Fig 2: impacts and intensification maps

Compiled on Tue Jul 23 10:39:21 2024 by jepa88

Contents


```
library(MyFunctions)

my_lib(
  c(
    "tidyverse","raster","cowplot","here","sf"
  )
)
```

```
## tidyverse    raster   cowplot      here        sf
##      TRUE      TRUE      TRUE      TRUE      TRUE
```

```
# Fix new updates of sf package
sf::sf_use_s2(use_s2 = FALSE)
```

Summary

Create figure 2 for NCBA based on O'Hara et al (2021) manuscript.

Methods

Get and Prepare Data

```
# Get O'hara data fro Figure 2

# Load raster data for impacts (Figure 2A and 2B)
```

```r
imp_count  <- raster(here('_output/rasters/impact_maps/impact_all_2013.tif'))

# Load raster data for species impacts (Figure 2B)
nspp <- raster(here('_output/rasters/n_spp_map.tif'))

#  Estimate values as O'hara et al
imp_pct <- imp_count / nspp


# Load raster data for number of species (Figure 2C)
incr <- raster(here('_output/rasters/intens_maps/intens_all_incr2.tif'))
decr <- raster(here('_output/rasters/intens_maps/intens_all_decr2.tif'))
nspp <- raster(here('_output/rasters/n_spp_map.tif'))

# Estimate intencity as per O'hara et al
int_pct <- (incr - decr) / nspp

# Load SAU EEZs we are interested in
# MyFunctions::my_sf("SAU") %>% arrange(name) %>% pull(name) %>% unique() # Check eez names
sau_sf <- MyFunctions::my_sf("SAU") %>%
  filter(name %in% c(
    "USA (East Coast)","USA (West Coast)","USA (Gulf of Mexico)","USA (Alaska, Arctic)","USA (Alaska, St
    "Hawaii Main Islands (USA)","Hawaii Northwest Islands (USA)","Puerto Rico (USA)" ,
    "Mexico (Pacific)","Mexico (Atlantic)",
    "Canada (Arctic)","Canada (East Coast)","Canada (Pacific)")) %>%
  st_transform(crs(imp_count))
```

```
## Reading layer 'SAUEEZ_July2015' from data source
##   '/Users/jepa88/Library/CloudStorage/OneDrive-UBC/Data/Spatial/SAU/SAU_Shapefile/SAUEEZ_July2015.shp
##   using driver 'ESRI Shapefile'
## Simple feature collection with 280 features and 7 fields
## Geometry type: MULTIPOLYGON
## Dimension:     XY
## Bounding box:  xmin: -180 ymin: -63.66443 xmax: 180 ymax: 87.02394
## Geodetic CRS:  WGS 84
```

```r
# Get land countries
# world_land %>% arrange(admin) %>% pull(admin) %>% unique()
world_land <- rnaturalearth::ne_countries(scale = 'medium', returnclass = c("sf")) %>%
  st_transform(4326) %>%
  filter(admin %in% c("Canada","United States of America","Puerto Rico","Mexico")) %>%
  st_shift_longitude()

# Get SAU codes for matching data
sau_codes <- my_data("sau_index") %>%
  dplyr::select(x = 1, everything()) %>%
  filter(x %in% sau_sf$eezid)
```

```
## Loading required package: janitor
```

```
##
## Attaching package: 'janitor'
```

```
## The following object is masked from 'package:raster':
##
##     crosstab

## The following objects are masked from 'package:stats':
##
##     chisq.test, fisher.test
```

```
# Load SAU as grid to extract data
# Transform SAU grid to a points sf
sau_sf <- st_as_sf(my_data("dbem_coords"),
                   coords = c("lon", "lat"),
                   crs = 4326) %>%
  st_transform(crs(imp_count)) %>%
  filter(index %in% sau_codes$index)


# Ohara's color pallet for figure 2C
### diverging color palette from ColorBrewer
div_pal <- c('#8e0152','#c51b7d','#de77ae','#f1b6da','#fde0ef',
             '#f7f7f7', ### mid color
             '#e6f5d0','#b8e186','#7fbc41','#4d9221','#276419') %>% rev()
```

Incorporate data into SAU shapefile

```
# Impacts(Figure 2A)
# Extract raster values at grid points of the SAU SF
sau_sf$impact_value <- extract(imp_count, sau_sf)

# n species(Figure 2B)
# Extract raster values at grid points of the SAU SF
sau_sf$impact_spp <- extract(imp_pct, sau_sf)



# intensity (Figure 2C)
# Extract raster values at grid points of the SF
sau_sf$intense <- extract(int_pct, sau_sf)


# Final details of shapefile projection
sau_oh_sf <- sau_sf %>%
  # Filter the region we want
  st_transform(4326) %>%
  st_shift_longitude()
```

