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Title Estimation of Equilibrium Reference Points for Fisheries

Version 0.1.19

Description Methods to estimate equilibrium reference points for fisheries data. Currently data must be converted into FLStock objects of the FLR (Fisheries Library in R) style, defined in the R package FLCore.

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msy-package

Estimation of equilibrium reference points for fisheries

Description

Methods to estimate equilibrium reference points for fisheries data. Currently data must be converted into FLStock objects of the FLR (Fisheries Library in R) style, defined in the R package FLCore

Details

Model fitting and simulation:

eqsr_fit	fitting stock recruit models to data
eqsim_run	simulation am 'equilibrium' population state

Plotting:

eqsr_plot	plot stock recruitment fit
eqsim_plot	plot summary of simulation showing reference points
eqsim_plot_range	plot summary of MSY ranges reference points

Example data:

icesStocks	A list of various stocks
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Author(s)

John Simmonds, Einar Hjorleifsson, Carmen Fernandez and Colin Millar.

References

ICES (2015) Report of the Workshop to consider F MSY ranges for stocks in ICES categories 1 and 2 in Western Waters (WKMSYREF4). [01 WKMSYREF4 Report.pdf](#)

ICES (2017) ICES fisheries management reference points for category 1 and 2 stocks. DOI: [10.17895/ices.pub.3036](#)

Buckland, S.T., K.P. Burnham & N.H. Augustin (1997). Model selection: An integral part of inference. *Biometrics* 53, 603-618. DOI: [10.2307/2533961](#)

To explore the code of the package see the GitHub repo: [ices-tools-prod/msy](#)

Bevholt	<i>stock recruitment function</i>
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Description

stock recruitment function

Usage

```
Bevholt(ab, ssb)
```

Arguments

ab	the model parameters
ssb	a vector of ssb

Value

log recruitment according to model

bevholt2	<i>stock recruitment function</i>
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Description

stock recruitment function

Usage

```
bevholt2(ab, ssb)
```

Arguments

ab	the model parameters
ssb	a vector of ssb

Value

log recruitment according to model

eqsim_ggplot *Plots of the results from eqsim*

Description

XXX

Usage

```
eqsim_ggplot(sim, Scale = 1, plotit = TRUE)
```

Arguments

sim	An object returned from the function eqsim_run
Scale	A value, the scaling on the yaxis
plotit	Boolean, if TRUE (default) returns a plot

Author(s)

Einar Hjorleifsson <einar.hjorleifsson@gmail.com>

eqsim_plot *Plots of the results from eqsim*

Description

XXX

Usage

```
eqsim_plot(sim, ymax.multiplier = 1.2, catch = TRUE)
```

Arguments

sim	An object returned from the function eqsim_run
ymax.multiplier	A value that acts as a multiplier of the maximum observed variable being plotted. E.g. 1.2 means that for each of the three panels a, b and c the ymax is set to 1.2 of the maximum observed recruitment, spawning stock biomass and yield (catch or landings, depending on user input).
catch	Boolean, if TRUE (default) returns a plot based on catch. If false returns a plot based on landings.

Author(s)

Einar Hjorleifsson <einar.hjorleifsson@gmail.com>

eqsim_plot_range *Calculate Fmsy range*

Description

XXX

Usage

```
eqsim_plot_range(sim, interval = 0.95, type = "median")
```

Arguments

sim	XXX
interval	XXX
type	XXX

eqsim_run *Simulates the Equilibrium Results for a Population.*

Description

Simulate a fish stock forward in time given biological parameters, fishery parameters and advice parameters.

