Example of Analyses with `funrar`

Matthias Grenié

21 novembre, 2016

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

```r
library(assertr)
library(dplyr)

# Compute Functional Uniqueness per site
site_rich = rowSums(subset_pres[, -c(1:3)])
names(site_rich) = subset_pres$GlobalID

site_coords = subset_pres[, 1:3]

make_index_df = function(mammal_funrar, index = "Ui") {
    species_index = mammal_funrar[[index]][[index]]

    names(species_index) = mammal_funrar[[index]]$species

    index_name = paste0("site_", index)

    site_index = data.frame(
        given_index = (as.matrix(subset_pres[, -c(1:3)]) %*%
                                      species_index) / site_rich,
        GlobalID = site_coords$GlobalID)

    colnames(site_index)[1] = index_name

    site_index = site_index %>%
        verify(nrow(.) == nrow(subset_pres)) %>%
        filter_(paste0("!is.na(", site_index,")")) %>%
        inner_join(site_coords, by = "GlobalID")

    return(site_index)
}

site_ui = make_index_df(mammal_funrar, "Ui")
```
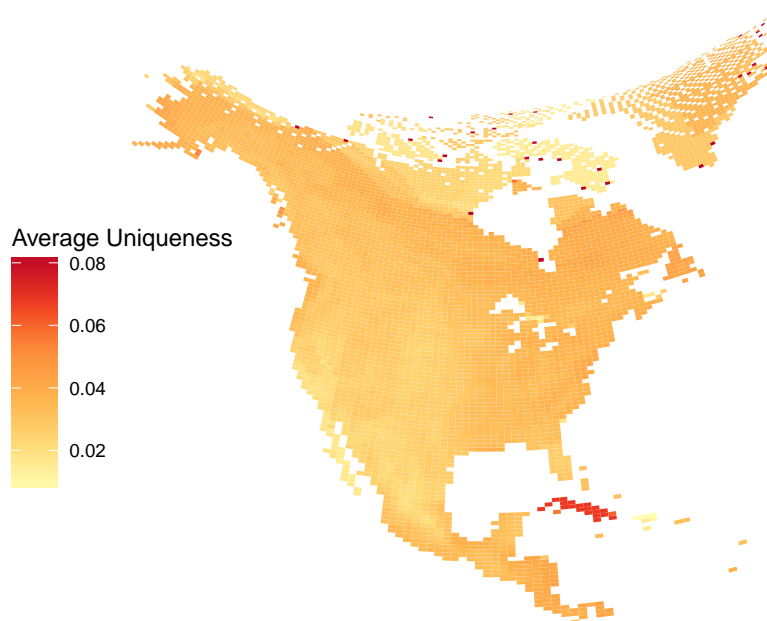
```r
ggplot(site_ui, aes(x = Longitude, y = Latitude, z = site_Ui)) +
    stat_summary_2d(bins = 150, color = NA) +
    coord_map("albers", at0 = 40, lat1 = 20, xlim = range(site_ui$Longitude),
```

```
        ylim = range(site_ui$Latitude)) +
    ggthemes::theme_map() +
    theme(legend.position = c(0.1, 0.2)) +
    labs(fill = "Average Uniqueness") +
    scale_fill_distiller(palette = "YlOrRd", direction = 1)
```

```
## Warning: `panel.margin` is deprecated. Please use `panel.spacing` property
## instead
```



Geographical Restrictedness

```
site_ri = make_index_df(mammal_funrar, "Ri")

ggplot(site_ri, aes(x = Longitude, y = Latitude, z = site_Ri)) +
