Package 'r4ss'

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Type Package

Title R Code for Stock Synthesis

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Description A collection of R functions for use with Stock Synthesis, a fisheries stock assessment modeling platform written in ADMB by Dr. Richard D. Methot at the NOAA Northwest Fisheries Science Center. The functions include tools for summarizing and plotting results, manipulating files, visualizing model parameterizations, and various other common stock assessment tasks.

License GPL-3

LazyLoad yes

URL https://github.com/r4ss

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R topics documented:

`r4ss-package` *R tools for Stock Synthesis*

Description

A collection of R functions for use with Stock Synthesis, a fisheries stock assessment modeling platform written in ADMB by Dr. Richard D. Methot at the NMFS Northwest Fisheries Science Center. The functions include tools for summarizing and plotting results, manipulating files, visualizing model parameterizations, and various other tasks.

Details

Package:	r4ss
Type:	Package
Version:	1.24.0
Date:	2015-12-15
License:	GPL-3
LazyLoad:	yes
URL:	https://github.com/r4ss/

Should be compatible with Stock Synthesis versions 3.20 through 3.30.

Author(s)

Ian G. Taylor, Ian J. Stewart, Allan C. Hicks, Tommy M. Garrison, Andre E. Punt, John R. Wallace, Chantel R. Wetzel, James T. Thorson, Yukio Takeuchi, Kotaro Ono, Cole C. Monnahan, Christine C. Stawitz, Z. Teresa A'mar, Athol R. Whitten, Kelli F. Johnson, Robbie L. Emmet, Sean C. Anderson, and other contributors. Package maintainer: Ian Taylor <Ian.Taylor@noaa.gov>

References

r4ss on GitHub: https://github.com/r4ss
Download Stock Synthesis: http://nft.nefsc.noaa.gov/

Examples

```
## Not run:
# read in the report file using SS_output
myreplist <- SS_output(dir='c:/SS/simple/')

# make a collection of plots using SS_plots
SS_plots(replist=myreplist)

## End(Not run)
```

`addSSsummarize` *Add a model to the list of models to compare*

Description

Adds specified quantities from any model to the list of models returned from `SSsummarize` for further comparison.

Usage

```
addSSsummarize(origModels, newModels)
```

Arguments

origModels	A list of models created by SSsummarize.
newModels	A list of models to add to the originals models list. Each new model is an element of the list, and is a list itself with possible components described in the details below.

Value

Returns list as is returned from SSsummarize, but contains additions for the new models.

Note

This function was made to compare TINSS results and SS results, and assumed that you would always start with a list of SS models output from SSsummarize. It has not been tested to see how it works when starting with an empty list.

Author(s)

Allan Hicks

See Also

SSsummarize SSplotComparisons

Examples

```
  ## Not run:
  ######################################
  #DO NOT RUN
tinss1 <- list(npars=A$fit$npar,maxgrad=A$fit$maxgrad,nsexes=1,
               #note, there is an estimated parameter called sd_sbt,
               #      but it is a single value
               SpawnBio=data.frame(c(1964,1965,A$yrs),
                                   c(A$sbo,A$sbo,A$sbt)*1e6,0,
                                   qnorm(0.025,c(A$so,A$so,A$sbt)*1e6,0),
                                   qnorm(0.975,c(A$so,A$so,A$sbt)*1e6,0)),
               Bratio=data.frame(A$yrs,A$sbt/A$sbo,0,
                                 qnorm(0.025,A$sbt/A$sbo,0),
                                 qnorm(0.975,A$sbt/A$sbo,0)),
               SPRratio=data.frame(A$yr,A$spr,0,qnorm(0.025,A$spr,0),
                                   qnorm(0.975,A$spr,0)),
               recruits=data.frame(A$yr,A$nt[,1]*1e6,0,qnorm(0.025,A$nt[,1]*1e5,0),
                                   qnorm(0.975,A$nt[,1]*1e6,0)),
               #I'm not sure exactly what wt are,
               #   but it is important to line them up correctly
               recdevs=data.frame(A$recYrs,A$wt),
               indices = data.frame(A$iyr,1e6*A$yt,1e6*A$qbt,
                                    rep(A$q,length(A$iyr)),rep(0.4,length(A$iyr)),
                                    rep(0,length(A$iyr)),rep(1,length(A$iyr)))
               )
```

```
tinss <- list(tinss1,tinss1)   #can add more models here


#add TINSS model to SS models already summarized
SSnTINSS <- addSSsummarize(models,tinss)
mcmcInd <- seq(burnin+1,nrow(A$mc.sbt),thin)
SSnTINSS$mcmc[[2]] <- data.frame(A$mc.sb0[mcmcInd],
                                 A$mc.sbt[mcmcInd,],
                                 A$mc.depl[mcmcInd,],
                                 A$mc.spr[mcmcInd,],
                                 A$mc.rt[mcmcInd,],
                                 log(A$mcmc[mcmcInd,"Ro"]*1e6),
                                 A$mcmc[mcmcInd,"msy"]*1e6)
names(SSnTINSS$mcmc[[2]]) <-
  c("SPB_Virgin",paste("SPB",A$yrs,sep="_"),
    paste("Bratio",A$yrs,sep="_"),
    paste("SPRratio",A$yr,sep="_"),
    paste("Recr",A$yr,sep="_"),"SR_R0","TotYield_MSY")
modelnames <- c("SS", "TINSS","TINSS.MLE")

SSplotComparisons(SSnTINSS, legendlabels=modelnames,
                  subplot=2,endyr=2011,mcmcVec=c(T,T,F))
title(main="MCMC")
SSplotComparisons(SSnTINSS, legendlabels=modelnames,
                  subplot=4,endyr=2011,mcmcVec=c(T,T,F))
title(main="MCMC")
################################################

## End(Not run)
```

---

bubble3 *Create a bubble plot.*

Description

Bubble plot based on function vaguely based on bubble by Edzer Pebesma in gstat package. By default, positive values have closed bubbles and negative values have open bubbles.

Usage

```
bubble3(x, y, z, col = 1, cexZ1 = 5, maxsize = NULL, do.sqrt = TRUE,
  bg.open = gray(0.95, 0.3), legend = TRUE, legendloc = "top",
  legend.z = "default", legend.yadj = 1.1, main = "", cex.main = 1,
  xlab = "", ylab = "", minnbubble = 3, xlim = NULL, ylim = NULL,
  axis1 = TRUE, xlimextra = 1, add = FALSE, las = 1, allopen = TRUE)
```

Arguments

x	Vector of x-values.
y	Vector of y-values.
z	Vector of bubble sizes, where positive sizes will be plotted as closed bubbles and negative as open unless allopen==TRUE.
col	Color for bubbles.
cexZ1	Character expansion (cex) value for a proportion of 1.0.
maxsize	Size of largest bubble. Prefered option is now an expansion factor for a bubble with z=1 (see cexZ1 above).
do.sqrt	Should size be based on the area? (Diameter proportional to sqrt(z)). Default=TRUE.
bg.open	background color for open bubbles (border will equal 'col')
legend	Add a legend to the plot?
legendloc	Location for legend (default='top')
legend.z	If a legend is added, what z values will be shown. Default is c(-3,-2,-1,.1,1,2,3) for Pearson-like quantities and a smaller range for proportions that are all less than 1.
legend.yadj	If a legend is added, how much should the y-axis be expanded to make space for it.
main	Title of plot. Default="".
cex.main	Charecter expansion for title. Default=1.
xlab	X-axis label.
ylab	Y-axis label.
minnbubble	Minimum number of unique x values below which extra space is added to horizontal axis (to make plot look better). Default = 8.
xlim	Optional limits on x-range.
ylim	Optional limits on y-range.
axis1	Show the horizontal axis on plot? Option allows turning off for use in multi-figure plots.
xlimextra	Extra space (see minnbubble above). Default = 1.
add	Add bubbles to existing plot? Default=FALSE.
las	Style of axis labels (see ?par for more info).
allopen	Should all bubbles be open (instead of just negative values)?

Author(s)

Ian Stewart and Ian Taylor

DoProjectPlots *Make plots from Rebuilder program*

Description

Make a set of plots based on output from Andre Punt's Rebuilder program.

Usage

```
DoProjectPlots(dirn = "C:/myfiles/", fileN = c("res.csv"), Titles = "",
  ncols = 200, Plots = list(1:25), Options = list(c(1:9)),
  LegLoc = "bottomright", yearmax = -1, Outlines = c(2, 2),
  OutlineMulti = c(2, 2), AllTraj = c(1, 2, 3, 4), AllInd = c(1, 2, 3, 4,
  5, 6, 7), BioType = "Spawning biomass", CatchUnit = "(mt)",
  BioUnit = "(mt)", BioScalar = 1, ColorsUsed = "default",
  Labels = "default", pdf = FALSE, pwidth = 6.5, pheight = 5, lwd = 2)
```

Arguments

dirn	Directory (or vector of directories) where rebuilder output files are stored.
fileN	Vector of filenames containing rebuilder output. Default=c("res.csv").
Titles	Titles for plots when using multiple filenames. Default="".
ncols	Number of columns to read in output file (fileN). Deafult=200.
Plots	List to get specific plots (currently 1 through 8). Default=list(1:25). If there are multiple files, supply a list of vectors, e.g. list(c(1,5),c(2:5))
Options	List to get specific strategies in the trajectory plots. Default=list(c(1:9)).If there are multiple files, supply a list of vectors, e.g. list(c(1,5),c(2:5))
LegLoc	Location for the legend (for plots with a legend). Default="bottomright".
yearmax	Maximum year to show in the plots. Set negative to show all years. Default=-1.
Outlines	Number of rows, columns for some of the plots. Default=c(2,2).
OutlineMulti	Number of rows, columns for other plots. Default=c(2,2).
AllTraj	Vector of trajectories to show. Default=c(1,2,3,4).
AllInd	Vector of individual plots to show. Default=c(1,2,3,4,5,6,7).
BioType	Label for biomass type. Default="Spawning biomass".
CatchUnit	Units of catch. Default="(mt)".
BioUnit	Units of biomass. Default="(mt)".
BioScalar	Scalar for biomass plot. Default=1.
ColorsUsed	Optional vector for alternative line colors. Default="default".
Labels	Optional vector for alternative legend labels. Default="default".
pdf	Option to send figures to pdf file instead of plot window in Rgui. Default=FALSE.
pwidth	Width of the plot window or PDF file (in inches). Default=7.
pheight	Height of the plot window or PDF file (in inches). Default=7.
lwd	Line width for many of the plot elements. Default=2.

Author(s)

Andre Punt, Ian Taylor

Examples

```
## Not run:
# example with one file
 DoProjectPlots(dirn="c:/myfiles/", Plots=1:8,
                Options=c(1,2,3,4,5,9), LegLoc="bottomleft")

# example with multiple files
 # Plots - set to get specific plots
 # Options - set to get specific strategies in the trajectory plots

 Titles <- c("Res1","Res2","Res3")
 Plots <- list(c(1:9),c(6:7))
 Options <- list(c(7:9,3),c(5,7))
 DoProjectPlots(fileN=c("res1.csv","res2.csv"),Titles=Titles,Plots=Plots,
                Options=Options,LegLoc="bottomleft",yearmax=-1,
                Outlines=c(2,2),OutlineMulti=c(3,3),AllTraj=c(1:4),
                AllInd=c(1:7),BioType="Spawning numbers",BioUnit="(lb)",
                BioScalar=1000,CatchUnit="(lb)",
                ColorsUse=rep(c("red","blue"),5),
                Labels=c("A","B","C","D","E","F"))

## End(Not run)
```

---

getADMBHessian *Read admodel.hes file*

Description

This function reads in all of the information contained in the admodel.hes file. Some of this is needed for relaxing the covariance matrix, and others just need to be recorded and rewritten to file so ADMB "sees" what it's expecting.

Usage

```
getADMBHessian(File, FileName)
```

Arguments

File	Directory in which .hes file is located.
FileName	Name of .hes file.

Value

A list with elements num.pars, hes, hybrid_bounded_flag, and scale.

Note

Also published here: http://www.admb-project.org/examples/admb-tricks/covariance-calculations

Author(s)

Cole Monnahan

See Also

read.admbFit, NegLogInt_Fn

IOTCmove *Make a map of movement for a 5-area Indian Ocean model*

Description

Run the SSplotMovementMap function with defaults related to a 5-area model for tunas in the Indian Ocean as discussed at the Indian Ocean Tuna Commission Working Party on Tropical Tunas in October, 2010. Obviously this is not useful for the majority of r4ss users, but it could serve as an example of how a wrapper function might be written for any other model.

Usage

```
IOTCmove(replist = NULL, moveage = 5, moveseas = 1, legend = FALSE,
  title = NULL, areanames = c("R1", "R2", "R3", "R4", "R5"), ...)
```

Arguments

replist	optional list created by SS_output
moveage	age for which movemement rates will be represented
moveseas	season for which movement rates will be represented
legend	add a legend to show the movement rate associated with the widest arrows
title	optional title to add at top of figure
areanames	vector of names for each area
...	Additional arguments can get passed to SSplotMovementMap

Author(s)

Ian Taylor

make_multifig *Create multi-figure plots.*

Description

Function created as an alternative to lattice package for multi-figure plots of composition data and fits from Stock Synthesis output.

Usage

```
make_multifig(ptsx, ptsy, yr, linesx = 0, linesy = 0, ptsSD = 0,
  sampsize = 0, effN = 0, showsampsize = TRUE, showeffN = TRUE,
  sampsizeround = 1, maxrows = 6, maxcols = 6, rows = 1, cols = 1,
  fixdims = TRUE, main = "", cex.main = 1, xlab = "", ylab = "",
  size = 1, cexZ1 = 1.5, bublegend = TRUE, maxsize = NULL,
  do.sqrt = TRUE, minnbubble = 8, allopen = TRUE, horiz_lab = "default",
  xbuffer = c(0.1, 0.1), ybuffer = c(0, 0.15), yupper = NULL,
  ymin0 = TRUE, axis1 = NULL, axis2 = NULL, linepos = 1, type = "o",
  polygons = TRUE, bars = FALSE, barwidth = "default", ptscex = 1,
  ptscol = 1, ptscol2 = 1, colvec = c(rgb(1, 0, 0, 0.7), rgb(0, 0, 1,
  0.7), rgb(0.1, 0.1, 0.1, 0.7)), linescol = c(rgb(0, 0.8, 0, 0.7), rgb(1, 0,
  0, 0.7), rgb(0, 0, 1, 0.7)), lty = 1, lwd = 2, pch = 1, nlegends = 3,
  legtext = list("yr", "sampsize", "effN"), legx = "default",
  legy = "default", legadjx = "default", legadjy = "default",
  legsize = c(1.2, 1), legfont = c(2, 1), venusmars = TRUE,
  sampsizeline = FALSE, effNline = FALSE, sampsizemean = NULL,
  effNmean = NULL, ipage = 0, scalebins = FALSE, sexvec = NULL,
  multifig_colpolygon = c("grey60", "grey80", "grey70"), multifig_oma = c(5,
  5, 5, 2) + 0.1, ...)
```

Arguments

ptsx	vector of x values for points or bars
ptsy	vector of y values for points or bars of same length as ptsx
yr	vector of category values (years) of same length as ptsx
linesx	optional vector of x values for lines
linesy	optional vector of y values for lines
ptsSD	optional vector of standard deviations used to plot error bars on top of each point under the assumption of normally distributed error
sampsize	optional sample size vector of same length as ptsx
effN	optional effective sample size vector of same length as ptsx
showsampsize	show sample size values on plot?
showeffN	show effective sample size values on plot?
sampsizeround	rounding level for sample size values

maxrows	maximum (or fixed) number or rows of panels in the plot
maxcols	maximum (or fixed) number or columns of panels in the plot
rows	number or rows to return to as default for next plots to come or for single plots
cols	number or cols to return to as default for next plots to come or for single plots
fixdims	fix the dimensions at maxrows by maxcols or resize based on number of elements in yr input.
main	title of plot
cex.main	character expansion for title
xlab	x-axis label
ylab	y-axis label
size	vector of bubbles sizes if making a bubble plot
cexZ1	Character expansion (cex) for point associated with value of 1.
bublegend	Add legend with example bubble sizes to bubble plots.
maxsize	maximum size of bubbles
do.sqrt	scale bubbles based on sqrt of size vector. see ?bubble3 for more info.
minnbubble	number of unique x values before adding buffer. see ?bubble3 for more info.
allopen	should all bubbles be open? see ?bubble3 for more info.
horiz_lab	axis labels set horizontal all the time (TRUE), never (FALSE) or only when relatively short ("default")
xbuffer	extra space around points on the left and right as fraction of total width of plot
ybuffer	extra space around points on the bottom and top as fraction of total height of plot
yupper	upper limit on ymax (applied before addition of ybuffer)
ymin0	fix minimum y-value at 0?
axis1	position of bottom axis values
axis2	position of left size axis values
linepos	should lines be added on top of points (linepos=1) or behind (linepos=2)?
type	type of line/points used for observed values (see 'type' in ?plot for details) on top of a grey polygon. Default is "o" for overplotting points on lines.
polygons	should polygons be added to the (turning off is required for sex-ratio plot)
bars	should the ptsx/ptsy values be bars instead of points (TRUE/FALSE) NOT CURRENTLY FUNCTIONAL
barwidth	width of bars in barplot, default method chooses based on quick and dirty formula also, current method of plot(...type='h') could be replaced with better approach
ptscex	character expansion factor for points (default=1)
ptscol	color for points/bars
ptscol2	color for negative value points in bubble plots
colvec	Vector of length 3 with colors for females, males, unsexed fish

linescol	color for lines
lty	line type
lwd	line width
pch	point character type
nlegends	number of lines of text to add as legends in each plot
legtext	text in legend, a list of length=nlegends. values may be any of 1. "yr", 2. "sampsize", 3. "effN", or a vector of length = ptsx.
legx	vector of length=nlegends of x-values of legends (default is first one on left, all after on right)
legy	vector of length=nlegends of y-values of legends (default is top for all plots)
legadjx	left/right adjustment of legends around legx
legadjy	left/right adjustment of legends around legy
legsize	font size for legends. default=c(1.2,1.0) (larger for year and normal for others)
legfont	font type for legends, same as "font" under ?par
venusmars	Label females and males with venus and mars symbols?
sampsizeline	show line for input sample sizes on top of conditional age-at-length plots (TRUE/FALSE/scalar, still in development)
effNline	show line for effective sample sizes on top of conditional age-at-length plots (TRUE/FALSE/scalar, still in development)
sampsizemean	mean input sample size value (used when sampsizeline=TRUE)
effNmean	mean effective sample size value (used when effNline=TRUE)
ipage	which page of plots when covering more than will fit within maxrows by maxcols.
scalebins	Rescale expected and observed proportions by dividing by bin width for models where bins have different widths? Caution!: May not work correctly in all cases.
sexvec	vector of sex codes if more than one present (otherwise NULL)
multifig_colpolygon	vector of polygon fill colors of length 3 (for females, males, and unsexed fish). Can be input to SS_plots and will be passed to this function via the ... argument.
multifig_oma	vector of outer margins. Can be input to SS_plots and will be passed to this function via the ... argument.
...	additional arguments (NOT YET IMPLEMENTED).

Author(s)

Ian Taylor

See Also

SS_plots,SSplotComps

`mcmc.nuisance` *Summarize nuisance MCMC output*

Description

Summarize nuisance MCMC output (used in combination with `mcmc.out` for key parameters).

