# R documentation

## of all in 'PBSawatea'

### July 26, 2018

# R topics documented:

| | |
|---|---|
| `PBSawatea-package` | *PBSawatea – Tools for Running Awatea and Visualizing the Results* |

## Description

**PBSawatea** contains R code to control the input to and output from the modelling of rockfish populations (e.g., Pacific Ocean Perch, *Sebastes alutus*) that occur along the British Columbia (BC) coast.

The model implementation uses a modified version of the Coleraine statistical catch-at-age software (Hilborn *et al.* 2003) called Awatea (Allan Hicks, IPHC, pers. comm.). Awatea template code is compiled by Automatic Differentiation Model Builder (ADMB) software (Otter Research 1999) to a 64-bit binary called 'awatea.exe'. Running the binary file, which contains ADMB libraries, provides (a) maximum posterior density estimates using a function minimiser and automatic differentiation, and (b) an approximation of the posterior distribution of the parameters using the Markov Chain Monte Carlo (MCMC) method, specifically using the Hastings-Metropolis algorithm (Gelman et al. 2004).

The running of Awatea is streamlined, using code written in R (R Development Core Team 2018) rather than manually manipulating the original Microsoft Excel implementation. Figures and tables of output are automatically produced through R using code adapted from the R packages **scape** (Magnusson 2009) and **plotMCMC** (Magnusson & Stewart 2007). We use the R function Sweave (Leisch 2008) in the package **utils** to automatically collate, via LaTeX (specifically pdflatex), the large amount of figures and tables into a single portable document file (.pdf) for each model run.

We provide master Sweave files in the folder `../library/PBSawatea/snw` to build the .pdf document. The code copies these to a local working directory if they are not already there.

## Author(s)

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Last modified `Rd: 2018-07-25`

## References

Gelman, A., Carlin, J.B., Stern, H.S, and Rubin, D.B. (2004) Bayesian data analysis, 2nd edition. Chapman and Hall/CRC, New York, 668 p.

Hilborn, R., Maunder, M., Parma, A., Ernst, B. Payne, J., and Starr, P. (2003) Coleraine: a generalized age-structured stock assessment model. *School of Aquatic and Fishery Sciences*, University of Washington, 54 p.

Leisch, F. (2008) Sweave, R package.

Magnusson, A. (2009) Scape – statistical catch-at-age plotting environment, R package.

Magnusson, A. and Stewart, I. (2007) MCMCscape – MCMC diagnostic plots. R package.

Otter Research Ltd. (1999) An introduction to AD Model Builder for use nonlinear modeling and statistics. Otter Research Ltd., British Columbia. 194 p.

R Development Core Team (2018) R: A language and environment for statistical computing. hrefhttps://www.r-project.org/R Foundation for Statistical Computing, Vienna, Austria.

---

allEqual                        *Are All Values Equal to the First?*

---

### Description

A short-cut function for all(x==x[1]), which asks are all values in $x$ equl to the first value in $x$.

### Usage

```
allEqual(x)
```

### Arguments

x                     vector of values.

### Value

TRUE or FALSE

### See Also

all, clearAll, clipVector

---

AWATEAdata-class                *S4: AWATEA Data Class*

---

### Description

The set of functions described here provide an easy method of dealing with a complicated scheme for manipulating data when using the catch-at-age model called **Awatea**, a variant of **Coleraine**. Awatea is maintained by Allan Hicks (University of Washington) and Paul Starr (Canadian Groundfish Research and Conservation Society).

To use **PBSawatea**'s management functions, the function runADMB calls readAD which creates an AWATEAdata object. The AWATEAdata object contains a distinct R environment where data are stored and accessed by various package functions.

### Details

An Awatea data file can be loaded into an AWATEAdata object using readAD, and if a complementary results file is available, the user can run reweight for a single re-weighting of the abundance data and the composition data.

Alternatively, starting with a single input data file, a user can run the function runADMB to perform multiple (iterative) re-weightings automatically.

## Objects from the Class

This S4 object can be created by calls of the form:

```
dat = new("AWATEAdata", txtnam=character(), input=character(), vlst=list(),
dnam=character(), nvars=numeric(), vdesc=character(), vars=list(),
gcomm=character(), vcomm=character(), resdat=list() , likdat=list(),
pardat=list(), stddat=list(), cordat=list(), evadat=list(),
reweight=list(), controls=list())
```

The function `readAD` populates the first nine slots of the S4 object by reading in an `Awatea` data file from the user's current working directory. If `Awatea` output files exist (with the same prefix as the input file and suffixes = {`.res`, `.lik`, `.par`, `.std`, `.cor`, `.eva`}), then slots `resdat`, `likdat`, `pardat`, `stddat`, `cordat`, and `evadat`, respectively, will also be populated.

## Slots

`txtnam` the file name (including extension) of the `Awatea` input data file.

`input` a string vector comprising the line-by-line information from the data file.

`vlst` a list named by line number (e.g. "L001:...") of comments and data.

`dnam` a vector of data descriptors referenced by numeric line number.

`nvars` a numeric scalar indicating the number of input variables.

`vdesc` as for dnam but indexed by variable identifier (e.g. "v001").

`vars` variable values indexed by variable identifier.

`gcomm` commented lines indexed by numeric line number.

`vcomm` value descriptors indexed by numeric line number.

`resdat` list of Awatea results from the file `results.dat` after calling `importRes`.

`likdat` list of MPD likelihoods from the file `likelihood.dat` after calling `importLik`.

`pardat` list of parameter values from the file `Awatea.par` after calling `importPar`.

`stddat` list of estimated parameter values from the file `Awatea.std` after calling `importStd`.

`cordat` list of correlation objects from the file `Awatea.cor` after calling `importCor`.

`evadat` eigenvalues of the Hessian from the file `Awatea.eva` after calling `importEva`.

`reweight` list of re-weighted abundance and composition data (see [reweight](reweight) for details).

`controls` list of control values from the ADMB input data.

## Methods

`fix, signature(x="AWATEAdata")` : replace data elements of an input list

`reweight, signature(x="AWATEAdata")` : reweight abundance and composition data

`view, signature(x="AWATEAdata")` : view the basic input list

`write, signature(x="AWATEAdata")` : write a new input data file

**Note**

Some of the output values in results.dat, likelihood.dat, Awatea.par, Awatea.std, and Awatea.cor contain redundant information.

**Author(s)**

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

**See Also**

readAD for loading the ADMB data file

importRes for reading in the file results.dat

importLik for reading in the file likelihood.dat

importPar for reading in the file Awatea.par

importStd for reading in the file Awatea.std

importCor for reading in the file Awatea.cor

importEva for reading in the file Awatea.eva

reweight for re-weighting abundance and composition data

runADMB for running the Awatea model through multiple iterations.

---

calc.projExpect                    *Calculate Expectations and Probabilities*

---

**Description**

Calculate the expectation of projection to reference, and probability of being greater than reference.

**Usage**

```
calc.projExpect  ( obj, projObj, refYrs  )
calc.projExpect2 ( obj, projObj, refList )
calc.projProbs   ( obj, projObj, refYrs  )
calc.projProbs2  ( obj, projObj, refList )
calc.refProbs    ( projObj=currentProj$B, refPlist=refPointsList )
calc.refProbsHist( projObj=currentProj$B,
   refPlist=refPointsHistList[c("blimHRP","btarHRP")] )
```

**Arguments**

| | |
|---|---|
| obj | matrix of biomass MCMCs. |
| projObj | matrix of biomass projections. |
| refYrs | numeric vector of reference years |
| refList | list of reference years (numeric vectors). |
| refPlist | list of reference points. |

## Details

```
calc.projExect....Calculate the expectation of projection to reference.
..................Compare reference years to projection years.
calc.projExect2...Calculate expectation (projection biomass / reference biomass).
calc.projProbs.....Calculate the probability of being greater than refYrs.
..................Compare reference years to projection years.
calc.projProbs2....Calculate the probability of being greater than refYrs.
..................Compare reference years to projection years.
calc.refProbs......Calculate the reference probabilities (based on calc.projProbs2).
calc.refProbsHist..Calculate the historical reference probabilities.
```

## Value

Decision tables

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified `Rd`: `2018-07-26`

## See Also

`calc.refVal`

---

| calc.refVal | *Calculate Reference Value for Performance Measure* |
|---|---|

---

## Description

Calculate the reference value for performance measures.

## Usage

```
calc.refVal(obj, refYrs, fun=mean)
```

## Arguments

| | |
|---|---|
| obj | scape Biomass matrix with $n$ rows and $m$ columns, where $n$ = number of MCMC samples, and $m$ = number of years. |
| refYrs | numeric years in reference period. |
| fun | the function to apply to reference period $i$. |

## Value

Returns a vector of length `nrow(obj)` reference values.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[calc.projExpect](), [findTarget]()

---

closeAllWin                          *Close All Open Devices*

---

## Description

Close all open devices.

## Usage

```
closeAllWin()
```

## See Also

[closeWin]()

---

compB0                          *Compare Reference Criteria and Points Relative to B0*

---

## Description

Compare COSWEIC reference criteria and DFO reference points relative to $B_0$.
The figure concept comes from Chris Woods (PBS).

## Usage

```
compB0(B, Mnams=NULL, ratios=c(0.4,0.8),
   include=list(A1=TRUE, A2=TRUE, SSPM=TRUE, Bmsy=TRUE, Bt=TRUE),
   t.yr=2011, boxwidth=0.6, figgy=FALSE, width=12, height=9,
   pngres=400, lang=c("e","f"), ...)
```

## Arguments

| | |
|---|---|
| B | list – list of list of MCMC samples (see **Details**); the first level of the list is the model run, while the second level contains MCMC samples (one of which should be $B_0$ which acts as the divisor to the other MCMCs). |
| Mnams | character – optional model names for the boxplot. |
| ratios | numeric – reference levels of $B_{MSY}$ (usually 0.4 and 0.8). |
| include | logical – list of logicals specifying whether to plot COSEWIC's reference criteria A1 and A2, the Schaefer surplus production model SSPM, the biomass at maximum sustainable yield Bmsy, and the biomass of a given time period Bt, where t.yr specifies the year. All values are cast in terms of $B_0$. |
| t.yr | numeric – numeric year that represents the time period for $B_t$. |
| boxwidth | numeric – width of the box in x-units. |
| figgy | logical – if TRUE, send figure to four output files (.eps, .pdf, .png, and .wmf). |
| width | numeric – width of the output files in inches. |
| height | numeric – height of the output files in inches. |
| pngres | numeric – resolution (pixels/inch) of the png file, if it's created. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| ... | additional values for [plotBox](plotBox)'s argument pars. |

## Details

An example of the input list B:
```
List of 2
..$ 29.01:List of 3
....$ B0.MCMC  : num [1:1000]
....$ Bt.MCMC  : num [1:1000]
....$ Bmsy.MCMC: num [1:1000]
..$ 30.01:List of 3
....$ B0.MCMC  : num [1:1000]
....$ Bt.MCMC  : num [1:1000]
....$ Bmsy.MCMC: num [1:1000]
```

The function creates a figure comparing COSEWIC criteria and reference points for the Schaefer surplus production model and specified ratios of $B_{MSY}$ from catch-at-age models. The coordinate space (*y*-axis) is relative to $B_0$.

## Value

Invisibly returns a list object of xBox and BarBox used to create the boxplot.

## Note

Uses a modified version of boxplot called [plotBox](plotBox).

## Author(s)

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Last modified Rd: 2018-07-25

## See Also

plotBox, importMCMC, msyCalc
plotmath, boxplot, bxp

---

cquantile                              *Running Quantile*

---

## Description

Creates a set of running quantiles from MCMC traces.
(Uses subfunction found in **coda**'s function cumuplot.)

## Usage

```
cquantile(z, probs)
cquantile.vec(z, prob)
```

## Arguments

z             an MCMC object.

probs         vector of quantiles.

prob          single quantile.

## Value

```
cquantile.......running quantile matrix
cquantile.vec...running quantile vector
```

## Note

Arni Magnusson describes a running quantile as:
"*the evolution of the sample quantiles as a function of the number of iterations*"

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

cumuplot, plotTracePOP

---

findTarget                                    *Find Time to Achieve a Target Reference Point*

---

### Description

Find the time (years) to achieve a recovery target (including a moving target) with a given confidence. Produce decision tables showing the probability of exceeding the reference point.

### Usage

```
findTarget(Vmat, yrU=as.numeric(dimnames(Vmat)[[2]]), yrG=90,
    ratio=0.5, target=B0.MCMC, conf=0.95, plotit=FALSE, retVal="N")
```

### Arguments

| | |
|---|---|
| Vmat | matrix of projected biomass values $B_{Nt}$, where $N$ = number of MCMCs and $t$ = projection year. |
| yrU | user-specified projection years. |
| yrG | number of years $G$ for a moving target window (*e.g.*, 3 YMR generations = 90y); might not work for all possibilities. |
| ratio | recovery target ratio $R$. |
| target | recovery target values $T_N$ <br> = B0.MCMC for ratios of $B_0$; <br> = Bmsy.MCMC for ratios of $B_{MSY}$; <br> = Bt.MCMC for moving window of $B_{N,t-G}$. |
| conf | confidence level $C$ required. |
| plotit | logical: if TRUE, plot the probability $p_t$ of exceeding target reference point. |
| retVal | character name of object to return: <br> retVal="N" : creates global object "Ttab" (see below); <br> retVal="p.hi" : creates global object "Ptab" (see below). |

### Details

As this function uses Bayesian output, there are $N$ (*e.g.*, 1000) values of some target $T_N$, which can remain fixed ($B_0$, $B_{MSY}$) or move forward in time $G$ years before the projection year $t$ (that is $T_{N,t-G}$). For simplification, we'll just call all targets $T_N$.

The probability of exceeding a target ratio $R$ is:

$$p_t = \frac{1}{N} \sum^{N} \left[ \frac{B_{Nt}}{T_N} > R \right],$$

where $R$ = target ratio of the reference point (*e.g.*, $0.4B_{MSY}$ ($R$=0.4), $0.2B_0$ ($R$=0.2), $0.5B_{t-G}$ ($R$=0.5) ).

At a glance, we can see for any given projection year $t$ whether the probability of achieving a target ratio is greater than the confidence required:

$$p_t \geq C,$$

where $C$ is the confidence level acceptable.

## Value

If `retVal="N"` then the function returns a data frame object called `"Ttab"` in the user's global environment. This table reports the number of years to achieve the target reference point at various catch levels with a specified confidence.

If `retVal="p.hi"` then the function returns a list object called `"Ptab"` in the user's global environment. This list contains data frames (tables) that report the probability of achieving various reference points at specified catch levels.

Any other `retVal` will return a list of the specified object, if it exists in the function.

## Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[runSweaveMCMC](runSweaveMCMC)

---

get.resFile                     *Get Awatea Results Files for Menu*

---

## Description

A function that retrieves the names of Awatea results files (`.res$`) for use in the `mainMenu` command. When choice is made, the function loads the results file and assigns it to the global environment as `currentRes`.

## Usage

```
get.resFile(resFile=NULL)
```

## Arguments

resFile            supposedly the name of a results file, but the code suggests that argument is
                   ignored.

## Value

A results file chosen from a menu.

## Note

AME: made changes so that options are compatible with those in `load.allResFiles`. Previously, trouble occurred when overwriting.

