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blmeco-package	<i>Data Sets and Functions Accompanying the Book Bayesian Data Analysis in Ecology Using Linear Models with R, BUGS and Stan</i>
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Description

Data sets and functions accompanying the book Bayesian data analysis in ecology using linear models with R, BUGS and STAN

Details

Package: blmeco
 Type: Package
 Version: 1.0
 Date: 2014-03-03
 License: GPL-2

See book

Author(s)

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References

Korner-Nievergelt et al. book

AICweights

Calculates AICc-weights for each model of a set of models

Description

Calculates AICc-weights for each model of a set of models

Usage

AICweights(models)

Arguments

models a vector of characters with the model names

Details

The AICc for small sample sizes is used (can also be applied for large samples)

Value

a vector of model weights

Note

The function uses the function AICc from the package MuMIn.

Author(s)

F. Korner

References

Burnham, KP and Anderson DR (2002) Model selection and multimodel inference, a practical information-theoretic approach. Springer, New York

Examples

```

data(periparusater)
dat<-periparusater
# preparation of the data
dat$age[dat$age==0] <- NA # replace 0 with NA
dat$age[dat$age==5] <- 4 # replace "after hatching year" with "non-hatching year"
dat$age <- factor(dat$age) # 3 = hatching year, 4 = non hatching year
dat$sex[dat$sex==0] <- NA # replace 0 by missing values
dat$sex <- factor(dat$sex) # 1 = males, 2 = females
# retain only those data where sex and age is not missing
dat <- dat[complete.cases(dat$sex, dat$age),]

mod1 <- lm(wing~sex+age, data=dat)
mod2 <- lm(wing~sex*age, data=dat)
AICweights(c("mod1", "mod2"))

```

anoctua

*Presence-absence data of Little owls in nest boxes***Description**

The data contains presence-absence data of Little owls in nest boxes and elevation

Usage

```
data(anoctua)
```

Format

A data frame with 361 observations on the following 3 variables.

Id nest box id

PA indicator of Little owl presence

elevation elevation (meters above sea level)

References

Gottschalk, T, Ekschmitt, K., Volters, V. (2011) Efficient placement of nest boxes for the little owl (Athene noctua). The Journal of Raptor Research 45: 1-14

Examples

```
data(anoctua)
```

blackstork	<i>Breeding success of Black storks in Latvia</i>
------------	---

Description

The data set contains number of nestlings in Blackstork (*Ciconia nigra*) nests.

Usage

```
data(blackstork)
```

Format

A data frame with 1130 observations on the following 3 variables.

nest number of nest (nest id)

year year

njuvs number of nestlings

Source

The data is property of Maris Stradz. Attention, this is a non-random subselection of the data available. Please, contact Maris Stradz, if you have interest in the whole data set. mstrazds@latnet.lv

Examples

```
data(blackstork)
```

compareqqnorm	<i>Produces QQ-plots of model residuals and of random normal samples</i>
---------------	--

Description

The function produces 9 QQ-Plots. One is for the residuals of a model. 8 of them are for a simulated sample of equal size as the first one but simulated from a normal distribution using `rnorm`. The QQ-plot for the residuals is placed at a random place within the 9 plots. If you immediately can find the QQ-Plot of the residuals, these may not be normally distributed. The place of residuals is printed to the R-console.

Usage

```
compareqqnorm(mod)
```

Arguments

mod a linear model (an `lm`-object or any other object of which `resid(mod)` gives a numeric vector of numbers)

Value

a plot is produced and a number is given which indicates the position of the residuals (1-3 corresponds to the first row, 4-6 to the second row and 7-9 to the third row)

Author(s)

F. Korner

Examples

```
y <- rexp(50)
mod <- lm(y~1)
compareqqnorm(mod)
```

cortbowl

stress hormone data of nestling barn owls which were either treated with a corticosterone-implant or with a placebo-implant as control

Description

The aim of the study was to look at the corticosterone increase due to the corticosterone implants. In each brood one or two nestlings were implanted with a corticosterone-implant and one or two nestlings with a placebo-implant (variable Implant). Blood samples were taken just before implantation (day 1), 2 and 20 days after implantation. In total we have 287 measurements of 151 individuals (variable Ring) of 54 broods.

Usage

```
data(cortbowl)
```

Format

A data frame with 287 observations on the following 6 variables.

