

# Reproductive maturity analysis results of *Patella* spp. in Madeira

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## 0.1 0. Imports and cleaning data

```
Mad_RAW <- readxl::read_excel("E:/Investigación/Repositorios/Lapacom/Data/ToAnalyze/Madeira/BD_LIMPETS_1")
Mad_RAW_Clean <- Mad_RAW %>% clean_names()

Mad_selected <- Mad_RAW_Clean %>%
  dplyr::select(species, year, month, total_length_mm, total_length_class_mm, weight_g, mature_imature,
    sampling_site, lat, long, protective_regime, proximity_human_settlements,
    accessibility, age_lt, age_months, age_class)

Mad_2sp <- Mad_selected %>%
  filter(species %in% c("Patella ordinaria", "Patella aspera")) %>%
  filter(!is.na(sampling_site) & trimws(sampling_site) != "") %>%
  mutate(across(where(is.character), as.factor),
    regulation_period = if_else(year < 2007, "Before", "After") %>% as.factor())

Mad_2sp_analisis <- Mad_2sp %>%
  filter(sampling_site %in% c("Porto Moniz", "Paúl do Mar", "Funchal", "Desertas",
    "Caníçal", "Santa Cruz", "Ribeira Brava", "São Vicente")) %>%
  mutate(
    across(where(is.character), as.factor),
    regulation_period = factor(regulation_period, levels = c("Before", "After"))
  )
```

```

Mad_2sp_analisis <- Mad_2sp_analisis %>%
  mutate(
    accessibility = case_when(
      protective_regime == "MPA" ~ "South",          # asignar categoría South a todas las MPA
      TRUE ~ as.character(accessibility)            # mantener el resto tal como está
    )
  ) %>%
  filter(!is.na(accessibility), accessibility %in% c("North", "South")) %>% # eliminar NA y "North-Sou
  mutate(
    accessibility = factor(accessibility, levels = c("North", "South"))      # asegurar orden y formato
  )
summary(Mad_2sp_analisis)

```

```

##          species          year      month      total_length_mm
## Patella aspera :16623   Min.   :1996   Min.   : 1.000   Min.   : 3.07
## Patella ordinaria:20576 1st Qu.:1999   1st Qu.: 4.000   1st Qu.:41.00
##                               Median :2009   Median : 6.000   Median :46.00
##                               Mean   :2008   Mean   : 5.727   Mean   :46.07
##                               3rd Qu.:2017   3rd Qu.: 7.000   3rd Qu.:50.83
##                               Max.   :2018   Max.   :12.000   Max.   :79.90
##
## total_length_class_mm  weight_g  mature_imature      sampling_site
## 45      : 2075         Min.   : 0.09   Imature: 3202   Porto Moniz :18524
## 46      : 2053         1st Qu.: 4.86   Mature :33997   Desertas    : 6659
## 47      : 2004         Median : 6.93                Paúl do Mar : 4353
## 43      : 1997         Mean   : 8.17                Caniçal     : 3246
## 44      : 1991         3rd Qu.: 9.88                Ribeira Brava: 1774
## 48      : 1976         Max.   :74.70                Funchal     : 1351
## (Other):25103         NA's   :2708                (Other)     : 1292
##
##          lat          long      protective_regime
## 32°51'50.0"N:18524 17°09'52.9"W:18524 Full access:30540
## 32°30'06.4"N: 6659 16°30'16.1"W: 6659 MPA          : 6659
## 32°45'53.5"N: 4353 17°14'07.5"W: 4353
## 32°44'48.2"N: 3246 16°41'42.1"W: 3246
## 32°40'19.8"N: 1774 17°04'07.7"W: 1774
## 32°38'10.4"N: 1351 16°56'05.5"W: 1351
## (Other)      : 1292 (Other)      : 1292
##
## proximity_human_settlements accessibility  age_lt      age_months
## Control: 6659                North:18869   Min.   : 0.1032   Min.   : 1.239
## Far      : 3246                South:18330  1st Qu.: 1.9872   1st Qu.: 23.846
## Near     :27294                Median : 2.4249   Median : 29.099
##                               Mean   : 2.5254   Mean   : 30.305
##                               3rd Qu.: 2.9135   3rd Qu.: 34.962
##                               Max.   :14.0200   Max.   :168.240
##
## age_class      regulation_period
## 23      : 2029   Before:14733
## 27      : 1870   After :22466
## 29      : 1821
## 28      : 1820
## 25      : 1817
## 26      : 1770
## (Other):26072

