

Arthropoda species assessment results

21 February, 2023

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Load the data

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

g_base <- g_base()

locations_shp <- sf::st_read("../data/arthropods_occurrences/arthropods_occurrences.shp")
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 7690 occurrences of 343 species that belong to 11 orders.

The unique locations are:

```

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

## [1] 1569

```

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")

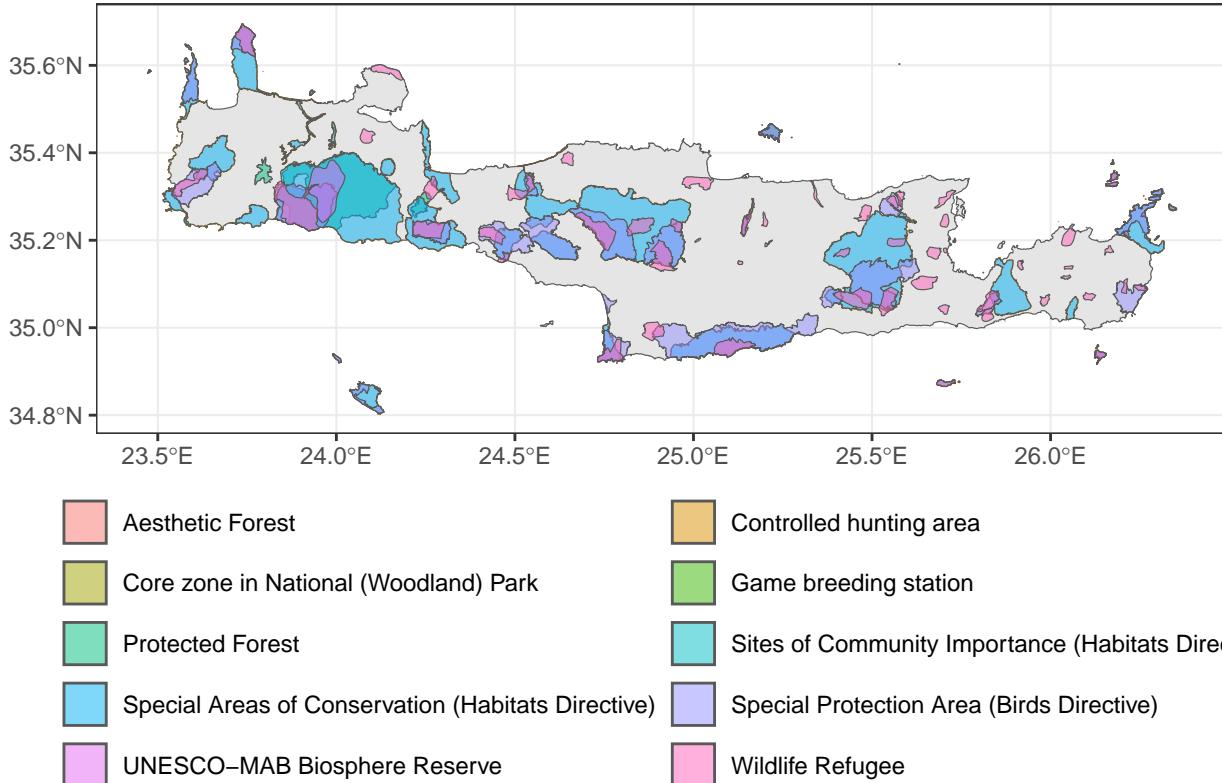
```

name	area
Aesthetic Forest	0.17 [km ²]
Sites of Community Importance (Habitats Directive)	0.34 [km ²]
Game breeding station	1.02 [km ²]
Controlled hunting area	11.59 [km ²]
Core zone in National (Woodland) Park	47.56 [km ²]
UNESCO-MAB Biosphere Reserve	88.65 [km ²]
Protected Forest	417.74 [km ²]
Wildlife Refugee	610.70 [km ²]
Special Protection Area (Birds Directive)	1261.78 [km ²]
Special Areas of Conservation (Habitats Directive)	2371.42 [km ²]
total protected (no overlap)	2900.59 [km ²]
total protected	4810.96 [km ²]
crete	8346.55 [km ²]

```
g_wdpa <- g_base +
  geom_sf(wdpa_crete, mapping=aes(fill=DESIG_ENG), alpha=0.5, size=0.1) +
  theme_bw() +
  theme(legend.position="bottom", legend.margin=margin()) +
  guides(fill=guide_legend(nrow=5, byrow=TRUE, title=""))
```

```
ggsave("../plots/wdpa_protected_aread.png", g_wdpa, device="png")
```

```
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"))

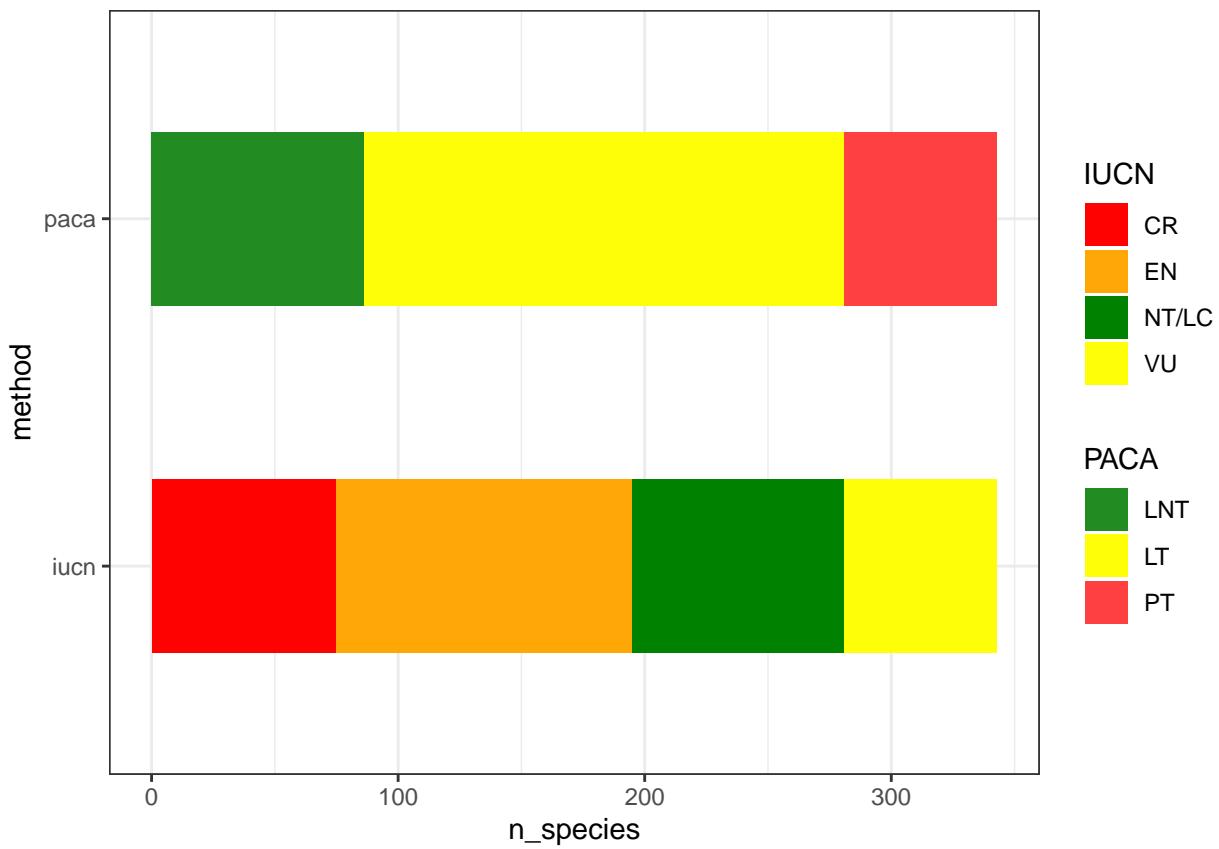
endemic_species_p <- endemic_species %>%
  group_by(paca) %>%
  summarise(n_species=n(), .groups="drop") %>%
#  rename("category"="paca") %>%
  mutate(method="paca") %>%
  mutate(proportion = round(n_species/sum(n_species), digits=2))

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

```



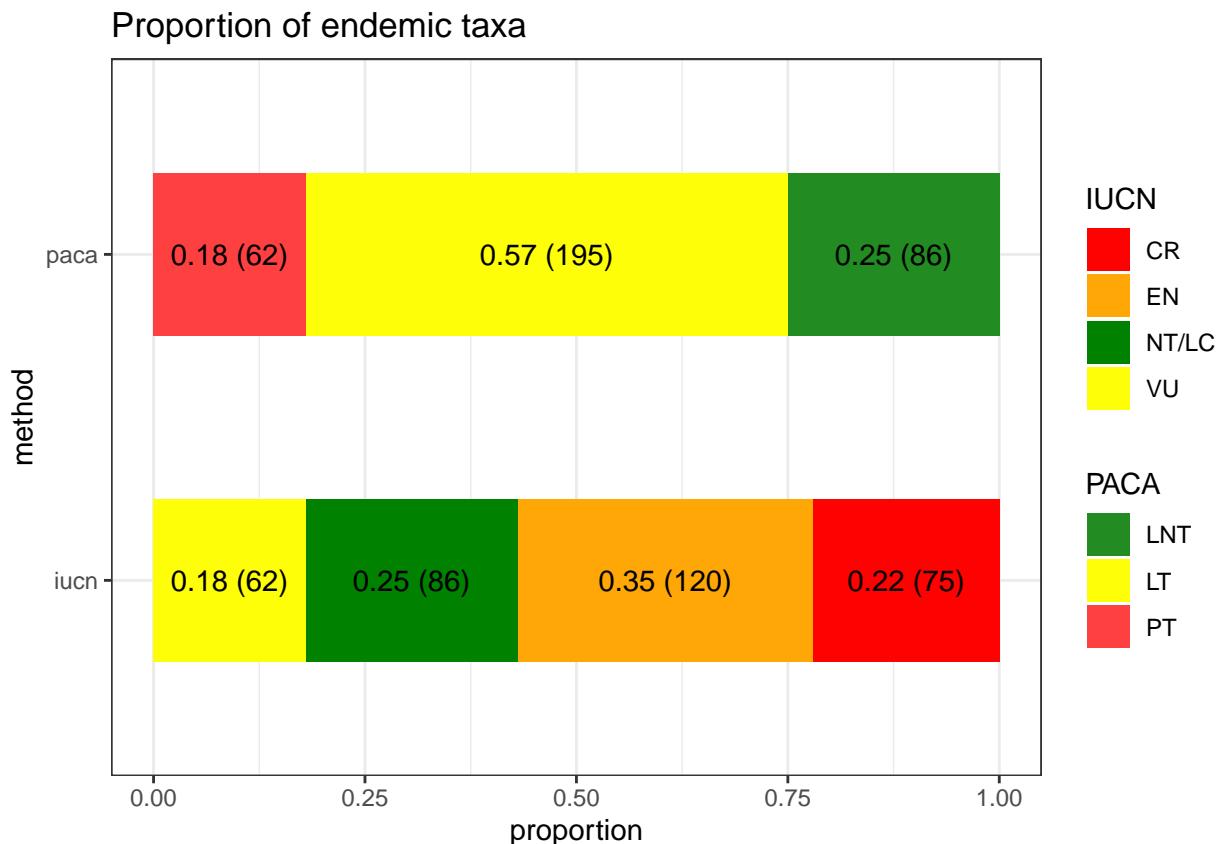
```

