

Package: multiStockassessment (via r-universe)

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Title Fitting Multiple State-Space Assessment Models

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Description Fitting multiple SAM models.

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Depends stockassessment (>= 0.12.2)

Imports TMB (>= 1.9.1), stockassessment (>= 0.12.4), grDevices, graphics, methods, stats, Matrix (>= 1.6-3)

LinkingTo TMB (>= 1.9.1), RcppEigen, stockassessment (>= 0.12.4)

Suggests parallel

URL https://github.com/calbertsen/multi_SAM

LazyData TRUE

Encoding UTF-8

BugReports https://github.com/calbertsen/multi_SAM/issues

Remotes github::fishfollower/SAM/stockassessment@refpoint

RoxygenNote 7.2.3

Repository <https://calbertsen.r-universe.dev>

RemoteUrl https://github.com/calbertsen/multi_SAM

RemoteRef shared_obs

RemoteSha d8692fe1c695cb1ca01277eaf769258922f0691a

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addTrans	<i>Add transparency to a color</i>
----------	------------------------------------

Description

Function to add transparency to a color

Usage

```
addTrans(name, alpha = 1)
```

Arguments

name	Name of color
alpha	Alpha level

Value

A hex color string

Author(s)

Christoffer Moesgaard Albertsen

c.msam	<i>Collect msam objects</i>
--------	-----------------------------

Description

Collect a number of msam objects into an msamset

Usage

```
## S3 method for class 'msam'  
c(...)
```

Arguments

...	msam objects
-----	--------------

Value

An msamset

catchplot.msam *Catch plot*

Description

Catch plot

Usage

```
## S3 method for class 'msam'
catchplot(fit, obs.show = TRUE, drop = 0, ...)
```

Arguments

fit	msam object
obs.show	Show observations in plot?
drop	Number of years to drop from the end
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

catchtable.msam *Catch Table*

Description

Catch Table

Usage

```
## S3 method for class 'msam'
catchtable(fit, obs.show = FALSE, returnList = FALSE, ...)
```

Arguments

fit	msam object
obs.show	should observed catches be included?
returnList	If true, a list of matrices is returned
...	Other parameters

Details

Table of predicted catch in weight

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

coef.msam

Extract parameter estimates of msam object

Description

Extract parameter estimates of msam object

Usage

```
## S3 method for class 'msam'  
coef(object, ...)
```

Arguments

object	msam object
...	extra arguments not used

Value

a vector of parameter estimates

Author(s)

Christoffer Moesgaard Albertsen

corplot.msam

Correlation and partial correlation plot between survival processes

Description

Correlation and partial correlation plot between survival processes

Usage

```
## S3 method for class 'msam'  
corplot(object, ...)
```

Arguments

object msam object
 ... Other parameters not currently used

Value

A matrix of correlations (lower triangular) and partial correlations (upper triangular)

Author(s)

Christoffer Moesgaard Albertsen

deterministicReferencepoints.msam
Deterministic reference points

Description

Deterministic reference points

Usage

```
## S3 method for class 'msam'
deterministicReferencepoints(
  fit,
  referencepoints,
  catchType = "catch",
  nYears = 300,
  Fsequence = seq(0, 2, len = 50),
  aveYears = lapply(fit, function(x) max(x$data$years) + (-9:0)),
  selYears = lapply(fit, function(x) max(x$data$years)),
  biasCorrect = FALSE,
  newton.control = list(),
  ...
)
```

Arguments

fit
 referencepoints

catchType

nYears

Fsequence

aveYears

selYears
biasCorrect
newton.control
...