## See Also

[mainMenu](), [importRes]()

---

getYrIdx                               *Select a Subset of Years for Plotting*

---

## Description

Select a subset of years for which many years are available. The default is to select 5-year increments.

## Usage

```
getYrIdx(yrNames, mod=5)
```

## Arguments

| | |
|---|---|
| yrNames | vector (character or numeric) of years. |
| mod | select the years modulo mod. |

## Value

Subset of input years that are modulo mod.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[findPat](), [pad0]()

---

gfcode                          *Code: Groundfish Species Codes and Names*

---

## Description

Data frame of groundfish species described primarily by Hart codes. The information resides in a
data table called C_Species in the relational database PacHarvest.

## Usage

```
data(gfcode)
```

## Format

Data frame comprising 549 rows (species) and 5 columns:

| | |
|---|---|
| code | Hart code |
| latin | scientific (latin) name |
| name | common species name |
| code2 | 2-letter code if available |
| code3 | 3-letter code if available |

## Details

The data frame comprises 5,49 rows (species) and 5 columns. Hart codes for fish species essentially
reference page numbers in Hart (1973).

Quick reference to species name: species["424",]$name yields Quillback rockfish.

Quick reference to latin name: species["424",]$latin yields Sebastes maliger.

## Source

Norm Olsen, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## References

Hart, J.L. (1973) Pacific Fishes of Canada. *Bulletin of the Fisheries Research Board of Canada* **180**,
740 pp.

---

 graphics                        *Open a Windows Device*

---

## Description

Open a windows device in portrait or landscape mode.

## Usage

```
graphics(view = "portrait")
```

## Arguments

view             if "portrait", set width = 8.5 in and height = 11 in
                 if "landscape", set width = 11 in and height = 8.5 in

## See Also

[resetGraph](resetGraph)

---

importCor                          *Import Awatea Correlation File*

---

## Description

Import an Awatea correlation file that results from an MPD minimisation.

## Usage

```
importCor(cor.file)
```

## Arguments

cor.file         correlation file (e.g., Awatea.cor).

## Details

Extracts the data from character vectors and makes various data objects.

## Value

The output is a list object with the following components:

cfile            character vector representing the file line-by-line

cor              data.frame of the correlation file

cor.mat          matrix representing the correlation matrix only

index            character vector used in the row and column names of cor and cor.mat

cor.name         Awatea parameter names in the correlation file

cor.value        Awatea parameter values in the correlation file

cor.std.dev      Awatea parameter standard deviations in the correlation file

hessian_log_determinant
                 log of the determinant of the hessian reported in the header

**Author(s)**

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

**See Also**

importPar, importRes, importStd

---

importEva                         *Import Awatea Hessian Eigenvalues*

---

**Description**

Import a vector of eigenvalues of the Hessian from an MPD analysis file (Awatea.eva).

**Usage**

```
importEva(eva.file)
```

**Arguments**

eva.file          vector of hessian eigenvalues; first element should be a positive definite number.

**Details**

The eigenvalues of the Hessian represent the 2nd derivatives of the negative log-likelihood function. If they are all positive it indicates a minimum. The first element of this vector should be positive definite before an MCMC is run.

**Value**

The output is a list object with only one component:

eva               a numeric vector representing the eigenvalues of the Hessian.

**Author(s)**

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

**See Also**

importCor, importLik, importPar, importRes, importStd

---

importLik                    *Import Awatea Likelihoods*

---

### Description

Import an Awatea file of the likelihoods from an MPD estimation.

### Usage

```
importLik(lik.file)
```

### Arguments

lik.file          likelihoods file (usually `likelihood.dat`)

### Details

Extracts the data from character vectors and makes various data objects.

### Value

The output is a list object with the following components:

| | |
|---|---|
| lik | character vector representing the file line-by-line |
| Total_likelihood | |
| | values of the final likelihood (objective function value) |
| Worst_gradient | worst gradient? |
| CPUE | commercial CPUE likelihood(s) |
| Survey_Index | survey index likelihood(s) |
| CA_Commercial | commercial catch-at-age likelihood(s) |
| CL_Commercial | commercial catch-at-length likelihood(s) |
| CA_survey | survey catch-at-age likelihood(s) |
| CL_no_sex_data_survey | |
| | likelihood(s) for catch-at-length from surveys with no sex data? |
| CL_data_survey | likelihood(s) for catch-at-length from surveys with sex data? |
| Von_B_Likelihood | |
| | von Bertalanffy likelihood |
| Priors | priors? |
| Penalty_for_U | penalty for U? |

### Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

[importCor](), [importPar](), [importRes](), [importStd]()

---

importMCMC.ddiff            *Import Functions for PJS Delay Difference Model*

---

### Description

Make a **plotMCMC** object identical in format to the result of importMCMC (or importProj) from PJS delay difference model output.
The difference is that $B$ is biomass defined by a delay difference model.

### Usage

```
importMCMC.ddiff()
importProj.ddiff(yrVal="2006")
```

### Arguments

yrVal            character year for delay-difference model (?).

### Value

importMCMC.ddiff returns a list object containing:
L...likelihood MCMCs,
P...parameter MCMCs,
B...spawning biomass MCMCs,
R...recruitment MCMCs.

importProj.ddiff returns a list object containing:
B...projected biomass,
Y...projected yields.

### Note

Get the biomass projection – PJS does 1 year ahead projection. The column "X" appears as the last column because trailing "," exist in the mcmcprojbiom.csv file.
Note also that "cat=" in .csv file becomes "cat." in read.table.

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

importMCMC, importProj, read.table

## importPar                    *Import Awatea Parameter File*

### Description

Import an Awatea file of all parameters resulting from an MPD minimisation.

### Usage

```
importPar(par.file)
```

### Arguments

par.file          parameter file (e.g., `Awatea.par`).

### Details

Extracts the data from character vectors and makes various data objects.

### Value

The output is a list object with the following components:

par                character vector representing the file line-by-line

npars              number of parameters reported in header

fval               objective function value reported in header

maxgrad            maximum gradient component reported in header

parameters         numerous reported parameters (e.g., `R0`) that will depend on the model

### Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

[importCor](), [importRes](), [importStd]()

---

importProjRec                          *Import Projected Recruitment*

---

**Description**

Import the projected recruitments (actually, the values are random normals $N(0, 1)$).

**Usage**

```
importProjRec(dir, info="", coda=FALSE, ngear=1, quiet=TRUE)
```

**Arguments**

dir                 directory where MCMC projections reside.

info                user-supplied information, if desired.

coda                logical: if TRUE, use the function mcmc in the package **coda** to generate MCMCs.

ngear               number of commercial gears

quiet               logical: if TRUE, print progress messages to the R console.

**Details**

The values saved by the Awatea code are random normals $N(0, 1)$, which for a particular MCMC sample are the same for all the catch strategies.

**Value**

A list object comprising:

B                   data frame of spawning biomass (dim = MCMC samples by projected years)

VB                  data frame of vulnerable biomass (dim = MCMC samples by projected years)

Y                   data frame of yield (dim = MCMC samples by projected years)

eps                 data frame of $\epsilon_t$ (dim = MCMC samples by projected years)

**Note**

The function importProj does not import recruitment residuals.

This function grabs the tempdev values from Awatea, which are just $N(0, 1)$ values, then multiplies them by $\sigma_R$ to yield $\epsilon_t \sim N(0, \sigma_R^2)$.

The parameter value for $\sigma_R$ can be found in
currentRes$extra$residuals$p_log_RecDev[6].

**Author(s)**

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

**See Also**

importProj
**coda**: mcmc

---

importRes                         *Import Coleraine Model Results (RH version)*

---

**Description**

Import Coleraine model results from `.res` file, and rearrange into a standard format suitable for
plotting.

**Usage**

```
importRes(res.file, info="", Dev=FALSE, CPUE=FALSE, Survey=FALSE,
    CAc=FALSE, CAs=FALSE, CLc=FALSE, CLs=FALSE, LA=FALSE, quiet=TRUE,
    extra=TRUE, sep=" ")
```

**Arguments**

| | |
|---|---|
| res.file | name of Coleraine model results file to import. |
| info | optional string containing information to store with model results. |
| Dev | logical: whether recruitment deviates were estimated in model. |
| CPUE | logical: whether model was fitted to catch-per-unit-effort data. |
| Survey | logical: whether model was fitted to survey abundance index data. |
| CAc | logical: whether model was fitted to commercial catch-at-age data. |
| CAs | logical: whether model was fitted to survey catch-at-age data. |
| CLc | logical: whether model was fitted to commercial catch-at-length data. |
| CLs | logical: whether model was fitted to survey catch-at-length data. |
| LA | logical: whether model was fitted to length-at-age data. |
| quiet | logical: whether to report progress while parsing file. |
| extra | logical: if TRUE, import likelihoods, parameters, priors, and recruitment residuals. |
| sep | the field separator character (usually " " or "\t"). |

**Details**

This function was modified from the original `importCol` function in the **scape** package to grab
extra data and to deal with anomalous characters in Coleraine results files.

**Value**

A list of class `list` containing at least N, B, and Sel. The other elements may or may not be included in the list, depending on how `importRes` was called:

| | |
|---|---|
| N | predicted numbers at age |
| B | predicted biomass, recruitment, and observed landings (year things) |
| Sel | predicted selectivity and observed maturity (age things) |
| Dev | predicted recruitment deviates from the stock-recruitment curve |
| CPUE, Survey | commercial and survey abundance index and fit |
| CAc, CAs | commercial and survey C@A (catch at age) and fit |
| CLc, CLs | commercial and survey C@L (catch at length) and fit |
| LA | observed L@A and fit |

**Note**

This import function is implemented for the Coleraine statistical catch-at-age software, and can serve as a template for **scape** users who would like to implement import functions for specific stock assessment software.

The functions `ll` (package **gdata**) and `head` are recommended for browsing model results, *e.g.* `ll(x.cod); ll(x.cod$N); head(x.cod$N)`.

**References**

Hilborn, R., Maunder, M., Parma, A., Ernst, B., Payne, J., and Starr, P. (2003) Coleraine: A generalized age-structured stock assessment model. User's manual version 2.0. *University of Washington Report* **SAFS-UW-0116**. Available at:
https://tinyurl.com/y83fwgeb.

**See Also**

importCor, importPar, importStd, runADMB, readAD, reweight
Import data:
read.table, readLines, scan
Overview of **scape** package:
scape-package

---

importStd | *Import Awatea Estimated Parameter File*

---

**Description**

Import an Awatea file of estimated parameters resulting from an MPD minimisation.

**Usage**

```
importStd(std.file, vnam="name")
```

## Arguments

| | |
|---|---|
| `std.file` | parameter file (e.g., `Awatea.std`). |
| `vnam` | field name listing parameter names in data file. |

## Details

Extracts the data from character vectors and makes various data objects.

## Value

The output is a list object with the following components:

| | |
|---|---|
| `std` | data.frame representation of the `.std` file |
| `parameters` | data.frame for each of the estimated parameters in `std` |

## Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

`importCor`, `importPar`, `importRes`

---

`load.allResFiles`     *Load All Awatea .res Files*

---

## Description

Load all Awatea `.res` files in the working directory into a list object.

## Usage

```
load.allResFiles(resList = NULL)
```

## Arguments

| | |
|---|---|
| `resList` | AME: sets directory to path above current and sets the pattern to `"results.dat$"`; probably deprecated. |

## Value

List of multiple calls to `importRes`.

## Note

If deprecated, remove from package **PBSawatea**.

**Author(s)**

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

**See Also**

[importRes](#)

---

MAfun                          *Calculate Mean Age by Year*

---

**Description**

Calculate mean ages from proportions-at-age (modified from a subfunction in `runADMB`).

**Usage**

```
MAfun(padata, brks=NULL)
```

**Arguments**

| | |
|---|---|
| padata | proportion-at-age data `CAc` or `CAs` from a call to `importRes`. |
| brks | breaks specified as numeric years to split the commercial data up into regimes that may account for index discontinuities (**not used**). |

**Details**

Mean age function supplied by Chris Francis (2011).
padata has fields:
Series...series identifier
Year.....numeric year
Age......age bin
Obs......observed proportions
Fit......predicted (fitted) proportions
SS.......sample size (effective $N$)

**Value**

List object of observed and expected mean ages, variance of expected ages, and a few bits and bobs.

**Author(s)**

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC.

**References**

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

**See Also**

runADMB, importRes

---

mainMenu                    *Create a Menu of Options and Actions*

---

**Description**

From a main menu, the user can choose various options and actions.
We tend to do everything from the command line so the menu functionality fosters the warning:
*CAVEAT EMPTOR*.

**Usage**

```
mainMenu()
loadMenu()
mpdMenu()
mcmcMenu()
utilMenu()
```

**Details**

**Main menu items:**
```
Import files
MPD plots
Plot all MPD graphs
Save all MPD plots to PNG
MCMC plots
Plot all MCMC plots
Save all MCMC plots to PNG
Close all graphics windows
Help & Utilities
```

**Load menu items:**
```
Get Awatea res file
Get Awatea MCMC file
Get Awatea projection file
Load all res files in working directory
Get PJS Delay Difference MCMC+Projection
```

**MPD menu items:**
```
Plot biomass, recruitment, catch
Plot numbers at age
Plot selectivity and maturity
Plot commercial catch-at-age results
Plot survey catch-at-age results
Plot survey catch-at-length results
Plot abundance index
```

```
All residual plots
Plot multi-panel biomass, recruitment, catch
Plot multi-panel exploitation rate
Plot alternative numbers at age
```

**MCMC menu items:**
```
Plot biomass and projections by policy
Probability of projection biomass > reference
Expectation of projection biomass / reference
Plot biomass posterior densities (plotDens)
Plot recruitment posterior densities (plotDens)
Plot parameter posterior densities (plotDens)
Plot cumulative quantiles (plotCumu)
Plot traces (plotTrace)
Plot PJS traces (plt.allTraces)
```

**Utils menu items:**
```
scape Help
plotMCMC Help
Portrait graphsheet
Landscape graphsheet
```

### See Also

[get.resFile](), [importRes]()

---

makeCmat                        *Make Column (Row) Matrix Using a Vector*

---

### Description

Covert a vector into a one-column (or one-row) matrix.

### Usage

```
makeCmat(x, colname = "Y")
makeRmat(x, rowname = "Y")
```

### Arguments

| | |
|---|---|
| x | vector (numeric or character) to convert to a matrix with dimensions ($n$,1) or (1,$n$). |
| colname | name of the single column in the matrix |
| rowname | name of the single row in the matrix |

## Details

R has a tendency to lose dimensionality when a matrix subset has one column or one row. The dimensionality can be retained using the argument `drop=FALSE`; however, there are time when a user cannot control operations using this trick (e.g., reading in a file). The functions `makeCmat` and `makeRmat` can restore dimensionality to a vector when needed.

## Value

A matrix with one column or one row, depending on the function.

## Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[runADMB](runADMB)

---

makeErrMat                      *Make Ageing Error Matrix for Awatea*

---

## Description

Make a simple ageing error matrix for Awatea.

## Usage

```
makeErrMat(N=60, ondiag=0.8, offdiag=0.1, corner=0.9)
```

## Arguments

| | |
|---|---|
| N | numeric scalar indicating number of age classes, which determines the dimension of the matrix. |
| ondiag | numeric value to appear along the matrix diagonal. |
| offdiag | numeric value to appear one cell to the left and right of the matrix diagonal. |
| corner | numeric value to appear in the top left and bottom right corners of the matrix. |

## Value

Simple symmetric ageing error matrix.

## Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[plotProp](plotProp), [weightBio](weightBio)

---

mochaLatte *Mock Lattice*

---

### Description

An attempt to simulate a lattice panel plot and gain greater control over the look of the figure without having to tweak endless sub-options.

### Usage

```
mochaLatte(dat, xfld, yfld, ffld, panel, strip=list(col=lucent("black", 0.5),
    bg=lucent("moccasin",0.5), height=0.1, cex=1.4), ...)
```

### Arguments

| | |
|---|---|
| dat | data.frame – object with fields that can be used as factors (without being factors) and fields with data to plot. |
| xfld | character – name of the field with x-values. |
| yfld | character – name of the field with y-values. |
| ffld | character – name of the field with 'factors' that will be represented in each panel. |
| panel | function – panel function that plots the data in some fashion. |
| strip | list – controls for strip along the top of each panel: outline colour (col), background colour (bg), height, and font size (cex). |
| ... | list – aditional arguments for plot, axis, and mtext. |

### Details

The function does not mock lattice, rather, it provides a *faux* lattice-like, panel-plotting framework that will undoubtedly evolve as it is used to replace other calls to lattice plots. There is no guarantee that this function is universally functional. But perhaps more importantly, it is an alternative to embracing ggplot.

### Value

Currently returns nothing.

### Note

The lattice package provides a versatile system that has evolved over many years; however, there is only so much time in a day that one can fiddle about with lattice options.

### Author(s)

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: 2018-05-24

## See Also

[plotChains](), [plotDensPOP](), [plotIndexNotLattice](), [plotTracePOP]()

---

msyCalc                     *Calculate the Maximum Sustainable Yield*

---

### Description

Load in `MSY.out` and calculate the MSY (maximum sustainable yield).

### Usage

```
msyCalc(dir = getwd(), error.rep = 1)
```

### Arguments

| | |
|---|---|
| dir | working directory. |
| error.rep | numeric: if 1, report errors (reaching bounds), if 0 do not. |

### Value

Returns a list object containing:
yield...maximum sustainable yield,
u.......exploitation rate at MSY,
VB......vulnerable biomass at MSY,
B.......spawning biomass at MSY,
nProj...numnber of projections needed to reach MSY.

### Note

See `msyTestCreating.r` for full details when figuring this out.

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

[findTarget]()

---

out.pmTables *Write Decision Tables to Comma-Delimited Files*

---

### Description

Write decision tables to comma-delimited text files (.csv).

### Usage

```
out.pmTables(obj, fileName="pm", dec=3)
```

### Arguments

| | |
|---|---|
| obj | list object containing tables (matrices or data frames). |
| fileName | prefix for output file names. |
| dec | number of decimal places to retain. |

### Value

Comma-delimited text files (.csv).

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

[write.table](), [writeList]()

---

panLab *Write Text to Figure in Relative (0:1) Coordinates*

---

### Description

Write text to a figure by first setting the coordinate space to lie between 0 and 1:
par(usr=c(0,1,0,1)).

### Usage

```
panLab(x, y, txt, ...)
```

### Arguments

| | |
|---|---|
| x | relative x-coordinate. |
| y | relative y-coordinate. |
| txt | text to add to figure. |
| ... | additional arguments sent to function text. |

## Note

Currently, this function does not reset the coordinate space to the original.
Use addLabel instead.

## See Also

addLabel, addLegend

---

panLegend                          *Place a Legend in a Figure using Relative (0:1) Coordinates*

---

## Description

Place a legend in a figure by first setting the coordinate space to lie between 0 and 1:
par(usr=c(0,1,0,1)).

## Usage

```
panLegend(x, y, legTxt, ...)
```

## Arguments

| | |
|---|---|
| x | relative x-coordinate. |
| y | relative y-coordinate. |
| legTxt | legend text to add to figure. |
| ... | additional arguments sent to function legend. |

## Note

Currently, this function does not reset the coordinate space to the original.
Use addLegend instead.

## See Also

addLabel, addLegend

---

plotACFs                          *Plot Autocorrelations for MCMC Parameters*

---

### Description

Plot ACFs for a set of estimated parameters from MCMC samples.

### Usage

```
plotACFs(mcmcObj, lag.max=60, lang="e")
```

### Arguments

| | |
|---|---|
| mcmcObj | list – collection of data frames from the MCMC, including P used by this function. |
| lag.max | numeric – maximum lag at which to calculate the autocorelation function (see [acf](#)). |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |

### Details

Extracts the estimated parameters from the data frame currentMCMC$P and displays the first lag.max lags using the acf function from the stats package.

### Value

Returns nothing at present.

### Note

*Caution* – (from plot.acf) The confidence interval plotted in plot.acf is based on an *uncorrelated* series and should be treated with appropriate caution. Using ci.type = "ma" may be less potentially misleading.

### Author(s)

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: 2018-07-25

### See Also

plotChains, plotCI

---

plotAges                    *Plot MPD Fits to Proportions-at-Age*

---

### Description

Plot the MPD model fits from Awatea to age data (commercial or survey) using the scape function
`plotCA`.

### Usage

```
plotAges(obj, what="c", maxcol=5, sexlab=c("Females","Males"),
   ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"), ...)
```

### Arguments

| | |
|---|---|
| obj | list – the MPD object created by the `importRes` function (e.g., `currentRes`). |
| what | character – letter: `"c"` for commercial proportions-at-age (pA) or `"s"` for survey pA. |
| maxcol | numeric – maximum number of columns for trellis plot |
| sexlab | character – label(s) to rename sex on the plot (e.g., a user may wish to rename "Unisex" to "Female"). |
| ptypes | character – plot types for the figures: eps = encapsulated postscript, png = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the png file. |
| lang | character – a vector of letters that denote the language for output: currently only `"e"` (english) and `"f"` (french). |
| ... | additional arguments for `plotCA` and internal control. |

### Details

The function drills down into the MPD object to extract data to pass to **scape**'s function `plotCA`.

If all goes well, `.eps` and `.png` files will be produced for each series and sex of the commercial `CAc`
and/or survey `CAs` data in the MPD object.

### Author(s)

[Rowan Haigh](#), Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: `2018-07-25`

### See Also

[`plotCA`](#), [`plt.bubbles`](#), [`plt.recdev`](#)

---

plotB2                          *Plot Biomass, Recruitment, and Landings (AME Version)*

---

### Description

Plot scape model predicted biomass, stock recruitment, and landings.

AME: This is an alteration of Arni Magnussons `plotB` function to accommodate PJS's request not to show biomass prior to fishery and survey indices period.

### Usage

```
plotB2(model, what="d", series=NULL, years=NULL, axes=TRUE, div=1,
       legend="bottom", main="", xlab="", ylab="", cex.main=1.2,
       cex.legend=1, cex.lab=1, cex.axis=0.8, las=1,
       tck=c(1,what=="d")/2, tick.number=5, lty.grid=3, col.grid="white",
       pch=16, cex.points=0.8, col.points="black", lty.lines=1:3,
       lwd.lines=2, col.lines="black", ratio.bars=3, col.bars="grey",
       plot=TRUE, ...)
```

### Arguments

| | |
|---|---|
| model | fitted `scape` model. |
| what | what to plot: `"d"`[efault], `"s"`[tock recruitment], or `"l"`[andings]. |
| series | vector of strings indicating which column names in `model$B` data frame to plot (all by default). |
| years | vector of numbers indicating which years to include (all by default). |
| axes | whether to plot axis values. |
| div | denominator to shorten values on the y axis, or a vector with two elements referring to x and y axis. |
| legend | legend location: `"bottom"`, `"left"`, `"top"`, `"right"`, or `""` to suppress legend. |
| main | main title. |
| xlab | x-axis label. |
| ylab | y-axis label. |
| cex.main | size of main title. |
| cex.legend | size of legend text. |
| cex.lab | size of axis labels. |
| cex.axis | size of tick labels. |
| las | orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical. |
| tck | tick mark length. |
| tick.number | number of tick marks. |
| lty.grid | line type of gridlines. |

| | |
|---|---|
| col.grid | color of gridlines. |
| pch | symbol for points. |
| cex.points | size of points. |
| col.points | color of points. |
| lty.lines | line type of main lines. |
| lwd.lines | line width of main lines. |
| col.lines | color of main lines. |
| ratio.bars | width of bars. |
| col.bars | color of bars. |
| plot | whether to draw plot. |
| ... | passed to xyplot and panel.superpose. |

## Details

The "d"[efault] plot shows spawning biomass and vulnerable biomass as lines, and landings as bars, on the same scale.

## Value

When plot=TRUE, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When plot=FALSE, a trellis object is returned.

## Note

The Args function from the **gdata** package is recommended for reviewing the arguments, instead of args.

## See Also

xyplot, panel.barchart, and panel.superpose are the underlying drawing functions.

plotCA, plotCL, plotIndex, and plotLA plot model fit and data.

plotB, plotN, and plotSel plot derived quantities.

scape-package gives an overview of the **scape** package.

---

| plotBars | *Barplots of Annual Age Proportions* |
|---|---|

---

**Description**

Plot barplots of specific-year age proportions.

**Usage**

```
plotBars(res, type="N", prop=TRUE, year=min(res[[type]][["Year"]]),
    sex=c(2,1), age=NULL, fill=c("orange", "cyan", "green"),
    eps=FALSE, png=FALSE, win=TRUE, pngres = 400, lang="e", ...)
```

**Arguments**

| | |
|---|---|
| res | Awatea results file from a call to `importRes`: `importRes("POPrun05/pop-3CD.05.01.res",Dev=T,CPUE=T,Survey=T,CAc=T,CAs=T)` |
| type | `character` – type of annual value (e.g., `"N"` = numbers, `"B"` = biomass). |
| prop | `logical` – if `TRUE`, convert values from `type` to proportions. |
| year | `numeric` – scalar or vector of years. |
| sex | `numeric` – sex code where 1 = males and 2 = females; note that Awatea uses females before males. |
| age | `numeric` – specify age vector if subset of available is desired. |
| fill | `character` – bar colour by sex for barplots (one colour per sex). |
| eps | `logical` – if `TRUE`, send figure to a postscript (`.eps`) file. |
| png | `logical` – if `TRUE`, send figure to a portable network graphics (`.png`) file. |
| win | `logical` – if `TRUE`, send figure to the R windows device. |
| pngres | `numeric` – resolution (pixels/inch) for the png file. |
| lang | `character` – a letter that denotes the language for output: currently only `"e"` (english) or `"f"` (french). |
| ... | extra parameters (not currently used). |

**Details**

The plot is used primarily to see how an age composition for a year compares with an equilibrium age structure (represented by an exponential decay from 1 using $e^{-M}$).

**Value**

Aside from the figure plots, the function invisibly returns a list of:

| | |
|---|---|
| dat | data file from `importRes` for the `type` and `year` specified. |
| mat | three-dimensional array (age, sex, year) for the year(s) specified. |
| xpos | x-position generated by barplot for the ages specified. |

## Author(s)

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: 2018-07-25

## See Also

plotBox, compB0

---

| plotBox | *Plot Boxes using Quantiles* |
|---|---|

---

## Description

Produce box-and-whisker plot(s) of the given (grouped) values. This function is simply a modified
version of boxplot that sets the whiskers to specified quantiles rather than 1.5 IRQ.

## Usage

```
plotBox(x, ..., range=1.5, width=NULL, varwidth=FALSE,
    notch=FALSE, outline=TRUE, names, plot=TRUE,
    border=par("fg"), col=NULL, log="",
    pars=list(boxwex=0.8, staplewex=0.5, outwex=0.5, whisklty=1),
    horizontal=FALSE, add=FALSE, at=NULL,
    quants = get("quants5"), outliers=FALSE)
```

## Arguments

x          for specifying data from which the boxplots are to be produced. Either a numeric
vector, or a single list containing such vectors. Additional unnamed arguments
specify further data as separate vectors (each corresponding to a component
boxplot). NAs are allowed in the data.

Arguments formula, data, codesubset, and na.action are itemized below in
**Notes**, but have not been tested for plotBox.

...          For the formula method, named arguments to be passed to the default method.

For the default method, unnamed arguments are additional data vectors (unless
x is a list when they are ignored), and named arguments are arguments and
graphical parameters to be passed to bxp in addition to the ones given by argu-
ment pars (and override those in pars). Note that bxp may or may not make
use of graphical parameters it is passed: see its documentation.

range          this determines how far the plot whiskers extend out from the box. If range is
positive, the whiskers extend to the most extreme data point which is no more
than range times the interquartile range from the box. A value of zero causes
the whiskers to extend to the data extremes.

width          a vector giving the relative widths of the boxes making up the plot.

| | |
|---|---|
| varwidth | if `varwidth` is TRUE, the boxes are drawn with widths proportional to the square-roots of the number of observations in the groups. |
| notch | if `notch` is TRUE, a notch is drawn in each side of the boxes. If the notches of two plots do not overlap this is 'strong evidence' that the two medians differ (Chambers *et al.*, 1983, p. 62). See `boxplot.stats` for the calculations used. |
| outline | if `outline` is not true, the outliers are not drawn (as points whereas S+ uses lines). |
| names | group labels which will be printed under each boxplot. Can be a character vector or an expression (see plotmath). |
| plot | if TRUE (the default) then a boxplot is produced. If not, the summaries which the boxplots are based on are returned. |
| border | an optional vector of colors for the outlines of the boxplots. The values in `border` are recycled if the length of `border` is less than the number of plots. |
| col | if `col` is non-null it is assumed to contain colors to be used to colour the bodies of the box plots. By default they are in the background colour. |
| log | character indicating if x or y or both coordinates should be plotted in log scale. |
| pars | a list of (potentially many) more graphical parameters, e.g., boxwex or `outpch`; these are passed to `bxp` (if `plot` is true); for details, see there.<br>Some explicit settings:<br>`boxwex` – a scale factor to be applied to all boxes. When there are only a few groups, the appearance of the plot can be improved by making the boxes narrower.<br>`staplewex` – staple line width expansion, proportional to box width.<br>`outwex` – outlier line width expansion, proportional to box width.<br>`whisklty` – whisker line type. |
| horizontal | logical indicating if the boxplots should be horizontal; default FALSE means vertical boxes. |
| add | logical, if true *add* boxplot to current plot. |
| at | numeric vector giving the locations where the boxplots should be drawn, particularly when add = TRUE; defaults to 1:n where n is the number of boxes. |
| quants | numeric vector of 5 quantiles to specify (i) the extent of the lowest whisker, (ii) the lower boundary of the box, (iii) the middle line of the box, (iv) the upper boundary of the box, and (v) the extent of the upper whisker. |
| outliers | logical: if TRUE show the outliers (but used primarily to suppress outliers when FALSE). |

### Details

The generic function boxplot currently has a default method (boxplot.default) and a formula interface (boxplot.formula).

If multiple groups are supplied either as multiple arguments or via a formula, parallel boxplots will be plotted, in the order of the arguments or the order of the levels of the factor (see factor).

Missing values are ignored when forming boxplots.

