

An overview of the status and management of the Skipjack Tuna (*Katsuwonus pelamis*) in the Atlantic Ocean

Final Report for ESM 211 - Applied Population Ecology

Caio Faro & Juan Carlos Villasenor-Derbez

March 20, 2017

```
suppressPackageStartupMessages({  
  library(readr)  
  library(tidyverse)  
  library(reshape)  
  library(popbio)  
  library(ggExtra)  
  library(knitr)  
  library(RobustRegression)  
  library(stargazer)  
})
```

A description of the conservation or management problem

Katsuwonus pelamis (Linnaeus, 1758), also known as Skipjack Tuna, is a fish from the Order Perciformes, under the Scombridae family. This family includes all mackerels, tunas, and bonitos. As other species in this family, *K. pelamis* has a pelagic affinity, often found in aggregations between 0 and 260 m deep and is mainly distributed in tropical waters –where they spawn– but is common to subtropical and temperate waters. Scombrids are also characterized for their fast growth rates and high mobility.

Unlike other Scombrids, *K. pelamis* is relatively small, with a mean length of 80 cm (max up to 110 cm). The maximum reported weight has been 34.5 Kg, and the maximum reported age has been 12 years. It reaches the sexual maturity around one year and 43 cm. It feeds mainly on fish and crustaceans, but squids and some mollusks also comprise part of their diet. Trophic ecology research indicates that they have a trophic level of $TL = 4.4 \pm 0.5$ ($M \pm SE$; Froese & Pauly, 2016).

Besides its populations being classified as Least Concern by CITES, there is a high uncertainty in population estimations, which may mask the real status. FAO reports increased landings in the last years, likely due to an increase in effort. Some regions are already showing the first signs of overfishing for this species.

Conservation or management problem

The Skipjack is a commercially important fish that sustain a high fishing effort around the world. It is currently the third most captured species of the world on average (FAO, 2016). Catches of skipjack tuna have been steadily increasing since 1950, reaching a global peak in 1991 at 1 674 970 t. (FAO, 2017). In the Atlantic Ocean the catches peaked on 2013 at 255,729.78 t. Guarantee that this fishery is sustainable is extremely important for the economy and food security.

Data

Our data comprise nominal catches data, effort and size for Skipjack Tuna on the Atlantic Ocean, reported by countries to the International Commission to the Conservation of the Atlantic Tuna (ICCAT). The data was updated on November 2016 and incorporates catches from 1950 to 2015.

Metadata

The data includes a total of 3,711 records of catch data, specified for 66 years (1950 - 2015). The data also includes information by Fleet (149), country (66 Flags), and Party (39). The effort data correspond to 40,646 records of catch data from 17 countries associated with the effort (fishing hours) for that fishing trip, from 2006 to 2015. The last dataset includes a total of 34,074,524 records of size of the Skipjack captured by 17 countries between 1964 and 1980. All the datasets also include ICCAT Area code to allow spatial identification. In order to control for different gear types, a column for Gear group is included. Stock source (Eastern and Western Atlantic) is also included.

Evidence for past trends

We explored the relationship between effort and time (**Fig?**) by fitting a linear model where coefficients were estimated by Ordinary Least Squares with heteroskedastic-robust standard errors, and tested the significance of the slope and intercept coefficients. Neither the intercept or slope showed significant change through time (**Table?**), indicating that fishing effort had remained relatively constant from 2006 to 2015 (**Fig?**).

```
skj <- read.csv("Effort_full.csv", stringsAsFactors = F) %>%
  mutate(CPUE = SKJ/Eff1) %>%
  filter(GearCode == "PS") %>%
  group_by(Year, Flag) %>%
  summarize(Effort = sum(Eff1))

ggplot(skj, aes(x = Year, y = Effort)) +
  geom_point() +
  geom_smooth(method = "lm") +
  theme_bw() +
  labs(y = "Effort (fishing hours)")
```

```
model <- lm(Effort~Year, skj)
```

```
stargazer(model,
  se = rse(model),
  t.auto = T,
  p.auto = T,
  header = F,
  single.row = T,
  title = "Regression coefficients for Fishing effort (hours) as a function of time. Numbers in
```

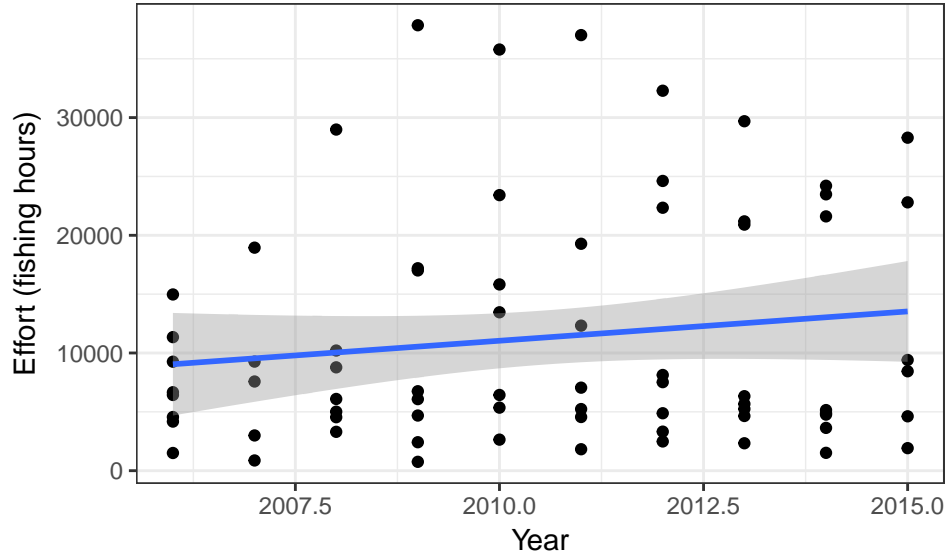


Figure 1: Total effort (fishing hours) by country through time.

