

Package ‘eHOF’

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Title Extended HOF (Huisman-Olff-Fresco) Models

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Suggests vegdata, vegan, knitr, testthat

LazyData yes

VignetteBuilder knitr

Description Extended and enhanced hierarchical logistic regression models (called Huisman-Olff-Fresco in biology, see Huisman et al. 1993 Journal of Vegetation Science <[doi:10.1111/jvs.12050](https://doi.org/10.1111/jvs.12050)>) models. Response curves along one-dimensional gradients including no response, monotone, plateau, unimodal and bimodal models.

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NeedsCompilation no

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HOF-package

Hierarchical logistic regression analysis

Description

The HOF package provides functions for hierarchical logistic regressions, extended to bimodal models and a bootstrap approach to guarantee model stability. Such hierarchical models are also known as HOF models (Huisman-Olff-Fresco 1993) and can be used e.g. to model species distribution along ecological gradients.

Details

The functions in the **eHOF** package contain tools to model Extended Huisman-Olff-Fresco-Models to bounded responses to any gradient. The gradients (x-values) are internally standardized to 0 to 1. Binary as well as continuous response values can be modelled.

Author(s)

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References

Huisman, J., Olff, H. & Fresco, L.F.M. (1993). A hierarchical set of models for species response analysis. *Journal of Vegetation Science* 4, 37-46. Jansen F, Oksanen J (2013) How to model species responses along ecological gradients - Huisman-Olff-Fresco models revisited. *Journal of Vegetation Science*. DOI: 10.1111/jvs.12050

acre

Vegetation plots from arable fields in North-Eastern Germany

Description

Species and Environmental Data from arable fields in North-Eastern Germany. The data contains 100 selected plots (rows) and 6 species (columns).

Usage

```
data(acre)
```

Format

Two data frames, one data frame called `acre` with 100 vegetation plots (rows). Species are named with 7 letter shortletters according to the taxonomic reference list GermanSL. Plant performance is given as presence-absence. The second data frame, named `acre.env` consists of plot information about date of survey, survey area, total plant cover and measured soil pH.

Details

Soil pH was measured in 1-mol KCl buffer solution.

References

Manthey, M. (2003). Vegetationsökologie der Acker und Ackerbrachen Mecklenburg-Vorpommerns. 209 p., Berlin [u.a.]: Cramer.

Examples

```
data(acre)
hist(acre.env$PH_KCL)
## Not run:
vignette('eHOF', 'eHOF')

## End(Not run)
```

autolayout

Automatically Specifying Complex Plot Arrangements

Description

Automatic version of function [layout](#) for given number of subplots. Defined matrix schemes for [layout](#) for up to 32 subfigures.

Usage

```
autolayout(N, byrow = TRUE, ...)
```

Arguments

N	number of subfigures
byrow	see matrix
...	additional arguments for layout or matrix .

Value

Returns the number of figures, N, see [layout](#).

Author(s)

Florian Jansen

See Also

[layout](#); [matrix](#)

Examples

```
for(i in sample(1:32, 1)) {  
  autolayout(i, byrow=TRUE)  
  layout.show(i)  
}
```

betaresp

Beta response models

Description

Generating beta response models. Implemented to compare the hierarchical logistic regression models with beta response models.

Usage

```
betaresp(x, p1, p2, alpha, gamma, hi)
```

Arguments

x	Gradient values
p1, p2	response endpoints
alpha, gamma	shape parameters of the response
hi	maximum height of response

Author(s)

Jari Oksanen

References

Jansen, F. & Oksanen, J. (2013) How to model species responses along ecological gradients? - Huisman-Olf-Fresco models revisited, *Journal of Vegetation Science* DOI: 10.1111/jvs.12050

Oksanen, J. & Minchin, P.R. (2002). Continuum theory revisited: what shape are species responses along ecological gradients? *Ecological Modelling* 157, 119-129.

Examples

```
x <- seq(0,3, len=201)  
m <- betaresp(x, 2, 0.8, 0.1, 0.5, 0.8)  
plot(m)
```

Description

Fit seven hierarchical logistic regression models and select the most appropriate model by information criteria and a bootstrap approach to guarantee model stability. The first five shapes are known as Huisman-Olff-Fresco (HOF) models in ecology (Huisman et al. 1993). Additionally the package provides two bimodal shapes.

