# Example of Analyses with funrar

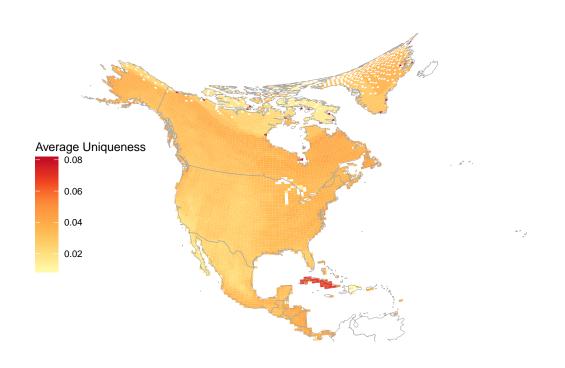
Matthias Grenié 18 janvier, 2017

With funrar you can compute Functional Rarity indices. We are using a North American Mammals datasets to show the kind of questions you can come up with.

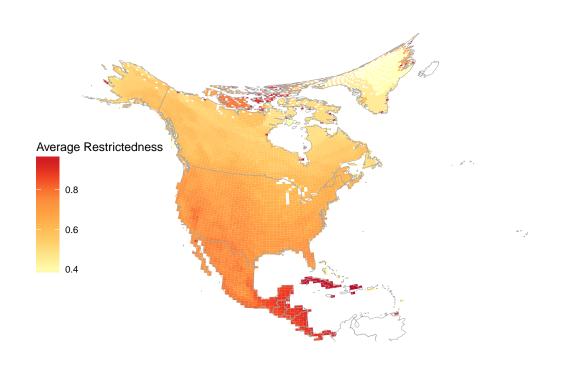
For example, you can try to map the hotspots of Regional Functional Uniqueness, i.e. the communities with highest number of functionally unique species (relatively to the whole species pool).

#### Hotspots

#### Functional Uniqueness

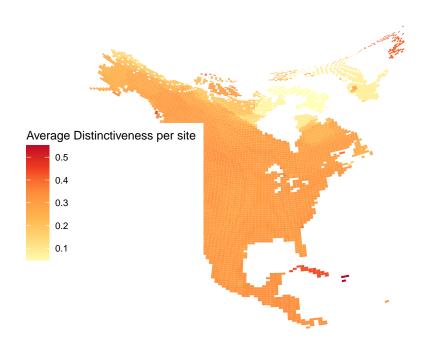


### Geographical Restrictedness



#### Functional Distinctiveness

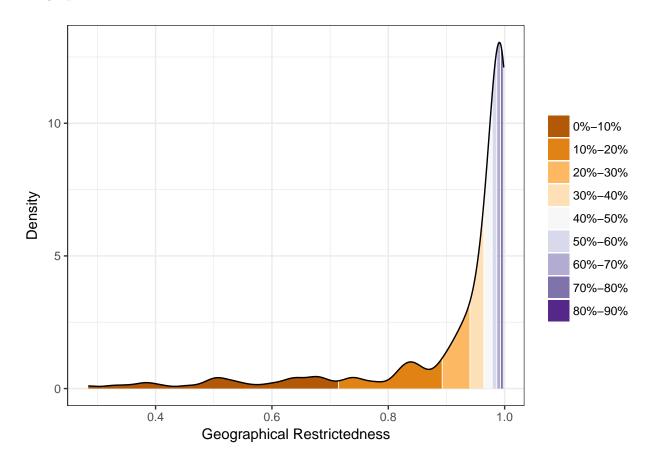
## Warning: Removed 552 rows containing non-finite values (stat\_summary2d).



