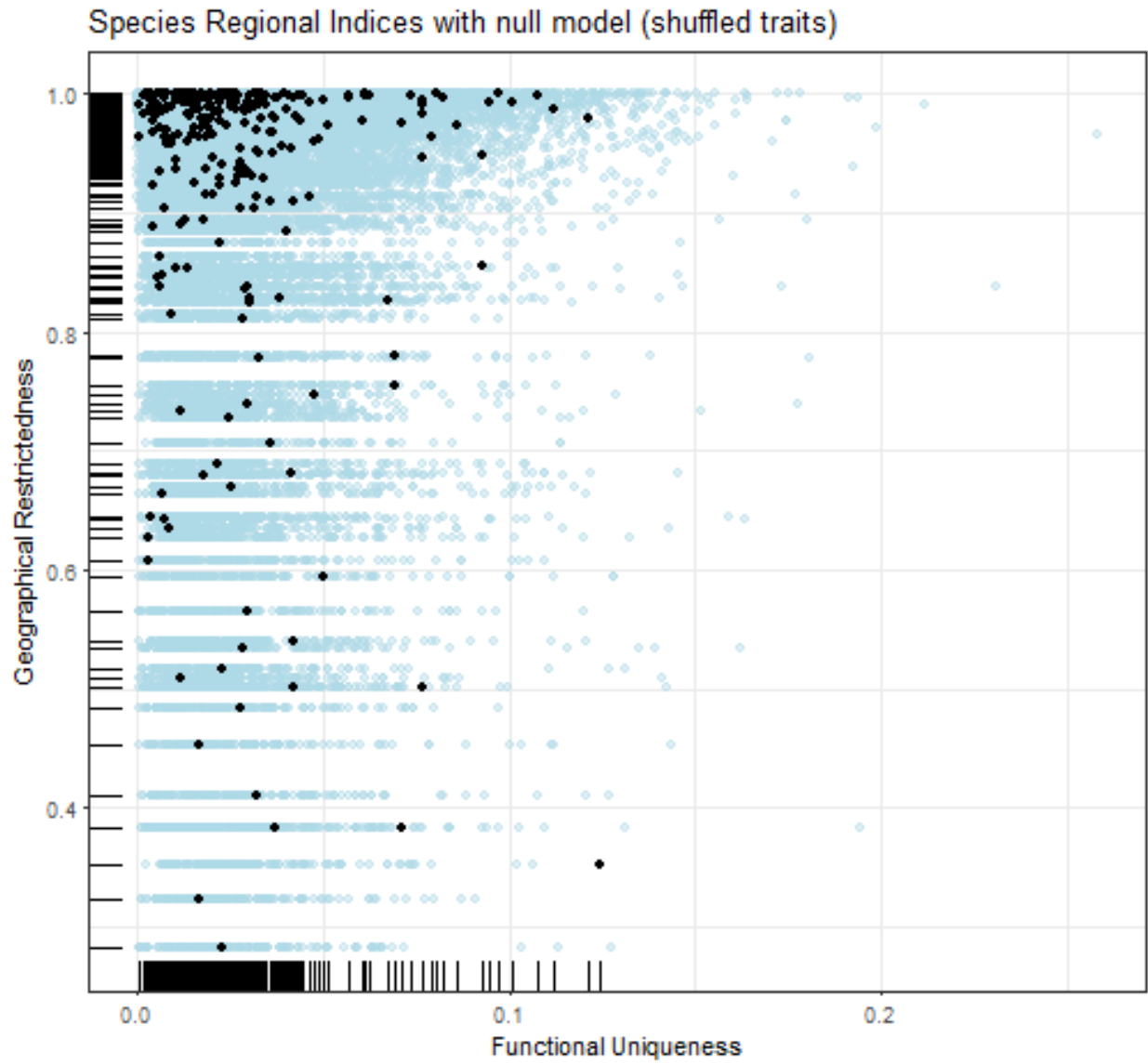


Functional Uniqueness



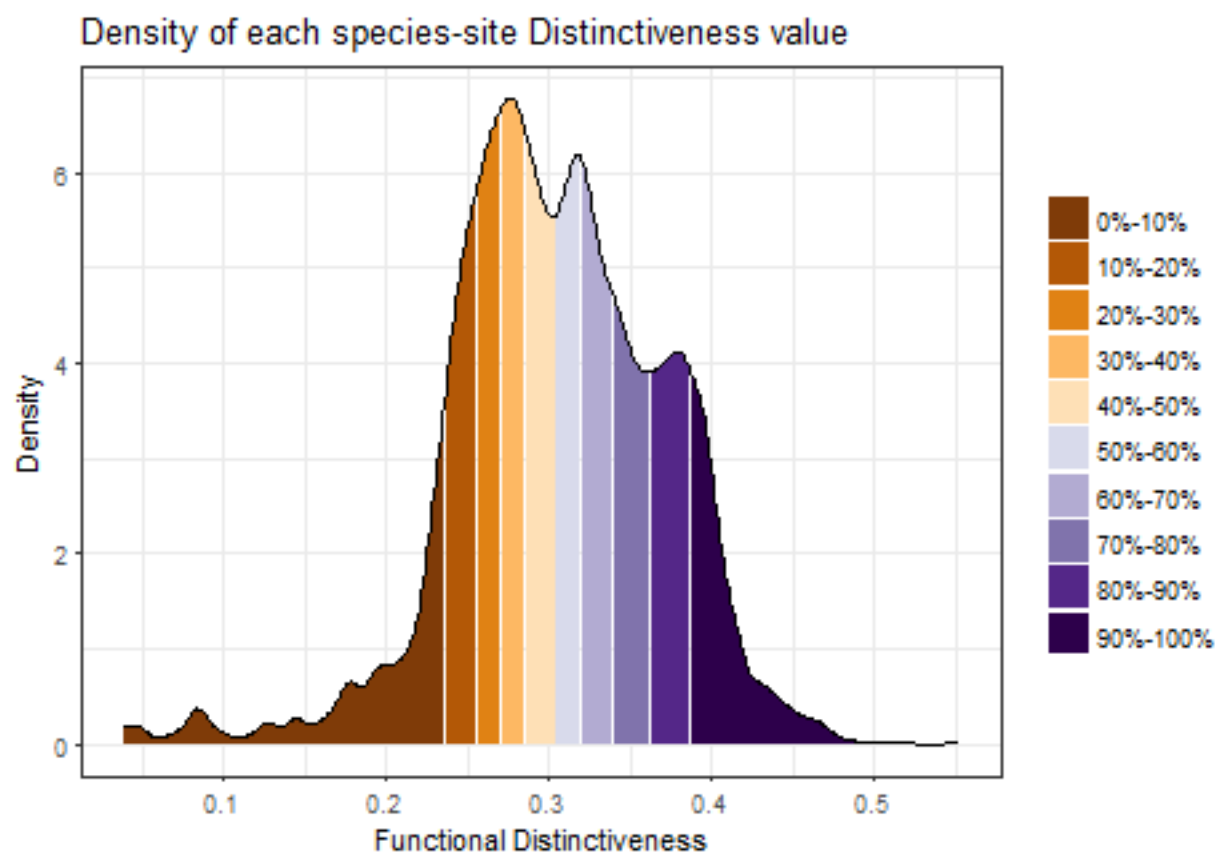
