ESM 211 Applied Population Ecology Final Paper

Fancy title about Skipjack, including scientific name and shit

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

Define the functions we will need

Age at length

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

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:

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

Define demographic parameters

```r
# 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 <- 1.39

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 ti

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 re
```

Table 1: Population matrix A. The inferior diagonal represents survivals, while the first row represents facundities.

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
0.25	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	0.25	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	0.25	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00

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}
0.00	0.00	0.00	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	0.00

Build a population vector

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

n <- n %>% {
  .$N}%>%
  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")
```

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

```r
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()
```

```r
A_min <- A

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

knitr::kable(A_min,
      digits = 2,
      col.names = paste0("$a_{",ages,"}$"),
      row.names = F,
```
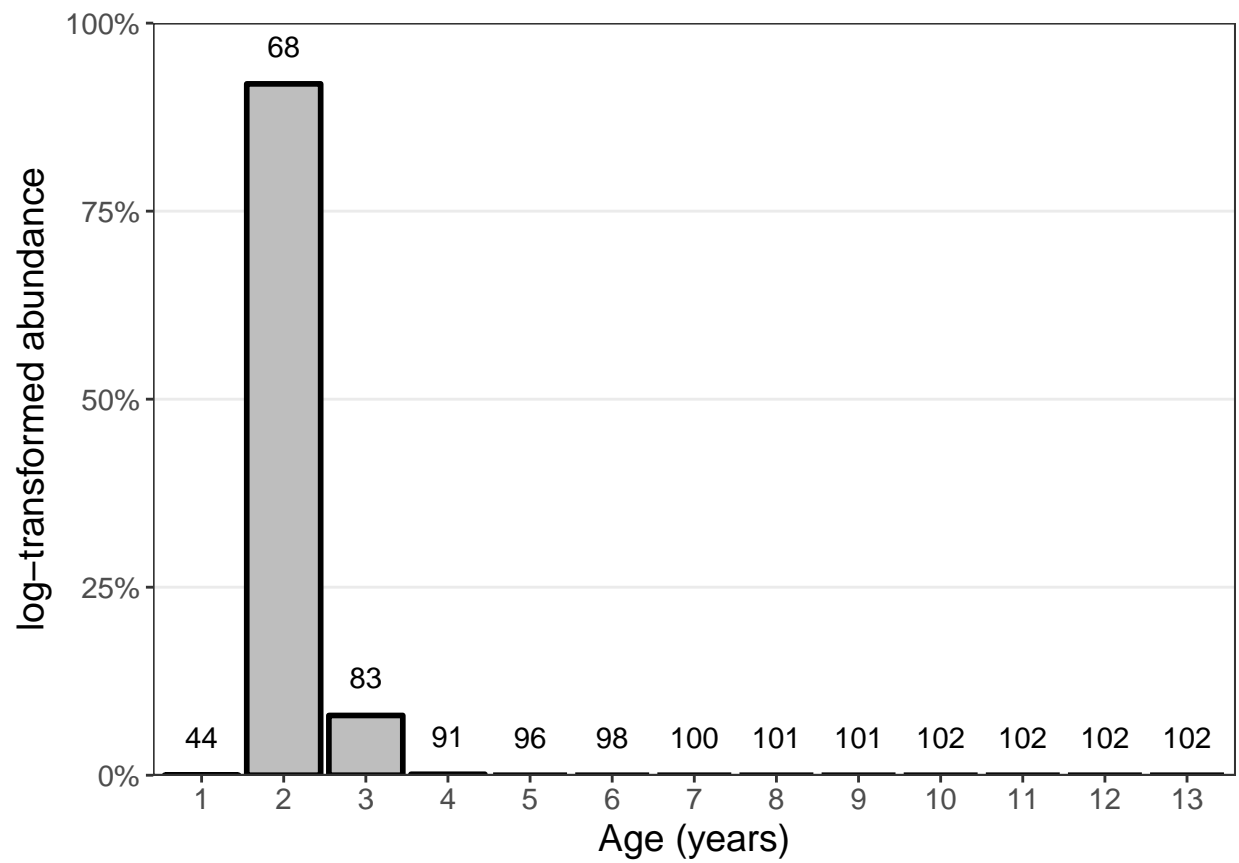
Figure 1: Initial population population structure, represented by ages (x-axis) and relative abundances (y-axis). Numbers above bars indicate the corresponding size (TL cm) for each age.
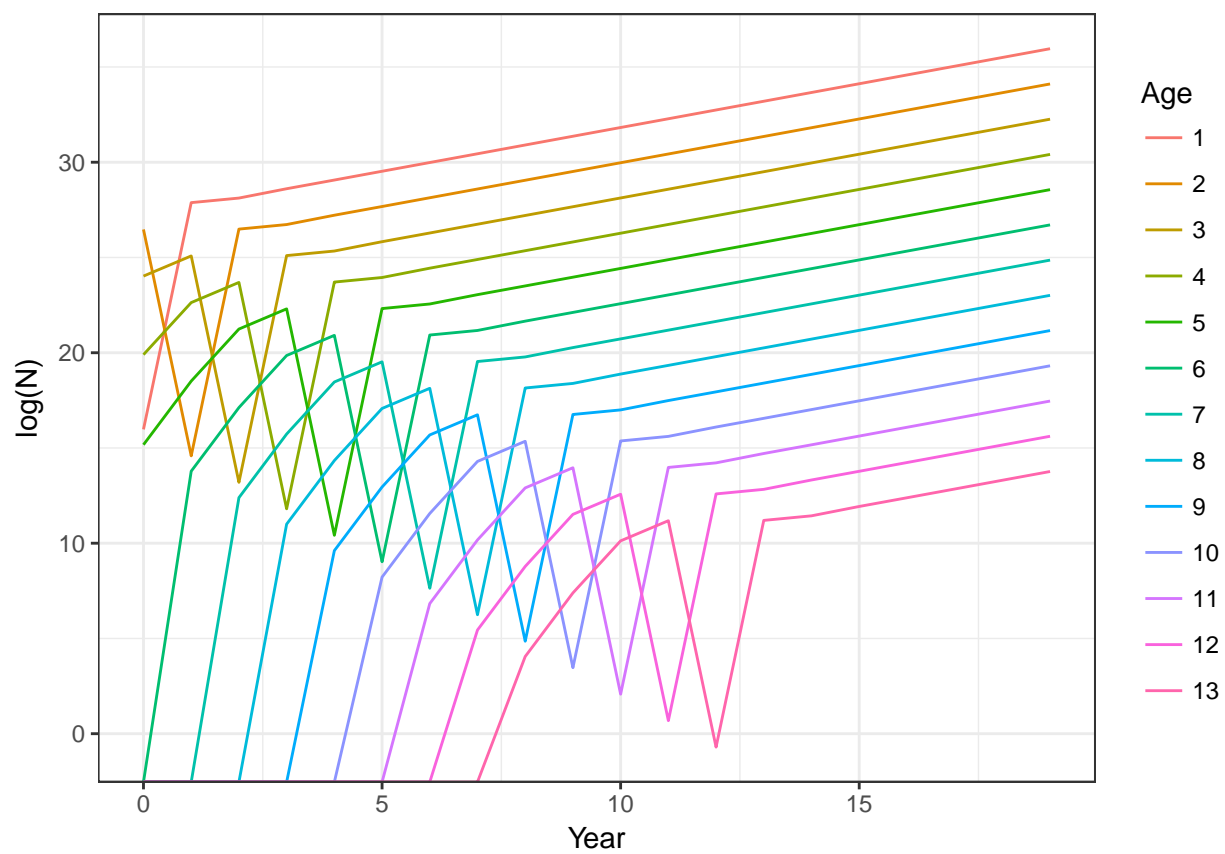
Figure 2: Figure 1 - Population size through time, represented by ages.

Table 2: 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 facundities.

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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	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	0.25	0.00

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

