

# Stable Populations Assignment

## European Doctoral School of Demography 2021

Liliana Patricia Calderón Bernal  
Gonzalo Daniel Garcia  
Ainhoa-Elena Leger  
Ozge Elif Ozer

29/3/2021

### Exercise 1: Everybody loves penguins

Here are two stage-classified matrices for the Emperor penguin. The life cycle diagram is given on the next-to-last page of the Jenouvrier et al. (2009) paper in the readings for the course. The first of these matrices was obtained under normal conditions, the other during an unusual warm event during which the penguin population declined by about 50%.

- (a) Write a program to project the population (for what seems like an interesting length of time) starting from several different initial conditions:

$\mathbf{n}(0)$  = one newborn baby penguin  
 $\mathbf{n}(0)$  = one breeding adult penguin  
 $\mathbf{n}(0)$  = a population with the stable stage distribution

Plot the results (plotting on a log scale will probably be particularly informative). Compare the fates of the population under the two different environmental conditions.

[Sol.]

We projected the following populations into the future:

$\mathbf{n}(0) = [1, 0, 0, 0, 0, 0]$   
 $\mathbf{n}(0) = [0, 0, 0, 0, 0, 1]$   
 $\mathbf{n}(0) = \mathbf{w}_1$  (i.e the right eigenvector corresponding to the dominant eigenvalue of the transition matrix) standardized to represent population proportions at all stages.

To this aim, we ‘matrix-multiply’ the vectors by the transition matrix  $\mathbf{A}$  under the two different environmental conditions. We can use this strategy to project the resulting populations forward again. Each time we do the multiplication step, we advance one year. The matrix population growth equation is