Functional Uniqueness and Geographical Restrictedness Biplot

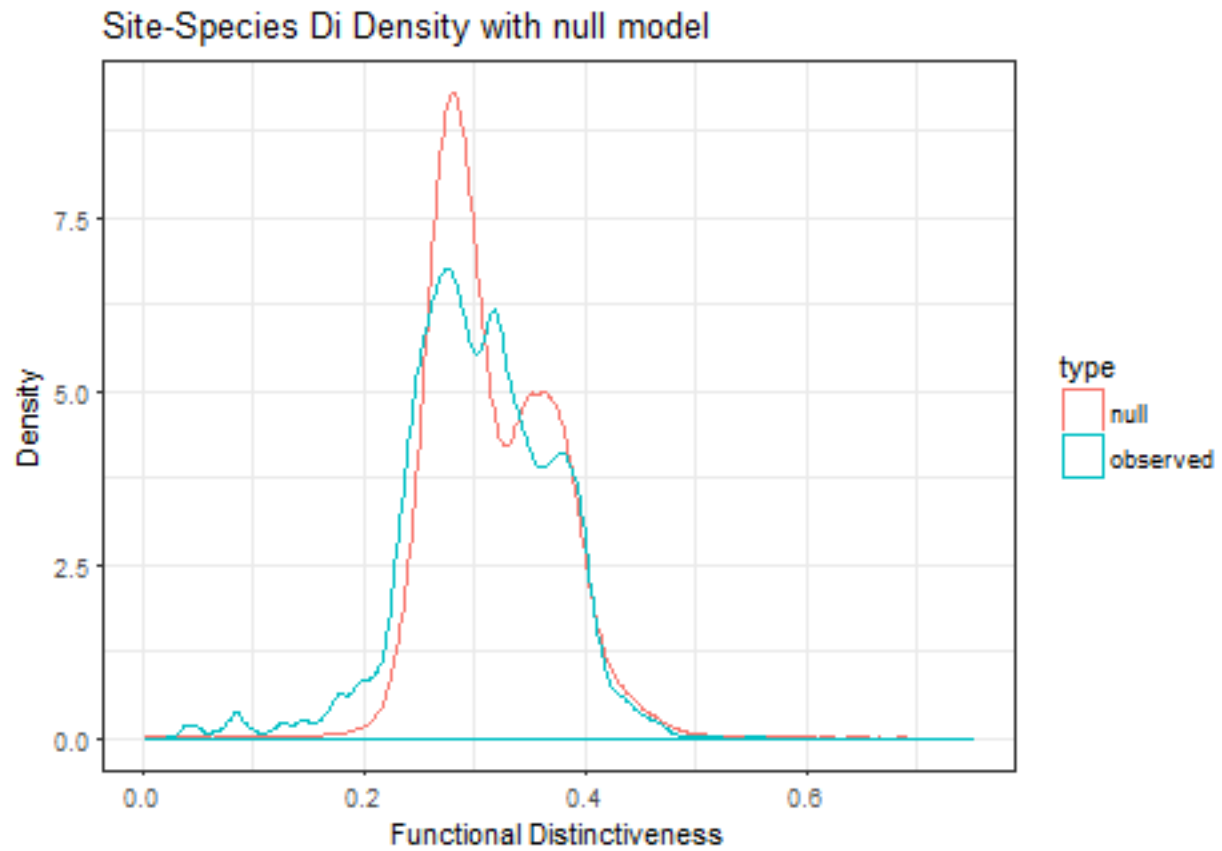




