Package 'fishdynr'

January 31, 2015

Type Package

Title fishdynr

Version 1.0

Date 2014-12-26

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Description Fisheries science related population dynamics models

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URL https://github.com/marchtaylor/fishdynr

R topics documented:

1

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cohortSim   *Simulation of a cohort*

Description

`cohortSim` simulates a single cohort

Usage

```
cohortSim(params, t_incr = 1)
```

Arguments

`params`	List of parameters to use in function
`t_incr`	Value to use a time increment (in years). Defaults to 1.

Details

`params` list should contain the following parameters:

- `species` Species name
- `growthFun` Name of growth function (e.g. "growth_VB" is the von Bertalanffy growth function)
- `amax` Maximum age
- `LWa` Length-weight relationship parameter a (weight~a*length^b)
- `LWb` Length-weight relationship parameter b (weight~a*length^b)
- `M` Natural mortality
- `F` Fishing mortality
- `N0` Number of individuals at time 0
- `matFun` Name of maturity function (e.g. "pmat_w" is a logistic function that includes width, w, of quantiles)
- `selectFun` Function to use for gear selection. Determines lengths vulnerable to fishing mortality (e.g. "gillnet" and "knife_edge" functions).
- `...` Other parameters for growth, maturity, and selectivity functions.

Value

A list

Examples

```
data(tilapia)
res <- cohortSim(tilapia, t_incr=.1)
plot(pcap ~ Lt, res, t="l")
plot(Lt ~ t, res, t="l")
plot(Wt ~ t, res, t="l")

plot(Bt ~ t, res, t="l")
lines(SBt ~ t, res, col=2)
```

```
plot(Bt ~ Lt, res, t="l")
lines(SBt ~ Lt, res, col=2)

plot(Yt ~ t, res, t="l")

plot(Nt ~ t, res, t="l", log="y")
lines(Nt.noF ~ t, res, col=2, lty=2)
```

---

gillnet   *gillnet selection*

Description

`gillnet` describes gillnet selection following Millar and Holst (1997). Possible selectivity distributions include normal (fixed width) and lognormal. [Note: others will be added]

Usage

```
gillnet(Lt, mesh_size, mesh_size1, select_dist, select_p1, select_p2)
```

Arguments

Lt	body size
mesh_size	mesh size
mesh_size1	smallest reference mesh size
select_dist	selectivity type ("normal_fixed", "lognormal")
select_p1	selectivity function parameter 1 (see Millar and Holst 1997)
select_p2	selectivity function parameter 2 (see Millar and Holst 1997)

References

Millar, R. B., & Holst, R. (1997). Estimation of gillnet and hook selectivity using log-linear models. ICES Journal of Marine Science: Journal du Conseil, 54(3), 471-477.

Examples

```
data(tilapia)
tilapia$selectFun="gillnet"
mesh_sizes <- c(60, 80, 100, 120)
for(i in seq(mesh_sizes)){
  tilapia$mesh_size <- mesh_sizes[i]
  res <- cohortSim(tilapia, t_incr=0.01)
  if(i == 1) plot(pcap ~ Lt, res, t="n")
  lines(pcap ~ Lt, res, col=i)
}
legend("topleft", legend=mesh_sizes,
  col=seq(mesh_sizes), lty=1,
  title="mesh size [mm]", bty="n"
)
```

growth_soVB	*seasonally oscillating von Bertalanffy growth function*

Description

`growth_soVB` describes the growth as a function of age (t) using the seasonally oscillating von Bertalanffy growth function (Somers 1988).

Usage

```
growth_soVB(Linf, K, t, t0, ts, C)
```

Arguments

Linf	Infinite length
K	growth constant
t	age
t0	(hypothetical) age at length zero
ts	summer point. Time of year (between 0 and 1) when growth oscillation cycle begins (sine wave term becomes positive)
C	oscillation strength. Varies between 0 and 1.

References

Somers, I. F. (1988). On a seasonally oscillating growth function. Fishbyte, 6(1), 8-11.

Examples

```
t <- seq(0,5,0.1)
L <- growth_soVB(Linf=100, K=0.5, t=t, t0=-0.2, ts=0.5, C=0.75)
plot(t, L, t="l")
```

growth_VB	*von Bertalanffy growth function*

Description

`growth_VB` describes the growth as a function of age (t) using the von Bertalanffy growth function

Usage

```
growth_VB(Linf, K, t, t0)
```

Arguments

Linf	Infinite length
K	growth constant
t	age
t0	(hypothetical) age at length zero

Examples

```
t <- seq(0,5,0.1)
L <- growth_VB(Linf=100, K=0.5, t=t, t0=-0.2)
plot(t, L, t="l")
```

---

knife_edge   *knife-edge selection*

Description

`knife_edge` describes knife-edge selection where probability of capture 100% after a minimum defined size. Provides a rough estimate of trawl-type selectivity.