## Value

List with the following components:

| | |
|---|---|
| stats | a matrix, each column contains the extreme of the lower whisker, the lower hinge, the median, the upper hinge and the extreme of the upper whisker for one group/plot. If all the inputs have the same class attribute, so will this component. |
| n | a vector with the number of observations in each group. |
| conf | a matrix where each column contains the lower and upper extremes of the notch. |
| out | the values of any data points which lie beyond the extremes of the whiskers. |
| group | a vector of the same length as out whose elements indicate to which group the outlier belongs. |
| names | a vector of names for the groups. |

## Additional arguments

Additional arguments used by boxplot but not tested in plotBox:

| | |
|---|---|
| formula..... | A formula, such as y ~ grp, where y is a numeric vector of data values to be split into groups according to the grouping variable grp (usually a factor). |
| data........ | A data.frame (or list) from which the variables in formula should be taken. |
| subset...... | An optional vector specifying a subset of observations to be used for plotting. |
| na.action... | A function which indicates what should happen when the data contain NAs. The default is to ignore missing values in either the response or the group. |

## References

Becker, R. A., Chambers, J. M. and Wilks, A. R. (1988) *The New S Language*. Wadsworth & Brooks/Cole.

Chambers, J. M., Cleveland, W. S., Kleiner, B. and Tukey, P. A. (1983) *Graphical Methods for Data Analysis*. Wadsworth & Brooks/Cole.

Murrell, P. (2005) *R Graphics*. Chapman & Hall/CRC Press.

See also boxplot.stats.

## See Also

See compB0 to show MCMC distributions of $B$ relative to $B_0$.

boxplot.stats which does the computation, bxp for the plotting and more examples; and stripchart for an alternative (with small data sets).

---

| plotBVBnorm | *Plot Spawning and Vulnerable Biomass Relative to Virgin* |
|---|---|

---

## Description

Plot spawning and vulnerable biomass boxplots relative to virgin levels $B_0$ and $V_0$, respectively.

## Usage

```
plotBVBnorm(mcmcObj,
    p=get("quants5"),
    xyType="quantBox",
    lineType=c(3,2,1,2,3),
    refLines=NULL, xLim=NULL, yLim=NULL,
    userPrompt=FALSE, save=TRUE, xLeg=0.05, yLeg=0.2,
    yaxis.by=0.05, tcl.val=-0.2,
    B.col="black", VB.col="black", ngear=1, lang="e", ...)
```

## Arguments

| | |
|---|---|
| mcmcObj | MCMC list object (currentMCMC). |
| p | quantiles to use in quantBox. |
| xyType | type of plot (currently only uses quantBox). |
| lineType | line types to use in quantBox. |
| refLines | reference lines to add to plot. |
| xLim | limits of the x-axis. |
| yLim | limits of the y-axis. |
| userPrompt | **not used** |
| save | **not used** |
| xLeg | x-coordinate for legend. |
| yLeg | y-coordinate for legend. |
| yaxis.by | increments along the y-axis to place tick marks. |
| tcl.val | tick length. |
| B.col | colour for spawning biomass. |
| VB.col | colour for vulnerable biomass. |
| ngear | number of commercial gear codes |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |
| ... | **not used** |

## Note

AME: tried in separate file, but then changed that to lattice and wouldn't be good format for Arni's boxplots.

Based on [plotVBcatch](#) (with some twerking).
currentRes1 is local currentRes.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified Rd: 2018-07-25

## See Also

plotVBcatch

---

| plotChains | *Plot Cumulative Frequency of MCMC Chains* |
|---|---|

---

## Description

Plot cumulative fequency of $n$ chains by partitioning one trace.
(Modified from the function plotTracePOP.)

## Usage

```
plotChains(mcmc, nchains=3, pdisc=0.1, axes=FALSE, same.limits=FALSE,
   between=list(x=axes,y=axes), div=1, span=1/4, log=FALSE,
   base=10, main=NULL, xlab=NULL, ylab=NULL, cex.main=1.2,
   cex.lab=1, cex.strip=0.8, cex.axis=0.8,
   las=0, tck=0.4, tick.number=5, lty.trace=1, lwd.trace=1,
   col.trace="grey", lty.median=1, lwd.median=1,
   col.median="black", lty.quant=2, lwd.quant=1,
   col.quant="black", plot=TRUE, probs=get("quants3"), lang="e", ...)
```

## Arguments

| | |
|---|---|
| mcmc | MCMC chain(s) as a vector, data frame or mcmc object. |
| nchains | number of chains to create from one trace. |
| pdisc | proportion of the initial trace to discard before creating chains. |
| axes | whether axis values should be plotted. |
| same.limits | whether panels should have same x-axis limits. |
| between | list with x and y indicating panel spacing. |
| div | denominator to shorten values on the y axis. |
| span | smoothness parameter (**not used**). |
| log | whether values should be log-transformed. |
| base | logarithm base. |
| main | main title. |

| | |
|---|---|
| `xlab` | x-axis title. |
| `ylab` | y-axis title. |
| `cex.main` | size of main title. |
| `cex.lab` | size of axis labels. |
| `cex.strip` | size of strip labels. |
| `cex.axis` | size of tick labels. |
| `las` | orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical. |
| `tck` | tick mark length. |
| `tick.number` | number of tick marks. |
| `lty.trace` | line type of trace. |
| `lwd.trace` | line width of trace. |
| `col.trace` | colour of trace. |
| `lty.median` | line type of median. |
| `lwd.median` | line width of median. |
| `col.median` | colour of median. |
| `lty.quant` | line type of quantile trace. |
| `lwd.quant` | line width of quantile trace. |
| `col.quant` | colour of quantile trace. |
| `plot` | whether to draw plot. |
| `probs` | quantile values for quantile trace. |
| `lang` | character – a letter that denotes the language for output: currently only `"e"` (english) or `"f"` (french). |
| `...` | passed to `panel.trace` (**not used**). |

## Value

When `plot=TRUE`, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When `plot=FALSE`, a trellis object is returned.

## Note

This idea stemmed from a discussion with PJS.

## Author(s)

Rowan Haigh, Program Head – Offshore Rockfish
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*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified `Rd`: 2018-07-25

## See Also

`plotTracePOP`, `plotDensPOP`

---

| plotCI | *Plot Confidence Intervals* |
|---|---|

---

### Description

Given a set of x and y values with upper and lower bounds, plot the points with the vertical limits.

### Usage

```
plotCI(x, y=NULL, ui, li, uiw=0.05, liw=uiw, clipNA=TRUE, gap=1,
    col=par("col"), barcol=col, lwd=par("lwd"), lty=par("lty"), ...)
```

### Arguments

| | |
|---|---|
| x,y | numeric – coordinates for the center of vertical limits. If only x is provided, x becomes y and x defaults to `1:length(x)`. |
| ui | numeric – vector of heights above the points (x,y). Set to NULL or NA to omit upper bars. |
| li | numeric – vector of heights below the points (x,y). Set to NULL or NA to omit lower bars. |
| uiw | numeric – width of the edge of the upper bar's head (inches). |
| liw | numeric – width of the edge of the lower bar's foot (inches). |
| clipNA | logical – if TRUE, remove NA values on either end of the points vector (x,y). |
| gap | numeric – vertical space between the points and the bars. |
| col | character – colour of the points. |
| barcol | character – colour of the bars. |
| lwd | numeric – line width of bars. |
| lty | numeric – line type for bars. |
| ... | additional parameters for plotting (e.g., bg for background colour of points) |

### Details

Used primarily to plot abundance indices and their confidence limits.

### Value

Invisibly returns a list of x and y.

### Note

This function offers a pale imitation of gplots::plotCI, and was created to reduce package dependenciesin PBSawatea.

## Author(s)

Rowan Haigh, Program Head – Offshore Rockfish
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Last modified Rd: 2018-05-23

## See Also

plotACFs, plotCPUE, plotMeanAge

---

plotCPUE                           *Plot CPUE and Add Error Bars*

---

## Description

Plot CPUE and fit with error bars.

## Usage

```
plotCPUE(obj, main="", save=NULL, bar=1.96, yLim=NULL,
    ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"), ...)
```

## Arguments

| | |
|---|---|
| obj | data frame of CPUE indices from Awatea's results file (*e.g.*, currentRes$CPUE). |
| main | character – title for figure |
| save | **not used** |
| bar | numeric – standard deviation of the normal distribution (1.96 is the approximate value of the 97.5 percentile point). |
| yLim | numeric – limits of the y-axis. |
| ptypes | character – plot types for the figures: eps = encapsulated postscript, png = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the png file. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| ... | **not used** |

## Value

A postscript file:
CPUEser.eps...CPUE indices with error bars.

## Note

Copied code from plotIndexNotLattice.

**Author(s)**

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: `2018-07-25`

**See Also**

[plotIndexNotLattice](#)

---

plotDensPOP                          *Plot MCMC Density (AME Version)*

---

**Description**

Plot Markov-chain Monte Carlo density. This is an approximation of the posterior probability density function.

**Usage**

```
plotDensPOP(mcmc, probs=get("quants3")[c(1, 3)], points=FALSE, axes=TRUE,
     same.limits=FALSE, between=list(x=axes,y=axes), div=1,
     log=FALSE, base=10, main=NULL, xlab=NULL, ylab=NULL,
     cex.main=1.2, cex.lab=1, cex.strip=0.8, cex.axis=0.7,
     las=0, tck=0.5, tick.number=5,
     lty.density=1, lwd.density=3, col.density="black",
     lty.median=2, lwd.median=1, col.median="darkgrey",
     lty.outer=3, lwd.outer=1, col.outer="darkgrey", pch="|",
     cex.points=1, col.points="black", plot=TRUE, MPD.height=0.04,
     mpd = mcmc[1, ], lang="e", ...)

plotDensPOPpars(mcmc, probs=get("quants3")[c(1, 3)], points=FALSE,
     axes=TRUE, same.limits=FALSE, between=list(x=axes,y=axes),
     div=1, log=FALSE, base=10, main=NULL, xlab=NULL, ylab=NULL,
     cex.main=1.2, cex.lab=1, cex.strip=0.8, cex.axis=0.7,
     las=0, tck=0.5, tick.number=5,
     lty.density=1, lwd.density=3, col.density="black",
     lty.median=2, lwd.median=1, col.median="darkgrey",
     lty.outer=3, lwd.outer=1, col.outer="darkgrey", pch="|",
     cex.points=1, col.points="black", plot=TRUE, MPD.height=0.04,
     mpd = mcmc[1, ], lang="e", ...)

plotDensPOPparsPrior(mcmc, probs=get("quants3")[c(1, 3)], points=FALSE,
     axes=TRUE, same.limits=FALSE, between=list(x=axes,y=axes),
     div=1, log=FALSE, base=10, main=NULL, xlab=NULL, ylab=NULL,
```

```
cex.main=1.2, cex.lab=1, cex.strip=0.8, cex.axis=0.7,
las=0, tck=0.5, tick.number=5,
lty.density=1, lwd.density=3, col.density="black",
lty.median=2, lwd.median=1, col.median="darkgrey",
lty.outer=3, lwd.outer=1, col.outer="darkgrey", pch="|",
cex.points=1, col.points="black", plot=TRUE, MPD.height=0.04,
mpd = mcmc[1, ], lang="e", ...)
```

## Arguments

| | |
|---|---|
| mcmc | numeric – MCMC chain(s) as a vector, data frame or mcmc object. |
| probs | numeric – vector of outer quantiles to draw, besides the median. |
| points | logical – whether data points should be plotted along the x axis. |
| axes | logical – whether axis values should be plotted. |
| same.limits | logical – whether panels should have same x-axis limits. |
| between | numeric – list with x and y indicating panel spacing. |
| div | numeric – denominator to shorten values on the x axis. |
| log | logical – whether values should be log-transformed. |
| base | numeric – logarithm base |
| main | character – main title |
| xlab | character – x-axis label |
| ylab | character – y-axis label |
| cex.main | numeric – size of main title |
| cex.lab | numeric – size of axis labels |
| cex.strip | numeric – size of strip labels |
| cex.axis | numeric – size of tick labels |
| las | numeric – orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical |
| tck | numeric – tick mark length |
| tick.number | numeric – number of tick marks |
| lty.density | numeric – line type of density curve |
| lwd.density | numeric – line width of density curve |
| col.density | character\|numeric – colour of density curve |
| lty.median | numeric – line type of median |
| lwd.median | numeric – line width of median |
| col.median | character\|numeric – colour of median |
| lty.outer | numeric – line type of outer quantiles |
| lwd.outer | numeric – line width of outer quantiles |
| col.outer | character\|numeric – colour of outer quantiles |
| pch | numeric – symbol for data points |

| | |
|---|---|
| cex.points | numeric – size of data points |
| col.points | character|numeric – colour of data points |
| plot | logical – whether to draw plot |
| MPD.height | numeric – how far up to put MPD |
| mpd | numeric – vector of MPD values (from which MCMC search starts) |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |
| ... | passed to densityplot and panel.densityplot. |

### Details

The function plotDensPOPpars differs from plotDensPOP only by a few tweaks to the internal list object myscales.
The function plotDensPOPparsPrior adds the priors automatically.

### Value

When plot=TRUE, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When plot=FALSE, a trellis object is returned.

### Note

The Args function from the **gdata** package is recommended for reviewing the arguments, instead of args.

AME: edited plotDens function to have less whitesapce, not repeat x-axis labels, and make y-axes the same scales. Cannot just do it through the options.

For Recruits and Biomass, use plotDensPOPpars for parameters. Tried y-axes the same scales, but 1973–1975 are so narrow that they make all the others really small: same.limits=TRUE, ylim=c(0, 0.0005).

### Author(s)

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Last modified Rd: 2018-07-25

### See Also

xyplot and panel.densityplot are the underlying drawing functions, and densplot is a similar non-trellis plot.

plotTrace, plotAuto, plotCumu, and plotSplom are diagnostic plots.

plotDens and plotQuant are posterior plots.

plotMCMC-package gives an overview of the package.

---

plotIndexNotLattice     *Plot Survey Indices*

---

### Description

Plot survey index series with error bars in a variety of ways (e.g., grouped, individually).

### Usage

```
plotIndexNotLattice(obj, main="", save=NULL,
    bar=1.96, ssnames=paste("Ser",1:9,sep=""),
    ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"), ...)
```

### Arguments

| | |
|---|---|
| obj | list – the MPD object created by the importRes function (e.g., currentRes). |
| main | character – title for figure |
| save | **not used** |
| bar | numeric – standard deviation of the normal distribution (1.96 is the approximate value of the 97.5 percentile point). |
| ssnames | character – survey series names for figure labelling and image creation. |
| ptypes | character – plot types for the figures: "eps" = encapsulated postscript, "png" = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the .png file. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| ... | **not currently used** |

### Value

Four series of encapsulated postscript (and portable network graphics) files:
survIndSer.eps....each survey panel focuses on the years of the survey;
survIndSer2.eps...each panel uses a fixed set of years that span all surveys;
survIndSer3.eps...one panel showing all series (incl. CPUE if used) normalised to their means;
survIndSer4-n.eps.seperate files for each index series *n*.

### Author(s)

Andrew M. Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified Rd: 2018-07-26

## See Also

[plt.idx](plt.idx)

---

plotMeanAge                 *Plot Mean Age*

---

## Description

Plot model MPD estimates of mean age and observed mean age (with 95% confidence interval).

