

# Steller sea lion matrix projection modeling

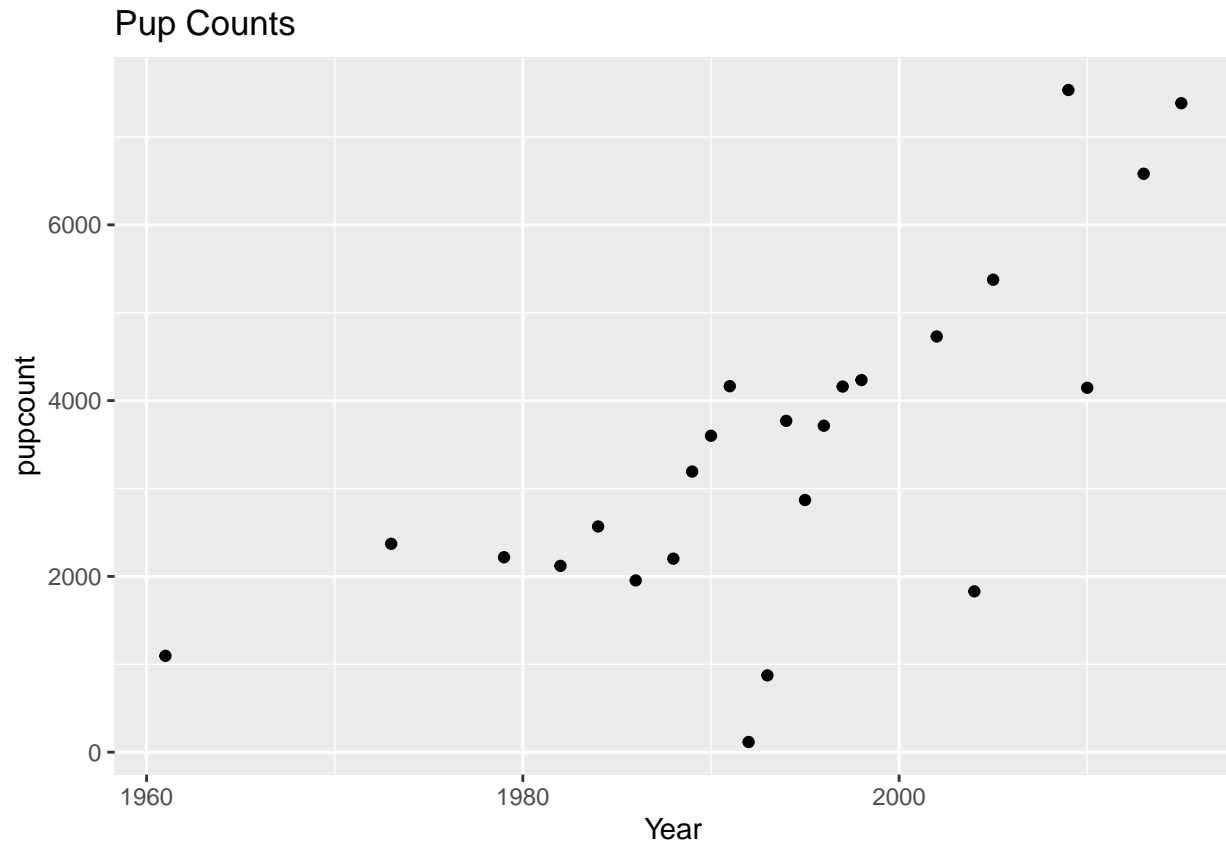
## Southeast AK Steller sea lions

### Pup counts

```
se_pups <- pups %>%  
  filter(rookery==1,  
         trendsite ==1,  
         regionnumb == 5) %>%  
  group_by(Year, sitename) %>%  
  summarize(pupcount = max(pupcount)) %>%  
  ungroup() %>%  
  group_by(Year) %>%  
  summarize(n = length(pupcount),  
            pupcount = sum(pupcount))
```

## `summarise()` has grouped output by 'Year'. You can override using the  
## ` .groups ` argument.

```
ggplot(se_pups) +  
  #geom_line(aes(x=Year,y=n))  
  geom_point(aes(x=Year,y=pupcount)) +  
  labs(title = "Pup Counts")
```



