

Arthropoda species assessment results

31 January, 2024

Contents

Load the data	1
Protected Areas	2
PACA - Preliminary Automated Conservation Assessment	4
IUCN categories per Order:	6
Categories of Coleoptera families	10
Hotspots and threatspots	12
Overlap of hotspots and threatspots with protected areas.	14
Wildlife refuges	17
Order locations overlap	19
EOO and AOO distributions	20
EOO and AOO relation	20
EOO area distribution	25
AOO area distribution	27
Digital Elevation Maps	31
Habitats	34
Summary	35

Load the data

```
library(tidyverse)
library(ggnewscale)
library(sf)
library(knitr)
library(kableExtra)
source("functions.R")

g_base <- g_base()

supplementary_material_1 <- readxl::read_excel("../data/Supplementary-material-1.xlsx", sheet="arthropods")

arthropods_occurrences <- st_as_sf(supplementary_material_1,
                                      coords=c("decimalLongitude", "decimalLatitude"),
                                      remove=F,
                                      crs="WGS84")

locations_shp <- arthropods_occurrences |>
```

```

dplyr::select(-bibliographicCitation) |>
  distinct()
locations_spatial <- sf::st_read("../results/locations_spatial/locations_spatial.shp")
locations_grid <- sf::st_read("../results/locations_grid/locations_grid.shp")
crete_shp <- sf::st_read("../data/crete/crete.shp")
endemic_species <- read_delim("../results/endemic_species_assessment.tsv", delim="\t")
clc_crete_shp <- st_read("../data/clc_crete_shp/clc_crete_shp.shp")
natura_crete <- sf::st_read("../data/natura2000/natura2000_crete.shp")
wdpa_crete <- sf::st_read("../data/wdpa_crete/wdpa_crete.shp")
natura_crete_land <- st_intersection(natura_crete, crete_shp)

# split the SPA SCI

natura_crete_land_sci <- natura_crete_land |> filter(SITETYPE=="B")

wildlife <- wdpa_crete |> filter(DESIG_ENG=="Wildlife Refugee")

## Hotspots and threatspots
endemic_hotspots <- st_read("../results/endemic_hotspots/endemic_hotspots.shp")
threatspots <- st_read("../results/threatspots/threatspots.shp")

```

There are 4924 occurrences of 343 species that belong to 11 orders.

The unique locations are:

```

st_coordinates(locations_shp) |> as.data.frame() |> distinct() |> nrow()

## [1] 1539

```

Protected Areas

```

wdpa_crete$area <- units::set_units(st_area(wdpa_crete), km^2)

wdpa_crete_all <- data.frame(name="total protected",
                                area=sum(wdpa_crete$area))

wdpa_crete_combine <- st_union(wdpa_crete) %>%
  st_make_valid() %>%
  st_as_sf() %>%
  filter(st_geometry_type(.) %in% c("MULTIPOLYGON"))

wdpa_crete_combine_area <- data.frame(name="total protected (no overlap)",
                                         area=sum(units::set_units(st_area(wdpa_crete_combine), km^2)))
crete_area <- data.frame(name="crete",
                           area=sum(units::set_units(st_area(crete_shp), km^2)))

protected_area <- wdpa_crete |>
  group_by(DESIG_ENG) |>
  summarise(area=sum(area)) |>
  st_drop_geometry() |>
  dplyr::rename("name"="DESIG_ENG") |>
  bind_rows(crete_area,wdpa_crete_all, wdpa_crete_combine_area) |>
  arrange(area) |>
  mutate(area=round(area,2))

```

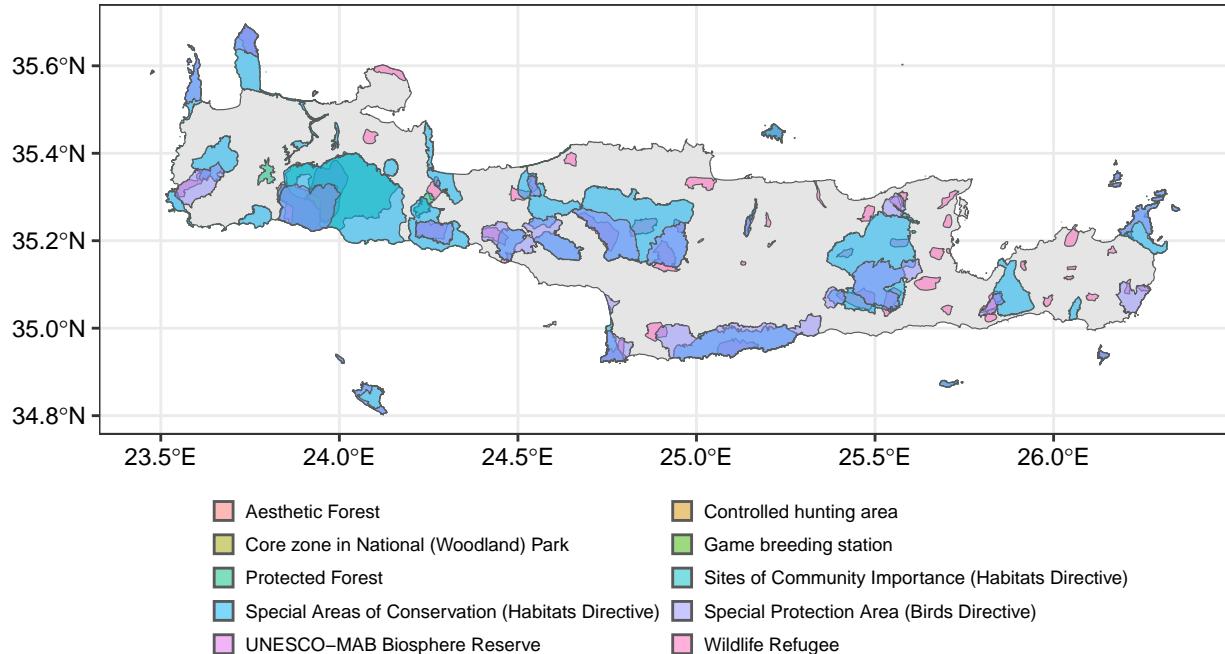
```

knitr::kable(protected_area, "latex")

\begin{table border="1">
| name | area |
| --- | --- |
| Aesthetic Forest | 0.17 [km2] |
| Sites of Community Importance (Habitats Directive) | 0.34 [km2] |
| Game breeding station | 1.02 [km2] |
| Controlled hunting area | 11.59 [km2] |
| Core zone in National (Woodland) Park | 47.56 [km2] |
| UNESCO-MAB Biosphere Reserve | 88.65 [km2] |
| Protected Forest | 417.74 [km2] |
| Wildlife Refugee | 610.70 [km2] |
| Special Protection Area (Birds Directive) | 1261.78 [km2] |
| Special Areas of Conservation (Habitats Directive) | 2371.42 [km2] |
| total protected (no overlap) | 2900.59 [km2] |
| total protected | 4810.96 [km2] |
| crete | 8346.55 [km2] |


g_wdpa


```



PACA - Preliminary Automated Conservation Assessment

The PACA categories results. LT = CR + EN, PT = VU, PNT = NT and LC.

```
iucn_color <- setNames(c("#FD0200", "#FEFE08", "#FFA706", "#008100"),
                        c("CR", "VU", "EN", "NT/LC"))
```

```
paca_color <- setNames(c("brown1", "#FEFE08", "forestgreen"),
                        c("PT", "LT", "LNT"))
```

```
endemic_species_p <- endemic_species |>
  group_by(paca) |>
  summarise(n_species=n(), .groups="drop") |>
#  rename("category"="paca") |>
  mutate(method="paca") |>
  mutate(proportion = round(n_species/sum(n_species), digits=2))
```

```
endemic_species_i <- endemic_species |>
  group_by(iucn) |>
  summarise(n_species=n(), .groups="drop") |>
#  rename("category"="iucn") |>
  mutate(method = "iucn") |>
  mutate(proportion = round(n_species/sum(n_species), digits=2))
#/>
#  bind_rows(endemic_species_p)
```

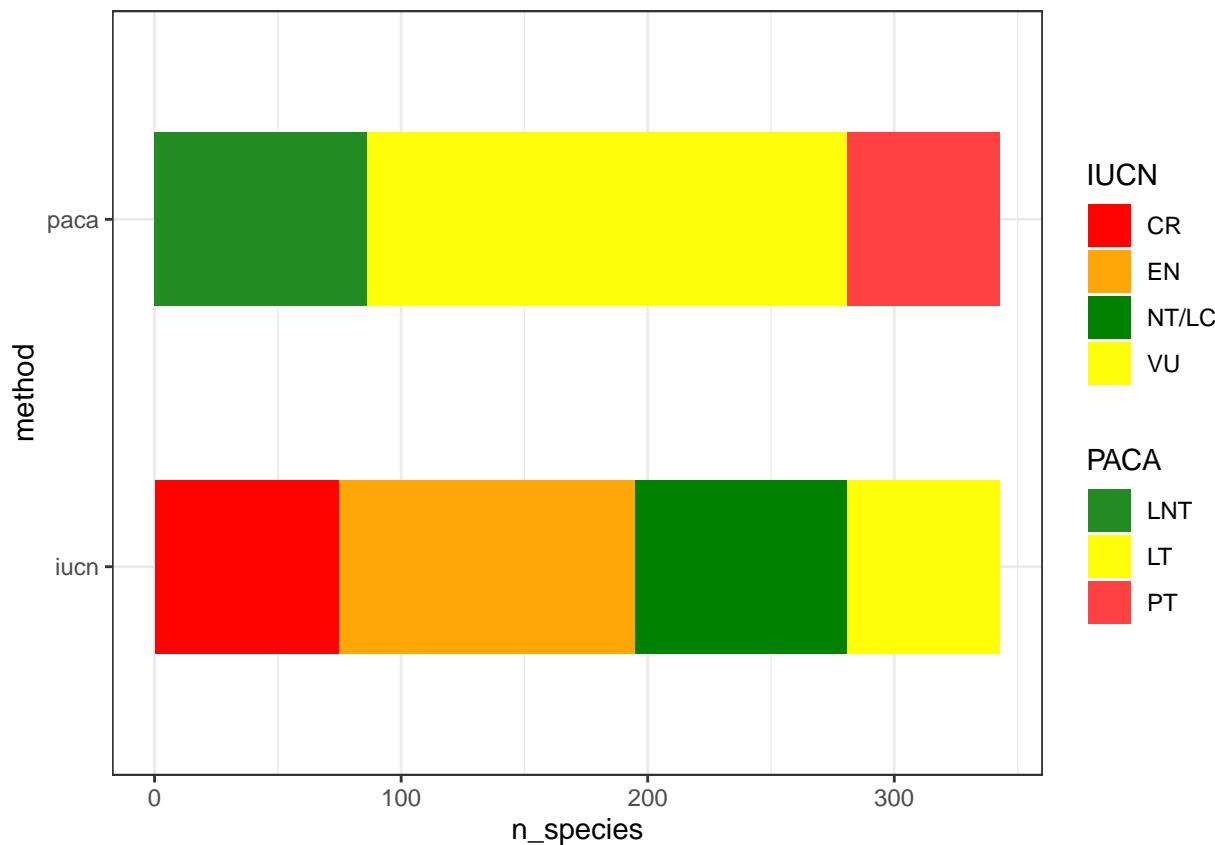
```
g_paca <- ggplot() +
  geom_col(data=endemic_species_i,
            aes(x=n_species, y=method, fill=iucn),
            width=0.5,
            position = position_stack(reverse = TRUE)) +
```

```

scale_fill_manual("IUCN", values=iucn_color) +
new_scale('fill') +
geom_col(data=endemic_species_p,
  aes(x=n_species,y=method, fill=paca),
  width=0.5,
  position = position_stack(reverse = TRUE)) +
scale_fill_manual("PACA", values=paca_color) +
#   guides(fill=guide_legend(override.aes = list(fill=c("PACA", "IUCN"),order=2))) +
theme_bw()

ggsave("../plots/bar_chart_paca.png",
  g_paca,
  width = 20,
  height = 15,
  units='cm',
  device="png")
g_paca

```



```

g_paca_p <- ggplot() +
  geom_col(data=endemic_species_i,
    aes(x=proportion,y=method, fill=iucn),
    width=0.5,
    position = position_stack(reverse = FALSE)) +
  geom_text(data=endemic_species_i, aes(x=proportion,y=method, fill=iucn,
    label = paste(proportion, " (", n_species, ")", sep="")),
    position = position_stack(vjust = .5)) +
  scale_fill_manual("IUCN", values=iucn_color) +

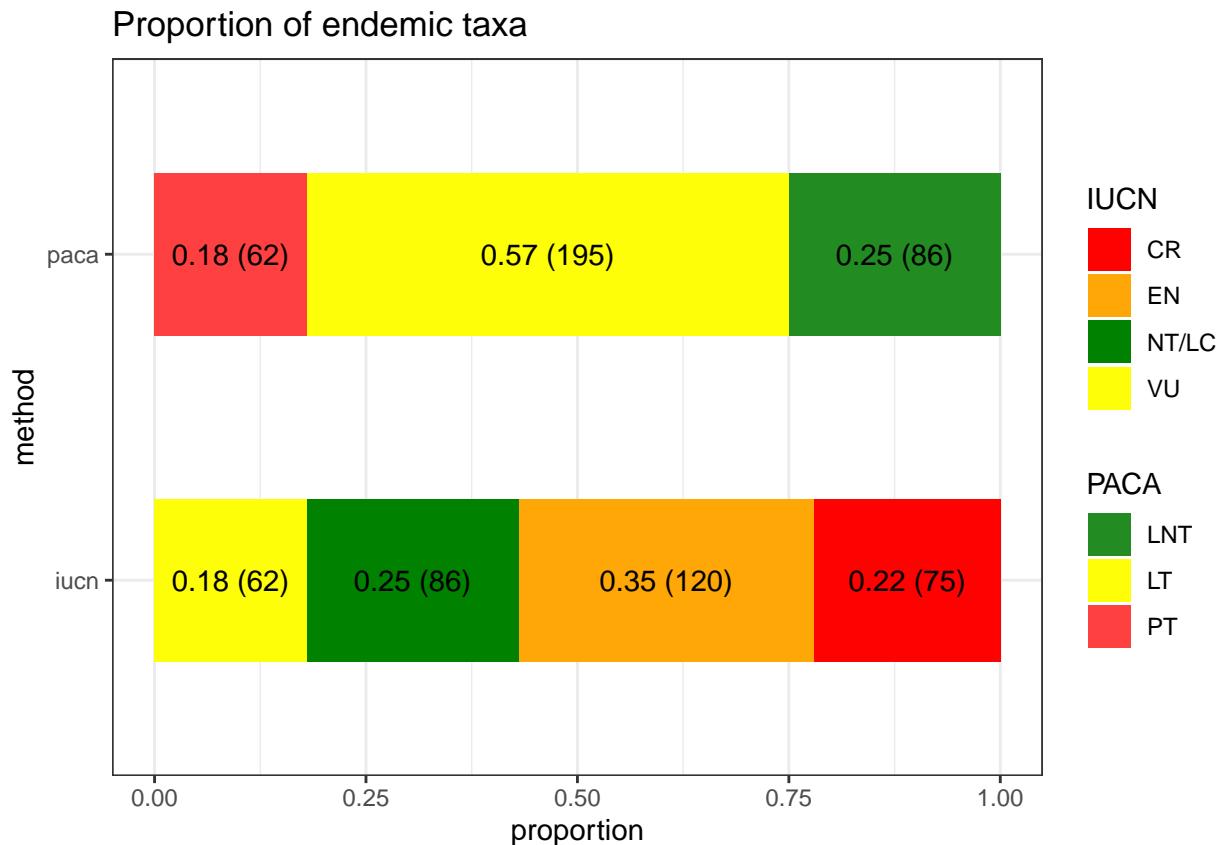
```

```

new_scale('fill') +
geom_col(data=endemic_species_p,
  aes(x=proportion,y=method, fill=paca),
  width=0.5,
  position = position_stack(reverse = FALSE)) +
geom_text(data=endemic_species_p, aes(x=proportion,y=method, fill=paca,
  label = paste(proportion, " (",n_species,")", sep="")),
  position = position_stack(vjust = .5)) +
scale_fill_manual("PACA", values=paca_color) +
ggtitle("Proportion of endemic taxa") +
# guides(fill=guide_legend	override.aes = list(fill=c("PACA", "IUCN"),order=2))) +
theme_bw()

ggsave("../plots/bar_chart_paca_proportion.png",
  g_paca_p,
  width = 20,
  height = 15,
  units='cm',
  device="png")
g_paca_p