```

## 0.2 1. Localización geográfica de los sitios de muestreo

```
# shapefiles and polígonos

world <- ne_countries(scale = 10, returnclass = "sf")
portugal_gadm <- geodata::gadm("PRT", level = 1, path = tempdir()) %>% st_as_sf()
portugal_mainland <- portugal_gadm %>% filter(!NAME_1 %in% c("Madeira", "Açores"))
madeira_sf <- portugal_gadm %>% filter(NAME_1 == "Madeira")
azores_sf <- portugal_gadm %>% filter(NAME_1 == "Açores")

# Coordenadas DMS a decimales
convert_dms_to_decimal <- function(dms) {
  parts <- str_match(dms, "(\\d+)°(\\d+)'(\\d+\\.?\\d*)\""?([NSEW])")
  deg <- as.numeric(parts[, 2])
  min <- as.numeric(parts[, 3])
  sec <- as.numeric(parts[, 4])
  dir <- parts[, 5]
  decimal <- deg + min / 60 + sec / 3600
  ifelse(dir %in% c("S", "W"), -decimal, decimal)
}

coords <- Mad_2sp_analisis %>%
  dplyr::select(sampling_site, lat, long, protective_regime) %>%
  distinct() %>%
  drop_na() %>%
  mutate(
    lat_dd = convert_dms_to_decimal(lat),
    long_dd = convert_dms_to_decimal(long)
  )

coords_sf <- st_as_sf(coords, coords = c("long_dd", "lat_dd"), crs = 4326)

etiquetas <- tibble::tibble(
  lugar = c("Portugal", "Selvagens", "Azores", "Canary Islands", "Morocco", "Gibraltar", "Spain"),
  lon = c(-10.5, -16.1, -26.0, -16.5, -8.5, -5.4, -6.5),
  lat = c(39.5, 31.0, 38.6, 29.2, 31.0, 36.1, 43.0)
)

# Mapas
map_region <- ggplot() +
  geom_sf(data = world, fill = "grey90", color = "darkgrey") +
  geom_sf(data = portugal_mainland, fill = "darkgrey") +
  geom_sf(data = madeira_sf, fill = "darkgrey") +
  geom_sf(data = azores_sf, fill = "darkgrey") +
  geom_text(data = etiquetas, aes(x = lon, y = lat, label = lugar),
    size = 3.2, fontface = "italic") +
  annotation_scale(location = "bl", width_hint = 0.3) +
  annotate("rect", xmin = -17.6, xmax = -16.2, ymin = 32.4, ymax = 33.2,
    fill = "grey", alpha = 0.3, color = "grey20", size = 0.7) +
  annotate("text", x = -20, y = 36, label = "Atlantic Ocean", angle = 45, size = 7,
    fontface = "italic", color = "gray30") +
  annotate("text", x = -17.0, y = 33.5, label = "Madeira", size = 3.2, fontface = "bold",
    color = "black") +
```

```

annotation_north_arrow(location = "tl", which_north = "true",
                        style = north_arrow_fancy_orienteering()) +
coord_sf(xlim = c(-30, -5), ylim = c(27, 44), expand = FALSE) +
labs(x = "Longitude", y = "Latitude") +
theme_minimal() +
theme(
  panel.grid.major = element_line(color = "darkgrey", size = 0.2),
  axis.title = element_blank(),
  plot.margin = margin(5, 5, 5, 5)
)

map_madeira <- ggplot() +
  geom_sf(data = madeira_sf, fill = "gray90", color = "darkgrey") +
  geom_sf(data = coords_sf, aes(color = sampling_site, shape=protective_regime), size = 3) +
  coord_sf(xlim = c(-17.6, -16.2), ylim = c(32.4, 33.2), expand = FALSE) +
  annotation_scale(location = "bl", width_hint = 0.3) +
  annotation_north_arrow(location = "tl", which_north = "true",
                        style = north_arrow_fancy_orienteering()) +
  labs(color = "Sitios de muestreo") +
  theme_minimal() +
  theme(legend.position = "bottom")

legend_b <- ggplotGrob(map_madeira) %>%
  gtable::gtable_filter("guide-box")
map_madeira_noleg <- map_madeira + theme(legend.position = "none")

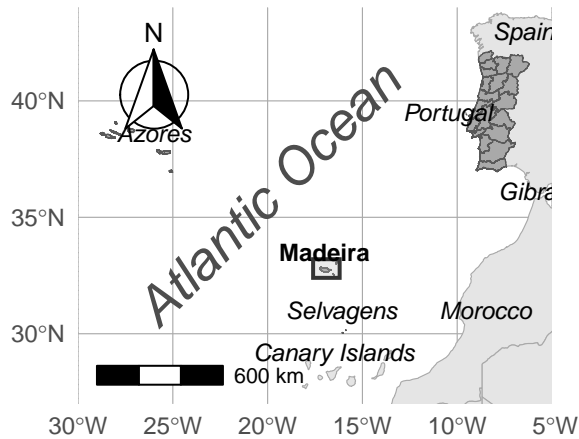
panel_maps <- plot_grid(
  map_region, map_madeira_noleg,
  labels = c("A", "B"),
  label_size = 14,
  ncol = 2,
  rel_widths = c(1, 1.2)
)

final_plot <- plot_grid(
  panel_maps,
  legend_b,
  ncol = 1,
  rel_heights = c(1, 0.1)
)

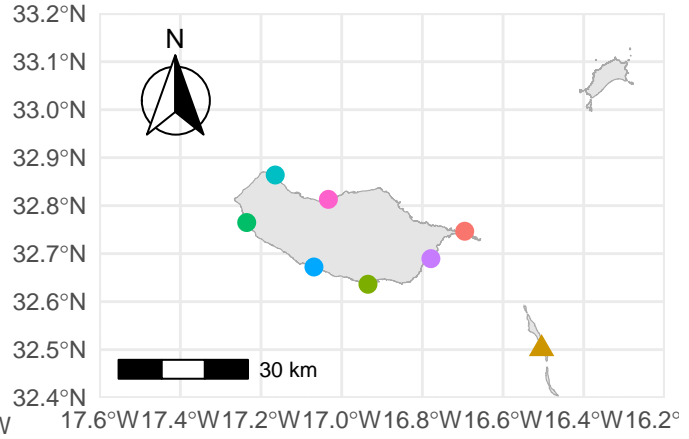
final_plot

```

A)



B)



● Caniçal    ● Funchal    ● Porto Moniz    ● Santa Cruz    ● protective\_regime  
● Desertas    ● Paúl do Mar    ● Ribeira Brava    ● São Vicente

```

madurez_prop_mensual_pr <- Mad_2sp_analisis %>%
  filter(!is.na(mature_imature)) %>%
  group_by(year, month, species, sampling_site, accessibility, protective_regime) %>%
  summarise(
    total = n(),
    maduros = sum(mature_imature == "Mature"),
    proporcion_madura = maduros / total,
    .groups = "drop"
  ) %>%
  mutate(
    grupo = interaction(species, protective_regime, sep = " - "),
    fecha = lubridate::make_date(year, month, 1) # For a continuous time axis
  )

# Visual style for protection regime plot
colores <- c(
  "Patella aspera - Full access" = "#D39C00",
  "Patella ordinaria - Full access" = "#0072B2",
  "Patella aspera - MPA" = "#D39C00",
  "Patella ordinaria - MPA" = "#0072B2"
)

lineas <- c(
  "Patella aspera - Full access" = "solid",
  "Patella ordinaria - Full access" = "solid",
  "Patella aspera - MPA" = "dotted",

