

# Examine stressor sensitivities

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```
# source('https://raw.githubusercontent.com/oharac/src/master/R/common.R')
```

```
library(MyFunctions)
```

```
my_lib(c("cowplot", "tidyverse", "wesanderson", "here"))
```

```
##      cowplot  tidyverse wesanderson      here
##      TRUE      TRUE      TRUE      TRUE
```

```
source(here::here('common_fxns.R'))
```

```
select <- dplyr::select
```

## Summary

Examine the results of the stressor sensitivity scripts from O'Hara et al 2021.

## Methods

### Species impacted by each stressor

Plotting the number of species impacted by each stressor and country. This plot includes species that:

- have an IUCN range map
- are in a comprehensively assessed taxon (and birds are seabirds)

- are threatened or near threatened (i.e. not LC or EX)
- are sensitive to at least one stressor in our study
- are present in the EEZs of Canada, Mexico and the USA (including Puerto Rico and Hawaii)

## Extract data

Because the original study is global, we had to first extract the data for only the North American countries we were interested in. For that we combined a series of data available in the repository. The sensitivity data has an `iucn_sid` category that can be match to the `range` data tha has an additional column for `eez`. The file `rgn_names_fixed.csv` has that information, note that the column `rgn_id = eez` in the `range` data. We selected the regions for 116 - Puerto Rico and Virgin Islands of the United States, 135 - Mexico, 163 - USA, 218 - Canada and further lumped regions 116 and 163 together. The analysis included only the species found in these regions.

```
# Get sensitivity data
sens_all_file <- here('_output', sprintf('spp_sensitivity_%s.csv', api_version))

sens_all_df <- read_csv(sens_all_file, col_types = cols('iucn_sid' = 'i')) %>%
  left_join(read_csv(here('_raw/stressor_names.csv')), by = 'stressor')

#### SELECT ONLY SPECIES FOUND IN NORTH AMERICAN EEZs

# For that we need to combine a series of data disperse in the repo
# range_from_rasts, gives us the range of each species per EEZ
range <- read_csv(here("_raw/range_from_rasts.csv"))

# Now we need to figure out what EEZ numbers we are interested in. Which means we need to find the data
# EEZ id and name. Turns out that the file rgn_names_fixed.csv has that information, note that the column

rgn_names <- read_csv(here("_spatial/rgn_names/rgn_names_fixed.csv")) %>%
  select(rgn_id, rgn_label) %>%
  distinct()

# Lets now filter out the EEZs we want
# rgn_names %>% arrange(rgn_label) %>% View()
# 116 - Puerto Rico and Virgin Islands of the United States
# 135 - Mexico
# 163 - USA
# 218 - Canada

# Select only the species from North America
na_spp_range <- range %>%
  filter(eez %in% c(116,135,163,218)) %>%
  rename('rgn_id' = 'eez') %>% # because the data have different column names
  left_join(rgn_names,
    by = "rgn_id") %>%
  mutate(rgn_label = ifelse(rgn_label == "Puerto Rico and Virgin Islands of the United States","United States of America",rgn_label)) %>%
  mutate(rgn_label = ifelse(rgn_label == "United States of America","USA",rgn_label)) %>%
  select(iucn_sid,rgn_label) %>%
  distinct()

# Get the sens data for those selected species
sens_na_df <- na_spp_range %>%
```

```
left_join(sens_all_df)
```

## Plot panel A

This section is the same as O'Hara *et al* (2021) with the only difference that we are focusing on the countries mentioned above and that the data (plots) are presented by country and not general