    stat_summary_2d(bins = 150, color = NA) +
    coord_map("albers", at0 = 40, lat1 = 20, xlim = range(site_ri$Longitude),
              ylim = range(site_ri$Latitude)) +
    ggthemes::theme_map() +
    theme(legend.position = c(0.1, 0.2)) +
    labs(fill = "Average Restrictedness") +
    scale_fill_distiller(palette = "YlOrRd", direction = 1)
```

```
## Warning: `panel.margin` is deprecated. Please use `panel.spacing` property
## instead
```
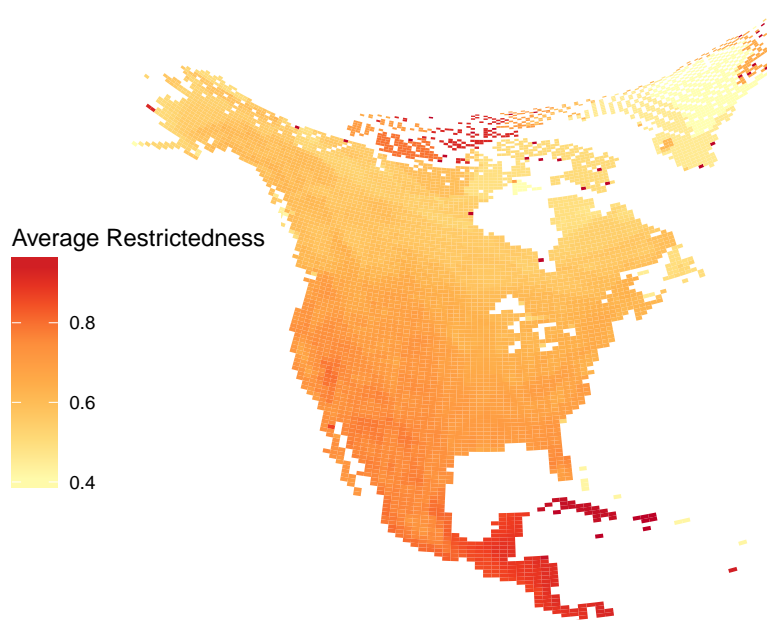
Functional Distinctiveness

```r
# Average Functional Distinctiveness
site_di = rowMeans(mammal_funrar$Di, na.rm = T) %>%
    as_data_frame() %>%
    mutate(GlobalID = rownames(.)) %>%
    rename(avg_Di = value) %>%
    inner_join(site_ri %>%
                   dplyr::select(GlobalID, Longitude, Latitude) %>%
                   mutate(GlobalID = as.character(GlobalID)),
