# Package ‘r4ss’

October 18, 2019

**Type** Package  
**Title** R Code for Stock Synthesis  
**Version** 1.36.1  
**Maintainer** Ian G. Taylor <Ian.Taylor@noaa.gov>  
**Depends** R (>= 2.10.0)  
**Imports** coda, corpcor, gdata, gplots, gtools, pso, truncnorm, kableExtra  
**Suggests** maps, testthat, knitr, rmarkdown, shiny  
**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  
**Encoding** UTF-8  
**LazyLoad** yes  
**URL** https://github.com/r4ss/r4ss  
**BugReports** https://github.com/r4ss/r4ss/issues  
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**VignetteBuilder** knitr  
**NeedsCompilation** no  
**Repository** CRAN  
**Date/Publication** 2019-10-18 04:50:02 UTC
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r4ss-package

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r4ss-package

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: 1.36.1
Date: 2019-10-16
License: GPL-3
LazyLoad: yes
URL: https://github.com/r4ss/

Should be compatible with Stock Synthesis versions 3.24 through 3.30 (specifically version 3.30.14.05, from September, 2019).

Author(s)


Package maintainer: Ian G. Taylor <Ian.Taylor@noaa.gov>

References

r4ss on GitHub: https://github.com/r4ss
Download Stock Synthesis: https://vlab.ncep.noaa.gov/web/stock-synthesis/home

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)

---

**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**

```r
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. Should be either a single value or vector of length equal to x, y, and z vectors.
- **cexZ1**: Character expansion (cex) value for a proportion of 1.0.
- **maxsize**: Size of largest bubble. Preferred 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.
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)
DoProjectPlots

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). Default=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

```r
## 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",ycremax=-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

Author(s)
Cole Monnahan

See Also
read.admbFit,NegLogInt_Fn
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, sampsize_label = "N=", effN_label = "effN=", 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, 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(1, 0, 0, 0.7)), linescol = c(rgb(0, 0.8, 0.7), rgb(0.1, 0.1, 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?
<table>
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<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sampsize_label</td>
<td>label on sampsize</td>
</tr>
<tr>
<td>effN_label</td>
<td>label on effN</td>
</tr>
<tr>
<td>sampsize_round</td>
<td>rounding level for sample size values</td>
</tr>
<tr>
<td>maxrows</td>
<td>maximum (or fixed) number or rows of panels in the plot</td>
</tr>
<tr>
<td>maxcols</td>
<td>maximum (or fixed) number or columns of panels in the plot</td>
</tr>
<tr>
<td>rows</td>
<td>number or rows to return as default for next plots to come or for single plots</td>
</tr>
<tr>
<td>cols</td>
<td>number or cols to return as default for next plots to come or for single plots</td>
</tr>
<tr>
<td>fixdims</td>
<td>fix the dimensions at maxrows by maxcols or resize based on number of elements in yr input.</td>
</tr>
<tr>
<td>main</td>
<td>title of plot</td>
</tr>
<tr>
<td>cex.main</td>
<td>character expansion for title</td>
</tr>
<tr>
<td>xlab</td>
<td>x-axis label</td>
</tr>
<tr>
<td>ylab</td>
<td>y-axis label</td>
</tr>
<tr>
<td>size</td>
<td>vector of bubbles sizes if making a bubble plot</td>
</tr>
<tr>
<td>cexZ1</td>
<td>Character expansion (cex) for point associated with value of 1.</td>
</tr>
<tr>
<td>bublegend</td>
<td>Add legend with example bubble sizes to bubble plots.</td>
</tr>
<tr>
<td>maxsize</td>
<td>maximum size of bubbles</td>
</tr>
<tr>
<td>do.sqrt</td>
<td>scale bubbles based on sqrt of size vector.</td>
</tr>
<tr>
<td>minnbubble</td>
<td>number of unique x values before adding buffer.</td>
</tr>
<tr>
<td>allopen</td>
<td>should all bubbles be open?</td>
</tr>
<tr>
<td>horiz_lab</td>
<td>axis labels set horizontal all the time (TRUE), never (FALSE) or only when relatively short (“default”)</td>
</tr>
<tr>
<td>xbuffer</td>
<td>extra space around points on the left and right as fraction of total width of plot</td>
</tr>
<tr>
<td>ybuffer</td>
<td>extra space around points on the bottom and top as fraction of total height of plot</td>
</tr>
<tr>
<td>yupper</td>
<td>upper limit on ymax (applied before addition of ybuffer)</td>
</tr>
<tr>
<td>ymin0</td>
<td>fix minimum y-value at 0?</td>
</tr>
<tr>
<td>axis1</td>
<td>position of bottom axis values</td>
</tr>
<tr>
<td>axis2</td>
<td>position of left size axis values</td>
</tr>
<tr>
<td>linepos</td>
<td>should lines be added on top of points (linepos=1) or behind (linepos=2)?</td>
</tr>
<tr>
<td>type</td>
<td>type of line/points used for observed values (see 'type' in ?plot for details) on top of a grey polygon. Default is &quot;o&quot; for overplotting points on lines.</td>
</tr>
<tr>
<td>polygons</td>
<td>should polygons be added to the (turning off is required for sex-ratio plot)</td>
</tr>
<tr>
<td>bars</td>
<td>should the ptsx/ptsy values be bars instead of points (TRUE/FALSE) NOT CURRENTLY FUNCTIONAL</td>
</tr>
<tr>
<td>barwidth</td>
<td>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</td>
</tr>
<tr>
<td>ptscex</td>
<td>character expansion factor for points (default=1)</td>
</tr>
</tbody>
</table>
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. "samp-size", 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
make_multifig_sexratio

Create multi-figure sex ratio plots.

Description

Modified version of `make_multifig` for multi-figure plots of sex ratio data with crude confidence intervals (+/- 1 se) and fits from Stock Synthesis output.

Usage

```r
make_multifig_sexratio(dbase, sexratio.option = 2, CI = 0.75,
                         sampsizeround = 1, maxrows = 6, maxcols = 6, rows = 1,
                         cols = 1, fixdims = TRUE, main = "", cex.main = 1, xlab = "",
                         ylab = "Fraction female", horiz_lab = "default", xbuffer = c(0.1,
                         0.1), ybuffer = "default", yupper = NULL, axis1 = NULL,
                         axis2 = NULL, ptscol = gray(0.5), linescol = 4,
                         lty = 1, lwd = 2, nlegends = 3, legtext = list("yr", "sampsize",
                         "effN"), legx = "default", legy = "default", legadjx = "default",
                         legadjy = "default", legsize = c(1.2, 1), legfont = c(2, 1),
                         ipage = 0, multifig_oma = c(5, 5, 5, 2) + 0.1, ...)```

Arguments

- `dbase`: element of list created by `SS_output` passed from `SSplotSexRatio`
- `sexratio.option` code to choose among (1) female: male ratio or (2) fraction females out of the total (the default)
- `CI`: confidence interval for uncertainty
- `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
- `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
**make_multifig_sexratio**

- `ybuffer`: extra space around points on the bottom and top as fraction of total height of plot. "default" will cause c(0,.15) for sexratio.option=1 and c(.15,.3) for sexratio.option=2.
- `yupper`: upper limit on ymax (applied before addition of ybuffer)
- `axis1`: position of bottom axis values
- `axis2`: position of left size axis values
- `ptscex`: character expansion factor for points (default=1)
- `ptscol`: color for points/bars
- `linescol`: color for fitted model
- `lty`: line type
- `lwd`: line width
- `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. "samp-size", 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
- `ipage`: which page of plots when covering more than will fit within maxrows by maxcols.
- `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).

**Details**

The SE of the sex ratio is crude and calculated as follows. First, assume a multinomial which as MLEs of proportions. Then use the delta method of the ratio F/M, using the MLE as the expected values and analytical variances and covariance between F and M. After some algebra this calculation reduces to: $\text{SE(F/M)} = \sqrt{(f/m)^2*(1-f/f*N) + (1-m/m*N) + 2/N})$. Confidence intervals created from these should be considered very crude and would not necessarily be appropriate for future alternative compositional likelihoods.

This function was derived from make_multifig and hence has a lot of overlap in functionality and arguments.

**Author(s)**

Cole Monnahan. Adapted from `make_multifig`.

**See Also**

`SS_plots,SSplotSexRatio`
mcmc.nuisance

**Summarize nuisance MCMC output**

**Description**

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

**Usage**

```r
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", "SSB", "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)
NegLogInt_Fn

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          Xaxis 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

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), StartFromPar = TRUE, Intern = TRUE, ReDoBiasRamp = FALSE, BiasRamp_linenum_Vec = NULL, CTL_linenum_Type = NULL, systemcmd = FALSE, exe = "ss")

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)
NegLogInt_Fn

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 ".cor" output file.

PAR_num_Vec
Vector giving the number in the ".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. Although this input is still required, it is no has the former input Version has been hardwired to Version = 1.

StartFromPar
Logical flag (TRUE or FALSE) saying whether to start each round of optimization from a ".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 instead of "shell". This may be required when running R in Emacs on Windows. Default = FALSE.

exe
SS executable name (excluding extension), either "ss" or "ss3". This string is used for both calling the executable and also finding the output files like ss.par. For 3.30, it should always be "ss" since the output file names are hardwired in the TPL code.

Author(s)
James Thorson

References

See Also
read.admbFit, getADMBHessian
PinerPlot

Examples

```r
## 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,
  Input_SD_Group_Vec=1,
  CTL_linenum_List=list(127:131),
  ESTPAR_numList=list(86:205),
  Int_Group_List=1,
  PAR_num_Vec=NA,
  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])),
  exact = FALSE, 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, add_cutoff = FALSE, cutoff_prob = 0.95,
  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. If `exact=FALSE`, this can be a substring of one of the SS parameter labels found in the Report.sso file. For instance, the default input 'R0' matches the parameter 'SR_LN(R0)'. If `exact=TRUE`, then `profile.string` needs to be an exact match to the parameter label.
- `profile.label`: Label for x-axis describing the parameter over which the profile was conducted.
- `exact`: Should the `profile.string` have to match the parameter label exactly, or is a substring OK.
- `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 likelihood components.
- `lty.total`: Line type for the total likelihood.
- `lwd`: Line width for the likelihood 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.
**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

```r
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.
- **...**: Additional inputs that will be passed to the function `plot(x, y, ylim=ylim,...)`
- **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.

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**

```r
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**

```r
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.
SSbiologytables

Author(s)

Arni Magnusson, Ian Taylor

selShapes

A Shiny app that displays various selectivity curves given parameters that would be input into SS

Description

Currently implemented only for

1. logistic (type 1)
2. double normal (type 24)

This could possibly be hosted on a Shiny server instead of within r4ss

Usage

selShapes()

Author(s)

Allan Hicks, Andrea Havron, Ian Taylor,
inspired by tcl/tk code written by Tommy Garrison

SSbiologytables

A function to create a table of biology for assessment reporting: length, weight, % mature, fecundity, and selectivity

Description

Takes the object created by SS_output to create table for reporting for West Coast groundfish. Works with Stock Synthesis versions 3.30.12 and later.