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
```

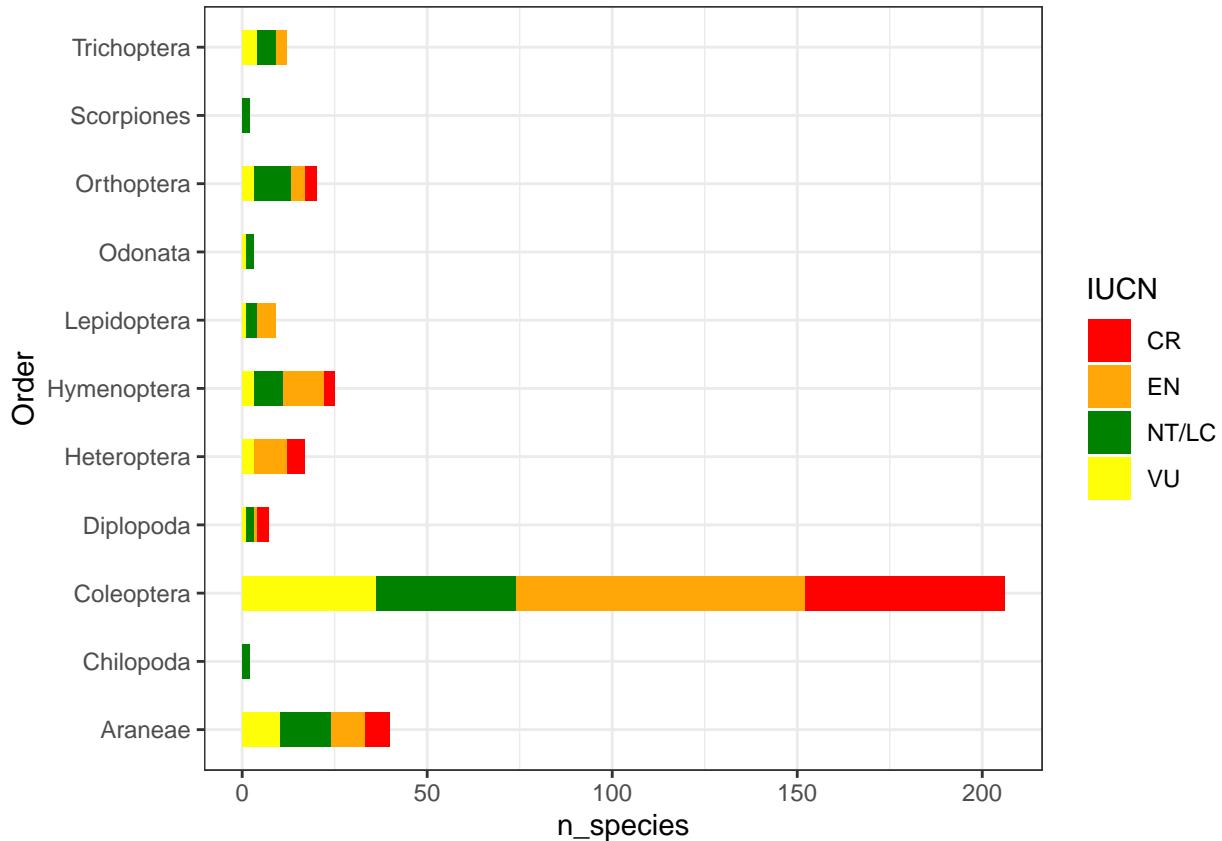


IUCN categories per Order:

```
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
```

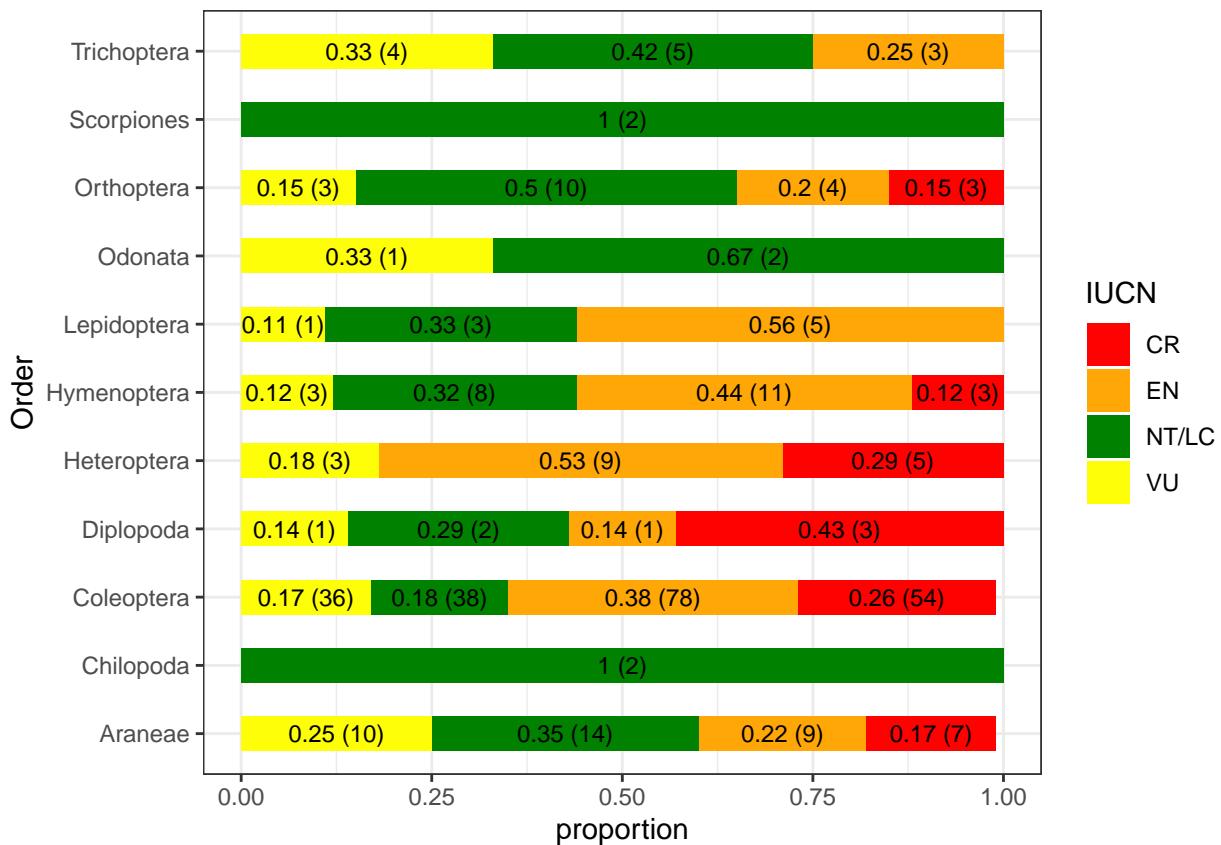


```

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:

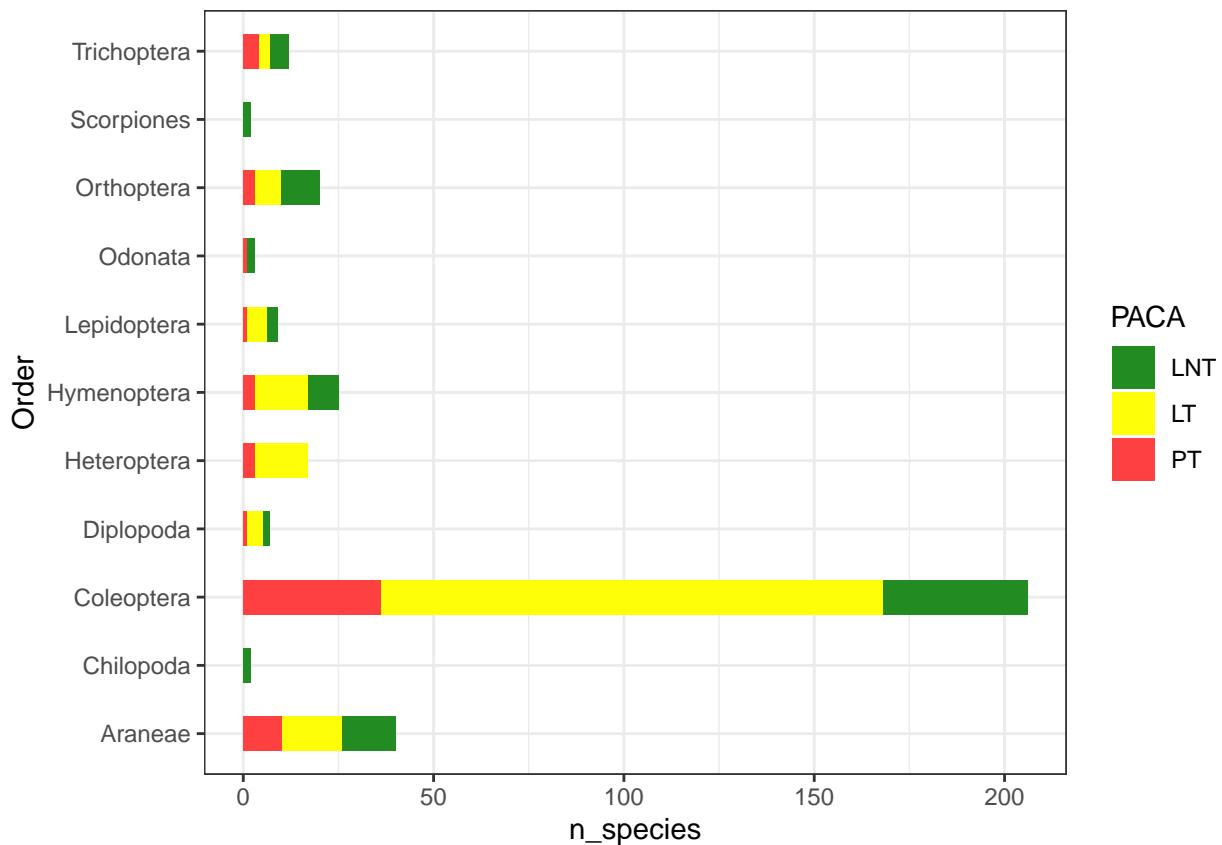
```

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,
       height = 15,
       units='cm',
       device="png")
g_paca_o