Table 1: Regression coefficients for Fishing effort (hours) as a function of time. Numbers in parenthesis are Standard Errors.

	<i>Dependent variable:</i>
	Effort
Year	498.467 (343.705)
Constant	−990,880.400 (690,769.600)
Observations	72
R ²	0.021
Adjusted R ²	0.007
Residual Std. Error	9,778.583 (df = 70)
F Statistic	1.496 (df = 1; 70)
<i>Note:</i> *p<0.1; **p<0.05; ***p<0.01	

We then used a larger dataset that included catches from 1950 to 2015, by country (Fig 2), and calculated the total catches by year (Fig. 3). We counted the unique countries that participated in the fishery or for which there is data (Figure 4), and used this as a proxy of total fishing effort. We then normalized total catches by dividing them by the number of countries participating in the fishery each year (Fig. 5). Here, we can see an increase in catches even after normalizing for our proxy of effort. For the Eastern stock (ATE), we see a steady increase since 1950, resulting in an order of magnitude higher values for 2015, as compared to 1950. On the other hand, the Western stock (WTE) does not show an increase of similar magnitude. Interannual variability in the data is in the order of 5,000 tonnes for ATE, and 1500 for ATW. Tables 2 and 3 present the regression coefficients for CPUE as a function of time, for each stock.

```
iccat <- read.csv("ICCAT Data_full.csv")

slope <- coefficients(model)[[2]]
intercept <- coefficients(model)[[1]]

countries <- iccat %>%
  group_by(YearC, Stock, Flag) %>%
  count() %>%
  group_by(YearC, Stock) %>%
  count()

iccat2 <- iccat %>%
  group_by(YearC, Stock, Flag) %>%
  summarize(Catch = sum(Qty_t)) %>%
  left_join(countries, by = c("YearC", "Stock")) %>%
  mutate(Effort = intercept + (slope * YearC),
         CPUE = Catch/Effort,
         CPUE2 = Catch / nn)

ggplot(data = iccat2, aes(x = YearC, y = Catch, color = Stock)) +
  geom_point() +
  theme_bw() +
  labs(x = "Year", y = "Catches (tonnes)") +
  scale_color_brewer(palette = "Set1") +
  removeGridX() +
  theme(text = element_text(size = 14))

iccat2 <- iccat %>%
  group_by(YearC, Stock) %>%
  summarize(Catch = sum(Qty_t)) %>%
  left_join(countries, by = c("YearC", "Stock")) %>%
  mutate(Effort = intercept + (slope * YearC),
         CPUE = Catch/Effort,
         CPUE2 = Catch / nn)

ggplot(data = iccat2, aes(x = YearC, y = Catch, color = Stock)) +
  geom_point() +
  theme_bw() +
  labs(x = "Year", y = "Catches (tonnes)") +
  scale_color_brewer(palette = "Set1")

ggplot(countries, aes(x = YearC, y = nn, color = Stock)) +
  geom_point() +
  theme_bw() +
  labs(x = "Year", y = "Number of countries \n in the fishery") +
```

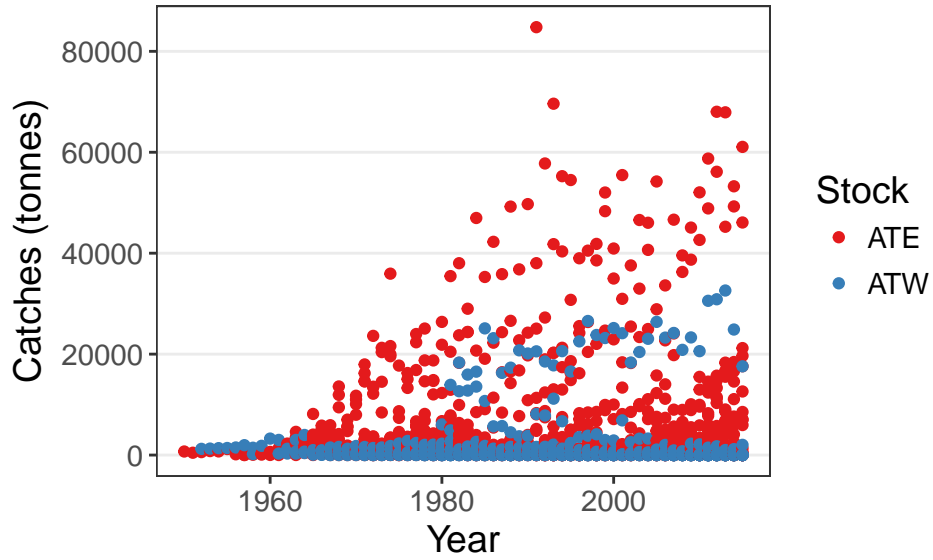


Figure 2: Annual catches (tonnes) of Skipjack by country, from two different stocks. Red points represent catches from the East Atlantic Stock (ATE) and blue points from the West Atlantic Stock (ATW).