Usage

```
mcmc.nuisance(directory = "c:/mydirectory/", run = "mymodel/",
  file = "posteriors.sso", file2 = "derived_posteriors.sso",
  bothfiles = FALSE, printstats = FALSE, burn = 0, header = TRUE,
  thin = 1, trace = 0, labelstrings = "all", columnnumbers = "all",
  sep = "")
```

Arguments

`directory`	Directory where all results are located, one level above directory for particular run.
`run`	Directory with files from a particular run.
`file`	File containing posterior samples for nuisance parameters. This could be posteriors.sso or something written by the function `SSgetMCMC`.
`file2`	Optional second file containing posterior samples for nuisance parameters. This could be derived_posteriors.sso.
`bothfiles`	TRUE/FALSE indicator on whether to read `file2` in addition to `file1`.
`printstats`	Return all the statistics for a closer look.
`burn`	Optional burn-in value to apply on top of the option in the starter file and `SSgetMCMC`.
`header`	Data file with header?
`thin`	Optional thinning value to apply on top of the option in the starter file, in the `mcsave` runtime command, and in `SSgetMCMC`.
`trace`	Plot trace for param # (to help sort out problem parameters).
`labelstrings`	Vector of strings that partially match the labels of the parameters you want to consider.
`columnnumbers`	Vector of column numbers indicating the columns you want to consider.
`sep`	Separator for data file passed to the `read.table` function.

Author(s)

Ian Stewart

See Also

`mcmc.out`, `SSgetMCMC`

mcmc.out *Summarize, analyze and plot key MCMC output.*

Description

Makes four panel plot showing trace plots, moving average, autocorrelations, and densities for chosen parameters from MCMC output.

Usage

```
mcmc.out(directory = "c:/mydirectory/", run = "mymodel/",
  file = "keyposteriors.csv", namefile = "postplotnames.sso",
  names = FALSE, headernames = TRUE, numparams = 1, closeall = TRUE,
  burn = 0, thin = 1, scatter = FALSE, surface = FALSE, surf1 = 1,
  surf2 = 2, stats = FALSE, plots = TRUE, header = TRUE, sep = ",",
  print = FALSE, new = T, colNames = NULL)
```

Arguments

directory	Directory where all results are located, one level above directory for particular run.
run	Directory with files from a particular run.
file	File containing posterior samples for key parameters. This could be written by the function SSgetMCMC.
namefile	The (optional) file name of the dimension and names of posteriors.
names	Read in names file (T) or use generic naming (F).
headernames	Use the names in the header of file?
numparams	The number of parameters to analyze.
closeall	By default close all open devices.
burn	Optional burn-in value to apply on top of the option in the starter file and SSgetMCMC.
thin	Optional thinning value to apply on top of the option in the starter file, in the -mcsave runtime command, and in SSgetMCMC.
scatter	Can add a scatter-plot of all params at end, default is none.
surface	Add a surface plot of 2-way correlations.
surf1	The first parameter for the surface plot.
surf2	The second parameter for the surface plot.
stats	Print stats if desired.
plots	Show plots or not.
header	Data file with header?
sep	Separator for data file passed to the read.table function.
print	Send to screen unless asked to print.
new	Logical whether or not to open a new plot window before plotting
colNames	Specific names of the file to extract and work with. NULL keeps all columns

Author(s)

Ian Stewart, Allan Hicks (modifications)

See Also

mcmc.nuisance, SSgetMCMC

Examples

```
## Not run:
    mcmc.df <- SSgetMCMC(dir="mcmcRun", writecsv=T,
                keystrings = c("NatM", "R0", "steep", "Q_extraSD"),
               nuisancestrings = c("Objective_function", "SPB_", "InitAge", "RecrDev"))
    mcmc.out("mcmcRun",run="",numparams=4,closeall=F)

#Or for more control
    par(mar=c(5,3.5,0,0.5),oma=c(0,2.5,0.2,0))
   mcmc.out("mcmcRun",run="",numparams=1,closeall=F,new=F,colNames=c("NatM_p_1_Fem_GP_1"))
    mtext("M (natural mortality)",side=2,outer=T,line=1.5,cex=1.1)

## End(Not run)
```

---

mountains *Make shaded polygons with a mountain-like appearance*

Description

Designed to replicate like the cool-looking Figure 7 in Butterworth et al. (2003).

Usage

```
mountains(zmat, xvec = NULL, yvec = NULL, zscale = 3, rev = TRUE,
  nshades = 100, axes = TRUE, xaxs = "i", yaxs = "i", xlab = "",
  ylab = "", las = 1, addbox = FALSE, ...)
```

Arguments

zmat	A matrix where the rows represent the heights of each mountain range
xvec	Optional input for the x variable
yvec	Optional input for the y variable
zscale	Controls the height of the mountains relative to the y-axis and max(zmat)
rev	Reverse the order of the display of yvec values.
nshades	Number of levels of shading
axes	Add axes to the plot?
xaxs	X-axis as internal or regular (see ?par for details)

yaxs	Y-axis as internal or regular (see ?par for details)
xlab	Optional label for x-axis
ylab	Optional label for y-axis
las	Xxis label style (see ?par for details). Default = 1 = horizontal axis labels.
addbox	Puts a box around the whole plot
...	Extra inputs passed to the plot command

Author(s)

Ian Taylor

References

Butterworth D.S., Ianelli J.N., Hilborn R. (2003) A statistical model for stock assessment of southern bluefin tuna with temporal changes in selectivity. South African Journal of Marine Science 25:331-362.

---

movepars *Explore movement parameterizations in a GUI*

Description

A function to visualize parameterization of movement in Stock Synthesis. It creates a GUI interface for movement exploration. Based on selectivity GUI by Tommy Garrison

Usage

```
movepars(nareas = 4, accuage = 40, season.duration = 1,
  min.move.age = 0.5)
```

Arguments

nareas	Number of areas
accuage	Accumulator age
season.duration	Length of season (annual rates are scaled by this value in SS).
min.move.age	Minimum age of movement.

Author(s)

Ian Taylor

NegLogInt_Fn *Perform SS implementation of Laplace Approximation*

Description

(Attempt to) perform the SS implementation of the Laplace Approximation from Thorson, Hicks and Methot (2014) ICES J. Mar. Sci.

Usage

```
NegLogInt_Fn(File = NA, Input_SD_Group_Vec, CTL_linenum_List, ESTPAR_num_List,
  PAR_num_Vec, Int_Group_List = list(1), Version = 1, StartFromPar = TRUE,
  Intern = TRUE, ReDoBiasRamp = FALSE, BiasRamp_linenum_Vec = NULL,
  CTL_linenum_Type = NULL, systemcmd = FALSE)
```

Arguments

File	Directory containing Stock Synthesis files (e.g., "C:/Users/James Thorson/Desktop/")
Input_SD_Group_Vec	Vector where each element is the standard deviation for a group of random effects (e.g., a model with a single group of random effects will have Input_SD_Group_Vec be a vector of length one)
CTL_linenum_List	List (same length as Input_SD_Group_Vec), where each element is a vector giving the line number(s) for the random effect standard deviation parameter or penalty in the CTL file (and where each line will correspond to a 7-parameter or 14-parameter line).
ESTPAR_num_List	List (same length as Input_SD_Group_Vec), where each element is a vector giving the parameter number for the random effect coefficients in that group of random effects. These "parameter numbers" correspond to the number of these parameters in the list of parameters in the "ss3.cor" output file.
PAR_num_Vec	Vector giving the number in the "ss3.par" vector for each random effect coefficient.
Int_Group_List	List where each element is a vector, providing a way of grouping different random effect groups into a single category. This is not used (but input is still required) when Version=1.
Version	Integer (options are 1, 5, and 6) giving the type of Laplace Approximation. I recommend 1.
StartFromPar	Logical flag (TRUE or FALSE) saying whether to start each round of optimization from a "ss3.par" file (I recommend TRUE)
Intern	Logical flag saying whether to display all ss3 runtime output in the R terminal
ReDoBiasRamp	Logical flag saying whether to re-do the bias ramp (using SS_fitbiasramp) each time Stock Synthesis is run.

`BiasRamp_linenum_Vec`
: Vector giving the line numbers from the CTL file that contain the information about the bias ramp.

`CTL_linenum_Type`
: Character vector (same length as `Input_SD_Group_Vec`), where each element is either "Short_Param", "Long_Penalty", "Long_Penalty". Default is NULL, and if not explicitly specified the program will attempt to detect these automatically based on the length of relevant lines from the CTL file.

`systemcmd`
: Should R call SS using "system" function intead of "shell". This may be required when running R in Emacs on Windows. Default = FALSE.

Author(s)

James Thorson

References

Thorson, J.T., Hicks, A.C., and Methot, R.D. 2014. Random effect estimation of time-varying factors in Stock Synthesis. ICES J. Mar. Sci.

See Also

`read.admbFit`, `getADMBHessian`

Examples

```
## Not run:
 direc <- "C:/Models/LaplaceApprox/base"  #need the full path because wd is changed in function
  if("Optimization_record.txt" %in% list.files(direc)) {
       file.remove(file.path(direc,"Optimization_record.txt"))
  }
  Opt = optimize(f=NegLogInt_Fn,
                 interval=c(0.001, 0.12),
                 maximum=FALSE,
                 File=direc,
                 CTL_linenum_List=list(127:131),
                 ESTPAR_num_List=list(86:205),
                 Int_Group_List=1,
                 PAR_num_Vec=NA,
                 Version=1, Intern=TRUE)

## End(Not run)
```

PinerPlot *Make plot of likelihood contributions by fleet*

Description

This style of plot was officially named a "Piner Plot" at the CAPAM Selectivity Workshop, La Jolla March 2013. This is in honor of Kevin Piner's contributions to interpreting likelihood profiles. He's surely not the first person to make such a plot but the name seems to have stuck.

Usage

```
PinerPlot(summaryoutput, plot = TRUE, print = FALSE,
  component = "Length_like",
  main = "Changes in length-composition likelihoods by fleet",
  models = "all", fleets = "all", fleetnames = "default",
  profile.string = "R0", profile.label = expression(log(italic(R)[0])),
  ylab = "Change in -log-likelihood", col = "default", pch = "default",
  lty = 1, lty.total = 1, lwd = 2, lwd.total = 3, cex = 1,
  cex.total = 1.5, xlim = "default", ymax = "default", xaxs = "r",
  yaxs = "r", type = "o", legend = TRUE, legendloc = "topright",
  pwidth = 6.5, pheight = 5, punits = "in", res = 300, ptsize = 10,
  cex.main = 1, plotdir = NULL, verbose = TRUE, fleetgroups = NULL,
  likelihood_type = "raw_times_lambda", minfraction = 0.01)
```

Arguments

summaryoutput	List created by the function SSsummarize.
plot	Plot to active plot device?
print	Print to PNG files?
component	Which likelihood component to plot. Default is "Length_like".
main	Title for plot. Should match component.
models	Optional subset of the models described in summaryoutput. Either "all" or a vector of numbers indicating columns in summary tables.
fleets	Optional vector of fleet numbers to include.
fleetnames	Optional character vector of names for each fleet.
profile.string	Character string used to find parameter over which the profile was conducted. Needs to match substring of one of the SS parameter labels found in the Report.sso file. For instance, the default input 'steep' matches the parameter 'SR_BH_steep'.
profile.label	Label for x-axis describing the parameter over which the profile was conducted.
ylab	Label for y-axis. Default is "Change in -log-likelihood".
col	Optional vector of colors for each line.
pch	Optional vector of plot characters for the points.
lty	Line total for the liklihood components.

lty.total	Line type for the total likelihood.
lwd	Line width for the liklihood components.
lwd.total	Line width for the total likelihood.
cex	Character expansion for the points representing the likelihood components.
cex.total	Character expansion for the points representing the total likelihood.
xlim	Range for x-axis. Change in likelihood is calculated relative to values within this range.
ymax	Maximum y-value. Default is 10% greater than largest value plotted.
xaxs	The style of axis interval calculation to be used for the x-axis (see ?par for more info)
yaxs	The style of axis interval calculation to be used for the y-axis (see ?par for more info).
type	Line type (see ?plot for more info).
legend	Include legend?
legendloc	Location of legend (see ?legend for more info).
pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	Point size for PNG file
cex.main	Character expansion for plot titles
plotdir	Directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	Return updates of function progress to the R GUI? (Doesn't do anything yet.)
fleetgroups	Optional character vector, with length equal to the number of declared fleets, where fleets with the same value are aggregated
likelihood_type	choice of "raw" or "raw_times_lambda" (the default) determines whether or not likelihoods plotted are adjusted by lambdas (likelihood weights)
minfraction	Minimum change in likelihood (over range considered) as a fraction of change in total likelihood for a component to be included in the figure.

Author(s)

Ian Taylor, Kevin Piner, Jim Thorson

References

Kevin Piner says that he's not the originator of this idea so Athol Whitten is going to add a reference here.

plotCI *Plot points with confidence intervals.*

Description

Given a set of x and y values and upper and lower bounds, this function plots the points with error bars. This was Written by Venables and modified to add access to ylim and contents.

Usage

```
plotCI(x, y = NULL, uiw, liw = uiw, ylo = NULL, yhi = NULL, ...,
  sfrac = 0.01, ymax = NULL, add = FALSE, col = "black")
```

Arguments

x	The x coordinates of points in the plot
y	The y coordinates of the points in the plot.
uiw	The width of the upper portion of the confidence region.
liw	The width of the lower portion of the confidence region.
ylo	Lower limit of y range.
yhi	Upper limit of y range.
sfrac	Fraction of width of plot to be used for bar ends.
ymax	Additional input for Upper limit of y range.
add	Add points and intervals to existing plot? Default=FALSE.
col	Color for the points and lines.
...	Additional inputs that will be passed to the function `plot(x,y,ylim=ylim,...)`

Author(s)

Bill Venables, Ian Stewart, Ian Taylor, John Wallace

r4ss_logo *Make a simple logo for r4ss organization on GitHub*

Description

I was tired of the automatically generated symbol that appeared by default.

Usage

```
r4ss_logo()
```

Author(s)

Ian Taylor

read.admbFit *Read ADMB .par and .cor files.*

Description

This function will parse the .par and .cor files to provide things like parameter estimates, standard deviations, and correlations. Required for Jim Thorson's Laplace Approximation but likely useful for other purposes.

Usage

```
read.admbFit(file)
```

Arguments

file	Name of ADMB executable such that files to read will have format file.par and file.cor.

Value

List of various things from these files.

Author(s)

James Thorson

See Also

getADMBHessian, NegLogInt_Fn

rich.colors.short *Make a vector of colors.*

Description

A subset of rich.colors by Arni Magnusson from the gplots package, with the addition of alpha transparency (which is now available in the gplots version as well)

Usage

```
rich.colors.short(n, alpha = 1)
```

Arguments

n	Number of colors to generate.
alpha	Alpha transparency value for all colors in vector. Value is passed to rgb function.

Author(s)

Arni Magnusson, Ian Taylor

`sel.line` *a function for drawing selecitivity curves*

Description

This function is primarily inteded for use by the selfit function.

Usage

```
sel.line(x, model, sp, min.dist, max.dist)
```

Arguments

`x`	vector of x values (age or length)
`model`	selectivity model "Double_Normal" or "Double_Logistic"
`sp`	vector of parameters
`min.dist`	minimum value for selectivity
`max.dist`	maximum value for selectivity

Author(s)

Tommy Garrison

See Also

`selfit`

Examples

```
## Not run:
plot(0, xlim = c(0, 50), ylim = c(0, 1),
xlab = 'Length', ylab = 'Selectivity', type = 'n',
xaxs = 'i', yaxs = 'i')
sel.line(model = 'Double_Normal', min.dist = 10, max.dist = 50,
sp = c(25, -0.5, 3, 3, -5, 0))

## End(Not run)
```

`selfit` *A function to visual parameterization of double normal and double logistic selectivity in Stock Synthesis*

Description

A GUI interface for exploring selectivity.

Usage

```
selfit(minLength = 10, maxLength = 65, silent = FALSE, init = NULL)
```

Arguments

`minLength`	Minimum size to show
`maxLength`	Maximum size to show
`silent`	T/F switch to return fit at the end
`init`	Optional initial values for the parameters

Author(s)

Tommy Garrison

See Also

`sel.line`

Examples

```
## Not run:
selfit()

## End(Not run)
```

`selfit_spline` *visualize parameterization of cubic spline selectivity in SS*

Description

A GUI interface for exploring spline selectivity.

Usage

```
selfit_spline(n = 4, minBin = 10, maxBin = 65, knots = NULL,
  slopevec = c(0.01, -0.01), params = NULL, dir = getwd(),
  silent = FALSE)
```

Arguments

`n`	Number of knots.
`minBin`	Minimum length or age to show.
`maxBin`	Maximum length or age to show.
`knots`	Vector giving location of each knot.
`slopevec`	Optional initial values parameters controlling slope at first and last knot.
`params`	Optional initial values for the parameters controlling selectivity at each knot.
`dir`	Directory in which the spline_selex executable is located (default = working directory).
`silent`	TRUE/FALSE switch to return fit at the end.

Author(s)

Ian Taylor

See Also

`selfit`

Examples

```
## Not run:
selfit_spline()

## End(Not run)
```

SSbootstrap *Fit models to parametric bootstraps*

Description

Run a series of models fit to parametric bootstrap data taken from data.ss_new. This is not yet a generalized function, just some example code for how to do a parametric bootstrap such as was done for the Pacific hake model in 2006.

Usage

```
SSbootstrap()
```

Note

Thanks to Nancie Cummings for inspiration.

Author(s)

Ian Taylor

References

http://www.pcouncil.org/wp-content/uploads/2006_hake_assessment_FINAL_ENTIRE.pdf
(A description is on page 41 and Figures 55-56 (pg 139-140) show some results.)

SSFishGraph *A function for converting Stock Synthesis output to the format used by FishGraph*

Description

Only skeleton of a function right now, needs work. Intended as a translator to convert the output from object created by SS_output to the format used by FishGraph.

Usage

```
SSFishGraph(replist, title = "SSv3 output", species = "some kind of fish")
```

Arguments

replist	Object created by SS_output
title	Title of output
species	Species name

Author(s)

Ian Taylor

References

A website related to FishGraph is http://r-forge.r-project.org/projects/fishgraph/

SSgetMCMC *Read MCMC output.*

Description

Reads the MCMC output (in the posteriors.sso and derived_posteriors.sso files) from one or more models.

Usage

```
SSgetMCMC(dir = NULL, verbose = TRUE, writecsv = FALSE,
  csv1 = "keyposteriors.csv", csv2 = "nuisanceposteriors.csv",
  keystrings = c("NatM", "R0", "steep", "RecrDev_2008", "Q_extraSD"),
  nuisancestrings = c("Objective_function", "SPB_", "InitAge", "RecrDev"),
  modelnames = "default", burnin = 0, thin = 1)
```

Arguments

dir	A string (or vector of strings) of the directory (or directories) with MCMC output.
verbose	TRUE/FALSE switch to get more or less information about the progress of the function.
writecsv	Write key parameters and certainty nuisance quantities to a CSV file.
csv1	First CSV file for key parameters.
csv2	Second CSV file for nuisance quantities.
keystrings	Vector of strings that partially match parameter names to write to the file csv1. This file intended to feed into mcmc.out.
nuisancestrings	Vector of strings that partially match derived quantity names to write to the file csv2. This file intended to feed into mcmc.nuisance.
modelnames	Either "default" or a vector of names to use in naming elements of list that is output by the function. Default is "model1", "model2", etc.
burnin	Optional burn-in value to apply on top of the option in the starter file.
thin	Optional thinning value to apply on top of the option in the starter file and in the -mcsave runtime command.

Author(s)

Ian Taylor

See Also

mcmc.out, mcmc.nuisance, SSplotPars

SSgetoutput *Get output from multiple Stock Synthesis models.*

Description

Apply the function SS_output multiple times and save output as individual objects or a list of lists.