Author(s)

Christoffer Moesgaard Albertsen

faytable.msam *F-at-age Table*

Description

F-at-age table

Usage

```
## S3 method for class 'msam'  
faytable(fit, returnList = FALSE, ...)
```

Arguments

<code>fit</code>	msam object
<code>returnList</code>	If true, a list of matrices is returned
<code>...</code>	Other parameters

Details

Table of estimated age-wise fishing mortality

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

fbarplot.msam *Fbar plot for msam object*

Description

Fbar plot for msam object

Usage

```
## S3 method for class 'msam'
fbarplot(
  fit,
  partial = FALSE,
  drop = 0,
  page = NULL,
  plot = TRUE,
  effectiveF = TRUE,
  add = FALSE,
  ex = numeric(0),
  ...
)
```

Arguments

fit	fitted msam object
partial	Should F for each age in Fbar range be added?
drop	Number of years to drop from the end
page	List of ages to be used per stock for partial = true. Defaults to all ages used to calculate Fbar.
...	plotting arguments

Author(s)

Christoffer Moesgaard Albertsen

fbartable.msam *Fbar Table*

Description

Fbar Table

Usage

```
## S3 method for class 'msam'
fbartable(fit, ...)
```


Arguments

fit	msam object
...	Other parameters

Details

Table of estimated average fishing mortalities

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

fitplot.msam	<i>Fit plot</i>
--------------	-----------------

Description

Fit plot

Usage

```
## S3 method for class 'msam'
fitplot(
  fit,
  stock,
  log = TRUE,
  fleets = lapply(attr(fit, "m_data")$sam, function(x) unique(x$aux[, "fleet"])),
  ...
)
```

Arguments

fit	msam object
stock	Stock to plot for
log	Plot on log-scale?
fleets	Fleets to plot
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

fselectivityplot.msam *F selectivity plot*

Description

F selectivity plot

Usage

```
## S3 method for class 'msam'
fselectivityplot(
  fit,
  cexAge = 1,
  type = c("bar", "line"),
  col = .plotcols.crp(length(fit)),
  ...
)
```

Arguments

fit	msam object
cexAge	size of Age label
type	bar for separate bar plots, line for overlaid line plots
col	Line colors for line plot
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

gen2PCA *Prepare allele matrix for PCA analysis*

Description

Prepare allele matrix for PCA analysis

Usage

```
gen2PCA(x, alleleMeans)
```

Arguments

x	output from linkread.gen
alleleMeans	Mean allele frequencies to impute. Is calculated if missing.

Value

allele data for PCA analysis

Author(s)

Christoffer Moesgaard Albertsen

grad

Calculate gradient of a function

Description

Calculate gradient of a function

Usage

```
grad(  
  func,  
  x,  
  h = abs(1e-04 * x) + 1e-04 * (abs(x) < sqrt(.Machine$double.eps/7e-07)),  
  ...  
)
```

Arguments

func	function
x	parameter values
...	passed to func

Value

gradient vector

Author(s)

Christoffer Moesgaard Albertsen

holdout	<i>Holdout forecast for validation</i>
---------	--

Description

Holdout forecast for validation

Usage

```
holdout(fit, nYears, ...)

## S3 method for class 'msam'
holdout(fit, nYears, forecastYears = 1, ncores = 1, ...)
```

Arguments

fit	msam fit
nYears	Number of years to hold out
...	Arguments passed to modelforecast

Value

A model forecast

Author(s)

Christoffer Moesgaard Albertsen

jacobian	<i>Calculate jacobian of a function</i>
----------	---

Description

Calculate jacobian of a function

Usage

```
jacobian(
  func,
  x,
  h = abs(1e-04 * x) + 1e-04 * (abs(x) < sqrt(.Machine$double.eps/7e-07)),
  ...
)
```

Arguments

func	function
x	parameter values
...	passed to func

Value

jacobian matrix

Author(s)

Christoffer Moesgaard Albertsen

jit.msam

Jitter runs

Description

Jitter runs

Usage

```
## S3 method for class 'msam'
jit(
  fit,
  nojit = 10,
  par = NULL,
  sd = 0.25,
  ncores = parallel::detectCores() - 1,
  silent = TRUE
)
```

Arguments

fit	a fitted model object as returned from sam.fit
nojit	a list of vectors. Each element in the list specifies a run where the fleets mentioned are omitted
par	initial values to jitter around. The default ones are returned from the defpar function
sd	the standard deviation used to jitter the initial values (most parameters are on a log scale, so similar to cv)
ncores	the number of cores to attempt to use

Details

...