```

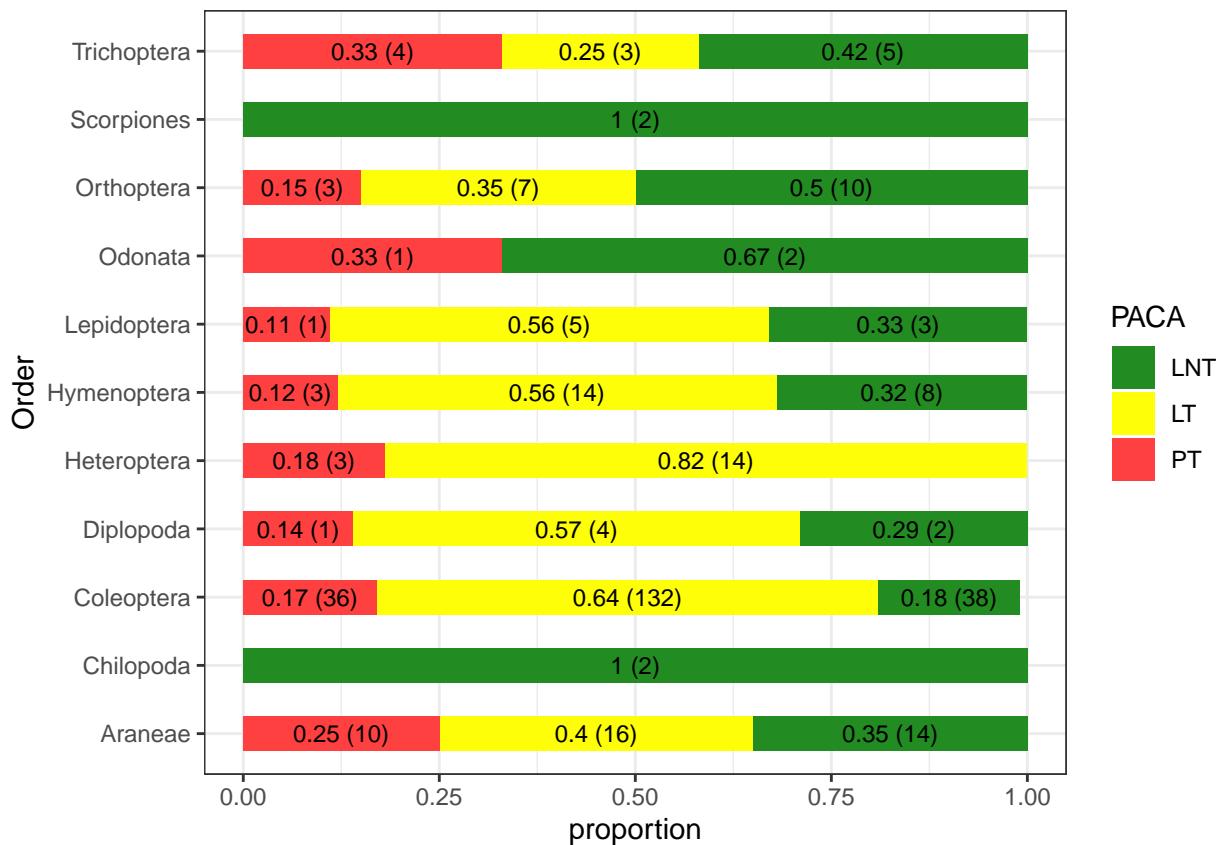


```

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

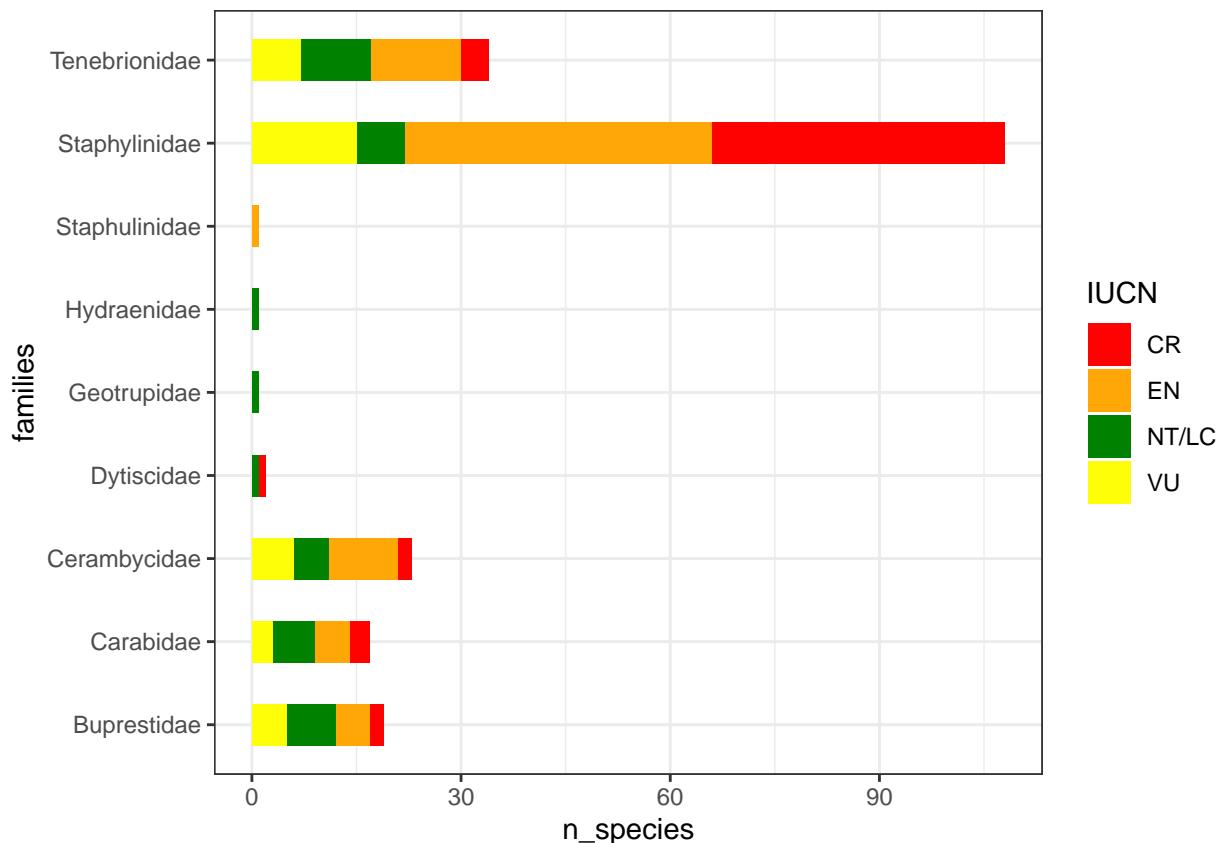
```

endemic_species_coleoptera <- endemic_species %>%
  filter(Order=="Coleoptera") %>%
  group_by(iucn, families) %>%
  summarise(n_species=n(), .groups="drop")

g_iucn_c <- ggplot() +
  geom_col(data=endemic_species_coleoptera,
            aes(x=n_species,y=families, 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

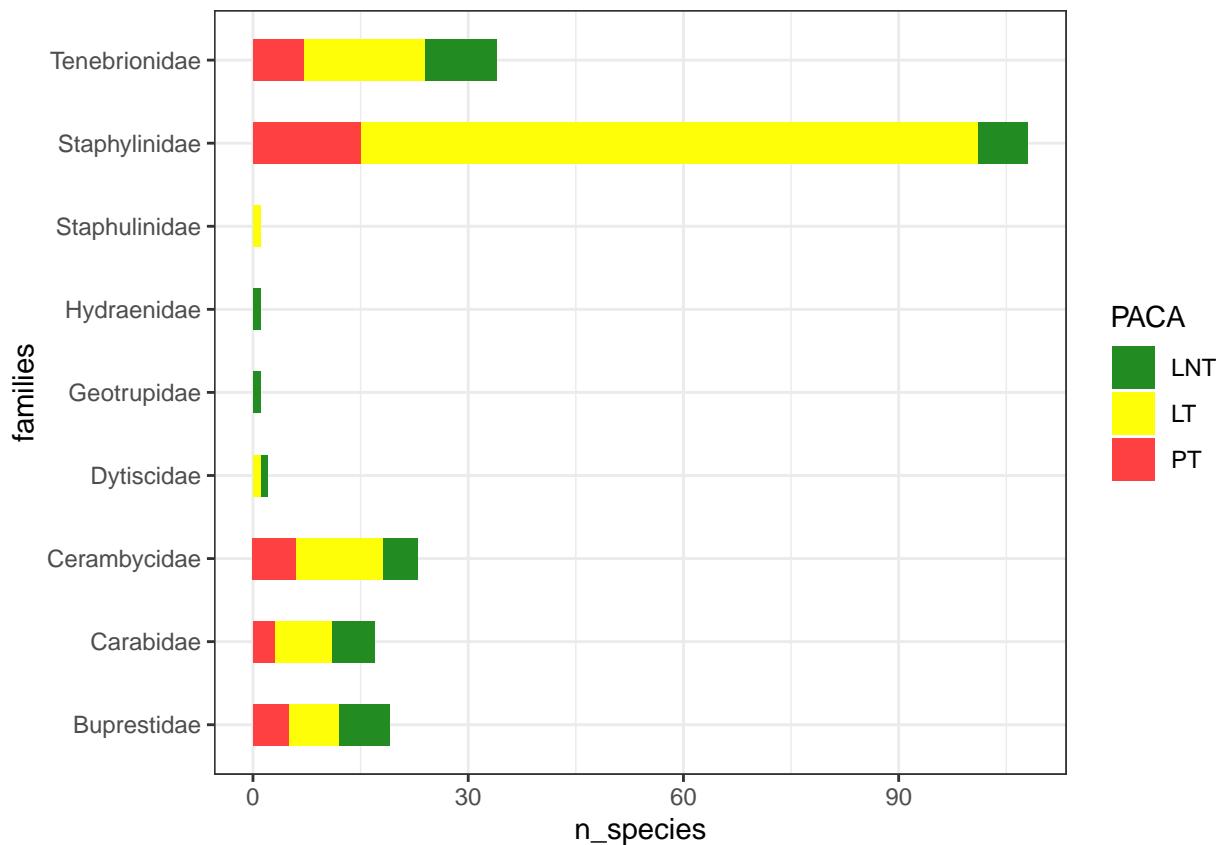
```

endemic_species_coleoptera_p <- endemic_species %>%
  filter(Order=="Coleoptera") %>%
  group_by(paca, families) %>%
  summarise(n_species=n(), .groups="drop")

g_iucn_c_p <- ggplot() +
  geom_col(data=endemic_species_coleoptera_p,
            aes(x=n_species,y=families, 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

```

Endemic hotspots

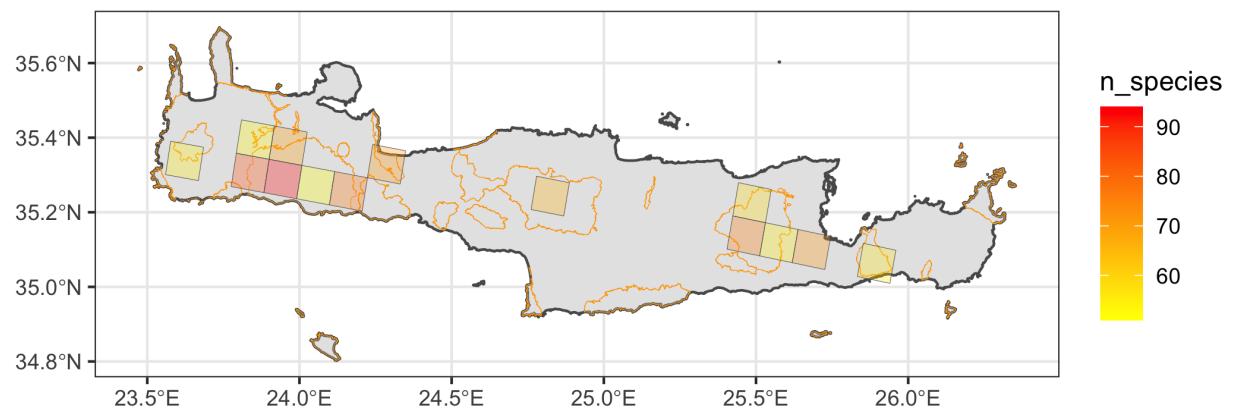


Figure 1: Crete endemic hotspots

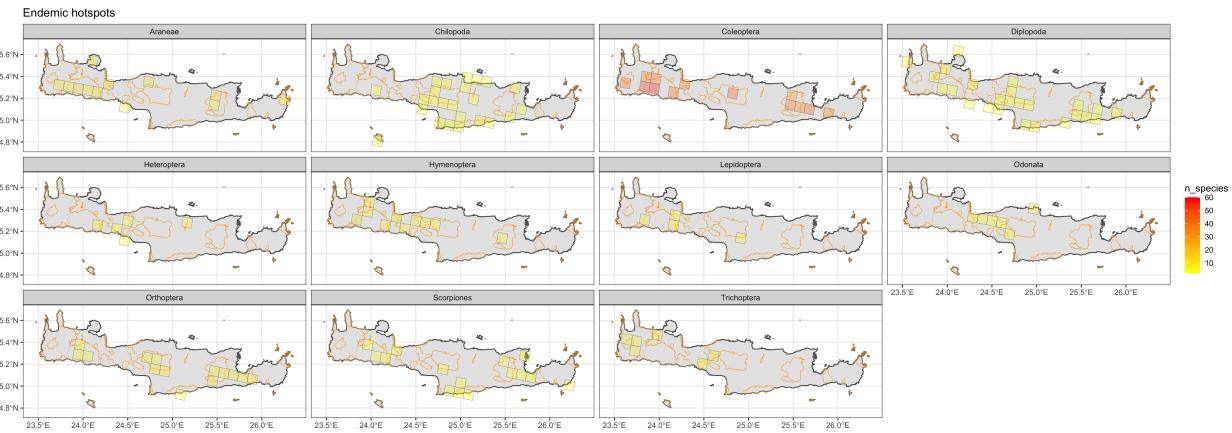
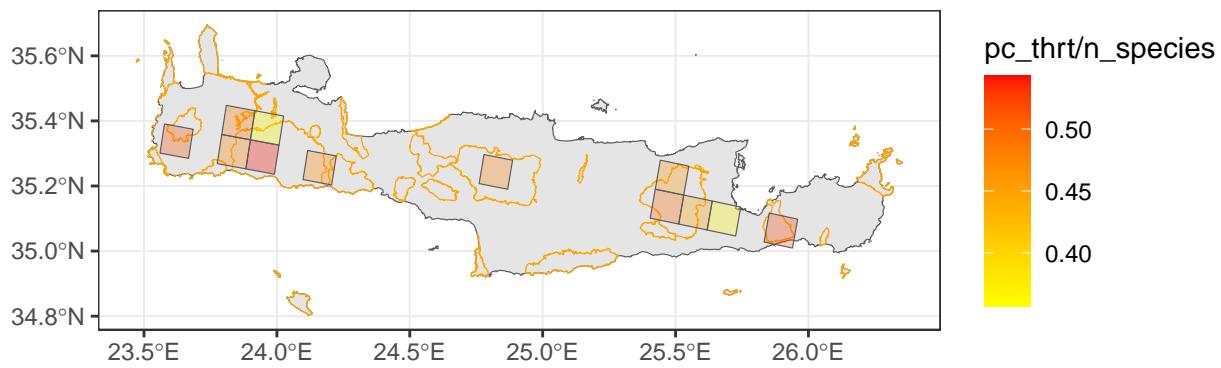