Usage

SSbiologytables(replist = NULL, printfolder = "tables",
               dir = "default", fleetnames = "default", selexyr = "default")
SSbootstrap

Arguments

replist List created by SS_output backslashes (or forwardslashes) and quotes necessary.

printfolder The sub-directory under ‘dir’ (see below) in which the PNG files will be located. The default sub-directory is "plots". The directory will be created if it doesn’t exist. If 'printfolder' is set to "", it is ignored and the PNG files will be located in the directory specified by 'dir'.

dir The directory in which a PDF file (if requested) will be created and within which the printfolder sub-directory (see above) will be created if png=TRUE. By default it will be the same directory that the report file was read from by the SS_output function. Alternatives to the default can be either relative (to the working directory) or absolute paths. The function will attempt to create the directory it doesn’t exist, but it does not do so recursively.

fleetnames Either the string "default", or a vector of characters strings to use for each fleet name. Default="default".

selexyr The year to summarize selectivity, the default is the final model yr strings to use for each fleet name. Default="default".

Value

A csv files containing biology and selectivity tables

Author(s)

Chantel Wetzel

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
SSexecutivesummary

A function to create a executive summary tables from an SS Report.sso file

Description

Reads the Report.sso within the directory and creates executive summary tables as required by the current Terms of Reference for West Coast groundfish. Works with Stock Synthesis versions 3.24U and later. Additionally, historical catch and numbers at ages tables are created.

Usage

SSexecutivesummary(dir, plotdir = "default", quant = 0.95, es.only = FALSE, tables = c("a", "b", "c", "d", "e", "f", "g", "h", "i", "catch", "numbers"), nsex = FALSE, endyr = NULL, verbose = TRUE)

Arguments

dir Locates the directory of the files to be read in, double backslashes (or forwardslashes) and quotes necessary.

plotdir Directory where the 'tables' directory will be created. The default is the dir location where the Report.sso file is located.

quant To calculate confidence intervals, default is set at 0.95

es.only TRUE/FALSE switch to produce only the executive summary tables will be produced, default is FALSE which will return all executive summary tables, historical catches, and numbers-at-ages

tables Which tables to produce (default is everything). Note: some tables depend on calculations related to previous tables, so will fail if requested on their own (e.g. Table 'f' can’t be created without also creating Table 'a')

nsex This will allow the user to calculate single sex values based on the new sex specification (-1) in SS for single sex models. Default value is FALSE. TRUE will not divide by 2.

deyr Optional input to choose a different ending year for tables (could be useful for catch-only updates)

verbose Return updates of function progress to the R console?

Value

A csv files containing executive summary tables.

References

(A description is on page 41 and Figures 55-56 (pg 139-140) show some results.)
SSgetMCMC

Description

Reads the MCMC output (in the posteriors.sso and derived_posteriors.sso files) from a model.

Usage

```
SSgetMCMC(dir = NULL, verbose = TRUE, writecsv = FALSE,
  postname = "posteriors.sso", derpostname = "derived_posteriors.sso",
  csv1 = "keyposteriors.csv", csv2 = "nuisanceposteriors.csv",
  keystrings = c("NatM", "R0", "steep", "RecrDev_2008", "Q_extraSD"),
  nuisancestrings = c("Objective_function", "SSB_", "InitAge",
                     "RecrDev"), burnin = 0, thin = 1)
```

Arguments

- `dir` Directory containing 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.
- `postname` Name of file with parameter posteriors (default matches "posteriors.sso" used by SS, but the user could change the name)
- `derpostname` Name of file with parameter posteriors (default matches "derived_posteriors.sso" used by SS, but the user could change the name)
- `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`.
- `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)

Chantel Wetzel

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 = TRUE, 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**

```r
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.

**Usage**

```r
SSMethodCond.TA1.8(fit, fleet, part = 0:2, seas = NULL, plotit = TRUE, printit = TRUE, datonly = FALSE, plotadj = !datonly, maxpanel = 1000, FullDiagOut = FALSE, ShowVersionB = FALSE, fleetnames = NULL)
```
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).

**printit**
if TRUE, print results to R console.

**datonly**
if TRUE, don’t show the model expectations

**plotadj**
if TRUE, plot the confidence intervals associated with the adjusted sample sizes (TRUE by default unless datonly = TRUE)

**maxpanel**
maximum number of panels within a plot

**FullDiagOut**
Print full diagnostics?

**ShowVersionB**
Report the Version B value in addition to the default?

**fleetnames**
Vector of alternative fleet names to draw from for plot titles and captions. It should have length equal to the number of fleets in the model, not the number of fleets considered in this function.

Details

The function outputs a multiplier, \( w \), (with bootstrap 95% confidence intervals) so that \( N2i = w \times N1i \), where \( N1i \) and \( N2i \) are the stage-1 and stage-2 multinomial sample sizes for the \( i \)th composition. Optionally makes a plot 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.

This function formerly reported 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). However, research by Punt (2015) found Version A to perform better and version B is no longer recommended and is only reported if requested by the user.

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.
Author(s)
Chris Francis, Andre Punt, Ian Taylor

References

See Also
SSMethod.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 multiplier, $w$ (with bootstrap 95% confidence interval), so that $N_{2y} = w \times N_{1y}$, where $N_{1y}$ and $N_{2y}$ 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 $N_{1y}$) 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, sexes = 0:3,
seas = NULL, method = NULL, plotit = TRUE, printit = TRUE,
datonly = FALSE, plotadj = !datonly, maxpanel = 1000,
fleetnames = NULL, label.part = TRUE, label.sex = TRUE,
set.pars = TRUE)
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).

sexes vector of one or more values for Sexes; analysis is restricted to composition data with one of these Sexes 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).

printit if TRUE, print results to R console.

datonly if TRUE, don’t show the model expectations

plotadj if TRUE, plot the confidence intervals associated with the adjusted sample sizes (TRUE by default unless datonly = 'TRUE')

maxpanel maximum number of panels within a plot

fleetnames Vector of alternative fleet names to draw from for plot titles and captions. It should have length equal to the number of fleets in the model, not the number of fleets considered in this function.

label.part Include labels indicating which partitions are included?

label.sex Include labels indicating which sexes are included?

set.pars Set the graphical parameters such as mar and mfrow. Can be set to FALSE in order to add plots from multiple calls to this function as separate panels in one larger figure.

Author(s)

Chris Francis, Andre Punt, Ian Taylor

References

SSmohnsrho

See Also

SSMethod.Cond.TA1.8

Examples

```r
## 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)
```

SSmohnsrho

Calculate Mohn’s Rho values for select quantities

Description

Function calculates: (1) a rho value for the ending year for each retrospective relative to the reference model, (2) a "Wood’s Hole Mohn’s Rho", and (3) an "Alaska Fisheries Science Center and Hurtado-Ferro et al. (2015) Mohn’s rho" (2) and (3) are based on all years between the reference and the retrospective run.

Usage

```r
SSmohnsrho(summaryoutput, endyrvec = NULL, startyr = NULL, verbose = TRUE)
```

Arguments

- `summaryoutput`: List created by SSsummarize. The expected order for the models are the full reference model, the retro -1, retro -2, and so forth.
- `endyrvec`: Single year or vector of years representing the final year of values to show for each model.
- `startyr`: Single year used to calculate the start of the Wood’s Hole Mohn’s Rho value across all years.
- `verbose`: Print messages when running the function?
**SSplotAgeMatrix**

**Author(s)**
Chantel R. Wetzel and Carey McGilliard

**References**

**Description**
Distribution of length at age or observed age at true age is represented as a histogram. Values are from the AGE_LENGTH_KEY and AGE_AGE_KEY sections of Report.sso ($ALK and $AAK in the list created by SS_output)

**Usage**
```r
SSplotAgeMatrix(replist, option = 1, slices = NULL, scale = NULL, plot = TRUE, print = FALSE, labels = c("Age", "Length", "True age", "Observed age", "for ageing error type", "Distribution of", "at"), pwidth = 6.5, pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1, mainTitle = TRUE, plotdir = "default")
```

**Arguments**
- **replist**: List created by SS_output
- **option**: Switch set to either 1 for length at true age or 2 for obs. age at true age
- **slices**: Optional input to choose which matrix (slice of the 3D-array) within $AAK or $ALK to plot. By default all slices will be shown. For ageing imprecision this should correspond to the ageing error matrix number. Distribution of length at age ($ALK) is ordered by season, sub-season, and then morph. A future version could allow subsetting plots by these dimensions.
- **scale**: Multiplier for bars showing distribution. Species with many ages benefit from expanded bars. NULL value causes function to attempt automatic scaling.
- **plot**: Plot to active plot device?
- **print**: Print to PNG files?
- **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
**SSplotBiology**

- `ptsiz`e: Point size for PNG file
- `cex.main`: Character expansion for plot titles
- `mainTitle`: Logical indicating if a title should be included at the top
- `plotdir`: directory where PNG files will be written. By default it will be the directory where the model was run.

**Author(s)**

Ian G. Taylor

**See Also**

*SSplotNumbers*

---

**SSplotBiology**  
*Plot biology related quantities.*

**Description**

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

**Usage**

```r
SSplotBiology(replist, plot = TRUE, print = FALSE, add = FALSE, 
subplots = 1:32, seas = 1, morphs = NULL, forecast = FALSE, 
minyr = -Inf, maxyr = Inf, colvec = c("red", "blue", "grey20"), 
ltyvec = c(1, 2), shadealpha = 0.1, imageplot_text = FALSE, 
imageplot_text_round = 0, 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", "Hermaphroditism transition rate", 
"Fraction females by age at equilibrium"), pwidth = 6.5, pheight = 5, 
punits = "in", res = 300, ptsiz = 10, cex.main = 1, 
mainTitle = TRUE, 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. Numbering of subplots is as follows:
- 1 growth curve only
- 2 growth curve with CV and SD
- 3 growth curve with maturity and weight
- 4 distribution of length at age (still in development)
- 5 length or wt at age matrix
- 6 maturity
- 7 fecundity from model parameters
- 8 fecundity at weight from BIOLOGY section
- 9 fecundity at length from BIOLOGY section
- 10 spawning output at length
- 11 spawning output at age
- 21 Natural mortality (if age-dependent)
- 22 Time-varying growth persp
- 23 Time-varying growth contour
- 24 plot time-series of any time-varying quantities
- 31 hermaphroditism transition probability
- 32 hermaphroditism cumulative probability

Additional plots not created by default
- 101 diagram with labels showing female growth curve
- 102 diagram with labels showing female growth curve & male offsets
- 103 diagram with labels showing female CV = f(A) (offset type 2)
- 104 diagram with labels showing female CV = f(A) & male offset (type 2)
- 105 diagram with labels showing female CV = f(A) (offset type 3)
- 106 diagram with labels showing female CV = f(A) & male offset (type 3)

seas which season to plot (values other than 1 only work in seasonal models but but maybe not fully implemented)
morphs Which morphs to plot (if more than 1 per sex)? By default this will be replist$mainmorphs
forecast Include forecast years in plots of time-varying biology?
minyr optional input for minimum year to show in plots
maxyr optional input for maximum year to show in plots
colvec vector of length 3 with colors for various points/lines
ltyvec vector of length 2 with lty for females/males in growth plots values can be applied to other plots in the future
shadealpha Transparency parameter used to make default shadecol values (see ?rgb for more info)
imageplot_text Whether to add numerical text to the image plots when using weight at age. Defaults to FALSE.
imageplot_text_round The number of significant digits to which the image plot text is rounded. Defaults to 0, meaning whole numbers. If all your values are small and there’s no contrast in the text, you might want to make this 1 or 2.
SSplotCatch