```



IUCN categories per Order:

```

endemic_species_s_i <- endemic_species |>
  group_by(iucn, order) |>
  summarise(n_species=n(), .groups="drop") |>

```

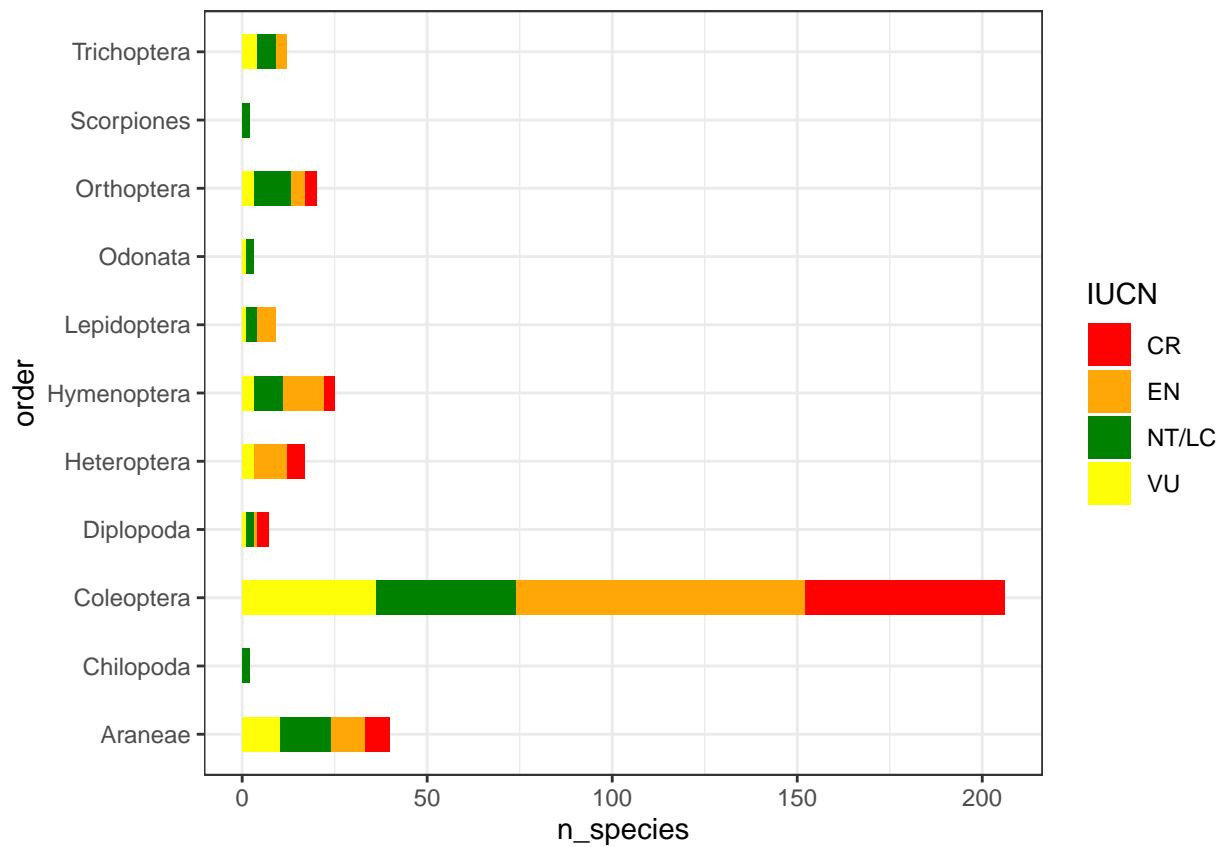
```

group_by(order) |>
  mutate(proportion = round(n_species/sum(n_species), digits=2))

g_iucn_o <- ggplot() +
  geom_col(data=endemic_species_s_i,
            aes(x=n_species,y=order, fill=iucn),
            width=0.5, show.legend=T)+ 
  scale_fill_manual("IUCN", values=iucn_color) +
  theme_bw()

ggsave("../plots/bar_chart_iucn_order.png",
       g_iucn_o,
       width = 20,
       height = 15,
       units='cm',
       device="png")
g_iucn_o

```



```

g_iucn_o_p <- ggplot() +
  geom_col(data=endemic_species_s_i,
            aes(x=proportion,y=order, fill=iucn),
            width=0.5, show.legend=T)+ 
  geom_text(data=endemic_species_s_i, aes(x=proportion,y=order, fill=iucn,
                                         label = paste(proportion, " (",n_species,")", sep="")),
            size=3,
            position = position_stack(vjust = .5)) +
  scale_fill_manual("IUCN", values=iucn_color) +

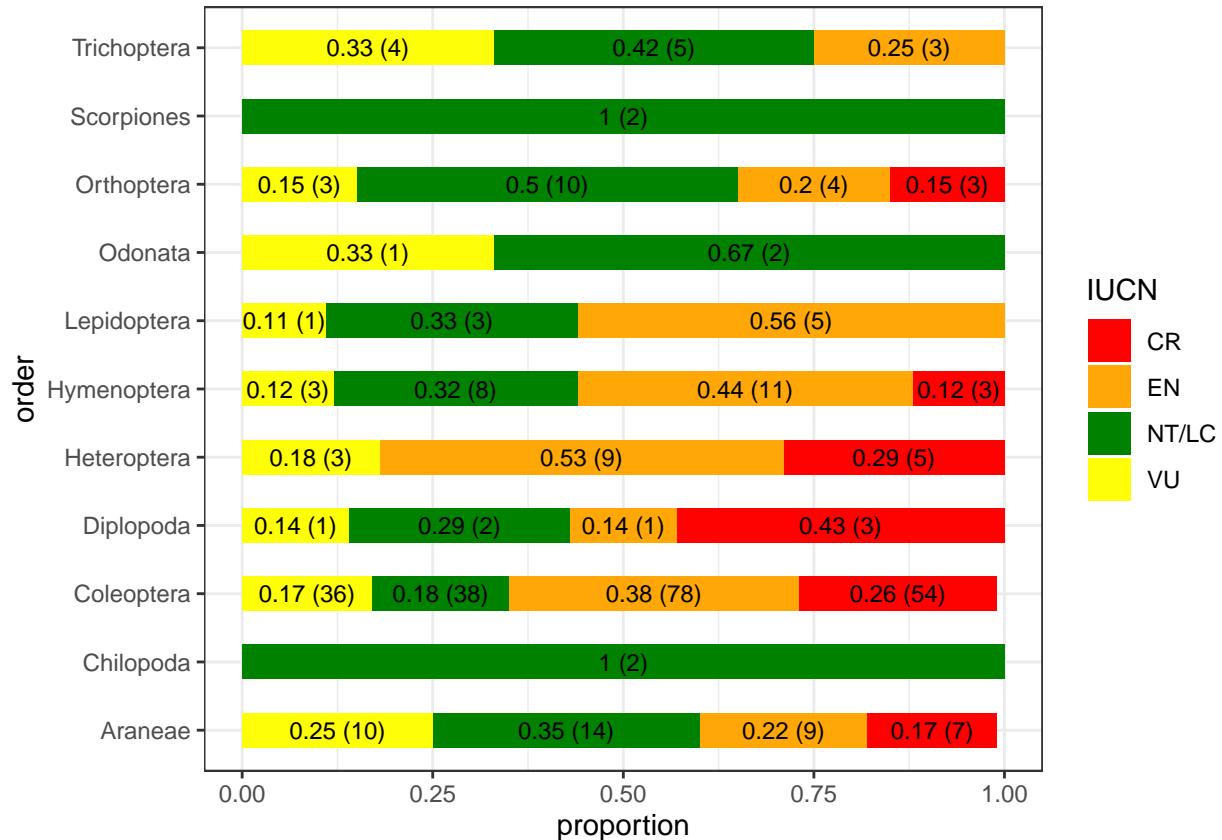
```

```

theme_bw()

ggsave("../plots/bar_chart_iucn_order_proportion.png",
       g_iucn_o_p,
       width = 20,
       height = 15,
       units='cm',
       device="png")
g_iucn_o_p

```



PACA categories per Order:

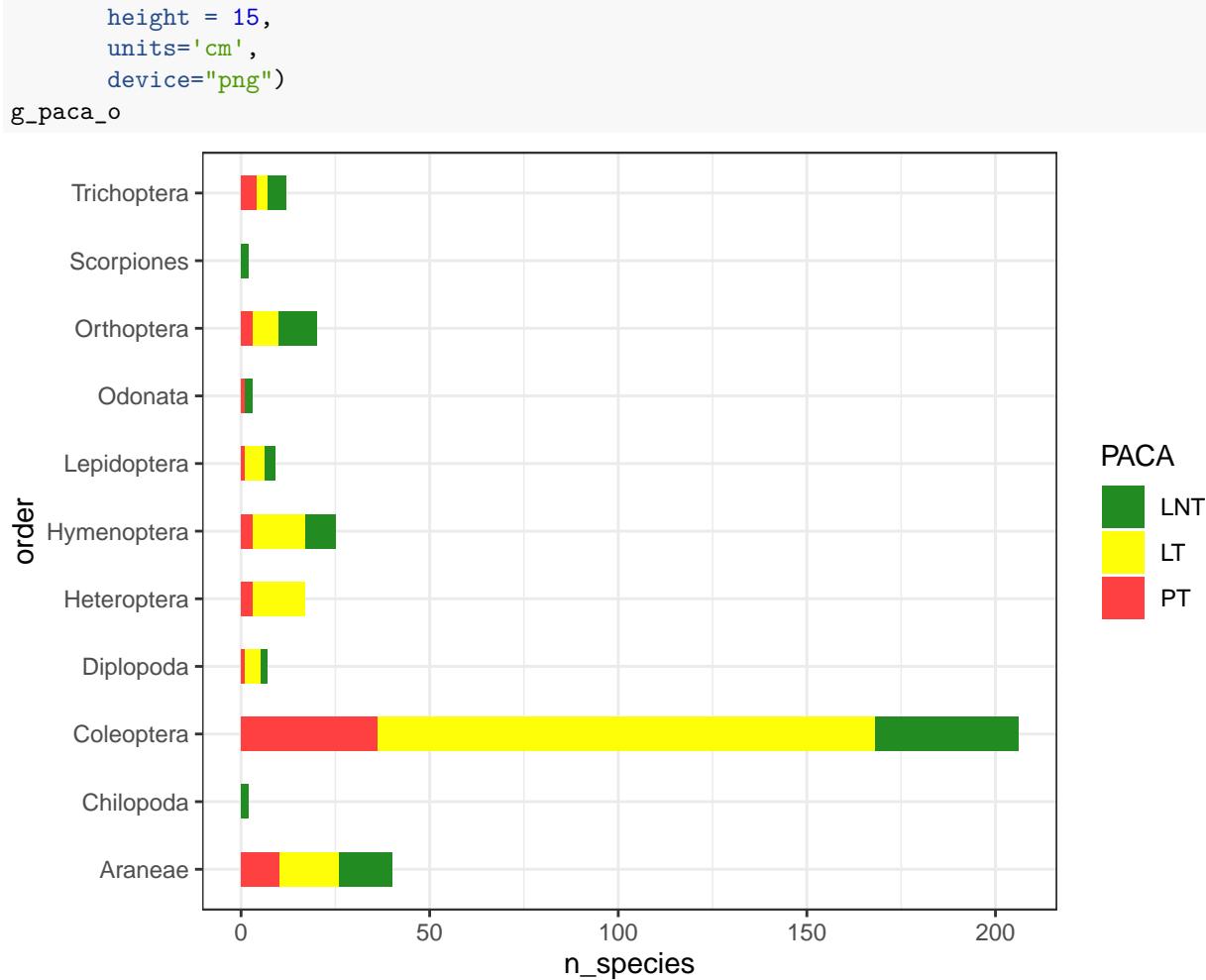
```

endemic_species_s_o <- endemic_species |>
  group_by(paca, order) |>
  summarise(n_species=n(), .groups="drop") |>
  mutate(paca = gsub("FALSE", "PNT", paca)) |>
  group_by(order) |>
  mutate(proportion = round(n_species/sum(n_species), digits=2))

g_paca_o <- ggplot() +
  geom_col(data=endemic_species_s_o, aes(x=n_species, y=order, fill=paca),
            width=0.5, show.legend=T) +
  scale_fill_manual("PACA", values=paca_color) +
  theme_bw()

ggsave("../plots/bar_chart_paca_order.png",
       g_paca_o,
       width = 20,