Figure 2: Crete endemic hotspots per order

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

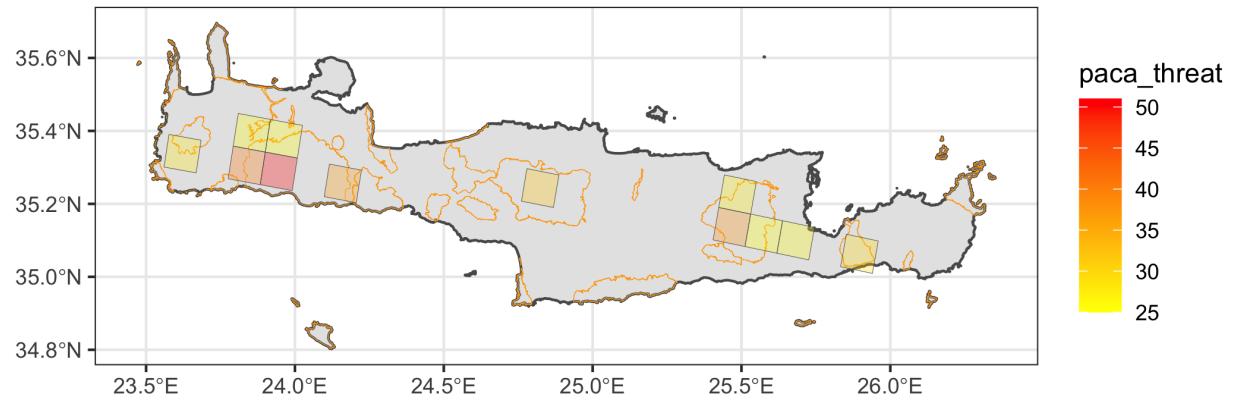


Figure 3: Crete endemic threatspots

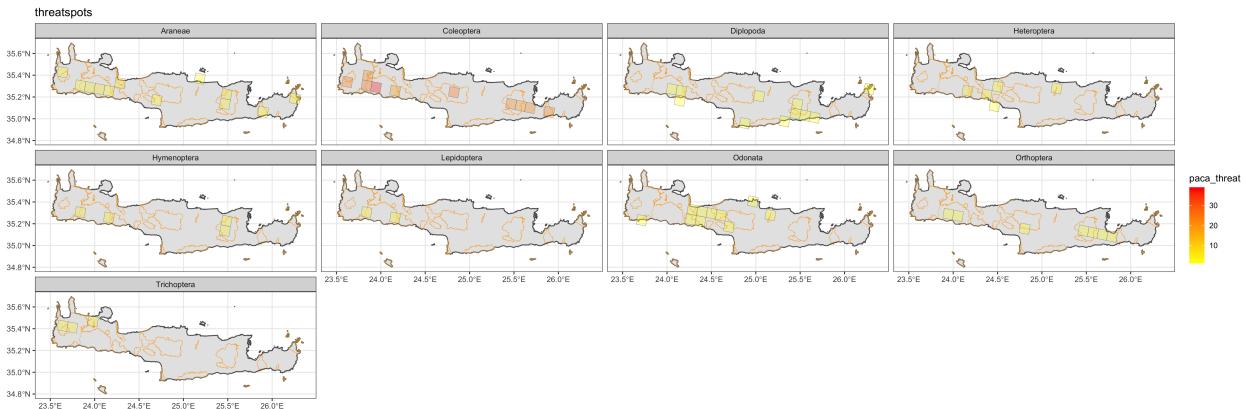


Figure 4: Crete endemic threatspots per order

Endemic hotspots and threatspots

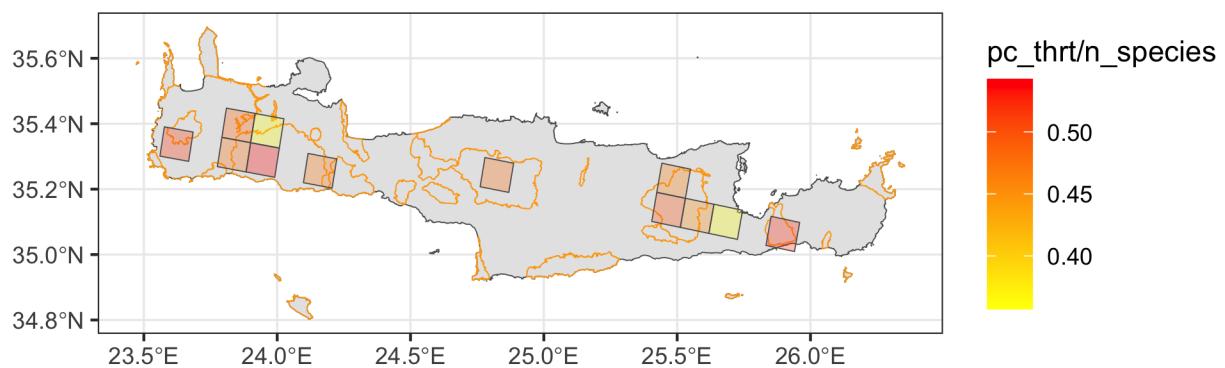


Figure 5: Overlap of hotspots with threatspots

```

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(sbspcsn %in% species_10_natura$subspeciesname) %>%
  group_by(CELLCOD) %>%
  summarise(n_species=n()) %>%
  filter(n_species>2)

species_10_natura_l_o <- locations_grid %>%
  filter(sbspcsn %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

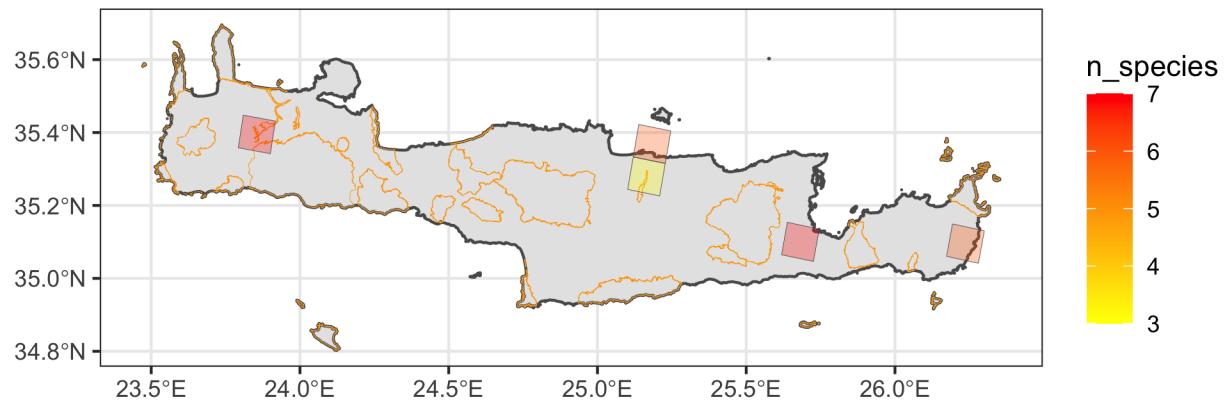


Figure 6: Hotspots of < 10% AOO overlap with Natura2000

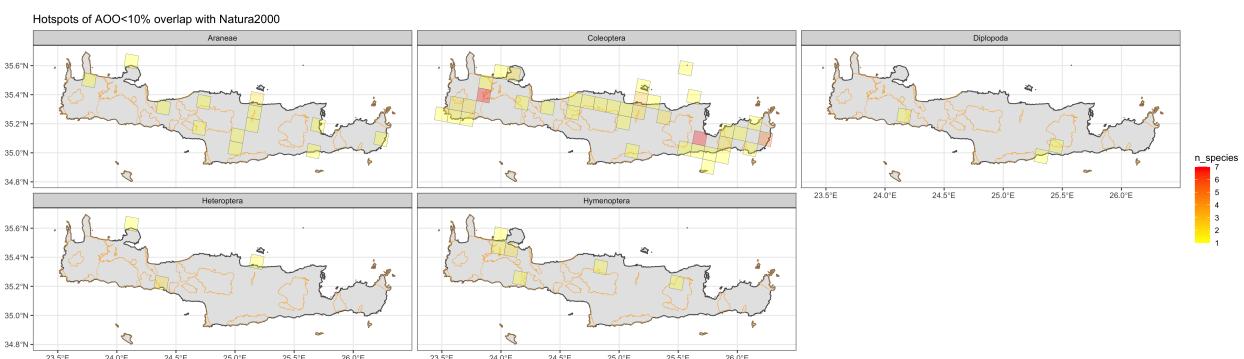


Figure 7: Hotspots of < 10% AOO overlap with Natura2000 per Order

```

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(CELLCOD %in% endemic_hotspots$CELLCODE) %>%
  distinct(CELLCOD, 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)

```

```
dpi = 300)
```

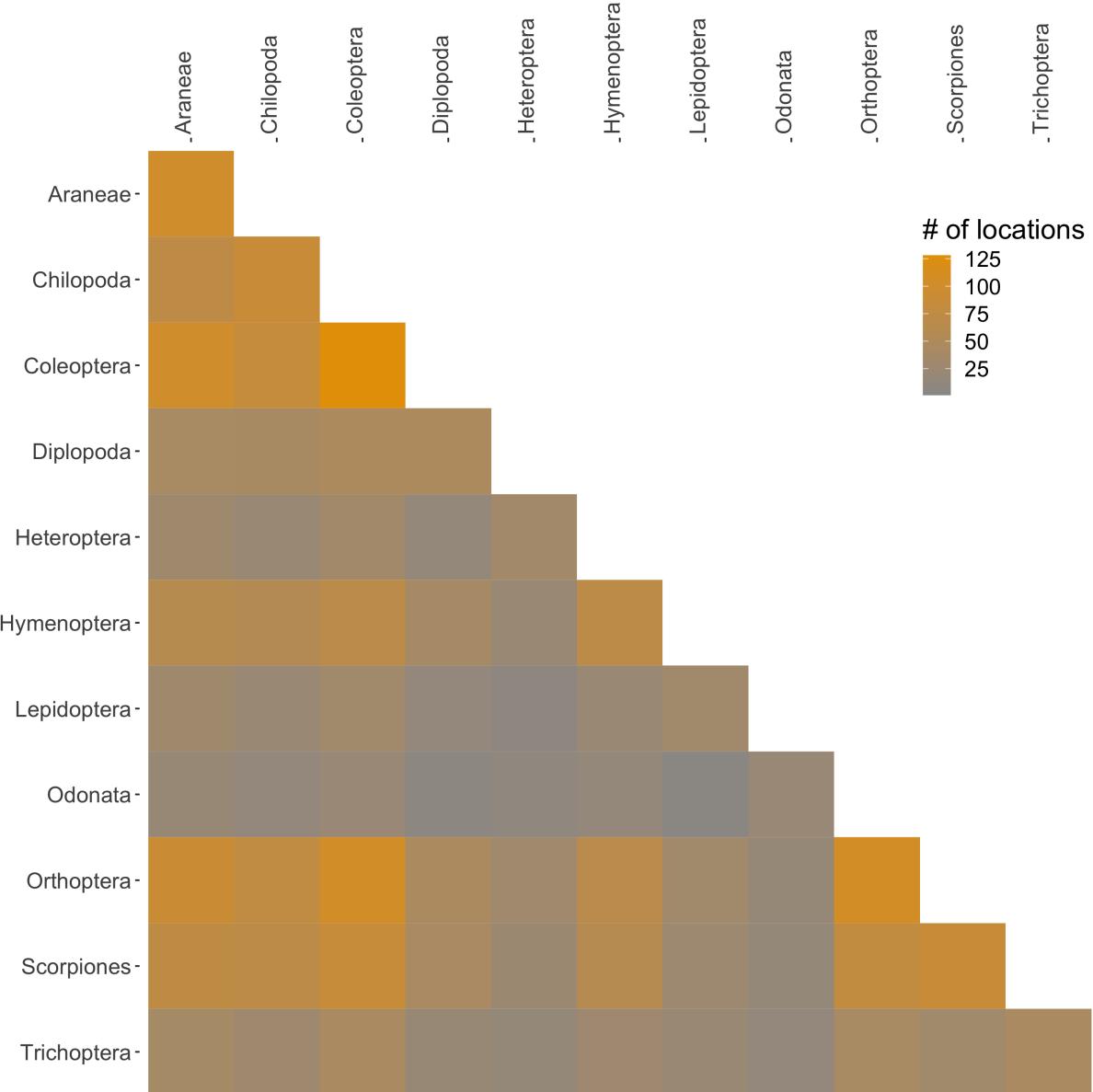


Figure 8: Shared locations of arthropod orders

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=aoe, y=eoo, color=iucn)) +  
  scale_color_manual("IUCN", values=iucn_color) +
```