Usage

```
SSgetoutput(keyvec = NULL, dirvec = NULL, getcovar = TRUE,
  getcomp = TRUE, forecast = FALSE, verbose = TRUE, ncols = 210,
  listlists = TRUE, underscore = FALSE, save.lists = FALSE)
```

Arguments

keyvec	A vector of strings that are appended to the output files from each model if models are all in one directory. Default=NULL.
dirvec	A vector of directories (full path or relative to working directory) in which model output is located. Default=NULL.
getcovar	Choice to read or not read covar.sso output (saves time and memory). Default=TRUE.
getcomp	Choice to read or not read CompReport.sso output (saves time and memory). Default=TRUE.
forecast	Choice to read or not read forecast quantities. Default=FALSE.
verbose	Print various messages to the command line as the function runs? Default=TRUE.
ncols	Maximum number of columns in Report.sso (same input as for SS_output). Default=210.
listlists	Save output from each model as a element of a list (i.e. make a list of lists). Default = TRUE.
underscore	Add an underscore '_' between any file names and any keys in keyvec. Default=FALSE.
save.lists	Save each list of parsed output as a .Rdata file (with default filenaming convention based on iteration and date stamp.

Author(s)

Ian Taylor

See Also

SS_output SSsummarize

SSmakeMmatrix *Convert a matrix of natural mortality values into inputs for Stock Synthesis*

Description

Inspired by Valerio Bartolino and North Sea herring

Usage

```
SSmakeMmatrix(mat, startyr, outfile = NULL, overwrite = FALSE,
  yrs.in.columns = TRUE)
```

Arguments

mat	a matrix of natural mortality by year and age, starting with age 0
startyr	the first year of the natural mortality values (no missing years)
outfile	optional file to which the results will be written
overwrite	if 'outfile' is provided and exists, option to overwrite or not
yrs.in.columns	an indicator of whether the matrix has years in columns or rows

Value

Prints inputs with option to write to chosen file

Author(s)

Ian Taylor

`SSMethod.Cond.TA1.8` *Apply Francis composition weighting method TA1.8 for conditional age-at-length fits*

Description

Uses an extension of method TA1.8 (described in Appendix A of Francis 2011) to do stage-2 weighting of conditional age at length composition data from a Stock Synthesis model. Outputs two versions (A and B) of a mutiplier, *w*, (with bootstrap 95% confidence intervals) so that *N2i* = *w* x *N1i*, where *N1i* and *N2i* are the stage-1 and stage-2 multinomial sample sizes for the *i*th composition. Optionally makes a plot (for version A) of observed and expected mean ages, with two alternative sets of confidence limits - based on *N1i* (thin lines) and *N2i* (thick lines) - for the observed values.

The two versions of w differ according to whether the calculated mean ages are indexed by year (version A) or by year and length bin (version B). Version A is recommended; version B is included for historical reasons.

CAUTIONARY/EXPLANATORY NOTE. The large number of options available in SS makes it very difficult to be sure that what this function does is appropriate for all combinations of options. The following notes (for version A) might help anyone wanting to check or correct the code.

1. The code first removes un-needed rows from database condbase.
2. The remaining rows of the database are grouped (indexed by vector indx) and relevant statistics (e.g., observed and expected mean age), and ancillary data, are calculated for each group (these are stored in pldat - one row per group).
3. If the data are to be plotted they are further grouped by fleet, with one panel of the plot per fleet.
4. A single multiplier, *w*, is calculated to apply to all the selected data.

Usage

```
SSMethod.Cond.TA1.8(fit, fleet, part = 0:2, seas = NULL, plotit = TRUE,
  maxpanel = 1000, FullDiagOut = FALSE)
```

Arguments

`fit`	Stock Synthesis output as read by r4SS function SS_output
`fleet`	vector of one or more fleet numbers whose data are to be analysed simultaneously (the output N multiplier applies to all fleets combined)
`part`	vector of one or more partition values; analysis is restricted to composition data with one of these partition values. Default is to include all partition values (0, 1, 2).
`seas`	string indicating how to treat data from multiple seasons 'comb' - combine seasonal data for each year and plot against Yr 'sep' - treat seasons separately, plotting against Yr.S If is.null(seas) it is assumed that there is only one season in the selected data (a warning is output if this is not true) and option 'comb' is used.

plotit	if TRUE, make an illustrative plot like one or more panels of Fig. 4 in Francis (2011).
maxpanel	maximum number of panels within a plot
FullDiagOut	Print full diagnostics?

Author(s)

Chris Francis, Andre Punt, Ian Taylor

References

Francis, R.I.C.C. (2011). Data weighting in statistical fisheries stock assessment models. Canadian Journal of Fisheries and Aquatic Sciences 68: 1124-1138.

See Also

SSMethod.TA1.8

SSMethod.TA1.8 *Apply Francis composition weighting method TA1.8*

Description

Uses method TA1.8 (described in Appendix A of Francis 2011) to do stage-2 weighting of composition data from a Stock Synthesis model. Outputs a mutiplier, *w* (with bootstrap 95 so that *N2y* = *w* x *N1y*, where *N1y* and *N2y* are the stage-1 and stage-2 multinomial sample sizes for the data set in year y. Optionally makes a plot of observed (with confidence limits, based on *N1y*) and expected mean lengths (or ages).

CAUTIONARY/EXPLANATORY NOTE. The large number of options available in SS makes it very difficult to be sure that what this function does is appropriate for all combinations of options. The following notes might help anyone wanting to check or correct the code.

1. The code first takes the appropriate database (lendbase, sizedbase, agedbase, or condbase) and removes un-needed rows.
2. The remaining rows of the database are grouped into individual comps (indexed by vector indx) and relevant statistics (e.g., observed and expected mean length or age), and ancillary data, are calculated for each comp (these are stored in pldat - one row per comp). If the data are to be plotted, the comps are grouped, with each group corresponding to a panel in the plot, and groups are indexed by plindx.
3. A single multiplier is calculated to apply to all the comps.

Usage

```
SSMethod.TA1.8(fit, type, fleet, part = 0:2, pick.gender = 0:3,
  seas = NULL, method = NULL, plotit = TRUE, maxpanel = 1000)
```

Arguments

fit	Stock Synthesis output as read by r4SS function SS_output
type	either 'len' (for length composition data), 'size' (for generalized size composition data), 'age' (for age composition data), or 'con' (for conditional age at length data)
fleet	vector of one or more fleet numbers whose data are to be analysed simultaneously (the output N multiplier applies to all fleets combined)
part	vector of one or more partition values; analysis is restricted to composition data with one of these partition values. Default is to include all partition values (0, 1, 2).
pick.gender	vector of one or more values for Pick_gender; analysis is restricted to composition data with one of these Pick_gender values. Ignored if type=='con'
seas	string indicating how to treat data from multiple seasons 'comb' - combine seasonal data for each year and plot against Yr 'sep' - treat seasons separately, plotting against Yr.S If is.null(seas) it is assumed that there is only one season in the selected data (a warning is output if this is not true) and option 'comb' is used.
method	a vector of one or more size-frequency method numbers (ignored unless type = 'size'). If !is.null(method), analysis is restricted to size-frequency methods in this vector. NB comps are separated by method
plotit	if TRUE, make an illustrative plot like one or more panels of Fig. 4 in Francis (2011).
maxpanel	maximum number of panels within a plot

Author(s)

Chris Francis, Andre Punt, Ian Taylor

References

Francis, R.I.C.C. (2011). Data weighting in statistical fisheries stock assessment models. Canadian Journal of Fisheries and Aquatic Sciences 68: 1124-1138.

See Also

SSMethod.Cond.TA1.8

Examples

```
## Not run:
Nfleet <- length(myreplist$FleetNames)
for (Ifleet in 1:Nfleet)
  SSMethod.TA1.8(myreplist,"len",fleet=Ifleet,maxpanel=maxpanel)
for (Ifleet in 1:Nfleet)
  SSMethod.TA1.8(myreplist,"age",fleet=Ifleet,maxpanel=maxpanel)
for (Ifleet in 1:Nfleet)
  SSMethod.TA1.8(myreplist,"size",fleet=Ifleet,maxpanel=maxpanel)
```

```
for (Ifleet in 1:Nfleet)
  SSMethod.TA1.8(myreplist,"con",fleet=Ifleet,maxpanel=maxpanel)
for (Ifleet in 1:Nfleet)
  SSMethod.Cond.TA1.8(myreplist,fleet=Ifleet,maxpanel=maxpanel)

## End(Not run)
```

SSplotBiology *Plot biology related quantities.*

Description

Plot biology related quantities from Stock Synthesis model output, including mean weight, maturity, fecundity, and spawning output.

Usage

```
SSplotBiology(replist, plot = TRUE, print = FALSE, add = FALSE,
  subplots = 1:14, seas = 1, colvec = c("red", "blue", "grey20"),
  shadealpha = 0.1, legendloc = "topleft", plotdir = "default",
  labels = c("Length (cm)", "Age (yr)", "Maturity",
  "Mean weight (kg) in last year", "Spawning output",
  "Length (cm, beginning of the year)", "Natural mortality",
  "Female weight (kg)", "Female length (cm)", "Fecundity",
  "Default fecundity label", "Year"), pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1, verbose = TRUE)
```

Arguments

replist	List created by SS_output
plot	Plot to active plot device?
print	Print to PNG files?
add	add to existing plot
subplots	vector controlling which subplots to create
seas	which season to plot (obviously only works in seasonal models, but maybe not fully implemented even then)
colvec	vector of length 3 with colors for various points/lines
shadealpha	Transparency parameter used to make default shadecol values (see ?rgb for more info)
legendloc	Location of legend (see ?legend for more info)
plotdir	Directory where PNG files will be written. by default it will be the directory where the model was run.
labels	Vector of labels for plots (titles and axis labels)

pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	Point size for PNG file
cex.main	Character expansion for plot titles
verbose	Return updates of function progress to the R GUI?

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_plots, SS_output

SSplotCatch *Plot catch related quantities.*

Description

Plot catch related quantities from Stock Synthesis output. Plots include harvest rate, continuous F, landings, and discard fraction.

Usage

```
SSplotCatch(replist, subplots = 1:15, add = FALSE, areas = 1,
  plot = TRUE, print = FALSE, type = "l", fleetlty = 1, fleetpch = 1,
  fleetcols = "default", fleetnames = "default", lwd = 3,
  areacols = "default", areanames = "default", minyr = NULL,
  maxyr = NULL, annualcatch = TRUE, forecastplot = FALSE,
  plotdir = "default", showlegend = TRUE, legendloc = "topleft",
  order = "default", xlab = "Year", labels = c("Harvest rate/Year",
  "Continuous F", "Landings", "Total catch", "Predicted Discards",
  "Discard fraction", "(mt)", "(numbers x1000)", "Observed and expected",
  "aggregated across seasons"), catchasnumbers = NULL, catchbars = TRUE,
  addmax = TRUE, ymax = NULL, pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1, verbose = TRUE)
```

Arguments

replist	List created by SS_output
subplots	Vector controlling which subplots to create
add	Add to existing plot? (not yet implemented)
areas	Optional subset of areas to plot for spatial models

plot	Plot to active plot device?
print	Print to PNG files?
type	Type parameter passed to plot function. Default "l" is lines only. Other options include "o" for overplotting points on lines.
fleetlty	Vector of line type by fleet
fleetpch	Vector of plot character by fleet
fleetcols	Vector of colors by fleet
fleetnames	Optional replacement for fleenames used in data file
lwd	Line width
areacols	Vector of colors by area. Default uses rich.colors by Arni Magnusson
areanames	Names for areas. Default is to use Area1, Area2,...
minyr	Optional input for minimum year to show in plots
maxyr	Optional input for maximum year to show in plots
annualcatch	Include plot of catch aggregated across seasons within each year
forecastplot	Add points from forecast years
plotdir	Directory where PNG or PDF files will be written. By default it will be the directory where the model was run.
showlegend	Put legend on plot
legendloc	Location of legend (see ?legend for more info)
order	Optional input to change the order of fleets in stacked plots.
xlab	x-label for all plots
labels	Vector of labels for plots (titles and axis labels)
catchasnumbers	Is catch in numbers instead of biomass? Should be set automatically if set to NULL. If fleets include a mix of biomass and numbers, then catch plots should be interpreted carefully.
catchbars	Show catch by fleet as barplot instead of stacked polygons? (default=TRUE)
addmax	Add a point on the y-axis for the maximum catch (default=TRUE)
ymax	Optional input for ymax value (can be used to add or subtract white space at the top of the figure)
pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	point size for PNG file
cex.main	Character expansion for plot titles
verbose	Report progress to R console?

Author(s)

Ian Taylor, Ian Stewart

See Also

SS_plots, SS_output

SSplotCohorts *Plot cumulative catch by cohort.*

Description

Cumulative catch contributions for each cohort are plotted based on estimated catch-at-age matrix and weight-at-age values by fleet. Curves are shown in units of both numbers and biomass.

Usage

```
SSplotCohorts(replist, subplots = 1:2, add = FALSE, plot = TRUE,
  print = FALSE, cohortcols = "default", cohortfrac = 1,
  cohortvec = NULL, cohortlabfrac = 0.1, cohortlabvec = NULL, lwd = 3,
  plotdir = "default", xlab = "Year", labels = c("Age",
  "Cumulative catch by cohort (in numbers x1000)",
  "Cumulative catch by cohort (x1000 mt)"), pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1, verbose = TRUE)
```

Arguments

replist	List created by SS_output
subplots	Vector controlling which subplots to create
add	Add to existing plot? (not yet implemented)
plot	Plot to active plot device?
print	Print to PNG files?
cohortcols	Vector of colors to show for each cohort. Default is range of colors shade indicating time period.
cohortfrac	What fraction of the cohorts to include in plot. If value < 1 is used, then cohorts are filtered to only include those with the highest maximum cumulative catch. Value will be overridden by cohortvec.
cohortvec	Optional vector of birth years for cohorts to include in plot. Value overrides cohortfrac.
cohortlabfrac	What fraction of the cohorts to label in plot. By default, top 10% of cohorts are labeled. Value will be overridden by cohortlabvec.
cohortlabvec	Optional vector of birth years for cohorts to label in plot. Value overrides cohortlabfrac.
lwd	Line width
plotdir	Directory where PNG or PDF files will be written. By default it will be the directory where the model was run.
xlab	x-label for all plots

labels	Vector of labels for plots (titles and axis labels)
pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	point size for PNG file
cex.main	Character expansion for plot titles (no titles in this function yet)
verbose	Report progress to R console?

Author(s)

Ian Taylor

See Also

SS_plots, SS_output

SSplotComparisons *plot model comparisons*

Description

Creates a user-chosen set of plots comparing model output from a summary of multiple models, where the collection was created using the SSsummarize function.

Usage

```
SSplotComparisons(summaryoutput, subplots = 1:20, plot = TRUE,
  print = FALSE, png = print, pdf = FALSE, models = "all",
  endyrvec = "default", indexfleets = NULL, indexUncertainty = FALSE,
  indexQlabel = TRUE, indexQdigits = 4, indexSEvec = "default",
  indexPlotEach = FALSE, labels = c("Year", "Spawning biomass (t)",
  "Relative spawning biomass", "Age-0 recruits (1,000s)",
  "Recruitment deviations", "Index", "Log index", "SPR ratio", "Density",
  "Management target", "Minimum stock size threshold", "Spawning output",
  "Harvest rate"), col = NULL, shadecol = NULL, pch = NULL, lty = 1,
  lwd = 2, spacepoints = 10, staggerpoints = 1, initpoint = 0,
  tickEndYr = TRUE, shadeForecast = TRUE, xlim = "default", ylimAdj = 1,
  xaxs = "r", yaxs = "r", type = "o", uncertainty = TRUE,
  shadealpha = 0.1, legend = TRUE, legendlabels = "default",
  legendloc = "topright", legendorder = "default", legendncol = 1,
  sprtarg = NULL, btarg = NULL, minbthresh = NULL, pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1,
  plotdir = NULL, filenameprefix = "", densitynames = c("SPB_Virgin",
  "R0"), densityxlabs = "default", densityscalex = 1, densityscaley = 1,
```

```
densityadjust = 1, densitysymbols = TRUE, densitytails = TRUE,
densitymiddle = FALSE, densitylwd = 1, fix0 = TRUE, new = TRUE,
add = FALSE, par = list(mar = c(5, 4, 1, 1) + 0.1), verbose = TRUE,
mcmcVec = "default")
```

Arguments

summaryoutput	List created by SSsummarize
subplots	Vector of subplots to be created.
plot	Plot to active plot device?
print	Send plots to PNG files in directory specified by plotdir?
png	Has same result as print, included for consistency with SS_plots.
pdf	Write output to PDF file? Can't be used in conjunction with png or print.
models	Optional subset of the models described in summaryoutput. Either "all" or a vector of numbers indicating columns in summary tables.
endyrvec	Optional single year or vector of years representing the final year of values to show for each model. By default it is set to the ending year specified in each model.
indexfleets	Vector of fleet numbers for each model for which to compare indices of abundance. Only necessary if any model has more than one index.
indexUncertainty	Show uncertainty intervals on index data? Default=FALSE because if models have any extra standard deviations added, these intervals may differ across models.
indexQlabel	Add catchability to legend in plot of index fits (TRUE/FALSE)?
indexQdigits	Number of significant digits for catchability in legend (if indexQlabel=TRUE)
indexSEvec	Optional replacement for the SE values in summaryoutput$indices to deal with the issue of differing uncertainty by models described above.
indexPlotEach	TRUE plots the observed index for each model with colors, or FALSE just plots observed once in black dots.
labels	Vector of labels for plots (titles and axis labels)
col	Optional vector of colors to be used for lines. Input NULL makes use of rich.colors.short function.
shadecol	Optional vector of colors to be used for shading uncertainty intervals. Input NULL makes use of rich.colors.short function with alpha transparency.
pch	Optional vector of plot character values
lty	Optional vector of line types
lwd	Optional vector of line widths
spacepoints	Number of years between points shown on top of lines (for long timeseries, points every year get mashed together)
staggerpoints	Number of years to stagger the first point (if spacepoints > 1) for each line (so that adjacent lines have points in different years)

initpoint	Year value for first point to be added to lines. Points added to plots are those that satisfy (Yr-initpoint)%%spacepoints == (staggerpoints*iline)%%spacepoints
tickEndYr	TRUE/FALSE switch to turn on/off extra axis mark at final year in timeseries plots.
shadeForecast	TRUE/FALSE switch to turn on off shading of years beyond the maximum ending year of the models
xlim	Optional x limits
ylimAdj	Multiplier for ylim parameter. Allows additional white space to fit legend if necessary. Default=1.
xaxs	Choice of xaxs parameter (see ?par for more info)
yaxs	Choice of yaxs parameter (see ?par for more info)
type	Type parameter passed to points (default 'o' overplots points on top of lines)
uncertainty	Show plots with uncertainty intervals? Either a single TRUE/FALSE value, or a vector of TRUE/FALSE values for each model, or a set of integers corresponding to the choice of models.
shadealpha	Transparency adjustment used to make default shadecol values (implemented as `adjustcolor(col=col, alpha.f=shadealpha)`)
legend	Add a legend?
legendlabels	Optional vector of labels to include in legend. Default is 'model1','model2',etc.
legendloc	Location of legend. See ?legend for more info.
legendorder	Optional vector of model numbers that can be used to have the legend display the model names in an order that is different than that which is represented in the summary input object.
legendncol	Number of columns for the legend.
sprtarg	Target value for SPR-ratio where line is drawn in the SPR plots and phase plot.
btarg	Target biomass value at which to show a line (set to 0 to remove)
minbthresh	Minimum biomass threshhold at which to show a line (set to 0 to remove)
pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	Point size for PNG file
cex.main	Character expansion for plot titles
plotdir	Directory where PNG or PDF files will be written. By default it will be the directory where the model was run.
filenameprefix	Additional text to append to PNG or PDF file names. It will be separated from default name by an underscore.
densitynames	Vector of names (or subset of names) of parameters or derived quantities contained in summaryoutput$pars$Label or summaryoutput$quants$Label for which to make density plots

densityxlabs	Optional vector of x-axis labels to use in the density plots (must be equal in length to the printed vector of quantities that match the densitynames input)
densityscalex	Scalar for upper x-limit in density plots (values below 1 will cut off the right tail to provide better contrast among narrower distributions
densityscaley	Scalar for upper y-limit in density plots (values below 1 will cut off top of highest peaks to provide better contrast among broader distributions
densityadjust	Multiplier on bandwidth of kernel in density function used for smoothing MCMC posteriors. See 'adjust' in ?density for details.
densitysymbols	Add symbols along lines in density plots. Quantiles are c(0.025,0.1,0.25,0.5,0.75,0.9,0.975).
densitytails	Shade tails outside of 95% interval darker in density plots?
densitymiddle	Shade middle inside of 95% interval darker in density plots?
densitylwd	Line width for density plots
fix0	Always include 0 in the density plots?
new	Create new empty plot window
add	Allows single plot to be added to existing figure. This needs to be combined with specific 'subplots' input to make sure only one thing gets added.
par	list of graphics parameter values passed to the par function
verbose	Report progress to R GUI?
mcmcVec	Vector of TRUE/FALSE values (or single value) indicating whether input values are from MCMC or to use normal distribution around MLE

Author(s)

Ian Taylor

See Also

SS_plots, SSsummarize, SS_output, SSgetoutput

SSplotComps *Plot composition data and fits.*

Description

Plot composition data and fits from Stock Synthesis output. Multi-figure plots depend on make_multifig.

