

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>

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| | |
|-----------|-------------------------------|
| cohortSim | <i>Simulation of a cohort</i> |
|-----------|-------------------------------|

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 ($\text{weight} \sim a * \text{length}^b$)
- LWb Length-weight relationship parameter b ($\text{weight} \sim a * \text{length}^b$)
- 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="1")
plot(Lt ~ t, res, t="1")
plot(Wt ~ t, res, t="1")

plot(Bt ~ t, res, t="1")
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 | <i>seasonally oscillating von Bertalanffy growth function</i> |
|-------------|---|

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 | <i>von Bertalanffy growth function</i> |
|-----------|--|

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 | <i>knife-edge selection</i> |
|------------|-----------------------------|

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 | <i>Optimization of fishing mortality</i> |
|----------------|--|

Description

Sets up an exploration of optimum fishing policy using the function [stockSim](#) (i.e. optimal time series of fishing mortalities, F_t , in order to maximize time series yield, Y_t). 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 minimum)
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="1", 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 ($\text{weight} \sim a \cdot \text{length}^b$)
- LWb Length-weight relationship parameter b ($\text{weight} \sim a \cdot \text{length}^b$)
- 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, F_t , 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 ($\text{weight} \sim a \cdot \text{length}^b$)
- LWb. Length-weight relationship parameter b ($\text{weight} \sim a \cdot \text{length}^b$)
- 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 [stretched 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 | <i>Yield-per-recruit</i> |
|-----|--------------------------|

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 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. |

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)
```

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