Brood id of brood

Ring id of individual

Implant a factor with levels C P; treatment: C=corticosterone treatment, P=placebo

Age age of nestling in days

days the day of the blood sample

totCort corticosterone measurement in the blood sample

References

Almasi, B., Roulin, A., Jenni-Eiermann, S., Breuner, C.W., Jenni, L., 2009. Regulation of free corticosterone and CBG capacity under different environmental conditions in altricial nestlings. *Gen. Comp. Endocr.* 164, 117-124.

Examples

```
data(cortbowl)
```

crosspoint	<i>Gives the x and y-coordinates of the cross point of two straight lines</i>
------------	---

Description

Calculates the x and y-coordinates of the cross point of two straight lines based on their intercepts and slopes

Usage

```
crosspoint(a1, b1, a2, b2)
```

Arguments

a1	intercept of first line
b1	slope of first line
a2	intercept of second line
b2	slope of second line

Value

a two column matrix with x- and y-coordinates of the cross point(s)

Author(s)

F. Korner

Examples

```
crosspoint(4, -0.1, 3, 0.1)
```

dispersion_glmer *Measures dispersion in a glmer-model*

Description

Computes the square root of the penalized residual sum of squares divided by n , the number of observations. This quantity may be interpreted as the dispersion factor of a binomial and Poisson mixed model. It may be used to correct standard errors of the model coefficients. But note that this post-hoc correction may be misleading because not all standard errors of the same model might need to be corrected by the same factor if the extra variance is explicitly included in the model structure (see e.g. Barry et al. 2003).

Usage

```
dispersion_glmer(modelglmer)
```

Arguments

modelglmer a model that has been fitted by glmer

Value

the square root of the scale parameter, according to recommendations by D. Bates, if its value is between 0.75 and 1.4, there may not be an overdispersion problem.

Such one number diagnostics should not be used as the only decision criterion. It can indicate overdispersion, but if it does not, it does not mean that the model fits the data well. Thorough residual analyses or posterior predictive model checking is still needed!

Author(s)

she or he is unfortunately unknown to us

References

This function has been posted on the R-helplist. It seems to have been written or motivated by D. Bates. Here is the URL, where we downloaded the function: <https://stat.ethz.ch/pipermail/r-sig-mixed-models/2011q1/015392.html>

Barry SC, Brooks SP, Catchpole EA, Morgan BJT (2003) The analysis of ring-recovery data using random effects. *Biometrics* 59:54-65.

Examples

```
## Not run:
data(swallowfarms)
dat <- swallowfarms
dat$colsize.z <- scale(dat$colsize) # scaled values for better model convergence
dat$dung.z <- scale(dat$dung)
dat$die <- dat$clutch - dat$fledge
```



```
mod <- glmer(cbind(fledge,die) ~ colsize.z + cow + dung.z + (1|farm) , data=dat, family="binomial")
dispersion_glmer(mod)

## End(Not run)
```

 ellenberg

Hohenheim groundwater table experiment of Heinz Ellenberg

Description

Heinz Ellenberg's historically important work on changes in the abundances of a community of grass species growing along experimental gradients of water table depth has played an important role in helping to identify the hydrological niches of plant species in wet meadows. The dataset comprises measurements taken from two similar experiments conducted in 1952 and 1953.

Usage

```
data(ellenberg)
```

Format

A data frame with 264 observations on the following 29 variables.

Year two levels: 1952 and 1953

Soil two levels: Loam and Sand

Water Average distance to groundwater in cm, 10 levels for 1952, 11 levels for 1953: (-5), 5, 20, 35, 50, 65, 80, 95, 110, 125, 140

Species 6 species in 1952 and 4 species in 1953. Species 1952: *Poa palustris*, *Festuca pratensis*, *Alopecurus pratensis*, *Dactylis glomerata*, *Arrhenatherum elatius*, *Bromus erectus*. Species 1953: *Alopecurus pratensis*, *Dactylis glomerata*, *Arrhenatherum elatius*, *Bromus erectus*.

Mi.g Individual yield of dried biomass in g in monocultures

Yi.g Individual yield of dried biomass in g in mixtures

Mono.area.m2 Area of the yields in monocultures, 0.383 m in year 1952, 0.5 m in year 1953

Mix.area.m2 Area of the yields in mixtures, 1.2 m in year 1952, 1.5 m in year 1953

Div Species richness, 6 in year 1952, 4 in year 1953

Moi.g.m2 Individual monoculture yields in m2

Yoi.g.m2 Individual mixture yields in m2

Mo.g.m2 Moi.g.m2 averaged over species by year, soil type and water level

Yo.g.m2 Yoi.g.m2 summed over species by year, soil type and water level

RYoi Individual relative yield observed (Yoi.g.m2/ Moi.g.m2)