```

```

"Patella ordinaria - MPA" = "dotted"
)

# Final plot: mature proportion by protection regime
MATURE_PROP_protreg <- ggplot(
  data = madurez_prop_mensual_pr,
  aes(x = fecha,
       y = proporcion_madura,
       color = grupo,
       linetype = grupo)) +

  geom_line(linewidth = 1) +

  geom_vline(
    xintercept = as.Date("2007-01-01"),
    linetype = "dashed",
    color = "black",
    linewidth = 0.7) +

  scale_color_manual(
    values = colores) +

  scale_linetype_manual(
    values = lineas) +

  scale_y_continuous(
    labels = scales::percent_format(accuracy = 1)) +

  scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
  scale_x_date(
    date_breaks = "2 year",
    date_labels = "%Y"
  ) +

  labs(
    x = "Date",
    y = "Mature Proportion (%)") +

  theme_minimal() +

  theme(
    legend.position = "bottom",
    legend.title = element_blank(),
    panel.grid.minor = element_blank()
  )

# Monthly proportion of mature individuals by accessibility
madurez_prop_mensual_ac <- Mad_2sp_analisis %>%
  filter(!is.na(mature_imature)) %>%
  group_by(year, month, species, sampling_site, accessibility, protective_regime) %>%
  summarise(
    total = n(),
    maduros = sum(mature_imature == "Mature"),

```

```

    proporcion_madura = maduros / total,
    .groups = "drop"
  ) %>%
  mutate(
    grupo = interaction(species, accessibility, sep = " - "),
    fecha = lubridate::make_date(year, month, 1) # For a continuous time axis
  )

# Visual style for accessibility plot
colores <- c(
  "Patella aspera - North" = "#D39C00",
  "Patella ordinaria - North" = "#0072B2",
  "Patella aspera - South" = "#D39C00",
  "Patella ordinaria - South" = "#0072B2"
)

lineas <- c(
  "Patella aspera - South" = "solid",
  "Patella ordinaria - South" = "solid",
  "Patella aspera - North" = "dotted",
  "Patella ordinaria - North" = "dotted"
)

# Final plot: mature proportion by accessibility
MATURE_PROP_ACC <- ggplot(
  madurez_prop_mensual_ac,
  aes(x = fecha,
       y = proporcion_madura,
       color = grupo,
       linetype = grupo)) +

  geom_line(
    linewidth = 1) +

  geom_vline(
    xintercept = as.Date("2007-01-01"),
    linetype = "dashed",
    color = "black",
    linewidth = 0.7) +

  scale_color_manual(
    values = colores) +

  scale_linetype_manual(
    values = lineas) +

  scale_y_continuous(
    labels = scales::percent_format(accuracy = 1)) +

  scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
  scale_x_date(
    date_breaks = "2 year",
    date_labels = "%Y"
  )

```

```

) +

labs(
  x = "Date",
  y = "Mature proportion (%)" +

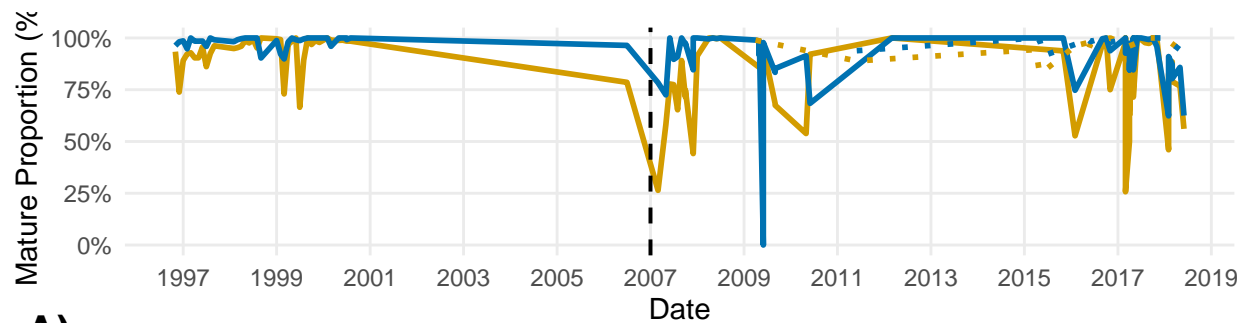
theme_minimal() +

theme(
  legend.position = "bottom",
  legend.title = element_blank(),
  panel.grid.minor = element_blank()
)

# Plot both panels (A and B)
plot_grid(
  MATURE_PROP_protreg, MATURE_PROP_ACC,
  labels = c("A", "B"),
  label_size = 16,
  label_x = 0.02,    # Horizontal alignment (closer to edge)
  label_y = 0.3,     # Vertical alignment
  hjust = 0,         # Left justified
  vjust = 1,         # Top justified
  ncol = 1,
  rel_heights = c(1, 1)
)

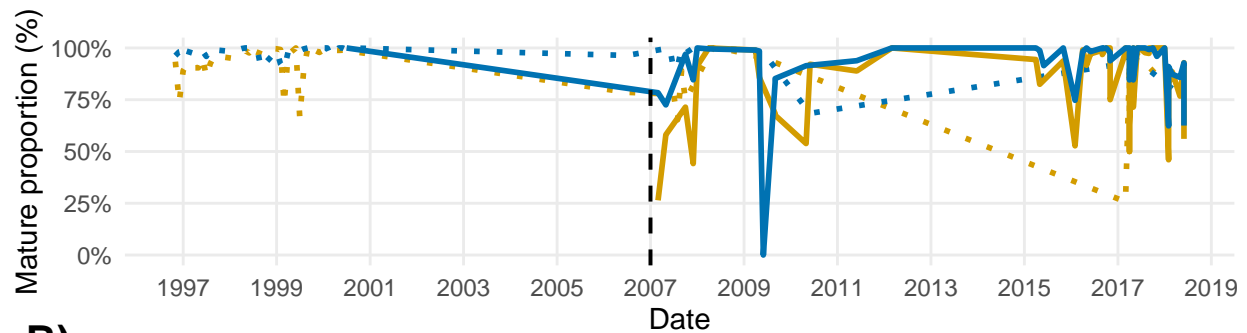
```