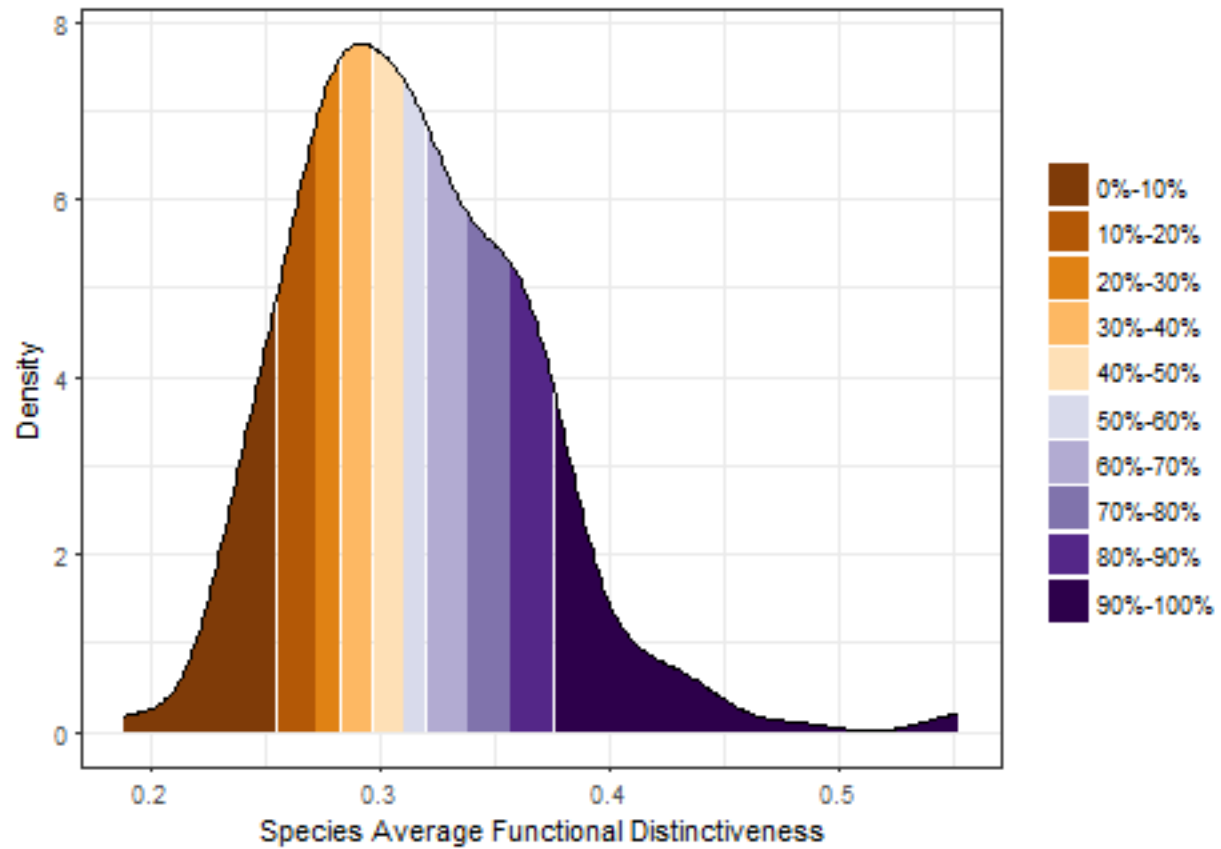
Functional Distinctiveness

For each site-species combination