Value

A "samset" object, which is basically a list of sam fits

lifeexpectancyplot.msam

Life expectancy plot

Description

Life expectancy plot

Usage

```
## S3 method for class 'msam'
lifeexpectancyplot(
  fit,
  atRecruit = TRUE,
  col = .plotcols.crp(length(fit)),
  ylimAdd = max(sapply(fit, function(x) x$conf$maxAge)),
  ...
)
```

Arguments

fit	msam object
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

lifeexpectancytable.msam

SSB Table

Description

Life expectancy Table

Usage

```
## S3 method for class 'msam'
lifeexpectancytable(fit, atRecruit = TRUE, ...)
```

Arguments

fit msam object
 ... Other parameters

Details

Table of estimated life expectancy.

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

modelforecast.msam *Forecast of a multiStockassessment*

Description

Forecast of a multiStockassessment

Usage

```
## S3 method for class 'msam'
modelforecast(
  fit,
  constraints = NULL,
  fscale = NULL,
  catchval = NULL,
  fval = NULL,
  nextssb = NULL,
  landval = NULL,
  nosim = 1000,
  year.base = unlist(min(sapply(fit, function(x) max(x$data$years)))),
  ave.years = lapply(fit, function(x) max(x$data$years) + (-9:0)),
  overwriteBioModel = FALSE,
  rec.years = lapply(fit, function(x) numeric(0)),
  label = NULL,
  overwriteSelYears = NULL,
  deterministicF = FALSE,
  processNoiseF = FALSE,
  fixedFdeviation = FALSE,
  useFHessian = FALSE,
  resampleFirst = !is.null(nosim) && nosim > 0,
  resampleParameters = FALSE,
```

```

    useModelLastN = TRUE,
    fixFirstN = FALSE,
    customSel = NULL,
    lagR = FALSE,
    splitLD = FALSE,
    addTSB = FALSE,
    biasCorrect = FALSE,
    returnAllYears = FALSE,
    returnObj = FALSE,
    progress = nosim > 0 && ncores == 1,
    estimate = median,
    silent = TRUE,
    newton_config = NULL,
    custom_pl = NULL,
    useNonLinearityCorrection = (nosim > 0 && !deterministicF),
    ncores = 1,
    ...
)

```

Arguments

```

fit
fscale
catchval
fval
nextssb
landval
nosim
year.base
ave.years
rec.years
label
overwriteSelYears

```

```

deterministicF
processNoiseF
customSel
lagR
splitLD
addTSB
biasCorrect
returnAllYears

```

Value

```
msamforecast
```

modeltable.msam	<i>Model table</i>
-----------------	--------------------

Description

Model table

Usage

```
## S3 method for class 'msam'  
modeltable(fits, ...)
```

Arguments

fits	msam object
...	extra arguments

Value

A matrix of model information

Author(s)

Christoffer Moesgaard Albertsen

modeltable.msamset	<i>Model table</i>
--------------------	--------------------

Description

Model table

Usage

```
## S3 method for class 'msamset'  
modeltable(fits, ...)
```

Arguments

fits	msamset object
...	extra arguments

Value

A matrix of model information

Author(s)

Christoffer Moesgaard Albertsen

multisam.fit

*Fit multiple SAM models with correlations***Description**

Fit multiple SAM models with correlated survival processes.