RYo RYoi summed over species by year, soil type and water level

Yei.g.m2 Individual expected yield in m2 (Moi.g.m2 * RYe)

Ye.g.m2 Yei.g.m2 summed over species by year, soil type and water level

RRY_o Rescaled relative yield observed (RY_{oi}/RY_o)
 ΔRY_{oi} Difference between relative observed yield and rescaled relative observed yield ($RY_{oi} - RRY_o$)
 ΔRY_o ΔRY_{oi} summed over species by year, soil type and water level
 RY_e Relative yield expected in mixtures ($1/Div$)
 ΔRY_e Difference between the rescaled relative yield observed and relative yield expected ($RRY_o - RY_e$)
 RYT Relative yield total summed over species by year, soil type and water level
 $level$ two levels: species and community
 NE Net Effect ($Y_o.g.m^2 - Y_e.g.m^2$)
 $TICE$ Trait-Independent Complementarity Effect ($Mo.g.m^2 * \Delta RY_o * Div$)
 SE Selection Effect ($NE - TICE$)
 $TDCE$ Trait-Dependent Complementarity Effect ($(Moi.g.m^2 - Mo.g.m^2) * (\Delta RY_{oi} - \Delta RY_o)$ summed over species by year, soil type and water level)
 DE Diversity effect ($SE - TDCE$)

Details

A detailed description of the data set can be found in the methods section of Hector et al. (2012).

Source

<http://www.plosone.org/article/info%3Adoi%2F10.1371%2Fjournal.pone.0043358>

References

- Ellenberg H (1953) Physiologisches und oekologisches Verhalten derselben Pflanzenarten. *Berichte der Deutschen Botanischen Gesellschaft* 65: 350-361
- Ellenberg H (1954) Ueber einige Fortschritte der kausalen Vegetationskunde. *Plant Ecology* 5/6: 199-211.
- Lieth H, Ellenberg H (1958) Konkurrenz und Zuwanderung von Wiesenpflanzen. Ein Beitrag zum Problem der Entwicklung neu angelegten Gruenlands. *Zeitschrift fuer Acker- und Pflanzenbau* 106: 205-223.
- Hector A, von Felten S, Hautier Y, Weilenmann M and Bruelheide H (2012) Effects of Dominance and Diversity on Productivity along Ellenberg's Experimental Water Table Gradients. *PlosOne* 7: e43358

Examples

`data(ellenberg)`

frogs

Counts of the number of frogs in a water body

Description

Counts of the number of frogs in ponds of the Canton Aargau, Switzerland.

Usage

```
data(frogs)
```

Format

A data frame with 481 observations on the following 10 variables.

count1 number of counted frogs during the first visit

count2 number of counted frogs uring the second visit

elevation elevation, meters above sea level

year year

fish presence of fish (1 = present, 0 = absent)

waterarea area of the water body in square meters

vegetation indicator of vegetation (1 = vegetation present, 0 = no vegetation present)

pondid name of the pond, corresponds to observation id

x x coordinate

y y coordinate

Details

The amphibian monitoring program started in 1999 and is mainly aimed to survey population trends of endangered amphibian species. Every year, about 30 water bodies in two or three randomly selected priority areas (out of ten priority areas of high amphibian diversity) are surveyed. Additionally, a random selection of water bodies that potentially are suitable for one of the endangered amphibian species but that do not belong to the priority areas were surveyed. Each water body is surveyed by single trained volunteer during two nocturnal visits per year. Volunteers recorded anurans by walking along the waters edge with precise rules for the duration of a survey taking account of the size of the surveyed water body and noting visual encounters and calls. As fare as possible, encountered individuals of the Pelophylax-complex were identified as Marsh Frog (*Pelophylax ridibundus*), Pool Frog (*P. lessonaea*) or hybrids (*P. esculentus*) based on morphological characteristics or based on their calls. In the given data set, however, these three taxa are lumped together.

Source

The data is provided by Isabelle Floess, Landschaft und Gewaesser, Kanton Aargau.

References

Schmidt, B. R., 2005: Monitoring the distribution of pond-breeding amphibians, when species are detected imperfectly. - Aquatic conservation: marine and freshwater ecosystems 15: 681-692.

Tanadini, L. G.; Schmidt, B. R., 2011: Population size influences amphibian detection probability: implications for biodiversity monitoring programs. - Plos One 6: e28244.

