

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.

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Encoding UTF-8

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

Imports methods, FLasher, data.table, foreach

Suggests knitr, rmarkdown, doParallel, icesAdvice

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

LazyData true

VignetteBuilder knitr

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

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

RemoteUrl <https://github.com/flr/a4adiags>

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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 additioned `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 by `nyears`.

Usage

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

Arguments

<code>stock</code>	Input <code>FLStock</code> object.
<code>indices</code>	Input <code>FLIndices</code> object.
<code>nyears</code>	Number of years for retrospective, defaults to 5.
<code>nsq</code>	Number of years for average biology and selectivity, defaults to 3.
<code>...</code>	Any submodels and other arguments for the call to <code>sca</code> .
<code>fixed.ks</code>	Is the number of knots in 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)
```

```

plota4aBioidx      plota4aBioidx Computes observed and expected FLIndexBiomass
                    from a4a fits plota4aBioidx(stock, fit, indices)
                    \itemstockInput FLStock object.
                    \itemfitobject a4a fit .
                    \itemindicesInput FLIndices object.
                    \itemnyearsNumber if years for retrospective, defaults to 5.
                    \itemn-sqNumber of years for average biology and selectivity,
                    defaults to 3.
                    \itemfixed.kIs the number of knots in splines with 'year'
                    constant?
                    ggplot plota4aBioidx Computes observed and expected
                    FLIndexBiomass from a4a fits
                    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)
                    plota4aBioidx(stock, fit, indices)

```

```
plotRunstest,a4aFitSA,FLIndices-method
```

Plot the runs test result for one or more time series

Description

Plot the runs test result for one or more time series

Usage

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

Arguments

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

Value

An object of class `ggplot2::gg`

Examples

```
data(sol274)
plotRunstest(fit, 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	An <i>FLIndices</i> object of the original observations.
y	A list containing <i>FLIndices</i> objects returned by <i>a4ahcxval</i> .
order	Order in which retrospective runs are stored, defaults to "inverse".

Value

A ggplot object

Examples

```
# SEE vignette
```

runstest, a4aFitSA, FLIndices-method

Computes Runs Test p-values

Description

Computes Runs Test p-values

Usage

```
## S4 method for signature 'a4aFitSA,FLIndices'
runstest(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
runstest(fit, indices)
#
runstest(index(fit), 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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