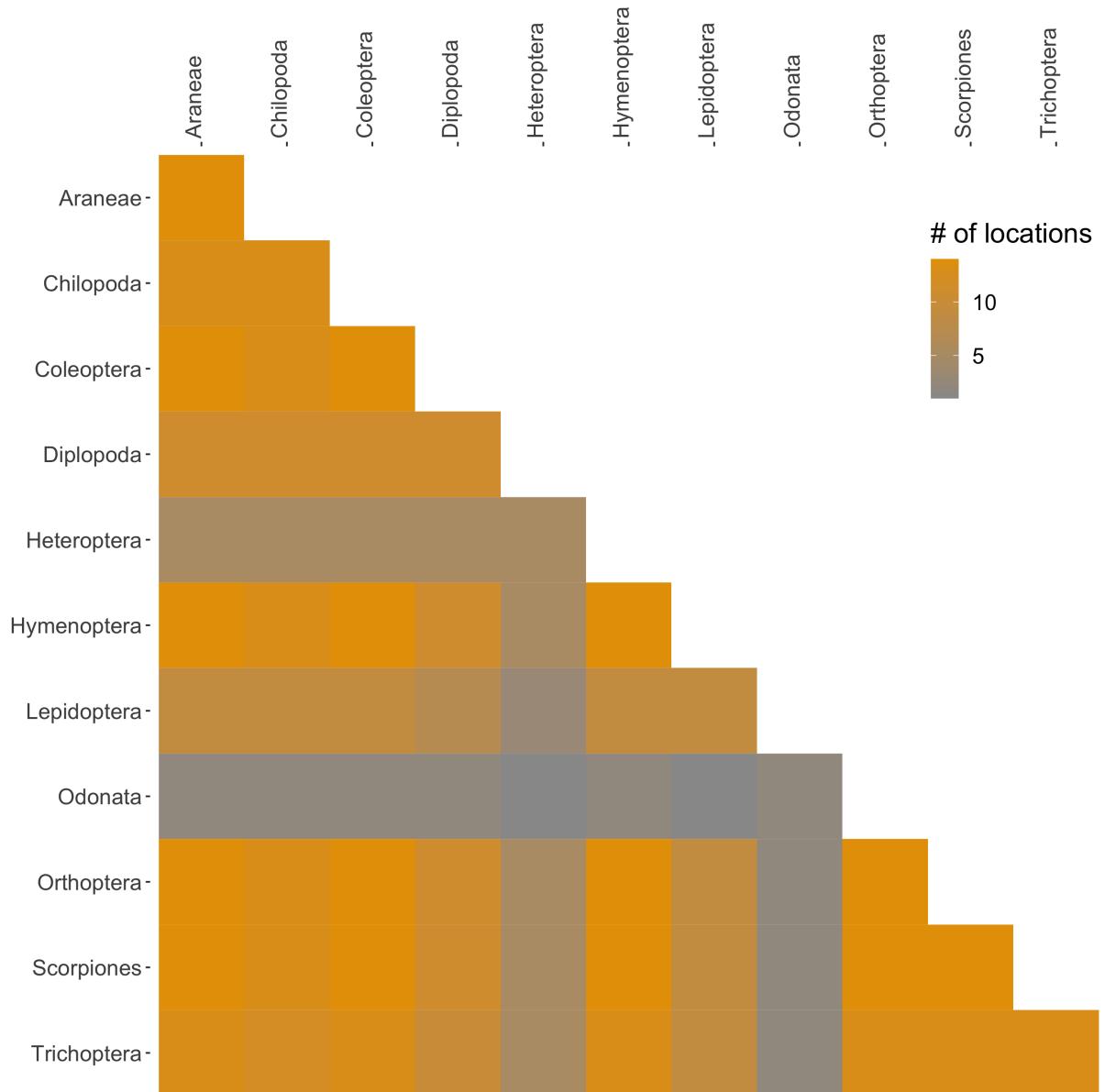


Figure 9: Shared hotspots of arthropod orders

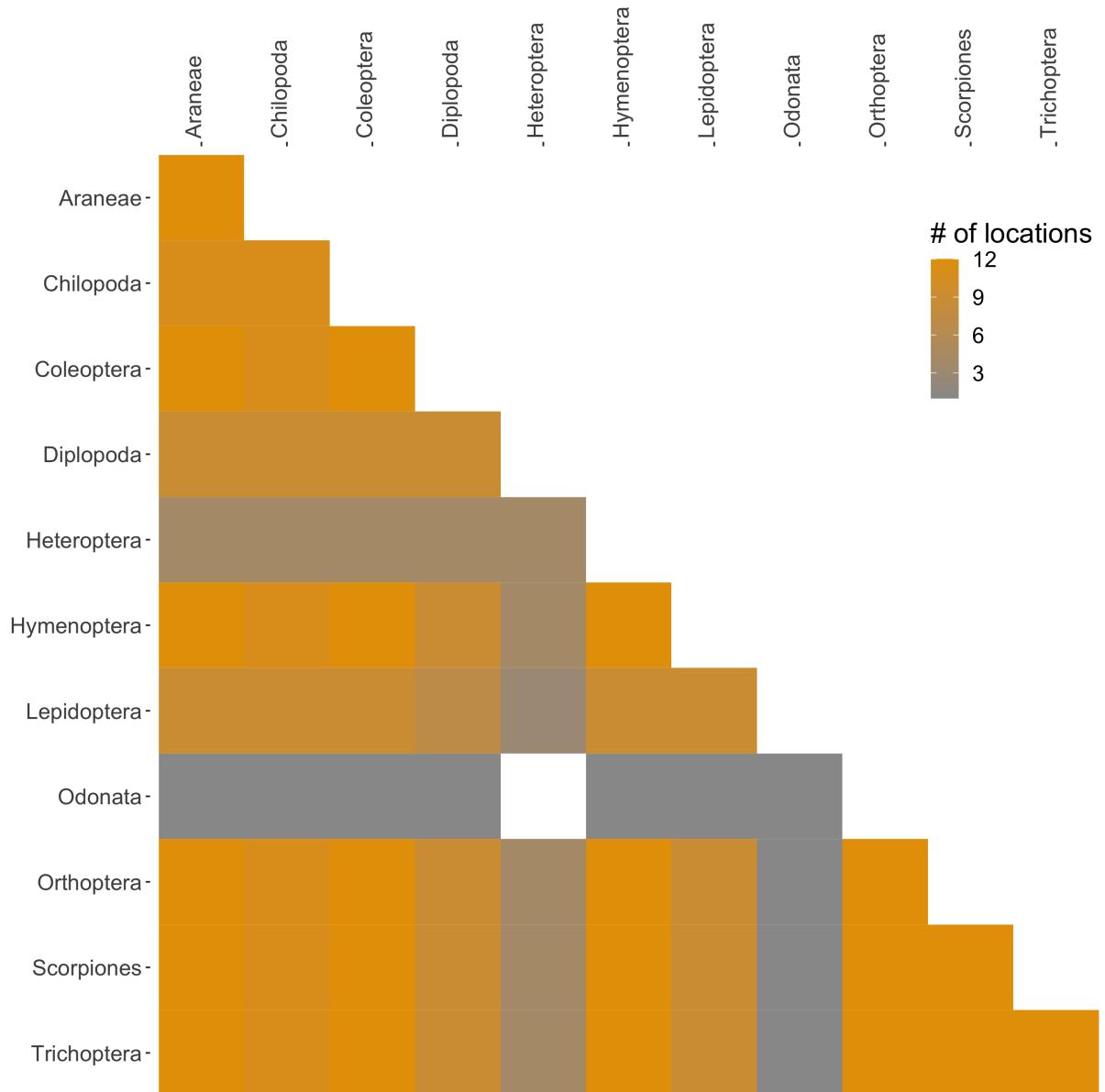


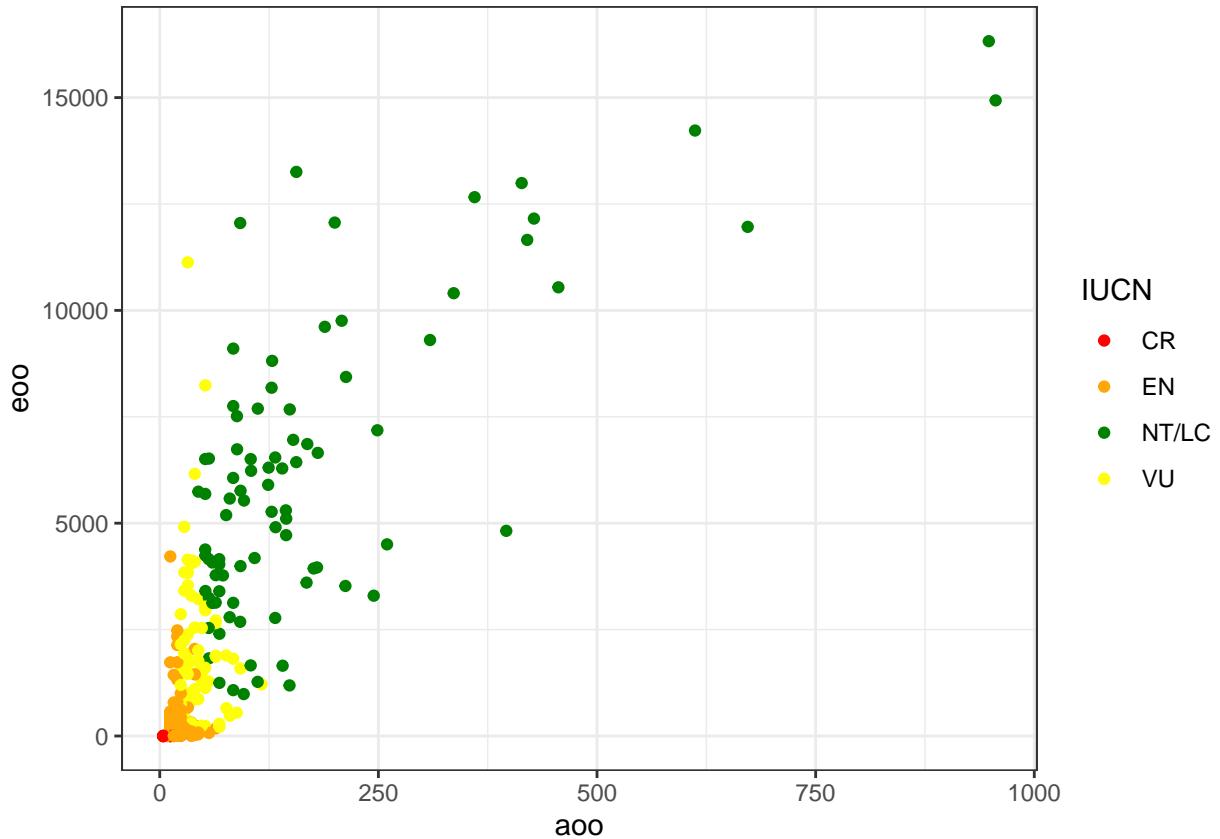
Figure 10: Shared threatspots of arthropod orders

```

    theme_bw()
ggsave("../plots/aoo-eoo_dist.png", plot=g_e_o, device="png")