```
# Change sens_all_df for sens_na_df below
spp_incl <- get_incl_spp() %>%
  filter(!is.na(stressor)) %>%
  filter(iucn_sid %in% sens_na_df$iucn_sid) # filter only species in the region

sens_df <- sens_na_df %>%
  filter(sens) %>%
  select(-code, -sens) %>%
  distinct() %>%
  filter(iucn_sid %in% spp_incl$iucn_sid) %>%
  mutate(category = tools::toTitleCase(category))

cat_sum_df <- sens_df %>%
  select(iucn_sid, rgn_label, category) %>% # added region
  group_by(category, rgn_label) %>% # added region
  summarize(n_spp = n_distinct(iucn_sid)) %>%
  arrange(desc(n_spp)) %>%
  mutate(str_desc = category)

plot1_df <- sens_df %>%
  group_by(str_desc, category, rgn_label) %>% # add region
  summarize(n_spp = n()) %>%
  ungroup() %>%
  bind_rows(cat_sum_df) %>%
  filter(str_desc != 'Ocean') %>%
  mutate(str_desc = ifelse(!str_detect(str_desc, '^Art'),
                           str_replace(str_desc, ' fishing$', ''), str_desc)) %>%
  mutate(str_desc = str_replace(str_desc, 'destructive ', 'destr. ')) %>%
  mutate(str_desc = ifelse(str_desc == category, paste0('(Total ', str_desc, ')'), str_desc)) %>%
  mutate(str_desc = ifelse(str_desc == 'Shipping', 'Shipping (Total Ocean-Based)', str_desc)) %>%
  # mutate(category = factor(category, levels = cat_sum_df$category)) %>%
  arrange(desc(category), n_spp) %>%
  mutate(stressor = fct_inorder(str_desc))

bar_pal1 <- c(viridisLite::viridis(n = 4, option = 'D'), 'grey90')

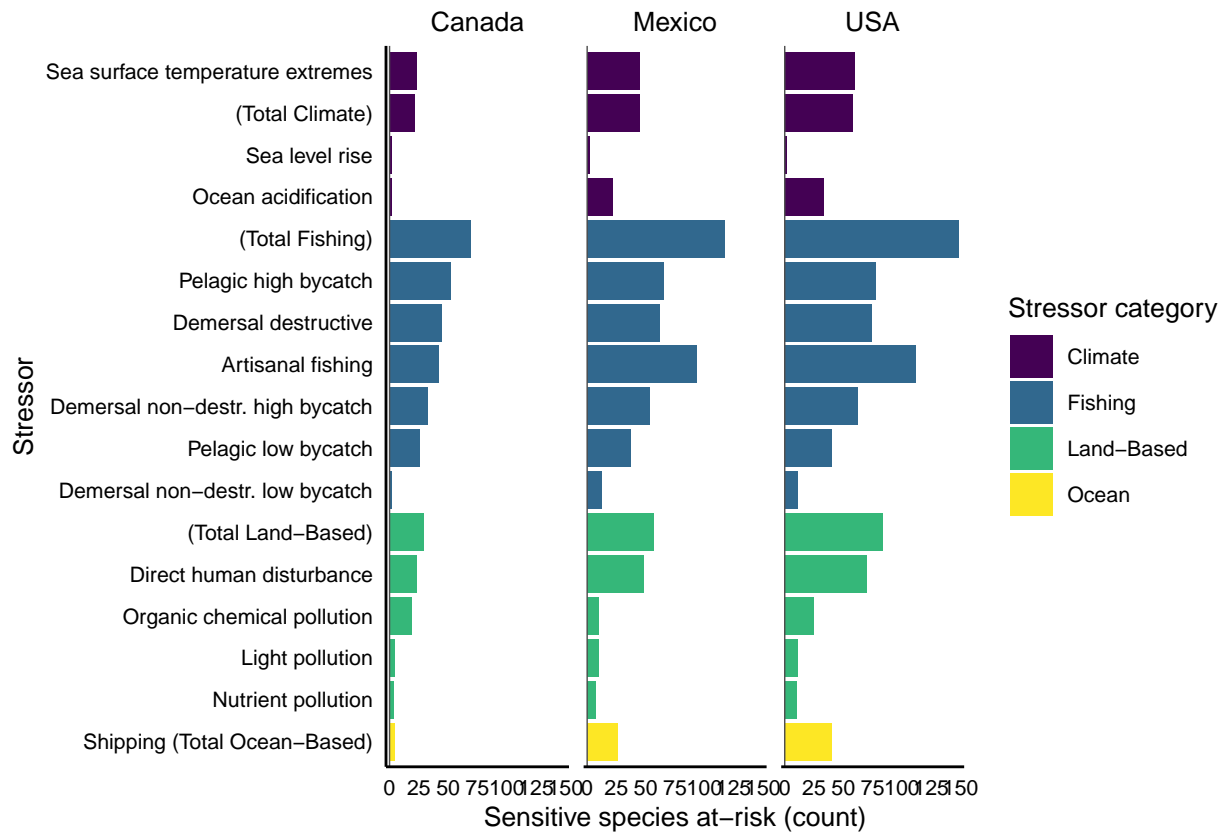
n_spp_str <- ggplot(plot1_df, aes(x = stressor, y = n_spp, fill = category)) +
  geom_col() +
  geom_hline(yintercept = 0, color = 'grey30', size = .25) +
  geom_rect(xmin = 1, xmax = 8, ymin = 600, ymax = 200,
            fill = 'white', color = 'grey90', size = .1) + ### suppress gridlines behind legend
  # scale_fill_viridis_d() +
  scale_fill_manual(values = bar_pal1) +
  labs(y = 'Sensitive species at-risk (count)',
       fill = 'Stressor category',
```