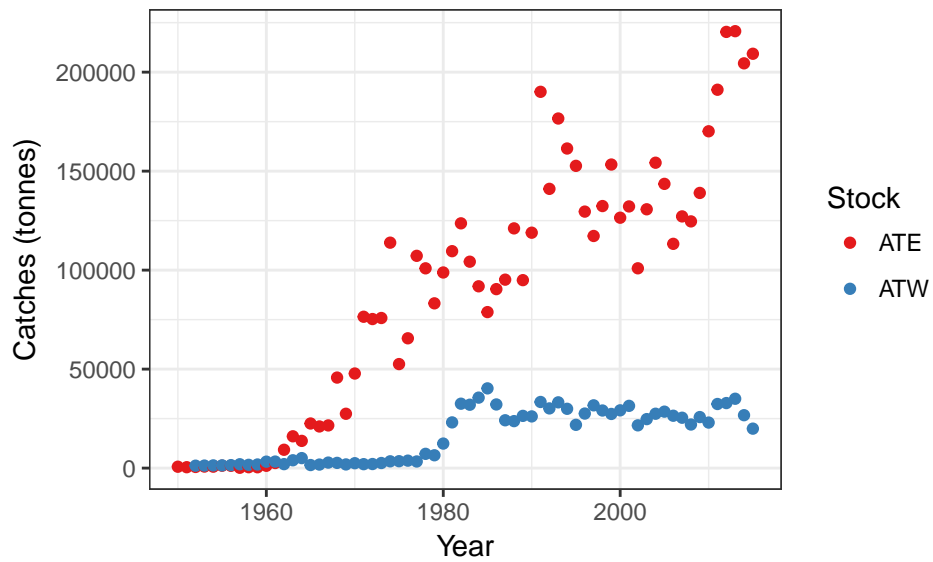


Figure 3: Total catches (tonnes) of skipjack per year from the two stocks available on the Atlantic Ocean.

```
scale_color_brewer(palette = "Set1")
```

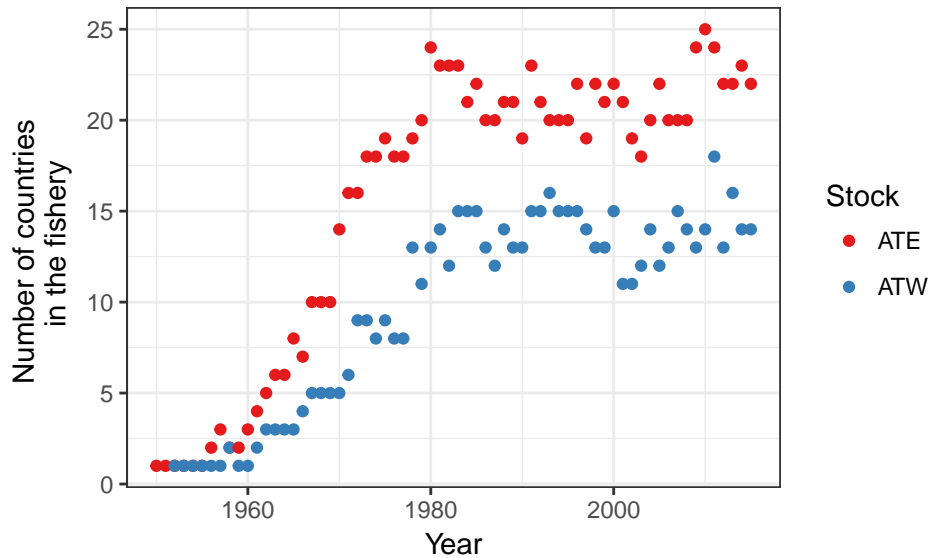


Figure 4: Number of countries involved on the harvest of the Skipjack on the East (ATE - red points) and West (ATW - blue points) Atlantic Ocean Stocks.

```
ggplot(data = iccat2, aes(x = YearC, y = CPUE2, color = Stock)) +
  geom_point() +
  theme_bw() +
  geom_smooth(method = "lm") +
  labs(x = "Year", y = "Catch per unit effort\n (tonnes / fishing countries)") +
  scale_color_brewer(palette = "Set1")
```

```
mod2 <- filter(iccat2, Stock == "ATW") %>%
  lm(formula = CPUE ~ YearC)
```

```
stargazer(mod2,
  se = rse(mod2),
  t.auto = T,
  p.auto = T,
  header = F,
  single.row = T,
  title = "Regression coefficients for Catch per unit effort (ATW) as a function of time. Number of countries")
```

```
mod2 <- filter(iccat2, Stock == "ATE") %>%
  lm(formula = CPUE ~ YearC)
```

```
stargazer(mod2,
  se = rse(mod2),
  t.auto = T,
  p.auto = T,
  header = F,
  single.row = T,
  title = "Regression coefficients for Catch per unit effort (ATE) as a function of time. Number of countries")
```

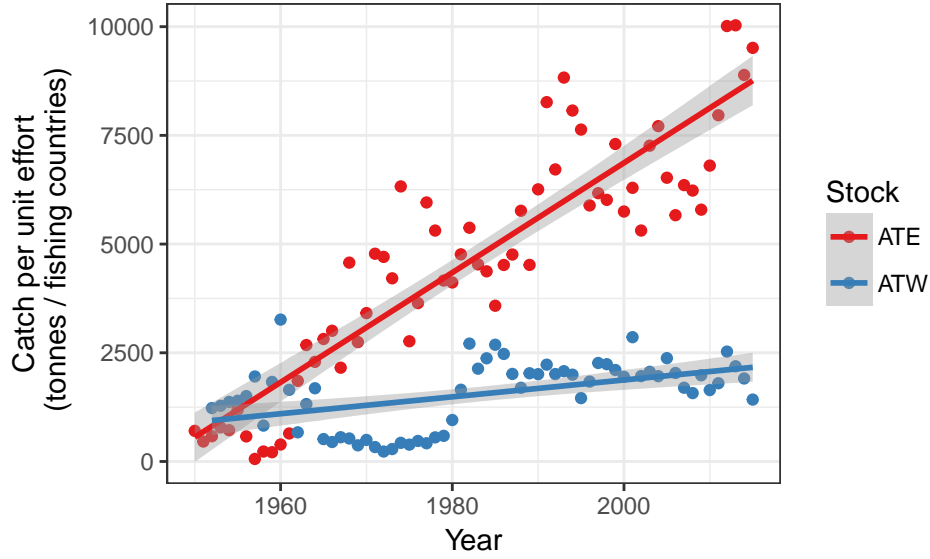


Figure 5: Annual mean catch (tonnes/country) of skipjack captured on from two stocks on the Atlantic Ocean. Red and blue points represent catches from the East Atlantic Stock and West Atlantic Stock, respectively. Colored lines represent the trend for mean catches per country from each stock.