```

g_e_o



```

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")

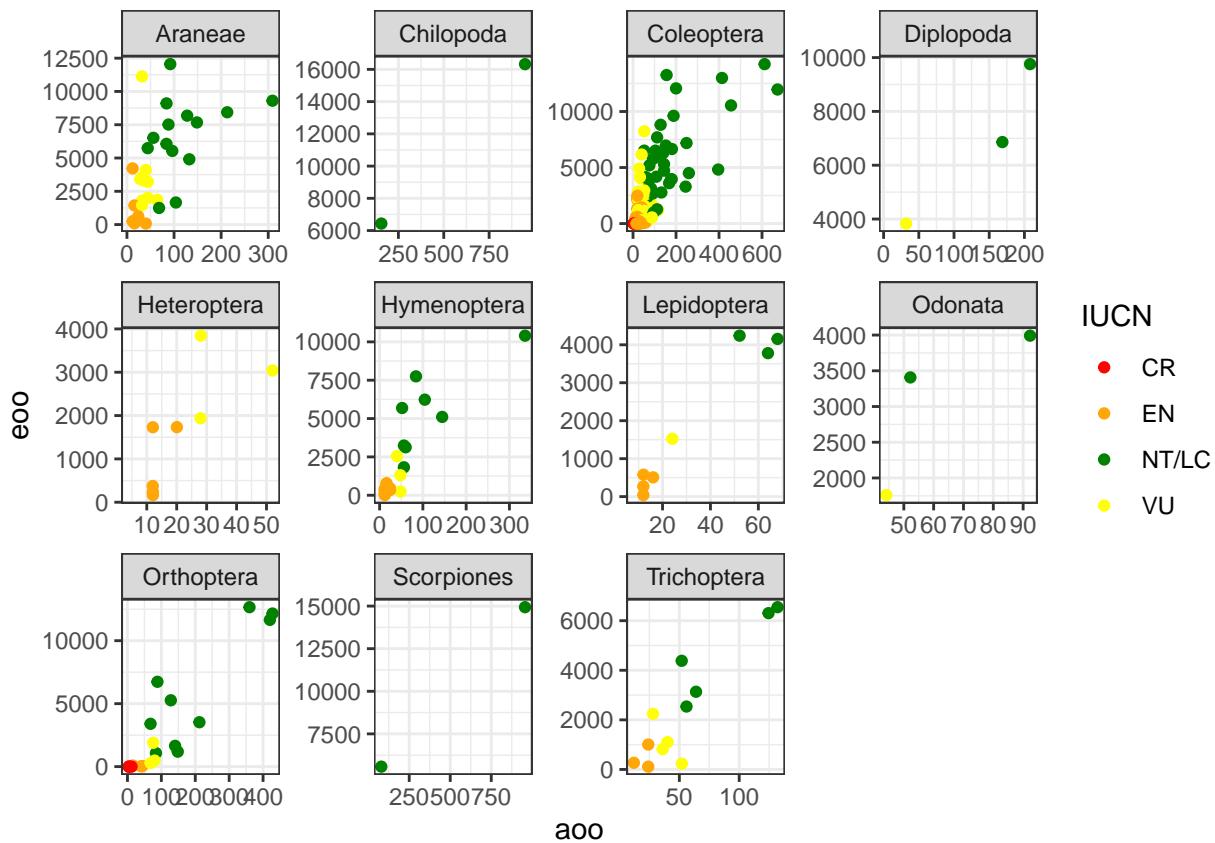
```

```

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

```

g_e_o_order

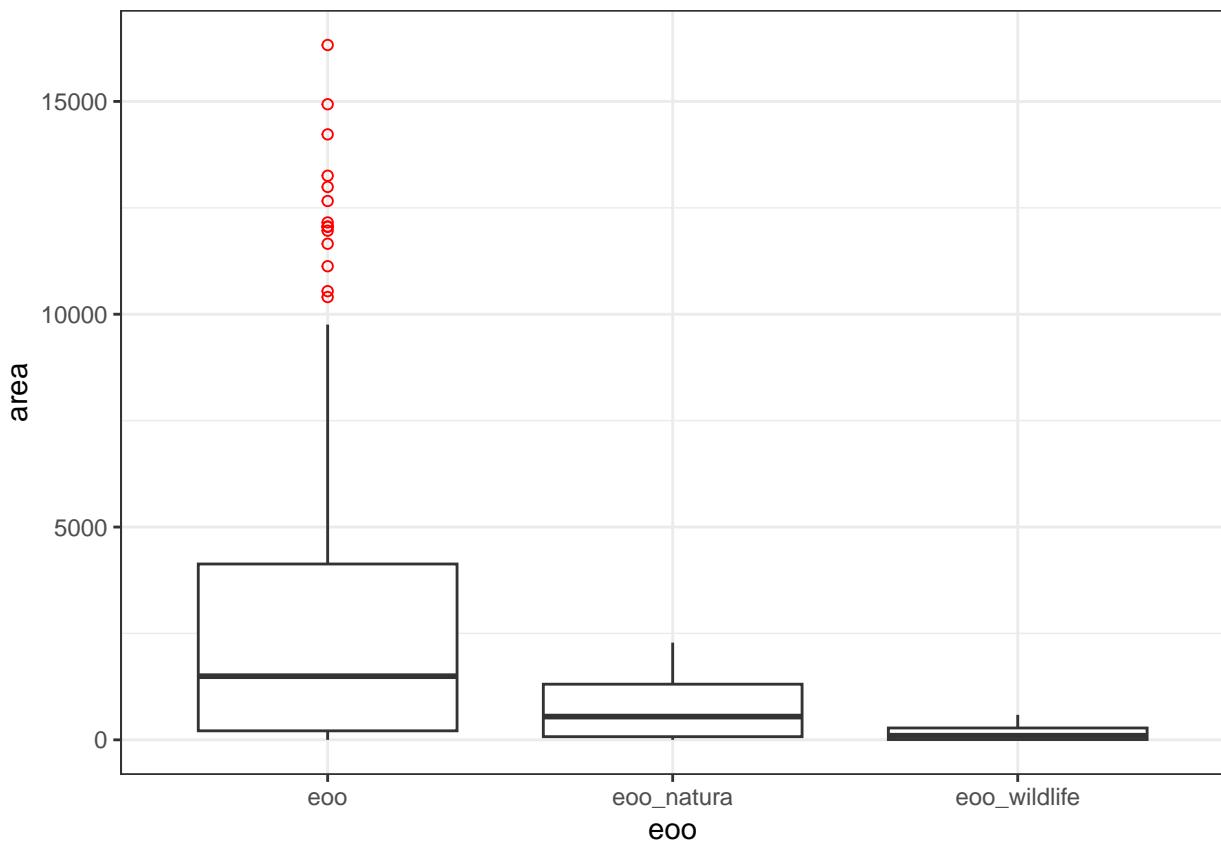


EOO area distribution

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

```
endemic_species_eoo <- endemic_species %>%
  dplyr::select(subspeciesname, 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(subspeciesname, 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")