Map them

Fig. 2A: map of impacted spp by count

```
fig_2a <- ggplot() +
  geom_sf(data = sau_oh_sf, aes(color = log10(impact_value)), size = 0.1) +
  geom_sf(data = world_land, aes(), color = "black") +
  scale_color_viridis_c(
    "Species affected\n(n)",
    breaks = c(0,0.5,1,1.5),
    labels = c(0,20,40,60),
    na.value = 'grey80') +
  theme_classic() +
  theme(plot.margin = unit(c(.05, 0, .05, 0), units = 'cm'),
        legend.background = element_blank(),
        legend.key.width = unit(.25, 'cm'),
        axis.text.x = element_blank(),
        legend.title = element_blank()
  ) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0))

fig_2a
```

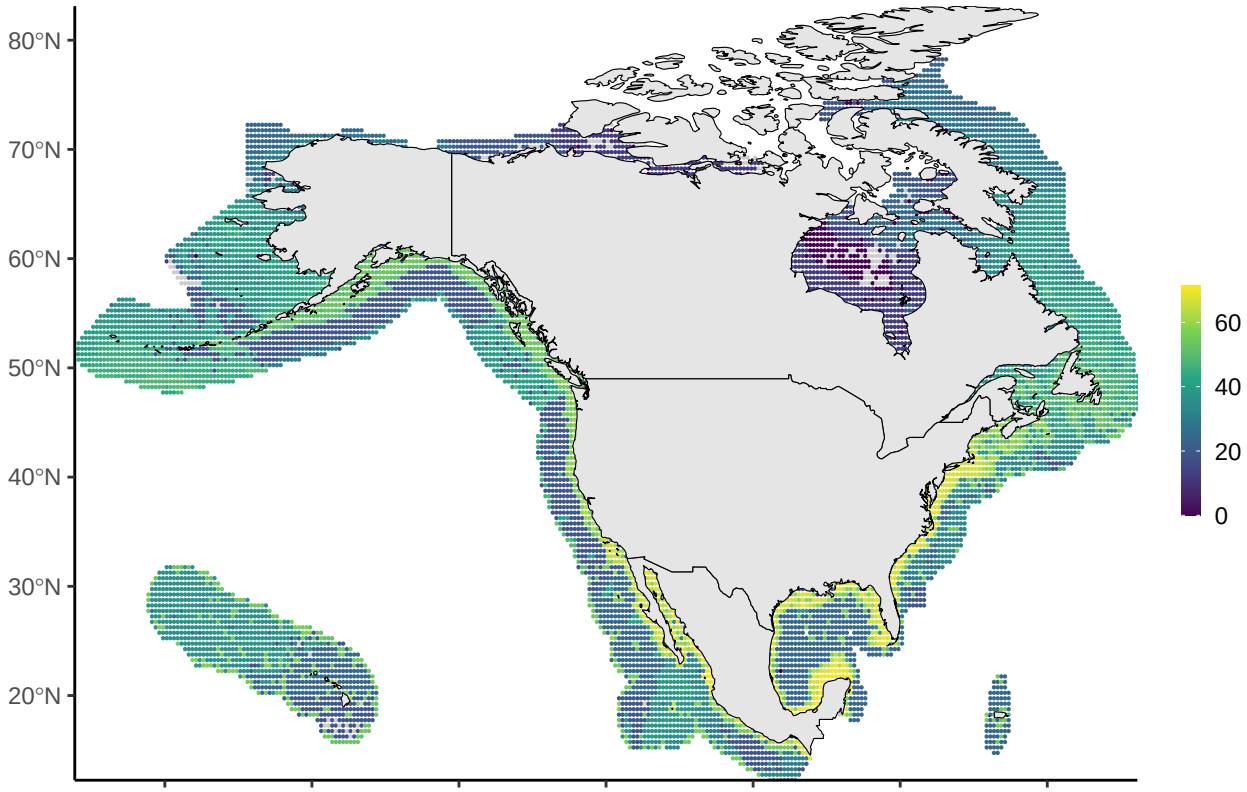


Fig. 2B: map of impacted species by percentage

```
fig_2b <-
  ggplot() +
  geom_sf(data = sau_oh_sf, aes(color = impact_spp), size = 0.1) +
  geom_sf(data = world_land, aes(), color = "black") +
  scale_color_viridis_c(
    "Species affected\n(%)",
    breaks = seq(0, 1, .25),
    labels = paste0(seq(0, 100, 25), '%'),
    na.value = 'grey80') +
  theme_classic() +
  theme(plot.margin = unit(c(.05, 0, .05, 0), units = 'cm'),
        legend.background = element_blank(),
        legend.key.width = unit(.25, 'cm'),
        axis.text.x = element_blank(),
        legend.title = element_blank()
  ) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0))
```

```
fig_2b
```