A)

— Patella aspera – Full access — Patella ordinaria – Full access - - Patella aspera – MPA - - Patella ordinaria – MPA



B)

- - Patella aspera – North - - Patella ordinaria – North — Patella aspera – South — Patella ordinaria – South

### 0.3 2. Monthly proportion of mature adults per year.

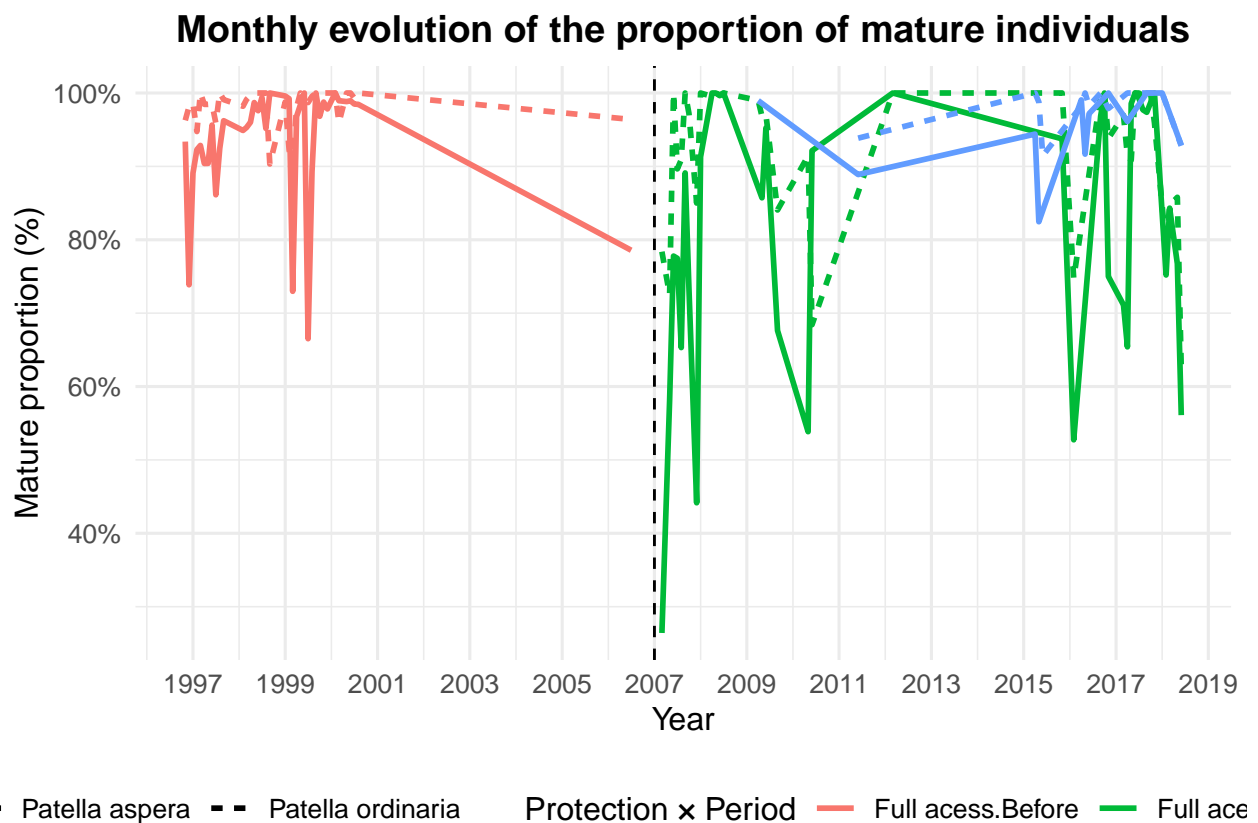
```
madurez_prop <- Mad_2sp_analisis %>%
  filter(!is.na(mature_imature)) %>%
  group_by(year, month, species, protective_regime, regulation_period) %>%
  summarise(
    total = n(),
    maduros = sum(mature_imature == "Mature"),
    prop_maduros = maduros / total,
    .groups = "drop"
  ) %>%
  mutate(fecha = make_date(year, month, 1))

ggplot(madurez_prop,
  aes(x = fecha, y = prop_maduros,
    color = interaction(protective_regime, regulation_period), linetype = species)) +
  geom_line(linewidth = 1) +
  geom_vline(xintercept = as.Date("2007-01-01"),
    linetype = "dashed", color = "black") +
  labs(
    title = "Monthly evolution of the proportion of mature individuals",
    x = "Year",
    y = "Mature proportion (%)",
    color = "Protection × Period",
  )
```

```

linetype = "Species"
) +
scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
scale_x_date(
date_breaks = "2 year",
date_labels = "%Y"
)+
theme_minimal(base_size = 12) +
theme(
legend.position = "bottom",
strip.text = element_text(face = "bold"),
plot.title = element_text(face = "bold", hjust = 0.5)
)