```



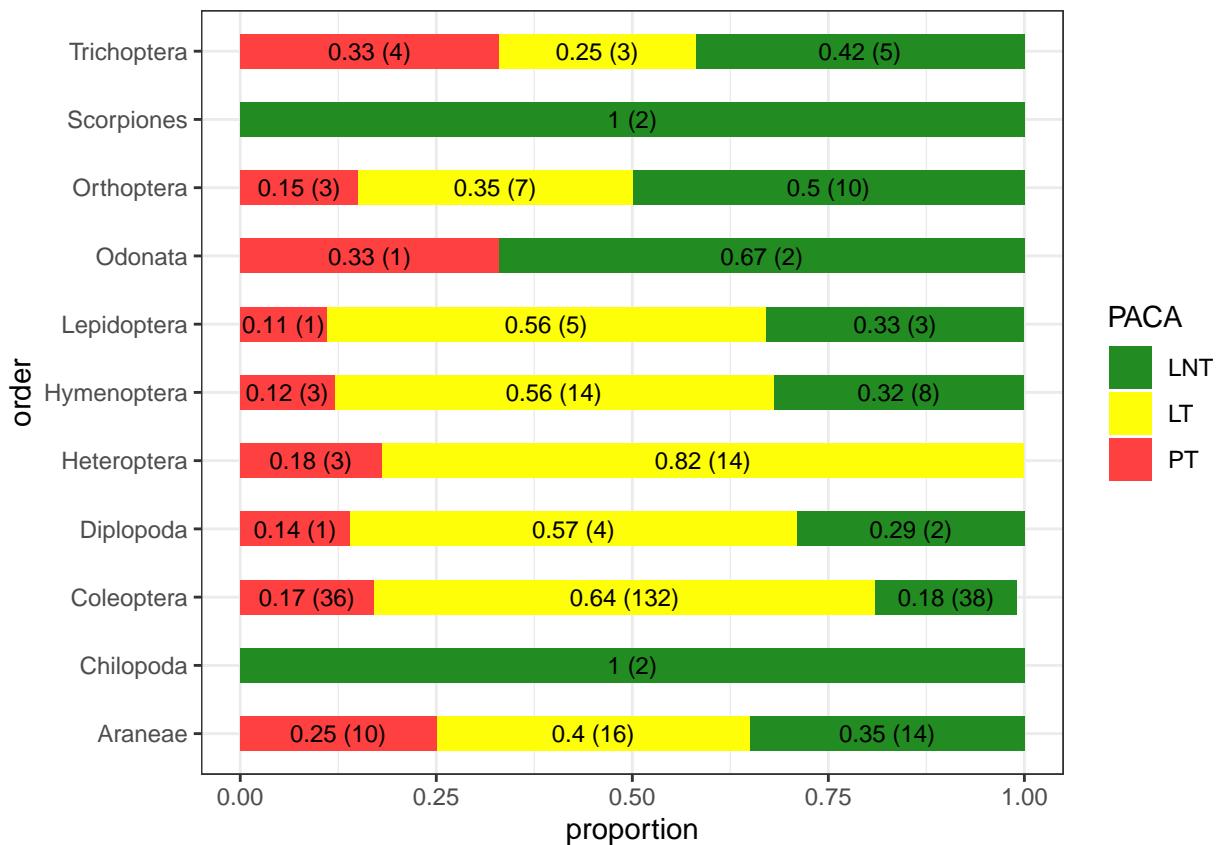
```

g_paca_o_p <- ggplot() +
  geom_col(data=endemic_species_s_o, aes(x=proportion,y=order, fill=paca),
            width=0.5, show.legend=T) +
  geom_text(data=endemic_species_s_o, aes(x=proportion,y=order, fill=paca,
                                         label = paste(proportion, " (", n_species, ")"), sep="")),
            size=3,
            position = position_stack(vjust = .5)) +
  scale_fill_manual("PACA", values=paca_color) +
  theme_bw()

ggsave("../plots/bar_chart_paca_order_proportion.png",
       g_paca_o_p,
       width = 20,
       height = 15,
       units='cm',
       device="png")

```

g_paca_o_p



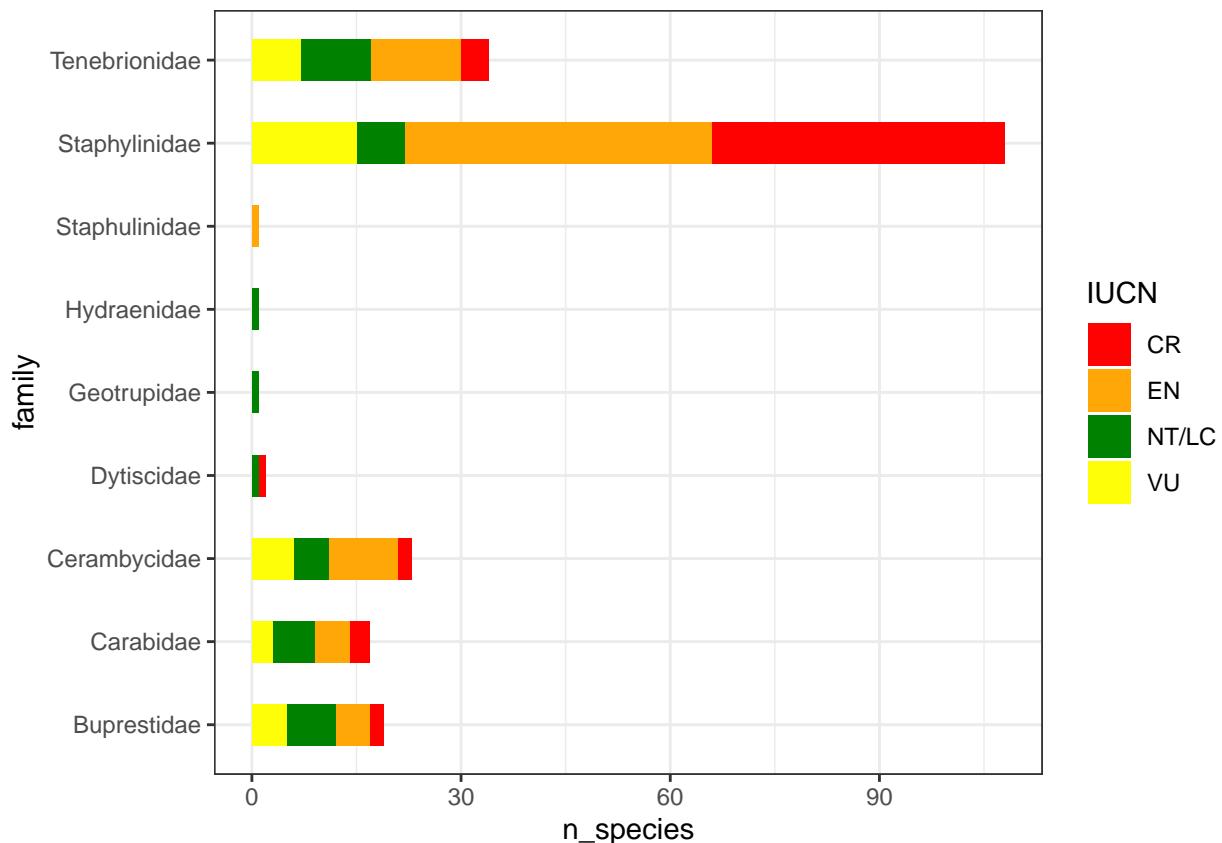
Categories of Coleoptera families

IUCN categories of the families of coleoptera

```
endemic_species_coleoptera <- endemic_species |>
  filter(order=="Coleoptera") |>
  group_by(iucn, family) |>
  summarise(n_species=n(), .groups="drop")

g_iucn_c <- ggplot() +
  geom_col(data=endemic_species_coleoptera,
            aes(x=n_species,y=family, fill=iucn),
            width=0.5, show.legend=T)+ 
  scale_fill_manual("IUCN", values=iucn_color) +
  theme_bw()

ggsave("../plots/bar_chart_iucn_coleoptera.png",
       g_iucn_c,
       width = 20,
       height = 15,
       units='cm',
       device="png")
g_iucn_c
```

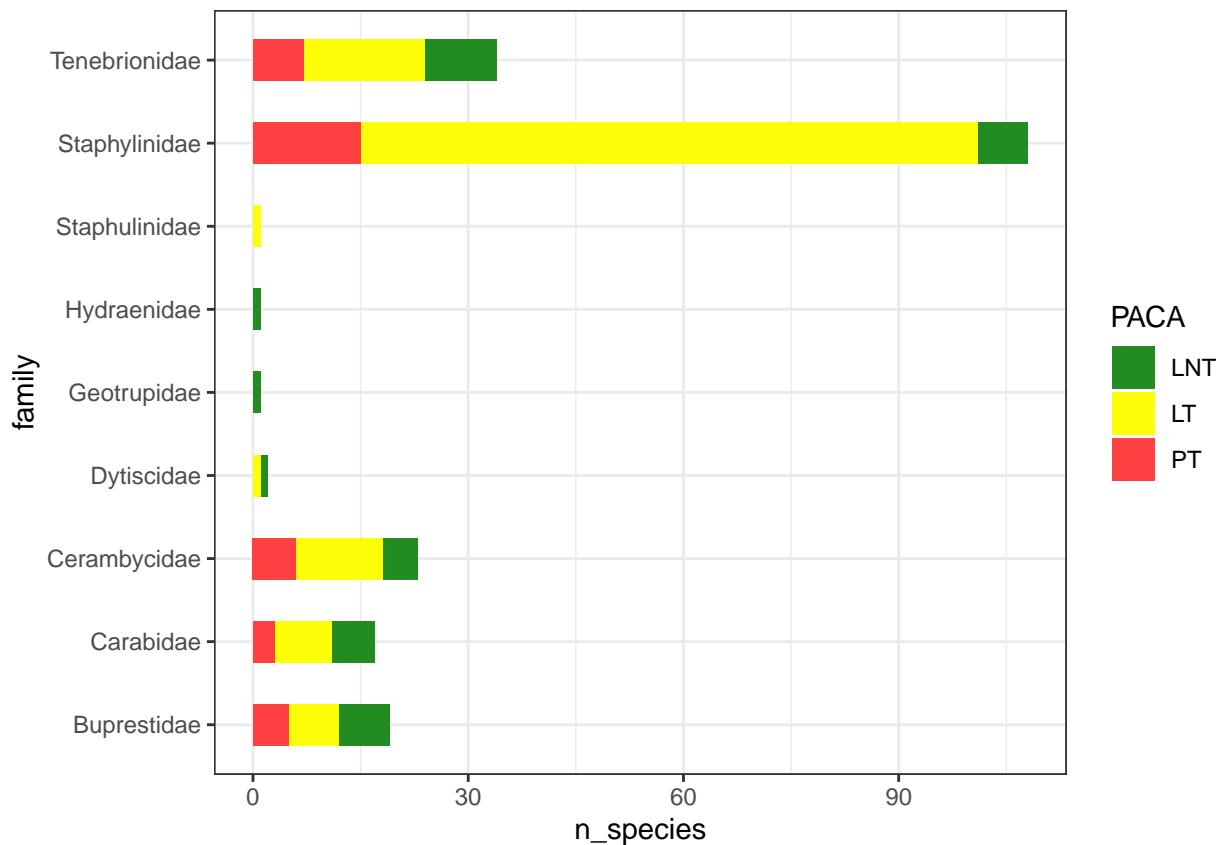


PACA categories of the families of coleoptera

```
endemic_species_coleoptera_p <- endemic_species |>
  filter(order=="Coleoptera") |>
  group_by(paca, family) |>
  summarise(n_species=n(), .groups="drop")

g_iucn_c_p <- ggplot() +
  geom_col(data=endemic_species_coleoptera_p,
            aes(x=n_species,y=family, fill=paca),
            width=0.5, show.legend=T)+ 
  scale_fill_manual("PACA", values=paca_color) +
  theme_bw()

ggsave("../plots/bar_chart_paca_coleoptera.png",
       g_iucn_c_p,
       width = 20,
       height = 15,
       units='cm',
       device="png")
g_iucn_c_p
```



Hotspots and threatspots

Here are the hotspots and threatspots of the analysis. Endemic hotspots are the grid cells that contain the 10% of the endemic species.

```

threatspots_lt <- threatspots |>
  filter(pc_thrt >= quantile(pc_thrt, 0.90))

intersection_spots <- endemic_hotspots |>
  st_drop_geometry() |>
  inner_join(threatspots_lt, by=c("CELLCODE" = "CELLCOD")) |>
  st_as_sf()

g_e_t <- g_base +
  geom_sf(intersection_spots, mapping=aes(fill=pc_thrt/n_species), alpha=0.3, size=0.1, na.rm = TRUE)
  gtitle("Endemic hotspots and threatspots")+
  scale_fill_gradient(low = "yellow", high = "red", na.value = "transparent")+
  theme_bw()

ggsave("../plots/crete-hotspots-threatspots.png", plot=g_e_t, device="png")

g_e_t

```

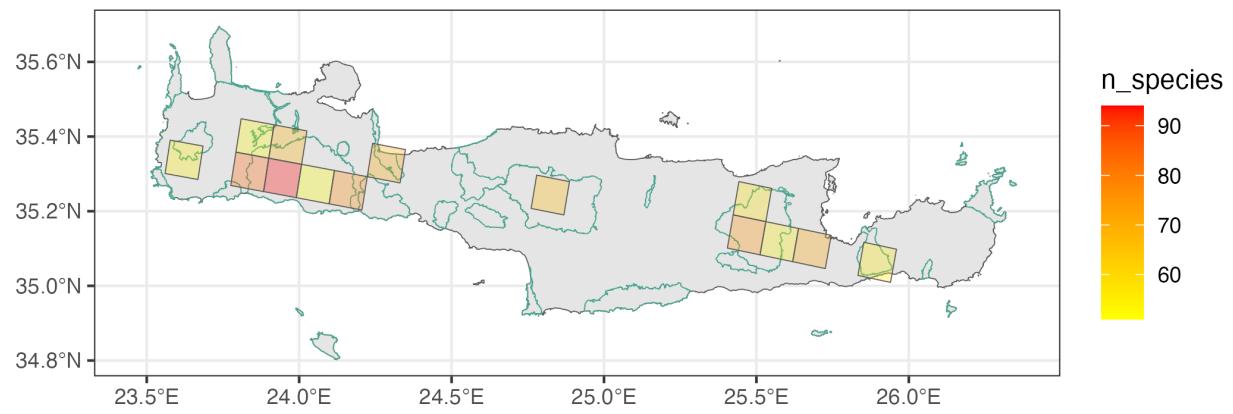


Figure 1: Crete endemic hotspots

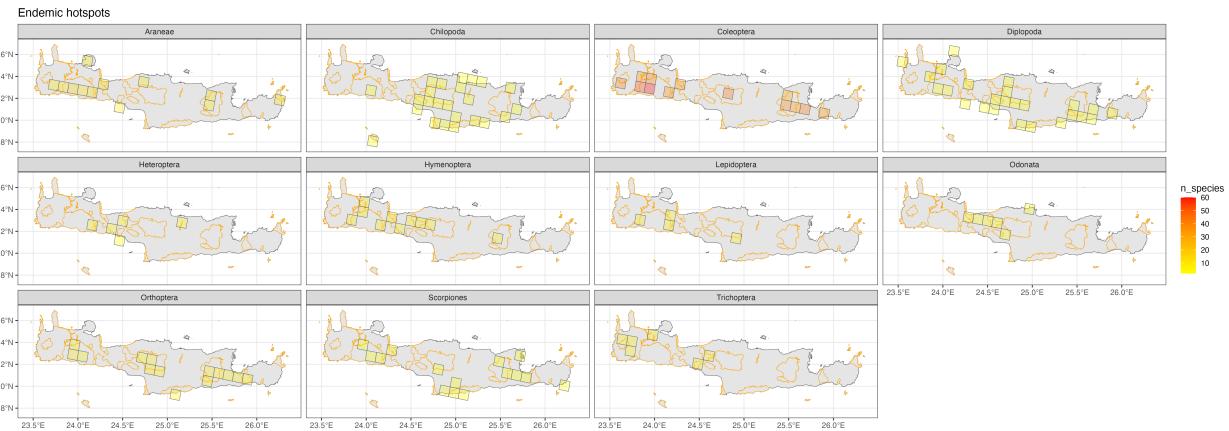
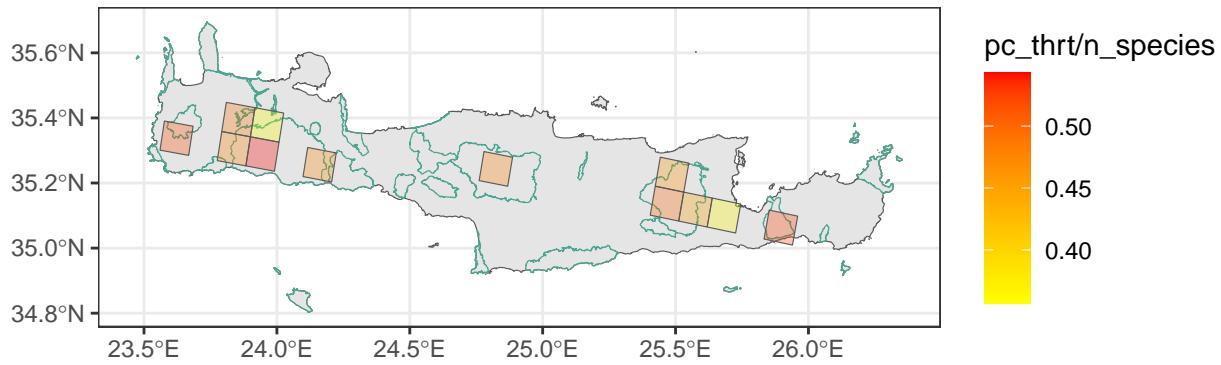


Figure 2: Crete endemic hotspots per order

Endemic hotspots and threatspots



The area of the intersection of hotspots and threatspots:

```
sum(units::set_units(st_area(intersection_spots), km^2))

## 1200.023 [km^2]
```

Overlap of hotspots and threatspots with protected areas.

