Example of Analyses with funrar

Matthias Grenié 06 décembre, 2016

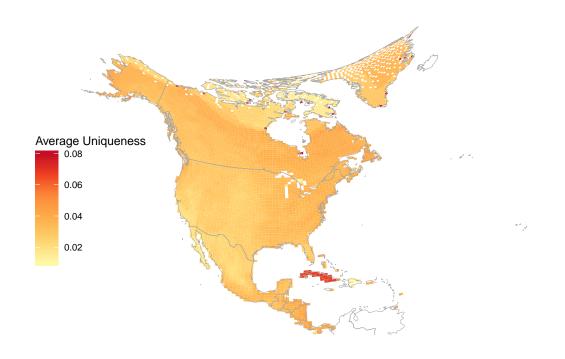
With funrar you can compute Functional Rarity indices. We are using a North American Mammals datasets to show the kind of questions you can come up with.

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).

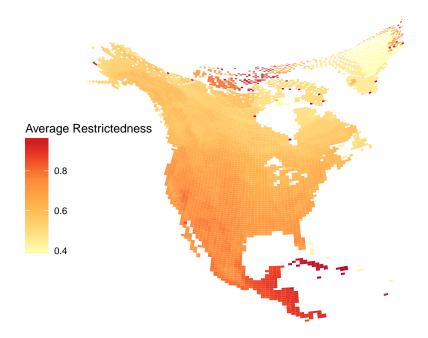
Hotspots

Functional Uniqueness

```
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$GlobalID)
    colnames(site_index)[1] = index_name
    site_index = site_index %>%
        verify(nrow(.) == nrow(subset_pres)) %>%
        filter_(paste0("!is.na(", site_index,")")) %>%
        inner_join(site_coords, by = "GlobalID")
   return(site_index)
}
site_ui = make_index_df(mammal_funrar, "Ui")
ggplot(site_ui, aes(x = Longitude, y = Latitude, z = site_Ui)) +
    stat_summary_2d(bins = 150, color = NA) +
    coord_map("albers", at0 = 40, lat1 = 20, xlim = range(site_ui$Longitude),
```



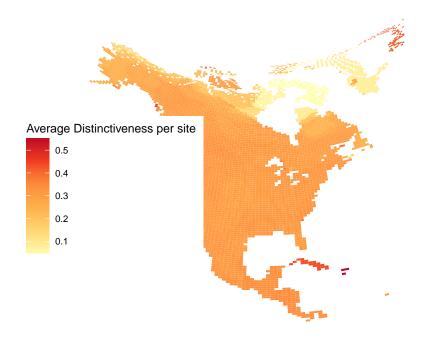
Geographical Restrictedness



Functional Distinctiveness

```
# Average Functional Distinctiveness
site_di = rowMeans(as.matrix(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 per site") +
    scale_fill_distiller(palette = "YlOrRd", direction = 1)
```

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



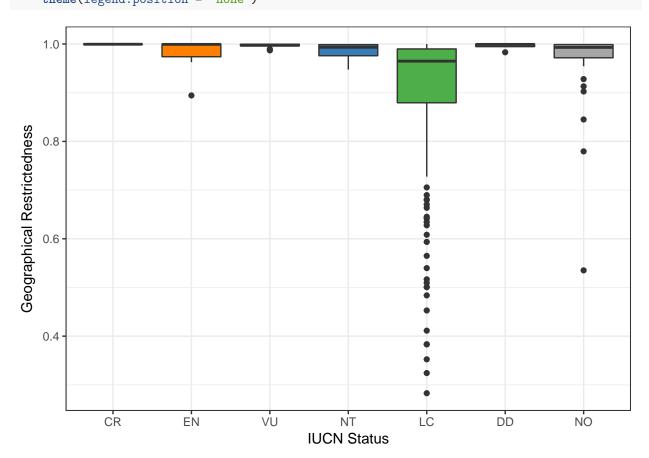
Relation between IUCN status and Functional Rarity Indices