Usage

```
knife_edge(Lt, knife_edge_size)
```

Arguments

Lt   body size

knife_edge_size

knife edge size. Minimum size at capture.

Examples

```
data(tilapia)
tilapia$selectFun="knife_edge"
knife_edge_sizes <- c(20, 25, 30, 35)
for(i in seq(knife_edge_sizes)){
  tilapia$knife_edge_size <- knife_edge_sizes[i]
  res <- cohortSim(tilapia, t_incr=0.01)
  if(i == 1) plot(pcap ~ Lt, res, t="n")
  lines(pcap ~ Lt, res, col=i)
}
legend("topleft", legend=knife_edge_sizes,
  col=seq(knife_edge_sizes), lty=1,
  title="min. size", bty="n"
)
```

---

optim.stockSim   *Optimization of fishing mortality*

Description

Sets up an exploration of optimum fishing policy using the function [stockSim](i.e. optimal time series of fishing mortalities, Ft, in order to maximize time series yield, Yt). The routine is described in further detail in Walters and Martell (2004).

Usage

```
optim.stockSim(Ft = 0, params, nyears = 100, envKt = 1, envSt = 1)
```

Arguments

Ft	time series vector for fishing mortality. If a single value, then the function assumes a constant fishing mortality for the entire simulation (default=0)
params	List of parameters to for the population. Applies a single cohort simulation for the initial population state using cohortSim function. See stockSim for details.
nyears	number of years in the simulation
envKt	time series vector for environmental effects to maximum recruitment (e.g. rmax in srrBH) (default=1).
envSt	time series vector for environmental effects to half maximum recruitment parameter (e.g. beta in srrBH) (default=1).

References

Walters, C. J., Martell, S. J., 2004. Fisheries ecology and management. Princeton University Press.

Examples

```
data(tilapia)
params <- tilapia
params$N0 <- 1e8
params$knife_edge_size <- 20
nyears <- 100
Ft <- rep(0.5, nyears)
envKt <- rep(1, nyears); envKt[30:50] <- 0.5
envSt <- runif(nyears, min=0.5, max=1.5)

# Optimization of Ft (will take some time to reach cost function mimimum)
out <- optim(
  par = Ft,  # initial guess
  fn = optim.stockSim,
  params = params,
  nyears = nyears,
  envKt = envKt,
  envSt = envSt,
  method = "L-BFGS-B",
  lower = 0,
  upper = 3,
  control = list(fnscale=-1, trace=4)
)

# optimum Ft series
plot(out$par, t="l")

# optimum Yt series
tmp <- stockSim(params, nyears=nyears, Ft=out$par, envKt=envKt, envSt=envSt)
plot(Yt ~ t, tmp, t="l")
sum(tmp$Yt/1e6, na.rm=TRUE)

# optimum yield versus stock biomass
plot(Yt ~ Bt, tmp)
fit <- lm(Yt ~ Bt, tmp)
abline(fit)
summary(fit)
```

```
plot(Bt ~ t, tmp, t="l", ylim=c(0, max(tmp$Bt)))
lines(Yt ~ t, tmp, col=2)
```

---

pmat_w   *Probability of maturity logistic function using quartile width*

Description

pmat_w describes the probability of maturity as a function of the size when 50% of the individuals in a population are mature and the width (in size) between 25% and 75% probability of maturity quartiles (after Heino et al. 2002).

Usage

```
pmat_w(Lt, Lmat, wmat)
```

Arguments

Lt   size for probability of maturity calculation

Lmat   size at 50% probability of maturity (i.e. "massive maturity")

wmat   width (in size) between 25% and 75% probability of maturity quartiles

References

Heino M, Dieckmann U, Godo OR (2002) Measuring probabilistic reaction norms for age and size at maturation. Evolution 56: 669-678.

Examples

```
L <- seq(1,20,0.1)
pmat1 <- pmat_w(L, Lmat=10, wmat=5)
pmat2 <- pmat_w(L, Lmat=10, wmat=2)
plot(L, pmat1, t="l", ylab="prob. of maturity")
lines(L, pmat2, lty=2)
legend("bottomright", legend=c("Lmat=10; wmat=5", "Lmat=10; wmat=2"),
 col=1, lty=1:2, bty="n")
```

---

srrBH   *Stock-recruitment relationship (Beverton-Holt type)*

Description

srrBH describes stock-recruitment relationship as the number of recruits resulting from a given spawning biomass.

