

Package: a4adiags (via r-universe)

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Title Additional Diagnostics for FL4a stock Assessment Models

Version 0.1.6

Description A series of extra diagnostics for the FL4a model, including prediction skill through restrospective prediction of model inputs and runs tests. Contains ggplot-based plot funtions of diagnostics outputs.

License EUPL

Depends R(>= 3.5.0), ggplot2, FLCore, ggplotFL, FL4a

Imports methods, FLasher, data.table, foreach

Suggests knitr, rmarkdown, doParallel, icesAdvice

VignetteBuilder knitr

Additional_repositories <http://flr-project.org/R>

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a4aBioidx	<i>a4aBioidx Computes observed and expected FLIndexBiomass from a4a fits</i>
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Description

a4aBioidx Computes observed and expected FLIndexBiomass from a4a fits

Usage

```
a4aBioidx(stock, fit, indices)
```

Arguments

stock	Input FLStock object.
fit	object a4a fit .
indices	Input FLIndices object.
nyears	Number if years for retrospective, defaults to 5.
nsq	Number of years for average biology and selectivity, defaults to 3.
fixed.ks	Is the number of knots is splines with 'year' constant?

Value

FLIndexBiomass

Examples

```
data(sol274)
# models
fmod <- ~te(replace(age, age > 8, 8), year, k = c(4, 22)) +
  s(replace(age, age > 8, 8), k=4) +
  s(year, k=22, by=as.numeric(age==1))
qmod <- list(~s(age, k=3), ~s(age, k=3))
vmod <- list(~s(age, k=3), ~s(age, k=3), ~s(age, k=3))
srmod <- ~factor(year)
# RUN a4a
fit <- sca(stock, indices, fmodel=fmod, qmodel=qmod, vmodel=vmod, sr=srmod)
idxs = a4aBioidx(stock,fit,indices)
idxs$"BTS"@index # observed
idxs$"BTS"@index.q # fitted stored here
```

a4ahcxval	<i>Compute a retrospective hindcast cross-validation of a4a stock and indices</i>
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Description

The output of a4ahcxval consist of a list with two elements, named 'stocks' and 'indices'. The first is an object of class FLStocks, each a peel from the retrospective run. The second element is a list of FLIndices object. The first FLIndices object, named 'data', is a copy of the input 'indices' argument, with the additoned catch.n slot, if originally missing. The next element, named as the final year of the data set, contains the naive prediction of the input FLIndices, while the remaining elements are the result of a hindcast prediction of the relevant indices, those within the year range of as set ny years.

Usage

```
a4ahcxval(stock, indices, nyears = 5, nsq = 3, check.ks = FALSE, ...)
```

Arguments

stock	Input FLStock object.
indices	Input FLIndices object.
nyears	Number if years for retrospective, defaults to 5.
nsq	Number of years for average biology and selectivity, defaults to 3.
...	Any submodels and other arguments for the call to <i>sca</i> .
fixed.ks	Is the number of knots is splines with 'year' constant?

Value

A list containing elements 'stocks', of class *FLStocks*, and 'indices', a list of *FLIndices* objects. See details for structure of this list.

Examples

```
data(sol274)
# models
fmod <- ~te(replace(age, age > 8, 8), year, k = c(4, 22)) +
  s(replace(age, age > 8, 8), k=4) +
  s(year, k=22, by=as.numeric(age==1))
qmod <- list(~s(age, k=3), ~s(age, k=3))
vmod <- list(~s(age, k=3), ~s(age, k=3), ~s(age, k=3))
srmod <- ~factor(year)
# RUN xval
xval <- a4ahcxval(stock, indices, fmodel=fmod, qmodel=qmod, vmodel=vmod, sr=srmod)
# PLOT result
plotXval(xval$indices)
```

mase2	<i>Adjusted mase function for dealing with NAs</i>
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Description

Adjusted mase function for dealing with NAs

Usage

```
mase2(ref, preds, order = "inverse")
```

Arguments

order	Order in which retrospective runs are stored, defaults to "inverse".
x	An <i>FLIndices</i> object of the original observations or xval\$indices.
y	A list containing of <i>FLIndices</i> objects returned by <i>a4ahcxval</i> .