with Geographical Restrictedness

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

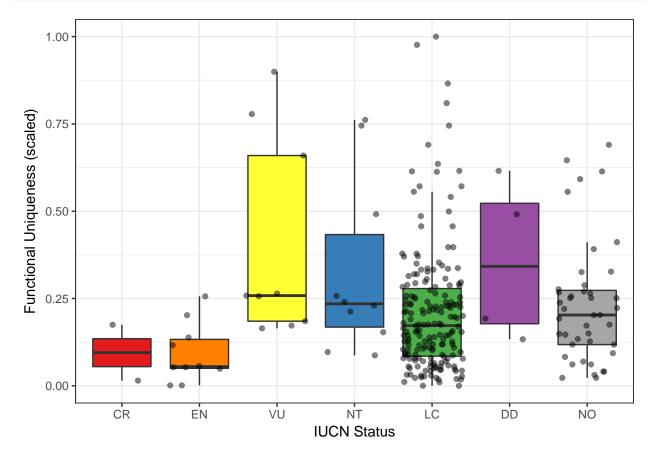
summary(species_status)

```
IUCN_status
##
      species
                              Ui
                                                               Ri
                               :0.0006121
                                            CR: 2
                                                                :0.2828
##
    Length: 265
                        Min.
                                                         Min.
    Class :character
                        1st Qu.:0.0115721
                                            EN: 10
                                                         1st Qu.:0.9242
    Mode :character
                                                         Median :0.9787
##
                        Median :0.0223622
                                            VU: 9
##
                        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
##
           :1.00000
##
    Max.
##
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")
```



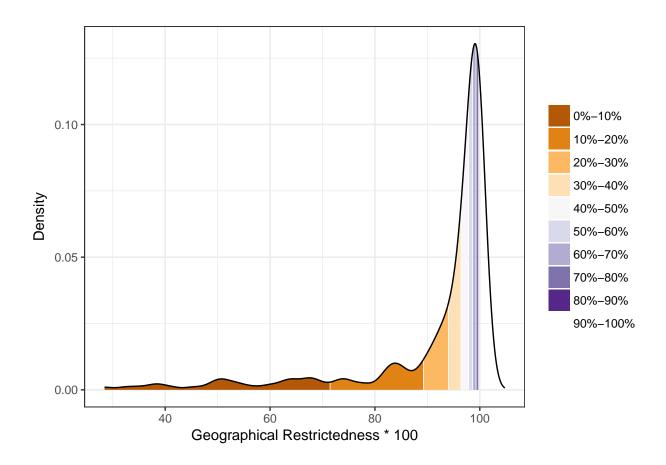
with Functional Uniqueness

```
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")
```