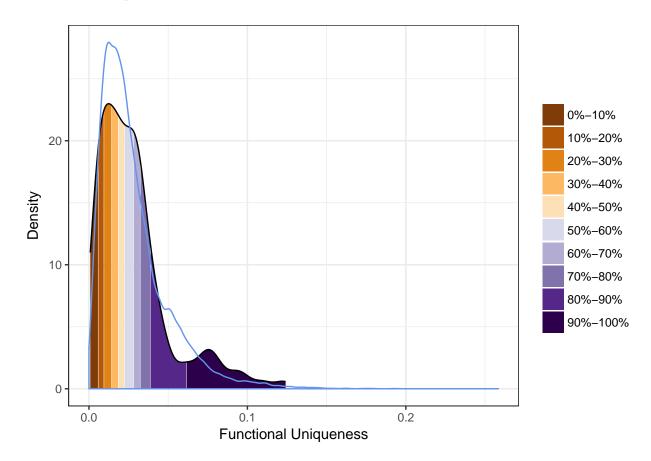
#### Total distribution of indices

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

### Geographical Restrictedness

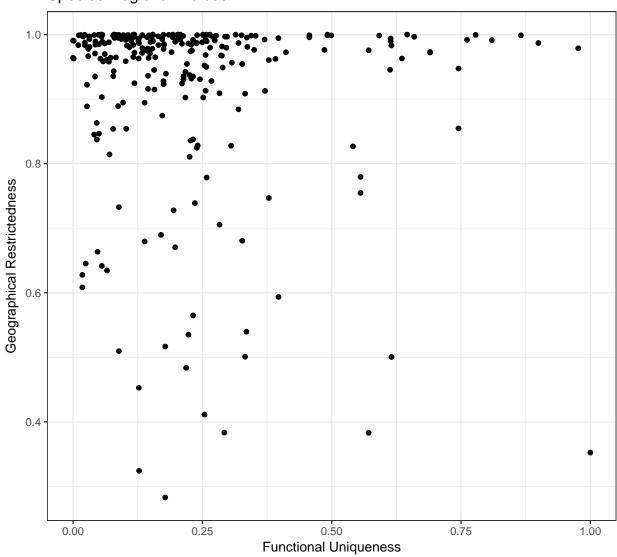


### Functional Uniqueness

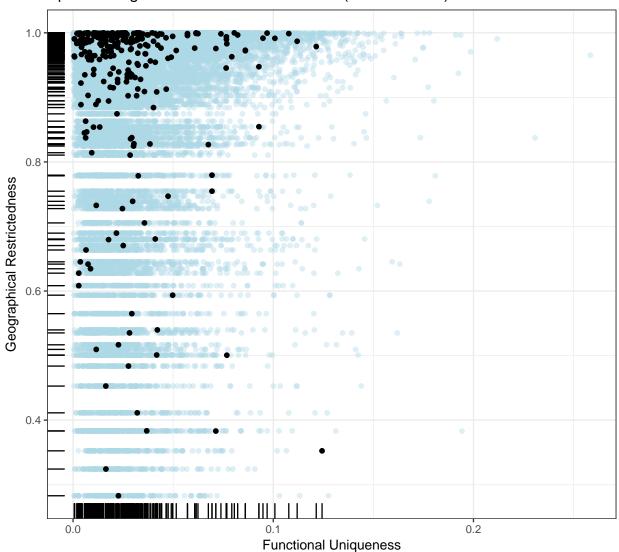


Biplot



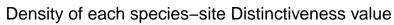


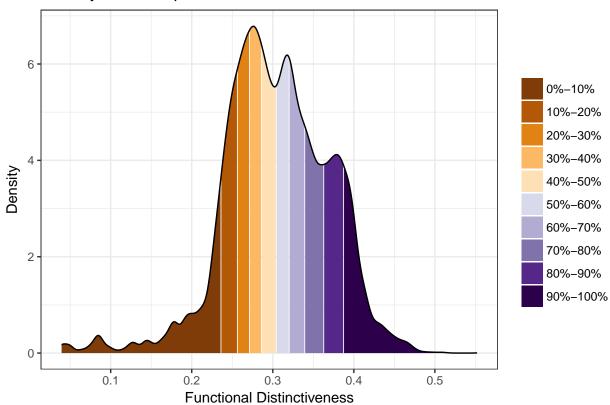
### Species Regional Indices with null model (shuffled traits)