Examples

```
data(frogs)
```

historyplot	<i>Function to plot history (trace) plots of the Markov chains obtained by STAN or by WinBUGS.</i>
-------------	--

Description

Draws history (trace) plots for the Markov chains in a STAN- or WinBUGS-object

Usage

```
historyplot(fit, parameter)
```

Arguments

fit	a model fit obtained by STAN or WinBUGS
parameter	the name, a character, of the parameter for which the history plot should be drawn

Details

can only handle one or two dimensional parameters up to now.

Value

gives a plot

Author(s)

Fraenzi Korner

Examples

```
## Not run:  
fit <- stan(...)  
historyplot(fit, parameter="alpha")  
  
## End(Not run)
```

loo.cv *Bayesian leave-one-out cross-validation*

Description

Bayesian leave-one-out cross-validation based on the log pointwise predictive density

Usage

```
loo.cv(mod, nsim = 100, bias.corr = FALSE)
```

Arguments

mod	an object obtained by the functions lm or glm
nsim	number of Monte Carlo simulations used to describe the posterior distributions. Computing time is large!
bias.corr	The leave-one-out cross-validation underestimates predictive fit because each prediction is conditioned n-1 data points. For large n this bias is negligible. For small n, a bias correction is recommended.

Details

For details see Gelman et al. (2014) p 175

Value

LOO.CV	leave-one-out cross-validation estimate of out-of-sample predictive fit, (log pointwise predictive density)
bias.corrected.LOO.CV	bias corrected leave-one-out cross-validation estimate of out-of-sample predictive fit, (log pointwise predictive density)
minus2times_lppd	-2*LOO.CV, transformed LOO.CV to scale of deviance
est.peff	estimate for the number of effective parameters

Author(s)

F. Korner

References

Gelman A, Carlin JB, Stern HS, Dunson DB, Vehtari A and Rubin DB (2014) Bayesian Data Analysis, Third edn. CRC Press.

See Also

[ocv](#)

Examples

```
## Not run:
x <- runif(20)
y <- 2+0.5*x+rnorm(20, 0, 1)
mod <- lm(y~x)
loo.cv(mod, bias.corr=TRUE) # increase nsim!!

## End(Not run)
```

mdat

Simulated set of correlated variables

Description

Simulated set of correlated variables. The code for the simulation is given in the details section.

Usage

```
data("mdat")
```

Format

A data frame with 100 observations on the following 6 variables.

```
y a numeric vector
x1 a numeric vector
x2 a numeric vector
x3 a numeric vector
x4 a numeric vector
x5 a numeric vector
```

Details

```
# data simulation library(MASS) Sigma <- matrix(c(1, -0.5, -0.8, -0.5, -0.9, -0.5, 1, 0.5, 0.3, 0.5, -
0.8, 0.5, 1, 0.2, 0.5, -0.5, 0.3, 0.2, 1, 0.5, -0.9, 0.5, 0.5, 0.5, 1), ncol=5, byrow=TRUE) set.seed(242)
X <- mvrnorm(n = 100, mu=runif(5, -1,1), Sigma=Sigma)
b_true <- c(3, 1.3, -0.5, 0.9, -1.3, 0.4) y_hat <- cbind(1, X) y <- y_hat + rnorm(100) dat <-
data.frame(y=y, x1=X[,1], x2=X[,2], x3=X[,3], x4=X[,4], x5=X[,5]) # end of data simulation —
```

Examples

```
data(mdat)
```

nightingales

Nightingale territory occupancy data

Description

Territory occupancy data indicating whether a Nightingale (*Luscinia megarhynchos*) was observed (1; 0 otherwise) in a given territory, year and during a given visit.

Usage

```
data(nightingales)
```

Format

Three-dimensional array containing 0 (i.e. not observed) and 1 (observed) with the three dimensions referring to

1st dimension the 1:55 territories

2nd dimension the 1:10 study years

3rd dimension the 1:8 visits

Source

The data is provided by PD Dr. Valentin Amrhein.

References

Roth T; Amrhein V (2010) Estimating individual survival using territory occupancy data on unmarked animals. *Journal of Applied Ecology* 47: 386-392.

Examples

```
data(nightingales)
```

ocv

Ordinary cross validation score

Description

Sum of squared differences between the out-of-data prediction and the observation for the leave-one-out cross validation for linear models with normal error structure (lm-objects)

Usage

```
ocv(mod)
```

Arguments

mod an lm-object

Value

the ordinary cross validation score

Author(s)

F. Korner

References

e.g. Wood, SN (2006) Generalized Additive Models, An Introduction with R. Chapman & Hall/CRC, London.

