Example of Analyses with `funrar`

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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).

Functional Uniqueness Hotspots

```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]

species_ui = mammal_funrar$Ui$Ui

names(species_ui) = mammal_funrar$Ui$species

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

site_ui = site_ui %>%
    verify(nrow(.) == nrow(subset_pres)) %>%
    filter(!is.na(site_Ui)) %>%
    inner_join(site_coords, by = "GlobalID")
```
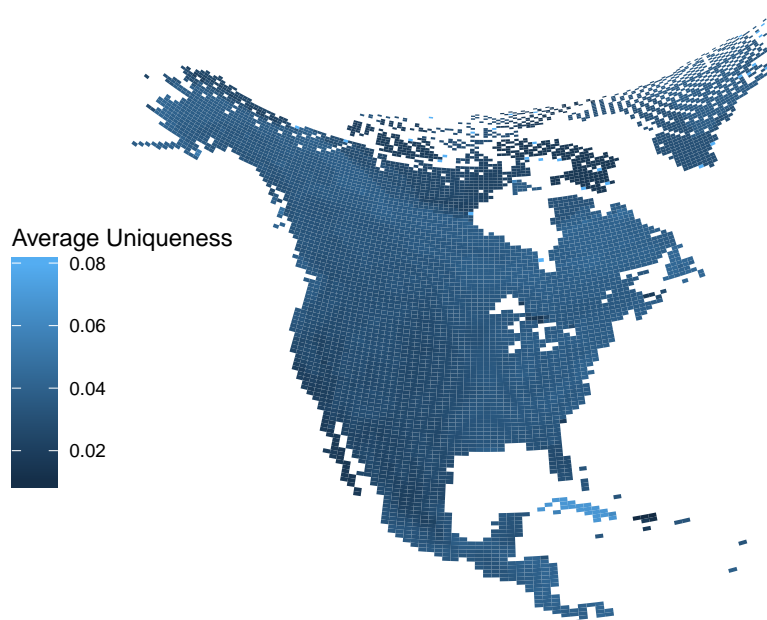
```r
ggplot(site_ui, aes(x = Longitude, y = Latitude, z = site_Ui)) +
    stat_summary_2d(bins = 150, color = NA) +
    coord_map("albers", at0 = 40, lat1 = 20, xlim = range(site_ui$Longitude),
              ylim = range(site_ui$Latitude)) +
    ggthemes::theme_map() +
    theme(legend.position = c(0.1, 0.2)) +
    labs(fill = "Average Uniqueness")
```

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

Average Uniqueness

Geographical Restrictedness Hotspots

Relation between IUCN status and Functional Rarity Indices

with Geographical Restrictedness

```
species_status = mammal_funrar$Ui %>%
    inner_join(subset_iucn_status %>%
                   dplyr::select(TaxonName, IUCN_status) %>%
                   mutate(species = gsub(" ", "_", TaxonName)) %>%
                   dplyr::select(-TaxonName),
               by = "species") %>%
    inner_join(mammal_funrar$Ri, by = "species") %>%
    mutate(IUCN_status = ifelse(is.na(IUCN_status), "NO",
                                as.character(IUCN_status)))
```

```
## 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))
```

```r
ggplot(species_status, aes(x = IUCN_status, y = Ri)) +
    geom_boxplot(aes(fill = IUCN_status)) +
    scale_fill_manual(values = status_values)
```
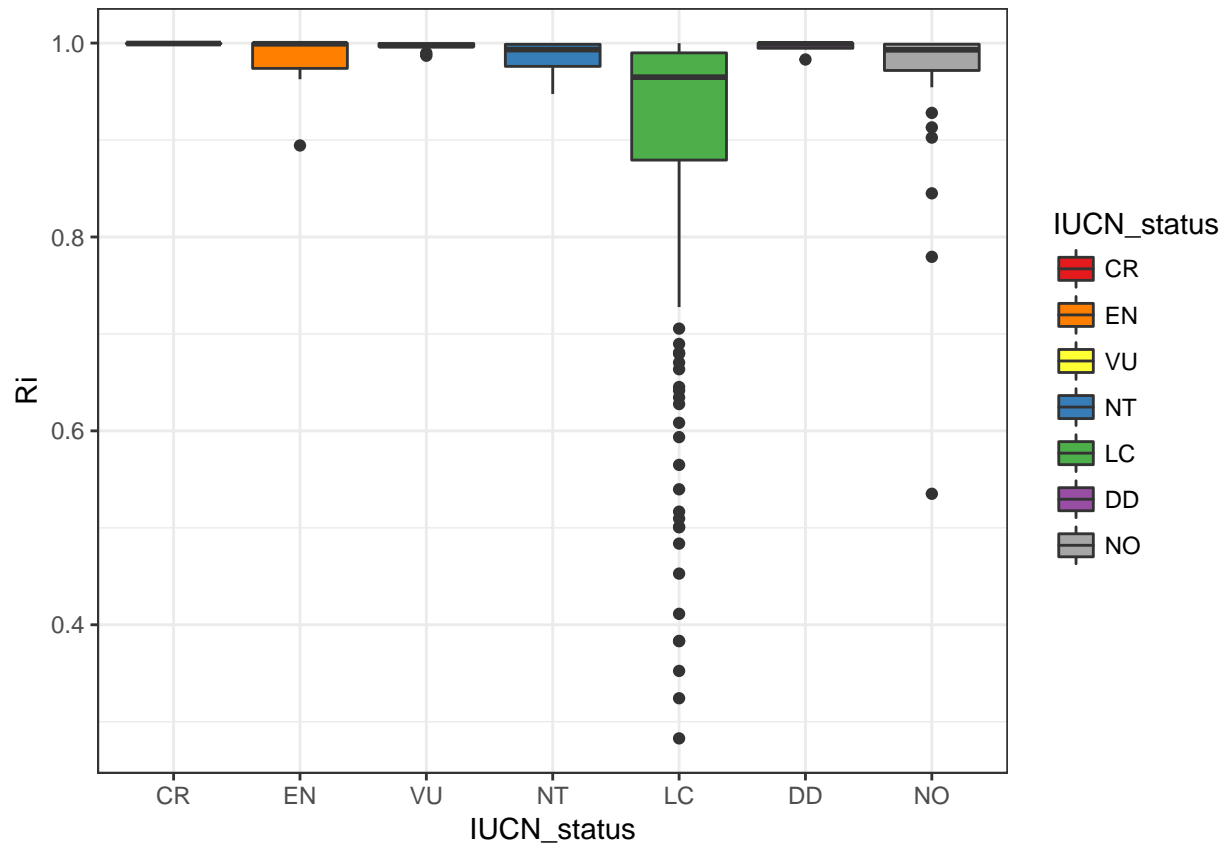

with Functional Uniqueness

```r
ggplot(species_status, aes(x = IUCN_status, y = Ui)) +
    geom_boxplot(aes(fill = IUCN_status)) +
    scale_fill_manual(values = status_values)
```