Usage

```
multisam.fit(  
  x,  
  formula = ~-1,  
  corStructure = suggestCorStructure(x, nAgeClose = 0),  
  usePartialCors = TRUE,  
  newtonsteps = 0,  
  rm.unidentified = FALSE,  
  nlminb.control = list(trace = 1, eval.max = 20000, iter.max = 20000),  
  lower = NULL,  
  upper = NULL,  
  starting = NULL,  
  community_formula = ~-1,  
  community_type = 1,  
  shared_data = NULL,  
  shared_keys = character(0),  
  shared_selectivity = 0,  
  shared_seasonality = 0,  
  shared_stockrecruitment = FALSE,  
  shared_oneFScalePars = FALSE,  
  shared_initN = FALSE,  
  shared_fleetParameters = c(),  
  shared_proportionalHazard = NULL,  
  shared_phmap = NULL,  
  skip_stock_observations = FALSE,  
  stockAreas = matrix(1, 1, length(x)),  
  genetics_data = prepareGenetics(),  
  genetics_dirichlet = FALSE,  
  genetics_spatialAge = TRUE,  
  genetics_independentStocks = TRUE,  
  initN = 0,  
  initF = FALSE,  
  parlist = NULL,  
  run = TRUE,  
  symbolicAnalysis = FALSE,
```

```

    fullDerived = FALSE,
    mohn = FALSE,
    ...
  )

```

Arguments

x	samset from the stockassessment package
formula	formula for covariance matrix covariates (See Details)
corStructure	symmetric boolean matrix. True if a (partial) correlation in survival should be fixed to zero between the corresponding age/stock combination
usePartialCors	if TRUE corStructure describes the partial correlations. If FALSE corStructure describes correlations.
newtonsteps	As for stockassessment::sam.fit
lower	As for stockassessment::sam.fit
upper	As for stockassessment::sam.fit
...	Additional arguments passed to TMB::MakeADFun

Details

Function to fit a multi-stock SAM model (Albertsen et al., 2018).

Value

A list of class msam and samset

Author(s)

Christoffer Moesgaard Albertsen

References

Albertsen, C. M., Nielsen, A. and Thygesen, U. H. (2018) Connecting single-stock assessment models through correlated survival. *ICES Journal of Marine Science*, 75(1), 235-244. doi: 10.1093/icesjms/fsx114

Examples

```

if(require(stockassessment)){
  data(nscodData)
  data(nscodConf)
  data(nscodParameters)
  fit <- sam.fit(nscodData, nscodConf, nscodParameters)
  fits <- c(fit)
  obj <- multisam.fit(fits)
}

```

ntable.msam

N Table

Description

N Table

Usage

```
## S3 method for class 'msam'  
ntable(fit, returnList = FALSE, ...)
```

Arguments

fit	msam object
returnList	If true, a list of matrices is returned
...	Other parameters

Details

Table of estimated numbers-at-age

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

parplot.msam

Parameter plot

Description

Parameter plot

Usage

```
## S3 method for class 'msam'  
parplot(fit, cor.report.limit = 0.95, ...)
```

Arguments

fit msam object
cor.report.limit
 Not used
... extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

partable.msam *Parameter table*

Description

Parameter table

Usage

```
## S3 method for class 'msam'  
partable(fit, ...)
```

Arguments

fit msam object
... Other parameters

Details

Table of estimated parameters

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

`plotit.msam`*Function to actually do the plotting*

Description

Function to actually do the plotting

Usage

```
## S3 method for class 'msam'
plotit(
  fit,
  what,
  x = lapply(attr(fit, "m_data")$sam, function(x) x$years),
  ylab = what,
  xlab = "Years",
  ex = numeric(0),
  trans = function(x) x,
  add = FALSE,
  ci = TRUE,
  cicol = gray(0.5, alpha = 0.5),
  addCI = NA,
  drop = 0,
  unnamed.basename = "current",
  xlim = NULL,
  ciAlpha = 0.3,
  col = .plotcols.crp(length(fit) + 1),
  extraLabel = NULL,
  addTotal = FALSE,
  onlyTotal = FALSE,
  legend.pos = "bottom",
  stocks = seq_len(length(fit) + addTotal),
  ...
)

## S3 method for class 'msamforecast'
plotit(
  fit,
  what,
  x = fit$data$years,
  ylab = what,
  xlab = "Years",
  ex = numeric(0),
  trans = exp,
  add = FALSE,
  ci = TRUE,
  cicol = gray(0.5, alpha = 0.5),
```

```

    addCI = NA,
    drop = 0,
    unnamed.basename = "current",
    xlim = NULL,
    addTotal = FALSE,
    onlyTotal = FALSE,
    ...
)