Examples

```
data(pondfrog1)
mod1 <- lm(log(frog+1)~ph, data=pondfrog1)
mod2 <- lm(log(frog+1)~waterdepth, data=pondfrog1)
ocv(mod1)
ocv(mod2)
```

parusmajor

Number of migrating Great tits

Description

Counts of Great tits (*Parus major*) observed at the mountain pass Ulmethoechi (BL, Switzerland) between 1982 and 2007 during fall migration.

Usage

```
data(parusmajor)
```

Format

A data frame with 434 observations on the following 3 variables.

year year
julian day of the year
count number of individuals counted

References

Korner-Nievergelt F, Korner-Nievergelt P, Baader E, Fischer L, Schaffner W, Kestenholz M (2007) Jahres- und tageszeitliches Auftreten von Singvoegeln auf dem Herbstzug im Jura (Ulmethoechi, Kanton Basel-Landschaft). *Der Ornithologische Beobachter* 104: 101-130.

Examples

```
data(parusmajor)
```

periparusater	<i>The data contain morphological measurements taken from museum skins of Coal tits (Periparus ater)</i>
---------------	--

Description

The data is part of the study by Korner-Nievergelt & Leisler (2004) Morphological convergence in conifer-dwelling passerines. Journal of Ornithology 145: 245-255.

Usage

```
data(periparusater)
```

Format

A data frame with 28 observations on the following 6 variables.

country country of origin of the individual

age numeric code for age categories as defined by www.euring.org, 3 = hatching year, 4 = not hatching year, 5 = after hatching year, 0 = missing

sex numeric code for sex as defined by www.euring.org, 1 = male, 2 = female, 0 = missing

weight body mass in g

P8 length of primary 8 in mm. Primary 8 is the third outermost wing feather often building the wing tip.

wing wing length in mm

References

Korner-Nievergelt & Leisler (2004) Morphological convergence in conifer-dwelling passerines. Journal of Ornithology 145: 245-255.

Examples

```
data(periparusater)
```

 pondfrog

Fake Data of the Numbers of Frogs in Ponds

Description

The data contain frog population sizes in different ponds with some characteristics of ponds. The data is simulated, thus the "true" model is known. The data can serve to play with different methods for doing model selection.

Usage

```
data(pondfrog)
```

Format

A data frame with 130 observations on the following 9 variables.

```
frog a numeric vector
fish a numeric vector
vegdensity a numeric vector
ph a numeric vector
surfacearea a numeric vector
waterdepth a numeric vector
region a factor with levels north south
height a numeric vector
temp a numeric vector
```

Details

The r-code for producing the pondfrog data is

```
set.seed(196453) n <- 130 # sample size height <- sample(150:1500,n) region <- sample(c("south",
"north"), n, replace=TRUE, prob=c(0.2, 0.8)) waterdepth <- sample(seq(0.3, 5.5, by=0.01), n) sur-
facearea <- sample(seq(3, 150), n) temp <- 20 - 0.01*height + 0.5*as.numeric(region=="south") -
0.005*waterdepth + 0.1*sqrt(surfacearea) + rnorm(n, 0, 1.5) ph <- 7.5 - 0.8 * as.numeric(region=="south")
+ rnorm(n, 0, 0.2) vegdensity.logitp <- -3.5+0.3*ph + 0.2*temp+rnorm(n,0,1) vegdensity.p <- plo-
gis(vegdensity.logitp) vegdensity <- rbinom(n, 1, prob=vegdensity.p) fish.logitp <- -4+0.3*ph +
0.2*waterdepth+rnorm(n,0,1) fish.p <- plogis(fish.logitp) fish <- rbinom(n, 1, prob=fish.p) frog.mu
<- exp(3.5 + 0.2*(temp-mean(temp)) + 0.2*(ph-mean(ph)) + 0.1*(ph-mean(ph))^2 - 0.3*(waterdepth-
mean(waterdepth)) - 0.5 * fish + 0.5*fish*vegdensity) frog <- rpois(n, lambda=frog.mu)
dat <- data.frame(frog=frog, fish=fish, vegdensity=vegdensity, ph=ph, surfacearea=surfacearea, wa-
terdepth=waterdepth, region=region, height=height, temp=temp)
```

Thus, the "true" model for the number of pondfrog (frog) is a Poisson model with log-link function and the following linear predictor:

$$3.5 + 0.2*(temp-mean(temp)) + 0.2*(ph-mean(ph)) + 0.1*(ph-mean(ph))^2 - 0.3*(waterdepth-mean(waterdepth)) - 0.5 * fish + 0.5*fish*vegdensity$$