```r
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()
```

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

```r
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() +
```
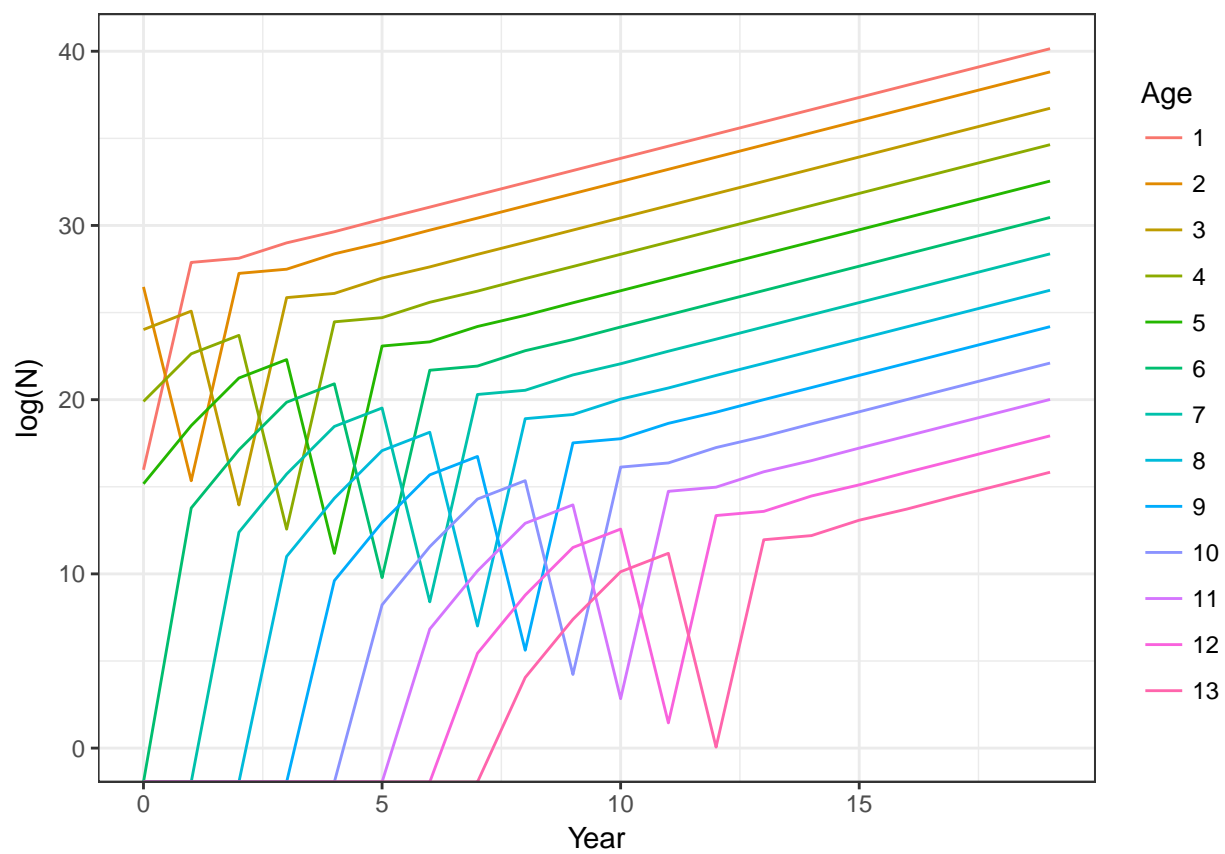
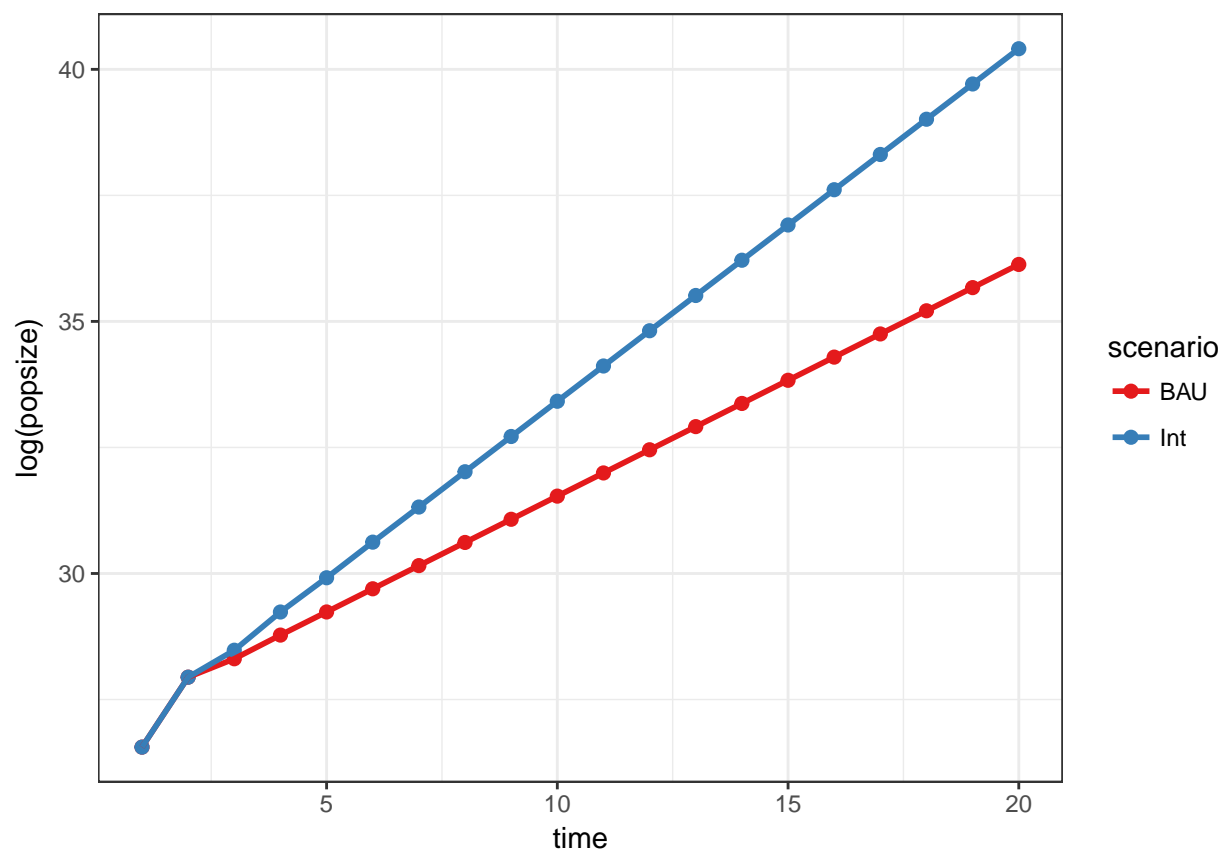Figure 3: Population size through time, represented by ages.

Figure 4: Total population size through time.