$$\mathbf{n}_{t+1} = \mathbf{A}\mathbf{n}_t.$$

We used the following code to project the populations 25 years forward.

```
##### Population projection for the next 25 years under Normal Conditions #####  
  
# Setting initial population in t = 0  
n0.a <- as.vector(c(1,0,0,0,0,0))  
n0.b <- as.vector(c(0,0,0,0,0,1))  
n0.c <- omega1.pen1.stand
```

```

# Preparing the matrix to collect projections over 25 years
periods <- 25
n.a <- matrix(NA,nrow=dim(U.pen1)[1],ncol=periods+1)
n.b <- matrix(NA,nrow=dim(U.pen1)[1],ncol=periods+1)
n.c <- matrix(NA,nrow=dim(U.pen1)[1],ncol=periods+1)

# Adding initial population to the matrix
n.a[,1] <- n0.a
n.b[,1] <- n0.b
n.c[,1] <- n0.c

### LOOP FOR POPULATION PROJECTION
for (t in 1:periods) { # use 't' as our looping variable

  ## Perform matrix multiplication for each year
  ## pen1 is matrix A under Normal Conditions
  n.a[,t+1] <- pen1 %*% n.a[,t]
  n.b[,t+1] <- pen1 %*% n.b[,t]
  n.c[,t+1] <- pen1 %*% n.c[,t]

}

##### Population projection for the next 25 years under Warm Conditions #####

# Setting initial population in t = 0
n0.a.2 <- as.vector(c(1,0,0,0,0,0,0))
n0.b.2 <- as.vector(c(0,0,0,0,0,0,1))
n0.c.2 <- omega1.pen2.stand

# Preparing the matrix to collect projections over 25 years
periods <- 25
n.a.2 <- matrix(NA,nrow=dim(U.pen2)[1],ncol=periods+1)
n.b.2 <- matrix(NA,nrow=dim(U.pen2)[1],ncol=periods+1)
n.c.2 <- matrix(NA,nrow=dim(U.pen2)[1],ncol=periods+1)

# Adding initial population to the matrix
n.a.2[,1] <- n0.a.2
n.b.2[,1] <- n0.b.2
n.c.2[,1] <- n0.c.2

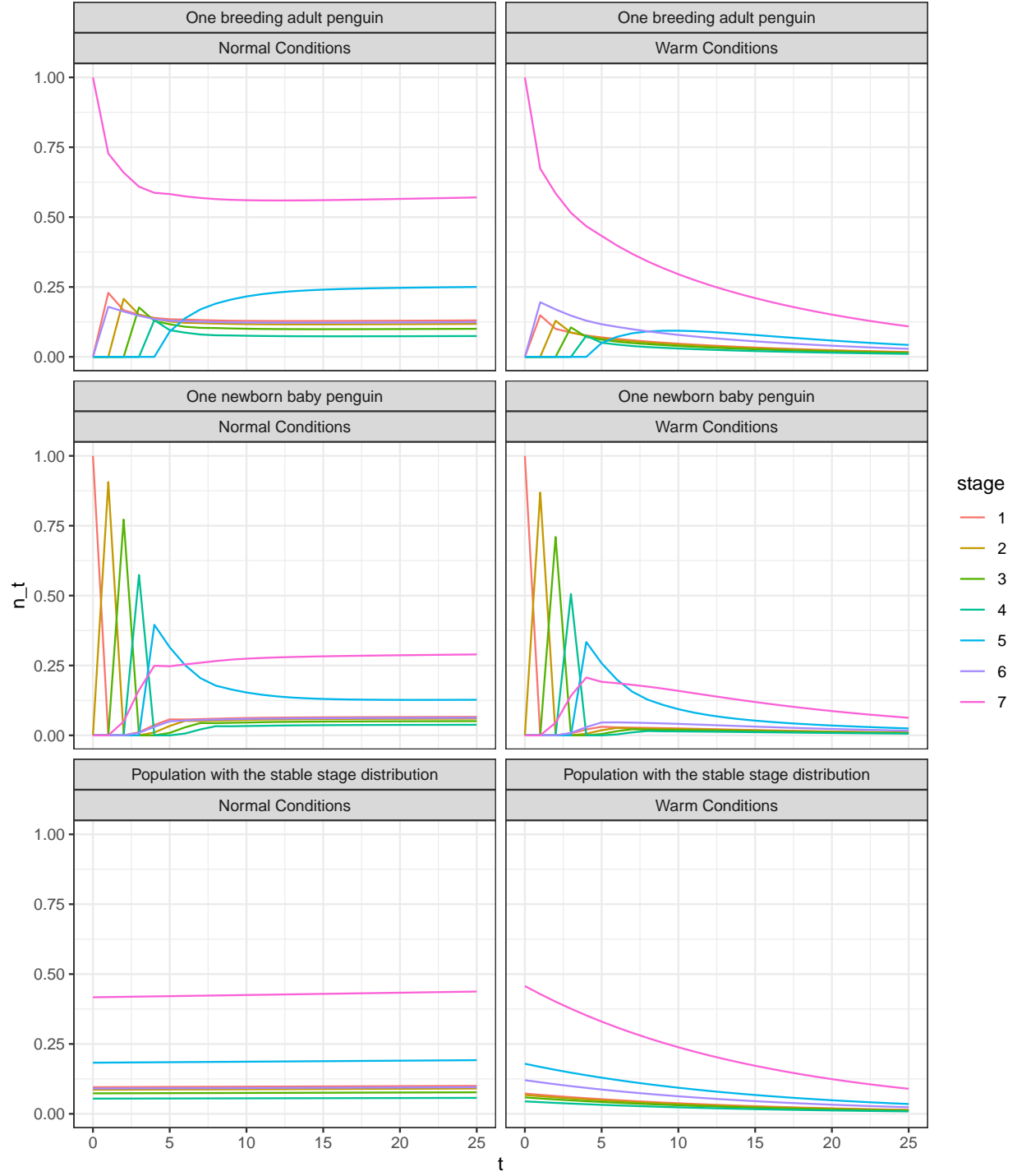
### LOOP FOR POPULATION PROJECTION
for (t in 1:periods) { # use 't' as our looping variable

  ## Perform matrix multiplication for each year
  ## pen2 is matrix A under Warm Conditions
  n.a.2[,t+1] <- pen2 %*% n.a.2[,t]
  n.b.2[,t+1] <- pen2 %*% n.b.2[,t]
  n.c.2[,t+1] <- pen2 %*% n.c.2[,t]

}

```

First we plot the distribution of each stage across time for the 3 different initial conditions and the 2 matrices:



As was expected, the penguin population in Warm conditions has a declining population projection in the long run. Compared to the population under Normal conditions, the stage 7 population does not stabilize in warm conditions.