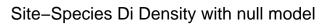


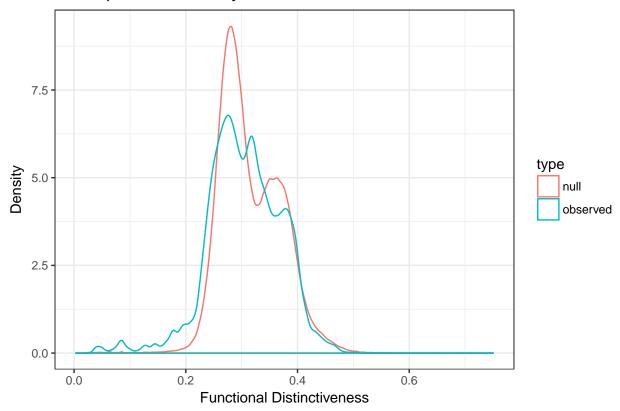
Functional Distinctiveness

For each site-species combination

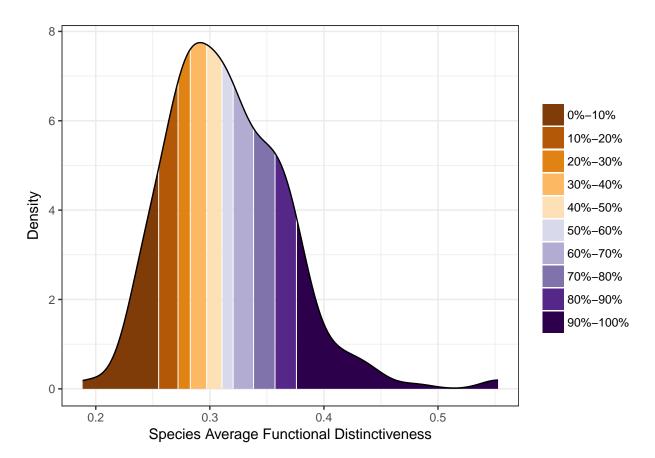






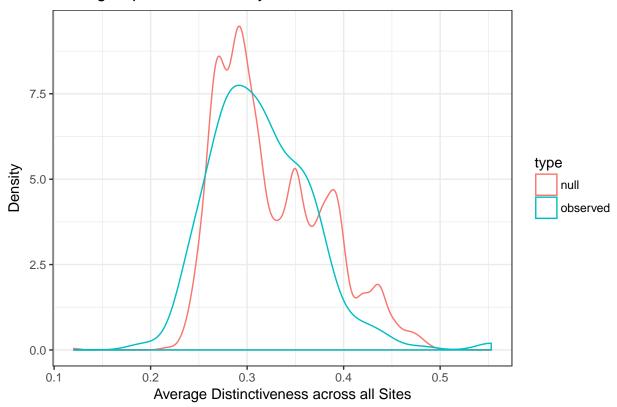


Average Distinctiveness of a species across all sites



- ## Warning: Removed 1 rows containing non-finite values (stat\_density).

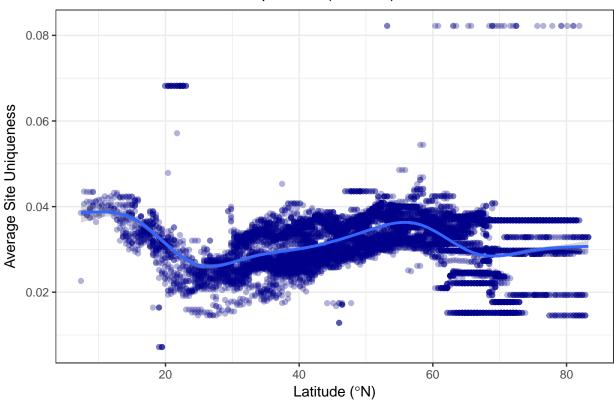
## Average Species Di Density with null model



#### Functional Uniqueness

## `geom\_smooth()` using method = 'gam'

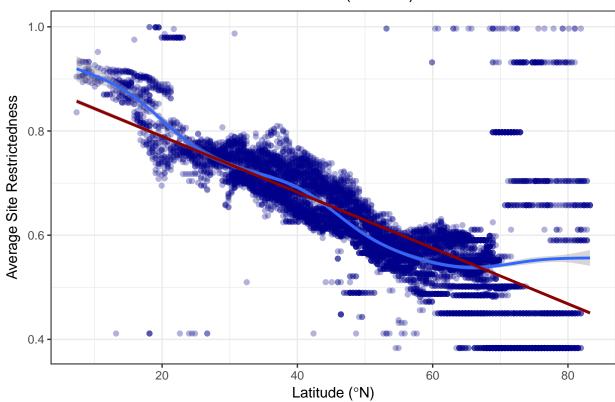
## Latitudinal Gradient of Uniqueness (n=9497)



#### ${\bf Geographical\ Restrictedness}$

## `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)

