Package ‘eHOF’

February 19, 2015

Version 1.5.7
Encoding UTF-8
Date Jan 2015
Title Extended hierarchical logistic regression (Huisman-Olff-Fresco) models
Author Florian Jansen, Jari Oksanen
Maintainer Florian Jansen <jansen@uni-greifswald.de>
Depends R (>= 2.5.0), mgcv, lattice
Suggests vegdata, vegan, knitr
LazyData yes
VignetteBuilder knitr
Description Extended and enhanced hierarchical logistic regression models, so-called Huisman-Olff-Fresco models. Response curves along one-dimensional gradients including no response, monotone, plateau, unimodal and bimodal models.
License GPL (>= 2)
NeedsCompilation no
Repository CRAN
Date/Publication 2015-01-14 19:32:20

R topics documented:

HOF-package ................................................................. 2
acre ............................................................. 2
autolayout ............................................................. 3
betaresp ................................................................. 4
HOF ................................................................. 5
mtf ................................................................. 7
Para ................................................................. 8
plot.HOF .............................................................. 9

Index 12
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 known as HOF models (Huisman-Olff-Fresco 1993).

Details

Package: HOF
Title: Extended Huisman-Olff-Fresco-Models
Author: Florian Jansen <jansen@uni-greifswald.de>
Jari Oksanen
Maintainer: Florian Jansen <jansen@uni-greifswald.de>
Depends: R (>= 2.0.0), vegdata
Suggests: vegan
URL: http://geobot.botanik.uni-greifswald.de/download

Author(s)

Florian Jansen <jansen@uni-greifswald.de> and Jari Oksanen

References


See Also

HOF

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


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, widths, heights, respect)

Arguments

N number of subfigures
byrow see matrix
widths a vector of values for the widths of columns on the device. Relative widths are specified with numeric values. Absolute widths (in centimetres) are specified with the lcm() function (see examples).
heights  a vector of values for the heights of rows on the device. Relative and absolute heights can be specified, see widths above.

respect  either a logical value or a matrix object. If the latter, then it must have the same dimensions as mat and each value in the matrix must be either 0 or 1.

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


Examples

```r
x <- seq(0.3, len=201)
m <- betaresp(x, 2, 0.8, 0.1, 0.5, 0.8)
plot(m)
```

HOF  
---
**Hierarchical logistic regression**

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

```r
## 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 "Deviance".
modeltypes  vector of model types, when only a subset of the six 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 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.

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


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", "RUMEACT", "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


Examples

data(mtf)

## 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

```r
## 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

If you want to obtain the model slope, you can use the undocumented function `Para.deriv(resp, p=modelparameter, newdata=x, type='slope')`.

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, calculate something like:

```
gradient <- seq(min(Para(resp)$range), max(Para(resp)$range), length.out=10000)
weighted.mean(gradient, predict(resp, newdata=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
estimated by non-parametric generalised additive models. Ecological Modelling, 157, 131-139.

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 "Deviance".
- **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 eight
- **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('MATREC', 'RUMEACT', '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:
# acid <- sample(rownames(acre)[acre.env$PH_KCL < 4.8], 1)
SpeciesFromAnAcidicPlot <- acre['57',] >0
mods.acidic <- HOF(acre[,SpeciesFromAnAcidicPlot],acre.env$PH_KCL,M=1,bootstrap=NULL)
SpeciesFromAnCalcaceousPlot <- acre[calc <-
    sample(rownames(acre)[acre.env$PH_KCL > 6], 1),] >0
mods.calc <- HOF(acre[,SpeciesFromAnCalcaceousPlot],acre.env$PH_KCL,M=1,bootstrap=NULL)

layout(2)
plot(mods.acidic, plottype='all', main='Plot with low pH')
abline(v=acre.env$PH_KCL[acre.env$RELEVE_NR == acid])
legend('topright',cex=.75, bty='n', lty=1:length(mods.acidic), col= c("black","red","green","blue","sienna","violet")[as.integer(factor(pick.model(mods.acidic)))]
, names(mods.acidic))
abline(v=acre.env$PH_KCL[acre.env$RELEVE_NR == acid])

plot(mods.calc, plottype='all', main='Plot with high pH')
legend('topleft',cex=.75, bty='n', lty=1:length(mods.acidic), col= c("black","red","green","blue","sienna","violet")[as.integer(factor(pick.model(mods.calc)))]
, names(mods.calc))
abline(v=acre.env$PH_KCL[acre.env$RELEVE_NR == calc])

## End(Not run)
Index

*Topic datasets
  acre, 2
  mtf, 7
*Topic misc
  autolayout, 3
*Topic models
  betaresp, 4
  HOF, 5
  Para, 8
*Topic model
  plot.HOF, 9
*Topic nonlinear
  betaresp, 4
  HOF, 5
*Topic package
  HOF-package, 2
*Topic regression
  betaresp, 4
  HOF, 5

acre, 2
autolayout, 3, 10

betaresp, 4
betaresponse (betaresp), 4
fitted.HOF (HOF), 5
HOF, 2, 5, 8, 11
HOF-package, 2
layout, 3, 4
matrix, 3, 4
mtf, 7

Para, 7, 8
pick.model, 6, 8
pick.model (HOF), 5
plot.betaresp (betaresp), 4
plot.HOF, 7, 9
predict.HOF (HOF), 5
print.betaresp (betaresp), 4
print.HOF (HOF), 5

vegan, 2
vegdata, 2