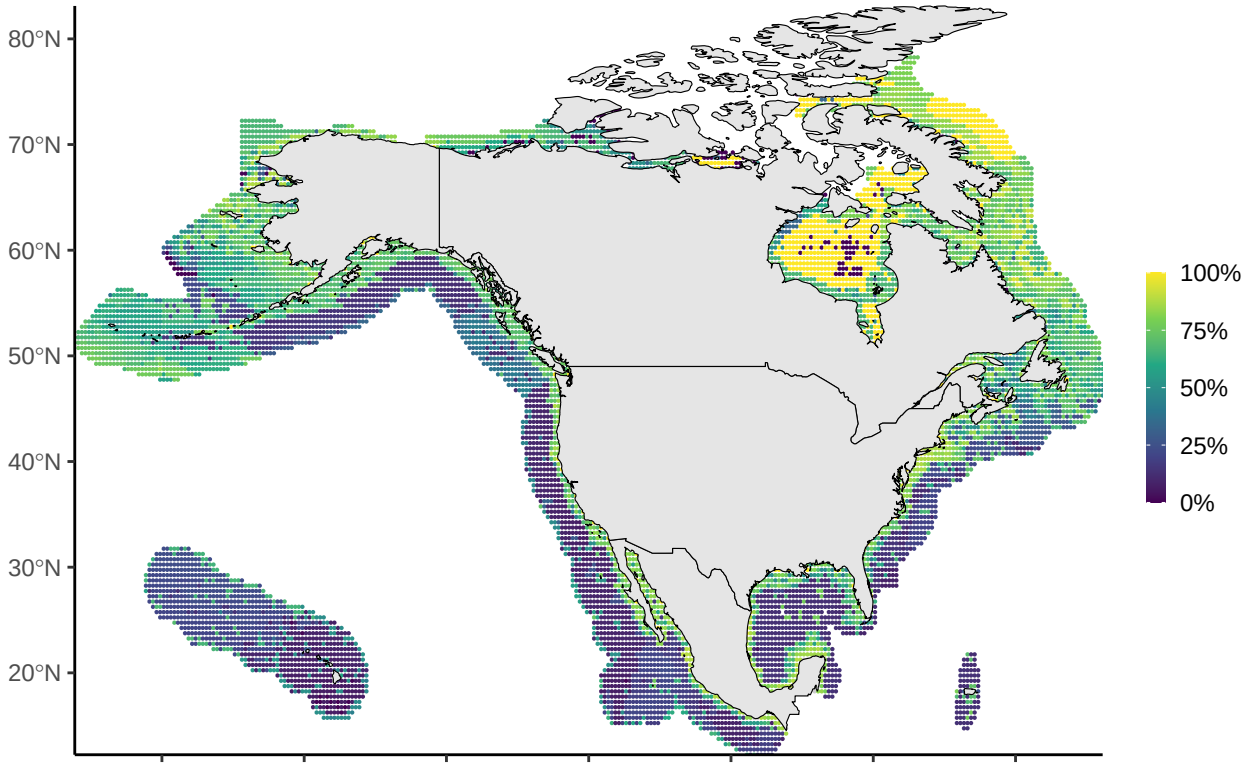
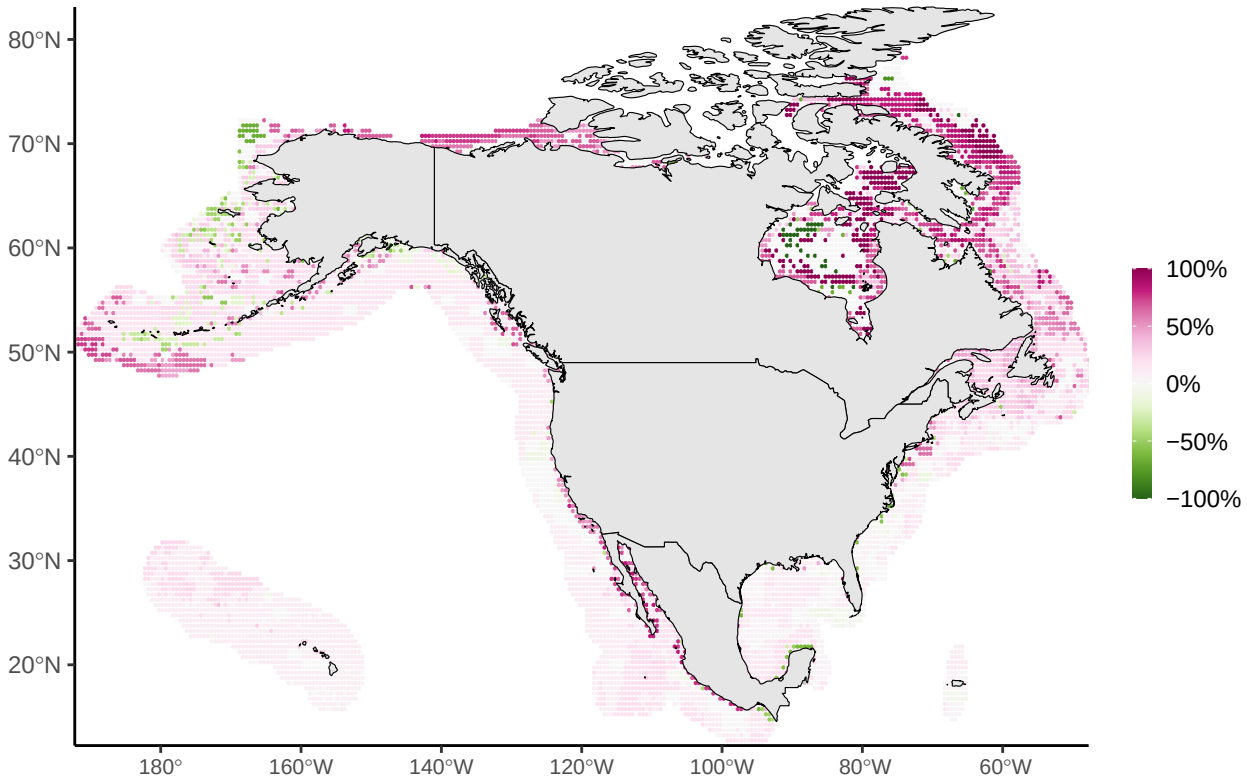