```

x = "Stressor") +
scale_y_continuous(expand = c(0.02, 0.02), limits = c(0, 150), breaks = seq(0, 150, 25)) +
coord_flip() +
# guides(fill = guide_legend(title.position = "top",
#                               # hjust = 1 # centres the title horizontally
#                               title.hjust = 1,
#                               label.position = "left"))) +
my_ggtheme_p(ax_tx_s = 8, ax_tl_s = 10, leg_tl_s = 10, leg_tx_s = 8, facet_tx_s = 10, hjust = 0.5, leg_pos
facet_wrap(~rgn_label)

n_spp_str

```



## Plot panel B

Number of stressor sensitivities per species. This does not indicate spatial co-occurrence of stressors, just whether a species is sensitive to one, two, or more stressors.

Here we maintain the analysis that the original authors did with the only difference that we do not filter out taxa, instead, we show all of them.

```

str_count_df <- spp_incl %>%
  group_by(iucn_sid, desc) %>%
  summarize(n_str = n_distinct(stressor),
            n_cat = n_distinct(category),
            strs = paste(unique(stressor), collapse = ', ')) %>%

```

```

ungroup()

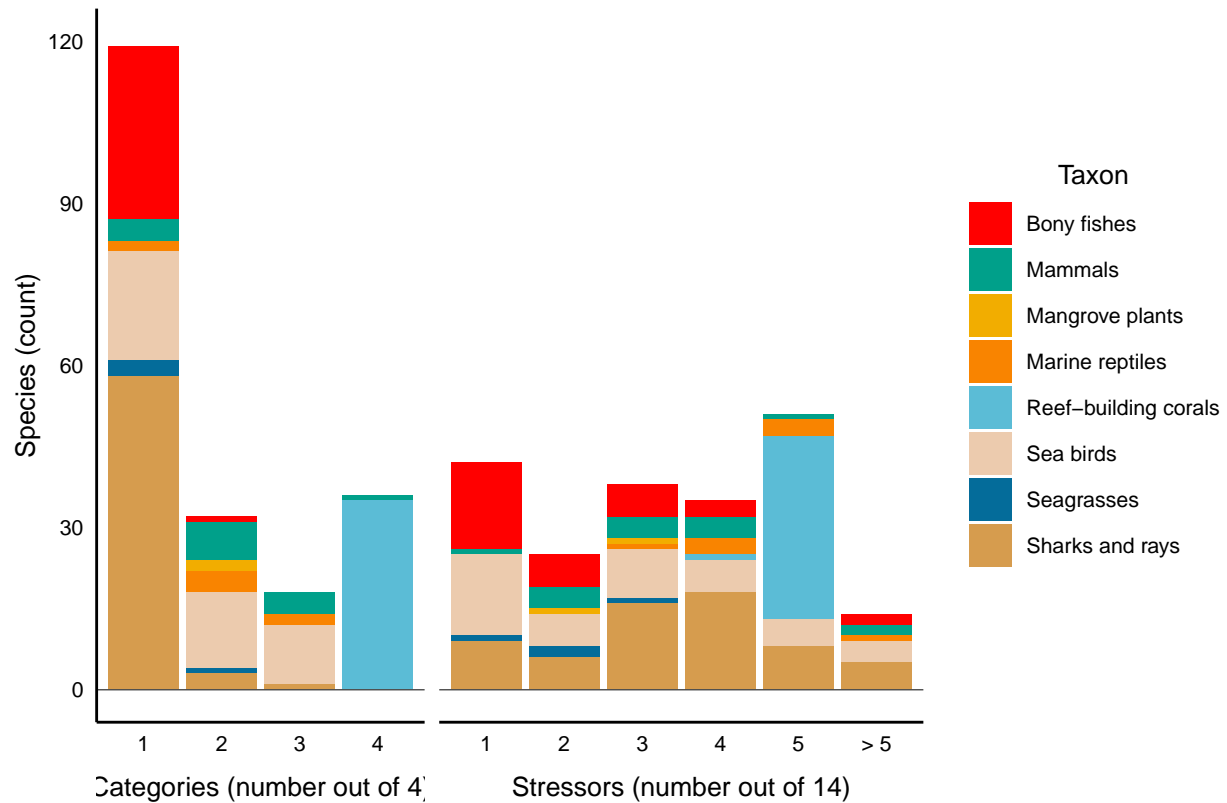
# Finalized dataframe for figure
plot2_df <- str_count_df %>%
  gather(key = type, value = ct, n_str, n_cat) %>%
  arrange(ct) %>%
  mutate(ct = as.character(ct),
         ct = ifelse(as.integer(ct) > 5, '> 5', ct),