## Usage

```
plotMeanAge(obj, useCA=TRUE, useSA=TRUE, CAnames, lang="e")
```

## Arguments

| | |
|---|---|
| obj | list – The model's MPD object, usually `currentRes`. |
| useCA | logical – if TRUE, then plot mean ages from the commercial fishery. |
| useSA | logical – if TRUE, then plot mean ages from the surveys. |
| CAnames | character – commercial fishery names, those that have composition (age) data. |
| lang | character – a letter that denotes the language for output: currently only `"e"` (english) or `"f"` (french). |

## Details

Provides a diagnostic plot, recommended by Francis (2011), that compares the model's calculated mean ages with observed mean ages for each abundance index.

## Value

Contrary to CRAN's phobia about polluting the user's working environment, the function assigns a mean-age object `MA.pjs` to the global environment, *and* dumps the object into an ASCII file (`MA.pjs.r`) and a binary file (`MA.pjs.rda`) in the MPD working directory. Stock assessments are messy and the user needs as much output as possible.

## Author(s)

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*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified `Rd`: `2018-07-26`

## References

Francis, R.I.C.C. (2011) Data weighting in statistical fisheries stock assessment models. *Can. J. Fish. Aquat. Sci.* **68**(6): 1124–1138.

## See Also

[importPar](), [importRes](), [MAfun](), [reweight]()

---

plotRmcmcPOP                          *Plot Recruitment Posterior Quantiles*

---

## Description

Plot recruitment posteriors quantiles as one graph over time.

## Usage

```
plotRmcmcPOP( obj,
    p=get("quants5"),
    xyType="quantBox",
    lineType=c(3,2,1,2,3),
    refLines=NULL, xLim=NULL, yLim=NULL,
    userPrompt=FALSE, save=TRUE, tcl.val=-0.2,
    yaxis.by=10000, yLab="Recruitment", lang="e", ...)
```

## Arguments

| | |
|---|---|
| obj | data.frame – MCMC data frame of $R$ (currentMCMC$R). |
| p | numeric – quantiles to use in quantBox. |
| xyType | character – type of plot (currently only uses quantBox). |
| lineType | numeric – line types to use in quantBox. |
| refLines | numeric – reference lines to add to plot. |
| xLim | numeric – limits of the x-axis. |
| yLim | numeric – limits of the y-axis. |
| userPrompt | logical – **not used** |
| save | logical – **not used** |
| tcl.val | numeric – tick length. |
| yaxis.by | numeric – increments along the y-axis to place tick marks. |
| yLab | character – label for the y-axis. |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |
| ... | additional arguments passed to the function rect. |

## Note

AME: Plot recruitment posteriors quantiles as one graph over time.
Already have the full posterior densities done.
Using plotBmcmcPOP as template, but will be simpler as no extra stuff. Probably not simplifying down as much as could due to time constraints.
Adding yLab and then using for exploitation plot also.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified Rd: 2018-07-26

## See Also

plotB2

---

| plotSnail | *Phase Plot of Exploitation vs. Biomass* |
|---|---|

---

## Description

Plot the historical progression of the ratio $u_t/u_{MSY}$ against $B_t/B_{MSY}$. Traditionally known as 'phase plots', some wine connoiseurs call these plots *snail trails*.

## Usage

```
plotSnail(BoverBmsy, UoverUmsy, p=c(0.1,0.9), xLim=NULL, yLim=NULL,
    Lwd=1.5, ngear=1, assYrs=2011, outs=FALSE, lang="e")
```

## Arguments

| | |
|---|---|
| BoverBmsy | numeric – matrix of $B_t$ over $B_{MSY}$. |
| UoverUmsy | numeric – matrix of $u_t$ over $u_{MSY}$. |
| p | numeric – quantiles to show the bulk of the distribution. |
| xLim | numeric – limits of the x-axis. |
| yLim | numeric – limits of the y-axis. |
| Lwd | numeric – line width of the snail trail. |
| ngear | numeric – number of commercial gears |
| assYrs | numeric – 'current' model years of past assessments. |
| outs | logical – if TRUE, extend the range of the quantile box whiskers to include the outliers (all data). |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |

## Details

The graph attempts to show the time history of the exploitation rate compared to the spawning biomass using a precautionary framework recast in Bayesian terms.

## Note

The term *snail trail* comes from PJS.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified Rd: 2018-07-26

## See Also

plotBVBnorm

---

plotTracePOP                              *Plot MCMC Traces (AME Version)*

---

## Description

Plot Markov-chain Monte Carlo traces. This is a diagnostic plot for deciding whether a chain shows unwanted trends by showing the trace of moving quantiles. (Modified from the **plotMCMC** function plotTrace.)

## Usage

```
plotTracePOP(mcmc, axes=FALSE, same.limits=FALSE,
          between=list(x=axes,y=axes), div=1, span=1/4, log=FALSE,
          base=10, main=NULL, xlab=NULL, ylab=NULL, cex.main=1.2,
          cex.lab=1, cex.strip=0.8, cex.axis=0.8,
          las=0, tck=0.5, tick.number=5, lty.trace=1, lwd.trace=1,
          col.trace="grey", lty.median=1, lwd.median=1,
          col.median="black", lty.quant=2, lwd.quant=1,
          col.quant="black", plot=TRUE, probs=get("quants3"),
          mpd=mcmc[1, ], lang="e", ...)
```

## Arguments

| | |
|---|---|
| mcmc | MCMC chain(s) as a vector, data frame or mcmc object. |
| axes | whether axis values should be plotted. |
| same.limits | whether panels should have same x-axis limits. |
| between | list with x and y indicating panel spacing. |
| div | denominator to shorten values on the y axis. |
| span | smoothness parameter (**not used**). |
| log | whether values should be log-transformed. |

| base | logarithm base. |
| --- | --- |
| main | main title. |
| xlab | x-axis title. |
| ylab | y-axis title. |
| cex.main | size of main title. |
| cex.lab | size of axis labels. |
| cex.strip | size of strip labels. |
| cex.axis | size of tick labels. |
| las | orientation of tick labels: 0=parallel, 1=horizontal, 2=perpendicular, 3=vertical. |
| tck | tick mark length. |
| tick.number | number of tick marks. |
| lty.trace | line type of trace. |
| lwd.trace | line width of trace. |
| col.trace | colour of trace. |
| lty.median | line type of median. |
| lwd.median | line width of median. |
| col.median | colour of median. |
| lty.quant | line type of quantile trace. |
| lwd.quant | line width of quantile trace. |
| col.quant | colour of quantile trace. |
| plot | whether to draw plot. |
| probs | quantile values for quantile trace. |
| mpd | vector of MPD values (from which MCMC search starts). |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |
| ... | passed to panel.trace (**not used**). |

## Value

When plot=TRUE, a trellis plot is drawn and a data frame is returned, containing the data used for plotting. When plot=FALSE, a trellis object is returned.

## Note

The Args function from the **gdata** package is recommended for reviewing the arguments, instead of args.

## Author(s)

Andrew M. Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

Rowan Haigh, Program Head – Offshore Rockfish
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Last modified Rd: 2018-07-26

## See Also

[xyplot](#) and [panel.loess](#) are the underlying drawing functions, and [traceplot](#) is a similar non-trellis plot.

[plotTrace](#), [plotAuto](#), [plotCumu](#), and [plotSplom](#) are diagnostic plots.

[plotDensPOP](#), [plotDens](#), [plotQuant](#), and [plotChains](#) are posterior plots.

[plotMCMC-package](#) gives an overview of the **plotMCMC** package.

---

plotTraj                          *Plot Median Trajectory*

---

## Description

Plot median trajectories from various MCMC runs in one figure.

## Usage

```
plotTraj(dat, index, traj="B", y0=FALSE, lab.stock,
    col=c("black","green4","blue","red","purple","orange"),
    png=FALSE, pngres=400, PIN=c(8,8), lang=c("e","f"), ...)
```

## Arguments

| | |
|---|---|
| dat | list – an object (currently called stock) generated by running Sweave code to compile a Results Appendix. The object stock comprises one or more stocks, identified at the first level in the list's hierarchy. |
| index | numeric – vector of indices pointing to runs that a user wishes to compare. For example, the index typically points to a base case and a number of sensitivity runs. |
| traj | character – vector of trajectory names (e.g., B = spawning biomass, Bt/B0 = spawning biomass depletion, etc.); options are limited. |
| y0 | logical – if TRUE, start the y-axis at 0. |
| lab.stock | character – name of stock to appear in the name of the png output file, if png=TRUE. |
| col | character – names of colours for each trajectory. |
| png | logical – if TRUE, send the figure output to a png device. |
| pngres | numeric – resolution (pixels/inch) for png file. |
| PIN | numeric – vector of width and height (inches) for png file. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| ... | list – additional arguments for lines (lty only) and legend. |

## Details

Trajectories are currently limited to objects in the `currentMCMC` object (`c("B","VB","R","U")`) and spawning biomass depletion (`Bt/B0`).

## Value

Assigns a trajectory `array` object to the global environment.

## Note

This function is geared for use after a number of Awatea model runs have been completed. The steps for creating one model run generally involve five stages – (i) reweighting abundance & composition data, (ii) MPD fit, (iii) MCMC fits, (iv) MSY calculations, and (v) projections. After a number of model runs have been generated, the results can be gathered and compared.

## Author(s)

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Last modified Rd: `2018-07-26`

## See Also

[runADMB](), [runMPD](), [runMCMC]()

---

| plotVBcatch | *Plot Vulnerable Biomass and Catch* |
|---|---|

---

## Description

Plot vulnerable biomass from posterior as boxplots, and add catch bars on same graph.

## Usage

```
plotVBcatch(obj, currentRes1=currentRes,
   p=get("quants5"),
   xyType="quantBox",
   lineType=c(3,2,1,2,3),
   refLines=NULL, xLim=NULL, yLim=NULL,
   userPrompt=FALSE, save=TRUE,
   xLab="Year",
   yLab="Catch and vulnerable biomass (t)",
   textLab=c("catch", "vulnerable"),
   yaxis.by=10000, tcl.val=-0.2,
   gear=1, lang="e", ...)
```

## Arguments

| | |
|---|---|
| obj | MCMC data frame of *VB* (currentMCMC$VB) |
| currentRes1 | list/scape object created by [importRes](#) |
| p | quantiles to use in quantBox |
| xyType | type of plot (currently only uses quantBox) |
| lineType | line types to use in quantBox |
| refLines | reference lines to add to plot |
| xLim | limits of the x-axis |
| yLim | limits of the y-axis |
| userPrompt | **not used** |
| save | **not used** |
| xLab | x-coordinates for labels |
| yLab | y-coordinates for labels |
| textLab | text labels to display on plot |
| yaxis.by | increments along the y-axis to place tick marks |
| tcl.val | tick length |
| gear | scalar: numeric gear code from subset 1 to Ngear |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |
| ... | additional arguments passed to the function rect |

## Note

This function is essentially a tweak of plotBmcmcPOP (AME), which is currenly dysfunctional and not used (RH).

## Author(s)

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Last modified Rd: 2018-07-26

## See Also

[plotB2](#)

---

plt.ageResidsPOP          *Plot Model Residuals*

---

## Description

Plot model residuals as boxplots or qq-plots.

## Usage

```
plt.ageResidsPOP  (obj, ages=c(2,60), pct=c(5,25,50,75,95),
   main=NULL, lang="e")

plt.ageResidsqqPOP(obj, ages=c(2,60), pct=c(5,25,50,75,95),
   main=NULL, lang="e")

plt.yearResidsPOP (obj, ages=c(2,60), pct=c(5,25,50,75,95),
   main=NULL, fill.in=TRUE, lang="e", ... )

plt.cohortResids  (obj, ages=c(2,59), pct=c(5,25,50,75,95),
   main=NULL, lang="e")
```

## Arguments

| | |
|---|---|
| obj | output from `stdRes.CA`. |
| ages | age classes to plot. |
| pct | quantiles to show in boxplot or qq-plot. |
| main | title for plot if desired. |
| fill.in | logical: if `TRUE`, add missing years to boxplot. |
| lang | character – a letter that denotes the language for output: currently only `"e"` (english) or `"f"` (french). |
| ... | additional arguments for `boxplot`. |

## Details

```
plt.ageResidsPOP.....plot age class residuals as boxplots.
plt.ageResidsqqPOP...plot age class residuals as qq-plot.
plt.yearResidsPOP....plot age residuals by year as boxplots.
plt.cohortResids.....plot age residuals by cohort as boxplots.
```

## Note

Some trouble noted adding text and legend.

## Author(s)

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Last modified Rd: `2018-07-26`

## See Also

`plt.allTraces`, `plt.expRate`, `plt.idx`, `plt.mcmcGraphs`, `plotIndexNotLattice`, `plotChains`, `plotCPUE`

---

| plt.allTraces | *Plot MCMC Traces* |
| --- | --- |

---

## Description

Plot traces from MCMC samples.

## Usage

```
plt.allTraces(obj, bioYrList=NULL, recYrList=NULL, save=TRUE)
```

## Arguments

| | |
| --- | --- |
| `obj` | vector of MCMC samples. |
| `bioYrList` | years to plot spawning biomass traces. |
| `recYrList` | years to plot recruitment traces. |
| `save` | logical: if TRUE, save figure to a raster file (`.jpg`). |

## Note

Appears to be some figure requested by PJS.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

`plotChains`

| plt.bubbles | *Plot Proportions-at-Age as Bubbles* |
|---|---|

### Description

Plot proportions-at-age by representing annual age distributions as proportional bubbles for model inputs and fits by sex and gear or survey.

### Usage

```
plt.bubbles(mpdObj, nsex=2, ptypes=tcall(PBSawatea)$ptype,
    pngres=400, redo.Graphs=TRUE, lang=c("e","f"))
```

### Arguments

| | |
|---|---|
| mpdObj | list – the MPD object created by the importRes function (e.g., currentRes). |
| nsex | numeric – number of sexes in the model |
| ptypes | character – plot types for the figures: ″eps″ = encapsulated postscript, ″png″ = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the .png file. |
| redo.Graphs | logical – if TRUE, re-create the figures. |
| lang | character – a vector of letters that denote the language for output: currently only ″e″ (english) and ″f″ (french). |

### Details

The function plt.bubbles loops through all the catch@age (CA) objects for commercial (CAc) and survey (CAs) observations and fits by sex and gear/survey to produce bubble plots of the proportions-at age.

### Author(s)

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Last modified Rd: 2018-07-26

### See Also

[plotCA](), [plt.recdev](), [plt.catch]()

***

plt.catch                                        *Plot Catch and Biomass History*

***

### Description

Plot catch and/or model biomass by year.

### Usage

```
plt.catch(years, Ct, xint=5, yint=250,
   ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"))


plt.biomass(years, Bt, xint=5, yint=2500,
   ptypes=tcall(PBSawatea)$ptype, pngres=400,
   pname="Bt", xlab="Year", ylab="Spawning biomass (t), Bt", lang=c("e","f"))
```

### Arguments

| | |
|---|---|
| years | numeric – vector of years |
| Ct | numeric – vector or matrix of annual catches; if a matrix, then rows=years and cols=gear. |
| Bt | numeric – vector or matrix of annual biomass; if a matrix, then rows=years and cols=gear. |
| xint | numeric – x-axis (year) intervals for small, unlabelled ticks |
| yint | numeric – y-axis (catch or biomass) intervals for small, unlabelled ticks |
| ptypes | character – plot types for the figures: eps = encapsulated postscript, png = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the png file. |
| pname | character – prefix name for an image file |
| xlab | character – label for the x-axis |
| ylab | character – label for the y-axis |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |

### Details

The function `plt.catch` plots catch as vertical bars and spits out two files named `catch.eps` and `catchsmall.eps` (and/or `.png` files).