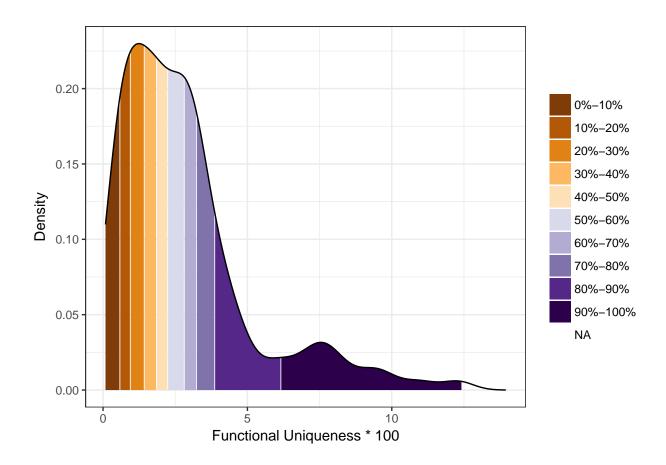
Total distribution of indices

Geographical Restrictedness



Functional Uniqueness

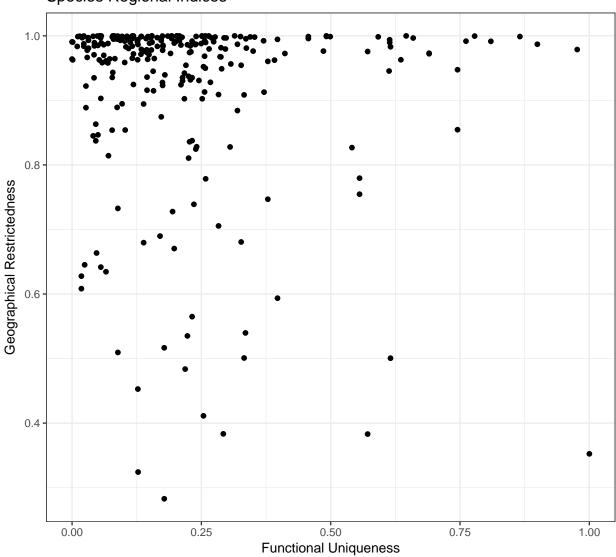
```
divr::make_quantile_density(species_status$Ui*100) +
    labs(x = "Functional Uniqueness * 100",
        y = "Density",
        fill = NULL)
```



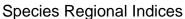
Biplot

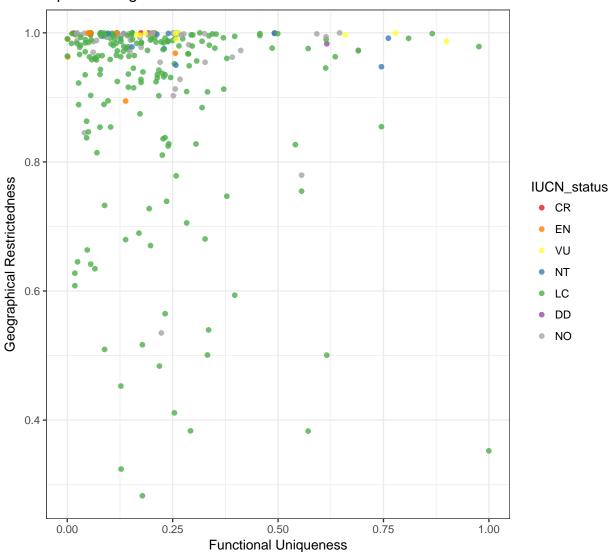
```
ggplot(species_status, aes(x = std_Ui, y = Ri)) +
    geom_point() +
    labs(x = "Functional Uniqueness",
        y = "Geographical Restrictedness",
        title = "Species Regional Indices")
```

Species Regional Indices

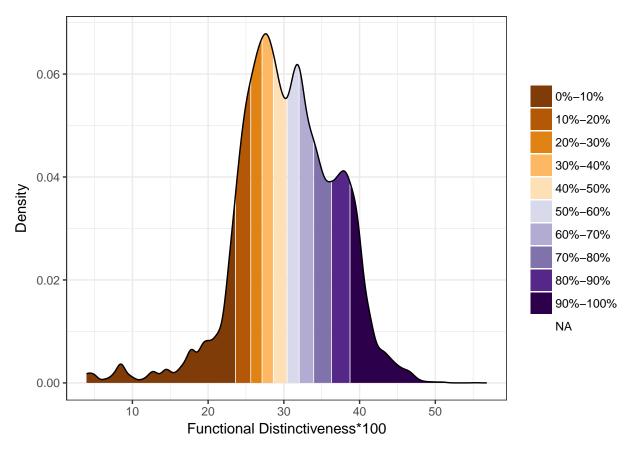


```
ggplot(species_status, aes(x = std_Ui, y = Ri, color = IUCN_status)) +
    geom_point(size = 1.5, alpha = 0.8) +
    scale_color_manual(values = status_values) +
    labs(x = "Functional Uniqueness",
        y = "Geographical Restrictedness",
        title = "Species Regional Indices")
```





Functional Distinctiveness



```
divr::make_quantile_density(colMeans(mammal_di, na.rm = TRUE) *100) +
    labs(x = "Species Average Functional Distinctiveness*100",
        y = "Density",
        fill = NULL)
```