- `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
- `mainTitle`: Logical indicating if a title should be included at the top
- `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**

```r
SSplotCatch(replist, subplots = 1:16, 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 = -Inf, maxyr = Inf, 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, should include all fleets (not just those with catch)
- `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?
**SSplotCohortCatch**

**Author(s)**

Ian Taylor, Ian Stewart

**See Also**

SS_plots, SS_output

---

**SSplotCohortCatch**  
_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**

SSplotCohortCatch(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.
SSplotComparisons

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)", "Fraction of unfished", "Age-0 recruits (1,000s)", "Recruitment deviations", "Index", "Log index", "1 - SPR", "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 = 1.05, xaxs = "i", yaxs = "i", type = "o", uncertainty = TRUE, shadealpha = 0.1, legend = TRUE,
legendlabels = "default", legendloc = "topright",
legendorder = "default", legendncol = 1, sprtarg = NULL,
btarget = NULL, minbthresh = NULL, pwidth = 6.5, pheight = 5,
punits = "in", res = 300, psize = 10, cex.main = 1,
plotdir = NULL, filenameprefix = "", densitynames = c("SSB_Virgin",
"R0"), densityxlabs = "default", rescale = TRUE, densscalesx = 1,
densscalesy = 1, densityadjust = 1, densitiesymbols = 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 = FALSE,
show_equilibrium = TRUE)

Arguments

summaryoutput List created by SSsummarize
subplots Vector of subplots to be created Numbering of subplots is as follows:

- 1 spawning biomass
- 2 spawning biomass with uncertainty intervals
- 3 biomass ratio (hopefully equal to fraction of unfished)
- 4 biomass ratio with uncertainty
- 5 SPR ratio
- 6 SPR ratio with uncertainty
- 7 F value
- 8 F value with uncertainty
- 9 recruits
- 10 recruits with uncertainty
- 11 recruit devs
- 12 recruit devs with uncertainty
- 13 index fits
- 14 index fits on a log scale
- 15 phase plot
- 16 densities
- 17 cumulative densities

Note that this represents a revision in the numbering for 7 and higher from the numbering used up to r4ss version 1.36.0 which was as follows:

- 18 F value with uncertainty
- 7 recruits
- 8 recruits with uncertainty
- 9 recruit devs
- 10 recruit devs with uncertainty
- 11 index fits
- 12 index fits on a log scale
- 13 phase plot
- 14 densities
- 15 cumulative densities

<table>
<thead>
<tr>
<th>Option</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>plot</code></td>
<td>Plot to active plot device?</td>
</tr>
<tr>
<td><code>print</code></td>
<td>Send plots to PNG files in directory specified by <code>plotdir</code>?</td>
</tr>
<tr>
<td><code>png</code></td>
<td>Has same result as <code>print</code>, included for consistency with <code>SS_plots</code>.</td>
</tr>
<tr>
<td><code>pdf</code></td>
<td>Write output to PDF file? Can't be used in conjunction with <code>png</code> or <code>print</code>.</td>
</tr>
<tr>
<td><code>models</code></td>
<td>Optional subset of the models described in <code>summaryoutput</code>. Either &quot;all&quot; or a vector of numbers indicating columns in summary tables.</td>
</tr>
<tr>
<td><code>endyrvec</code></td>
<td>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.</td>
</tr>
<tr>
<td><code>indexfleets</code></td>
<td>Vector of fleet numbers for each model for which to compare indices of abundance. Only necessary if any model has more than one index.</td>
</tr>
<tr>
<td><code>indexUncertainty</code></td>
<td>Show uncertainty intervals on index data? Default=FALSE because if models have any extra standard deviations added, these intervals may differ across models.</td>
</tr>
<tr>
<td><code>indexQlabel</code></td>
<td>Add catchability to legend in plot of index fits (TRUE/FALSE)?</td>
</tr>
<tr>
<td><code>indexQdigits</code></td>
<td>Number of significant digits for catchability in legend (if <code>indexQlabel=TRUE</code>)</td>
</tr>
<tr>
<td><code>indexSEvec</code></td>
<td>Optional replacement for the SE values in <code>summaryoutput$indices</code> to deal with the issue of differing uncertainty by models described above.</td>
</tr>
<tr>
<td><code>indexPlotEach</code></td>
<td>TRUE plots the observed index for each model with colors, or FALSE just plots observed once in black dots.</td>
</tr>
<tr>
<td><code>labels</code></td>
<td>Vector of labels for plots (titles and axis labels)</td>
</tr>
<tr>
<td><code>col</code></td>
<td>Optional vector of colors to be used for lines. Input NULL makes use of <code>rich.colors.short</code> function.</td>
</tr>
<tr>
<td><code>shadecol</code></td>
<td>Optional vector of colors to be used for shading uncertainty intervals. Input NULL makes use of <code>rich.colors.short</code> function with alpha transparency.</td>
</tr>
<tr>
<td><code>pch</code></td>
<td>Optional vector of plot character values</td>
</tr>
<tr>
<td><code>lty</code></td>
<td>Optional vector of line types</td>
</tr>
<tr>
<td><code>lwd</code></td>
<td>Optional vector of line widths</td>
</tr>
<tr>
<td><code>spacepoints</code></td>
<td>Number of years between points shown on top of lines (for long timeseries, points every year get mashed together)</td>
</tr>
<tr>
<td><code>staggerpoints</code></td>
<td>Number of years to stagger the first point (if <code>spacepoints &gt; 1</code>) for each line (so that adjacent lines have points in different years)</td>
</tr>
<tr>
<td><code>initpoint</code></td>
<td>Year value for first point to be added to lines. Points added to plots are those that satisfy <code>(Yr-initpoint)%%spacepoints == (staggerpoints*iline)%%spacepoints</code></td>
</tr>
<tr>
<td><code>tickEndYr</code></td>
<td>TRUE/FALSE switch to turn on/off extra axis mark at final year in timeseries plots.</td>
</tr>
<tr>
<td><code>shadeForecast</code></td>
<td>TRUE/FALSE switch to turn on/off shading of years beyond the maximum ending year of the models</td>
</tr>
<tr>
<td><code>xlim</code></td>
<td>Optional x limits</td>
</tr>
<tr>
<td>Variable</td>
<td>Description</td>
</tr>
<tr>
<td>------------</td>
<td>---------------------------------------------------------------------------------------------------------------------------------------------</td>
</tr>
<tr>
<td>ylimAdj</td>
<td>Multiplier for ylim parameter. Allows additional white space to fit legend if necessary. Default=1.05.</td>
</tr>
<tr>
<td>xaxs</td>
<td>Choice of xaxs parameter (see ?par for more info)</td>
</tr>
<tr>
<td>yaxs</td>
<td>Choice of yaxs parameter (see ?par for more info)</td>
</tr>
<tr>
<td>type</td>
<td>Type parameter passed to points (default 'o' overplots points on top of lines)</td>
</tr>
<tr>
<td>uncertainty</td>
<td>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.</td>
</tr>
<tr>
<td>shadealpha</td>
<td>Transparency adjustment used to make default shadecol values (implemented as adjustcolor(col=col, alpha.f=shadealpha))</td>
</tr>
<tr>
<td>legend</td>
<td>Add a legend?</td>
</tr>
<tr>
<td>legendLabels</td>
<td>Optional vector of labels to include in legend. Default is 'model1','model2',etc.</td>
</tr>
<tr>
<td>legendloc</td>
<td>Location of legend. Either a string like &quot;topleft&quot; or a vector of two numeric values representing the fraction of the maximum in the x and y dimensions, respectively. See ?legend for more info on the string options.</td>
</tr>
<tr>
<td>legendorder</td>
<td>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.</td>
</tr>
<tr>
<td>legendncol</td>
<td>Number of columns for the legend.</td>
</tr>
<tr>
<td>sprtarg</td>
<td>Target value for SPR-ratio where line is drawn in the SPR plots and phase plot.</td>
</tr>
<tr>
<td>btarg</td>
<td>Target biomass value at which to show a line (set to 0 to remove)</td>
</tr>
<tr>
<td>minbthresh</td>
<td>Minimum biomass threshold at which to show a line (set to 0 to remove)</td>
</tr>
<tr>
<td>pwidth</td>
<td>Width of plot</td>
</tr>
<tr>
<td>pheight</td>
<td>Height of plot</td>
</tr>
<tr>
<td>punits</td>
<td>Units for PNG file</td>
</tr>
<tr>
<td>res</td>
<td>Resolution for PNG file</td>
</tr>
<tr>
<td>ptsize</td>
<td>Point size for PNG file</td>
</tr>
<tr>
<td>cex.main</td>
<td>Character expansion for plot titles</td>
</tr>
<tr>
<td>plotdir</td>
<td>Directory where PNG or PDF files will be written. By default it will be the directory where the model was run.</td>
</tr>
<tr>
<td>filenameprefix</td>
<td>Additional text to append to PNG or PDF file names. It will be separated from default name by an underscore.</td>
</tr>
<tr>
<td>densitynames</td>
<td>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</td>
</tr>
<tr>
<td>densityxlabs</td>
<td>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)</td>
</tr>
<tr>
<td>rescale</td>
<td>TRUE/FALSE control of automatic rescaling of units into thousands, millions, or billions</td>
</tr>
<tr>
<td>densitiescalex</td>
<td>Scalar for upper x-limit in density plots (values below 1 will cut off the right tail to provide better contrast among narrower distributions</td>
</tr>
</tbody>
</table>
SSplotComparisons

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
show_equilibrium Whether to show the equilibrium values for SSB. For some model comparisons, these might not be comparable and thus useful to turn off. Defaults to TRUE.

Author(s)
Ian G. Taylor, John R. Wallace

See Also
SS_plots, SSsummarize, SS_output, SSgetoutput

Examples

```r
## Not run:
# directories where models were run need to be defined
dir1 <- 'c:/SS/mod1'
dir2 <- 'c:/SS/mod2'