Fig. 2C: map of intensification by percentage

```
fig_2c <-
  ggplot() +
  geom_sf(data = sau_oh_sf, aes(color = intense), size = 0.1) +
  geom_sf(data = world_land, aes(), color = "black") +
  scale_color_gradientn(
    "Intensification\n(%)",
    colors = div_pal,
    breaks = seq(-1, 1, .5),
    labels = paste0(seq(-100, 100, 50), '%'),
    na.value = 'grey80') +
  theme_classic() +
  theme(plot.margin = unit(c(.05, 0, .05, 0), units = 'cm'),
        legend.background = element_blank(),
        legend.key.width = unit(.25, 'cm'),
        axis.text.x = element_text(size = 8),
        legend.title = element_blank()
  ) +
  scale_x_continuous(expand = c(0, 0)) +
  scale_y_continuous(expand = c(0, 0))

fig_2c
```



Combine into one figure

```
fig2 <-
ggdraw() +
  draw_plot(fig_2a,  x = .0001, y = 0.67, width = 1, height = .33) +
  draw_plot(fig_2b,  x = .01, y = 0.34, width = 1, height = .33) +
  draw_plot(fig_2c,  x = .003, y = 0.01, width = 1, height = .33) +
  # draw_plot(fig2a_legend, x = .89, y = 0.67, width = .1, height = .32) +
  # draw_plot(fig2b_legend, x = .895, y = 0.34, width = .1, height = .32) +
  # draw_plot(fig2c_legend, x = .9, y = 0.00, width = .1, height = .32) +
  draw_label('A', x = .1, y = .97, vjust = 0, size = 9, color = 'grey20', fontface = 'bold') +
  draw_label('B', x = .1, y = .65, vjust = 0, size = 9, color = 'grey20', fontface = 'bold') +
  draw_label('C', x = .1, y = .33, vjust = 0, size = 9, color = 'grey20', fontface = 'bold') +
  draw_label('Species impacted\n(count)', x = .92, y = .82, hjust = 0.5, vjust = 1,
             size = 8, color = 'grey20', fontface = 'bold', angle = 270) +
  draw_label('Species impacted\n(percent)', x = .92, y = .50, hjust = 0.5, vjust = 1,
             size = 8, color = 'grey20', fontface = 'bold',angle = 270) +
  draw_label('Intensification\n(percent)', x = .91, y = .18, hjust = 0.5, vjust = 1,
             size = 8, color = 'grey20', fontface = 'bold',angle = 270)

ggsave(plot = fig2, filename = "ncba_fig2.pdf",
       height = 20, width = 15, units = 'cm', dpi = 150)

print(fig2)
```