Under Normal conditions, in both cases when we start with only newborns or when we start with a breeding adult penguin, the population stabilizes rather quickly around periods 5 and 10 (depending on each stage). What we found interesting about these populations is that under Normal conditions is the stage 5 the one that takes much longer to stabilize.

- (b) Find the population growth rate  $\lambda$ , the stable stage distribution  $\mathbf{w}$ , and the reproductive value distribution  $\mathbf{v}$  for each matrix. Make some plots; make some comparisons.

[Sol.]

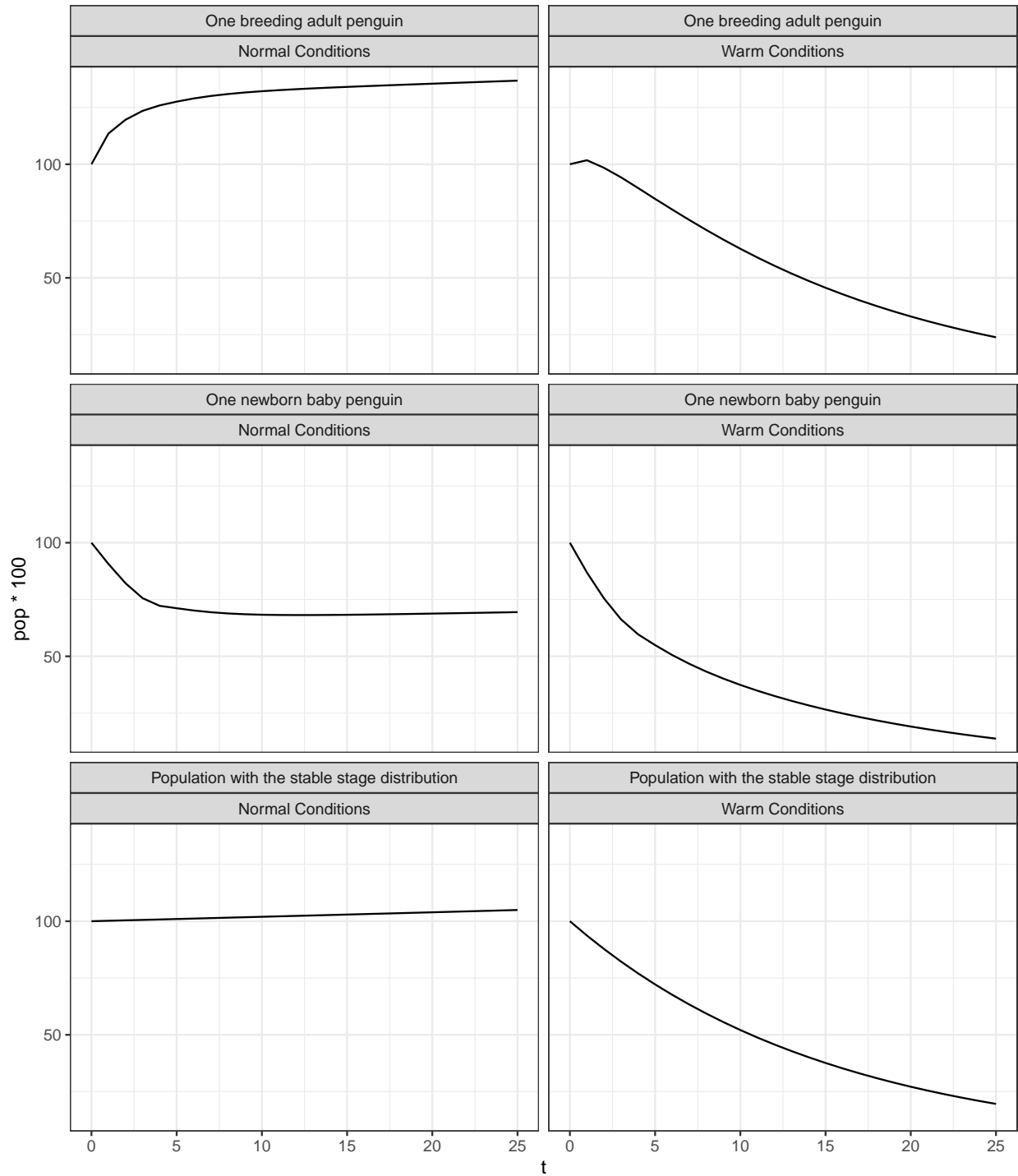
For the matrix on Normal conditions we have the following results:

- Rate of growth: 1.00192737796366+0i
- Stable Stage distribution: 0.194440489963298+0i, 0.175901830790301+0i, 0.149580062517039+0i, 0.110954052067729+0i, 0.373173973271385+0i, 0.184964925313631+0i, 0.850350284936257+0i
- Reproductive value distribution: 0.277988893150835+0i, 0.307286719789979+0i, 0.326397257241825+0i, 0.319780416181722+0i, 0.292201270312972+0i, 0.484018240807112+0i, 0.547582982944706+0i

And for the matrix on Warm conditions:

- Rate of growth: 0.93688602955638+0i
- Stable Stage distribution: -0.139427539561691+0i, -0.12930984698589+0i, -0.112735465879544+0i, -0.0857351021417296+0i, -0.344220488555178+0i, -0.231497307704186+0i, -0.878464787832999+0i
- Reproductive value distribution: 0.299560273857171+0i, 0.322999005163846+0i, 0.337410300336863+0i, 0.329843613943409+0i, 0.304221577800046+0i, 0.471005898376633+0i, 0.518551289509912+0i

We can plot the full population for each temperature and initial condition. We are representing here the sum of all stages for each period:



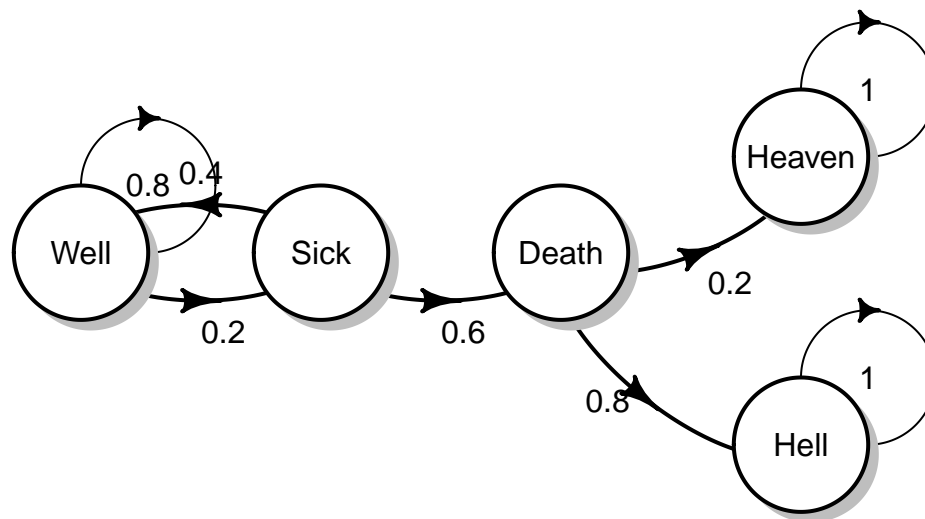
From this plot we can appreciate that the Warm conditions matrix is one such that population is declining in the long run ( $0.93688602955638 + 0i < 1$ ). While for the Normal conditions matrix, the rate of growth under stable stage distribution is greater than 1 but very low.

Another insight from the plots is that when the initial condition is the one where we have only newborns, then the population declines in the first periods until stabilizes (except when temperature conditions are warm).

## Exercise 2: The Irish tea-towel problem

In an airport in Belfast, I found a souvenir tea-towel, inscribed with a verse identified as “Irish philosophy”. See the figure. It looks like an incidence-based health model to me.

- (a) Create a life cycle graph for this system, based on your interpretation of the verse.



- (b) Identify the transient and absorbing states.

[Sol.]