Usage

```
## Default S3 method:
HOF(occ, grad, M = max(occ), y.name, family=binomial, lim=100,
    bootstrap=100, test=c('AICc', 'BIC', 'AIC', 'Dev'),
    modeltypes=eHOF.modelnames, ...)
## S3 method for class 'data.frame'
HOF(veg, grad, M, freq.limit = 10, ...)
## S3 method for class 'HOF'
pick.model(object, level = 0.95, test = c("AICc", "BIC", "AIC", "Dev"),
    modeltypes, penal = 'df', gam = FALSE, selectMethod = c('bootselect.lower',
    'bootselect.always', 'IC.weight', 'pick.model'), silent = FALSE, ...)
## S3 method for class 'HOF'
fitted(object, model, ...)
## S3 method for class 'HOF'
predict(object, model, newdata, ...)
```

Arguments

occ	species occurrences (=response) vector.
veg	vegetation data frame. Either as matrix with species in columns and plots in rows, or in Turboveg format.
grad	gradient data vector.
M	maximum attainable value in the HOF model, similar to binomial denominator.
y.name	name of the species.
family	error distribution. Alternatives are binomial, poisson and gaussian.
lim	limiting criterion for minimization function, see details.
bootstrap	number of bootstrap samplings to check model robustness, see details.
freq.limit	lowest frequency of species analysed.
object	HOF model object, results from function HOF. Either for a single species or a list for several species.
level	probability for model selection (1-P) for F or Chisq tests.
test	information criterion for model selection. Alternatives are "AICc", "BIC", "AIC" or just "Dev"iance.

modeltypes	vector of model types, when only a subset of the seven implemented modeltypes should be considered.
penal	penalty term for model types, default is the number of model parameter.
gam	calculate AIC of GAM model and compare it with HOF models.
selectMethod	choose the model type selection method in case of divergence of the most frequent bootstrapped model or the one with highest information criterion weight from the primary chosen type.
silent	messages about selectMethod
newdata	vector of gradient values for prediction.
model	You can specify the HOF model type to be used, otherwise it is selected through function pick.model .
...	further arguments passed to or from other methods

Details

The minimization function changed compared to package `gravy` (Oksanen 2002) from `nlm` to `nlminb` to be able to set a limit for estimated parameters (default= -100 to 100). The old models III and V have been often too sharp, `lim=Inf` will produce results similar to `gravy`. Function [pick.model](#) finds the most adequate modeltype according to the chosen Information Criterion (AICc is default). Function `fitted` returns the fitted values for the used gradient, and `predict` for any values in `newdata`.

To improve and check model stability a bootstrapping mechanism is implemented in function `HOF`. If the initially chosen model type is different from the most frequent one, the latter will be chosen by default. Bootstrapping is done with `sample(length(grad), replace = TRUE)`.

Value

`HOF.fit` returns an object of class "HOF" which contains the parameters of the call, the fitting results for every model type and a vector of chosen model types from bootstrapping.

Author(s)

Florian Jansen, Jari Oksanen

References

- Jansen, F. & Oksanen, J. (2013) What shape are species responses along ecological gradients? - Huisman-Olf-Fresco models revisited. *Journal of Vegetation Science*, DOI: 10.1111/jvs.12050
- Oksanen, J. & Minchin, P.R. (2002). Continuum theory revisited: what shape are species responses along ecological gradients? *Ecological Modelling* 157, 119-129.
- Huisman, J., Olf, H. & Fresco, L.F.M. (1993). A hierarchical set of models for species response analysis. *Journal of Vegetation Science* 4, 37-46.

See Also

[plot.HOF](#) provides advanced plotting schemes for HOF models. [Para](#) derives model parameters like optimum, niche (width), slope etc.