Value

A ggplot object

plota4aBioidx	<i>plota4aBioidx</i> Computes observed and expected <i>FLIndexBiomass</i> from <i>a4a</i> fits <code>plota4aBioidx(stock, fit, indices)</code> \itemstockInput <i>FLStock</i> object. \itemfitobject <i>a4a</i> fit . \itemindicesInput <i>FLIndices</i> object. \itemnyearsNumber if years for retrospective, defaults to 5. \itemnsqNumber of years for average biology and selectivity, defaults to 3. \itemfixed.ksIs the number of knots is splines with 'year' constant? <code>ggplot plota4aBioidx</code> Computes observed and expected <i>FLIndexBiomass</i> from <i>a4a</i> fits <code>data(sol274)</code> # models <code>fmod <- ~te(replace(age, age > 8, 8), year, k = c(4, 22)) + s(replace(age, age > 8, 8), k=4) + s(year, k=22, by=as.numeric(age==1))</code> <code>qmod <- list(~s(age, k=3), ~s(age, k=3))</code> <code>vmod <- list(~s(age, k=3), ~s(age, k=3), ~s(age, k=3))</code> <code>srmod <- ~factor(year)</code> # RUN <i>a4a</i> fit <code><- sca(stock, indices, fmodel=fmod, qmodel=qmod, vmodel=vmod, sr=srmod)</code> <code>idxs = a4aBioidx(stock, fit, indices)</code> <code>plota4aBioidx(stock, fit, indices)</code>
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plotRunstest,a4aFitSA,FLIndices-method

plotRunstest Plot the runs test result for one or more time series

Description

plotRunstest Plot the runs test result for one or more time series

Usage

```
## S4 method for signature 'a4aFitSA,FLIndices'
plotRunstest(fit, obs, combine = TRUE)
```

Arguments

fit	The result of a model fit.
obs	The observations used in the fit.
combine	Should ages be combined by addition, defaults to TRUE.
...	Extra arguments.

Value

An object of class ggplot2::gg

Examples

```
data(sol274)
plotRunstest(sol274fit, indices)
```

plotXval2

Plot of FLIndices cross-validation by retrospective hindcast

Description

Plot of FLIndices cross-validation by retrospective hindcast

Usage

```
plotXval2(x, y = "missing", order = "inverse")
```

Arguments

x	default output of \$indices from <i>a4ahcxval</i> , else <i>FLIndices</i> with observations.
y	Default missing, else list containing <i>FLIndices</i> objects returned by .
order	Order in which retrospective runs are stored, defaults to "inverse".

Value

A ggplot object

Examples

```
# SEE vignette
```

```
runtest,a4aFitSA,FLIndices-method
```

Computes Runs Test p-values

Description

Computes Runs Test p-values

Usage

```
## S4 method for signature 'a4aFitSA,FLIndices'
runtest(fit, obs, combine = TRUE)
```

Arguments

fit	The result of a model fit.
obs	The observations used in the fit.
combine	Should ages be combined by addition, defaults to TRUE.
...	Extra arguments.

Value

A list with elements 'p.values' and 'pass'.

Examples

```
data(sol274)
# Call on a a4aFitSA object
runtest(sol274fit, indices)
#
runtest(index(sol274fit), lapply(indices, index))
```

sol274*Data from the 2020 ICES stock assessment of North Sea sole (sol.27.4)*

Description

```
fmod <- ~te(replace(age, age > 8, 8), year, k = c(4, 22)) + s(replace(age, age > 8, 8), k=4) + s(year,
k=22, by=as.numeric(age==1))
```

Format

Objects of class FLStock, FLIndices and a4aFitSA

Details

```
qmod <- list(~s(age, k=3), ~s(age, k=3))
vmod <- list( ~s(age, k=3), ~s(age, k=3), ~s(age, k=3))
srmod <- ~factor(year)
```

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