Examples

```
data(pondfrog)
pairs(pondfrog)
```

pondfrog1

Fake Data: Number of Frogs in Ponds

Description

Simulated data of which the true model is known. Can be used to play with model selection. This is a simplified version of the pondfrog -example (see pondfrog)

Usage

```
data(pondfrog1)
```

Format

A data frame with 130 observations on the following 4 variables.

frog a numeric vector

ph a numeric vector

waterdepth a numeric vector

temp a numeric vector

Details

The code used to simulate the data was: `set.seed(333) frog.mu <- exp(3.5 + 0.2*(temp-mean(temp))+0.1*(ph-mean(ph)) - 0.3*(waterdepth-mean(waterdepth))) frog <- rpois(n, lambda=frog.mu)`

For the simulation of the explanatory variables, see help file for the pondfrog data

Examples

```
data(pondfrog1)
pairs(pondfrog1)
```

redstart	<i>Common Redstart (Phoenicurus phoenicurus) counts</i>
----------	---

Description

Counts of Common Redstart (*Phoenicurus phoenicurus*) breeding pairs between 1993-1996 in a small part of Switzerland.

Usage

```
data(redstart)
```

Format

Data frame with 342 observations and the following 5 columns:

counts count of Common Redstart breeding pairs in each 1 km² plot

x x-coordinate in CH1903-LV03 (EPSG: 21781)

y y-coordinate in CH1903-LV03 (EPSG: 21781)

elevation average elevation in m.

forests forest cover

Source

Swiss Breeding Bird Atlas 1993-1996 (Swiss Ornithological Institute): <http://www.vogelwarte.ch>

References

Schmid H., Luder R., Naef-Daenzer B., Graf R., Zbinden N. (1998) Schweizer Brutvogelatlas. Verbreitung der Brutvoegel in der Schweiz und im Fuerstentum Liechtenstein 1993-1996. Schweizerische Vogelwarte, Sempach.

Examples

```
data(redstart)
```

resprouts	<i>Survival data of tree sprouts</i>
-----------	--------------------------------------

Description

Number of tree sprouts that survived a management fire and the time since the last fire.

Usage

```
data(resprouts)
```

Format

A data frame with 41 observations on the following 4 variables.

treatment time since last fire in months

plot_ID plot name

pre number of tree sprouts before the fire

post number of tree sprouts after the fire, survivors

References

Walters, G (2012) Customary fire regimes and vegetation structure in Gabon's Bateke Plateaux. *Human Ecology* 40: 943-955

Examples

```
data(resprouts)
```

roostingsiteuse	<i>Roosting site use by little owls</i>
-----------------	---

Description

Locations of roosting sites of little owls obtained by telemetry data

Usage

```
data(roostingsiteuse)
```

Format

A data frame with 42 observations on the following 5 variables.

roosting.loc a factor with 4 levels
 roostingnum roosting site number
 temp ambient temperature in degree celsius
 familynum number of the family
 indnum number of the individual

References

Bock, A., Naef-Daenzer, B., Keil, H., Korner-Nievergelt, F., Perrig, M., Grueebler, M. U. (2013) Roost site selection by Little Owls *Athene noctua* in relation to environmental conditions and life history stages. *Ibis* 155: 847-856.

Examples

```
data(roostingsiteuse)
```

spermdepletion	<i>Sperm depletion data in a hermaphrodite sea slug</i>
----------------	---

Description

Data of experiment 1 in Anthes et al. (2014) to measure the depletion rate of sperms in a hermaphrodite sea slug.

Usage

```
data(spermdepletion)
```

Format

A data frame with 264 observations on the following 6 variables.

donor the id of the focal sperm donor
 matingN the number of the mating in the sequences of matings
 totalsperm number of sperms transferred to the receiver
 MeanPairSize mean of the weight of the two slugs of the pair
 RelativeDonorSize a relative size measurement of the donor, see Anthes et al. (2014)
 Dec_duration duration of mating in decimal minutes

References

Anthes N, Werminghausen J, Lange R (2014) Large donors transfer more sperm, but depletion is faster in a promiscuous hermaphrodite. *Behavioural Ecology and Sociobiology* 68: 477-483.

Examples

```
data(spermdepletion)
```

```
survival_swallows      Telemetry data of Barn swallow fledglings
```

Description

Capture-histories (obtained by radio-telemetry) of Barn swallows during their first 17 days after fledging. To simplify the example (for didactical reasons), only the first broods were selected.