Examples

```
data(acre)
sel <- c('MATRREC', 'RUMECT', 'SILENOC', 'APHAARV', 'MYOSARV', 'DESUSOP', 'ARTE#VU')
mo <- HOF(acre[,match(sel, names(acre))], acre.env$PH_KCL, M=1, bootstrap=NULL)
mo
```

mtf

Species Data and Altitude from Mt. Field, Tasmania

Description

Species and Environmental Data from Mt. Field, Tasmania. The `acre` data frame has 100 selected sites (rows) and 6 species (columns). Data frame `mtf.env` has only one variable: Altitude above sea level (in meters) for each site. The data are a subset of well drained sites from a more extensive data set.

Usage

```
data(mtf)
```

Format

The species data frame contains the following species:

EPACSERP a numeric vector

CYATPETI a numeric vector

NOTHCUNN a numeric vector

POA.GUNN a numeric vector

BAUERUBI a numeric vector

References

Minchin, P.R. (1989). Montane vegetation of the Mt. Field massif, Tasmania: a test of some hypotheses about properties of community patterns. *Vegetatio* 83, 97.110.

Examples

```
data(mtf)
```

Para

*Curve parameters of eHOF models***Description**

Derive common shape parameters from the different model types. Calculate a set of parameters (see values below) from eHOF models.

Usage

```
## S3 method for class 'HOF'
Para(resp, model, newdata = NULL, ...)
## S3 method for class 'HOF.list'
Para(resp, ...)
```

Arguments

resp	response model results, see HOF .
model	response model type. If not specified, the output of pick.model will be used.
newdata	new gradient vector.
...	further arguments passed to or from other methods, e.g. for pick.model .

Details

For models VI and VII Para will give you two expectancy values for the ranges left and right of the pessimum between the model optima. If you want to have the overall expectancy value, use:
`gradient <- seq(min(Para(resp)$range), max(Para(resp)$range), length.out=10000) weighted.mean(gradient,`

Value

species	Name or abbreviat of the species.
abund sum	Abundance sum, i.e. sum of all response values divided by M.
range	Range of x values.
model	Model type, if not specified the result of pick.model .
para	Model parameters (a to d).
M	Maximum response value, specified in the HOF function call.
mini	Location of the minimum, i.e. the gradient value, where the response is lowest, for model VI and VII the lowest response between the two optima.
pess	Lowest estimated response value.
top	Highest estimated response value(s).
opt	Location of the optimum, i.e. the gradient value, where the species response is highest. NA for model I and an optimum interval for model type III.
expect	Expectancy value, i.e. average x value under the model curve).

max slope	Highest slope, i.e. maximum of the first derivation of the curve.
centralBorder	Following Heegard, the central borders are calculated as the gradient values, where the response reaches " $\exp(-1/2)$ " of the top.
outerBorder	Following Heegard, the outer borders of the species niche are calculated as the gradient values, where the response reaches $\exp(-2)$ of the top.
raw mean	Average of measured x values.

Author(s)

Florian Jansen

References

Heegard, E. (2002) The outer border and central border for species-environmental relationships estimated by non-parametric generalised additive models. *Ecological Modelling*, 157, 131-139.
 Damgaard, C. (2006) Modelling ecological presence-absence data along an environmental gradient: threshold levels of the environment. *Environ Ecol Stat* 13:229-236.

Para_deriv *Curve derivatives of eHOF models*

Description

Slope and inflection points for the eHOF model types.

Usage

```
Para_deriv(resp, newdata = NULL, model = NULL, p, type = c("slope", "inflection"), ...)
```

Arguments

resp	response model results, see HOF .
newdata	new gradient vector, if NULL a vector with 10000 values within gradient range will be used
model	response model type. If not specified, the output of pick.model will be used.
p	Vector of model parameters. If not specified, <code>resp\$models[[model]]\$par</code> will be used.
type	Output type: slope or inflection points of model curves
...	further arguments passed to or from other methods, e.g. for pick.model .

Value

For slope a vector of slopes for all newdata points. Inflection points are the extremes of the second derivative.

Author(s)

Florian Jansen

References

Peper, J., Jansen, F., Pietzsch, D., Manthey, M. 2011. Patterns of plant species turnover along grazing gradients. *Journal of Vegetation Science* 22: 457–466.

plot.HOF

Plot Hierarchical Logistic Regression Models

Description

Plot single or multiple HOF models with or without model parameters.