Usage

```
SSplotComps(replist, subplots = c(1:21, 24), kind = "LEN", sizemethod = 1,
  aalyear = -1, aalbin = -1, plot = TRUE, print = FALSE,
  fleets = "all", fleetnames = "default", sexes = "all", yupper = 0.4,
  datonly = FALSE, samplesizeplots = TRUE, compresidplots = TRUE,
  bub = FALSE, showyears = TRUE, showsampsize = TRUE, showeffN = TRUE,
  sampsizeline = FALSE, effNline = FALSE, minnbubble = 3,
  pntscalar = NULL, scalebubbles = FALSE, cexZ1 = 1.5, bublegend = TRUE,
  colvec = c(rgb(1, 0, 0, 0.7), rgb(0, 0, 1, 0.7), rgb(0.1, 0.1, 0.1, 0.7)),
  linescol = c(rgb(0, 0.5, 0, 0.7), rgb(0.8, 0, 0, 0.7), rgb(0, 0, 0.8, 0.7)),
  axis1 = NULL, axis2 = NULL, blue = rgb(0, 0, 1, 0.7), red = rgb(1, 0,
  0, 0.7), pwidth = 6.5, pheight = 5, punits = "in", ptsize = 10,
  res = 300, plotdir = "default", cex.main = 1, linepos = 1,
  fitbar = FALSE, do.sqrt = TRUE, smooth = TRUE, cohortlines = c(),
  labels = c("Length (cm)", "Age (yr)", "Year", "Observed sample size",
  "Effective sample size", "Proportion", "cm", "Frequency", "Weight", "Length",
  "(mt)", "(numbers x1000)", "Stdev (Age) (yr)", "Conditional AAL plot, "),
  printmkt = TRUE, printsex = TRUE, maxrows = 6, maxcols = 6,
  maxrows2 = 2, maxcols2 = 4, rows = 1, cols = 1, andre_oma = c(3, 0,
  3, 0), andrerows = 3, fixdims = TRUE, fixdims2 = FALSE,
  maxneff = 5000, verbose = TRUE, scalebins = FALSE, addMeans = TRUE,
  ...)
```

Arguments

replist	list created by SSoutput
subplots	vector controlling which subplots to create
kind	indicator of type of plot can be "LEN", "SIZE", "AGE", "cond", "GSTAGE", "L[at]A", or "W[at]A".
sizemethod	if kind = "SIZE" then this switch chooses which of the generalized size bin methods will be plotted.
aalyear	Years to plot multi-panel conditional age-at-length fits for all length bins; must be in a "c(YYYY,YYYY)" format. Useful for checking the fit of a dominant year class, critical time period, etc. Default=-1.
aalbin	The length bin for which multi-panel plots of the fit to conditional age-at-length data will be produced for all years. Useful to see if growth curves are ok, or to see the information on year classes move through the conditional data. Default=-1.
plot	plot to active plot device?
print	print to PNG files?
fleets	optional vector to subset fleets for which plots will be made
fleetnames	optional vector of fleet names to put in the labels
sexes	which sexes to show plots for. Default="all" which will include males, females, and unsexed. This option is not fully implemented for all plots.
yupper	upper limit on ymax for polygon/histogram composition plots

datonly	make plots of data without fits as well as data with fits?
samplesizeplots	make sample size plots?
compresidplots	make plots of residuals for fit to composition data?
bub	make bubble plot for numbers at age or size?
showyears	Add labels for years to sample size plots?
showsampsize	add sample sizes to plot
showeffN	add effective sample sizes to plot
sampsizeline	show line for input sample sizes on top of conditional age-at-length plots (TRUE/FALSE, still in development)
effNline	show line for effective sample sizes on top of conditional age-at-length plots (TRUE/FALSE, still in development)
minnbubble	number of unique x values before adding buffer. see ?bubble3 for more info.
pntscalar	This scalar defines the maximum bubble size for bubble plots. This option is still available but a better choice is to use cexZ1 which allow the same scaling throughout all plots.
scalebubbles	scale data-only bubbles by sample size, not just proportion within sample? Default=FALSE.
cexZ1	Character expansion (cex) for point associated with value of 1.
bublegend	Add legend with example bubble sizes to bubble plots.
colvec	Vector of length 3 with colors for females, males, unsexed fish
linescol	Color for lines on top of polygons
axis1	position of bottom axis values
axis2	position of left size axis values
blue	What color to use for males in bubble plots (default is slightly transparent blue)
red	What color to use for females in bubble plots (default is slightly transparent red)
pwidth	default width of plots printed to files in units of punits. Default=7.
pheight	default height width of plots printed to files in units of punits. Default=7.
punits	units for pwidth and pheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
ptsize	point size for plotted text in plots printed to files (see help("png") in R for details). Default=12.
res	resolution of plots printed to files. Default=300
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
cex.main	character expansion parameter for plot titles
linepos	should lines be added before points (linepos=1) or after (linepos=2)?
fitbar	show fit to bars instead of points
do.sqrt	scale bubbles based on sqrt of size vector. see ?bubble3 for more info.

smooth	add loess smoother to observed vs. expected index plots and input vs. effective sample size?
cohortlines	optional vector of birth years for cohorts for which to add growth curves to numbers at length bubble plots
labels	vector of labels for plots (titles and axis labels)
printmkt	show market categories in plot titles?
printsex	show gender in plot titles?
maxrows	maximum (or fixed) number or rows of panels in the plot
maxcols	maximum (or fixed) number or columns of panels in the plot
maxrows2	maximum number of rows for conditional age at length plots
maxcols2	maximum number of columns for conditional age at length plots
rows	number or rows to return to as default for next plots to come or for single plots
cols	number or cols to return to as default for next plots to come or for single plots
andre_oma	Outer margins passed to Andre's multi-panel conditional age-at-length plots.
andrerows	Number of rows of Andre's conditional age-at-length plots within each page. Default=3.
fixdims	fix the dimensions at maxrows by maxcols or resize based on number of years of data
fixdims2	fix the dimensions at maxrows by maxcols in aggregate plots or resize based on number of fleets
maxneff	the maximum value to include on plots of input and effective sample size. Occasionally a calculation of effective N blows up to very large numbers, rendering it impossible to observe the relationship for other data. Default=5000.
verbose	return updates of function progress to the R GUI?
scalebins	Rescale expected and observed proportions by dividing by bin width for models where bins have different widths? Caution!: May not work correctly in all cases.
addMeans	Add parameter means in addition to medians for MCMC posterior distributions in which the median and mean differ.
...	additional arguments that will be passed to the plotting.

Author(s)

Ian Taylor

See Also

SS_plots, make_multifig

SSplotData *Timeline of presence/absence of data by type, year, and fleet.*

Description

Plot shows graphical display of what data is being used in the model. Some data types may not yet be included. Note, this is based on output from the model, not the input data file.

Usage

```
SSplotData(replist, plot = TRUE, print = FALSE, plotdir = "default",
  fleetcol = "default", datatypes = "all", fleets = "all",
  fleetnames = "default", ghost = FALSE, pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1,
  margins = c(5.1, 2.1, 2.1, 8.1), cex = 2, lwd = 12, verbose = TRUE)
```

Arguments

replist	list created by SS_output
plot	plot to active plot device?
print	print to PNG files?
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
fleetcol	Either the string "default", or a vector of colors to use for each fleet.
datatypes	Either the string "all", or a vector including some subset of the following: "catch", "cpue", "lendbase", "sizedbase", "agedbase", "condbase", "ghostagedbase", "ghostcondbase", "ghostlendbase", "ladbase", "wadbase", "mnwgt", "discard", "tagdbase1", "tagdbase2".
fleets	Either the string "all", or a vector of numerical values, like c(1,3), listing fleets or surveys to be included in the plot.
fleetnames	A vector of alternative names to use in the plot. By default the parameter names in the data file are used.
ghost	TRUE/FALSE indicator for whether to show presence of composition data from ghost fleets (data for which the fit is shown, but is not included in the likelihood calculations).
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
margins	margins of plot (passed to par() function), which may need to be increased if fleet names run off right-hand margin

cex	Character expansion for points showing isolated years of data
lwd	Line width for lines showing ranges of years of data
verbose	report progress to R GUI?

Author(s)

Ian Taylor, Chantel Wetzel

See Also

SS_plots, SS_output, SS_readdat

SSplotDiscard *Plot fit to discard fraction.*

Description

Plot fit to discard fraction from Stock Synthesis output file.

Usage

```
SSplotDiscard(replist, subplots = 1:2, plot = TRUE, print = FALSE,
  plotdir = "default", fleets = "all", fleetnames = "default",
  datplot = FALSE, labels = c("Year", "Discard fraction", "Total discards",
  "for"), yhi = 1, col1 = "blue", col2 = "black", pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1,
  verbose = TRUE)
```

Arguments

replist	List created by SS_output
subplots	Vector of which plots to make (1 = data only, 2 = with fit). If plotdat = FALSE then subplot 1 is not created, regardless of choice of subplots.
plot	Plot to active plot device?
print	Print to PNG files?
plotdir	Directory where PNG files will be written. by default it will be the directory where the model was run.
fleets	Optional vector to subset fleets for which plots will be made
fleetnames	Optional replacement for fleenames used in data file
datplot	Make data-only plot of discards? This can override the choice of subplots.
labels	Vector of labels for plots (titles and axis labels)
yhi	Maximum y-value to include in plot (all data included regardless). Default = 1.
col1	First color to use in plot (for expected values)
col2	Second color to use in plot (for observations and intervals)

pwidth	Width of plot
pheight	Height of plot
punits	Units for PNG file
res	Resolution for PNG file
ptsize	Point size for PNG file
cex.main	Character expansion for plot titles
verbose	Report progress to R GUI?

Author(s)

Ian G. Taylor, Ian J. Stewart, Robbie L. Emmet

See Also

SS_plots

SSplotIndices *Plot indices of abundance and associated quantities.*

Description

Plot indices of abundance and associated quantities.

Usage

```
SSplotIndices(replist, subplots = 1:9, plot = TRUE, print = FALSE,
  fleets = "all", fleetnames = "default", smooth = TRUE, add = FALSE,
  datplot = FALSE, labels = c("Year", "Index", "Observed index",
  "Expected index", "Log index", "Log observed index", "Log expected index",
  "Standardized index", "Catchability (Q)", "Time-varying catchability",
  "Vulnerable biomass", "Catchability vs. vulnerable biomass"),
  col1 = "default", col2 = "default", col3 = "blue", col4 = "red",
  pch1 = 21, pch2 = 16, cex = 1, bg = "white", legend = TRUE,
  legendloc = "topright", seasnames = NULL, pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1, addmain = TRUE,
  plotdir = "default", minyr = NULL, maxyr = NULL,
  maximum_ymax_ratio = Inf, show_input_uncertainty = TRUE, verbose = TRUE,
  ...)
```

Arguments

replist	list created by SS_output
subplots	vector controlling which subplots to create
plot	plot to active plot device?
print	print to PNG files?

fleets	optional vector to subset fleets for which plots will be made
fleetnames	optional replacement for fleenames used in data file
smooth	add smoothed line to plots of observed vs. expected sample sizes
add	add to existing plot (not yet implemented)
datplot	make plot of data only?
labels	vector of labels for plots (titles and axis labels)
col1	vector of colors for points in each season for time series plot. Default is red for single season models and a rainbow using the rich.colors.short function for multiple seasons.
col2	vector of colors for points in each season for obs. vs. exp. plot. Default is blue for single season models and a rainbow using the rich.colors.short function for multiple seasons.
col3	color of line showing expected index in time series plot. Default is blue.
col4	color of smoother shown in obs. vs. exp. plots. Default is red.
pch1	single value or vector of plotting characters (pch parameter) for time-series plots of index fit. Default=21.
pch2	single value or vector of plotting characters (pch parameter) for sample size plots of index fit. Default=16.
cex	character expansion factor for points showing observed values. Default=1.
bg	Background color for points with pch=21.
legend	add a legend to seasonal colors (only for seasonal models)
legendloc	add a legend to seasonal colors (default is "topright")
seasnames	optional vector of names for each season to replace defaults if a legend is used
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
addmain	switch which allows the plot title to be left off
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
minyr	First year to show in plot (for zooming in on a subset of values)
maxyr	Last year to show in plot (for zooming in on a subset of values)
maximum_ymax_ratio	Maximum allowed value for ymax (specified as ratio of y), which overrides any value of ymax that is greater (default = Inf)
show_input_uncertainty	switch controlling whether to add thicker uncertainty interval lines indicating the input uncertainty relative to the total uncertainty which may result from estimating a parameter for extra standard deviations
verbose	report progress to R GUI?
...	Extra arguments to pass to calls to plot

Author(s)

Ian Stewart, Ian Taylor, James Thorson

See Also

SS_plots, SS_output

SSplotMCMC_ExtraSelex *Plot uncertainty around chosen selectivity ogive from MCMC.*

Description

Plot uncertainty in selectivity from an MCMC output for whichever fleet/year was chosen in the optional extra "more stddev reporting"

Usage

```
SSplotMCMC_ExtraSelex(post, add = FALSE, nsexes = 1, shift = 0,
  fleetname = "default", col = "blue")
```

Arguments

post	A data frame containing either derived_posteriors.sso or a good subset of it. This can be an element of the list created by the the SSgetMCMC function.
add	TRUE/FALSE option to add results to an existing plot.
nsexes	Number of sexes in the model (should match model values but is only used in the title).
shift	Optional adjustment to the x values to avoid overlap of intervals when overplotting on an existing plot.
fleetname	Optional input to make the title better. Default will be something like "Fleet 1", using the numbering from the model.
col	Color for points and lines.

Author(s)

Ian Taylor

SSplotMnwt *Plot mean weight data and fits.*

Description

Plot mean weight data and fits from Stock Synthesis output. Intervals are based on T-distributions as specified in model.

Usage

```
SSplotMnwt(replist, subplots = 1:2, ymax = NULL, plot = TRUE,
  print = FALSE, fleets = "all", fleetnames = "default",
  datplot = FALSE, labels = c("Year", "discard", "retained catch",
  "whole catch", "Mean individual body weight (kg)", "Mean weight in", "for"),
  col1 = "blue", col2 = "black", pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1,
  plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SS_output
subplots	Vector of which plots to make (1 = data only, 2 = with fit). If plotdat = FALSE then subplot 1 is not created, regardless of choice of subplots.
ymax	Optional input to override default ymax value.
plot	plot to active plot device?
print	print to PNG files?
fleets	optional vector to subset fleets for which plots will be made
fleetnames	optional replacement for fleenames used in data file
datplot	Make data-only plot of discards? This can override the choice of subplots.
labels	vector of labels for plots (titles and axis labels)
col1	first color to use in plot (for expected values)
col2	second color to use in plot (for observations and intervals)
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Taylor, Ian Stewart

See Also

SS_plots, SS_output

SSplotMovementMap *Show movement rates on a map.*

Description

Make a map with colored spatial cells and add arrows representing movement rates between cells.

Usage

```
SSplotMovementMap(replist = NULL, xlim, ylim, polygonlist, colvec,
  land = "grey", xytable = NULL, moveage = 5, moveseas = 1,
  lwdscale = 5, legend = TRUE, title = NULL, areanames = NULL,
  cex = 1)
```

Arguments

replist	optional list created by SS_output
xlim	range of longitude values in the map
ylim	range of latitude values in the map
polygonlist	a list of data frames, each with two columns representing the longitude and latitude values of the colored polygons. The order of elements in the list should match the numbering of areas in the SS model.
colvec	vector of colors for each polygon (if replist is provided)
land	color of landmasses in the map
xytable	data frame of latitude and longitude values which will be connected by the arrows representing movement rates. The order should match the order of areas in polygonlist and in the SS model. Not necessary if no arrows are shown on the map.
moveage	age for which movemement rates will be represented
moveseas	season for which movement rates will be represented
lwdscale	scaling factor for arrows in the plot. The largest rate of movement shown will be scaled to have a line width equal to this value.
legend	add a legend to show the movement rate associated with the widest arrows
title	optional title to be added above map
areanames	optional vector of names to be shown on map at coordinates matching xytable values
cex	character expansion to apply to text shown by areanames (if used)

Note

Inspired by plots of MULTIFAN-CL movement patterns presented by Adam Langley

Author(s)

Ian Taylor

See Also

SS_output, SSplotMovementRates, IOTCmove

SSplotMovementRates *Plot movement rates from model output*

Description

Plots estimated movement rates in final year for each area/seaon with movement as reported in Report.sso. If movement is time-varying, an additional figure shows pattern across years.

Usage

```
SSplotMovementRates(replist, plot = TRUE, print = FALSE, subplots = 1:2,
  plotdir = "default", colvec = "default", ylim = "default",
  legend = TRUE, legendloc = "topleft", moveseas = "all",
  min.move.age = 0.5, pwidth = 6.5, pheight = 5, punits = "in",
  res = 300, ptsize = 10, cex.main = 1, verbose = TRUE)
```

Arguments

replist	list created by SS_output
plot	plot to active plot device?
print	print to PNG files?
subplots	which subplots to create
plotdir	where to put the plots (uses model directory by default)
colvec	vector of colors for each movement rate in the plot
ylim	optional input for y range of the plot. By default plot ranges from 0 to 10% above highest movement rate (not including fish staying in an area).
legend	add a legend designating which color goes with which pair of areas?
legendloc	location passed to legend function (if used)
moveseas	choice of season for which movemement rates are shown
min.move.age	Minimum age of movement (in future will come from Report file)
pwidth	width of plot
pheight	height of plot

punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	Character expansion parameter for plot titles
verbose	Print information on function progress.

Author(s)

Ian Taylor

See Also

SS_output, SSplotMovementRates, IOTCmove

Examples

```
  ## Not run:
    SSplotMovementRates(myreplist)

## End(Not run)
```

SSplotNumbers *Plot numbers-at-age related data and fits.*

Description

Plot numbers-at-age related data and fits from Stock Synthesis output. Plots include bubble plots, mean age, equilibrium age composition, sex-ratio, and ageing imprecision patterns.

Usage

```
SSplotNumbers(replist, subplots = 1:9, plot = TRUE, print = FALSE,
  numbers.unit = 1000, areas = "all", areanames = "default",
  areacols = "default", pntscalar = 2.6, bub.bg = gray(0.5, alpha = 0.5),
  bublegend = TRUE, period = c("B", "M"), add = FALSE,
  labels = c("Year", "Age", "True age (yr)", "SD of observed age (yr)",
  "Mean observed age (yr)", "Mean age (yr)", "mean age in the population",
  "Ageing imprecision", "Numbers at age at equilibrium",
  "Equilibrium age distribution", "Sex ratio of numbers at age (males/females)",
  "Length", "Mean length (cm)", "mean length (cm) in the population",
  "expected numbers at age", "Beginning of year", "Middle of year",
  "expected numbers at length",
  "Sex ratio of numbers at length (males/females)",
  "Sex ratio of numbers at length (females/males)"), pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1,
  plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SSoutput
subplots	vector controlling which subplots to create
plot	plot to active plot device?
print	print to PNG files?
numbers.unit	Units for numbers. Default (based on typical Stock Synthesis setup) is thousands (numbers.unit=1000).
areas	optional subset of areas to plot for spatial models
areanames	names for areas. Default is to use Area1, Area2,...
areacols	vector of colors by area
pntscalar	maximum bubble size for bubble plots; each plot scaled independently based on this maximum size and the values plotted. Often some plots look better with one value and others with a larger or smaller value. Default=2.6
bub.bg	background color for bubbles (no control over black border at this time)
bublegend	Add legend with example bubble sizes?
period	indicator of whether to make plots using numbers at age just from the beginning ("B") or middle of the year ("M") (new option starting with SSv3.11)
add	add to existing plot? (not yet implemented)
labels	vector of labels for plots (titles and axis labels)
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_output, SS_plots

SSplotPars *Plot distributions of priors, posteriors, and estimates.*

Description

Make multi-figure plots of prior, posterior, and estimated asymptotic parameter distributions. MCMC not required to make function work.

