

Pink salmon analyses for paper

09-28-2015

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

Data Processing

Brief descriptions of pink salmon dataset are as follows:

3. 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, $\log(\text{Recruits}/\text{Spawners})$.

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

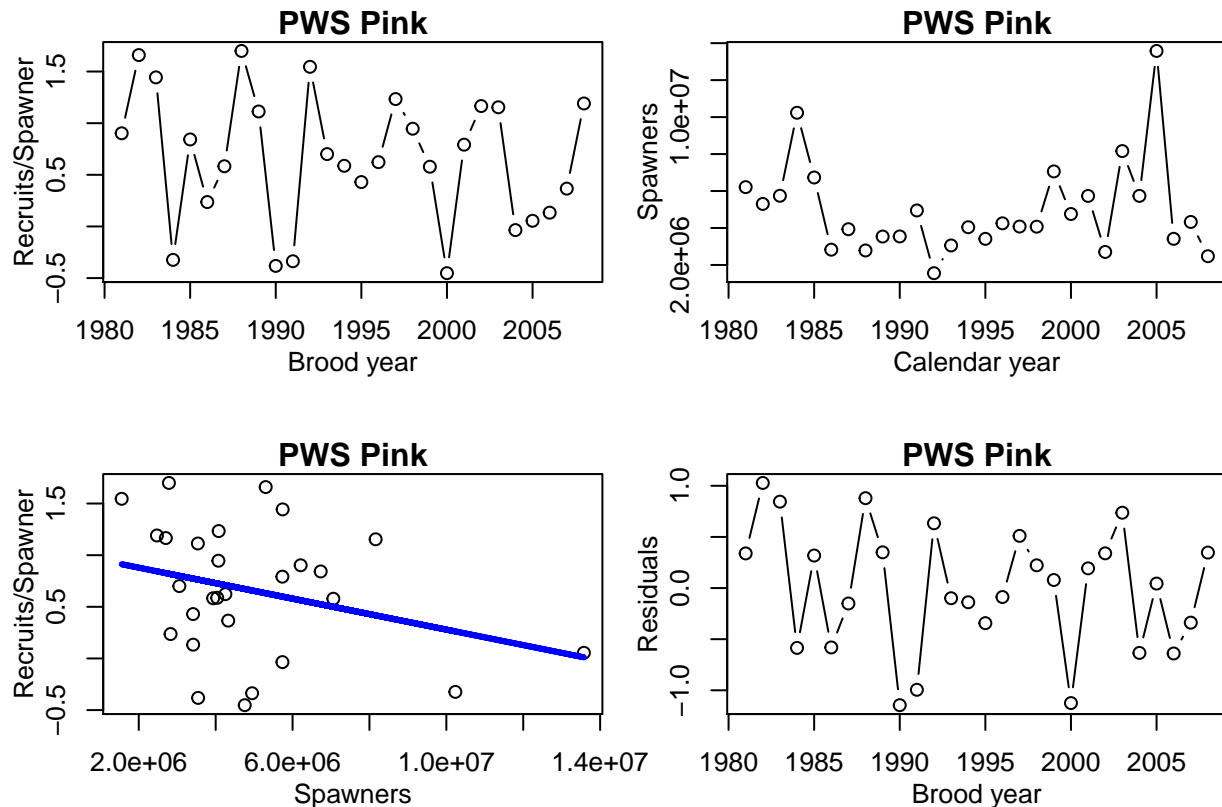
par(mfrow = c(2,2),mgp=c(2,1,0),mai=c(0.8,0.6,0.2,0.05))
plot(1981:2008,Y, xlab="Brood year",ylab="Recruits/Spawner",main="PWS Pink",type="b")

# 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 recruitment

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()
```

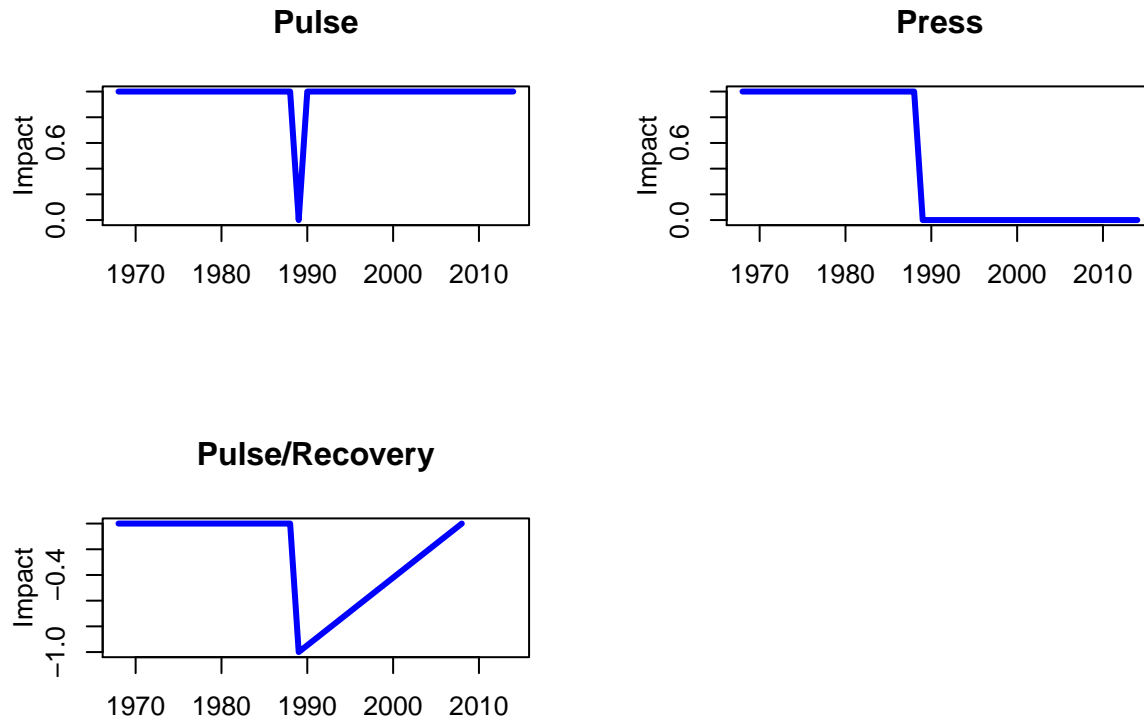
Model	AICc	Coef
Density dependence only (Ricker b)	58.735	NA
Null model	58.622	NA

Hypothesis 1: EVOS had a negative impact on pink salmon productivity

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")
```



```

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	56.737	-1.26537695
EVOS.press.lag1	59.236	-0.59517298
EVOS.pulseRecovery.lag1	58.65	0.56010922
EVOS.pulse.lag2	58.133	-1.08237836
EVOS.press.lag2	61.719	-0.00813342
EVOS.pulseRecovery.lag2	61.472	0.15542919

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 2: Wild pink salmon productivity in PWS has been negatively 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 competition with juvenile wild pink salmon increases AICc, and doesn't improve the fit of the model.

Hypothesis 3: Wild pink salmon productivity in PWS has been negatively 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.

Hypothesis 4: Wild pink salmon productivity in PWS has been largely shaped by changing ocean conditions (SST, PDO)

```
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()

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.

As an update, 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.

`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