```



#### 0.4 3. Comparación antes y después de 2007

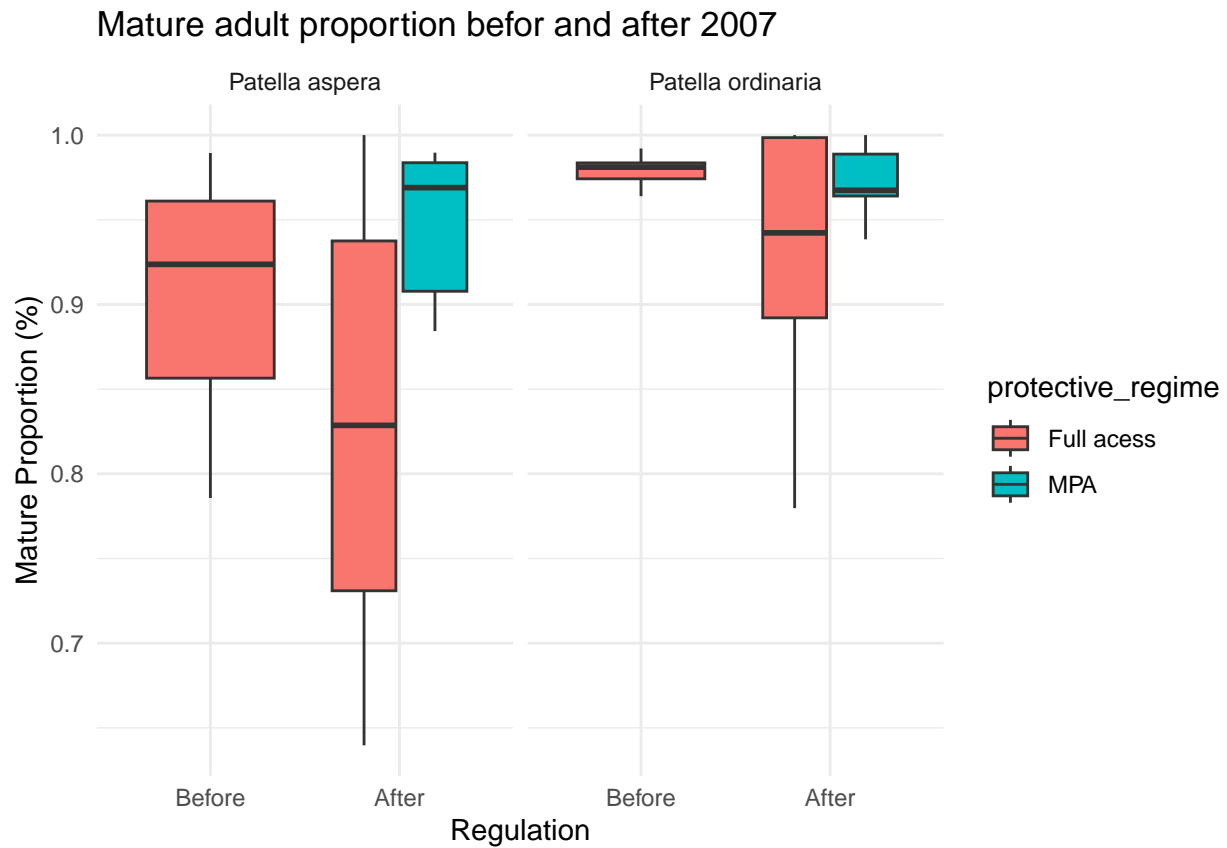
```

madurez_yearly <- madurez_prop %>%
  group_by(year, species, protective_regime, regulation_period) %>%
  summarise(prop_m = mean(prop_maduros, na.rm = TRUE), .groups = "drop")

ggplot(madurez_yearly, aes(x = regulation_period, y = prop_m, fill = protective_regime)) +
  geom_boxplot() +
  facet_wrap(~species) +

```

```
labs(title = "Mature adult proportion befor and after 2007", y = "Mature Proportion (%)", x = "Regulation",
theme_minimal())
```