Table 2: Regression coefficients for Catch per unit effort (ATW) as a function of time. Numbers in parenthesis are Standard Errors.

<i>Dependent variable:</i>	
CPUE	
YearC	0.169** (0.077)
Constant	-330.174** (148.574)
Observations	64
R ²	0.005
Adjusted R ²	-0.011
Residual Std. Error	42.775 (df = 62)
F Statistic	0.342 (df = 1; 62)
<i>Note:</i> *p<0.1; **p<0.05; ***p<0.01	

Table 3: Regression coefficients for Catch per unit effort (ATE) as a function of time. Numbers in parenthesis are Standard Errors.

<i>Dependent variable:</i>	
CPUE	
YearC	0.936** (0.425)
Constant	-1,826.342** (819.463)
Observations	66
R ²	0.007
Adjusted R ²	-0.008
Residual Std. Error	210.258 (df = 64)
F Statistic	0.475 (df = 1; 64)
<i>Note:</i> *p<0.1; **p<0.05; ***p<0.01	

Description of the model(s) used to project the population, and the sources of information about the model parameters

Qualitative description of population structure

For our analyses, we use a age structured model.

As previously mentioned, our data is composed by length data, which we transformed into expected age using the transformed Von Bertalanffy function

$$A = \frac{1}{-K} \times \log\left(1 - \left(\frac{L}{L_{inf}}\right)\right) + t_0$$

Where:

- A = age (years)
- K = growth rate
- L = length (cm)
- L_{inf} = asymptotic length (cm)

The model can then be made into a function as follows:

```
# Convert length to age using von bertalanffy model, solving for A
length2age <- function(length, l_inf, K, t_o){
  age <- (1/-K)*(log(1-(length/L_inf))) + t_o
  return(age)
}
```

Length at age

Solving for L in the equation above, we obtain:

$$L = l_{inf}(1 - \exp^{-K(A-t_o)})$$

Which can be made into a function as:

```
# Convert age to length using von bertalanffy model
age2length <- function(age, l_inf, K, t_o){
  length <- l_inf*(1-exp(-K*(age-t_o)))
  return(length)
}
```

Fecundity at length

$$f = 10^{(a+(b*\log_{10}(L*10)))}$$

Where:

- f = fecundity (number of eggs)
- a = **NAME HERE**
- b = **NAME HERE**
- L = length (cm)

As a function, this takes the form:


```
#Convert length to fecundity (number of eggs)
fecundity <- function(length, a, b){
  f <- 10^(a+(b*log10(length*10)))
  return(f)
}
```

Description of the demographic information

For this report, we used data from the literature:

- Mortality: $Z = 1.69$ (Garbin & Castello, 2014)
- Fecundity: $a = -1.33354$, $b = 3.238$ (from FISHBASE)
- von Bertalanffy growth parameters: $L_{\infty} = 102.0$, $K = 0.55$, $t_0 = -0.02$ (Uchiyama & Struhsaker, 1981)

A life-cycle diagram for your species

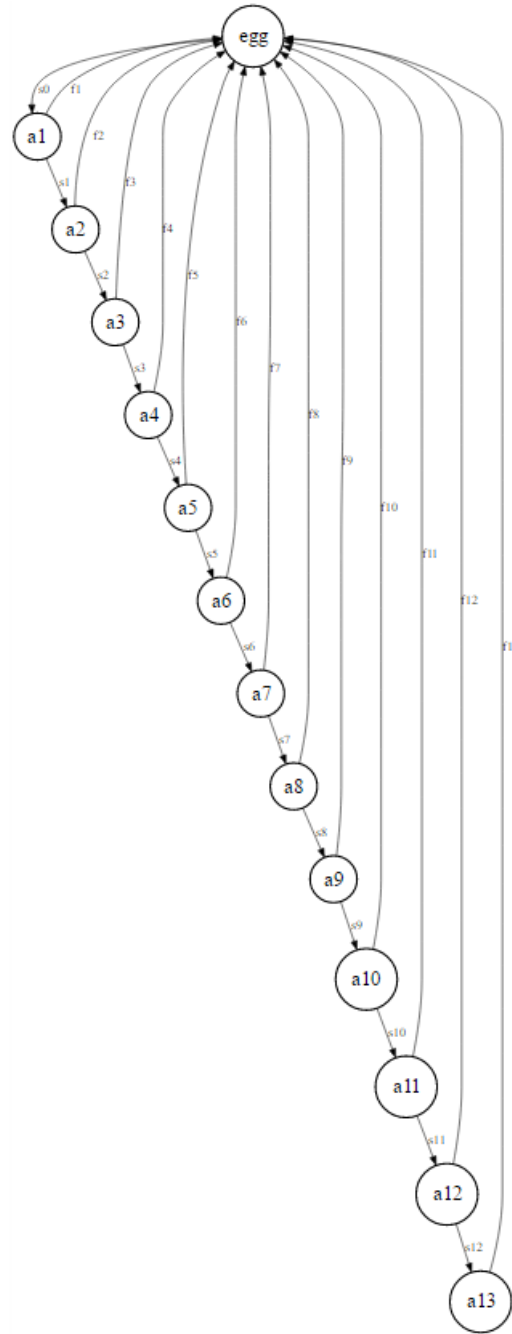


Figure 6: Life-cycle diagram for Skipjack tuna (*Katsuwonus pelamis*). S indicates survival, and f indicates fecundity.