Usage

```
eqsim_run(
  fit,
  bio.years = c(-5, -1) + FLCore::dims(fit$stk)$maxyear,
  bio.const = FALSE,
  sel.years = c(-5, -1) + FLCore::dims(fit$stk)$maxyear,
  sel.const = FALSE,
  Fscan = seq(0, 2, len = 40),
  Fcv = 0,
  Fphi = 0,
  SSBcv = 0,
  rhologRec = TRUE,
  Blim,
  Bpa,
  recruitment.trim = c(3, -3),
```

```

Btrigger = 0,
Nrun = 200,
process.error = TRUE,
verbose = TRUE,
extreme.trim = c(0, 1),
R.initial = mean(fit$rby$rec),
keep.sims = FALSE
)

```

Arguments

<code>fit</code>	A list returned from the function <code>fitModels</code>
<code>bio.years</code>	The years to sample maturity, weights and M from, given as a vector of length 2, i.e. <code>c(2010, 2015)</code> select from the years 2010 to 2015 inclusive.
<code>bio.const</code>	A flag (default FALSE), if TRUE mean of the biological values from the years selected are used
<code>sel.years</code>	The years to sample the selection patterns from, given as a vector of length 2, i.e. <code>c(2010, 2015)</code> select from the years 2010 to 2015 inclusive.
<code>sel.const</code>	A flag (default FALSE), if TRUE mean of the selection patterns from the years selected are used
<code>Fscan</code>	F values to scan over, i.e. <code>seq(0, 2, by = 0.05)</code>
<code>Fcv</code>	Assessment error in the advisory year
<code>Fphi</code>	Autocorrelation in assessment error in the advisory year
<code>SSBcv</code>	Spawning stock biomass error in the advisory year
<code>rhologRec</code>	A flag for recruitment autocorrelation, default (TRUE), or a vector of numeric values specifying the autocorrelation parameter for the residuals for each SR model.
<code>Blim</code>	SSB limit reference point
<code>Bpa</code>	SSB precautionary reference point
<code>recruitment.trim</code>	A numeric vector with two log-value clipping the extreme recruitment values from a continuous lognormal distribution. The values must be set as <code>c("high", "low")</code> .
<code>Btrigger</code>	If other than 0 (default) the target F applied is reduced by <code>SSB/Btrigger</code> . This is the "ICES Advice Rule".
<code>Nrun</code>	The number of years to run in total (the last 50 years from that will be retained to compute equilibrium values from)
<code>process.error</code>	Use stochastic recruitment or mean recruitment? TRUE (default) uses the predictive distribution of recruitment, model estimate of recruitment + simulated observation error. FALSE uses model prediction of recruitment with no observation error.
<code>verbose</code>	Flag, if TRUE (default) indication of the progress of the simulation is provided in the console. Useful to turn to FALSE when knitting documents.

<code>extreme.trim</code>	a pair of quantiles (low, high) which are used to trim the equilibrium catch values, across simulations within an F scenario, when calculating the mean catch and landings for that F scenario. These mean values calculated across simulations within an F scenario are used to find which F scenario gave the maximum catch. <code>extreme.trim</code> can therefore be used to stabilise the estimate of mean equilibrium catch and landings by F scenario. The default is <code>c(0, 1)</code> which includes all the data and is effectively an untrimmed mean.
<code>R.initial</code>	Initial recruitment for the simulations. This is common across all simulations. Default = mean of all recruitments in the series.
<code>keep.sims</code>	Flag, if TRUE returns a matrix of population trajectories for each value of F in Fscan (see examples).

Details

Details of the steps required to evaluate reference points are given in ICES (2017). While, details of the calculation of MSY ranges is given in ICES (2015).

Value

A list containing the results from the forward simulation and the reference points calculated from it.

References

ICES (2015) Report of the Workshop to consider F MSY ranges for stocks in ICES categories 1 and 2 in Western Waters (WKMSYREF4). [01 WKMSYREF4 Report.pdf](#)

ICES (2017) ICES fisheries management reference points for category 1 and 2 stocks. DOI: [10.17895/ices.pub.3036](#)

See Also

[eqsr_fit](#) fits multiple stock recruitment models to a data set.

[eqsr_plot](#) plots the results from `eqsr_fit`.

[eqsim_plot](#) summary plot of the forward simulation showing estimates of various reference points.