# read two models
mod1 <- SS_output(dir=dir1)
mod2 <- SS_output(dir=dir2)

# create list summarizing model results
mod.sum <- SSsummarize(list(mod1, mod2))

# plot comparisons
SSPlotComparisons(mod.sum, legendlabels=c("First model", "Second model"))

# Example showing comparison of MLE to MCMC results where the mcmc would have
```
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, aggregates_by_mkt = FALSE, 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, 0.8, 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, mainTitle = FALSE, ...)

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?

showsampsizes

add sample sizes to plot

showeffN

add effective sample sizes to plot

aggregates_by_mkt

separate plots of aggregates across years into different plots for each market category (retained, discarded)?

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.

ptnscalar

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.
SSplotComps

<table>
<thead>
<tr>
<th>Variable</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>colvec</td>
<td>Vector of length 3 with colors for females, males, unsexed fish</td>
</tr>
<tr>
<td>linescol</td>
<td>Color for lines on top of polygons</td>
</tr>
<tr>
<td>axis1</td>
<td>position of bottom axis values</td>
</tr>
<tr>
<td>axis2</td>
<td>position of left size axis values</td>
</tr>
<tr>
<td>blue</td>
<td>What color to use for males in bubble plots (default is slightly transparent blue)</td>
</tr>
<tr>
<td>red</td>
<td>What color to use for females in bubble plots (default is slightly transparent red)</td>
</tr>
<tr>
<td>pwidth</td>
<td>default width of plots printed to files in units of punits. Default=7.</td>
</tr>
<tr>
<td>pheight</td>
<td>default height width of plots printed to files in units of punits. Default=7.</td>
</tr>
<tr>
<td>punits</td>
<td>units for pwidth and pheight. Can be &quot;px&quot; (pixels), &quot;in&quot; (inches), &quot;cm&quot; or &quot;mm&quot;. Default=&quot;in&quot;.</td>
</tr>
<tr>
<td>ptsize</td>
<td>point size for plotted text in plots printed to files (see help(&quot;png&quot;) in R for details). Default=12.</td>
</tr>
<tr>
<td>res</td>
<td>resolution of plots printed to files. Default=300</td>
</tr>
<tr>
<td>plotdir</td>
<td>directory where PNG files will be written. by default it will be the directory where the model was run.</td>
</tr>
<tr>
<td>cex.main</td>
<td>character expansion parameter for plot titles</td>
</tr>
<tr>
<td>linepos</td>
<td>should lines be added before points (linepos=1) or after (linepos=2)?</td>
</tr>
<tr>
<td>fitbar</td>
<td>show fit to bars instead of points</td>
</tr>
<tr>
<td>do.sqrt</td>
<td>scale bubbles based on sqrt of size vector. see ?bubble3 for more info.</td>
</tr>
<tr>
<td>smooth</td>
<td>add loess smoother to observed vs. expected index plots and input vs. effective sample size?</td>
</tr>
<tr>
<td>cohortlines</td>
<td>optional vector of birth years for cohorts for which to add growth curves to numbers at length bubble plots</td>
</tr>
<tr>
<td>labels</td>
<td>vector of labels for plots (titles and axis labels)</td>
</tr>
<tr>
<td>printmkt</td>
<td>show market categories in plot titles?</td>
</tr>
<tr>
<td>printsex</td>
<td>show sex in plot titles?</td>
</tr>
<tr>
<td>maxrows</td>
<td>maximum (or fixed) number or rows of panels in the plot</td>
</tr>
<tr>
<td>maxcols</td>
<td>maximum (or fixed) number or columns of panels in the plot</td>
</tr>
<tr>
<td>maxrows2</td>
<td>maximum number of rows for conditional age at length plots</td>
</tr>
<tr>
<td>maxcols2</td>
<td>maximum number of columns for conditional age at length plots</td>
</tr>
<tr>
<td>rows</td>
<td>number or rows to return to as default for next plots to come or for single plots</td>
</tr>
<tr>
<td>cols</td>
<td>number or cols to return to as default for next plots to come or for single plots</td>
</tr>
<tr>
<td>andre_oma</td>
<td>Outer margins passed to Andre’s multi-panel conditional age-at-length plots.</td>
</tr>
<tr>
<td>andrerows</td>
<td>Number of rows of Andre’s conditional age-at-length plots within each page. Default=3.</td>
</tr>
<tr>
<td>fixdims</td>
<td>fix the dimensions at maxrows by maxcols or resize based on number of years of data</td>
</tr>
<tr>
<td>fixdims2</td>
<td>fix the dimensions at maxrows by maxcols in aggregate plots or resize based on number of fleets</td>
</tr>
</tbody>
</table>
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.

mainTitle: Logical indicating if a title for the plot should be produced

... 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", subplot = 1:2, fleetcol = "default", datatypes = "all", fleets = "all", fleetnames = "default", ghost = FALSE, pwidth = 6.5, pheight = 5, punits = "in", res = 300, psize = 10, cex.main = 1, margins = c(5.1, 2.1, 2.1, 8.1), cex = 2, lwd = 12, maxsize = 1, alphasize = 1, mainTitle = FALSE, 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.
subplot: vector controlling which subplots to create. Currently there are only 2 subplots:
• 1 equal size points showing presence/absence of data type by year/fleet
• 2 points scaled to indicate quantity or precision of data

defleetcol Either the string "default", or a vector of colors to use for each fleet. If tagging data is included, an additional color needs to be added for the tag releases which are not assigned to a fleet.

datatypes Either the string "all", or a vector including some subset of the following: "catch", "cpue", "lendbase", "sizdbase", "agedbase", "condbase", "ghostagedbase", "ghostcondbase", "ghostlendbase", "ladbase", "wadbase", "mnwgt", "discard", "tagrelease", and "tagdbase1".

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

ptsz size 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

maxsize The size (cex) of the largest bubble in the datasize plot. Default is 1.

alphasize The transparency of the bubbles in the datasize plot. Defaults to 1 (no transparency). Useful for models with lots of overlapping points.

mainTitle TRUE/FALSE switch to turn on/off the title on the plot.

verbose report progress to R GUI?

Author(s)
Ian Taylor, Chantel Wetzel, Cole Monnahan

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, ymax = NULL, 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 which will always be included in the plot (all data included regardless). Default = 1 so that discard fractions are always plotted on a 0-1 range, but total discard amounts which are greater than this value will exceed it.
ymax  Optional maximum y-value to include (useful if upper tails on discard amounts are very high)
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?
SSplotIndices

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 with or without model fit as well as other diagnostic plots such as observed vs. expected index and plots related to time-varying catchability (if present).

Usage

SSplotIndices(replist, subplots = c(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, mainTitle = 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 Numbering of subplots is as follows:
- 1 index data by fleet
- 2 index data with fit by fleet
- 3 observed vs expected index values with smoother
- 4 index data by fleet on a log scale (lognormal error only)
- 5 index data with fit by fleet on a log scale (lognormal error only)
- 6 log(observed) vs log(expected) with smoother (lognormal error only)
- 7 time series of time-varying catchability (only if actually time-varying)
- 8 catchability vs. vulnerable biomass (if catchability is not constant)
- 9 comparison of all indices
plot to active plot device?
print to PNG files?
optional vector to subset fleets for which plots will be made
optional replacement for fleenames used in data file
add smoothed line to plots of observed vs. expected sample sizes
add to existing plot (not yet implemented)
make plot of data only?
vector of labels for plots (titles and axis labels)
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.
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.
color of line showing expected index in time series plot. Default is blue.
color of smoother shown in obs. vs. exp. plots. Default is red.
single value or vector of plotting characters (pch parameter) for time-series plots of index fit. Default=21.
single value or vector of plotting characters (pch parameter) for sample size plots of index fit. Default=16.
character expansion factor for points showing observed values. Default=1.
Background color for points with pch=21.
add a legend to seasonal colors (only for seasonal models)
add a legend to seasonal colors (default is "topright")
optional vector of names for each season to replace defaults if a legend is used
width of plot
height of plot
units for PNG file
resolution for PNG file
point size for PNG file
character expansion for plot titles
switch which allows the plot title to be left off
directory where PNG files will be written. by default it will be the directory where the model was run.
First year to show in plot (for zooming in on a subset of values)
Last year to show in plot (for zooming in on a subset of values)
Maximum allowed value for ymax (specified as ratio of y), which overrides any value of ymax that is greater (default = Inf)
**SSplotMCMC_ExtraSelex**

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 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, psize = 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
psize 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?
SSplotMovementMap

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 movement 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

SSplotMovementRates  

Plot movement rates from model output

Description

Plots estimated movement rates in final year for each area/season 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 movement rates are shown
min.move.age  
Minimum age of movement (in future will come from Report file)
pwidth  
width of plot
**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**

```r
SSplotNumbers(replist, subplots = 1:10, 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", "Fraction female in numbers at age", 
"Length", "Mean length (cm)", "mean length (cm) in the population", 
"expected numbers at age", "Beginning of year", "Middle of year", 
"expected numbers at length", "Fraction female in numbers at length"), 
pwidth = 6.5, pheight = 5, punits = "in", res = 300, 
ptsize = 10, cex.main = 1, plotdir = "default", 
mainTitle = FALSE, verbose = TRUE)
```

**Author(s)**

Ian Taylor

**See Also**

`SS_output`, `SSplotMovementRates`

**Examples**

```r
## Not run:
SSplotMovementRates(myreplist)
## End(Not run)
```
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)
bub.legend 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.
mainTitle Logical indicating if a title should be included at the top
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(replist, xlab = "Parameter value", ylab = "Density", showmle = TRUE, showpost = TRUE, showprior = TRUE, showinit = TRUE, showdev = FALSE, 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, add = FALSE, pdf = FALSE, pwidth = 6.5, pheight = 5, punits = "in", ptsize = 10, returntable = FALSE, strings = c(), exact = FALSE, newheaders = NULL)

Arguments

replist List produced by SS_output.
xlab Label on horizontal axis.
ylab Label on vertical axis.
showmle Show MLE estimate and asymptotic variance estimate with blue lines?
showpost Show posterior distribution as bar graph if MCMC results are available in replist?
showprior Show prior distribution as black line?
showinit Show initial value as red triangle?
showdev Include devs in the plot?
showlegend Show the legend?
fitrange Fit range tightly around MLE & posterior distributions, instead of full parameter range?
xaxis Parameter input for x-axis. See ?par for more info.
xlim Optional x-axis limits to be applied to all plots. Otherwise, limits are based on the model results.
ylim Optional y-axis limits to be applied to all plots. Otherwise, limits are based on the model results.
verbose Controls amount of text output (maybe).
nrows How many rows in multi-figure plot.
ncols How many columns in multi-figure plot.
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)", exact = FALSE,
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", "InitEQ_Regime", "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", "Initial equilibrium 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, add_cutoff = FALSE,
cutoff_prob = 0.95, 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. If
                exact=FALSE, this can be a 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'. If exact=TRUE, then profile.string needs to be an exact match
                to the parameter label.
profile.label   Label for x-axis describing the parameter over which the profile was conducted.
exact           Should the profile.string have to match the parameter label exactly, or is a
                substring OK.
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 likelihood components.

**lty.total**  
Line type for the total likelihood.

**lwd**  
Line width for the likelihood 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.

**add_cutoff**  
Add dashed line at ~1.92 to indicate 95 based on common cutoff of half of chi-squared of p=.95 with 1 degree of freedom: 0.5*qchisq(p=cutoff_prob,df=1). The probability value can be adjusted using the cutoff_prob below.

**cutoff_prob**  
Probability associated with add_cutoff above.

**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**.
**SSplotRecdevs**

**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**

```r
SSplotRecdevs(replist, subplots = 1:3, plot = TRUE, print = FALSE, add = FALSE, uncertainty = TRUE, minyr = -Inf, maxyr = Inf, 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?

- **minyr**  
  optional input for minimum year to show in plots

- **maxyr**  
  optional input for maximum year to show in plots

- **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)
SSplotRetroRecruits

```r
ylab
main
plotdir
pwidth
pheight
punits
res
ptsize
cex.main
verbose
```

optional y-axis label (if the season names aren’t informative enough)
title for plot
directory where PNG files will be written. by default it will be the directory where the model was run.
width of plot
height of plot
units for PNG file
resolution for PNG file
point size for PNG file
character expansion for plot titles
report progress to R GUI?