Usage

```
data(survival_swallows)
```

Format

The format is: List of 8 \$ CH : int [1:322, 1:18] 1 1 1 1 1 1 1 1 ... capture histories of 322 individuals \$ I : int 322, number of individuals \$ K : int 18, capture occasions (inclusive the first capture) \$ carez : num [1:322], covariate, intensity of care by the parents \$ year : num [1:322] index of year (4 years study) \$ agec : num [1:18] covariate age of the fledglings, centered \$ family: num [1:322] index of the family (group the individuals belong to) \$ nfam : num 72, number of families

Details

Day 0 is the day of marking the individuals.

Source

The data has been collected by Martin Grueebler and Beat Naef-Daenzer.

Grueebler, M.U., Naef-Daenzer, B. 2008: Fitness consequences of pre- and post-fledging timing decisions in a double-brooded passerins. *Ecology* 89:2736-2745.

Grueebler, M.U., Naef-Daenzer, B. 2010: Survival benefits of post-fledging care: experimental approach to a critical part of avian reproductive strategies. *J. Anim. Ecol.* 79:334-341.

Examples

```
data(survival_swallows)
```

`swallowfarms`*Number of fledged Barn Swallows per nest*

Description

This is an adapted data set from Grueebler et al. (2010) on Barn Swallow *Hirundo rustica* nestling survival (we have selected a non-random sample to be able to fit a simple model; hence, the results do not add unbiased knowledge about the swallow biology!). For 63 swallow broods we know the clutch size and the number of the nestlings that fledged. The broods came from 51 farms, thus some farms had more than one brood. There are three predictors measured at the level of the farm: colony size (the number of swallow broods on that farm), cow (whether there are cows on the farm or not), and dungheap (the number of dungheaps within 500 m of the farm).

Usage

```
data(swallowfarms)
```

Format

A data frame with 63 observations on the following 6 variables.

farm farm id

colsize number of swallow broods on the farm

cow indicator of cows on the farm

dung number of dungheaps on the farm

clutch clutch size

fledge number of nestlings that survived to fledging

References

Grueebler MU, Korner-Nievergelt F, von Hirschheydt J (2010) The reproductive benefits of livestock farming in barn swallows *Hirundo rustica*: quality of nest site or foraging habitat? *Journal of Applied Ecology* 47:1340-1347

Examples

```
data(swallowfarms)
```

`swallows`*Data set with number of nesting swallows per barn*

Description

Number of barn swallows and house martins nesting per barn with some characteristics of the barn.

Usage

```
data(swallows)
```

Format

A data frame with 27 observations on the following 6 variables.

`farm` indicator of the farm

`nhirrus` number of active barn swallow nests

`ndelurb` number of active house martin nests

`ncows` number of cows in the barn

`nesting_aid` a factor with levels `artif_nest`=artificial nests were put up, `both` both artificial nests and supporting material has been provided, `none` nothing has been done to support swallow nesting, `support` supporting material has been provided

`ndayempty` number of days the barn was empty, i.e. the cows have been on the meadow.

References

Willi T, Korner-Nievergelt F, Grueebler MU (2011) Rauchschwalben *Hirundo rustica* brauchen Nutztiere, Mehlschwalben *Delichon urbicum* Nisthilfen. *Der Ornithologische Beobachter* 108: 215-224

Examples

```
data(swallows)
```

`triplot.normal.knownvariance`*Draw prior, data and posterior for a known variance normal distribution example*

Description

The function draws a normal prior distribution, the data and the posterior distribution in one plot. It serves as a tool to explore the influence of different prior on a hypothetical set of normally distributed data

Usage

```
triplot.normal.knownvariance(theta.data, variance.known, n, prior.theta, prior.variance,
  legend = TRUE, ylim = c(0, max(yposterior)), legend.bty="n")
```

Arguments

theta.data	mean of the data
variance.known	known variance
n	sample size
prior.theta	mean of the prior distribution
prior.variance	variance of the prior distribution
legend	logical, if TRUE (default) a legend is drawn
ylim	ylim of the plot
legend.bty	box type of legend

Author(s)

Fraenzi Korner-Nievergelt

References

Gelman, A., J. B. Carlin, H. S. Stern and D. B. Rubin (2004). Bayesian Data Analysis. New York, Chapman & Hall/CRC.