         ct = fct_inorder(ct),
         type = ifelse(type == 'n_str', 'Stressors (number out of 14)', 'Categories (number out of 4)')
         desc = str_to_sentence(desc)
         )

# Set color
bar_pal2 <- c(wes_palette("Darjeeling1"),wes_palette("Darjeeling2"))

n_str_spp <-
  ggplot(plot2_df, aes(x = ct)) +
  geom_bar(position = 'stack', aes(fill = desc)) +
  geom_hline(yintercept = 0, color = 'grey30', size = .25) +
  theme(strip.placement = 'outside') +
  my_ggtheme_p(ax_tx_s = 8,ax_tl_s = 10,leg_tl_s = 10,leg_tx_s = 8,facet_tx_s = 10,hjust = 0.5, leg_pos
  scale_fill_manual(values = bar_pal2) +
  scale_y_continuous(breaks = seq(0,120,30),limits = c(0,120)) +
  labs(y = 'Species (count)',
       fill = 'Taxon',
       x = "") +
  facet_grid(~ type, scales = 'free_x', space = 'free_x', switch = 'x')

n_str_spp

```



## Combine both plots

```
fig1 <- ggdraw() +
  draw_plot(n_spp_str, x = 0, y = .40, height = .60, width = 1) +
  draw_plot(n_str_spp, x = 0, y = 0, height = .40, width = 1) +
  draw_label('A', x = 0.002, y = .99, hjust = 0, vjust = 1,
    size = 10) +
  draw_label('B', x = 0.002, y = .42, hjust = 0, vjust = 1,
    size = 10)

fname <- here('ms_figs/ncba_stressors_fig.png')

ggsave(plot = fig1, filename = fname,
  width = 20, height = 15, units = 'cm', dpi = 300)

fig1
```