We make up the transition probabilities and plot the life cycle graph with them. In our life cycle, the individuals start as sick or well and then they can either change between these two states, or the sick ones can die. As it can be seen, similar to “Well” and “Sick”, “Death” is a transient state. After death, people can go to hell or heaven. “Hell” and “Heaven” as it can be seen from the graph are two absorbing states. Therefore, at the end we have an absorbing Markov Chain.

- (c) Make up some transition probabilities (your choice) and calculate mean occupancy times and the probabilities of ending up in Heaven or Hell.

[Sol.]

### Transition probabilities

We included these in the probability matrix from the previous question.

## Mean occupancy time

Since this is an absorbing Markov chain with two absorbing states at the end of the lifecycle, we need to extract the transient matrix and mortality vector. We can calculate these with the transition probabilities matrix that we used for the Markov chain earlier.

Following the formulae for calculating the fundamental matrix,  $N$ , we end up with the  $a$  matrix that shows mean occupancy times at each stage.

By looking at this matrix, we can see that if your initial state is well, you can revisit this state 8.33 times on average, and this number is 3.33 for people whose initial state is sickness. For instance, death is a stage that can be visited only once. To calculate the probability of ending up in heaven or hell, we can make rows with the transient states, and columns with the absorbing states as follow;

	Hell	Heaven
Well	0.0	0.0
Sick	0.0	0.0
Death	0.8	0.2

## Exercise 3: An extra problem about Sweden

Sweden has an unusually long sequence of mortality and fertility data. There are two text files (`parray.txt` and `fertarray.txt`) in the Calculation Materials folder. One has survival probabilities as a function of age, the other has fertility as a function of age; one column for each year from 1891 to 2007.

- (a) Write a program to use this information to create an age-classified projection matrix  $\mathbf{A}$  for each year.

[Sol.]

We created a list `A.y` collecting annual age-classified projection matrices  $\mathbf{A}$ , consisting of fertility in the first row and survival probabilities on the subdiagonal. In total, the list contains 117 elements corresponding to the years of the time period considered.

```
# Grab number of years
years <- c(1891:2007)
nby <- length(years)

# Initialize the list with annual A matrices as elements
A.y <- replicate(nby, diag(111), simplify=F)

### LOOP FOR ANNUAL AGE-CLASSIFIED PROJECTION MATRIX
for (i in 1:nby) { # use 't' as our looping variable

  ## Extract each year survival and fertility
  surv.y <- surv[,i]
  fert.y <- fert[,i]

  ## Creating matrix A for year i
  # survival probabilities
  A <- diag(surv.y)
  # fertility
  A <- rbind(t(fert.y), cbind(A,rep(0,111)))

  ## Saving A in the list
  A.y[[i]] <- A
}
```

- (b) Compute the population growth rate  $\lambda_1$  and the corresponding right and left eigenvectors  $\mathbf{w}_1$  and  $\mathbf{v}_1$  for each year.

[Sol.]

From the previously created list `A.y` we extracted for every year the population growth rate  $\lambda_1$ , the stable stage distribution  $\mathbf{w}_1$  and the reproductive values  $\mathbf{v}_1$ . The  $\lambda_1$  values are saved in a vector `lambda1` (length 117), the vectors  $\mathbf{w}_1$  in a matrix `omega1` (dimension 112x117) and the  $\mathbf{v}_1$  in a matrix `v1` (dimension 112x117).

```
# Initialize vectors and matrices to use in the loop
A.eigen <- matrix(NA, 112, nby)
lambda1.position <- rep(0, nby)
lambda1 <- rep(0, nby)
omega1 <- matrix(0, 112, nby)
v1 <- matrix(0, 112, nby)

### LOOP FOR ANNUAL EIGENVALUES, LEFT AND RIGHT EIGENVECTORS
for(i in 1:nby) { # use 't' as our looping variable

  ## POPULATION GROWTH RATE (dominant eigenvalue)
  # Extract eigen-values (lambdas) from A for every year
  A.eigen[,i] <- eigen(A.y[[i]])$values
  # Find the one that checks Perron-Frobenius
  lambda1.position[i] <- which.max(abs(A.eigen[,i]))
  # Keep the dominant eigenvalue, lambda1
  lambda1[i] <- A.eigen[lambda1.position[i],i]

  ## STABLE POPULATION VECTOR (right eigenvector)
  omega1[,i] <- eigen(A.y[[i]])$vectors[,lambda1.position[i]]

  ## REPRODUCTIVE VALUE (left eigenvector)
  v1[,i] <- eigen(t(A.y[[i]]))$vectors[,lambda1.position[i]]

}

length(lambda1)
```

```
[1] 117
```

```
dim(omega1)
```

```
[1] 112 117
```

```
dim(v1)
```

```
[1] 112 117
```