               by = "GlobalID")

ggplot(site_di, aes(x = Longitude, y = Latitude, z = avg_Di)) +
    stat_summary_2d(bins = 150, color = NA) +
    coord_map("albers", at0 = 40, lat1 = 20, xlim = range(site_di$Longitude),
              ylim = range(site_di$Latitude)) +
    ggthemes::theme_map() +
    theme(legend.position = c(0.1, 0.2)) +
    labs(fill = "Average Distinctiveness") +
    scale_fill_distiller(palette = "YlOrRd", direction = 1)
```

```
## Warning: `panel.margin` is deprecated. Please use `panel.spacing` property
## instead
```

```
## Warning: Removed 552 rows containing non-finite values (stat_summary2d).
```
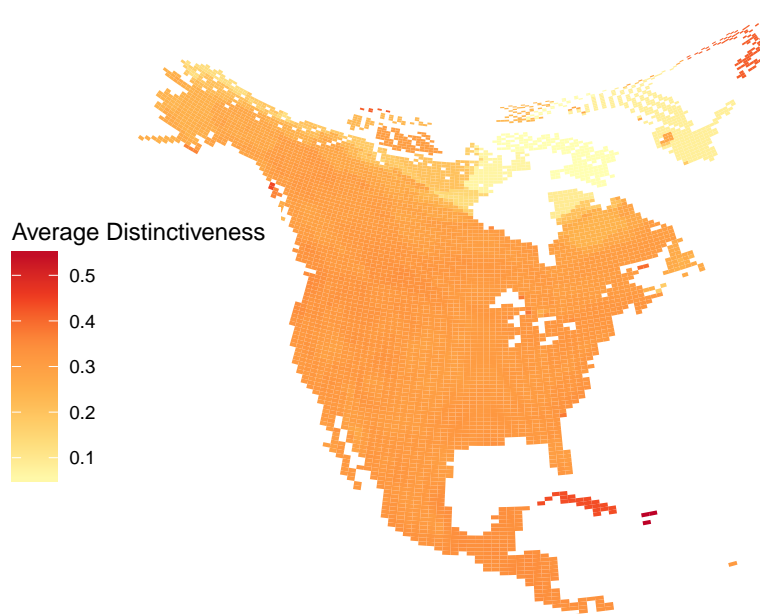
Relation between IUCN status and Functional Rarity Indices

with Geographical Restrictedness

```r
species_status = mammal_funrar$Ui %>%
    # Add IUCN status
    inner_join(subset_iucn_status %>%
