SSHI sockeye exploratory analyses (stage 1)

2019-07-11

This document summarizes some quick exploratory analyses of Fraser sockeye survival indices. all code and associated data can be found here

```r
# load required packages and functions
library(ersst)     # see: [https://github.com/michaelmalick/r-ersst](https://github.com/michaelmalick/r
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------------------------------

## v ggplot2 3.1.1     v purrr   0.2.5
## v tibble  2.1.1     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

## Warning: package 'ggplot2' was built under R version 3.5.2

## Warning: package 'tibble' was built under R version 3.5.2

## Warning: package 'dplyr' was built under R version 3.5.1

## -- Conflicts -----------------------------------------------------------------------
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()    masks stats::lag()
```

```r
library(viridis)
```

```
## Loading required package: viridisLite
```

```r
library(plyr)
```

```
## --------------------------------------------------------------------------

## You have loaded plyr after dplyr - this is likely to cause problems.
## If you need functions from both plyr and dplyr, please load plyr first, then dplyr:
## library(plyr); library(dplyr)

## --------------------------------------------------------------------------

##
## Attaching package: 'plyr'

## The following objects are masked from 'package:dplyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize

## The following object is masked from 'package:purrr':
##
##     compact
```

```r
source("functions.R")
source("sst_anomalies.R")

# load Fraser sockeye brood table,  recent missing estimates of effective female spawners were added to
raw_brood_table <- read.delim("data/fraser_brood_table.txt")

# clean up brood table
brood_table <- subset(raw_brood_table, BY < 2013) # drop incomplete brood years
```

```r
brood_table <- subset(brood_table, BY > 1949) #  and pre-1950
brood_table <- subset(brood_table, stock_name != "Cultus") #  drop cultus which does not have recruitmer
brood_table$efs <-as.numeric(levels(brood_table$total_effective_female_spawner))[brood_table$total_effe
```

Warning: NAs introduced by coercion

```r
brood_table$tas <-as.numeric(levels(brood_table$total_adult_spawner))[brood_table$total_adult_spawner]
```

Warning: NAs introduced by coercion

```r
brood_table$age.51 <- 0
brood_table$lnRS <-log(brood_table$recruits_no_jacks/brood_table$efs)
brood_table <- brood_table[!is.na(brood_table$lnRS),]
brood_table <- brood_table[brood_table$lnRS != "-Inf",]
brood_table<-brood_table[!is.na(brood_table$Stock.ID),]

# add columns with ocean entry age proportions
brood_table$ocean_0 <- (brood_table$age.21+brood_table$age.31+brood_table$age.41+brood_table$age.51)/bro
brood_table$ocean_1 <- (brood_table$age.32+brood_table$age.42+brood_table$age.52+brood_table$age.62)/bro
brood_table$ocean_2 <- (brood_table$age.43+brood_table$age.53+brood_table$age.63)/brood_table$total_rec

# 1st marine year SST
raw.clim <- read.csv(file="data/sst_yr_1_stock_anomalies.csv",header=TRUE)
head(raw.clim)
```

```
##   Year  sst_raw sst_anomaly Stock.ID
## 1 1950 10.49967 -1.36446262        1
## 2 1951 11.10579 -0.75834071        1
## 3 1952 11.22971 -0.63442207        1
## 4 1953 11.77355 -0.09058153        1
## 5 1954 11.22206 -0.64206584        1
## 6 1955 10.89087 -0.97326181        1
```

```r
early.sst <- clim.wgt.avg(brood.table = brood_table,
                          env.data = raw.clim,
                          env.covar = "sst_anomaly",
                          type = "first_year",
                          out.covar = "early_sst")

# Pink competitors (empirical data through 2015, extrapolated based on last four years of data for odd a
raw.comp <- read.csv(file="data/pink_abundance_2017_12_08.csv",header=TRUE)
extrap_pinks <- matrix(NA,4,16,dimnames = list(seq(1:4),colnames(raw.comp)))
extrap_pinks[1:4,1] <- c(2016,2017,2018,2019)
extrap_pinks[1:4,16] <- c(median(raw.comp$Total[c(57,59,61,63)]),
                          median(raw.comp$Total[c(58,60,62,64)]),
                          median(raw.comp$Total[c(57,59,61,63)]),
                          median(raw.comp$Total[c(58,60,62,64)]))

raw.comp <- rbind(raw.comp,extrap_pinks)
head(raw.comp)
```

```
##   Year Korea    Japan      M.I      WKam      EKam       WAK      SPen
## 1 1952     0 1.812361 26.28340  97.91619 16.229050 4.0461507 2.692169
## 2 1953     0 2.045614 44.40180 208.59244 26.562273 0.2906501 5.981372
## 3 1954     0 1.651938 46.24121  59.52690 13.443398 4.0461507 4.774613
## 4 1955     0 4.158328 78.63593 117.27708 28.467828 0.2906501 5.622972
```

