# Pink salmon analyses for paper

*03-28-2016*

This represents an outline / summary of the pink salmon analyses for the Ward et al. paper.

## Data Processing

```
## Warning: package 'readxl' was built under R version 3.2.4
```

### Brief descriptions of pink salmon dataset are as follows:

#### PWS pink salmon

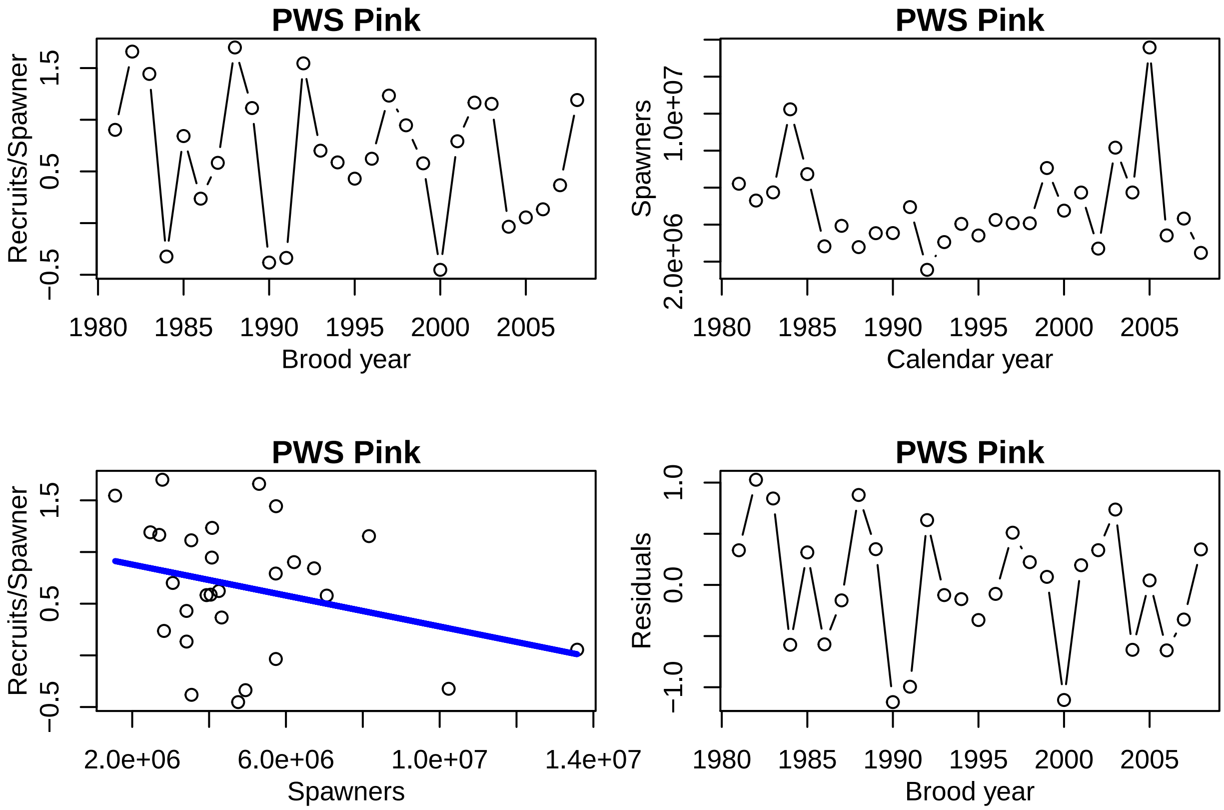
R/S is calculated as brood year returns / escapement. These are columns 'H' and 'L' from the 'Database' sheet of '2015_PWS_Pink_Wild_forecast-FINAL.xlsm'.

**Read in the data. All datasets have been trimmed to start at Brood Year 1968. We'll primarily use data 1980 or 1981 - 2008, because those are the span of years with R/S and covariates known (hatchery releases before 1980 incomplete).**

```
pink = read_excel("../../data/salmon data/data for analysis/PWS_Wild_Pink_final.xlsx")
```