                   dplyr::select(TaxonName, IUCN_status) %>%
                   mutate(species = gsub(" ", "_", TaxonName)) %>%
                   dplyr::select(-TaxonName),
               by = "species") %>%
    # Add Geographical Restrictedness
    inner_join(mammal_funrar$Ri, by = "species") %>%
    mutate(IUCN_status = ifelse(is.na(IUCN_status), "NO",
                                as.character(IUCN_status))) %>%
    mutate(std_Ui = (Ui - min(Ui))/(max(Ui) - min(Ui)))
```

```
## 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
```

```r
species_status$IUCN_status = factor(species_status$IUCN_status,
                                    levels = names(status_values))
```

```
summary(species_status)
```

```
##     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
##
```

```
ggplot(species_status, aes(x = IUCN_status, y = Ri)) +
    geom_boxplot(aes(fill = IUCN_status)) +
    scale_fill_manual(values = status_values) +
    labs(x = "IUCN Status",
         y = "Geographical Restrictedness") +
    theme(legend.position = "none")
```
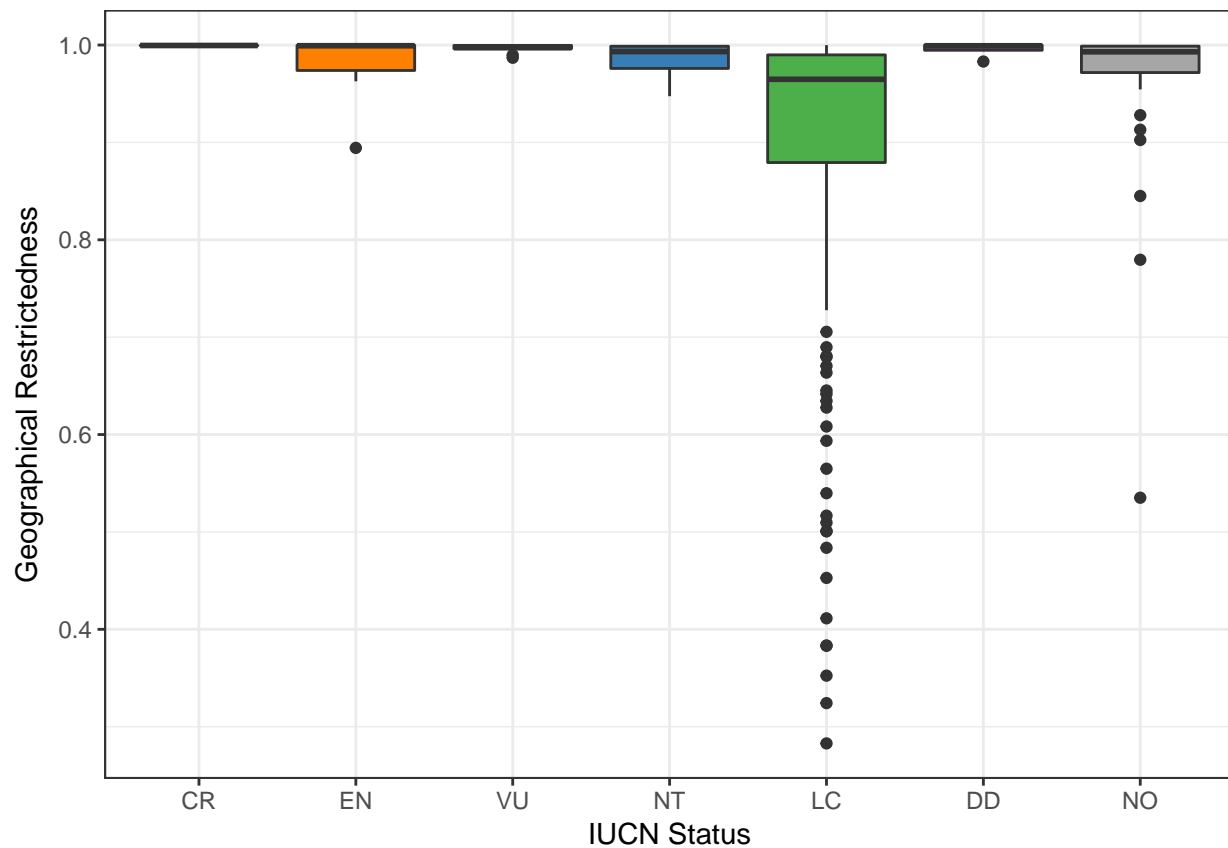
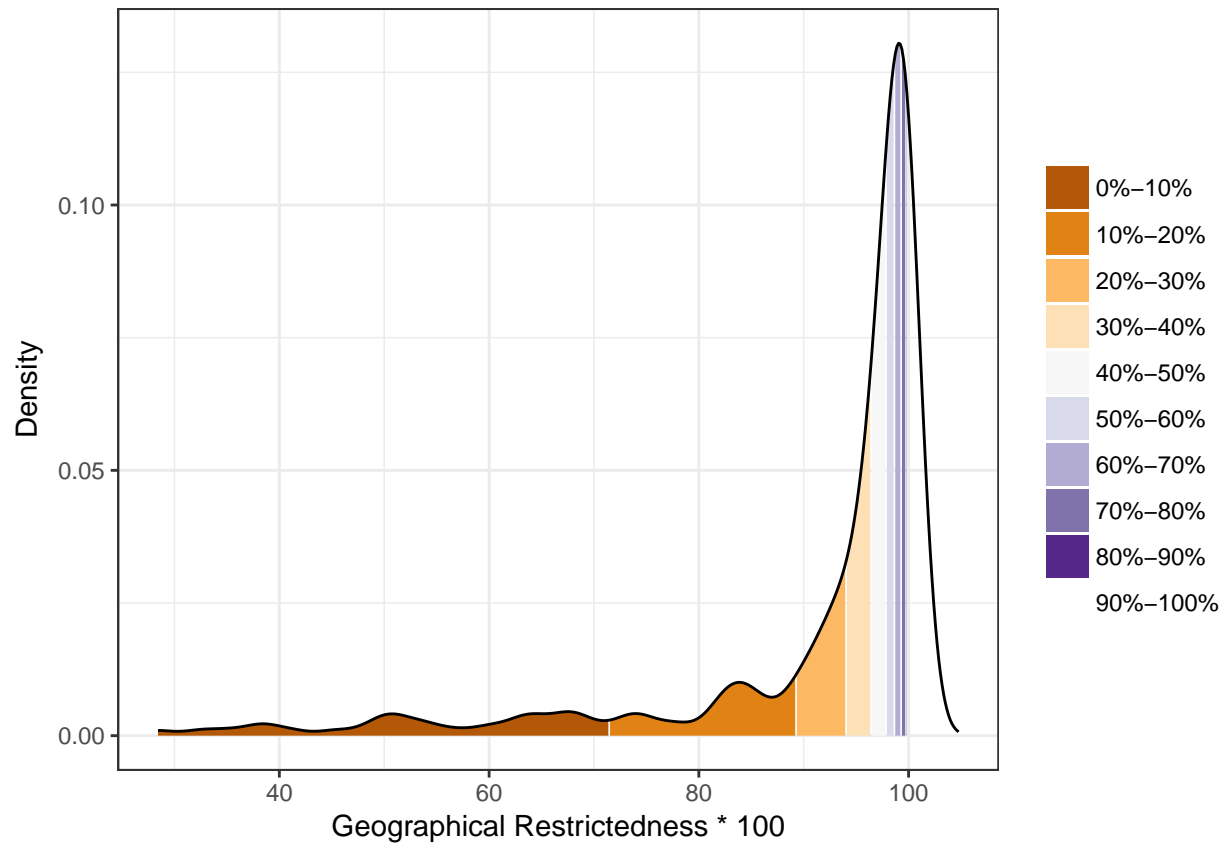**with Functional Uniqueness**

```
ggplot(species_status, aes(x = IUCN_status, y = std_Ui)) +
    geom_boxplot(aes(fill = IUCN_status), outlier.colour = NA) +
    geom_jitter(alpha = 0.5) +
    scale_fill_manual(values = status_values) +
    labs(x = "IUCN Status",
         y = "Functional Uniqueness (scaled)") +
    theme(legend.position = "none")
```
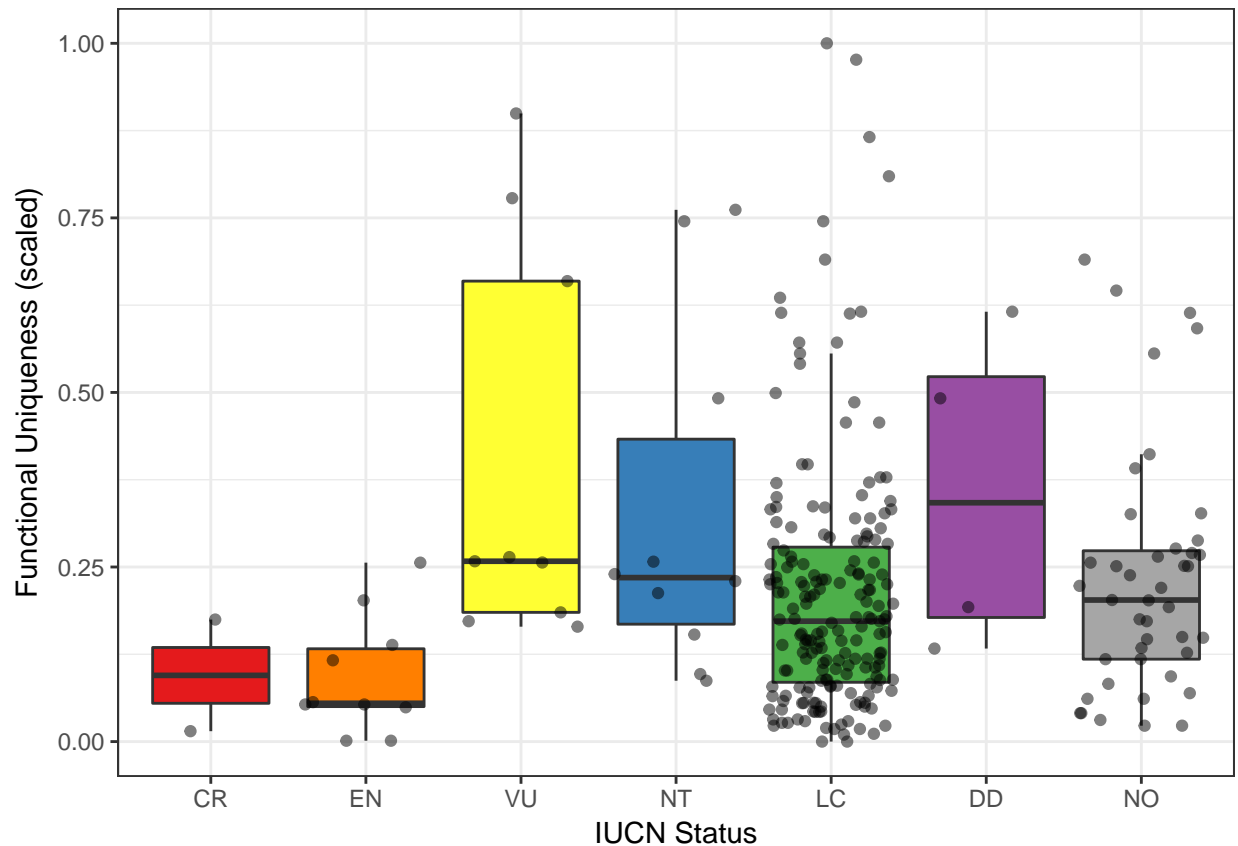

Total distribution of indices
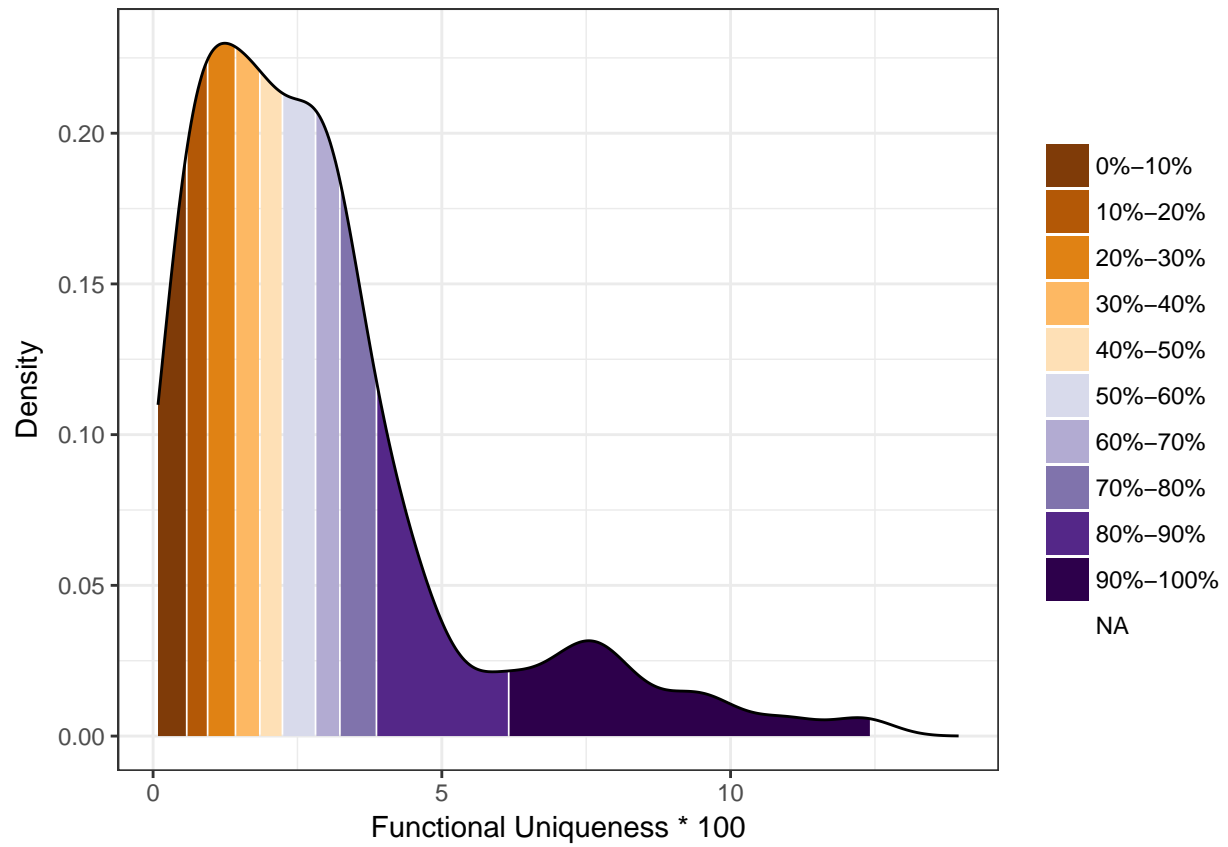
Geographical Restrictedness

```
divr::make_quantile_density(species_status$Ri*100) +