## 0.5 4. Estacionalidad y periodos de veda

```
madurez_mes <- madurez_prop %>%
  group_by(month, species, protective_regime) %>%
  summarise(prop_m = mean(prop_maduros, na.rm = TRUE), .groups = "drop")

periodos <- tibble(
  month = 1:12,
  periodo = case_when(
    month %in% 4:9 ~ "Exploitation",
    TRUE ~ "Reproductive"
  )
)

madurez_mes_plot <- madurez_mes %>%
  left_join(periodos, by = "month")

ggplot(madurez_mes_plot, aes(x = month, y = prop_m,
  color = protective_regime,
  linetype = species)) +
```

```

# Fondo por periodo con baja opacidad
geom_tile(aes(x = month, fill = periodo, y = 0.5), height = 1, alpha = 0.1,
          inherit.aes = FALSE, show.legend = FALSE) +

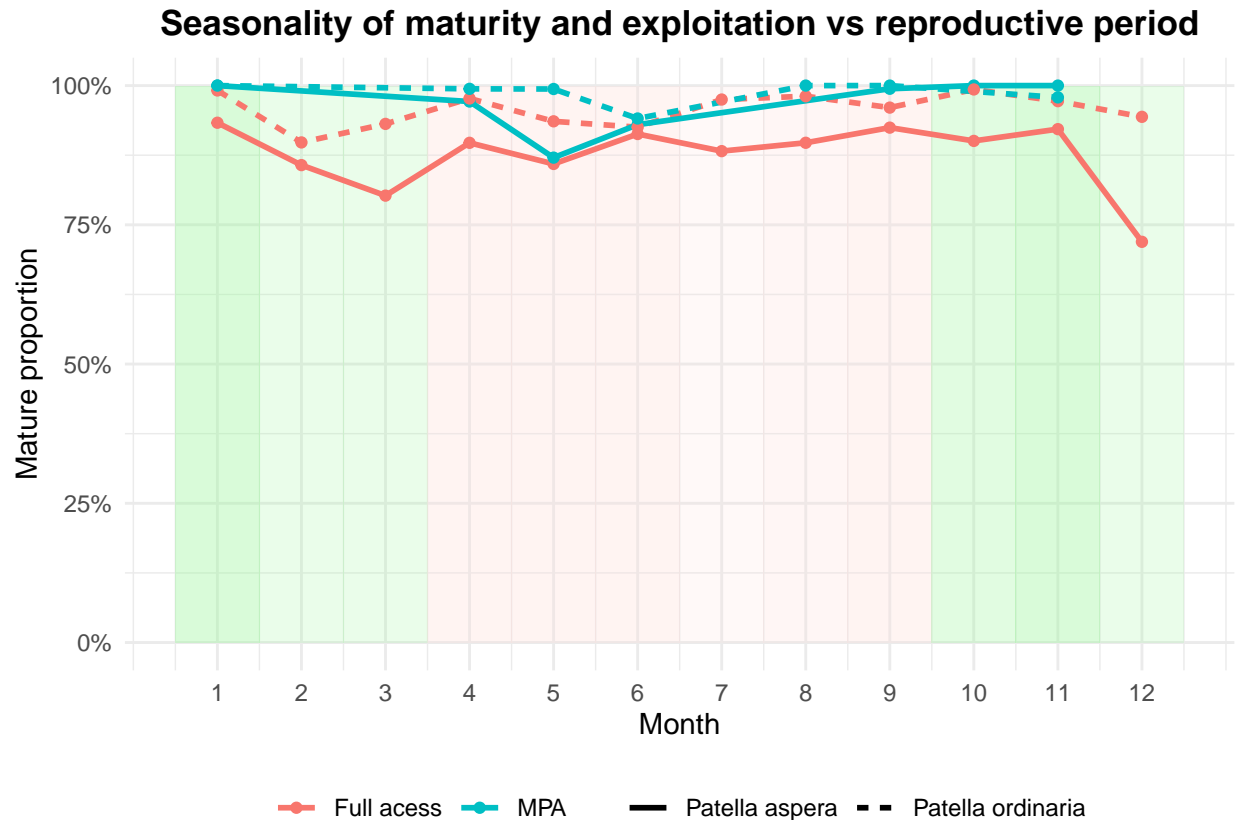
# Línea y puntos
geom_line(linewidth = 1) +
geom_point(size = 1.5) +

# Escalas
scale_x_continuous(breaks = 1:12) +
scale_y_continuous(labels = scales::percent_format(accuracy = 1)) +
scale_fill_manual(values = c("Exploitation" = "mistyrose",
                             "Reproductive" = "palegreen")) +

# Etiquetas
labs(title = "Seasonality of maturity and exploitation vs reproductive period",
     x = "Month", y = "Mature proportion") +

# Tema limpio
theme_minimal() +
theme(
  legend.title = element_blank(),
  legend.box = "horizontal",
  legend.position = "bottom",
  plot.title = element_text(face = "bold", hjust = 0.5)
)

```



## 0.6 5. Modelo GLM binomial para evaluar efecto MPA y regulación

### 0.6.1 Patella aspera

```
# Modelo sobre datos individuales para Patella aspera
modelo_comparado_pa <- Mad_2sp_analisis %>%
  filter(species == "Patella aspera", !is.na(mature_imature)) %>%
  mutate(
    maduro = mature_imature == "Mature",
    grupo = case_when(
      protective_regime == "Full access" & regulation_period == "Before" ~ "FA_Before",
      protective_regime == "Full access" & regulation_period == "After" ~ "FA_After",
      protective_regime == "MPA" & regulation_period == "After" ~ "MPA_After"
    ),
    grupo = factor(grupo, levels = c("FA_Before", "FA_After", "MPA_After"))
  ) %>%
  glm(maduro ~ grupo, data = ., family = binomial())
# Resultados del modelo (odds ratios con IC 95%)
broom::tidy(modelo_comparado_pa, exponentiate = TRUE, conf.int = TRUE)
```

```
## # A tibble: 3 x 7
##   term                estimate std.error statistic    p.value conf.low conf.high
##   <chr>                <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
```

```
## 1 (Intercept)      13.9      0.0503      52.3  0          12.6      15.3
## 2 grupoFA_After    0.261      0.0583     -23.1  1.24e-117    0.232      0.292
## 3 grupoMPA_After   1.46       0.0945      4.03  5.53e- 5     1.22      1.77
```

```
em_pa <- emmeans(modelo_comparado_pa, ~ grupo, type = "response")

contrastes_interes_pa <- contrast(em_pa, method = list(
  "FA_Before vs FA_After" = c(1, -1, 0),
  "FA_Before vs MPA_After" = c(1, 0, -1),
  "FA_After vs MPA_After" = c(0, 1, -1)
), type = "response")

# Convertir resultados de emmeans a data frame
contrastes_df_pa <- as.data.frame(summary(contrastes_interes_pa))

# Formatear columnas:
# - Redondear todas las columnas numéricas excepto p.value
# - Formatear p.value en notación científica
tabla_formateada_pa <- contrastes_df_pa %>%
  mutate(
    across(where(is.numeric) & !matches("p.value"), ~ round(., 3)),
    p.value = format(p.value, scientific = TRUE, digits = 6)
  )

# Mostrar como flextable con título
flextable(tabla_formateada_pa) %>%
  set_caption(caption = "Marginal Effects (EMMEANS) - Patella aspera")
```

Table 1: Marginal Effects (EMMEANS) - Patella aspera

contrast	odds.ratio	SE	df	null	z.ratio	p.value
FA_Before vs FA_After	3.834	0.223	Inf	1	23.057	1.23952e-117
FA_Before vs MPA_After	0.683	0.065	Inf	1	-4.032	5.52690e-05
FA_After vs MPA_After	0.178	0.015	Inf	1	-20.246	3.88032e-91