```
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")
```
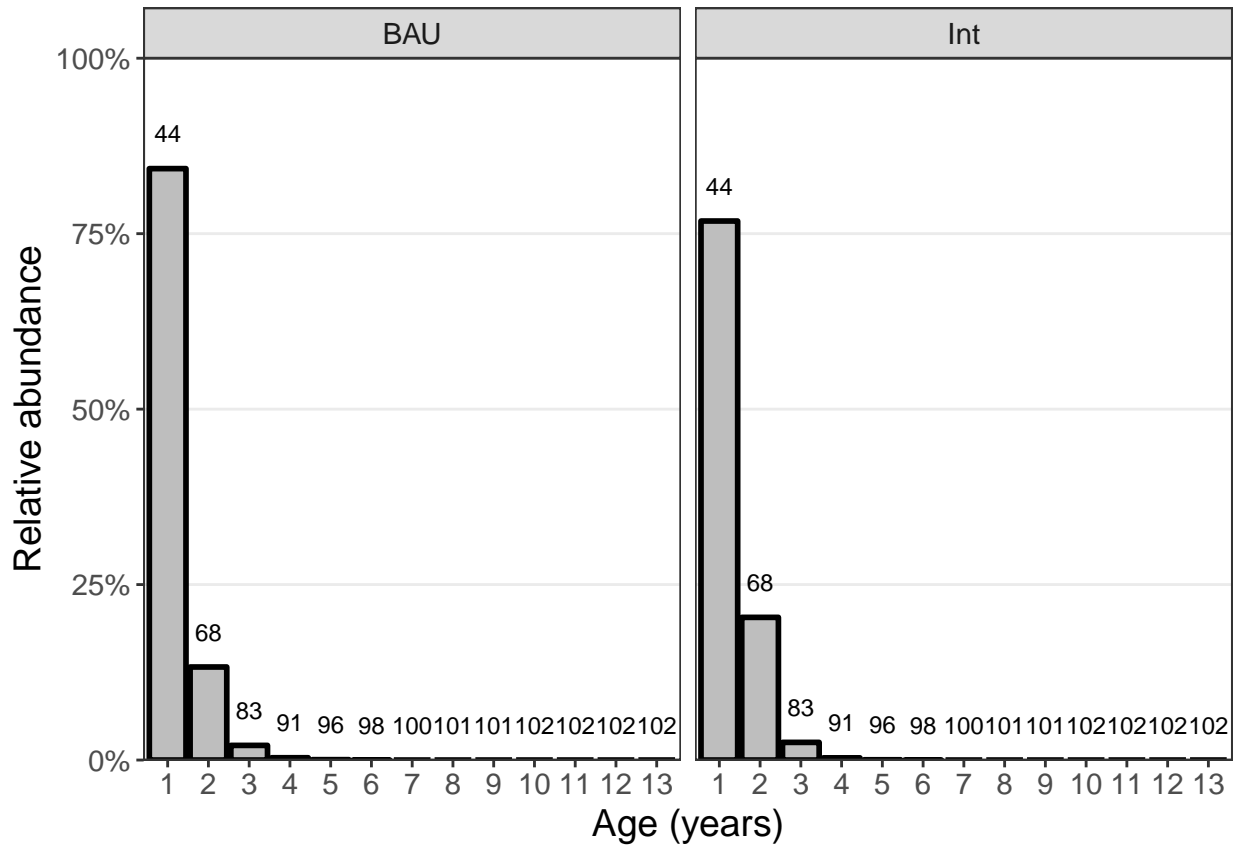

Figure 5: Stable stage population structure, represented by ages (x-axis) and relative abundances (y-axis). Numbers above bars indicate the corresponding size (TL cm) for each age.

```
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")
```