Natura2000

Here are the hotspots that overlap with Natura2000:

```
endemic_hotspots_natura <- st_intersection(endemic_hotspots, natura_crete_land_sci)
print("Total area of endemic hotspots")

## [1] "Total area of endemic hotspots"

sum(units::set_units(st_area(endemic_hotspots), km^2))

## 1400.024 [km^2]

print("Overlap area of endemic hotspots with Natura2000 sci")

## [1] "Overlap area of endemic hotspots with Natura2000 sci"
```

threatspots

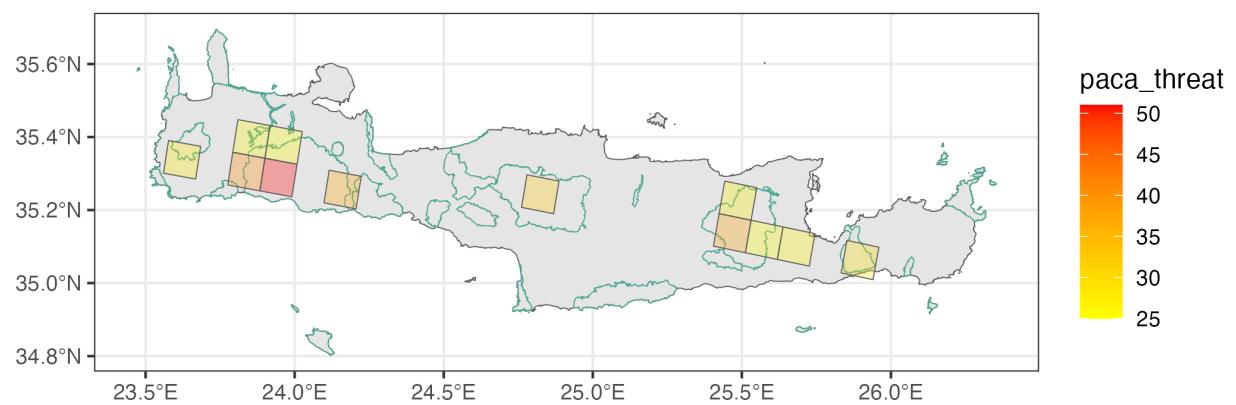


Figure 3: Crete endemic threatspots

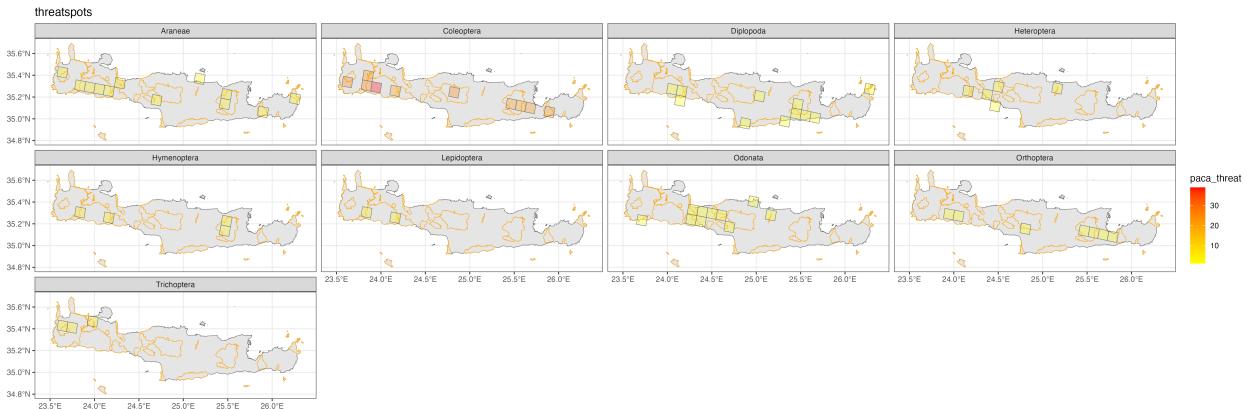


Figure 4: Crete endemic threatspots per order

Endemic hotspots and threatspots

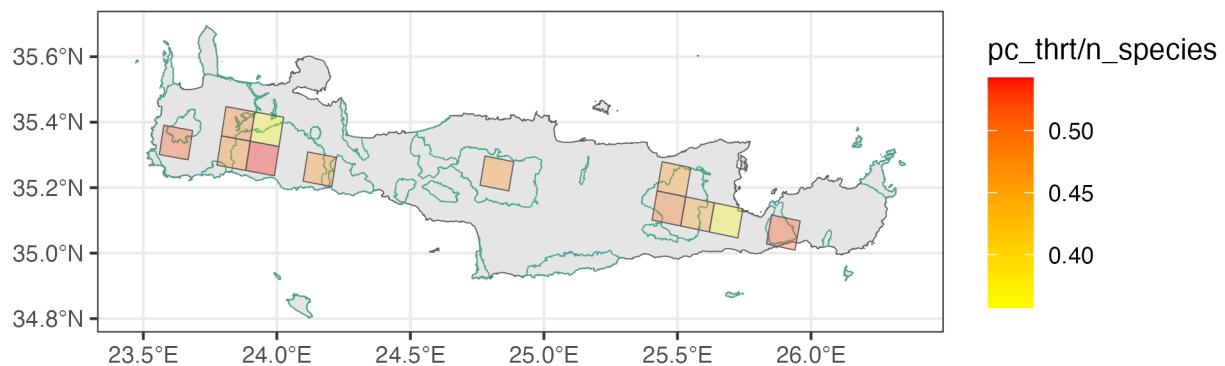


Figure 5: Overlap of hotspots with threatspots

```

sum(units::set_units(st_area(endemic_hotspots_natura), km^2))

## 858.1585 [km^2]

threatspots with Natura2000
threatspots_natura <- st_intersection(threatspots_lt, natura_crete_land_sci)

print("Total area of threatspots as they were inferred with the PACA method")

## [1] "Total area of threatspots as they were inferred with the PACA method"
sum(units::set_units(st_area(threatspots_lt), km^2))

## 1200.023 [km^2]

print("Overlap area of the PACA threatspots")

## [1] "Overlap area of the PACA threatspots"
sum(units::set_units(st_area(threatspots_natura), km^2))

## 721.4383 [km^2]

```

The threatened species that have AOO < 10% overlap with Natura2000.

```

species_10_natura <- endemic_species |>
  mutate(aoo_natura_percent=round(aoo_natura/aoe, digits=4)) |>
  filter(aoo_natura_percent<0.1 & threatened==T)

species_10_natura_l <- locations_grid |>
  filter(scntfcN %in% species_10_natura$subspeciesname) |>
  group_by(CELLCOD) |>
  summarise(n_species=n()) |>
  filter(n_species>2)

species_10_natura_l_o <- locations_grid |>
  filter(scntfcN %in% species_10_natura$subspeciesname) |>
  group_by(CELLCOD, order) |>
  summarise(n_species=n(), .groups="drop")

table(species_10_natura$order)

##
##      Araneae Coleoptera Heteroptera Hymenoptera
##          6         31          2          2

```

Wildlife refuges

```

endemic_hotspots_wild <- st_intersection(endemic_hotspots, wildlife)

print("Overlap area of endemic hotspots with Wildlife Refuges")

## [1] "Overlap area of endemic hotspots with Wildlife Refuges"
sum(units::set_units(st_area(endemic_hotspots_wild), km^2))

## 143.1965 [km^2]

```

Hotspots of AOO<10% overlap with Natura2000

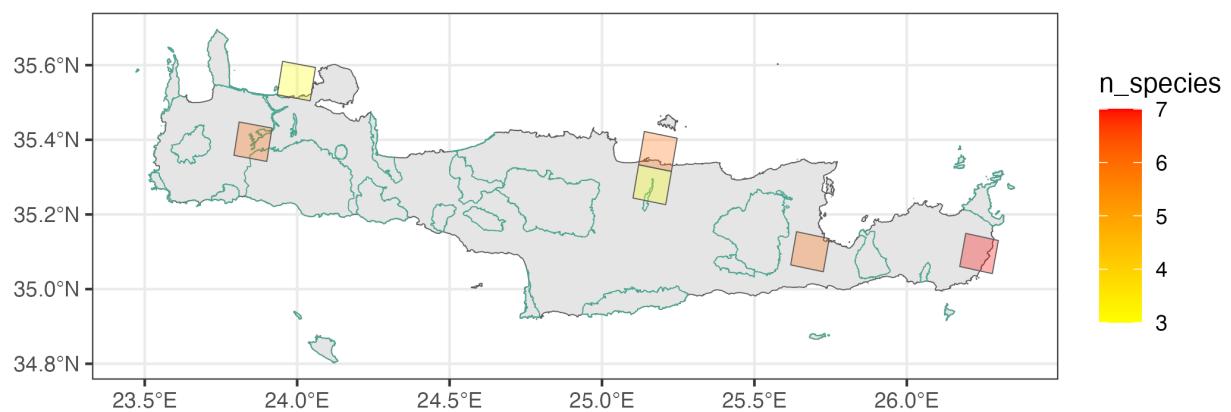


Figure 6: Hotspots of < 10% AOO overlap with Natura2000

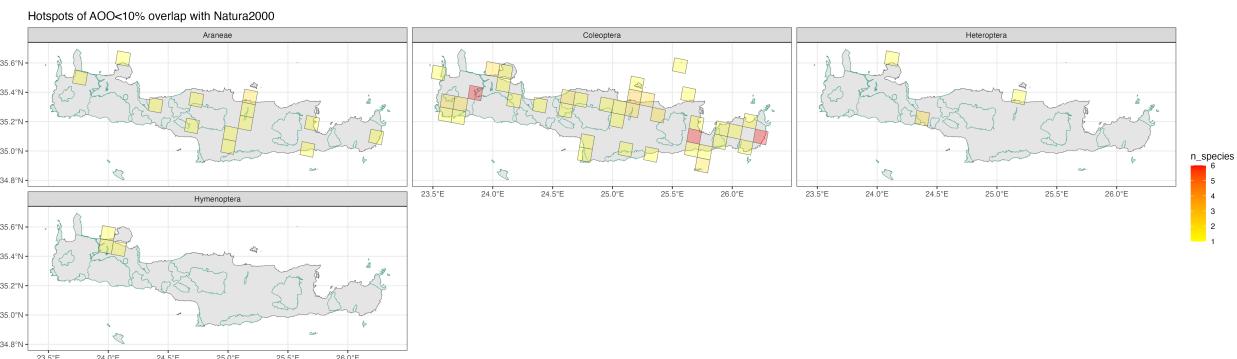


Figure 7: Hotspots of < 10% AOO overlap with Natura2000 per Order

threatspots with Wildlife Refuges

```
threatspots_wild <- st_intersection(threatspots_lt, wildlife)

print("Overlap area of the PACA threatspots with Wildlife Refuges")

## [1] "Overlap area of the PACA threatspots with Wildlife Refuges"
sum(units::set_units(st_area(threatspots_wild), km^2))

## 129.9314 [km^2]
```

Order locations overlap

Here we calculate the overlaps of locations and hotspots of the different orders.

```
# Overlap of all locations
heatmaps_l <- heatmaps(locations_grid)

ggsave("../plots/order_location_heatmap.png",
      plot = heatmaps_l[[2]],
      width = 25,
      height = 25,
      units='cm',
      device = "png",
      dpi = 300)

# Overlap of hotspots
endemic_hotspots_o <- locations_grid |>
  filter(CELLCODE %in% endemic_hotspots$CELLCODE) |>
  distinct(CELLCODE, order)

heatmaps_hotspots <- heatmaps(endemic_hotspots_o)

ggsave("../plots/order_hotspot_heatmap.png",
      plot = heatmaps_hotspots[[2]],
```

```

width = 25,
height = 25,
units='cm',
device = "png",
dpi = 300)

# Overlap of threatspots
threatspots_o <- locations_grid |>
  filter(CELLCOD %in% threatspots_lt$CELLCOD) |>
  distinct(CELLCOD, order)

heatmaps_threatspots <- heatmaps(threatspots_o)

ggsave("../plots/order_threatspots_heatmap.png",
  plot = heatmaps_threatspots[[2]],
  width = 25,
  height = 25,
  units='cm',
  device = "png",
  dpi = 300)

```

EOO and AOO distributions

EOO and AOO relation

The relation of EOO and AOO per IUCN category

```

g_e_o <- ggplot() +
  geom_point(endemic_species,mapping = aes(x=aoo, y=eoo, color=iucn)) +
  scale_color_manual("IUCN", values=iucn_color) +
  theme_bw()
ggsave("../plots/aoo-eoo_dist.png", plot=g_e_o, device="png")

g_e_o