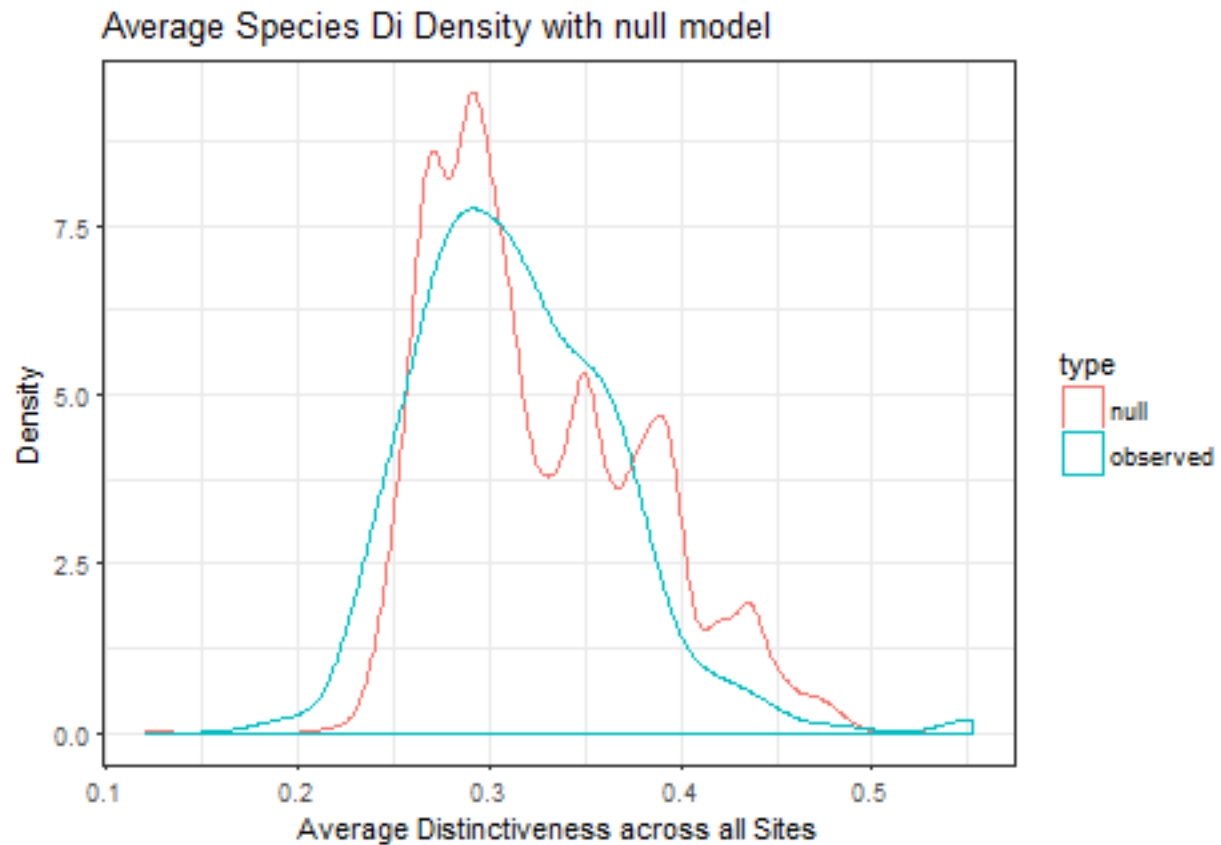




Average Distinctiveness of a species across all sites