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```
## 5 1956      0 3.633480 105.00509  85.05538  4.439488 4.0461507 5.976094
## 6 1957      0 2.414860  68.69835 168.91125 78.790918 0.2906501 2.701325
##         Kod       CI      PWS     SEAK      NBC      SBC       WA
## 1  6.572562 4.3626918 3.386470 19.85095 9.952010  4.925796 0.000000
## 2  7.270872 1.3019509 3.188460 11.45334 3.745838 16.400000 5.294486
## 3 10.919343 4.6650066 4.295368 18.35103 8.724543  3.155473 0.000000
## 4 13.431398 2.6683939 4.295368 19.06637 3.775723 12.902005 3.820964
## 5  5.058095 3.5666173 5.916931 26.24360 9.546154  2.326438 0.000000
## 6  6.736866 0.8040015 1.492568 14.82025 4.974572  8.402024 2.996358
##     Total
## 1 198.0298
## 2 336.5291
## 3 179.7950
## 4 294.4130
## 5 260.8135
## 6 362.0340
```

```r
np.pink <- pink.wgt.avg(brood.table = brood_table,
                        pink.data = raw.comp,
                        pink.covar = "Total",
                        type = "second_year",
                        out.covar = "np_pinks")


# merge datasets
master.1 <- merge(brood_table, early.sst, by=c("BY","Stock.ID"),all.x=T)
master.bt <- merge(master.1, np.pink, by=c("BY","Stock.ID"),all.x=T)
master.bt <- master.bt[order(master.bt$Stock.ID),]

# add derived columns
master.bt_w_cov <- ddply(master.bt, .(Stock.ID), transform,
                         early_sst_stnd = scale(early_sst)[ , 1],
                         np_pinks_stnd = scale(np_pinks)[ , 1])


# export to output
write.csv(master.bt_w_cov, "data/master_brood_table_covar.csv", row.names=FALSE)

# create data frame with normalized survival indices
survial_indices <- ddply(master.bt_w_cov, c("stock_name"),function(x) {
                     ricker_fit <- lm(x$lnRS~x$efs,na.action=na.exclude)
                     ricker_resid <- scale(resid(ricker_fit))
                     ricker_fit_cov <- lm(x$lnRS~x$efs+x$np_pinks_stnd+x$early_sst_stnd,na.action=
                       ricker_cov_resid <- scale(resid(ricker_fit_cov))
                     lnRS <- scale(x$lnRS)
                     brood_year <- x$BY
                     xx <- data.frame(brood_year,ricker_resid,ricker_cov_resid,lnRS)
    })
survial_indicesL<-gather(survial_indices,survival_index,value,ricker_resid:lnRS)

# create data frame with covariate effects
cov_effects <- ddply(master.bt_w_cov, c("stock_name"),function(x) {
                  ricker_fit_cov <- lm(x$lnRS~x$efs+x$np_pinks_stnd+x$early_sst_stnd,na.action=na.e
                    pink <- ricker_fit_cov$coefficients[3]
                    sst <- ricker_fit_cov$coefficients[4]
                  xx <- data.frame(pink,sst)
```

```
    })
cov_effectsL<-gather(cov_effects,covariate,value,pink:sst)
```

plot point estiamtes of covariate effects