Usage

```
SSplotPars(dir = "c:/path/", repfile = "Report.sso",
  xlab = "Parameter value", ylab = "Density", postfile = "posteriors.sso",
  showpost = TRUE, showprior = TRUE, showmle = TRUE, showinit = TRUE,
  showrecdev = TRUE, priorinit = TRUE, priorfinal = TRUE,
  showlegend = TRUE, fitrange = FALSE, xaxs = "i", xlim = NULL,
  ylim = NULL, verbose = TRUE, nrows = 3, ncols = 3, ltyvec = c(1, 1,
  3, 4), colvec = c("blue", "red", "black", "gray60", rgb(0, 0, 0, 0.5)),
  new = TRUE, pdf = FALSE, pwidth = 6.5, pheight = 5, punits = "in",
  ptsize = 10, returntable = FALSE, strings = c(), exact = FALSE,
  newheaders = NULL, burn = 0, thin = 1, ctlfile = "control.ss_new")
```

Arguments

dir	Directory where all files are located.
repfile	Name of report file. Default="Report.sso".
xlab	Label on horizontal axis.
ylab	Label on vertical axis.
postfile	Name of MCMC posteriors file (not required). Default="posteriors.sso".
showpost	Show posterior distribution as bar graph? Default=TRUE.
showprior	Show prior distribution as black line? Default=TRUE.
showmle	Show MLE estimate and asymptotic variance estimate with blue lines? Default=TRUE.
showinit	Show initial value as red triangle? Default=TRUE.
showrecdev	Include recdevs in the plot? Default=TRUE.
priorinit	TRUE/FALSE for prior probability at initial value (not implemented).
priorfinal	TRUE/FALSE for prior probability at final value (not implemented).
showlegend	Show the legend? Default=TRUE.
fitrange	Fit range tightly around MLE & posterior distributions, instead of full parameter range? Default=FALSE.
xaxs	Parameter input for x-axis. See ?par for more info. Default="i".
xlim	Optional x-axis limits to be applied to all plots. Otherwise, limits are based on the model results. Default=NULL.

ylim	Optional y-axis limits to be applied to all plots. Otherwise, limits are based on the model results. Default=NULL.
verbose	Controls amount of text output (maybe). Default=TRUE.
nrows	How many rows in multi-figure plot. Default=3.
ncols	How many columns in multi-figure plot. Default=3.
ltyvec	Vector of line types used for lines showing MLE and prior distributions and the median of the posterior distribution
colvec	Vector of colors used for lines and polygons showing MLE, initial value, prior, posterior, and median of the posterior.
new	Open new window for plotting? Default=TRUE.
pdf	Write to PDF file instead of R GUI? Default=FALSE.
pwidth	Default width of plots printed to files in units of punits. Default=7.
pheight	Default height width of plots printed to files in units of punits. Default=7.
punits	Units for pwidth and pheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
ptsize	Point size for plotted text in plots printed to files (see help("png") in R for details). Default=12.
returntable	Return table of parameter info? Default=FALSE.
strings	Subset parameters included in the plot using substring from parameter names (i.e. "SR" will get "SR_R0" and "SR_steep" if they are both estimated quantities in this model). Default=c().
exact	Should strings input match parameter names exactly? Otherwise substrings are allowed. Default=FALSE.
newheaders	Optional vector of headers for each panel to replace the parameter names. Default=NULL.
burn	Additional burn-in applied to MCMC posteriors. Default=0.
thin	Additional thinning applied to MCMC posteriors. Default=1.
ctlfile	Specify control file to get min and max recdev values (otherwise assumed to be -5 and 5). Default="control.ss_new".

Author(s)

Ian Taylor

Examples

```
## Not run:
pars <- SSplotPars(dir='c:/SS/Simple/')

# strings can be partial match
pars <- SSplotPars(dir='c:/SS/Simple/',strings=c("steep"))

## End(Not run)
```

SSplotProfile *Plot likelihood profile results*

Description

Makes a plot of change in negative-log-likelihood for each likelihood component that contributes more than some minimum fraction of change in total.

Usage

```
SSplotProfile(summaryoutput, plot = TRUE, print = FALSE, models = "all",
  profile.string = "steep", profile.label = "Spawner-recruit steepness (h)",
  ylab = "Change in -log-likelihood", components = c("TOTAL", "Catch",
  "Equil_catch", "Survey", "Discard", "Mean_body_wt", "Length_comp", "Age_comp",
  "Size_at_age", "SizeFreq", "Morphcomp", "Tag_comp", "Tag_negbin",
  "Recruitment", "Forecast_Recruitment", "Parm_priors", "Parm_softbounds",
  "Parm_devs", "F_Ballpark", "Crash_Pen"), component.labels = c("Total",
  "Catch", "Equilibrium catch", "Index data", "Discard", "Mean body weight",
  "Length data", "Age data", "Size-at-age data", "Generalized size data",
  "Morph composition data", "Tag recapture distribution", "Tag recapture total",
  "Recruitment", "Forecast recruitment", "Priors", "Soft bounds",
  "Parameter deviations", "F Ballpark", "Crash penalty"), minfraction = 0.01,
  sort.by.max.change = TRUE, col = "default", pch = "default", lty = 1,
  lty.total = 1, lwd = 2, lwd.total = 3, cex = 1, cex.total = 1.5,
  xlim = "default", ymax = "default", xaxs = "r", yaxs = "r",
  type = "o", legend = TRUE, legendloc = "topright", pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1,
  plotdir = NULL, verbose = TRUE, ...)
```

Arguments

summaryoutput	List created by the function SSsummarize.
plot	Plot to active plot device?
print	Print to PNG files?
models	Optional subset of the models described in summaryoutput. Either "all" or a vector of numbers indicating columns in summary tables.
profile.string	Character string used to find parameter over which the profile was conducted. Needs to match substring of one of the SS parameter labels found in the Report.sso file. For instance, the default input 'steep' matches the parameter 'SR_BH_steep'.
profile.label	Label for x-axis describing the parameter over which the profile was conducted.
ylab	Label for y-axis. Default is "Change in -log-likelihood".
components	Vector of likelihood components that may be included in plot. List is further refined by any components that are not present in model or have little change over range of profile (based on limit minfraction). Hopefully this doesn't need to be changed.

component.labels
: Vector of labels for use in the legend that matches the vector in components.

minfraction
: Minimum change in likelihood (over range considered) as a fraction of change in total likelihood for a component to be included in the figure.

sort.by.max.change
: Switch giving option to sort components in legend in order of maximum amount of change in likelihood (over range considered). Default=TRUE.

col
: Optional vector of colors for each line.

pch
: Optional vector of plot characters for the points.

lty
: Line total for the liklihood components.

lty.total
: Line type for the total likelihood.

lwd
: Line width for the liklihood components.

lwd.total
: Line width for the total likelihood.

cex
: Character expansion for the points representing the likelihood components.

cex.total
: Character expansion for the points representing the total likelihood.

xlim
: Range for x-axis. Change in likelihood is calculated relative to values within this range.

ymax
: Maximum y-value. Default is 10% greater than largest value plotted.

xaxs
: The style of axis interval calculation to be used for the x-axis (see ?par for more info)

yaxs
: The style of axis interval calculation to be used for the y-axis (see ?par for more info).

type
: Line type (see ?plot for more info).

legend
: Include legend?

legendloc
: Location of legend (see ?legend for more info).

pwidth
: Width of plot

pheight
: Height of plot

punits
: Units for PNG file

res
: Resolution for PNG file

ptsize
: Point size for PNG file

cex.main
: Character expansion for plot titles

plotdir
: Directory where PNG files will be written. by default it will be the directory where the model was run.

verbose
: Return updates of function progress to the R GUI? (Doesn't do anything yet.)

...
: Additional arguments passed to the plot command.

Note

Someday the function SS_profile will be improved and made to work directly with this plotting function, but they don't yet work well together. Thus, even if SS_profile is used, the output should be read using SSgetoutput or by multiple calls to SS_output.

Author(s)

Ian Taylor, Ian Stewart

See Also

SSsummarize, SS_profile, SS_output, SSgetoutput

SSplotRecdevs *Plot recruitment deviations*

Description

Plot recruitment deviations and associated quantities including derived measures related to bias adjustment.

Usage

```
SSplotRecdevs(replist, subplots = 1:3, plot = TRUE, print = FALSE,
  add = FALSE, uncertainty = TRUE, forecastplot = FALSE, col1 = "black",
  col2 = "blue", col3 = "green3", col4 = "red", legendloc = "topleft",
  labels = c("Year", "Asymptotic standard error estimate",
  "Log recruitment deviation",
  "Bias adjustment fraction, 1 - stddev^2 / sigmaR^2"), pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1,
  plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SSoutput
subplots	vector controlling which subplots to create
plot	plot to active plot device?
print	print to PNG files?
add	add to existing plot (not yet implemented)
uncertainty	include plots showing uncertainty?
forecastplot	include points from forecast years?
col1	first color used
col2	second color used
col3	third color used
col4	fourth color used
legendloc	location of legend. see ?legend for more info
labels	vector of labels for plots (titles and axis labels)
pwidth	width of plot
pheight	height of plot

punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Taylor, Ian Stewart

See Also

SS_plots, SS_fitbiasramp

SSplotRecdist *Plot of recruitment distribution among areas and seasons*

Description

Image plot shows fraction of recruitment in each combination of area and season. This is based on the RECRUITMENT_DIST section of the Report.sso file.

Usage

```
SSplotRecdist(replist, plot = TRUE, print = FALSE, areanames = NULL,
  seasnames = NULL, xlab = "", ylab = "",
  main = "Distribution of recruitment by area and season",
  plotdir = "default", pwidth = 6.5, pheight = 5, punits = "in",
  res = 300, ptsize = 10, cex.main = 1, verbose = TRUE)
```

Arguments

replist	list created by SS_output
plot	plot to active plot device?
print	print to PNG files?
areanames	optional vector to replace c("Area1","Area2",...)
seasnames	optional vector to replace c("Season1","Season2",...)
xlab	optional x-axis label (if the area names aren't informative enough)
ylab	optional y-axis label (if the season names aren't informative enough)
main	title for plot
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.

pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
verbose	report progress to R GUI?

Author(s)

Ian Taylor

See Also

SS_plots, SSplotRecdevs

SSplotRetroRecruits *Make squid plot of retrospectives of recruitment deviations.*

Description

Inspired by Jim Ianelli and named by Sean Cox, the squid plot is a way to examine retrospective patterns in estimation of recruitment deviations.

Usage

```
SSplotRetroRecruits(retroSummary, endyrvec, cohorts, ylim = NULL,
  uncertainty = FALSE, labels = c("Recruitment deviation",
  "Recruitment (billions)", "relative to recent estimate", "Age"),
  main = "Retrospective analysis of recruitment deviations",
  mcmcVec = FALSE, devs = TRUE, relative = FALSE, labelyears = TRUE,
  legend = FALSE, leg.ncols = 4)
```

Arguments

retroSummary	List object created by SSsummarize that summarizes the results of a set of retrospective analysis models.ss
endyrvec	Vector of years representing the final year of values to show for each model.
cohorts	Which cohorts to show in plot.
ylim	Limits of y-axis.
uncertainty	Show uncertainty intervals around lines? (This can get a bit busy.)
labels	Vector of plot labels.
main	Title for plot.

mcmcVec	Either vector of TRUE/FALSE values indicating which models use MCMC. Or single value applied to all models.
devs	Plot deviations instead of absolute recruitment values?
relative	Show deviations relative to most recent estimate or relative to 0.
labelyears	Label cohorts with text at the end of each line?
legend	Add a legend showing which color goes with which line (as alternative to labelyears).
leg.ncols	Number of columns for the legend.

Author(s)

Ian Taylor

References

Ianelli et al. (2011) Assessment of the walleye pollock stock in the Eastern Bering Sea. http://www.afsc.noaa.gov/REFM/docs/2011/EBSpollock.pdf. (Figure 1.31, which is on an absolute, rather than log scale.)

See Also

SSsummarize

Examples

```
## Not run:
# run retrospective analysis
SS_doRetro(olddir='2013hake_12',years=0:-10)
# read in output
retroModels <- SSgetoutput(dirvec=paste('retrospectives/retro',-10:0,sep=''))
# summarize output
retroSummary <- SSsummarize(retroModels)

# set the ending year of each model in the set
endyrvec <- retroModels[[1]]$endyr-10:0
# make comparison plot
pdf('retrospectives/retrospective_comparison_plots.pdf')
SSplotComparisons(retroSummary,endyrvec=endyrvec,new=FALSE)
dev.off()

# make Squid Plot of recdev retrospectives
pdf('retrospectives/retrospective_dev_plots.pdf',width=7,height=10)
par(mfrow=c(2,1))
# first scaled relative to most recent estimate
SSplotRetroRecruits(retroSummary, endyrvec=endyrvec, cohorts=1999:2012,
                    relative=TRUE, legend=FALSE)
# second without scaling
SSplotRetroDevs(retroSummary, endyrvec=endyrvec, cohorts=1999:2012,
                relative=FALSE, legend=FALSE)
dev.off()
```

```
## End(Not run)
```

SSplotSelex *Plot selectivity*

Description

Plot selectivity, including retention and other quantities, with additional plots for time-varying selectivity.

Usage

```
SSplotSelex(replist, infotable = NULL, fleets = "all",
  fleetnames = "default", sizefactors = c("Lsel"), agefactors = c("Asel",
  "Asel2"), years = "endyr", season = 1, sexes = "all",
  selexlines = 1:6, subplot = 1:25, skipAgeSelex10 = TRUE, plot = TRUE,
  print = FALSE, add = FALSE, labels = c("Length (cm)", "Age (yr)",
  "Year", "Selectivity", "Retention", "Discard mortality"), col1 = "red",
  col2 = "blue", lwd = 2, fleetcols = "default", fleetpch = "default",
  fleetlty = "default", spacepoints = 5, staggerpoints = 1,
  legendloc = "bottomright", pwidth = 7, pheight = 7, punits = "in",
  res = 300, ptsize = 12, cex.main = 1, showmain = TRUE,
  plotdir = "default", verbose = TRUE)
```

Arguments

replist	List created by SS_output
infotable	Optional table of information controlling appearance of plot and legend. Is produced as output and can be modified and entered as input.
fleets	Optional vector to subset fleets for which to make plots
fleetnames	Optional replacement for fleenames used in data file
sizefactors	Which elements of the factors column of SIZE_SELEX should be included in plot of selectivity across multiple fleets?
agefactors	Which elements of the factors column of AGE_SELEX should be included in plot of selectivity across multiple fleets?
years	Which years for selectivity are shown in multi-line plot (default = last year of model).
season	Which season (if seasonal model) for selectivity shown in multi-line plot (default = 1).
sexes	Optional vector to subset genders for which to make plots (1=females, 2=males)
selexlines	Vector to select which lines get plotted. values are 1. Selectivity, 2. Retention, 3. Discard mortality, 4. Keep = Sel*Ret, 5. Dead = Sel*(Ret+(1-Ret)*Mort).

subplot	Vector controlling which subplots to create
skipAgeSelex10	Exclude plots for age selectivity type 10 (selectivity = 1.0 for all ages beginning at age 1)?
plot	Plot to active plot device?
print	Print to PNG files?
add	Add to existing plot (not yet implemented)
labels	vector of labels for plots (titles and axis labels)
col1	color for female growth curve
col2	color for male growth curve
lwd	Line widths for plots
fleetcols	Optional vector of colors for each fleet (in multi-fleet plots)
fleetpch	Optional vector of plot characters for each fleet (in multi-fleet plots)
fleetlty	Optional vector of line types for each fleet (in multi-fleet plots)
spacepoints	number of years between points shown on top of lines (for long timeseries, points every year get mashed together)
staggerpoints	number of years to stagger the first point (if spacepoints > 1) for each line (so that adjacent lines have points in different years)
legendloc	location of legend. See ?legend for more info.
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
showmain	Include main title at top of plot?
plotdir	Directory where PNG files will be written. By default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_plots, SS_output

SSplotSpawnrecruit *Plot spawner-recruit curve.*

Description

Plot spawner-recruit curve based on output from Stock Synthesis model.

Usage

```
SSplotSpawnrecruit(replist, subplot = 1:2, add = FALSE, plot = TRUE,
  print = FALSE, xlim = NULL, ylim = NULL,
  xlab = "Spawning biomass (mt)", ylab = "Recruitment (1,000s)",
  bioscale = "default", plotdir = "default", pwidth = 6.5, pheight = 5,
  punits = "in", res = 300, ptsize = 10, cex.main = 1, verbose = TRUE,
  colvec = c("blue", "green3", "black", "red"), legend = TRUE,
  legendloc = "topleft", minyr = "default", textmindev = 0.5,
  virg = TRUE, init = TRUE, forecast = FALSE)
```

Arguments

replist	list created by SS_output
subplot	vector of which subplots to show. 1=plot without labels, 2=plot with year labels.
add	add to existing plot?
plot	plot to active plot device?
print	print to PNG files?
xlim	optional control of x range
ylim	optional control of y range
xlab	x-axis label
ylab	y-axis label
bioscale	multiplier on spawning biomass, set to 0.5 for single-sex models
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
verbose	report progress to R GUI?
colvec	vector of length 4 with colors for 3 lines and 1 set of points
legend	add a legend to the figure?

legendloc	location of legend. See ?legend for more info
minyr	minimum year of recruitment deviation to show in plot
textmindev	minimum recruitment deviation for label to be added so only extreme devs are labeled (labels are added to first and last years as well). Default=0.7.
virg	add point for equilibrium conditions (x=B0,y=R0)
init	add point for initial conditions (x=B1,y=R1), only appears if this point differs from virgin values
forecast	include forecast years in the curve?

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_plots, SS_output

SSplotSPR *Plot SPR quantities.*

Description

Plot SPR quantities, including 1-SPR and phase plot.

Usage

```
SSplotSPR(replist, add = FALSE, plot = TRUE, print = FALSE,
  uncertainty = TRUE, subplots = 1:4, forecastplot = FALSE,
  col1 = "black", col2 = "blue", col3 = "green3", col4 = "red",
  sprtarg = "default", btarg = "default", labels = c("Year", "SPR",
  "1-SPR"), pwidth = 6.5, pheight = 5, punits = "in", res = 300,
  ptsize = 10, cex.main = 1, plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SSoutput
add	add to existing plot (not yet implemented)
plot	plot to active plot device?
print	print to PNG files?
uncertainty	include plots showing uncertainty?
subplots	vector controlling which subplots to create
forecastplot	Include forecast years in plot?
col1	first color used
col2	second color used

col3	third color used
col4	fourth color used
sprtarg	F/SPR proxy target. "default" chooses based on model output.
btarg	target depletion to be used in plots showing depletion. May be omitted by setting to NA. "default" chooses based on model output.
labels	vector of labels for plots (titles and axis labels)
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_plots, SS_output

SSplotSummaryF *Plot the summary F (or harvest rate).*

Description

Plots the summary F (or harvest rate) as set up in the starter file Needs a lot of work to be generalized

Usage

```
SSplotSummaryF(replist, yrs = "all", Ftgt = NA,
  ylab = "Summary Fishing Mortality", plot = TRUE, print = FALSE,
  plotdir = "default", verbose = TRUE, uncertainty = TRUE, pwidth = 6.5,
  pheight = 5, punits = "in", res = 300, ptsize = 10)
```

Arguments

replist	List created by SS_output
yrs	Which years to include.
Ftgt	Target F where horizontal line is shown.
ylab	Y-axis label.
plot	Plot to active plot device?
print	Print to PNG files?
plotdir	Directory where PNG files will be written. By default it will be the directory where the model was run.
verbose	Verbose output to R console?
uncertainty	Show 95% uncertainty intervals around point estimates?
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file

Author(s)

Allan Hicks

See Also

SSplotTimeseries, ~~~

SSplotTags *Plot tagging data and fits*

Description

Plot observed and expected tag recaptures in aggregate and by tag group.