```

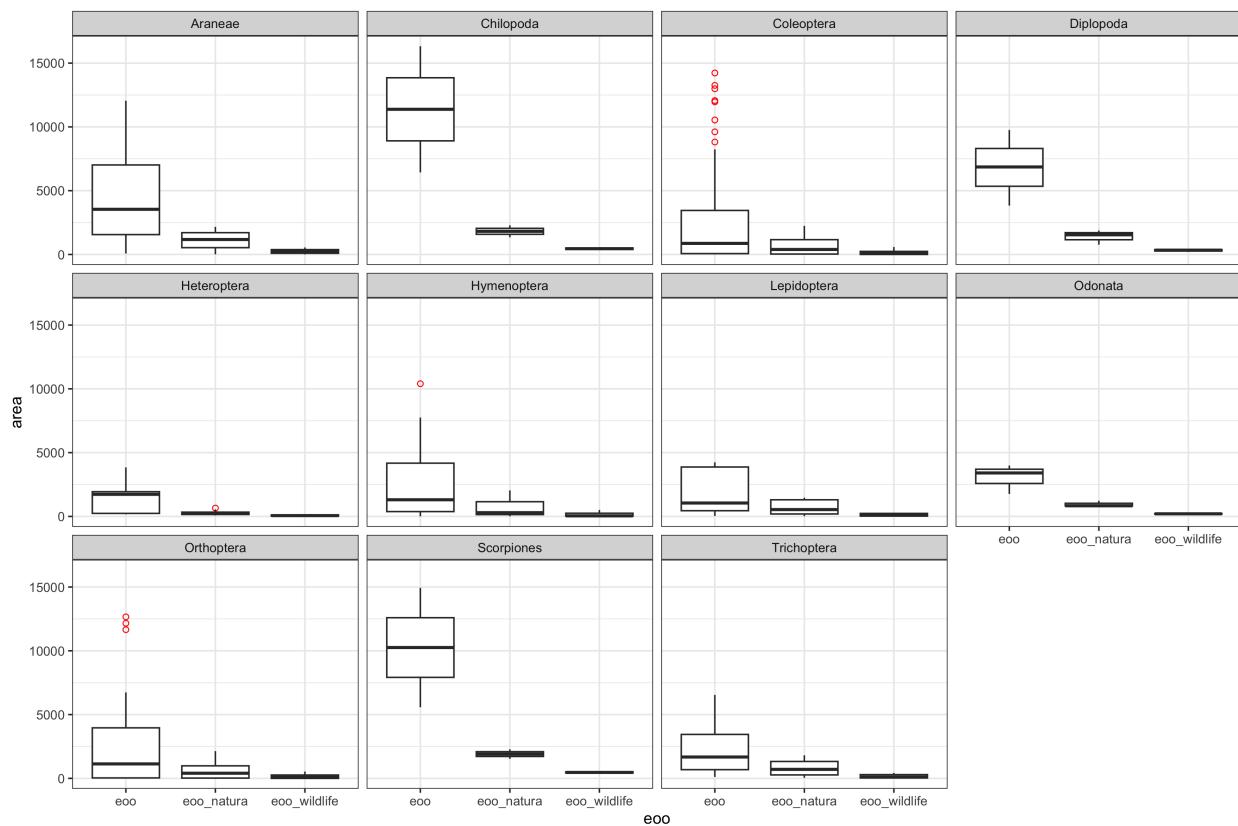


Figure 11: Distributions of EOO and overlaps per Order

AOO area distribution

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

```

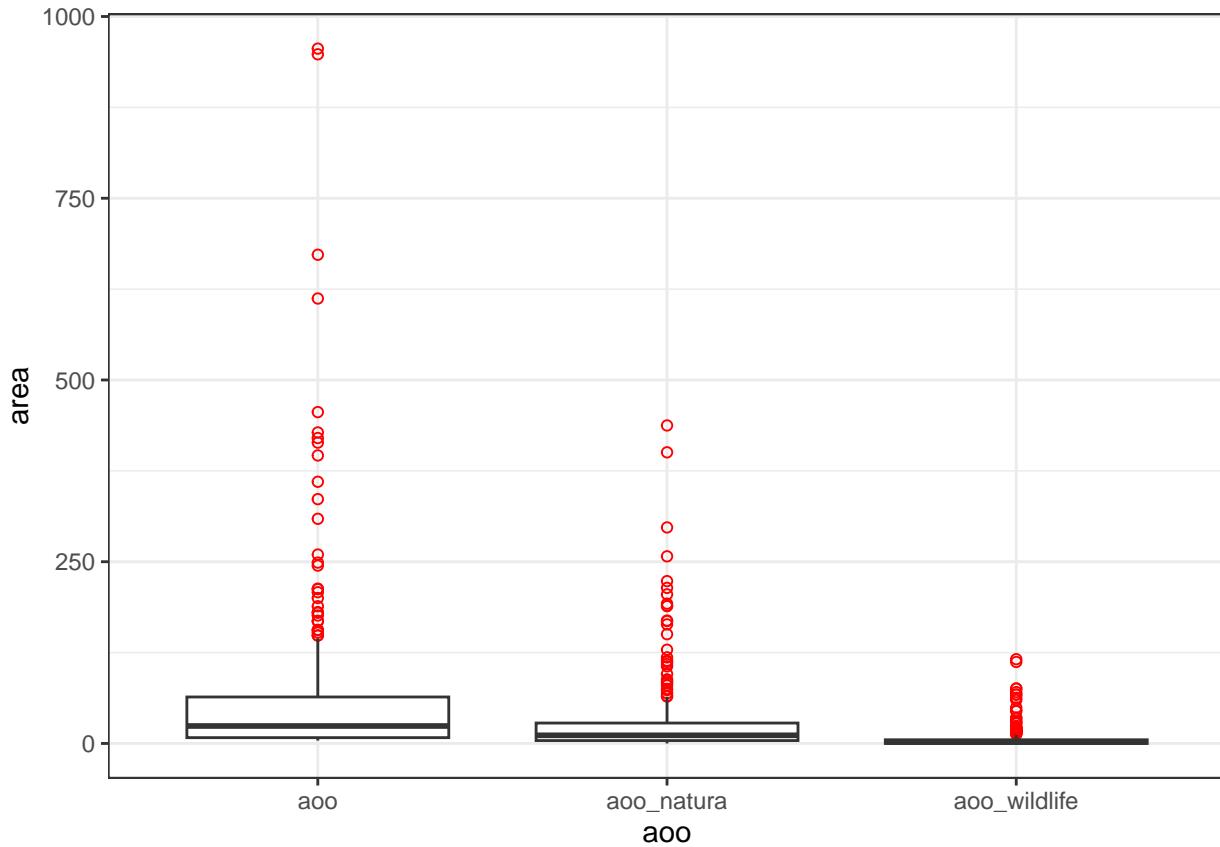
endemic_species_aoo <- endemic_species %>%
  dplyr::select(subspeciesname, aoo, aoo_natura,aoo_wildlife) %>%
  pivot_longer(cols=c(aoo,aoo_natura, aoo_wildlife),
               names_to="aoo",
               values_to="area")

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(subspeciesname, 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))

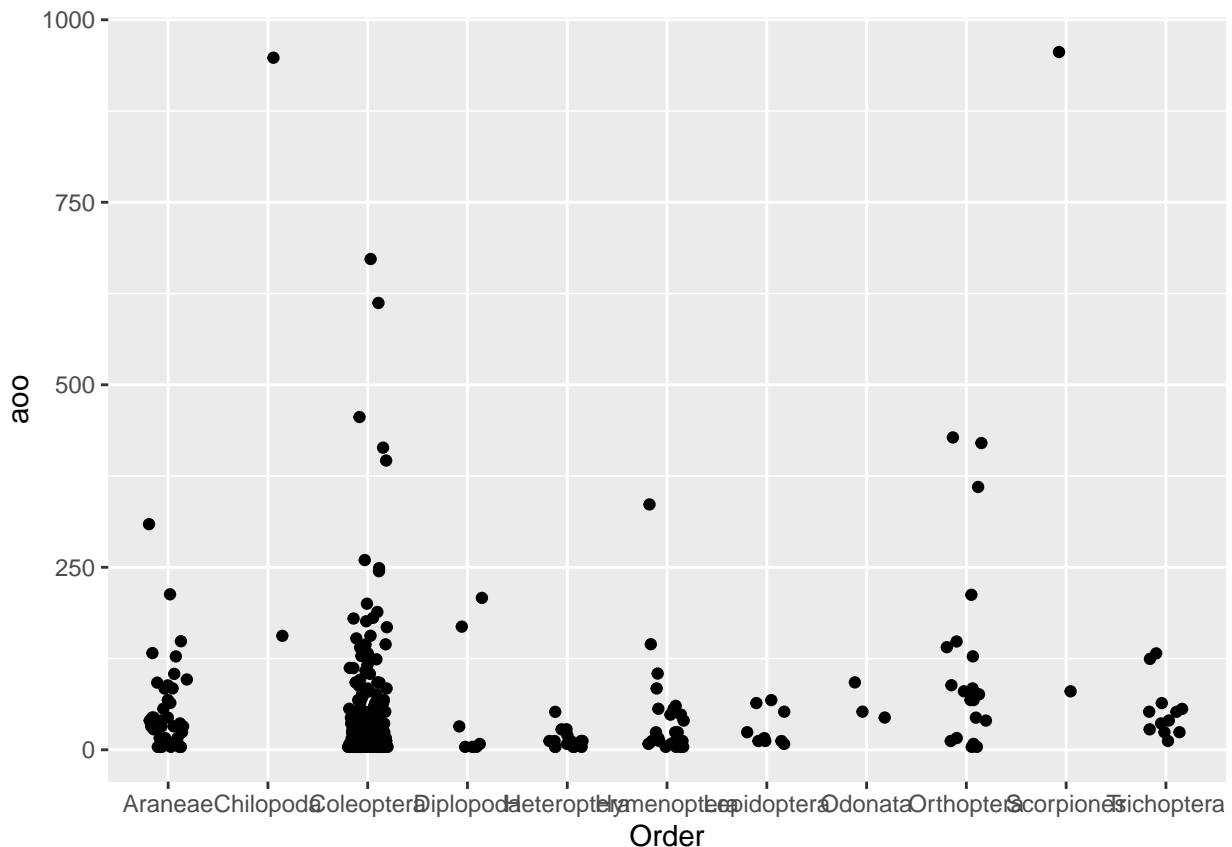
```

```

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

```

p



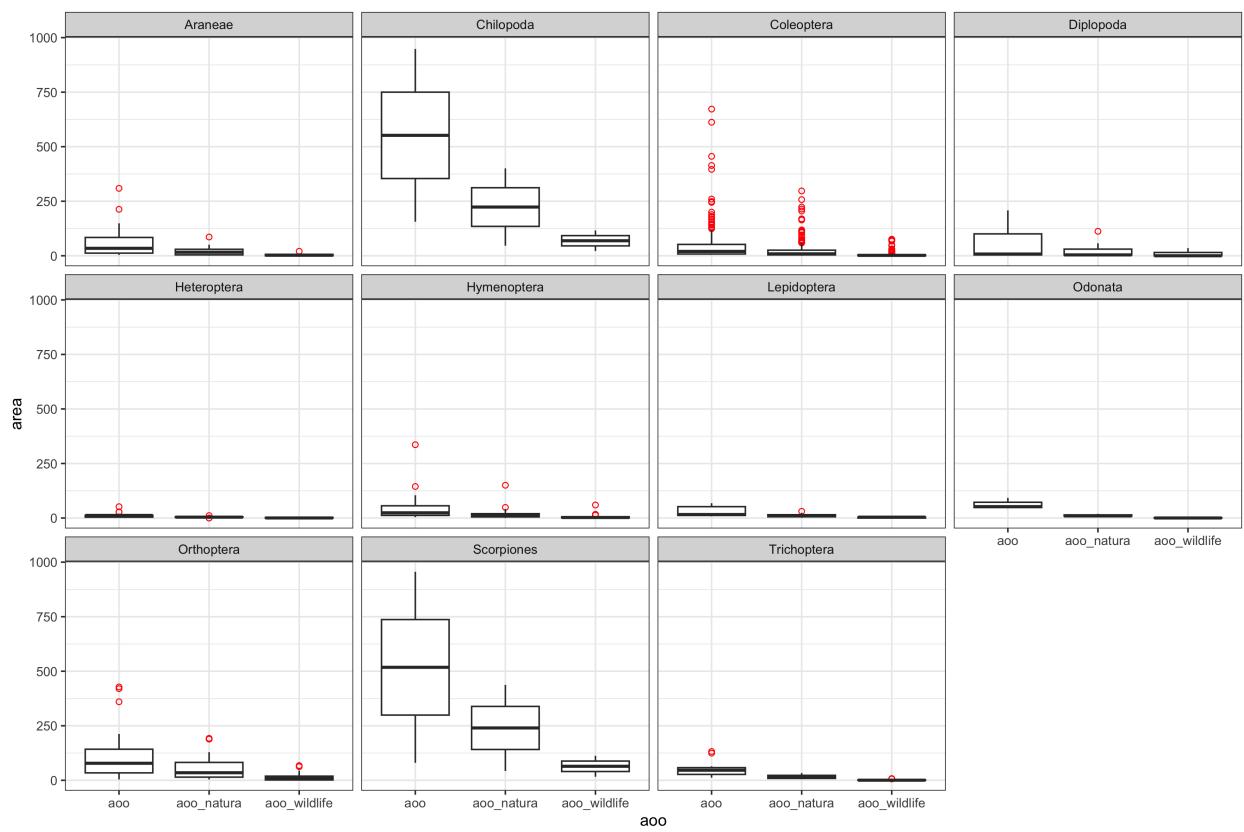


Figure 12: Distributions of AOO and overlaps per Order

Digital Elevation Maps

```
locations_spatial_d <- locations_spatial %>%
  st_drop_geometry() %>%
  dplyr::select(-Order) %>%
  left_join(endemic_species, by=c("sbspcsn"="subspeciesname")) %>%
  mutate(elevation_bin=cut(elevation,
                           breaks=seq.int(from=0, to=2500, by=400),
                           dig.lab = 5))

locations_spatial_d_b <- locations_spatial_d %>%
  distinct(sbspcsn, elevation_bin) %>%
  group_by(elevation_bin) %>%
  summarise(n_species=n())

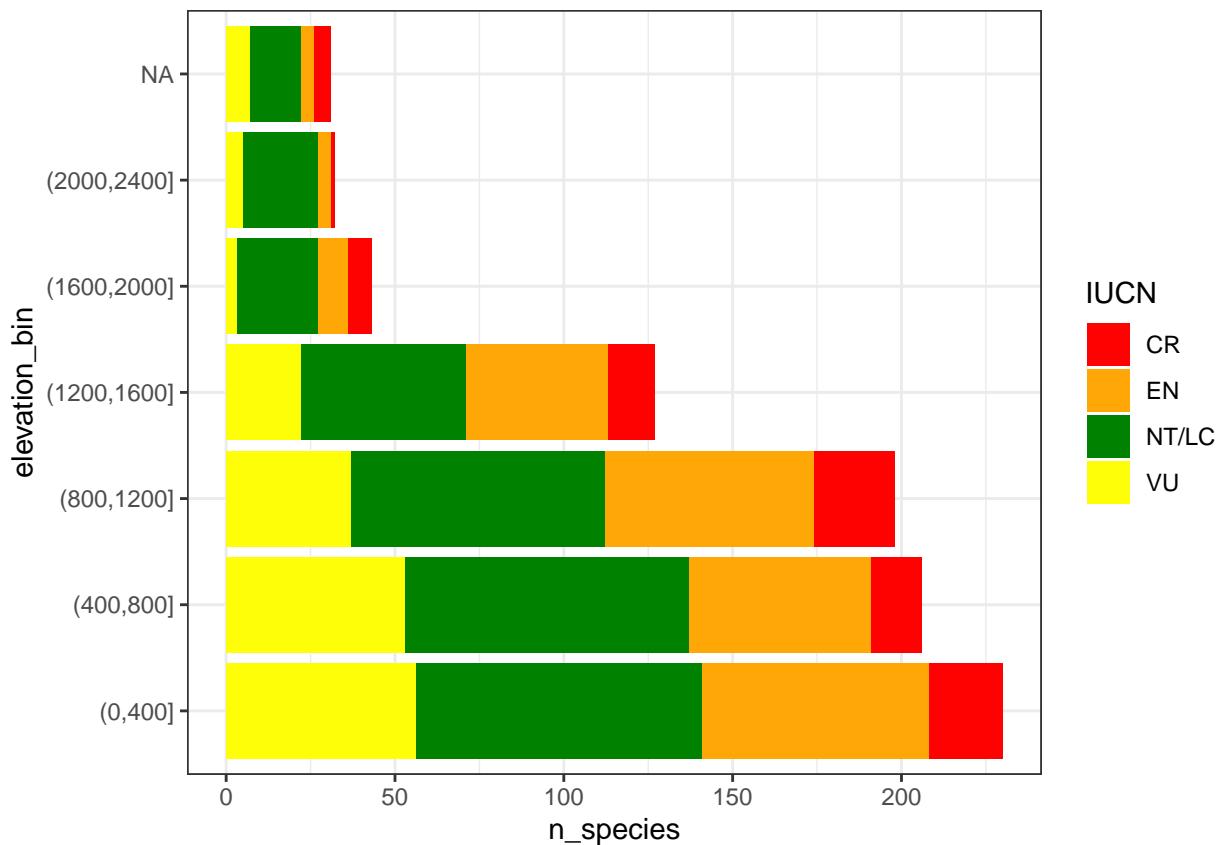
locations_spatial_d_b_i <- locations_spatial_d %>%
  distinct(sbspcsn, elevation_bin, iucn) %>%
  group_by(elevation_bin, iucn) %>%
  summarise(n_species=n(), .groups="drop")

locations_spatial_d_b_o <- locations_spatial_d %>%
  distinct(sbspcsn, 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=elevation),
               outlier.colour = "red",
               outlier.shape = 1) +
  theme_bw()
ggsave("../plots/elevation_iucn.png", plot=g_elev, device="png")

g_elev