```

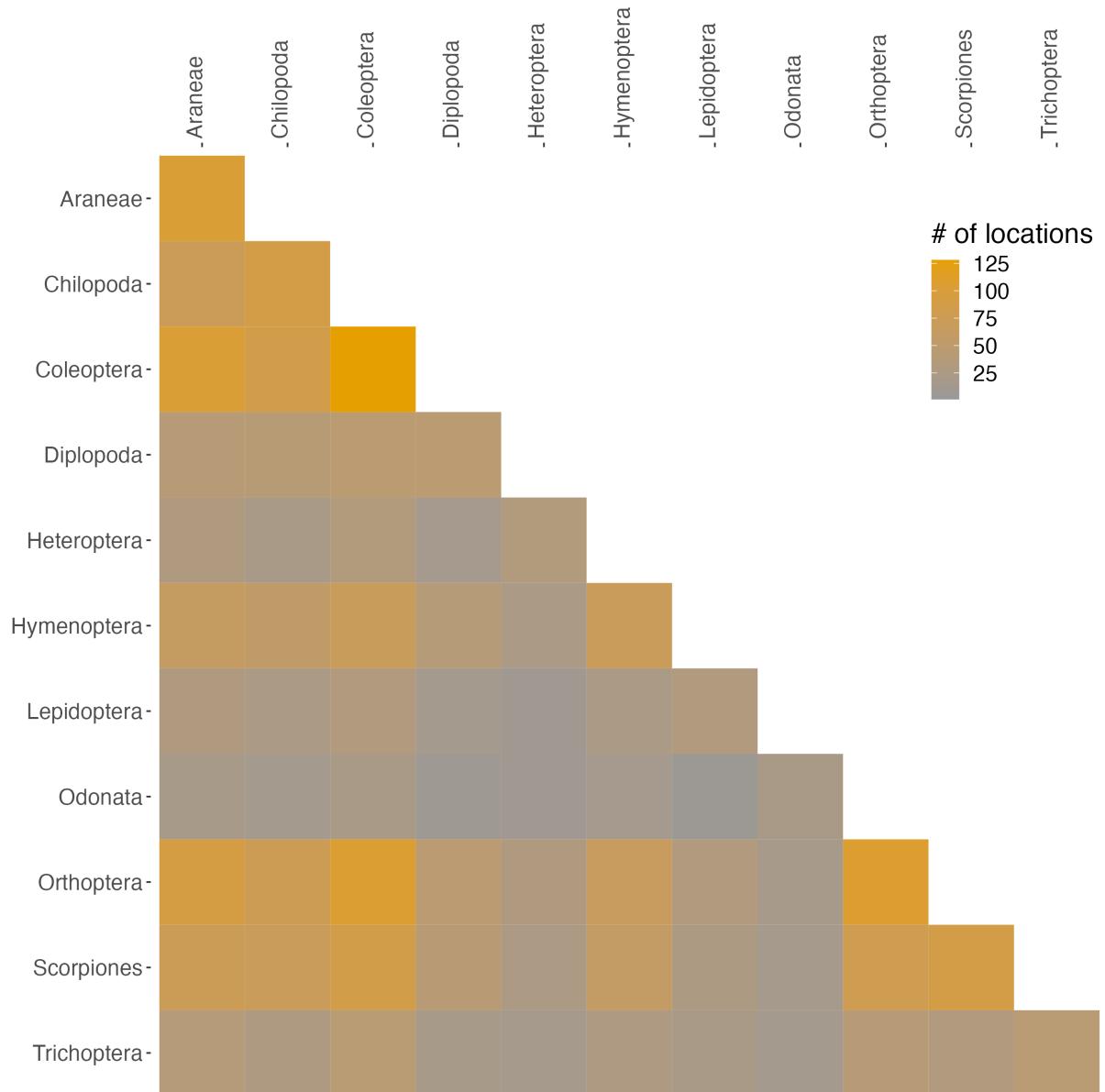


Figure 8: Shared locations of arthropod orders

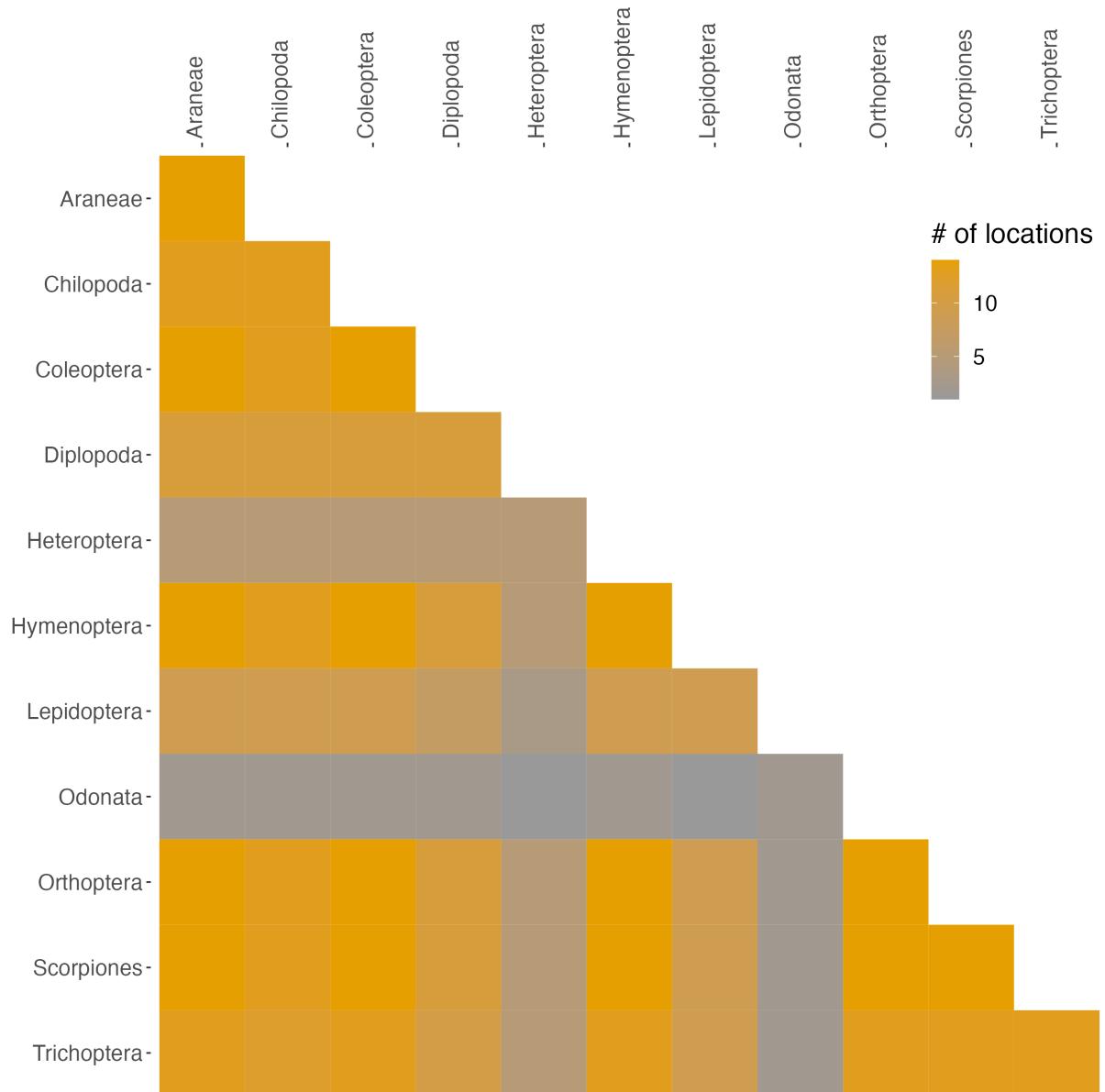


Figure 9: Shared hotspots of arthropod orders

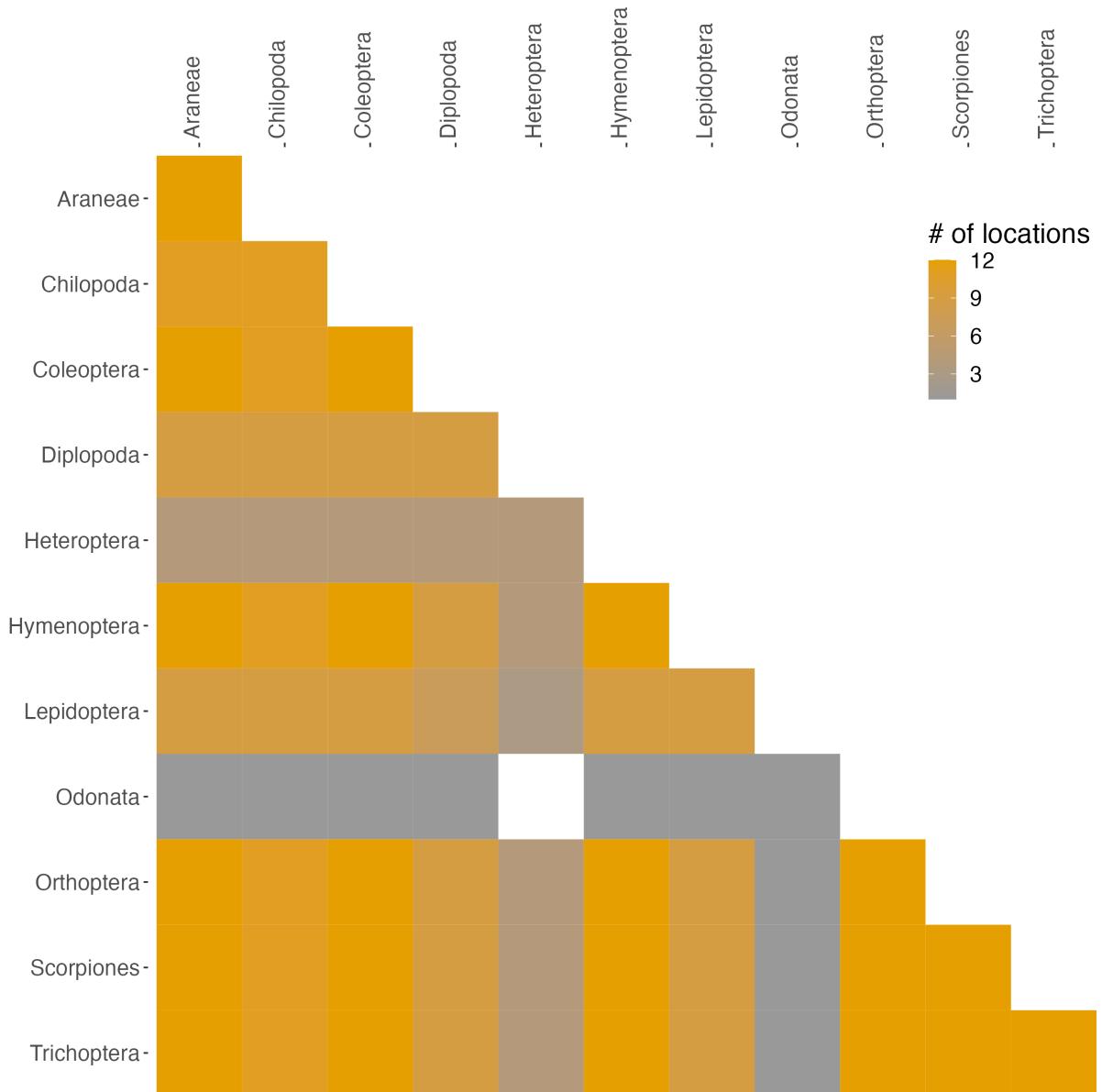
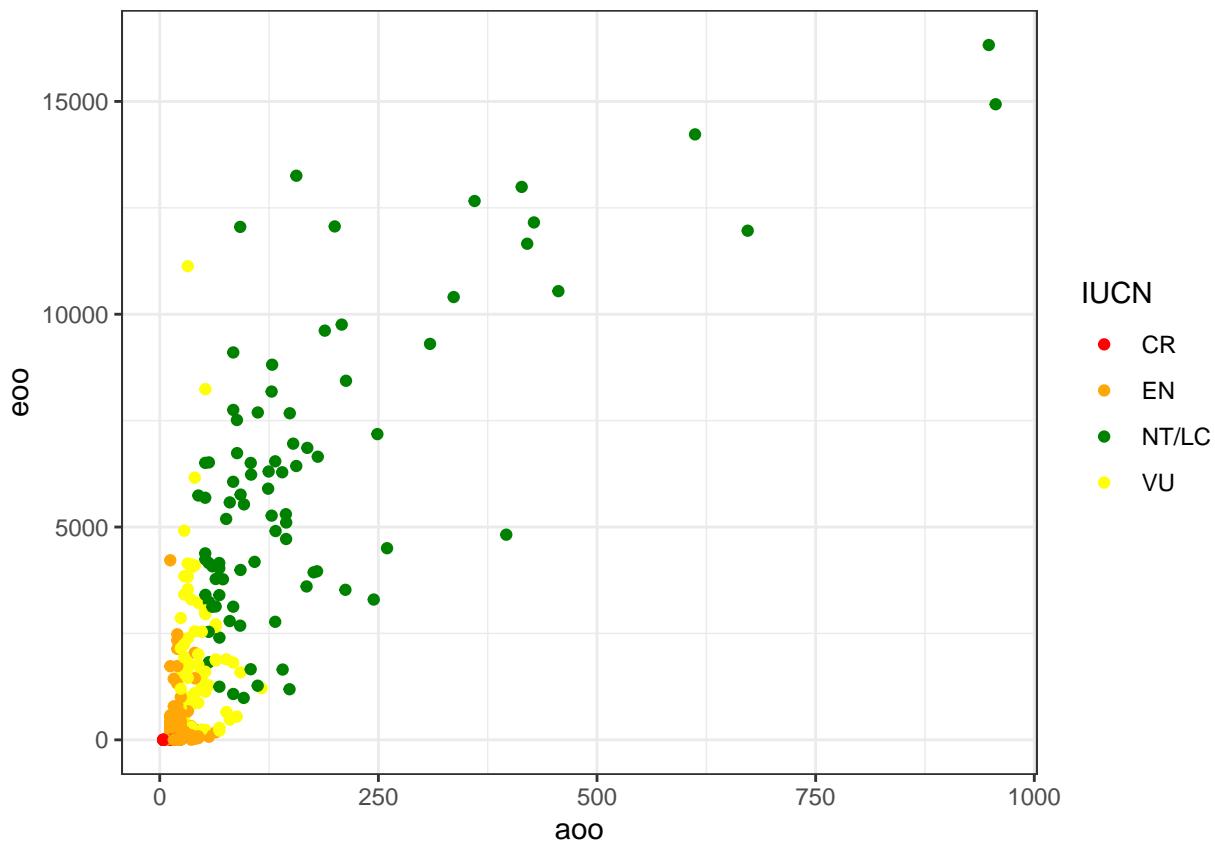


Figure 10: Shared threatspots of arthropod orders



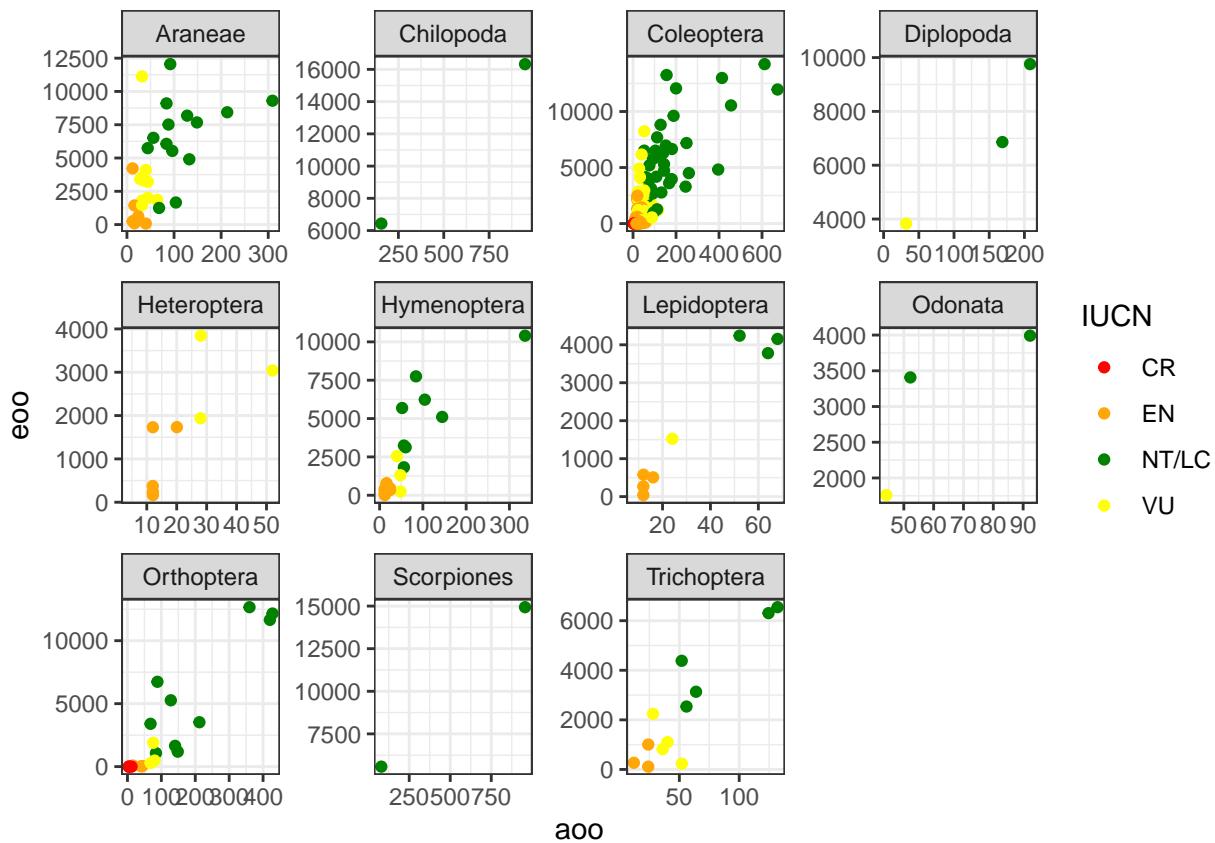
```

g_e_o_order <- ggplot() +
  geom_point(endemic_species, mapping = aes(x=aoo, y=eoo, color=iucn)) +
  scale_color_manual("IUCN", values=iucn_color) +
  theme_bw() +
  facet_wrap(vars(order), ncol=4, scales = "free")

ggsave("../plots/aoo-eoo_order.png",
       plot=g_e_o_order,
       device="png",
       height = 20,
       width = 20,
       units="cm")

g_e_o_order