The function `plt.biomass` plots biomass as points and allows more flexibility to handle various biomass inputs (e.g., $B_t$, $B_t/B_0$, $V_{tg}/V_{0g}$).

### Author(s)

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Last modified Rd: 2018-07-26

### See Also

plt.cpue, plt.recdev, plt.bubbles

---

| plt.cpue | *Plot CPUE Fits* |
|---|---|

---

### Description

Plot CPUE fits to annual indices (only if the model uses CPUE).

### Usage

```
plt.cpue(cpueObj, ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"))
```

### Arguments

| | |
|---|---|
| cpueObj | data.frame – a CPUE object created by the importRes function (e.g., currentRes$CPUE). |
| ptypes | character – plot types for the figures: "eps" = encapsulated postscript, "png" = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the .png file. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |

### Details

The function plt.cpue is only activated in the Sweave routine if the Awatea model uses CPUE. The image file created is called CPUEfit.eps (and/or .png) and shows the model fit through the CPUE points.

### Author(s)

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Last modified Rd: 2018-07-26

### See Also

plt.catch, plt.recdev, plt.bubbles

---

plt.expRate                 *Plot Exploitation Rate*

---

### Description

Plot exploitation rate against year.

### Usage

```
plt.expRate(obj, yLim=c(0,0.5), xLim=c(1954,2005))
```

### Arguments

| | |
|---|---|
| obj | an object from `load.allResFiles`. |
| yLim | limits of the y-axis. |
| xLim | limits of the x-axis. |

### Details

Simple points and lines plot.

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

[plt.idx](plt.idx)

---

plt.idx                 *Plot Survey Index Residuals*

---

### Description

Plot the survey index residuals as a quantile-quantile plot (see [qqnorm](qqnorm)).

### Usage

```
plt.idx(obj, main="Residuals", save=NULL, ssnames=paste("Ser",1:9,sep=""),
   ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"), ...)
```

## Arguments

| | |
|---|---|
| obj | data.frame – data with columns Year, stdRes, and Fit. |
| main | character – title for the plot |
| save | logical – if TRUE, save the figure to a raster file (.png). |
| ssnames | character – survey series names for figure labelling and image creation. |
| ptypes | character – plot types for the figures: "eps" = encapsulated postscript, "png" = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the .png file. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| ... | **not used** |

## Details

QQ-plots show sample quantiles vs. theoretical quantiles.

## Note

The save option has been disabled for some reason.

## Author(s)

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Last modified Rd: 2018-07-26

## See Also

plt.stdResids, plotIndexNotLattice

---

| plt.mpdGraphs | *Plot a Set of Figures for MPD and MCMC Runs* |
|---|---|

---

## Description

Plot a set of encapsulated postscript (.eps) and portable network graphics (.png) figures for the MPD (mode of the posterior distribution) and MCMC (Monte Carlo Markoff Chain) results.

**Usage**

```
plt.mpdGraphs(obj, save=FALSE, ssnames=paste("Ser",1:9,sep=""),
   ptypes=tcall(PBSawatea)$ptype, pngres=400, ngear=1,
   pchGear=seq(21,20+ngear,1), ltyGear=seq(1,ngear,1),
   colGear=rep(c("black","blue"),ngear)[1:ngear], lang=c("e","f"))

plt.mcmcGraphs(mcmcObj, projObj=NULL, mpdObj=NULL, save=FALSE,
   ptypes=tcall(PBSawatea)$ptype, pngres=400, ngear=1,
   ylim.recruitsMCMC=NULL, ylim.exploitMCMC=NULL,
   ylim.VBcatch=NULL, ylim.BVBnorm=NULL,
   xlim.snail=NULL, ylim.snail=NULL,
   plotPolicies=names(projObj$Y[1:6]),
   onePolicy=names(projObj$Y[2]), mpd=list(),
   SAR.width=7.5, SAR.height=4, trevObj=NULL, lang=c("e","f"))
```

**Arguments**

| | |
|---|---|
| obj | list – an Awatea MPD results object (*e.g.*, currentRes) |
| save | logical – **not used** *deprecated* |
| ssnames | character – survey series names for figure labelling and image creation |
| ptypes | character – plot types for the figures: eps = encapsulated postscript, png = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the png file. |
| ngear | numeric – number of commercial gears |
| pchGear, ltyGear, colGear | |
| | numeric\|character – symbols, line types, and colours for plotting data by commercial gear. |
| mcmcObj | list – an Awatea MCMC object (*e.g.*, currentMCMC) |
| projObj | list – an Awatea projected biomass object (*e.g.*, currentProj) |
| mpdObj | list – an Awatea MPD results object (*e.g.*, currentRes) |
| ylim.recruitsMCMC | |
| | numeric – y-limits for the recruitsMCMC plot |
| ylim.exploitMCMC | |
| | numeric – y-limits for the recruitsMCMC plot |
| ylim.VBcatch | numeric – y-limits for the VBcatch plot |
| ylim.BVBnorm | numeric – y-limits for the BVBnorm plot |
| xlim.snail | numeric – x-limits for the snail-trail plot |
| ylim.snail | numeric – y-limits for the snail-trail plot |
| plotPolicies | numeric – six-policies projections to plot |
| onePolicy | numeric – the one policy from the above six to use for some figures |
| mpd | list – list of MPD values for parameters, biomass, and recruitment |
| SAR.width | numeric – width (inches) of an output WMF file for SAR figures |

| | |
|---|---|
| SAR.height | numeric – height (inches) of an output WMF file for SAR figures |
| trevObj | data.frame – various MCMC values suggested by Trevor Davies (Dalhousie) for comparison: c("h", "M_1", "M_2", "B0", "MSY", "Bmsy", "umsy"). |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |

## Details

Creates a whole heap of encapsulated postscript (.eps) and/or portable network graphics (.png) files, depending on the plot types specified in ptypes. Due to endless problems with postscript files (not to mention their potentially humungous sizes), .png files are favoured for stock assessment documents by the CSAP/CSAS office.

As of July 2018, english plot are dumped into the current working directory (as per usual) while french plots, using the same file names, are dumped into a subdirectory called 'french'.

## Value

**plt.mpdGraphs** creates the following EPS (and/or PNG) files:
exploit.eps............annual exploitation rate,
recruits.eps...........annual recruitment at age 1,
selectivity.eps........selectivity curves for commercial gear(s) and survey(s),
ageComm.eps............fits to annual commercial age composition (panel plots),
ageSurv.eps............fits to annual survey age composition (panel plots),
survIndSer.eps.........four figures of survey indices (calls plotIndexNotLattice),
CPUEser.eps............CPUE indices with error bars (calls plotCPUE),
commAgeResids.eps......standardised age residuals for commercial gear by sex,
survAgeResidsSer.eps...standardised age residuals for surveys by sex,
meanAge.eps............mean age for catch and surveys,
stockRecruit.eps.......stock recruitment function.

**plt.mcmcGraphs** creates the following postscript files:
recruitsMCMC.eps.......boxplots of annual MCMC recruitment,
exploitMCMC.eps........boxplots of annual MCMC exploitation rate,
pdfParameters.eps......density panel plots of MCMC parameter priors and posteriors,
pdfBiomass.eps.........density panel plots of annual female spawning biomass,
pdfRecruitment.eps.....density panel plots of annual recuitment,
selectivityMCMC.eps....**not currently implemented**,
traceBiomass.eps.......panel plots of annual spawning biomass with running quantiles,
traceRecruits.eps......panel plots of annual recruitmwent traces with running quantiles,
traceParams.eps........panel plots of parameter traces with running quantiles,
splitChain.eps.........panel plots of cumulative parameter estimate chains,
VBcatch.eps............boxplots of annual vulnerable biomass and barplots of catch,
BVBnorm.eps............spawning and vulnerable biomass relative to their virgin levels,
Bproj.eps..............boxplots of spawning biomass – MCMCs and projections,
Rproj.eps..............boxplots of recruitment – MCMCs and projections,
RprojOnePolicy.eps.....boxplots of recruitment for one catch policy,
snail.eps..............time series of $u_t/u_{MSY}$ *vs.* $B_t/B_{MSY}$,

```
pairs[1,...,n].eps.....pairs plot of parameter MCMC samples (6 pars/page).
pairsMSY.eps...........pairs plot of MCMC samples for MSY-related parameters.
```

### Note

The function is currently set up to send figures to encapsulated postscript (eps) and/or portable network graphics (png) files only. If a user wants other file types (e.g., windows metafiles), then additional lines of code need to be added to invoke the appropriate device(s).

### Author(s)

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Last modified Rd: `2018-07-25`

### See Also

`plt.mcmcGraphs`, `plotIndexNotLattice`, `plotCPUE`, `plotChains`, `plotSnail`

---

| plt.numR | *Plot Numbers at Age at Equilibrium* |
|---|---|

---

### Description

Plot numbers at age at equilibrium. Plot recruitment (age 1). (*possibly deprecated*)

### Usage

```
plt.numR(obj, minYr = NULL)
```

### Arguments

| | |
|---|---|
| `obj` | an Awatea results object from `load.allResFiles`. |
| `minYr` | minimum year to display in plot. |

### Note

Not sure what this plot is used for (RH). Appears to be called only in the `menuFuns.r` module (which has not been used for centuries).

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

### See Also

`plotRmcmcPOP`

---

plt.quantBio                    *Plot Quantile Boxes of MCMC and Projected Biomass*

---

**Description**

Plots MCMC and projected biomass as quantile boxes, the former in black, the latter in red.

**Usage**

```
plt.quantBio(obj, projObj=NULL, policy=NULL,
     p=get("quants5"), xyType="lines",
     lineType=c(3,2,1,2,3), refLines=NULL,
     xLim=NULL, yLim=NULL, userPrompt=FALSE,
     save=TRUE, yaxis.lab="Spawning biomass", lang="e")

plt.quantBioBB0(obj, projObj=NULL, policy=NULL,
     p=get("quants5"), xyType="lines",
     lineType=c(3,2,1,2,3), refLines=NULL,
     xLim=NULL, yLim=NULL, userPrompt=FALSE, save=TRUE,
     main="", cex.main="", tcl.val=-0.2,
     xaxis.by=1, yaxis.by=10000, xaxis.lab="Year",
     yaxis.lab="Spawning biomass", lang="e")
```

**Arguments**

| | |
|---|---|
| obj | an Awatea MCMC object (*e.g.*, currentMCMC). |
| projObj | an Awatea projected biomass object (*e.g.*, currentProj). |
| policy | numeric vector specifying catch policy. |
| p | quantiles to use from the biomass samples. |
| xyType | string specifying type of plot. |
| lineType | line types for the quantiles if xyType="lines". |
| refLines | reference points. |
| xLim | limits of the x-axis. |
| yLim | limits of the y-axis. |
| userPrompt | logical: if TRUE prompts user before figure is drawn. |
| save | logical: if TRUE save figure as a raster file .png. |
| main | character string specifying a title for the plot. |
| cex.main | font size for figure title. |
| tcl.val | tick length. |
| xaxis.by | tick mark intervals for x-axis. |
| yaxis.by | tick mark intervals for y-axis. |
| xaxis.lab | label for x-axis. |
| yaxis.lab | label for y-axis. |
| lang | character – a letter that denotes the language for output: currently only "e" (english) or "f" (french). |

## Value

List of the reconstructed (MCMC) and projected results.

## Note

`plt.quantBioBB0` performs similarly as for `plt.quantBio` but uses $B_t/B_0$ instead of $B_t$.

## Author(s)

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Last modified Rd: `2018-07-26`

## See Also

`plotVBcatch`, `plotBVBnorm`, `plotRmcmcPOP`

---

| plt.recdev | *Plot Recruitment Deviations and ACF* |
|---|---|

---

## Description

Plot recruitment deviations, the auto-correlation function of recuritment deviations, or the initial age deviations.

## Usage

```
plt.recdev(logRecDev, xint=5,
   ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"))

plt.recdevacf(logRecDev, muC, logvC, A, years, yr1,
  ptypes=tcall(PBSawatea)$ptype, pngres=400, redo.Graphs=TRUE, lang=c("e","f"))

plt.initagedev(logInitAgeDev,
   ptypes=tcall(PBSawatea)$ptype, pngres=400, lang=c("e","f"))
```

## Arguments

| | |
|---|---|
| `logRecDev` | `numeric` – vector of log recruitment deviations created by the `importRes` function (e.g., `currentRes$Dev$Annual`). |
| `logInitAgeDev` | `numeric` – vector of log initial age deviations created by the `importRes` function (e.g., `currentRes$Dev$Initial`). |
| `muC` | `numeric` – age at full selectivity for commercial gear created by the `importRes` function (e.g., `currentRes$extra$parameters$Sfullest`). |

| | |
|---|---|
| logvC | numeric – log variance of commercial gear selectivity (left side) created by the `importRes` function (e.g., `currentRes$extra$parameters$log_varLest`). |
| A | numeric – maximum age in the model (plus class) |
| years | numeric – years covered by the population model reconstruction |
| yr1 | numeric – first year of age data |
| xint | numeric – x-axis (year) intervals for small, unlabelled ticks |
| ptypes | character – plot types for the figures: `"eps"` = encapsulated postscript, `"png"` = portable network graphics. |
| pngres | numeric – resolution (pixels/inch) for the `.png` file. |
| lang | character – a vector of letters that denote the language for output: currently only `"e"` (english) and `"f"` (french). |
| redo.Graphs | logical – if TRUE, re-create the figures. |

## Details

The function `plt.recdev` plots annual log recruitment deviations.

The function `plt.recdevacf` plots the auto-correlation function (first 30 lags) for the log recuritment deviations.

The function `plt.initagedev` plots the initial age deviation for each age in the model.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

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Last modified Rd: `2018-07-26`

## See Also

[plt.catch](#), [plt.cpue](#), [plt.bubbles](#)

---

| | |
|---|---|
| plt.ssbVbCatch | *Plot Annual Spawning and Vulnerable Biomass* |

---

## Description

Plot MPD values of spawning biomass (SB) and vulnerable biomass(VB), as well as catch, against year.

## Usage

```
plt.ssbVbCatch(obj, x1=1966, xLim=c(1954,2005), yLim=c(0,25000))
```

## Arguments

| | |
|---|---|
| `obj` | an Awatea results object from `load.allResFiles`. |
| `x1` | year to start plotting SB and VB lines. |
| `xLim` | limits of the x-axis. |
| `yLim` | limits of the y-axis. |

## Note

This analysis uses the MPD (mode of the posterior distribution) values for $B$ and $V$.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[load.allResFiles](#), [get.resFile](#), [plt.expRate](#)

---

| | |
|---|---|
| plt.stdResids | *Plot Diagnostics for Standardised Residuals* |

---

## Description

Plot standardised residuals against year, fitted value, and theoretical residuals.