Projections of the model, typically including a baseline scenario and one or more management or environmental change scenarios

Description of the demographic information

- Mortality: $Z = 1.69$ and $M = 0.63$ (Garbin & Castello, 2014)
- Fecundity: $a = -1.33354$, $b = 3.238$ (from FISHBASE)
- von Bertalanffy growth parameters: $L_{inf} = 102.0$, $K = 0.55$, $t_0 = -0.02$ (Uchiyama & Struhsaker, 1981)

Define demographic parameters

```
# Or from Us and Stiurskjgfas, 1981
L_inf <- 102
K <- 0.55
t_0 <- -0.02

# Fecundity parameters
fec_a <- -1.33354
fec_b <- 3.238

# Mortality
m <- 0.63
z <- 1.69
```

Create the matrix

```
A <- matrix(0, 13, 13) #initial empty matrix with all 0

# Populate matrix with mortality
for (i in 2:13){
  A[i,i-1] <- exp(-z)
}

# Populate matrix with fecundity
ages <- seq(1,13)
lengths <- age2length(ages, L_inf, K, t_0)
A[1,] <- fecundity(lengths, fec_a, fec_b) * 0.5 * 1e-7 #Multiply fecundity times 0.5 (F:M = 1:1) and times 1e-7

colnames(A) <- ages
rownames(A) <- ages

kable(A,
      digits = 2,
      col.names = paste0("$a_{",ages,"}$"),
      row.names = F,
      caption = "Population matrix A. The inferior diagonal represents survivals, while the first row represents fecundity")
```

Table 4: Population matrix A. The inferior diagonal represents survivals, while the first row represents fecundities.

a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}	a_{12}	a_{13}
0.83	3.51	6.47	8.79	10.36	11.35	11.95	12.31	12.51	12.64	12.71	12.75	12.77
0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00

Build the population vector

```
load("size_dist_1980.RData") #This is the n-vector for 1980, loads it to a vector called n

n <- n %>% {
  .$N*0.5}%>%
  c(rep(0, times = 8))

data.frame(N = n,
            Age = ages) %>%
  mutate(N = N/sum(N)) %>%
  ggplot(aes(x = Age, y = N)) +
  geom_bar(stat = "identity", fill = "gray", color = "black", size = 1) +
  geom_text(aes(x = Age, y = N + 0.05, label = formatC(lengths, digits = 0, format = "f")))) +
  theme_bw() +
  scale_x_continuous(expand = c(0.01, 0.01), breaks = seq(1, 13)) +
  scale_y_continuous(expand = c(0, 0), limits = c(0, 1), labels = scales::percent) +
  removeGridX() +
  theme(text = element_text(size = 14)) +
  labs(x = "Age (years)", y = "log-transformed abundance")
```

Asymptotic analysis of the matrix

```
project <- popbio::pop.projection(A, n, 20)
```

Lambda

$\lambda = 1.4181528$

```
plot(project$pop.changes, type = "b", xlab = "Iterations", ylab = "Lambda")
```

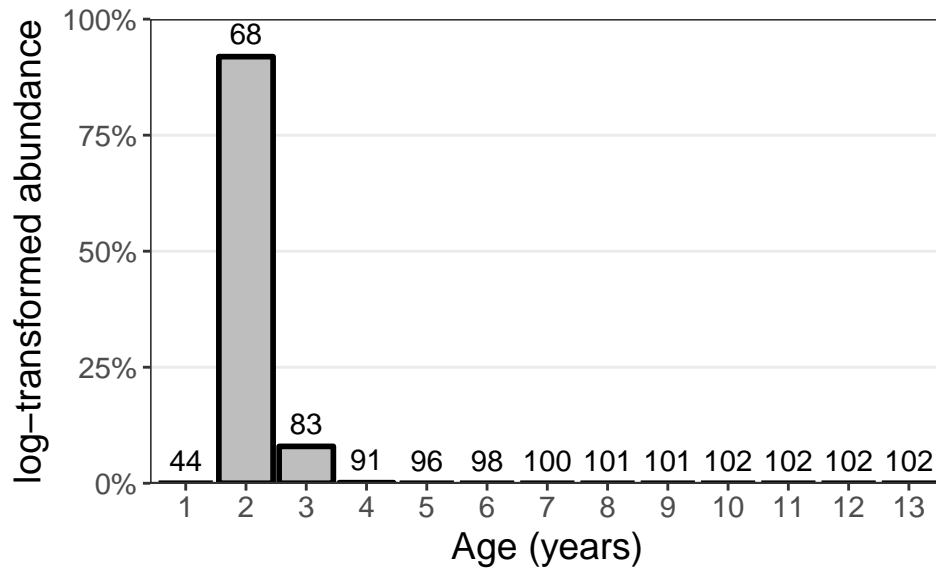


Figure 7: Initial population population structure, represented by ages (x-axis) and relative abundances (y-axis). Numbers above bars indicate the corresponding size (TL cm) for each age.

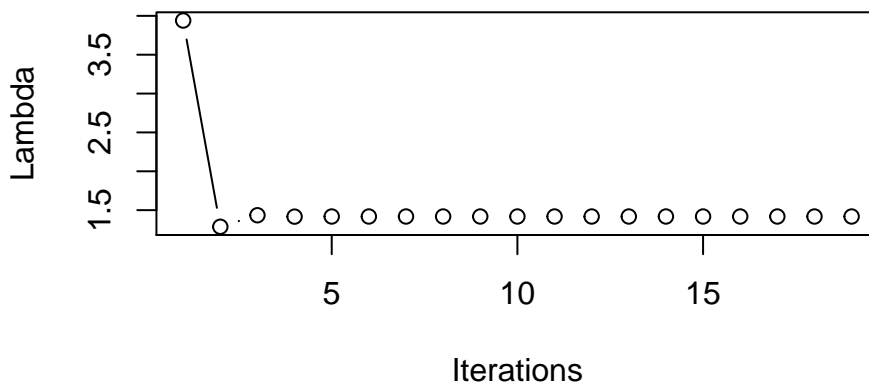


Figure 8: Figure 3 - Convergence of λ through time.