Plot the response, log(Recruits/Spawners).

```
subset = which(pink$BroodYear%in%seq(1981,2008))
Y = log(as.numeric(pink$RecPerSpawn[subset])) # log(R/S)

par(mfrow = c(2,2),mgp=c(2,1,0),mai=c(0.8,0.6,0.2,0.05))
plot(1981:2008,Y, xlab="Brood year",ylab="Recruits/Spawner",main="PWS Pink",type="b")

# Plot the predictor, number of spawners.
X = as.numeric(pink$Escapement[subset]) # number of spawners
plot(1981:2008,X, xlab="Calendar year",ylab="Spawners",main="PWS Pink",type="b")

# Plot the data, as log(Recruits/Spawners) versus Spawners over the period we're using,
# 1981-2008. This is the same formulation as the Ricker model assumes (below).
plot(X,Y, xlab="Spawners",ylab="Recruits/Spawner",main="PWS Pink")
# fit linear model
lines(X, predict.lm(lm(Y~X),newdata=data.frame(X)), col="blue",lwd=3)

# Plot the residuals from the regression of log(Recruits/Spawners) versus Spawners over
# the period we're using, 1981-2008. This is the same formulation as the Ricker
# model assumes (below).

Y = log(as.numeric(pink$RecPerSpawn[subset])) # log(R/S)
X = as.numeric(pink$Escapement[subset]) # number of spawners
mod = lm(Y~X)
plot(1981:2008,mod$residuals, xlab="Brood year",ylab="Residuals",main="PWS Pink",type="b")
```




## Modeling recruiutment

We'll conduct this analysis using the Ricker stock-recruit model, which is equivalent to a linear regression model,
$log(R/S)_t = a_i + b_i * S_t + c_i * X_t + e_i$

where $a_i$ represents the population-specific intercept, $b_i$ is a density-dependent parameter (generally negative), $c_i$ is an optional coefficient(s) incorporating a time-varying covariate $X_t$, and $e_i$ is an error term. Simple models for the error are IID white noise, which we'll adopt here.

### Constructing the basic (null) model with no covariates.

We'll start with just using data 1981-2008, and spawners as a predictor of recruitment. Recruits / spawner is not modeled as an autoregressive state-space process, but all uncertainty is assumed to have arisen from measurement and observation error. Hypotheses for mechanistic relationships are discussed and evaluated below.

```
subset = which(pink$BroodYear%in%seq(1981,2008))

Y = log(as.numeric(pink$RecPerSpawn[subset])) # log(R/S)
X = as.numeric(pink$Escapement[subset]) # number of spawners
nT = length(Y)
```

```
# fit in initial Ricker S-R state space model
cMat = matrix(NA, nrow=1, ncol = nT)
```

```
cMat[1,] = X
Covar = matrix(list(0),1,1)
Covar[1,1] = "Spawners"
models = list()
```

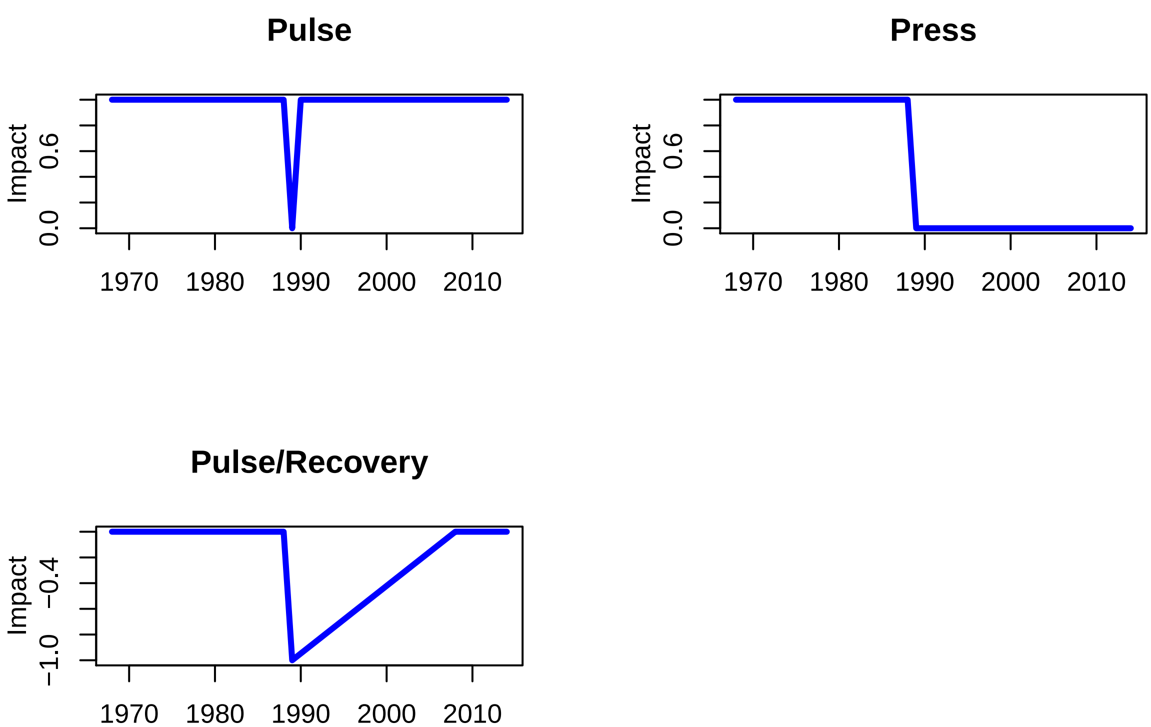
| Model | AICc | Coef |
|---|---|---|
| Density dependence only (Ricker b) | 58.735 | NA |
| Null model | 58.622 | NA |