Author(s)
Ian Taylor

See Also
SS_plots, SSplotRecdevs

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
deyrvec
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

```r
## 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
df('retrospectives/retrospective_comparison_plots.pdf')
SSplotComparisons(retroSummary,endyrvec=endyrvec,new=FALSE)
dev.off()

# make Squid Plot of recdev retrospectives
df('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)
de.v.off()

## End(Not run)

---

### SSplotSelex

**Plot selectivity**

#### Description

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

#### Usage

```r
SSplotSelex(replist, infotable = NULL, fleets = "all",
fleetnames = "default", sizefactors = c("Lsel"),
agefactors = c("Asel", "Asel2"), years = "endyr", minyr = -Inf,
maxyr = Inf, season = 1, sexes = "all", selexlines = 1:6,
subplot = 1:25, skipAgeSel10 = 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,
peight = 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).
- **minyr**: Optional input for minimum year to show in plots
maxyr optional input for maximum year to show in plots
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)
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
SSplotSexRatio  
Plot sex-ratio data and fits for two sex models

**Description**

Plot sex-ratio data and fits from Stock Synthesis output. Multi-figure plots depend on make_multifig. The confidence intervals around the observed points are based on a Jeffreys interval calculated from the adjusted input sample size (with a floor of 1).

**Usage**

```r
SSplotSexRatio(replist, kind = "AGE", sexratio.option = 2, CI = 0.75,
plot = TRUE, print = FALSE, fleets = "all",
fleetnames = "default", yupper = 4, linescol = rgb(0.6, 0, 0.9,
0.7), lwd = 2, axis1 = NULL, axis2 = NULL, pwidth = 6.5,
phheight = 5, punits = "in", ptsize = 10, res = 300,
plotdir = "default", cx.main = 1, labels = c("Length (cm)",
"Age (yr)", "Sex ratio (females:males)", "Fraction female"),
maxrows = 6, maxcols = 6, rows = 1, cols = 1, fixdims = TRUE,
verbose = TRUE, mainTitle = FALSE, ...)
```

**Arguments**

- **replist**: list created by SSoutput
- **kind**: indicator of type of plot can be "LEN", "SIZE", "AGE", "cond", "GSTAGE", "L[lat]A", or "W[lat]A".
- **sexratio.option**: code to choose among (1) female: male ratio or (2) fraction females out of the total
- **CI**: confidence interval for uncertainty
- **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
- **yupper**: upper limit on ymax (only applies for sexratio.option == 1)
- **linescol**: Color for line showing expected value (default is purple)
- **lwd**: line width
- **axis1**: position of bottom axis values
- **axis2**: position of left size axis values
- **pwidth**: default width of plots printed to files in units of punits. Default=7.
- **phheight**: default height width of plots printed to files in units of punits. Default=7.
- **punits**: units for pwidth and phheight. Can be "px" (pixels), "in" (inches), "cm" or "mm". Default="in".
SSplotSpawnrecruit

```r
ptsizesize for plotted text in plots printed to files (see help("png") in R for details). Default=12.
resresolution of plots printed to files. Default=300
plotdirdirectory where PNG files will be written. by default it will be the directory where the model was run.
cex.maincharacter expansion parameter for plot titles
labelsvector of labels for plots (titles and axis labels)
maxrowsmaximum (or fixed) number or rows of panels in the plot
maxcolsmaximum (or fixed) number or columns of panels in the plot
rowsnumber or rows to return to as default for next plots to come or for single plots
colsnumber or cols to return to as default for next plots to come or for single plots
fixdimsfix the dimensions at maxrows by maxcols or resize based on number of years of data
verbosereturn updates of function progress to the R GUI?
mainTitleLogical indicating if a title for the plot should be produced
...
```

Author(s)

Cole Monnahan, Ian Taylor

References


See Also

`SS_plots`, `make_multifig_sexratio`

SSplotSpawnrecruit  Plot spawner-recruit curve.

Description

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

Usage

SSplotSpawnrecruit(replist, subplot = 1:3, add = FALSE, plot = TRUE,
   print = FALSE, xlim = NULL, ylim = NULL,
   labels = c("Spawning biomass (mt)", "Recruitment (1,000s)",
   "Spawning output", expression(paste("Spawning output (relative to ",
   italic(B)[0], ", ")")), expression(paste("Recruitment (relative to ",
   italic(R)[0], ", ")")), "Log recruitment deviation"),
   bioscale = "default", plotdir = "default", pwidth = 6.5,
   pheight = 5, punits = "in", res = 300, ptsize = 10,
   verbose = TRUE, colvec = c("blue", "black", "black", gray(0, 0.7)),
   ltyvec = c(1, 2, 1, NA), ptcol = "default", legend = TRUE,
   legendloc = NULL, minyr = "default", textmindev = 0.5,
   relative = FALSE, expected = TRUE, estimated = TRUE,
   bias_adjusted = TRUE, show_env = TRUE, 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
labels vector containing x-axis label for models with spawning biomass in metric tons,
y-axis label, and alternative x-axis for models with a fecundity relationship making spawning output not equal to spawning biomass.
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
verbose report progress to R GUI?
colvec vector of length 4 with colors for 3 lines and 1 set of points (where the 4th value for the points is the color of the circle around the background color provided by ptcol
ltyvec vector of length 4 with line types for the 3 lines and 1 set of points, where the points are disconnected (lty=NA) by default
SSplotSPR

ptcol  vector or single value for the color of the points, "default" will by replaced by a vector of colors of length equal to nrow(replist$recruit)
legend  add a legend to the figure?
legendloc  location of legend. By default it is chosen as the first value in the set of "topleft", "topright", "bottomright" that results in no overlap with the points in the plot, but the user can override this with their choice of location. See ?legend for more info on the options.
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.
relative  scale both axes so that B0 and R0 are at 1 to show spawning output and recruitment relative to the equilibrium
expected  show line for expected recruitment (stock-recruit curve)
estimated  show points for estimated recruitment values (including deviations)
bias_adjusted  show lines for bias adjusted expected recruitment
show_env  add line for expected recruitment with environmental variability
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.
btarget  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**

```r
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,
  taggroups = 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)
taggroups which tag groups to include in the plots. Default=NULL causes all groups to be included.
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".
ptsiz: 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 = 1, minyr = -Inf, maxyr = Inf, 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. Default = 1. Previously this was set to 0.5 for single-sex models, and 1.0 for all others, but now single-sex models are assumed to use the -1 option for Nsexes in the data file so the scaling is done automatically by SS.
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?
btarget 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 = 1:3, refpoints = c("MSY", "Btgt", "SPR", "Current"), add = FALSE, plot = TRUE, print = FALSE, labels = c("Fraction unfished", "Equilibrium yield (mt)", "Total biomass (mt)", "Surplus production (mt)"), col = "blue", col2 = "black", 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 Numbering of subplots is as follows:
  • 1 yield curve
  • 2 yield curve with reference points
  • 3 surplus production vs. biomass plots (Walters et al. 2008)
refpoints character vector of which reference points to display in subplot 2, from the options ‘MSY’, ‘Btgt’, and ‘SPR’.
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 for equilibrium plot
col2 line color for dynamic surplus production plot
lty line type (only applied to equilibrium yield plot at this time)
lwd line width (only applied to equilibrium 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?
**SSsummarize**

**Author(s)**

Ian Stewart, Ian Taylor

**References**


**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, one for each model. The individual lists can be created by SS_output or the list of lists can be created by SSgetoutput (which iteratively calls SS_output).
- **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  Quanitle for lower bound on calculated intervals. Default = 0.025 for 95% intervals.

upperCI  Quanitle 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

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
SStimeseries

A function to create a time-series table from an SS Report.sso file

Description

Reads the Report.sso within the directory and creates a time-series table as required by the current Terms of Reference for West Coast groundfish. Table includes the historical and the forecast years for the model. Works with Stock Synthesis versions 3.24U and later.

Usage

SStimeseries(dir, plotdir = "default", nsex = FALSE)

Arguments

- dir: Locates the directory of the files to be read in, double backslashes (or forwardslashes) and quotes necessary.
- plotdir: Directory where the table will be saved. The default saves the table to the dir location where the Report.sso file is located.
- nsex: This will allow the user to calculate single sex values based on the new sex specification (-1) in SS for single sex models. Default value is FALSE. TRUE will not divide by 2.

Value

A csv file containing a time-series of total biomass, summary biomass, spawning biomass or output, relative depletion, total dead catch the SPR, and the exploitation.

Author(s)

Chantel Wetzel
SS_unavailableSpawningOutput

*Plot unavailable spawning output*

**Description**

Calculate and plot the unavailable spawning output—separating out ones that are unavailable because they're too small to be selected from ones that are too big to be selected.

**Usage**

```r
SS_unavailableSpawningOutput(replist, plot = TRUE, print = FALSE, plotdir = "default", pwidth = 6.5, pheight = 5, punits = "in", res = 300, ptsize = 10, cex.main = 1)
```

**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.
- `pwidth`: Width of plot
- `pheight`: Height of plot
- `punits`: Units for PNG file
- `res`: Resolution for PNG file
- `ptsise`: Point size for PNG file
- `cex.main`: Character expansion for plot titles

**Author(s)**

Megan Stachura, Andrew Cooper, Andi Stephens, Neil Klaer, Ian G. Taylor

---

**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.
SS_changepars

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, newprior = NULL, newprsd = NULL,
newprtype = NULL, estimate = NULL, 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 lower 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 high 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.
newprior     Vector of new prior 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.
newprsd      Vector of new prior sd 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.
newprtype    Vector of new prior type. 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.
SS_changepars

estimate  Optional vector or single value of TRUE/FALSE for which parameters are to be estimated. Changes sign of phase to be positive or negative. Default NULL causes no change to phase.

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 remaining parameters, where the vector of values needs to be in the same order as either linenums or strings.

Author(s)
Ian Taylor, Christine Stawitz, Chantel Wetzel

See Also
SS_parlines, SS_profile

Examples

```r
## Not run:
SS_changepars(dir='C:/ss/SSv3.30.03.05_May11/Simple - Copy',
strings=c("steep","sigmaR"), newvals=c(.4,.6))
## parameter names in control file matching input vector 'strings' (n=2):
## [1] "SR_BH_steep" "SR_sigmaR"
## These are the ctl file lines as they currently exist:
## LO HI INIT PRIOR PR_type SD PHASE env-var use_dev dev_minyr dev_maxyr
## 95 0.2 1 0.613717 0.7 0.05 1 4 0 0 0 0
## 96 0.0 2 0.600000 0.8 0.80 0 -4 0 0 0 0
## dev_stddev Block Block_Fxn Label Linenum
## 95 0 0 0 SR_BH_steep 95
## 96 0 0 0 SR_sigmaR 96
## line numbers in control file (n=2):
## [1] 95 96
##
## wrote new file to control_modified.ss with the following changes:
## oldvals newvals oldphase newphase oldlos newlos oldhis newhis comment
## 1 0.613717 0.4 4 -4 0.2 0.2 1 1 # SR_BH_steep
## 2 0.600000 0.6 -4 -4 0.0 0.0 2 2 # 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,
exefile = "ss", 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.
exefile Executable file found in directory with model files. On Windows systems, this value will be automatically updated if a single executable exists in the directory of model files. Input exefile=NULL if the executable is in your path and doesn’t need copying.
extras Additional commands to use when running SS. Default = "-nox" will reduce the amount 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
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",
exclude_forecast = FALSE, 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.

exclude_forecast  Exclude forecast values in the estimation of alternative bias adjustment inputs?