```
## 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).
```

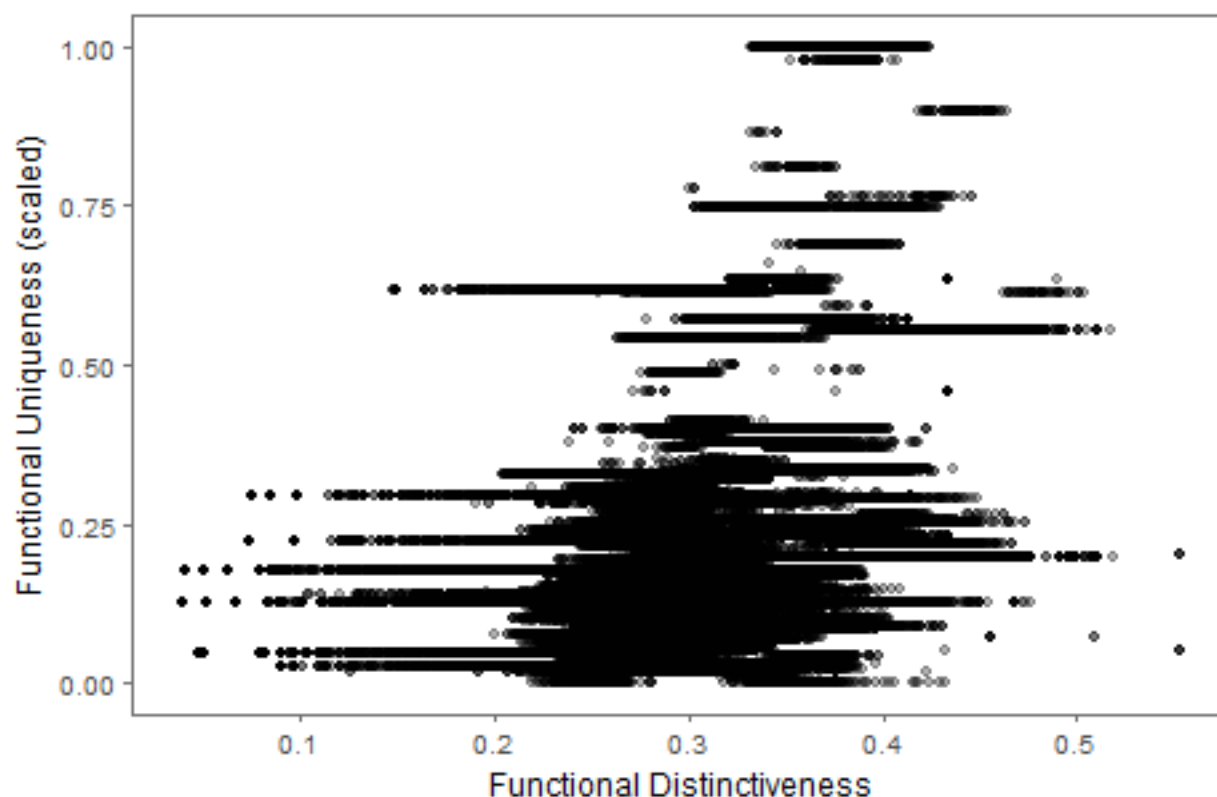


Functional Distinctiveness and other indices biplots

```
## 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)
```

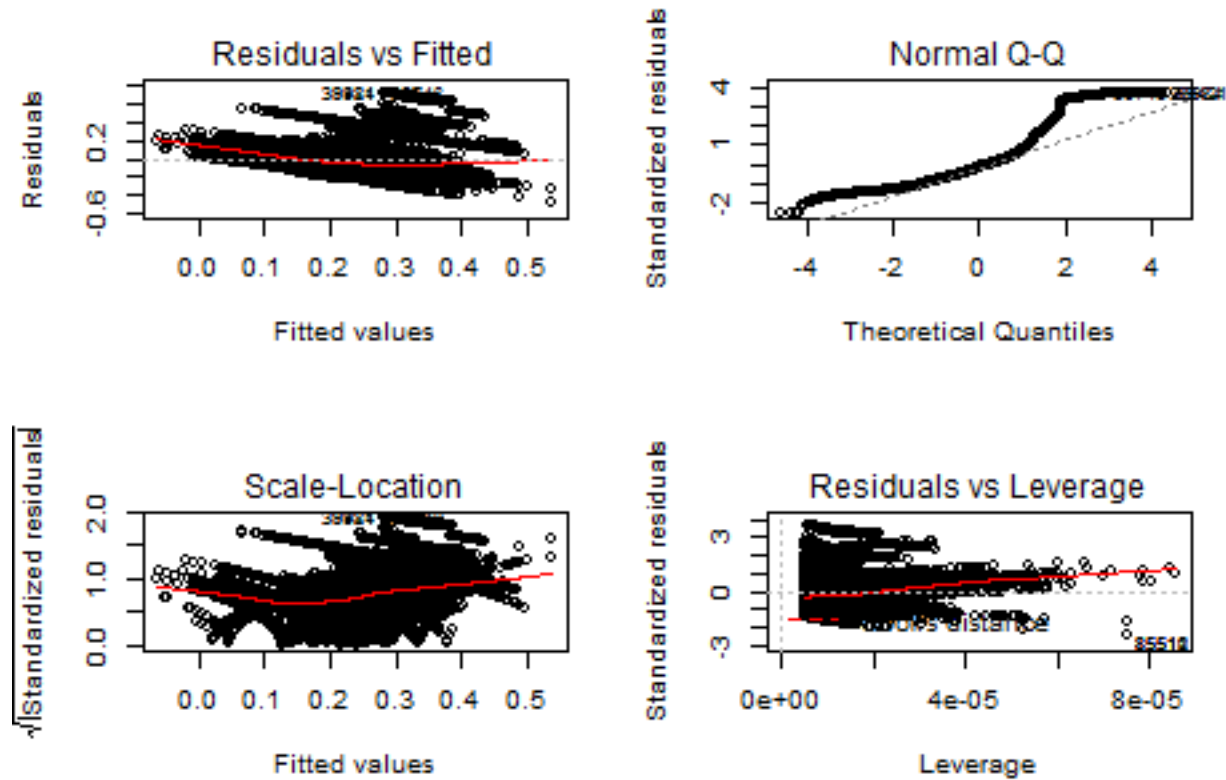
```
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.48486 -0.13026 -0.03203  0.06274  0.71942
