

Examine stressor sensitivities

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Contents

Summary	1
Methods	1
Species impacted by each stressor	1
Number of stressor sensitivities per species	4

```
# 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.

Methods

Species impacted by each stressor

Plotting the number of species impacted by each stressor. 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

```

# 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", "Puerto Rico and Virgin Islands of the United States", rgn_label))
  select(iucn_sid, rgn_id, rgn_label)

# Get species names
# iucn_comp_assessed_2020_1 <- read_csv("_data/iucn_comp_assessed_2020-1.csv")

# Get the sens data for those selected species
sens_na_df <- na_spp_range %>%
  left_join(sens_all_df)

#### ---- Done North America Selection ####
# Continue with O'Hara's original code

# 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)

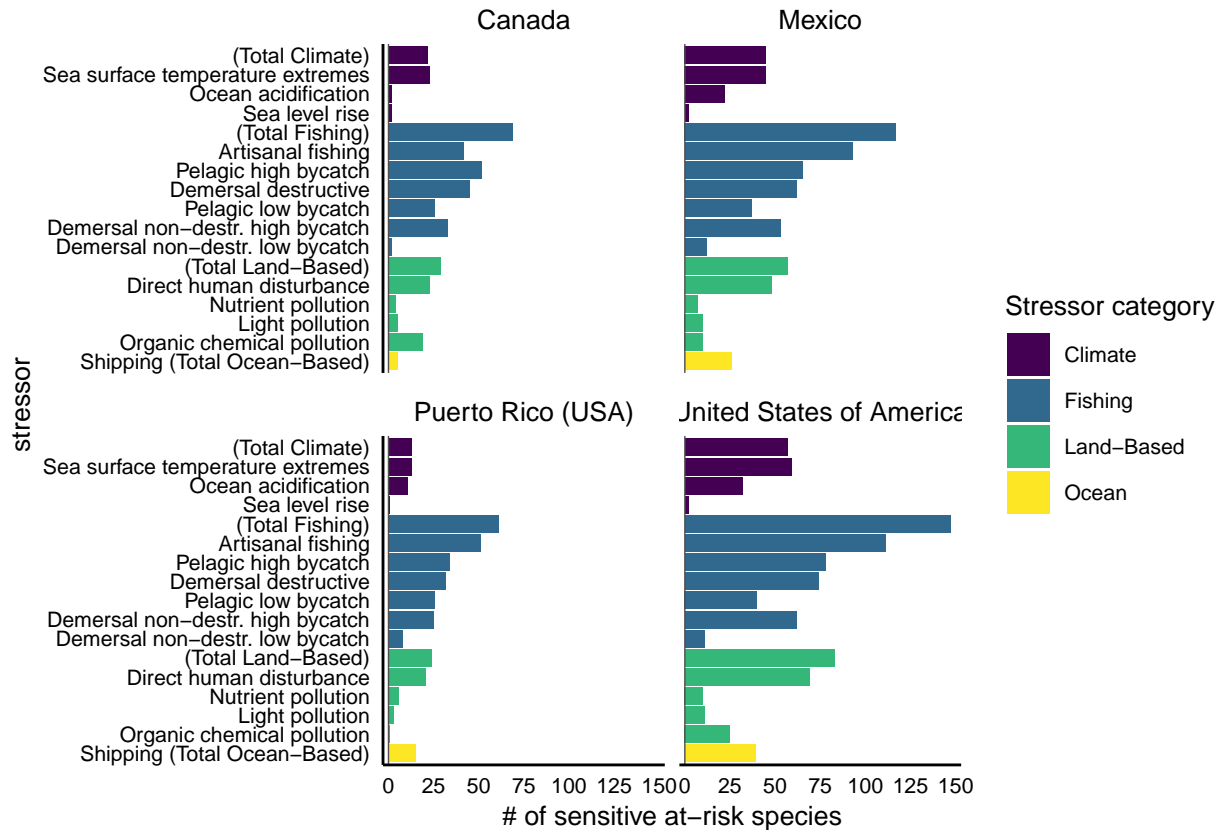
plot1_df <- sens_df %>%
  group_by(str_desc, category, rgn_label) %>% # add region
  summarize(n_spp = n()) %>%
  ungroup() %>%
  bind_rows(cat_sum_df) %>%
  filter(str_desc != 'Ocean') %>%
  mutate(str_desc = ifelse(!str_detect(str_desc, '^Art'),
                           str_replace(str_desc, ' fishing$',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

# bar_pal <- c('grey10', 'grey60', 'grey35', 'grey85')
bar_pal1 <- c(viridisLite::viridis(n = 4, option = 'D'), 'grey90')

n_spp_str <- ggplot(plot1_df, aes(x = stressor, y = n_spp, fill = category)) +
  # ggtheme_plot(base_size = 9) +
  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 = '# of sensitive at-risk species',
       fill = 'Stressor category') +
  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

```



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.