## 0.6.2 Patella ordinaria

```
modelo_comparado_po <- Mad_2sp_analisis %>%
  filter(species == "Patella ordinaria", !is.na(mature_imature)) %>%
  mutate(
    maduro = mature_imature == "Mature",
    grupo = case_when(
```

```

protective_regime == "Full access" & regulation_period == "Before" ~ "FA_Before",
protective_regime == "Full access" & regulation_period == "After" ~ "FA_After",
protective_regime == "MPA" & regulation_period == "After" ~ "MPA_After"
),
grupo = factor(grupo, levels = c("FA_Before", "FA_After", "MPA_After"))
) %>%
glm(maduro ~ grupo, data = ., family = binomial())
# Resultados del modelo (odds ratios con IC 95%)
broom::tidy(modelo_comparado_po, exponentiate = TRUE, conf.int = TRUE)

```

```

## # A tibble: 3 x 7
##   term                estimate std.error statistic  p.value conf.low conf.high
##   <chr>                <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)         61.1      0.0864     47.6 0      51.8      72.7
## 2 grupoFA_After       0.161     0.0938    -19.5 2.43e-84  0.134     0.193
## 3 grupoMPA_After      0.285     0.117     -10.8 5.22e-27  0.226     0.358

```

```

em_po <- emmeans(modelo_comparado_po, ~ grupo, type = "response")

contrastes_interes_po <- contrast(em_po, method = list(
  "FA_Before vs FA_After" = c(1, -1, 0),
  "FA_Before vs MPA_After" = c(1, 0, -1),
  "FA_After vs MPA_After" = c(0, 1, -1)
), type = "response")

em_po <- emmeans(modelo_comparado_po, ~ grupo, type = "response")

contrastes_interes_po <- contrast(em_po, method = list(
  "FA_Before vs FA_After" = c(1, -1, 0),
  "FA_Before vs MPA_After" = c(1, 0, -1),
  "FA_After vs MPA_After" = c(0, 1, -1)
), type = "response")

# Convertir resultados de emmeans a data frame
contrastes_df_po <- as.data.frame(summary(contrastes_interes_po))

# Formatear columnas:
# - Redondear todas las columnas numéricas excepto p.value
# - Formatear p.value en notación científica
tabla_formateada_po <- contrastes_df_po %>%
  mutate(
    across(where(is.numeric) & !matches("p.value"), ~ round(., 3)),
    p.value = format(p.value, scientific = TRUE, digits = 6)
  )

# Mostrar como flextable con título
flextable(tabla_formateada_po) %>%
  set_caption(caption = "Marginal Effects (EMMEANS) - Patella ordinaria")

```

Table 2: Marginal Effects (EMMEANS) - Patella ordinaria

contrast	odds.ratio	SE	df	null	z.ratio	p.value
FA_Before vs FA_After	6.206	0.582	Inf	1	19.459	2.43274e-84
FA_Before vs MPA_After	3.511	0.410	Inf	1	10.762	5.21739e-27
FA_After vs MPA_After	0.566	0.049	Inf	1	-6.586	4.50338e-11

## 0.7 6. Gráfico de odds ratios del modelo de implementacion de MPA y regulaciones.

```
# Obtener resultados tidy para ambas especies
po_df <- broom::tidy(modelo_comparado_po, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)") %>%
  mutate(
    term = dplyr::recode(term,
                        "grupoFA_After" = "Full access (After)",
                        "grupoMPA_After" = "MPA (After)"),
    species = "Patella ordinaria"
  )

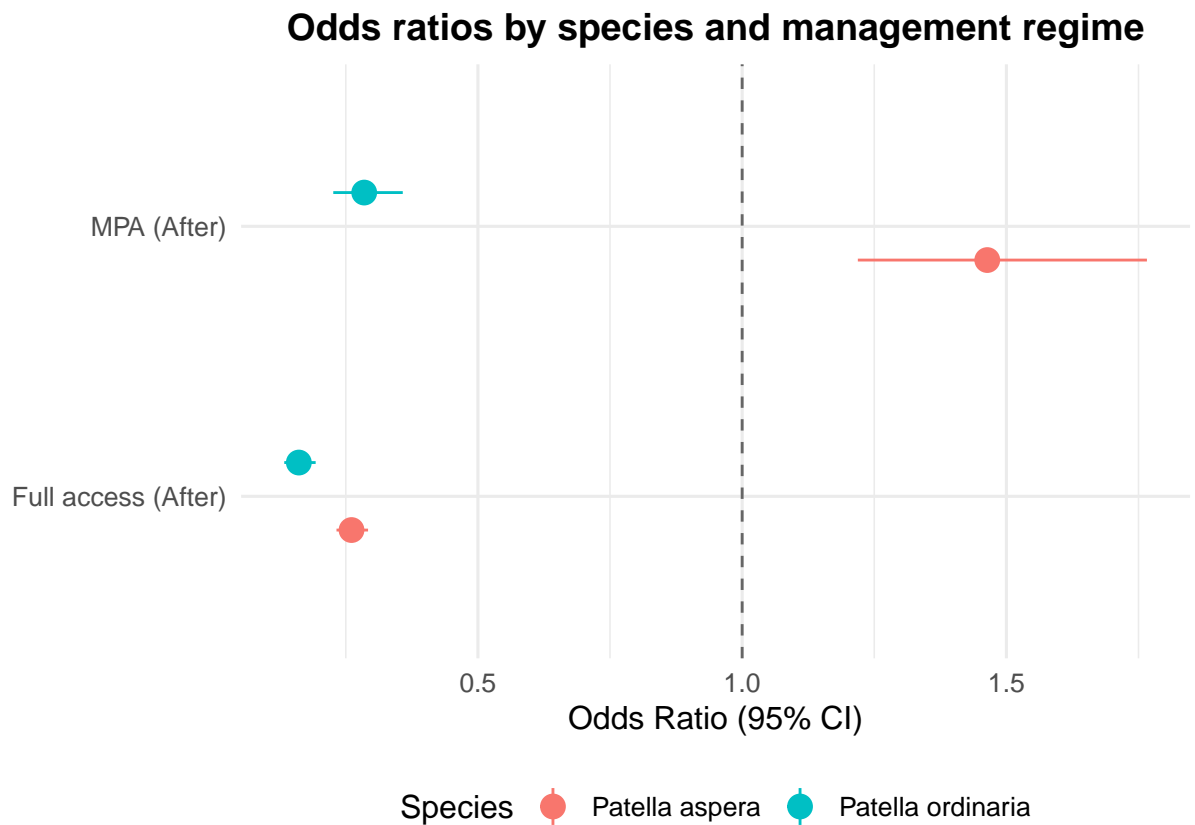
pa_df <- broom::tidy(modelo_comparado_pa, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)") %>%
  mutate(
    term = dplyr::recode(term,
                        "grupoFA_After" = "Full access (After)",
                        "grupoMPA_After" = "MPA (After)"),
    species = "Patella aspera"
  )

# Combinar en un solo data frame
odds_df <- bind_rows(po_df, pa_df)

# Graficar
ggplot(odds_df, aes(x = term, y = estimate, ymin = conf.low, ymax = conf.high, color = species)) +
  geom_pointrange(position = position_dodge(width = 0.5), size = 0.8) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "gray40") +
  coord_flip() +
  labs(
    title = "Odds ratios by species and management regime",
    x = "", y = "Odds Ratio (95% CI)", color = "Species"
  ) +
  theme_minimal(base_size = 12) +
  theme(
    plot.title = element_text(face = "bold", hjust = 0.5),
```



```
legend.position = "bottom"
)
```