Sensitivity

```
sensitivity(A) %>%
  image2(box.offset=.1)
```

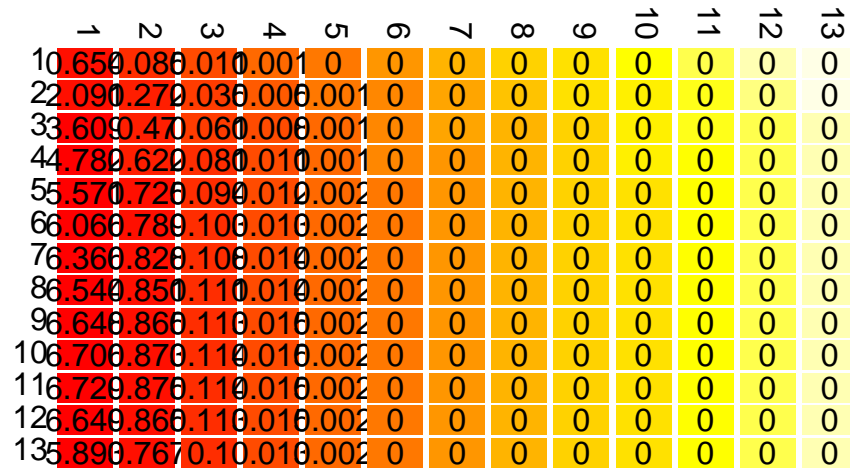


Figure 9: Figure 5 - Sensitivity matrix.

Elasticity

```
elasticity(A) %>%
  image2(box.offset = 0.1)
```

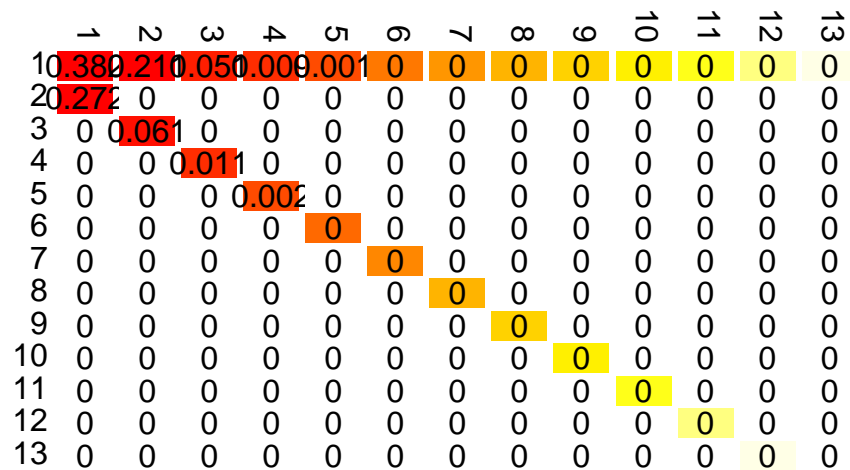


Figure 10: Figure 6 - Elasticity matrix.

Interpretation of the asymptotic results

The $\lambda = 1.47$ shows that the population is projected to grow at rate of 47%. The result of the sensitivity analysis suggest that is most effective to intervene on the early ages. Since the species mature early (between ages 1 and 2), there is no necessity of conserving the old/big individuals that have higher fecundity, because the younger ones (in quantity) can provide enough eggs to maintain the population.

Project the population

We projected the population, stratified by ages, for 20 years in the future. The population seems to have a positive trend, which shows the population is increasing. ##### Project the population

```
project <- popbio::pop.projection(A, n, 20)
```

```
project$stage.vectors %>%  
  as.data.frame() %>%  
  mutate(Age = as.factor(seq(1,13))) %>%  
  gather(Year, N, -Age) %>%  
  mutate(Year = as.numeric(as.character(Year))) %>%  
  select(Year, Age, N) %>%  
  ggplot(aes(x = Year, y = log(N), color = Age)) +  
  geom_line() +  
  theme_bw()
```

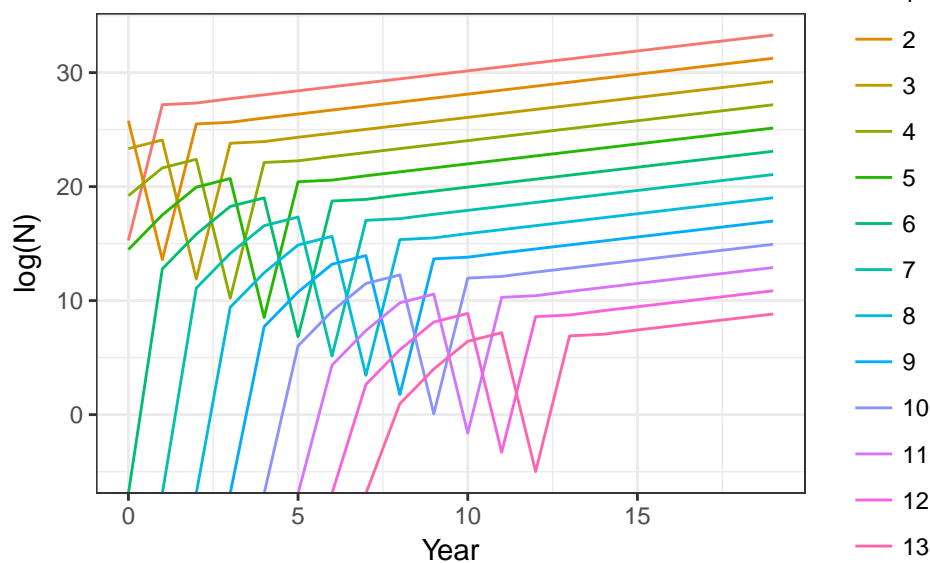


Figure 11: Figure 1 - Population size through time, represented by ages.