```
# spp_incl <- get_incl_spp() %>%
# filter(!is.na(stressor))

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 = ', ')) %>%
  # group_by(desc) %>%
  # mutate(desc = ifelse(n_distinct(iucn_sid) < 50, 'other', desc)) %>%
  ungroup() # %>%
  # mutate(desc = str_replace(desc, 'mangrove plants', 'mangroves'),
  #         desc = str_replace(desc, 'reef-building ', ''),
  #         desc = str_replace(desc, 'marine reptiles', 'reptiles'),
  #         desc = str_replace(desc, 'sharks and rays', 'sharks/rays'))

# taxon_order <- str_count_df %>%
# filter(desc != 'other') %>%
# group_by(desc) %>%
# summarize(n = n_distinct(iucn_sid)) %>%
```

```

#   arrange(desc(n)) %>%
#   .$desc %>%
#   c(., 'other')

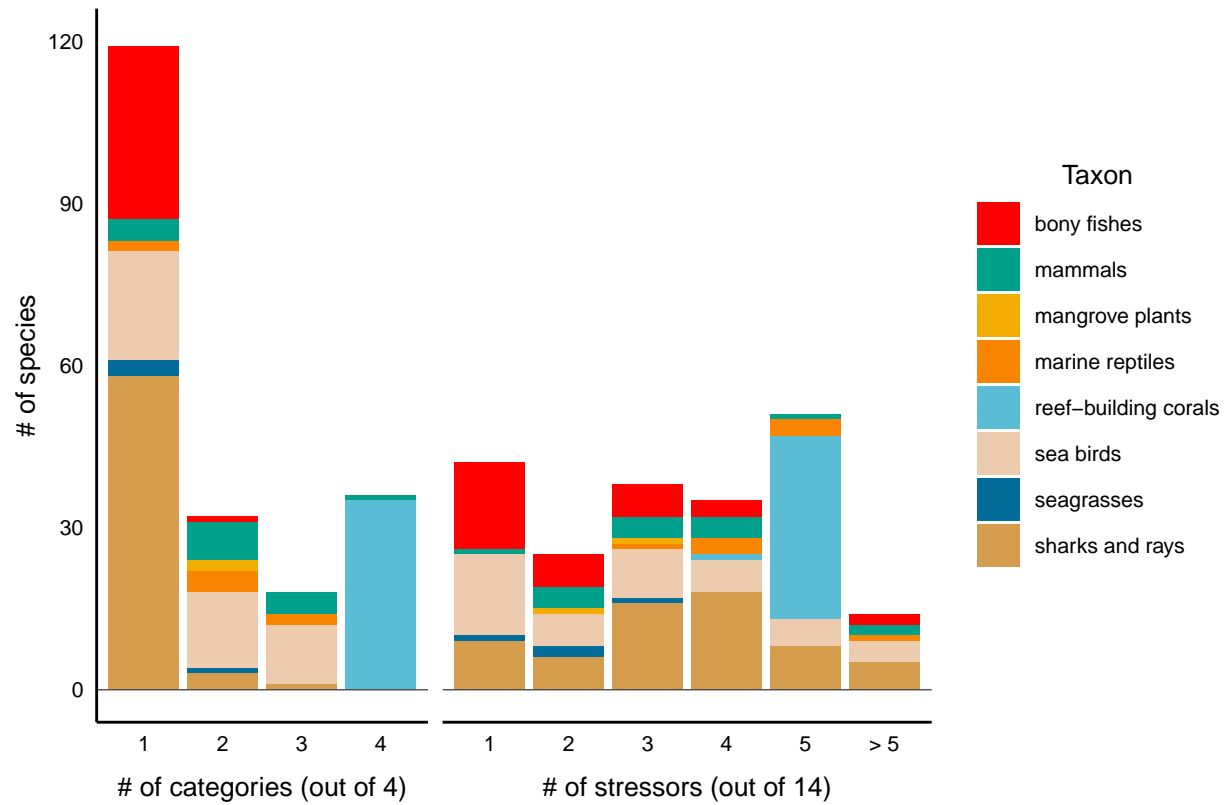
plot2_df <- str_count_df %>%
  gather(key = type, value = ct, n_str, n_cat) %>%
  arrange(ct) %>%
  mutate(ct = as.character(ct),
         ct = ifelse(as.integer(ct) > 5, '> 5', ct),
         ct = fct_inorder(ct),
         type = ifelse(type == 'n_str', '# of stressors (out of 14)', '# of categories (out of 4)')) # %>%
  # mutate(desc = factor(desc, levels = taxon_order))

bar_pal2 <- c(wes_palette("Darjeeling1"), wes_palette("Darjeeling2"))
# bar_pal <- c(viridisLite::viridis(n = 6, option = 'D')[c(2,4,6,3,5)], 'grey90')
# bar_pal <- c(viridisLite::viridis(n = 5, option = 'D')[c(1,3,5,2,4)], 'grey90')
# bar_pal <- c('grey10', 'grey50', 'grey80', 'grey30', 'grey50', 'grey90')

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
  # guides(fill = guide_legend(title.position = "top",
  #                               # hjust = 1 # centres the title horizontally
  #                               title.hjust = .6,
  #                               ncol = 1,
  #                               label.position = "left")) +
  scale_fill_manual(values = bar_pal2) +
  scale_y_continuous(breaks = seq(0,120,30), limits = c(0,120)) +
  labs(y = '# of species',
       fill = 'Taxon',
       x = "") +
  facet_grid(~ type, scales = 'free_x', space = 'free_x', switch = 'x')

n_str_spp

```



```
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_fig1_spp_stressor_sens.png')

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

fig1
```