## Hypothesis 2: Potential impacts of EVOS

The EVOS spill occurred in 1989. Pink typically migrate to the ocean the year after spawning occurs, and return to spawn in June-Oct.

We'll include the impacts of the EVOS spill. We'll do this 3 ways: creating a pulse impact, a press impact, and a press impact followed by a recovery back to the original state. The form of the recovery was assumed to be linear over a 20 - year period.

```
par(mfrow = c(2,2),mgp=c(2,1,0))
plot(pink$BroodYear, 1-pink$EVOS.pulse.lag0, xlab = "", ylab = "Impact",
     main = "Pulse",col="blue",lwd=3,type="l")
plot(pink$BroodYear, 1-pink$EVOS.press.lag0, xlab = "", ylab = "Impact",
     main = "Press",col="blue",lwd=3,type="l")
plot(pink$BroodYear, pink$EVOS.pulseRecovery.lag0, xlab = "", ylab = "Impact",
     main = "Pulse/Recovery",col="blue",lwd=3,type="l")
```



```r
library(MARSS)
covar.names = c("EVOS.pulse.lag0","EVOS.press.lag0","EVOS.pulseRecovery.lag0",
"EVOS.pulse.lag1","EVOS.press.lag1","EVOS.pulseRecovery.lag1",
"EVOS.pulse.lag2","EVOS.press.lag2","EVOS.pulseRecovery.lag2")
# fit in initial Ricker S-R state space model

cMat = matrix(NA, nrow=2, ncol = nT)
cMat[1,] = X
Yall = rbind(Y)

# Coefficients matrix. cMat Matrix is dimensioned
# cmat.row x cmat.col, and Covar needs to be dimensioned
# cmat.row x n.responses
evos.models = list()
```

| Model | AICc | Coef |
|---|---|---|
| EVOS.pulse.lag0 | 61.48 | 0.30850133 |
| EVOS.press.lag0 | 60.246 | -0.46012745 |
| EVOS.pulseRecovery.lag0 | 59.827 | 0.43599061 |
| EVOS.pulse.lag1 | 59.602 | 0.88347187 |
| EVOS.press.lag1 | 61.674 | -0.05393094 |
| EVOS.pulseRecovery.lag1 | 61.489 | 0.14111885 |
| EVOS.pulse.lag2 | 61.522 | -0.25704189 |
| EVOS.press.lag2 | 61.415 | -0.18737395 |
| EVOS.pulseRecovery.lag2 | 61.168 | 0.2353661 |

These results show that in general, adding EVOS as a pulse impact (lag.0, in 1989) improves the fit of the model and lowers AIC.

# Hypothesis 3: Wild pink salmon productivity in PWS has been affected by changing ocean conditions

```r
library(MARSS)
covar.names = c("SST.pink.lag0","SST.pink.lag1","Upwelling.winter.lag1",
"Upwelling.winter.lag2","Upwelling.spring.lag1","Upwelling.spring.lag2")
# fit in initial Ricker S-R state space model

cMat = matrix(NA, nrow=2, ncol = nT)
cMat[1,] = X
Yall = rbind(Y)

# Coefficients matrix. cMat Matrix is dimensioned
# cmat.row x cmat.col, and Covar needs to be dimensioned
# cmat.row x n.responses
enviro.models = list()
```

```r
kable(m)
```

| Model | AICc | Coef |
|---|---|---|
| SST.pink.lag0 | 61.448 | 0.04932262 |
| SST.pink.lag1 | 59.045 | 0.24868091 |
| Upwelling.winter.lag1 | 61.726 | 0.00051707 |
| Upwelling.winter.lag2 | 61.707 | -0.00040973 |
| Upwelling.spring.lag1 | 61.7 | 0.00087154 |
| Upwelling.spring.lag2 | 61.286 | 0.00588347 |

These results show that in these indices of SST and Upwelling on pink salmon increases AICc, worsening the fit of the model.