Minimum catch size

This time we projected the population for 30 years in the future with a management intervention on the minimum size of capture (Figure X) set at 67 cm (upper limit of age = 1) based on the sensitivity analysis. Our projection assumes total compliance on the intervention, which means the fishing pressure is equal to 0. Therefore, the total mortality (Z) is equal to the natural mortality (M) for individuals of age 1. By protecting individuals of age 1 (the age at which they reach maturity), we observe a faster recovery in the fishery. This can be observed by comparing the $\log(N) = 40$ at year 22, which is now reached at year 18 for one-year olds.

Additionally, in the context of the entire stock, Figure 3 shows that with the management intervention total skipjack population recovers faster.

```
A_min <- A

A_min[2, 1] <- exp(-m)

knitr::kable(A_min,
  digits = 2,
  col.names = paste0("$a_{", ages, "}"),
  row.names = F,
  caption = "Population matrix  $\hat{A}$ , modifying mortality of age 1 organisms through a minimum
```

Table 5: Population matrix \hat{A} , modifying mortality of age 1 organisms through a minimum catch size set at 67 cm. The inferior diagonal represents survivals, while the first row represents fecundities.

a_1	a_2	a_3	a_4	a_5	a_6	a_7	a_8	a_9	a_{10}	a_{11}	a_{12}	a_{13}
0.83	3.51	6.47	8.79	10.36	11.35	11.95	12.31	12.51	12.64	12.71	12.75	12.77
0.53	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18	0.00
0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.18

```
project_min <- popbio::pop.projection(A_min, n, 20)
```

```
project_min$stage.vectors %>%
  as.data.frame() %>%
  mutate(Age = as.factor(seq(1, 13))) %>%
  gather(Year, N, -Age) %>%
  mutate(Year = as.numeric(as.character(Year))) %>%
  select(Year, Age, N) %>%
  ggplot(aes(x = Year, y = log(N), color = Age)) +
  geom_line() +
  theme_bw()
```

```
tot1 <- project$pop.sizes
tot2 <- project_min$pop.sizes
time <- seq(1:20)
```

```
data.frame(time, BAU = tot1, Int = tot2) %>%
  gather(scenario, popsize, -time) %>%
  ggplot(aes(x = time, y = log(popsize), color = scenario)) +
  geom_point(size = 2) +
  geom_line(size = 1) +
```

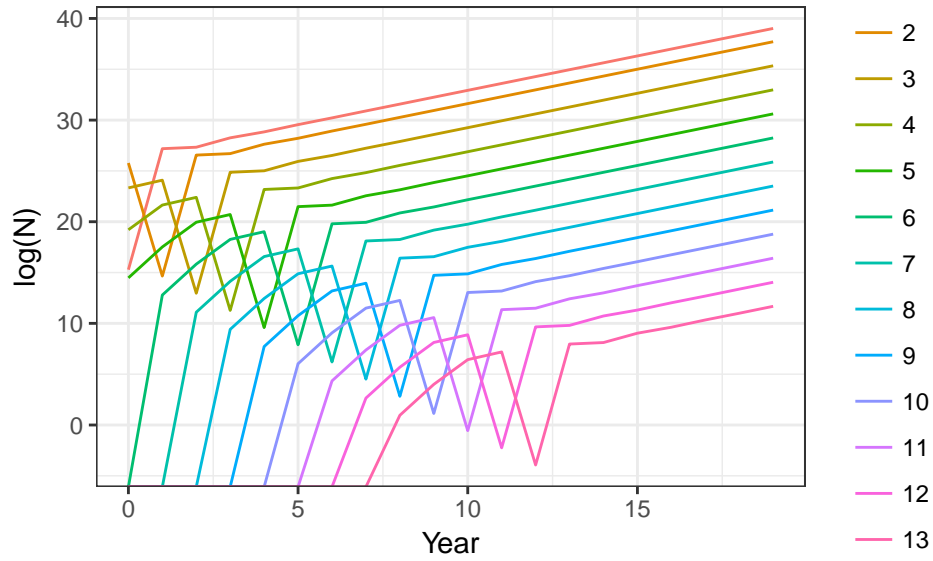


Figure 12: Population size through time, represented by ages.

```
theme_bw() +
scale_color_brewer(palette = "Set1")
```