- (c) This is a lot of information. To summarize the population structure, compute and plot the early-age dependency ratio and the old-age dependency ratio calculated from  $\mathbf{w}$ .

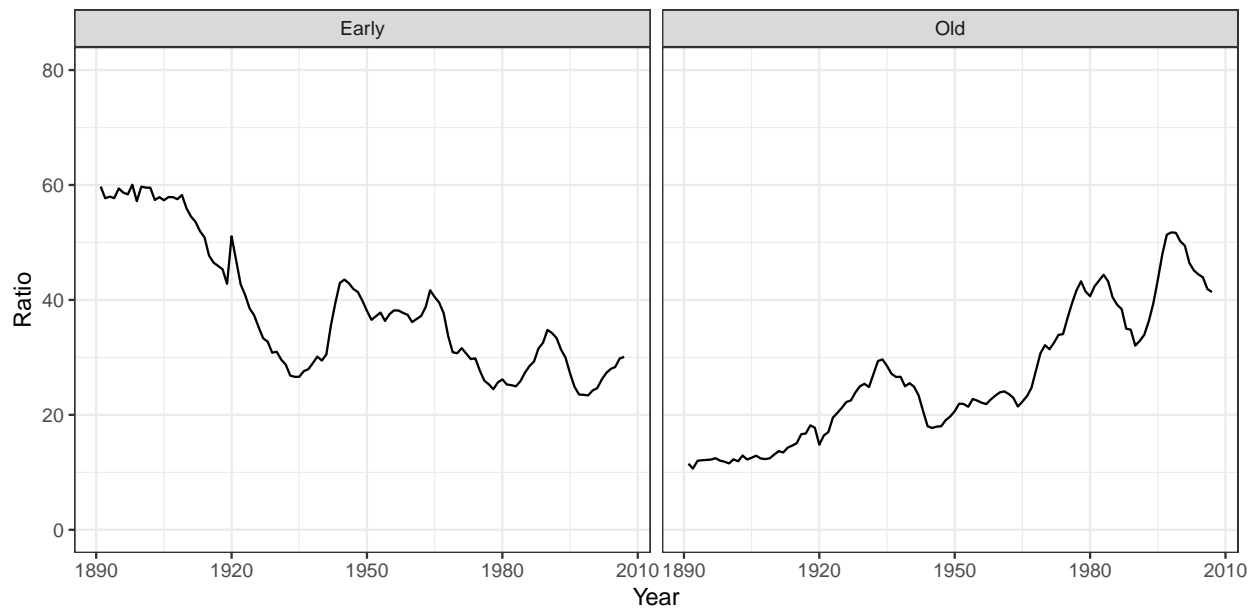
[The dependency ratio is the ratio of population numbers during dependent ages (0-15 and older than 65) to the numbers in productive years (16-65). The early age and late age ratios just look at those portions of the dependent population. ]

[Sol.]

The decreasing early-age dependency ratio and the increasing old-age dependency ratio show that more people are moving out of the working age range than into it. In 1981, the early-age dependency ratio was 60 youth for every 100 working-age people. This dropped to 30 youth in 2007. The opposite trend is evident for



seniors. For every 100 working-age people, there were 10 seniors in 1981 and 40 in 2007. However, the trends are very wiggly and would need some smoothing. So one should be careful in interpreting variations in the short term.



## References

Jenouvrier, Stéphanie, Hal Caswell, Christophe Barbraud, Marika Holland, Julianne Stroeve, and Henri Weimerskirch. 2009. "Demographic Models and Ipcc Climate Projections Predict the Decline of an Emperor Penguin Population." *Proceedings of the National Academy of Sciences* 106 (6): 1844–7.