```

```
## 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 ***
```

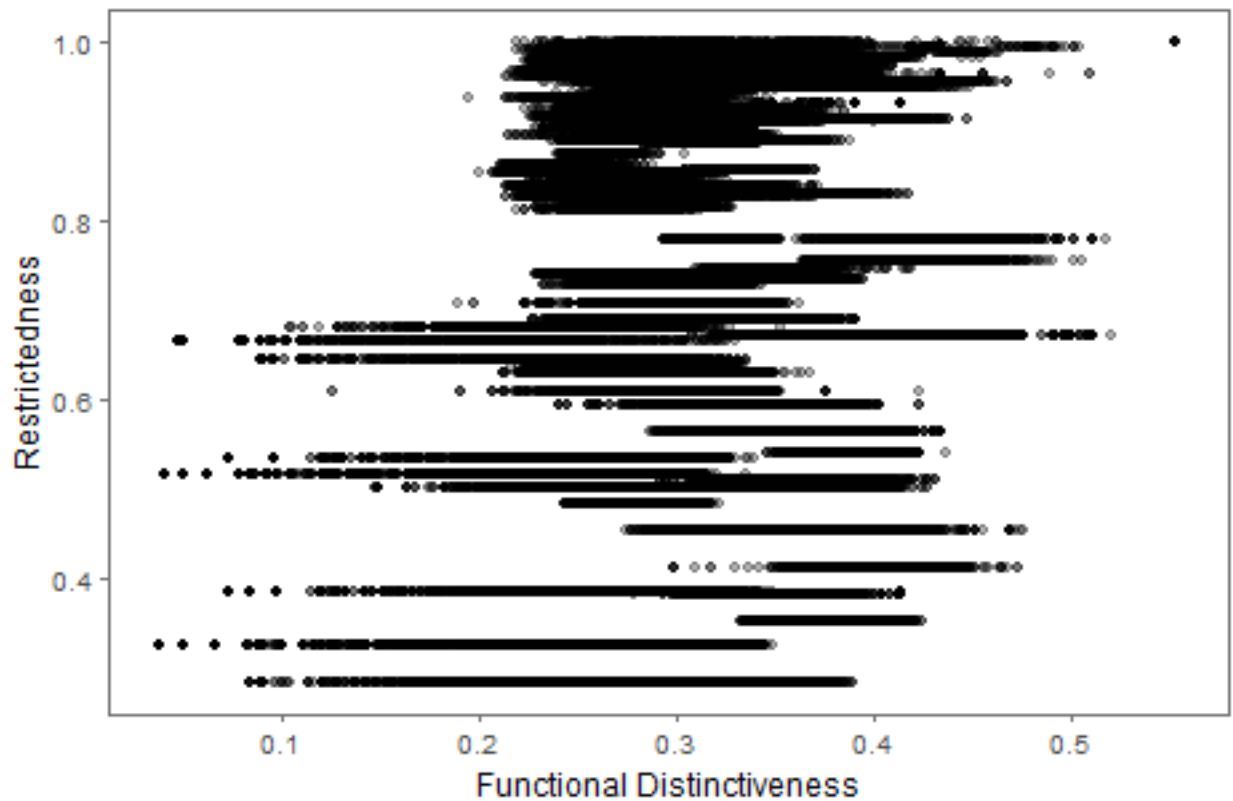
```
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```



```
##
## 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
```



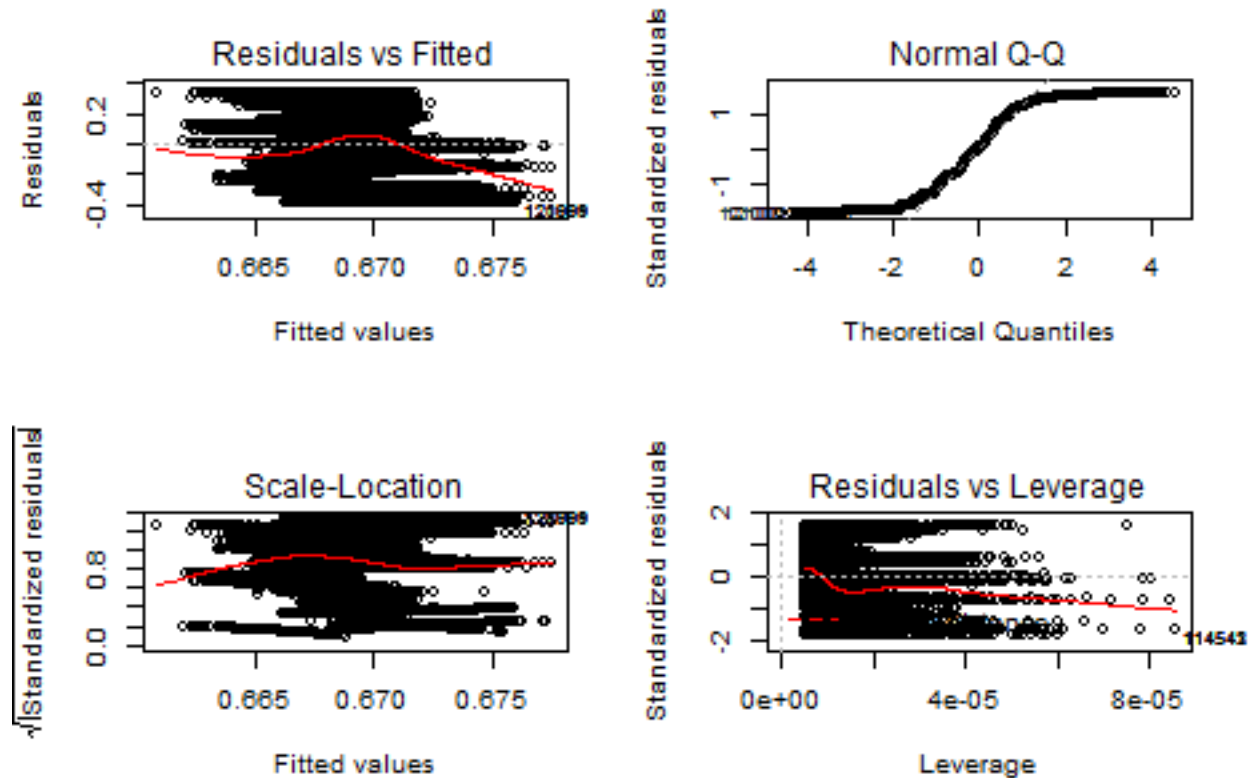