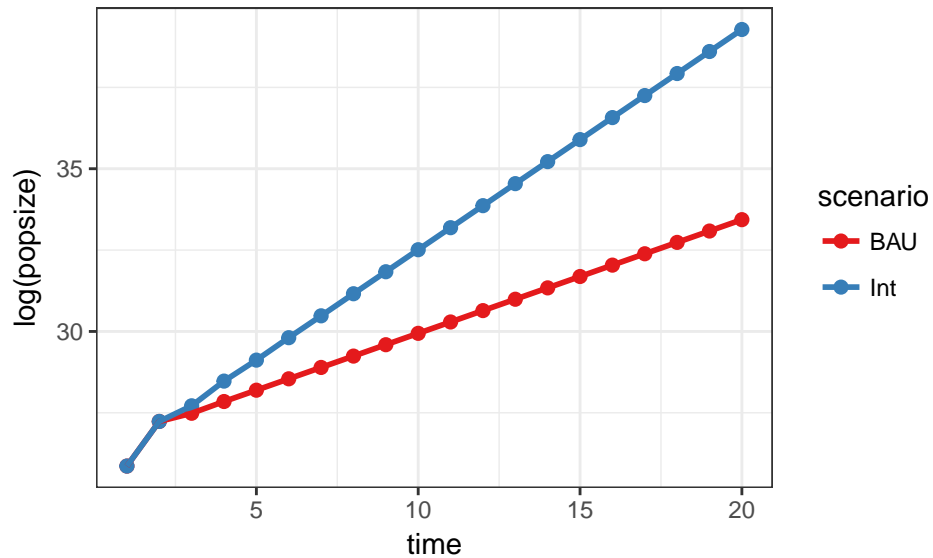


Figure 13: Total population size through time.

```
data.frame(Age = ages, BAU = project$stable.stage, Int = project_min$stable.stage) %>%
  gather(scenario, N, -Age) %>%
  ggplot(aes(x = Age, y = N)) +
  geom_bar(stat = "identity", fill = "gray", color = "black", size = 1) +
  facet_grid(~scenario, scales = "free_y") +
  geom_text(aes(x = Age, y = N + 0.05, label = formatC(age2length(Age, L_inf, K, t_0), digits = 0, for
  theme_bw() +
  scale_x_continuous(expand = c(0.01, 0.01), breaks = seq(1, 13)) +
```

```
scale_y_continuous(expand = c(0, 0), limits = c(0, 1), labels = scales::percent) +
removeGridX() +
theme(text = element_text(size = 14)) +
labs(x = "Age (years)", y = "Relative abundance")
```

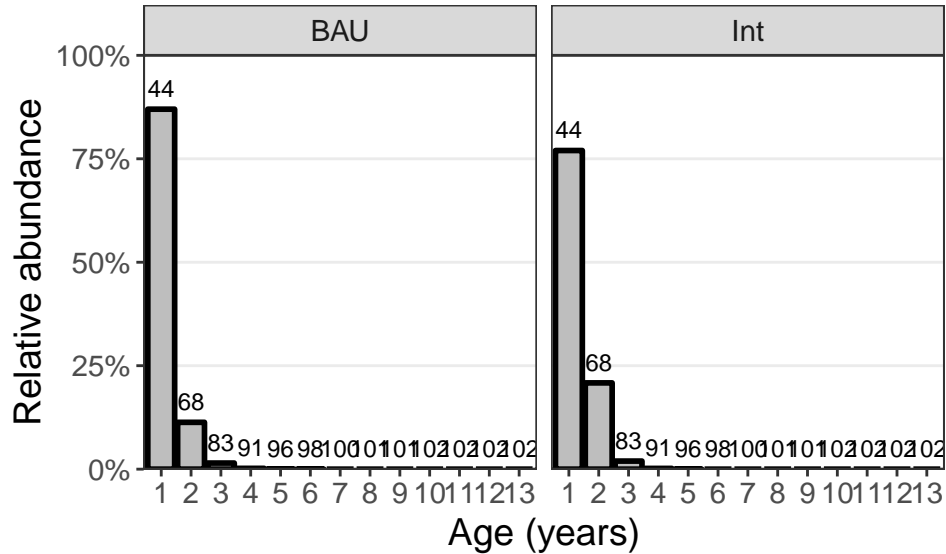
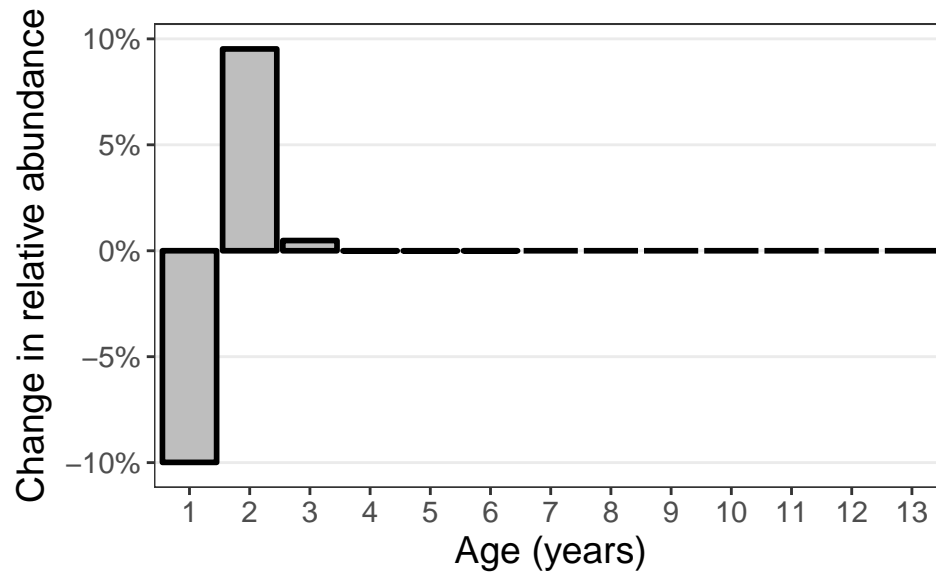


Figure 14: Stable stage population structure, represented by ages (x-axis) and relative abundances (y-axis). Numbers above bars indicate the corresponding size (TL cm) for each age.

```
data.frame(Age = ages, BAU = project$stable.stage, Int = project_min$stable.stage) %>%
mutate(Diff = Int - BAU) %>%
ggplot(aes(x = Age, y = Diff)) +
geom_bar(stat = "identity", fill = "gray", color = "black", size = 1) +
theme_bw() +
scale_x_continuous(expand = c(0.01, 0.01), breaks = seq(1, 13)) +
scale_y_continuous(expand = c(0.01, 0.01), labels = scales::percent) +
removeGridX() +
theme(text = element_text(size = 14)) +
labs(x = "Age (years)", y = "Change in relative abundance")
```



A description of the impacts of the modeled management actions or environmental scenarios

A conclusion discussing how the model results address the conservation/management problem.

References

- <http://www.iucnredlist.org/details/170310/0>
- https://www.iccat.int/Documents/SCRS/ExecSum/SKJ_ENG.pdf
- Froese, R. and D. Pauly. Editors. 2016.FishBase. World Wide Web electronic publication. www.fishbase.org, (10/2016)