See Also

[dnorm](#)

Examples

```
triplot.normal.knownvariance(theta.data=10, n=20, variance.known=5,
  prior.theta=0, prior.variance=100)
```

WAIC

Watanabe-Akaike or widely applicable information criterion (WAIC)

Description

WAIC is a more fully Bayesian approach for estimating the out-of-sample expectation based on the log pointwise posterior predictive density

Usage

```
WAIC(mod, bsim = NA, nsim = 100)
```

Arguments

<code>mod</code>	an object of class <code>lm</code> , <code>glm</code> or <code>mer</code>
<code>bsim</code>	an object of class <code>simMer</code> (optional), if provided computing time is reduced.
<code>nsim</code>	number of simulations used to describe the posterior distributions, if <code>bsim</code> is provided, this number is taken from <code>bsim</code> .

Details

We implemented the formulas given in Gelman et al. (2014) p 173. We hope that the implementation is correct! For hierarchical (mixed) models, the function gives the WAIC that measures predictive fit for the groups in the data (not for new groups). For hierarchical models the predictive fit could be measured for each level of the data. But this flexibility is not yet implemented in the WAIC function.

Value

<code>lppd</code>	log pointwise posterior predictive density: the logarithms of the predictive density integrated over the posterior distribution of the model parameters summed over all observations.
<code>pwaic1</code>	an estimate for the number of effective parameters
<code>pwaic2</code>	a second estimate for the number of effective parameters
<code>WAIC1</code>	WAIC based on <code>pwaic1</code>
<code>WAIC2</code>	WAIC based on <code>pwaic2</code>

Author(s)

F. Korner

References

- Gelman, A., Carlin, J.B., Stern, H.S., Dunson, D.B., Vehtari, A. & Rubin, D.B. (2014) Bayesian Data Analysis, Third edn. CRC Press.
- Watanabe, S. (2010) Applicable Information Criterion in Singular Learning Theory. *Journal of Machine Learning Research*, 11, 3571-3594.

Examples

```
data(pondfrog1)
mod1 <- glm(frog ~ ph + waterdepth + temp, data=pondfrog1, family=poisson)
mod2 <- glm(frog ~      + waterdepth + temp, data=pondfrog1, family=poisson)
mod3 <- glm(frog ~ ph +          + temp, data=pondfrog1, family=poisson)
mod4 <- glm(frog ~ ph + waterdepth      , data=pondfrog1, family=poisson)
WAIC(mod1)
WAIC(mod2)
WAIC(mod3)
WAIC(mod4)
```

wildflowerfields	<i>Territory numbers of Whitethroat in wildflowerfields</i>
------------------	---

Description

Number of territories of Whitethroat in wildflowerfields of different ages. The data has been collected by J-L Zollinger.

Usage

```
data(wildflowerfields)
```

Format

A data frame with 136 observations on the following 8 variables.

field field id

year year

age age of the wildflower field in years

bp number of territories of whitethroats *Sylvia communis*

X x-coordinate

Y y-coordinate

size area of the field in ares (a, 10 x 10 m)

Nspec number of species

References

Zollinger J-L, Birrer S, Zbinden N, Korner-Nievergelt F (2013) The optimal age of sown field margins for breeding farmland birds. *Ibis* 155: 779-791

Examples

```
data(wildflowerfields)
```

`wingbowl`*Growth rate data of Barn owl nestlings and corticosterone*

Description

The data contains wing length measurements of Barn owl nestlings that were either treated with a corticosterone or a placebo implant.

Usage

```
data(wingbowl)
```

Format

A data frame with 209 observations on the following 7 variables.

Brood brood id

Ring individual id

Age1 age of the individual at the day it received the implant, in days

Implant type of implant: C = corticosterone, P = placebo

days number of days after the implant

Age age of the nestling at the day of the wing length measurement, in days

Wing wing length measurement in mm

References

AlmaisB, Roulin A, Korner-Nievergelt F, Jenni-Eiermann S, Jenni L (2012) Coloration signals the ability to cope with elevated stress hormones: effects of corticosterone on growth of barn owls are associated with melanism. *Journal of Evolutionary Biology* 25: 1189-1199

Examples

```
data(wingbowl)
```

`yellow_bellied_toad`*Site-occupancy data for Yellow-bellied toads*

Description

Site-occupancy data indicating whether Yellow-bellied toads (*Bombina variegata*) were observed (1; 0 otherwise) in a given site and during a given visit.

Usage

```
data(yellow_bellied_toad)
```

Format

List with 2 items

y Two-dimensional matrix with the observed absence (0) or presence (1) of Yellow-bellied toads for a given territory (rows) and visit (columns).

DAY integer vector containing the day of the year for each observation.

Source

The data is provided by Isabelle Floess, Landschaft und Gewaesser, Kanton Aargau.

Examples

```
data(yellow_bellied_toad)
```

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