```

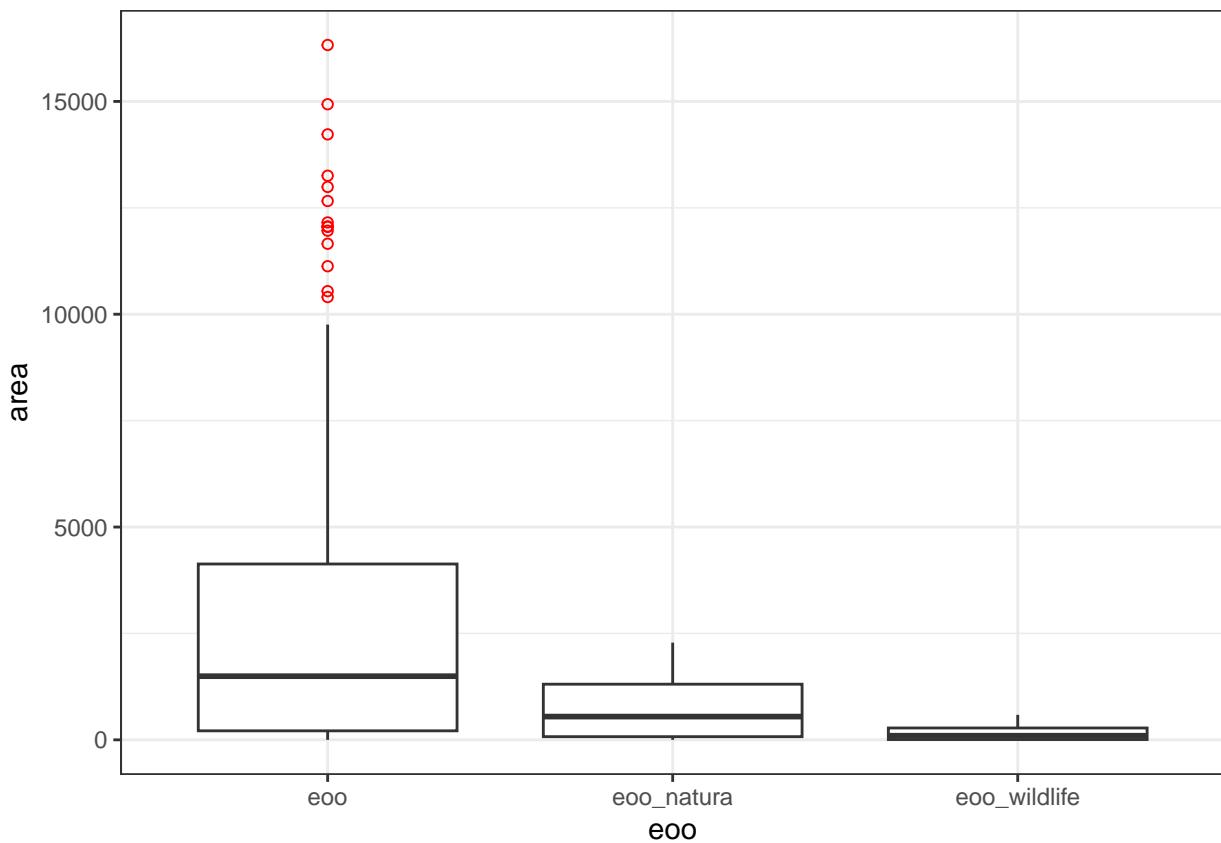


EOO area distribution

EOO area distribution and the differences with the EOO overlap with Natura2000 and wildlife refugees.

```
endemic_species_eoo <- endemic_species |>
  dplyr::select(scientificName, eoo, eoo_natura, eoo_wildlife) |>
  pivot_longer(cols = c(eoo, eoo_natura, eoo_wildlife),
               names_to = "eoo",
               values_to = "area")

g_eoo_b <- ggplot() +
  geom_boxplot(endemic_species_eoo,
               mapping = aes(x=eoo, y=area),
               outlier.colour = "red",
               outlier.shape = 1) +
  theme_bw()
ggsave("../plots/eoo_dist_boxplot.png", plot=g_eoo_b, device="png")
g_eoo_b
```



```
tapply(endemic_species_eoo$area, endemic_species_eoo$eoo, summary)
```

```
## $eoo
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
##      0.0   211.7 1495.6  2790.5 4131.6 16325.5       91
##
## $eoo_natura
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
##      0.00   74.52 546.39  724.80 1307.95 2284.09       91
##
## $eoo_wildlife
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.    NA's
##      0.000  7.734 97.394 154.770 278.703 587.257       91
```

Examine the differences of EOO area per Order.

```
endemic_species_eoo_o <- endemic_species |>
  dplyr::select(scientificName, order, eoo, eoo_natura, eoo_wildlife) |>
  pivot_longer(cols=c(eoo, eoo_natura, eoo_wildlife),
               names_to="eoo",
               values_to="area")

g_eoo_b_o <- ggplot() +
  geom_boxplot(endemic_species_eoo_o,
               mapping = aes(x=eoo, y=area),
               outlier.colour = "red",
               outlier.shape = 1) +
  theme_bw()
```

```

facet_wrap(vars(order), ncol=4, scales = "fixed")

ggsave("../plots/eoo_dist_boxplot_o.png",
       plot=g_eoo_b_o,
       device="png",
       height = 20,
       width = 30,
       units="cm")

```

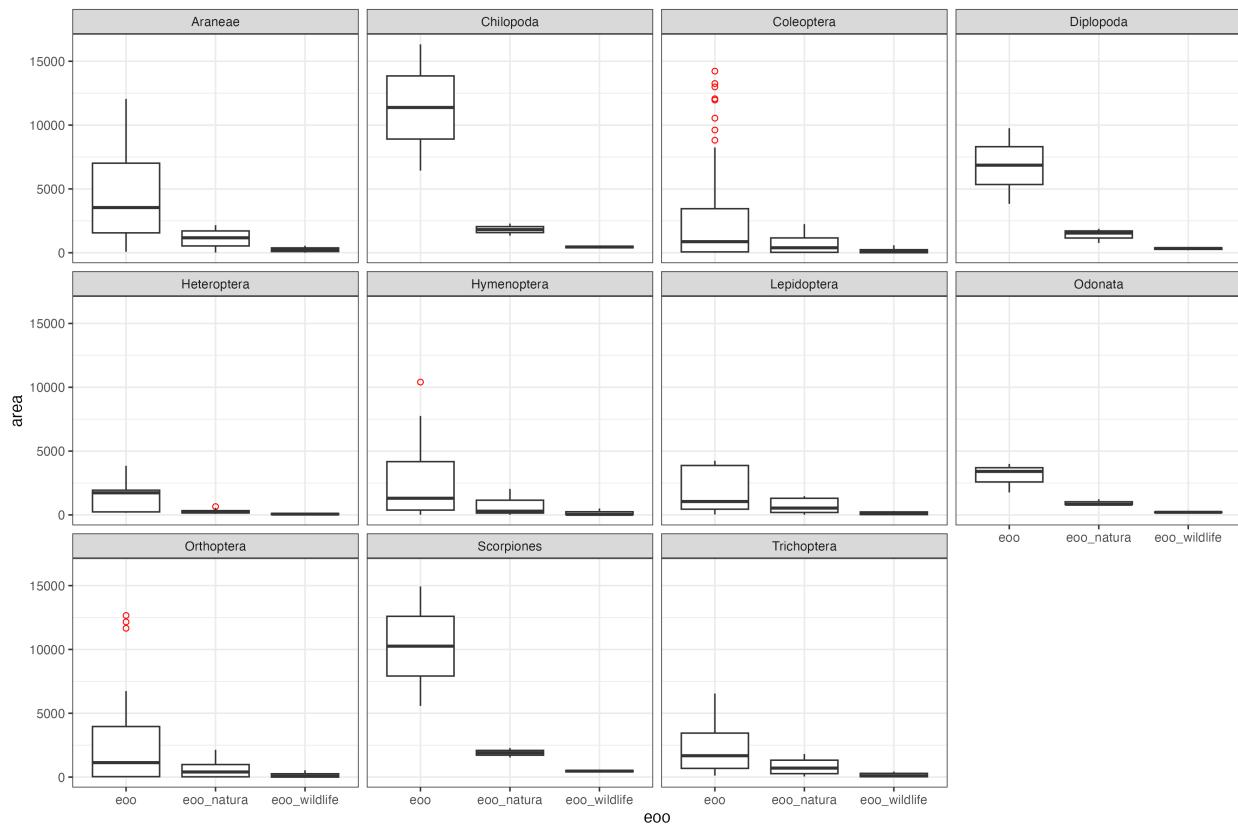


Figure 11: Distributions of EOO and overlaps per Order

AOO area distribution

AOO area distribution and the differences with the AOO overlap with Natura2000 and wildlife refugees.

```

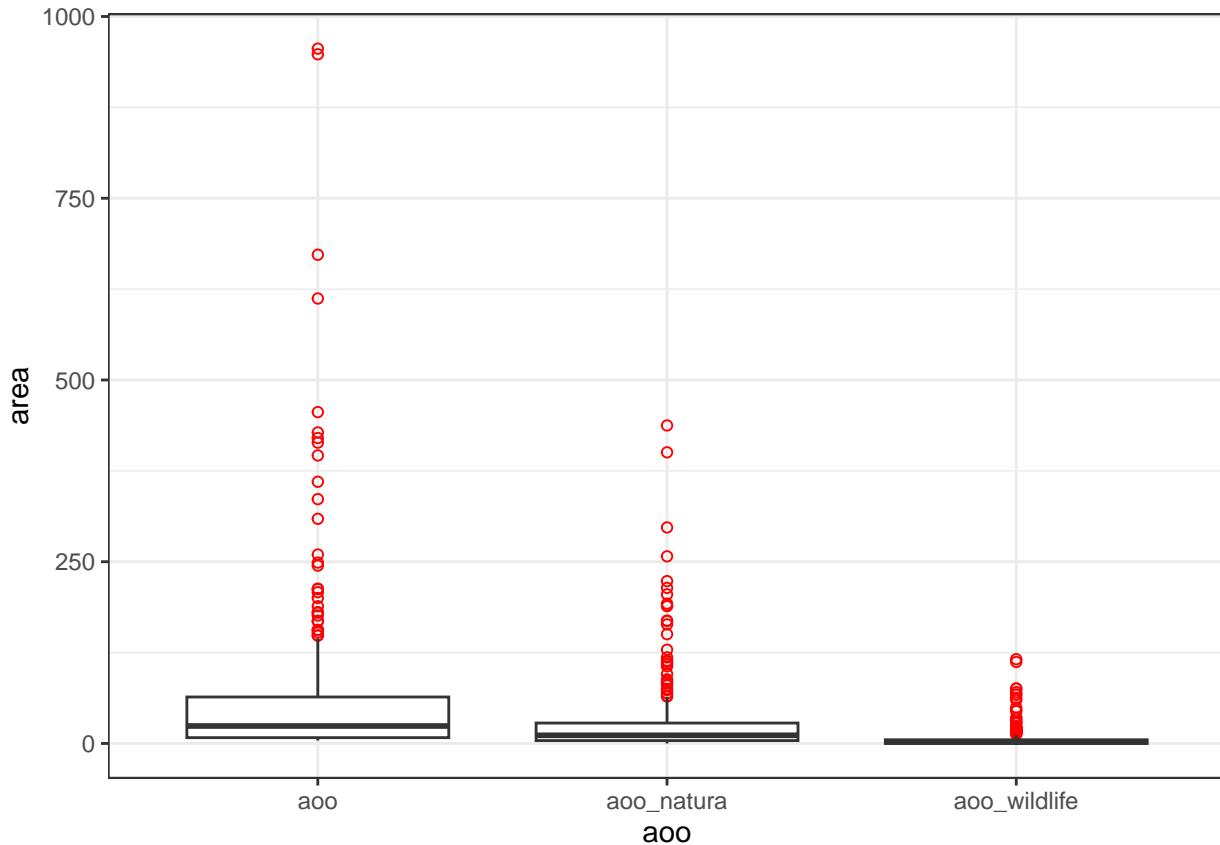
endemic_species_aoo <- endemic_species |>
  dplyr::select(scientificName, aoo, aoo_natura,aoo_wildlife) |>
  pivot_longer(cols=c(aoo,aoo_natura, aoo_wildlife),
               names_to="aoo",
               values_to="area")

g_aoo_b <- ggplot() +
  geom_boxplot(endemic_species_aoo,
               mapping = aes(x=aoo, y=area),
               outlier.colour = "red",
               outlier.shape = 1) +
  theme_bw()

```

```
ggsave("../plots/aoo_dist_boxplot.png", plot=g_aoo_b, device="png")
```

```
g_aoo_b
```



```
tapply(endemic_species_aoo$area, endemic_species_aoo$aoo, summary)
```

```
## $aoo
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##      3.998   8.021  24.038  58.517  63.959 955.818
##
## $aoo_natura
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##      0.000   4.006  11.244  27.177  28.091 437.461
##
## $aoo_wildlife
##      Min. 1st Qu. Median     Mean 3rd Qu.    Max.
##      0.000   0.000   1.987   6.255   5.063 115.928
```

Examine the differences of AOO area per Order.

```
endemic_species_aoo_o <- endemic_species |>
  dplyr::select(scientificName, order, aoo, aoo_natura,aoo_wildlife) |>
  pivot_longer(cols=c(aoo,aoo_natura, aoo_wildlife),
               names_to="aoo",
               values_to="area")

g_aoo_b_o <- ggplot() +
  geom_boxplot(endemic_species_aoo_o,
```

```

        mapping = aes(x=aoo, y=area),
        outlier.colour = "red",
        outlier.shape = 1) +
      theme_bw() +
    facet_wrap(vars(order), ncol=4, scales = "fixed")

ggsave("../plots/aoo_dist_boxplot_o.png",
       plot=g_aoo_b_o,
       device="png",
       height = 20,
       width = 30,
       units="cm")