```

Arguments

fit	msam fit
what	variable to plot
x	x-axis values
ylab	y-axis label
xlab	x-axis label
ex	extra years to add
trans	function to transform variable to plot
add	If false a new plot is created. If true everything is added to the previous plot-
ci	Add confidence intervals?
cicol	Color of confidence intervals
addCI	Not used
drop	Number of years to drop from the end
unnamed.basename	not used
xlim	x-axis limits. If null, the range of x is used.
ciAlpha	Alpha channel value of confidence interval color
col	line colors
extraLabel	Not used
...	Other arguments

```
print.msam          Print result from multisam.fit
```

Description

Print output from multisam.fit

Usage

```
## S3 method for class 'msam'
print(x, ...)
```

Arguments

x A msam object
 ... Other parameters passes to logLik

print.msamcoef *Print msam coef object*

Description

Print msam coef object

Usage

```
## S3 method for class 'msamcoef'
print(x, ...)
```

Arguments

x msamcoef object
 ... Not used

Author(s)

Christoffer Moesgaard Albertsen

read.gen *Read genepop data files*

Description

Read genepop data files

Usage

```
read.gen(
  f,
  pop.names,
  sort.loci = FALSE,
  sort.individuals = FALSE,
  NAlleleKeep = NA
)
```


Arguments

f file name
pop.names population names. If missing, the ID of the last individual is used
sort.loci Should loci be sorted by names?
sort.individuals Should individuals be sorted by id?

Value

an allele array

Author(s)

Christoffer Moesgaard Albertsen

replot.msam *Recruitment plot*

Description

Recruitment plot

Usage

```
## S3 method for class 'msam'  
replot(fit, ...)
```

Arguments

fit msam object
... extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

rectable.msam	<i>Recruitment Table</i>
---------------	--------------------------

Description

Recruitment Table

Usage

```
## S3 method for class 'msam'  
rectable(fit, ...)
```

Arguments

fit	msam object
...	Other parameters

Details

Table of estimated recruitment to the fisheries.

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

simulate.msam	<i>Simulate from a msam object</i>
---------------	------------------------------------

Description

Simulate from a msam object

Usage

```
## S3 method for class 'msam'  
simulate(  
  object,  
  nsim = 1,  
  seed = NULL,  
  full.data = TRUE,  
  ready.to.fit = FALSE,  
  ...  
)
```

Arguments

object	msam object result from multisam.fit
nsim	Number of simulations
seed	random number seed
full.data	should a full data set for sam.fit be returned?
...	Other arguments not used

Value

a list of lists.

Author(s)

Christoffer Moesgaard Albertsen

 srplot.msam

Stock-recruitment plot

Description

Stock-recruitment plot

Usage

```
## S3 method for class 'msam'
srplot(
  fit,
  textcol = "red",
  add = FALSE,
  col = .plotcols.crp(length(fit)),
  ...
)
```

Arguments

fit	msam object
textcol	Text color
add	Should the figure be added to a current plot?
col	Line colors
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

ssbplot.msam	<i>SSB plot</i>
--------------	-----------------

Description

SSB plot

Usage

```
## S3 method for class 'msam'  
ssbplot(fit, ...)
```

Arguments

fit	msam object
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

ssbtable.msam	<i>SSB Table</i>
---------------	------------------

Description

SSB Table

Usage

```
## S3 method for class 'msam'  
ssbtable(fit, ...)
```

Arguments

fit	msam object
...	Other parameters

Details

Table of estimated spawning stock biomasses.