    labs(x = "Geographical Restrictedness * 100",
         y = "Density",
         fill = NULL)
```
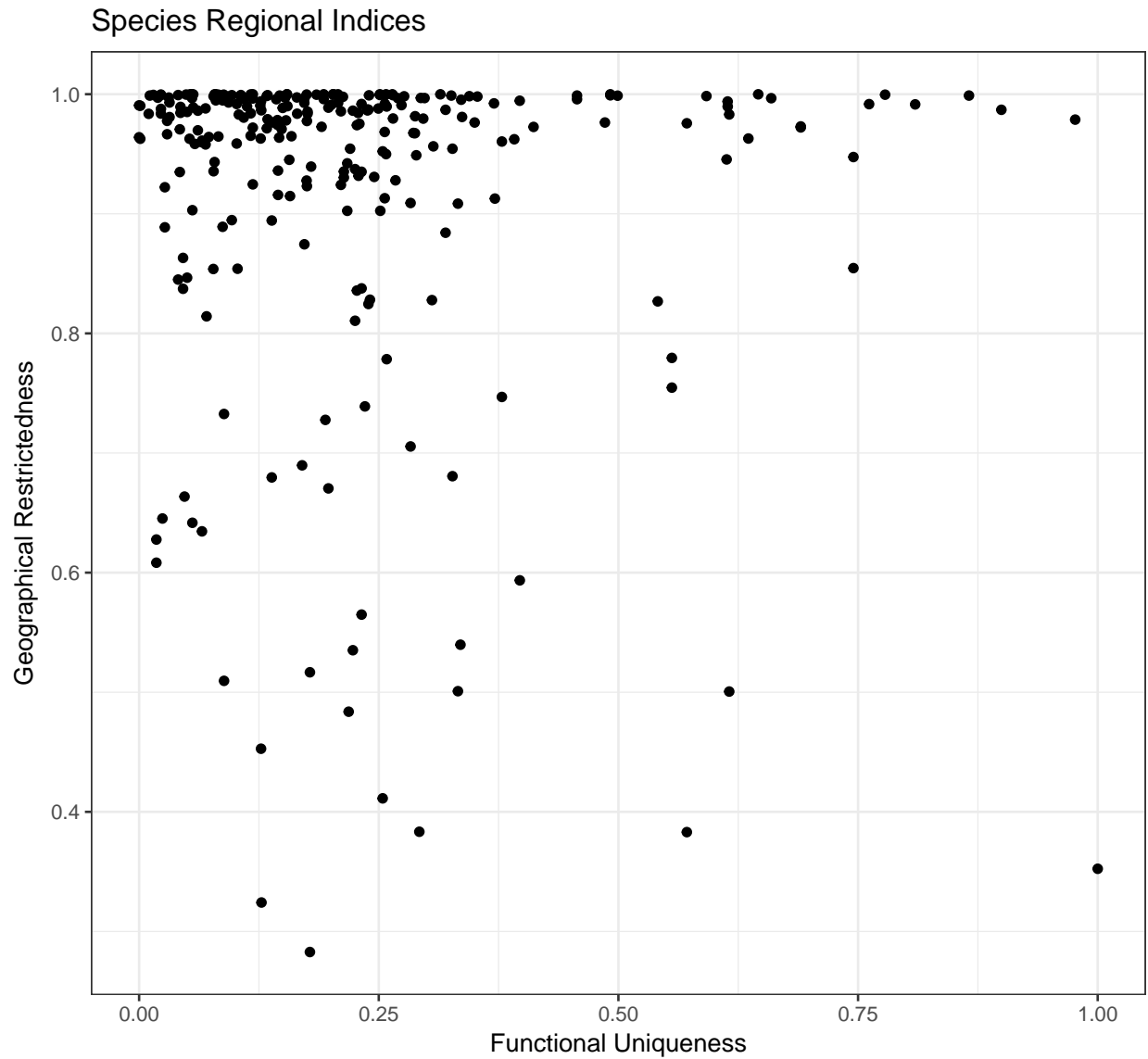
Functional Uniqueness

```r
divr::make_quantile_density(species_status$Ui*100) +
    labs(x = "Functional Uniqueness * 100",
        y = "Density",
        fill = NULL)
```

Biplot

```
ggplot(species_status, aes(x = std_Ui, y = Ri)) +
    geom_point() +
    labs(x = "Functional Uniqueness",
         y = "Geographical Restrictedness",
         title = "Species Regional Indices")
```

Species Regional Indices


```r
ggplot(species_status, aes(x = std_Ui, y = Ri, color = IUCN_status)) +
    geom_point(size = 1.5, alpha = 0.8) +
    scale_color_manual(values = status_values) +
    labs(x = "Functional Uniqueness",
        y = "Geographical Restrictedness",
        title = "Species Regional Indices")
```

Species Regional Indices