Usage

```
srrBH(rmax = 1000, beta = 500, SB = 500)
```

Arguments

rmax	maximum recruitment level
beta	parameter describing steepness of relationship. Specifically, beta describes the point where the number of spawned eggs results in half the maximum number of recruits, rmax
SB	spawning biomass of the adult population

Value

Number of recruited individuals

References

Beverton, R. J., Holt, S. J., 1957. On the dynamics of exploited fish populations

Examples

```
SB <- seq(0,1e11,,100)
rmax = 2e8
beta = 1e10
Nrecr <- srrBH(rmax, beta, SB)
plot(SB, Nrecr, t="l", ylim=c(0, rmax))
abline(h=rmax, lty=2, col=8)
lines(x=c(0, beta, beta), y=c(rmax/2, rmax/2, 0), lty=2, col=8)
text(x=0, y=rmax*0.95, labels="rmax", col=8, pos=4)
text(x=beta, y=rmax/2, labels="rmax/2", pos=4, col=8)
text(x=beta, y=0, labels="beta", pos=4, col=8)
```

---

stockSim   *Simulation of a stock*

Description

stockSim simulates a stock using variable fishing mortality and stock recruitment relationship

Usage

```
stockSim(params, nyears = 100, Ft = 0, envKt = 1, envSt = 1)
```

Arguments

params	List of parameters for the population. Applies a single cohort simulation for the initial population state using cohortSim function
nyears	number of years in the simulation
Ft	time series vector for fishing mortality. If a single value, then the function assumes a constant fishing mortality for the entire simulation (default=0)
envKt	time series vector for environmental effects to maximum recruitment (e.g. rmax in srrBH) (default=1).
envSt	time series vector for environmental effects to half maximum recruitment parameter (e.g. beta in srrBH) (default=1).

Details

params list should contain the following parameters:

- species Species name
- growthFun Name of growth function (e.g. "growth_VB" is the von Bertalanffy growth function)
- amax Maximum age
- LWa Length-weight relationship parameter a (weight~a*length^b)
- LWb Length-weight relationship parameter b (weight~a*length^b)
- M Natural mortality
- F Fishing mortality
- N0 Number of individuals at time 0
- matFun Name of maturity function (e.g. "pmat_w" is a logistic function that includes width, w, of quantiles)
- selectFun Function to use for gear selection. Determines lengths vulnerable to fishing mortality (e.g. "gillnet" and "knife_edge" functions).
- srrFun Stock-recruitment relationship function (e.g. "srrBH").
- fec Number of eggs produced per weight [g] of mature female (For use in srrFun).
- ... Other parameters for growth, maturity, and selectivity functions.

For fitting an optimal time series of fishing mortalities, Ft, see optim.stockSim (Walters and Martell, 2004).

Value

A list

- Btc matrix. Stock biomass by time (rows) and cohort (columns).
- Ytc matrix. Fishery yield by time (rows) and cohort (columns).
- Bt vector. Stock biomass by time.
- Yt vector. Fishery yield by time.
- Nt vector. Stock size (in numbers) by time.
- Ct vector. Fishery catch (in numbers) by time.

References

Walters, C. J., Martell, S. J., 2004. Fisheries ecology and management. Princeton University Press.

Examples

```
data(tilapia)
params <- tilapia
params$knife_edge_size <- 20
params$N0 <- 1e8
nyears <- 50
Ft <- rep(0.5, nyears)
envKt <- rep(1, nyears); envKt[20:35] <- 0.5
envSt <- runif(nyears, min=0.5, max=1.5)
tmp <- stockSim(Ft=Ft, params=params, nyears=nyears, envKt=envKt, envSt=envSt)
plot(tmp$Bt, t="l")
plot(tmp$Yt, t="l")
sum(tmp$Yt/1e6, na.rm=TRUE)
```

tilapia	*Parameter list for Oreochromis niloticus (Nile tilapia)*

Description

The `tilapia` data set contains a list of parameters used by other functions in the `fishdynr` package.