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

suggestCorStructure *Suggest correlation structure*

Description

Construct valid (band) correlation structures for multisam.fit

Usage

```
suggestCorStructure(  
  x,  
  nAgeClose = 1,  
  noConnection = FALSE,  
  onlyCloseAge = TRUE,  
  noCorInArea = TRUE,  
  onlyCorInArea = FALSE,  
  noCorBetween = matrix(0, 0, 2)  
)
```

Arguments

x	a samset
nAgeClose	Number of close ages to correlate
noConnection	If TRUE, no correlations
onlyCloseAge	If TRUE, age classes no less than nAgeClose are un-correlated
noCorInArea	If TRUE, age classes in same area/stock are un-correlated
onlyCorInArea	If TRUE, only age classes in same area/stock are correlated
noCorBetween	matrix of area/stock numbers that should not be correlated

Value

A boolean matrix

Author(s)

Christoffer Moesgaard Albertsen

summary.msam	<i>Summary of msam object</i>
--------------	-------------------------------

Description

Summary of msam object

Usage

```
## S3 method for class 'msam'
summary(object, returnList = FALSE, digits = c(0, 0, 3), ...)
```

Arguments

object	msam object
returnList	If true, a list of table is returned
digits	digits for rounding output. Vector of length 3 corresponding to recruitment, ssb, and fbar.
...	not used

Value

a summary table

Author(s)

Christoffer Moesgaard Albertsen

tableit	<i>Table helper</i>
---------	---------------------

Description

Table helper

Usage

```
tableit(
  fit,
  what,
  x = lapply(attr(fit, "m_data")$sam, function(x) x$years),
  trans = function(x) x,
  returnList = FALSE,
  ...
)
```

```
## S3 method for class 'msam'
tableit(
  fit,
  what,
  x = lapply(attr(fit, "m_data")$sam, function(x) x$years),
  trans = function(x) x,
  returnList = FALSE,
  addTotal = FALSE,
  ...
)
```

Arguments

fit	msam object
what	quoted name of what to extract
x	rownames of table
trans	function to be applied
returnList	If true, a list of matrices is returned
...	extra arguments not used

Value

matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

tsbplot.msam	<i>TSB plot</i>
--------------	-----------------

Description

TSB plot

Usage

```
## S3 method for class 'msam'
tsbplot(fit, ...)
```

Arguments

fit	msam object
...	extra arguments for plotting

Author(s)

Christoffer Moesgaard Albertsen

tsbtable.msam	<i>TSB Table</i>
---------------	------------------

Description

TSB Table

Usage

```
## S3 method for class 'msam'
tsbtable(fit, ...)
```

Arguments

fit	msam object
...	Other parameters

Details

Table of estimated total stock biomasses.

Value

A matrix of estimates and confidence intervals

Author(s)

Christoffer Moesgaard Albertsen

yearslostplot.msam	<i>Life Years lost to fishing plot</i>
--------------------	--

Description

Life Years lost to fishing plot

Usage

```
## S3 method for class 'msam'
yearslostplot(fit, cause = c("Fishing", "Other", "LifeExpectancy"), ...)
```


Arguments

fit	msam object
...	extra arguments for plotting

Author(s)

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ypr.msam	<i>Yield per recruit calculation</i>
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Description

Yield per recruit calculation

Usage

```
## S3 method for class 'msam'
ypr(
  fit,
  Flimit = 2,
  Fdelta = 0.01,
  aveYears = lapply(attr(fit, "m_data")$sam, function(x) min(15, length(x$years))),
  ageLimit = 100,
  ...
)
```

Arguments

fit	msam object
Flimit	Upper limit for Fbar
Fdelta	increments on the Fbar axis
aveYears	A list/vector of same length as the number of stocks with number of years to average over
ageLimit	Oldest age used
...	not used

Value

A list of samypr objects

Author(s)

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