[eqsim_plot_range](#) summary plots of the forward simulation showing the estimates of MSY ranges (ICES, 2015)

[msy-package](#) gives an overview of the package.

Examples

```
## Not run:
data(icesStocks)
FIT <- eqsr_fit(icesStocks$saiNS,
              nsamp = 1000,
              models = c("Ricker", "Segreg"))

SIM <-
  eqsim_run(
    FIT,
```

```

    bio.years = c(2004, 2013),
    sel.years = c(2004, 2013),
    Fcv = 0.24,
    Fphi = 0.42,
    Blim = 106000,
    Bpa = 200000,
    Fscan = seq(0, 1.2, len = 40)
  )

# extract trajectories
ssbsim <- SIM$rbya$ssb
years <- SIM$rbya$simyears
models <- SIM$rbya$srmodels$model
Ftarget <- SIM$rbya$Ftarget

Fval <- which(Ftarget == 0)
Fval <- which(Ftarget > .3)[1]
x <- ssbsim[Fval,,]
df <- data.frame(year = 1:nrow(x),
                 ssb = c(x),
                 sim = rep(1:ncol(x), each = nrow(x)),
                 model = rep(models, each = nrow(x)))
xyplot(ssb ~ year | model, groups = sim, data = df, type = "l", col = grey(0.5, alpha = 0.5))

fit <- density(x[x>1e-3], from = 0)
plot(fit$x, fit$y*mean(x>1e-3), col="red", type = "l")
lines(x = 0, y = mean(x<=1e-3), type = "h", lwd = 3)

## End(Not run)

```

eqsr_fit

Stock recruitment fitting

Description

Fits one or more stock recruitment relationship to data contained in an FLStock object. If more than one stock recruit relationship is provided, the models are weighted based on smooth AIC weighting (See Buckland et al., 1997).

Usage

```

eqsr_fit(
  stk,
  nsamp = 1000,
  models = c("Ricker", "Segreg", "Bevholt"),
  id.sr = FLCore::name(stk),
  remove.years = NULL,
  rshift = 0
)

```


Arguments

stk	FLStock object
nsamp	Number of samples (iterations) to take from the stock recruitment fit (default is 1000). If 0 (zero) then only the fits to the data are returned and no simulations are made.
models	A character vector containing stock recruitment models to use in the model averaging. User can set any combination of "Ricker", "Segreg", "Bevholt", "Smooth_hockey".
id.sr	A character vector specifying an id or name for the stock recruitment fit being run. The default is to use the slot "name" in the stk parameter is provided
remove.years	A vector specifying the years to remove from the model fitting.
rshift	lag ssb by additional years (default = 0). As an example, for some herring stocks, age 1 (1 winter ring) fish were spawned 2 years previously, in this case, rshift = 1.

Value

A list containing the following objects:

- 'sr.sto' data.frame containing the alpha (a), beta (b), cv and model names. The number of rows correspond to the value set of 'nsamp' in the function call.
- 'sr.det' The parameters in the stock recruitment model corresponding to the "best fit" of any given model.
- 'stk' An FLStock object, same as provided as input by the user.
- 'rby' A data.frame containing the recruitment (rec), spawning stock biomass (ssb) and year used in the fitting of the data.
- 'id.sr' A string containing run name (taken from the 'id.sr' argument)

References

Buckland, S.T., K.P. Burnham & N.H. Augustin (1997). Model selection: An integral part of inference. *Biometrics* 53, 603-618. DOI: [10.2307/2533961](https://doi.org/10.2307/2533961)

See Also

[eqsr_plot](#) plots a simulation of predictive recruitment from the fit, and shows a summary of the contributions of each stock recruitment model to the model average fit.

