Coastal Coho Salmon Life Cycle Modeling



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Northern California Life Cycle Monitoring Stations



Freshwater Creek Life Cycle Monitoring Station



Area: 92 km² Anadromous habitat: 14.5 km

Freshwater Creek Life Cycle Monitoring Station



Permanent weir located near upper extent of tidally influenced habitat

Freshwater Creek Life Cycle Monitoring Station



Antennas located throughout the basin and in wood creek marsh in the stream estuary ecotone











Early Emigrants

- Missed by spring migrant trapping
- Early emigrants account for up to 29% of fall tagged fish (2010-2015)
 - Up to 70+% in some Washington streams (Bennett et. al. 2014)
- Many rear in the estuary and associated tidally influenced habitat



Study Goals

1. Build a stage structured population model for Freshwater Creek CA

1. Quantify early emigration contribution to population dynamics

1. Identify limiting stages

1. Quantify population response to alternative restoration scenarios

Basic Model Framework

- Modified Leslie matrix design
- Survival and early emigration quantified at the reach scale
- 6 reaches and estuary included
- Density dependent functions to model changes in productivity and capacity
- Life stage survival quantified by data from Freshwater Creek LCM



Adults

Quantifying Model Parameters

 Cormack-Jolly-Sebert modeling using Program Mark and standard statistical methods



- CDFW data:
 - Overwinter survival
 - Early emigration parameters
 - Marine survival
 - Carrying capacity
 - Spring/Summer survival
 - Fecundity + (Shapivalov and Taft 1954)
- Literature values used for stages with incomplete/missing data:
 - Egg survival (Moring and Lantz, 1975)

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CJS Modeling Results

Overwinter Survival & Probability of Early Emigration:

- Both are highly variable between years
- Best fitting models vary from year to year
 - Multiple drivers: may be different from one year to the next
 - Length
 - Watershed area
 - Specific reach (habitat)
 - Mainstem vs. Tributaries





The Code Slide

cor.matrix <- matrix(0,nrow=6,ncol=6)
for(i in 1:6){
 for(ii in 1:6){
 mod <- cor.test(ow.1[,i],ow.1[,ii])
 if(mod\$p.value < 0.1){
 cor.matrix[i,ii] <- mod\$estimate}
 }}
 names <- c("BHH","LMS","MMS","UMS","CLO","SFO")
 rownames(cor.matrix) <- paste(names)</pre>

cor.matrix

corrmx <- cor.matrix# correlation matrix

colnames(cor.matrix) <- paste(names)

eig <- eigen(corrmx) #get them eigens

W <- eig\$vectors # Makes matrix of eigen Vectors: W

D <- eig\$values # Makes matrix of eigen Values: D

D12 <- sqrt(abs(matrix(diag(D),nrow=np))) # D12 is a matrix of the square root of the eigen values on diagonal, the rest of the elements are zero

C12 <- W%*%D12%*%t(W) # Generates the square root of correlation matrix corrmx

results <- matrix(NA,nrow=tmax,ncol=np) colnames(results) <- paste(names)

for(tt in 1:tmax){ # Loop for each years vital rates

normvals <- matrix(rnorm(np)) #makes a set of random standard normal values

corrnorms <- C12%*%normvals #make them norms into correlated norms bhh.vr <- betaval(vrmeans[1],vrvars[1],normfx(corrnorms[1])) #converts each normal into the beta equivalent via the Cumultive distribution value lms.vr <- betaval(vrmeans[2],vrvars[2],normfx(corrnorms[2])) if(Nt[5]>10){

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total.ad <- round(Nt[5]) #this is the total number of adults returning to spawn

fems <- sum(rbinom(total.ad,1,0.5)) # This is the total number of those that are female

if(fems<1){fems<-1} # This is just so the code doesn't break down if by statistical anomaly there are no females

f.lengths <- rnorm(fems,66.90909,5.933774) #normally distributed lengths of all the females

egg.counts <- sapply(f.lengths,l.egg) #applying the length to egg function to the length of each female

f <- sum(egg.counts)/fems #getting the average egg count for the cohort scour<- sum(rbinom(fems,1,0.85))/fems # calculating the redd mortality rate due to scour (nickelson and lawson 1998)

 $if(scour==0)\{scour<-0.85\}$

fem.pct <- fems/total.ad #percentage of the adults that are female Fert <- f*fem.pct*scour #fertility rate }else{Fert <- f*0.5*.85}

M <- matrix(data=c(0, 0, 0, 0, Fert, Y1, 0, 0, 0, 0, 0, Y2n, 0, 0, 0, 0, Y2e, 0, 0, 0, 0, 0, Y3n, Y3e, 0





Population Trajectory and Extinction Probability Simulated population runs to 50 years

Metrics:

- Extinction Threshold= 20 > Spawners for 3 consecutive years
- Average spawner escapement over the last 10 years of simulation





No Early Emigrants

Early Emigrant Model Credit: Paul Vecsei



No Early Emigrants

Early Emigrant Model

Slow water - Survival Relationship and Restoration Scenarios

- Winter slow water habitat associated with overwinter survival (In prep: John Deibner-Hansen Masters Thesis)
- Incorporate additions of slow water habitat into modeling scenarios (Solazzi 2000)
- Variable configurations
- Little data for how estuary restoration affects early emigrants
 - Modeled under three scenarios:
 - + Productivity
 - + Capacity
 - +Productivity + Capacity

Simulated Restoration Scenarios



Conclusions:

Early emigrant life history is important for population viability

Managing for multiple life history patterns is important for individual populations ability to cope with annual variability and extreme environmental events

Early emigrant estimates represent minimums:

- Stream estuary ecotone provides productive habitat for smolt emigrants on their way to the ocean
- Estuary restoration efforts provide additional off channel refugia during winter high flows

Further study of coho usage of SEE needed to improve parameter estimates (+productivity? +capacity? Overwinter survival?)

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Questions?