```

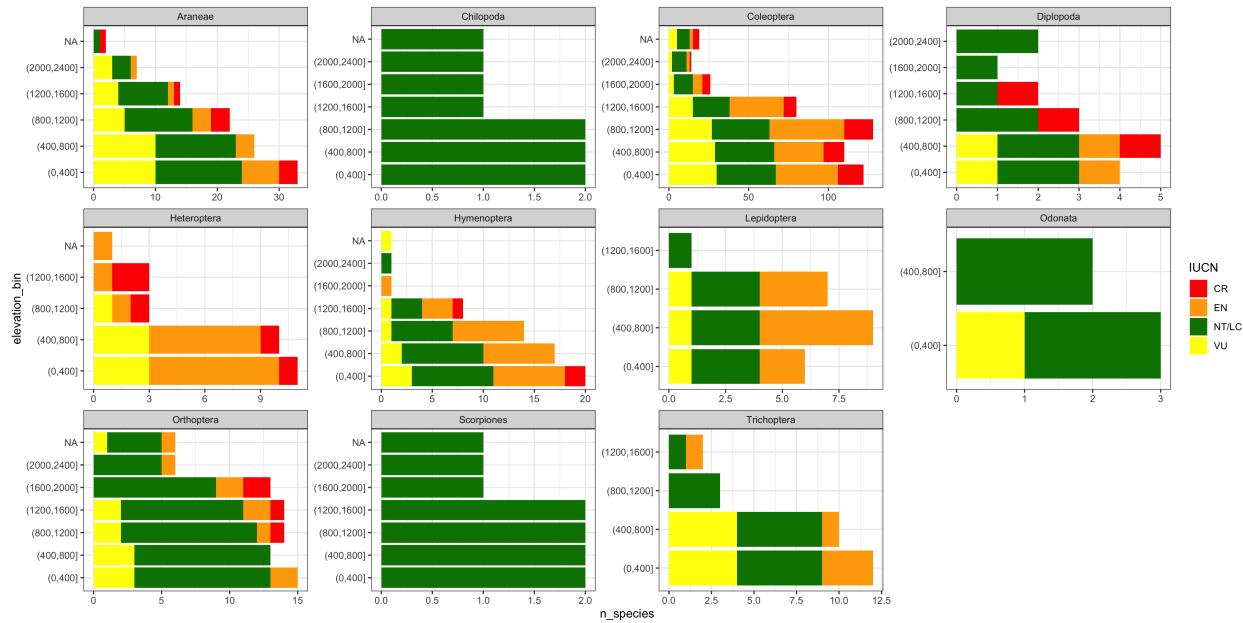
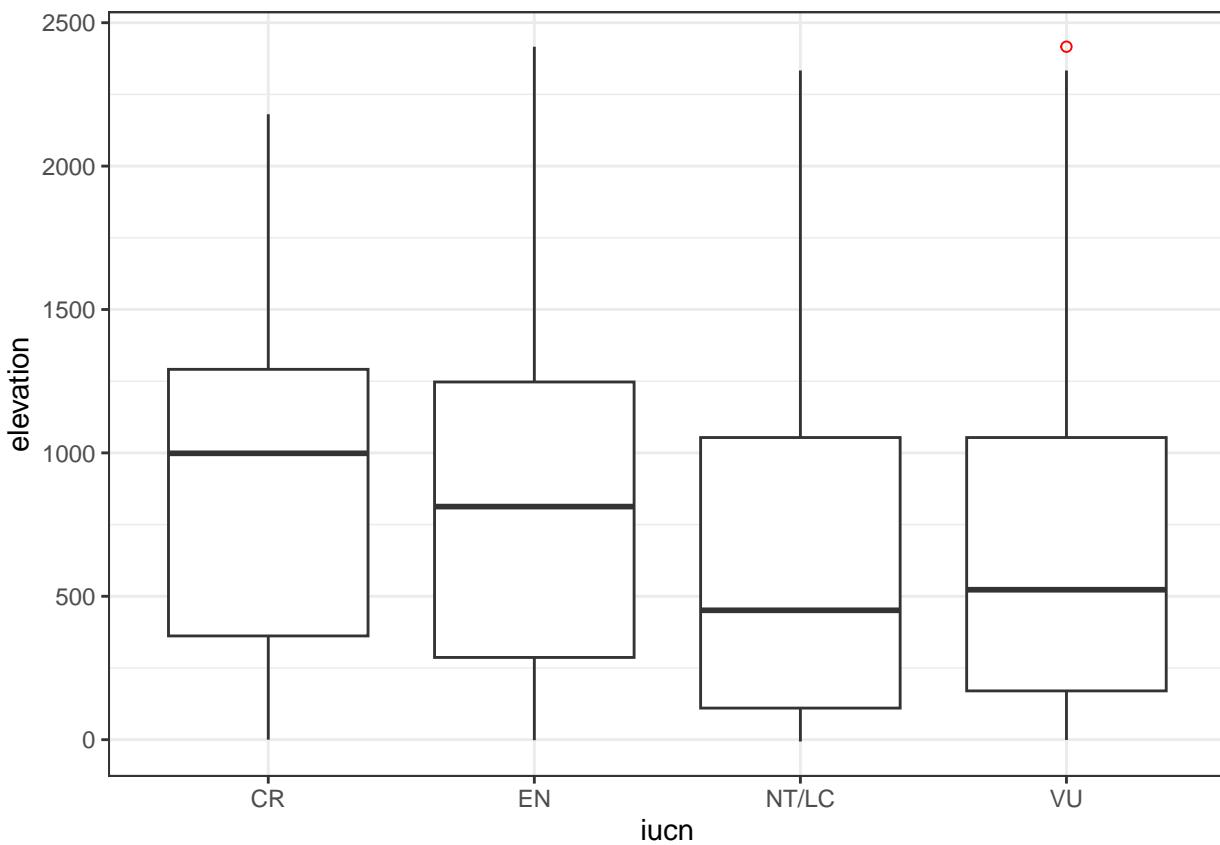


Figure 13: Altitude bins and the species that occur



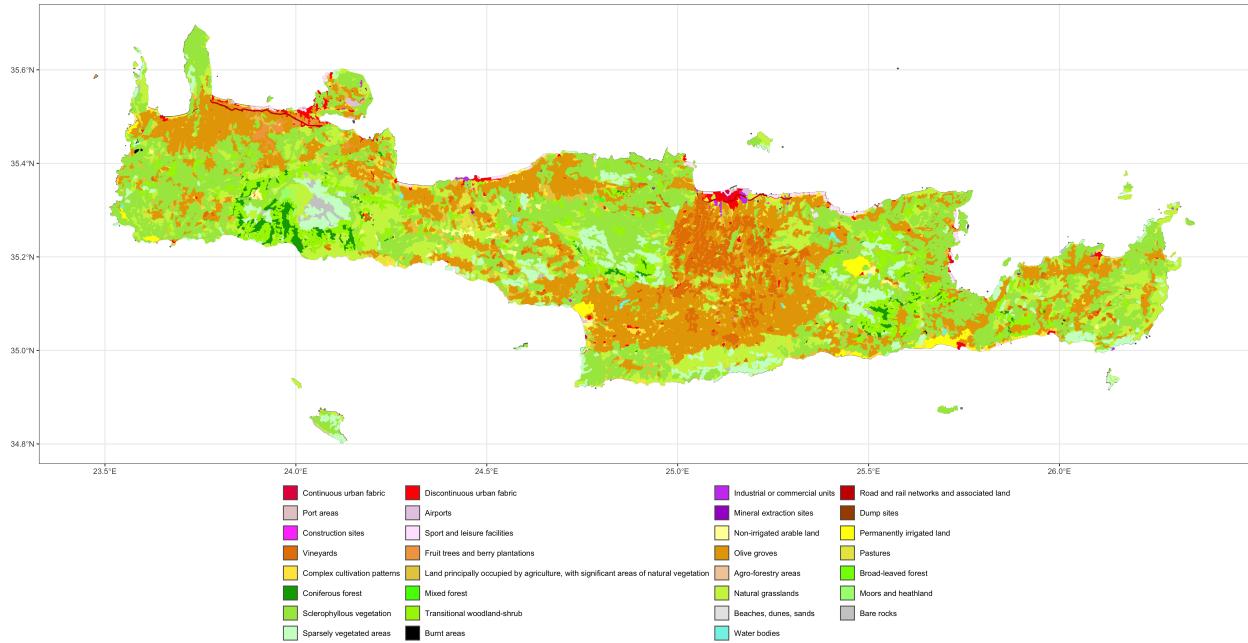


Figure 14: CORINE Land Cover 2018 (LABEL 3) in Crete

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
Agricultural areas	3618.20	301.93	57.42	275.12	240.07
Artificial surfaces	181.13	5.02	3.63	4.95	3.01
Forest and semi natural areas	4508.42	2040.26	545.58	1092.09	945.18
Water bodies	6.74	2.50	1.80	0.99	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
Agro-forestry areas	1.23	NA	NA	NA	NA
Airports	13.17	NA	NA	NA	NA
Bare rocks	63.46	61.15	4.03	33.83	7.82
Beaches, dunes, sands	4.03	NA	NA	NA	NA
Broad-leaved forest	70.72	14.71	1.42	19.18	16.95
Burnt areas	4.10	NA	NA	NA	NA
Complex cultivation patterns	443.16	54.19	7.39	29.28	20.44
Coniferous forest	219.01	181.81	58.94	143.79	125.10
Construction sites	3.35	0.32	0.57	0.32	0.32
Continuous urban fabric	8.98	NA	NA	NA	NA
Discontinuous urban fabric	101.66	2.63	1.45	3.54	2.37
Dump sites	0.85	NA	NA	NA	NA
Fruit trees and berry plantations	50.13	NA	NA	NA	NA
Industrial or commercial units	19.12	0.39	0.94	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
Mineral extraction sites	5.85	NA	NA	NA	NA
Mixed forest	10.21	2.69	0.01	0.65	0.65
Moors and heathland	12.97	12.97	0.00	12.93	12.15
Natural grasslands	1459.26	569.92	138.29	241.79	198.54
Non-irrigated arable land	32.50	12.86	0.45	8.24	8.24
Olive groves	2137.66	111.93	33.20	140.09	117.85
Pastures	59.25	15.11	1.81	8.50	8.05
Permanently irrigated land	55.79	21.25	0.57	18.66	18.66
Port areas	0.95	NA	NA	NA	NA
Road and rail networks and associated land	6.53	0.10	0.03	0.08	0.08
Sclerophyllous vegetation	2007.26	718.71	241.57	374.81	363.67
Sparingly vegetated areas	339.06	259.03	42.55	108.89	80.79
Sport and leisure facilities	20.68	NA	NA	NA	NA
Transitional woodland-shrub	318.34	217.42	58.77	155.67	139.21
Vineyards	179.91	4.94	1.66	4.75	4.75
Water bodies	6.74	2.50	1.80	0.99	0.31

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

```
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 %>%
  mutate(lon=st_coordinates(locations_shp)[,1],
```

```

    lat=st_coordinates(locations_shp)[,2]) %>%
distinct(Order,lon,lat) %>%
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$subspeciesname)),
                           sites = nrow(unique(st_coordinates(locations_shp))),
                           occurrences = nrow(locations_shp),
                           locations = length(unique(locations_grid$CELLCOD)))

```

Order	taxa	sites	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/LC	n. species VU	proportion_CR	proportion_EN	proportion_NT/LC	proportion_VU	threatened	proportion_threatened	
total	343	1569	7690	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	254	559	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	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA	
Coleoptera	206	9497	4037	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	203	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	48	70	21	NA	1	3	NA	0.50	0.17	5	9	NA	3	0.29	0.51	NA	0.18	17	1.0000000	
Homoptera	29	153	329	71	5	14	3	0.32	0.56	0.12	3	11	2	5	0.12	0.44	0.32	0.12	17	0.6800000	
Lepidoptera	9	40	69	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	29	50	20	NA	2	NA	0.67	NA	0.33	NA	NA	NA	NA	NA	NA	NA	NA	NA		
Orthoptera	20	118	101	10	1	3	1	0.25	0.51	0.11	3	1	10	1	0.13	0.25	0.20	0.14	10	0.5000000	
Scorpiones	2	243	508	88	2	NA	NA	1.00	NA	NA	NA	NA	NA	2	NA	NA	NA	1.00	NA	0	0.0000000
Trichoptera	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	

```
total_row <- cbind(total_data, total_paca, total_iucn)

total_summary <- rbind(total_row, order_total)
write_delim(total_summary, "../results/total_summary.tsv", delim="\t")

kbl(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
```