Examples

```
data(icesStocks)
FIT <- eqsr_fit(icesStocks$saiNS,
               nsamp = 0,
               models = c("Ricker", "Segreg"))

# summary of individual fits
FIT$sr.det
```

```

eqsr_plot(FIT)

# fit a bounded segmented regression
Segreg_bounded <- function(ab, ssb) {
  ab$b <- min_ssb + ab$b
  Segreg(ab, ssb)
}
min_ssb <- min(FLCore::ssb(icesStocks$saiNS))

FIT <- eqsr_fit(icesStocks$saiNS,
               nsamp = 0,
               models = c("Segreg", "Segreg_bounded"))

# summary of individual fits
FIT$sr.det
FIT$sr.det$b[2] + min_ssb
eqsr_plot(FIT)

## Not run:
FIT <- eqsr_fit(icesStocks$saiNS,
               nsamp = 2000,
               models = c("Segreg", "Segreg_bounded"))

# summary of individual fits
FIT$sr.det
eqsr_plot(FIT)

## End(Not run)

```

eqsr_plot

Plot Simulated Predictive Distribution of Recruitment

Description

Plot Simulated Predictive Distribution of Recruitment

Usage

```

eqsr_plot(
  fit,
  n = 20000,
  x.mult = 1.1,
  y.mult = 1.4,
  ggPlot = FALSE,
  Scale = 1
)

```

Arguments

<code>fit</code>	an fitted stock recruit model returned from <code>eqsr_fit</code>
<code>n</code>	Number of random recruitment draws to plot
<code>x.mult</code>	max value for the y axis (ssb) as a multiplier of maximum observed ssb
<code>y.mult</code>	max value for the x axis (rec) as a multiplier of maximum observed rec
<code>ggPlot</code>	Flag, if FALSE (default) plot using base graphics, if TRUE do a ggplot
<code>Scale</code>	Numeric value for scaling variables in plot.

Value

NULL produces a plot

See Also

[eqsr_fit](#) Fits several stock recruitment models to a data set and calculates the proportion contribution of each model based on a bootstrap model averaging procedure.

Examples

```
## Not run:
data(icesStocks)
FIT <- eqsr_fit(icesStocks$saiNS,
               nsamp = 1000,
               models = c("Ricker", "Segreg"))

eqsr_plot(FIT, n = 20000)

# Scale argument only available for ggPlot = TRUE
eqsr_plot(FIT, n = 20000, ggPlot = TRUE, Scale = 1000)

## End(Not run)
```

icesStocks

icesStocks

Description

A list FLStock object for various stocks

Usage

```
icesStocks
```

Format

a list

Author(s)

NA

Source

NA

initial	<i>Get starting values for models</i>
---------	---------------------------------------

Description

Starting values for hockey stick models

Usage

initial(model, data)

Arguments

model	XXX
data	XXX

Value

vector of starting values

llik	<i>the log-likelihood of the recruit function</i>
------	---

Description

the log-likelihood of the recruit function

Usage

llik(param, data, model, logpar = FALSE)

Arguments

param	the model parameters
data	the rec and ssb data
model	the stock recruit model to use
logpar	are the parameters on the log scale

Value

the log-likelihood

loader	<i>Progress function</i>
--------	--------------------------

Description

Non exported function, plots the progress of an iterative procedure using "[=>]", "[==>]", etc.

Usage

loader(p)

Arguments

p	Value
---	-------

Ricker	<i>stock recruitment function</i>
--------	-----------------------------------

Description

stock recruitment function

Usage

Ricker(ab, ssb)

Arguments

ab	the model parameters
ssb	a vector of ssb

Value

log recruitment according to model

Segreg *stock recruitment function*

Description

stock recruitment function

Usage

Segreg(ab, ssb)

Arguments

ab the model parameters
ssb a vector of ssb

Value

log recruitment according to model

segreg2 *stock recruitment function*

Description

stock recruitment function

Usage

segreg2(ab, ssb)

Arguments

ab the model parameters
ssb a vector of ssb

Value

log recruitment according to model

Smooth_hockey	<i>stock recruitment function</i>
---------------	-----------------------------------

Description

stock recruitment function

Usage

```
Smooth_hockey(ab, ssb, gamma = 0.1)
```

Arguments

ab	the model parameters
ssb	a vector of ssb
gamma	a smoother parameter

Value

log recruitment according to model

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