

# futR

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## R futR

futR() is a generic Rpackage for fitting recruitment models to stock assessment estimates of spawning stock biomass and recruitment with or without climate covariates. The recruitment model is based on Template Model Builder (TMB) and formulations follow Maunder and Desrioso (2011) using a generalized three parameter stock-recruitment model with environmental covariates (Deriso 1980; Schnute 1985). This includes Ricker (logistic), Beverton Holt, log-linear, and log-linear with biomass lagged by year 'y-1'. The model can be fit with and without random effects on spawning stock biomass (SSB) and recruitment (R) (i.e., measurement error on SSB and rec) using the methods of Porch and Laretta (2016) and with the optional unbiased estimate of sigma (sensu Ludwid and Walters 1981, Porch and Laretta 2016). Environmental covariates are optional but can be included as main effects or as interactions.

For more information see Holsman et al. 2020 Climate and trophic controls on groundfish recruitment in Alaska.

## Installing futR()

The package can be installed from github using the devtools package:

```
install.packages("devtools")
```

The projection package can then be installed to R directly:

```
devtools::install_github("kholmsan/futR")
```

## Fitting Recruitment:

The base function for fitting recruitment requires a data.frame of recruitment and spawning biomass:

```
# rm(list=ls())

# -----
# 1. Set things up
# -----

# e.g.,
main <- getwd()
setwd(main)

# load data, packages, setup, etc.
source("R/make.R")
```

```
#-----
# 2. Compile futR
#-----

compile('src/futR.cpp') # this will generate warnings - they can be ignored if "0" is returned
```

## Options

Now we can fit a set of models with and without covariates. There are various switches for fitting models:

### Recruitment formulations (rectype):

1. Linear ( $\gamma = 0$ )
2. Beverton Holt ( $\gamma = -1$ )
3. Ricker ( $0 < \gamma < 1$ ) ;  $\gamma$  is estimated (tMethod):
  - a. link = cloglog
  - b. link = logit
4. Exponential ( $\gamma=1$ ,  $b<0$ )

### Observation error options (sigMethod):

0. No observation error ( $\tau = 0$ )
1. estimate sigma, random effects on SSB if  $\tau > 0$ ,  $\tau$  input
2. unbiased sigma estimate,  $\tau$  input
3. as in 1 but with defined measurement error for rec (indep of random effects on Spawners/SSB)
4. as in 1 but with defined measurement error for rec and Spawners/SSB)

### Link options (tMethod):

1. cloglog link ( $g = 1 - \exp(-\exp(\gamma))$ )
2. logit link ( $g = \exp(\gamma)/(1 + \exp(\gamma))$ )

### Environmental effects (if set to “TRUE” in estparm):

- beta = effects on effective number of spawners
- lambda = effects on post-spawning success (e.g., age 0 survival)

## Fit recruitment

Let's start with some base models:

```
# 4.1 First run with no observation error on SSB:
# makeDat will make the input values, data, and phases for the model:
datlist <- makeDat(
  tauIN      = 1,
  sigMethod  = 1,
  tMethod    = 1,
  estparams  = estparams,
```

```

        typeIN      = 4,
        rec_years    = rec$years,
        Rec          = rec$Robs,
        SSB          = rec$SSB,
        sdSSB        = rec$sdSSB,
        sdRec        = rec$sdRobs,
        covars       = NULL,
        covars_sd    = NULL)

# run the basic model
mm1      <- runmod(dlistIN=datlist,version="src/futR",recompile=T,simulate=TRUE)
df1      <- data.frame(estimate=as.vector(mm1$sim), parameter=names( mm1$mle)[row
densityplot( ~ estimate | parameter, data=df1, layout=c(5,1),ylim=c(0,10))

#now change tau
datlist$rs_dat$tau <- 0.000001

# re-run the model with tau
mm1_t0    <- runmod(dlistIN=datlist,version="futR",recompile=F,simulate=TRUE)
df1_t0    <- data.frame(estimate=as.vector(mm1_t0$sim), parameter=names( mm1_t0$mle)
densityplot( ~ estimate | parameter, data=df1_t0, layout=c(5,1),ylim=c(0,10))

```