Usage

```
SSplotTags(replist = replist, subplots = 1:8, latency = NULL, rows = 1,
  cols = 1, tagrows = 3, tagcols = 3, plot = TRUE, print = FALSE,
  pntscalar = 2.6, minnbubble = 8, pwidth = 6.5, pheight = 5,
  punits = "in", ptsize = 10, res = 300, cex.main = 1, col1 = rgb(0,
  0, 1, 0.7), col2 = "red", col3 = "grey95", col4 = "grey70",
  labels = c("Year", "Frequency", "Tag Group",
  "Fit to tag recaptures by tag group",
  "Post-latency tag recaptures aggregated across tag groups",
  "Observed tag recaptures by year and tag group",
  "Residuals for post-latency tag recaptures: (obs-exp)/sqrt(exp)",
  "Observed and expected post-latency tag recaptures by year and tag group"),
  plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SS_output
subplots	vector controlling which subplots to create
latency	period of tag mixing to exclude from plots (in future could be included in SS output)
rows	number or rows of panels for regular plots
cols	number or columns of panels for regular plots
tagrows	number or rows of panels for multi-panel plots
tagcols	number or columns of panels for multi-panel plots
plot	plot to active plot device?
print	print to PNG files?
pntscalar	maximum bubble size for balloon plots; each plot scaled independently based on this maximum size and the values plotted. Often some plots look better with one value and others with a larger or smaller value. Default=2.6
minnbubble	minimum number of years below which blank years will be added to bubble plots to avoid cropping
pwidth	default width of plots printed to files in units of punits. Default=7.
pheight	default height width of plots printed to files in units of punits. Default=7.
punits	units for pwidth and pheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
ptsize	point size for plotted text in plots printed to files (see help("png") in R for details). Default=12.
res	resolution of plots printed to files. Default=300
cex.main	character expansion parameter for plot titles
col1	color for bubbles
col2	color for lines with expected values
col3	shading color for observations within latency period
col4	shading color for observations after latency period
labels	vector of labels for plots (titles and axis labels)
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	return updates of function progress to the R GUI?

Author(s)

Andre Punt, Ian Taylor

See Also

SS_plots, SS_output

SSplotTimeseries *Plot timeseries data*

Description

Plot timeseries data contained in TIME_SERIES output from Stock Synthesis report file. Some values have optional uncertainty intervals.

Usage

```
SSplotTimeseries(replist, subplot, add = FALSE, areas = "all",
  areacols = "default", areanames = "default", forecastplot = TRUE,
  uncertainty = TRUE, bioscale = "default", minyr = NULL, maxyr = NULL,
  plot = TRUE, print = FALSE, plotdir = "default", verbose = TRUE,
  btarg = "default", minbthresh = "default", xlab = "Year",
  labels = NULL, pwidth = 6.5, pheight = 5, punits = "in", res = 300,
  ptsize = 10, cex.main = 1)
```

Arguments

replist	list created by SS_output
subplot	number controlling which subplot to create
add	add to existing plot? (not yet implemented)
areas	optional subset of areas to plot for spatial models
areacols	vector of colors by area. Default uses rich.colors by Arni Magnusson
areanames	names for areas. Default is to use Area1, Area2,...
forecastplot	add points from forecast years
uncertainty	add intervals around quantities for which uncertainty is available
bioscale	scaling for spawning biomass by default it will be set to 0.5 for single-sex models, and 1.0 for all others
minyr	optional input for minimum year to show in plots
maxyr	optional input for maximum year to show in plots
plot	plot to active plot device?
print	print to PNG files?
plotdir	directory where PNG or PDF files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?
btarg	Target depletion to be used in plots showing depletion. May be omitted by setting to 0. "default" chooses value based on modeloutput.
minbthresh	Threshold depletion to be used in plots showing depletion. May be omitted by setting to 0. "default" assumes 0.25 unless btarg in model output is 0.25 in which case minbthresh = 0.125 (U.S. west coast flatfish).

xlab	x axis label for all plots
labels	vector of labels for plots (titles and axis labels)
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
cex.main	character expansion for plot titles

Author(s)

Ian Taylor, Ian Stewart

See Also

SS_plots, SS_output

SSplotYield *Plot yield and surplus production.*

Description

Plot yield and surplus production from Stock Synthesis output. Surplus production is based on Walters et al. (2008).

Usage

```
SSplotYield(replist, subplots = 1:2, add = FALSE, plot = TRUE,
  print = FALSE, labels = c("Relative depletion", "Equilibrium yield (mt)",
  "Total biomass (mt)", "Surplus production (mt)"), col = "blue", lty = 1,
  lwd = 2, cex.main = 1, pwidth = 6.5, pheight = 5, punits = "in",
  res = 300, ptsize = 10, plotdir = "default", verbose = TRUE)
```

Arguments

replist	list created by SS_output
subplots	vector controlling which subplots to create
add	add to existing plot? (not yet implemented)
plot	plot to active plot device?
print	print to PNG files?
labels	vector of labels for plots (titles and axis labels)
col	line color (only applied to equilbrium yield plot at this time)
lty	line type (only applied to equilbrium yield plot at this time)

lwd	line width (only applied to equilbrium yield plot at this time)
cex.main	character expansion for plot titles
pwidth	width of plot
pheight	height of plot
punits	units for PNG file
res	resolution for PNG file
ptsize	point size for PNG file
plotdir	directory where PNG files will be written. by default it will be the directory where the model was run.
verbose	report progress to R GUI?

Author(s)

Ian Stewart, Ian Taylor

References

Walters, Hilborn, and Christensen, 2008, Surplus production dynamics in declining and recovering fish populations. Can. J. Fish. Aquat. Sci. 65: 2536-2551

See Also

SS_plots, SS_output

SSsummarize *Summarize the output from multiple Stock Synthesis models.*

Description

Summarize various quantities from the model output collected by SSgetoutput and return them in a list of tables and vectors.

Usage

```
SSsummarize(biglist, sizeselfactor = "Lsel", ageselfactor = "Asel",
  selfleet = NULL, selyr = "startyr", selgender = 1,
  SpawnOutputUnits = NULL, lowerCI = 0.025, upperCI = 0.975)
```

Arguments

biglist	A list of lists created by SSgetoutput.
sizeselfactor	A string or vector of strings indicating which elements of the selectivity at length output to summarize. Default=c("Lsel").
ageselfactor	A string or vector of strings indicating which elements of the selectivity at age output to summarize. Default=c("Asel").
selfleet	Vector of fleets for which selectivity will be summarized. NULL=all fleets. Default=NULL.
selyr	String or vector of years for which selectivity will be summarized. NOTE: NOT CURRENTLY WORKING. Options: NULL=all years, "startyr" = first year.
selgender	Vector of genders (1 and/or 2) for which selectivity will be summarized. NULL=all genders. Default=NULL.
SpawnOutputUnits	Optional single value or vector of "biomass" or "numbers" giving units of spawning for each model.
lowerCI	Quantile for lower bound on calculated intervals. Default = 0.025 for 95% intervals.
upperCI	Quantile for upper bound on calculated intervals. Default = 0.975 for 95% intervals.

Author(s)

Ian Taylor

See Also

SSgetoutput

SStableComparisons *make table comparing quantities across models*

Description

Creates a table comparing key quantities from multiple models, which is a reduction of the full information in various parts of the list created using the SSsummarize function.

Usage

```
SStableComparisons(summaryoutput, models = "all", likenames = c("TOTAL",
  "Survey", "Length_comp", "Age_comp", "priors", "Size_at_age"),
  names = c("R0", "steep", "NatM", "L_at_Amax", "VonBert_K", "SPB_Virg",
  "Bratio_2015", "SPRratio_2014"), digits = NULL, modelnames = "default",
  csv = FALSE, csvdir = "workingdirectory",
  csvfile = "parameter_comparison_table.csv", verbose = TRUE,
  mcmc = FALSE)
```

Arguments

summaryoutput	list created by SSsummarize
models	optional subset of the models described in summaryoutput. Either "all" or a vector of numbers indicating columns in summary tables.
likenames	Labels for likelihood values to include, should match substring of labels in summaryoutput$likelihoods.
names	Labels for parameters or derived quantities to include, should match substring of labels in summaryoutput$pars or summaryoutput$quants.
digits	Optional vector of the number of decimal digits to use in reporting each quantity.
modelnames	optional vector of labels to use as column names. Default is 'model1','model2',etc.
csv	write resulting table to CSV file?
csvdir	directory for optional CSV file
csvfile	filename for CSV file
verbose	report progress to R GUI?
mcmc	summarize MCMC output in table?

Author(s)

Ian Taylor

See Also

SSsummarize, SSplotComparisons, SS_output

SS_changepars *Change parameters, bounds, or phases in the control file.*

Description

Loops over a subset of control file to change parameter lines. Current initial value, lower and upper bounds, and phase can be modified, but function could be expanded to control other columns. Depends on SS_parlines. Used by SS_profile and the **ss3sim** package.

Usage

```
SS_changepars(dir = NULL, ctlfile = "control.ss_new",
  newctlfile = "control_modified.ss", linenums = NULL, strings = NULL,
  newvals = NULL, repeat.vals = FALSE, newlos = NULL, newhis = NULL,
  estimate = FALSE, verbose = TRUE, newphs = NULL)
```

Arguments

dir	Directory with control file to change.
ctlfile	Control file name. Default="control.ss_new".
newctlfile	Name of new control file to be written. Default="control_modified.ss".
linenums	Line numbers of control file to be modified. Either this or the strings argument are needed. Default=NULL.
strings	Strings (with optional partial matching) indicating which parameters to be modified. This is an alternative to linenums. strings correspond to the commented parameter names included in control.ss_new, or whatever is written as comment at the end of the 14 number parameter lines. Default=NULL.
newvals	Vector of new parameter values. Default=NULL. The vector can contain NA values, which will assign the original value to the given parameter but change the remainder parameters, where the vector of values needs to be in the same order as either linenums or strings.
repeat.vals	If multiple parameter lines match criteria, repeat the newvals input for each line.
newlos	Vector of new lo bounds. Default=NULL. The vector can contain NA values, which will assign the original value to the given parameter but change the remainder parameters, where the vector of values needs to be in the same order as either linenums or strings.
newhis	Vector of new hi bounds. Must be the same length as newhis Default=NULL. The vector can contain NA values, which will assign the original value to the given parameter but change the remainder parameters, where the vector of values needs to be in the same order as either linenums or strings.
estimate	Vector of TRUE/FALSE for which changed parameters are to be estimated. Default=FALSE. Can also be NULL.
verbose	More detailed output to command line. Default=TRUE.
newphs	Vector of new phases. Can be a single value, which will be repeated for each parameter, the same length as newvals, where each value corresponds to a single parameter, or NULL, where the phases will not be changed. If one wants to strictly turn parameters on or off and not change the phase in which they are estimated use estimate = TRUE or estimate = FALSE, respectively. The vector can contain NA values, which will assign the original value to the given parameter but change the remainder parameters, where the vector of values needs to be in the same order as either linenums or strings.

Author(s)

Ian Taylor, Christine Stawitz

See Also

SS_parlines, SS_profile

Examples

```
## Not run:
SS_changepars(dir='Y:/ss/SSv3.03a/Simple/',ctlfile='Control.SS_New',
              strings=c('SR_steep','SR_sigmaR'),newvals=c(.35,.6))
# [1] wrote new file to Control_Modified.SS
#    oldvals newvals oldphase newphase     comment
# 1 0.609048    0.35        4       -4  # SR_steep
# 2 0.600000    0.60       -4       -4 # SR_sigmaR

## End(Not run)
```

SS_doRetro *Run retrospective analyses*

Description

Do retrospective analyses by creating new directories, copying model files, and iteratively changing the starter file to set the number of years of data to exclude.

Usage

```
SS_doRetro(masterdir, oldsubdir, newsubdir = "retrospectives",
  subdirstart = "retro", years = 0:-5, overwrite = TRUE,
  extras = "-nox", intern = FALSE, CallType = "system",
  RemoveBlocks = FALSE)
```

Arguments

masterdir	Directory where everything takes place.
oldsubdir	Subdirectory within masterdir with existing model files.
newsubdir	Subdirectory within masterdir where retrospectives will be run. Default is 'retrospectives'.
subdirstart	First part of the pattern of names for the directories in which the models will actually be run.
years	Vector of values to iteratively enter into the starter file for retrospective year. Should be zero or negative values.
overwrite	Overwrite any input files with matching names in the subdirectories where models will be run.
extras	Additional commands to use when running SS. Default = "-nox" will reduce the amound of command-line output.
intern	Display runtime information from SS in the R console (vs. saving to a file).
CallType	Either "system" or "shell" (choice depends on how you're running R. Default is "system".

RemoveBlocks Logical switch determining whether specifications of blocks is removed from top of control file. Blocks can cause problems for retrospective analyses, but the method for removing them is overly simplistic and probably won't work in most cases. Default=FALSE.

Author(s)

Ian Taylor, Jim Thorson

See Also

SSgetoutput

Examples

```
## Not run:
 # note: don't run this in your main directory--make a copy in case something goes wrong
  mydir <- "C:/Simple"

  ## retrospective analyses
  SS_doRetro(masterdir=mydir, oldsubdir="", newsubdir="retrospectives", years=0:-5)

 retroModels <- SSgetoutput(dirvec=file.path(mydir, "retrospectives",paste("retro",0:-5,sep="")))
  retroSummary <- SSsummarize(retroModels)
  endyrvec <- retroSummary$endyrs + 0:-5
 SSplotComparisons(retroSummary, endyrvec=endyrvec, legendlabels=paste("Data",0:-5,"years"))

## End(Not run)
```

SS_fitbiasramp *Estimate bias adjustment for recruitment deviates*

Description

Uses standard error of estimated recruitment deviates to estimate the 5 controls for the bias adjustment in Stock Synthesis

Usage

```
SS_fitbiasramp(replist, verbose = FALSE, startvalues = NULL,
  method = "BFGS", twoplots = TRUE, transform = FALSE, plot = TRUE,
  print = FALSE, plotdir = "default", shownew = TRUE, oldctl = NULL,
  newctl = NULL, altmethod = "nlminb", pwidth = 6.5, pheight = 5,
  punits = "in", ptsize = 10, res = 300, cex.main = 1)
```

Arguments

replist	Object created using SS_output
verbose	Controls the amount of output to the screen. Default=FALSE.
startvalues	A vector of 5 values for the starting points in the minimization. Default=NULL.
method	A method to apply to the 'optim' function. See ?optim for options. Default="BFGS". By default, optim is not used, and the optimization is based on the input altmethod.
twoplots	Make a two-panel plot showing devs as well as transformed uncertainty, or just the second panel in the set? Default=TRUE.
transform	An experimental option to treat the transform the 5 quantities to improve minimization. Doesn't work well. Default=FALSE.
plot	Plot to active plot device?
print	Print to PNG files?
plotdir	Directory where PNG files will be written. By default it will be the directory where the model was run.
shownew	Include new estimated bias adjustment values on top of values used in the model? (TRUE/FALSE)
oldctl	Optional name of existing control file to modify. Default=NULL.
newctl	Optional name of new control file to create from old file with estimated bias adjustment values. Default=NULL.
altmethod	Optimization tool to use in place of optim, either "nlminb" or "psoptim". If not equal to either of these, then optim is used.
pwidth	Default width of plots printed to files in units of punits. Default=7.
pheight	Default height width of plots printed to files in units of punits. Default=7.
punits	Units for pwidth and pheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
ptsize	Point size for plotted text in plots printed to files (see help("png") in R for details). Default=12.
res	Resolution of plots printed to files. Default=300.
cex.main	Character expansion for plot titles.

Author(s)

Ian Taylor

References

Methot, R.D. and Taylor, I.G., 2011. Adjusting for bias due to variability of estimated recruitments in fishery assessment models. Can. J. Fish. Aquat. Sci., 68:1744-1760.

See Also

SS_output

SS_ForeCatch *Create table of fixed forecast catches*

Description

Processing values of dead or retained bimoass from timeseries output to fit the format required at the bottom of the forecast file. This can be used to map the catches resulting from forecasting with a particular harvest control rule into a model representing a different state of nature. This is a common task for US west coast groundfish but might be useful elsewhere.

Usage

```
SS_ForeCatch(replist, yrs = 2017:2026, average = FALSE,
  avg.yrs = 2010:2014, total = NULL, digits = 2, dead = TRUE)
```

Arguments

replist	List created by SS_output
yrs	Range of years in which to fill in forecast catches from timeseries
average	Use average catch over a range of years for forecast (as opposed to using forecast based on control rule)
avg.yrs	Range of years to average over
total	Either single value or vector of annual total forecast catch used to scale values (especially if values are from average catches). For west coast groundfish, total might be ACL for next 2 forecast years
digits	Number of digits to round to in table
dead	TRUE/FALSE switch to choose dead catch instead of retained catch.

Author(s)

Ian G. Taylor

See Also

SS_readforecast, SS_readforecast

Examples

```
## Not run:
  # create table for next two hears based on
  SS_ForeCatch(base,               # object created by SS_output
               yrs=2015:2016,      # years with fixed catch
               average=TRUE,       # catch by fleet from average catch
                                   # (not harvest control rule)
               avg.yrs=2010:2014,  # use average of catches over past 5 years
```

```
                total=c(6.6,6.8))   # scale totals equal to ACLs (from John DeVore)

    # create table based on harvest control rule projection in SS
    # that can be mapped into an alternative state of nature
    SS_ForeCatch(low_state,          # object created by SS_output for low state
                yrs=2017:2026,       # forecast period after fixed ACL years
                average=FALSE)       # use values forecast in SS, not historic catch


## End(Not run)
```

SS_html *Create HTML files to view figures in browser.*

Description

Writes a set of HTML files with tabbed navigation between them. Depends on SS_plots with settings in place to write figures to PNG files. Should open main file in default browser automatically.

Usage