## 0.8 7. Efecto de la accesibilidad (conectividad)

Evaluate the effect of geographic accessibility (North/South) on the proportion of mature individuals, considering the interaction with:

protective regime (Total access / MPA)

regulatory period (Before / After)

### 0.8.1 Efecto de la accesibilidad en zonas Full access – Patella ordinaria

```
resumen_acc_po <- Mad_2sp_analisis %>%
  filter(
    species == "Patella ordinaria",
    protective_regime == "Full access",
    !is.na(mature_imature),
    !is.na(accessibility)
  ) %>%
  mutate(
    maduro = mature_imature == "Mature"
```

```

) %>%
group_by(accessibility) %>%
summarise(
  maduros = sum(maduro),
  total = n(),
  .groups = "drop"
) %>%
mutate(
  accessibility = factor(accessibility, levels = c("North", "South"))
)

modelo_acc_po <- glm(
  cbind(maduros, total - maduros) ~ accessibility,
  data = resumen_acc_po,
  family = binomial()
)

broom::tidy(modelo_acc_po, exponentiate = TRUE, conf.int = TRUE)

```

```

## # A tibble: 2 x 7
##   term                estimate std.error statistic   p.value conf.low conf.high
##   <chr>              <dbl>    <dbl>    <dbl>   <dbl>   <dbl>   <dbl>
## 1 (Intercept)        43.4      0.0646     58.3 0      38.3     49.3
## 2 accessibilitySouth  0.187    0.0758    -22.1 1.34e-108 0.161    0.217

```

## 0.8.2 Efecto de accesibilidad en zonas Full access – Patella aspera

```

resumen_acc_pa <- Mad_2sp_analisis %>%
  filter(
    species == "Patella aspera",
    protective_regime == "Full access",
    !is.na(mature_imature),
    !is.na(accessibility)
  ) %>%
  mutate(
    maduro = mature_imature == "Mature"
  ) %>%
  group_by(accessibility) %>%
  summarise(
    maduros = sum(maduro),
    total = n(),
    .groups = "drop"
  ) %>%
  mutate(
    accessibility = factor(accessibility, levels = c("North", "South"))
  )

modelo_acc_pa <- glm(
  cbind(maduros, total - maduros) ~ accessibility,
  data = resumen_acc_pa,
  family = binomial()
)

```

```
)
```

```
broom::tidy(modelo_acc_pa, exponentiate = TRUE, conf.int = TRUE)
```

```
## # A tibble: 2 x 7
```

```
##   term                estimate std.error statistic    p.value conf.low conf.high
##   <chr>                <dbl>    <dbl>    <dbl>    <dbl>    <dbl>    <dbl>
## 1 (Intercept)          10.1      0.0390     59.2 0      9.36     10.9
## 2 accessibilitySouth   0.331    0.0512    -21.6 1.82e-103 0.299     0.366
```

## 0.9 8. Gráfico de odds ratios de modelos de accesibilidad

```
# Patella ordinaria
```

```
res_po <- broom::tidy(modelo_acc_po, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)") %>%
  mutate(species = "Patella ordinaria")
```

```
# Patella aspera
```

```
res_pa <- broom::tidy(modelo_acc_pa, exponentiate = TRUE, conf.int = TRUE) %>%
  filter(term != "(Intercept)") %>%
  mutate(species = "Patella aspera")
```

```
# Unimos ambos modelos
```

```
res_combinado <- bind_rows(res_po, res_pa) %>%
  dplyr::mutate(term = dplyr::recode(term,
    "accessibilitySouth" = "South vs North"
  ))
```

```
# Gráfico
```

```
ggplot(res_combinado, aes(x = term, y = estimate, ymin = conf.low, ymax = conf.high, color = species)) +
  geom_pointrange(position = position_dodge(width = 0.6), size = 0.9) +
  geom_hline(yintercept = 1, linetype = "dashed", color = "gray50") +
  coord_flip() +
  labs(
    title = "Odds Ratios - Efecto de accesibilidad (Full access)",
    x = "", y = "Odds Ratio (IC 95%)", color = "Especie"
  ) +
  theme_minimal(base_size = 12) +
  theme(
    plot.title = element_text(face = "bold", hjust = 0.5),
    legend.position = "bottom"
  )
```