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


See Also

SS_output
SS_ForeCatch  

Create table of fixed forecast catches

Description

Processing values of dead or retained biomass 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 = 2019:2030, average = FALSE, avg.yrs = 2014:2018, total = NULL, digits = 2, dead = TRUE, zeros = FALSE)

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.
zeros  Include entries with zero catch (TRUE/FALSE)

Author(s)

Ian G. Taylor

See Also

SS_readforecast, SS_readforecast

Examples

## Not run:
# create table based on average over past 5 years
SS_ForeCatch(base, yrs = 2019:2020, average = TRUE, # object created by SS_output
              avg.yrs = 2014:2018, # years with fixed catch
total = NULL, # catch by fleet from average catch
digits = 2, # object created by SS_output
dead = TRUE, # object created by SS_output
zeros = FALSE) # object created by SS_output
avg.yrs = 2014:2018) # use average of catches over past 5 years

# create table with pre-defined totals where the first 2 years
# are based on current harvest specifications and the next 10 are set to some
# new value (with ratio among fleets based on average over past 5 years)
SS_ForeCatch(base, # object created by SS_output
  yrs = 2019:2020, # years with fixed catch
  average = TRUE, # catch by fleet from average catch
  avg.yrs = 2014:2018, # use average of catches over past 5 years
  total = c(rep(241.3, 2), rep(300, 10))) # total

# 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=2019:2030, # forecast period after fixed ACL years
  average=FALSE) # use values forecast in SS, not historic catch

## End(Not run)
SS_makedatlist

**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_makeHTMLdiagnostictable

Make html diagnostic tables

Description
Creates html tables that show diagnostic outputs, including status checks, gradients, and correlations.

Usage
SS_makeHTMLdiagnostictable(replist, plotdir = NULL, gradmax = 0.001)

Arguments
replist  List item representing stock assessment model output list (SS_output)
plotdir  Directory where the text files containing the tables will be written. By default it will be the directory where the model was run.
gradmax  the largest gradient value for estimated parameter; the default is 1E-3

Value
a three-element vector; the first element is the name of the html table file, the second is the table caption, and the third is the category of output type
**SS_output**

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

**Author(s)**

Christine Stawitz

**See Also**

[SS_plots()], [SS_output()], [SS_html()]

**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**

```r
SS_output(dir = "C:/myfiles/mymodels/myrun/", dir.mcmc = NULL,
    repfile = "Report.sso", compfile = "CompReport.sso",
    covarfile = "covar.sso", forefile = "Forecast-report.sso",
    wtfile = "wtatage.ss_new", warnfile = "warning.sso", 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**: Directory containing the Stock Synthesis model output. Forward slashes or double backslashes and quotes are necessary. This can also be either an absolute path or relative to the working directory.
- **dir.mcmc**: Optional directory containing MCMC output. This can either be relative to dir, such that file.path(dir, dir.mcmc) will end up in the right place, or an absolute path.
- **repfile**: Name of the big report file (could be renamed by user).
- **compfile**: Name of the composition report file.
- **covarfile**: Name of the covariance output file.
- **forefile**: Name of the forecast file.
- **wtfile**: Name of the file containing weight at age data.
- **warnfile**: Name of the file containing warnings.
**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.

**forecast**  Read the forecast-report file?

**warn**  Read the Warning.sso file?

**covar**  Read covar.sso to get variance information and identify bad correlations?

**readwt**  Read the weight-at-age file?

**checkcor**  Check for bad correlations?

**cormax**  The specified threshold for defining high correlations. A quantity with any correlation above this value is identified.

**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).

**printhighcor**  The maximum number of high correlations to print to the R GUI.

**printlowcor**  The maximum number of low correlations to print to the R GUI.

**verbose**  Return updates of function progress to the R GUI?

**printstats**  Print summary statistics about the output to the R GUI?

**hidewarn**  Hides some warnings output from the R GUI.

**NoCompOK**  Allow the function to work without a CompReport file.

**aalmaxbinrange**  The largest length bin range allowed for composition data to be considered as conditional age-at-length data.

---

**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**

```r
## Not run:  
# read model output  
myreplist <- SS_output(dir='c:/SS/Simple/')  
# make a bunch of plots  
SS_plots(myreplist)  

# read model output and also read MCMC results (if run), which in
```
### 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

```r
SS_parlines(ctlfile = "control.ss_new", dir = NULL, version = "3.30", verbose = TRUE, active = 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.
- **version**: SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
- **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.

### 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`
- `SS_readctl`
- `SS_readctl_3.24`
Examples

```r
## Not run:
parlines <- SS_parlines(ctlfile='c:/ss/Simple/Control.SS_New')
head(parlines)
# 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)
```

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

```r
SS_plots(replist = NULL, plot = 1:25, 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 = TRUE, datplot = TRUE, 
          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, 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 = -Inf, maxyr = Inf, sexes = "all", scalebins = FALSE,
```

SS_plots

plot many quantities related to output from Stock Synthesis
scalebubbles = FALSE, tslabels = NULL, catlabels = NULL, 
maxsize = 1, ...)

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. Current grouping of plots is as follows:
1. Biology
2. Selectivity and retention
3. Timeseries
4. Recruitment deviations
5. Recruitment bias adjustment
6. Spawner-recruit
7. Catch
8. SPR
9. Discards
10. Mean weight
11. Indices
12. Numbers at age
13. Length comp data
14. Age comp data
15. Conditional age-at-length data
16. Length comp fits
17. Age comp fits
18. Conditional age-at-length fits
19. Francis and Punt conditional age-at-length comp fits
20. Mean length-at-age and mean weight-at-age
21. Tags
22. Yield
23. Movement
24. Data range
25. Diagnostic tables

print Deprecated input for backward compatibility, 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 The sub-directory under 'dir' (see below) in which the PNG files will be located. The default sub-directory is "plots". The directory will be created if it doesn't exist. If 'printfolder' is set to "", it is ignored and the PNG files will be located in the directory specified by 'dir'. 
dir  The directory in which a PDF file (if requested) will be created and within
which the printfolder sub-directory (see above) will be created if png=TRUE.
By default it will be the same directory that the report file was read from by
the SS_output function. Alternatives to the default can be either relative (to the
working directory) or absolute paths. The function will attempt to create the
directory it doesn’t exist, but it does not do so recursively.

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. De-
default="default".

fleettle  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. De-
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 de-
finite hessian in model? Default=TRUE.

forecastplot  Include forecast years in the timeseries plots and plots of time-varying quan-
tities? Default=TRUE.

datplot  Plot the data by itself? This is useful in document preparation, but doesn’t
change across alternative model runs with the same data, so can be committed
to save time once the plots have been created once. Setting datplot=FALSE
is equivalent to leaving off plots 15 and 16. Default=TRUE.

Natageplot  Plot the expected numbers at age bubble plots and mean-age time series? De-
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 scal-
ing 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 omitted by setting to NA.
minbthresh  Threshold depletion to be used in plots showing depletion. May be omitted by setting to NA.

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 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.

**mainTitle**
Logical indicating if a title should be included at the top

**cex.main**
Character expansion parameter for plot titles (not yet implemented for all plots). Default=1.

**selexlines**
Vector controlling 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 and time-varying plots

**maxyr**
Last year to show in time-series and time-varying plots. This can either be an alternative to, or redundant with, the forecastplot input.

**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.
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 = "ss.par", parlinenum = NULL, parstring = NULL, dircopy = TRUE, exe.delete = FALSE, model = "ss", extras = "-nox", systemcmd = FALSE, saveoutput = TRUE, overwrite = TRUE, whichruns = NULL, SSversion = "3.30", prior_check = TRUE, read_like = TRUE, 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 ("parfile_original_backup.sso", which is automatically copied from original parfile) for all runs instead of the par file from each successive run
parfile Name of par file to use (for 3.30 models, this needs to remain 'ss.par'). When globalpar=TRUE, the backup copy of this is used for all runs.
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 = "ss".
extras Additional commands to use when running SS. Default = "-nox" will reduce the amount of command-line output.
systemcmd Should R call SS using "system" function instead 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 interrupted or some runs fail to converge. Must be a subset of 1:n, where n is the length of profilevec.
SSversion SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
prior_check Check to make sure the starter file is set to include the prior likelihood contribution in the total likelihood. Default = TRUE.
read_like Read the table of likelihoods from each model as it finishes. Default = TRUE. Changing to FALSE should allow the function to play through even if something is wrong with reading the table.
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

```R
# 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, 0.1)
Nprofile <- length(h.vec)

# run SS_profile command
profile <- SS_profile(dir=mydir, # directory
    model="ss",
    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 from SS*

**Description**

Read Stock Synthesis control file into list object in R. This function is a wrapper which calls either SS_readctl_3.24 or SS_readctl_3.30 (not yet written). This setup allows those functions to be cleaner (if somewhat redundant) than a single function that attempts to do everything.

**Usage**