```
SS_html(replist = NULL, plotdir = "plots", plotInfoTable = NULL,
  title = "SS Output", width = 500, openfile = TRUE, multimodel = FALSE,
  filenotes = NULL, verbose = TRUE)
```

Arguments

replist	Object created by SS_output
plotdir	Directory where PNG files are located.
plotInfoTable	CSV file with info on PNG files. By default, the plotdir directory will be searched for files with name beginning 'plotInfoTable*'
title	Title for HTML page.
width	Width of plots (in pixels).
openfile	Automatically open index.html in default browser?
multimodel	Override errors associated with plots from multiple model runs. Only do this if you know what you're doing.
filenotes	Add additional notes to home page.
verbose	Display more info while running this function?

Note

By default, this function will look in the directory where PNG files were created for CSV files with the name 'plotInfoTable...' written by 'SS_plots. HTML files are written to link to these plots and put in the same directory. Please provide feedback on any bugs, annoyances, or suggestions for improvement.

Author(s)

Ian Taylor

See Also

SS_plots, SS_output

SS_makedatlist *make a list for SS data*

Description

create a list similar to those built by SS_readdat which can be written to a Stock Synthesis data file using SS_writedat. In hindsight, this function doesn't seem very useful and I haven't taken time to describe the arguments below.

Usage

```
SS_makedatlist(styr = 1971, endyr = 2001, nseas = 1,
  months_per_seas = 12, spawn_seas = 1, Nfleet = 1, Nsurveys = 1,
  N_areas = 1, fleetnames = c("fishery1", "survey1"), surveytiming = 0.5,
  areas = 1, units_of_catch = 1, se_log_catch = 0.01, Ngenders = 2,
  Nages = 40, init_equil = 0, catch = NULL, CPUE = NULL,
  N_discard_fleets = 0, discard_data = NULL, meanbodywt = NULL,
  DF_for_meanbodywt = 30, lbin_method = 2, binwidth = 2,
  minimum_size = 2, maximum_size = 90, comp_tail_compression = -1e-04,
  add_to_comp = 1e-04, max_combined_lbin = 0, lbin_vector = seq(22, 90,
  2), lencomp = NULL, agebin_vector = 1:25,
  ageerror = data.frame(rbind(0:40 + 0.5, 0.001, 0:40 + 0.5, seq(0.525, 2.525,
  0.05))), agecomp = NULL, Lbin_method = 3, max_combined_age = 1,
  MeanSize_at_Age_obs = NULL, N_environ_variables = 0, N_environ_obs = 0,
  N_sizefreq_methods = 0, do_tags = 0, morphcomp_data = 0)
```

Arguments

styr	start year of the model
endyr	end year of the model
nseas	number of seasons
months_per_seas	vector of months per season
spawn_seas	spawning season
Nfleet	number of fishing fleets
Nsurveys	number of surveys
N_areas	number of areas
fleetnames	names of fleets and surveys (alphanumeric only, no spaces or special characters)

surveytiming	vector of survey timings
areas	area definitions for each fleet and survey
units_of_catch	units of catch for each fleet
se_log_catch	Uncertainty in catch (standard error in log space) for each fleet
Ngenders	Number of genders.
Nages	Number of ages.
init_equil	Initial equilibrium catch for each fleet
catch	Catch data
CPUE	Indices of abundance (if present).
N_discard_fleets	Number of fleets with discard data.
discard_data	Discard data (if exists).
meanbodywt	Mean body weight data (if exists)
DF_for_meanbodywt	Degrees of freedom for mean body weight t-distribution.
lbin_method	Method for entering length bins. (1=use databins; 2=generate from binwidth,min,max below; 3=read vector). Not sure if all options implemented.
binwidth	Bin width for length bins.
minimum_size	Lower bound of length bins.
maximum_size	Upper bound of length bins.
comp_tail_compression	Value below which tails of composition data will be compressed (negative to turn off).
add_to_comp	Robustifying constant added to multinomial composition likelihoods.
max_combined_lbin	Maximum length bin below which length composition data will have genders combined.
lbin_vector	Vector of length bins.
lencomp	Length composition data (if exists).
agebin_vector	Vector of age bins.
ageerror	Ageing error matrices.
agecomp	Age composition data (if exists).
Lbin_method	Method of specifying length bins in conditional age-at-length data.
max_combined_age	Maximum age below which age composition data will have genders combined.
MeanSize_at_Age_obs	Data on mean size at age (if exists).
N_environ_variables	Number of environmental variables.
N_environ_obs	Number of environmental observations.
N_sizefreq_methods	Number of size frequency methods. NOT IMPLEMENTED YET.
do_tags	Include tag data? NOT IMPLEMENTED YET.
morphcomp_data	Morph composition data. NOT IMPLEMENTED YET.

Author(s)

Ian Taylor

See Also

SS_readdat, SS_writedat

SS_output *A function to create a list object for the output from Stock Synthesis*

Description

Reads the Report.sso and (optionally) the covar.sso, CompReport.sso and other files files produced by Stock Synthesis and formats the important content of these files into a list in the R workspace. A few statistics unavailable elsewhere are taken from the .par and .cor files. Summary information and statistics can be returned to the R console or just contained within the list produced by this function.

Usage

```
SS_output(dir = "C:/myfiles/mymodels/myrun/", model = "ss3",
  repfile = "Report.sso", compfile = "CompReport.sso",
  covarfile = "covar.sso", forefile = "Forecast-report.sso",
  wtfile = "wtatage.ss_new", ncols = 200, forecast = TRUE, warn = TRUE,
  covar = TRUE, readwt = TRUE, checkcor = TRUE, cormax = 0.95,
  cormin = 0.01, printhighcor = 10, printlowcor = 10, verbose = TRUE,
  printstats = TRUE, hidewarn = FALSE, NoCompOK = FALSE,
  aalmaxbinrange = 4)
```

Arguments

dir	Locates the directory of the files to be read in, double backslashes (or forward-slashes) and quotes necessary.
model	Name of the executable (leaving off the .exe). Deafult="ss3"
repfile	Name of the big report file (could be renamed by user). Default="Report.sso".
compfile	Name of the composition report file. Default="CompReport.sso".
covarfile	Name of the covariance output file. Default="covar.sso".
forefile	Name of the forecast file. Default="Forecast-report.sso".
wtfile	Name of the file containing weight at age data. Default="wtatage.ss_new".
ncols	The maximum number of columns in files being read in. If this value is too big the function runs more slowly, too small and errors will occur. A warning will be output to the R command line if the value is too small. It should be bigger than the maximum age + 10 and the number of years + 10. Default=200.
forecast	Read the forecast-report file? Default=TRUE.

warn	Read the Warning.sso file? Default=TRUE.
covar	Read covar.sso to get variance information and identify bad correlations? Default=TRUE.
readwt	Read the weight-at-age file? Default=TRUE.
checkcor	Check for bad correlations? Default=TRUE.
cormax	The specified threshold for defining high correlations. A quantity with any correlation above this value is identified. Default=0.95.
cormin	The specified threshold for defining low correlations. Only quantities with all correlations below this value are identified (to find variables that appear too independent from the model results). Default=0.01.
printhighcor	The maximum number of high correlations to print to the R GUI. Default=10.
printlowcor	The maximum number of low correlations to print to the R GUI. Default=10.
verbose	Return updates of function progress to the R GUI? Default=TRUE.
printstats	Print summary statistics about the output to the R GUI? Default=TRUE.
hidewarn	Hides some warnings output from the R GUI. Default=FALSE.
NoCompOK	Allow the function to work without a CompReport file. Default=FALSE.
aalmaxbinrange	The largest length bin range allowed for composition data to be considered as conditional age-at-length data. Default=4.

Value

Many values are returned. Complete list would be quite long, but should probably be created at some point in the future.

Author(s)

Ian Stewart, Ian Taylor

See Also

SS_plots

Examples

```
  ## Not run:
    myreplist <- SS_output(dir='c:/SS/SSv3.10b/Simple/')

## End(Not run)
```

SS_parlines *Get parameter lines from Stock Synthesis control file*

Description

A simple function which takes as input the full path and filename of a control file for input to Stock Synthesis. Ideally, a Control.SS_New file will be used, so that it represents what SS thinks the inputs are, and not what the user thinks the inputs are.

Usage

```
SS_parlines(ctlfile = "C:/myfiles/mymodels/myrun/control.ss_new",
  dir = NULL, verbose = TRUE, active = FALSE, print14 = FALSE)
```

Arguments

ctlfile	File name of control file including path.
dir	Alternative input of path, where file is assumed to be "control.ss_new". Default=NULL.
verbose	TRUE/FALSE switch for amount of detail produced by function. Default=TRUE.
active	Should only active parameters (those with positive phase) be output? Default=FALSE.
print14	Print 14 columns or just 7 (TRUE/FALSE)

Details

It returns a table which should contain one line for each parameter in the model. Currently, only the first 7 values are returned, because all parameters have those values. In the future, extended parameter lines could be returned.

Parameter lines are identified as those which have 7 or 14 numeric elements followed by a non-numeric element. It's possible that this system could break down under certain circumstances

Author(s)

Ian Taylor

See Also

SS_changepars

Examples

```
## Not run:
x <- SS_parlines(ctlfile='Y:/ss/SSv3.03a/Simple/Control.SS_New')
head(x)
#       LO    HI     INIT PRIOR PR_type   SD PHASE             Label Line_num
# 42  0.05  0.15  0.10000  0.10       0  0.8    -3  NatM_p_1_Fem_GP_1       42
```

```
# 43  0.05  0.15  0.10000  0.10       0  0.8    -3  NatM_p_2_Fem_GP_1       43
# 44  1.00 45.00 32.28100 36.00       0 10.0     2 L_at_Amin_Fem_GP_1       44
# 45 40.00 90.00 71.34260 70.00       0 10.0     4 L_at_Amax_Fem_GP_1       45
# 46  0.05  0.25  0.15199  0.15       0  0.8     4 VonBert_K_Fem_GP_1       46
# 47  0.05  0.25  0.10000  0.10       0  0.8    -3  CV_young_Fem_GP_1       47

## End(Not run)
```

SS_plots *plot many quantities related to output from Stock Synthesis*

Description

Creates a user-chosen set of plots, including biological quantities, time series, and fits to data. Plots are sent to R GUI, single PDF file, or multiple PNG files. This is now just a wrapper which calls on separate functions to make all the plots.

Usage

```
SS_plots(replist = NULL, plot = 1:24, print = NULL, pdf = FALSE,
  png = TRUE, html = png, printfolder = "plots", dir = "default",
  fleets = "all", areas = "all", fleetnames = "default",
  fleetcols = "default", fleetlty = 1, fleetpch = 1, lwd = 1,
  areacols = "default", areanames = "default", verbose = TRUE,
  uncertainty = TRUE, forecastplot = FALSE, datplot = FALSE,
  Natageplot = TRUE, samplesizeplots = TRUE, compresidplots = TRUE,
  comp.yupper = 0.4, sprtarg = "default", btarg = "default",
  minbthresh = "default", pntscalar = NULL, bub.scale.pearson = 1.5,
  bub.scale.dat = 3, pntscalar.nums = 2.6, pntscalar.tags = 2.6,
  minnbubble = 8, aalyear = -1, aalbin = -1, aalresids = TRUE,
  maxneff = 5000, cohortlines = c(), smooth = TRUE, showsampsize = TRUE,
  showeffN = TRUE, sampsizeline = FALSE, effNline = FALSE,
  showlegend = TRUE, pwidth = 6.5, pheight = 5, punits = "in",
  ptsize = 10, res = 300, cex.main = 1, selexlines = 1:6, rows = 1,
  cols = 1, maxrows = 4, maxcols = 4, maxrows2 = 2, maxcols2 = 4,
  andrerows = 3, tagrows = 3, tagcols = 3, fixdims = TRUE, new = TRUE,
  SSplotDatMargin = 8, filenotes = NULL, catchasnumbers = NULL,
  catchbars = TRUE, legendloc = "topleft", minyr = NULL, maxyr = NULL,
  sexes = "all", scalebins = FALSE, scalebubbles = FALSE,
  tslabels = NULL, catlabels = NULL, ...)
```

Arguments

replist	List created by SS_output
plot	Plot sets to be created, see list of plots below. Use to specify only those plot sets of interest, e.g., c(1,2,5,10). Plots for data not available in the model run will automatically be skipped, whether called or not.

print	Deprecated input for backward compatability, now replaced by png = TRUE/FALSE.
pdf	Send plots to PDF file instead of R GUI?
png	Send plots to PNG files instead of R GUI?
html	Run SS_html on completion? By default has same value as png.
printfolder	Name of subfolder to create within the working directory into which any PNG files specified by print will be saved. By default the working directory is used with no subfolder. Default="".
dir	The directory in which any PNG files requested by print are created. By default it will be the same directory that the report file was read from by the SS_output function. Default="default".
fleets	Either the string "all", or a vector of numerical values, like c(1,3), listing fleets or surveys for which plots should be made. By default, plots will be made for all fleets and surveys. Default="all".
areas	Either the string "all", or a vector of numerical values, like c(1,3), listing areas for which plots should be made in a multi-area model. By default, plots will be made for all areas (excepting cases where the function has not yet been updated for multi-area models). Default="all".
fleetnames	Either the string "default", or a vector of characters strings to use for each fleet name. Default="default".
fleetcols	Either the string "default", or a vector of colors to use for each fleet. Default="default".
fleetlty	Vector of line types used for each fleet in some plots. Default=1.
fleetpch	Vector of point types used for each fleet in some plots. Default=1.
lwd	Line width for some plots. Default=1.
areacols	Either the string "default", or a vector of colors to use for each area. Default="default".
areanames	Optional vector of names for each area used in titles. Default="default".
verbose	Return updates of function progress to the R GUI? Default=T.
uncertainty	Include values in plots showing estimates of uncertainty (requires positive definite hessian in model and covar=T in SS_output)? Default=T.
forecastplot	Include forecast years in the plots? Obviously requires forecast options to have been used in the model. Default=T.
datplot	Plot the data by itself? This is useful in document preparation. Setting datplot=F is equivalent to leaving off plots 15 and 16. Default=F.
Natageplot	Plot the expected numbers at age bubble plots and mean-age time series? Default=T.
samplesizeplots	Show sample size plots? Default=T.
compresidplots	Show residuals for composition plots?
comp.yupper	Upper limit on ymax for polygon/histogram composition plots. This avoids scaling all plots to have max=1 if there is a vector with only a single observed fish in it. Default=0.4.

sprtarg	Specify the F/SPR proxy target. Default=0.4.
btarg	Target depletion to be used in plots showing depletion. May be omitted by setting to NA. Default=0.4.
minbthresh	Threshold depletion to be used in plots showing depletion. May be omitted by setting to NA. Default=0.25.
pntscalar	This scalar defines the maximum bubble size for bubble plots. This option is still available but a better choice is to use bub.scale.pearson and bub.scale.dat, which are allow the same scaling throughout all plots.
bub.scale.pearson	Character expansion (cex) value for a proportion of 1.0 in bubble plot of Pearson residuals. Default=1.5.
bub.scale.dat	Character expansion (cex) value for a proportion of 1.0 in bubble plot of composition data. Default=3.
pntscalar.nums	This scalar defines the maximum bubble size for numbers-at-age and numbers-at-length plots.
pntscalar.tags	This scalar defines the maximum bubble size for tagging plots.
minnbubble	This defines the minimum number of years below which blank years will be added to bubble plots to avoid cropping. Default=8.
aalyear	Years to plot multi-panel conditional age-at-length fits for all length bins; must be in a "c(YYYY,YYYY)" format. Useful for checking the fit of a dominant year class, critical time period, etc. Default=-1.
aalbin	The length bin for which multi-panel plots of the fit to conditional age-at-length data will be produced for all years. Useful to see if growth curves are ok, or to see the information on year classes move through the conditional data. Default=-1.
aalresids	Plot the full set of conditional age-at-length Pearson residuals? Turn to FALSE if plots are taking too long and you don't want them.
maxneff	The maximum value to include on plots of input and effective sample size. Occasionally a calculation of effective N blows up to very large numbers, rendering it impossible to observe the relationship for other data. Default=5000.
cohortlines	Optional vector of birth years for cohorts for which to add growth curves to numbers at length bubble plots. Default=c().
smooth	Add loess smoother to observed vs. expected index plots and input vs. effective sample size? Default=T.
showsampsize	Display sample sizes on composition plots? Default=T.
showeffN	Display effective sample sizes on composition plots? Default=T.
sampsizeline	show line for input sample sizes on top of conditional age-at-length plots (TRUE/FALSE, still in development)
effNline	show line for effective sample sizes on top of conditional age-at-length plots (TRUE/FALSE, still in development)
showlegend	Display legends in various plots? Default=T.
pwidth	Width of plots printed to files in units of punits. Default recently changed from 7 to 6.5.

pheight	Height width of plots printed to files in units of punits. Default recently changed from 7 to 5.0
punits	Units for pwidth and pheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
ptsize	Point size for plotted text in plots printed to files (see help("png") in R for details). Default recently changed from 12 to 10.
res	Resolution of plots printed to files. Default=300.
cex.main	Character expansion parameter for plot titles (not yet implemented for all plots). Default=1.
selexlines	Vector controling which lines should be shown on selectivity plots if the model includes retention. Default=1:5.
rows	Number of rows to use for single panel plots. Default=1.
cols	Number of columns to use for single panel plots. Default=1.
maxrows	Maximum number of rows to for multi-panel plots. Default=4.
maxcols	Maximum number of columns for multi-panel plots. Default=4.
maxrows2	Maximum number of rows for conditional age-at-length multi-panel plots. Default=2.
maxcols2	Maximum number of rows for conditional age-at-length multi-panel plots. Default=4.
andrerows	Number of rows of Andre's conditional age-at-length plots within each page. Default=3.
tagrows	Number of rows for tagging-related plots. Default=3.
tagcols	Number of columns for tagging-related plots. Default=3.
fixdims	Control whether multi-panel plots all have dimensions equal to maxrows by maxcols, or resized within those limits to fit number of plots. Default=T.
new	Open a new window or add to existing plot windows. Default=T.
SSplotDatMargin	Size of right-hand margin in data plot (may be too small if fleet names are long)
filenotes	Optional vector of character strings to be added to intro HTML page (if created) with notes about the model.
catchasnumbers	Is catch input in numbers instead of biomass? Default=F.
catchbars	show catch by fleet as barplot instead of stacked polygons (default=TRUE)
legendloc	Location for all legends. Default="topleft".
minyr	First year to show in time-series plots (changes xlim parameters).
maxyr	Last year to show in time-series plots (changes xlim parameters).
sexes	Which sexes to show in composition plots. Default="all".
scalebins	Rescale expected and observed proportions in composition plots by dividing by bin width for models where bins have different widths? Caution!: May not work correctly in all cases.
scalebubbles	scale data-only bubbles by sample size, not just proportion within sample? Default=FALSE.

tslabels	Either NULL to have default labels for timeseries plots or a vector of appropriate length (currently 11) with labels for each figure
catlabels	Either NULL to have default labels for catch plots or a vector of appropriate length (currently 10) with labels for each figure
...	Additional arguments that will be passed to some subfunctions.

Author(s)

Ian Stewart, Ian Taylor

References

Walters, Hilborn, and Christensen, 2008, Surplus production dynamics in declining and recovering fish populations. Can. J. Fish. Aquat. Sci. 65: 2536-2551.

See Also

SS_output, SSplotBiology, SSplotCatch, SSplotComps, SSplotDiscard, SSplotIndices, SSplotMnwt, SSplotNumbers, SSplotRecdevs, SSplotSelex, SSplotSpawnrecruit, SSplotSPR, SSplotTags, SSplotTimeseries, SSplotYield

---

SS_profile *Run a likelihood profile in Stock Synthesis.*

Description

Iteratively changes the control file using SS_changepars.

Usage