Functional Distinctiveness vs. Geographical Restrictedness



```
## 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
```

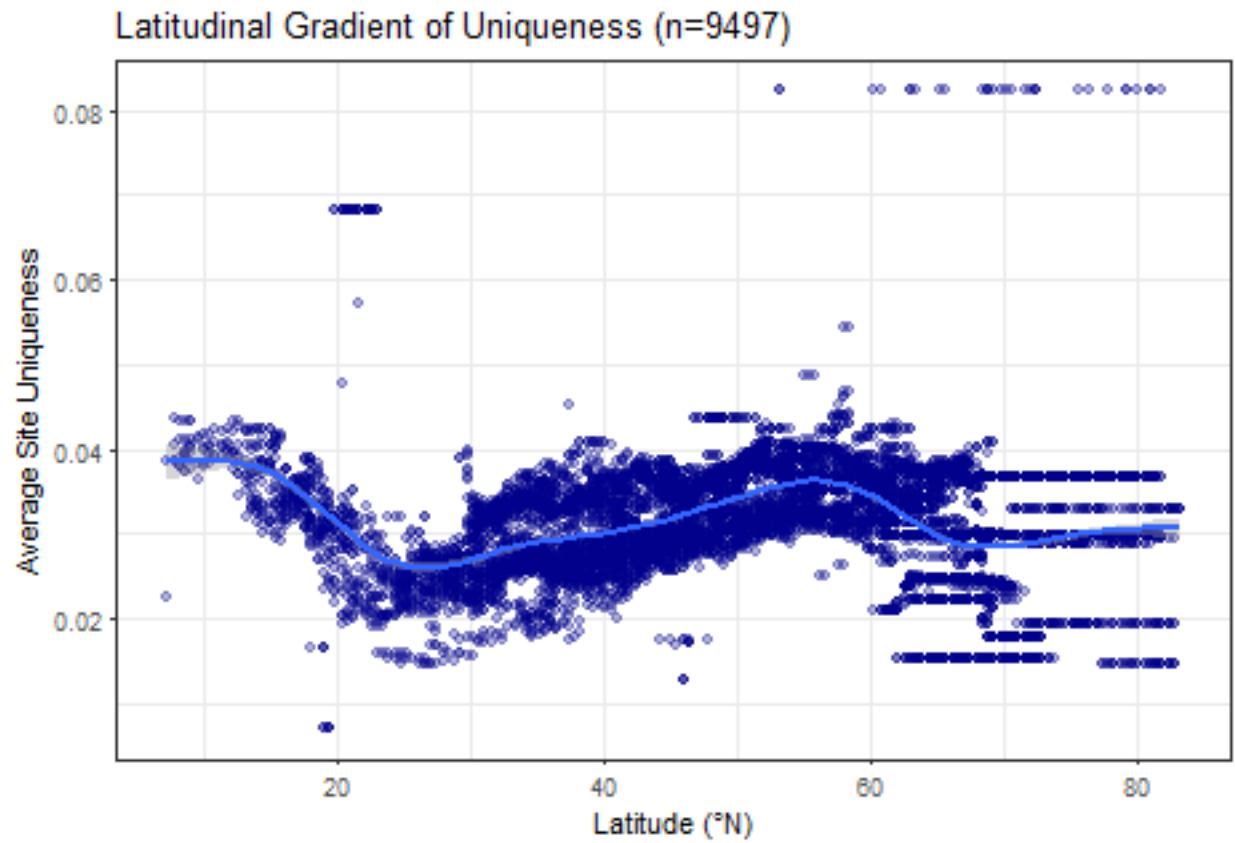
```
##
## Residual standard error: 0.2128 on 207226 degrees of freedom
## Multiple R-squared: 9.834e-05, Adjusted R-squared: 9.351e-05
## F-statistic: 20.38 on 1 and 207226 DF, p-value: 6.352e-06
```