```

```

p <- ggplot(endemic_species, mapping=aes(x=order, y=aoo)) +
  geom_jitter(position=position_jitter(0.2))

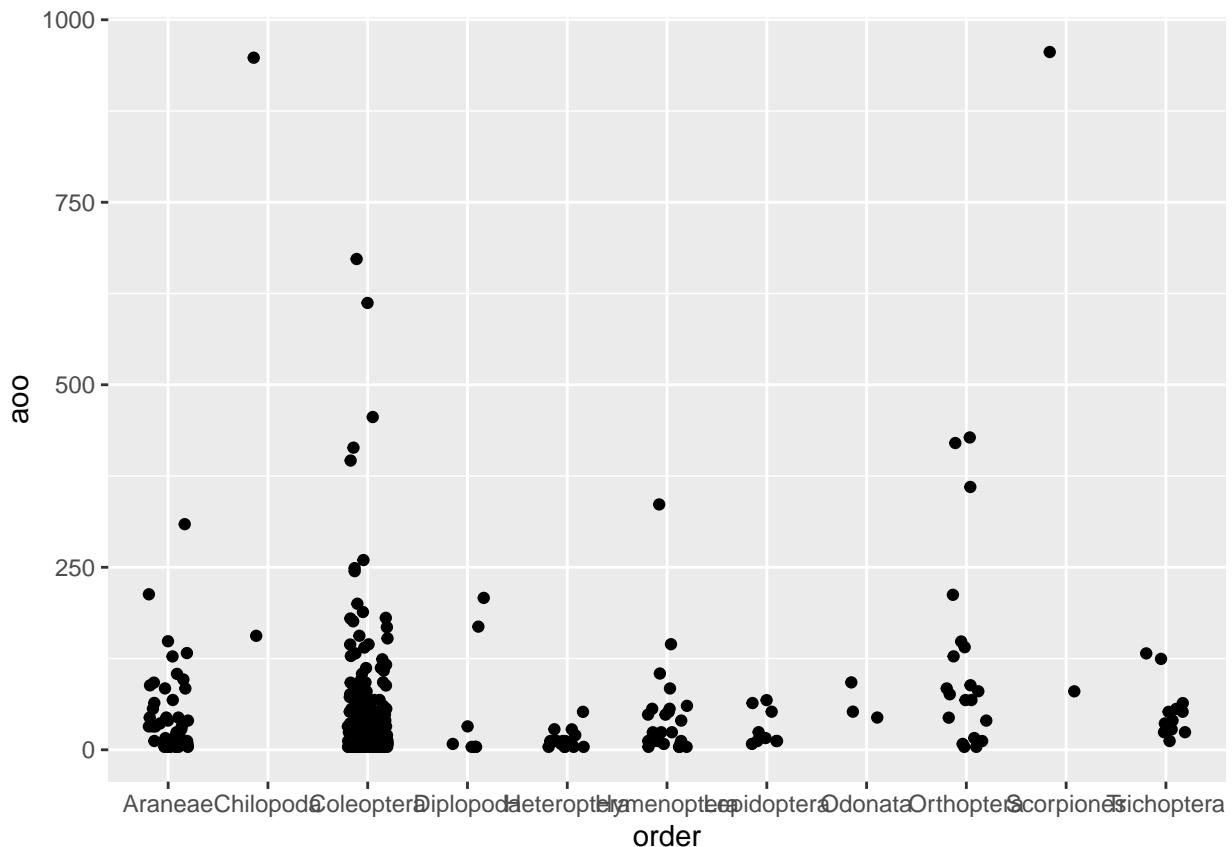
```

```

ggsave("../plots/aoo_dist_stripplot-o.png",
       plot=p,
       device="png",
       height = 20,
       width = 30,
       units="cm")

```

p



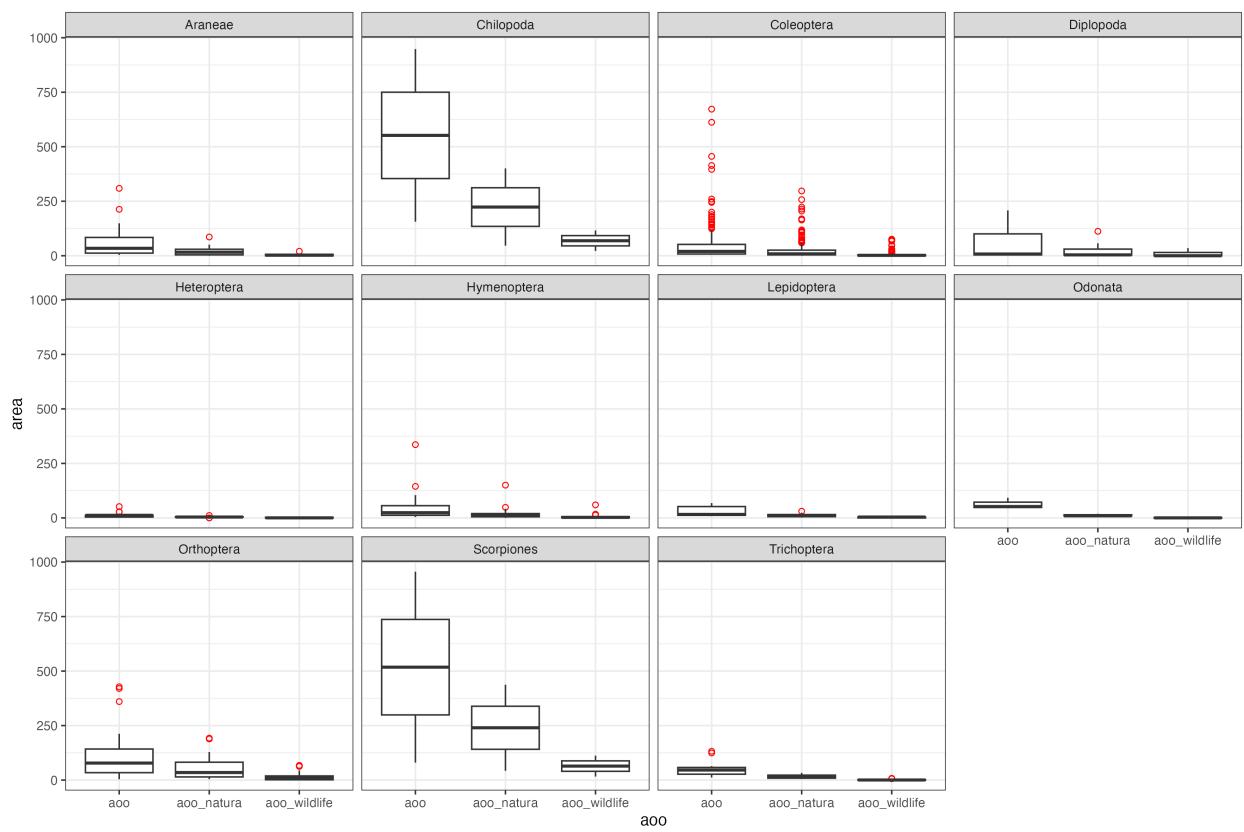


Figure 12: Distributions of AOO and overlaps per Order

Digital Elevation Maps

```
locations_spatial_d <- locations_spatial |>
  st_drop_geometry() |>
  dplyr::select(-order) |>
  left_join(endemic_species, by=c("scntfcN"="scientificName")) |>
  mutate(elevation_bin=cut(elevatn,
                           breaks=seq.int(from=0, to=2500, by=400),
                           dig.lab = 5))

locations_spatial_d_b <- locations_spatial_d |>
  distinct(scntfcN, elevation_bin) |>
  group_by(elevation_bin) |>
  summarise(n_species=n())

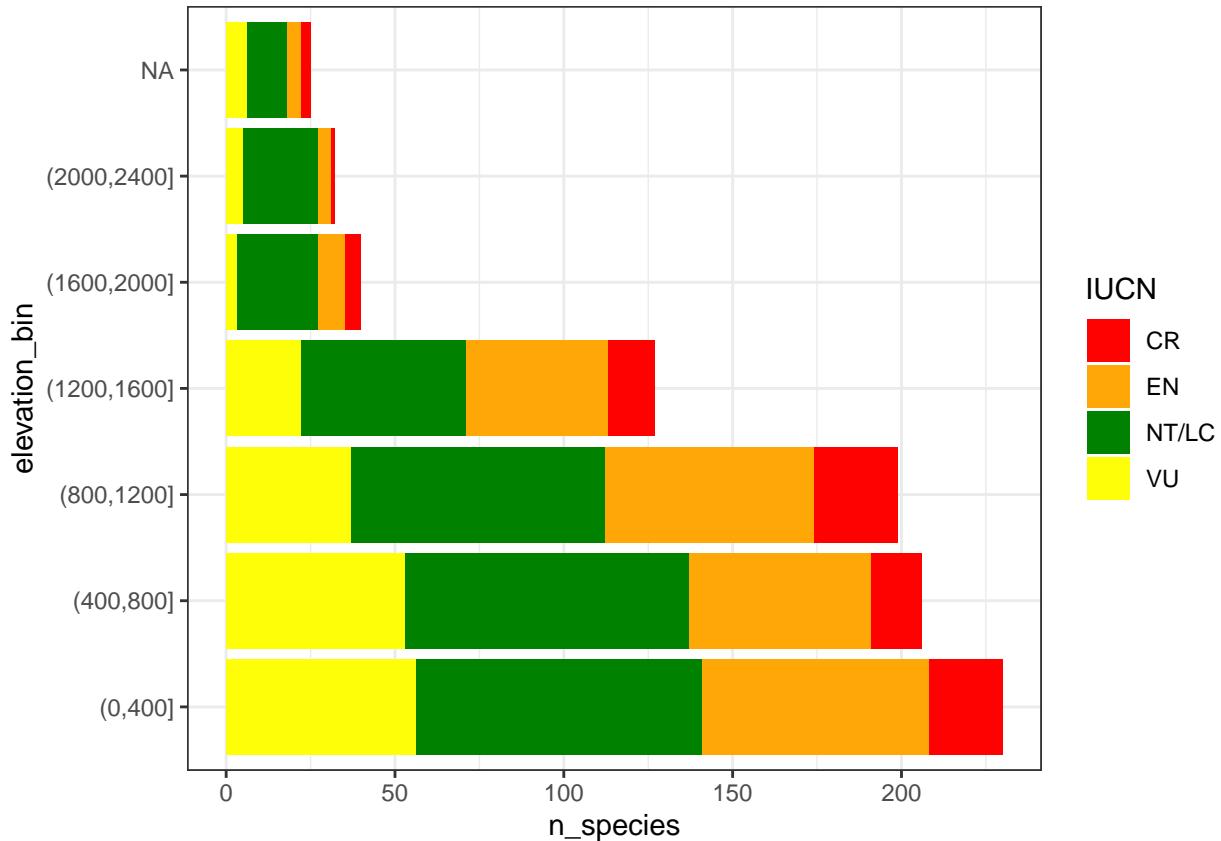
locations_spatial_d_b_i <- locations_spatial_d |>
  distinct(scntfcN, elevation_bin, iucn) |>
  group_by(elevation_bin, iucn) |>
  summarise(n_species=n(), .groups="drop")

locations_spatial_d_b_o <- locations_spatial_d |>
  distinct(scntfcN, elevation_bin, iucn, order) |>
  group_by(elevation_bin, iucn, order) |>
  summarise(n_species=n(), .groups="drop")

g_humb <- ggplot() +
  geom_col(locations_spatial_d_b_i,
           mapping=aes(x=n_species, y= elevation_bin, fill=iucn)) +
  scale_fill_manual("IUCN", values=iucn_color) +
  theme_bw()

ggsave("../plots/elevation_humb.png",
       plot=g_humb,
       device="png")

g_humb
```



```

g_humb_o <- ggplot() +
  geom_col(locations_spatial_d_b_o,
           mapping=aes(x=n_species, y= elevation_bin, fill=iucn)) +
  theme_bw() +
  scale_fill_manual("IUCN", values=iucn_color) +
  facet_wrap(vars(order), ncol=4, scales = "free")

ggsave("../plots/elevation_humb_o.png",
       plot=g_humb_o,
       height = 20,
       width = 40,
       units="cm",
       device="png")

g_elev <- ggplot() +
  geom_boxplot(locations_spatial_d,
               mapping = aes(x=iucn, y=elevatn),
               outlier.colour = "red",
               outlier.shape = 1) +
  theme_bw()
ggsave("../plots/elevation_iucn.png", plot=g_elev, device="png")

g_elev

```

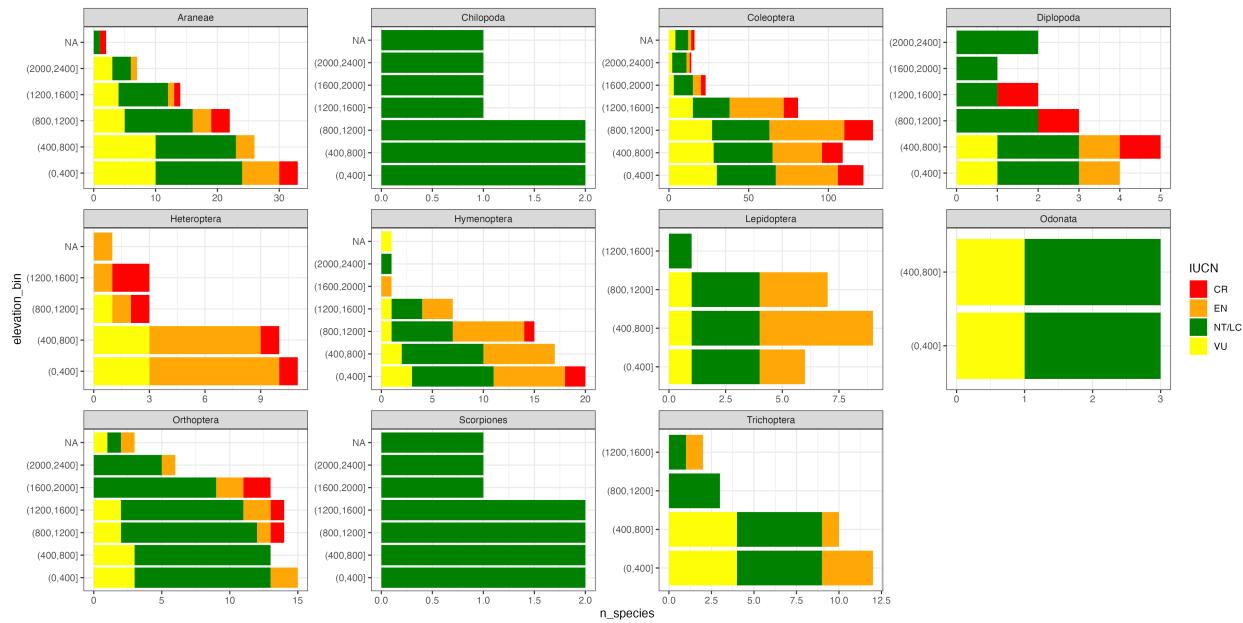
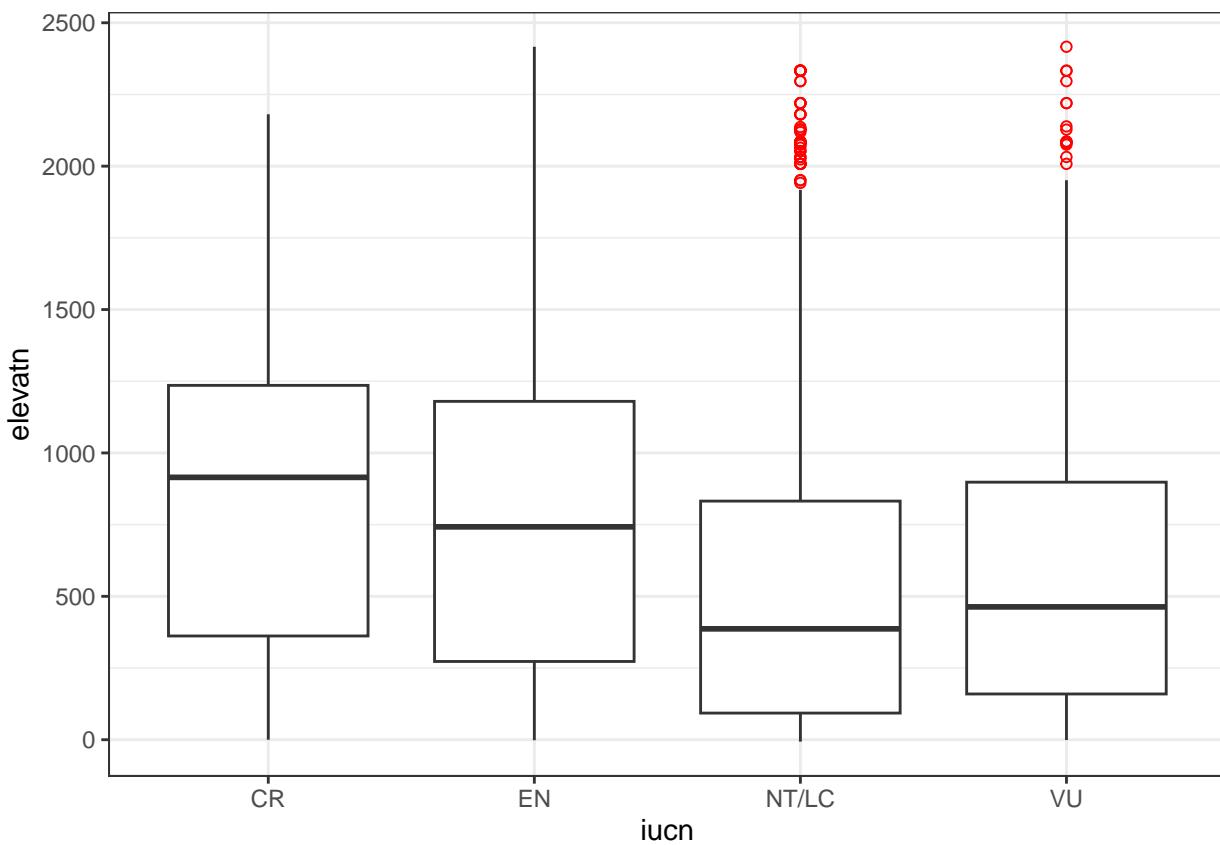