# Hypothesis 4: Wild pink salmon productivity in PWS has been impacted by predation and competition from juvenile pink (hatchery) or chum salmon

```
library(MARSS)
covar.names = c("juv.hatchRelPink.lag0","juv.hatchRelChum.lag0","juv.wildChumRun.lag1")#,"juv.wildCohoR
# fit in initial Ricker S-R state space model

cMat = matrix(NA, nrow=2, ncol = nT)
cMat[1,] = X
Yall = rbind(Y)
# Coefficients matrix. cMat Matrix is dimensioned
# cmat.row x cmat.col, and Covar needs to be dimensioned
# cmat.row x n.responses
juvComp.models = list()
```

```
kable(m)
```

| Model | AICc | Coef |
|---|---|---|
| juv.hatchRelPink.lag0 | 58.926 | 0 |
| juv.hatchRelChum.lag0 | 61.386 | 0 |
| juv.wildChumRun.lag1 | 61.552 | 1.5e-07 |

These results show that in these indices of pink and chum salmon juvenile competion with juvenile wild pink salmon increases AICc, and doesn't improve the fit of the model.

# Hypothesis 5: Wild pink salmon productivity in PWS has been impacted by predation and competition from adult pink salmon

```
library(MARSS)
pink$ad.totalPinkRun.lag1 = pink$ad.wildPinkRun.lag1 + pink$ad.hatchPinkRun.lag1
covar.names = c("ad.hatchRelPink.lag1",
```

```
"ad.hatchRelChum.lag1","ad.wildChumRun.lag2",
"ad.wildPinkRun.lag1","ad.hatchPinkRun.lag1","ad.totalPinkRun.lag1")
# fit in initial Ricker S-R state space model

cMat = matrix(NA, nrow=2, ncol = nT)
cMat[1,] = X
Yall = rbind(Y)

# Coefficients matrix. cMat Matrix is dimensioned
# cmat.row x cmat.col, and Covar needs to be dimensioned
# cmat.row x n.responses
adComp.models = list()
```

| Model | AICc | Coef |
|---|---|---|
| ad.hatchRelPink.lag1 | 60.445 | 0 |
| ad.hatchRelChum.lag1 | 61.717 | 0 |
| ad.wildChumRun.lag2 | 61.693 | -2e-08 |
| ad.wildPinkRun.lag1 | 61.597 | -1e-08 |
| ad.hatchPinkRun.lag1 | 60.11 | -1e-08 |
| ad.totalPinkRun.lag1 | 60.728 | -1e-08 |

These results show that in these indices of pink and chum salmon adult predation with juvenile wild pink salmon increases AICc.

As an update to the changing ocean conditions hypotheses, we can also explore whether these same correlations hold for the longer time series, going back to 1968.

```
subset = which(pink$BroodYear%in%seq(1968,2008))

Y = log(as.numeric(pink$RecPerSpawn[subset])) # log(R/S)
X = as.numeric(pink$Escapement[subset]) # number of spawners
nT = length(Y)
```

```
library(MARSS)
covar.names = c("SST.pink.lag0","SST.pink.lag1","Upwelling.winter.lag1",
"Upwelling.winter.lag2","Upwelling.spring.lag1","Upwelling.spring.lag2")
# fit in initial Ricker S-R state space model

cMat = matrix(NA, nrow=2, ncol = nT)
cMat[1,] = X
Yall = rbind(Y)

# Coefficients matrix. cMat Matrix is dimensioned
# cmat.row x cmat.col, and Covar needs to be dimensioned
# cmat.row x n.responses
enviro.models = list()
```

So what this illustrates is that SST outperforms the null model when the longer time series is included – but has had little explanatory power since the regime shift.

```r
kable(m)
```

| Model | AICc | Coef |
|---|---|---|
| SST.pink.lag0 | 92.776 | 0.07015537 |
| SST.pink.lag1 | 85.532 | 0.39046457 |
| Upwelling.winter.lag1 | 93.096 | -0.00116151 |
| Upwelling.winter.lag2 | 91.743 | -0.00517887 |
| Upwelling.spring.lag1 | 92.92 | 0.00329952 |
| Upwelling.spring.lag2 | 92.986 | 0.0036167 |
| Null model | 90.573 | NA |