Latitudinal Gradients

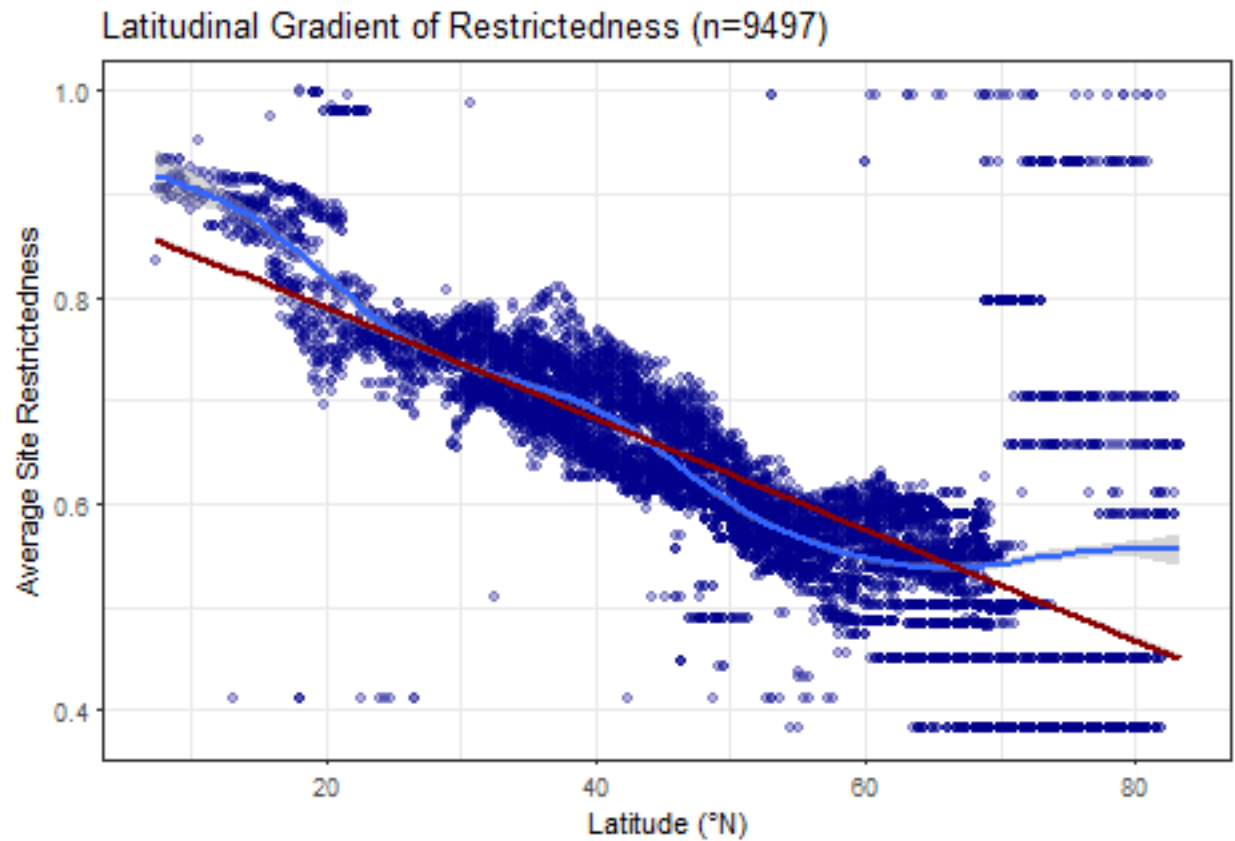
Functional Uniqueness

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



Geographical Restrictedness

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



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)