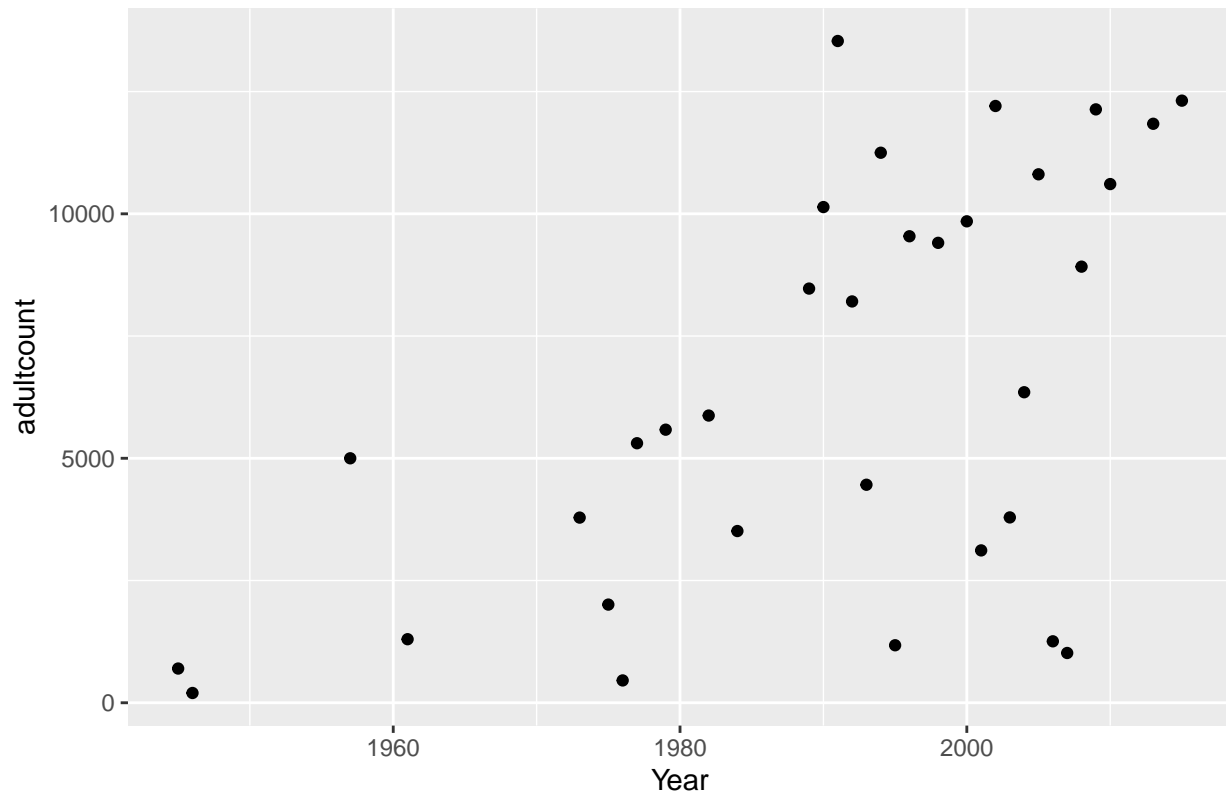
### Non-pup counts

```
se_nonpups <- nonpups %>%
  filter(#rookery==1,
         trendsite ==1,
         regionnumb == 5) %>%
  group_by(Year, sitename) %>%
  summarize(adultcount = max(adultcount)) %>%
  ungroup() %>%
  group_by(Year) %>%
  summarize(n = length(adultcount),
            adultcount = sum(adultcount))

## `summarise()` has grouped output by 'Year'. You can override using the
## `.groups` argument.

ggplot(se_nonpups) +
  geom_point(aes(x=Year,y=adultcount)) +
  labs(title = "Counts of Non-pups")
```

## Counts of Non-pups



```
#ggplot(se_nonpups) +  
# geom_line(aes(x=Year,y=n))
```

## Stage-structured population projection model

$$\begin{bmatrix} N_{pups,t+1} \\ N_{np,t+1} \end{bmatrix} = \begin{bmatrix} 0 & f \\ \phi_p & \phi_{np} \end{bmatrix} \begin{bmatrix} N_{pups,t} \\ N_{np,t} \end{bmatrix}$$

```
NO <- c(1000,2500)  
NO
```

```
## [1] 1000 2500
```

```
fec <- 0.25 # 63% pregnancy rate * 0.5 for males * 80% for immature animals  
phi1 <- 0.6 # avg. of Forester Island rates for males & females  
phi2 <- 0.9 # avg. of FI males/females juvs & adults given stable age distribution
```

```
X <- matrix(c(0,fec,  
             phi1, phi2),byrow=TRUE,nrow=2)
```

```
X
```

```
##      [,1] [,2]  
## [1,]  0.0 0.25  
## [2,]  0.6 0.90
```

```
#X*N
```

```
N1 <- X %*% NO  
N1
```

```
##      [,1]
## [1,]  625
## [2,] 2850
```

```
pups <- 0.25*N0[2]
pups
```

```
## [1] 625
```

```
nonpups <- 0.6*N0[1] + 0.9*N0[2]
nonpups
```

```
## [1] 2850
```

## Do a population projection for 40 years

```
Nstore <- matrix(rep(NA,80),byrow=TRUE,ncol=2)
Nstore[1,] <- N0
head(Nstore)
```

```
##      [,1] [,2]
## [1,] 1000 2500
## [2,]   NA   NA
## [3,]   NA   NA
## [4,]   NA   NA
## [5,]   NA   NA
## [6,]   NA   NA
```

```
for (t in 2:40)
  Nstore[t,] <- X%*%Nstore[t-1,]
head(Nstore)
```

```
##      [,1]      [,2]
## [1,] 1000.0000 2500.00
## [2,]  625.0000 2850.00
## [3,]  712.5000 2940.00
## [4,]  735.0000 3073.50
## [5,]  768.3750 3207.15
## [6,]  801.7875 3347.46
```

```
tail(Nstore)
```

```
##      [,1]      [,2]
## [35,] 2773.143 11577.51
## [36,] 2894.376 12083.64
## [37,] 3020.910 12611.90
## [38,] 3152.976 13163.26
## [39,] 3290.815 13738.72
## [40,] 3434.679 14339.33
```

## Population growth rate

“ (sum(Nstore[40,])/sum(Nstore[39,]) eigen(X) library(popbio) eigen.analysis(X) “