## Usage

```
plt.stdResids(obj, pct=c(5,25,50,75,95),
     main=NULL, yLim=NULL, xLim=xLim, lang="e")
```

## Arguments

| | |
|---|---|
| `obj` | `data.frame` – data with columns `Year`, `stdRes`, and `Fit`. |
| `pct` | `numeric` – percentiles to display as horizontal lines on the quantile-quantile plot. |
| `main` | `character` – title for the figure. |
| `yLim` | `numeric` – limits of the y-axis. |
| `xLim` | `numeric` – limits of the x-axis. |
| `lang` | `character` – a letter that denotes the language for output: currently only `"e"` (english) or `"f"` (french). |

## Details

Figure provides three panels of standardised residuals *vs.*
(i) years, (ii) fitted or predicted values, and (iii) theoretical quantiles.

### Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: `2018-07-26`

### See Also

[`plt.ssbVbCatch`](#)

---

| readAD | *Read ADMB Input and Create AWATEA Class Object* |
|---|---|

---

### Description

Read the ADMB input file and create an `AWATEA` class object.

### Usage

```
readAD(txt)
```

### Arguments

txt                string name of an Awatea input file.

### Details

The Awatea input file contains headers (lines prefixed with `"#"`) and data that are read sequentially into the model by the binary executable `Awatea.exe`.

### Value

An `AWATEA` class cobject with the slots:
txtnam.....character: name of the input file,
input......character: vector of strings that are the lines of the input file,
vlst.......list: each line of the input file with a label specifying line number and
...........indicating whether the line is a Comment or Data,
dnam.......character: vector of strings specifying data contents labelled by line number,
nvars......numeric: number of data variables,
vdesc......character: vector of strings specifying data contents labelled by
...........variable number (*e.g.*, v001),
vars.......list: numeric values of data labelled by variable number,
gcomm......character: vector of comments labelled by line number,
vcomm......character: vector of variable names labelled by line number,
output.....list: Awatea results file imported by function [`importRes`](#),
reweight...list: empty (later populated by function [`reweight`](#)).

### Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC.

### References

Hilborn, R., Maunder, M., Parma, A., Ernst, B. Payne, J., and Starr, P. (2003) Coleraine: a generalized age-structured stock assessment model. School of Aquatic and Fishery Sciences, University of Washington, 54 p.

### See Also

[runADMB](), [reweight]()

---

refPoints                                          *Calculate Reference Points*

---

### Description

Calculate reference points relative to either $B_{MSY}$ or $B_0$.

### Usage

```
refPoints(mcmcObj=currentMCMC, projObj=currentProj,
          msyObj=currentMSY, refLevels=c(0.4,0.8,1))

refPointsB0(mcmcObj=currentMCMC, projObj=currentProj,
          B0Obj=B0.MCMC, refLevels=B0refLevels, refNames=B0refNames)

refPointsHist(mcmcObj=currentMCMC, HRP.YRS)
```

### Arguments

| | |
|---|---|
| mcmcObj | MCMC list object (*e.g.*, currentMCMC). |
| projObj | projected biomass list object (*e.g.*, currentProj). |
| msyObj | MSY list object (*e.g.*, currentMSY). |
| refLevels | reference levels relative to $B_{MSY}$ (or $B_0$). |
| B0Obj | vector of $B_0$ MCMC values (*e.g.*, B0.MCMC). |
| refNames | names of the $B_0$ reference levels refLevels. |
| HRP.YRS | list of limit and target years for *B* (spawning biomass) and *u* (exploitation rate); names(HRP.YRS) = c("blimYrs", "btarYrs", "ulimYrs", "utarYrs"). |

### Value

List of reference points relative to either $B_{MSY}$ or $B_0$.

## Note

Call from Sweave as `refPoints()` or, in full:
`refPoints(currentMCMC, currentProj, currentMSY, refLevels=c(0.4,0.8,1))`

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[calc.refVal](calc.refVal)

---

reweight            *Reweight Abundance and Composition Data*

---

## Description

Weight the abundance data by adjusting survey and CPUE CVs, and weight the composition data by adjusting the effective sample size $N$.

## Usage

```
reweight(obj, cvpro=FALSE, mean.age=TRUE, ...)
```

## Arguments

obj          an `AWATEA` class object created initially by `readAD`.

cvpro        CV process error added to CV observation error: $c_t = \sqrt{c_o^2 + c_p^2}$;

                 if `FALSE` index CVs are reweighted using the standard deviation of normalized residuals.

mean.age     logical: if `TRUE`, use mean-age residuals to reweight the effective $N$ for the age composition data (see Francis 2011);

                 if `FALSE`, reweight $N$ using $\Sigma(P(1-P))/\Sigma(O-P)^2$, where $O$ = observed proportions-at age and $P$ = predicted/fitted proportions-at-age.

...             additional arguments to `reweight`.

## Details

For the reweight to work, a corresponding Awatea results file (`.res`) with the same prefix as the input file must be available in the working directory before calling `readAD`. This will populate the `output` slot with fitted data that the reweight needs.

## Value

An AWATEA class cobject with the slots outlined in readAD with the following slot populated by this function:

reweight...list of reweight results:

..nrwt.....the number of the current reweighting,

..survey...survey indices with CV values (observed, fitted, normalised residuals, reweighted),

..cpue.....if used in the model, CPUE indices with CV values (as above),

..wNcpa....reweigthed effective $N$ for commercial compositions (proportions-at-age),

..wNspa....reweigthed effective $N$ for survey compositions,

..SDNR.....standard deviation of normalised residuals for abundance and composition data,

..wj.......weights for composition data from a mean-age weighted calculation (Francis 2011).

## Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC.

## References

Francis, R.I.C.C. (2011, in press) Data weighting in statistical fisheries stock assessment models. *Canadian Journal of Fisheries and Aquatic Sciences*.

## See Also

runADMB, readAD, stdRes.CA, stdRes.index

---

runADMB                              *Run AD Model Builder Code for Awatea*

---

## Description

Run compiled AD Model Builder code called Awatea to reconstruct a population trajectory for a marine fish stock.

## Usage

```
runADMB(
  filename.ext, wd=getwd(),
  strSpp="XYZ", runNo=1, rwtNo=0,
  doMPD=FALSE, N.reweight=0, cvpro=FALSE, mean.age=TRUE,
  doMCMC=FALSE, mcmc=1e6, mcsave=1e3, ADargs=NULL, verbose=FALSE,
 doMSY=FALSE, msyMaxIter=15000., msyTolConv=0.01, endStrat=0.301, stepStrat=0.001,
  delim="-", clean=FALSE, locode=FALSE,
  awateaPath="C:/Users/haighr/Files/Projects/ADMB/Coleraine",
 codePath="C:/Users/haighr/Files/Projects/R/Develop/PBSawatea/Authors/Rcode/develop",
  ...
)
```

**Arguments**

| | |
|---|---|
| `filename.ext` | character file name including its extension. |
| `wd` | character string specifying the working directory, if different from the current working directory. |
| `strSpp` | character string 3-letter code of the species. |
| `runNo` | numeric: the model run number. |
| `rwtNo` | numeric: the reweight number. |
| `doMPD` | logical: if TRUE, perform an MPD analysis. |
| `N.reweight` | numeric: the number of reweights to perform in the MPD analysis. |
| `cvpro` | numeric/logical: CV process error added to CV observation error: $c_t = \sqrt{c_o^2 + c_p^2}$; <br> if `cvpro` vector is shorter than `Nsurvey + Ncpue`, it is repeated to match the number of survey series and CPUE series used to index abundance. <br> If `cvpro==FALSE`, index CVs are reweighted using the standard deviation of normalized residuals; <br> note that `cvpro=0` is not the same as `cvpro=FALSE`. |
| `mean.age` | logical: if TRUE, use mean-age residuals to reweight the effective $N$ for the age composition data (see Francis 2011); <br> if FALSE, reweight $N$ using $\Sigma(P(1-P))/\Sigma(O-P)^2$, where $O$ = observed proportions-at age and $P$ = predicted/fitted proportions-at-age. |
| `doMCMC` | logical: if TRUE, perform an MCMC analysis. |
| `mcmc` | numeric: number of MCMC iterations to perform. |
| `mcsave` | numeric: frequency of MCMC iterations to save. |
| `ADargs` | character: additional arguments for a call to Awatea. |
| `verbose` | logical: if TRUE, spew Awatea messages to the R console. |
| `doMSY` | logical: if TRUE, perform an MSY analysis. |
| `msyMaxIter` | numeric: maximum iterations for the MSY calculations. |
| `msyTolConv` | numeric: tolerance for convergence in the MSY calculations. |
| `endStrat` | numeric: maximum fishing mortality for the MSY analysis. |
| `stepStrat` | numeric: fishing mortality step size for the MSY analysis. |
| `delim` | character that delimits the components of the `filename` prefix. |
| `clean` | logical: if TRUE, clean all Awatea files before running an MPD analysis. |
| `locode` | logical: if TRUE, source local code located at `codePath`. |
| `awateaPath` | character: system path to the `Awatea.exe` executable (using path delimiter '/'). |
| `codePath` | character: system path to **PBSawatea** source code (using path delimiter '/'). |
| `...` | additional arguments (not currently used for any purpose). |

**Details**

This function is primarily used to automate MPD reweightings and to perform the MSY calculations. MCMCs are better run from a command line console on a supercomputer as they generally require $> 12$h to complete.

Once an MCMC has been created, the user can run various projections separately using
`awatea -ind filename.ext -mceval`
on the command line.

**Text Output Files Produced**

`Results.dat` contains an exhaustive listing of the maximum likelihood estimates for the model and derived parameters, a re-listing of some of the data and fixed parameters, and a listing of most of the prediction made. This includes numbers at age, fecundity, vulnerable biomass, survey trajectories, and so on. It is always placed in the same directory as the text input file. If there is an existing `Results.dat` file in that directory, it will be overwritten.

Other output files generated during the parameter estimation process include
`Awatea.par` (contains the maximum likelihood estimates of the free parameters),
`Awatea.cor` (shows standard deviation and correlations between the estimated parameters), and
`Awatea.std` (standard deviation of the estimated parameters).

Be aware that using argument `ADargs=list("-nohess")` will shorten the time to perform an MPD (useful if there will be multiple re-weightings), but the output files `Awatea.cor` and `Awatea.std` will **not** be produced.

**Note**

Be careful when setting the `clean` argument to `TRUE`. Some of the patterns for matching to Awatea files might inadvertently clean non-related files. The patterns are currently set to:
`"^Awatea"`, `"^admodel"`, `"\\.pst$"`, `"\\.out$"`, `"\\.rpt$"`, `"\\.tmp$"`,
`"^variance$"`, `"^results.dat$"`, `"^likelihood.dat$"`

**Author(s)**

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC.

**References**

Edwards, A.M., Haigh, R., and Starr, P.J. (2012a) Stock assessment and recovery potential assessment for Yellowmouth Rockfish (*Sebastes reedi*) along the Pacific coast of Canada. *Canadian Science Advisory Secretariat, Research Document* **2012/095**: iv + 188p.

Edwards, A. M., Haigh, R., and Starr, P.J. (2013a) Pacific Ocean Perch (*Sebastes alutus*) stock assessment for the north and west coasts of Haida Gwaii, British Columbia. *Fisheries and Oceans Canada. Canadian Science Advisory Secretariat Research Document* **2013/092**: vi + 126p.

Edwards, A. M., Haigh, R., and P. J. Starr, P.J. (2013b) Pacific Ocean Perch (*Sebastes alutus*) stock assessment for the west coast of Vancouver Island, British Columbia. *Fisheries and Oceans Canada. Canadian Science Advisory Secretariat Research Document* **2013/093**: vi + 135p.

Edwards, A.M., Starr, P.J., and Haigh, R. (2012b) Stock assessment for Pacific Ocean Perch (*Sebastes alutus*) in Queen Charlotte Sound, British Columbia. *Canadian Science Advisory Secretariat, Research Document* **2011/111**: viii + 172p.

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

Hilborn, R., Maunder, M., Parma, A., Ernst, B. Payne, J., and Starr, P. (2003) Coleraine: a generalized age-structured stock assessment model. School of Aquatic and Fishery Sciences, University of Washington, 54p.

### See Also

importRes, readAD, reweight, runSweave

---

runSweave            *Run Customised Sweave Files for Awatea MPD Runs*

---

### Description

Create and run customised Sweave files for `Awatea` MPD runs.

### Usage

```
runSweave( wd = getwd(), strSpp="XYZ",
   filename = "spp-area-00.txt",
   runNo   = 1,
   rwtNo   = 0,
   running.awatea =0,
   Nsex    = 2,
   Ncpue   = 0,
   Nsurvey = 3,
   Ngear   = 1,
   NCAset  = 1,
   Snames  = paste0("Ser",1:Nsurvey),
   SApos   = rep(TRUE,Nsurvey),
   Cnames  = paste0("Gear",1:Ngear),
   CApos   = rep(TRUE,Ngear),
   delim   = "-",
   debug   = FALSE,
   locode  = FALSE,
   codePath=
    "C:/Users/haighr/Files/Projects/R/Develop/PBSawatea/Authors/Rcode/develop",
   sexlab  = c("Females","Males"),
   resdoc  = FALSE,
   redo.Graphs = TRUE,
   ptype   = "png",
   lang    = c("e","f")
)
runMPD(prefix=c("spp","area"), runs=1, rwts=0, ...)
```

**Arguments**

| | |
|---|---|
| wd | character – working directory in which Awatea input files occur. |
| strSpp | character – three-letter code that identifies the species. |
| filename | character – name of Awatea input file. |
| runNo | numeric – the run number that identifies a unique combination of input values. |
| rwtNo | numeric – the reweight number of the MPD run to build and collate figures. |
| running.awatea | numeric – if 0 load a previous .rep file, if 1 re-run Awatea |
| Nsex | numeric – number of sexes; if $> 1$ then the routine will activate Sweave lines with the prefix @rmsex, otherwise the lines are removed. |
| Ncpue | numeric – number of CPUE series; if $>= 1$ then the routine will activate Sweave lines with the prefix @rmcpue, otherwise the lines are removed. |
| Nsurvey | numeric – number of survey series. |
| Ngear | numeric – number of commercial gear series. |
| NCAset | numeric – number of commercial catch-age-age plot sets (separate figures). It is best to limit the number of panels (years) per page to 20; therefore NCAset=1 for $\leq 20$ CA years, NCAset=2 for $\leq 40$ CA years, and so on. |
| Snames | character – survey names for figure labelling and image creation. |
| SApos | logical – vector of length Nsurvey denoting which surveys have ageing data. |
| Cnames | character – gear names for figure labelling and image creation. |
| CApos | logical – vector of length Ngear denoting which commercial gears have ageing data. |
| delim | character – that delimits the components of the filename prefix. |
| debug | logical – if TRUE, function only builds the target .Snw file but does not execute it. |
| locode | logical – if TRUE, source local code located at codePath. |
| codePath | character – system path to **PBSawatea** source code (using path delimiter '/'). |
| sexlab | character – labels for the sexes in figures. |
| resdoc | logical – if TRUE, the routine will remove Sweave lines with the prefix @rmresdoc (denoting either working paper or research document), otherwise the lines are activated. |
| redo.Graphs | logical – if TRUE, re-create the figures. |
| ptype | character – plot type for the figures: "png" = portable network graphics, "eps" = encapsulated postscript. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| | —— runMPD —— |
| prefix | character – vector of filename prefix components delimited by delim. |
| runs | numeric – vector of run number(s) for runNo in runSweave. |
| rwts | numeric – vector of reweight number(s) for rwtNo in runSweave. |
| ... | arguments passed on to the function runSweave. |

**Details**

The values specified by the arguments (or derived variables) are directly substituted into the Sweave file `run-master.Snw` wherever similarly named variables preceded by the @ symbol occur. Some primary substitutions when building the temporary Sweave file (`tfile`):

```
tfile = gsub("@cwd",wd,tfile)
tfile = gsub("@model.name",model.name,tfile)
tfile = gsub("@run.dir",run.dir,tfile)
tfile = gsub("@fig.dir",mpd.dir,tfile)
tfile = gsub("@running.awatea",running.awatea,tfile)
tfile = gsub("@redo.Graphs",redo.Graphs,tfile)
tfile = gsub("@sexlab",deparse(sexlab),tfile)
tfile = gsub("@sppcode",strSpp,tfile)
tfile = gsub("@ptype",ptype,tfile)
tfile = gsub("@lang",deparse(lang),tfile)
```

Additionally, if Sweave lines are preceded by the following control variables (prefixed '@rm'), the lines are either activated or removed depending on function argument inputs.

| Sweave control | function argument | activate when | remove when |
|---|---|---|---|
| @rmsex | Nsex | >1 | 1 |
| @rmcpue | Ncpue | >0 | 0 |
| @rmCA | sum(CApos) | >0 | 0 |
| @rmSA | sum(SApos) | >0 | 0 |
| @rmCSA | sum(CApos)+sum(SApos) | >0 | 0 |
| @rmCA1 | NCAset | 1 | !=1 |
| @rmCA2 | NCAset | 2 | !=2 |
| @rmresdoc | resdoc | FALSE | TRUE |
| @rmROL | strSpp=="ROL" | FALSE | TRUE |

The wrapper function `runMPD` essentially loops through `runSweave` using (`i in runs`) and (`j in rwts`).