- species. Species name
- growthFun. Name of growth function ("growth_VB" is von Bertalanffy growth function)
- K. Growth constant (for use in von Bertalanffy growth function))
- Linf. Infinite length (for use in von Bertalanffy growth function)
- t0. (hypothetical) time when length equals zero (for use in von Bertalanffy growth function)
- amax. Maximum age
- LWa. Length-weight relationship parameter a (weight~a*length^b)
- LWb. Length-weight relationship parameter b (weight~a*length^b)
- M. Natural mortality
- F. Fishing mortality
- N0. Number of individuals at time 0
- matFun. Name of maturity function ("pmat_w" is a logistic function that includes width, w, of quantiles)
- Lmat. Length at maturity (i.e. where probability of being mature is 50 (for use in "pmat_w" function)
- wmat. Width of length between 25 of transition from immature to mature (for use in "pmat_w" function)
- fec. Number of eggs produced per weight [g] of mature female
- selectFun. Function to use for gear selection. Determines lengths vulnerable to fishing mortality.
- select_p1. Parameter 1 used in "gillnet" selectivity function
- select_p2. Parameter 2 used in "gillnet" selectivity function
- mesh_size. Mesh size [streched length in mm] used in "gillnet" selectivity function
- mesh_size1. Mesh size of smallest reference net used in fitting "gillnet" selectivity function
- select_dist. Distribution type used in "gillnet" selectivity function
- knife_edge_size. Minimum length selected by "knife_edge" selectivity function
- srrFun. Function used for stock-recruitment relationship
- rmax. Maximum recruitment parameter used in "srrBH" stock-recruitment (Beverton-Holt)
- beta. "beta" parameter used in "srrBH" stock-recruitment (Beverton-Holt)

Usage

```
data(tilapia)
```

Format

A list containing parameters used on other `fishdynr` functions

Examples

```
data(tilapia)
res <- cohortSim(tilapia, t_incr=0.1)
plot(Lt ~ t, res, t="l")
```

---

ypr   *Yield-per-recruit*

Description

Sets up an yield-per-recruit exploration by adjusting fishing mortality and selectivity using the cohortSim function

Usage

```
ypr(params, adj.params)
```

Arguments

params   List of parameters for the population. Applies a single cohort simulation for the
                initial population state using cohortSim function

adj.params   List of 2 parameters combinations to use for yield per recruit analysis. In
                the case of trawl-type selectivity, these should be levels for F and knife-edge
                length at capture. For gillnet-type selectivity, these should be levels for F and
                mesh_size.

Value

A list of parameter combinations used in the yield-per-recruit exploration, plus matrix output for
yield (Y) and spawning stock biomass (SB) given the parameter combinations (adj.params.comb).

Examples

```
# Trawl-type
data(tilapia)
n <- 30
adj.params <- list(F=seq(0,3,,n), knife_edge_size=seq(0,tilapia$Linf,,n))
res <- ypr(params=tilapia, adj.params)
pal <- colorRampPalette(c(
 rgb(1,0.5,0.5), rgb(1,1,0.5), rgb(0.5,1,1), rgb(0.5,0.5,1)
))
op <- par(mfcol=c(1,2))
# Yield
image(x=res$F, y=res$knife_edge, z=res$Y, col=pal(100))
contour(x=res$F, y=res$knife_edge, z=res$Y, add=TRUE)
mtext("Yield", line=0.5, side=3)
# Relative spawning biomass
SB_F0 <- res$SB[which(res$F==0),1]
image(x=res$F, y=res$knife_edge, z=res$SB/SB_F0, col=pal(100))
contour(x=res$F, y=res$knife_edge, z=res$SB/SB_F0, add=TRUE)
mtext("Rel. Spawning Biomass", line=0.5, side=3)
par(op)
```

```
# Gillnet-type
data(tilapia)
tilapia$selectFun <- "gillnet"
n <- 30
adj.params <- list(F=seq(0,3,,n), mesh_size=seq(60,160,,n))
res <- ypr(params=tilapia, adj.params)
pal <- colorRampPalette(c(
 rgb(1,0.5,0.5), rgb(1,1,0.5), rgb(0.5,1,1), rgb(0.5,0.5,1)
))
op <- par(mfcol=c(1,2))
# Yield
image(x=res$F, y=res$mesh_size, z=res$Y, col=pal(100))
contour(x=res$F, y=res$mesh_size, z=res$Y, add=TRUE)
mtext("Yield", line=0.5, side=3)
# Relative spawning biomass
SB_F0 <- res$SB[which(res$F==0),1]
image(x=res$F, y=res$mesh_size, z=res$SB/SB_F0, col=pal(100))
contour(x=res$F, y=res$mesh_size, z=res$SB/SB_F0, add=TRUE)
mtext("Rel. Spawning Biomass", line=0.5, side=3)
par(op)
```

Index