Usage

```
## S3 method for class 'HOF'
plot(x, marginal = c('bar', 'rug', 'hist', 'points', 'n'), boxp = TRUE,
     las.h = 1, yl, main, model, test = 'AICc', modeltypes, onlybest = TRUE, penal, para =
     FALSE, gam.se = FALSE, color, newdata = NULL, lwd=1, leg = TRUE, add=FALSE, xlabel, ...)
## S3 method for class 'HOF.list'
plot(x, plottype = c("layout", "lattice", "all") , xlabel = NULL,
     test = 'AICc', modeltypes, border.top = 0.1, color, yl, leg = FALSE, ...)
```

Arguments

x	an object from HOF(spec, ...).
marginal	type of marginal representation for occurrences/absences.
boxp	plotting of horizontal boxplots
las.h	orientation of axes labels (0 = vertical, 1 = horizontal)
yl	range of y axis, useful for rare species. Must be given as fraction of M (between 0 and 1).
main	optional plot title
model	specific HOF model used, if not selected automatically.
test	test for model selection. Alternatives are "AICc" (default), "F", "Chisq", "AIC", "BIC" and "Dev"iance.
modeltypes	vector of suggested model types
onlybest	plot only the best model according to chosen Information criterion. If set to FALSE all calculated models will be plotted, but the best model with a thicker line.
penal	penalty term for model types, default is the number of model parameter

para	should model parameters (optima, raw.mean, niche,..) be plotted.
gam.se	plotting of two times standard error of predict.gam as confidence interval
color	model line color, vector of length seven
newdata	curves are plotted for original x-values. Otherwise you have to provide a vector with new gradient values.
leg	legend for model type (and parameters)
lwd	line width of model curve(s)
plottype	plottype, see details
add	add to existing plot
xlabel	x axis label
border.top	height of top border for legend
...	further arguments passed to or from other methods.

Details

Plottype layout will give a normal plot for a single species, or if the HOF object contains several species, the graphics display will be divided by [autolayout](#). Multiple species can also be plotted by a lattice xyplot and plotted with plot.HOF for every species. The third option (plottype='all') plots all selected species on the same graph which might be useful to evaluate e.g. the species within one vegetation plot, see examples.

A rug adds a rug representation (1-d plot) of the data to the plot. A rug plot is a compact way of illustrating the marginal distributions of x. Positions of the data points along x and y are denoted by tick marks, reminiscent of the tassels on a rug. Rug marks are overlaid onto the axis. A `dit='bar'` plot will display the original response values. For binary data this will be identical to rug.

Author(s)

Florian Jansen

References

de la Cruz Rot M (2005) Improving the Presentation of Results of Logistic Regression with R. Bulletin of the Ecological Society of America 86: 41-48

See Also

[HOF](#)

Examples

```
data(acre)
sel <- c('MATRREC', 'RUMECT', 'SILENOC', 'APHAARV', 'MYOSARV', 'DESUSOP', 'ARTE#VU')
mo <- HOF(acre[match(sel, names(acre))], acre.env$PH_KCL, M=1, bootstrap=NULL)
par(mar=c(2,2,1,.1))
plot(mo, para=TRUE)

# An example for plottype='all' to show species responses for the species within
```

```
# the most acidic and the most calcareous vegetation plot.
## Not run:
allSpeciesFromAnAcidicPlot <- acre['57',] > 0
mods.acidic <- HOF(acre[,allSpeciesFromAnAcidicPlot],acre.env$PH_KCL,M=1,bootstrap=NULL)
allSpeciesFromAnCalcareousPlot <- acre['87',] > 0
mods.calc <- HOF(acre[,allSpeciesFromAnCalcareousPlot],acre.env$PH_KCL,M=1,bootstrap=NULL)

autolayout(2)
plot(mods.acidic, plottype='all', main='Plot with low pH')
abline(v=acre.env$PH_KCL[acre.env$RELEVE_NR == '57'])
  names(mods.acidic)

plot(mods.calc, plottype='all', main='Plot with high pH')
abline(v=acre.env$PH_KCL[acre.env$RELEVE_NR == '87'])
  names(mods.calc)

## End(Not run)
```

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