**Value**

A customised Sweave file for `runNo` and `rwtNo` is created in a subdirectory (e.g., `./PSARC13/SGR/Data/Awatea/CST/SGRrun11/MPD.11.03`) from where it is run.

`runMPD` produces multiple Sweave documents and PDF files.

**Note**

Example Sweave files (`run-master.Snw`) can be found in the library directory: `.../R/.../library/PBSawatea/snw/`

**Author(s)**

Rowan Haigh, Program Head – Offshore Rockfish
Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC

*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified Rd: 2018-07-25

## See Also

runSweaveMCMC, runADMB

---

runSweaveMCMC                     *Run Customised Sweave Files for Awatea MCMC Runs*

---

## Description

Create and run customised Sweave files for Awatea MCMC runs.

## Usage

```
runSweaveMCMC (wd=getwd(), strSpp="XYZ",
   filename="spp-area-00.txt",
   runNo   = 1,
   rwtNo   = 0,
   running.awatea=0,
   Nsex    = 2,
   Ncpue   = 0,
   Nsurvey = 3,
   Ngear   = 1,
   Snames  = paste0("Ser",1:Nsurvey),
   SApos   = rep(TRUE,Nsurvey),
   Cnames  = paste0("Gear",1:Ngear),
   CApos   = rep(TRUE,Ngear),
   mcsub   = 1:1000,
   delim   = "-",
   locode  = FALSE,
   codePath=
    "C:/Users/haighr/Files/Projects/R/Develop/PBSawatea/Authors/Rcode/develop",
   histRP  = FALSE,
   wpaper  = FALSE,
   resdoc  = FALSE,
   redo.Graphs = TRUE,
   skip.last.year = TRUE,
   ptype   = "png",
   domeS   = FALSE,
   lang    = c("e","f")
)
runMCMC(prefix=c("spp","area"), runs=1, rwts=0, ...)
```

**Arguments**

| | |
|---|---|
| wd | character – working directory in which Awatea input files occur. |
| strSpp | character – three-letter code that identifies the species. |
| filename | character – name of Awatea input file. |
| runNo | numeric – the run number that identifies a unique combination of input values. |
| rwtNo | numeric – the reweight number of the MPD run to build and collate figures. |
| running.awatea | numeric – if 0 load a previous .rep file, if 1 re-run Awatea |
| Nsex | numeric – number of sexes; if $> 1$ then the routine will activate Sweave lines with the prefix @rmsex, otherwise the lines are removed. |
| Ncpue | numeric – number of CPUE series; if $>= 1$ then the routine will activate Sweave lines with the prefix @rmcpue, otherwise the lines are removed. |
| Nsurvey | numeric – number of survey series. |
| Ngear | numeric – number of commercial gear series. |
| Snames | character – survey names for figure labelling and image creation. |
| SApos | logical – vector of length Nsurvey denoting which surveys have ageing data. |
| Cnames | character – gear names for figure labelling and image creation. |
| CApos | logical – vector of length Ngear denoting which commercial gears have ageing data. |
| mcsub | numeric – vector of subsamples to select from the MCMC sample chain. |
| delim | character – that delimits the components of the filename prefix. |
| locode | logical – if TRUE, source local code located at codePath. |
| codePath | character – system path to **PBSawatea** source code (using path delimiter '/'). |
| histRP | logical – if TRUE, the routine will activate Sweave lines with the prefix @rmhrp (denoting historical reference points), otherwise the lines are removed. |
| wpaper, resdoc | logical – if TRUE, the routine will remove Sweave lines with the prefix @rmresdoc (denoting either working paper or research document), otherwise the lines are activated. Note that both wpaper and resdoc change the output file name. |
| redo.Graphs | logical – if TRUE, recreate all the figures (.eps, .wmf, .png). |
| skip.last.year | logical – if TRUE, remove the last year of projections (set to FALSE for POP 5ABC in 2010) |
| ptype | character – plot type for the figures: "png" = portable network graphics, "eps" = encapsulated postscript. |
| domeS | logical – if TRUE, estimate the right-hand side of the selectivity curve, i.e., assume dome-shaped selectivity. |
| lang | character – a vector of letters that denote the language for output: currently only "e" (english) and "f" (french). |
| | —— runMCMC —— |
| prefix | character – vector of filename prefix components delimited by delim. |
| runs | numeric – vector of run number(s) for runNo in runSweaveMCMC. |
| rwts | numeric – vector of reweight number(s) for rwtNo in runSweaveMCMC. |
| ... | arguments passed on to the function runSweaveMCMC. |

**Details**

The values specified by the some of the arguments (and derived variables) are directly substituted into the Sweave file `run-masterMCMC.Snw` wherever similarly named variables preceded by the `@` symbol occur. Some primary substitutions when building the temporary Sweave file (`tfile`):

```
tfile = gsub("@cwd",wd,tfile)
tfile = gsub("@model.name",model.name,tfile)
tfile = gsub("@run.dir",run.dir,tfile)
tfile = gsub("@fig.dir",mc.dir,tfile)
tfile = gsub("@mpd.dir",mpd.dir,tfile)
tfile = gsub("@msy.dir",msy.dir,tfile)
tfile = gsub("@prj.dir",prj.dir,tfile)
tfile = gsub("@running.awatea",running.awatea,tfile)
tfile = gsub("@redo.Graphs",redo.Graphs,tfile)
tfile = gsub("@skip.last.year",skip.last.year,tfile)
tfile = gsub("@mcsub",deparse(mcsub),tfile)
tfile = gsub("@nsex",Nsex,tfile)
tfile = gsub("@ngear",Ngear,tfile)
tfile = gsub("@sppcode",strSpp,tfile)
tfile = gsub("@ptype",ptype,tfile)
tfile = gsub("@lang",deparse(lang),tfile)
```

Additionally, if Sweave lines are preceded by the following control variables (prefixed '@rm'), the lines are either activated or removed depending on function argument inputs.

| Sweave control | function argument | activate when | remove when |
|---|---|---|---|
| @rmsex | Nsex | >1 | 1 |
| @rmcpue | Ncpue | >0 | 0 |
| @rmCA | sum(CApos) | >0 | 0 |
| @rmSA | sum(SApos) | >0 | 0 |
| @rmhrp | histRP | TRUE | FALSE |
| @rmresdoc | wpaper\|\|resdoc | FALSE | TRUE |
| @rmROL | strSpp=="ROL" | FALSE | TRUE |
| @rmdome | domeS | TRUE | FALSE |

The function `runSweaveMCMC` will incorporate various supplementary tex files (history and results) if they are available in the working directory. The results files must be named to match the run number (runNo) if they are to be incorporated into the MCMC tex document, and are substituted in the `run-masterMCMC.tex` build wherever the placeholder fields `@resultsMPD`, `@resultsMPDfigs`, `@resultsMPDtabs`, and `@resultsMCMC` occur. Only the run number is used when naming the supplementary tex files (see table below) as the species and area already determine the Awatea project structure and the reweight number is likely chosen by the user to represent the run results. As an example, MCMC results for a coastwide (CST) Silvergray Rockfish (SGR) stock assessment might include any of the following files depending on whether the output is for an informal MCMC summary, a working paper (WP), or a research document (RD):

| **LaTeX file** (`.tex`) | **Placeholder** | **Contents** |
|---|---|---|

| runHistory | — | Summary of all model runs for CST SGR. |
| resultsMPD-run16 | @resultsMPD | Summary of MPD results for Run 16 (WP/RD). |
| resultsMPDfigs-run16 | @resultsMPDfigs | Selected MPD figures created by `run-master.Snw`. |
| resultsMPDtabs-run16 | @resultsMPDtabs | Selected MPD tables created by `run-master.Snw`. |
| resultsMCMC-run16 | @resultsMCMC | Summary of MCMC results for Run 16 (WP/RD). |

The wrapper function `runMCMC` essentially loops through `runSweaveMCMC` using `(i in runs)` and `(j in rwts)`.

### Value

A customised Sweave file for `runNo` and `rwtNo` is created in a subdirectory (e.g., `./PSARC13/SGR/Data/Awatea/CST/SGRrun11/MCMC.11.03`) from where it is run.

`runMCMC` produces multiple Sweave documents and PDF files.

### Note

Example Sweave files (`run-masterMCMC.Snw`) can be found in the library directory: `paste0(system.file(package="PBSawatea"),"/snw")`

### Author(s)

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Pacific Biological Station (PBS), Fisheries & Oceans Canada (DFO), Nanaimo BC
*locus: Institute of Ocean Sciences (IOS), Sidney BC*
Last modified `Rd: 2018-07-25`

### See Also

runSweave, runADMB

---

srFun    *Stock Recruitment Function*

---

### Description

Take a vector of spawners in year $t$-1 and calculate recruits in year $t$.

### Usage

```
srFun(spawners, h = h.mpd, R0 = R0.mpd, B0 = B0.mpd)
```

## Arguments

| | |
|---|---|
| spawners | a vector of spawners where either : |
| | each element corresponds to spawners in year $t$-1 or |
| | the vector calculates a single year but multiple MCMCs. |
| h | steepness parameter value. |
| R0 | recruitment at $t = 0$ (virgin conditions). |
| B0 | spawning biomasss at virgin conditons. |

## Details

(AME wording) To input a vector of spawners in year $t$-1 and calculate recruits in year $t$. Output for recruits is vector, each element corresponds to spawners the the year before, so will usually want to shift the output by 1 so that recruits in year t are based on spawners in year $t$-1.

Can also have each input as a vector (used when calculating a single year but multiple MCMCs, as in first year of projections is based on penultimate year of MCMC calcualtions).

## Value

A vector of recruitments in year $t$.

## Note

This function was originally a subfunction in `plt.mpdGraphs`.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[plt.mpdGraphs](plt.mpdGraphs)

---

| | |
|---|---|
| stdRes.CA | *Calculate Standardised Residuals for Robust Normal Likelihood* |

---

## Description

Calculate the standardised residuals for Awatea's implementation of the Fournier *robustified* normal likelihood for proportions-at-length.
Based on PJS's summary of the CASAL document and ACH's change to length.

## Usage

```
stdRes.CA(obj, trunc=3, myLab="Age Residuals", prt=TRUE)
```

## Arguments

| | |
|---|---|
| obj | scape/list object of Awatea's results file (.res). |
| trunc | maximum standardised residual; values greater than this are set to trunc. |
| myLab | general label for the output. |
| prt | logical: if TRUE, print the results. |

## Value

List object of standardised residuals.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[stdRes.index](), [importRes](), [reweight]()

---

| stdRes.index | *Calculate Standardised Residuals for Abundance Indices* |
|---|---|

---

## Description

Calculate the standardised residuals for commercial and survey indices.

## Usage

```
stdRes.index(obj, label=NULL, prt=TRUE)
```

## Arguments

| | |
|---|---|
| obj | data frame of observed and fitted index values from Awatea's results file (.res). |
| label | general label for the output. |
| prt | logical: if TRUE, print the results. |

## Value

Input data frame with additional column of standardised residuals.

## Author(s)

Andrew Edwards, Pacific Biological Station, Fisheries and Oceans Canada, Nanaimo BC

## See Also

[stdRes.CA](), [importRes](), [reweight]()

---

tabSAR                        *Make Files of Reference Point Tables*

---

### Description

Generate comma-delimited, two-dimensional output tables (`.csv`) from objects reporting probabilities and times for DFO reference points and COSEWIC critera.

### Usage

```
tabSAR(models=paste("input-ymr",pad0(c(29,30),2),pad0(1,2),sep="."),
    pnam="refProbs3Gen90", tnam=c("Ttab0.5","Ttab0.8","Ttab0.95"),
    cats=seq(0, 2500, 500), digits=2)
```

### Arguments

| | |
|---|---|
| models | names of binary system files that store the decision tables. |
| pnam | name of list object containing matrices of reference probabilities. |
| tnam | names of matrices reporting times to reach reference points/criteria. |
| cats | catch strategies (subset) to report in output tables. |
| digits | number of digits to retain after the decimal. |

### Details

At the moment, the reference point objects are a list of matrices for the probabilities and individual matrices for the times to reach the references. The latter should also be a list of matrices to parallel the probability object.

### Value

No value is returned in R; however, comma-delimited text files (`.csv`) are created in the user's working directory. The probaility tables have the suffix `_prob.csv` while the time-to-target tables have the suffix `_targ.csv`.

### Note

The subset of the master decision tables in the stock assessment are primarily used in the SAR (Science Advisory Report) for managers.

### Author(s)

Rowan Haigh, Pacific Biological Station, Fisheries and Oceans Canada, Nanimo BC

### See Also

refPoints, findTarget,
cat, round, pad0, show0

---

tex.that.vec                    *Tex That Vector*

---

### Description

Convert a vector to a phrase 'x, y, and z' for use in Sweave.

### Usage

```
tex.that.vec(vec, simplify=TRUE)
```

### Arguments

vec         numeric|character – an R vector to summarise in Sweave.

simplify    logical – if TRUE, remove duplicated values and sort the unique values.

### Details

Primarily a utility function for use in Sweave where one wishes to convert a vector of items into a phrase for a beautiful sentence.

### Value

Returns a single-element character string that summarises the vector.

### Note

This function was a pre-cursor to the more advanced texThatVec in PBStools; however, PBSawatea currently only needs PBSmodelling in an effort to reduce dependencies.

*Aside*: Dependence only on PBSmodelling is also the reason that the PBStools function .flush.cat is reproduced in PBSawatea as .flash.cat.

### Author(s)

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Last modified Rd: 2018-05-24

### See Also

panLab, readAD, tabSAR

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