```r
SS_readctl(file, version = NULL, verbose = TRUE, echoall = FALSE, 
nseas = 4, N_areas = 1, Nages = 20, Ngenders = 1, 
Npopbins = NA, Nfleet = 2, Nsurveys = 2, N_tag_groups = NA, 
N_CPUE_obs = NA, use_datlist = FALSE, datlist = NULL, 
ptype = TRUE)
```

**Arguments**

- **file**: Filename either with full path or relative to working directory.
- **version**: SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
- **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.
<table>
<thead>
<tr>
<th>Parameter</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>nseas</code></td>
<td>number of season in the model. This information is not explicitly available in control file</td>
</tr>
<tr>
<td><code>N_areas</code></td>
<td>number of spatial areas in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>Nages</code></td>
<td>oldest age in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>Ngenders</code></td>
<td>number of genders in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>Npopbins</code></td>
<td>number of population bins in the model. This information is also not explicitly available in control file and this information is only required if length based maturity vector is directly supplied (Maturity option of 6), and not yet tested</td>
</tr>
<tr>
<td><code>Nfleets</code></td>
<td>number of fisheries in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>Nsurveys</code></td>
<td>number of survey fleets in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>N_tag_groups</code></td>
<td>number of tag release groups in the model. This information is also not explicitly available in control file</td>
</tr>
<tr>
<td><code>N_CPUE_obs</code></td>
<td>number of CPUE observations.</td>
</tr>
<tr>
<td><code>use_datlist</code></td>
<td>LOGICAL if TRUE, use datlist to derive parameters which can not be determined from control file</td>
</tr>
<tr>
<td><code>datlist</code></td>
<td>list or character. if list : produced from SS_writedat or character : file name of dat file.</td>
</tr>
<tr>
<td><code>ptype</code></td>
<td>include a column in the output indicating parameter type? (Can be useful, but causes problems for SS_writectl.) Only possible to use for 3.24 control files.</td>
</tr>
</tbody>
</table>

**Author(s)**

Ian G. Taylor, Yukio Takeuchi, Neil L Klaer

**See Also**

`SS_readctl_3.24, SS_readdat, SS_readdat_3.24`

**Description**

Read Stock Synthesis (version 3.24) control file into list object in R. This function comes with its wrapper function SS_readctl that calls SS_readctl_3.24 (this function) or SS_readctl_3.30 (to be available in future).
Usage

SS_readctl_3.24(file, verbose = TRUE, echoall = FALSE,
version = "3.24", nseas = 4, N_areas = 1, Nages = 20,
Ngenders = 1, Npopbins = NA, Nfleets = 2, Nsurveys = 2,
Do_AgeKey = FALSE, N_tag_groups = NA, N_CPUE_obs = c(0, 0, 9, 12),
use_datlist = FALSE, datlist = NULL, ptype = TRUE)

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.
version SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
nseas number of seasons in the model. This information is not explicitly available in control file
N_areas number of spatial areas in the model. Default = 1. This information is also not explicitly available in control file
Nages oldest age in the model. This information is also not explicitly available in control file
Ngenders number of genders in the model. This information is also not explicitly available in control file
Npopbins number of population bins in the model. This information is also not explicitly available in control file and this information is only required if length based maturity vector is directly supplied (Maturity option of 6), and not yet tested
Nfleets number of fisheries in the model. This information is also not explicitly available in control file
Nsurveys number of survey fleets in the model. This information is also not explicitly available in control file
Do_AgeKey Flag to indicate if 7 additional ageing error parameters to be read set 1 (but in fact any non zero numeric in R) or TRUE to enable to read them 0 or FALSE (default) to disable them. This information is not explicitly available in control file, too.
N_tag_groups number of tag release group. Default =NA. This information is not explicitly available control file. This information is only required if custom tag parameters is enabled (TG_custom=1)
N_CPUE_obs numeric vector of length=Nfleets+Nsurveys containing number of data points of each CPUE time series
use_datlist LOGICAL if TRUE, use datlist to derive parameters which can not be determined from control file
datlist list or character. if list : produced from SS_writedat or character : file name of dat file.
ptype include a column in the output indicating parameter type? (Can be useful, but causes problems for SS_writectl.)
\texttt{SS\_readctl\_3.30}

\textbf{Author(s)}
Yukio Takeuchi, Neil Klaer, Iago Mosqueira, and Kathryn Doering

\textbf{See Also}
\texttt{SS\_readctl}, \texttt{SS\_readdat} \texttt{SS\_readdat\_3.24}, \texttt{SS\_readdat\_3.30}, \texttt{SS\_readstarter}, \texttt{SS\_readforecast}, \texttt{SS\_writestarter}, \texttt{SS\_writeforecast}, \texttt{SS\_writedat}

---

\textbf{Description}
Read Stock Synthesis (version 3.30) control file into list object in R. This function comes with its wrapper function \texttt{SS\_readctl} that calls \texttt{SS\_readctl\_3.24} or \texttt{SS\_readctl\_3.30} (this function).

\textbf{Usage}

\begin{verbatim}
SS\_readctl\_3.30(file, verbose = TRUE, echoall = FALSE,
version = "3.30", nseas = 4, N\_areas = 1, N\_ages = 20,
Ngenders = 1, N\_popbins = NA, N\_fleet = 2, N\_surveys = 2,
Do\_AgeKey = FALSE, N\_tag\_groups = NA, N\_CPUE\_obs = c(0, 0, 9, 12),
use\_datlist = FALSE, datlist = NULL)
\end{verbatim}

\textbf{Arguments}

- \textit{file} Filename either with full path or relative to working directory.
- \textit{verbose} Should there be verbose output while running the file? Default=TRUE.
- \textit{echoall} Debugging tool (not fully implemented) of echoing blocks of data as it is being read.
- \textit{version} SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
- \textit{nseas} number of seasons in the model. This information is not explicitly available in control file
- \textit{N\_areas} number of spatial areas in the model. Default = 1. This information is also not explicitly available in control file
- \textit{N\_ages} oldest age in the model. This information is also not explicitly available in control file
- \textit{Ngenders} number of genders in the model. This information is also not explicitly available in control file
- \textit{N\_popbins} number of population bins in the model. This information is also not explicitly available in control file
- \textit{N\_fleet} number of population bins in the model. This information is also not explicitly available in control file and this information is only required if length based maturity vector is directly supplied (Maturity option of 6), and not yet tested
**Nfleet**
number of fisheries in the model. This information is also not explicitly available in control file.

**Nsurveys**
number of survey fleets in the model. This information is also not explicitly available in control file.

**Do_AgeKey**
Flag to indicate if 7 additional ageing error parameters to be read set 1 (but in fact any non zero numeric in R) or TRUE to enable to read them 0 or FALSE (default) to disable them. This information is not explicitly available in control file, too.

**N_tag_groups**
number of tag release group. Default = NA. This information is not explicitly available control file. This information is only required if custom tag parameters is enabled (TG_custom=1)

**N_CPUE_obs**
umeric vector of length=Nfleet+Nsurveys containing number of data points of each CPUE time series

**use_datlist**
LOGICAL if TRUE, use datlist to derive parameters which can not be determined from control file

**datlist**
list or character. If list, should be a list produced from SS_writedat. If character, should be the file name of an SS data file.

**Author(s)**
Neil Klaer, Yukio Takeuchi, Watal M. Iwasaki, and Kathryn Doering

**See Also**
SS_readctl, SS_readdat, SS_readdat_3.24, SS_readdat_3.30, SS_readctl_3.24, SS_readstarter, SS_readforecast, SS_writestarter, SS_writeforecast, SS_writedat

---

**SS_readdat**
*read Stock Synthesis data file*

**Description**
Read Stock Synthesis data file into list object in R. This function is a wrapper which calls SS_readdat_2.00, SS_readdat_3.00, SS_readdat_3.24, or SS_readdat_3.30 (and potentially additional functions in the future). This setup allows those functions to be cleaner (if somewhat redundant) than a single function that attempts to do everything. Returned datlist is mostly consistent across versions.

**Usage**
SS_readdat(file, version = NULL, verbose = TRUE, echoall = FALSE, section = NULL)
Arguments

- **file**: Filename either with full path or relative to working directory.
- **version**: SS version number. Currently "2.00", "3.00", "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
- **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 G. Taylor, Allan C. Hicks, Neil L. Klaer, Kelli F. Johnson, Chantel R. Wetzel

See Also

- SS_readdat_2.00
- SS_readdat_3.00
- SS_readdat_3.24
- SS_readdat_3.30
- SS_readctl
- SS_readctl_3.24
- SS_readstarter
- SS_readforecast
- SS_writestarter
- SS_writeforecast
- SS_writedat

Description

Read Stock Synthesis (version 2.00) data file into list object in R. This function was formerly called SS_readdat. That name is now used for a wrapper function that calls either SS_readdat_2.00, SS_readdat_3.00, SS_readdat_3.24 or SS_readdat_3.30 (and potentially additional functions in the future).

Usage

```r
SS_readdat_2.00(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). ## needs to be added
Author(s)
Ian G. Taylor, Yukio Takeuchi, Z. Teresa A’mar, Neil L. Klaer

See Also
SS_readdat, SS_readdat_3.30 SS_readstarter, SS_readforecast, SS_writestarter, SS_writeforecast, SS_writedat

Description
Read Stock Synthesis (version 3.00) data file into list object in R. This function was formerly called SS_readdat. That name is now used for a wrapper function that calls either SS_readdat_3.24 or SS_readdat_3.30 (and potentially additional functions in the future).

Usage
SS_readdat_3.00(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 G. Taylor, Yukio Takeuchi, Z. Teresa A’mar

See Also
SS_readdat, SS_readdat_3.30 SS_readstarter, SS_readforecast, SS_writestarter, SS_writeforecast, SS_writedat
**SS_readdat_3.24**

*read data file from SS version 3.24*

---

**Description**

Read Stock Synthesis (version 3.24) data file into list object in R. This function was formerly called SS_readdat. That name is now used for a wrapper function that calls either SS_readdat_3.24 or SS_readdat_3.30 (and potentially additional functions in the future).

**Usage**

```r
SS_readdat_3.24(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 G. Taylor, Yukio Takeuchi, Z. Teresa A’mar, Kelli F. Johnson, Chantel R. Wetzel

**See Also**

- SS_readdat, SS_readdat_3.30
- SS_readstarter, SS_readforecast, SS_writestarter, SS_writeforecast, SS_writedat

---

**SS_readdat_3.30**

*read data file from SS version 3.30*

---

**Description**

Read Stock Synthesis (version 3.30) data file into list object in R. This function was formerly called SS_readdat. That name is now used for a wrapper function that calls either SS_readdat_3.24 or SS_readdat_3.30 (and potentially additional functions in the future).
Usage

SS_readdat_3.30(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 G. Taylor, Yukio Takeuchi, Z. Teresa A’mar, Chris J. Grandin, Kelli F. Johnson, Chantel R. 
    Wetzel

See Also

SS_readdat, SS_readdat_3.30, SS_readstarter, SS_readforecast, SS_writestarter, 
SS_writeforecast, 
SS_writedat

SS_readforecast  
read forecast file

Description

read Stock Synthesis forecast file into list object in R

Usage

SS_readforecast(file = "forecast.ss", Nfleets, Nareas, nseas, 
    version = "3.30", readAll = FALSE, verbose = TRUE)

Arguments

file Filename either with full path or relative to working directory.
Nfleets Number of fleets (not required in 3.30).
Nareas Number of areas (not required in 3.30).
nseas number of seasons (not required in 3.30).
version SS version number. Currently only "3.24" or "3.30" are supported, either as 
    character or numeric values (noting that numeric 3.30 = 3.3).
**Description**
read Stock Synthesis starter file into list object in R

**Usage**
```r
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_writestarter`, `SS_writeforecast`, `SS_writedat`
SS_readwtatage  
*Read weight-at-age data file*

**Description**

Read in a weight-at-age data file into a data frame in R.

**Usage**

`SS_readwtatage(file = "wtatage.ss", verbose = TRUE)`

**Arguments**

- **file**: A relative or full path to the weight-at-age file. The default value is `wtatage.ss`.
- **verbose**: A logical value specifying if output should be printed to the screen. The default is `verbose = TRUE`.

**Value**

Returns a data frame with a variable number of columns based on the number of ages that are included in the file. Though, the first columns will always be Yr, Seas, Sex, Bio_Pattern, BirthSeas, and Fleet. The seventh column will be age zero. The last or next to last column will be the maximum age included in the weight-at-age data. For SS version 3.30 and greater, the last column will be a column of comments.

SS_read_summary  
*read ss_summary file*

**Description**

read Stock Synthesis ss_summary.sso file into list object in R

**Usage**

`SS_read_summary(file = "ss_summary.sso")`

**Arguments**

- **file**: Filename either with full path or relative to working directory.