Figure 13: Altitude bins and the species that occur



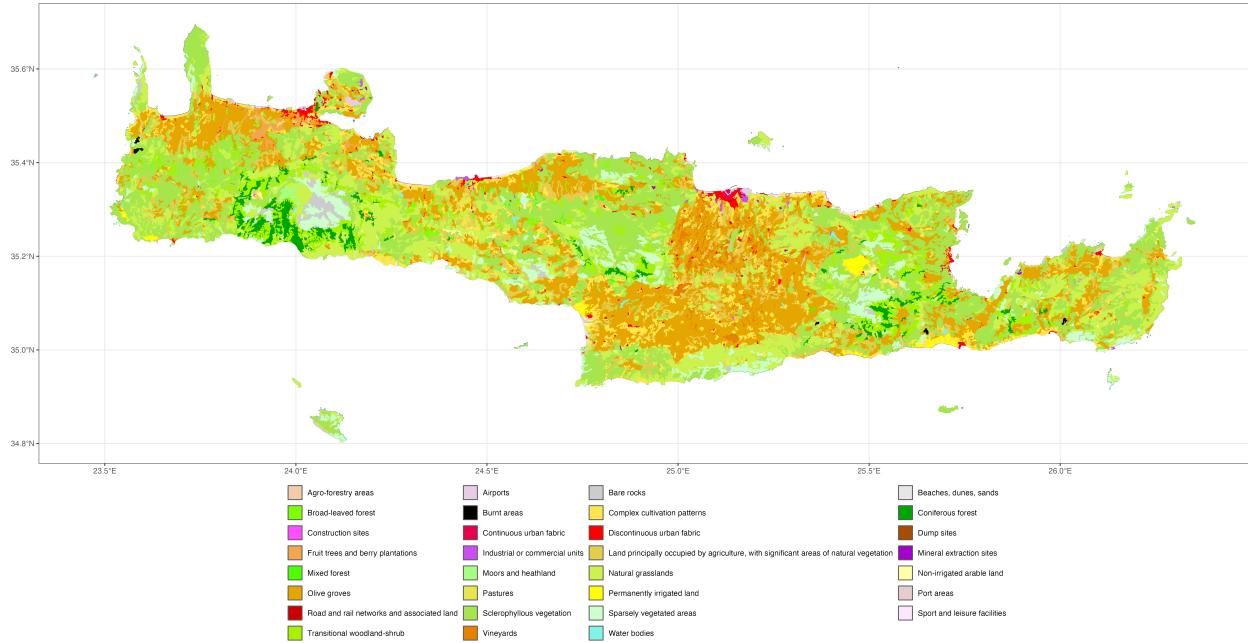


Figure 14: CORINE Land Cover 2018 (LABEL 3) in Crete

Habitats

```
clc_crete_label1 <- read_delim("../results/clc_crete_LABEL1.tsv", delim="\t") |>
  mutate(across(where(is.numeric), ~ round(.x,digits=2)))
```

```
knitr::kable(clc_crete_label1, "latex")
```

LABEL1	total_area	natura2000	wildlife	hotspots	threatspots	wege_kba
Agricultural areas	3618.20	301.93	57.42	275.12	240.07	301.11
Artificial surfaces	181.13	5.02	3.63	4.95	3.01	4.56
Forest and semi natural areas	4508.42	2040.26	545.58	1092.09	945.18	1058.80
Water bodies	6.74	2.50	1.80	0.99	0.31	0.31

```
clc_crete_label2 <- read_delim("../results/clc_crete_LABEL2.tsv", delim="\t") |>
  mutate(across(where(is.numeric), ~ round(.x,digits=2)))
```

```
knitr::kable(clc_crete_label2, "latex")
```

LABEL3	total_area	natura2000	wildlife	hotspots	threatspots	wege_kba
Agro-forestry areas	1.23	NA	NA	NA	NA	NA
Airports	13.17	NA	NA	NA	NA	NA
Bare rocks	63.46	61.15	4.03	33.83	7.82	7.82
Beaches, dunes, sands	4.03	NA	NA	NA	NA	NA
Broad-leaved forest	70.72	14.71	1.42	19.18	16.95	16.95
Burnt areas	4.10	NA	NA	NA	NA	NA
Complex cultivation patterns	443.16	54.19	7.39	29.28	20.44	28.15
Coniferous forest	219.01	181.81	58.94	143.79	125.10	127.55
Construction sites	3.35	0.32	0.57	0.32	0.32	0.32
Continuous urban fabric	8.98	NA	NA	NA	NA	NA
Discontinuous urban fabric	101.66	2.63	1.45	3.54	2.37	3.92
Dump sites	0.85	NA	NA	NA	NA	NA
Fruit trees and berry plantations	50.13	NA	NA	NA	NA	NA
Industrial or commercial units	19.12	0.39	0.94	0.25	0.25	0.25
Land principally occupied by agriculture, with significant areas of natural vegetation	658.57	75.06	12.32	64.14	60.62	72.02
Mineral extraction sites	5.85	NA	NA	NA	NA	NA
Mixed forest	10.21	2.69	0.01	0.65	0.65	2.17
Moors and heathland	12.97	12.97	0.00	12.93	12.15	12.15
Natural grasslands	1459.26	569.92	138.29	241.79	198.54	252.95
Non-irrigated arable land	32.50	12.86	0.45	8.24	8.24	8.24
Olive groves	2137.66	111.93	33.20	140.09	117.85	157.94
Pastures	59.25	15.11	1.81	8.50	8.05	9.71
Permanently irrigated land	55.79	21.25	0.57	18.66	18.66	18.66
Port areas	0.95	NA	NA	NA	NA	NA
Road and rail networks and associated land	6.53	0.10	0.03	0.08	0.08	0.08
Sclerophyllous vegetation	2007.26	718.71	241.57	374.81	363.67	405.68
Sparingly vegetated areas	339.06	259.03	42.55	108.89	80.79	90.40
Sport and leisure facilities	20.68	NA	NA	NA	NA	NA
Transitional woodland-shrub	318.34	217.42	58.77	155.67	139.21	142.82
Vineyards	179.91	4.94	1.66	4.75	4.75	4.93
Water bodies	6.74	2.50	1.80	0.99	0.31	0.31

LABEL2	total_area	natura2000	wildlife	hotspots	threatspots	wege_kl
Arable land	88.29	34.11	1.03	26.90	26.90	26.90
Artificial, non-agricultural vegetated areas	20.68	NA	NA	NA	NA	NA
Forests	299.93	199.20	60.36	163.62	142.70	146.00
Heterogeneous agricultural areas	1102.96	130.00	19.71	93.42	81.06	100.00
Industrial, commercial and transport units	39.77	0.65	0.97	0.33	0.33	0.33
Inland waters	6.74	2.50	1.80	0.99	0.31	0.31
Mine, dump and construction sites	10.05	0.57	1.15	0.32	0.32	0.32
Open spaces with little or no vegetation	410.66	322.04	46.58	143.27	88.91	98.50
Pastures	59.25	15.11	1.81	8.50	8.05	9.71
Permanent crops	2367.70	122.71	34.87	146.30	124.06	164.00
Scrub and/or herbaceous vegetation associations	3797.83	1519.02	438.63	785.19	713.57	813.00
Urban fabric	110.63	2.63	1.45	3.54	2.37	3.92

```
clc_crete_label3 <- read_delim("../results/clc_crete_LABEL3.tsv", delim="\t") |>
  mutate(across(where(is.numeric), ~ round(.x,digits=2)))
```

```
kbl(clc_crete_label3) |> kable_styling(latex_options = "scale_down")
```

Summary

A summary table of each order.

```
order_taxa <- endemic_species |>
  group_by(order) |>
  summarise(taxa=n())

order_sites <- locations_shp |>
  distinct(order,decimalLatitude,decimalLongitude) |>
  group_by(order) |>
```

```

    summarise(sites=n())

order_occ <- locations_shp |>
  group_by(order) |>
  summarise(occurrences=n()) |>
  st_drop_geometry()

order_locations <- locations_grid |>
  distinct(CELLCOD, order) |>
  group_by(order) |>
  summarise(locations=n())

order_iucn <- endemic_species_s_i |>
  pivot_wider(names_from=iucn,
              values_from=c(n_species,proportion),
              id_cols=order) |>
  group_by(order) |>
  rowwise() |>
  mutate(threatened=sum(n_species_EN,n_species_VU,n_species_CR,na.rm=TRUE),
         proportion_threatened=threatened/sum(n_species_EN,n_species_VU,n_species_CR,`n_species_NT/L`))

order_paca <- endemic_species_s_o |>
  pivot_wider(names_from=paca,
              values_from=c(n_species,proportion),
              id_cols=order)

order_total_l <- list(order_taxa,order_sites,order_occ,order_locations,order_iucn,order_paca)

order_total <- order_total_l |> reduce(full_join, by="order")

total_iucn <- endemic_species_i |>
  pivot_wider(names_from=iucn,
              values_from=c(n_species,proportion)) |>
  dplyr::select(-method) |>
  rowwise() |>
  mutate(threatened=sum(n_species_EN,n_species_VU,n_species_CR,na.rm=TRUE),
         proportion_threatened=threatened/sum(n_species_EN,n_species_VU,n_species_CR,`n_species_NT/L`))

total_paca <- endemic_species_p |>
  pivot_wider(names_from=paca,
              values_from=c(n_species,proportion)) |>
  dplyr::select(-method)

total_data <- data.frame(order="total",
                           taxa = length(unique(endemic_species$scientificName)),
                           sites = nrow(unique(st_coordinates(locations_shp))),
                           occurrences = nrow(locations_shp),
                           locations = length(unique(locations_grid$CELLCOD)))

total_row <- cbind(total_data, total_paca, total_iucn)

total_summary <- rbind(total_row, order_total)

```

order	taxa	ctoz	occurrences	locations	n. species_LNT	n. species_LT	n. species_PT	proportion_LNT	proportion_LT	proportion_PT	n. species_CR	n. species_EN	n. species_NT/UC	n. species_VU	proportion_CR	proportion_EN	proportion_NT/UC	proportion_VU	threatened	proportion_threatened
total	343	1539	4924	135	85	195	62	0.25	0.27	0.18	75	120	86	62	0.22	0.25	0.25	0.18	257	0.7492711
Arisaeidae	40	253	523	102	14	16	10	0.35	0.40	0.25	7	9	14	10	0.17	0.22	0.35	0.25	26	0.6500000
Archaeognatha	1	1	1	1	1	1	1	1.00	1.00	1.00	NA	NA	NA	NA	1.00	1.00	1.00	1.00	1	1.0000000
Coleoptera	206	925	2584	128	38	132	36	0.18	0.64	0.17	54	78	38	36	0.26	0.28	0.18	0.17	168	0.8153340
Diplopoda	7	74	101	46	2	4	1	0.29	0.57	0.14	3	1	2	1	0.43	0.14	0.29	0.14	5	0.7142875
Heteroptera	17	46	138	21	NA	1	3	NA	0.50	0.18	5	9	NA	3	0.29	0.51	NA	0.18	17	1.0000000
Homoptera	29	363	259	71	5	14	3	0.32	0.56	0.12	3	11	3	2	0.12	0.44	0.32	0.12	17	0.6800000
Lepidoptera	9	40	65	32	3	5	1	0.33	0.56	0.11	NA	5	3	1	NA	0.56	0.33	0.14	6	0.6666667
Odonata	3	18	49	20	NA	2	NA	0.67	NA	0.33	NA	NA	NA	NA	0.67	0.33	1	NA	0.3333333	
Ostracoda	29	363	527	101	10	11	3	0.24	0.51	0.11	3	11	10	3	0.13	0.29	0.29	0.14	10	0.5000000
Scorpiones	2	240	254	88	2	NA	NA	1.00	NA	NA	NA	NA	NA	NA	1.00	NA	NA	0	0.0000000	
Tischoptera	12	66	157	43	5	3	4	0.42	0.25	0.33	NA	3	5	4	NA	0.25	0.42	0.33	7	0.5833333

```
write_delim(total_summary, "../results/total_summary.tsv", delim="\t")
```

```
tbl(total_summary) |> kable_styling(latex_options = "scale_down")
```

AOO distribution summaries

```
summary(endemic_species$aoo)
```

```
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
```

```
##    3.998   8.021  24.038  58.517  63.959 955.818
```

```
sd(endemic_species$aoo)
```

```
## [1] 109.1561
```

```
summary(endemic_species$aoo_natura)
```

```
##      Min. 1st Qu. Median   Mean 3rd Qu.   Max.
```

```
##    0.000   4.006  11.244  27.177  28.091 437.461
```

```
sd(endemic_species$aoo_natura)
```

```
## [1] 50.96666
```