```
SS_profile(dir = "C:/myfiles/mymodels/myrun/",
  masterctlfile = "control.ss_new", newctlfile = "control_modified.ss",
  linenum = NULL, string = NULL, profilevec = NULL, usepar = FALSE,
  globalpar = FALSE, parfile = NULL, parlinenum = NULL,
  parstring = NULL, dircopy = TRUE, exe.delete = FALSE, model = "ss3",
  extras = "-nox", systemcmd = FALSE, saveoutput = TRUE,
  overwrite = TRUE, whichruns = NULL, verbose = TRUE)
```

Arguments

dir	Directory where input files and executable are located.
masterctlfile	Source control file. Default = "control.ss_new"
newctlfile	Destination for new control files (must match entry in starter file). Default = "control_modified.ss".
linenum	Line number of parameter to be changed. Can be used instead of string or left as NULL.

string	String partially matching name of parameter to be changed. Can be used instead of linenum or left as NULL.
profilevec	Vector of values to profile over. Default = NULL.
usepar	Use PAR file from previous profile step for starting values?
globalpar	Use global par file for all runs instead of the par file from each successive run
parfile	Name of par file to use (Ian says "I don't remember how this interacts with the globalpar input")
parlinenum	Line number in par file to change.
parstring	String in par file preceding line number to change.
dircopy	Copy directories for each run? NOT IMPLEMENTED YET.
exe.delete	Delete exe files in each directory? NOT IMPLEMENTED YET.
model	Name of executable. Default = "ss3".
extras	Additional commands to use when running SS. Default = "-nox" will reduce the amound of command-line output.
systemcmd	Should R call SS using "system" function intead of "shell". This may be required when running R in Emacs. Default = FALSE.
saveoutput	Copy output .SSO files to unique names. Default = TRUE.
overwrite	Overwrite any existing .SSO files. Default = TRUE. If FALSE, then some runs may be skipped.
whichruns	Optional vector of run indices to do. This can be used to re-run a subset of the cases in situations where the function was interupted or some runs fail to converge. Must be a subset of 1:n, where n is the length of profilevec.
verbose	Controls amount of info output to command line. Default = TRUE.

Note

The starting values used in this profile are not ideal and some models may not converge. Care should be taken in using an automated tool like this, and some models are likely to require rerunning with alternate starting values.

Also, someday this function will be improved to work directly with the plotting function SSplotProfile, but they don't yet work well together. Thus, even if SS_profile is used, the output should be read using SSgetoutput or by multiple calls to SS_output before sending to SSplotProfile.

Author(s)

Ian Taylor

See Also

SSplotProfile, SSgetoutput, SS_changepars, SS_parlines

Examples

```
  ## Not run:
# note: don't run this in your main directory
# make a copy in case something goes wrong
mydir <- "C:/ss/Simple - Copy"

# the following commands related to starter.ss could be done by hand
# read starter file
starter <- SS_readstarter(file.path(mydir, 'starter.ss'))
# change control file name in the starter file
starter$ctlfile <- "control_modified.ss"
# make sure the prior likelihood is calculated
# for non-estimated quantities
starter$prior_like <- 1
# write modified starter file
SS_writestarter(starter, dir=mydir, overwrite=TRUE)

# vector of values to profile over
h.vec <- seq(0.3,0.9,.1)
Nprofile <- length(h.vec)

# run SS_profile command
profile <- SS_profile(dir=mydir, # directory
                      # "NatM" is a subset of one of the
                      # parameter labels in control.ss_new
                      model="ss3_safe",
                      masterctlfile="control.ss_new",
                      newctlfile="control_modified.ss",
                      string="steep",
                      profilevec=h.vec)


# read the output files (with names like Report1.sso, Report2.sso, etc.)
profilemodels <- SSgetoutput(dirvec=mydir, keyvec=1:Nprofile)
# summarize output
profilesummary <- SSsummarize(profilemodels)

# OPTIONAL COMMANDS TO ADD MODEL WITH PROFILE PARAMETER ESTIMATED
MLEmodel <- SS_output("C:/ss/SSv3.24l_Dec5/Simple")
profilemodels$MLE <- MLEmodel
profilesummary <- SSsummarize(profilemodels)
# END OPTIONAL COMMANDS

# plot profile using summary created above
SSplotProfile(profilesummary,           # summary object
              profile.string = "steep", # substring of profile parameter
              profile.label="Stock-recruit steepness (h)") # axis label

# make timeseries plots comparing models in profile
SSplotComparisons(profilesummary,legendlabels=paste("h =",h.vec))
```

```
## End(Not run)
```

`SS_readctl` *read control file*

Description

read Stock Synthesis control file into list object in R

Usage

```
SS_readctl(file)
```

Arguments

`file`	Filename either with full path or relative to working directory.

Details

This function is not fully implemented. The logic to figure out all the details of a Stock Synthesis control file is very complex, so this function may be completed in a way that is not totally consistent with the other similar files. Or it may never be completed at all. The functions `SS_changepars` and `SS_parlines` offer alternatives for working with SS control files.

Author(s)

Ian Taylor

See Also

`SS_changepars`, `SS_parlines`, `SS_readstarter`, `SS_readforecast`, `SS_readdat`, `SS_writestarter`, `SS_writeforecast`, `SS_writedat`, `SS_writectl`

`SS_readdat` *read data file*

Description

read Stock Synthesis data file into list object in R

Usage

```
SS_readdat(file, verbose = TRUE, echoall = FALSE, section = NULL)
```

Arguments

file	Filename either with full path or relative to working directory.
verbose	Should there be verbose output while running the file? Default=TRUE.
echoall	Debugging tool (not fully implemented) of echoing blocks of data as it is being read.
section	Which data set to read. Only applies for a data.ss_new file created by Stock Synthesis. Allows the choice of either expected values (section=2) or bootstrap data (section=3+). Leaving default of section=NULL will read input data, (equivalent to section=1).

Author(s)

Ian Taylor

See Also

SS_readstarter, SS_readforecast, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

---

SS_readforecast *read forecast file*

Description

read Stock Synthesis forecast file into list object in R

Usage

```
SS_readforecast(file = "forecast.ss", Nfleets, Nareas, verbose = TRUE)
```

Arguments

file	Filename either with full path or relative to working directory.
Nfleets	Number of fleets.
Nareas	Number of areas.
verbose	Should there be verbose output while running the file?

Author(s)

Ian Taylor

See Also

SS_readstarter, SS_readdat, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

SS_readstarter *read starter file*

Description

read Stock Synthesis starter file into list object in R

Usage

```
SS_readstarter(file = "starter.ss", verbose = TRUE)
```

Arguments

file	Filename either with full path or relative to working directory.
verbose	Should there be verbose output while running the file?

Author(s)

Ian Taylor

See Also

SS_readforecast, SS_readdat, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

SS_recdevs *Insert a vector of recruitment deviations into the control file.*

Description

A function to insert a vector of recruitment deviations into the control file for simulation studies. This can also be achieved by using the .par file, but Ian Taylor prefers this approach for no good reason.

Usage

```
SS_recdevs(fyr, lyr, ctl = NULL, recdevs = NULL, rescale = TRUE,
  scaleyrs = NULL, dir = "working_directory", ctlfile = "control.ss_new",
  newctlfile = "control_modified.ss", verbose = TRUE, writectl = TRUE,
  returnctl = FALSE, newmaxbias = NULL)
```

Arguments

fyr	First year of the recdev vector.
lyr	Last year of the recdev vector.
ctl	Either NULL to read anew or an already read control file. Default=NULL.
recdevs	Either NULL to generate anew or an already generated vector of recdevs. Default=NULL.
rescale	Should the recdevs be rescaled to have mean = 0 and std. deviation = sigmaR? Default=TRUE.
scaleyrs	Vector of years over which rescaling (if chosen) should occur.
dir	Directory where files are located. Default is to use the working directory in use by R. Default="working_directory".
ctlfile	Name of control file to modify. Default="control.ss_new".
newctlfile	Name of new file to output modified control file. Default="control_modified.ss".
verbose	Verbose output to R command line? Default=TRUE.
writectl	Write new file? Default=TRUE.
returnctl	Return contents ctl file as an object in the R workspace. Default=FALSE.
newmaxbias	Replace the maximum bias adjustment fraction with any non-NULL value. Default=NULL.

Author(s)

Ian Taylor

SS_RunJitter *Iteratively apply the jitter option in SS*

Description

Iteratively runs SS model with different jittered starting parameter values (jitter value must be manually set in starter.ss). Output files are renamed in the format Report1.sso, Report2.sso, etc.

Usage

```
SS_RunJitter(mydir, model = "ss3",
  extras = "-nohess -cbs 500000000 -gbs 500000000", Njitter, Intern = TRUE,
  systemcmd = FALSE, printlikes = TRUE)
```

Arguments

mydir	Directory where model files are located
model	Executable name
extras	Additional command line arguments passed to executable
Njitter	Number of jitters, or a vector of jitter iterations. If `length(Njitter) > 1` only the iterations specified will be ran, else `1:Njitter` will be executed.
Intern	Show command line info in R console or keep hidden (Internal=TRUE)
systemcmd	Option to switch between 'shell' and 'system'
printlikes	Print likelihood values to console

Value

A vector of likelihoods for each jitter iteration.

Author(s)

James T. Thorson, Kelli F. Johnson

SS_splitdat *Split apart bootstrap data to make input file.*

Description

A function to split apart bootstrap data files created in data.ss_new. To get bootstraps, the input "N bootstrap file to produce" in starter.ss needs to be 3 or greater.

Usage

```
SS_splitdat(inpath = "working_directory", outpath = "working_directory",
  inname = "data.ss_new", outpattern = "BootData", number = FALSE,
  verbose = TRUE, fillblank = TRUE, MLE = TRUE, inputs = FALSE,
  notes = "")
```

Arguments

inpath	Directory containing the input file. By default the working directory given by getwd() is used. Default="working_directory".
outpath	Directory into which the output file will be written. Default="working_directory".
inname	File name of input data file to be split. Default="Data.SS_New".
outpattern	File name of output data file. Default="BootData".
number	Append bootstrap number to the file name chosen in `outpattern`? Default=F.
verbose	Provide richer command line info of function progress? Default=TRUE.
fillblank	Replace blank lines with "#". Helps with running on linux. Default=TRUE.

MLE	Grab the maximum likelihood values from the second block in Data.SS_New (instead of bootstrap values or copies of inputs)? Default=TRUE.
inputs	Grab the copy of the input values values from the first block in Data.SS_New (instead of MLE or bootstrap values)? Default=F.
notes	Notes to the top of the new file (comment indicator "#C" will be added). Default="".

Author(s)

Ian Taylor

SS_varadjust *Modify variance and sample size adjustments in the control file*

Description

Function has not been fully tested yet

Usage

```
SS_varadjust(dir = "C:/myfiles/mymodels/myrun/", ctlfile = "control.ss_new",
  newctlfile = "control_modified.ss", keyword = "Variance_adjustments",
  newtable = NULL, newrow = NULL, rownumber = NULL, maxcols = 100,
  overwrite = FALSE, verbose = TRUE)
```

Arguments

dir	Directory with control file to change.
ctlfile	Control file name. Default="control.ss_new".
newctlfile	Name of new control file to be written. Default="control_modified.ss".
keyword	Keyword to use as reference for start of section on variance adjustments
newtable	Optional table of new variance adjustment values
newrow	Optional vector of new variance adjustment values for a particular row
rownumber	Which of the 6 rows to replace with 'newrow' if present?
maxcols	Maximum number of columns to search among (may need to increase from default if you have a huge number of fleets)
overwrite	Overwrite file if it exists?
verbose	TRUE/FALSE switch for amount of detail produced by function. Default=TRUE.

Author(s)

Ian Taylor

See Also

SS_parlines, SS_changepars

SS_writectl *write control file*

Description

Write Stock Synthesis control file. Like SS_readctl, this function is not fully developed.

Usage

```
SS_writectl(ctllist, outfile, overwrite = F, verbose = T)
```

Arguments

ctllist	List object created by SS_readctl.
outfile	Filename for where to write new control file.
overwrite	Should existing files be overwritten? Default=F.
verbose	Should there be verbose output while running the file? Default=T.

Author(s)

Ian Taylor

See Also

SS_readstarter, SS_readforecast, SS_readdat, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

SS_writedat *write data file*

Description

write Stock Synthesis data file from list object in R which was probably created using SS_readdat

Usage

```
SS_writedat(datlist, outfile, overwrite = FALSE, verbose = TRUE)
```

Arguments

datlist	List object created by SS_readdat.
outfile	Filename for where to write new data file.
overwrite	Should existing files be overwritten? Default=FALSE.
verbose	Should there be verbose output while running the file?

Author(s)

Ian Taylor

See Also

SS_makedatlist, SS_readstarter, SS_readforecast, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

---

SS_writeforecast *write forecast file*

Description

write Stock Synthesis forecast file from list object in R which was probably created using SS_readforecast

Usage

```
SS_writeforecast(mylist, dir = NULL, file = "forecast.ss",
  overwrite = FALSE, verbose = TRUE)
```

Arguments

mylist	List object created by SS_readforecast.
dir	Directory for new forecast file. Default=NULL (working directory).
file	Filename for new forecast file. Default="forecast.ss".
overwrite	Should existing files be overwritten? Default=FALSE.
verbose	Should there be verbose output while running the file? Default=TRUE.

Author(s)

Ian Taylor

See Also

SS_readstarter, SS_readforecast, SS_readdat, SS_readctl, SS_writestarter, SS_writedat, SS_writectl

SS_writestarter *write starter file*

Description

write Stock Synthesis starter file from list object in R which was probably created using SS_readstarter

Usage

```
SS_writestarter(mylist, dir = NULL, file = "starter.ss",
  overwrite = FALSE, verbose = TRUE, warn = TRUE)
```

Arguments

mylist	List object created by SS_readstarter.
dir	Directory for new starter file. Default=NULL (working directory).
file	Filename for new starter file. Default="starter.ss".
overwrite	Should existing files be overwritten? Default=FALSE.
verbose	Should there be verbose output while running the file? Default=TRUE.
warn	Print warning if overwriting file?

Author(s)

Ian Taylor

See Also

SS_readstarter, SS_readforecast, SS_readctl, SS_writestarter, SS_writeforecast, SS_writedat, SS_writectl

SS_write_length.fit *Write length.fit file to be used by the MFCL length-comp viewer.*

Description

Writes files in the format used by the MFCL length-composition viewer. Inspired by Simon Hoyle's demonstration. Still needs work.

Usage

```
SS_write_length.fit(replist = NULL, outfile = "length.fit",
  compfile = "CompReport.sso", dir = "default", overwrite = FALSE,
  verbose = TRUE)
```

Arguments

replist	List created by SS_output
outfile	Name of file to create.
compfile	SS output file with composition data info.
dir	Directory where stuff happens. Defaults to directory where model was run.
overwrite	Overwrite existing file?
verbose	More verbose info on progress of the function?

Author(s)

Ian Taylor

References

http://www.multifan-cl.org/, http://www.spc.int/OceanFish/en/ofpsection/sam/research/272-mfcl-viewer

---

stackpoly *modified from "stackpoly" by Jim Lemon from "plotrix" package*

Description

Plot one or more columns of numeric values as the top edges of polygons instead of lines.

Usage

```
stackpoly(x, y, main = "", xlab = "", ylab = "", xat = NA,
  xaxlab = NA, xlim = NA, ylim = NA, lty = 1, border = NA, col = NA,
  axis4 = F, x.hash = NULL, density = 20, ...)
```

Arguments

x	A numeric data frame or matrix with the 'x' values. If 'y' is NULL, these will become the 'y' values and the 'x' positions will be the integers from 1 to dim(x)[1].
y	The 'y' values.
main	The title for the plot.
xlab	x axis labels for the plot.
ylab	y axis labels for the plot.
xat	Where to put the optional xaxlabs.
xaxlab	Optional labels for the x positions.
xlim	Optional x limits.
ylim	Optional y limits.

lty	Line type for the polygon borders.
border	Color for the polygon borders.
col	Color to fill the polygons. If NULL, 'rainbow' will be called to generate the colors. If NA, the polygons will not be filled.
axis4	option to add an axis on the right hand side.
x.hash	values from x for which the bars have hash marks instead of solid fill
density	density value for hashed areas
...	Additional arguments passed to 'plot'.

Author(s)

Jim Lemon, Ian Taylor

References

https://cran.r-project.org/package=plotrix

TSCplot *Create a plot for the TSC report*

Description

Creates a plot of catch and spawning biomass from the output of SS_output for the NOAA TSC report.

Usage

```
TSCplot(SSout, yrs = "default", ylimBar = "default", ylimDepl = c(0,
  1.025), colBar = "yellow", cexBarLabels = 1.1, cex.axis = 1.1,
  space = 0, pchDepl = 19, colDepl = "red", lwdDepl = 3,
  shiftDepl = 0.25, pchSpace = 5, ht = 4, wd = 7, labelLines = 2.8,
  makePDF = NULL, makePNG = NULL, MCMC = F)
```

Arguments

SSout	The output from SS_output
yrs	The vector of years to plot
ylimBar	y-axis limits for catch barplot
ylimDepl	y-axis limits for depletion line
colBar	colors of the bars
cexBarLabels	character expansion for the labels underneath the bars (years)
cex.axis	character expansion for the axis labels
space	space between bars (see space argument of barplot)

pchDepl	character type for points on the depletion line
colDepl	color of the points on the depletion line
lwdDepl	width of the depletion line
shiftDepl	shift from beginning of the year for the points on the depletion line. Helps to guide the eye for exactly which year it corresponds to.
pchSpace	number of years between points on the depletion line. Higher numbers help tidy up the plot when plotting many years.
ht	Height of the plot in inches
wd	Width of the plot in inches
labelLines	line argument for mtext to move the axis labels
makePDF	filename for a pdf file. If NULL it does not make a pdf. Can specify a pdf filename or a png filename. Not both at the same time.
makePNG	filename for a png image. If NULL it does not make a png. Can specify a pdf filename or a png filename. Not both at the same time.
MCMC	If TRUE, will use mcmc results. It needs a list element called 'mcmc' on SSout.

Details

It creates a plot on the current graphics device, in a pdf file, or as a png image of the figure used in the TSC report produced by the NWFSC. It expects the SS results read in by SS_output. If MCMC results are to be plotted, a 'mcmc' list element should be added using the SSgetMCMC function. See the examples below.

Value

Returns a data frame with the years, spawning biomass, depletion, and total dead catch.

Author(s)

Allan Hicks

See Also

SS_output SSgetMCMC

Examples

```
## Not run:
#####################################
#DO NOT RUN
  library(r4ss)
  update_r4ss_files()

  # ** CHANGE TO THE BASE DIRECTORY
  directory <- "C:\NOAA2011\Dover\Models\base_20110701"
```

```
base <- SS_output(dir=directory,covar=F,verbose=F)

#show the plot in R
TSCplot(base)
TSCplot(base,yrs=2000:2011,pchSpace = 1)
#Create the plot as a PNG file
TSCplot(base,makePNG="C:\NOAA2012\Assessments\TSCdover.png")
#Create the plot as a PDF file
TSCplot(base,makePDF="C:\NOAA2012\Assessment\TSCdover.pdf")

# ** Hake model with MCMC results
SSdir <- "C:/NOAA2012/Hake/Models"
base <- SS_output(dir=paste(SSdir,"81_base_MCMC",sep="/"),covar=F)
tmp <- SSgetMCMC(dir=paste(SSdir,"81_base_MCMC",sep="/"),writecsv=F)
base$mcmc <- data.frame(tmp$model1)
TSCplot(base,ylimDepl = c(0,1.25),pchSpace=1,MCMC=T)


  ###############################################

## End(Not run)
```

`update_r4ss_files` *Old function to updates r4ss files, deprecated in favor of devtools method*

Description

Left in place only as a pointer to the new installation approach.

Usage

```
update_r4ss_files(...)
```

Arguments

`...`	Any arguments that you would have passed to the function.

Author(s)

Ian Taylor

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