**Value**

Output will be a list with four elements, header, likelihoods, parameters, and derived_quants. Each is a data frame with rownames indicating the quantity shown in each row.
SS_recevs

Author(s)
Ian Taylor

See Also
SS_output, SS_readforecast, SS_readdat, SS_readstarter

Examples

```r
## Not run:
summary <- SS_read_summary(file='c:/mymodel/ss_summary.sso')
## End(Not run)
```

SS_recevs

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

```r
SS_recevs(fyr, lyr, ctl = NULL, recevs = 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 recevs vector.
- **lyr**
  Last year of the recevs vector.
- **ctl**
  Either NULL to read anew or an already read control file. Default=NULL.
- **recevs**
  Either NULL to generate anew or an already generated vector of recevs. Default=NULL.
- **rescale**
  Should the recevs 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". 
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 = "ss", extras = "-nohess", 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, Ian G. Taylor
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. The function can either create a file for just the input data (if inputs=TRUE), a file for just the MLE values (if MLE = TRUE), or separate files for each of the bootstraps (if inputs=FALSE and MLE=FALSE).

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".
SS_tune_comps

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_tune_comps

Calculate new tunings for length and age compositions

Description
Creates a table of values that can be copied into the SS control file for SS 3.30 models to adjust the input sample sizes for length and age compositions based on either the Francis or McAllister-Ianelli tuning.

Usage
SS_tune_comps(replist, fleets = "all", option = "Francis", digits = 6, write = TRUE)

Arguments
- replist: List output from SS_output
- fleets: Either the string 'all', or a vector of fleet numbers
- option: Which type of tuning: 'none', 'Francis', or 'MI'
- digits: Number of digits to round numbers to
- write: Write suggested tunings to a file 'suggested_tunings.ss'

Details
Note: starting with SS version 3.30.12, the "Length_Comp_Fit_Summary" table in Report.sso is already in the format required to paste into the control file to apply the McAllister-Ianelli tuning. However, this function provides the additional option of the Francis tuning and the ability to compare the two approaches. Also note, that the Dirichlet-Multinomial likelihood is an alternative approach that allow the tuning factor to be estimated rather than iteratively tuned.
Value

Returns a table that can be copied into the control file. If write=TRUE then will write the values to a file (currently hardwired to go in the directory where the model was run and called "suggested_tunings.ss")

Author(s)

Ian G. Taylor

References


See Also

SSMethod.TA1.8

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, maxrows = 100, overwrite = FALSE, version = "3.30", 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 in 3.24 models (may need to increase from default if you have a huge number of fleets)
maxrows: Maximum number of rows to search among in 3.30 models (may need to increase from default if you have a huge number of fleets).

overwrite: Overwrite file if it exists?

version: SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).

verbose: TRUE/FALSE switch for amount of detail produced by function. Default=TRUE.

Author(s)

Ian G. Taylor, Gwladys I. Lambert

See Also

SS_tune_comps, SS_parlines, SS_changepars

Examples

```r
## Not run:
# load model output into R
replist <- SS_output(dir='c:/model/')

# get new variance adjustments
varadjust <- SS_tune_comps(replist, option="Francis")
print(varadjust)

# write new table to file
SS_varadjust(dir=replist$inputs$dir, newctlfile="new_control.ss",
             newtable=varadjust, overwrite=FALSE)

## End(Not run)
```

Description

Write Stock Synthesis control file from list object in R which was probably created using SS_readctl. This function is a wrapper which calls either SS_writectl_3.24 or SS_writectl_3.30 (and potentially additional functions in the future).

Usage

```r
SS_writectl(ctllist, outfile, version = NULL, overwrite = FALSE,
             verbose = TRUE)
```
**Arguments**

- **ctllist**: List object created by `SS_readctl`.
- **outfile**: Filename for where to write new control file.
- **version**: SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3). Defaults to NULL, which means that the function will attempt to determine the version from `ctllist`.
- **overwrite**: Should existing files be overwritten? Defaults to FALSE.
- **verbose**: Should there be verbose output while running the file? Defaults to TRUE.

**Author(s)**

Ian G. Taylor, Yukio Takeuchi, Gwladys I. Lambert, Kathryn Doering

**See Also**

- `SS_writedat_3.24`
- `SS_writedat_3.30`
- `SS_readctl`
- `SS_makectl`
- `SS_readstarter`
- `SS_writestarter`
- `SS_readforecast`
- `SS_writeforecast`

---

**Description**

Write Stock Synthesis control file from list object in R which was probably created using `SS_readctl`.

**Usage**

```r
SS_writectl_3.24(ctllist, outfile, overwrite = FALSE, verbose = TRUE,
                 nseas = 1, N_areas = 1, Do_AgeKey = FALSE)
```

**Arguments**

- **ctllist**: List object created by `SS_readctl`.
- **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?
- **nseas**: Number of season in the model. This information is not explicitly available in control file
- **N_areas**: Number of spatial areas in the model. This information is also not explicitly available in control file
- **Do_AgeKey**: Flag to indicate if 7 additional ageing error parameters to be read set 1 (but in fact any non zero numeric in R) or TRUE to enable to read them 0 or FALSE (default) to disable them. This information is not explicitly available in control file, too.
**Author(s)**

Yukio Takeuchi

**See Also**

SS_readctl, SS_readctl_3.24, SS_readstarter, SS_writectl_3.30

---

**SS_writectl_3.30**

*write control file for SS version 3.30*

**Description**

write Stock Synthesis control file from list object in R which was created using SS_readctl. This function is designed to be called using SS_writectl and should not be called directly.

**Usage**

SS_writectl_3.30(ctllist, outfile, overwrite, verbose)

**Arguments**

- **ctllist**: List object created by SS_readctl.
- **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)**

Kathryn Doering, Yukio Takeuchi, Neil Klaer, Watal M. Iwasaki

**See Also**

SS_readctl, SS_readctl_3.30, SS_readstarter, SS_readforecast, SS_writestarter, SS_writeforecast, SS_writedat
SS_writedat  write Stock Synthesis data file

Description
Write Stock Synthesis data file from list object in R which was probably created using SS_readdat. This function is a wrapper which calls either SS_writedat_3.24 or SS_writedat_3.30 (and potentially additional functions in the future). This setup allows those functions to be cleaner (if somewhat redundant) than a single function that attempts to do everything.

Usage
SS_writedat(datlist, outfile, version = "3.30", overwrite = FALSE, faster = FALSE, verbose = TRUE)

Arguments
- datlist: List object created by SS_readdat (or by SS_readdat_3.24 or SS_readdat_3.24)
- outfile: Filename for where to write new data file.
- version: SS version number. Currently only "3.24" or "3.30" are supported, either as character or numeric values (noting that numeric 3.30 = 3.3).
- overwrite: Should existing files be overwritten? Default=FALSE.
- faster: Speed up writing by writing length and age comps without aligning the columns (by using write.table instead of print.data.frame)
- verbose: Should there be verbose output while running the file?

Author(s)
Ian G. Taylor, Yukio Takeuchi, Gwladys I. Lambert

See Also
SS_writedat_3.24, SS_writedat_3.30, SS_readdat, SS_makedatlist, SS_readstarter, SS_writestarter, SS_readforecast, SS_writeforecast

SS_writedat_3.24  write data file for SS version 3.24

Description
Write Stock Synthesis data file from list object in R which was probably created using SS_readdat (which would have called on SS_readdat_3.24).
**Usage**

```r
definition = SS_writedat_3.24(datlist, outfile, overwrite = FALSE, faster = 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.
- `faster`: Speed up writing by writing length and age comps without aligning the columns (by using `write.table` instead of `print.data.frame`).
- `verbose`: Should there be verbose output while running the file?

**Author(s)**

Ian G. Taylor, Yukio Takeuchi, Gwladys I. Lambert, Kelli F. Johnson, Chantel R. Wetzel

**See Also**

- `SS_writedat`, `SS_writedat_3.30`, `SS_readdat`, `SS_makedatlist`, `SS_readstarter`, `SS_writestarter`, `SS_readforecast`, `SS_writeforecast`

---

**Description**

Write Stock Synthesis data file from list object in R which was probably created using `SS_readdat` (which would have called on `SS_readdat_3.30`).

**Usage**

```r
definition = SS_writedat_3.30(datlist, outfile, overwrite = FALSE, faster = 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.
- `faster`: Speed up writing by writing length and age comps without aligning the columns (by using `write.table` instead of `print.data.frame`).
- `verbose`: Should there be verbose output while running the file?
SS_writeforecast

Author(s)
Ian G. Taylor, Yukio Takeuchi, Gwladys I. Lambert, Kelli F. Johnson, Chantel R. Wetzel

See Also
SS_writedat, SS_writedat_3.24, SS_readdat, SS_makedatlist, SS_readstarter, SS_writestarter, SS_readforecast, SS_writeforecast

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",
       writeAll = FALSE, overwrite = FALSE, verbose = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>mylist</td>
<td>List object created by SS_readforecast.</td>
</tr>
<tr>
<td>file</td>
<td>Filename for new forecast file. Default=&quot;forecast.ss&quot;.</td>
</tr>
<tr>
<td>writeAll</td>
<td>Should the function continue even if Forecast=0 (at which point SS stops reading, and remaining elements in list may not be available, depending on settings used in SS_readforecast)</td>
</tr>
<tr>
<td>overwrite</td>
<td>Should existing files be overwritten? Default=FALSE.</td>
</tr>
<tr>
<td>verbose</td>
<td>Should there be verbose output while running the file? Default=TRUE.</td>
</tr>
</tbody>
</table>

Author(s)
Ian Taylor

See Also
SS_readstarter, SS_readforecast, SS_readdat, SS_writestarter, SS_writedat
**SS_writestarter**  
(write starter file)

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

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

**Arguments**
- `mylist`  
  List object created by **SS_readstarter**.
- `dir`  
- `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_writestarter**, **SS_writeforecast**, **SS_writedat**

**SS_writewtatage**  
(Write weight-at-age file)

**Description**
Write Stock Synthesis weight-at-age file from R object that was probably created using **SS_readwtatage**

**Usage**
```r
SS_writewtatage(mylist, dir = NULL, file = "wtatage.ss",
overwrite = FALSE, verbose = TRUE, warn = TRUE)
```
Arguments

- **mylist**: Object created by `SS_readwtatage`.
- **dir**: A file path to the directory of interest. Typically used with `file`, an additional input argument, to specify input and output file paths. The default value is `dir = NULL`, which leads to using the current working directory, and thus, full file paths should not be specified for other arguments as they will be appended to `dir`.
- **file**: Filename for new weight-at-age file, which will be appended to `dir` to create a full file path. Default=`"wtatage.ss"`.
- **overwrite**: A logical value specifying if the existing file(s) should be overwritten. The default value is `overwrite = FALSE`.
- **verbose**: A logical value specifying if output should be printed to the screen. The default is `verbose = TRUE`.
- **warn**: A logical value specifying if a warning should be generated if overwriting `file`. The default value is `warn = TRUE`.

Author(s)

Kelli Faye Johnson

See Also

`SS_readwtatage`

Description

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

Usage

```r
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 \texttt{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 \texttt{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 \texttt{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 \texttt{SS\_output}. If MCMC results are to be plotted, a ’mcmc’ list element should be added using the \texttt{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

\texttt{SS\_output} \texttt{SSgetMCMC}
Examples

```r
## 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)
```
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