

# Package ‘fishdynr’

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**License** MIT + file LICENSE

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cohortSim	<i>Simulation of a cohort</i>
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## 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="1")
lines(SBt ~ Lt, res, col=2)

plot(Yt ~ t, res, t="1")

plot(Nt ~ t, res, t="1", log="y")
lines(Nt.noF ~ t, res, col=2, lty=2)

```

fecW\_LM

*Fecundity and function of weight***Description**

fecW\_LM is a linear model describing fecundity (number of eggs) as a function of individual weight

**Usage**

```
fecW_LM(fec_a = 0, fec_b = 1, Wt = 500)
```

**Arguments**

fec_a	intercept
fec_b	slope
Wt	individual weight (from cohortSim function)

**Value**

Number of eggs per individual

**Examples**

```

data(tilapia)
res <- cohortSim(tilapia, t_incr=0.1)
plot(Neggst ~ Wt, res) # Number of eggs as a function of ind. weight
plot(res$t, res$Neggst*res$pmat*res$Nt) # total population fecundity by age

```

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	<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")
```

---

growth_VB2	<i>von Bertalanffy growth function (using L0)</i>
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## Description

growth\_VB2 describes the growth as a function of age (t) using the von Bertalanffy growth function. The function differs slightly from [growth\\_VB](#) by using L0 instead of t0 to describe the growth function origin

## Usage

```
growth_VB2(Linf, K, t, L0)
```

**Arguments**

Linf	Infinite length
K	growth constant
t	age
L0	(hypothetical) length at time zero

**Examples**

```
t <- seq(0,5,0.1)
L <- growth_VB2(Linf=100, K=0.5, t=t, L0=10)
plot(t, L, t="l", ylim=c(0,110), xaxs="i", yaxs="i")
points(0,10); abline(h=100, lty=2, col=8)
```

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knife_edge	<i>knife-edge selection</i>
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**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"
)
```

---

logisticSelect	<i>logistic selection</i>
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### Description

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

### Usage

```
logisticSelect(Lt, L50, wqs)
```

### Arguments

Lt	body size
L50	length at first capture (i.e. where prob. of capture equals 50%)
wqs	width between 25% and 75% probability of capture

### Examples

```
data(tilapia)
tilapia$selectFun="logisticSelect"
tilapia$L50 <- 20
WQS <- c(0, 3, 6)
COL <- rainbow(3)
for(i in seq(WQS)){
  tilapia$wqs <- WQS[i]
  res <- cohortSim(tilapia, t_incr=0.01)
  if(i == 1) plot(pcap ~ Lt, res, t="n")
  lines(pcap ~ Lt, res, col=COL[i])
}
legend("bottomright", legend=paste(WQS, c(" ('knife-edge')", "", "")), sep=""),
  col=COL, lty=1,
  title="Width between 25% and 75%", bty="n"
)
lines(c(0,tilapia$L50,tilapia$L50), c(0.5,0.5,0), col=1, lty=2)
text(20,.5,bquote("L"[50]), pos=4, col=1, font=1)
```

---

optim.stockSim	<i>Optimization of fishing mortality</i>
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### 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, env_at = 1, env_bt = 1,
  opt = "sum", disc.rate = 0.02)
```

## 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 <a href="#">cohortSim</a> function. See <a href="#">stockSim</a> for details.
nyears	number of years in the simulation
env_at	time series vector for environmental effects to maximum recruitment (e.g. <a href="#">srrFecBH_a</a> in <a href="#">srrFecBH</a> ) (default=1).
env_bt	time series vector for environmental effects to maximum recruitment (e.g. <a href="#">srrFecBH_b</a> in <a href="#">srrFecBH</a> ) (default=1).
opt	what should be optimized ("sum", "sum.log", "sum.disc")
disc.rate	discount rate (default = 0.02)

## References

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

## Examples

```
set.seed(1)
data(tilapia)
params <- tilapia
params$knife_edge_size <- 20
params$N0 <- 1e9
nyears <- 50
Ft <- rep(0.5, nyears)
env_at <- runif(nyears, min=0.5, max=1.5)
env_bt <- rep(1, nyears); env_bt[20:35] <- 0.5

# 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,
  env_at = env_at,
  env_bt = env_bt,
  opt = "sum.log", # optimize the sum of log yield
  method = "L-BFGS-B",
  lower = 0,
  upper = 2,
  control = list(fnscale=-1, trace=4)
)

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



```
# optimum Yt series
tmp <- stockSim(params, nyears=nyears, Ft=out$par, env_at=env_at, env_bt=env_bt)
plot(Yt ~ t, tmp, t="l")
sum(tmp$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	<i>Stock-recruitment relationship (Beverton-Holt type)</i>
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---

## 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)
```

---

srrFecBH	<i>Stock-recruitment relationship using fecundity (Beverton-Holt type)</i>
----------	--

---

**Description**

srrFecBH describes stock-recruitment relationship as the number of recruits resulting from a given number of eggs produced by the population.

**Usage**

```
srrFecBH(srrFecBH_a, srrFecBH_b, neggs)
```

**Arguments**

srrFecBH_a	long-term mean survival parameter
srrFecBH_b	carrying capacity parameter
neggs	number of eggs spawned

**Value**

Number of recruited individuals

**References**

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

**Examples**

```
n <- 100
neggs <- seq(0,1e8,,n)
srrFecBH_a = 0.2
srrFecBH_b = 1e7/srrFecBH_a
Nrecr <- srrFecBH(srrFecBH_a, srrFecBH_b, neggs)
plot(neggs, Nrecr, t="l", ylim=c(0, srrFecBH_b*srrFecBH_a))
abline(0, srrFecBH_a, col=8, lty=2)
abline(h=srrFecBH_b*srrFecBH_a, lty=2, col=8)
```

---

stockSim	<i>Simulation of a stock</i>
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---

**Description**

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

**Usage**

```
stockSim(params, nyears = 100, Ft = 0, env_at = 1, env_bt = 1)
```

## Arguments

params	List of parameters for the population. Applies a single cohort simulation for the initial population state using <a href="#">cohortSim</a> 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)
env_at	time series vector for environmental effects to maximum recruitment (e.g. <a href="#">srrFecBH_a</a> in <a href="#">srrFecBH</a> ) (default=1).
env_bt	time series vector for environmental effects to half maximum recruitment parameter (e.g. <a href="#">srrFecBH_b</a> in <a href="#">srrFecBH</a> ) (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 ( $\text{weight} \sim a * \text{length}^b$ )
- 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).
- srrFun Stock-recruitment relationship function (e.g. "srrFecBH").
- fec Number of eggs produced per weight [g] of mature female (For use in [srrFecFun](#)).
- ... 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 <- 1e9
nyears <- 50
Ft <- rep(0.5, nyears)
env_at <- runif(nyears, min=0.5, max=1.5)
env_bt <- rep(1, nyears); env_bt[20:35] <- 0.5
tmp <- stockSim(Ft=Ft, params=params, nyears=nyears, env_at=env_at, env_bt=env_bt)
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="1")
```

---

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

<code>params</code>	List of parameters for the population. Applies a single cohort simulation for the initial population state using <code>cohortSim</code> function
<code>adj.params</code>	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)
```

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